Structural and functional characterization of natural alleles of potato (*Solanum tuberosum* L.) invertases associated with tuber quality traits

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HIER MEIN GEHEIMNIS. ES IST GANZ EINFACH: MAN SIEHT NUR MIT DEM HERZEN GUT. DAS WESENTLICHE IST FÜR DIE AUGEN UNSICHTBAR...

AUS DER KLEINE PRINZ VON ANTOINE DE SAINT-EXUPÉRY

ABSTRACT

The starch and sugar content of potato tubers are model traits for a candidate gene approach towards understanding the molecular basis of quantitative trait loci (QTL) because carbohydrate metabolism is one of the best studied plant processes at the functional level. Many genes of potato and other plant species involved in carbohydrate metabolism and transport have been cloned and functionally characterized. The starch and sugar content influences the nutritional quality of fresh potatoes and processed products, such as potato chips and French fries. Biochemical and genetic data suggest that genes encoding invertases (β-D-fructofuranosidase) participate in the control of starch and sugar content of the potato tubers. In this context, the focus was on invertases, which are ubiquitous enzymes hydrolyzing sucrose into the reducing sugars glucose and fructose. Under cold storage, reducing sugars accumulate in a genotype dependent manner in tubers (cold sweetening). High reducing sugar levels result in a reduction of potato chips quality e.g. darker chips colour, bitter taste, and a higher acrylamide concentration.

In this PhD work natural alleles of potato invertases, found previously to be significantly associated with tuber starch and sugar content (LI ET AL., 2005, 2008), were characterized at the molecular and biochemical level. Starting point was the PCR based cloning of cDNAs encoded by the five known potato invertase genes *Pain-1* on chromosome III, *invGE* and *invGF* on chromosome IX, and *pCD111* and *pCD141* on chromosome X, which resulted in 64 distinct alleles. Phenetic tree analysis based on amino acid similarity separated the alleles of cell wall and vacuolar invertases into two classes. This was also in line with the genomic organization of the different invertase loci. The genomic structures of the *Pain-1* locus and the gene pair *pCD111/pCD141* were unravelled by isolation and sequence analysis of corresponding BACs. The genes *pCD111* and *pCD141* consist each of six exons and five introns, and are arranged in a direct tandem repeat. The gene *Pain-1* comprises seven exons and six introns without a tandem duplication. Furthermore, structural alterations due to allelic invertase amino acid sequence variation were clarified by 3D-model analysis. Alleles associated with superior potato chips quality showed charge differences in the putative sucrose binding site possibly resulting in a lower conversion of sucrose in reducing sugars, which could influence potato chips quality. To test whether allele specific amino acid variations lead to altered enzyme activities, potato invertases were assayed in the yeast invertase mutant *SUC2*. Measurements of enzyme affinity to sucrose (K_m) and rate of sucrose conversion (v_{max}) did not show differences between vacuolar and cell wall-bound invertase alleles, which could explain the association with chips quality. Expression analysis revealed genotype specific transcription patterns of the alleles from different invertase isoforms.

In conclusion, at this point no definite statement on the functional impact of the characterized invertase alleles on potato chips quality is possible. The results of this study show that invertase regulation takes place at the transcript as well as at the protein level, is genotype specific and depends on allelic sequence variation. This work is a first example of a multi-pronged approach to dissect the natural variation of sugar and starch content in potato at molecular level.

Zusammenfassung

Stärke- und Zuckergehalt von Kartoffelknollen sind ausgezeichnete Beispiele, die molekularen Grundlagen von *quantitative trait loci* (QTLs*)* mittels Kandidatengenen zu identifizieren, da der Kohlenhydratstoffwechsel auf funktionaler Ebene einer der best untersuchten Prozesse in pflanzlichen Organismen ist. So wurden viele Gene aus Kartoffel und anderen Pflanzen, die mit dem Kohlenhydratstoffwechsel und -transport verbundenen sind, kloniert und hinsichtlich ihrer Funktion analysiert. Stärke- und Zuckergehalt beeinflussen unmittelbar die Qualität frischer Kartoffeln und weiter verarbeiteter Kartoffelprodukte wie zum Beispiel Kartoffelchips und Pommes Frites. Biochemische und genetische Daten deuten darauf hin, dass Invertase (β-D-fructofuranosidase) an der Kontrolle des Stärke- und Zuckergehaltes von Kartoffelknollen beteiligt ist. Deshalb wurde der Focus dieser Arbeit auf Invertasen gelegt, die universell verbreitet sind und Saccharose in die reduzierenden Zucker Glukose und Fruktose spalten. Eine durch Kaltlagerung bedingte Erhöhung an reduzierenden Zuckern in der Knolle ist abhängig von der Kartoffelsorte und äußert sich in einer Verschlechterung der Kartoffelchipsqualität, zum Beispiel dunklerer Farbe, bitterer Geschmack und einer höheren Konzentration von Acrylamid.

In dieser Doktorarbeit wurden natürlich vorkommende Allele von Kartoffelinvertasen, welche signifikant mit dem Stärke- und Zuckergehalt von Kartoffelknollen assoziiert sind (LI ET AL., 2005, 2008), hinsichtlich ihrer molekularen und biochemischen Eigenschaften charakterisiert. Die analysierten Gene waren *Pain-1* auf Chromosom III, *invGE* und *invGF* auf Chromosom IX, und *pCD111* und *pCD141* auf Chromosom X. Durch Klonieren von cDNA der fünf bekannten Invertasegene aus Kartoffel mittels PCR, konnten 64 Allele der unterschiedlichen Gene identifiziert werden. Weiterhin zeigte eine *phenetic tree*- Analyse, basierend auf Aminosäureähnlichkeiten der verschiedenen Invertaseisoformen, dass vakuoläre und apoplastische Invertasen in separate Klassen gegliedert werden können. Diese Einteilung wurde durch die unterschiedliche Genstruktur und -organisation der Isoformen, welche durch Isolation und Sequenzierung von entsprechenden BACs gewonnen wurde, bestätigt. So weisen die Gene *pCD111* und *pCD141* jeweils sechs Exons und fünf Introns auf und sind in einer direkten Tandem-Reihung angeordnet. Das Gen *Pain-1* enthält sieben Exons und sechs Introns, ohne ein Tandemduplikat aufzuweisen. Weiterhin wurden die durch allelische Aminosäuren ausgelösten strukturellen Veränderungen der Invertaseallele, mittels 3D-Analyse veranschaulicht. Allele, die nachweislich mit einer guten Kartoffelchipsqualität assoziiert sind, zeichneten sich durch Ladungsveränderungen in der potenziellen Saccharose-Bindedomäne des Enzyms aus. Diese Veränderungen führen möglicherweise zu einer verringerten Saccharosebindung und einer geringeren Konzentration an Glukose und Fruktose, was wiederum die Qualität von Kartoffelchips beeinflusst. Weiterführend wurde überprüft, ob allelspezifische

Aminosäurenvariationen zu einer veränderten Enzymaktivität führen können. Hierzu wurden die Enzymaffinität zu Saccharose (K_m) und die Rate der Saccharoseumwandlung (v_{max}) von Invertaseallelen aus Kartoffel mit Hilfe der Hefemutante *SUC2* analysiert. Die Messungen zeigten keine biochemischen Unterschiede zwischen apoplastischen und vakuolären Invertaseallelen, welche die Assoziation mit Kartoffelchipsqualität hätten erklären können.

Zusätzlich wurde mittels Expressionsanalyse veranschaulicht, dass allelische Transskriptionsmuster verschiedener Invertaseisoformen genotypspezifisch sind.

Zusammenfassend ist fest zu stellen, dass an diesem Punkt der Arbeit keine absolute Aussage über den funktionalen Einfluss der beschriebenen Invertaseallele auf Kartoffelchipsqualität möglich ist. Die Ergebnisse dieser Doktorarbeit zeigen, dass Invertaseregulation sowohl auf Transskript- als auch auf Proteinebene erfolgt, genotypspezifisch ist und von der Sequenzvariation der Allele abhängt. Diese Arbeit ist ein erstes Beispiel für einen ebenenübergreifenden Ansatz, die natürlich vorkommende Variation des Stärke- und Zuckergehalts in Kartoffelknollen auf molekularer Ebene zu entschlüsseln.

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Abbreviations

112 A1 NE	yeast expression vector
%	percent
°C	degree celsius
µg	microgram
µl	microliter
3'	three prime end of a DNA fragment
5'	five prime end of a DNA fragment
aa	amino acid
BAC	bacterial artificial chromosome
BNA	Böhm-Nordkartoffel Agrarproduktion GbR, 29574 Ebstorf
Btn	Biotin
bp	base pair(s)
ca.	circa
cDNA	complementary deoxyribonucleic acid
cM	centi Morgan
cm	centimeter
CQA	potato chips quality in autumn after harvest
CQS	potato chips quality in spring after 3-4 months of cold storage
DNA	deoxyribonucleic acid
DNAse	desoxyribonuclease
dNTP	deoxynucleosidetriphosphate
E.coli	*Escherichia coli*
e.g.	exempli gratia (Lat.) for example
EP	electrostatic potential
eQTLs	expression QTLs
EST	expressed sequence tag
et al.	*Et alii/et aliae* (Lat.) and others
EtBr	ethidium bromide
EtOH	ethanol
F1	first filial generation after cross
FAO	Food and agriculture organization of the United Nations
Fru	fructose
g	gram
Glc	glucose
GUS	β-glucoronidase
h	hour(s)
I	Inosin
InDels	insertions, deletions
INV	invertase
Inv-CW	cell wall-bound invertase
Inv-N	neutral invertase
Inv-V	vacuolar invertase

kb	kilo base pair(s)
kDa	kilo dalton
K_m	Michaelis constant
l	liter
LB medium	Luria Bertani medium
LD	linkage disequilibrium
M	molar
mg	milligram
min	minute(s)
mM	millimolar
mm	millimeter
MPIMP	Max-Planck-Institute for Molecular Plant Physiology/Golm
MPIZ	Max-Planck-Institute for Plant Breeding Research/Köln
mRNA	messenger ribonucleic acid
ng	nanogram
nm	nanometer
NOR	NORIKA GmbH, 18190 Groß Lüsewitz
OD	optical density
PAGE	polyacrylamide gel electrophoresis
PCR	polymerase chain reaction
PFGE	pulse field gel electrophoresis
pH	negative decimal log. of the H^+ concentration
pmol	picomolar
qRT-PCR	quantitative reverse transcription PCR
QTL	quantitative trait locus/loci
RFLP	restriction fragment length polymorphism
RNA	ribonucleic acid
rpm	rounds per minute
RT	room temperature
S.	Solanum
SAR	SAKA-RAGIS Pflanzenzucht GbR, Zuchtstation Windeby, 24340 Windeby/Eckernförde
SDS	sodium dodecil sulfate
sec	second(s)
SNP	single nucleotide polymorphisms
SSCP	single stranded conformation polymorphism
ssp.	subspecies
SUC	sucrose
TSC	tuber starch content
TSY	tuber starch yield
U	unit(s)
V	volt
v_{max}	maximal velocity
WT	wild type

Abbreviations for nucleic acids

A	Adenine
T	Tymidine
C	Cytosine
G	Guanine

Abbreviations for amino acids

A	Alanine
C	Cysteine
D	Aspartate
E	Glutamate
F	Phenylalanine
G	Glycine
H	Histidine
I	Isoleucine
K	Lysine
L	Leucine
M	Methionine
N	Asparagine
P	Proline
Q	Glutamine
R	Arginine
S	Serine
T	Threonine
V	Valine
W	Tryptophane
Y	Tyrosine

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1 Introduction

1.1 The potato

The potato (*Solanum tuberosum*) originated in the highlands of South America, where it has been cultivated for more than 8,000 years. Spanish explorers introduced the plant into Europe in the 16th century as a botanical curiosity (BRÜCHER, 1975). By the 19th century it was cultivated throughout the continent, providing an abundant and inexpensive food source. Today the potato is the fourth most important food crop in the world following wheat, maize and rice (www.cipotato.org). More than one-third of the global potato output now comes from developing countries, comparing to just 11% in the early 1960s. According to the latest FAO data from 2007 (Food and agriculture organization of the United Nations; http://faostat.fao.org), potato production worldwide stands at 322 million tons and covers more than 19 million hectares. China is now the world's largest potato producer with 70 million tons yearly. Although potato production in Europe has fallen since the early 1960s, this decline has been more than offset by the growth in Asia, Africa, and Latin America, thereby explaining the global rise in global potato tonnage. Because of its importance, potato became an object for extensive genetic studies increasing its resistance to pathogens, as well as improving cooking and nutrition qualities like the starch/sugar content and potato chips quality.

The genus *Solanum* contains seven cultivated and 228 wild species. The potato genome occurs in a range of chromosome numbers from 2n=24 (diploid) in for example. *S. stenotomum*, *S. phureja,* and *S. ajanhuiri*, 3n=36 (triploid) in *S. caucha,* and *S. juzepczukii*, 4n=48 in *S. tuberosum* ssp. *tuberosum* and *S. tuberosum* ssp. *andigena*, 5n=60 (pentaploid) in *S. curtilobum* to 6n=72 (hexaploid) in *S. demissum* (HAWKES, 1990).

The cultivated potato was named by Carl von Linné from a specimen grown in Europe and the scientific name *Solanum tuberosum* is presently used to include domesticated potatoes from South America, Europe and the USA and derivates of them in the rest of the world (INGRAM & WILLIAMS, 1991).

The cultivated potato (*S. tuberosum* ssp. *tuberosum*) is far from being an ideal species for genetic analysis due to its tetraploidy with tetrasomic inheritance. In addition, the high heterozygosis, the owing to inbreeding depression after repeated selfing, and multiple allelism generating a multitude of genotypes that are difficult to distinguish by comparing expected with observed segregation ratios complicates molecular analysis. An allele at any given locus

can occur in four allelic states: simplex (present one time at the locus), duplex (present two times), triplex (present three times) and quadruplex (present four times, homozygous state). Therefore, at any given genetic locus, up to four different alleles are possible. Nevertheless, the use of molecular markers enables the selection of favourable genotypes at an early time point in the potato breeding process.

1.2 Crosstalk between starch and sugar metabolism and the phenomenon of cold sweetening

As described above, potato is economically highly important. Being a staple food, potato is not only grown as a vegetable for table use but also processed into French fries and potato chips and used for dried products and starch production. In developed countries, up to 66% of potato in everyday diet is consumed in processed form. Consumers demands for convenient food at home, fast food in restaurants and snacking gave rise to a wide variety of processed products. These include potato chips, French fries, and various other frozen products, dehydrated potato products, as well as chilled-peeled and canned potatoes. Potato chips are thinly sliced potatoes, which are fried at high temperatures in different types of vegetable oil. The biggest problem of potato chips quality is the consumer's preference on fry colour, which is 'light-golden'. Fry colour is strongly dependent upon the reducing sugar concentration in tubers. But also other factors like variety characteristics, maturity at harvest, and ethylene in the storage atmosphere contribute to potato chips quality. A high reducing sugar content in tubers causes major problems for food processing because high frying temperatures lead to the non-enzymatic Maillard reaction between free aldehyde groups of the reducing sugars glucose and fructose and free α-amino groups of amino acids and proteins (SHALLENBERGER ET AL., 1959). With increasing concentration of reducing sugars in the raw tuber, chips and French fries colour changes from light yellow to dark brown and the fried products get a bitter taste (ROE ET AL., 1990). This process also attracts further attention because of the discovery that acrylamide, a potential neurotoxin and group 2A potential carcinogen, is formed from asparagine and reducing sugars via an N-glycoside intermediate in a side step of the Maillard reaction (MOTTRAM ET AL., 2002; CHUDA ET AL., 2003; OHARA-TAKADA ET AL., 2005; MATSUURA-ENDO ET AL., 2006).

The accumulation of reducing sugars in plants at low temperatures is a widespread and well-established phenomenon, often referred to as cold-induced sweetening or cold sweetening (MÜLLER-THURGAU, 1882). In mature potato tubers, which are stored in the cold to prevent tuber sprouting and loss of moisture, a shift in the balance between starch degradation and

glycolysis occurs, which leads to sucrose accumulation. Sucrose is then enzymatically converted into the reducing sugars glucose and fructose, which interfere with potato chips quality.

The sugar and starch metabolism is one of the best studied processes in plants. In higher plants, starch and sucrose are the primary products of photosynthetic carbon fixation. Starch is synthesized as an intermediate deposit in the chloroplasts, and stored in non-photosynthetic organs in amyloplasts. Sucrose is synthesized in the cytosol, transiently stored in the vacuole and exported via the phloem to sink tissues. For long-term storage sucrose can be converted into polymers such as starch, triacyl glycerides, polypeptides, or secondary compounds, enabling plants to cope with environmental biotic or abiotic challenges (STURM ET AL., 1999). In most plants, sucrose is the major form how carbon is transported from source to sink organs because of the non-reducing nature of the disaccharide, in which glucose and fructose are linked (α1→β2); (ARAI ET AL., 1991). Sucrose and the cleavage products glucose and fructose are the central molecules for carbohydrate translocation, metabolism, and sensing in higher plants (ROITSCH & GONZÁLEZ, 2004).
Starch may be degraded either hydrolytically or phosphorolytically (MALONE ET AL., 2006). The products are exported from the amyloplast either as hexose phosphates via the glucose phosphate-phosphate translocator or as free sugars via the glucose and/or maltose transporters (SMITH ET AL., 2005). Once in the cytosol, these metabolites are converted to sucrose via sucrose phosphate synthase (KRAUSE ET AL., 1998). Subsequently, a proportion of the sucrose may be hydrolysed to glucose and fructose by acid invertase (GREINER ET AL., 1999; WINTER & HUBER, 2000).

Several mechanisms have been proposed to explain the sugar accumulation during cold storage in plants (Figure 1.1). An early suggestion is that sweetening occurs because the entry of hexose phosphates into glycolysis is restricted at low temperatures. Therefore, the products of starch breakdown are directed into the pathway of sucrose synthesis (AP REES ET AL., 1981). Other studies implied that cold-induced sweetening requires long-term changes. ISHERWOOD ET AL. (1976) demonstrated that sugar accumulation is delayed several days following transfer to low temperatures. This delay may be associated with changes in gene expression involved in cold acclimation (VAN BUSKIRK & THOMASHOW, 2006).
A precise explanation how low temperatures may stimulate sugar accumulation is still unclear, but several possibilities have been suggested. One is that sugar accumulation requires the induction of starch degrading enzymes. It has been reported that enzyme activities of

endo- and exo-amylase (COCHRANE ET AL., 1991) and starch phosphorylase (CLAASSEN ET AL., 1993) were increased during cold storage leading to increased formation of hexose phosphates. However, this cold induction of starch degrading enzymes was not observed consistently because most studies failed to discriminate between different isoenzymes that might contribute to the overall amylolytic and phosphorylytic activity (MALONE ET AL., 2006). A second possibility is that sugar accumulation requires an increased activity of enzymes involved in sucrose synthesis. DEITING ET AL. (1998) showed a temperature dependence of a novel form of sucrose phosphate synthase accompanied by sugar accumulation. Another possibility suggests that the formation of glucose and fructose might be required to promote sugar accumulation by removing sucrose. DUPLESSIS ET AL. (1996) reviewed the potential of the so-called 'alternative pathway' (cyanine resistant respiration) in the starch to sucrose conversion. Low temperatures activate the alternative pathway, which leads to decreased ATP levels and simultaneous increase in sucrose concentration. This sucrose becomes the substrate for vacuolar acid invertase resulting in the accumulation of reducing sugars. However, the physiological sense of soluble sugar accumulation during cold temperatures is presumably frost protection for plant tissues (PRESSEY, 1966, 1969).

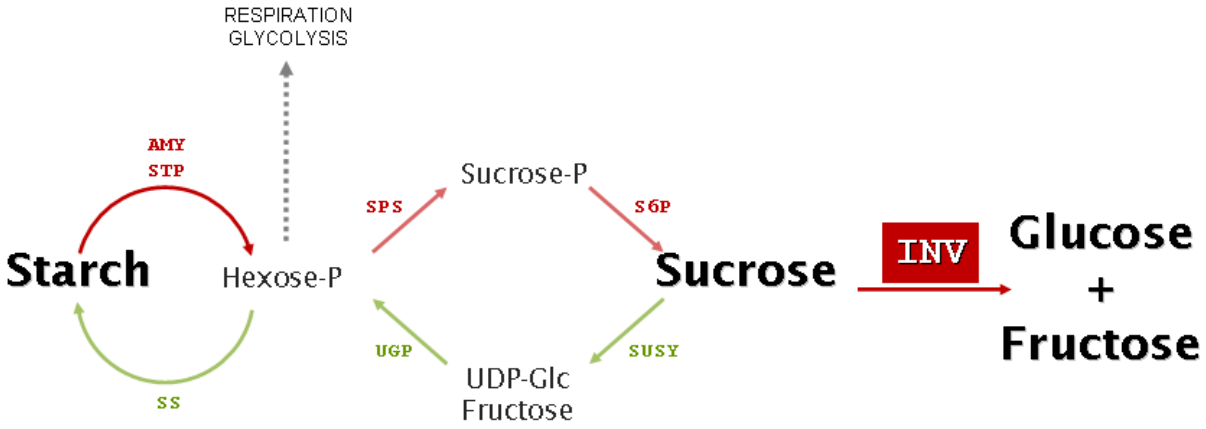


Figure 1.1: Simplified schematic overview of starch and sugar metabolism. Starch is degraded by endo- and exo-amylase (AMY) as well as by starch phosphorylase (STP). Products of these reactions are hexose phosphates (hexose-P), which can be shunted into glycolysis and respiration, or converted in starch by the action of starch synthase (SS). Another possibility is the synthesis of sucrose phosphate (sucrose-P) by sucrose phosphate synthase (SPS). Sucrose-P is then converted by sucrose 6-phosphatase (S6P) to sucrose. Sucrose can be degraded by sucrose synthase (SuSy) leading to the production of UDP-glucose and fructose. UDP-glucose is the substrate of UDP-glucose phosphatase leading to hexose-P. Another possibility of sucrose breakdown is the hydrolysis by invertases leading to the reducing sugars glucose and fructose, which mainly account for potato chips quality.

Cleavage of sucrose is mediated either by sucrose synthase (SuSy, EC 2.4.1.13) or by invertases (EC 3.2.1.26, β-fructosidase, β-fructofuranosidase). The reversible cleavage by sucrose synthase into UDP-glucose and fructose conserves the α1→β2 glycosidic bond energy of sucrose. By contrast, invertases catalyze the irreversible hydrolysis yielding glucose

and fructose. The impact of SuSy and invertases in carbon partitioning are not clearly defined. Depending on the plant organ, tissue, and species, SuSy and invertases fulfil divergent functions and importance in the breakdown of sucrose. It is generally accepted that SuSy acts predominately in growing sink organs, whilst levels in photosynthetic source tissues are low (AP REES, 1984). In the developing potato tuber, the vast majority of sucrose degradation is catalyzed by SuSy, while invertases play only a significant role at the beginning of tuberization (APPELDOORN ET AL., 1997). The crucial role of SuSy in sucrose breakdown in tubers is its importance of sucrose mobilization for the synthesis of storage compounds as well as its predominance in determining the potato tuber sink strength (HEIM ET AL., 1993; SEBKOVA ET AL., 1993; ZRENNER ET AL., 1995).

Although studies suggest the major role of SuSy in sink strength regulation, also the participation of invertases in this process was demonstrated suggesting especially cell wall invertase isoforms as main determinants of sink strength. ROITSCH (1999) und ROITSCH ET AL. (2000) showed that cell wall invertase regulates sink strength especially during the initial stages of sink development. The essential role of cell wall-bound invertase isoforms in regulating phloem unloading and sink strength has been analysed in transgenic carrot plants (STURM & TANG 1999; TANG ET AL. 1999). Using antisense suppression of cell wall-bound invertases under the control of the 35S-CaMV promoter dominantly active in carrot tap roots resulted in lowered carbohydrate content in roots and increased leaf-to-root ratio. STITT & SONNEWALD (1995) demonstrated the induction of sink metabolism in source leaves of transgenic plants by over-expression of a yeast invertase. Another study showed that cell wall-bound invertase isoforms of maize play an important role in sucrose partitioning of the developing maize endosperm (MILLER & CHOUREY, 1992). In the developing seed coat of faba bean seeds, a correlation of the cell wall-bound invertases activity and high levels of hexoses in the cotyledons and in the apoplastic space has been determined (WEBER ET AL., 1995). Additionally, invertases serve as regulators of sucrose movement and utilization beyond developmental processes. As shown elsewhere they play an important role in pathogen defence responses (KOCAL ET AL., 2009) and cold protection (PRESSEY, 1966, 1969). In mature tubers invertase influences the accumulation of the reducing sugars glucose and fructose in response to cold storage. Several studies demonstrated the influence of low temperature on increasing invertase activity (ROREM & SCHWIMMER, 1963; PRESSEY & SHAW, 1966) and invertase transcript up-regulation (ZRENNER ET AL., 1996; ZHOU ET AL., 2004; BAGNARESI ET AL., 2008).

1.3 Invertases

As described above, the accumulation of reducing sugars in mature tubers is due to invertase activity rather than to SuSy induced sucrose cleavage.

Invertases are ubiquitous enzymes in plants and occur in several isoforms. Based on their solubility, subcellular localization, pH optimum, and isoelectric point, three different types of invertase isoenzymes can be distinguished: vacuolar, cell wall-bound, and neutral invertases (Figure 1.2).

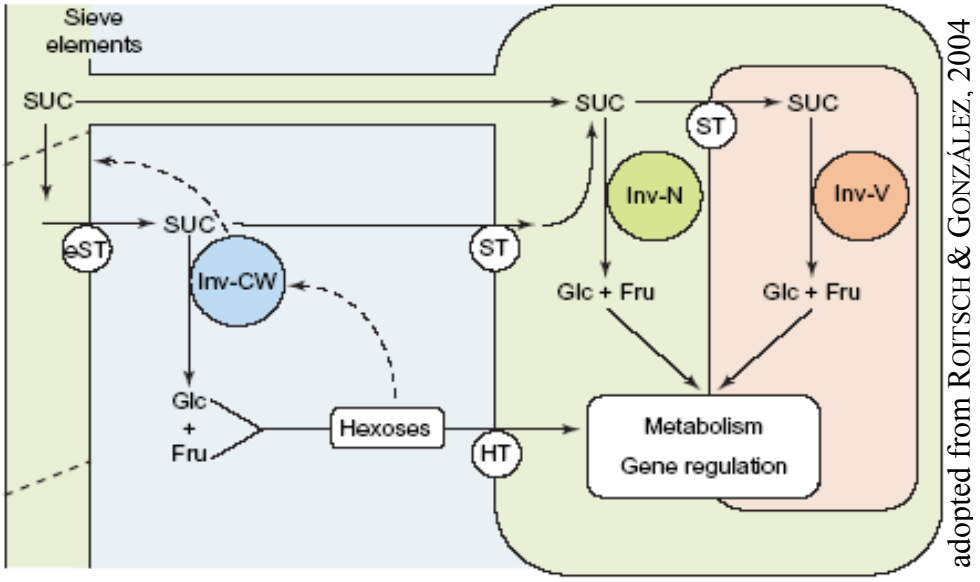


Figure 1.2: Subcellular location of invertase isoenzymes and phloem unloading pathways. Sucrose can be hydrolysed by different invertase isoforms depending on the mechanism of phloem unloading in the sink tissue. In symplastically isolated tissues, sucrose is unloaded from the sieve elements of the phloem into the apoplast by an assumed efflux sucrose transporter (eST). Once arrived in the apoplast, sucrose can be cleaved by a cell wall-bound invertase (Inv-CW). The resulting hexoses will be transported into the sink cell by a hexose transporter (HT). Alternatively, sucrose can be transported into the sink cells by a sucrose transporter (ST). Sucrose can be unloaded in the sink cells through the apoplasm or by plasmodesmata. In the cytosol sucrose can be cleaved by neutral invertase (Inv-N) or sucrose synthase (SuSy). Sucrose is also stored in the vacuole for sucrose utilization and remobilization for metabolic processes. In the vacuole sucrose can be hydrolysed by vacuolar invertase (Inv-V). The hexoses glucose and fructose, which resulted from sucrose cleavage, are not only substrates for heterotrophic growth but also function as regulators of gene expression. Invertases also play a role in sink strength regulation maintaining and stimulating the enhancement of the flow of assimilates from source to sink. Abbreviations: SUC=sucrose, Glc=glucose, Fru=fructose.

Vacuolar and cell wall-bound invertases have similar enzymatic and biochemical properties and share two conserved amino acid motifs. Both types of invertases are β-fructofuranosidases, which act in an acidic pH optimum and are able to convert other fructofuranosidases such as stachyose and raffinose. The conversion of alternative substrates is less efficient than sucrose cleavage. Another interesting fact is that vacuolar and cell wall-bound invertases are glycoproteins (STOMMEL & SIMON, 1990). Glycosylation of vacuolar and extracellular glycoproteins is fairly different. Most of the vacuolar glycoproteins described so

far were found to be N-glycosylated with modified N-glycans containing fucose and/or xylose residues, but without terminal glucosamine residues. In contrast, extracellular glycoproteins were found to be N-glycosylated mostly by complex-type N-glycans including large structures with terminal fucose and galactose residues (RAYON ET AL., 1998). Both types of glycoproteins are post-Golgi modified, leading to protein maturation in the vacuole or in the extracellular compartment. It was shown that N-glycosylation in plants plays an important role in the induction of correct folding, the biological activity of the protein, and prevention of proteolytic degradation (reviewed in RAYON ET AL., 1998). FAYE & CHRISPEELS (1989) demonstrated the proteolytic degradation of unglycosylated cell wall-bound invertase of carrot in the secretory pathway or immediately after its arrival in the cell wall. Furthermore, N-linked oligosaccharides may contain targeting information or may be involved in protein recognition (RAYON ET AL., 1998). Glycosylation of acid invertases is required for their transport across either the plasma membrane or the tonoplast, according their localization in the apoplast or the vacuole.

Invertase isoenzymes are encoded by small gene families. The genomic organization and exon/intron structure seems to be conserved between monocotyledons and dicotyledons (reviewed in TYMOWSKA-LALANNE & KREIS, 1998 and ROITSCH & GONZÁLES, 2004). Plant invertases isolated to date have fairly similar structures and consist of six to eight exons. A special feature is the presence of a mini exon of only nine nucleotides that was found in all invertase genes except *InvDC1* of carrot (RAMLOCH-LORENZ ET AL., 1993; LORENZ ET AL., 1995; SIMPSON ET AL., 2000). The mini exon, one of the smallest known, encodes the three amino acids DPN of the highly conserved β-fructosidase motif N-DNP-G/A that spans three exons and is found in invertases from plants, bacteria, and yeasts (reviewed in ROITSCH & GONZÁLES, 2004). BOURNAY ET AL. (1996) observed that under cold stress the mini exon of the *pCD111* potato cell wall invertase was skipped in an alternative splicing event. The functional relevance of the splicing effect was not investigated.

Acid invertases share another conserved peptide domain, which belongs to the active site of the enzyme. Within this domain WECxDF x stands for valine in vacuolar invertases while it is proline in cell wall-bound invertases (periplasmatic), (TYMOWSKA-LALANNE & KREIS, 1998; STURM, 1999). This conserved single amino acid difference determines the distinctly more acidic pH optimum of cell wall-bound invertases and their substrate specificity (GOETZ & ROITSCH, 1999).

Vacuolar and cell wall-bound invertases are synthesized as preproproteins with a leading sequence that is cleaved off during transport and protein maturation. The leader sequence

separates in two fragments, a signal peptide and an N-terminal extension. The signal peptide is required for entry into the endoplasmatic reticulum (ER) and consists of a basic region, a hydrophobic core of approximately 20 amino acids, and a polar region. The N-terminal extension is characteristic for all known vacuolar invertases and might be involved in the regulation of enzymatic activity, folding and stability of the polyprotein, or in vacuolar targeting (reviewed in TYMOWSKA-LALANNE & KREIS, 1998). Additionally, vacuolar invertases contain a C-terminal extension, not present in cell wall-bound invertases. This extension might be also involved in vacuolar targeting of the enzyme (BEDNAREK & RAIKHEL, 1992). Mature invertases show a molecular mass in the range of 60kDa.

Vacuolar invertases, also referred to as soluble acid invertases, are characterized by an acidic pH optimum of 5.0-5.5 and are localized in the vacuole (BOLLER & KENDE, 1979). They are crucial in determining the level of sucrose stored in the vacuole and in remobilization of sucrose for metabolic processes. Another well studied function is the regulation of the sugar balance in fruit tissues of tomato and mature potato tubers (OHYAMA et al., 1995; SCHOLES ET AL., 1996; GREINER ET AL., 1998). In potato one locus on chromosome III is known to encode vacuolar invertase. This locus is named *Pain-1*. To date, no information about genomic sequence, exon/intron structure and gene organization is available. Searching for orthologous genes in the syntenic tomato genome resulted in one EST on tomato chromosome III (www.sgn.cornell.edu). The activity of vacuolar invertases is correlated with the hexose/sucrose ratio in cold stored tubers (PRESSEY & SHAW, 1966), which leads to an increased accumulation of glucose and fructose in mature tubers. However, RICHARDSON ET AL. (1990) showed that there is no correlation between invertase activity and the total amount of accumulated sugars. Similarly, while antisense inhibition of invertase results in a decrease in the amount of hexoses and an increase in the amount of sucrose it does not affect the total amount of sugars accumulated (ZRENNER ET AL., 1996). The reducing sugars, increased during tuber cold storage due to cold protection, interfere with the trait potato chips quality that is analyzed in this study. The gene *Pain-1* is known to be differentially expressed during tuber cold storage (ZRENNER ET AL., 1996; ZHOU ET AL., 2004; BAGNARESI ET AL., 2008), showing transcript accumulation under the latter conditions.

Cell wall-bound invertases, also referred to as insoluble acid invertases, extracellular and periplasmatic invertases, are characterized by a low pH optimum of 3.5-5.0. They are localized in the apoplast and ionically bound to the cell wall. Cell wall-bound invertases cleave sucrose on its way from sieve elements of the phloem to the apoplast. The cleavage products glucose and fructose are then transported into the sink cells by hexose transporters.

In potato two different loci encoding cell wall-bound invertases are known. The first locus is *Inv$_{ap}$-b* on chromosome IX, which consists of two invertase genes *invGE* and *invGF* linked in a direct tandem repeat and separated by approximately 2.3kb from each other (MADDISON ET AL., 1999). The locus has a size of approximately 8.6kb. The genes *invGE* and *invGF* exhibit a similar exon/intron structure composed of six exons and five introns. The second locus of cell wall-bound invertases is *Inv$_{ap}$-a* on chromosome X, which consist of two genes *pCD111* and *pCD141*. Comparative analysis of the potato genetic map revealed that the gene pair *pCD111/pCD141* on chromosome X arose by partial chromosome duplication of the gene pair *invGE/invGF* of chromosome IX, and, therefore, might also be organized in a direct tandem repeat (GEBHARDT ET AL., 2003; FRIDMAN ET AL., 2003).

The third type of invertases are neutral invertases, also known as alkaline or cytoplasmatic invertases because of their pH optimum between 6.8 and 8.0, and their localization in the cytoplasm. Limited information about the physiological function is available due to the labile nature of this invertase isoform and low enzyme activity. In contrast to acidic invertases, neutral invertases are not glycosylated and preferentially or solely hydrolyse sucrose. Therefore, they are no fructofuranosidases, which also convert substrates such as stachyose and raffinose like described for vacuolar and cell wall-bound invertase isoenzymes. Neutral invertases are strongly inhibited by their cleavage products but not by heavy metals. The latter observation suggests marked differences in the catalytic site compared to acidic invertases. Neutral invertases were only found in cyanobacteria and plants suggesting an origin from orthologous prokaryotic genes after endosymbiosis (VARGAS ET AL., 2003). Native polypeptides of neutral invertase are homotetramers composed of subunits with a molecular mass of 54 to 65kDa (ROSS ET AL., 1996), except the enzyme of carrot (LEE & STURM, 1996). In potato no locus for neutral invertase was detected so far and no sequence information is available.

1.4 The genetic map of potato

The potato map is one of the most highly marker-saturated maps among the crop plant species. Initially, two potato maps were constructed concurrently using RFLP markers on different genetic backgrounds (BONIERBALE ET AL., 1988; GEBHARDT ET AL., 1989). These maps were then compared with each other and also aligned to the tomato RFLP map (GEBHARDT ET AL., 1991; TANKSLEY ET AL., 1992). Comparative mapping revealed that the genomes of potato and tomato are co-linear except for paracentric inversions of five chromosome arms (BONIERBALE ET AL., 1988; TANKSLEY ET AL., 1992). Comparison of the potato genetic map with the physical map of the sequenced *Arabidopsis* genome displayed syntenic relationships between circa 40% of the potato genetic map and circa 50% of the physical map of this very distantly related plant species (GEBHARDT ET AL., 2003). With the development of new molecular markers, the potato map was enriched, and at the moment it is based on more than 350 markers, which cover approximately 90% of the potato genome (GEBHARDT & VALKONEN, 2001). Molecular markers originate from natural DNA variation present in a population of individuals of the same species. The molecular basis of the variations are point mutations (SNP, single nucleotide polymorphisms), and insertions, deletions (InDels), or inversions of DNA fragments in one allele versus another.

The existence of highly marker saturated potato maps allows localizing many genes on the twelve potato chromosomes, and markers linked to these genes can be used to perform positive marker-assisted selection. Potato function maps have been constructed for pathogen resistance (GEBHARDT & VALKONEN, 2001), and for tuber traits e.g. tuber starch content (FREYRE & DOUCHES, 1994; SCHÄFER-PREGL ET AL., 1998), chips colour (FREYRE & DOUCHES, 1994), and cold sweetening (MENÉNDEZ ET AL., 2002), and many more traits (reviewed in GEBHARDT ET AL., 2004). Integration of positional information on genetic factors controlling agronomic characteristics results in potato function maps as a basis for innovative approaches improving breeding. Understanding the molecular basis of complex traits and the underlying genes and proteins will enable combination of favourable alleles in improvement programs, leading to ‘precision breeding’.

- **Quantitative trait loci (QTL)**

The starch and sugar content of potato tubers are quantitative traits. These physiological characteristics show continuous or quantitative phenotypic variation because phenotypic expression is controlled by more than one gene. Additionally, environment has a large influence. The precise number of the genes involved in a quantitative trait is usually not

known. The loci where such genes are located in the genome are referred to 'quantitative trait loci' (QTL), (GELDERMANN, 1975). The traits can be genetically dissected using linkage maps that are based on molecular markers (reviewed by TANKSLEY, 1993).
Structures and functions of proteins encoded by a QTL are unknown. It is assumed that DNA polymorphisms must exist in the gene(s) responsible for the observed QTL effect. These DNA polymorphisms are the molecular basis for phenotypic selection of superior genotypes by breeding. In contrast to many mutations with drastic effects on the phenotype, the molecular and functional variability present in genes controlling QTL operates under field conditions and, therefore, should not have severe effects on fitness.

QTL maps are the first step toward the identification of the responsible genes, either by positional cloning or by candidate gene approach.
QTLs for tuber starch and sugar content or chips colour have been mapped in potato (DOUCHES & FREYRE, 1994; SCHÄFER-PREGL ET AL., 1998; MENÉNDEZ ET AL., 2002). A number of candidate genes have been identified regarding the fact of co-localisation with QTLs or their position on molecular maps, as well as being functional in the biosynthesis, degradation, or transport of starch and sugars in potato and other plants (CHEN ET AL., 2001, MENÉNDEZ ET AL., 2002). Among others, invertase genes were identified as positional candidates for cold-sweetening QTLs.

- **Association genetics based on candidate genes**

Association genetics based on candidate genes is one approach aiming towards the improvement of crop breeding programs ('precision breeding'). The candidate gene approach is based on the knowledge of a gene's function controlling the trait of interest. Additionally, co-localization of a functional candidate gene with a QTL for the trait of interest leads to a positional candidate (PFLIEGER ET AL., 2001).
Association analysis was performed for potato vacuolar invertase and cell wall-bound invertase isoforms due to the fact of being functional candidates in the tuber sugar metabolism as well as their co-localization with QTLs for tuber sugar content (CHEN ET AL., 2001; MENÉNDEZ ET AL., 2002).
The locus *Pain-1* on chromosome III codes for a vacuolar invertase isoform. Association analysis of allelic *Pain-1* fragments revealed strong associations of the SSCP fragment *Pain1-9a* (*8c, 5c*) with potato chips quality after cold storage, explaining 10.4% of the phenotypic variance (LI ET AL., 2008). This marker allele also showed association with chips quality without cold storage, tuber starch content and tuber starch yield (Table 1.1). Furthermore, a

negative association of the allelic *Pain-1* fragment *Pain1-5b* with potato chips quality after cold storage was detected, which explains 2.5% of the phenotypic variance. This SSCP fragment is also negatively associated with tuber starch content (Table 1.1).

In addition, association analysis was carried out for the genes *invGE*, *invGF* and *pCD141*, which encode cell wall-bound invertase isoforms. LI ET AL. (2005, 2008) showed that *invGE* and *invGF* allelic fragments, which were in linkage disequilibrium, were associated with better potato chips quality. The SSCP fragments *invGE-6f* and *invGF-4d* explain 2.8% of phenotypic variance of potato chips quality after tuber cold storage (Table 1.1). Additionally, theses alleles displayed association with better potato chips quality without cold storage, The genes *invGE* and *invGF* co-localize with a QTL for starch and sugar content of potato tubers *Sug9a* (CHEN ET AL., 2001; MENÉNDEZ ET AL., 2002).

Analysis of allelic fragments of the gene *pCD141* revealed a negative association of one SSCP fragment *pCD141-3c* with potato chips quality without cold storage, after storage in the cold and tuber starch yield (LI ET al., 2008; Table 1.1).

Table 1.1: Invertase-trait association of tetraploid potato genotypes (Li et al., 2008).

Invertase genes	Chr. no.	Marker allele	CQA q (R^2)	CQS q (R^2)	TSC q (R^2)	TSY q (R^2)
Pain-1	III	*Pain1-5b* *Pain1-9a (8c, 5c)*	ns 0.001 (4.4) ↑	0.048 (2.5) ↓ 0.000 (10.4) ↑	0.002 (5.3) ↓ 0.000 (12.0) ↑	ns 0.003(5.3) ↑
invGE/ invGF	IX	*invGE-6f (invGF-4d)*	0.034 (2.2) ↑	0.040 (2.8) ↑	ns	ns
pCD111/ pCD141	X	*pCD141-3c*	0.008 (3.1) ↓	0.028 (3.1) ↓	0.007 (4.2) ↓	ns

Associations q>0.05 are significant, ns=not significant (q<0.05). The amount of variance (in %) explained by the marker allele is given by the R^2 statistic. Marker fragments shown in parenthesis are in nearly absolute LD, having identical or highly similar distribution in the population and show similar associations. ↑↓: direction of effect. ↑ the marker allele has a positive effect on the trait. ↓ the marker allele has a negative effect on the trait.

Association of one marker allele with more than one trait might be explained by the involvement of the same gene in multiple metabolic pathways interconnecting these complex traits. The pleiotropic effects of individual alleles always have the same direction, either positive (more starch, less reducing sugars, better potato chips quality) or negative (less starch, more reducing sugars, inferior chips quality).

1.5 Objectives of this thesis

Based on the previous studies of QTL detection for potato tuber starch and sugar content as well as association analysis of candidate genes of the starch and sugar metabolism, invertases were found to fulfil criteria being positional and functional candidates. Objective of this study was the identification and characterization of allelic variation of vacuolar and cell wall-bound invertase isoforms contributing to the important agronomic trait potato chips quality. The project aims can be summarized as follows (i) identification of alleles of all three known potato invertase loci *Pain-1*, Inv_{ap}-*b* and Inv_{ap}-*a*; (ii) analysis of putative effects of allele specific amino acid differences using 3D structural comparison; (iii) biochemical analysis of invertase alleles and (iv) allele specific differential expression analysis.
Figure 1.3 shows the aspects dealt with in each of the following chapters.

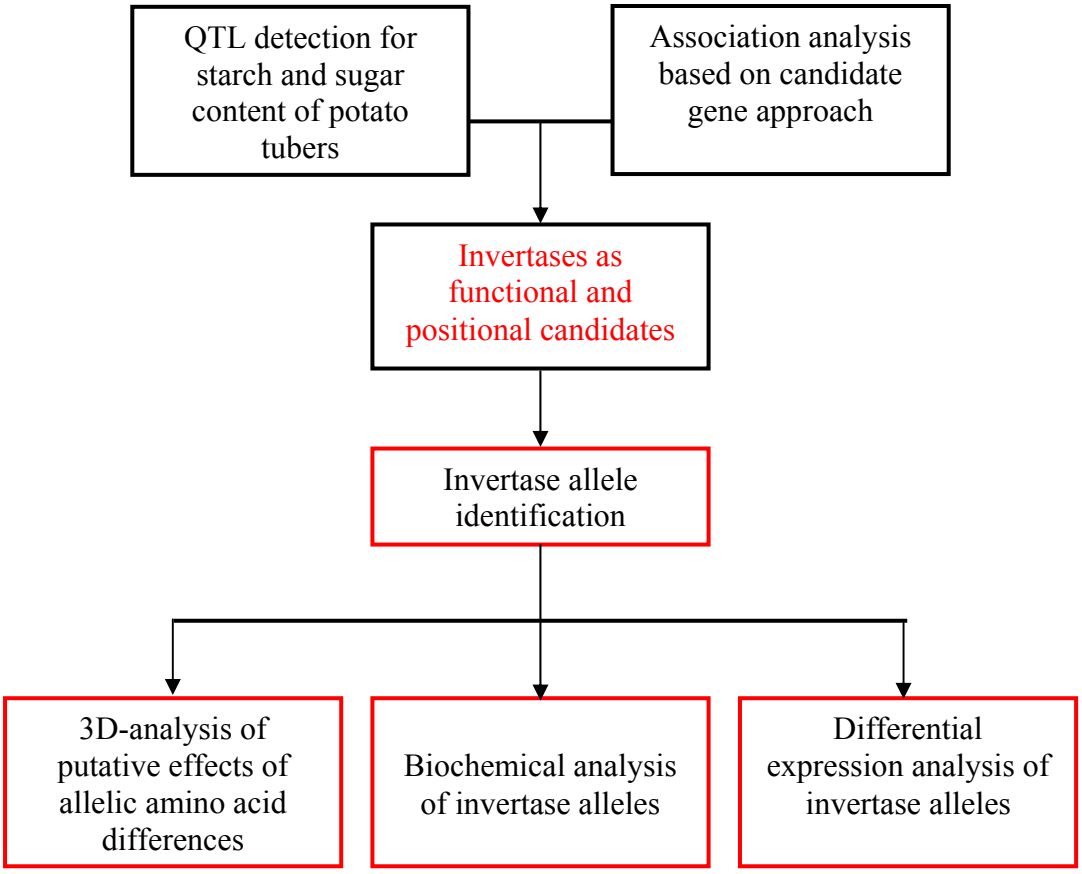


Figure 1.3: Strategy of the PhD work. The black boxes contain aspects, for which information was available. The red boxes contain aims of the study, which were set to elucidate the impact of different alleles of invertase isoforms on the analyzed trait potato chips quality.

The present study pursues to elucidate whether natural allelic variation of functional potato alleles within different genotypes can be identified and to what extent this natural variation

accounts for the observed phenotypic diversity of the selected genotypes regarding the trait chips quality. In consequence, the question arises whether allelic variation manifests at the functional level resulting in phenotypic diversity and whether these functional differences can be characterized, like observed in tomato for the fruit sugar content (FRIDMAN ET AL., 2004). This work will show whether natural variation of potato invertases is responsible for part of the phenotypic variation of tuber starch and sugar content, ultimately of potato chips quality.

2 Materials and Methods

2.1 Materials

2.1.1 Chemicals and Antibiotics

The chemicals and antibiotics (Table 2.1.1) were purchased from the following suppliers: Amersham Pharmacia Biotec (Braunschweig), Carl Roth GmbH (Karlsruhe), Difco Laboratories (Detroit, Michigan, USA), Invitrogen GmbH (Karlsruhe), Merck, Feinchemikalien und Laborbedarf (Darmstadt), Roche (Mannheim), and Sigma-Aldrich Chemie GmbH (Taufkirchen).

Table 2.1.1: Antibiotics.

Antibiotics	Solvent	Final conc. for selection on LB
Ampicillin (Amp)	H_2O	100µg/ml
Chloramphenicol (Cam)	Ethanol	12,5mg/l
Tetracyclin (Tet)	H_2O	12,5mg/l

2.1.2 Buffers and Culture Media

Stock solutions of the following buffers and culture media were prepared as described by SAMBROOK & RUSSELL (2001): DNA loading buffer, SDS, TAE, TBS, LB, YPD and SC medium. All media and solutions were made with highly purified Milli-Q-water (Millipore, Bedford, USA). Whenever required, the solutions were autoclaved for 20min at 121°C.

2.1.3 Restriction enzymes, nucleic acid modifying enzymes and kits

Restriction enzymes and corresponding buffers were used from New England BioLabs GmbH (Schwalbach/Taunus), MBI Fermentas GmbH (St. Leon-Rot) and Roche (Mannheim).

Nucleic modifying enzymes were used from:

DNA-*free*™ Kit (Ambion, Cambridgeshire, UK)

Fast Start High Fidelity PCR System (Roche, Mannheim)

KOD Hot Start DNA Polymerase (Novagen, Darmstadt)

Ribonuclease Inhibitor (Roche, Mannheim)

RNase H (Roche, Mannheim)

Superscript™ II reverse transcriptase (Invitrogen, Karlsruhe)

Taq DNA Polymerase (PLUTHERO, 1993)

T4 DNA ligase (Invitrogen, Karlsruhe)

The following commercial reagents and kits were used:

Bio-Safe™ Coomassie G-250 stain (Bio-Rad, Hercules, USA)

ExoSAP-IT® (USB Corporation, Cleveland, USA)

First Strand cDNA Synthesis kit (Invitrogen, Karlsruhe)

High Pure PCR Purification kit (Roche, Mannheim)

LiCrosolv® (Merck KGaA, Darmstadt)

Miniprep® Kit/Midiprep® (Qiagen, Hilden)

P3504 Ponceau S (Sigma-Aldrich Chemie GmbH, Taufkirchen)

pGEM® - T and pGEM® - T Easy Vectors (Promega, Mannheim)

Power SYBR® Green PCR Master Mix (Applied Biosystems, Carlsbad, USA)

Protein Assay (Bio-Rad, Hercules, USA)

PSQ 96 SNP Reagent Kit (Biotage AB, Uppsala, Sweden)

PureLink™ Plant RNA Reagent (Invitrogen, Karlsruhe)

RNAwiz™ (Ambion, Cambridgeshire, UK)

Streptavidin-coated Super Paramagnetic beads (Amersham Biosciences, Sweden)

ToTally RNA™ (Ambion, Cambridgeshire, UK)

2.1.4 Oligonucleotides

Synthetic oligonucleotides were purchased from Invitrogen (Karlsruhe), Sigma-Aldrich Chemie GmbH (Taufkirchen), and Operon Biotechnologies GmbH (Köln). The primers used in this study are listed in the following Tables.

Table 2.1.2: Primers used for molecular cloning of PCR products.

Name	Primer sequence in 5'-3' orientation
ZrPain-F	ATGGCCACGCAGTACC
PainUni-R	GATGAATTACAAGTCTTGCAAGGG
PainNotI_F	CCCCGCGGCCGCATGGCCACGCAGTACC
PainNotI_R	ATATGCGGCCGCGATGAATTACAAGTCTGG
PainBamHI_R	CCCCGGATCCGATGAATTACAAGTCTTGCAAGGG
PainGeno_For	GGGATTAACATGAGATCGTGTG
PainGeno_Rev	CCTGTACAGATGCCCATCCC
invGE-F-fulgth	ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGGT
invGE-R-fulgth	TTAGTGCATCTTAGGTACATCCATGCTCCAAGC
ENotI_F	GATTGCGGCCGCATGGAATTATTTATGAAAAGC
ENotI_R	CCCCGCGGCCGCTTAGTGCATCTTAGGTACATCC
invGF-F-fulgth	ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAG
invGF-R-fulgth	TCAATATTGTATCTTAGCTTTGCCCATACTCCATGC
FNotI_F	CCCCGCGGCCGCATGGATTATTCATCTAATTC
FBamHI_R	CCCCGGATCCTCAATATTGTATCTTAGCTTTGCCC
CD111fl_F	ATGGATTGTTTAAAAAAGTCTTCTC
CD111fl_R	TCAATAAGAAGAGTGACCAAATGACCAATTCA
CD141fl_F	ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTT
CD141fl_R	CTAGTGCAACTTTGCATTAGCCATGCTCCAAGC

Table 2.1.3: Primers used for colony-PCR and for sequencing of constructs and PCR products.

Name	Primer sequence in 5'-3' orientation
T7	GTAATACGACTCACTATAGGGC
SP6P	TATTTAGGTGACACTATAG
Adh1-Prom	CTCACCATATCCGCAATGAC
Adh1-Term	CTTGAGTAACTCTTTCCTGTAGGTC
G112_1	GGTCAGGTTGCTTTCTCAGGTATAG
G112_2	GAGAGTAGTGTGCGTGAATGAAGG
G112_3	CAGAACAGAAATGCAACGCG
G112_4	CCCAGTCACGACGTTGTAAAAC
G112_5	CCAACAAAGAATCTATACTTC
G112_6	CGACGCTCAAGTCAGAGGTGG
G112_7	GCTCGTTACAGTCCGGTGCG
G112_8	CATTGCGGATATGGTGAGACAAC
G112_9	GCGCATCACCAACATTTTCTG
G112_10	CTGACAGTTACCAATGCTTAATC
PGo2	GCCTCCCATTACACATTCCTC
PGo3	GGTAAAACGGGTATTGCACTTG
PGo3N	GATCCTCTCCTTCTAGACTGGGTC
PGo4	GCATCAAAGACATTTTATGACCCG
EGo2	CTATTACTGTCAACAATGTTCATAGAAC
EGo3	GTCCTTAAGAATAGCCTTGATG
EGo2N	GCACCAATGTATTATAATGGAG
EGo2_67.11_41	GACTTGCCGTCTTCAAATGC
FGo2	CAATCTCAAAATGCTGTAAATGTTC
FGo3	GTATGGATCTTACTCGATTTGAG
Pain_SEQ3	GTAACATATCACTAGTAAAATTTG
Pain_SEQ4	CCCTGAGAAACACCTCTTGAC
Pain_SEQ5	CCGGTGACACTGATGATTATGTAC
Pain_SEQ6	CAAGGAGGAAGAACAGTCATAAC
Pain_SEQ7	GGTCCCAAAATGCCTCTGC
Pain_SEQ12	GAAAGCTCCATGAAATCTAATGTC
Pain_SEQ11	CTTATCCCGGTACTAATTATTAATC
Pain_SEQ13	GATCTCGCTCGCCTCCCTC
25_SEQ3	GTAAACAATTGGTTCAATGGCC
25.12_CheckG	GTATGGATCTTACTCGATTTGAG
A60_For	CCATTGTACCACAAGGGATG
A60_Rev	CCCACATACCCGTACCCG
A60_SEQ3	GAGACCCGACTACTGCTTGG
A60_2F1	CCCATTACACATTCCTCCCG
A60_2SEQ4	GGTTCAATTGAGCTACTCCATG
34.1_For	GCATGCGGTTCCGGGTAC
34.1_Rev	CTGCAGCTGAGTCAACATGGAG
40.58_For	GAAGCCTCATTTGAAGTGGAC
40.58_Rev1	GCAACTCCCGGAGCCACTG
40.58_Rev2	CTCATCGAATGTTTTTCACCG
51.81_For	GGGACCATTTGGTGTCGTTG
36.1_SEQ3R	CCAGTATGAGGAGATGAATGAAG
36.1_3Nr4-F1	GCTCTTCTCTTTGGGGTTTAG
37.17_revG	CCTGTAACTTCAACCTTTTCACC
47.17_Rev	GTCCTTGGATACGGCATGGC
51.5_T-Rev	CTTCGTTGTTTCTTCGGGTC
35.83_For	CAGAGGCTCCGGGAGTTGC
F_SEQ3	GGACTGATATGTATGCACAAGATG
P54_SEQ3	GCTATTGGATGAAGTGCTGC
CD111_SEQ2	GTAAATGGATCAAGCCCGATAAC
CD141_SEQ2	GAGGAATCATAGGGGAAAGG
S21_For	CCGAGGCCGAGGCTACCTTAAAGAAGC
S21_Rev	CCCCATAACCTTTTAGCACCGCCTACC

Table 2.1.4.: Primers used for pyrosequencing analysis of the *Pain-1* locus on chromosome III.

Name	Primer sequence in 5'-3' orientation
Pyro_Pain_F	GGGACCATTTGGTGTCGTTG
Pyro_Pain_RB	(Btn)GCAAAGCTCTCCACAATTGAG
Pyro_PainTher_F	GCCTTTTGCCATGGTTCCTG
Pyro_PainTherRB	(Btn)GCAGTGGTCGGGTCTCTAAAGTC
Pyro_PainP40_RB	(Btn)CTGAGTCAACATGGAGTAGC
Pyro_PainP40_F	GGATTGGGGAAACTGATAG
Pyro_PainP40_Seq	CAGTGCTTTACGACAAGAAG
Pyro_PainTheSeq	CCGGTGACACTGATGATTATG
Pyro_PainDiaSq1	GAGCTAACGCCAGTTTACTTC
Pyro_PainDiaSq2	CATTTCTAAAGGAGCTGATGG
51.83_PyroF	CAAAATCTTGCGTACCCCACCAAC
51.83_PyroRevBi	(Btn)GTTTCATAAACAAGTGCAATACCCG
51.89_PyroF	CAGCTGCTCTACTAGTGGAGG
51.89_PyroRevBi	(Btn)GAGTCTCAGCTCGGCCATC
51.814_PyroF	CCTCAGAGGCTCCGGG
51.814_PyrRevBi	(Btn)CAATAATCTCATCGAATGTTTTTC
Seq_51.814Pyro	GGGAGITGCTAAACAAGTT

Table 2.1.5: Primers used for pyrosequencing analysis of the gene *invGE* on chromosome IX.

Name	Primer sequence in 5'-3' orientation
invGE-F-fulgth	CAATATCTTTCTCCAAAATCAC
PyroE_ParentsRB	(Btn)GCCCAAACAATATTGCCC
PyroE_PSNP58Seq	GGGTTTAGAAATTTATTTATTTTG
PyroE_PSNP108Se	GGGGTGTTTGCTTCTCATAATA
PyroE_SatF	GCAAGGGAGAAATGTTTGAAG
PyroE_SatRBio	(Btn)GTCTCATGGTAGATCTTCTAGCATC
PyroE_Sat6fSeq	AAGGAATCTCAGCATCACAG
PyroE_Sat4Seq	CGACTATCCAAGGTGGGCT
PyroE_Sat3Seq	GCTTGGICCCATTTGGGCTT
PyroE_Ther_F	GGTTCTCATGTGCTCAGATG
PyroE_TherRBio	(Btn)GTGCATCTTAGGTACATCCATG
PyroE_Ther1Seq	CTGAGACAATCACAATTGAGAC
PyroE_Ther6fSeq	GTAGCTGAGAGTTTTGGTGCTG
PyroE_Ther2Seq	GGATATGTAGATGTAGATTTAGTAGAC
PyroE_Dia_F	CCTTAAGAATAGCCTTGATGTT
PyroE_Dia_RBio	(Btn)CTCCCTTGCTCAACTTCTTG
PyroE_Dia3Seq	CCTGATAACAATTCTATCGATG
PyroE_Dia2Seq	CTCGAICITAGTGGTAAACA
PyroE_Dia6fSeq	GAATTCAAGCTATTCCGC

Table 2.1.6: Primers used for pyrosequencing analysis of the gene *invGF* on chromosome IX.

Name	Primer sequence in 5'-3' orientation
PyroF_4d_F	GATCCAATGTTTTTCTGGCTG
PyroF_4d-RBio	(Btn)GATCCAATGTTTTTCTGGCTG
PyroF_Sat_F	GGACTTAATCAATTGGATCAAT
PyroF_Sat_RBio	(Btn)CAGGCTTGATCCAATCACG
PyroF_Sat2Seq	GATCAATTIGGTACITGGTCTG
PyroF_Sat3Seq	GCIAACCAAACTCAAGTTCAAA
PyroF_SNP58Seq	CCAGTTATCTTAGTTTGCTTTTT
PyroF_SNP96Seq	CAATAATGTTGTTTTTGCTTCTC
PyroF_SNP111Seq	GCTTCTCAIAAAGTTTTTATT
PyroF_P40/54_F	GACTCAAGGGTGCAGATGTACAAG
PyroF_P40/54_RB	(Btn)CCTCGATGTTATACATGTCTTTCC
PyroF_P40Seq	CTGGATTTGTGGATGTTGATTT
PyroF_P54Seq	GCACAACAAAATTACAAGGTTC

Table 2.1.7: Primers used for expression analysis of the gene *invGF* on chromosome IX.

Name	Primer sequence in 5'-3' orientation
F1_F	ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAG
F_Expr_Rev	GTTACCAGGTAGAATAGTTGC

Table 2.1.8: Primers used for association analysis.

Name	Primer sequence in 5'-3' orientation
pCD141_3F	ACAAGTTTGGATAAGGCAGAG
pCD141_3R	TAGAGTCTCAATTGTGATTCTCTCC

Table 2.1.9: Primers used for quantification of real-time PCR products in SYBR® Green based detection assays.

Name	Primer sequence in 5'-3' orientation
Pyro_Pain_F	GGGACCATTTGGTGTCGTTG
Pyro_Pain_R	GCAAAGCTCTCCACAATTGAG
EF1α_F (NICOT ET AL., 2005)	ATTGGAAACGGATATGCTCCA
EF1α_R	TCCTTACCTGAACGCCTGTCA
L2_For (NICOT ET AL., 2005)	GGCGAAATGGGTCGTGTTAT
L2_Rev	CATTTCTCTCGCCGAAATCG

Table 2.1.10: Primers used for BAC analysis and sequencing, colony-lift, and Southern blot analysis.

Name	Primer sequence in 5'-3' orientation
A) Primers for probes:	
Pain1-5f	CGGAATTGGATTGTGGAATTG
Pain1-5r	TGGCGTTAGCTCAGATAGCTT
Pain_SondF1	CAATACAATCCAGATTCAGCTATTTG
Pain_SondR	CTGCAGCTGAGTCAACATGGAGTAG
CD111S2_For	CCTAGCAAAAATCGAAGAATTATGTG
CD111S1_Rev	CTTGTACATTGTCTTATCATTCTTG
pCD141_3F	ACAAGTTTGGATAAGGCAGAG
pCD141_3R	TAGAGTCTCAATTGTGATTCTCTCC
B) Primers for BAC sequencing	
37_F1	GCTGATTGGTTAGGTTGACTG
37_R1	CATACCGTTAATCCAGTTTTTAG
37_F2 NEW	CAGATTGATCATTCGGTAGTGG
37_R2	GTAAAGATCAGCCCAACTAGG
37_F3	GCCAAAATATATGACGTAAAGATG
37_R3	CCAATTTCCAGTACCGGG
37_F4	CAAACATCCCTCAAGCCTAAG
37_R4	GGAACAATTGAGATTTGATTAGTC
37_R4N	GACTCACCATTTGGATCTGTTG
37_F5	GAGGAATAAAGAAAAGTCAAAATG
37_F6	CACTTTTCAATGATGATAACGACG
37_F7	CATGAGTTGGTTCCCATTAGAAAC
37_F8	GTTATTCATAGACACAAGAAAAAGC
163_R1	CCTTGAGGCATCGGAACAC
146_F1	CCTATGCATACTACACTTCGATC
146_F4	
146_R3	
146_F5	
239_Seq7	GTCCACTTCAAATGAGGCTTC
P40_BACcheck_R	GTTCATCCAATTTTTTTGAGG
Seq8	GATGGATTGGGGAAACTGATAG
Seq9	CCGTAAAATCATCAAATCTATG
Seq10	GTCCATACCTGTACAGATGCCC
BAC_CD111_For	GAATTGGTCATTTGGTCACTCTTCTTATTG
BAC_CD111_Rev	GTGTGAAGCATTAACGCCATTGTTGAAAG
BAC_CD141_For	CAACAATGGCGCGGAGAGAATCACAATTG
BAC_CD141_Rev	CTAACATCAACATGGCTAGTAGTAGATTGC

2.1.5 Plasmids

Plasmids used for molecular cloning of cDNA and genomic DNA fragments are listed below.

Table 2.1.11: List of used vectors.

Vector	Supplied/provided by	Resistance
pGEM®-T Vector System	Promega	amp^R
pGEM®-T Easy Vector System	Promega	amp^R
112 A1 NE	Lothar Willmitzer, MPI for Molecular Plant Physiology/Golm	amp^R

2.1.6 Bacterial strains

For standard cloning electrocompetent or chemical competent cells (Invitrogen, Karlsruhe) of *Escherichia coli* (*E. coli*) strains DH5α and DH10B were used (HANAHAN, 1983).

MAX Efficiency® DH5α™ Competent cells:
F- φ 80*lac*ZΔM15 Δ(*lac*ZYA-*arg*F) U169 *rec*A1 *end*A1 *hsd*R17 (r_k-, m_k+) *pho*A *sup*E44 λ- *thi*-1 *gyr*A96 relA1

ElectroMAX™ DH10B™ Cells:
F- *mcr*A Δ(*mrr-hsd*RMS-*mcr*BC) φ 80*lac*ZΔM15 Δ*lac*X74 *rec*A1 *end*A1 *ara*D139 Δ(*ara, leu*)7697 *gal*U *gal*K λ- rpsL *nup*G

2.1.7 Yeast strains

In this work the yeast invertase mutant strain *SUC2* (GOZALBO & HOHMANN, 1989), and as a wild type reference the yeast strain *FY 1679* were used. Both strains were obtained from EUROSCARF: European *Saccharomyces Cerevisiae* Archives for Functional Analysis, Frankfurt.

SUC2=YIL162w: BY4741; Mat a; his3D1; leu2D0; met15D0; ura3D0; YIL162w::kanMX4

FY1679: MATa/MATα; ura3-52; trp1Δ63/TRP1; leu2Δ1/LEU2; his3Δ200/HIS3; GAL2/GAL2

2.1.8 Plant Material

Potato (*Solanum tuberosum* L.) plants used in this study were obtained from the companies SAKA-RAGIS Pflanzenzucht (SAR), Böhm-Nordkartoffel Agrarproduktion (BNA), and NORIKA (NOR). The genotypes resulted from a number of crosses amoung different varieties and breeding clones and were selected to represent the variation at the invertase loci, which were the objects of interest in this study. The following tetraploid cultivars were used: 'Satina' (SAR), 'Diana' (SAR), 'Theresa' (BNA), 'Saturna' (BNA), and 'Desireé'.
Furthermore, the diploid potato genotypes P18, P40, and P54 were included because they were used as parents for mapping QTLs and candidate genes for cold sweetening of potato tubers (MENÉNDEZ ET AL., 2002).

2.2 Methods

2.2.1 Plant work

Potato tubers were germinated after the tuber dormancy period (storage at 4°C) of ca. 3 months. In some cases tuber dormancy were broken by the application of a solution containing 10g thio-urea and 2mg giberelline in 1l H_2O. Tubers were cut at the navel and incubated in the solution for 20min at RT. Afterwards the tubers were dried over night, planted in pots containing a mixture of peat and soil, and placed in a warm surrounding.
The plants were either grown in greenhouse (temperature day: 20-24°C; temperature night: 18°C; light: 6-21:00 o'clock) or in Saran-houses under natural occuring conditions through May to September. Leaf and flower material were taken during all stages, whereas tubers were only selected after natural total tuber ripening. For further analysis tubers were stored at 4°C in dark environment.

2.2.2 Bacterial work

E. coli was incubated at 37°C with LB media over night (SAMBROOK & RUSSELL, 2001). Plate incubation was performed with LB media + 1% agar, liquid cultures were incubated on a shaker (200rpm).

Transformation of constructs was performed as described by HANAHAN (1983).

2.2.3 Yeast work

The yeast strains used in this study were grown on media with a suitable carbohydrate source (2%) depending on the genotype of the strain. The invertase mutant strain *SUC2* was grown on YPD media at 30°C overnight. The wild type strain *FY 1679* was either grown on YPD media or selective media (SD) with 2% sucrose as carbohydrate source. Transformed *SUC2* yeast strains were only grown on selective SD media with sucrose as carbohydrate source. Plate incubation was performed with yeast media + 2% agar, liquid cultures were incubated on a shaker (200rpm).

For functional complementation the invertase mutant strain *SUC2* was used. Yeast transformation was performed using a simplified method described by GIETZ & SCHIESTL (1995). The strain was grown in YPD media as a 5ml overnight culture. The next day a 50ml flask with YPD was inoculated with 1ml of the overnight culture and shaken for 3-5h at 30°C. Afterwards the culture was centrifuged at 4000rpm for 5min at RT and the pellet was washed

in 25ml H_20 and centrifuged again. The washed pellet was resuspended in 1ml 100mM LiAc, transferred to a 1,5ml tube and centrifuged at 13,000rpm for 10sec. After discarding the supernatant the pellet was resupended in 500µl 100mM LiAc.
The transformation reaction contained following components.

Table 2.2.1.: Components of the transformation reaction.

Component	Volume for one transformation
PEG 3000 (50%)	240µl
1M LiAc (pH 8.5)	35µl
ss-herring sperm (2mg/ml, denaturated at 100°C and kept on ice)	50µl
SUC2 yeast mutant	50µl

The concentration of the plasmid used for transformation varied between 0.8-1.5µg. 350µl of the transformation reaction were added to the plasmid (in 50µl), mixed and incubated for 30min at 30°C. Afterwards the reaction was incubated for 25-30min at 42°C and centrifuged at 13,000 for 10sec. The pellet was resuspended either in 150µl 1M sorbitol or in 150µl H_2O, plated on selective SD plates and incubated at 30°C between 3 and 5d. Transformants were transferred to fresh selective SD plates and check on their inserts using colony PCR.

2.2.4 Molecular biological methods

If not indicated otherwise, the methods applied in this study were taken from SAMBROOK & RUSSELL (2001) using standard procedures.

2.2.4.1 Genomic DNA extraction from leaf tissue

Young, healthy potato leaves were harvested and immidately frozen in liquid nitrogen. Frozen samples were freezedried (Eps1-15, Typ 1815, Christ Gefriertrocknung GmbH, Osterode) and stored in air-tight containers at –20°C. Total genomic DNA was extracted from 0.3-0.4g freeze dried leave material according to BORMANN ET AL. (2004).

2.2.4.2 Plasmid DNA isolation from bacteria

Small scale and midi scale plasmid isolation from *E. coli* were performed using the column-based Plasmid Isolation Mini or Midi Kit (Qiagen, Hilden) according to the supplier's protocol.
Isolation of BAC DNA has been adapted by customers from the Qiagen® Plasmid Midi Kit protocol. The procedure has been used to isolate 50-200kb BAC DNA of two potato-BAC

libraries BA and BC (BALLVORA ET AL., 2002, 2007). The yield of BAC DNA from a 100ml culture was up to 25µg.

2.2.4.3 Separation of DNA fragments by agarose gel electrophoresis

DNA fragments were mixed with DNA loading buffer and analyzed by agarose gel electrophoresis. The agarose concentration depended on the size of the fragments to be resolved. Electrophoresis was performed at 5V/cm using TAE buffer. Different DNA size markers were used to estimate the size of DNA fragments. The Fermentas ladders 100bp plus and 1kb were used. After electrophoresis, DNA was visualized on a transilluminator under UV light (254nm).

2.2.4.4 Separation of DNA fragments using pulse field gel electrophoresis (PFGE)

Pulse field gel electrophoresis (PFGE) was used to estimate the size of BAC inserts. 20µg of BAC DNA in a 25µl reaction was digested with NotI and incubated for 4h at 37°C. After inactivation of the reaction at 65°C for 15min, 5µl of the reaction were loaded on a 1% agarose gel to check the restriction reaction.

Preparation of the PFGE gel:

A 1% PFGE gel was prepared using Gold Agarose and 0.5x TAE buffer. After loading 20µl of the samples and the Fermentas markers lambda ladder and mid range, the slots were sealed with liquid gel and put in the PFGE chamber.

Running of the PFGE gel:

2.5l of 0.5x TAE buffer was filled in the PFGE chamber and cooled for 20min to 11-14°C. The machine settings were:

initial time	5sec
final	15sec
run	14h
voltage	5V/cm
incl. angle	120
pump	80

After the run, the PFGE gel was stained in a 2% EtBr solution for 1h. BAC DNA fragments were visualized on a transilluminator under UV light (254nm).

2.2.4.5 Purification of PCR products and gel-extracted DNA fragments

PCR products, gel-extracted PCR products and restriction digested products were either purified using the Roche High Pure PCR Purification Kit or using the Qiagen PCR Purification Kit following the supplier's protocol. PCR products for sequencing were purified using ExoSAP-IT®.

2.2.4.6 Total RNA extraction from leaf and floral tissue

Total RNA from leaves and inflorescences were extracted using the ToTally RNA Isolation Kit from Ambion following the manufacturer's protocol. Additionally, the RNA was purified from possible genomic DNA contaminations using the DNA-*free*™ Kit purchased from Ambion. The concentration and quality of the RNA was determined by measuring the ratios of absorbance A_{260nm}/A_{280nm} which should be between 1.8 and 2.0 and A_{260nm}/A_{230nm} which should be between 2 and 3 using the Nanodrop ND-1000 spectrophotometer (Peclab, Erlangen). The integrity of the RNA was tested by running a 1% agarose gel which were loaded with 300-500ng of total RNA that was mixed with 5µl of DNA loading dye. Total RNA was stored at –80°C.

2.2.4.7 Total RNA extraction from tuber tissue

Total RNA from tubers was extracted using the Plant RNA Isolation Kit from Invitrogen following the manufacturer's protocol. Small amounts of tubers were grinded in liquid nitrogen using mortal and pistil. Larger amounts of tuber tissue were crushed in liquid nitrogen cooled cylinders using the Retsch® Schwingmühle MM400 (Retsch GmbH, Haan) following the manufacturer's protocol.

Total RNA from tubers was further purified through additional precipitation steps: a high salt precipitation to remove polysaccharides and a lithium chloride precipitation to remove high molecular weight RNA. The RNA solution was adjusted to a total volume of 1ml by adding RNase free water. 250µl of isopropanol and 250µl of high salt solution (1.2M sodium citrate, 0.8M sodium chloride) were added, mixed and incubated on ice for 2h. The RNA was recovered by centrifugation at 13,000rpm for 30min at 4°C. The supernatant was removed and the pellet was rinsed with 70% ethanol, and centrifuged at 13,000rpm for 5min at 4°C. After removing the ethanol, the pellet was air-dried and dissolved in an appropriate volume of RNase free water to achieve a minimum concentration of 200ng/µl of total RNA.

The precipitation of high molecular weight RNA was done using 0.5 volume of 5M LiCl. The solution was mixed and kept on ice over night in the 4°C room. The RNA was recovered by

centrifugation at 13,000rpm for 30min at 4°C. After removal of the supernatant, the pellet was rinsed with 70% ethanol and centrifuged again at 13000rpm for 5min at 4°C. The ethanol was removed, the pellet air-dried and dissolved with RNase free water to a final volume of 20 to 50µl depending on the pellet size. Additionally, the RNA was purified from possible genomic DNA contaminations using the DNA-*free*™ Kit purchased from Ambion. The concentration and quality of the RNA was determined by measuring the ratios of absorbance A_{260nm}/A_{280nm} which should be between 1.8 and 2.0 and A_{260nm}/A_{230nm} which should be between 2 and 3 using the Nanodrop ND-1000 spectrophotometer (Peclab, Erlangen). The integrity of the RNA was tested by running a 1% agarose gel which were loaded with 300-500ng of total RNA that was mixed with 5µl of DNA loading dye. Total RNA was stored at –80°C.

2.2.4.8 cDNA synthesis

For first strand cDNA synthesis 2.0µg of total RNA was used to synthesize cDNA by reverse transcription using 200U of Superscript™ II reverse Transcriptase (Invitrogen, Karlsruhe) per reaction and oligo$(dT)_{16-18}$ primers (500ng), (Roche, Mannheim) as priming method. cDNA synthesis was performed according to the manufacturer's protocol and additional treated with RNase H (Roche, Mannheim) for 20min at 37°C.
Synthesized first strand cDNA was either used for moleular cloning (1µl per reaction) or in qRT-PCR (2.5µl of a 1:100 dilution).

2.2.4.9 Standard Polymerase Chain Reaction (PCR)

PCR reactions were performed in different thermal cyclers. The following machines were used.

Table 2.2.2: PCR machines.

Machine	Provided by
MJ Research DNA Engine Tetrad®4 peltier thermal cycler	Biozym, Hess. Oldendorf
Biometra® T1–Thermocycler	Biomedizinische Analytik GmbH, Göttingen
Biometra® T3–Thermocycler	Biomedizinische Analytik GmbH, Göttingen
Labcycler	Sensoquest Biomedizinische Elektronik, Göttingen

For standard reactions and colony-PCR *Thermus aquaticus* DNA Polymerase (*Taq*-DNA Polymerase) was used. *Taq*-DNA Polymerase was prepared described by PLUTHERO (1993). For high accuracy PCR reaction (cloning), the proof-reading Roche Fast Start High Fidelity PCR System and the proof-reading KOD Hot Start DNA Polymerase (Novagen, Darmstadt) were used.

Standard PCR reactions were performed as follows:

Table 2.2.3: Standard PCR reaction using *Taq*-DNA Polymerase

Concentration	Reagent
50-200ng	Template (genomic DNA, plasmid DNA, cDNA, bacterial or yeast colony)
2.5µl	10x PCR buffer (without $MgCl_2$)
3mM	$MgCl_2$
25mM	dNTP
10-25pmol	Primer 1
10-25pmol	Primer 2
0.5-0.7µl	*Taq*-DNA Polymerase (0.025-0.05U/µl)
adjust to 25µl	

Before using bacterial colonies for PCR, colonies were picked from the plate, resuspended in 15µl H_2O and denaturated at 95°C for 10min. Afterwards 1µl of the denaturated colony was used for PCR.

Before using yeast colonies for PCR, fresh grown colonies were picked and resuspended in 15µl 2mM NaOH and denaturated at 95°C for 10min. Afterwards 1µl of the denaturated colony was used for PCR.

PCR program:	Initial denaturation	94°C for 3min
	Denaturation	94°C for 30sec
	Annealing	55-65°C for 30sec
	Elongation	1min/1kb
	Final extension	72°C for 10min
	Number of cycles	30-50

Table 2.2.4: Standard PCR reaction using Roche Fast Start High Fidelity PCR System

Concentration	Reagent
50-200ng	Template (genomic DNA, plasmid DNA, cDNA)
2.5µl	10x PCR buffer (without $MgCl_2$)
3mM	$MgCl_2$
25mM	dNTP
10-25pmol	Primer 1
10-25pmol	Primer 2
0.25µl	Fast Start High Fidelity Polymerase (2.5U)
adjust to 25µl	

PCR program:	Initial denaturation and activation	94°C for 2min	
	Denaturation	94°C for 15sec	10x
	Annealing	55-65°C for 30sec	
	Elongation	1min/1kb	
	Denaturation	94°C for 15sec	
	Annealing	55-65°C for 30sec	20x
	Elongation	1min20sec/1kb	
	Final extension	68°C for 10min	
	Number of cycles	30	

Table 2.2.5: Standard PCR reaction using Novagen KOD Hot Start DNA Polymerase

Concentration	Reagent
50-200ng	Template (genomic DNA, plasmid DNA, cDNA)
2.5µl	10x PCR buffer (without $MgCl_2$)
1mM	$MgSO_4$
25mM	dNTP
10-25pmol	Primer 1
10-25pmol	Primer 2
0.5µl	KOD Hot Start DNA Polymerase(0.5U)
adjust to 25µl	

PCR program:	Initial denaturation and activation	94°C for 2min
	Denaturation	94°C for 15sec
	Annealing	55-65°C for 30sec
	Elongation	1min/1kb
	Number of cycles	30-50

2.2.4.10 Molecular cloning of cDNA constructs for yeast *SUC2* transformation

Unless otherwise described, cloning strategies performed in this study included directional cloning of PCR products into pGEM®-T Vector System or pGEM®-T Easy Vector System (Promega, Mannheim). All reactions were performed following the manufacturer's protocol. All constructs were verified by sequencing. Alleles were defined as sequences, which were found twice in two independent PCRs. In some cases where sequences varied a lot, the allelic consensus sequence was used for allele definition.

Production of the final expression vector constructs for yeast transformation was performed using the 112 A1 NE yeast expression vector (Appendix A 2) kindly provided by Lothar Willmitzer's Group, MPI for Molecular Plant Physiology/Golm. 112 A1 NE inserts are driven under the control of the constitutive strongly expressed *Adh1* promoter. The vector, originally

an *E. coli* vector, also includes the *Adh1* terminator, an ampicillin resistance for *E. coli* selection, and tryptophane for yeast selection. pGEM®-T constructs bearing invertase alleles were amplified using proof-reading high fidelity *Taq*-Polymerase (Roche, Mannheim) to insert specific cloning sites. Alleles of the loci *Pain-1* and *invGF* were amplified with primers inserting *Not*I and *Bam*HI restriction sites for sticky end ligation into the vector 112 A1 NE. *Pain-1* and *invGF* PCR products as well as the vector were digested with the corresponding restriction enzymes, followed by ligation of the linearized vector with the digested PCR products. Alleles of the *invGE* locus were amplified with primers inserting only *Not*I restriction sites because a *BamH*I restriction site is included in the gene. *invGE* PCR products as well as the vector were digested with *Not*I restriction enzyme, followed by blunt end ligation of the linearized vector with the digested PCR product. 112 A1 NE constructs were verified by sequencing.

All constructs generated in this study are indicated in the Table below.

Table. 2.2.6: Overview of generated constructs.

Gene	Vector	Primer pairs used (Table 2.1.2)
Initial cloning of invertase alleles:		
Pain-1	pGEM®-T/ T Easy	ZrPain-F/ PainUni-R
invGE	pGEM®-T/ T Easy	invGE-F-fulgth/ invGE-R-fulgth
invGF	pGEM®-T/ T Easy	invGF-F-fulgth/ invGF-R-fulgth
pCD111	pGEM®-T/ T Easy	CD111fl_F/ CD111fl_R
pCD141	pGEM®-T/ T Easy	CD141fl_F/ CD141fl_R
Cloning of constructs for yeast transformation:		
Pain-1	112 A1 NE	PainNotI_R/ PainBamHI_R
invGE	112 A1 NE	ENotI_F/ ENotI_R
invGF	112 A1 NE	FNotI_F/ FBamHI_R

The presence of the transformed plasmid was tested via colony-PCR using a primer that was located in the backbone of the vector and a second primer localized within the insert sequence (Table 2.1.3, primer pair T7/SP6P).

2.2.4.11 Quantitative real-time PCR

Quantitative real-time PCR (qRT-PCR) was performed using a Mastercycler® ep *realplex* (Eppendorf, Hamburg). Primers were tested for undesired primer dimer formation by melting curve analysis (55°C to 95°C with a heating rate of 0,1°Cs^{-1} and continuous fluorescence measurement) using the Power SYBR® Green PCR Master Mix (Applied Biosystems,). For standard curves tuber cDNA of the 4th week of cold storage were diluted 1:10, 1:100 and 1:1000. Total invertase transcripts were quantified using the primer pair Pyro_Pain_F/Pyro_Pain_R in a PCR with a 100 fold template dilution. The quantification of

the normalization gene *ef1-α* (elongation factor 1-α, NICOT ET AL, 2005) was calculated based on a 100 fold dilution series of the samples also tested with *Pain-1* transcript primer (qRT-primer are listed in Table 2.1.9). Additionally, the normalization gene *L2* (cytoplasmic ribosomal protein, NICOT ET AL, 2005) were used for samples of the cultivar 'Theresa'. Determined *L2* values were similar to values of the gene *ef1-α*, and in the course of the work *ef1-α* was used for subsequent qRT-PCR.

Plant material for quantitative expression analysis was grown in three independent biological replicates, from which two were used for all analysed samples. In case of high variances within the measured values, the third replicate was also tested. qRT-PCR reactions of each of the biological replicates were done in technical duplicates.

Table 2.2.7: Reaction setup for qRT-PCR

Concentration	Reagent	Volume
1:10, 1:100, 1:1000	cDNA	2.5µl
2x	Power SYBR® Green PCR Master Mix	12.5µl
10pmol	Primer 1	2µl
10pmol	Primer 2	2µl
fill to 25µl with H_2O		

PCR program for qRT-PCR of invertase transcripts:

Initial denaturation	95°C for 10min
Denaturation	95°C for 15sec
Annealing	55°C for 30sec
Elongation	72°C for 45sec
melting curve analysis	
Number of cycles	50

PCR program for qRT-PCR of the normalization gene *EF1α*:

Initial denaturation	95°C for 10min
Denaturation	95°C for 15sec
Annealing	60°C for 30sec
Elongation	72°C for 45sec
melting curve analysis	
Number of cycles	40-50

2.2.4.12 Sequencing

DNA sequencing was performed by the MPIZ DNA core facility on Applied Biosystems (Weiterstadt) Abi Prism 377, 3100 and 3730 sequencers using BigDye-terminator v3.1. chemistry. Premixed reagents were purchased from Applied Biosystems. Sequences were analysed with the software Chromas Pro version 1.33 (share-it, Cologne) or the Lasergene software.

2.2.4.13 Pyrosequencing

Pyrosequencing is a robust and quantitative method of DNA sequencing based on real-time detection of pyrophosphate, which is released as a result of nucleotide incorporation in a the 'sequencing by synthesis' reaction (RONAGHI ET AL., 1996). 'Sequencing by synthesis' involves taking a single strand of the DNA to be sequenced and then synthesizing its complementary strand enzymatically. The pyrosequencing method is based on detecting the activity of DNA polymerase with another chemiluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step. The template DNA is immobilized, and solutions of A, C, G, and T nucleotides are added and removed after the reaction, sequentially. Light is produced only when the nucleotide solution complements the first unpaired base of the template. The sequence of solutions, which produce chemiluminescent signals, allows the determination of the sequence of the template. The templates for pyrosequencing can be made both by solid phase template preparation (Streptavidin coated magnetic beads) and enzymatic template preparation (Apyrase+Exonuclease). In this study, Streptavidin coated magnetic beads were used.

PCR conditions:

The primers used for pyrosequencing analysis are listed in the Tables 2.4.1 for the *Pain1* locus on chromosome III, 2.4.2 for the *invGE* locus on chromosome IX and 2.4.3 for the *invGF* locus on chromosome IX.

PCR setup and conditions are listed in Table 2.10.

Solid phase template preparation for single-stranded DNA template:

Table 2.2.8: Reaction setup for pyrosequencing

Volume	Reagent
20µl	PCR product
15µ	H_2O (LiCroSolv Merck)
40µl	Binding buffer (10mM Tris-HCl, 2M NaCl, 1mM EDTA, 0.1% Tween 20; pH 7.6)
5µl	Streptavidin-coated Super Paramagnetic beads

The reaction mixture was incubated for 5min on a shaker at RT. The Streptavidin-template complex was captured using the PSQ96 Sample Prep tool (Biotage AB, Uppsala, Sweden) and single-stranded template was generated by washing in 70% EtOH for 3sec, in 0.2M NaOH for 5sec followed by washing in washing buffer (10mM Tris acetate pH 7.6) for 10sec. 1µl of the sequencing primer (0.25mM) was annealed to the immobilized template in 39µl annealing buffer (20mM Tris acetate, 2mM Mg acetate, pH 7.6) and heated at 80°C for 2min followed by slow cooling to room temperature.

Pyrosequencing:

The sequencing reaction was performed automatically with the PSQ 96 system (Biotage AB, Uppsala, Sweden) at 28°C using a SNP reagent kit according to the manufacturer's protocol. The ssDNA template is hybridized to a sequencing primer and incubated with the enzymes DNA polymerase, ATP sulfurylase, luciferase and apyrase, and with the substrates adenosine 5´ phosphosulfate (APS) and luciferin. The four enzyme mixture, the substrates and the four separate deoxynucleotide triphosphates were loaded into the reagent cartridge (PSQ 96 SNP Reagent Kit, Biotage AB, Uppsala, Sweden).

1. The addition of one of the four deoxynucleotide triphosphates initiates the second step. DNA polymerase incorporates the correct, complementary dNTPs onto the template. This incorporation releases pyrophosphate (PPi) stoichiometrically.

2. ATP sulfurylase quantitatively converts PPi to ATP in the presence of adenosine 5´ phosphosulfate. This ATP acts as fuel to the luciferase-mediated conversion of luciferin to oxyluciferin that generates visible light in amounts that are proportional to the amount of ATP. The light produced in the luciferase-catalyzed reaction is detected by a camera and analyzed in a program.

3. Unincorporated nucleotides and ATP are degraded by the apyrase, and the reaction can restart with another nucleotide.

The following Tables contain information about primers used in the pyrossequencing assay for detection of more than one SNP to dissect the corresponding alleles due to the complexity of the approach. Tables for the dissection of two alleles are not shown because the setup is described in the corresponding result section.

Table 2.2.9: Primers used in the pyrosequencing assay of *invGE* alleles from the tetraploid cultivars.

Genotype	Allele	SNP position	Allele specific SNP	Sequencing primer
			E_SA/E_SN1/E_SN2/E_SN3	
'Satina'	*E_SA*	SNP 1237	**T**/G/G/G	PyroE_Sat6fSeq
	E_SN1	SNP 1366	A/**G**/A/A	PyroE_Sat4Seq
	E_SN2	SNP 1379	C/C/**T**/C	PyroE_Sat3Seq
	E_SN3	SNP 1216	A/A/A/**G**	PyroE_Dia_F
			E_DA/E_DN1/E_DN2	
'Diana'	*E_DA*	SNP 1086	**A**/T/T	PyroE_Dia6fSeq
	E_DN1	SNP 1117	T/**C**/T	PyroE_Dia2Seq
	E_DN2	SNP 924	T/T/**C**	PyroE_Dia3Seq
			E_TA/E_TN1/E_TN2/E_TN3	
'Theresa'	*E_TA*	SNP 1615	**A**/T/T/T	PyroE_Ther6fSeq
	E_TN1	SNP 1720	C/**A**/C/C	PyroE_Ther1Seq
	E_TN2	SNP 1553	T/T/**C**/T	PyroE_Ther2Seq
	E_TN3	SNP 1473	T/T/T/**G**	PyroE_Ther_F

For PCR fragment amplification the following primers were used (Table 2.1.5): 'Satina': PyroE_SatF/PyroE_SatRBio; 'Diana': PyroE_Dia_F/PyroE_Dia_RBio; 'Theresa': PyroE_Ther_F/PyroE_TherRBio.

Table 2.2.10: Primers used in the pyrosequencing assay of *invGE* alleles from the diploid genotypes.

Genotype	Allele	SNP position	Allele specific SNP	Sequencing primer
P18	*E_P18N1*	SNP 108	A	PyroE_PSNP108Se
	E_P18N2		T	
P40	*E_P40N1*	SNP 58	C	PyroE_PSNP58Seq
	E_P40N2		T	
P54	*E_P54N1*	SNP 58	C	PyroE_PSNP58Seq
	E_P54N2		T	

For PCR fragment amplification the following primers were used (Table 2.1.5): P18, P40, P54: invGE-F-fulgth/PyroE_ParentsRB.

Table 2.2.11: Primers used in the pyrosequencing assay of *invGF* alleles from the tetraploid cultivars.

Genotype	Allele	SNP position	Allele specific SNP	Sequencing primer
			F_SN1/F_SN2/F_SN3/F_SN4	
'Satina'	*F_SN1*	SNP 111	**T**/C/C/C	PyroF_SNP111Seq
	F_SN2	SNP 459	C/**T**/C/C	PyroF_Sat2Seq
	F_SN3	SNP 378	A/A/**G**/A	PyroF_Sat3Seq
	F_SN4	SNP 96	C/C/C/**T**	PyroF_SNP96Seq
'Diana'	*F_DN1*	SNP 96	**T**	PyroF_SNP96Seq
	F_DN2		**C**	
'Theresa'	*F_TN1*	SNP 96	**T**	PyroF_SNP96Seq
	F_TN2		**C**	

For PCR fragment amplification the following primers were used (Table 2.1.6): 'Satina': PyroF_Sat_F/PyroF_Sat_RBio and PyroF_4d_F/PyroF_4d-RBio for the alleles *F_SN1* and *F_SN4*; 'Diana' and 'Theresa': PyroF_4d_F/PyroF_4d-RBio.

Table 2.2.12: Primers used in the pyrosequencing assay of *invGF* alleles from the diploid genotypes.

Genotype	Allele	SNP position	Allele specific SNP	Sequencing primer
P40	*F_P40N1* *F_P40N2*	SNP 1534	G A	PyroF_P40Seq
P54	*F_P54N1* *F_P54N2*	SNP 1446	T C	PyroF_P54Seq

For PCR fragment amplification the following primers were used (Table 2.1.6): P40 and P54: PyroF_P40/54_F/ PyroF_P40/54_RB.

2.2.4.14 Single stranded conformation polymorphism (SSCP) analysis

SSCP is the electrophoretic separation of single-stranded nucleic acids based on subtle differences in sequence (often a single base pair), which results in a different secondary structure and a measurable difference in mobility through a gel.

Background:

The mobility of double-stranded DNA in gel electrophoresis is dependent on strand size and length but is relatively independent of the particular nucleotide sequence. The mobility of single strands, however, is noticeably affected by very small changes in sequence, possibly one changed nucleotide out of several hundred. Small changes are noticeable because of the relatively unstable nature of single-stranded DNA; in the absence of a complementary strand, the single strand may experience intrastrand base pairing, resulting in loops and folds that give the single strand a unique 3D structure, regardless of its length. A single nucleotide change could dramatically affect the strand's mobility through a gel by altering the intrastrand base pairing and its resulting 3D-conformation (MELCHER, 2003).

Single-strand conformation polymorphism analysis takes advantage of this quality of single-stranded DNA. First announced in 1989 as a new means of detecting DNA polymorphisms, or sequence variations, SSCP analysis offers an inexpensive, convenient, and sensitive method for determining genetic variation (SUNNUCKS ET AL., 2000).

Like restriction fragment length polymorphisms (RFLPs), SSCPs are allelic variants of inherited, genetic traits that can be used as genetic markers. Unlike RFLP analysis, however, SSCP analysis can detect DNA polymorphisms and mutations at multiple places in DNA fragments (ORITA ET AL., 1989). As a mutation scanning technique, though, SSCP is more often used to analyze the polymorphisms at single loci, especially when used for medical diagnoses (SUNNUCKS ET AL., 2000).

The SSCP analysis of the invertase genes *invGE* and *invGF* was published by LI ET AL. (2005). The invertase genes *Pain-1* and *pCD141* were analyzed also by LI ET AL. (2008). Primers for *pCD141* (pCD141_3F/pCD141_3R) were generated in the course of this work (Table 2.1.8).
SSCP procedure was performed as described in the cited publications.

2.2.4.15 BAC DNA library screens

BAC library screens were performed using two different libraries (supplied by LION Bioscience AG, Heidelberg). The first library, so called 'BA' library (BALLVORA ET AL., 2002), was constructed from partially *Hind*III digested high-molecular weight genomic DNA of the potato genotype P6/210 in the binary vector pCLD04541. P6/210 is a F1 hybrid of the parental clones P41 (H79.1506/1) and P40 (H80.696/4), (RITTER ET AL., 1991).The BAC library consists of approximately 100.000 clones with an average insert size of 70kb. With the size of a haploid potato genome being approximately 109 base pairs, the genome coverage was 6-7 times per hapliod genome.
The second BAC library, so called 'BC' library (BALLVORA ET AL., 2007), was constructed from partially *Eco*RI digested genomic P6/210 DNA in the binary vector pBeloBAC11. The average insertion size was 80kb, corresponding to an, on average, 8-fold coverage of the potato genome.
Library screens were performed using a set of four filters carrying ≈100,000 clones.

Preparation of radioactively-labeled probes and DNA hybridisation:
200ng of gel-purified or ExoSAP-IT® purified PCR products were diluted up to a final volume of 12µl and 2.5µl buffer A1 (0.2mM dTTP, 0.2mM dCTP, 0.2mM dGTP; Invitrogen, Karlsruhe), 2.5µl DNaseI DNA Polymerase (Invitrogen, Karlsruhe) and 3µl α32 pdATP were added. The reaction was incubated at 16°C for 1h. The probe was purified on a Sephadex-G50 column (Amersham Biosciences, Sweden) and heated at 95°C for 5min.

Pre-hybridisation and hybridisation were carried out in hybridisation solution (20x SSPE [3M NaCl, 0.2M NaH_2PO_4, 20mM EDTA pH 7.0], 100x Denhardts, 10% SDS) in glass tubes (30cm x 4cm) at 65°C under continuous rotation in a hybridisation oven (Bachofer, Reutlingen). Pre-hybridisation was performed at least for 1h before hybridisation or overnight. Probe hybridisation was carried out overnight.

After hybridisation the filter was washed accordingly:

1. 50ml 2x SSPE + 0.1% SDS at 65°C for 10-15min
2. 50ml 1x SSPE + 0.1% SDS at 65°C for 10min
3. 50ml 0.2x SSPE + 0.1% SDS at 65°C for 10min

The filter was wrapped in thin plastic foil (Saran wrap) and exposed overnight either to a phospoimager screen (Molecular Dynamics) in a cassette at RT or to film (Kodak® X-Omat AR Film, XAR 5, 35x43cm (Sigma-Aldrich Chemie GmbH, Steinheim) in a cassette at -70°C.

The *Pain-1* locus of BC library clones BC14 and BC17 was custom sequenced by GATC Biotech, Konstanz using primer walking as sequencing method. Full-length BAC insert sequencing was performed for the *Pain-1* clones BC2 (insert size: 75kb), BC14 (insert size: 75kb), and BC15 (insert size: 97kb), and for the BC clone BC3 (insert size: 130kb) for the genes *pCD111* and *pCD141*. Full-length BAC insert sequencing was carried out by MWG Biotech AG, Ebersberg using the 454 sequencing technique on the GS FLX system.

2.2.4.16 Colony-lift

The colony-lift is an easy method to confirm hybridisation positive BAC clones. For this purpose single colonies from hybridisation positive BAC clones were grown on selective LB plates (BA BACs: Tet; BC BACs: Cam) at 37°C overnight. To transfer the DNA, Amersham Hybond^{TM} – N^+ membrane (GE Healthcare, Buckinhamshire, UK) was placed on the plate and then stripped off again. The membrane was washed accordingly:

1. once 10% SDS for 3min
2. once denaturation solution (1.5M NaCl; 0.5M NaOH) for 5min
3. twice neutralisation solution (1.5M NaCl; 0.5M Tris-HCl pH 8.0) for 5min

After washing, the membrane was air-dried (ca. 15min) and then cross linked with a UV crosslinker (Stratagene) by applying 120,000J x cm^{-2} of energy. The membrane was wrapped in thin plastic foil (Saran wrap) and stored in the refrigerator at 4°C.

Preparation of radioactively-labelled probes and DNA hybridisation:

Previously described in 2.2.4.15.

2.2.4.17 Southern blot analysis

Southern analysis was performed according to SAMBROOK ET AL. (1998). 20ng of purified BAC DNA were digested to completion with *Hind*III, *Sma*I and *Bam*HI for 4h.

DNA separation and blotting onto membranes:

Digested BAC DNA was subsequently mixed with loading buffer, loaded on a 1% agarose gel and separated for 5h at 70V via electrophoresis. After the run, the gel was stained in a 2% EtBr solution for 15min at RT and DNA was visualized on a transilluminator under UV light (254nm). The gel was destained in H_2O for 20min at RT.

DNA was transferred on Amersham Hybond^{TM} – N^+ membrane for 18h at RT using 0.4M NaOH buffer. After the transfer procedure DNA was cross linked to the filter with a UV crosslinker (Stratagene) by applying 120,000J x cm^{-2} of energy. The blot was wrapped in thin plastic foil (Saran wrap) and stored in the refrigerator at 4°C.

Preparation of radioactively-labelled probes and DNA hybridisation:

Previously described in 2.2.4.15.

2.2.5 Three-dimensional modelling of invertase alleles

3D-modelling was performed by Pawel Durek, MPIMP/Golm. The modelling of the allelic invertase molecular structure was based on the invertase 3D and crystal structure of cyanobacteria (ALBERTO ET AL., 2004). The models are comparative, superimposing two allelic sequences. Differences of the alleles are highlighted. The modelling was applied for associated and non associated *Pain-1* alleles of the tetraploid potato cultivars 'Satina' and 'Diana'. The models include the putative sucrose binding site with the substrate sucrose. In addition to the structural visualization of amino acid exchanges, also the electrostatic potential (EP) of the molecules was mapped at pH 4.7 mimicking the vacuolar and apoplastic conditions.

All models were predicted by homology modelling applying the automated structure prediction server 3djigsaw (BATES ET AL., 2001). Subsequently, the models were prepared for continuum electrostatics calculation utilizing the PDB2PQR package (Version: 1.3.0) (DOLINSKY ET AL., 2004). For the calculation, the AMBER force field and the protonation states at pH 4.7 were used (LI H. ET AL., 2005), to reflect the proper vacuolar and apoplastic acidity. The isoelectric surfaces were computed by the adaptive Poisson-Boltzmann Solver (APBS) (BAKER ET AL., 2001) utilizing standard parameters at the temperature of 298K. The

comparison of the isoelectic surfaces revealed no significant changes upon lowering the temperature parameter. The isoelectric surfaces were visualized by PyMol (DELANO, 2002).

The allelel models were superimposed by Swiss-PDB Viewer (GUEX ET AL., 1997). Differences between structures were marked by color-code as judged by the RMSs between the structures and visualized by PyMol. In Figures deep blue colour indicates highly similar protein regions, whilst red characterizes high structural differences.

2.2.6 Biochemical methods

2.2.6.1 Protein extraction from yeast

50ml of yeast cultures were grown for 72h at 30°C on a shaker (200rpm). Cells were harvested $OD_{600} \approx 2.3$ by centrifugation at 4,000rpm, for 10min, at 4°C. The pellet was washed with 25ml cold dest. H_2O and centrifuged again (4,000rpm, for 10min, at 4°C). The pellet was kept on ice and resuspended in 4ml cold protein extraction buffer (25mM Tris phosphate pH 6.7; 10mM glycerol, 0.1mM DTT, 1mM EDTA, 2% Protease Inhibitor Cocktail for general use (Sigma, St. Louis, USA). After adding half of the solution volume of acid washed glass beads (425-600 micron, Sigma-Aldrich Chemie GmbH, Taufkirchen), the tubes were vortexed for 10min in time intervals of 2min, keeping the solutions on ice in between. After this procedure a centrifugation followed at 6,000rpm for 10min at 4°C. The supernatant were loaded on PD-10 columns (GE Healthcare, Buckinhamshire, UK) equilibrated with protein extraction buffer without protease inhibitors. Proteins were eluted from the column by adding 2ml of protein extraction buffer without protease inhibitors and kept on ice.

Determination of the protein concentration using the Bradford assay:

The protein concentration was determinded using the Bradford assay (BRADFORD, 1976) with Bradford dye reagent (Protein assay, Bio-Rad, Hercules, USA). 2-10µl of the protein extracts were added to 198-190µl H_2O and 800µl of Bradford dye reagent. The mixture was incubated for 10-15min at RT and extinction was measured at 595nm against a blank (200µl H_2O + 800µl dye) and bovine serum albumin as a standard.

2.2.6.2 Enzymatic assay of invertase

The enzymatic invertase assay was performed using a modified protocol of ZRENNER ET AL. (1995). The principle of the enzymatic reaction is the following:

Figure 2.2.1: Simplified scheme of the principle of invertase reaction.

For a 100µl invertase assay reaction 20µg of total yeast protein extracts were used. The reaction components were the following:

Table 2.2.13: Reaction setup for invertase assay.

Concentration	Component
20µg	total yeast protein extract
20mM	NaOAc (pH 4.7)
2.5-120mM	sucrose
fill up to 100µl with H_2O	

The reaction was incubated for 1h at 30°C for invertase alleles from the genes *Pain-1*, *invGE,* and *invGF*. Additionally, invertase alleles from the *Pain-1* locus were incubated for 1:30h at 4°C. After incubation 10µl of 1M $NaHPO_4$ (pH 7.2) were added and the reaction was stopped by heating at 95°C for 10min. Blanks had the same reaction mixture, but were heat inactivated without incubation.
It was checked that the assay was linear with time for at least 90min, and was linearly dependent on the amount of protein in the crude extract added up to 50µg.

The quantitative, enzymatic determination of glucose was performed using the enzymes hexokinase (HK) and glucose-6-phosphate dehydrogenase (G6PDH). The principle of the reaction is the following:

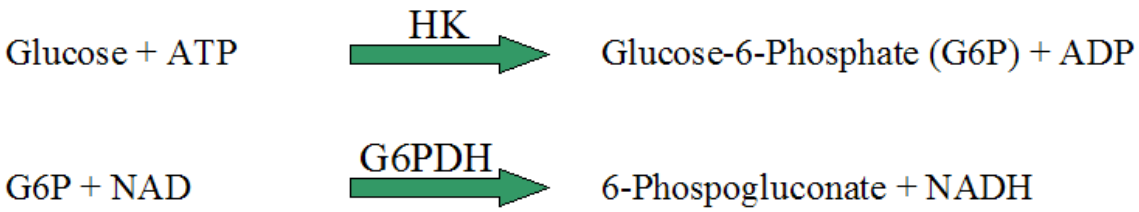


Figure 2.2.2: Simplified scheme of the NADH coupled glucose detection.

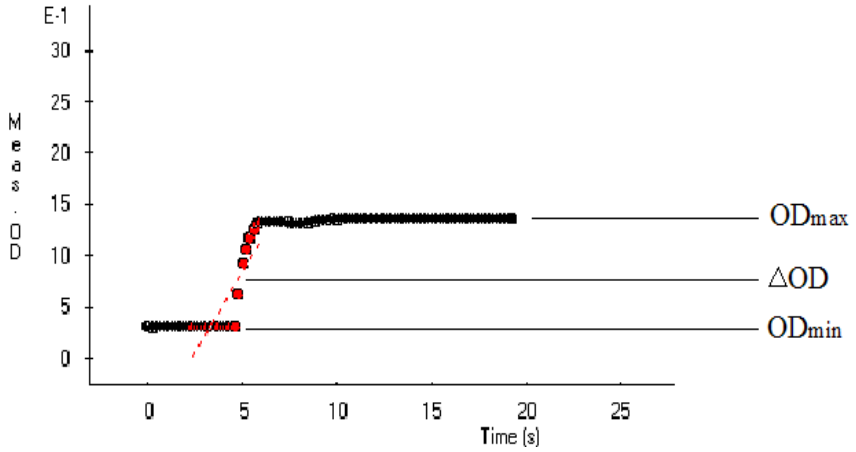
Glucose is phosphorylated by adenosine triphosphate (ATP) in the reaction catalyzed by hexokinase (HK). Glucose-6-phosphate (G6P) is then oxidized to 6-phospho-gluconate in the presence of the oxidized nicotinamide adenine dinucleotide (NAD) in a reaction catalyzed by glucose-6-phosphate dehydrogenase (G6PDH). During this oxidation, an equimolar amount of NAD is reduced to NADH. The consequent increase in absorbance at 340nm is directly proportional to glucose concentration.

The components of a 300µl reaction were the following:

Table 2.2.14: Reaction setup for glucose determination.

Stock concentration/storage	Final concentration	Volume/reaction
1M Imidazol pH 6,9 HCl / 4°C	100mM	30µl
1M $MgCl_2$ / RT	5mM	1.5µl
100mM NADP+ / -20°C	2mM	6µl
100mM ATP / -20°C	1mM	3µl
G6PDH from yeast (400U/ml) / 4°C	2U	5µl
Enzymatic invertase reaction / -20°C		10µl
fill up to 294µl with H_2O		

G6PDH was directly resuspended in the reaction components after spinning out of ammonium sulphate. HK (300U/ml) was also spun out of ammonium sulphate and resuspended in 6µl of the reaction components without G6PDH. The reaction was started by adding HK to the assay and absorbance was measured at 340nm. For absorbance measurements, a plate reader was used and OD_{min} and OD_{max} values were determined resulting in ΔOD used for calculation



nmol Glc/mg protein/h = ΔOD/5.3/A*B*C/D/E

Figure 2.2.3: Overview of plate reader output and glucose calculation. 5.3=millimolar extinction coefficient of NAD+, NADH, NADP+ or NADPH at 340nm using the 96 well plate. A=volume of invertase reaction for glucose detection, B=total volume of invertase reaction, C=total volume of glucose detection reaction, D=protein concentration used in invertase assay, E=incubation time of invertase assay.

Calculated glucose concentrations were blotted against all tested sucrose concentrations and tested for Michaelis-Menten kinetics. Transforming the measured values by Lineweaver-Burk plot, led to the determination of the Michaelis constant (K_m) and the maximal velocity (v_{max}) of invertase reaction. The K_m value describes the affinity of an enzyme to its substrate. K_m is inversely proportional to the substrate affinity, and is for a one-substrate reaction independent of the enzyme concentration. The enzymatic substrate conversion increases with increasing substrate concentration until the enzyme is saturated. This characteristic is described by the maximum velocity (v_{max}). In contrast to K_m, v_{max} depends on the enzyme concentration. Both biochemical characteristics vary with pH, with temperature and with the structure of the substrate.

Calculation of the significance values for the biochemical parameters

The significance values for differences between the K_m and v_{max} values measured for the *Pain-1* alleles at 30°C and 4°C, and for the alleles of the genes *invGE* and *invGF* at 30°C were calculated by Benjamin Stich, MPIZ/Köln.

In a first step, K_m and v_{max} estimates were calculated for each of the two biological replicates and the three technical replicates. These estimates were then used in a mixed-model context to examine:

(i) the presence of differences between the alleles in each of the four experiments (*Pain-1* assay at 30°C and 4°C, *invGE* assay at 30°C, *invGF* assay at 30°C):

$$Y = \mu + \text{allele} + \text{allele:biolrep} + \text{error},$$

where μ was the general mean, allele an effect for the allele (without wild type reference *FY 1679*), and allele:biolrep was an effect for the biological replicate nested within the allele effect. Allele was regarded as fixed and allele:biolrep as random.

(ii) the influence of the temperature regime (*Pain-1* assay at 30°C and 4°C):

$$Y = \mu + \text{tempreg} + \text{allele} + \text{temprep*allele} + \text{tempreg:allele:biolrep} + \text{error},$$

where tempreg was the effect for the temperature regime, and temprep*allele the interaction between the temperature regime and the allele. Tempreg and tempreg*allele were regarded as fixed.

(iii) the influence of the location of the proteins (vacuolar vs. cell wall-bound):

$$Y = \mu + \text{loc} + \text{loc:allele:biolrep} + \text{error},$$

where loc was the effect for the location of the protein, which was regarded as fixed.

(iv) the presence of differences between all examined alleles:

$$Y = \mu + allele + allele:biolrep + error.$$

For fixed effects, a Wald-F-test was performed.

2.2.6.3 Protein separation by SDS-PAGE and Western blot analysis

Protein separation by SDS-PAGE:

The protein extracts were prepared for SDS-PAGE (LAEMMLI, 1970) by adding SDS sample buffer and by heating the samples at 95°C for 10min to denature the proteins.

The extracts were applied onto precast 4-12% Bis-Tris gradient gels (NuPAGE®, Invitrogen, Carlsbad, USA) and were separated in MOPS running buffer (Invitrogen, Carlsbad, USA) at 200V in XCell SureLock™ Mini-Cells (Invitrogen, Karlsruhe). The following molecular weight markers were used:

1. Spectra™ Multicolor Broad Range Protein Ladder (10-260kDa), (MBI Fermentas GmbH (St. Leon-Rot)
2. MagicMark™ XP Western Protein Standard (Invitrogen, Carlsbad, USA)

After the run the gels were stained with Coomassie Brilliant Blue (Bio-Safe™ Coomassie G-250 stain, Bio-Rad, Hercules, USA) to detect the proteins. Gels for blotting were not stained.

Western blot analysis:

The protein extracts were blotted on Amersham Hybond-P PVDF Membrane (GE Healthcare, Buckinhamshire, UK) by wet electrotransfer using a blotting module (XCell™ II Blot Module, Invitrogen, Carlsbad, USA) according to the manufacturer's insructions. After blotting, the protein transfer onto the membrane was visualized with P3504 Ponceau S (Sigma-Aldrich Chemie GmbH, Steinheim) and after destaining and TBS (50mM Tris-HCl pH 7.5, 150mM NaCl) washing, the membrane was incubated in blocking solution (TBS + 3% non-fat dried milk powder) for 1h at RT and continuously shaking. For primary antibody reaction, the membrane was incubated with polyclonal anti-invertase antibodies overnight at RT on a shaker.

Table 2.2.15: Anti-invertase antibodies used in Western blot analysis.

Antibody	Concentration	Supplied/provided by
25kDa vacuolar invertase carrot isoform I	1:400	Arnd Sturm(former member of the Friedrich Miescher Institut, Basel, Switzerland)
43kDa vacuolar invertase carrot isoform I	1:500	
vacuolar invertase carrot isoform I	1:1000	Heather A. Ross (Scottish Crop Research Institute, Dundeé, Scotland)
vacuolar invertase carrot isoform II	1:1000	
58kDa vacuolar invertase potato	1:200	

All antibodies were used in TBS + 1.5% non-fat dried milk powder.

As a secondary antibody the ECL^{TM} Anti-rabbit IgG Horseradish Peroxidase linked whole antibody (from donkey, GE Healthcare, Buckinghamshire, UK) in a concentration 1:10000 in TBS without milk powder was used and incubated for 1h at RT on a shaker. For visualisation, the Amersham ECL Plus Western Blotting Detection Reagents (GE Healthcare, Buckinghamshire, UK) was used according to the manufacturer's protocol.

3 Results

3.1 The *Pain-1* locus on chromosome III

The *Pain-1* locus encodes a soluble acid invertase, which is located in the vacuole. The pH optimum of the corresponding enzyme ranges between 4.5 and 5.0 (TYMOWSKA-LALANNE & KREIS, 1998). cDNAs of several potato soluble acid invertases have been cloned and proteins were partially characterized at functional level (ZHOU ET AL., 2004; accession L29099, ZRENNER ET AL., 1996; accession X70368, ZHANG ET AL., unpublished; accession AY341425, MATSUURA-ENDO ET AL., 2006 unpublished; accession DQ478950).

3.1.1 Structural characterization of the *Pain-1* locus

3.1.1.1 Molecular cloning of *Pain-1* invertase cDNA alleles from tuber tissue

Soluble acid invertase transcripts are strongly induced during tuber cold storage (ZRENNER ET AL., 1996; BAGNARESI ET AL., 2008). Therefore, molecular cloning of *Pain-1* alleles was performed using potato tubers stored for four weeks at 4°C in the dark.

Using the full-length *Pain-1* specific primers ZrPain-F/PainUni-R (chapter 2, Table 2.1.2), cDNA invertase alleles were cloned and sequenced from the three tetraploid potato cultivars 'Satina', 'Diana', and 'Theresa', and from three diploid potato genotypes P18, P40, and P54. The tetraploid genotypes are representatives for the associated SSCP fragments of the *Pain-1* gene (LI ET AL., 2008; Table 3.1.1) and, therefore, were chosen in this study. Phenotypic characterization of potato chips quality from the cultivars showed variability within the trait (Table 3.1.2). The diploid potato genotypes were included because they were used as parents for mapping QTLs and candidate genes for cold sweetening of potato tubers (MENÉNDEZ ET AL., 2002).

Table 3.1.1: Distribution of the associated SSCP fragments *Pain1-5c, Pain1-8c* and *Pain1-9a* present in the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'.

Genotype	*Pain1-5c*	*Pain1-8c*	*Pain1-9a*
'Satina'	0	1	1
'Diana'	1	1	1
'Theresa'	0	0	0

0=SSCP fragment is absent, 1=SSCP fragment is present.

Table 3.1.2: Potato chips colour scores for the cultivars 'Satina', 'Diana', and 'Theresa'.

Genotype	CQA	CHS
'Satina'	3.33	0.83
'Diana'	7.83	4.67
'Theresa'	6.83	3.00

Potato chips quality was assessed by visually scoring the chips colour after deep frying of 1.2-2.0mm tuber slices in oil at 160-180°C for 2-3min (PUTZ, 1989), using a 1-9 colour scale. 1=very dark chips colour, very bad chips quality; 9=very light yellow chips colour, very good chips quality. CQA refers to the chips quality after harvest in autumn; CQS refers to the chips quality in spring after tuber cold storage for 3-4 months.

Out of 80 cloned cDNA sequences per genotype, a sequence was defined as an allele when it was found twice in two independent PCRs. Additionally, the consensus sequence of all alleles found in one genotype was used for allele definition when variable sequence polymorphisms occurred.

Pain-1 invertase alleles obtained from each genotype are listed in Table 3.1.3.

Table 3.1.3: Overview of *Pain-1* alleles.

Genotype	Full-length clones	*Pain-1* alleles
'Satina'	9	*Pain_SA*
		Pain_SN
'Diana'	16	*Pain_DA*
		Pain_DN1
		Pain_DN2
'Theresa'	8	*Pain_TN1*
		Pain_TN2
P18	7	*Pain_P18N1*
		Pain_P18N2
P40	8	*Pain_P40N1*
		Pain_P40N2
P54	6	*Pain_P54N*

The full-length clone number refers to the number of fully sequenced clones from each genotype used for allele definition. Allele names refer to the identification of associated *Pain-1* alleles, described in section 3.1.1.2. The **'**A' in the allele name stands for 'association with better potato chips quality', and refers to clones containing SNP 1544. The 'N' in the allele name means 'not associated' with better potato chips quality.

From all six genotypes analyzed in this study, 12 *Pain-1* alleles were identified.

3.1.1.1.1 cDNA alleles of the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'[1]

From nine full-length cDNA clones of the genotype 'Satina' two different alleles *Pain_SA* and *Pain_SN* were defined. Cloning and sequencing of 'Diana' cDNA resulted in 16 full-length clones, from which three different *Pain-1* alleles *Pain_DA*, *Pain_DN1,* and *Pain_DN2* were identified. For the cultivar 'Theresa' eight full-length clones were obtained. Two different alleles *Pain_TN1* and *Pain_TN2* were defined.

[1] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: 'Satina' (Appendix A 3.1.1), 'Diana' (Appendix A 3.1.2), 'Theresa' (Appendix A 3.1.3). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *Pain_SA* (Appendix A 3.1.4), *Pain_SN* (Appendix A 3.1.5), *Pain_DA* (Appendix A 3.1.6), *Pain_DN1* (Appendix A 3.1.7), *Pain_DN2* (Appendix A 3.1.8), *Pain_TN1* (Appendix A 3.1.9), *Pain_TN2* (Appendix A 3.1.10).

Comparing all seven alleles at the nucleotide level (Appendix A 3.1.11), 26 single nucleotide polymorphisms (SNPs) were detected. Ten of them resulted in an amino acid exchange (Table 3.1.4; Figure 3.1.1).

Table 3.1.4: SNPs present in 'Satina', 'Diana', and 'Theresa' alleles.

Position of cDNA SNP	*Pain_SA*	*Pain_SN*	*Pain_DA*	*Pain_DN1*	*Pain_DN2*	*Pain_TN1*	*Pain_TN2*	aa
32	C	T	C	T	C	T	C	C/T P11L
75	C	T	C	T	C	T	C	s.
174	G	A	G	A	G	A	G	s.
213	A	G	G	G	G	G	G	s.
280	G	G	A	G	G	G	G	A/G I94V
528	T	A	T	A	T	A	T	s.
552	C	T	C	T	T	T	T	s.
612	A	A	A	A	G	A	G	s.
718	A	G	A	G	G	G	G	A/G I240V
741	T	C	C	C	C	C	C	s.
777	T	T	T	T	C	T	C	s.
1068	C	C	C	C	G	C	G	C/G N356K
1212	G	G	G	G	G	G	A	s.
1316	C	C	T	C	C	C	C	T/C V439A
1143	C	G	G	G	G	G	G	s.
1544	A	C	A	C	C	C	C	A/C K515T
1574	A	A	A	A	T	A	T	A/T Y525F
1596	T	C	T	C	T	C	T	s.
1629	T	C	T	C	T	C	T	s.
1661	A	A	A	A	G	A	G	A/G Q554R
1689	G	G	A	G	G	G	G	s.
1749	T	T	C	T	T	T	T	s.
1830	C	C	C	C	C	C	T	s.
1843	G	T	G	T	G	T	G	T/G S615A
1857	C	C	T	C	C	C	C	s.
1895	G	A	G	A	G	A	G	A/G Q632R

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured. SNP 1544 (blue) was used to assign the associated SSCP fragments to a cloned allele (section 3.1.1.2) as well as for pyrosequencing analysis (section 3.1.2.1).

The two alleles of 'Satina' had a total of 14 SNPs, of which five caused an amino acid exchange. In the three 'Diana' allelic sequences 21 SNPs occurred, from which ten resulted in an amino acid substitution. The two 'Theresa' alleles differed in 15 SNPs. Six of them led to amino acid exchanges.

The amino acid alignment highlights the differences of all seven *Pain-1* alleles from the three tetraploid potato cultivars (Figure 3.1.1). The comparison of these deduced protein sequences revealed ten variable amino acid positions in the different genotypes.

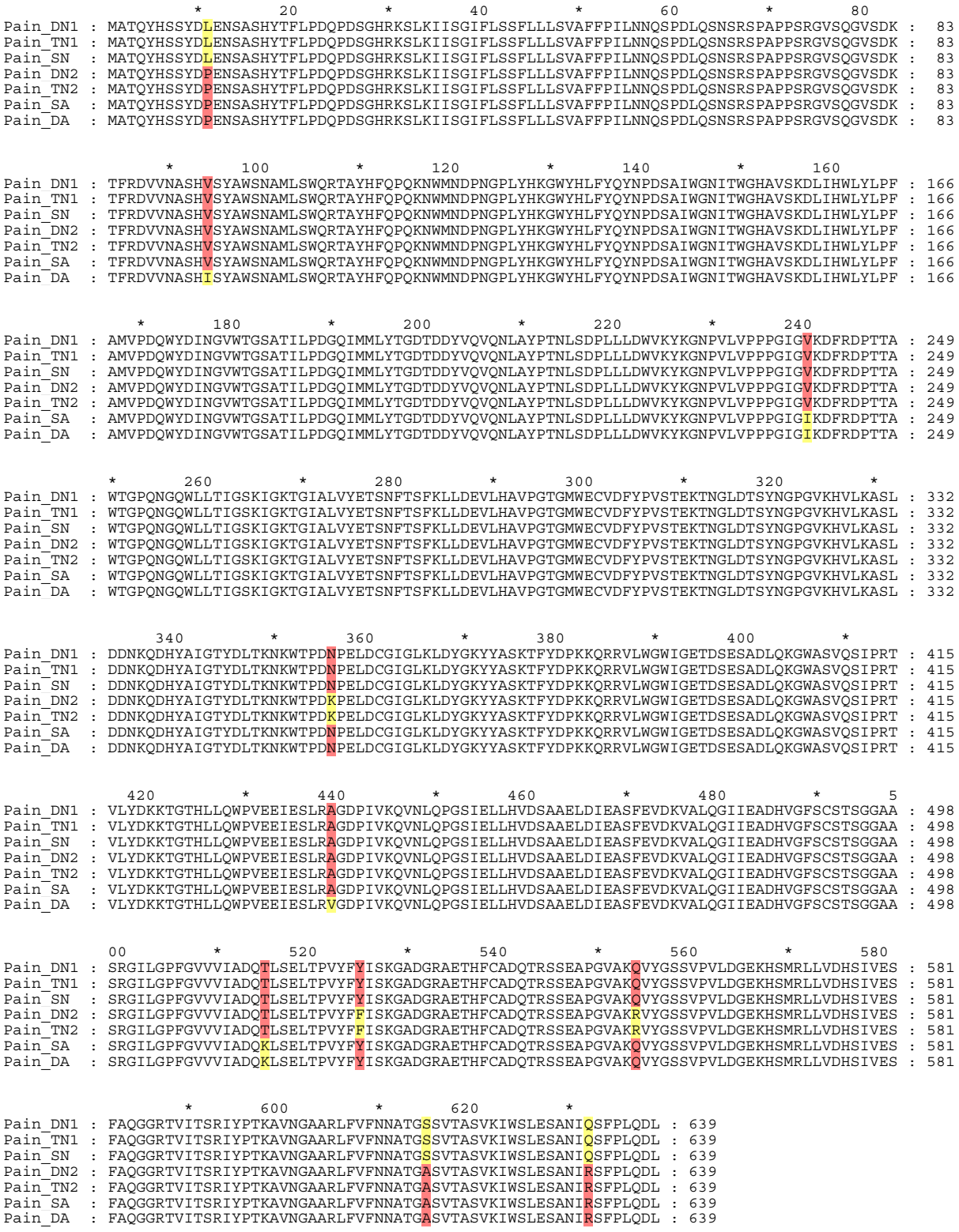


Figure 3.1.1: Amino acid alignment of *Pain-1* alleles from the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'. Amino acid exchanges are highlighted in colour.

Comparison of allelic cDNA sequences of the *Pain-1* gene from the three tetraploid cultivars revealed that different genotypes harbour amino acid sequence identical alleles. 'Satina', 'Diana', and 'Theresa' share one identical allele (*Pain_SN=Pain_DN1=Pain_TN1*). Furthermore, 'Diana', and 'Theresa' contain another allele identical at amino acid level (*Pain_DN2=Pain_TN2*).

3.1.1.1.2 cDNA alleles of the diploid potato genotypes P18, P40, and P54[2]

Cloning and sequencing of P18 cDNA resulted in seven full-length clones, from which two different alleles *Pain_P18N1* and *Pain_P18N2* were identified. In the case of P40 two alleles *Pain_P40N1* and *Pain_P40N2* out of eight full-length clones were found. From the genotype P54 six full-length clones were obtained. All six clones exhibited the same amino acid sequence. The P54 allele was named *Pain_P54N*.

The nucleotide sequence comparison (Appendix A 3.1.20) of the alleles described above detected 47 SNPs, from which 20 resulted in amino acid exchanges (Table 3.1.5; Figure 3.1.2).

Table 3.1.5: SNPs present in P18, P40, and P54 alleles.

Position of cDNA SNP	*Pain_P18N1*	*Pain_P18N2*	*Pain_P40N1*	*Pain_P40N2*	*Pain_P54N*	aa
18	T	T	C	C	T	s.
21	C	C	A	A	C	s.
32	C	T	C	C	T	C/T P11L
74	C	C	A	A	C	C/A P25H
75	C	C	C	C	T	s.
93	G	G	A	A	G	s.
97	C	C	A	C	C	A/C I33L
130	T	T	C	C	T	T/C F44L
145	G	G	T	T	G	G/T V49L
149	C	C	T	T	C	C/T A50V
174	G	A	G	G	A	s.
189	G	G	A	A	G	s.
196	T	T	G	G	T	T/G S66A
200	G	G	A	G	G	A/G H67R

[2] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: P18 (Appendix A 3.1.12), P40 (Appendix A 3.1.13), P54 (Appendix A 3.1.14). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *Pain_P18N1* (Appendix A 3.1.15), *Pain_P18N2* (Appendix A 3.1.16), *Pain_P40N1* (Appendix A 3.1.17), *Pain_P40N2* (Appendix A 3.1.18), *Pain_P54N* (Appendix A 3.1.19).

Position of cDNA SNP	*Pain_P18N1*	*Pain_P18N2*	*Pain_P40N1*	*Pain_P40N2*	*Pain_P54N*	aa
280	A	G	G	G	G	A/G I94V
369	T	T	T	C	T	s.
528	T	A	T	T	A	s.
534	T	T	T	G	T	s.
552	C	T	T	T	T	s.
591	C	C	T	T	C	s.
612	A	A	G	G	A	s.
637	A	A	G	G	A	T/A T213A
718	A	G	G	G	G	A/G I240V
723	G	A	G	G	G	s.
834	C	C	C	A	C	s.
852	G	G	A	G	G	s.
927	T	T	T	C	T	s.
1050	C	T	C	C	C	s.
1161	A	A	G	A	A	s.
1267	G	G	A	G	G	A/G R423G
1316	T	C	C	C	C	T/C V439A
1340	T	T	C	C	T	T/C V447A
1359	A	A	A	G	A	s.
1522	G	G	G	A	G	G/A V508I
1544	A	C	C	C	C	A/C K515T
1596	T	C	T	T	C	s.
1603	G	G	C	G	G	C/G Q535E
1629	T	C	T	T	C	s.
1640	A	A	T	T	A	A/T E547V
1683	C	C	C	G	C	s.
1689	A	G	G	G	G	s.
1698	G	A	G	G	A	s.
1749	C	T	T	T	T	s.
1776	G	G	A	G	G	s.
1843	G	T	G	G	T	G/T A615S
1857	T	C	C	C	C	s.
1895	G	A	G	G	A	G/A R632Q

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured. SNP 1544 (blue) was used to assign the associated SSCP fragments to a cloned allele (section 3.1.1.2) as well as for pyrosequencing analysis (section 3.1.2.1).

From 17 SNPs of the two P18 alleles, seven caused an amino acid exchange. In the two P40 allelic sequences 14 SNPs occurred, from which five resulted in an amino acid substitution.

The amino acid alignment of all five *Pain-1* alleles of the three diploid genotypes showed the variability of positions where amino acids differed (Figure 3.1.2).

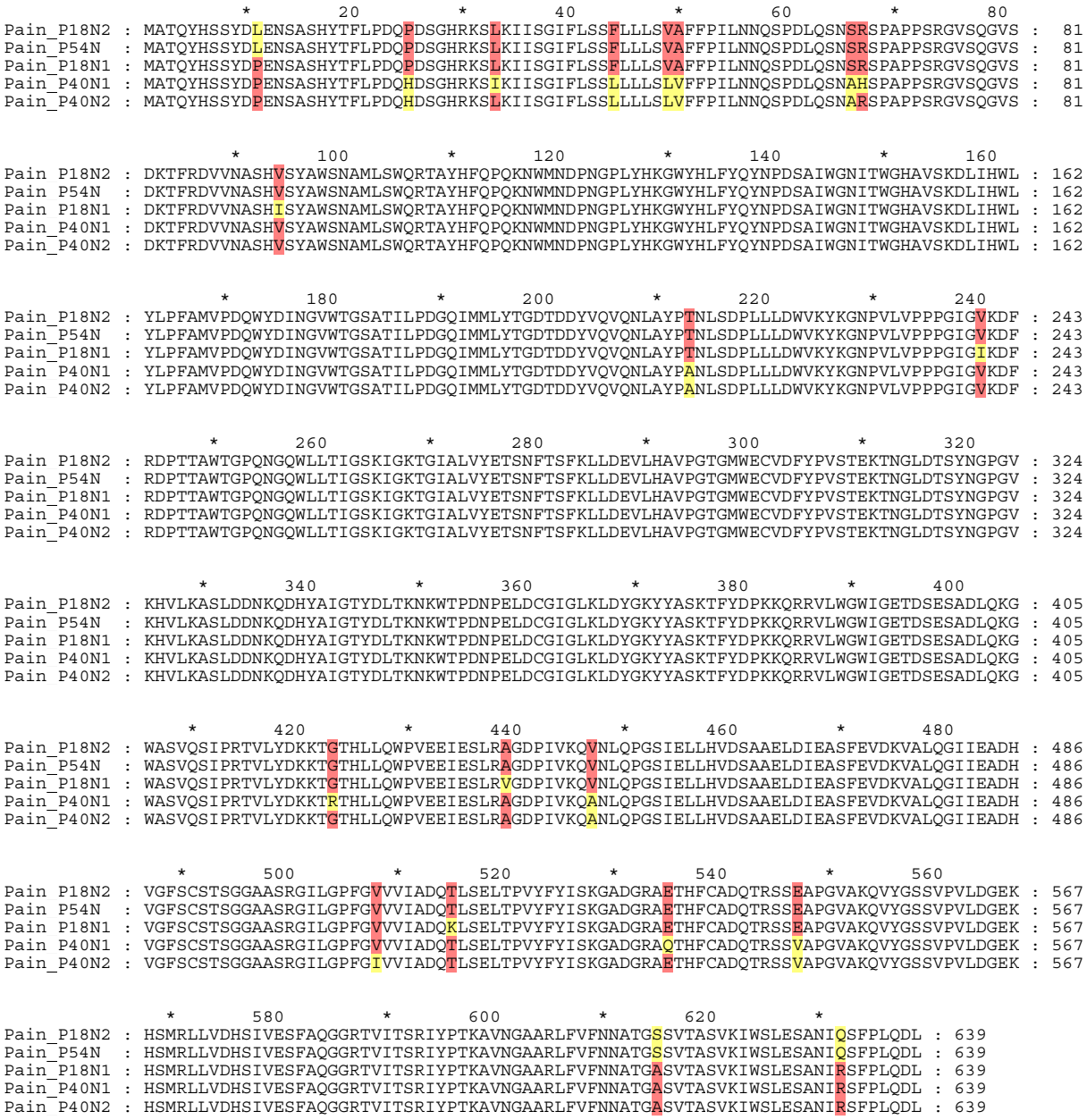


Figure 3.1.2: Amino acid alignment of the *Pain-1* alleles from the diploid genotypes P18, P40, and P54. Amino acid exchanges are highlighted in colour.

The amino acid alignment of the five *Pain-1* alleles of the diploid genotypes showed that P18 and P54 contain an allele identical at amino acid level (*Pain_P18N2=Pain_P54N*).

3.1.1.1.3 Amino acid alignment of all *Pain-1* invertase alleles of the analyzed potato genotypes

Multiple alignment of allelic *Pain-1* deduced protein sequences revealed partially overlapping amino acid polymorphisms between the tetraploid and diploid genotypes. Several amino acid exchanges occurred in different genotypes at the same position. Intriguingly, the two P40

alleles *Pain_P40N1* and *Pain_P40N2* showed less similarity to the alleles retrieved from the other genotypes (Figure 3.1.3; Figure 3.1.4).

```
                  *        20         *        40         *        60         *        80
Pain_DA     : MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_P18N1  : MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_SA     : MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_DN2    : MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_TN2    : MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_SN     : MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_P54N   : MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_P18N2  : MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_TN1    : MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_DN1    : MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVS :  81
Pain_P40N1  : MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVS :  81
Pain_P40N2  : MATQYHSSYDPENSASHYTFLPDQHDSGHRKSLKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNARSPAPPSRGVSQGVS :  81

                  *       100         *       120         *       140         *       160
Pain_DA     : DKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_P18N1  : DKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_SA     : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_DN2    : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_TN2    : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_SN     : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_P54N   : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_P18N2  : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_TN1    : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_DN1    : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_P40N1  : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162
Pain_P40N2  : DKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWL : 162

                *       180         *       200         *       220         *       240
Pain_DA     : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDF : 243
Pain_P18N1  : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDF : 243
Pain_SA     : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDF : 243
Pain_DN2    : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_TN2    : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_SN     : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_P54N   : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_P18N2  : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_TN1    : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_DN1    : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_P40N1  : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243
Pain_P40N2  : YLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDF : 243

              *       260         *       280         *       300         *       320
Pain_DA     : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_P18N1  : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_SA     : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_DN2    : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_TN2    : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_SN     : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_P54N   : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_P18N2  : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_TN1    : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_DN1    : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_P40N1  : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324
Pain_P40N2  : RDPTTAWTGPQNGQWLLTIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGV : 324

                *       340         *       360         *       380         *       400
Pain_DA     : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_P18N1  : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_SA     : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_DN2    : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_TN2    : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_SN     : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_P54N   : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_P18N2  : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_TN1    : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_DN1    : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_P40N1  : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405
Pain_P40N2  : KHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWGWIGETDSESADLQKG : 405

              *       420         *       440         *       460         *       480
Pain_DA     : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_P18N1  : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_SA     : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_DN2    : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_TN2    : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_SN     : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_P54N   : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_P18N2  : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_TN1    : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_DN1    : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_P40N1  : WASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
Pain_P40N2  : WASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADH : 486
```

```
                *       500         *       520         *       540         *       560
Pain_DA     : VGFSCSTSGGAASRGILGPFGVVVIADQKLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_P18N1  : VGFSCSTSGGAASRGILGPFGVVVIADQKLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_SA     : VGFSCSTSGGAASRGILGPFGVVVIADQKLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_DN2    : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEK : 567
Pain_TN2    : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEK : 567
Pain_SN     : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_P54N   : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_P18N2  : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_TN1    : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_DN1    : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEK : 567
Pain_P40N1  : VGFSCSTSGGAASRGILGPFGVVVIADQTLSELTPVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEK : 567
Pain_P40N2  : VGFSCSTSGGAASRGILGPFGIVVIADQTLSELTPVYFYISKGADGRAETHFCADQTRSSVAPGVAKQVYGSSVPVLDGEK : 567

                *       580         *       600         *       620         *
Pain_DA     : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_P18N1  : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_SA     : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_DN2    : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_TN2    : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_SN     : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL : 639
Pain_P54N   : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL : 639
Pain_P18N2  : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL : 639
Pain_TN1    : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL : 639
Pain_DN1    : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL : 639
Pain_P40N1  : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
Pain_P40N2  : HSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL : 639
```

Figure 3.1.3: Amino acid alignment of all cloned *Pain-1* invertase alleles. Amino acid exchanges are highlighted in colour.

Protein sequence comparison of the deduced *Pain-1* alleles from all analyzed genotypes showed that amino acids differed at 23 positions, of which five were genotype specific and occurred only once.

3.1.1.1.4 Phenetic trees of all *Pain-1* invertase alleles of the analyzed potato genotypes

In addition to the multiple amino acid alignment (section 3.1.1.1.3), the phenetic tree analysis was applied to group the invertase alleles according to similarity at amino acid as well as at nucleotide level. Using the neighbour-joining method, the allelic classification visualized that *Pain-1* alleles from all analyzed potato genotypes grouped in two clades and four to five subclades (Figure 3.1.4, Figure 3.1.5).

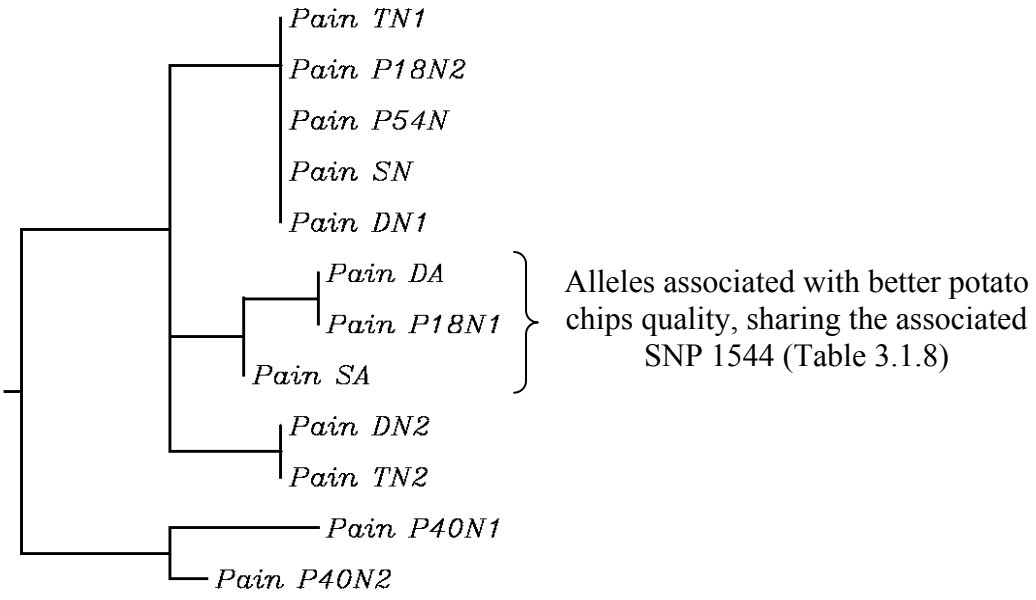


Figure 3.1.4: Amino acid based phenetic tree (Neighbour-joining method) of all cloned *Pain-1* invertase alleles.

The first clade includes alleles from the genotypes 'Satina', 'Diana', 'Theresa', P18, and P54. The first subclade of the first clade consists of five alleles from five different genotypes. The alleles *Pain_SN*, *Pain_DN1*, *Pain_TN1*, *Pain_P18N2,* and *Pain_P54N* have the same amino acid sequence, although polymorphisms in the corresponding nucleotide sequences occurred (Figure 3.1.5).

The second subclade consists of the alleles *Pain_SA* and *Pain_DA*, which are associated with better potato chips quality. The two alleles are not identical at the amino acid level but possess cDNA SNP 1544 that is associated with better potato chips quality (section 3.1.1.2). The allele *Pain_P18N1* of the diploid genotype P18 has an identical amino acid sequence to *Pain_DA*.

The third subclade includes the two alleles *Pain_DN2* and *Pain_TN2,* which have the same amino acid sequence.

The second main clade consists of the two outlaying P40 alleles *Pain_P40N1* and *Pain_P40N2*. The two alleles show the highest diversity compared to the other cloned alleles.

Cloning and sequencing of *Pain-1* alleles showed that tetraploid and diploid genotypes contain alleles identical in their amino acid sequence but different at nucleotide level. The following Table 3.1.6 summarizes the nucleotide comparison of amino acid identical alleles of different genotypes. The allelic nucleotide sequence was defined based on the consensus sequence of multiple alignment of full-length clones obtained from each genotype (Table 3.1.3). Although SNPs are present at positions in the corresponding cDNA, the nucleotide polymorphisms resulted in one and the same amino acid sequence.

Table 3.1.6: Genotype specific nucleotide differences of alleles identical at amino acid level (Appendix A 3.1.21)**.**

A) Comparison of the alleles *Pain_SN*, *Pain_DN1*, *Pain_TN1*, *Pain_P18N2,* and *Pain_P54N*.

Position of cDNA SNP	*Pain_SN*	*Pain_DN1*	*Pain_TN1*	*Pain_P18N2*	*Pain_P54N*
75	T	T	T	C	T
486	A	G	G	G	G
723	G	G	G	A	G
1050	C	C	C	T	C
1236	T	C	T	T	T

B) Alleles of the alleles *Pain_DA* and *Pain_P18N1*.

Position of cDNA SNP	*Pain_DA*	*Pain_P18N1*
816	G	A
1698	A	G

C) Comparison of the alleles *Pain_DN2* and *Pain_TN2*.

Position of cDNA SNP	Pain_DN2	Pain_TN2
1830	C	T

The nucleotide polymorphisms between all *Pain-1* (Appendix A 3.1.21) were visualized using the phenetic tree analysis (Figure 3.1.5).

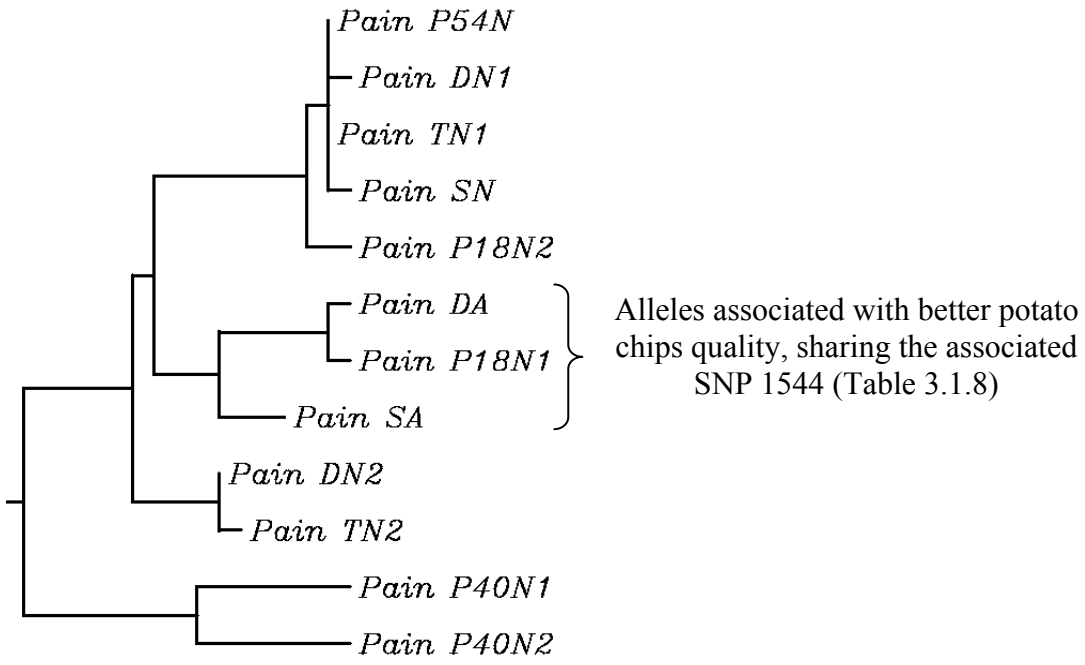


Figure 3.1.5: Nucleotide sequence based phenetic tree (Neighbour-joining method) of all cloned *Pain-1* invertase alleles.

Allele specific SNPs were detected in at least two sequences and used for comparing the allelic nucleotide polymorphisms. The two phenetic trees are very similar, just displaying more subclades due to a higher number of nucleotide polymorphisms compared to the amino acid exchanges (Figure 3.1.4).

3.1.1.2 Identification of associated *Pain-1* alleles

The *Pain-1* locus maps to potato chromosome III (CHEN ET AL., 2001) in a region associated with tuber quality traits where a QTL for potato tuber sugar content, *Sug3a*, was identified (MENÉNDEZ ET AL., 2002). In the latter study, the *Pain-1* gene was not mapped directly in the mapping population used, but was considered as a candidate gene for the QTL *Sug3a*.

Single-strand conformation polymorphism (SSCP) analysis revealed an association of *Pain-1* SSCP fragments with starch and sugar content of potato tubers. SSCP fragments found to be associated with better potato chips quality were named *Pain1-5c, Pain1-8c* and *Pain1-9a* (LI ET AL., 2008). The occurrence of these fragments in the genotypes was highly correlated indicating that the three fragments are in nearly absolute LD, and suggesting that these allelic fragments correspond to the same associated *Pain-1* invertase allele. The associated SSCP fragments are present in the cultivars ‘Satina’, ‘Diana’, and absent in ‘Theresa’ (Table 3.1.7).

Table 3.1.7: Associated SSCP fragments *Pain1-5c, Pain1-8c* and *Pain1-9a* present in 'Satina', 'Diana', and 'Theresa'.

Genotype	*Pain1-5c*	*Pain1-8c*	*Pain1-9a*
'Satina'	0	1	1
'Diana'	1	1	1
'Theresa'	0	0	0

0=SSCP fragment is absent, 1=SSCP fragment is present.

To assign a cloned invertase allele (section 3.1.1.1) to the corresponding associated SSCP fragments, two groups, each consisting of 15 potato genotypes that were scored either positive (present) or negative (absent) for the associated SSCP fragments, were used to identify the corresponding SNPs.

Based on multiple nucleotide alignment (Appendix A 3.1.22) of the three cultivars 'Satina', 'Diana', and 'Theresa', the cDNA SNP 1544 was selected present in 'Satina' and 'Diana', and absent in 'Theresa' referring to the SSCP fragment distribution (Table 3.1.7). The distribution of SNP 1544, which causes an amino acid exchange of threonine (T) in the non associated to lysine (K) in the associated alleles is shown in Table 3.1.8.

Table 3.1.8: Comparison and distribution of associated SSCP fragments and SNP 1544.

A) Genotypes scored negative for associated SSCP fragments

Genotype	SSCP			SNP 1544
	Pain1-5c	*Pain1-8c*	*Pain1-9a*	
'Leyla' (St01)	0	0	0	C
'Marabel' (St02)	0	0	0	C
'Solara' (St03)	0	0	0	C
'Vitara' (St04)	0	0	0	C
'Ponto' (St06)	0	0	0	C
'Marlen' (St08)	0	0	0	C
'Eldena' (St09)	0	0	0	C
'Theresa' (St10)	0	0	0	C
'Goldika' (St11)	0	0	0	C
'Saturna' (St12)	0	0	0	C
'Karlena' (St14)	0	2	0	C
'Kolibri' (St15)	0	2	0	C
'Terra' (St18)	0	0	0	C
'Solist' (St19)	0	2	0	C
'Melina' (St20)	0	2	0	C

B) Genotypes scored positive for associated SSCP fragments

Genotype	SSCP			SNP 1544
	Pain1-5c	***Pain1-8c***	***Pain1-9a***	
'Milva' (St05)	1	0	1	C/A
'Tomensa' (St07)	1	0	1	C/A
'Fasan' (St16)	1	2	1	C
'Apart' (St24)	0	1	1	C/A
'Diana' (St28)	1	1	1	C/A
'Orlando' (St31)	1	0	1	C/A
'Satina' (St33)	0	1	1	C/A
B05	1	1	1	C/A
B07	1	0	1	C/A
B16	1	1	1	C
B17	1	1	1	C/A
B30	1	0	1	C
B32	1	1	1	C/A
B38	1	1	1	C/A

St=potato cultivars defined as standards, B=BNA breeding clones, 0=SSCP fragment is absent, 1=SSCP fragment is present, 2=SSCP fragment could not be analyzed properly, SNP 1544=analyzed SNP for association with better potato chips quality, C=cytosine, A=adenine.

All genotypes, which scored negative for the associated SSCP fragments (Table 3.1.8 A), contain the nucleotide C at cDNA SNP position 1544. Genotypes, which scored positive for associated SSCP fragments (Table 3.1.8 B), show a C/A-polymorphism nearly equally distributed as the corresponding SSCP fragments. Three out of 14 analyzed genotypes did not display the C/A-polymorphism.

For further analysis and molecular description of the cloned *Pain-1* alleles, the term 'associated with better potato chips quality' is used for alleles of phenotypically characterized genotypes displaying the C/A-polymorphism at cDNA position 1544.

This polymorphism results in an amino acid substitution at position 515 of the corresponding protein sequence, exchanging threonine (T) in the non associated invertase alleles to lysine (K) in the associated *Pain-1* alleles. To study the effects of the amino acid differences of cloned *Pain-1* alleles, analysis was continued with 3D-modelling (section 3.1.1.3) and functional characterization (section 3.1.2).

3.1.1.3 Three-dimensional modelling of *Pain-1* alleles

3D-modelling was performed by Pawel Durek, MPIMP/Golm. The modelling of the allelic invertase molecular structure was based on the invertase 3D and crystal structure of cyanobacteria (ALBERTO ET AL., 2004). The models are comparative, superimposing two allelic sequences. Differences of the alleles are highlighted. The modelling was applied for associated and non associated *Pain-1* alleles of the tetraploid potato cultivars 'Satina' and 'Diana'. The models include the putative sucrose binding site with the substrate sucrose. In

addition to the structural visualization of amino acid exchanges, also the electrostatic potential (EP) of the molecules was mapped at pH 4.7 mimicking the vacuolar conditions.

3.1.1.3.1 Structural modelling of alleles of the cultivars 'Satina' and 'Diana'

In the first analysis of allelic molecular structures, the two 'Satina' alleles *Pain_SA* and *Pain_SN,* and the three 'Diana' alleles *Pain_DA*, *Pain_DN1,* and *Pain_DN2* were used. The models compare the allelic sequences with each other, meaning that one sequence superimposes the other and vice versa. Based on multiple alignment (Figure 3.1.1) of the allelic protein sequences, regions, which are affected directly or indirectly by amino acid exchanges, were identified (Figure 3.1.6; Figure 3.1.7).

Amino acid region	Affected surface area
225-236	1
512-518	2
479-500	3
529-531	4

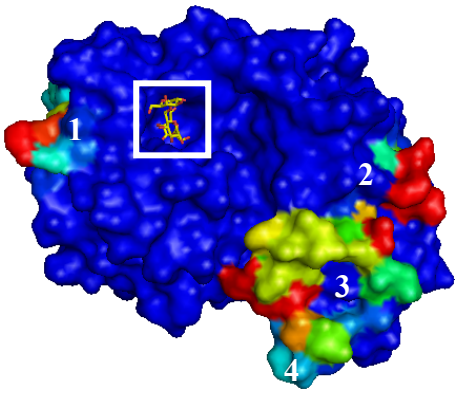


Figure 3.1.6: Correlation of amino acid regions or exchanges and affected surface areas of *Pain-1* alleles. Amino acids are numbered based on the multiple sequence alignment (Figure 3.1.1). Areas are numbered from 1-4. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (weak). The putative sucrose binding site with the substrate sucrose is framed.

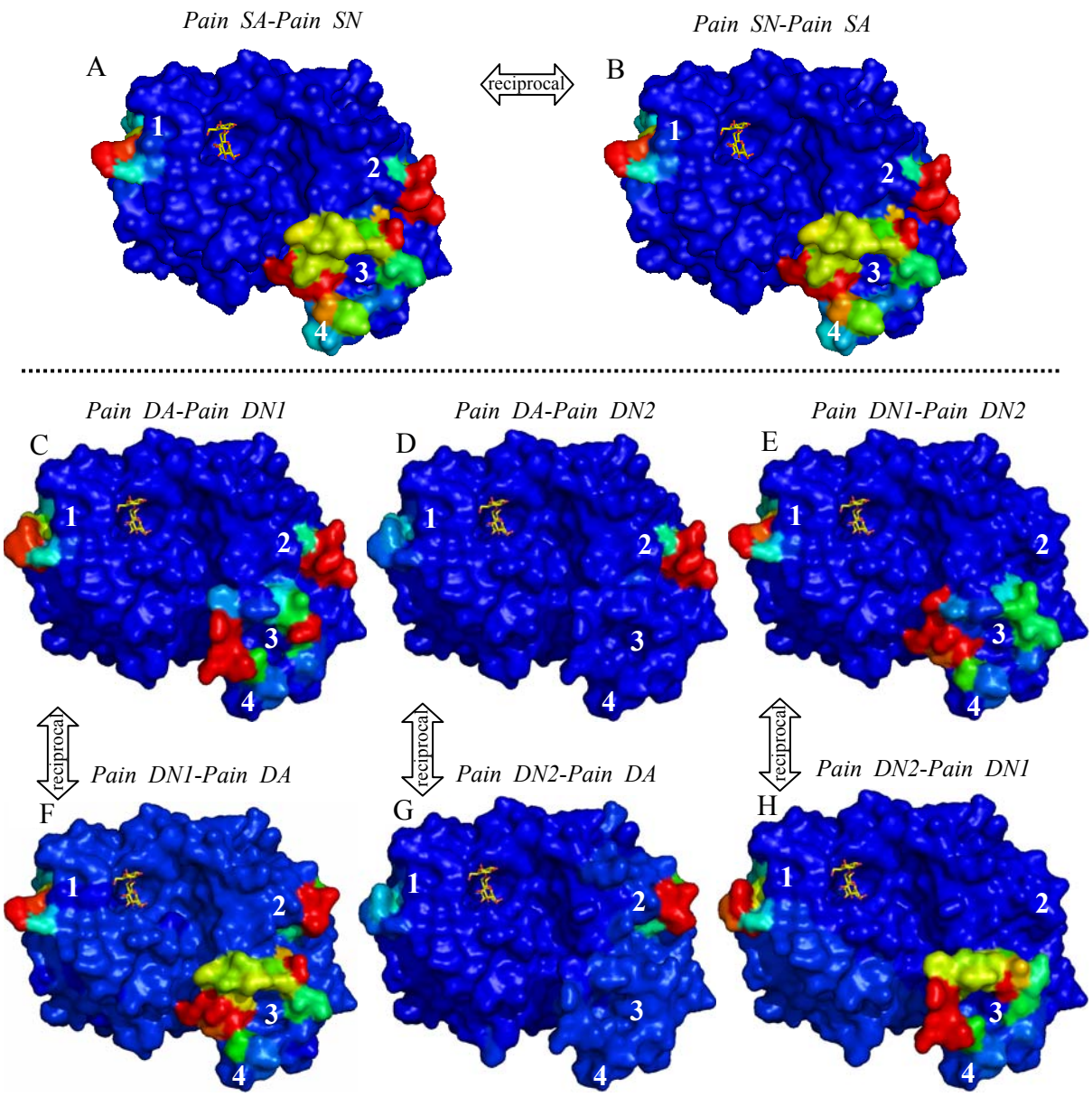


Figure 3.1.7: Structural comparison of 'Satina' alleles *Pain_SA*, *Pain_SN,* and 'Diana' alleles *Pain_DA*, *Pain_DN1, Pain_DN2*. A: *Pain_SA* superimposes *Pain_SN*. **B:** *Pain_SN* superimposes *Pain_SA*. **C:** *Pain_DA* superimposes *Pain_DN1*; **D:** *Pain_DA* superimposes *Pain_DN2*; **E:** *Pain_DN1* superimposes *Pain_DN2*; **F:** *Pain_DN1* superimposes *Pain_DA*; **G:** *Pain_DN2* superimposes *Pain_DA*; **H:** *Pain_DN2* superimposes *Pain_DN1*. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (weak).

The models of the invertase molecules of the alleles *Pain_SA* and *Pain_SN* and *Pain_DA*, *Pain_DN1,* and *Pain_DN2* showed structural differences on the enzyme's surface. All analyzed molecules possess similar affected surface areas (area definition: Figure 3.1.6). Surface area 1 differs in all represented models, but is less distinctive between the alleles *Pain_DA* and *Pain_DN2* (Figure 3.1.7 D, G). Region 1, defined by the amino acids 225-236, manifests sterical differences although amino acids in the corresponding region do not differ between the alleles. The same observations were made for the surface areas 3 and 4, defined by amino acids 479-500 and 529-531 respectively, where the alleles display identical amino

acid sequences. These areas are affected indirectly by other amino acid substitutions leading to a variable folding of the protein. Accountable amino acids are subject of ongoing investigations.

Region 2 is defined by amino acids 512-518 showing a lysine (K) in the associated alleles *Pain_SA* and *Pain_DA,* and a threonine (T) in the alleles *Pain_SN, Pain_DN1,* and *Pain_DN2* at position 515. The corresponding nucleotide SNP 1544 was found to be associated with better potato chips quality (section 3.1.1.2). The structural modification 2 is absent in the models E and H (Figure 3.1.7) because of the absence of SNP 1544 in the superimposed alleles *Pain_DN1* and *Pain_DN2*.

The structural effects caused by allelic sequences resulted in invertase folding variations of the *Pain-1* molecules. The function of all identified variable surface areas is unknown.

3.1.1.3.2 Modelling the electrostatic potential (EP) of alleles of the cultivars 'Satina' and 'Diana'

The mapping of the EP of the *Pain-1* alleles *Pain_SA*, *Pain_SN*, *Pain_DA*, *Pain_DN1,* and *Pain_DN2* revealed charge differences of the molecules at pH 4.7 (Figure 3.1.8).

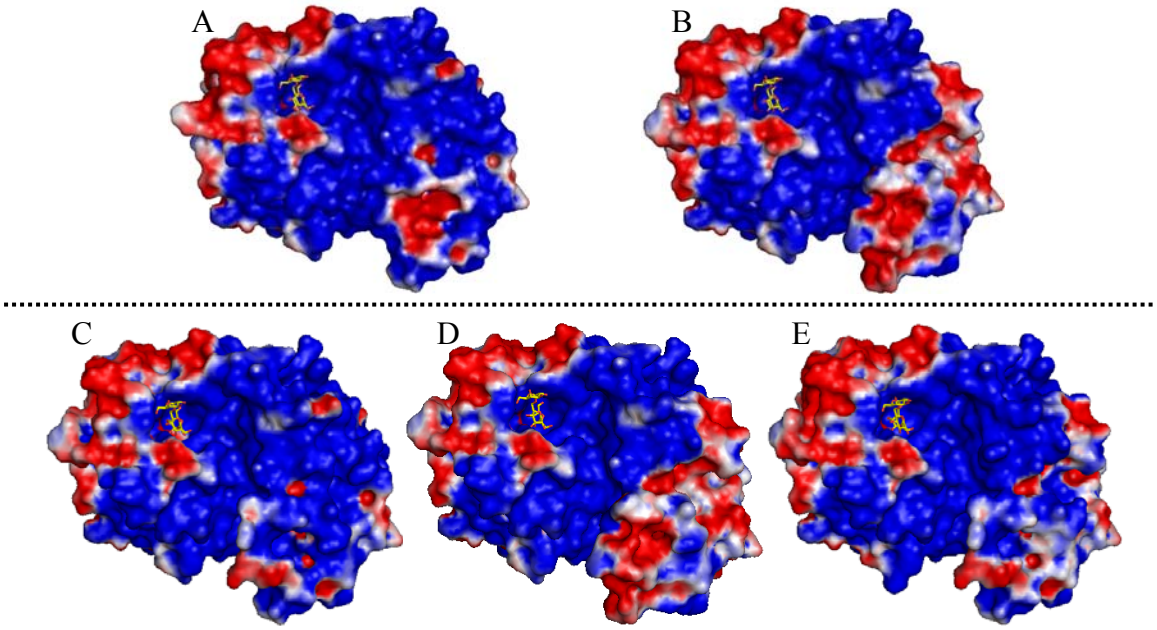


Figure 3.1.8: EP of the alleles *Pain_SA*, *Pain_SN*, *Pain_DA*, *Pain_DN1,* and *Pain_DN2*. A: *Pain_SA*. **B:** *Pain_SN*. **C:** *Pain_DA;* **D:** *Pain_DN1;* **E:** *Pain_DN2*. Red: negatively charged; blue: positively charged; white: neutrally charged.

The EP modelling of the two alleles from the cultivar 'Satina' showed that *Pain_SA* is more positively charged than *Pain_SN* (Figure 3.1.8 A, B). The three 'Diana' alleles also exhibit charge differences to each other. The allele *Pain_DN1* (Figure 3.1.8 D) possesses an extended

negative charge in comparison to the other two alleles (C, E). The EP of the allele *Pain_DA* (C) showed more positive charges in regions where allele *Pain_DN2* was more neutral.

Focusing on the EP of the putative sucrose binding site

The putative sucrose binding site (Figure 3.1.6) is positively charged matching the partial negative charge of the substrate sucrose due to the hydroxyl groups.

Zooming into the putative sucrose binding domain revealed charge differences between the molecules *Pain_SA* (A), *Pain_SN* (B), *Pain_DA* (C), *Pain_DN1* (D), and *Pain_DN2* (E); (Figure 3.1.9).

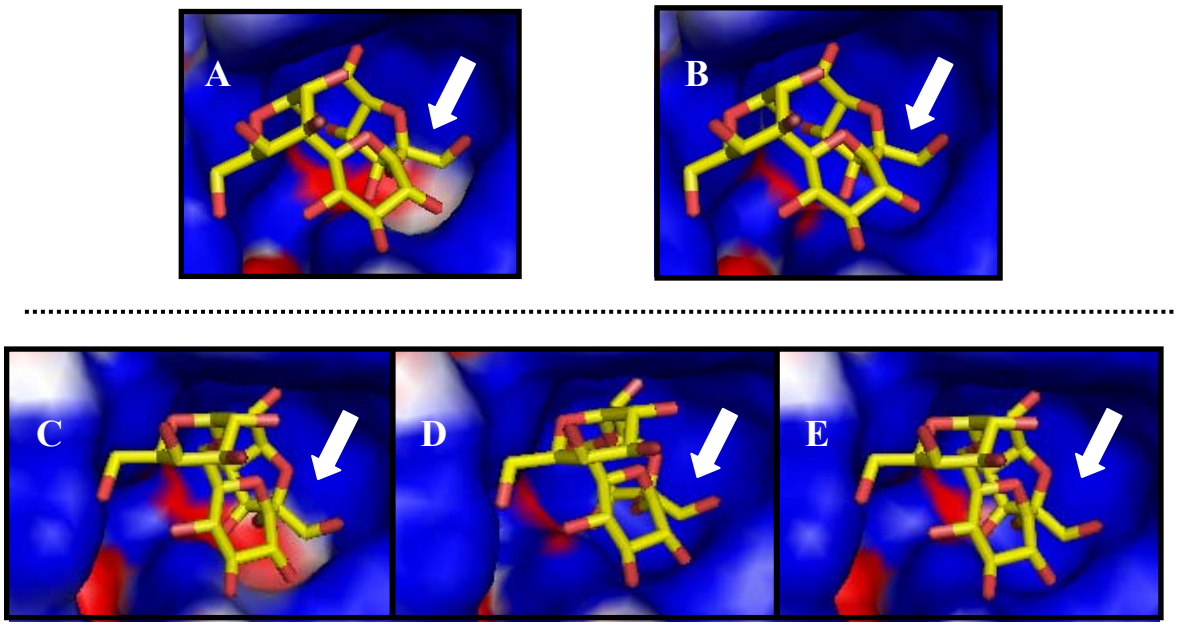


Figure 3.1.9: Focusing of the EP of the putative sucrose binding site of the alleles of the cultivars 'Satina' and 'Diana'. A: *Pain_SA*; **B:** *Pain_SN;* **C:** *Pain_DA,* **D:** *Pain_DN1,* **E:** *Pain_DN2.* Red: negatively charged; blue: positively charged; white: neutrally charged.

Close-up views of the putative sucrose binding domain revealed strong charge changes between the molecules *Pain_SA* (A) and *Pain_SN* (B) (Figure 3.1.9). The site of the associated allele *Pain_SA* is characterized by a neutral to negative charge composition compared to the positive charge of the allele *Pain_SN*. The EP of the putative sucrose binding site of the three 'Diana' alleles also showed apparent changes of charge. The EP of the associated allele *Pain_DA* (C) switched from a positive to a neutral/negative charge. The charge of the alleles *Pain_DN1* (D), and *Pain_DN2* (E) differed not visibly.

3.1.1.3.3 Overview of 3D-modelling analysis of *Pain-1* alleles

3D-modelling is a tool to gain first insights in the possible consequences of different invertase alleles. The models nicely show that amino acid exchanges manifest on the surface of the enzyme. However, no effect on the structure of the putative sucrose binding domain was

detected in any of the modelled molecules. The characterization of the EP showed differences in charge among the analyzed proteins. A dramatic charge difference of the putative sucrose binding site was observed in the associated alleles *Pain_SA* and *Pain_DA* (Figure 3.1.9 A, C). The EP switched from positive to neutral. The EP changes could not be correlated to amino acid exchanges nearby the sucrose binding site. The causative amino acids were not yet analyzed, but are subject of ongoing investigations in the research project.

3.1.1.4 Genomic organization of the *Pain-1* locus

❖ **BAC library screens**

High density BAC library screens with two different PCR generated probes were performed to determine the genomic sequence of the *Pain-1* locus. Using the primers Pain1-5f/Pain1-5r (LI ET AL., 2005; chapter 2, Table 2.1.10A), Probe 1 was generated, which consists of exon and intron based sequences of *Pain-1*. Probe 2 only consists of exon based sequences and was amplified with the primers Pain_SondF1/Pain_SondR (chapter 2, Table 2.1.10A).

The screening of two different BAC libraries (BA and BC, BALLVORA ET AL., 2002, 2007) constructed with genomic DNA of the same diploid genotype resulted in 21 positive BAC clones (Table 3.1.9).

Table 3.1.9: Positive BAC clones.

Library	**BAC clones**	
BA BAC library	BA1: Plate 32N19	
	BA2: Plate 128A5	
	BA3: Plate 213B14	
BC BAC library	BC1: Plate 14O7	BC10: Plate 47C9
	BC2: Plate 21K3	BC11: Plate 57A16
	BC3: Plate 27G10	BC12: Plate 57P6
	BC4: Plate 32J7	BC13: Plate 68K22
	BC5: Plate 34G11	BC14: Plate 149O15
	BC6: Plate 34O24	BC15: Plate 216L1
	BC7: Plate 35N9	BC16: Plate 223N21
	BC8: Plate 35E21	BC17: Plate 239N10
	BC9: Plate 45P17	BC18: Plate 244C12

BACs are numbered and their position in the *E. coli* microtiter plates is listed.

Following the hybridisation, clones from the BC library for sequencing were selected based on the results of PCR, colony-lift, and Southern blot. Out of 18 hybridization positive *Pain-1* BC BAC clones, eight clones were found positive for full-length PCR amplification using

Pain-1 specific primers. All analyzed clones were colony-lift positive and eight BACs were Southern blot positive (Table 3.1.10; Figure 3.1.10).

Table 3.1.10: Summary of the results for BAC insert sequencing.

BC clones	Filter hybridisation	PCR	Colony-lift	Southern blot
BC1: Plate 14O7	yes	no	yes	no
BC2: Plate 21K3	yes	no	yes	yes
BC3: Plate 27G10	yes	no	yes	yes
BC4: Plate 32J7	yes	no	yes	no
BC5: Plate 34G11	yes	yes	yes	yes
BC6: Plate 34O24	yes	no	yes	no
BC7: Plate 35N9	yes	no	yes	no
BC8: Plate 35E21	yes	no	yes	yes
BC9: Plate 45P17	yes	yes	not analyzed	not analyzed
BC10: Plate 47C9	yes	no	yes	no
BC11: Plate 57A16	yes	no	yes	not analyzed
BC12: Plate 57P6	yes	no	yes	no
BC13: Plate 68K22	yes	no	yes	no
BC14: Plate 149O15	yes	no	yes	no
BC15: Plate 216L1	yes	no	yes	no
BC16: Plate 223N21	yes	yes	yes	yes
BC17: Plate 239N10	yes	no	yes	yes
BC18: Plate 244C12	yes	yes	yes	yes

For PCR reaction Probe 1 (Pain1-5f/Pain1-5r, chapter 2, Table 2.1.10A), Probe 2 (Pain_SondF1/Pain_SondR, chapter 2, Table 2.1.10A), or *Pain-1* full-length primers (ZrPain-F/PainUni-R, chapter 2, Table 2.1.2) were used. Colony-lift and Southern blot hybridisation were performed using Probe 1.

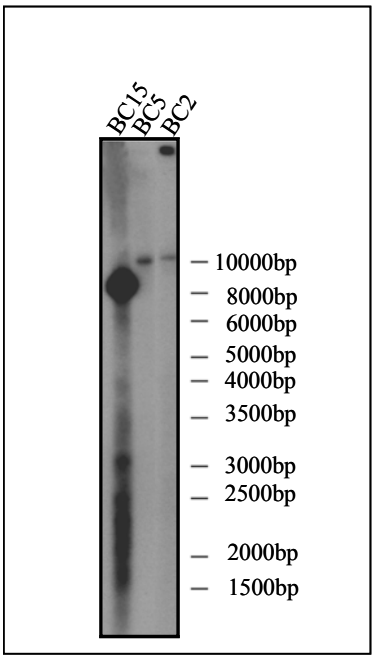


Figure 3.1.10: Southern blot analysis of *Sma*I digested BC BAC clones. The pattern of this first line was only represented by the BAC BC15. The restriction pattern of BC5 was also observed for the clones BC12 and BC14. The BC2 pattern was also detected for the BACs BC8 and BC13.

The *Pain-1* locus of BC library clones BC14 and BC17 was custom sequenced by GATC Biotech, Konstanz using primer walking as sequencing method. Full-length BAC insert sequencing was performed for the clones BC2 (insert size: 75kb), BC14 (insert size: 75kb), and BC15 (insert size: 97kb), which showed differential restriction patterns in Southern blot

analysis (Figure 3.1.10) suggesting different *Pain-1* alleles or gene loci. Full-length BAC insert sequencing was carried out by MWG Biotech AG, Ebersberg using the 454 sequencing technique on the GS FLX system. The BAC clones BC14 and BC15 as well as BC17 harboured the same genomic invertase allele. BAC clone BC2 was found invertase negative, meaning that no invertase sequence was detected.

The genomic sequences of the *Pain-1* gene received by different sequencing technologies differed in one to six nucleotides in the second intron of the gene. The sequences resulted from primer walking showed more nucleotide differences than sequences obtained by 454 sequencing.

❖ BAC Annotation

Full-length sequencing of the BAC inserts revealed sequence and structural information of *Pain-1* and of genes flanking the *Pain-1* locus. Since the BAC clones BC14 and BC15 contained the same genomic *Pain-1* invertase sequence, only the annotation of BC14 is shown (Table 3.1.11).

Table 3.1.11: BC14 sequence annotation.

Strand	Apollo name	Position on the BAC insert (bp)	Description
+	gene 10	9,298-13,989	putative retrotransposon protein
+	gene 20	15,377-16,656	unknown
+	gene 30	31,121-33,084	putative transposon protein
+	gene 40	33,625-35,078	putative transposase
+	gene 50	74,626-78,901	putative retroelement polyprotein
-	gene 60	6,138-5,488	putative reverse transcriptase
-	**gene 70**	**61,166-57,216**	**invertase *Pain-1***, beta-fructofuranosidase (glucoside hydrolase family 32)

BAC annotation was carried out using the software Apollo Genome Annotation and Curation Tool, version 1.9.8. The invertase gene was named 'gene 70' in the Apollo BAC sequence characterization. The invertase gene is written in bold.

The screened BAC libraries BA and BC harbour genomic DNA of the same diploid genotype P6/210, which is a hybrid derived from the cross of the parental genotypes P40 x P41 (LEISTER ET AL., 1996). The genotype P40 was also selected in this study for invertase allele characterization. The sequence alignment of the two P40 cDNA alleles with the protein sequence of the gene 70 (*Pain-1*) from BAC BC14, which is identical to the *Pain-1* genomic sequences of the BACs BC 15 and BC17, showed no sequence identity (Appendix A 3.1.23). Therefore, the detected BAC allele for the gene *Pain-1* originates from the other parental genotype P41.

❖ Genomic structure of the *Pain-1* gene

The exon and intron organization of the *Pain-1* gene was determined using multiple sequence alignment of *Pain-1* cDNA alleles and the genomic *Pain-1* sequence of BAC BC14 (Appendix A 3.1.24[3]).

The *Pain-1* gene consists of seven exons and six introns and has a length of 3951bp (Figure 3.1.11).

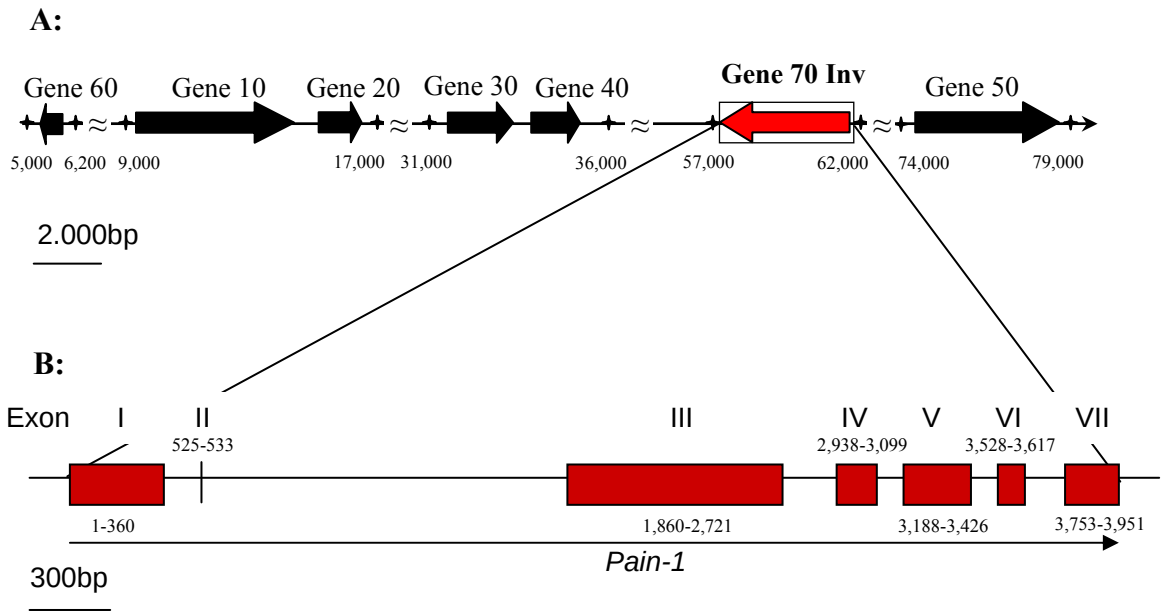


Figure 3.1.11: Position of the *Pain-1* gene within the sequenced BAC insert of BC14 (A) and genomic organization of the *Pain-1* gene (B). A: The direction of the annotated genes (Table 3.1.11) is indicated by arrows. ➡: 5'-3' orientation (+ strand); ⬅ : 3'-5' orientation (- strand). The lengths are given in base pairs. **B:** Exons are drawn in red and numbered from I to VII, the length is given in base pairs. The arrow demonstrates the length of the gene without promoter and terminator sequences.

It is known from potato invertase loci encoding insoluble acid isoforms that two genes are linked in direct tandem repeat (MADDISON ET AL., 1999). The genes organized in this way are either separated by 2,3kb (MADDISON ET AL., 1999) or by 8kb (chapter 3.3, Figure 3.3.12). The insert of BAC BC14, which has a length of 75kb contained no second invertase gene. Within the BAC insert *Pain-1* gene surrounding sequences should allow to detect a probable tandem repeat organization if present (Figure 3.1.10 A). This possibility was excluded for the *Pain-1* locus.

The range of *Pain-1* exons and introns are summarized in Table 3.1.12.

[3] The alignment program Multalin version 5.4.1 (http://bioinfo.genetoul.fr) used revealed problems in the comparison of the genomic *Pain-1* sequence with the *Pain-1* cDNA sequence. The mini-exon II was not aligned properly, one additional nucleotide occurred.

Table 3.1.12: Ranges of the exons and introns of the *Pain-1* gene.

Exon number	Range (bp)	Intron number	Range (bp)
I	1-360	I	361-524
II	525-533	II	534-1859
III	1,860-2,721	III	2,722-2,937
IV	2,938-3,099	IV	3,100-3,187
V	3,188-3,426	V	3,427-3,527
VI	3,528-3,617	VI	3,618-3,752
VII	3,753-3,951		

Plant invertases isolated to date have fairly similar structures and consist of six to eight exons (reviewed in TYMOWSKA-LALANNE & KREIS, 1998). The genes contain one extremely small exon (exon II), which only codes for the core tripeptide DPN of the conserved β-fructosidase motif NDPNG (TYMOWSKA-LALANNE & KREIS, 1998).

3.1.2 Functional characterization of the *Pain-1* gene

3.1.2.1 Differential expression analysis of *Pain-1* alleles during cold storage of potato tubers

Plant invertases are influenced by a variety of intra- and extracellular factors. It has been shown that invertases are regulated by temperature. ROREM & SCHWIMMER (1963) first demonstrated that temperature affects the level of invertase activity. Invertase activity is always detectable in potato tubers, but the highest level is measured when tubers have been stored at low temperature (PRESSEY, 1966). ZHOU ET AL. (1994) detected soluble acid invertase transcripts in potato tubers stored at 1°C, but not in those stored at 10°C. Strongly induced transcript accumulation of soluble acid invertase was also shown for tuber samples stored at 4°C after 7-10 days (ZRENNER ET AL., 1996; BAGNARESI ET AL., 2008).

Expression analysis was performed with two biological replicates of potato tubers stored for 1, 2, 3, and 4 weeks at 4°C in the dark as well as with potato tuber samples frozen in liquid nitrogen directly after harvest and kept at -80°C.

Two different strategies were used to define the allelic expression pattern. The first strategy was based on pyrosequencing analysis to separate the different *Pain-1* alleles within a genotype. The pyrosequencing analysis was performed using cDNA from tubers stored for 0-4 weeks at 4°C in the dark, and tuber genomic DNA to determine the allele dosage. Comparison of both samples revealed specific expression patterns not just for each genotype but also between different alleles of the same genotype. In the following Figures the relationship between the presence of alleles in the genome and their transcription levels are illustrated. Accordingly, both values are shown together in terms of the relative expression level.

Additionally, plasmids harbouring one allele of complementary SNPs of corresponding genotypes were mixed in different ratios to monitor the accuracy of pyrosequencing analysis. Plasmid based measurements, working as positive controls, showed that SNP depending variations of ±5% occurred. Values of cDNA and genomic dosages of the analysed alleles as determined by pyrosequencing were corrected for the observed SNP specific variations.

qRT-PCR was carried out as second strategy to measure the total amount of invertase transcript levels during the applied cold storage period of four weeks.

3.1.2.2.1 Expression pattern of *Pain-1* alleles in tubers of the tetraploid cultivar 'Satina'

The cultivar 'Satina' is tetraploid. Potentially four different *Pain-1* alleles can occur. Cloning and sequencing of 'Satina' cDNA resulted in two different alleles *Pain_SA* and *Pain_SN*.
In a pyrosequencing assay the alleles were analyzed on the basis of the A/C polymorphism of the associated SNP at cDNA position 1544 (Table 3.1.4). This SNP allows the comparison of the expression of *Pain_SA,* which exhibits the allele specific nucleotide A against the allelic fraction containing nucleotide C. The nucleotide C fraction can contain up to three different alleles, due to the ploidy state of the cultivated potatoes but is only represented by *Pain_SN*.
The pyrosequencing analysis was performed using cDNA from cold stored tubers and tuber genomic DNA to measure the dosages of the alleles (Figure 3.1.12).

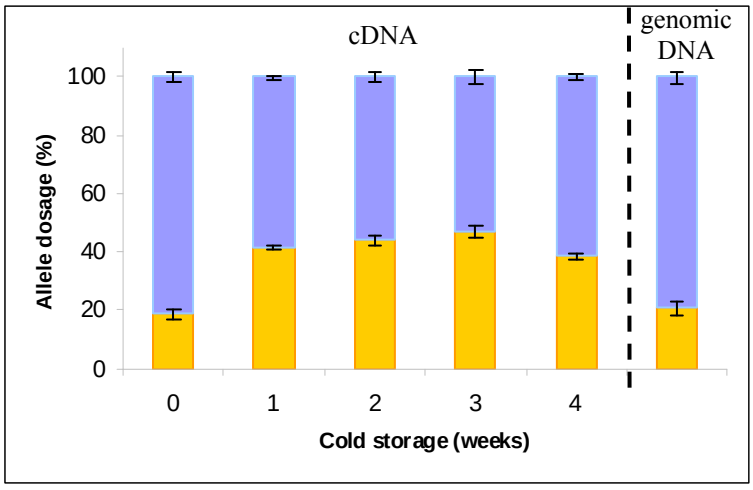


Figure 3.1.12: Pyrosequencing analysis of the alleles *Pain_SA* and *Pain_SN* of the cultivar 'Satina'.
: *Pain_SA;* **:** *Pain_SN.* For allele discrimination the primers Pyro_Pain_F/Pyro_Pain_RB (chapter 2, Table 2.1.4) were used. The primer Pyro_Pain_F was also used as sequencing primer. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of tubers. Percentages of the expression level of the cold stored samples are related to the genomic dosage of the alleles. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Standard deviations are derived from two biological replicates done in technical triplicates.

From ‘Satina’ two *Pain-1* alleles were identified. Pyrosequencing analysis of genomic tuber DNA revealed that the associated allele *Pain_SA* represents 25% of the potential four *Pain-1* alleles in the genotype ‘Satina’ (Figure 3.1.11). If the alleles were transcribed according to the genomic allele dosage, *Pain_SA* is expected to contribute 25% of the total transcripts and *Pain_SN* 75%. Comparison of allele dosage and allele transcription revealed that the alleles *Pain_SA* and *Pain_SN* differed in their abundance during tuber cold storage. The expression level of *Pain_SA* increased during tuber cold storage relative to *Pain_SN*. Maximal expression level was at ≈43% in the 3rd week of cold storage.

Transferring the information about allelic distribution from pyrosequencing analysis to the total amount of invertase transcript levels from qRT-PCR resulted in detailed expression pattern during tuber cold storage (Figure 3.1.13).

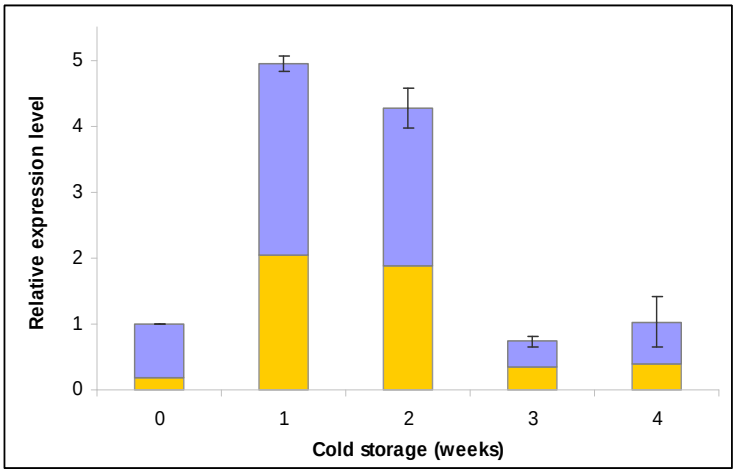


Figure 3.1.13: Overview of the expression pattern during tuber cold storage combining allelic distribution and total invertase transcript analysis of the cultivar ‘Satina’. **:** *Pain_SA*; **:** *Pain_SN*. The quantification of total invertase transcript was performed using the primers Pyro_Pain_F/Pyro_Pain_R (chapter 2, Table 2.1.9) in qRT-PCR analysis. Total transcript data were normalized with the reference gene *EF1α*. The relative expression level was calculated by defining transcript data of 0 weeks of cold storage as ‘1’. All other transcript data were related to this time point. Allelic distribution was calculated by relating the pyrosequencing data to the total transcript data. Standard deviations derived from two biological replicates done in technical duplicates. Standard deviations represent the variation within the replicates of the total transcripts, standard deviations for allele specific expression are shown in Figure 3.1.12.

qRT-PCR analysis showed an approximately four fold induction of total invertase transcripts after one week of tuber cold storage at 4°C (Figure 3.1.13). Transcript up-regulation declined in the 3rd and 4th week of cold storage to levels similar to samples not stored in the cold.

Expression analysis of the associated ‘Satina’ allele *Pain_SA,* which was found in one genomic dosage revealed an up-regulation up to 43% during tuber cold storage. Total invertase transcripts were induced up to four fold during the applied cold storage period. In

consequence tuber cold storage leads to a relative induction of the *Pain_SA* expression in contrast to the remaining allelic fraction in the tetraploid genotype 'Satina'.

3.1.2.2.2 Expression pattern of *Pain-1* alleles in tubers of the tetraploid cultivar 'Diana'

Referring to the cultivar tetraploidy, 'Diana' can consist of four possible *Pain-1* alleles. In this study three different alleles *Pain_DA, Pain_DN1*, and *Pain_DN2* were found. The expression of the three alleles was analyzed by tracing allele specific SNPs (Table 3.1.4; Table 3.1.13), which were used in pyrosequencing assays (Figure 3.1.14).

Table 3.1.13: Overview of allele specific SNPs analyzed by pyrosequencing.

Allele	SNP position	Allele specific SNP
		Pain_DA/*Pain_DN1*/*Pain_DN2*
Pain_DA	SNP 1544	**A**/C/C
Pain_DN1	SNP 1596	T/**C**/T
Pain_DN2	SNP 1574	A/A/**T**

SNP positions refer to cDNA sequence where '1' represents the adenine of the start codon ATG. Primers used for pyrosequencing are listed in chapter 2, Table 2.1.4 (Pyro_Pain_F/Pyro_Pain_RB; sequencing primer Pyro_Pain_F). Allele specific SNPs are highlighted in bold capitals.

Pyrosequencing analysis was performed using cDNA from cold stored tubers and tuber genomic DNA to measure the dosages of the alleles (Figure 3.1.13).

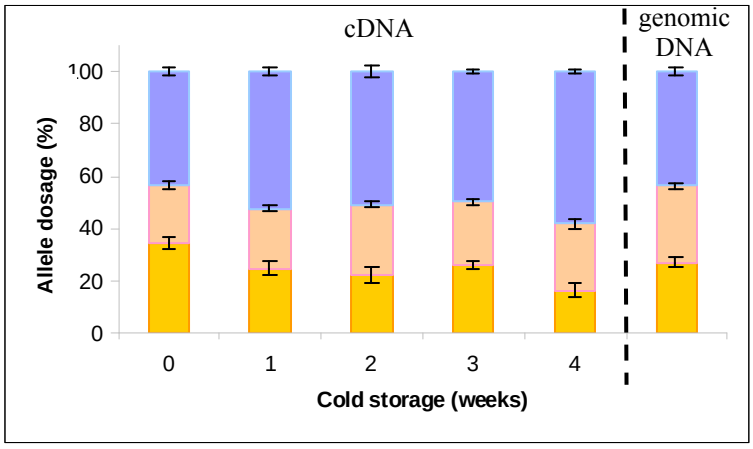


Figure 3.1.14: Pyrosequencing analysis of the alleles *Pain_DA, Pain_DN1,* and *Pain_DN2* of the cultivar 'Diana'. **:** *Pain_DA*; **:** *Pain_DN1*, **:** *Pain_DN2.* In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of tubers. Percentages of the expression level of the cold stored samples are related to the genomic dosage of the alleles. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Standard deviations are derived from two biological replicates done in technical triplicates.

Pyrosequencing analysis of genomic DNA showed that the 'Diana' alleles *Pain_DA* and *Pain_DN2* are present in simplex (25%), whilst *Pain_DN1* occurs in duplex (50%).

The allele *Pain_DN1* displays at SNP position 1596 the nucleotide C but it might be possible that this fraction, representing half of the allelic entity, contains more than one allele because

of tetraploidy. If the alleles were transcribed according to their allele dosage, *Pain_DA* and *Pain_DN2* are expected to contribute 25% of the total transcripts and *Pain_DN2* 50%.
The expression of the associated allele *Pain_DA* changed in tubers during cold treatment from 38% before storage to a level of 18% in tubers stored in the cold for four weeks. *Pain_DN1* was the most prevalent allele of the cultivar 'Diana' and was expressed from approximately 40% (0 weeks) up to 60% (4 weeks). The expression level of the third allele *Pain_DN2* did not show strong variation during tuber cold storage. The level of expression remained stable between 20 and 25%, and, therefore, similar to the genomic dosage.

Relating the pyrosequencing data to the total amounts of invertase transcripts obtained by qRT-PCR resulted in detailed information about invertase expression during tuber cold storage (Figure 3.1.15).

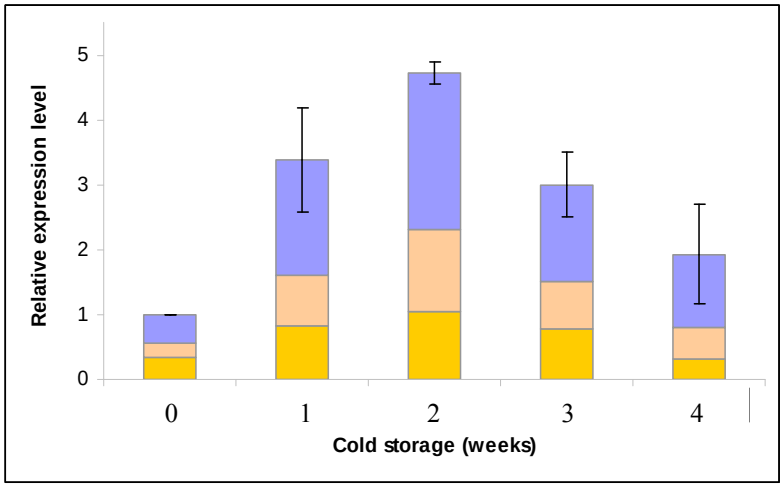


Figure 3.1.15: Overview of the expression pattern during tuber cold storage combining allelic distribution and total invertase transcript analysis of the cultivar 'Diana'. **:** *Pain_DA;* **:** *Pain_DN1;* **:***Pain_DN2.* The quantification of total invertase transcript was performed using the primers Pyro_Pain_F/Pyro_Pain_R (chapter 2, Table 2.1.9) in qRT-PCR analysis. Total transcript data were normalized with the reference gene *EF1α* (section 2, Table 2.1.9). The relative expression level was calculated by defining transcript data of 0 weeks of cold storage as '1'. All other transcript data were related to this time point. Allelic distribution was calculated by relating the pyrosequencing data to the total transcript data. Standard deviations derived from two biological replicates done in technical duplicates. Standard deviations represent the variation within the replicates of the total transcripts, standard deviations for allele specific expression are shown in Figure 3.1.14.

qRT-PCR analysis showed an approximately 2.5 fold induction of total invertase transcript after one week of tuber cold storage (Figure 3.1.15). The transcript level increased in the 2nd week of cold storage up to about four fold compared to the control samples (no cold storage). In the 3rd and 4th week of storage the relative expression level declined but remained higher compared to levels in tubers not stored in the cold.

The expression of 'Diana' alleles during cold storage differed not strongly compared to their genomic dosages. Total invertase transcripts were induced up to three fold after the 1st and 2nd week of tuber cold storage.

3.1.2.2.3 Expression pattern of *Pain-1* alleles in tubers of the tetraploid cultivar 'Theresa'

From the tetraploid cultivar 'Theresa' two different alleles *Pain_TN1* and *Pain_TN2* were obtained by cDNA cloning and sequencing. These two alleles were analyzed by means of the discriminative SNP at cDNA position 612 by pyrosequencing analysis (Figure 3.1.16). *Pain_TN1* has nucleotide A at SNP position 612, whilst *Pain_TN2* has nucleotide G (Table 3.1.4).

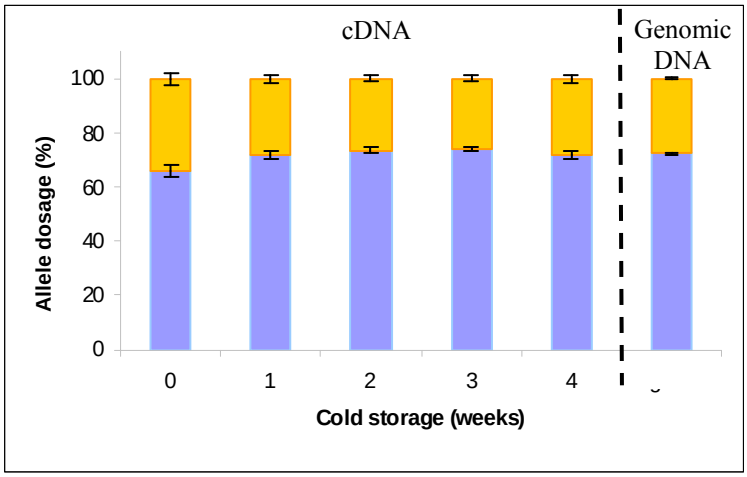


Figure 3.1.16: Pyrosequencing analysis of the alleles *Pain_TN1* and *Pain_TN2* of the cultivar 'Theresa'. **:** *Pain_TN2;* **:** *Pain_TN1*. For allele discrimination the primers Pyro_PainTher_F/Pyro_PainTherRB (chapter 2, Table 2.1.4) were used. The primer Pyro_PainTheSeq was used as sequencing primer. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of tubers. Percentages of the expression level of the cold stored samples are related to the genomic dosage of the alleles. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Standard deviations are derived from two biological replicates done in technical triplicates.

Pyrosequencing analysis of genomic DNA showed that the allele *Pain_TN2* is present in simplex (25%) and the allele *Pain_TN1* in triplex (75%). If the alleles were transcribed according to the allele dosage, *Pain_TN1* is expected to contribute 75% of the total transcripts, and *Pain_TN2* 25%. Both alleles showed little changes in their presence in cDNA samples and their expression remained at similar levels during tuber cold treatment.

The expression level of *Pain_TN2* changed marginal during tuber cold storage compared with samples not stored at 4°C. *Pain_TN1* was the prevalent allele during tuber cold storage.

Referring to 'Theresa's' tetraploidy, it is possible that the triplex fraction represented by *Pain_TN1* consists of more than one allele.

Pyrosequencing analysis gave information of allele expression during tuber cold storage. Transferring this allelic pattern to the total amount of invertase transcripts led to a detailed overview of *Pain-1* allele expression (Figure 3.1.17).

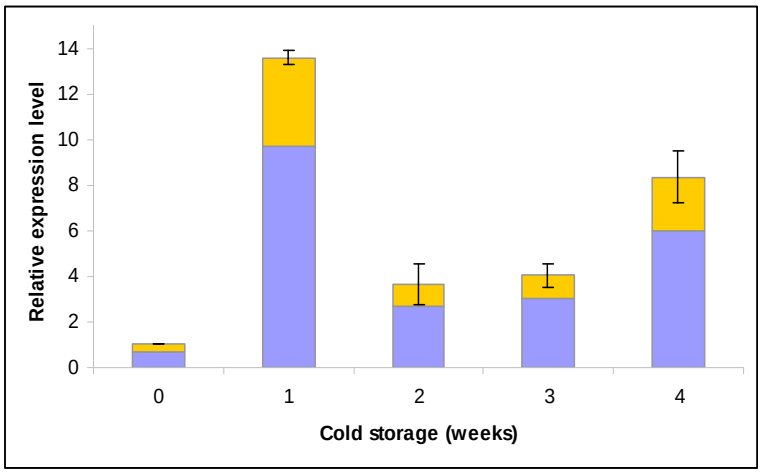


Figure 3.1.17: Overview of the expression pattern during tuber cold storage combining allelic distribution and total invertase transcript analysis of the cultivar 'Theresa'. : *Pain_TN2*; : *Pain_TN1*. The quantification of total invertase transcript was performed using the primers Pyro_Pain_F/Pyro_Pain_R (chapter 2, Table 2.1.9) in qRT-PCR analysis. Total transcript data were normalized with the reference gene *EF1α* (chapter 2, Table 2.1.9). The relative expression level was calculated by defining transcript data of 0 weeks of cold storage as '1'. All other transcript data were related to this time point. Allelic distribution was calculated by relating the pyrosequencing data to the total transcript data. Standard deviations derived from three biological replicates done in technical duplicates. Standard deviations represent the variation within the replicates of the total transcripts, standard deviations for allele specific expression are shown in Figure 3.1.16.

qRT-PCR analysis showed an about 12 fold induction of total invertase transcript after the 1st week of tuber cold storage (Figure 3.1.17). Transcript up-regulation declined in the 2nd and 3rd week of cold storage to levels remaining higher than in control tubers (no cold storage). In the 4th week of cold treatment invertase transcripts increased again up to seven fold compared to control samples.

Expression analysis of both alleles of the cultivar 'Theresa' revealed no relevant changes of allele distribution in cold stored tubers. An intense up-regulation of total invertase transcripts was observed after the 1st week of tuber cold storage. The cultivar 'Theresa' is the only genotype analyzed, where total invertase transcripts increased again after four weeks at 4°C storage.

3.1.2.2.4 Expression pattern of *Pain-1* alleles in tubers of the diploid genotype P18

The differentiation between the two P18 alleles *Pain_P18N1* and *Pain_P18N2* relied on the C/A polymorphism of SNP at cDNA position 1544 using pyrosequencing analysis (Figure 3.1.18). The allele *Pain_P18N1* exhibits at SNP 1544 the nucleotide A, whilst allele *Pain_P18N2* consists of the nucleotide C (Table 3.1.5).

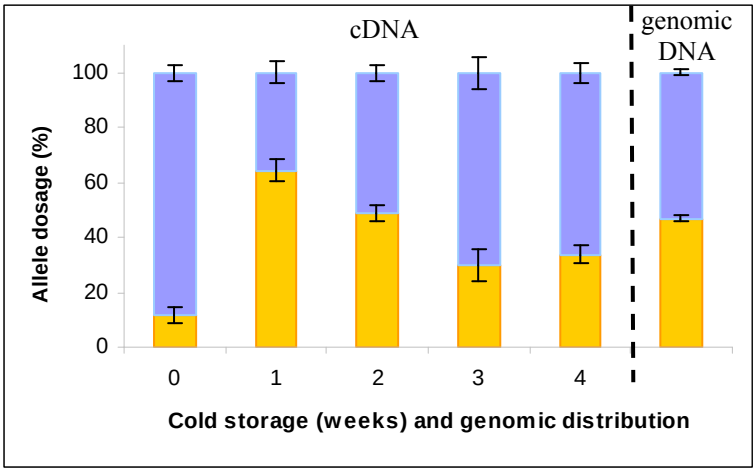


Figure 3.1.18: Pyrosequencing analysis of the alleles *Pain_P18N1* and *Pain_P18N2* of the genotype P18. **:** *Pain_P18N1;* **:** *Pain_P18N2.* For allele discrimination the primers Pyro Pyro_Pain_F/Pyro_Pain_RB (chapter 2, Table 2.1.4) were used. The primer Pyro_Pain_F was also used as sequencing primer. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of tubers. Percentages of the expression level of the cold stored samples are related to the genomic dosage of the alleles. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Standard deviations are derived from two biological replicates done in technical triplicates.

Pyrosequencing analysis of genomic DNA showed that both P18 alleles are present in duplex (50%) as expected for a heterozygous diploid genotype. Pyrosequencing analysis of cDNA samples showed a strong increase of allele *Pain_P18N1* after one week of tuber cold storage (Figure 3.1.18). Expression level was 50% higher than in tubers that were not stored in the cold. *Pain_P18N1* up-regulation declined in the 2nd, 3rd, and 4th week of cold storage to level ranging from about 30 to 50% of total expression.

Analyzing the relative expression level of P18 allele transcripts by transferring pyrosequencing data to qRT-PCR analysis showed that expression pattern changed during tuber cold storage (Figure 3.1.19).

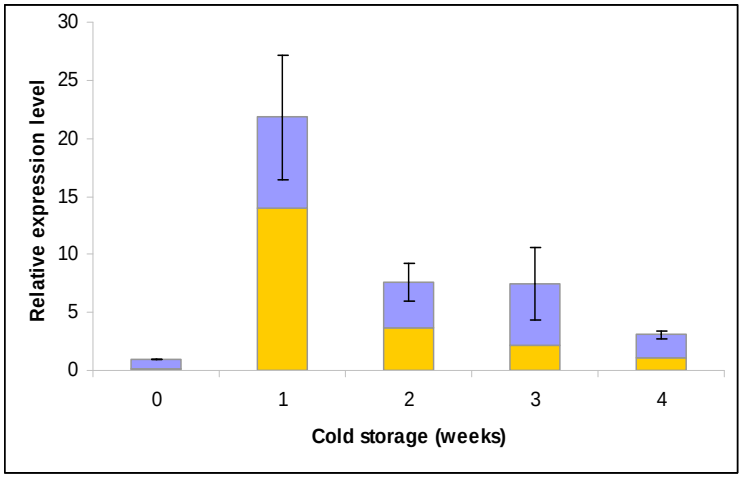


Figure 3.1.19: Overview of the expression pattern during tuber cold storage combining allelic distribution and total invertase transcript analysis of the potato genotype P18. **:** *Pain_P18N1*; **:** *Pain_P18N2.* The quantification of total invertase transcript was performed using the primers Pyro_Pain_F/Pyro_Pain_R (chapter 2, Table 2.1.9) in qRT-PCR analysis. Total transcript data were normalized with the reference gene *EF1α* (chapter 2, Table 2.1.9). The relative expression level was calculated by defining transcript data of 0 weeks of cold storage as '1'. All other transcript data were related to this time point. Allelic distribution was calculated by relating the pyrosequencing data to the total transcript data. Standard deviations derived from two biological replicates done in technical duplicates. Standard deviations represent the variation within the replicates of the total transcripts, standard deviations for allele specific expression are shown in Figure 3.1.18.

qRT-PCR analysis demonstrated that total invertase transcripts were strongly induced after one week of tuber cold storage at 4°C (Figure 3.1.19). Transcript up-regulation occurred up to 20 fold compared to control tubers (0 weeks). The relative expression level showed an about eight fold induction in the 2nd and 3rd week and decreased toward the end of cold storage.

Expression analysis of P18 invertase transcripts revealed an up-regulation of allele *Pain_P18N1* up to about 50% as well as an intense induction of total transcripts after one week of tuber cold storage. The diploid genotype P18 showed the highest accumulation of invertase transcripts (up to ≈20 fold) due to cold storage compared to control samples of all tested potato genotypes. Comparing the expression levels of the alleles *Pain_P18N1* and *Pain_DA,* which are identical at amino acid level, showed that expression of *Pain_DA* in contrast to *Pain_P18N1* was not effected by tuber cold storage (Figure 3.1.14). *Pain_DA* was found to be associated with better potato chips quality.

3.1.2.2.5 Expression pattern of *Pain-1* alleles in tubers of the diploid genotype P40

Pyrosequencing analysis of the P40 allele specific SNP at cDNA position 1267 were used to separate the alleles *Pain_P40N1* and *Pain_P40N2* (Figure 3.1.20). *Pain_P40N1* is characterized by adenine at SNP position 1267, whilst *Pain_P40N2* shows guanine (Table 3.1.5).

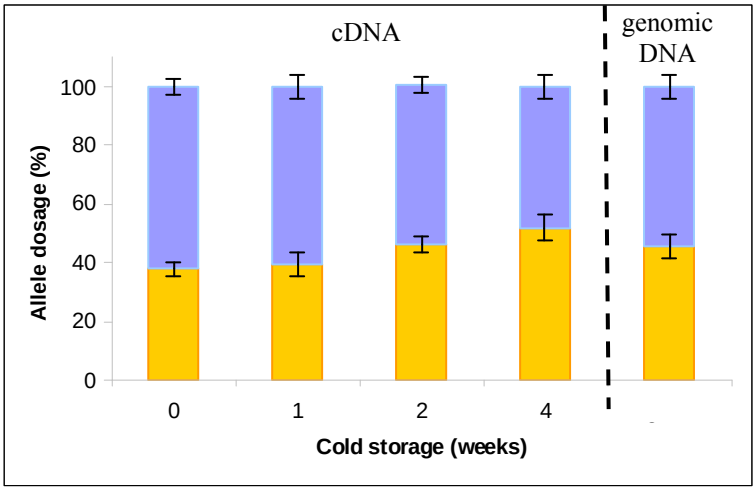


Figure 3.1.20: Pyrosequencing analysis of the alleles *Pain_P40N1* and *Pain_P40N2* of the genotype P40. **:** *Pain_P40N1;* **:** *Pain_P40N2.* For allele discrimination the primers Pyro_PainP40_F/Pyro_PainP40_RB were used. The primer Pyro_PainP40_Seq was used as sequencing primer (chapter 2, Table 2.1.4). In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of tubers. Percentages of the expression level of the cold stored samples are related to the genomic dosage of the alleles. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Standard deviations are derived from two biological replicates done in technical triplicates.

Pyrosequencing analysis of genomic DNA showed that both P 40 alleles are present in duplex (50%) as expected for a heterozygous diploid genotype. Pyrosequencing analysis of cDNA samples revealed a slight but continuous increase of allele *Pain_P40N1* during tuber cold storage (Figure 3.1.20). Expression levels ranged from about 38% in control samples up to 50% in tubers stored in the cold for four weeks. Tuber tissues stored for three weeks were not analyzed in pyrosequencing assay due to sample limitation.

Relating the pyrosequencing data to the total amounts of invertase transcripts obtained by qRT-PCR resulted in detailed information about invertase expression during tuber cold storage (Figure 3.1.21).

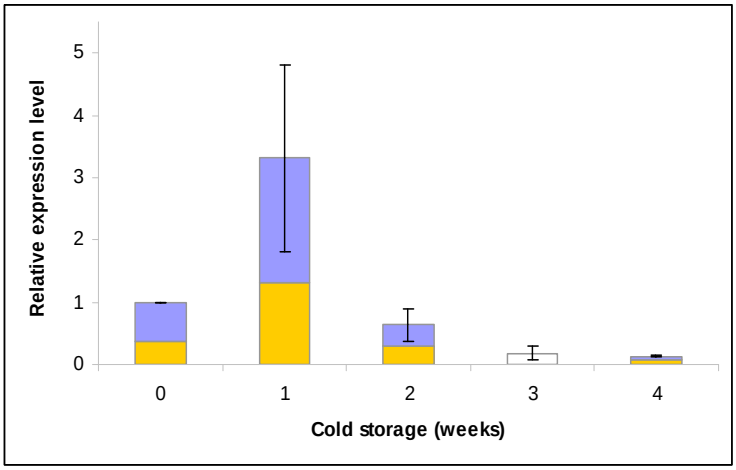


Figure 3.1.21: Overview of the expression pattern during tuber cold storage combining allelic distribution and total invertase transcript analysis of the potato genotype P40. **:** *Pain_P40N1*; **:** *Pain_P40N2*. The quantification of total invertase transcript was performed using the primers Pyro_Pain_F/Pyro_Pain_R (chapter 2, Table 2.1.9) in qRT-PCR analysis. Total transcript data were normalized with the reference gene *EF1α* (chapter 2, Table 2.1.9). The relative expression level was calculated by defining transcript data of 0 weeks of cold storage as '1'. All other transcript data were related to this time point. Allelic distribution was calculated by relating the pyrosequencing data to the total transcript data. The 3rd week of tuber cold storage was not analyzed by pyrosequencing due to samples limitations. The bar of total invertase transcripts, therefore, is left empty. Standard deviations derived from two biological replicates done in technical duplicates. Standard deviations represent the variation within the replicates of the total transcripts, standard deviations for allele specific expression are shown in Figure 3.1.20.

Monitoring the relative expression level of total invertase transcripts showed an about 2.5 fold induction after one week of tuber cold storage at 4°C (Figure 3.1.21). Transcript up-regulation declined in the 2nd, 3rd, and 4th week of cold storage to levels lower than in control tubers that were not stored in the cold.

Expression analysis of both P40 alleles revealed slight changes of allele distribution in cold stored tubers. Allele *Pain_P40N1* expression increased during cold storage from about 38% to 50%. Up-regulation of total invertase transcripts was observed after one week of cold treatment up to 2.5 fold. The relative expression level of total transcripts declined dramatically from the 2nd to the 4th week of tuber cold storage.

3.1.2.2 Functional complementation of the yeast invertase mutant *SUC2*

Plant invertases are functional in heterologous systems (FRIDMAN ET AL., 2004). Therefore, the model organism yeast (*Saccharomyces cerevisae*) was used to analyze potato invertase alleles. The yeast invertase mutant *SUC2* lacks invertase activity and uses glucose as carbohydrate source. Transforming *SUC2* with *Pain-1* cDNA alleles resulted in yeast transformants that were able to grow on sucrose as sole carbohydrate source, indicating functional complementation of the *SUC2* mutation.

The *Pain-1* cDNA alleles listed below were used for complementation of *SUC2* (Figure 3.1.22) and subsequent analysis of invertase activity (section 3.1.2.3).

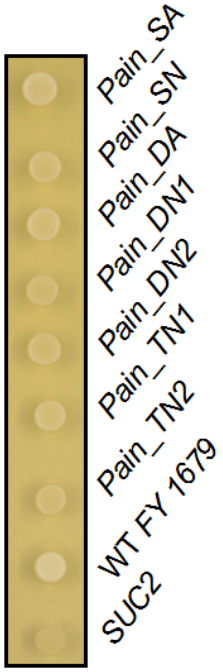
Genotype	Allele name	*SUC2* complementation
'Satina'	*Pain_SA*	 Representative yeast transformants complemented with invertase alleles of the cultivars 'Satina', 'Diana', and 'Theresa' were spotted on solid yeast minimal broth with 2% sucrose as carbon source. The wild type *FY 1479* was plated as positive control, whilst the invertase mutant *SUC2* was the negative control. Growth of all complemented yeast transformants was quantified (Figure 3.1.23).
	Pain_SN	
'Diana'	*Pain_DA*	
	Pain_DN1	
	Pain_DN2	
'Theresa'	*Pain_TN1*	
	Pain_TN2	
P18	*Pain_P18N1*	
	Pain_P18N2	
P40	*Pain_P40N1*	
	Pain_P40N2	
P54	*Pain_P54N*	

Figure 3.1.22: cDNA alleles used for *SUC2* complementation and *SUC2* transformants on solid yeast minimal media.

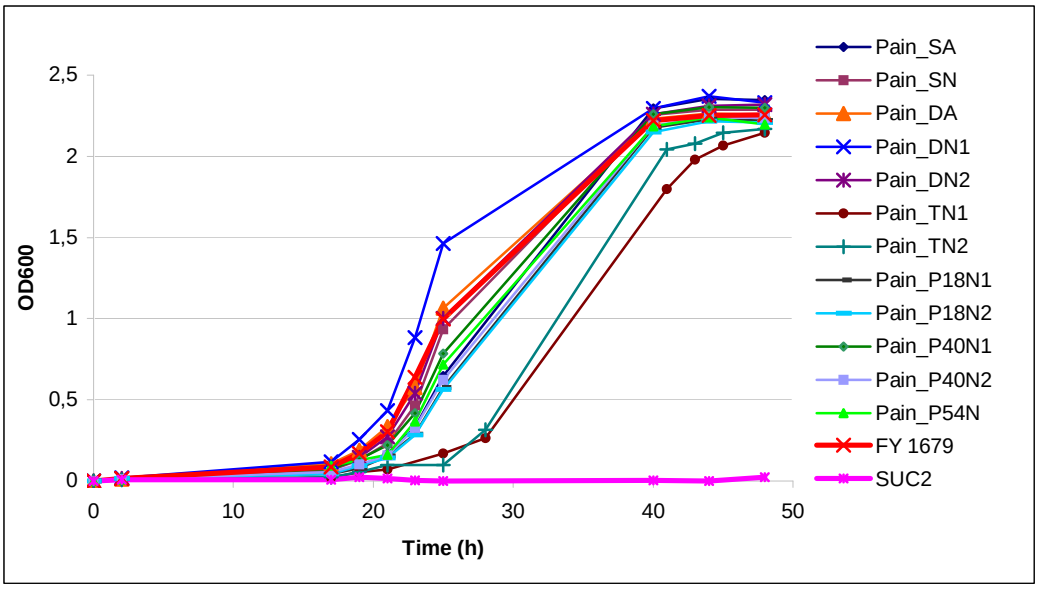


Figure 3.1.23: Growth of complemented *SUC2* transformants. Yeast reference strain *FY 1679* (red), yeast invertase mutant strain *SUC2* (pink), and *Pain-1* transformants were grown in yeast minimal media with 2% sucrose as the sole carbon source. OD600 is plotted against growth time in hours. OD600 values represent the means of two replicates. Standard deviations were less than 20% of mean.

All *SUC2* invertase transformants exhibited substantial growth on sucrose. 'Satina' and 'Diana' alleles and alleles of the diploid genotypes P18, P40, and P54 complemented the invertase deficiency of the yeast strain better than the alleles of 'Theresa'. However, it was not possible to correlate the altered complementation efficiency to quantitative invertase protein differences using immunoblot studies (section 3.1.2.4; Figure 3.1.25).

3.1.2.3 Biochemical characterization of *Pain-1* alleles

Putative 3D-models of allelic *Pain-1* molecules (3.1.1.3) indicated structural and electrostatical differences between the alleles, which could cause functional differences. To test, whether structural characteristics might influence enzymatic activity of *Pain-1* invertase alleles, biochemical characterization was performed.

From yeast *SUC2* transformants complemented with *Pain-1* cDNA alleles total protein was extracted. To test soluble acid invertase activity, a modified protocol based on ZRENNER ET AL. (1995) was used. Invertase assays were carried out at 30°C. Additionally, *Pain-1* alleles were assayed at 4°C. The analysis at 4°C was performed to study possible differences of enzyme kinetics due to allelic amino acid composition in response to cold storage conditions. It was previously reported that cold storage influences transcriptional changes regarding vacuolar invertases (ZRENNER ET AL., 1996; ZHOU ET AL., 2004; BAGNARESI ET AL., 2008), but no study investigated the effect of low temperatures on the enzyme activity itself. The *Pain-1* alleles displayed in Table 3.1.14 were used for biochemical characterization at 30°C and 4°C.

Table 3.1.14: *Pain-1* alleles used for biochemical characterization.

Tetraploid genotypes	Allele	Diploid genotypes	Allele
'Satina'	*Pain_SA*	P18	*Pain_P18N1*
	Pain_SN		*Pain_P18N2*
'Diana'	*Pain_DA*	P40	*Pain_P40N1*
	Pain_DN1		*Pain_P40N2*
	Pain_DN2	P54	*Pain_P54N*
'Theresa'	*Pain_TN1*		
	Pain_TN2		

The biochemical parameters Michaelis constant (K_m) and the maximal velocity (v_{max}) of invertase reaction were determined.

Results of the biochemical analysis at 30°C and 4°C are shown in Table 3.1.15.

Table 3.1.15: K_m (mM) and v_{max} (mmol/h*mg protein^{-1}) of *Pain-1* invertase alleles at 30°C and 4°C.

Genotype	Allele	K_m (30°C)	K_m (4°C)	v_{max} (30°C)	v_{max} (4°C)
'Satina'	*Pain_SA*	22.1±1.4	2.3±0.3	4.7±1.0	1.7±0.1
	Pain_SN	23.0±1.4	3.5±0.3	4.1±1.0	1.5±0.1
'Diana'	*Pain_DA*	19.9±1.4	4.0±0.3	12.4±0.8	2.8±0.1
	Pain_DN1	19.6±1.4	2.7±0.3	11.2±0.8	2.7±0.1
	Pain_DN2	15.6±1.4	3.7±0.3	6.2±1.0	2.2±0.1
'Theresa'	*Pain_TN1*	19.8±1.4	3.0±0.3	3.4±1.0	1.5±0.1
	Pain_TN2	21.6±1.4	na	2.0±1.4	na
P18	*Pain_P18N1*	20.4±1.4	2.7±0.3	5.5±1.0	2.1±0.1
	Pain_P18N2	16.9±1.4	4.7±0.4	2.7±1.0	1.9±0.1
P40	*Pain_P40N1*	17.2±1.4	3.4±0.3	5.8±1.0	2.1±0.1
	Pain_P40N2	14.9±1.4	4.4±0.3	6.8±1.0	2.6±0.1
P54	*Pain_P54N*	19.1±1.4	2.7±0.4	3.7±1.0	1.6±0.1
FY 1679		21.0±1.6	21.1±2.5	23.9±4.5	7.7±0.9

Standard deviations are derived from three biological replicates for the associated alleles *Pain_SA* and *Pain_DA*, and the wild type reference strain *FY 1679,* and from two biological replicates for the other alleles done in technical replicates to obtain six measurements. To make assays of different invertase isoforms comparable, the yeast reference strain *FY 1679* was used as positive control.

Tables 3.1.16, 3.1.17, 3.1.18 and 3.1.19 summarize the significance values for differences between the K_m and v_{max} values measured for the *Pain-1* alleles at 30°C and 4°C. The statistical calculation was performed by Benjamin Stich, MPIZ/Köln.

Table 3.1.16: Overview of statistical significance levels of K_m values from the *Pain-1* invertase alleles at 30°C.

Allele	*Pain SA*	*Pain SN*	*Pain DA*	*Pain DN1*	*Pain DN2*	*Pain TN1*	*Pain TN2*	*Pain P18N1*	*Pain P18N2*	*Pain P40N1*	*Pain P40N2*	*Pain P54N*
Pain SA	---	0.63	0.28	0.22	0.0058	0.26	0.79	0.39	0.019	0.028	0.0029	0.15
Pain SN	---	---	0.13	0.10	0.0024	0.12	0.47	0.20	0.008	0.011	0.0012	0.067
Pain DA	---	---	---	0.89	0.048	0.98	0.40	0.80	0.15	0.20	0.024	0.71
Pain DN1	---	---	---	---	0.06	0.91	0.33	0.70	0.19	0.25	0.03	0.81
Pain DN2	---	---	---	---	---	0.051	0.009	0.03	0.53	0.42	0.71	0.095
Pain TN1	---	---	---	---	---	---	0.38	0.78	0.16	0.21	0.025	0.73
Pain TN2	---	---	---	---	---	---	---	0.55	0.032	0.045	0.0047	0.23
Pain P18N1	---	---	---	---	---	---	---	---	0.09	0.13	0.015	0.53
Pain P18N2	---	---	---	---	---	---	---	---	---	0.86	0.32	0.27
Pain P40N1	---	---	---	---	---	---	---	---	---	---	0.25	0.35
Pain P40N2	---	---	---	---	---	---	---	---	---	---	---	0.048
Pain P54N	---	---	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

Table 3.1.17: Overview of statistical significance levels of K_m values from the *Pain-1* invertase alleles at 4°C.

Allele	*Pain SA*	*Pain SN*	*Pain DA*	*Pain DN1*	*Pain DN2*	*Pain TN1*	*Pain TN2*	*Pain P18N1*	*Pain P18N2*	*Pain P40N1*	*Pain P40N2*	*Pain P54N*
Pain SA	---	0.014	0.0019	0.36	0.0078	0.11	na	0.298	0.0003	0.023	0.0004	0.34
Pain SN	---	---	0.24	0.080	0.65	0.33	na	0.1	0.026	0.798	0.06	0.14
Pain DA	---	---	---	0.0099	0.47	0.053	na	0.013	0.21	0.16	0.44	0.022
Pain DN1	---	---	---	---	0.042	0.43	na	0.89	0.0012	0.13	0.0021	0.89
Pain DN2	---	---	---	---	---	0.18	na	0.052	0.066	0.49	0.15	0.079
Pain TN1	---	---	---	---	---	---	na	0.51	0.0058	0.46	0.012	0.57
Pain TN2	---	---	---	---	---	---	---	na	na	na	na	na
Pain P18N1	---	---	---	---	---	---	---	---	0.0014	0.16	0.0027	0.98
Pain P18N2	---	---	---	---	---	---	---	---	---	0.017	0.59	0.0028
Pain P40N1	---	---	---	---	---	---	---	---	---	---	0.038	0.2085
Pain P40N2	---	---	---	---	---	---	---	---	---	---	---	0.0055
Pain P54N	---	---	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

Table 3.1.18: Overview of statistical significance levels of v_{max} values from the *Pain-1* invertase alleles at 30°C.

Allele	*Pain SA*	*Pain SN*	*Pain DA*	*Pain DN1*	*Pain DN2*	*Pain TN1*	*Pain TN2*	*Pain P18N1*	*Pain P18N2*	*Pain P40N1*	*Pain P40N2*	*Pain P54N*
Pain SA	---	0.696	5.80 E-05	0.0003	0.29	0.38	0.15	0.58	0.177	0.43	0.15	0.52
Pain SN	---	---	3.01E-05	0.0001	0.16	0.62	0.25	0.35	0.32	0.25	0.077	0.79
Pain DA	---	---	---	0.32	0.0004	1.35E-05	3.11E-05	0.0002	6.2E-06	0.0002	0.0009	1.98E-05
Pain DN1	---	---	---	---	0.0021	5.26E-05	9.68E-05	0.0007	2.28E-05	0.0012	0.0049	7.98E-05
Pain DN2	---	---	---	---	---	0.0653	0.03	0.599	0.026	0.77	0.68	0.1
Pain TN1	---	---	---	---	---	---	0.44	0.16	0.61	0.11	0.03	0.81
Pain TN2	---	---	---	---	---	---	---	0.067	0.72	0.047	0.016	0.34
Pain P18N1	---	---	---	---	---	---	---	---	0.068	0.813	0.356	0.249
Pain P18N2	---	---	---	---	---	---	---	---	---	0.044	0.012	0.46
Pain P40N1	---	---	---	---	---	---	---	---	---	---	0.49	0.16
Pain P40N2	---	---	---	---	---	---	---	---	---	---	---	0.048
Pain P54N	---	---	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

Table 3.1.19: Overview of statistical significance levels of v_{max} values from the *Pain-1* invertase alleles at 4°C.

Allele	*Pain SA*	*Pain SN*	*Pain DA*	*Pain DN1*	*Pain DN2*	*Pain TN1*	*Pain TN2*	*Pain P18N1*	*Pain P18N2*	*Pain P40N1*	*Pain P40N2*	*Pain P54N*
Pain SA	---	0.06	4.05 E-06	8.19 E-06	0.0093	0.22	na	0.013	0.25	0.013	3.20 E-05	0.55
Pain SN	---	---	3.74 E-07	6.11 E-07	0.0003	0.5	na	0.0003	0.0097	0.0003	2.18 E-06	0.23
Pain DA	---	---	---	0.41	0.0006	1.22 E-06	na	0.0003	5.86 E-05	0.0003	0.2	4.80 E-06
Pain DN1	---	---	---	---	0.0019	2.20E-06	na	0.0008	0.0002	0.0008	0.58	9.54 E-06
Pain DN2	---	---	---	---	---	0.0012	na	0.78	0.12	0.77	0.0073	0.0052
Pain TN1	---	---	---	---	---	---	na	0.0015	0.037	0.0015	7.64 E-06	0.56
Pain TN2	---	---	---	---	---	---	---	na	na	na	na	na
Pain P18N1	---	---	---	---	---	---	---	---	0.17	0.99	0.0034	0.0069
Pain P18N2	---	---	---	---	---	---	---	---	---	0.18	0.0005	0.12
Pain P40N1	---	---	---	---	---	---	---	---	---	---	0.0034	0.0067
Pain P40N2	---	---	---	---	---	---	---	---	---	---	---	3.14 E-05
Pain P54N	---	---	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

The 30°C assay of *Pain-1* alleles showed that the substrate affinity ranged between 15mM of the allele *Pain_P40N2* and 23mM of the allele *Pain_SN*. Maximal velocities of the alleles varied between 2mmol*h^{-1}*mg $protein^{-1}$ in the case of the allele *Pain_TN2* and 12mmol*h^{-1}*mg $protein^{-1}$ for the allele *Pain_DA*. The enzymatic characteristics of the analyzed alleles from the cultivar 'Satina' *Pain_SA* and *Pain_SN* showed no significant differences. In the K_m and v_{max} values of the cultivar 'Diana' differences were displayed in respect to the allele *Pain_DN2*. *Pain_DN2* showed the highest substrate affinity with a K_m of approximately 16mM, and the slowest substrate conversion with a v_{max} of around 6mmol*h^{-1}*mg $protein^{-1}$. The other two analyzed alleles *Pain_DA* and *Pain_DN1* displayed substrate affinities of approximately 20mM and maximal velocities of around 12mmol*h^{-1}*mg $protein^{-1}$. Comparison of the associated *Pain-1* alleles *Pain_SA* and *Pain_DA,* which are not identical at amino acid level, revealed no significant differences regarding their affinity to sucrose, but showed strong differences in the rate of sucrose conversion. The allele *Pain_DA* converts sucrose approximately 2.5 times faster than the allele *Pain_SA*.

Looking at the other analyzed *Pain-1* alleles, the two 'Theresa' alleles showed similar enzymatic characteristics and did not differ significantly. K_m values varied from 20 to 21mM, and v_{max} values ranged from 2 to 3mmol*h^{-1}*mg $protein^{-1}$. Biochemical analysis of the alleles

from the diploid potato genotypes P18 and P40 did not display any significant K_m and v_{max} differences. K_m and v_{max} values of *Pain_P18N1* and *Pain_P18N2* ranged from 17 to 20mM, and 3 to 5.5mmol*h^{-1}*mg $protein^{-1}$, respectively. The alleles *Pain_P40N1* and *Pain_P40N2* displayed substrate affinities between 15 and 17mM, and v_{max} values between 6 and 7mmol*h^{-1}*mg $protein^{-1}$.

Biochemical analysis of the enzymatic characteristics of the *Pain-1* alleles at 4°C showed a dramatic increase in the enzyme's affinity to sucrose. The K_m values decreased approximately 5.5 times compared to K_m values measured at 30°C. Also the maximal velocities of the alleles were affected at 4°C. By trend v_{max} values were around 2mmol*h^{-1}*mg $protein^{-1}$.

Additionally, biochemical characteristics were determined for two nucleotide variants of the 'Satina' allele *Pain_SN* to measure codon influences in the heterologous system yeast. The variants differed in one to three nucleotides to *Pain_SN* (Table 3.1.20), (Appendix A 3.1.25).

Table 3.1.20: SNPs of the nucleotide variants of the allele *Pain_SN*.

SNP position	*Pain_SN*	*Pain_SN**	*Pain_SN***
69	T	T	C
75	T	C	T
1050	C	T	C
1350	A	G	A

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. The nucleotide exchanges are synonymous, not causing an amino acid exchange.

It was shown that all nucleotide variants of *Pain_SN* displayed similar K_m and v_{max} values (Table 3.1.21), showing that a codon usage independent comparison of different alleles was possible.

Table 3.1.21: K_m (mM) and v_{max} (mmol/h*mg $protein^{-1}$) of *Pain-SN1* nucleotide variants at 30°C and 4°C.

Allele	K_m (30°C)	K_m (4°C)	v_{max} (30°C)	v_{max} (4°C)
Pain SN	23.0±1.4	3.5±0.3	4.1±1.0	1.5±0.1
*Pain SN**	23.0±1.7	3.0±0.3	5.7±1.0	1.8±0.1
*Pain SN***	24.5±1.5	2.5±0.4	7.8±1.4	1.7±0.1

Standard deviations are derived from two biological replicates done in technical triplicates.

The Tables 3.1.22 and 23 summarize the significance values for differences between the K_m and v_{max} values measured for the nucleotide variants of the allele *Pain_SN* at 30°C and 4°C. The statistical calculation was performed by Benjamin Stich, MPIZ/Köln.

Table 3.1.22: Overview of statistical significance levels of K_m values from the *Pain-SN1* nucleotide variants at 30°C and 4°C.

	30°C			4°C		
Allele	*Pain SN*	*Pain SN**	*Pain SN***	*Pain SN*	*Pain SN**	*Pain SN***
Pain SN	---	0.1	0.48	---	0.28	0.06
*Pain SN**	---	---	0.53	---	---	0.35
*Pain SN***	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

Table 3.1.23: Overview of statistical significance levels of v_{max} values from the *Pain-SN1* nucleotide variants at 30°C and 4°C.

	30°C			4°C		
Allele	*Pain SN*	*Pain SN**	*Pain SN***	*Pain SN*	*Pain SN**	*Pain SN***
Pain SN	---	0.27	0.048	---	0.04	0.084
*Pain SN**	---	---	0.24	---	---	0.83
*Pain SN***	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are orange coloured, no significant differences are described by P-values >0.05.

3.1.2.4 Western blot analysis

To analyze, whether the observed differences of invertase enzyme activity and yeast growth behaviour are not due to changes in protein quantity, immunoblot quantification was performed.

As a loading control the blotted membrane was stained with Ponceau S (Figure 3.1.24). The concentration of total yeast protein extract was the same within the loaded samples.

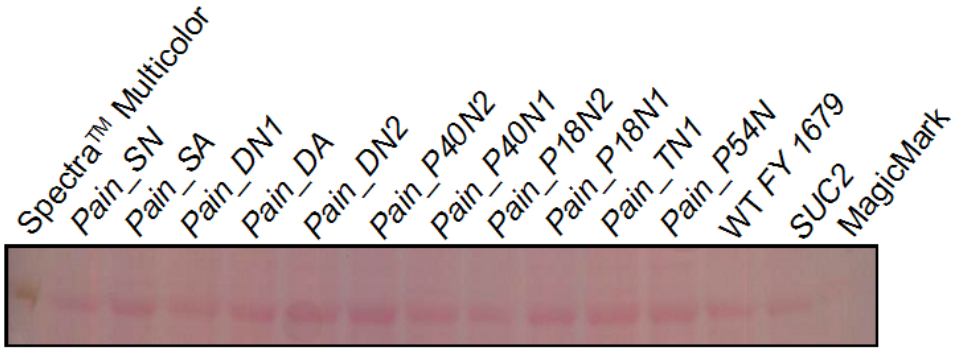


Figure 3.1.24: Ponceau S stained blot membrane. The corresponding alleles are given by their name above every lane. 15µg of total protein were loaded. A representative protein band out of the blotted membrane is shown as loading control.

From all tested invertase antibodies (chapter 2, Table 2.2.15), the antibody against a 58kDa vacuolar invertase of potato (BURCH ET AL., 1992) detected *Pain-1* protein most reliable and, therefore, was used in subsequent Western blot analysis. The invertase protein content of a set of allelic *Pain-1* yeast *SUC2* transformants was analyzed representatively (Figure 3.1.25).

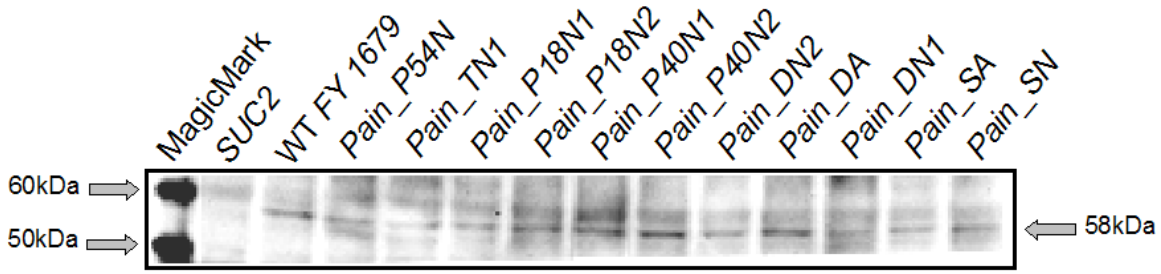


Figure 3.1.25: Western blot analysis of *Pain-1* alleles using an antibody against a 58kDa vacuolar invertase of potato. The corresponding alleles are given by their name above every lane. 15µg of total protein were loaded. Additionally, yeast invertase mutant *SUC2* and yeast reference strain WT *FY 1679* were blotted. Left arrows stand for size bands of the MagicMark Marker, the right arrow refers to the 58kDa band where the invertase protein was detected.

Western blot analysis showed that invertase protein content of *SUC2* transformants containing different *Pain-1* alleles did not differ significantly. Additionally, the invertase of the yeast reference strain WT *FY 1679* was detected by the potato antibody compared to the yeast invertase mutant *SUC2* where no protein was detectable.

3.2 The *Invap-b* locus on chromosome IX

The *Inv$_{ap}$-b* locus was intensively studied and described by MADDISON ET AL., (1999). The locus consists of two invertase genes *invGE* and *invGF* linked in direct tandem repeat and has a size of approximately 8.6kb. Both genes exhibit a similar exon/intron structure composed of six exons and five introns. This exon/intron structure is identical to the two potato cell wall-bound invertases *pCD111* and *pCD141* on chromosome X (HEDLEY ET AL., 1993, 1994), and slightly different from the *Pain-1* invertase gene on chromosome III (ZHOU ET AL., 1994). Expression analysis showed *invGE* transcription in the leaf, stem, root, tuber, and floral tissue, whilst *invGF* expression is restricted to floral tissues (MADDISON ET AL., 1999).
The genes *invGE* and *invGF* encode cell wall-bound invertase isoforms. These acidic insoluble invertases act in a pH optimum range of 4.5 to 5.0 and are functional in the apoplast (TYMOWSKA-LALANNE & KREIS, 1998).

3.2.1 Structural characterization of the genes *invGE* and *invGF*

3.2.1.1 Identification of associated *invGE* and *invGF* alleles

The *Inv$_{ap}$-b* locus maps to potato chromosome IX (CHEN ET AL., 2001) in a region associated with tuber quality trait,s where a QTL for potato tuber sugar content, *Sug9a*, was identified (MENÉNDEZ ET AL., 2002). In the latter study, the genes *invGE* and *invGF* were directly mapped in the mapping population used and showed linkage to the QTL *Sug9a.*

Single-strand conformation polymorphism (SSCP) analysis revealed an association of *invGE* and *invGF* alleles with starch and sugar content of potato tubers. SSCP fragments found to be associated with better potato chips quality were named *invGE-6f* and *invGF-4d,* respectively (LI ET AL., 2005). The occurrence of those fragments in the genotypes was highly correlated indicating that *invGE-6f* and *invGF-4d* are in LD. The analysis of protein sequences of allelic *invGE-6f* fragments revealed a unique histidine instead of proline at amino acid position 368 (LI ET AL., 2005). *invGE-6f* fragments containing histidine at posititon 368 were associated with better potato chips quality. Histidine 368 is encoded by the cDNA SNP at nucleotide position 1103* (section 3.2.1.2, Table 3.2.3) where cytosine changes to adenine. Therefore, cloned *invGE* cDNA alleles were named based on the presence (A) or absence (N) of SNP 1103*.
Assigning cloned *invGF* alleles to the SSCP fragment *invGF-4d* and detecting the underlying SNPs are subject of ongoing investigations in the research project.

3.2.1.2 Molecular cloning of *invGE* and *invGF* invertase cDNA alleles

Regarding *invGE* and *invGF* expression patterns (MADDISON ET AL., 1999), molecular cloning of *invGE* alleles was performed using leaf and floral tissue, whilst *invGF* allele cloning was initially carried out with floral tissue. During this study *invGF* alleles were obtained also from leaf material demonstrating that the restriction of floral *invGF* expression is genotype dependent.

❖ **Genotype dependent *invGF* expression in leaves**

Following the approach to detect *invGF* transcripts as described by MADDISON ET AL. (1999), gene specific primers amplifying a small fragment of the gene from the tetraploid genotypes 'Désirée', 'Saturna', 'Diana', 'Theresa', and from the diploid genotypes P40 and P54 were designed. MADDISON ET AL. (1999) restricted the expression analysis consisting of a histochemical GUS assay of *invGF* expression in transgenic plants and RT-PCR from mature flowers, flower bud, source, and sink leaf, respectively to the genotypes 'Désirée' and 'Saturna'. The *invGF* primers (chapter 2, Table 2.1.7) were selected spanning from exon I to exon III, which should generate a product of 402bp from cDNA. In contrast, any product generated from contaminating genomic DNA would include sequences from two intermediate introns and the mini-exon II, amounting to 704bp. RT-PCR with the latter primers using total RNA prepared from both mature flowers and leaves as template generated a product of the expected size (Figure 3.2.1) indicating expression of *invGF* in these organs.

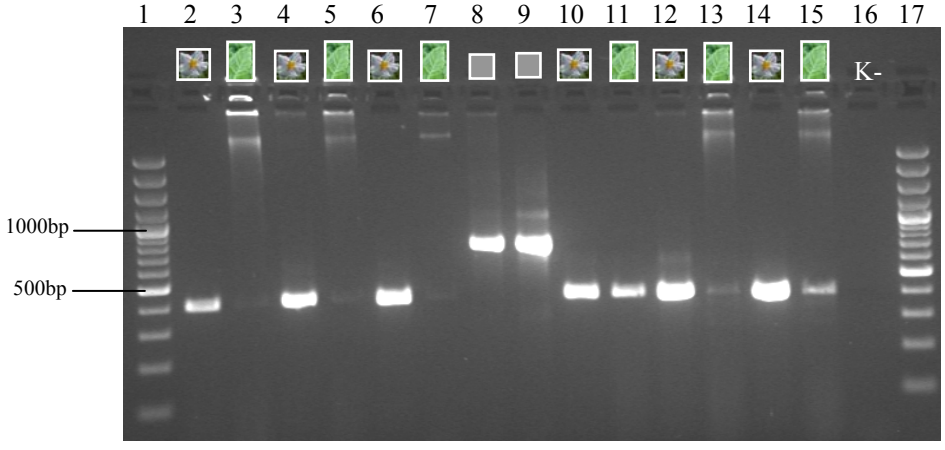


Figure 3.2.1: Amplification of a 402bp *invGF* fragment following the approach described by MADDISON ET AL. (1999). As template cDNA from leaves and flowers, and genomic DNA from leaves were used. cDNA template from flowers, cDNA template from leaves, genomic DNA from leaves. Lane 1: Fermentas ladder 100bp plus , lane 2: floral cDNA 'Saturna', lane 3: leaf cDNA 'Saturna', lane 4: floral cDNA 'Désirée', lane 5, leaf cDNA 'Désirée', lane 6: floral cDNA P40, lane 7: leaf cDNA P40, lane 8: genomic DNA P40, lane 9: genomic DNA 'Diana', lane 10: floral cDNA 'Diana', lane 11: leaf cDNA 'Diana', lane 12: floral cDNA 'Theresa', lane 13: leaf cDNA 'Theresa', lane 14: floral cDNA P54, lane 15: leaf cDNA P54, lane 16: negative control for leaf cDNA, lane 17: Fermentas ladder 100bp plus.

To obtain full-length *invGF* alleles, PCR amplification using full-length gene specific primers was accomplished. cDNA and genomic DNA of flowers and leaves from the genotypes ‘Satina’, ‘Diana’, ‘Theresa’, P18, P40, and P54 served as template. Additionally, full-length PCR was carried out for cDNA and genomic DNA from flowers and leaves of the cultivar ‘Saturna’ (Figure 3.2.2).

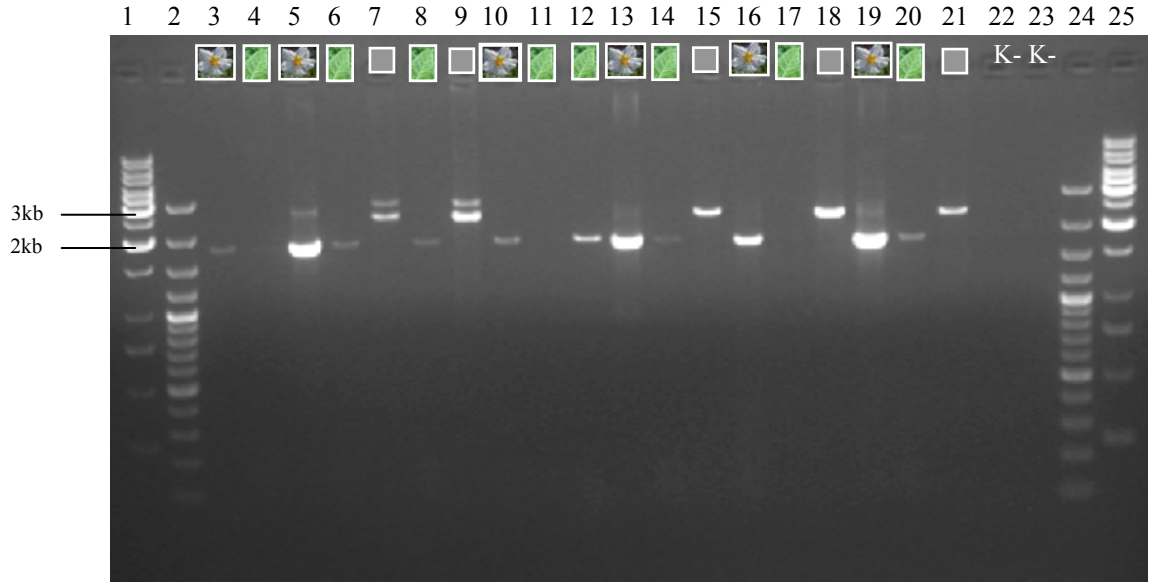


Figure 3.2.2: Full-length amplification of the gene *invGF* in different genotypes. As template cDNA from leaves and flowers, and genomic DNA from leaves were used. Full-length amplification was carried out using specific *invGF* primers (chapter 2, Table 2.1.2, invGF-F-fulgth/invGF-R-fulgth). A positive control was included using specific primers for the gene *pCD141* (chapter 2, Table 2.1.2, CD141fl_F/CD141fl_R) and cDNA from leaves to check cDNA integrity (lane 12). cDNA template from flowers, cDNA template from leaves, genomic DNA from leaves. Lane1: 1kb Fermentas ladder, lane 2: Fermentas ladder 100bp plus, lane 3: floral cDNA ‘Satina’, lane 4: leaf cDNA ‘Satina’, lane 5: floral cDNA ‘Diana’, lane 6: leaf cDNA ‘Diana’, lane 7: genomic DNA ‘Diana’, lane 8: leaf cDNA ‘Theresa’, lane 9: genomic DNA ‘Theresa’, lane 10: floral cDNA ‘Saturna’, lane 11: leaf cDNA ‘Saturna’, lane 12: leaf cDNA ‘Saturna’ with *pCD141* specic primers as positive control, lane 13: floral cDNA P18, lane 14: leaf cDNA P18, lane 15: genomic DNA P18, lane 16: floral cDNA P40, lane 17: leaf cDNA P40, lane 18: genomic DNA P40, lane 19: floral cDNA P54, lane 20: leaf cDNA P54; lane 21: genomic DNA P54, lane 22: negative control for leaf cDNA, lane 23: negative control for genomic DNA, lane 24: Fermentas ladder 100bp plus, lane 25: 1kb Fermentas ladder.

Both PCRs with short and full-length primers revealed genotype depending *invGF* expression. *invGF* transcripts were detected in leaves of the genotypes ‘Diana’, ‘Theresa’, P18, and P54. The gene specific expression in the genotypes ‘Diana’ and P54 were stronger compared to ‘Theresa’ and P18. The genotype ‘Satina’ showed a very weak *invGF* expression (Figure 3.2.2 lane 4), No *invGF* transcripts were detectable in ‘Désirée’ (Figure 3.2.1 lane 5), ‘Saturna’ (Figure 3.2.1 lane 3, Figure 3.2.2 lane 11), and P40 (Figure 3.2.1 lane 7, Figure 3.2.2 lane 17).

Cloning and sequencing of the entire RT-PCR products confirmed their identity to and, therefore, its origin from *invGF*.

❖ *invGE* and *invGF* cDNA alleles

Using full-length gene specific primers, cDNA invertase alleles of *invGE* and *invGF* were cloned and sequenced from the three tetraploid cultivars 'Satina', 'Diana', and 'Theresa' and from three diploid potato genotypes P18, P40, and P54.

All tetraploid genotypes harbour the associated SSCP fragments of the genes *invGE* and *invGF* (LI ET AL., 2005; Table 3.2.1) and, therefore, were chosen in this study. The diploid genotypes were included because they were parents of the QTL analysis for cold sweetening of potato tubers (MENÉNDEZ ET AL., 2002).

Table 3.2.1: Distribution of the associated SSCP fragments *invGE-6f* and *invGF-4d* present in the genotypes 'Satina', 'Diana', and 'Theresa'.

Genotype	*invGE-6f*	*invGF-4d*
'Satina'	1	1
'Diana'	1	1
'Theresa'	1	1

1=SSCP fragment is present.

Out of 80 cloned cDNA sequences per genotype, a sequence was defined as an allele when it was found twice in two independent PCRs[4]. The consensus sequence of all alleles found in one genotype was then used for allele definition when variable sequence polymorphisms occurred.

invGE and *invGF* invertase alleles obtained from each genotype are listed in Table 3.2.2.

Table 3.2.2: Overview of *invGE* and *invGF* alleles.

Genotype	Full-length *invGE* clones	*invGE* alleles	Full-length *invGF* clones	*invGF* alleles
'Satina'	10	*E_SA* *E_SN1* *E_SN2* *E_SN3*	14	*F_SN1* *F_SN2* *F_SN3* *F_SN4*
'Diana'	8	*E_DA* *E_DN1* *E_DN2*	4	*F_DN1* *F_DN2*
'Theresa'	19	*E_TA* *E_TN1* *E_TN2* *E_TN3*	4	*F_TN1* *F_TN2*
P18	9	*E_P18N1* *E_P18N2*	2	*F_P18N*
P40	8	*E_P40N1* *E_P40N2*	4	*F_P40N1* *F_P40N2*
P54	5	*E_P54N1* *E_P54N2*	10	*F_P54N1* *F_P54N2*

The 'A' in the allele name stands for 'association with better potato chips quality' and refers to clones containing SNP 1103* (Table 3.2.3), which leads to a histidine at protein position 368. The 'N' in the allele name means 'not associated' with tuber starch and sugar content. The full-length clone number refers to the number of fully sequenced clones from each genotype used for allele definition. PCR amplification was carried out using gene specific full-length primers: *invGE*-invGE-F-fulgth/invGE-R-fulgth (chapter 2, Table 2.1.2); *invGF*-invGF-F-fulgth/invGF-R-fulgth (chapter 2, Table 2.1.2).

From all six genotypes analyzed in this study, 17 *invGE* and 13 *invGF* alleles were identified.

[4] Exceptions are listed in Appendix A 3.2.

3.2.1.2.1 *invGE* cDNA alleles of the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'[5]

Cloning and sequencing of 'Satina' cDNA resulted in ten full-length clones, from which four *invGE* alleles *E_SA, E_SN1, E_SN2,* and *E_SN3* were defined. From the genotype 'Diana' eight full-length clones were obtained, and of those three different alleles *E_DA, E_DN1,* and *E_DN2* were identified. For the cultivar 'Theresa' 19 full-length clones were isolated and four alleles *E_TA, E_TN1, E_TN2,* and *E_TN3* were defined.

The nucleotide sequence comparison (Appendix A 3.2.13) of the alleles described above detected 125 SNPs, which resulted in 43 amino acid exchanges (Table 3.2.3; Figure 3.2.3).

Table 3.2.3: SNPs present in 'Satina', 'Diana', and 'Theresa' alleles

Position cDNA SNP	*E SA*	*E SN1*	*E SN2*	*E SN3*	*E DA*	*E DN1*	*E DN2*	*E TA*	*E TN1*	*E TN2*	*E TN3*	aa
58	T	C	C	T	T	C	C	T	T	C	C	T/C F20L
85	A	G	G	A	A	G	G	A	G	G	G	A/G K29G
86	A	G	G	A	A	G	G	A	G	G	G	s.
95	G	C	C	C	G	C	C	C	C	C	C	G/C G32A
106	G	A	A	A	G	A	A	A	A	A	A	s.
108	T	T	A	T	T	T	A	T	T	T	T	A/T V36I
133	G	G	G	G	G	G	G	G	G	G	C	C/G P45A
135	T	T	T	A	T	T	T	A	T	T	T	s.
162	T	T	T	T	T	T	T	T	G	T	T	s.
163	G	G	G	A	G	G	G	A	G	G	G	A/G S55G
187	C	C	C	T	C	C	C	T	T	T	C	T/C Y63H
204	T	T	T	T	T	T	T	T	A	T	T	s.
231	A	A	A	A	A	A	A	A	G	A	A	s.
276	T	C	C	C	T	C	C	C	C	C	T	s.
345	C	T	T	T	C	T	T	T	T	T	T	s.
351	C	T	T	T	C	T	T	T	T	T	T	s.
390	C	A	A	A	C	A	A	A	A	A	A	s.
402	T	A	A	T	T	A	A	T	T	A	A	s.
411	G	A	A	A	G	G	A	A	A	G	A	s.
414	T	C	C	T	T	C	C	T	T	C	T	s.
415	G	G	A	G	G	G	A	G	G	G	G	A/G I139V
420	T	C	C	C	T	C	C	C	C	C	C	s.
429	T	C	C	C	T	C	C	C	C	C	C	s.

[5] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: 'Satina' (Appendix A 3.2.1), 'Diana' (Appendix A 3.2.2), 'Theresa' (Appendix A 3.2.3). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *E_SA* (Appendix A 3.2.4), *E_SN1* (Appendix A 3.2.5), *E_SN3* (Appendix A 3.2.6), *E_DA* (Appendix A 3.2.7), *E_DN1* (Appendix A 3.2.8), *E_TA* (Appendix A 3.2.9), *E_TN1* (Appendix A 3.2.10), *E_TN2* (Appendix A 3.2.11), *E_TN3* (Appendix A 3.2.12). For the alleles *E_SN2* and *E_DN2* only one sequence was obtained, respectively. It has been shown that both alleles are real because allele specific SNPs were detected by pyrosequencing assay of cDNA and genomic DNA.

Position cDNA SNP	*E SA*	*E SN1*	*E SN2*	*E SN3*	*E DA*	*E DN1*	*E DN2*	*E TA*	*E TN1*	*E TN2*	*E TN3*	aa
444	T	C	C	C	T	C	C	C	C	C	C	s.
451	A	T	T	T	A	T	T	T	T	T	T	T/C T151S
456	A	A	A	G	A	A	A	G	G	A	A	s.
462	A	A	A	G	A	A	A	G	G	A	A	s.
465	C	T	T	T	C	T	T	T	T	T	T	s.
471	C	A	G	A	C	A	A	A	A	A	A	s.
477	A	G	G	G	A	G	G	G	A	G	G	s.
495	G	A	A	A	G	A	A	A	A	A	A	s.
511	G	A	A	A	G	A	A	A	A	A	A	G/A V171I
519	C	T	T	T	C	T	T	T	T	T	T	s.
531	G	G	A	G	G	G	A	G	G	G	G	s.
538	A	G	G	G	A	G	G	G	G	G	G	A/G I180V
540	T	T	A	A	T	A	A	A	T	A	T	s.
576	T	T	T	T	T	T	T	T	T	T	C	s.
588	T	A	A	T	T	A	A	T	T	A	A	s.
597	T	C	C	C	T	C	C	C	C	C	C	s.
598	G	C	C	C	G	C	C	C	C	C	C	s.
599	T	A	A	A	T	A	A	A	A	A	A	T/A V200Q
607	G	C	C	C	G	C	C	C	C	C	C	G/C V203L
615	G	A	A	A	G	A	A	A	A	A	A	s.
639	A	A	C	A	A	A	C	A	A	A	A	C/A N213K
645	A	A	A	A	A	A	A	A	T	A	A	T/A S215R
658	T	T	T	T	T	T	G	T	T	T	T	G/T V220L
688	G	G	A	G	G	G	A	G	G	G	G	A/G T230A/V
689	T	C	C	C	T	C	C	C	C	C	C	T/C V230A/T
702	C	T	T	T	C	T	T	T	T	T	T	s.
753	C	C	C	T	C	T	C	T	T	T	T	s.
768	T	A	A	A	T	A	A	A	A	A	A	T/A N256K
774	T	T	T	T	T	A	T	T	T	A	T	s.
780	T	C	C	C	T	C	C	C	C	C	C	s.
807	---	A	A	---	---	---	A	---	---	---	---	K269
808	---	A	A	---	---	---	A	---	---	---	---	K269
809	---	A	A	---	---	---	A	---	---	---	---	K269
810*	T	A	T	T	T	T	T	T	T	T	T	A/T K270N
817*	T	C	C	C	T	T	C	T	C	T	T	C/T H273Y
855*	T	G	T	G	T	G	G	T	T	G	G	T/G D285E
858*	C	T	T	T	C	T	T	C	T	T	T	s.
864*	T	T	T	T	T	T	A	T	T	T	T	s.
870*	C	T	T	T	C	T	T	C	T	T	T	s.
884*	G	A	A	A	G	A	A	G	A	A	A	G/A R295K

Position cDNA SNP	*E SA*	*E SN1*	*E SN2*	*E SN3*	*E DA*	*E DN1*	*E DN2*	*E TA*	*E TN1*	*E TN2*	*E TN3*	aa
909*	C	C	C	C	C	C	C	C	C	C	T	s.
924*	T	T	T	T	T	T	C	T	T	T	T	s.
926*	G	C	C	C	G	C	C	G	C	C	C	s.
927*	T	G	G	G	T	G	G	T	G	G	G	T/G C309S
945*	T	C	C	C	T	C	C	T	C	C	C	s.
975*	T	C	C	T	T	C	C	T	T	C	C	s.
981*	T	C	C	C	T	C	C	T	C	C	C	s.
983*	C	C	C	C	C	C	T	C	C	C	C	T/C L328P
986*	C	T	T	T	C	T	T	C	T	T	T	s.
987*	T	G	G	G	T	G	G	T	G	G	G	T/G T329M
1005*	G	A	A	A	G	A	A	G	A	A	A	s.
1010*	G	G	G	G	G	G	G	G	C	G	G	C/G A337G
1016*	C	C	C	C	C	C	C	C	T	C	C	T/C I340T
1017*	C	A	A	A	C	A	A	C	A	A	A	s.
1065*	T	T	T	A	T	T	T	T	A	T	T	s.
1068*	A	T	A	A	A	A	A	A	A	A	A	s.
1083*	G	G	G	A	G	G	G	G	A	G	G	s.
1086*	A	T	T	T	A	T	T	A	T	T	T	s.
1101*	T	C	C	C	T	C	C	T	C	C	C	s.
1103*	A	C	C	C	A	C	C	A	C	C	C	A/C H368P
1110*	T	T	T	C	T	T	T	T	T	T	T	s.
1117*	T	T	T	T	T	C	T	T	T	C	T	s.
1149*	C	C	A	A	C	A	A	C	A	A	A	s.
1152*	A	G	A	A	A	A	A	A	A	A	A	s.
1158*	A	G	G	G	A	G	G	A	G	G	G	s.
1167*	C	T	T	T	C	T	T	C	T	T	T	s.
1168*	---	---	A	---	---	A	A	---	---	A	---	I389
1169*	---	---	T	---	---	T	T	---	---	T	---	I389
1170*	---	---	T	---	---	T	T	---	---	T	---	I389
1179**	T	C	C	C	T	C	C	T	C	C	C	s.
1182**	C	C	C	C	C	C	C	C	C	C	G	G/C K394N
1191**	G	G	G	G	G	G	G	G	A	G	G	s.
1216**	A	A	A	G	A	A	A	A	G	A	A	G/A E406K
1237**	T	G	G	G	T	G	G	T	G	G	G	T/G S413A
1254**	A	G	G	G	A	G	G	A	G	G	G	s.
1257**	T	C	C	C	T	C	C	T	C	C	C	s.
1272**	G	G	A	G	G	G	A	G	G	G	G	s.
1276**	A	G	A	A	A	A	A	A	A	A	A	G/A E426K
1278**	A	G	G	G	A	G	G	A	G	G	G	s.
1281**	T	C	C	C	T	C	C	T	C	C	C	s.
1299**	T	A	A	A	T	A	A	T	A	A	A	T/A N433K
1305**	T	C	C	T	T	C	C	T	C	C	C	s.
1332**	C	C	C	C	C	C	T	C	C	C	C	s.
1335**	A	T	A	T	A	A	A	A	T	A	A	s.
1365**	A	G	A	A	A	A	G	A	A	A	A	s.

Position cDNA SNP	*E SA*	*E SN1*	*E SN2*	*E SN3*	*E DA*	*E DN1*	*E DN2*	*E TA*	*E TN1*	*E TN2*	*E TN3*	aa
1379**	C	C	T	C	C	T	C	C	C	T	T	T/C V460A
1380**	A	G	G	G	A	G	G	A	G	G	G	
1384**	T	T	T	G	T	T	T	T	T	T	T	G/T V462L
1395**	A	A	A	G	A	A	A	A	G	A	A	s.
1410**	T	C	C	C	T	C	C	T	C	C	C	s.
1413**	A	A	A	A	A	A	G	A	A	A	A	s.
1427**	G	G	G	G	G	G	G	G	G	G	A	A/G Q476R
1456**	G	A	G	G	G	G	G	G	G	G	G	A/G I486V
1476**	T	T	T	T	T	T	T	T	T	T	G	s.
1556**	T	T	C	T	T	C	C	T	T	C	T	C/T T519M
1617**	A	T	T	T	A	T	T	A	T	T	T	s.
1653**	A	G	G	G	A	G	G	A	G	G	G	s.
1659**	A	G	G	G	A	G	G	A	G	G	G	s.
1665**	T	T	T	T	T	C	C	T	T	T	C	s.
1666**	G	A	A	A	G	A	A	G	A	A	A	G/A D556N
1692**	T	C	T	T	T	T	T	T	T	T	T	s.
1723**	C	C	C	C	C	C	C	C	A	C	C	A/C I575L

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. * and **: SNP positions changed because of amino acid insertions, numbers refer to alignment nomenclature and not to the SNP positions of the cDNA for standardized comparison. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are coloured in orange.

The four 'Satina' alleles displayed a total of 95 SNPs, of which 30 caused an amino acid exchange. In the three allelic sequences of 'Diana' 87 SNPs occurred, from which 26 resulted in an amino acid exchange. The four 'Theresa' alleles differed in 70 SNPs. 22 of them led to an amino acid exchanges. The alleles *E_SN1*, *E_SN2*, and *E_DN2* contain the additional amino acid lysine (K) at position 259. An amino acid insertion also occurs at position 390* where the alleles *E_SN2*, *E*_DN1, *E_DN2*, and *E_TN2* contain an additional isoleucine (I).

The amino acid alignment shows the polymorphisms between all 11 *invGE* alleles from the three tetraploid potato cultivars. The comparison of these deduced protein sequences revealed 42 variable amino acid positions in the different genotypes, which are highlighted in colour (Figure 3.2.3).

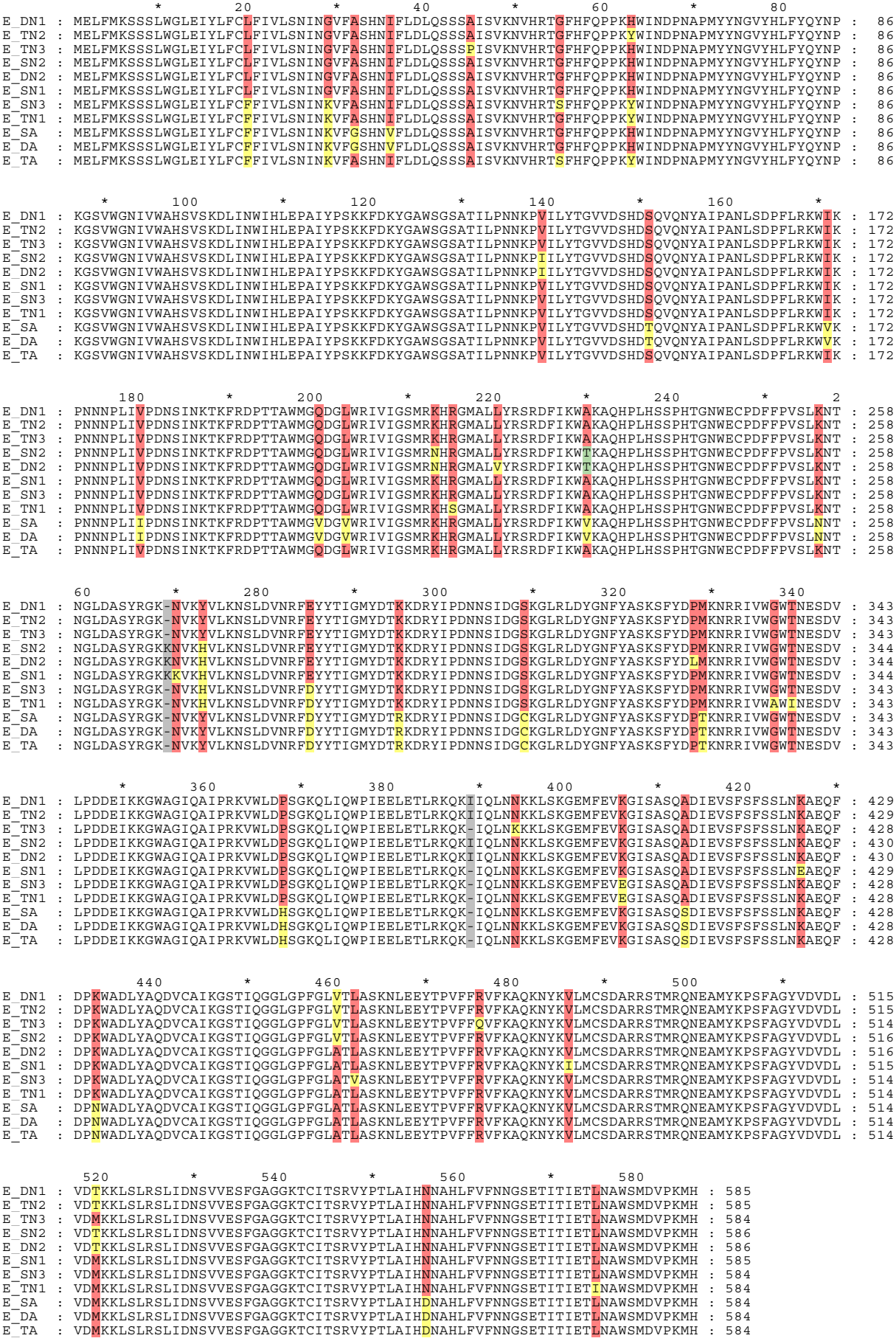

E_DN1 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_TN2 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNP : 86
E_TN3 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSPISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_SN2 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_DN2 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_SN1 : MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_SN3 : MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNP : 86
E_TN1 : MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNP : 86
E_SA : MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_DA : MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNP : 86
E_TA : MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNP : 86
E_DN1 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_TN2 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_TN3 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_SN2 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_DN2 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_SN1 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_SN3 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_TN1 : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_SA : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVK : 172
E_DA : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVK : 172
E_TA : KGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSATILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIK : 172
E_DN1 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_TN2 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_TN3 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_SN2 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_DN2 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALVYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_SN1 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_SN3 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_TN1 : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_SA : PNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNT : 258
E_DA : PNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNT : 258
E_TA : PNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNT : 258
E_DN1 : NGLDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 343
E_TN2 : NGLDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 343
E_TN3 : NGLDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 343
E_SN2 : NGLDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 344
E_DN2 : NGLDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDLMKNRRIVWGWTNESDV : 344
E_SN1 : NGLDASYRGKKKVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 344
E_SN3 : NGLDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDV : 343
E_TN1 : NGLDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDV : 343
E_SA : NGLDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDV : 343
E_DA : NGLDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDV : 343
E_TA : NGLDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDV : 343
E_DN1 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQF : 429
E_TN2 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQF : 429
E_TN3 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQK-IQLNKKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQF : 428
E_SN2 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQF : 430
E_DN2 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQF : 430
E_SN1 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNEAEQF : 429
E_SN3 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQF : 428
E_TN1 : LPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQF : 428
E_SA : LPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQF : 428
E_DA : LPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQF : 428
E_TA : LPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQK-IQLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQF : 428
E_DN1 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 515
E_TN2 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 515
E_TN3 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFQVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_SN2 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 516
E_DN2 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 516
E_SN1 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKILMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 515
E_SN3 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLATVASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_TN1 : DPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_SA : DPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_DA : DPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_TA : DPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDL : 514
E_DN1 : VDTKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 585
E_TN2 : VDTKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 585
E_TN3 : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 584
E_SN2 : VDTKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 586
E_DN2 : VDTKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 586
E_SN1 : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 585
E_SN3 : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH : 584
E_TN1 : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH : 584
E_SA : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH : 584
E_DA : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH : 584
E_TA : VDMKKLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH : 584

Figure 3.2.3: Amino acid alignment of 'Satina', 'Diana', and 'Theresa' *invGE* alleles. Amino acid exchanges are shown in colour. Additional amino acids are coloured in grey bars. At protein position 230 three different amino acids are displayed.

The amino acid alignment of *invGE* alleles of the tetraploid genotypes showed that 'Satina' and 'Diana' contain an allele identical at amino acid level (*E_SA=E_DA*).

3.2.1.2.2 *invGE* cDNA alleles of the diploid potato genotypes P18, P40, and P54[6]

From the genotype P18 nine full-length clones were obtained, and of those two alleles *E_P18N1* and *E_P18N2* were defined. Cloning and sequencing of P40 cDNA resulted in eight full-length clones, from which two different alleles *E_P40N1* and *E_P40N2* were identified. From the genotype P54 five full-length clones were isolated, and two alleles *E_P54N1* and *E_P54N2* were determined.

The alleles contain at nucleotide level (Appendix A 3.2.23) 48 SNPs. These sequence polymorphisms caused 23 amino acid exchanges (Table 3.2.4; Figure 3.2.4).

Table 3.2.4: SNPs present in P18, P40, and P54 alleles.

Position cDNA SNP	*E_P18N1*	*E_P18N2*	*E_P40N1*	*E_P40N2*	*E_P54N1*	*E_P54N2*	aa
58	C	C	C	T	C	T	T/C F20L
83	A	A	A	A	A	T	T/A I28N
85	G	G	G	A	G	A	A/G K29G
86	G	G	G	A	G	A	A/G K29G
108	A	T	A	T	T	T	s.
187	C	T	C	C	C	A	T/A/C Y63N/H
255	T	T	T	C	T	T	s.
402	A	A	A	T	A	T	s.
411	A	G	A	A	G	A	s.
414	C	C	C	T	C	T	s.
415	A	G	A	G	G	G	A/G I139V
426	C	C	C	T	C	C	s.
456	A	A	A	G	A	G	s.
462	A	A	A	G	A	G	s.
531	A	G	A	G	G	G	s.
540	A	A	A	T	A	T	s.
565	A	A	A	G	A	G	G/A E189K
619	G	G	G	A	G	G	A/G I207V
639	C	A	C	A	A	A	C/A N213K

[6] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: P18 (Appendix A 3.2.14), P40 (Appendix A 3.2.15), P54 (Appendix A 3.2.16). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *E_P18N1* (Appendix A 3.2.17), *E_P18N2* (Appendix A 3.2.18), *E_P40N1* (Appendix A 3.2.19), *E_P40N2* (Appendix A 3.2.20), *E_P54N1* (Appendix A 3.2.21), *E_P54N2* (Appendix A 3.2.22).

Position cDNA SNP	*E_P18N1*	*E_P18N2*	*E_P40N1*	*E_P40N2*	*E_P54N1*	*E_P54N2*	aa
645	A	A	A	A	A	G	s.
688	A	G	A	G	G	G	A/G T230A
753	C	T	C	T	T	C	s.
774	T	A	T	T	A	T	s.
807	A	---	A	---	---	---	K259
808	A	---	A	---	---	---	K259
809	A	---	A	---	---	---	K259
817*	C	T	C	C	T	C	T/C Y273H
855*	G	G	G	T	G	T	T/G D285E
975*	C	C	C	T	C	T	s.
1031*	T	T	T	T	T	G	G/T G344V
1101*	C	C	C	T	C	C	s.
1117*	T	C	T	T	C	T	s.
1168*	A	A	A	---	A	---	I389
1169*	T	T	T	---	T	---	I389
1170*	T	T	T	---	T	---	I389
1216**	A	A	A	G	A	G	G/A E406K
1272**	A	G	A	G	G	G	s.
1335**	A	A	A	T	A	T	s.
1379**	T	T	T	C	T	C	C/T A460V
1395**	A	A	A	G	A	G	s.
1462**	A	A	A	C	A	A	s.
1464**	G	G	G	A	G	G	A/G L488M
1471**	G	G	G	G	G	A	A/G N491D
1556**	C	C	C	T	C	T	T/C M519T
1616**	G	G	G	A	G	G	A/G D539G
1652**	C	C	C	C	C	T	T/C M551T
1665**	T	T	T	T	C	T	s.
1712**	C	C	C	T	C	C	T/C I561T

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. * and **: SNP positions changed because of amino acid insertions, numbers refer to alignment nomenclature and not to the SNP positions of the cDNA for standardized comparison. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are coloured in orange.

In the two allelic sequences of P18 12 SNPs occurred, from which five resulted in an amino acid exchange. The two P40 alleles differed in 30 SNPs. 14 of them led to changes in the protein sequence. From 26 SNPs of the two P54 alleles, 13 caused an amino acid substitution. The alleles *E_P18N1* and *E_P40N1* contain the additional amino acid lysine (K) at position 259. An amino acid insertion also occurs at position 390*, where the alleles *E_P18N1*, *E_P18N2, E_P40N1*, and *E_P54N1* contain an additional isoleucine (I).

The amino acid alignment displays the differences of the six cloned *invGE* alleles from the three diploid potato genotypes (Figure 3.2.4). The comparison of the protein sequences revealed 22 variable amino acid positions.

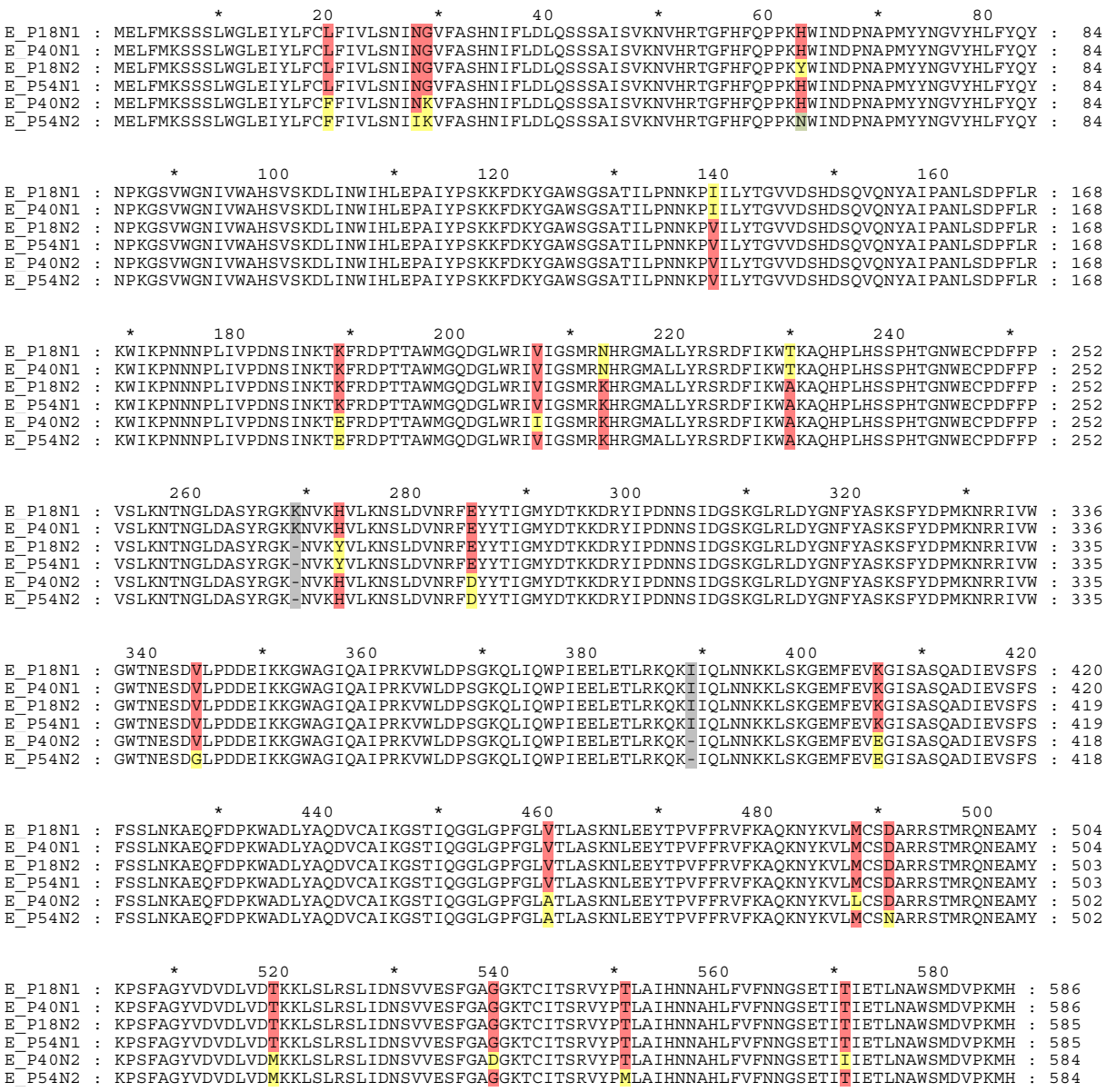
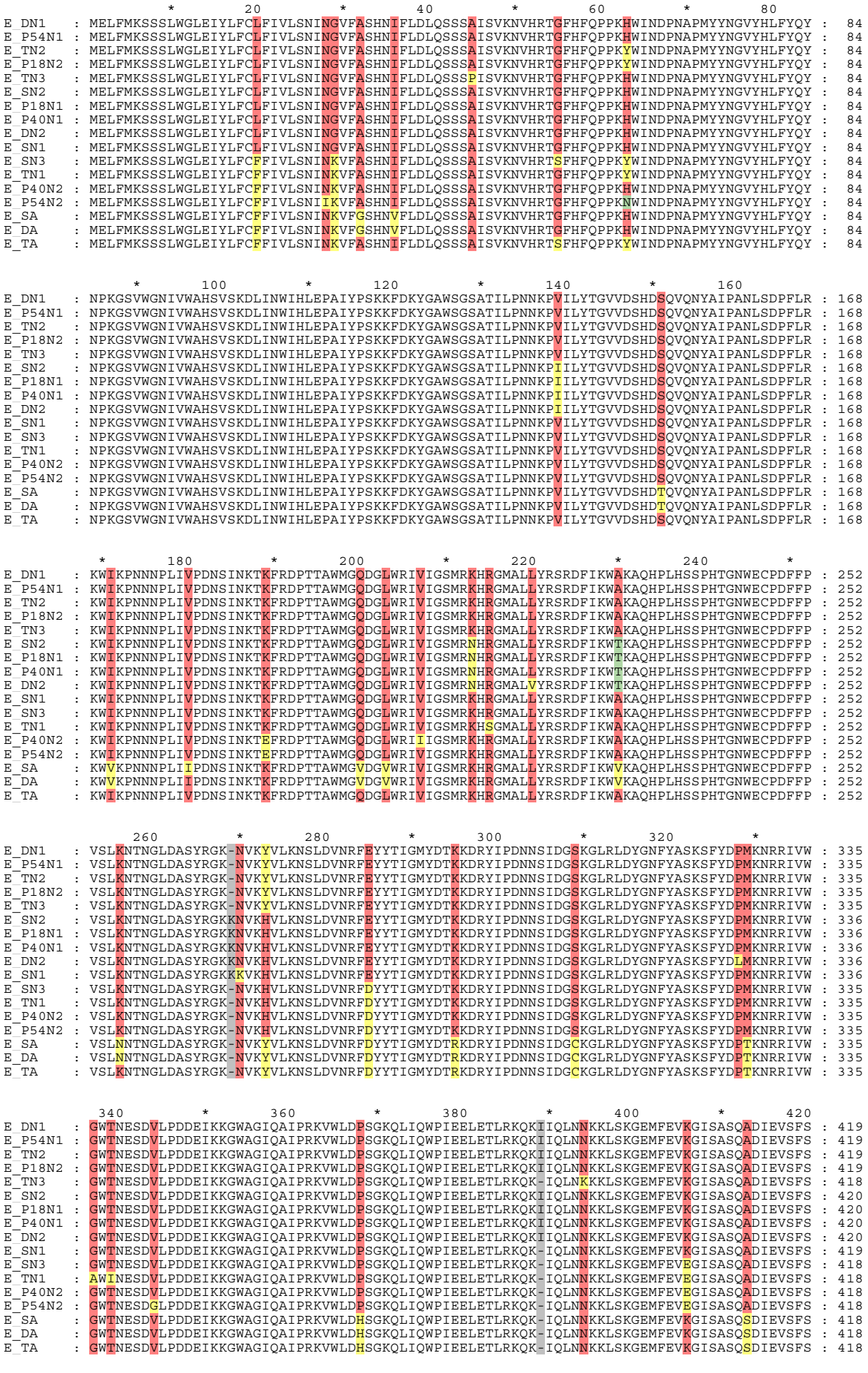


Figure 3.2.4: Amino acid alignment of P18, P40, and P54 *invGE* alleles. Amino acid exchanges are shown in colour. Additional amino acids are coloured in grey bars. At protein position 63 three different amino acids are displayed.

3.2.1.2.3 Amino acid alignment of all *invGE* invertase alleles of the analyzed potato genotypes

Multiple alignment of allelic *invGE* protein sequences revealed 53 variable amino acid polymorphisms between six genotypes (Figure 3.2.5). 21 amino acid exchanges were found to be genotype specific occurring only once.



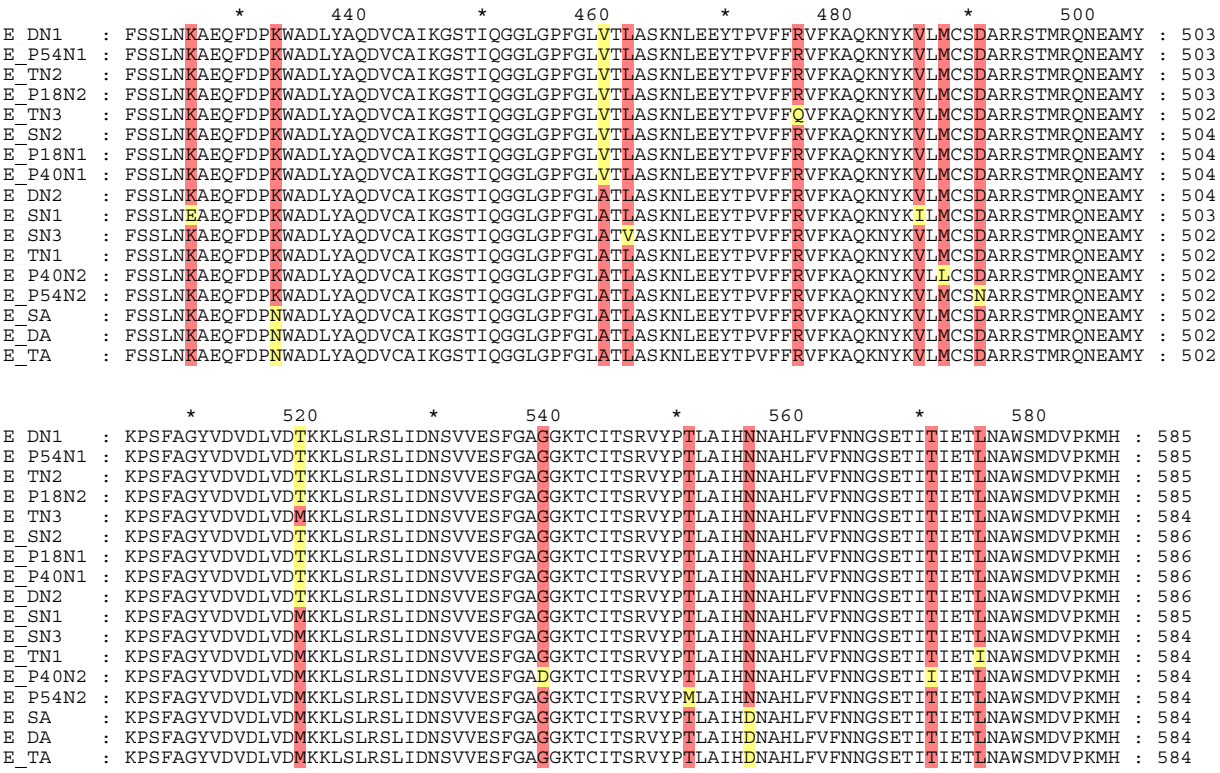


Figure 3.2.5: Amino acid alignment of all cloned *invGE* alleles of all genotypes. Amino acid exchanges are shown in colour. Additional amino acids are coloured in grey bars. At protein positions 63 and 230 three different amino acids are displayed.

Comparison of allelic cDNA sequences of the *invGE* gene from the three tetraploid and the three diploid genotypes revealed that different genotypes harbour amino acid sequence identical alleles. The alleles *E_SN2*, *E_P18N1,* and *E_P40N1*, the alleles *E_DN1* and *E_P54N1,* and the alleles *E_TN2* and *E_P18N2* have the same amino acid sequences.

3.2.1.2.4 Phenetic trees of all *invGE* invertase alleles of the analyzed potato genotypes

In addition to the multiple amino acid alignment (3.2.1.2.3), the phenetic tree analysis was applied to group the invertase alleles according to their similarity at amino acid as well as at nucleotide level. Using the neighbour-joining method, the allelic classification visualized that *invGE* alleles from all six genotypes group in two clades and multiple subclades (Figure 3.2.6, Figure 3.2.7).

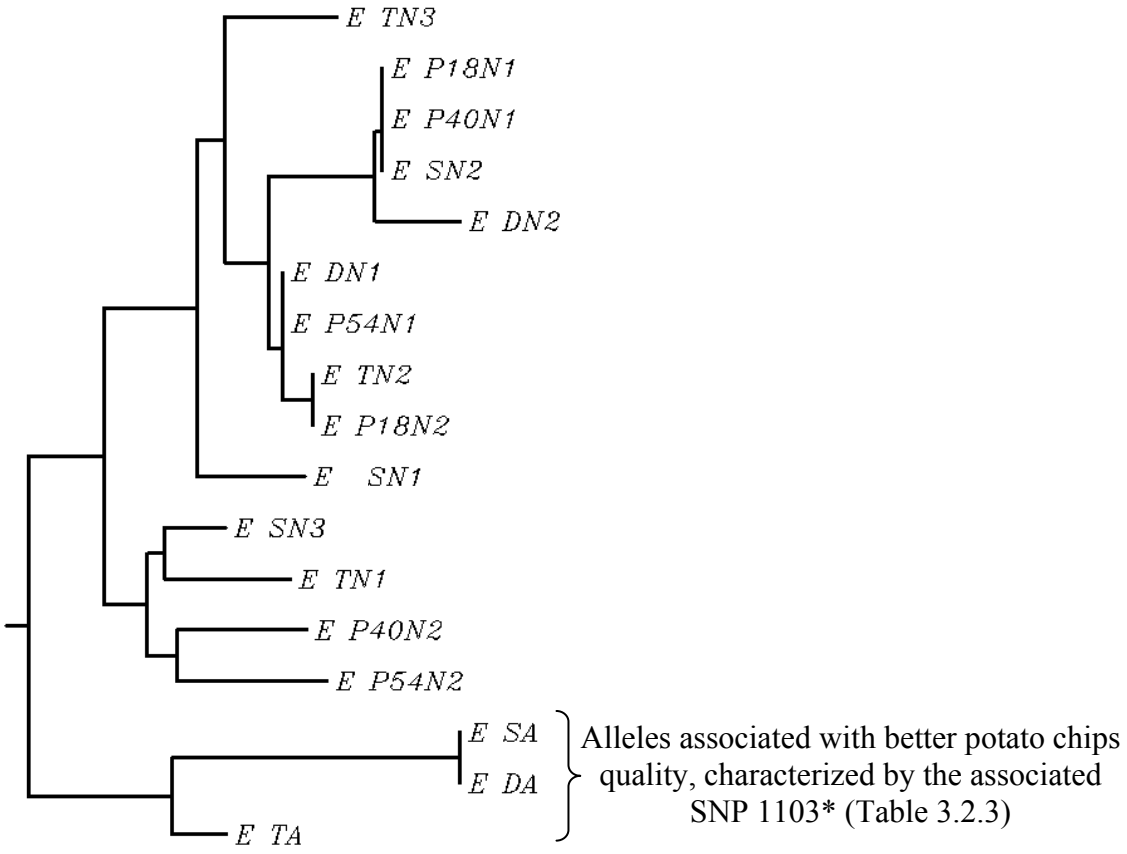


Figure 3.2.6: Amino acid based phenetic tree (Neighbour-joining method) of all cloned *invGE* invertase alleles.

The amino acid based phenetic tree has two clades. One clade contains most of the *invGE* alleles, and the other one the alleles *E_SA*, *E_DA*, and *E_TA,* which were found to be associated with superior potato chips quality.

The first clade then splits into diverse subclades due to the high number of amino acid polymorphisms between the different genotypes, although different genotypes contain amino acid sequence identical alleles. The alleles *E_SN2*, *E_P18N1,* and *E_P40N1*, the alleles *E_DN1* and *E_P54N1,* and the alleles *E_TN2* and *E_P18N2* have the same amino acid sequences.

The second clade consists of the alleles *E_SA*, *E_DA*, and *E_TA.* The two alleles *E_SA* and *E_DA* are identical at amino acid level, whilst *E_TA* differs in its amino acid sequence compared to the other two. However, all three alleles are characterized by the nucleotide adenine at cDNA SNP 1103* (Table 3.2.3), which is associated with better potato chips quality.

Cloning and sequencing of *invGE* alleles showed that different genotypes contain alleles identical at amino acid level but different regarding their nucleotide sequence. The allelic nucleotide composition was defined based on the consensus sequence of multiple alignments

of full-length clones obtained from each genotype (Table 3.2.2). Although SNPs are present at the mentioned cDNA positions, the nucleotide polymorphisms resulted in one and the same amino acid sequence.

Nucleotide comparison (Appendix A 3.2.24) showed that the associated alleles *E_SA* and *E_DA* consist of an identical nucleotide sequence as well as the alleles *E_TN2* and *E_P18N2*. The nucleotide sequences of the alleles and *E_P18N1* and *E_P40N1* are also identical, whilst the sequence of *E_SN2* differs at position 471. At position 471 a synonymous nucleotide exchange from A in the alleles *E_P18N1* and *E_P40N1* to G in allele *E_SN2* arose. Also one synonymous nucleotide variation was detected between the alleles *E_DN1* and *E_P54N1*. Allele *E_DN1* contains nucleotide A and allele *E_P54N1* consists of nucleotide G at position 1408**. Allele specific SNPs were detected in at least two sequences and used for comparing the allelic nucleotide polymorphisms.

The phenetic tree analysis showed the nucleotide polymorphisms between all alleles of the six different genotypes (Figure 3.2.7).

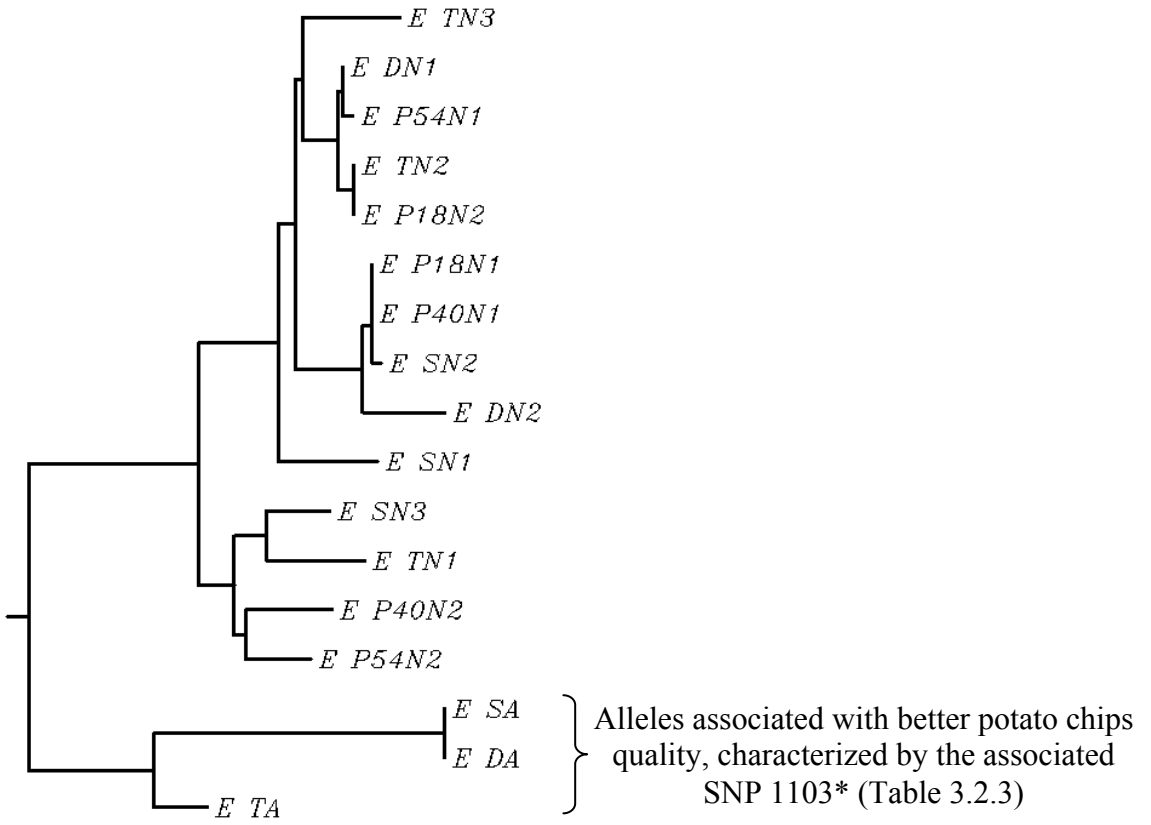


Figure 3.2.7: Nucleotide sequence based phenetic tree (Neighbour-joining tree) of all cloned *invGE* invertase alleles.

Although being very similar, the nucleotide based tree is characterized by an extended number of subclades due to a higher number of nucleotide polymorphisms in contrast to the amino acid based phenetic tree (Figure 3.2.6).

3.2.1.2.5 *invGF* cDNA alleles of the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'[7]

From the genotype 'Satina' 14 full-length clones were obtained, and of those four different alleles *F_SN1*, *F_SN2*, *F_SN3*, and *F_SN4* were identified. For 'Diana' four full-length clones were isolated, and two alleles *F_DN1* and *F_DN2* were determined. Cloning and sequencing of 'Theresa' cDNA resulted in four full-length clones, from which two *invGF* alleles *F_TN1* and *F_TN2* were defined.

The nucleotide comparison (Appendix A 3.2.35) of the alleles described above detected 86 SNPs, of which 19 were non synonymous and caused amino acid exchanges (Table 3.2.5; Figure 3.2.8).

Table 3.2.5: SNPs present in 'Satina', 'Diana', and 'Theresa' alleles.

Position cDNA SNP	*F_SN1*	*F_SN2*	*F_SN3*	*F_SN4*	*F_DN1*	*F_DN2*	*F_TN1*	*F_TN2*	aa
28	G	G	G	G	A	G	G	G	A/G T10A
58	A	A	A	G	A	A	G	A	G/A V20I
96	C	C	C	T	T	C	T	C	s.
111	T	C	C	C	C	C	C	C	s.
117	G	A	A	A	A	A	A	A	s.
141	A	C	A	C	C	A	C	A	A/C Q47H
162	C	C	C	T	T	C	T	C	s.
223	G	A	G	G	G	G	G	G	A/G I75V
225	C	T	T	C	C	C	C	C	s.
228	C	C	C	T	T	T	T	T	s.
249	C	C	C	C	C	T	C	T	s.
255	T	C	C	C	C	C	C	C	s.
273	T	C	T	C	C	T	C	T	s.
279	T	T	T	T	T	G	T	G	s.
345	C	T	T	T	T	C	T	C	s.
351	C	A	A	A	A	A	A	A	s.
363	C	C	C	T	T	C	T	C	s.
369	G	G	G	A	A	G	A	G	s.
378	A	A	G	A	A	A	A	A	s.

[7] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: 'Satina' (Appendix A 3.2.25), 'Diana' (Appendix A 3.2.26), 'Theresa' (Appendix A 3.2.27). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *F_SN1* (Appendix A 3.2.28), *F_SN2* (Appendix A 3.2.29), *F_SN3* (Appendix A 3.2.30), *F_SN4* (Appendix A 3.2.31), *F_DN2* (Appendix A 3.2.32), *F_TN1* (Appendix A 3.2.33), *F_TN2* (Appendix A 3.2.34). For the allele *F_DN1* two nucleotide sequences were obtained, from which one showed an alternative stop codon leading to no termination of the sequence. Therefore, the nucleotide alignment of both sequences is not shown. *F_DN1* specific SNPs were shown to be real by pyrosequencing analysis of cDNA and genomic DNA.

Position cDNA SNP	*F_SN1*	*F_SN2*	*F_SN3*	*F_SN4*	*F_DN1*	*F_DN2*	*F_TN1*	*F_TN2*	aa
381	T	T	T	A	A	T	A	T	s.
405	G	G	G	A	A	G	A	G	s.
429	A	A	A	A	A	T	A	A	s.
432	A	A	A	G	G	A	G	A	s.
438	C	C	C	T	T	C	T	C	s.
459	C	T	C	C	C	C	C	C	s.
466	A	A	A	G	G	A	G	G	A/G I156V
478	T	G	G	A	A	T	A	T	T/G/A L160V/I
489	A	T	T	T	T	A	T	A	s.
491	T	T	T	T	T	T	T	C	C/T H164Y
495	C	C	C	A	A	T	A	T	s.
519	C	C	T	C	C	C	C	T	s.
542	C	A	A	C	C	C	C	C	A/C D181A
546	C	T	T	C	C	T	C	T	s.
555	G	A	G	G	G	G	G	G	s.
579	C	T	T	C	C	C	C	C	s.
582	A	A	A	T	T	A	T	A	s.
630	G	A	A	A	G	A	A	A	s.
651	T	A	A	T	T	T	T	T	s.
663	A	A	A	A	A	A	A	G	s.
672	T	T	T	C	C	T	C	T	s.
675	C	C	T	C	C	C	C	C	s.
717	T	T	T	C	C	T	C	C	s.
729	C	T	T	T	T	T	T	T	s.
750	C	T	T	C	C	C	C	C	s.
753	T	T	T	C	C	T	C	T	s.
778	A	A	A	C	C	A	C	A	s.
779	T	T	T	A	A	T	A	T	T/A I260Q
799	T	T	T	C	C	T	C	T	s.
801	T	T	T	C	C	T	C	T	C/T H267Y
805	T	T	T	T	T	T	T	A	A/T N269Y
820	A	A	A	A	A	A	A	G	G/A G274S
864	C	T	C	C	C	C	C	C	s.
876	G	A	A	A	A	A	A	A	s.
885	T	T	T	C	C	T	C	C	s.
886	G	G	G	A	A	G	A	G	A/G I296V
888	T	T	T	A	A	T	A	A	s.
903	T	T	C	T	T	T	T	T	s.
933	T	T	T	C	C	T	C	T	s.
958	A	A	A	T	T	A	T	A	T/A S320T
970	A	A	A	C	C	A	C	A	C/A P324T
981	C	C	C	T	T	C	T	C	s.
1029	G	A	A	G	G	G	G	G	s.
1038	T	T	T	C	C	T	C	T	s.
1041	G	G	G	T	T	G	T	G	s.
1047	A	A	A	A	A	A	A	G	s.

Position cDNA SNP	*F_SN1*	*F_SN2*	*F_SN3*	*F_SN4*	*F_DN1*	*F_DN2*	*F_TN1*	*F_TN2*	aa
1089	C	C	C	T	T	T	T	C	s.
1108	G	G	G	A	A	A	A	A	G/A V370I
1113	G	G	A	A	A	A	A	A	s.
1164	T	T	T	C	C	T	C	T	s.
1170	A	A	A	G	G	A	G	G	s.
1173	A	A	A	G	G	G	G	G	s.
1206	A	A	A	G	G	A	G	G	s.
1263	A	A	A	G	G	A	G	G	s.
1271	C	C	C	C	C	C	C	T	T/C L424S
1279	T	T	T	C	C	C	C	T	T/C S427P
1320	C	C	C	C	C	T	C	C	s.
1323	G	G	G	A	A	G	A	G	s.
1335	A	A	A	T	T	T	T	A	s.
1452	T	T	T	C	C	T	C	C	s.
1458	C	C	C	T	T	C	T	C	s.
1536	A	A	A	A	A	T	A	A	s.
1623	G	G	G	G	G	A	G	G	s.
1636	T	T	T	T	T	C	T	T	s.
1638	G	G	G	G	G	G	G	A	s.
1650	G	G	G	C	C	C	C	G	G/C E550D
1745	G	G	G	G	G	G	G	A	s.

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are coloured in orange.

The four 'Satina' alleles differed in 70 SNPs, 14 of those led to amino acid exchanges. In the two allelic sequences of 'Diana' 47 SNPs were found, from which nine resulted in an amino acid substitution. The two alleles of 'Theresa' had a total of 47 SNPs, and 14 of those resulted in an amino acid difference.

The amino acid alignment shows the polymorphisms of all eight *invGF* alleles from the three tetraploid potato cultivars. The comparison of deduced protein sequences revealed 19 variable amino acid positions in the different genotypes displayed in coloured columns (Figure 3.2.8).

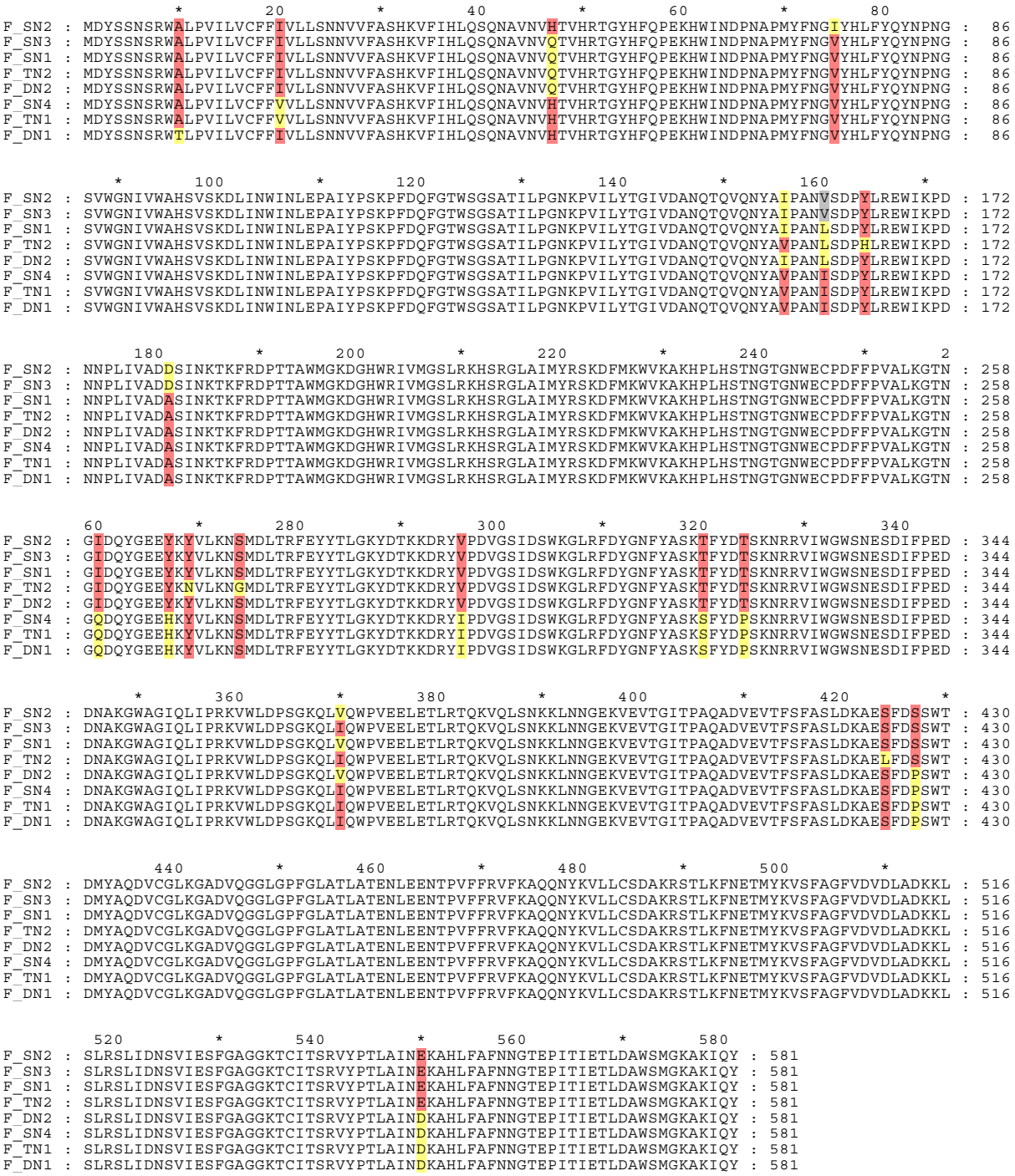


Figure 3.2.8: Amino acid alignment of 'Satina', 'Diana', and 'Theresa' *invGF* alleles. Amino acid exchanges are highlighted in colour. At protein position 160 three different amino acids are displayed.

Comparison of allelic cDNA sequences of the gene *invGF* from the three tetraploid cultivars revealed that the 'Satina' allele *F_SN4* and the 'Theresa' allele *F_TN1* are identical at amino acid level.

3.2.1.2.6 *invGF* cDNA alleles of the diploid potato genotypes P18, P40, and P54[8]

From P18 two full-length clones were isolated, and one allele *F_P18N* was determined. 20 partial sequenced P18 clones showed identical sequences to *F_P18N* but exhibited frame shifts or other modifications and, therefore, were not completely sequenced. From the genotype P40 four full-length clones were obtained, and of those two different alleles *F_P40N1* and *F_P40N2* were identified. Cloning and sequencing of P54 cDNA resulted in ten full-length clones, from which two *invGF* alleles *F_P54N1* and *F_P54N2* were defined.

31 SNPs for all alleles of the diploid genotypes were detected by nucleotide sequence comparison (Appendix A 3.2.43). Six of the identified polymorphisms caused an amino acid exchange (Table 3.2.6; Figure 3.2.9).

Table 3.2.6: SNPs present in P18, P40, and P54 alleles.

Position cDNA SNP	*F_P18N*	*F_P40N1*	*F_P40N2*	*F_P54N1*	*F_P54N2*	aa
111	T	T	C	T	T	s.
223	G	G	A	G	G	s.
225	C	C	T	C	C	T/C I75V
255	T	T	C	T	T	s.
351	C	C	A	C	C	s.
363	C	C	T	C	C	s.
542	C	C	A	C	C	A/C D181A
546	C	C	T	C	C	s.
579	C	C	T	C	C	s.
630	G	G	A	G	G	s.
651	T	T	A	T	T	s.
717	T	T	C	T	T	s.
729	C	C	T	C	C	s.
750	C	C	T	C	C	s.
791	G	G	A	G	G	A/G D264G
942	T	T	C	T	T	s.
1089	T	T	C	T	T	s.
1090	C	C	G	C	C	G/C A364P
1206	A	A	G	A	A	s.
1224	A	G	A	A	G	s.
1238	C	T	C	C	T	T/C I413T
1242	T	T	C	T	T	s.
1263	G	A	A	G	A	s.
1320	C	T	C	C	T	s.
1386	G	A	A	G	A	s.
1446	T	C	C	T	C	s.
1452	C	C	T	C	C	s.
1534	G	G	A	G	G	s.
1536	T	T	A	T	T	A/T T512A
1668	G	A	G	G	A	s.
1677	T	C	C	T	C	s.

[8] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: P18 (Appendix A 3.2.36), P40 (Appendix A 3.2.37), P54 (Appendix A 3.2.38). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *F_P18N* (Appendix A 3.2.39), *F_P40N2* (Appendix A 3.2.40), *F_P54N1* (Appendix A 3.2.41), *F_P54N2* (Appendix A 3.2.42).

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are coloured in orange.

In the two allelic sequences of P40 27 SNPs occurred, six of those resulted in an amino acid exchange. The two P54 alleles differed in eight SNPs, and of those one led to an exchange in the amino acid sequence.

The amino acid alignment of the five *invGF* alleles from the three diploid potato genotypes showed the variability of six positions where amino acids differed (Figure 3.2.9).

```
                 *        20         *        40         *        60         *        80
F_P40N1 : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P54N2 : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P18N  : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P54N1 : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P40N2 : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNP :  84

              *       100         *       120         *       140         *       160
F_P40N1 : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P54N2 : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P18N  : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P54N1 : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P40N2 : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168

            *       180         *       200         *       220         *       240         *
F_P40N1 : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P54N2 : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P18N  : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P54N1 : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P40N2 : IKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252

               260         *       280         *       300         *       320         *
F_P40N1 : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P54N2 : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P18N  : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P54N1 : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P40N2 : ALKGTNGIDQYDEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336

             340         *       360         *       380         *       400         *       420
F_P40N1 : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVIFSFASLD : 420
F_P54N2 : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVIFSFASLD : 420
F_P18N  : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_P54N1 : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_P40N2 : ESDIFPEDDNAKGWAGIQLIPRKVWLDASGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420

                 *       440         *       460         *       480         *       500
F_P40N1 : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P54N2 : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P18N  : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P54N1 : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P40N2 : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504

              *       520         *       540         *       560         *       580
F_P40N1 : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P54N2 : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P18N  : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P54N1 : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P40N2 : GFVDVDLTDKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
```

Figure 3.2.9: Amino acid alignment of P18, P40, and P54 *invGF* alleles. Amino acid exchanges are highlighted in colour.

Comparison of allelic cDNA sequences of the gene *invGF* from the three diploid genotypes revealed that the alleles *F_P18N* and *F_P54N1,* and the alleles *F_P40N1* and *F_P54N2* are identical at amino acid level.

3.2.1.2.7 Amino acid alignment of all *invGF* invertase alleles of the analyzed potato genotypes

The variability of amino acid positions, which exhibit exchanges was visualized by multiple sequence alignment of *invGF* invertase alleles (Figure 3.2.10). Several amino acid exchanges occur in different genotypes at the same position.

```
                 *        20         *        40         *        60         *        80
F_SN2    : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNP :  84
F_P40N2  : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNP :  84
F_SN3    : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P40N1  : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P54N2  : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P54N1  : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_P18N   : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_SN1    : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_TN2    : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_DN2    : MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_SN4    : MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_TN1    : MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84
F_DN1    : MDYSSNSRWTLPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNP :  84

                    *       100         *       120         *       140         *       160
F_SN2    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREW : 168
F_P40N2  : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_SN3    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREW : 168
F_P40N1  : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P54N2  : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P54N1  : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_P18N   : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_SN1    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_TN2    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAVPANLSDPHLREW : 168
F_DN2    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREW : 168
F_SN4    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREW : 168
F_TN1    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREW : 168
F_DN1    : NGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATILPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREW : 168

                  *       180         *       200         *       220         *       240         *
F_SN2    : IKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P40N2  : IKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_SN3    : IKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P40N1  : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P54N2  : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P54N1  : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_P18N   : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_SN1    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_TN2    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_DN2    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_SN4    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_TN1    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252
F_DN1    : IKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPV : 252

                 260         *       280         *       300         *       320         *
F_SN2    : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P40N2  : ALKGTNGIDQYDEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_SN3    : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P40N1  : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P54N2  : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P54N1  : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_P18N   : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_SN1    : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_TN2    : ALKGTNGIDQYGEEYKNVLKNGMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_DN2    : ALKGTNGIDQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSN : 336
F_SN4    : ALKGTNGQDQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSN : 336
F_TN1    : ALKGTNGQDQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSN : 336
F_DN1    : ALKGTNGQDQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSN : 336

                340         *       360         *       380         *       400         *       420
F_SN2    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_P40N2  : ESDIFPEDDNAKGWAGIQLIPRKVWLDASGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_SN3    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_P40N1  : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVIFSFASLD : 420
F_P54N2  : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVIFSFASLD : 420
F_P54N1  : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_P18N   : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_SN1    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_TN2    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_DN2    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_SN4    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_TN1    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
F_DN1    : ESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNKKLNNGEKVEVTGITPAQADVEVTFSFASLD : 420
```

```
                  *       440         *       460         *       480         *       500
F_SN2    : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P40N2  : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_SN3    : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P40N1  : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P54N2  : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P54N1  : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_P18N   : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_SN1    : KAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_TN2    : KAELFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_DN2    : KAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_SN4    : KAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_TN1    : KAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504
F_DN1    : KAEQFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFA : 504

                *       520         *       540         *       560         *       580
F_SN2    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P40N2  : GFVDVDLTDKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_SN3    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P40N1  : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P54N2  : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P54N1  : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_P18N   : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_SN1    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_TN2    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_DN2    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_SN4    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_TN1    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
F_DN1    : GFVDVDLADKKLSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY : 581
```

Figure 3.2.10: Amino acid alignment of all cloned *invGF* invertase alleles. Amino acid exchanges are highlighted in colour. At protein position 160 three different amino acids are displayed.

Protein sequence comparison of the deduced *invGF* alleles from all analyzed genotypes showed that amino acids differed at 23 positions, of which eight were genotype specific and occurred only once.

3.2.1.2.8 Phenetic trees of all *invGF* invertase alleles of the analyzed potato genotypes

The further characterization of *invGF* alleles included, besides multiple amino acid alignment (section 3.2.1.2.7), a phenetic tree analysis in order to group the invertase alleles according to their similarity at amino acid as well as at nucleotide level. The neighbour-joining method was used for allelic classification and showed that *invGF* alleles from all analyzed potato genotypes group in different clades and subclades (Figure 3.2.11, Figure 3.2.12).

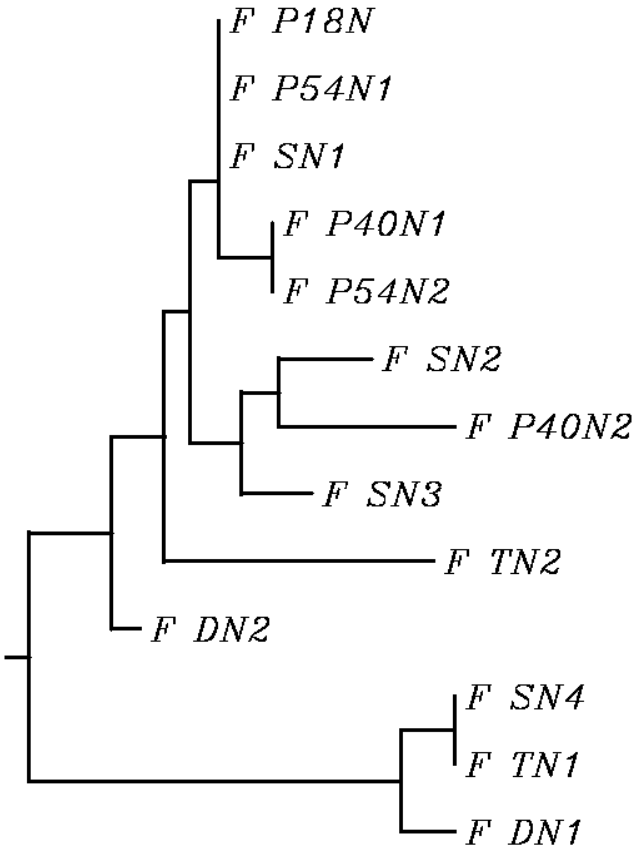


Figure 3.2.11: Amino acid based phenetic tree (Neighbour-joining method) of all cloned *invGF* invertase alleles.

The amino acid based phenetic tree splits into two main clades, from which the first one contains most of the *invGF* alleles. It is build of quite diverse subclades due to the high number of amino acid polymorphisms between the different genotypes. Amino acid comparison revealed sequence identical alleles in different genotypes. The alleles *F_SN1*, *F_P18N,* and *F_P54N1*, and the alleles *F_P40N1* and *F_P54N2* show the same amino acid sequence.

The second clade consists of the alleles *F_SN4*, *F_DN1*, and *F_TN1*. The two alleles *F_SN4* and *F_TN1* are identical at amino acid level, whilst *F_DN1* differs in its amino acid sequence.

Cloning and sequencing of *invGF* alleles showed that different genotypes contain alleles identical at amino acid level but different at nucleic acid level (Appendix A 3.2.44). Table 3.2.7 shows a nucleotide comparison of amino acid identical alleles of different genotypes. The allelic nucleotide sequence was defined based on the consensus sequence of multiple alignments of full-length clones obtained from each genotype (Table 3.2.2). Although SNPs are present at the mentioned cDNA positions the nucleotide polymorphisms resulted in one and the same amino acid sequence.

Table 3.2.7: Genotype specific nucleotide differences of alleles *F_SN1*, *F_P18N,* and *F_P54N1*.

Position of cDNA SNP	*F_SN1*	*F_P18N*	*F_P54N1*
117	G	A	A
876	G	A	A
1089	C	T	T
1113	G	A	A
1173	A	G	G
1242	C	T	T
1263	A	G	G
1386	A	G	G
1446	C	T	T
1452	T	C	C
1536	A	T	T
1677	C	T	T

Nucleotide sequence comparison showed that the alleles *F_P40N1* and *F_P54N2,* and the alleles *F_SN4* and *F_TN1* were identical.The nucleotide sequences of the alleles *F_P18N* and *F_P54N1* were also identical, whilst the sequence of *F_SN1* differed in 12 positions. Allele specific SNPs were detected in at least two sequences and used for comparing the allelic nucleotide polymorphisms.

The nucleotide polymorphisms between all *invGF* alleles of the six analyzed genotypes were visualized using the phenetic tree analysis (Figure 3.2.12).

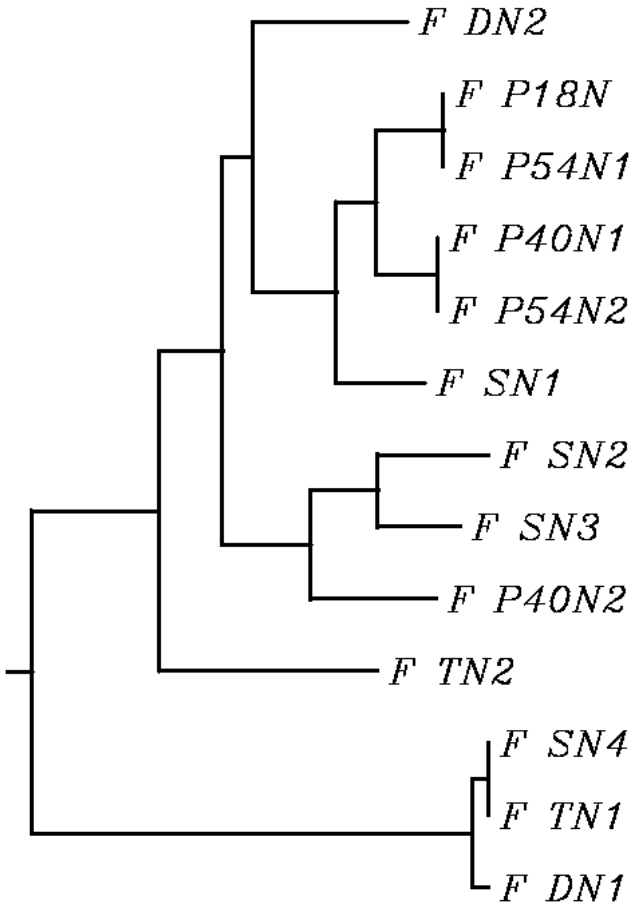


Figure 3.2.12: Nucleotide sequence based phenetic tree (Neighbour-joining tree) of all cloned *invGF* invertase alleles.

The alleles group regarding their similarity in the same clades and sublcades as observed in the amino acid sequences based phenetic tree (Figure 3.2.11). Subclades are more subdivided because of nucleotide polymorphisms.

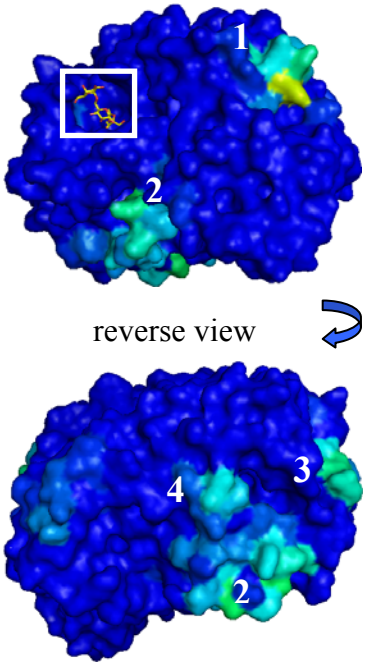
3.2.1.3 Three-dimensional modelling of *invGE* and *invGF* alleles

The 3D-modelling was performed by Pawel Durek, MPIMP/Golm. The allelic invertase molecular structures were modelled after the invertase 3D and crystal structure of cyanobacteria (ALBERTO ET AL., 2004). The models are comparative, superimposing two allelic sequences. Differences of the alleles are highlighted. The models include the putative sucrose binding site with the substrate sucrose. In addition to the structural visualization of amino acid exchanges, also the electrostatic potential (EP) of the molecules was mapped at pH 4.7 mimicking the apoplastic conditions.

- **Structural modelling of *invGE* alleles of the cultivars 'Satina' and 'Theresa'**

Analysis of allelic molecular structures was performed with the associated 'Satina' allele *E_SA* compared to the allele *E_SN3,* and with the associated 'Theresa' allele *E_TA* compared to the allele *E_TN1*. The models contrast the allelic sequences with each other, meaning that

one sequence superimposes the other and vice versa (Figure 3.2.14). Based on protein sequence alignments (Figure 3.2.3), regions, which are affected directly or indirectly by amino acid exchanges, were identified (Figure 3.2.13).



Amino acid region	Affected surface area
460-466	1
254-256 264-266 295-310	2
224-227	3
328-329	4

Figure 3.2.13: Correlation of amino acid regions and affected surface areas of *invGE* alleles. Amino acids are numbered based on the multiple sequence alignment (Figure 3.2.3). Surface effects of the variable amino acids are weak, therefore the reverse view of the molecule is also shown to depict all surface modifications. Areas are numbered from 1-4. Yellow: intermediate structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from yellow (intermediate) to blue (no difference). The putative sucrose binding site with the substrate sucrose is framed.

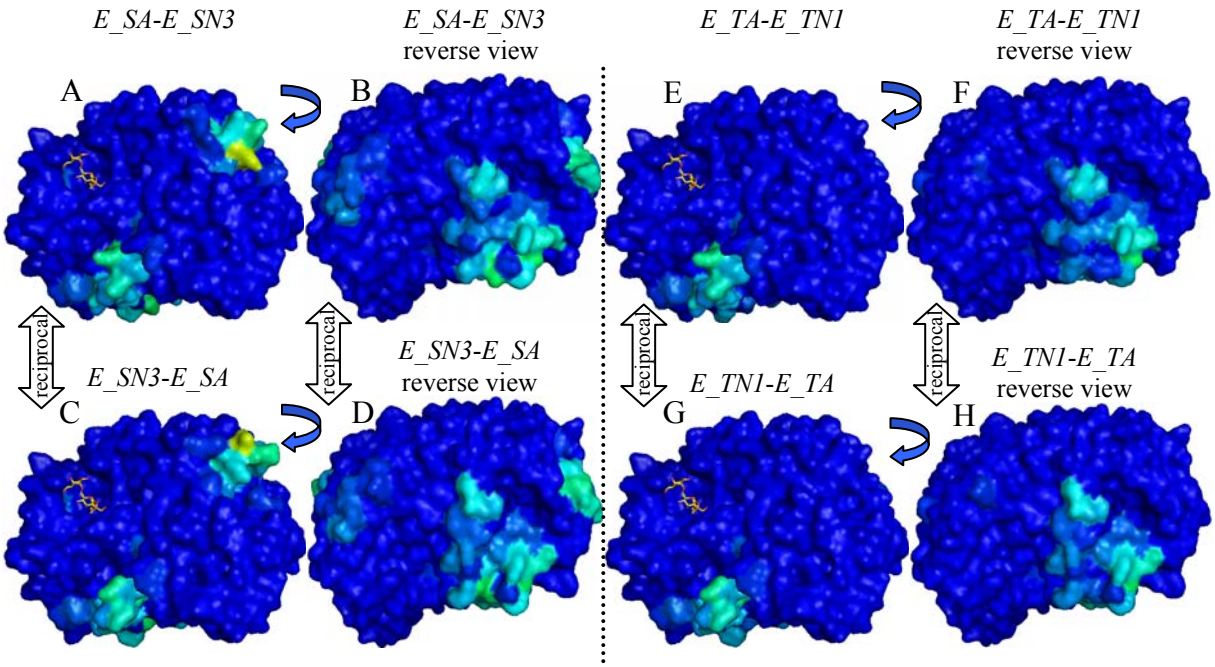


Figure 3.2.14: Structural comparison of 'Satina' alleles *E_SA*, *E_SN3* and 'Theresa' alleles *E_TA*, *E_TN1*. **A:** *E_SA* superimposes *E_SN3*; **B:** *E_SA* superimposes *E_SN3,* reverse view; **C:** *E_SN3* superimposes *E_SA*; **D:** *E_SN3* superimposes *E_SA*, reverse view; **E:** *E_TA* superimposes *E_TN1*; **F:** *E_TA* superimposes *E_TN1,* reverse view; **G:** *E_TN1* superimposes *E_TA*; **H:** *E_TN1* superimposes *E_TA*, reverse view. Yellow: intermediate structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from yellow (intermediate) to blue (no difference).

The models of the invertase alleles *E_SA*, *E_SN3* and *E_TA*, *E_TN1* showed structural differences on the enzyme's surface. The analysis of the allelic molecules *E_SA* and *E_SN3* revealed differences in regions 1, 2, 3, and 4 (Figure 3.2.13). Area 1 is defined by amino acids 460-466 showing alanine (A) in allele *E_SA* and valine (V) in allele *E_SN3* at position 462. Three amino acid exchanges between the two alleles occur in region 2 where at positions 256, 295 and 309 the protein sequence differs. The allele *E_SA* contains at position 256 asparagine (N) versus lysine (K) in allele *E_SN3*, at position 295 arginine (R) versus lysine (K), and at position 309 cysteine (C) versus serine (S). Region 3 is defined by amino acids 224-227. Here, the protein sequences of both 'Satina' alleles are identical. In the vicinity of this region, at position 230, an exchange from valine (V) to alanine (A) in the alleles *E_SA* and *E_SN3* respectively, occurs. This difference might influence surrounding areas and lead to variable protein folding. Amino acids 328 and 329 determine region 4, where at position 329 an amino acid exchange from threonine (T) in allele *E_SA* to methionine (M) in allele *E_SN3* appears.
The models of the two 'Theresa' alleles *E_TA* and *E_TN1* show surface differences in the regions 2 and 4. Differences are absent in area 1 and 3 because of identical amino acid composition of both alleles. In region 2, which is defined by amino acids 254-256, 264-266, and 295-310 two amino acid exchanges occur. The allele *E_TA* contains at position 295 arginine (R) versus lysine (K) in allele *E_TN1*, and at position 309 cysteine (C) versus serine (S). These two substitutions are also present in allele *E_SA* from 'Satina'.

- **Comparison of 3D-structures of of the'Satina' and 'Theresa' *invGE* alleles, which are associated with better chips quality**

The tetraploid potato cultivars 'Satina' and 'Theresa' harbour alleles, which are not identical at amino acid level but exhibit the nucleotide adenine at cDNA SNP 1103* (Table 3.2.3), which is associated with better potato chips quality. Comparison of the 3D-structures of *Pain_SA* and *Pain_TA* molecules revealed minor surface differences between the two protein models (Figure 3.2.15).

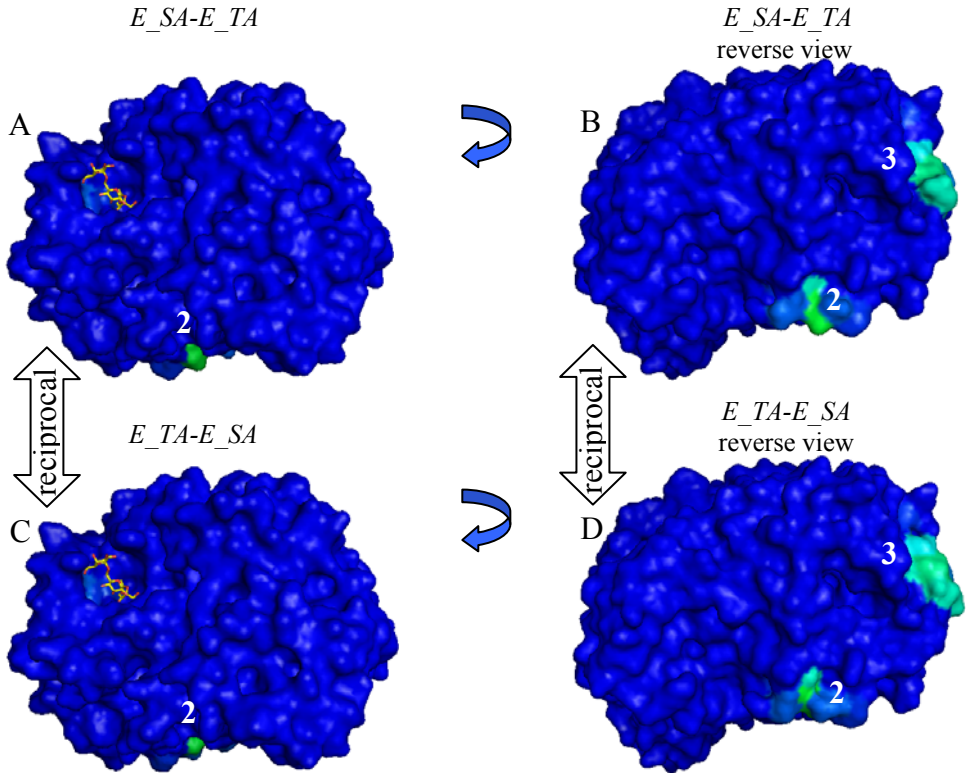


Figure 3.2.15: Comparative 3-D structures of the associated alleles *E_SA* and *E_TA*. A: *E_SA* superimposes *E_TA*; **B:** *E_SA* superimposes *E_TA,* reverse view; **C:** *E_TA* superimposes *E_SA*; **D:** *E_TA* superimposes *E_SA*, reverse view. Green: weak structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from green (weak) to blue (no difference).

Alleles *E_SA* and *E_TA* differ at 11 amino acid positions. The models of both allelic molecules revealed weak structural differences on the enzyme's surface in regions 2 and 3. Region 2 is defined by three amino acid stretches 254-256, where at position 256 an amino acid exchange was detected. The allele *E_SA* exhibits asparagine (N), whilst *E_TA* has lysine (K). Except this exchange, both alleles are identical in region 2 explaining the limited extension of this area compared to the other analyzed molecules (Figure 3.2.14). Region 3, defined by the amino acids 224-227, is identical in both alleles. The visible structural effect might be caused by the altered sequence at position 230 in the vicinity of region 3, which substitutes valine (V) to alanine (A) in the alleles *E_SA* and *E_TA*.

- **Modelling the electrostatic potential (EP) of *invGE* alleles from the cultivars 'Satina' and 'Theresa'**

The mapping of the EP of the *invGE* alleles *E_SA, E_SN3, E_TA,* and *E_TN1* revealed minor charge differences of the molecules at pH 4.7 (Figure 3.2.16).

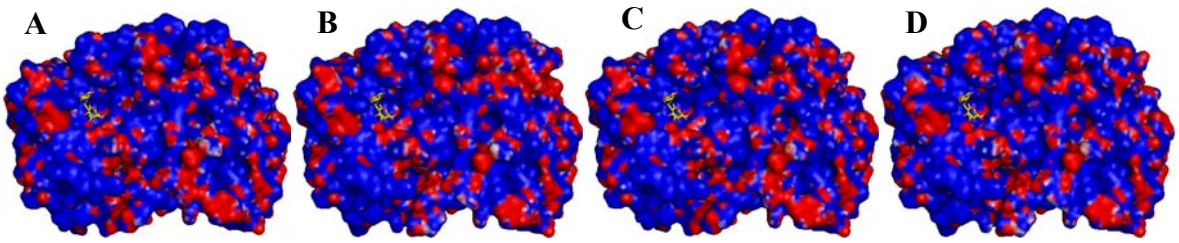


Figure 3.2.16: EP of the 'Satina' and 'Theresa' alleles. A: *E_SA*; **B:** *E_SN3*; **C:** *E_TA;* **D**: *E_TN1*. Red: negatively charged; blue: positively charged; white: neutrally charged.

Focusing on the EP of the putative sucrose binding site

The putative sucrose binding site (Figure 3.2.13) is positively charged matching the partial negative charge of the substrate sucrose due to its hydroxyl groups.

Zooming into the putative sucrose binding domain revealed weak charge differences between the molecules *E_SA* (A) and *E_SN3* (B). The alleles *E_TA* (C) and *E_TN1* (D) showed no visible differences (Figure 3.2.17).

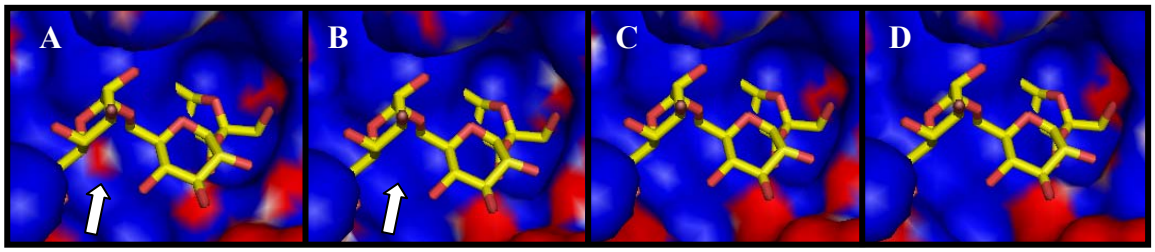
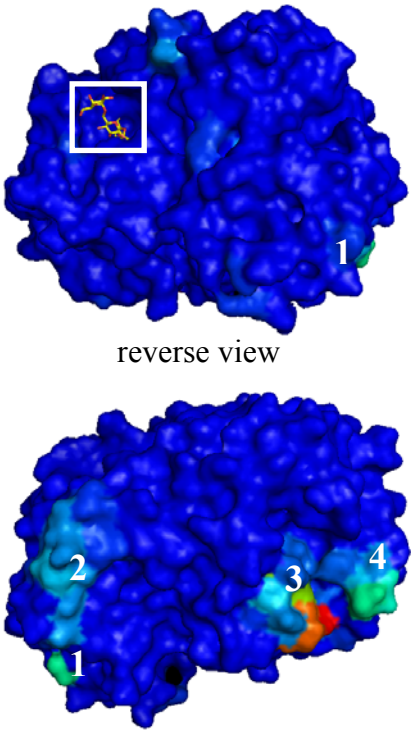


Figure 3.2.17: Focusing on the EP of the putative sucrose binding site of the 'Satina' and 'Theresa' alleles. A: *E_SA*; **B:** *E_SN3*; **C:** *E_TA;* **D**: *E_TN1*. Red: negatively charged; blue: positively charged; white: neutrally charged.

The EP changes of the putative sucrose binding site of the two alleles from 'Satina' were weak. The EP of the associated allele *E_SA* (A) exhibits a small negatively charged area compared to the allele *E_SN3* (B). The charge of the 'Theresa' alleles *E_TA* (C) and *E_TN1* (D) were similar.

- **Structural modelling of *invGF* alleles of the cultivar 'Satina'**

Molecular analysis of allelic structures was conducted using the two 'Satina' alleles *F_SN3* and *F_SN4*. The models compare the allelic sequences with each other by means of superimposing sequences of the different alleles (Figure 3.2.19). Doing so, differences between the alleles are visualized. Multiple alignment (Figure 3.2.8) of allelic protein sequences allowed to identify the regions, which are directly or indirectly affected by amino acid exchanges (Figure 3.2.18).



Amino acid region	Affected surface area
416/417	1
382-385	2
260-267	3
196-198	4

Figure 3.2.18: Correlation of amino acid regions and affected surface areas of *invGF* alleles. Amino acids are numbered based on the multiple sequence alignment (Figure 3.2.8). Surface effects of the variable amino acids are weak, therefore the reverse view of the molecule is also shown to depict all surface modifications. Areas are numbered from 1-4. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (no difference). The putative sucrose binding site with the substrate sucrose is framed.

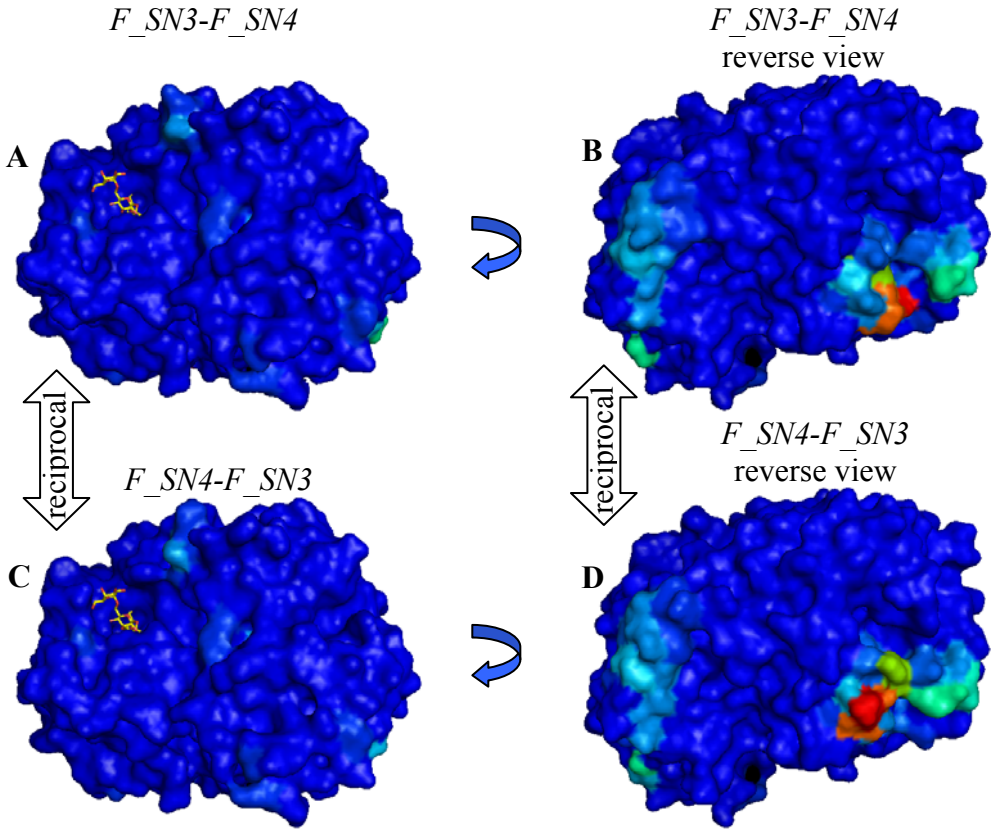


Figure 3.2.19: Structural comparison of 'Satina' alleles *F_SN3* and *F_SN4*. A: *F_SN3* superimposes *F_SN4*; **B:** *F_SN3* superimposes *F_SN4,* reverse view; **C:** *F_SN4* superimposes *F_SN3*; **D:** *F_SN4* superimposes *F_SN3*, reverse view. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (no difference).

The molecular models of the 'Satina' alleles *F_SN3* and *F_SN4* showed structural differences on the enzyme's surface. Those differences were assigned to regions 1, 2, 3, and 4 (Figure 3.2.18). Area 1 is characterized by amino acids 416 and 417 exhibiting no differences between the two alleles. Region 2 is determined by the amino acids 382-385. Both alleles are identical in this region. Also area 4 consists of identical amino acids at positions 196-198. Although amino acids in the corresponding regions 1, 2, and 4 do not differ between the alleles, sterical differences occur. The reasons for the mild structural effects may be surrounding allelic sequences causing a variable lobing of the corresponding regions of the putative 3D invertase structure.

Region 3, which is defined by the amino acids 260-267 shows exchanges between the alleles. The allele *F_SN3* contains at position 260 isoleucine (I) versus glutamine (Q) in allele *F_SN4* and at position 267 tyrosine (Y) versus histidine (H).

- **Modelling the electrostatic potential (EP) of *invGF* alleles from the cultivar 'Satina'**

The mapping of the EP of the *invGF* alleles *F_SN3* and *F_SN4* revealed minor charge differences of the molecules at pH 4.7 (Figure 3.2.20).

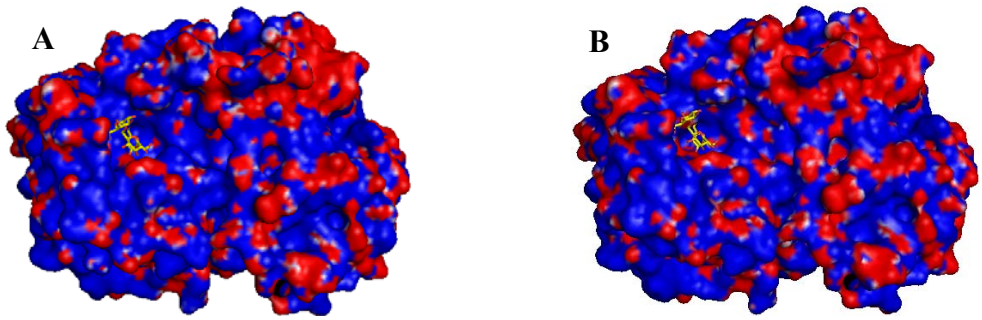


Figure 3.2.20: EP of the alleles *F_SN3* and *F_SN4*. A: *F_SN3*; **B:** *F_SN4*. Red: negatively charged; blue: positively charged; white: neutrally charged.

Focusing on the EP of the putative sucrose binding site

The putative sucrose binding site (Figure 3.2.18) has a positive charge matching the partial negative charge of the substrate sucrose due to its hydroxyl groups.

Zooming into the putative sucrose binding domain revealed charge differences between the molecules *F_SN3* (Figure 3.2.21, A) and *F_SN4* (Figure 3.2.21, B).

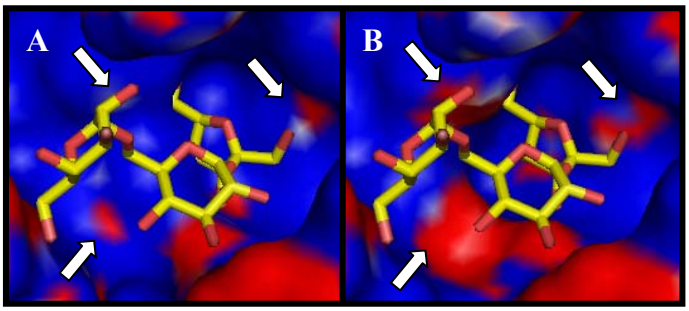


Figure 3.2.21: Focusing of the EP of the putative sucrose binding site of the alleles *F_SN3* and *F_SN4*. A: *F_SN3*; **B:** *F_SN4*. Red: negatively charged; blue: positively charged; white: neutrally charged.

The EP of the allele *F_SN4* (B) switched from a positive to a more negative charge caused by its allelic composition.

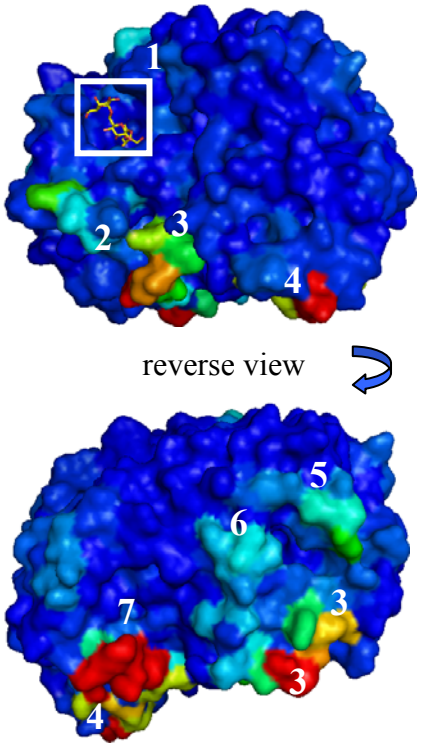
❖ Comparison of 3D-structures of *invGE* and *invGF* alleles

Association analysis showed that two SSCP fragments of the genes *invGE* (*invGE-6f*) and *invGF* (*invGF-4d*) are associated with better potato chips quality. These fragments are in LD showing nearly identical distributions within the population used (LI ET AL., 2005). Amino acid alignments (Figure 3.2.3) and phenetic tree analysis (Figure 3.2.6) showed the similarity of the three associated *invGE* alleles. Also three alleles of the gene *invGF* show high similarity to each other (Figure 3.2.8) and group in a separate clade compared to the other *invGF* alleles (Figure 3.2.11). Out of these three *invGF* alleles, which showed similar grouping as the associated *invGE* alleles and, therefore, might represent the associated *invGF* alleles, the allele *F_SN4* was selected for comparative 3D-modelling.

The associated *invGE* alleles *E_SA* and *E_TA* were compared against *F_SN4,* which was found to be amino acid and nucleotide identical to *F_TN1*. The *invGF* alleles *F_SN4, F_DN1,* and *F_TN1* are distinctive from the other *invGF* alleles.

Comparison of the 3D molecular structures of *E_SA* and *F_SN4,* and of *E_TA* and *F_SN4* revealed similar surface differences of both analyzed groups due to minor structural differences between the two associated *invGE* alleles *E_SA* and *E_TA*. The structural models are shown representatively from the comparison of *E_SA* and *F_SN4*.

A multiple alignment (Appendix A 3.2.45) of the allelic protein sequences allowed the identification of regions, which are directly or indirectly affected by amino acid exchanges (Figure 3.2.22).



Amino acid region	Affected surface area
86-89	1
133-135 210-213	2
262-268 300-309	3
419/420 476-480	4
133-136	5
326-329	6
510-519	7

Figure 3.2.22: Correlation of amino acid regions and affected surface areas of comparative *invGE* and *invGF* alleles. Amino acids are numbered based on multiple sequence alignment (Appendix A 3.2.19). The reverse view of the molecule is shown because of the manifestation of allelic amino acid differences at the whole surface. Areas are numbered from 1-7. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (no difference). The putative sucrose-binding site with the substrate sucrose is framed.

Comparison of the 3D molecular structures of *E_SA* and *F_SN4,* and of *E_TA* and *F_SN4* revealed surface differences between both analyzed enzymes (Figure 3.2.23).

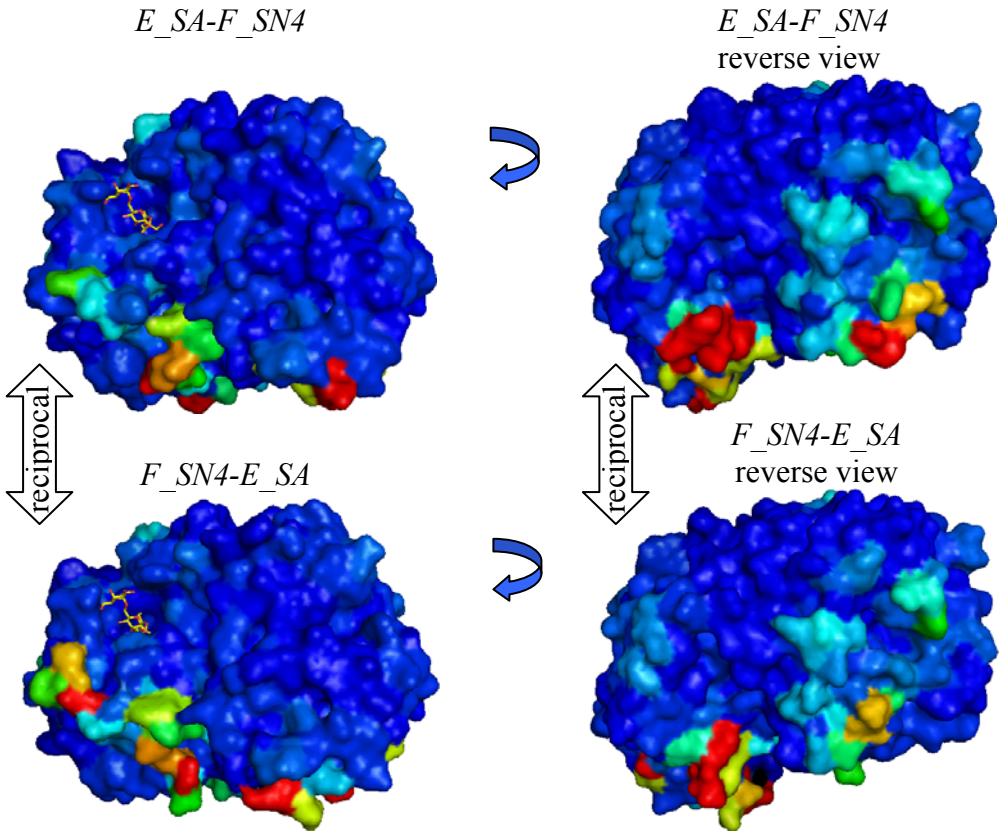


Figure 3.2.23: Structural comparison of *invGE* allele *E_SA* and *invGF* allele *F_SN4*. A: *E_SA* superimposes *F_SN4*; **B:** *E_SA* superimposes *F_SN4,* reverse view; **C:** *F_SN4* superimposes *E_SA*; **D:** *F_SN4* superimposes *E_SA*, reverse view. Red: strong structural differences; blue: no structural differences; all colours in between represent a transition of structural differences from red (strong) to blue (no difference).

The analysis of the corresponding allelic molecules revealed differences in the regions 1, 2, 3, 4, 5, 6, and 7 (area definition: Figure 3.2.22). Region 1 is defined by the amino acids 86-89. At position 87 an amino acid exchange occurs between both alleles. The allele *E_SA* contains lysine (K), whilst *F_SN4* consists of asparagine (N). The amino acids 133-135 and 210-213 represent the surface area 2. Amino acid exchanges at positions 135 and 211 cause structural differences. The allelic sequences change from asparagine (N135) in allele *E_SA* to glycine (G135) in allele *F_SN4*. At position 211 *E_SA* exhibits methionine (M) compared to leucine (L) in *F_SN4*. Region 3 is defined by the amino acids 262-268 and 300-309. Five regional amino acid exchanges are found between the two alleles. Protein sequence comparison revealed the following *E_SA* to *F_SN4* exchanges: A267Q, N302V, N303G, G307S and C308W. In the surface area 4 two amino acid substitutions occur. The first exchange is at position 420 where *E_SA* possesses serine (S), whilst *F_SN4* has alanine (A). The second exchange at position 480 shows a difference from lysine (K) in *E_SA* to glutamine (Q) in *F_SN4*. Region 5 is definded by the amino acids 133-136. At position 135 *E_SA* contains asparagine (N), *F_SN4* consists of lycine (G). The amino acids 326-329 are located in region 6 where an exchange at position 328 from threonine (T) in *E_SA* to serine (S) in *F_SN4* occurs. Region 7 is defined by the amino acids 510-519. In this area two exchanges at positions 515 and 517 were detected. The allele *E_SA* contains at position 515 valine (V) compared to alanine (A) in *F_SN4* and at position 517 a methionine (M), whilst *F_SN4* does not exhibit a comparable residue at this position.
The amino acid exchanges in the described regions manifest sterically and influence the lobing of the putative invertase molecules.

3.2.2 Functional characterization of the genes *invGE* and *invGF*

3.2.2.1 Differential expression analysis of *invGE* and *invGF* alleles

Referring to the expression pattern of the genes *invGE* and *invGF* observed by MADDISON ET AL. (1999), allele specific expression analysis was carried out in pyrosequencing assays using leaf tissues for *invGE* analysis and floral tissues for *invGF* characterization.

The pyrosequencing analysis was performed using cDNA from leaves and flowers and leaf and floral genomic DNA to determine the relative frequency of *invGE* and *invGF* alleles. Comparison of both samples revealed specific expression patterns not just for each genotype but also between different alleles of the same genotype. In the following Figures the relationship between the presence of alleles in the genome and their transcription levels are

illustrated. Accordingly, both values are shown together in terms of the relative expression level.

Additionally, plasmids harbouring one allele of complementary SNPs of corresponding genotypes were mixed in different ratios to monitor the accuracy of pyrosequencing analysis. Plasmid based measurements, working as positive controls, showed that SNP dependent variations of ±5% occurred. Values of cDNA and genomic dosages of the analysed alleles as determined by pyrosequencing were corrected for the observed SNP specific variations.

3.2.2.1.1 Expression patterns of *invGE* alleles in leaves of the tetraploid genotypes

By means of pyrosequencing the distribution of allele specific SNPs was analyzed (Table 3.2.3). The following Table 3.2.8 displays an overview of the SNPs selected from each tetraploid cultivar.

Table 3.2.8: Allele specific SNPs analyzed by pyrosequencing.

Genotype	Allele	SNP position	Allele specific SNP
'Satina'			*E_SA/E_SN1/E_SN2/E_SN3*
	E_SA	SNP 1237	**T**/G/G/G
	E_SN1	SNP 1366	A/**G**/A/A
	E_SN2	SNP 1379	C/C/**T**/C
	E_SN3	SNP 1216	A/A/A/**G**
'Diana'			*E_DA/E_DN1/E_DN2*
	E_DA	SNP 1086	**A**/T/T
	E_DN1	SNP 1117	T/**C**/T
	E_DN2	SNP 924	T/T/**C**
'Theresa'			*E_TA/E_TN1/E_TN2/E_TN3*
	E_TA	SNP 1615	**A**/T/T/T
	E_TN1	SNP 1720	C/**A**/C/C
	E_TN2	SNP 1553	T/T/**C**/T
	E_TN3	SNP 1473	T/T/T/**G**

SNP positions refer to cDNA sequence where '1' represents the adenine of the start codon ATG. Primers used for pyrosequencing are listed in chapter 2 (Table 2.1.5 and Table 2.2.9). Allele specific SNPs are highlighted in bold capitals.

The pyrosequencing analysis was performed using cDNA from leaves and leaf genomic DNA to measure the dosages of the alleles (Figure 3.2.24).

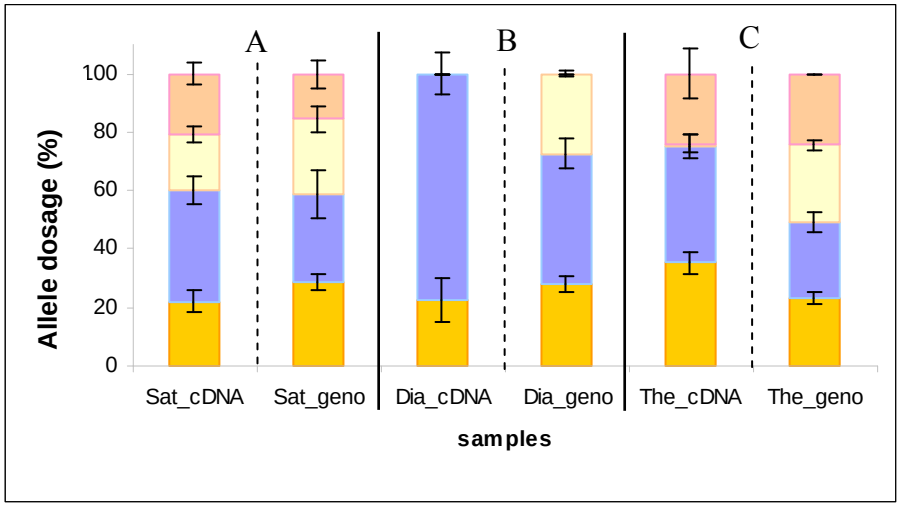


Figure 3.2.24: Pyrosequencing analysis of *invGE* alleles from the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'. A: Pyrosequencing of 'Satina' alleles. : *E_SA*; : *E_SN1*; : *E_SN2*; : *E_SN4*. **B:** Pyrosequencing of 'Diana' alleles. : *E_DA*; : *E_DN1*; : *E_DN2*. **C:** Pyrosequencing of 'Theresa' alleles. : *E_TA*; : *E_TN1*; : *E_TN2*; : *E_TN3*. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of leaves. Percentages of the expression level of the cDNA samples are related to the genomic dosage of the alleles. Standard deviations are derived from two biological replicates done in technical triplicates.

Pyrosequencing analysis of genomic DNA showed that the three associated alleles *E_SA*, *E_DA*, and *E_TA* from the different cultivars are present in simplex (25%) in the corresponding genotype. For the cultivar 'Satina' four *invGE* alleles were found. If the alleles were transcribed according to the allele dosage, each allele is expected to contribute 25% of the total transcripts. Comparison of genomic allele dosage and allele transcription revealed that the alleles *E_SN1* and *E_SN4* were slightly over-represented, whilst the alleles *E_SA* and *E_SN2* were less abundant in cDNA samples.

In the cultivar 'Diana' three alleles were identified. Pyrosequencing analysis of genomic 'Diana' DNA showed allele dosages of 25% *E_DA*, 25% *E_DN2* and 50% of *E_DN1*.

However, the fraction represented by *E_DN1* could consist of two alleles since 'Diana' is tetraploid. In the pyrosequencing assay of 'Diana' leaf cDNA no transcripts for the allele *E_DN2* were detected due to a transcription rate below detection level, whilst the cDNA fraction represented by *E_DN1* showed a strong over-representation up to 80%. The abundance of the associated allele *E_DA* decreased from 25% of its genomic dosage to approximately 20% in cDNA.

The cultivar 'Theresa' has four *invGE* alleles *E_TA, E_TN1, E_TN2*, and *E_TN3*. Each allele is present in simplex (25%). Pyrosequencing analysis of leaf cDNA showed that the transcripts of the allele *E_TN3* were below the detection level. The abundance of the associated allele *E_TA* increased slightly from 25% genomic dosage to about 38% in leaf

cDNA. The strongest uprating was observed for the allele *E_TN1* that increased up to 40% when compared to the genomic dosage. Expression of the allele *E_TN2* did not differ compared to its genomic dosage and remained at 25%.

3.2.2.1.2 Expression pattern of *invGE* alleles in leaves of the diploid genotypes

For allele specific separation within the diploid potato genotypes P18, P40, and P54 allele specific SNPs were identified based on multiple nucleotide alignments (Table 3.2.4). SNP at position 108 was used to separate the two P18 alleles *E_P18N1* and *E_P18N2*. Using the SNP at position 58 the P40 alleles *E_P40N1*, *E_P40N2* and the P54 alleles *E_P54N1*, *E_P54N2* were distinguished (Table 3.2.9).

Table 3.2.9: Allele specific SNPs analyzed by pyrosequencing.

Genotype	Allele	SNP position	Allele specific SNP
P18	*E_P18N1* *E_P18N2*	SNP 108	A T
P40	*E_P40N1* *E_P40N2*	SNP 58	C T
P54	*E_P54N1* *E_P54N2*	SNP 58	C T

SNP positions refer to cDNA sequence where '1' represents the adenine of the start codon ATG. Primers used for pyrosequencing are listed in chapter 2 (Table 2.1.5 and Table 2.2.10).

Pyrosequencing analysis was performed using cDNA from leaves (Figure 3.2.25).

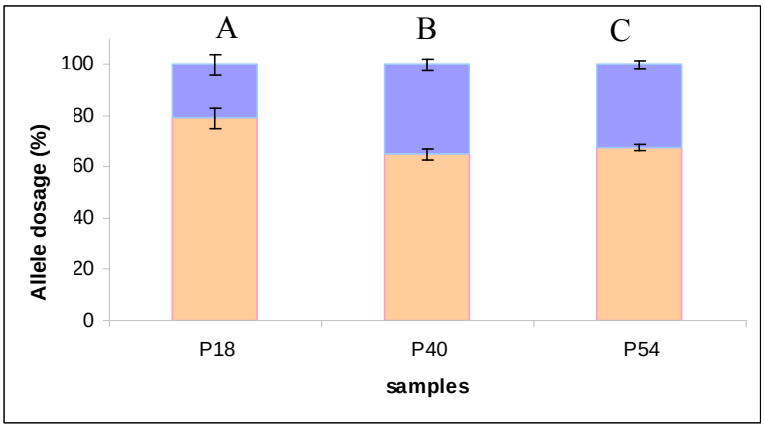


Figure 3.2.25: Pyrosequencing analysis of *invGE* alleles from the diploid genotypes P18, P40, and P54. A: Pyrosequencing of P18 alleles. : *E_P18N1*; : *E_P18N2*. **B:** Pyrosequencing of P40 alleles. : *E_P40N1*; : *E_P40N2*. **C:** Pyrosequencing of P54 alleles. : *E_P54N1*; : *E_P54N2*. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. Percentages of the expression level of the cDNA samples are related to the genomic allelic distribution being 50% because of the heterozygous diploid genotype. Genomic DNA of the corresponding genotypes was not analyzed in pyrosequencing assay. Standard deviations are derived from two biological replicates done in technical triplicates.

The three potato genotypes are diploid, meaning that they can be homozygous harbouring one *invGE* allele or heterozygous consisting of two *invGE* alleles. For P18, P40, and P54 two different *invGE* alleles were identified, respectively. Consequently, each allele per genotype is

present at 50%. Pyrosequencing analysis of leaf cDNA showed transcriptional changes of the genotype specific *invGE* alleles compared to their allele dosage. The allele *E_P18N1* revealed an increased abundance from 50% of its genomic distribution to 80% in cDNA.

In P40 the allele *E_P40N1* was under-represented in cDNA samples compared to its genomic dosage, whilst the allele *E_P40N2* showed an abundance increase up to 62% compared to its genomic dosage.

The two P54 alleles exhibit a similar expression pattern to P40. The allele order was inverted meaning that *E_P54N1* was over-represented, whilst *E_P54N2* was under-represented compared to the genomic allele dosage.

3.2.2.1.3 Expression pattern of *invGF* alleles in fowers of the tetraploid genotypes

Allele specific SNPs were selected based on multiple nucleotide alignment to separate different *invGF* alleles in the tetraploid genotypes (Table 3.2.5). The following Table 3.2.10 summarizes the selected SNPs from each cultivar.

Table 3.2.10: Allele specific SNPs analyzed by pyrosequencing.

Genotype	Allele	SNP position	Allele specific SNP
			F_SN1/F_SN2/F_SN3/F_SN4
'Satina'	*F_SN1*	SNP 111	**T**/C/C/C
	F_SN2	SNP 459	C/**T**/C/C
	F_SN3	SNP 378	A/A/**G**/A
	F_SN4	SNP 96	C/C/C/**T**
'Diana'	*F_DN1*	SNP 96	**T**
	F_DN2		**C**
'Theresa'	*F_TN1*	SNP 96	**T**
	F_TN2		**C**

SNP positions refer to cDNA sequence where '1' represents the adenine of the start codon ATG. Primers used for pyrosequencing are listed in chapter 2 (Table 2.1.6 and Table 2.2.11). Allele specific SNPs are highlighted in bold capitals.

The pyrosequencing analysis was performed using cDNA and genomic DNA from flowers to measure the dosages of the alleles (Figure 3.2.26).

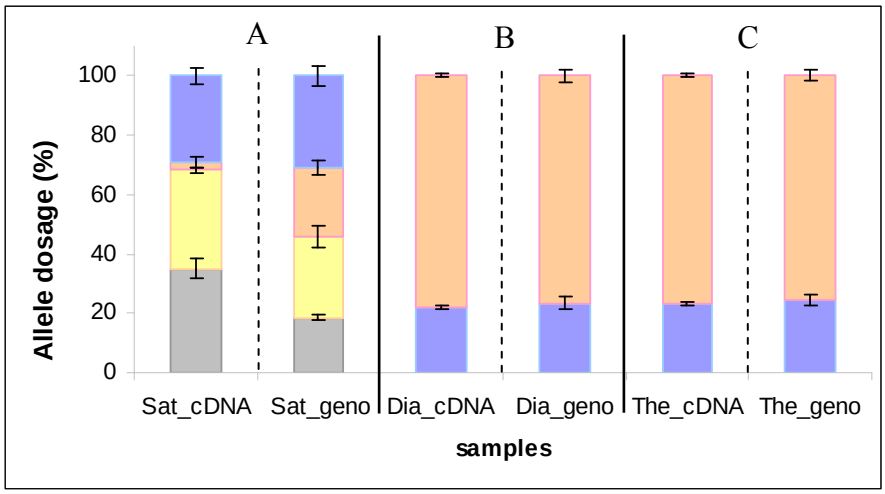


Figure 3.2.26: Pyrosequencing analysis of *invGF* alleles from the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'. A: Pyrosequencing of 'Satina' alleles. : *F_SN1*; : *F_SN2*; : *F_SN3*; : *F_SN4*. **B:** Pyrosequencing of 'Diana' alleles. : *F_DN1*; : *F_DN2*. **C:** Pyrosequencing of 'Theresa' alleles. : *F_TN1*; : *F_TN2*. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of flowers. Percentages of the expression level of the cDNA samples are related to the genomic allelic distribution. Standard deviations are derived from two biological replicates done in technical triplicates.

For the cultivar 'Satina' four *invGF* alleles were found. If the alleles were transcribed according to the allele dosage, each allele is expected to contribute 25% of the total transcripts. In the cDNA pyrosequencing assay marginal transcript was detectable for the allele *F_SN3*. The alleles *F_SN1* and *F_SN2* were more abundant in cDNA compared to their genomic dosage, whilst the presence of allele *F_SN4* remained stable at 25% according to its genomic distribution.

In the cultivar 'Diana' two alleles were identified. The allele *F_DN1* was present in simplex (25%), whilst the allele *F_D*N2 was triplex (75%). However, *F_DN2* could possibly consist of up to three diverse alleles due to the tetraploidy of 'Diana'. Pyrosequencing of flower cDNA revealed no differences in the expression pattern of both alleles compared to their genomic dosage.

The alleles *F_TN1* and *F_TN2* were defined for the cultivar 'Theresa'. The allele *F_TN1* existed in simplex (25%), whilst the allele *F_TN2* was present in triplex (75%). Considering the tetraploidy, the fraction represented by the allele *F_TN2* might consist of more than one allele. Similar to the expression pattern of the two 'Diana" alleles, also the 'Theresa' alleles did not show any changes in their expression compared to their genomic dosage.

3.2.2.1.4 Expression pattern of *invGF* alleles in flowers of the diploid genotypes

From the potato genotype P18 one *invGF* allele was identified, whilst for P40 and P54 two alleles were found. In the pyrosequencing assay the distribution of allele specific SNPs were

analyzed (Table 3.2.6). In the following Table 3.2.11 discriminative SNPs of P40 and P54 alleles are listed.

Table 3.2.11: Allele specific SNPs analyzed by pyrosequencing.

Genotype	Allele	SNP position	Allele specific SNP
P40	*F_P40N1* *F_P40N2*	SNP 1534	G A
P54	*F_P54N1* *F_P54N2*	SNP 1446	T C

SNP positions refer to cDNA sequence where 1 represents the adenine of the start codon ATG. Primers used for pyrosequencing are listed in chapter 2 (Table 2.1.6 and Table 2.2.12).

The pyrosequencing analysis was performed using cDNA and genomic DNA from flowers to measure the dosages of the alleles (Figure 3.2.27)

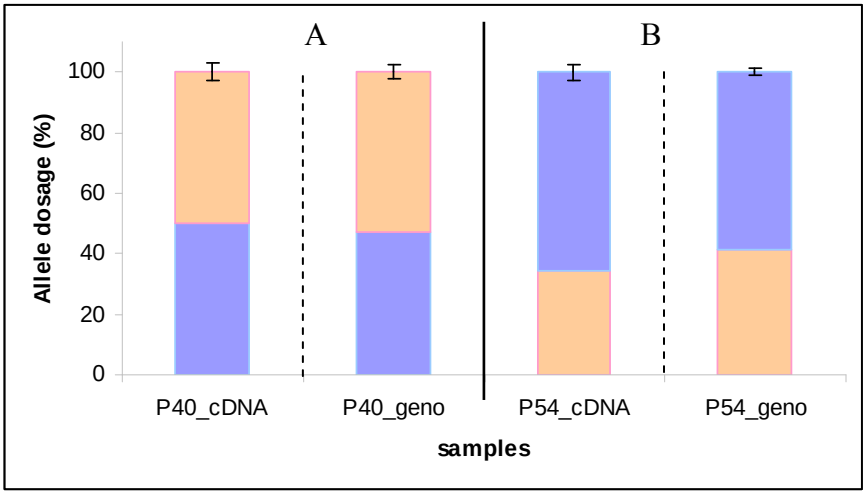


Figure 3.2.27: Pyrosequencing analysis of *invGF* alleles from the diploid genotypes P40 and P54. A: Pyrosequencing of P40 alleles. : *F_P40N1*; : *F_P40N2*. **B:** Pyrosequencing of P54 alleles. : *F_P54N1*; : *F_P54N2*. 100% is defined as the sum of alternative peaks measuring allele specific SNPs. In addition to pyrosequencing analysis of cDNA samples, the genomic dosage of the alleles was determined using genomic DNA of flowers. Percentages of the expression level of the cDNA samples are related to the genomic allelic distribution. Standard deviations are derived from two biological replicates done in technical triplicates.

Regarding the diploidy of the potato genotypes, the two alleles per genotype are expected to be equally frequent at genomic level. The expression pattern of the two P40 alleles *F_P40N1* and *F_P40N2* remained unchanged compared to their genomic dosage. Transcript levels of both alleles were consistent at approximately 50%.

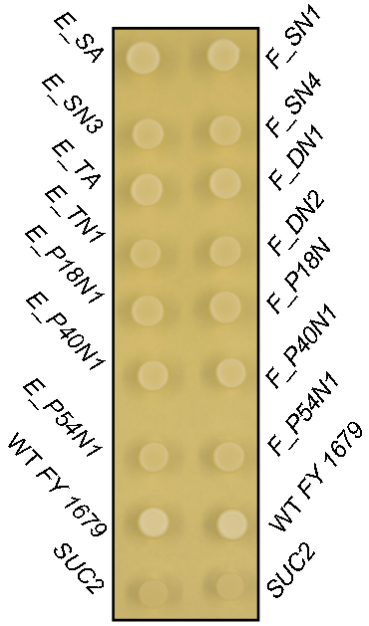
In P54 the allele *F_P54N1* showed a decreased abundance of 15% compared to its genomic dosage. The allele *F_P54N2* was over-represented up to approximately 65% in cDNA compared to its genomic dosage.

3.2.2.2 Functional complementation of the yeast invertase mutant *SUC2*

Similar to the previous functional complementation analysis of the yeast invertase mutant *SUC2* with *Pain-1* cDNA alleles (section 3.1.2.2), cDNA alleles of the genes *invGE* and *invGF* were used for yeast transformation. Transforming *SUC2* with *invGE* and *invGF* cDNA alleles resulted in yeast transformants that were able to grow on sucrose as carbohydrate source, indicating functional complementation of the *SUC2* mutation.

The *invGE* and *invGF* cDNA alleles listed below (Figure 3.2.28) were used for complementation of *SUC2* and subsequent analysis of invertase activity (section 3.2.2.3).

Genotype	***invGE* alleles**
'Satina'	*E_SA*
	E_SN1
	E_SN3
'Theresa'	*E_TA*
	E_TN1
P18	*E_P18N1*
P40	*E_P40N1*
	E_P40N2
P54	*E_P54N1*
	E_P54N2
	***invGF* alleles**
'Satina'	*F_SN1*
	F_SN2
	F_SN3
	F_SN4
'Diana'	*F_DN1*
	F_DN2
P18	*E_P18N*
P40	*F_P40N1*
	F_P40N2
P54	*F_P54N1*
	F_P54N2



Representative yeast transformants complemented with *invGE* and *invGF* invertase alleles were spotted on solid yeast minimal broth with 2% sucrose as carbon source. The wild type *FY 1479* was plated as positive control, whilst the invertase mutant *SUC2* was the negative control.

Figure 3.2.28: cDNA alleles used for *SUC2* complementation and *SUC2* transformants on solid yeast minimal media.

All *SUC2* invertase transformants exhibited substantial growth on sucrose and were used for the biochemical characterization of the *invGE* and *invGF* alleles. The potato alleles complemented the invertase deficiency of the yeast mutant not this good as the wild type *FY 1479* and displayed less colonies.

3.2.2.3 Biochemical characterization of *invGE* and *invGF* alleles

Putative 3D-models of allelic *invGE* and *invGF* molecules (section 3.2.1.3) indicated structural and electrostatical differences between the alleles, which could cause functional

differences. To test, whether structural characteristics might influence enzymatic activity of *invGE* and *invGF* invertase alleles, biochemical characterization was performed.

From yeast *SUC2* transformants complemented with *invGE* and *invGF* cDNA alleles, total protein was extracted. To test invertase activity, a modified protocol based on ZRENNER ET AL. (1995) was used. Invertase assays were carried out at 30°C. The *invGE* and *invGF* alleles displayed in Table 3.2.12 were used for biochemical characterization.

Table 3.2.12: *invGE* and *invGF* alleles used for biochemical characterization.

Genotype	*invGE* alleles	Genotype	*invGF* alleles
'Satina'	*E_SA* *E_SN1* *E_SN3*	'Satina'	*F_SN1* *F_SN2* *F_SN3* *F_SN4*
'Theresa'	*E_TA* *E_TN1*	'Diana'	*F_DN1* *F_DN2*
P18	*E_P18N1*	P18	*F_P18N*
P40	*E_P40N1* *E_P40N2*	P40	*F_P40N1* *F_P40N2*
P54	*E_P54N1* *E_P54N2*	P54	*F_P54N1* *F_P54N2*

The biochemical parameters Michaelis constant (K_m) and the maximal velocity (v_{max}) of invertase reaction were determined.

K_m values are independent from the enzyme concentration, whereas v_{max} values depend on the enzyme concentration. Due to the lack of an appropriate antibody against *invGE* and *invGF* cell wall-bound invertase isoforms, immunoblot analysis could not be performed (section 3.2.2.4). Therefore, v_{max} values of *invGE* and *invGF* alleles cannot be taken into account until protein quantification can be carried out.

❖ Biochemical characterization of *invGE* alleles

Results of the biochemical analysis for *invGE* alleles are shown in Table 3.2.13.

Table 3.2.13: K_m (mM) of *invGE* invertase alleles.

Genotype	*invGE* allele	K_m
'Satina'	*E_SA* *E_SN1* *E_SN3*	19.66±0.93 16.99±0.85 23.97±0.93
'Theresa'	*E_TA* *E_TN1*	21.32±0.93 18.64±0.85
P18	*E_P18N1*	24.4±0.93
P40	*E_P40N1* *E_P40N2*	17.13±0.85 17.1±0.85
P54	*E_P54N1* *E_P54N2*	22.73±0.85 19.51±0.85
FY 1679		24.25±2.5

Standard deviations are derived from three biological replicates for the associated alleles *E_SA* and *E_TA*, and the wild type reference strain *FY 1679* and from two biological replicates for the other alleles done in technical replicates to obtain six measurements. To make assays of different invertase isoforms comparable, the yeast reference strain *FY 1679* was used as positive control.

Table 3.2.14 summarizes the significance values for differences between the K_m values measured for the *invGE* alleles. The statistical calculation was performed by Benjamin Stich, MPIZ/Köln.

Table 3.2.14: Statistical significance levels of K_m values from the *invGE* invertase alleles.

Allele	*E_SA*	*E_SN1*	*E_SN3*	*E_TA*	*E_TN1*	*E_P18N1*	*E_P40N1*	*E_P40N2*	*E_P54N1*	*E_P54N2*
E_SA	---	0.056	0.006	0.23	0.43	0.0036	0.067	0.065	0.032	0.91
E_SN1	---	---	0.0001	0.0050	0.19	7.66E-05	0.92	0.93	0.0004	0.06
E_SN3	---	---	---	0.067	0.001	0.75	0.0002	0.0001	0.34	0.004
E_TA	---	---	---	---	0.055	0.038	0.006	0.006	0.29	0.18
E_TN1	---	---	---	---	---	0.0006	0.23	0.22	0.005	0.48
E_P18N1	---	---	---	---	---	---	8.97E-05	8.70E-05	0.21	0.002
E_P40N1	---	---	---	---	---	---	---	0.98	0.0005	0.07
E_P40N2	---	---	---	---	---	---	---	---	0.0005	0.067
E_P54N1	---	---	---	---	---	---	---	---	---	0.02
E_P54N2	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are coloured in orange, no significant differences are described by P-values >0.05.

The K_m values of the 'Satina' alleles *E_SA* and *E_SN1* differed not significantly but showed a significant difference to *E_SN3*. The allele *E_SN3* revealed the highest K_m of approximately 24mM meaning that this allele shows a lower affinity to its substrate sucrose compared to the other two 'Satina' alleles.

K_m values of the two 'Theresa' alleles did not differ significantly. The allele *E_TA* had a K_m value of approximately 21mM, whilst the K_m of allele *E_TN1* was around 19mM.

Comparison of K_m values of the two P40 alleles *E_P40N1* and *E_P40N2* revealed no significant change in enzyme affinity to its substrate. K_m values of both enzymes were approximately 17mM.

The K_m values of P54 alleles *E_P54N1* and *E_P54N2* differed significantly. *E_P54N1* displayed a K_m value around 23mM and *E_P54N2* of approximately 20mM. The K_m value of the yeast wild type reference strain *FY 1679* was approximately 24mM.

❖ Biochemical characterization of *invGF* alleles

Results of the biochemical analysis for invGF alleles are shown in Table 3.2.15

Table 3.2.15: K_m (mM) of *invGF* invertase alleles.

Genotype	*invGF* allele	K_m
'Satina'	*F_SN1*	12.72±1.41
	F_SN2	12.30±1.41
	F_SN3	14.73±1.41
	F_SN4	17.71±1.23
'Diana'	*F_DN1*	13.10±1.41
	F_DN2	14.45±1.45
P18	*F_P18N*	13.90±1.41
P40	*F_P40N1*	21.41±1.41
	F_P40N2	17.03±1.41
P54	*F_P54N1*	18.02±1.41
	F_P54N2	16.65±1.41
FY 1679		20.1±3.1

Standard deviations are derived from two biological replicates done in technical triplicates. To make assays of different invertase isoforms comparable, the yeast reference strain *FY 1679* was used as positive control.

Table 3.2.16 summarizes the significance values for differences between the K_m values measured for the *invGF* alleles. The statistical calculation was performed by Benjamin Stich, MPIZ/Köln.

Table 3.2.16: Statistical significance levels of K_m values from the *invGF* invertase alleles.

Allele	*F SN1*	*F SN2*	*F SN3*	*F SN4*	*F DN1*	*F DN2*	*F P18N*	*F P40N1*	*F P40N2*	*F P54N1*	*F P54N2*
F_SN1	---	0.83	0.33	0.02	0.87	0.41	0.56	0.0009	0.05	0.02	0.07
F_SN2	---	---	0.24	0.01	0.71	0.31	0.44	0.0006	0.035	0.014	0.05
F_SN3	---	---	---	0.14	0.03	0.1	0.06	0.07	0.72	0.12	0.35
F_SN4	---	---	---	---	0.03	0.11	0.06	0.07	0.72	0.87	0.58
F_DN1	---	---	---	---	---	0.51	0.68	0.001	0.07	0.03	0.1
F_DN2	---	---	---	---	---	---	0.8	0.005	0.23	0.1	0.3
F_P18N	---	---	---	---	---	---	---	0.003	0.14	0.06	0.2
F_P40N1	---	---	---	---	---	---	---	---	0.048	0.11	0.034
F_P40N2	---	---	---	---	---	---	---	---	---	0.63	0.85
F_P54N1	---	---	---	---	---	---	---	---	---	---	0.51
F_P54N2	---	---	---	---	---	---	---	---	---	---	---

Significant differences are defined by P-values <0.05 and are coloured in orange, no significant differences are described by P-values >0.05.

The K_m values of the 'Satina' alleles *F_SN1*, *F_SN2*, and *F_SN3* were similar, whilst the K_m value of allele *F_SN4* differed significantly. The allele *F_SN4* showed the lowest substrate affinity compared to the other 'Satina' alleles characterized by a K_m value of approximately 18mM. The enzymatic characteristics of the two 'Diana' alleles *F_DN1* (13mM) and *F_DN2* (≈14mM) were similar to each other, no significant differences were detected.

The K_m values of the P40 alleles *F_P40N1* and *F_P40N2* differed significantly. The allele *F_P40N1* displayed a lower affnity (≈21mM) to sucrose than allele *F_P40N2* (≈17mM). The K_m values of the two P54 alleles *F_P54N1* and *F_P54N2* showed similarity to each other, no enzymatic differences were observed. The K_m value of *F_P54N1* was 18mM and of *F_P54N2* approximately 17mM. The K_m value of the yeast wild type reference strain *FY 1679* was approximately 20mM.

❖ Comparison of biochemical *invGE* and *invGF* characteristics

Both *invGE* and *invGF* genes encode cell wall-bound invertase isoforms functional in the apoplast. Biochemical analysis of *invGE* and *invGF* alleles showed differences in enzyme affinity to the substrate sucrose. The significance values for differences between the K_m values measured for *invGE* alleles compared to *invGF* alleles are listed in Table 3.2.17.

Table 3.2.17: Statistical significance levels of K_m values from the *invGE* and *invGF* invertase alleles.

Allele	*E SA*	*E SN1*	*E SN3*	*E TA*	*E TN1*	*E P18N1*	*E P40N1*	*E P40N2*	*E P54N1*	*E P54N2*
F_SN1	0.002	0.029	4.30 E-05	0.0005	0.005	3.08 E-05	0.026	0.026	0.0003	0.004
F_SN2	0.001	0.019	3.03 E-05	0.0003	0.003	2.19 E-05	0.016	0.017	0.0002	0.003
F_SN3	0.016	0.215	0.0002	0.003	0.043	0.0002	0.192	0.196	0.003	0.049
F_SN4	0.28	0.685	0.0042	0.0669	0.595	0.0028	0.739	0.728	0.1027	0.8082
F_DN1	0.001	0.042	5.71 E-05	0.001	0.0072	4.07 E-05	0.037	0.038	0.001	0.007
F_DN2	0.017	0.205	0.0003	0.004	0.0438	0.0002	0.183	0.187	0.004	0.051
F_P18N	0.007	0.099	0.0001	0.002	0.0179	8.31 E-05	0.087	0.089	0.001	0.018
F_P40N1	0.358	0.025	0.18	0.953	0.1351	0.125	0.029	0.028	0.512	0.051
F_P40N2	0.16	0.985	0.002	0.036	0.3699	0.0015	0.957	0.968	0.049	0.506

Significant differences are defined by P-values <0.05 and are coloured in orange, no significant differences are described by P-values >0.05.

Significant differences in K_m values were detected for the *invGE* and *invGF* alleles of the cultivar 'Satina'. The alleles *E_SA* and *E_SN1* were significantly different to *F_SN1*, *F_SN2*, and *F_SN3*, whilst *F_SN4* showed no significant differences. The allele *E_SN3* differed significantly from all four *invGF* alleles.

Biochemical analysis of the P18 *invGE* and *invGF* alleles showed significant differences for both alleles. The allele *E_P40N1* converted sucrose with a lower affinity than the allele *F_P40N2*. The *invGF* alleles of P54 possessed a slightly lower affinity to sucrose than the P54 *invGE* alleles.

3.2.2.4 Western blot analysis of *invGE* and *invGF* invertase proteins

To analyze whether the observed differences of invertase activity of *invGE* and *invGF* alleles are due to changes in protein quantity, it is necessary to perform immunoblot quantification. From all invertase antibodies tested (chapter 2, Table 2.2.15), no satisfiying *invGE* and *invGF* protein detection pattern were obtained. Therefore, a specific antibody against potato invertases was custom produced by BioGenes, Gesellschaft für Biopolymere mbH (Berlin) and is subject of ongoing investigations of this project.

3.3 The *Invap-a* locus on chromosome X

The *Inv$_{ap}$-a* locus consists of the two invertase genes *pCD111* and *pCD141,* and encodes cell wall-bound invertase isoforms. These acidic insoluble invertases act in a pH optimum range of 3.5 to 5.1, and are functional in the apoplast (HEDLEY ET AL., 1993, 1994). cDNA of *pCD111* (incomplete sequence; accession: Z21486) and *pCD141* (accession: Z22645) have been cloned and structurally characterized (HEDLEY ET AL. 1993, 1994).

3.3.1 Structural characterization of the genes *pCD111* and *pCD141*

3.3.1.1 Molecular cloning of *pCD111* and *pCD141* invertase cDNA alleles from leaf tissue

Using full-length gene specific primers, cDNA invertase alleles of *pCD111* and *pCD141* were cloned and sequenced from the three tetraploid potato cultivars 'Satina', 'Diana' and 'Theresa', and from the three diploid potato genotypes P18, P40, and P54. The tetraploid genotypes were selected based on the presence of the associated SSCP fragment from the *pCD141* gene (LI ET AL., 2008; Table 3.3.1) and, therefore, were chosen in this study. The diploid potato genotypes were included because they were used as parents for mapping QTLs and candidate genes for cold sweetening of potato tubers (MENÉNDEZ ET AL., 2002).

Table 3.3.1: Distribution of the associated SSCP fragment *pCD141_3c* present in the tetraploid genotypes 'Satina', 'Diana', and 'Theresa'.

Genotype	*pCD141-3c*
'Satina'	1
'Diana'	0
'Theresa'	0

0=SSCP fragment is absent, 1=SSCP fragment is present. Primers used for the amplification of the fragment *pCD141-3* are listed in chapter 2 (Table 2.1.8).

Out of 40 cloned cDNA sequences per genotype, a sequence was defined as an allele when it was detected twice in two independent PCRs[9]. Additionally, the consensus sequence of all alleles found in one genotype was used for allele definition when variable sequence polymorphisms occurred. For the genes *pCD111* and *pCD141* not every allele was detected twice in two independent PCRs due to the focus on the genes *Pain-1* (section 3.1), *invGE*, and *invGF* (section 3.2) because at the beginning of this work less information about association and putative allelic effects on potato chips quality of *pCD111* and *pCD141* was available.
pCD111 and *pCD141* invertase alleles obtained from each genotype are listed in Table 3.3.2.

[9] Exceptions are listed in Appendix A 3.3.

Table 3.3.2: Overview of *pCD111* and *pCD141* alleles.

Genotype	Full-length clones	*pCD111* alleles	Full-length clones	*pCD141* alleles
'Satina'	5	*pCD111_S1* *pCD111_S2* *pCD111_S3*	6	*pCD141_S1* *pCD141_S2* *pCD141_S3*
'Diana'	1	*pCD111_D1*	5	*pCD141_D1* *pCD141_D2*
'Theresa'	4	*pCD111_T1* *pCD111_T2*	6	*pCD141_T1* *pCD141_T2* *pCD141_T3*
P18	0	0	5	*pCD141_P18_1* *pCD141_P18_2*
P40	1	*pCD111_P40_1*	2	*pCD141_P40_1*
P54	3	*pCD111_P54_1* *pCD111_P54_2*	4	*pCD141_P54_1* *pCD141_P54_2*

The full-length clone number refers to the number of fully sequenced clones from each genotype used for allele definition. PCR amplification was carried out using gene specific full-length primers: *pCD111*-CD111fl_F/CD111fl_R (chapter 2, Table 2.1.2), *pCD141*-CD141fl_F/CD141fl_R (chapter 2, Table 2.1.2).

In 'Theresa', P18, and P40 cDNA sequences were found, which contained internal frame shifts and missing or modified start or stop codons in gene *pCD111*. These sequences were excluded from the analysis. From all six genotypes selected in this study, nine *pCD111* and 13 *pCD141* alleles were identified

3.3.1.1.1 *pCD111* cDNA alleles of the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'[10]

From five full-length cDNA clones of the genotype 'Satina' three different alleles *pCD111_S1, pCD111_S2*, and *pCD111_S3* were identified. For the cultivar 'Diana' one full-length clone was obtained and named *pCD111_D1*. Cloning and sequencing of 'Theresa' cDNA resulted in four full-length clones, from which two *pCD111* alleles *pCD111_T1* and *pCD111_T2* were defined.

Comparing all six alleles at nucleotide level (Appendix A 3.3.6), 47 single nucleotide polymorphisms (SNPs) were detected, 30 of them resulted in an amino acid exchange (Table 3.3.3; Figure 3.3.1).

[10] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: 'Satina' (Appendix A 3.3.1), 'Theresa' (Appendix A 3.3.2). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *pCD111_S1* (Appendix A 3.3.3), *pCD111_S2* (Appendix A 3.3.4), *pCD111_T2* (Appendix A 3.3.5). For the alleles *pCD111_S3*, *pCD111_D1,* and *pCD111_T1* only one nucleotide sequence was obtained, respectively.

Table 3.3.3: SNPs present in 'Satina', 'Diana', and 'Theresa' *pCD111* alleles.

Position of cDNA SNP	*pCD111 S1*	*pCD111 S2*	*pCD111 S3*	*pCD111 D1*	*pCD111 T1*	*pCD111 T2*	aa
181	A	A	A	A	C	A	C/A Q61N
183	A	T	A	A	A	T	A/T K61N
207	C	C	T	T	C	C	s.
267	T	T	A	A	A	T	s.
303	C	C	G	G	C	C	s.
357	T	C	T	T	T	C	s.
478	A	G	G	G	G	G	A/G N160D
635	G	A	G	G	G	A	G/A G212E
640	C	A	C	C	C	A	C/A Q214K
668	A	G	A	A	A	G	A/G K223R
670	A	G	A	A	A	G	A/G N224D
675	C	C	C	C	A	C	C/A L225F
691	A	G	A	A	A	G	A/G I231V
693	T	C	T	T	T	C	T/C I231V
697	C	G	C	C	C	G	C/G H233D
750	T	C	T	T	T	C	s.
780	G	A	G	G	G	A	s.
815	C	C	T	T	T	C	T/C V272A
858	A	C	A	A	C	C	s.
865	A	A	A	A	C	A	C/A Q289K
866	T	A	T	T	A	A	T/A I289K
897	A	C	A	A	A	C	s.
920	G	T	G	G	G	G	G/T W307
924	G	C	G	G	G	C	G/C K308N
939	C	C	T	T	C	C	s.
972	T	T	C	C	T	T	s.
977	C	T	C	C	C	T	C/T P326L
981	C	G	C	C	C	G	C/G S327R
1039	G	G	A	A	G	G	G/A V347I
1056	A	G	G	G	A	G	s.
1081	T	C	T	T	T	C	s.
1104	G	G	A	A	G	G	s.
1110	G	G	A	A	G	G	s.
1141	C	C	T	T	C	C	C/T L381F
1143	A	A	T	T	A	A	A/T L381F

Position of cDNA SNP	*pCD111 S1*	*pCD111 S2*	*pCD111 S3*	*pCD111 D1*	*pCD111 T1*	*pCD111 T2*	aa
1182	G	C	C	C	C	C	G/C K394N
1245	T	C	C	C	T	C	s.
1252	T	T	T	T	A	T	A/T T418S
1273	C	C	C	C	A	C	A/C T425P
1286	A	A	G	A	A	A	A/G N429S
1292	A	C	C	C	A	C	A/C D431A
1334	C	C	C	C	T	C	T/C M445T
1401	G	A	G	G	G	A	s.
1426	G	G	A	A	G	G	G/A A476T
1432	G	A	G	G	G	A	G/A D478N
1464	A	A	C	C	A	A	s.
1538	T	C	C	C	C	C	T/C I513T

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured.

The six *pCD111* alleles from the three tetraploid potato cultivars displayed 47 SNPs resulting in 26 variable amino acid positions because at protein sequence positions 61 and 289 three different amino acids are displayed (Figure 3.3.1). The three alleles of 'Satina' had a total of 41 SNPs, of which 24 caused an amino acid exchange. In the two allelic sequences of 'Theresa' 29 SNPs occurred, from which 19 resulted in amino acid substitutions.

The amino acid alignment shows the polymorphisms of all six *pCD111* alleles from the three tetraploid potato cultivars. The comparison of these deduced protein sequences revealed variable amino acid positions in the different genotypes seen in red, yellow, and grey (Figure 3.3.1).

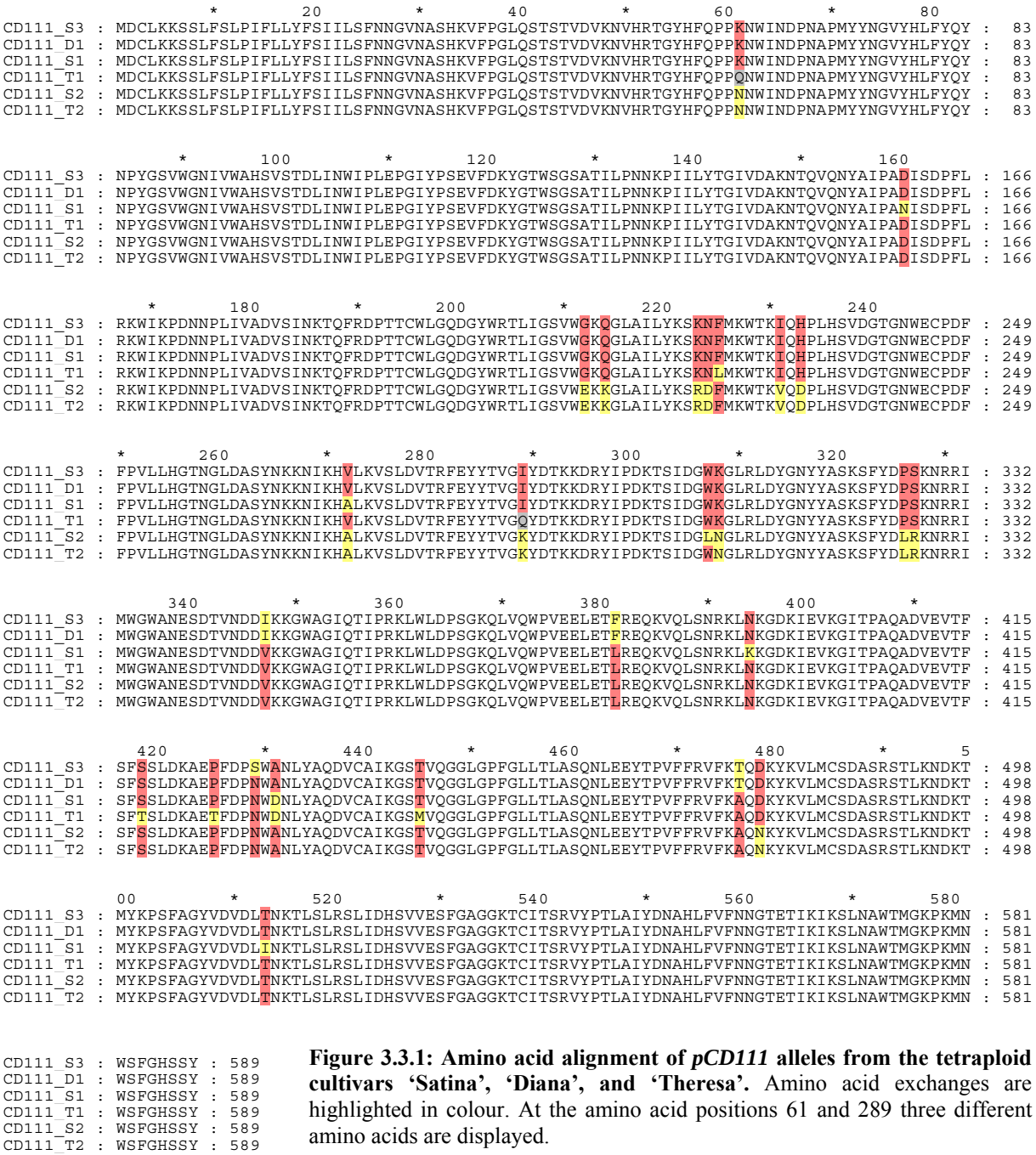


Figure 3.3.1: Amino acid alignment of *pCD111* alleles from the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'. Amino acid exchanges are highlighted in colour. At the amino acid positions 61 and 289 three different amino acids are displayed.

Comparison of allelic cDNA sequences of the gene *pCD111* from the three tetraploid cultivars revealed that none of the six alleles is present in different genotypes.

3.3.1.1.2 pCD111 cDNA alleles of the diploid potato genotypes P18, P40, and P54[11]

From the genotype P18 no full-length cDNA alleles were obtained. The cloned sequences either did not feature the start codon of the gene, or the reading frame was shifted resulted in a sequence, which could not be used for further analysis. Cloning and sequencing of P40 cDNA

[11] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: P54 (Appendix A 3.3.7). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *pCD111_P54_1* (Appendix A 3.3.8). For the alleles *pCD111_P40_1* and *pCD111_P54_2* only one full-length nucleotide sequence was obtained, respectively.

produced one full-length clone. The allele was named *pCD111_P40_1*. In P54 three full-length clones were found, and two different alleles, *pCD111_P54_1* and *pCD111_P54_2,* were identified.

The nucleotide sequence comparison (Appendix A 3.3.9) of the alleles described above detected 42 SNPs. 22 of them led to amino acid exchanges (Table 3.3.4; Figure 3.3.2).

Table 3.3.4: SNPs present in P40 and P54 alleles.

Position of cDNA SNP	*pCD111_P40_1*	*pCD111_P54_1*	*pCD111_P54_2*	aa
183	A	T	T	A/T K61N
207	T	C	C	s.
267	A	T	T	s.
303	G	C	G	s.
357	T	C	C	s.
360	C	C	T	s.
389	C	C	T	C/T P133L
407	A	A	C	A/C K136T
421	T	T	C	T/C Y141H
633	G	G	C	G/C W211C
635	G	A	A	G/A G212E
640	C	A	A	C/A Q214K
668	A	G	G	A/G K223R
670	A	G	G	A/G N224D
691	A	G	G	s.
693	T	C	C	T/C I231V
697	C	G	G	C/G H233D
750	T	C	C	s.
780	G	A	G	s.
815	T	C	T	C/T A272V
858	A	C	C	s.
866	T	A	A	T/A I289K
897	A	C	C	s.
924	G	C	G	C/G N308K
939	T	C	C	s.
972	C	T	T	s.
977	C	T	T	C/T P326L
981	C	G	G	C/G S327R
1039	A	G	G	A/G I347V
1081	T	C	C	s.
1104	A	G	G	s.
1110	A	G	G	s.

Position of cDNA SNP	*pCD111_P40_1*	*pCD111_P54_1*	*pCD111_P54_2*	aa
1141	T	C	C	s.
1143	T	A	A	T/A F381L
1302	T	T	C	s.
1382	A	A	G	A/G Q461R
1401	G	A	A	s.
1404	G	G	A	s.
1426	A	G	G	A/G T476A
1432	G	A	G	A/G N478D
1464	C	A	A	s.
1757	G	A	A	G/A R586H

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured.

In the two P54 allelic sequences *pCD111_P54_1* and *pCD111_P54_2* 10 SNPs occurred. Eight of them caused an amino acid substitution.

The amino acid alignment of the P40 allele *pCD111_P40_1,* and the P54 alleles *pCD111_P54_1* and *pCD111_P54_2* showed 22 polymorphisms. (Figure 3.3.2).

```
                    *        20         *        40         *        60         *        80
CD111_P541 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81
CD111_P542 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81
CD111_P401 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFY :  81

                  *       100         *       120         *       140         *       160
CD111_P541 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_P542 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILLNNTPIILHTGIVDAKNTQVQNYAIPADIS : 162
CD111_P401 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162

                *       180         *       200         *       220         *       240
CD111_P541 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243
CD111_P542 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVCEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243
CD111_P401 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGN : 243

                  *       260         *       280         *       300         *       320
CD111_P541 : WECPDFFPVLLHGTNGLDASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFY : 324
CD111_P542 : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_P401 : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324

                    *       340         *       360         *       380         *       400
CD111_P541 : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_P542 : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_P401 : DPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSNRKLNKGDKIEVKGIT : 405

                  *       420         *       440         *       460         *       480
CD111_P541 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCS : 486
CD111_P542 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASRNLEEYTPVFFRVFKAQDKYKVLMCS : 486
CD111_P401 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCS : 486

                    *       500         *       520         *       540         *       560
CD111_P541 : DASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_P542 : DASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_P401 : DASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567

                  *       580
CD111_P541 : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_P542 : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_P401 : KSLNAWTMGKPKMNWSFGRSSY : 589
```

Figure 3.3.2: Amino acid alignment of *pCD111* alleles from the diploid genotypes P40 and P54. Amino acid exchanges are highlighted in colour.

3.3.1.1.3 Amino acid alignment of all *pCD111* invertase alleles of the analyzed potato genotypes

Multiple alignment of the nine *pCD111* deduced protein sequences revealed partially overlapping amino acid polymorphisms between the tetraploid and diploid genotypes (Figure 3.3.3). Several amino acid exchanges occur in different genotypes at the same position. The comparison of the protein sequences showed that amino acids differed at 32 positions, of which 17 were genotype specific and occurred only once.

```
                    *        20         *        40         *        60         *        80
CD111_S3   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFY :  81
CD111_P401 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFY :  81
CD111_D1   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFY :  81
CD111_S1   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFY :  81
CD111_T1   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPQNWINDPNAPMYYNGVYHLFY :  81
CD111_S2   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81
CD111_T2   : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81
CD111_P541 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81
CD111_P542 : MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFY :  81

                        *       100         *       120         *       140         *       160
CD111_S3   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_P401 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_D1   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_S1   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPANIS : 162
CD111_T1   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_S2   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_T2   : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_P541 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILPNNKPIILYTGIVDAKNTQVQNYAIPADIS : 162
CD111_P542 : QYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSATILLNNTPIILHTGIVDAKNTQVQNYAIPADIS : 162

                    *       180         *       200         *       220         *       240
CD111_S3   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGN : 243
CD111_P401 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGN : 243
CD111_D1   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGN : 243
CD111_S1   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGN : 243
CD111_T1   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNLMKWTKIQHPLHSVDGTGN : 243
CD111_S2   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243
CD111_T2   : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243
CD111_P541 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243
CD111_P542 : DPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVCEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGN : 243

                        *       260         *       280         *       300         *       320
CD111_S3   : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_P401 : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_D1   : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_S1   : WECPDFFPVLLHGTNGLDASYNKKNIKHALKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_T1   : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGQYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324
CD111_S2   : WECPDFFPVLLHGTNGLDASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGLNGLRLDYGNYYASKSFY : 324
CD111_T2   : WECPDFFPVLLHGTNGLDASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFY : 324
CD111_P541 : WECPDFFPVLLHGTNGLDASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFY : 324
CD111_P542 : WECPDFFPVLLHGTNGLDASYNKKNIKHVLKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFY : 324

                    *       340         *       360         *       380         *       400
CD111_S3   : DPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_P401 : DPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_D1   : DPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_S1   : DPSKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLKKGDKIEVKGIT : 405
CD111_T1   : DPSKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_S2   : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_T2   : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_P541 : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405
CD111_P542 : DLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSNRKLNKGDKIEVKGIT : 405

                      *       420         *       440         *       460         *       480
CD111_S3   : PAQADVEVTFSFSSLDKAEPFDPSWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCS : 486
CD111_P401 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCS : 486
CD111_D1   : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCS : 486
CD111_S1   : PAQADVEVTFSFSSLDKAEPFDPNWDNLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCS : 486
CD111_T1   : PAQADVEVTFSFTSLDKAETFDPNWDNLYAQDVCAIKGSMVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCS : 486
CD111_S2   : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCS : 486
CD111_T2   : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCS : 486
CD111_P541 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCS : 486
CD111_P542 : PAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASRNLEEYTPVFFRVFKAQDKYKVLMCS : 486
```

```
                *       500         *       520         *       540         *       560
CD111_S3   : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_P401 : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_D1   : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_S1   : DASRSTLKNDKTMYKPSFAGYVDVDLLINKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_T1   : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_S2   : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_T2   : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_P541 : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567
CD111_P542 : DASRSTLKNDKTMYKPSFAGYVDVDLLTNKTLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKI : 567

                *       580
CD111_S3   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_P401 : KSLNAWTMGKPKMNWSFGRSSY : 589
CD111_D1   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_S1   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_T1   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_S2   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_T2   : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_P541 : KSLNAWTMGKPKMNWSFGHSSY : 589
CD111_P542 : KSLNAWTMGKPKMNWSFGHSSY : 589
```

Figure 3.3.3: Amino acid alignment of all cloned *pCD111* invertase alleles. Amino acid exchanges are highlighted in colour. At the amino acid positions 61 and 289 three different amino acids are displayed.

Comparison of cDNA sequences revealed that the alleles *pCD111_T2* and *pCD111_P54_1* are identical at amino acid level.

3.3.1.1.4 Phenetic trees of all *pCD111* invertase alleles of the analyzed potato genotypes

In addition to the multiple amino acid alignment (3.3.1.1.3), the phenetic tree analysis was used to group the invertase alleles according to similarity. Using the neighbour-joining method showed that *pCD111* alleles from all analyzed potato genotypes grouped in two clades and five subclades (Figure 3.3.4).

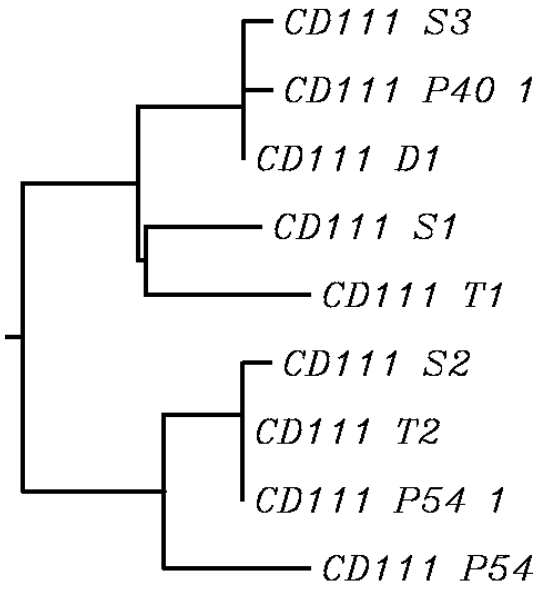


Figure 3.3.4: Amino acid based phenetic tree (Neighbour-joining tree) of all cloned *pCD111* invertase alleles.

The first clade includes alleles *pCD111_S1*, *pCD111_S3*, *pCD111_D1*, *pCD111_T1*, and *pCD111_P40_1*. The second clade consists of *pCD111_S2*, *pCD111_T2*, and the two alleles from the diploid genotype P54 *pCD111_P54_1* and *pCD111_P54_2*. Most alleles of both

clades differ in one or more amino acid positions. The alleles *pCD111_T2* and *pCD111_P54_1* are identical at amino acid level.

Cloning and sequencing of *pCD111* alleles showed that the tetraploid genotype 'Theresa' and the diploid genotype P54 contained an allele identical in amino acid sequence but different at nucleotide level. The following Table 3.3.5 summarizes the nucleotide comparison of the two amino acid identical alleles *pCD111_T2* and *pCD111_P54_1*. The allelic nucleotide sequence was defined based on the consensus sequence of the alignment of full-length clones obtained from each genotype (Table 3.3.2). Although SNPs are present at four positions in the cDNAs, the nucleotide polymorphisms resulted in one and the same amino acid sequence.

Table 3.3.5: Genotype specific nucleotide differences of alleles identical at amino acid level.

Position of cDNA SNP	*pCD111_T2*	*pCD111_P54_1*
21	C	T
111	A	T
681	A	G
801	G	A

The nucleotide polymorphisms between all *pCD111* (Appendix A 3.3.10) were visualized using the phenetic tree analysis (Figure 3.3.5).

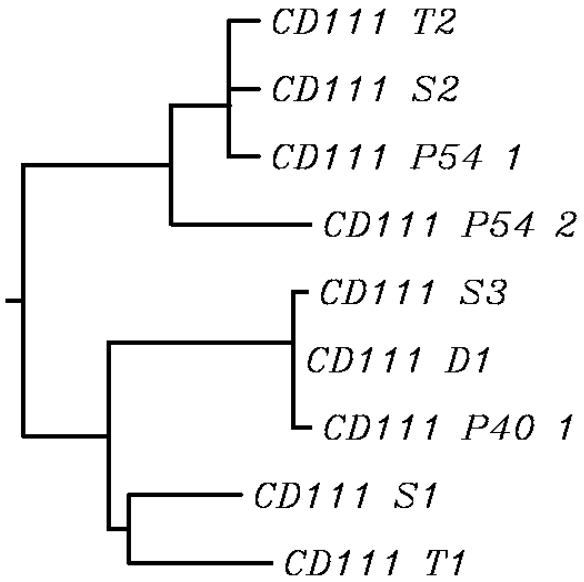


Figure 3.3.5: Nucleotide sequence based phenetic tree (Neighbour-joining tree) of all cloned *pCD111* invertase alleles.

The two phenetic trees are very similar, just displaying more subclades due to a higher number of nucleotide polymorphisms as compared to the amino acid exchanges (Figure 3.3.4).

3.3.1.1.5 *pCD141* cDNA alleles of the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'[12]

Cloning and sequencing of cDNA of the cultivar 'Satina' resulted in six full-length clones, from which three *pCD141* alleles *pCD141_S1*, *pCD141_S2*, and *pCD141_S3* were identified. For the cultivar 'Diana' five full-length clones were obtained, and of those two different alleles *pCD141_D1* and *pCD141_D2* were defined. From the cultivar 'Theresa' six full-length clones were isolated and led to the definition of three different alleles *pCD141_T1*, *pCD141_T2*, and *pCD141_T3*.

At nucleotide level (Appendix A 3.3.19) the alleles contain 62 SNPs but not all of them are causative for amino acid exchanges (Table 3.3.6; Figure 3.3.6).

Table 3.3.6: SNPs present in 'Satina', 'Diana', and 'Theresa' *pCD141* alleles.

Position cDNA SNP	*pCD141 S1*	*pCD141 S2*	*pCD141 S3*	*pCD141 D1*	*pCD141 D2*	*pCD141 T1*	*pCD14 1T2*	*pCD141 T3*	aa
57	C	T	C	C	C	T	C	C	s.
140	C	T	C	C	C	T	C	C	T/C V47A
178	C	C	T	C	C	C	C	C	C/T P60S
186	C	T	C	C	C	T	C	C	s.
207	T	T	T	C	C	T	C	C	s.
276	C	T	T	T	T	T	T	T	s.
280	A	G	G	G	G	G	G	G	A/G I94V
378	C	C	C	T	T	C	T	T	s.
426	C	T	T	T	T	C	T	T	s.
440	C	C	C	G	G	C	G	G	C/G A147G
444	T	C	C	T	T	T	T	T	s.
462	T	C	T	C	C	C	C	C	s.
474	G	A	G	G	G	G	G	G	s.
483	G	A	G	G	G	G	G	G	G/A M161I
508	A	A	A	A	A	A	A	G	A/G I170V
582	A	A	A	C	C	A	C	C	s.
601	G	G	A	G	G	G	G	G	G/A G201R
621	T	T	T	A	A	A	A	A	s.
624	G	G	G	C	C	C	C	C	s.
667	A	G	A	A	A	A	A	A	A/G N223D

[12] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: 'Satina' (Appendix A 3.3.11), 'Diana' (Appendix A 3.3.12), 'Theresa' (Appendix A 3.3.13). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *pCD141_S2* (Appendix A 3.3.14), *pCD141_S3* (Appendix A 3.3.15), *pCD141_D1* (Appendix A 3.3.16), *pCD141_T1* (Appendix A 3.3.17), *pCD141_T2* (Appendix A 3.3.18). For the alleles *pCD141_S1, pCD141_D2,* and *pCD141_T3* only one full-length nucleotide sequence was obtained, respectively.

Position cDNA SNP	*pCD141 S1*	*pCD141 S2*	*pCD141 S3*	*pCD141 D1*	*pCD141 D2*	*pCD141 T1*	*pCD14 1T2*	*pCD141 T3*	aa
673	A	G	A	A	A	A	A	A	A/G N225D
714	A	C	A	A	A	A	A	A	s.
717	T	C	C	C	C	C	C	C	s.
720	C	G	C	C	C	C	C	C	s.
765	A	G	A	A	A	A	A	A	s.
775	G	A	G	G	G	G	G	G	G/A D259N
798	T	T	T	C	C	C	C	C	s.
843	T	T	T	A	A	A	A	A	s.
862	A	G	A	A	A	A	A	A	A/G I288V
889	A	A	A	C	C	C	C	C	s.
891	G	A	A	G	G	G	G	G	s.
892	C	T	T	T	T	T	T	T	C/T H298Y
905	A	A	A	G	G	G	G	G	A/G N302S
939	T	T	T	C	C	C	C	C	s.
980	G	A	G	G	G	G	G	G	G/A S327N
1029	T	T	G	T	T	T	T	T	s.
1030	C	G	G	G	G	G	G	G	C/G R344V
1031	G	T	T	T	T	T	T	T	G/T R344V
1059	C	T	C	C	C	C	C	C	s.
1096	T	C	C	C	C	C	C	C	T/C S366P
1135	T	T	C	T	T	T	T	T	s.
1188	G	A	G	G	G	G	G	G	s.
1224	A	T	A	A	A	A	A	A	s.
1255	G	A	A	A	A	A	A	A	G/A A419T
1266	A	T	T	C	C	C	C	C	A/T E422D
1277	T	C	C	C	C	C	C	C	T/C L426P
1368	C	C	C	A	A	A	A	A	s.
1416	T	T	T	C	C	C	C	C	s.
1434	A	A	A	T	T	T	T	T	A/T Q478H
1446	G	A	A	A	A	A	A	A	s.
1467	C	T	T	C	C	C	C	C	s.
1503	T	C	C	T	T	T	T	T	s.
1541	C	C	C	C	T	C	C	C	C/T A514V
1542	A	G	G	G	G	G	G	G	s.
1560	T	T	T	C	C	C	C	C	s.
1582	G	G	G	A	A	A	A	A	G/A V528I
1614	G	A	A	A	A	A	A	A	s.
1629	G	G	G	A	A	A	A	A	s.
1641	A	G	G	G	G	G	G	G	s.
1674	C	A	A	A	A	A	A	A	s.
1680	C	C	T	C	C	C	C	C	s.
1683	T	C	C	C	C	C	C	C	s.

SNP position numbering refers to cDNA sequence where ‘1’ represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured.

The eight *pCD141* alleles of the tetraploid cultivars differed in 62 SNPs, from which 23 resulted in an amino acid substitution. From 41 SNPs of the three ‘Satina’ alleles, 17 caused an amino acid exchange. The two ‘Diana’ alleles possessed two SNPs, from which one resulted in an amino acid substitution. The three ‘Theresa’ alleles differed in nine SNPs. Three of them led to an amino acid exchange.

The amino acid alignment highlights the differences of all cloned *pCD141* alleles from the three tetraploid potato cultivars (Figure 3.3.6). Positions of genotype dependent amino acid exchanges were revealed.

```
                  *        20         *        40         *        60         *        80
CD141_T2 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_T3 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_D1 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_D2 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_T1 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_S2 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_S3 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPSKNWINDPNGPMYYNGVYHLFYQY :  83
CD141_S1 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQY :  83

                  *       100         *       120         *       140         *       160
CD141_T2 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYL : 166
CD141_T3 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYL : 166
CD141_D1 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYL : 166
CD141_D2 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYL : 166
CD141_T1 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYL : 166
CD141_S2 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANISDPYL : 166
CD141_S3 : NPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYL : 166
CD141_S1 : NPKGAIWGNIIWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYL : 166

                *       180         *       200         *       220         *       240
CD141_T2 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_T3 : RKWVKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_D1 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_D2 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_T1 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_S2 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSDKDFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_S3 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDRNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249
CD141_S1 : RKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPD : 249

              *       260         *       280         *       300         *       320         *
CD141_T2 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_T3 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_D1 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_D2 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_T1 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_S2 : FFPVSLKNKNGLDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRR : 332
CD141_S3 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332
CD141_S1 : FFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKHFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRR : 332

                340         *       360         *       380         *       400         *
CD141_T2 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_T3 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_D1 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_D2 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_T1 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_S2 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_S3 : ILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415
CD141_S1 : ILLGWANESDTRDNDVRKGWAGVHPIPRKIWLDSSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGITVAQADVEVI : 415

              420         *       440         *       460         *       480         *       5
CD141_T2 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNET : 498
CD141_T3 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNET : 498
CD141_D1 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNET : 498
CD141_D2 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNET : 498
CD141_T1 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNET : 498
CD141_S2 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNET : 498
CD141_S3 : FSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNET : 498
CD141_S1 : FSFASLEKAELFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNET : 498
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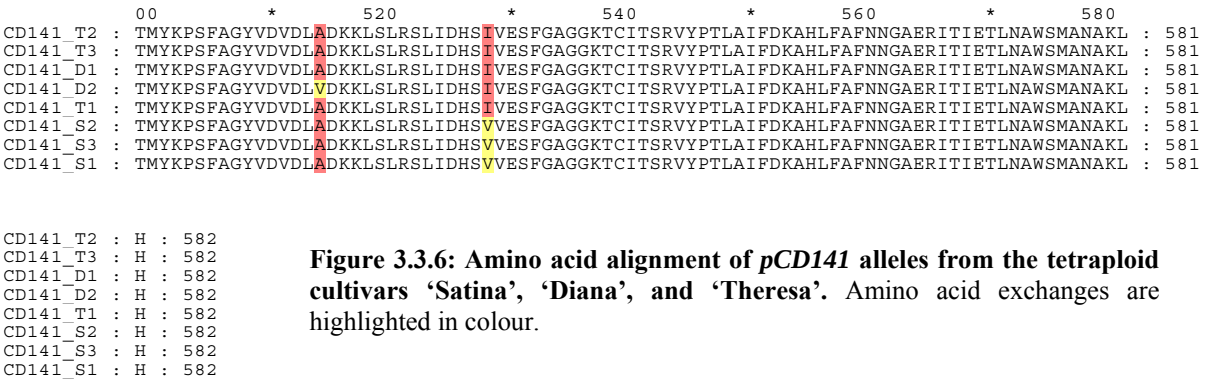

Figure 3.3.6: Amino acid alignment of *pCD141* alleles from the tetraploid cultivars 'Satina', 'Diana', and 'Theresa'. Amino acid exchanges are highlighted in colour.

Comparison of allelic amino acid sequences from the tetraploid cultivars revealed that the genotypes 'Diana' and 'Theresa' harbour an allele identical at amino acid level (*CD141_D1=CD141_T2*).

3.3.1.1.6 pCD141 cDNA alleles of the diploid potato genotypes P18, P40, and P54[13]

From the genotype P18 five full-length clones were obtained, from which two different cDNA alleles *pCD141_P18_1* and *pCD141_P18_2* were identified. Cloning and sequencing of P40 cDNA resulted in two full-length clones identical at amino acid level. The allele was named *pCD141_P40_1*. Sequence comparison suggested a second P40 allele but the clones harbouring an allelic sequence either did not feature the start codon of the gene or the reading frame was shifted, and, therefore, were not used in further analysis. From the genotype P54 four full-length clones were isolated, from which two different alleles *pCD141_P54_1* and *pCD141_P54_2* were defined.

The alleles contain at nucleotide level 64 SNPs (Appendix A 3.3.28). These sequence polymorphisms can cause amino acid exchanges (Table 3.3.7; Figure 3.3.7).

Table 3.3.7: SNPs present in P18, P40, and P54 *pCD141* alleles.

Position of cDNA SNP	*pCD141 P18_1*	*pCD141 P18_2*	*pCD141 P40_1*	*pCD141 P54_1*	*pCD141 P54_2*	aa
57	T	C	C	C	C	s.
101	T	T	T	T	C	T/C A34V
140	T	C	C	C	C	T/C V47A
141	T	T	T	T	A	s.
153	T	T	T	C	T	s.

[13] Alleles of each genotype were defined by alignment of all fully sequenced cDNA clones: P18 (Appendix A 3.3.20), P40 (Appendix A 3.3.21), P54 (Appendix A 3.3.22). The nucleotide sequence for one allele was defined by aligning all obtained nucleotide sequences for this allele and using the consensus sequence when SNPs occurred: *pCD141_P18_1* (Appendix A 3.3.23), *pCD141_P18_2* (Appendix A 3.3.24), *pCD141_P40_1* (Appendix A 3.3.25), *pCD141_P54_1* (Appendix A 3.3.26), *pCD141_P54_2* (Appendix A 3.3.27). For the allele *pCD141_P40_2* only one full-length nucleotide sequence was obtained.

Position of cDNA SNP	*pCD141 P18_1*	*pCD141 P18_2*	*pCD141 P40_1*	*pCD141 P54_1*	*pCD141 P54_2*	aa
186	T	C	C	C	C	s.
195	C	C	C	T	C	s.
207	C	T	C	C	T	s.
231	T	C	T	T	C	s.
276	T	C	T	T	C	s.
378	C	C	T	C	C	s.
440	C	C	G	C	C	G/C G147A
444	C	C	T	T	T	s.
462	T	T	C	C	C	s.
582	A	C	C	C	C	s.
585	A	T	A	T	T	s.
621	T	A	A	T	T	s.
624	G	G	C	G	G	s.
701	A	T	A	A	A	A/T H234I
714	G	G	A	A	A	s.
717	C	C	C	C	T	s.
720	G	C	C	G	G	s.
761	C	C	C	C	T	C/T S254L
765	G	A	A	G	G	s.
775	A	G	G	A	A	A/G N259D
798	T	T	C	T	T	s.
843	T	A	A	A	A	s.
862	G	A	A	A	A	G/A V288I
889	A	A	C	A	A	C/A K297Q
891	A	G	G	A	A	s.
895	T	A	T	T	T	T/A F299I
905	A	A	G	A	A	A/G N302S
913	A	A	A	A	G	A/G I305V
939	T	T	C	T	T	s.
980	A	G	G	G	G	A/G N327S
1043	T	T	T	T	C	T/C V348A
1143	A	T	T	T	T	s.
1146	G	A	A	A	A	s.
1158	A	G	G	G	G	s.
1188	A	A	G	G	G	s.
1192	G	G	G	A	A	G/A E398K
1224	A	T	A	A	A	s.
1266	T	T	C	T	T	s.
1368	A	C	A	C	C	s.
1390	T	G	T	T	T	T/G L464V
1412	T	T	T	T	C	T/C F417S
1416	C	T	C	T	C	s.

Position of cDNA SNP	*pCD141 P18_1*	*pCD141 P18_2*	*pCD141 P40_1*	*pCD141 P54_1*	*pCD141 P54_2*	aa
1417	A	A	A	A	C	s.
1429	A	G	G	G	G	A/G T477A
1434	T	A	T	T	T	T/A H478Q
1446	G	A	A	G	G	s.
1452	T	T	T	T	C	s.
1461	C	C	C	T	C	s.
1467	C	T	C	C	C	s.
1503	T	C	T	T	T	s.
1542	A	G	G	G	G	s.
1560	T	T	C	T	T	s.
1582	G	G	A	G	G	G/A V528I
1587	G	G	G	C	G	s.
1602	T	T	C	C	T	s.
1613	C	C	C	C	T	C/T T538I
1629	G	G	A	G	G	s.
1641	G	G	G	A	G	s.
1673	C	C	C	T	C	T/C V558A
1674	A	A	A	G	A	s.
1683	C	C	C	C	T	s.
1689	G	G	G	A	G	s.

SNP position numbering refers to cDNA sequence where '1' represents the adenine of the start codon ATG and the polymorphism is described. aa=amino acid exchanges ; s.=synonymous nucleotide exchange that does not lead to an amino acid exchange. Non synonymous nucleotide exchanges lead to an amino acid exchange and are orange coloured.

The five alleles obtained from the three diploid genotypes differed in 64 SNPs, from which 21 resulted in an amino acid exchange. The two P18 alleles differed in 30 SNPs. Nine of them led to an amino acid substitution. In the two P54 allelic sequences 18 SNPs occurred, from which four resulted in an amino acid exchange.

Multiple alignment of the protein sequences of all alleles from the three potato genotypes P18, P40, and P54 showed the variability of positions where amino acids differed (Figure 3.3.7).

```
                    *        20          *        40          *        60          *        80
CD141_P182 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFY :  81
CD141_P401 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFY :  81
CD141_P181 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFY :  81
CD141_P541 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFY :  81
CD141_P542 : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKAYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFY :  81

                   *       100         *       120         *       140         *       160
CD141_P182 : QYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMS : 162
CD141_P401 : QYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPANMS : 162
CD141_P181 : QYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMS : 162
CD141_P541 : QYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMS : 162
CD141_P542 : QYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPANMS : 162

                  *       180         *       200         *       220         *       240
CD141_P182 : DPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKIPLHSAPGTG : 243
CD141_P401 : DPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTG : 243
CD141_P181 : DPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTG : 243
CD141_P541 : DPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTG : 243
CD141_P542 : DPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTG : 243

                 *       260         *       280         *       300         *       320
CD141_P182 : NWECPDFFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYIPDNTSIDGWKGLRLDYGNYYASKTF : 324
CD141_P401 : NWECPDFFPVSLKNKDGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTF : 324
CD141_P181 : NWECPDFFPVSLKNKNGLDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTF : 324
CD141_P541 : NWECPDFFPVSLKNKNGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTF : 324
CD141_P542 : NWECPDFFPVLLKNKNGLDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSVDGWKGLRLDYGNYYASKTF : 324

               *       340         *       360         *       380         *       400
CD141_P182 : FDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGI : 405
CD141_P401 : FDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGI : 405
CD141_P181 : FDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGEKVEIKGI : 405
CD141_P541 : FDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGKKVEIKGI : 405
CD141_P542 : FDSGKNRRILLGWANESDTVDNDARKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLNNKKLNKGKKVEIKGI : 405

                 *       420         *       440         *       460         *       480
CD141_P182 : TVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNVEEYTPVFFRIFKAQDKYKVLMC : 486
CD141_P401 : TVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMC : 486
CD141_P181 : TVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKTHDKYKVLMC : 486
CD141_P541 : TVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMC : 486
CD141_P542 : TVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVSFRIFKAHDKYKVLMC : 486

              *       500         *       520         *       540         *       560
CD141_P182 : SDASRSSLKNETTMYKPSFAGYVDVDLADKKLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERIT : 567
CD141_P401 : SDASRSSLKNETTMYKPSFAGYVDVDLADKKLSLRSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERIT : 567
CD141_P181 : SDASRSSLKNETTMYKPSFAGYVDVDLADKKLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERIT : 567
CD141_P541 : SDASRSSLKNETTMYKPSFAGYVDVDLADKKLSLRSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFVFNNGAERIT : 567
CD141_P542 : SDASRSSLKNETTMYKPSFAGYVDVDLADKKLSLRSLIDHSVVESFGAGGKICITSRVYPTLAIFDKAHLFAFNNGAERIT : 567

            *       580
CD141_P182 : IETLNAWSMANAKLH : 582
CD141_P401 : IETLNAWSMANAKLH : 582
CD141_P181 : IETLNAWSMANAKLH : 582
CD141_P541 : IETLNAWSMANAKLH : 582
CD141_P542 : IETLNAWSMANAKLH : 582
```

Figure 3.3.7: Amino acid alignment of *pCD141* alleles from the diploid genotypes P18, P40, and P54. Amino acid exchanges are highlighted in colour.

Comparison of allelic cDNA sequences of the gene *pCD141* from the three diploid genotypes revealed that none of the five alleles is present in different genotypes.

3.3.1.1.7 Amino acid alignment of all *pCD141* invertase alleles of the analyzed potato genotypes

The variability of amino acid positions, which exhibit exchanges, was visualized by multiple sequence alignment of *pCD141* invertase alleles (Figure 3.3.8). Several amino acid exchanges occur in different genotypes at the same position. The comparison of the protein sequences showed that amino acids differed at 35 positions, of which 25 were genotype specific and occurred only once.

Comparison of allelic amino acid sequences from the three tetraploid and the three diploid genotypes revealed that the genotypes ‘Diana’, ‘Theresa’, and P40 harbour an allele identical at amino acid level (*CD141_D1=CD141_T2=CD141_P40_1*).

```
                    *        20         *        40         *        60         *        80
CD141_S1    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_S3    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPSKNWINDPNGPMYYNGVYHLF :  80
CD141_P182  : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_T2    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_T3    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_D1    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_D2    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_P401  : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_T1    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_S2    : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_P181  : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_P541  : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80
CD141_P542  : MEILRRSSSLWVLPILLLCFFINNGVFVDASHKAYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLF :  80

                    *       100         *       120         *       140         *       160
CD141_S1    : YQYNPKGAIWGNIIWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_S3    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_P182  : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_T2    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPAN : 160
CD141_T3    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPAN : 160
CD141_D1    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPAN : 160
CD141_D2    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPAN : 160
CD141_P401  : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDGNKTQVQNYAIPAN : 160
CD141_T1    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_S2    : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_P181  : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_P541  : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160
CD141_P542  : YQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSATILPGNKPVILYTGIVDANKTQVQNYAIPAN : 160

                    *       180         *       200         *       220         *       240
CD141_S1    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_S3    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDRNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_P182  : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKIPLHSAP : 240
CD141_T2    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_T3    : MSDPYLRKWVKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_D1    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_D2    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_P401  : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_T1    : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_S2    : ISDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSDKDFMKWTKAKHPLHSAP : 240
CD141_P181  : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_P541  : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
CD141_P542  : MSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAP : 240
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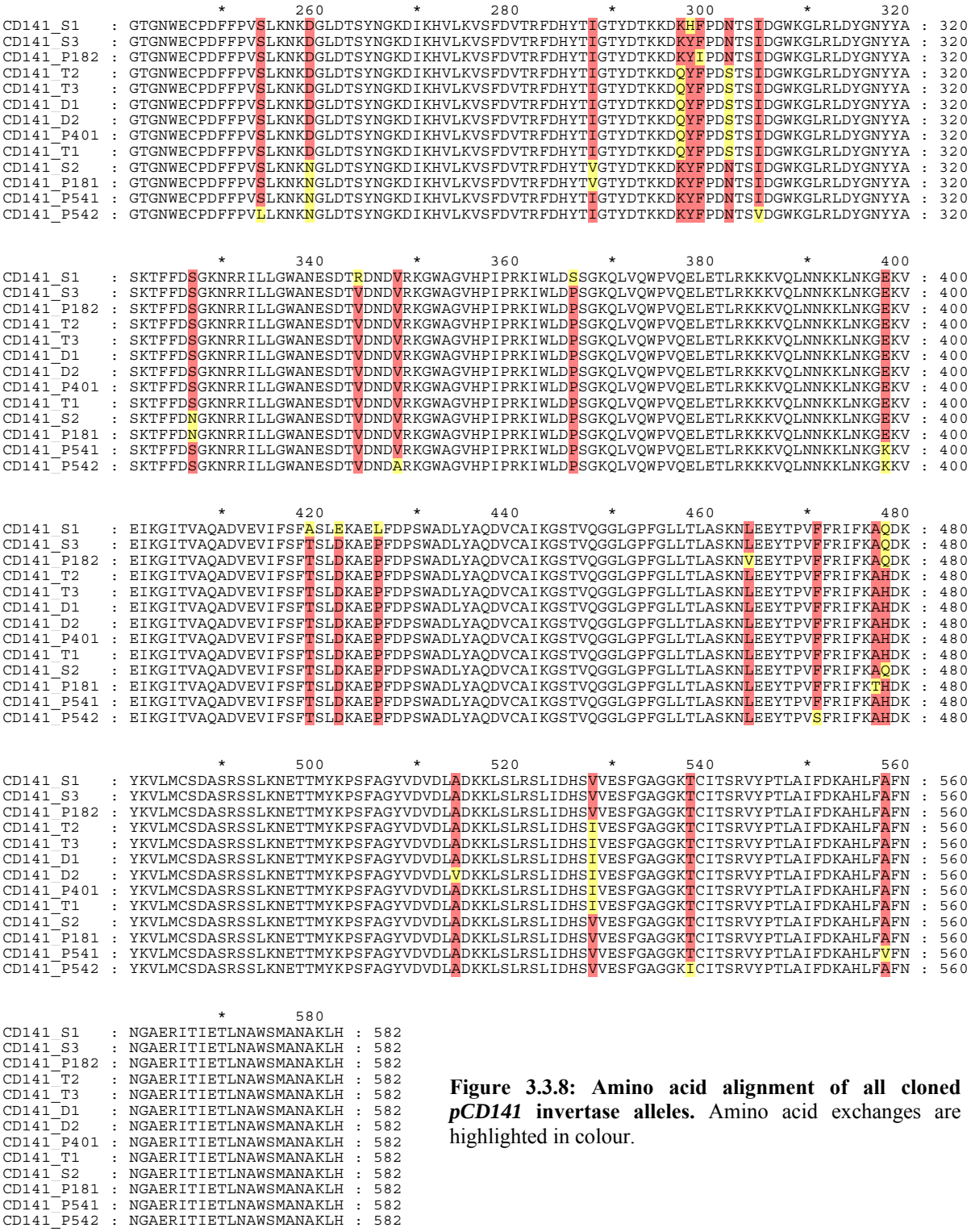

Figure 3.3.8: Amino acid alignment of all cloned *pCD141* invertase alleles. Amino acid exchanges are highlighted in colour.

3.3.1.1.8 Phenetic trees of all pCD141 invertase alleles of the analyzed potato genotypes

To further characterize the invertase alleles in addition to the multiple amino acid alignment (3.3.1.1.7), a phenetic tree analysis was used. Similarity based grouping of *pCD141* alleles using the neighbour-joining method visualized a complex distribution, resulting in two clades and multiple subclades (Figure 3.3.9).

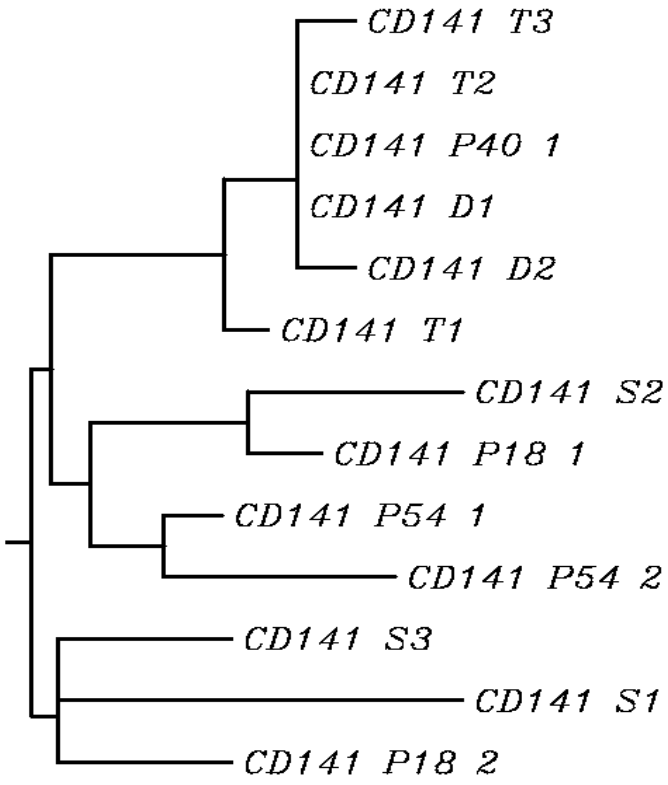

Figure 3.3.9: Amino acid based phenetic tree (Neighbour-joining tree) of all cloned *pCD141* invertase alleles.

The phenetic tree as well as the multiple amino acid alignment revealed the high diversity within the cloned *pCD141* alleles from six different genotypes. The alleles group in two different clades from which the first one consists of two subclades dividing further on.

The first subclade of the first main clade comprises the two 'Diana' alleles, the three 'Theresa' alleles as well as the allele of the diploid potato genotype P40. The alleles *pCD141_D1*, *pCD141_T2*, and *pCD141_P40_1* are identical at amino acid level and, therefore, group together. The second subclade of the first main clade consists of the alleles *pCD141_S2*, *pCD141_P18_1*, and of the two P54 alleles *pCD141_P54_1* and *pCD141_P54_2*. The second main clade contains the alleles *pCD141_S1*, *pCD141_S3*, and *pCD141_P18_2*.

Cloning and sequencing of *pCD141* alleles showed that the alleles *pCD141_D1*, *pCD141_T2*, and *pCD141_P40_1* are identical at amino acid level. Comparison of the nucleotide

sequences revealed that *pCD141_P40_1* differs in one SNP at cDNA position 1602. The P40 allele contains at the given position nucleotide C, whilst *pCD141_D1* and *pCD141_T2* exhibit the nucleotide T.

The nucleotide polymorphisms between all *pCD141* (Appendix A 3.3.29) were visualized using the phenetic tree analysis (Figure 3.3.10).

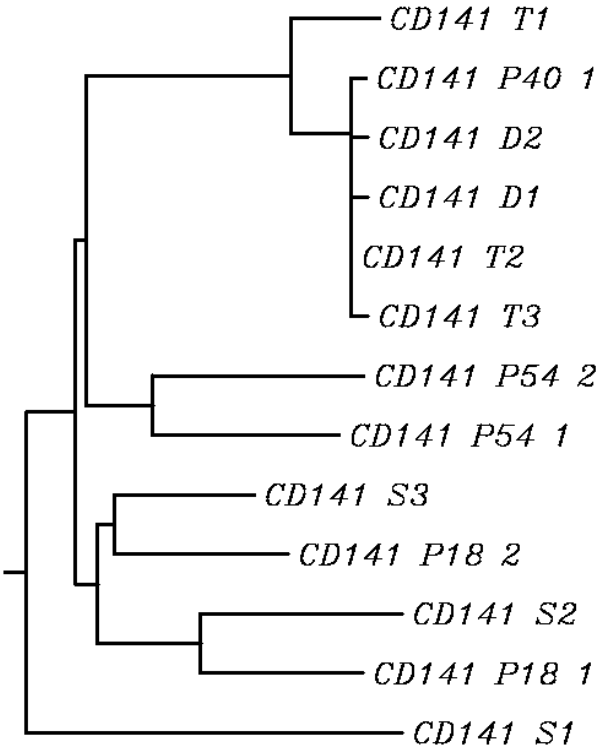

Figure 3.3.10: Nucleotide sequence based phenetic tree (Neighbour-joining tree) of all cloned *pCD141* invertase alleles.

The alleles group regarding their similarity in the same clades and subclades as observed in the amino acid sequences based phenetic tree (Figure 3.3.9). Subclades are more subdivided because of nucleotide polymorphisms.

3.3.1.2 Classification of alleles of the genes *pCD111* and *pCD141*

The genes *pCD111* and *pCD141* map to potato chromosome X (CHEN ET AL., 2001) in a region associated with tuber quality traits where a QTL for potato tuber sugar content, *Sug10a*, was identified (MENÉNDEZ ET AL., 2002). In the latter study, the genes *pCD111* and *pCD141* (referred to Inv_{ap}-*a*) were directly mapped, and showed linkage to the QTL *Sug10a.*

Single-strand conformation polymorphism (SSCP) analysis was carried out for the gene *pCD141* and revealed an association of *pCD141* SSCP fragments with starch and sugar content of potato tubers (LI ET AL., 2008). The SSCP fragment *pCD141_3c* was found to have a negative effect on potato chips quality and tuber starch content. To assign one of the cloned

pCD141 allele (section 3.3.1.1.5/6) to the corresponding associated SSCP fragment, 12 potato cultivars from BNA, SARA, and NOR, respectively were analyzed. To date in none of these 36 genotypes, defined as standards and characterized regarding *pCD141_3c* distribution, associated SNPs could be identified. This is a subject of ongoing investigations in the research project.

3.3.1.3 Genomic organization of the *Invap-a* locus

❖ **BAC library screens**

The genomic sequence and gene organization of the gene pair *pCD111/pCD141* were identified using high density BAC library screens with two different PCR generated probes. Using the primers CD111S2_For/CD111S1_Rev and pCD141-3F/pCD141-3R (chapter 2, Table 2.1.10A), Probe 1 for the gene *pCD111* and Probe 2 for the gene *pCD141* were generated. Both probes consisted of exon based sequences (HEDLEY ET AL. 1993, 1994) of the genes *pCD111* and *pCD141*, respectively.

The screening of two different BAC libraries (BA and BC, BALLVORA ET AL. 2002, 2007) constructed with genomic DNA of the same diploid genotype resulted in six positive BAC clones for the gene *pCD141* (Table 3.3.8). From the *pCD141* positive BACs one clone (BAC BC3) showed full-length PCR amplification of the gene *pCD111*. BAC screens with the specific *pCD111* Probe 1 were negative.

Table 3.3.8: Positive BAC clones for the genes *pCD111* and *pCD141*.

Library	BAC clones *pCD141*	PCR *pCD141*	PCR *pCD111*
BA BAC library	BA1: Plate 28K15	yes	not analyzed
	BA2: Plate 40M19	yes	not analyzed
	BA3: Plate 59E10	yes	not analyzed
BC BAC library	BC1: Plate 37C23	yes	no
	BC2: Plate 146K10	yes	no
	BC3: Plate 163L15	yes	no

PCR for the genes *pCD111* and *pCD141* were performed with gene specific full-length gene primers: *pCD111*-CD111fl_F/CD111fl_R (chapter 2, Table 2.1.2), *pCD141*-CD141fl_F/CD141fl_R (chapter 2, Table 2.1.2). Positive BACs are numbered and their position in the *E. coli* microtiter plate is listed.

BAC library screening and full-length PCR amplification of *pCD111* and *pCD141* within BAC BC3 suggested that this clone contains both invertase genes of interest. BAC insert (size: 130kb) sequencing was carried out by MWG Biotech AG, Ebersberg using the 454 sequencing technique on the GS FLX system.

❖ BAC Annotation

Full-length sequencing of the BAC insert revealed sequence and structural information of the genes *pCD111* and *pCD141* and of flanking genes (Table 3.3.9).

Table 3.3.9: BC3 sequence annotation.

Strand	Apollo name	Position on the BAC insert (bp)	Description
+	gene 10	2,068-2454	response to auxin stimulus
+	gene 20	4,655-13,035	kinesin
+	**gene 30**	**31,961-36,971**	**cell wall invertase *pCD111,*** beta-fructofuranosidase (glycoside hydrolase family 32)
+	**gene 40**	**44,311-48,793**	**cell wall invertase *pCD141***, beta-fructofuranosidase (glycoside hydrolase family 32)
+	gene 50	62,479-64,535	GTP-binding protein
+	gene 60	69,953-71,012	unknown
+	gene 70	73,520-74,558	putative integral membrane family protein
+	gene 80	75,343-78,806	putative RNA-binding protein
+	gene 90	85,626-88,464	putative embryo defective protein
+	gene 100	122,735-125,703	unknown
-	gene 110	54,022-51,302	putative ribosomal protein
-	gene 120	58,824-55,722	putative esterase lipase
-	gene 130	68,349-66,377	putative dynamin
-	gene 140	81,608-80,442	unknown
-	gene 150	94,506-89,268	DNA-binding protein
-	gene 160	109,512-106,330	Pre-mRNA splicing factor

The invertase genes were named ‘gene 30’ (*pCD111*) and ‘gene 40’ (*pCD141*) in the Apollo BAC sequence characterization. BAC annotation was carried out using the software Apollo Genome Annotation and Curation Tool, version 1.9.8. Both invertase genes are written in bold.

The screened BAC libraries BA and BC harbour genomic DNA of the same diploid genotype P6/210, which is a hybrid derived from the cross of the parental genotypes P40 x P41 (LEISTER ET AL., 1996). The genotype P40 was also selected in this study for invertase allele characterization. Sequence alignments of P40 cDNA alleles from *pCD111* and *pCD141* with the genomic sequences of the genes 30 (*pCD111,* Appendix A 3.3.30) and 40 (*pCD141,* Appendix A 3.3.31) from the BAC BC3 showed no sequence identity. Since only one P40 cDNA allele from *pCD111* and *pCD141* respectively, was cloned it is possible that the second not detected P40 allele corresponds to the BAC sequences, or that the detected BAC allele for the genes *pCD111* and *pCD141* originate from the other parental genotype P41.

❖ Structural characterization of the genes *pCD111* and *pCD141*

The exon and intron organization of the genes *pCD111* and *pCD141* was determined by aligning the *pCD111* (Appendix A 3.3.32[14]) and *pCD141* (Appendix A 3.3.33[15]) cDNA alleles and the genomic sequences of the corresponding genes from BAC BC3. Both genes consist of six exons and five introns (Figure 3.3.11). The gene *pCD111* has a length of 5012bp, whilst the gene size of *pCD141* is 4478bp.

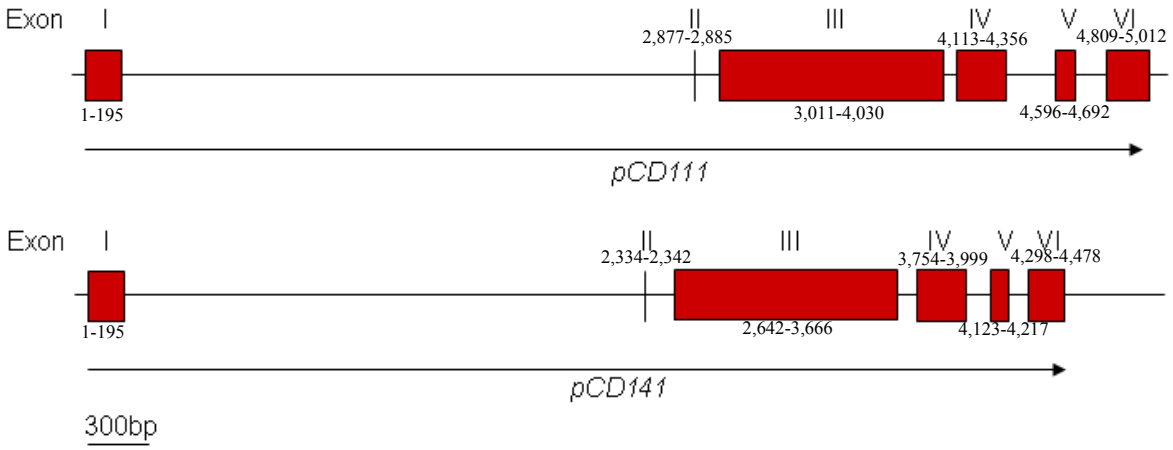

Figure 3.3.11: Genomic organization of the genes *pCD111* and *pCD141*. Exons are drawn in red and numbered from I to VI. The arrows symbolize the whole length of the particular gene without promoter and terminator sequences.

The range of individual *pCD111* and *pCD141* exons and introns are summarized in Table 3.3.10.

Table 3.3.10: Ranges of exons and introns of the genes *pCD111* and *pCD141*.

Exon number	Range (bp)	Intron number	Range (bp)
pCD111			
I	1-195	I	196-2,876
II	2,877-2,885	II	2,886-3,010
III	3,011-4,030	III	4,031-4,112
IV	4,113-4,356	IV	4,357-4,595
V	4,596-4,692	V	4,693-4,808
VI	4,809-5,012		
pCD141			
I	1-195	I	196-2,333
II	2,334-2,342	II	2,343-2,641
III	2,642-3,666	III	3,667-3,753
IV	3,754-3,999	IV	4,000-4,122
V	4,123-4,217	V	4,218-4,297
VI	4,298-4,478		

[14] The alignment program Multalin version 5.4.1 (http://bioinfo.genetoul.fr) used revealed problems in the comparison of the genomic *pCD141* sequence with the *pCD141* cDNA sequence due to SNPs in both sequences. The mini-exon II was not aligned properly, two additional nucleotides occurred, whilst another one was connected with the first exon.

[15] As described above in footnote 14.

It is known from the literature that the genomic structure of higher plant invertases is fairly conserved and consists of six to eight exons. As it is the case for the invertases *Pain-1* (chapter 3.1), *invGE* and *invGF* (chapter 3.2), also the genes *pCD111* and *pCD141* show this exon-intron structure and exhibit the extremely small exon II, which only codes for the core tripeptide DPN of the conserved β-fructosidase motif NDPNG (TYMOWSKA-LALANNE & KREIS, 1998).

It has been shown that potato invertase loci encoding cell wall-bound isoforms are characterized by a direct tandem repeat organization where two linked genes are separated by about 2,3kb (MADDISON ET AL., 1999). The *Inv$_{ap}$-a* locus consisting of the gene pair *pCD111/pCD141* showed this kind of genomic structure with approximately 8kb separating the corresponding invertase genes (Figure 3.3.12).

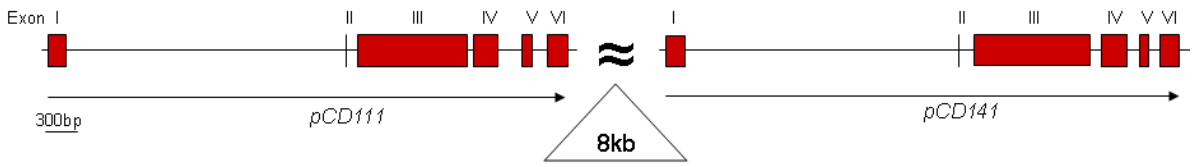

Figure 3.3.12: Tandem repeat linkage of the genes *pCD111* and *pCD141*. Exons are drawn in red and numbered from I to VI. The arrows symbolize the whole length of the genes without promoter and terminator sequences.

4 Discussion[16]

4.1 The physiological impact of potato invertases on tuber chips quality

The interest of this study was to characterize the underlying mechanisms of the trait 'potato chips quality', which is influenced by the starch and sugar content of potato tubers. A high content of the reducing sugars glucose and fructose, which are accumulating during tuber cold storage (cold-sweetening), results in inferior chips quality e.g. a dark colour, a bitter taste and a high acrylamide concentration. Starch and sugar content of potato tubers are quantitative traits, which can be considered as model traits using the candidate gene approach to unravel the molecular basis of quantitative trait loci (QTL). QTL for tuber starch and sugar content or potato chips colour have been mapped in potato (DOUCHES & FREYRE, 1994; MENÉNDEZ ET AL., 2002). A number of candidate genes have been identified regarding the fact of their co-localisation with QTLs on molecular maps, as well as being functional in the biosynthesis, degradation, or transport of starch and sugars in potato and other plants (CHEN ET AL., 2001; MENÉNDEZ ET AL., 2002). Among others, invertase genes were identified as positional candidates for cold-sweetening QTLs. Furthermore, association analysis showed a significant correlation between alleles of vacuolar and cell wall-bound invertase isoforms and better potato chips quality as well as other tuber traits (LI ET AL., 2005, 2008). In potato three invertase loci *Pain-1*, Inv_{ap}-*a* and Inv_{ap}-*b* are known. The gene *Pain-1* on chromosome III encodes a vacuolar invertase. The two gene pairs *invGE/invGF* of the locus Inv_{ap}-*b* and *pCD111/pCD141* of the locus Inv_{ap}-*a* on potato chromosomes IX and X respectively, code for cell wall-bound invertase isoforms. The genes *invGE* and *invGF* are linked in a direct tandem repeat and separated by approximately 2.3kb from each other. The size of the Inv_{ap}-*b* locus is approximately 8.6kb (MADDISON ET AL., 1999). Comparative analysis of the potato genetic map revealed that the gene pair *pCD111/pCD141* on chromosome X arose by partial chromosome duplication of the gene pair *invGE*/*invGF* of chromosome IX and, therefore, might also be organized in a direct tandem repeat (GEBHARDT ET AL., 2003; FRIDMAN ET AL., 2003). The present study showed that the genes *pCD111/pCD141* are arranged in a direct tandem repeat and separated by approximately 8kb. The size of the Inv_{ap}-*a* locus is approximately 17.5kb (chapter 3.3, section 3.3.1.3).

[16] Due to the complexity of the present work, a summary of the project and the main results were included to facilitate reading and understanding.

Besides being positional candidates, invertases are also functional candidates. Invertases are enzymes, which catalyze the last step in the carbohydrate breakdown chain. The products of the invertase reaction are the reducing sugars glucose and fructose, which directly interfere with potato chips quality (SHALLENBERGER ET AL., 1959). In consequence invertases fulfil both criteria, being candidate genes in the genetic and biochemical sense.

Part of the phenotypic differences of potato chips quality can be explained by allelic variation of invertases as identified by association analysis (LI ET AL., 2005, 2008). FRIDMAN ET AL. (2004) identified the tomato invertase gene *LIN5* as causal for the QTL *Brix9-2-5* for sugar yield of tomato fruits, comparing differences between *LIN5* alleles of the cultivated tomato (*Solanum lycopersicum*) and of wild species (*Solanum pennellii*). The tomato fruits of the wild species showed a dramatic reduction of the sugar content compared to fruits of the cultivated tomato. The present study aimed to elucidate whether allelic variation of functional potato invertase alleles in different genotypes can be identified and to what extent this natural variation accounts for the observed phenotypic diversity regarding chips quality. The question was whether allelic variation manifested itself at functional level as functional differences that could be characterized, like observed in tomato for the fruit sugar content (FRIDMAN ET AL., 2004).

To analyze allelic composition and functional relevance of invertase alleles, six different genotypes were selected. Based on association analysis the tetraploid cultivars ‘Satina’, ‘Diana’, and ‘Theresa’ were chosen due to the presence or absence of associated invertase SSCP fragments (LI ET AL., 2005, 2008). Additionally, three diploid potato genotypes were analyzed previously being used as parents for mapping QTLs and candidate genes for cold sweetening of potato tubers (MENÉNDEZ ET AL., 2002).

4.2 Structural characterization of potato invertase alleles

Invertase alleles of the five genes *Pain-1*, *invGE/invGF*, and *pCD111/pCD141* were structurally analyzed focusing on their cDNA and genomic sequences, their exon/intron structures and their gene organization. Additionally, *Pain-1* and *invGE/invGF* alleles were characterized using 3D-modelling to visualize putative effects of allelic amino acid differences. The genes *pCD111* and *pCD141* were not modelled because less information about association and putative allelic effects on potato chips quality was available at the beginning of this work.

❖ Molecular cloning of invertase cDNA alleles

cDNA alleles of *Pain-1* were isolated from tuber tissue, *invGE*, *pCD111*, and *pCD141* cDNA alleles were obtained from leaf tissue. In the case of *invGF,* alleles were isolated using floral as well as leaf tissue. In the following Table 4.1 all invertase cDNA alleles cloned from the six genotypes are listed.

Table 4.1: Overview of isolated invertase cDNA alleles.

Genotype	***Pain-1* alleles**	***invGE* alleles**	***invGF* alleles**	***pCD111* alleles**	***pCD141* alleles**
'Satina'	2	4	4	3	3
'Diana'	3	3	2	1	2
'Theresa'	2	4	2	2	3
P18	2	2	1	0	2
P40	2	2	2	1	1
P54	1	2	2	2	2

PCR based cDNA cloning of the five known potato invertase genes *Pain-1* on chromosome III, *invGE/invGF* on chromosome IX and *pCD111/pCD141* on chromosome X resulted in 64 distinct alleles.

Specific PCR amplification of the five invertase genes *Pain-1*, *invGE*, *invGF*, *pCD111*, and *pCD141* was indicated by the presence of corresponding alleles amplified in one course of PCR using a given gene specific primer pair. In Table 4.2 the sequences of full-length primers for all five genes are listed showing gene specific sequence polymorphisms that resulted in gene specific amplification.

Table 4.2: Full-length primers used for gene specific PCR amplification.

Invertase gene	Chr. number	Forward primer (in 5'-3'orientation)	Reverse primer (in 5'-3'orientation)
Pain-1	III	ATG GCC ACG CAG TAC C	GAT GAA TTA CAA GTC TTG CAA GGG
invGE	IX	ATG GAA TTA TTT ATG AAA AGC TCT TCT CTT TGG GGG T	TTA GTG CAT CTT AGG TAC ATC CAT GCT CCA AGC
invGF	IX	ATG GAT TAT TCA TCT AAT TCT CGT TGG GCT TTG CCA G	TCA ATA TTG TAT CTT AGC TTT GCC CAT ACT CCA TGC
pCD111	X	ATG GAT TGT TTA AAA AAG TCT TCT C	TCA ATA AGA AGA GTG ACC AAA TGA CCA ATT CA
pCD141	X	ATG GAG ATT TTA AGA AGA TCT TCT TCT CTT TGG GTT	CTA GTG CAA CTT TGC ATT AGC CAT GCT CCA AGC

In the course of cloning and sequencing of cDNA alleles, quite a number of singular nucleotide variants (singletons) or non functional clones showing internal frame shifts and missing start and stop codons, were isolated. As the cloning of cDNA alleles was PCR based, a proofreading *Taq*-Polymerase, which is characterized by a high fidelity (approximately $5.5x10^{-5}$ mismatches per base pair per PCR cycle) was used to minimize PCR derived errors. Hereby four times better amplification results compared to common *Taq* DNA-Polymerase were achieved. Sequence reliability was similar to other commercially available proof-reading polymerases (i.e. *Pfu* DNA-Polymerase: $1.5x10^{-5}$ errors per base pair per PCR cycle, Invitrogen, Karlsruhe). Another source of *in-vitro* invertase sequence variability might have been the conversion of RNA to cDNA by Superscript II (Invitrogen, Karlsruhe), which possesses an error rate of $1x10^{-4}$ per nucleotide.

Randomly occurring sequencing errors were eliminated by checking forward and reverse sequence of the affected area. Furthermore, in the present study PCR did not show equal amplification of invertase alleles, and allele detection needed several PCRs. This phenomenon is known as allelic dropout and was observed in diverse studies in human genetics as well as in plant microsatellite genotyping (FINDLAY ET AL., 1995; TABERLET ET AL., 1996, BROQUET & PETIT, 2004; ZHANG ET AL., 2006; SOULSBURRY ET AL., 2007). Allelic dropout is the failure of PCR amplification of one allele in a heterozygous organism. Therefore, allele identification might be incomplete, and there is the possibility that not all existing invertase alleles of one genotype have been detected. Another aspect of allele mining by PCR was the definition of cDNA alleles, which were not detected as actively transcribed by pyrosequencing analysis of cDNA (section 3.2.2.1.1, Figure 3.2.24). A low number of cDNA clones represented these alleles and some occurred only once in PCR amplification. However, pyrosequencing analysis of genomic DNA showed that the SNPs specific for those alleles are present at genomic level, representing an existing allele of the genotype but is transcribed at such a low level, therefore not being detectable by cDNA pyrosequencing analysis. This is consistent with the rare amplification of these alleles by PCR.

Allele mining for each invertase gene was achieved by using tissues where invertase expression has been demonstrated (ZRENNER ET AL., 1996; MADDISON ET AL., 1999; HEDLEY ET AL., 1993, 1994). For the gene *invGF,* MADDISON ET AL. (1999) detected expression exclusively in floral tissues. Expression profiles of the tomato and the *Arabidopsis invGF* orthologs, *LIN7* and *ATβFRUCT2* respectively, showed also restriction of transcripts to floral tissues (FRIDMAN ET AL., 2003). In contrast to these findings, this study showed that *invGF* expression occurred also cultivar dependent in leaves (section 3.2.1.2, Figures 3.2.1 and 3.2.2). *invGF* alleles isolated from leaves and flowers were identical at amino acid level as well as in their nucleotide sequence.

It has to be pointed out that in the course of this study invertase allele mining using three tetraploid cultivars resulted in a tremendous allelic variation not expected by SSCP analysis that was earlier applied on 240 tetraploid potato cultivars (LI ET AL., 2005, 2008). Besides non synonymous allele specific SNPs, which caused amino acid exchanges, quite a number of synonymous SNPs occurred, leading to alleles identical at amino acid level. As synonymous SNPs do not cause amino acid substitutions, the function of the corresponding protein should not be affected. Nevertheless, several studies in humans showed that synonymous SNPs produced altered mRNA secondary structures affecting mRNA degradation and modification (e.g. splicing) as well as resulting in a reduced amount of translated protein (NACKLEY ET AL., 2006; reviewed in CHAMARY ET AL., 2006). Additionally, KIMCHI-SARFATY ET AL. (2007) showed that synonymous SNPs also affect enzymatic substrate specificities. In this respect, haplotypes showing synonymous SNPs accompanied by similar mRNA and protein levels, led to altered enzyme conformation because of rare codons, resulting from synonymous polymorphisms that affected the timing of co-translational folding and, therefore, the structure of the enzyme. Whether synonymous SNPs detected in potato invertase alleles also alter mRNA secondary structure, mRNA degradation, translation and enzyme conformation needs further investigation.

- **Phenetic tree analysis of invertase cDNA alleles from all five potato invertase genes**

The phenetic tree analysis was applied to group all alleles obtained from the five potato invertase genes according to their similarity at amino acid level (Figure 4.1). This allowed getting an impression of the grouping between the invertase isoforms as well as the clustering of associated and not associated alleles of the latter isoforms to each other.

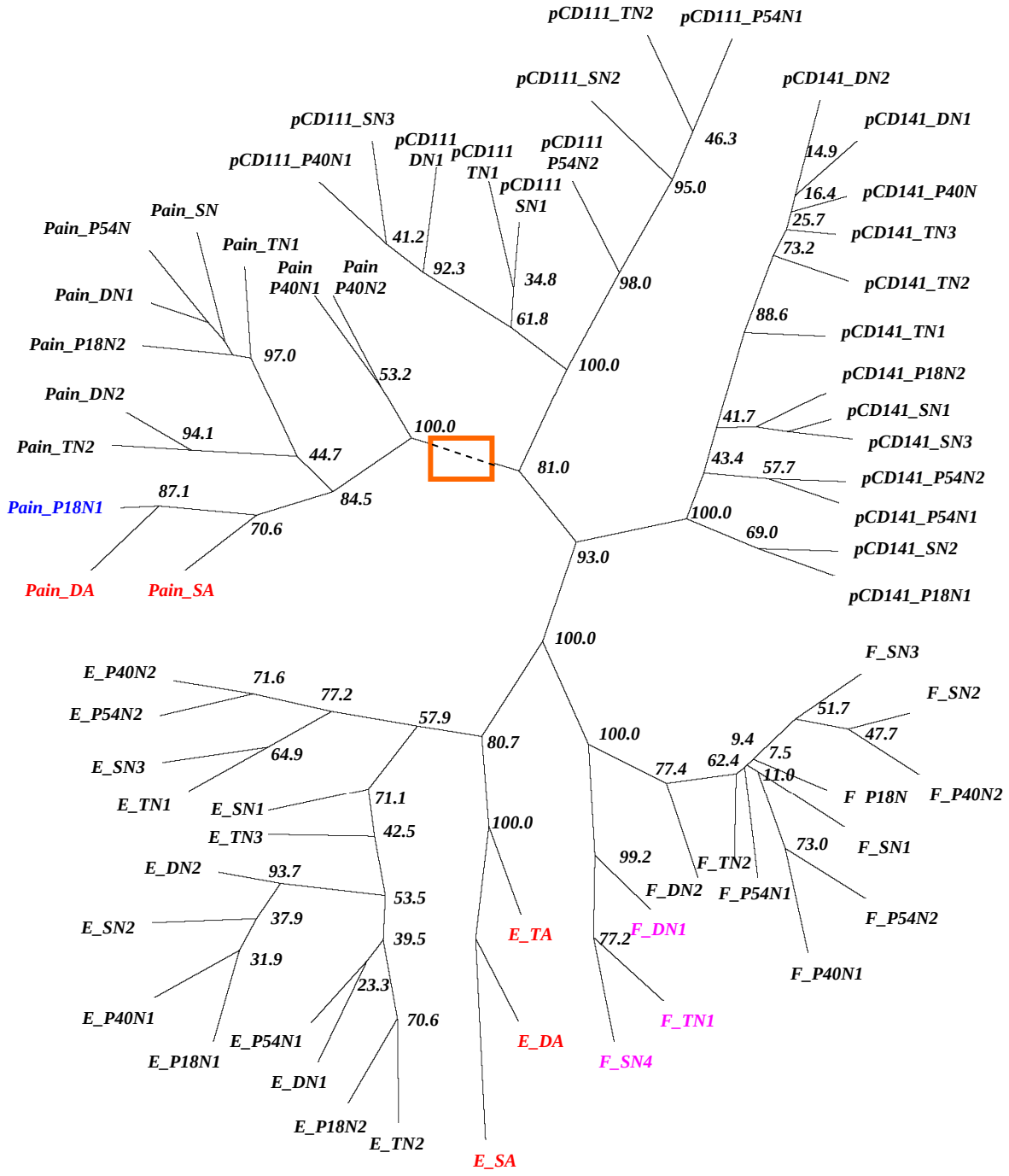

Figure 4.1: Amino acid based phenetic tree of all cloned invertase cDNA alleles. The tree was generated using the maximum parsimony method. A total of 100 bootstrapping runs were performed, and the percent reliability is indicated next to each branch. Allele names comprise the invertase gene, genotype and allele type. Alleles found to be associated with better potato chips quality are coloured in red. The allele *Pain_P18N1*, which is amino acid sequence identical to *Pain_DA* was not tested by association analysis and, therefore, is coloured in blue. The three *invGF* alleles *F_SN4*, *F_DN1*, and *F_TN1* are thought to be representatives of the associated SSCP fragment *invGF-4d* because of similar grouping as observed for the associated *invGE* alleles *E_SA*, *E_DA*, and *E_TA*. The three *invGF* alleles are coloured in pink. ☐ The boxed area reflects a truncated branch – this is due to the relatively distant clustering of vacuolar *Pain-1* alleles compared to cell wall-bound invertase isoforms (*invGE*, *invGF*, *pCD111*, and *pCD141*) because of weak sequence homology.

The phenetic tree of invertase alleles generated in this study revealed that the alleles from the different loci group separately. The analysis showed that the gene *Pain-1* is more similar to

the genes *pCD111* and *pCD141* because of closer branching distance in contrast to the genes *invGE* and *invGF*. Peptide based comparison of the different potato invertase isoforms revealed that the cell wall-bound invertases *invGE, invGF, pCD11,1* and *pCD141* share an amino acid sequence homology of approximately 73%, whilst the vacuolar invertase *Pain-1* displayed a homology of around 38% to the cell wall-bound isoforms explaining the distant clustering. This is in agreement with previous studies where comparison of amino acid sequences of plant invertases demonstrated that cell wall and vacuolar invertases belong to two different classes (TYMOWSKA-LALANNE & KREIS, 1998). Therefore, invertase amino acid sequences of the same isoform originating from different species are more similar to each other than sequences of different isoforms from one and the same species.

❖ **Genomic characterization of the genes *Pain-1*, *pCD111*, and *pCD141***

The next step was to elucidate the genomic structures of the genes *Pain-1*, *pCD111*, and *pCD141*. Therefore, high density BAC library screens were performed using two different BAC libraries constructed with genomic DNA of the same diploid genotype (BALLVORA ET AL., 2002, 2007).

Information about genomic potato invertase organization was only available for the genes *invGE* and *invGF* on chromosome IX. MADDISON ET AL. (1999) showed that the Inv_{ap}-*b* locus consists of the genes *invGE* and *invGF* linked in a direct tandem repeat and separated by approximately 2.3kb from each other. Both genes exhibit a similar exon/intron structure composed of six exons and five introns. The size of the Inv_{ap}-*b* locus is approximately 8.6kb (MADDISON ET AL., 1999). Comparative analysis of the potato genetic map revealed that the genome segment harbouring the genes *pCD111* and *pCD141* on chromosome X is related to a genome segment containing the genes *invGE* and *invGF* of chromosome IX, and, therefore, might also be organized in a direct tandem repeat (GEBHARDT ET AL., 2003; FRIDMAN ET AL., 2003). Corresponding studies of orthologous invertase genes of tomato revealed that the syntenic tomato locus to *invGE/invGF*, *LIN5/LIN7* on chromosome IX, also displays the linkage of both genes in a direct tandem repeat (FRIDMAN ET AL., 2003). The tomato invertase genes *LIN8* and *LIN6* on tomato chromosome X, which are orthologs of the potato genes *pCD111* and *pCD141* on potato chromosome X, are also arranged in this manner. Known genomic organizations of above described potato and tomato invertase genes strongly encouraged the expectation that the potato genes *pCD111* and *pCD141* are also linked in a direct tandem repeat.

Sequencing of a BAC insert harbouring the genes *pCD111* and *pCD141* confirmed the latter spatial organization of both genes (section 3.3.1.3, Figures 3.3.11 and 3.3.12) as observed for

their tomato orthologs *LIN8* and *LIN6*. Furthermore, it could be shown that the genes *pCD111* and *pCD141* are separated from each other by approximately 8kb, whilst the tomato genes *LIN8* and *LIN6* are divided by 7,2kb. Additionally, the tomato locus *LIN8/LIN6* is flanked upstream by a kinesin, and downstream by a 40S ribosomal gene. These two genes were also detected flanking the potato gene pair *pCD111/pCD141* of the Inv_{ap}-*a* locus in the same orientation. The size of the Inv_{ap}-*a* locus is approximately 17.5kb.

The potato invertase genes *invGE* and *invGF* as well as the tomato invertase genes *LIN5*, *LIN7*, and *LIN6* consist of six exons and five introns. The tomato invertase gene *LIN8* displays five exons and four introns. However, genomic characterization of the potato genes *pCD111* and *pCD141* showed that both contain six exons and five introns.

The size of the exons and introns is not conserved between different potato invertase genes, except the nine base pair mini-exon II, and varies from 9 to 1,026 and from 83 to 2,682 nucleotides, respectively.

The gene *Pain-1* on chromosome III codes for a vacuolar invertase in contrast to *invGE/invGF* and *pCD111/pCD141*, which all encode cell wall-bound invertase isoforms. One interest of this study was whether *Pain-1* is differently organized than the other two known invertase loci. Searching for *Pain-1* tomato orthologs resulted in one EST on tomato chromosome III (www.sgn.cornell.edu). By sequencing BAC inserts harbouring the *Pain-1* gene no second invertase was detected. Within the BAC inserts *Pain-1* gene surrounding sequences should allow to detect a possible tandem repeat organization (section 3.1.1.4, Figure 3.1.11 A). This possibility was excluded for the *Pain-1* locus. Furthermore, in the corresponding flanking regions no kinesin or ribosomal genes as observed for the genes *pCD111/pCD141* were detected. The *Pain-1* gene consists of seven exons and six introns, and, therefore, has an additional exon and intron when compared to the other four known potato invertase genes. Analysis of invertase isoforms from different species like *Arabidopsis thaliana*, carrot, tomato, maize, tobacco, mung bean, and pea demonstrated that invertases vary in their exon/intron composition (TYMOWSKA-LALANNE & KREIS, 1998). All potato invertases contain the conserved exon II, which only consists of nine nucleotides. This mini-exon, one of the smallest exons known in plants, encodes the residues DPN of the highly conserved β-fructosidase motif, NDPNG (TYMOWSKA-LALANNE & KREIS, 1998). The β-fructosidase motif of the genes *invGE*, *invGF*, and *pCD111* is represented by NDPNA rather than NDPNG. The other potato invertases *Pain-1* and *pCD141* display the residues NDPNG. BOURNAY ET AL. (1996) observed that under cold stress the mini-exon of the *pCD111* cell

wall invertase was skipped in an alternative splicing event. The functional relevance of the splicing effect was not investigated.

Comparison of the amino acid sequences of plant invertases demonstrated that cell wall and vacuolar invertases belong to two different classes (TYMOWSKA-LALANNE & KREIS, 1998). Corresponding invertase amino acid sequences of the same isoform originating from different species are more similar to each other than sequences of different isoforms from one and the same species are. Additionally, typical vacuolar invertase peptide regions or residues were identified that are absent in cell wall-bound isoforms. The peptide domain WECxDF, which is conserved among plant invertases, where x=valine in vacuolar and x=proline in cell wall-bound invertases (TYMOWSKA-LALANNE & KREIS, 1998; STURM, 1999) was also present in the different invertase isoforms of potato.

- **Structural 3D-analysis of invertase cDNA alleles**

In collaboration with Pawel Durek (MPIMP/Golm) the structural consequences of allelic invertase sequence variation was explored by applying a 3D-modelling analysis. The modelling of the allelic invertase structure was based on the 3D crystal structure of cyanobacteria invertase (ALBERTO ET AL., 2004). The models presented included the putative sucrose binding domain. In addition to the structural visualization of amino acid exchanges, also the electric potential (EP) of *Pain-1* and *invGE/invGF* alleles was mapped at pH 4.7 mimicking the vacuolar and apoplastic environment.

The analysis of the molecular structure of the associated 'Satina' *Pain-1* allele *Pain_SA* compared to *Pain_SN3* and of the associated 'Diana' allele *Pain_DA* compared to *Pain_DN1* and *Pain_DN2* showed that amino acid exchanges were manifested on the surface of the enzyme. None of the modelled molecules showed structural differences within the putative sucrose binding domain (section 3.1.1.3.1, Figure 3.1.7).

Comparative models of 'Diana' alleles revealed that models of the two not associated alleles *Pain_DN1* and *Pain_DN2* differed less from each other compared to the associated allele (*Pain_DA* vs. *Pain_DN1*; *Pain_DA* vs. *Pain_DN2*). The SNP 1544 present in the alleles *Pain_SA* and *Pain_DA*, which was found to be associated with better potato chips quality, had a direct effect on the molecule's surface.

The characterization of the EP showed charge differences among the protein models. The putative sucrose binding site was positively charged matching the partial negative charge of the substrate sucrose due to the hydroxyl groups. A dramatic charge difference of the putative sucrose binding site was observed in the associated *Pain-1* alleles *Pain_SA* and *Pain_DA*, which are not amino acid identical but share the associated SNP at cDNA position 1544

(section 3.1.1.3.2, Figure 3.1.9). The EP switched from positive to neutral compared to the not associated *Pain-1* alleles. The EP changes could not be correlated to amino acid exchanges near the sucrose binding site. The causative amino acids were not yet analyzed, but are subject of ongoing investigations in the research project. Whether these EP differences of the associated alleles compared to the EP of the not associated alleles might influence enzymatic activity remains unclear. Possible effects of the neutral charge might be a weaker binding of sucrose and, therefore, a reduced conversion of sucrose into the reducing sugars glucose and fructose, which influence negatively potato chips quality. This would support the hypothesis that sequence variation of potato invertases leads to functional variation and that in consequence associated alleles produce less reducing sugars in tubers and thus a good potato chips quality.

Modelling *invGE* alleles from the cultivars 'Satina' and 'Theresa' revealed similar molecular structures of the investigated alleles (section 3.2.1.3, Figure 3.2.14). Only slight differences were visible. Comparative modelling of the associated *invGE* alleles *E_SA* and *E_TA* did not reveal strong differences (Figure 3.2.15). Superimposing the associated *invGE* allele *E_SA* and the *invGF* allele *F_SN4* showed strong structural differences (Figure 3.2.23). The strong structural effects are likely caused by sequence divergence of the two genes. Even though the latter belong to the same locus and arose from gene duplication (GEBHARDT ET AL., 2003; FRIDMAN ET AL., 2003), *invGE* and *invGF* proteins are only 74% similar to each other (MADDISON ET AL., 1999).

EP analysis of *invGE* alleles (Figure 3.2.16 and 3.2.17) revealed only weak charge differences of the associated 'Satina' allele *E_SA,* which showed a small negatively charged area compared to the allele *E_SN3.* The associated 'Theresa' allele *E_TA* which differs in its amino acid sequences to *E_SA* but contains the associated SNP 1103*, exhibited no charge differences of the putative sucrose binding site compared to *E_TN1*.

For the gene *invGF* two alleles of the cultivar 'Satina' *F_SN3* and *F_SN4* were modelled (section 3.2.1.3, Figure 3.2.19). Comparison of both allelic structures showed differences among the molecules. EP analysis showed that especially the putative sucrose binding domain displayed visible changes of its charge between the two alleles. In the allele *F_SN4* the EP of the putative domain switched from positive to negative, influencing possible interactions of substrate and enzyme (Figure 3.2.21). As reported for the *Pain-1* and *invGE* alleles, EP changes are not directly mediated by amino acid exchanges nearby the binding site. It is most likely that surrounding amino acid exchanges cause the charge shift.

In conclusion, 3D-modelling is a tool to gain first insights in the possible structural consequences of different invertase alleles. The models nicely showed that amino acid exchanges can modify the surface of the enzyme. However, no effect on the structure of the putative sucrose binding domain was detected in any of the modelled molecules, but an effect on the charge was observed. The putative sucrose binding site exposed areas of neutral and positive charges in the associated *Pain-1* and *invGE* alleles, *Pain-SA*, *Pain_DA,* and *E_SA*, and in the putative associated *invGF* allele *F_SN4*. Whether these EP differences of the alleles influence enzymatic activity remains unclear. To address this question a biochemical characterization was carried out (*Pain-1*: section 3.1.2.3; *invGE/invGF*: section 3.2.2.3) to determine whether differences in enzymatic activity are present between invertase alleles. The corresponding results will be discussed in one of the following section (4.3: Biochemical analysis of *Pain-1*, *invGE,* and *invGF* alleles).

Extracellular invertase from yeast and alkaline invertase from *Vicia faba* are known to act as oligomers (KERN ET AL., 1992; ROSS ET AL., 1996). Due to 3D-analysis, it might be possible that the vacuolar and cell wall-bound potato invertases might also function as a higher complex of several monomers. ROSS ET AL. (1996) did not investigate the role of allelic subunits in the alkaline invertase complex. Supported by putative 3D structural analysis, there is the possibility that invertase enzyme complexes are formed by allelic proteins (Pawel Durek, personal communication). Considering this information, it is comprehensive that conformational and electrostatic changes on the enzyme's surface affect invertase enzyme complex formation and might lead to altered enzyme activity as reported for other studies about complex formation of enzymes (TETLOW ET AL., 2004a; TETLOW ET AL., 2004b; TETLOW ET AL., 2008).

4.3 Functional characterization of potato invertase alleles

The expression of single genotype specific *Pain-1, invGE*, and *invGF* alleles was quantified with pyrosequencing using cDNA. Allele specific transcript abundance was compared to the genomic allele dosages as determined by pyrosequencing using genomic DNA. Additionally, total amounts of *Pain-1* transcripts during tuber cold storage were determined using qRT-PCR.

Pyrosequencing is a robust and quantitative sequencing method, based on real-time detection of pyrophosphate, which is released as a result of nucleotide incorporation in a sequencing-by-synthesis reaction (RONAGHI ET AL., 1996). Assessing allele frequencies in large genomic DNA pools by pyrosequencing has demonstrated the high level of accuracy of this method. WASSON ET AL. (2002) reported the reliable detection of allele frequency differences of 4% between DNA pools from human populations. This result was confirmed by NEVE ET AL. (2002) who estimated that, for large DNA pools, allele frequencies that differ by ±5.2% would be significant. Because of its high accuracy, pyrosequencing has been considered as the method of choice for genotyping SNPs in polyploid species. For example, RICKERT ET AL. (2002) and OEFNER (2002) have shown that the different heterozygous states of a binary SNP in tetraploid potato could reliably be distinguished. Furthermore, RICKERT ET AL. (2002) showed that 82% of the polymorphic sites tested were amenable to allelic discrimination by pyrosequencing, which is by far better than any other SNP genotyping method. Another advantage of pyrosequencing is the possibility to determine multiple SNP frequencies in a single measurement, allowing analysis of more than two alleles simultaneously.

The biochemical analysis of invertase cDNA alleles was performed using yeast as heterologous expression system. The complementation of a yeast invertase mutant with potato cDNA alleles allowed expression of single alleles and their characterization. Invertase activities were assayed to determine substrate affinities (K_m) and reaction rates (v_{max}).

The genes *pCD111* and *pCD141* were not functionally analyzed because of limited information concerning association and putative allelic effects on potato chips quality at the beginning of this work.

In a simple scenario, one can imagine several functional characteristics of an invertase allele influencing positively potato chips quality. Even though potato chips quality is a multigenic trait, invertase was the first gene studied at functional level in terms of allelic differences contributing to this trait. Possible features of a superior allele are summarized in Figure 4.2.

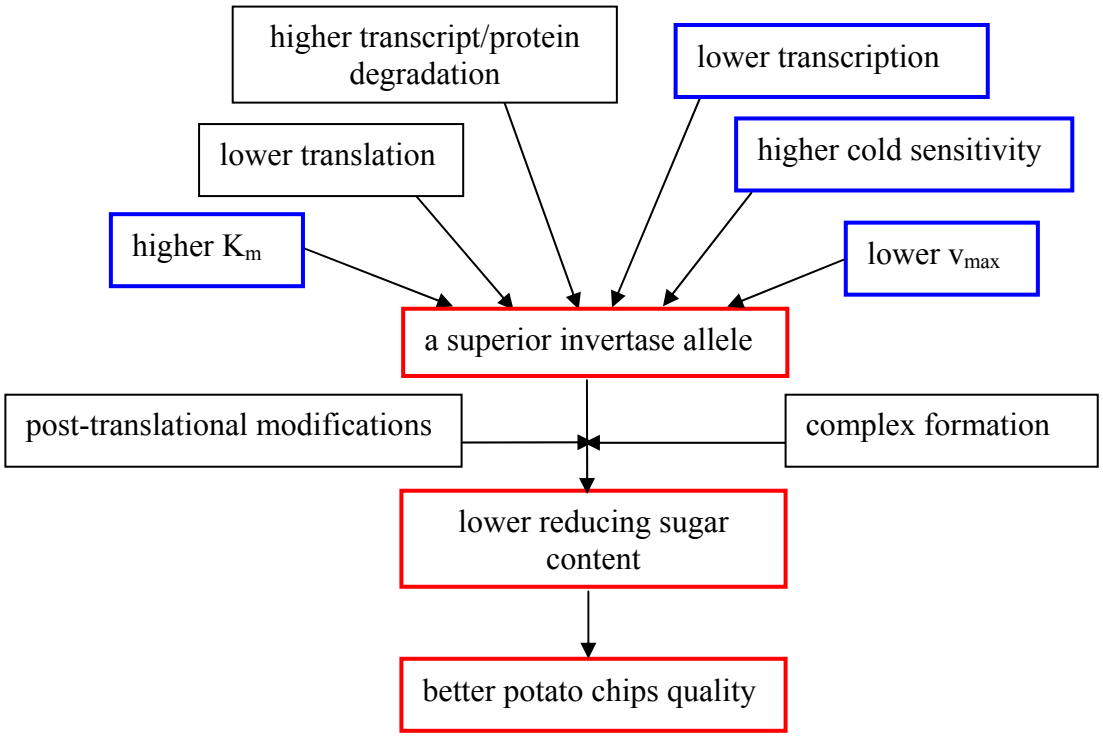

Figure 4.2: Simplified scheme displaying features of an 'ideal' invertase allele acting positively on potato chips quality. Red boxes indicate desired phenotypic traits influenced by a superior invertase allele. Blue boxes represent functional characteristics that were studied during this work.

A superior invertase allele should lead to a low reducing sugar content, which in consequence gives rise to a good potato chips quality. Allelic effects can occur at transcriptional, translational, post-translational, and biochemical level. In this agreement, a superior invertase allele would be sparsely transcribed and translated, displaying low protein abundance, and, therefore, having a poor contribution to overall invertase activity consequently leading to a reduced sucrose conversion. Additionally, high levels of transcript and protein degradation would also contribute to low protein content. In addition, a superior invertase allele could be characterized by a high K_m value meaning a low affinity to sucrose combined with a low v_{max} value indicating a slow conversion of sucrose. These biochemical characteristics can be even more prevalent in a cold environment applied to potato tubers to prevent them from sprouting. However, other post-translational modifications like N-glycosylation, protein folding, or allelic complex formation are further possibilities in influencing a superior invertase allele resulting in lower reducing sugar content and, therefore, better potato chips quality.

In the course of this work, out of the mentioned features characterizing a superior invertase allele, allele specific expression and allelic biochemical characteristics were determined to prove whether such alleles are present.

❖ **Expression analysis of *Pain-1*, *invGE,* and *invGF* alleles**

Besides the possibility of an altered enzymatic activity, sequence variation can also manifest at expression level. A simple assumption consist of a low transcription level of a superior invertase allele resulting in low translation rate contributing to a lower extent to overall invertase activity due to limited enzyme abundance. In the latter case lower invertase protein levels due to a reduced allelic expression would lead to superior chips quality (Figure 4.2).

Differential expression analysis was performed monitoring the genes *Pain-1, invGE,* and *invGF*. The study of the expression followed different purposes. The gene *Pain-1* is known to be differentially expressed during tuber cold storage (ZRENNER ET AL., 1996; ZHOU ET AL., 2004; BAGNARESI ET AL., 2008). Using pyrosequencing, genotype specific allelic transcription patterns during a cold storage time course of four weeks were determined compared to additional measured genomic dosages of the alleles. Total amounts of *Pain-1* transcripts during tuber cold storage were measured using qRT-PCR.

The expression of *invGE* and *invGF* alleles was detected by pyrosequencing analysis in comparison to the allelic genomic dosage determined by pyrosequencing using genomic DNA as template.

Expression analysis of *Pain-1*, *invGE,* and *invGF* alleles revealed differential transcriptional regulations of particular alleles. Allele specific expression is a common fact and several studies showed such a regulation on transcriptional level (reviewed in KNIGHT, 2004). Studies in octoploid strawberry showed allele specific expression of a pathogenesis-related gene induced by fungal infection causing fruit rot (SCHAART ET AL., 2005). SPRINGER & STUPAR (2007) used allele specific expression assays to profile the relative allelic expression in seedling tissue derived from maize hybrids. They found evidence for regulatory variation that contributes to biased allelic expression between genotypes and between tissues. Studies in mammals during early stages of development demonstrated the importance of allele specific expression implicating imprinting mechanisms (SZABO & MANN, 1995).

The alleles *Pain_SA* and *Pain_DA* were derived from the genotypes ‘Satina’ and ‘Diana’. It could be shown that the two alleles, having different amino acid sequences but being associated with better potato chips quality, were differentially expressed during tuber cold storage when compared to their genomic dosage (section 3.1.2.1, Figures 3.1.12 and 3.1.14). Whilst *Pain_SA* showed an up-regulation in its expression of approximately 18%, the allele *Pain-DA* revealed a permanent reduction of expression during the cold storage course of four weeks resulting in an overall decrease up to 20% compared to samples that were not stored in the cold. The diploid potato genotype P18 harbours an allele with identical amino acid

sequence to the associated allele *Pain_DA*. The allele *Pain_P18N1* showed a strong transcript increase after one week of tuber cold storage (section 3.1.2.1, Figure 3.1.18). Expression level was 50% higher than in tubers that were not stored in the cold. The differential expression of the associated allele *Pain_SA* and the allele *Pain_P18N1,* which is identical at amino acid level to the associated allele *Pain_DA,* showed that these allelic transcripts are influenced by low temperature leading to higher abundance during tuber cold storage than expected from their genomic dosage. This observation is in contradiction with the hypothesis that a superior invertase allele is characterized by transcriptional regulation implicating a lower expression (Figure 4.2). The associated allele *Pain_DA* exhibited a lower transcription level during tuber cold storage showing the lowest abundance after four weeks in the cold. This is in agreement with the assumption mentioned above that superior alleles display low amounts of transcripts, protein and, therefore, a lower enzymatic activity. However, the impact of the 'Diana' allele on overall invertase activity remains unclear since no methods are available to measure the activity of single allelic invertases *in vivo*. Additionally, tissue or clonal specific enzyme activity due to transcriptional changes in specific tissues or single cells might contribute to altered expression patterns and, therefore, lead to a quite variable enzyme activity.

The other alleles not associated with superior chips quality of the genotypes 'Diana', 'Theresa', and P40 revealed no relevant changes in their expression pattern during tuber cold storage. The allelic expression remained similar compared to the genomic dosage of the alleles.

Allelic differences and the contrasting observations regarding expression of the associated alleles at transcript level might be due to the individual genetic background. Genotype specific transcription factors and other regulatory elements as well as allele specific promoter sequences can result in differences of allele expression. Additionally, observations of allele specific expression patterns are limited due to the limited number of analyzable genotypes in the course of this work.

Using qRT-PCR, total *Pain-1* transcripts were quantified during tuber cold storage. ZRENNER ET AL. (1996) detected soluble acid invertase transcripts after 44h of tuber cold treatment at 4°C using Northern blots. Transcript levels reached a maximum after seven days of cold storage, followed by a decrease throughout the next two to six weeks. In contrast, BAGNARESI ET AL. (2008) detected an increase of soluble acid invertase transcripts at week two to four of cold storage.

In this study expression analysis showed an intense up-regulation of *Pain-1* transcripts after one to two weeks of tuber cold storage at 4°C. After the first week of cold treatment P18

transcripts showed the highest level of relative expression compared to all other analyzed genotypes (section 3.1.2.1, Figure 3.1.19). The cultivar 'Theresa' was the only genotype where total invertase transcripts increased again after four weeks of tuber cold storage (section 3.1.2.1, Figure 3.1.17).

The results of the expression analysis of the soluble acid invertase *Pain-1* are in agreement with earlier observations by ZRENNER ET AL. (1996) and BAGNARESI ET AL. (2008). Additionally, it was demonstrated that in different genotypes *Pain-1* alleles were strongly cold influenced regarding their expression, whilst others showed minor changes or stayed unaffected compared to their genomic distribution (section 3.1.2.1, Figures 3.1.14 and 3.1.16).

Pyrosequencing of *invGE* and *invGF* alleles of leaf and floral tissue respectively, showed that genotype specific alleles are differentially expressed compared to their genomic dosage. The question might arise how alleles analyzed in leaves and flowers might contribute to chips quality when not acting directly in the potato tuber. Association analysis of *invGE* and *invGF* genes revealed positive correlations between corresponding allelic fragments and potato chips quality (LI ET AL., 2005). Expression profiles investigated by MADDISON ET AL. (1999) using GUS histochemical expression analysis showed that *invGE* is expressed in several tissues and also under the 'eyes' of the tuber. In this study, none of the six selected genotypes allowed *invGE* transcript amplification using cDNA synthesized from mature tuber 'eye' RNA. Therefore, leaf tissue has been chosen to identify *invGE* alleles as well as to study their expression. It might be possible that mature tubers were not the appropriate source for *invGE* allele mining even though MADDISON ET AL. (1999) also used mature tubers but from a different cultivar. In this study mature tubers were used to extract RNA. Following the study's approach analyzing potato chips quality before and after tuber cold storage, tubers were directly processed after harvest or stored in the cold for one to four weeks. MADDISON ET AL. (1999) also showed that *invGF* expression is restricted to floral tissues in the cultivars 'Désirée' and 'Saturna', which was shown to be not consistent with findings concerning some of the selected genotypes in this study where *invGF* expression was also detected in leaves (section 3.2.1.2, Figures 3.2.1, 3.2.2).

Reasons for the lack of *invGE* transcripts in potato tubers might also be that under the latter conditions *invGE* expression is below the detection limit due to time-dependent expression pattern. Cell wall-bound invertases are known to play an important role in tuber initiation. MINHAS & SAINI (2004/5) showed that under tuber-inducing conditions cell wall invertase activity increases up to 74% during the stolon to tuber transition period. Cell wall-bound invertase has been recognized as a key enzyme in apoplastic phloem unloading, which

switches in the developing tuber to the symplastic mode resulting in the primary function of sucrose synthase (SuSy) in sucrose cleavage. Cell wall invertases regulate the import of the reducing sugars glucose and fructose, which are used for starch synthesis in stolon tips. Assuming a superior invertase allele, less transcribed and translated resulting in low protein abundance accompanied by low activity, might lead to retarded sucrose cleavage and, therefore, less import of sugars in the initiated tuber. Additionally, a less active invertase allele in the apoplast might influence sink strength in a way that phloem unloading is decelerated and further tuber storage compounds are less abundant. Besides playing an important role in tuber initiation, cell wall invertases are generally believed as main determinants of sink strength especially during the initial stages of sink development (ROITSCH, 1999; ROITSCH ET AL., 2000). Various experimental approaches have been used to demonstrate the importance of cell wall-bound invertase isoforms for assimilate partitioning and determining sink strength. These include inhibition of storage tissue development in carrot roots by antisense repression of cell wall invertase (STURM & TANG, 1999; TANG ET AL., 1999), increase in potato tuber size by over-expression of cell wall invertase (TAUBENBERGER ET AL., 1999), arrested seed development in maize mutant lacking cell wall invertase (MILLER & CHOUREY, 1992), induction of sink metabolism in source leaves of transgenic plants by over-expression of a yeast invertase (STITT & SONNEWALD, 1995), and specific expression of a cell wall invertase during pre-storage phase in the thin walled parenchyma of faba bean seed coat (WEBER ET AL., 1995).

A possible explanation for the association of *invGF* alleles transcribed in flowers and leaves might be the fact of LD with associated *invGE* alleles detected in SCCP based analysis (LI ET AL., 2005). It might be comprehensive to think of a haplotype block associated with better chips quality including both genes *invGE* and *invGF*.

The associated *invGE* alleles correlated with better potato chips quality (LI ET AL., 2005) revealed minor changes in their expression in leaves compared to their genomic dosage (section 3.2.2.2.1, Figure 3.2.24). The 'Satina' allele *E_SA* and the 'Diana' allele *E_DA,* which are identical in their nucleotide and amino acid sequences, are present in simplex (25%) in the corresponding genotypes. Allele expression was reduced by 5% to a level of 20% in leaves. The associated 'Theresa' allele *E_TA,* which is present in simplex (25%) and is different in its amino acid sequence to *E_SA* and *E_DA,* showed a slight expression induction up to 35% in leaves. Transcripts for the 'Diana' allele *E_DN2* and the 'Theresa' allele *E_TN3* were not detected in pyrosequencing analysis possibly due to transcripts below the detection level. These findings indicated an allele specific expression of invertase genes in

potato. Whether this differential expression of *invGE* alleles influences potato chips quality remains unclear since no transcripts in tubers were detectable.

The *invGE* alleles of the diploid potato genotypes P18, P40, and P54 were differentially expressed in leaves as expected from their genomic dosage (section 3.2.2.1.2, Figure 3.2.25). Transcripts of the alleles *E_P18N1*, *E_P40N2*, and *E_P54N1* were more abundant, whilst the other alleles were less present compared to the genomic distribution.

Pyrosequencing based expression analysis of *invGF* alleles showed that the alleles *F_SN4*, *F_DN1*, and *F_TN1,* which group separately from the other *invGF* alleles were not expressed differentially in flowers compared to their genomic dosage (section 3.2.2.1.3, Figure 3.2.26). All three alleles are present in simplex (25%) in the corresponding genotypes. The 'Satina' allele *F_SN4* and the 'Theresa' allele *F_TN1* are identical at nucleotide and amino acid level. It is speculated that *F_SN4*, *F_DN1*, and *F_TN1* might refer to the *invGF-4d* SSCP fragment, which was found to be associated with better potato chips quality. The speculation is based on the fact that the three alleles show the same separation like the associated *invGE* alleles *E_SA*, *E_DA,* and *E_TA* in phenetic tree analysis (*invGE*: section 3.2.1.2.4, Figure 3.2.6; *invGF*: section 3.2.1.2.8, Figure 3.2.11). Additionally, the 'Satina' allele *F_SN3* showed a strong decrease in transcripts, whilst *F_SN1* was the prevalent allele in flowers compared to the allelic genomic distribution. The allocation of the alleles from the genotypes 'Diana', 'Theresa', and P40 did not differ. The two alleles of P54 revealed minor changes, the allele *F_P54N1* was decreased, whilst the allele *F_P54N2* was increased compared to their genomic distribution.

In conclusion, expression pattern of *Pain-1*, *invGE,* and *invGF* alleles of six genotypes did not correlate with association analysis, which was based on 240 tetraploid individuals (LI ET AL., 2005, 2008). The observation of genotype and invertase gene dependent transcriptional changes might be due to the genetic background. Since no allelic promoters or transcription factors and other modifiers were analyzed in this study the impact of these on allelic invertase expression cannot be clearly assessed. Nevertheless, the results showed that invertase genes are expressed in a genotype specific manner and that associated alleles followed divergent expression patterns. As expression QTLs (eQTLs) are an emerging field of interest in plants such analysis will be an interesting extension of the results gained in the present study, although expression data could not directly be linked to protein abundance and/or enzymatic activity.

❖ **The heterologous system yeast**

Aiming at the biochemical characterization of single invertase alleles, the use of a heterologous system was necessary to separate alleles from each other. With the knowledge that plant invertases are functional in yeast (FRIDMAN ET AL., 2004), the yeast invertase mutant *SUC2* (GOZALBO & HOHMANN, 1989), which lacks invertase activity was chosen for potato invertase allele expression. FRIDMAN ET AL. (2004) demonstrated the functional complementation of a yeast mutant with tomato cell wall-bound invertases. In this study it was shown that also a vacuolar invertase isoform complements the yeast *SUC2* mutant phenotype. All *SUC2* transformants harbouring *Pain-1, invGE*, and *invGF* cDNA alleles were able to grow on sucrose as sole carbohydrate source indicating functional complementation. The cDNA alleles of all three different genes were expressed under the control of the constitutive promoter *Adh1* to obtain high amounts of potato invertase protein.

With respect to the yeast and potato codon usages, it was found that the translation efficiency between both systems is different leading to less potato invertase protein depending on the allelic nucleotide sequence. It was tried to balance this translation deficiencies by incubation of complemented yeast strains for three days achieving equal amounts of potato invertase protein. Immunoblot analysis of *Pain-1* yeast transformants reflected the equal distribution of allelic invertase proteins (section 3.1.2.4, Figures 3.1.24 and3.1.25).

In yeast, two invertase isoforms occur, which are encoded by the same gene, but originate from differential splicing events. One isoform is active, N-glycosylated, and extracellular, the other isoform is inactive, nonglycosylated, and located in the cytoplasm. The extracellular yeast invertase is targeted for secretion by a signal peptide, which is then removed by a peptidase. Plant vacuolar and cell wall-bound invertases are synthesized as prepropeptides (TYMOWSKA-LALANNE & KREIS, 1998). These peptides consist of N-terminal extensions up to 100 amino acid residues in length, which harbour a signal peptide and an N-terminal propeptide (STURM, 1999). The signal peptide is required for the entry in the endoplasmatic reticulum (ER), which leads to the secretory pathway. The N-terminal propeptide as well as a C-terminal extension, the latter being characteristic for vacuolar invertases, are thought to act as vacuolar sorting signals (MATSUOKA & NAKAMURA, 1991). Figure 4.3 illustrates vacuolar and cell wall-bound preproproteins and included domains (adopted from TYMOWSKA-LALANNE & KREIS, 1998; STURM, 1999).

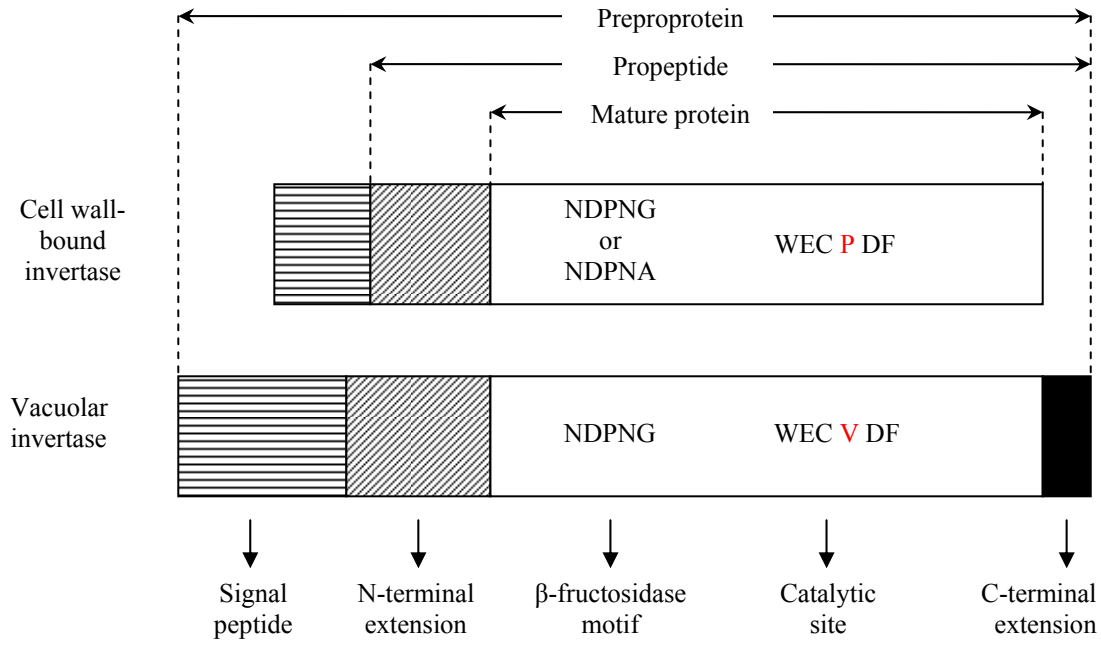

Figure 4.3: Schematic comparison of vacuolar and cell wall-bound preproprotein invertases. The preproprotein sequence includes the signal peptide, N- and C-terminal extensions and the mature protein. The peptide sequences NDPNG/NDPNA and $WEC^{P}/_{V}DF$ represent the β-fructosidase motif and the catalytic site, respectively.

Since yeast has no vacuole or a similar compartment, the question arises how vacuolar allelic potato invertases are processed and targeted in yeast to remain functional. This question can not be answered although functional complementation of the yeast invertase mutant was achieved.

Yeast invertase is known to be an oligomeric glycoprotein with 14 potential N-glycosylation sites located in the sequence (REDDY ET AL., 1999). The carbohydrate chains play a role in structure, function, stability, and folding of glycoproteins (KERN ET AL., 1992). In the yeast Golgi apparatus, N-glycosylation is achieved by a varying number of extended outer polymannose chains, yielding a high-mannose-type glycolysated protein with an average of nine to ten oligosaccharides per peptide chain. The glycosylated proteins are strongly heterogeneous in their carbohydrate content. Studies with yeast invertase demonstrated that glycosylation is a prerequisite for the oligomerization of the enzyme beyond the state of the active dimer. It was shown that core-glycosylation of yeast invertase is necessary for tetramer and octamer formation (KERN ET AL., 1992).

In plants, vacuolar and cell wall-bound invertases are glycosylated, whilst cytoplasmatic invertase isoforms are not glycosylated (STOMMEL & SIMON, 1990). Glycosylation of vacuolar and extracellular glycoproteins are different from each other. Most of the vacuolar glycoproteins described so far were found to be N-glycosylated with modified N-glycans containing fucose and/or xylose residues, but devoid of terminal glucosamine residues. In

contrast, extracellular glycoproteins were found to be N-glycosylated mostly by complex-type N-glycans including large structures with terminal fucose and galactose residues (RAYON ET AL., 1998). Both types of glycoproteins are post-Golgi modified leading to protein maturation in the vacuole or in the extracellular compartment. It was shown that N-glycosylation in plants plays an important role in prevention of proteolytic degradation, induction of correct folding, and biological activity of the protein. Furthermore, N-linked oligosaccharides may contain targeting information, or may be involved in protein recognition (RAYON ET AL., 1998). FAYE & CHRISPEELS (1989) found that unglycosylated cell wall-bound invertase of carrot was degraded in the secretory pathway or immediately after attaining the cell wall. As indicated above, N-glycosylation of proteins in plants is more complex than in yeast. It might be possible that the analyzed potato invertase alleles were not modified according their original status in the heterologous system yeast. Following the argumentation that N-glycosylation plays an important role in correct protein folding, yeast modified potato alleles might not be able to fold correctly. Due to possible folding deficiencies and less complex N-glycosylation, which both is crucial for enzyme activity, it might be also reasonable that measured potato invertase activity does not reflect the native situation in potato. Additionally, the invertase oligomerizaion must be considered. Yeast invertase was found to be a mixture of dimers, tetramers, and octamers (KERN ET AL., 1992). Studies in *Vicia faba* on alkaline invertase assumed that this enzyme acts as a homotetramer (ROSS ET AL., 1996). Considering this information, it might be possible that soluble acid invertases as well as cell wall-bound invertase isoforms might also function in a complex of subunits. In none of the mentioned oligomeric analysis, the role of allelic monomers was investigated. Assuming that a functional potato invertase complex is build of different allelic subunits in different ratios, yeast transformants containing only one allele do not allow the assembly of 'multi-allelic' complexes. VEITIA ET AL. (2008) reviewed cellular reactions to gene dosage imbalances and suppose that stoichiometric imbalances in macromolecular complexes are source of dosage-dependent phenotypes. In this context, it might be reasonable that putative invertase complexes being 'mono-allelic' in yeast do not reflect the *in vivo* situation in potato.

- **Biochemical analysis of *Pain-1*, *invGE*, and *invGF* alleles**

Biochemical analysis of plant invertases in heterologous systems was successfully demonstrated for a tomato cell wall-bound invertase isoform by FRIDMAN ET AL. (2004). In that study an invertase allele originating from a wild species (*S. pennellii*), which is barely functional indicated by low fruit sugar content was compared to the homologous invertase allele of the cultivated tomato (*S. lycopersicum*). In contrast, the present study aimed towards

the characterization of functional potato invertase alleles from different genotypes to detect allelic enzyme activities. The possible functional variability of invertases operates under field conditions and, therefore, should not have severe effects on fitness and might be difficult to detect.

Using yeast, the challenge was to determine possible minor enzymatic allelic differences.

The heterologous system yeast made it possible to measure enzyme activity of single potato invertase alleles. The enzymatic parameters Michaelis constant (K_m) and maximal velocity (v_{max}) of the invertase reaction were determined.

The biochemical analysis was carried out for 14 *Pain-1*, 10 *invGE,* and 11 *invGF* invertase alleles. For alleles of the genes *invGE* and *invGF* of the *Inv$_{ap}$-b* locus only K_m values are presented because of missing a suitable antibody for determination of the invertase protein levels to evaluate v_{max} values, which are enzyme dependent.

Considering ideal biochemical characteristics of a superior invertase allele, a high K_m value demonstrating the low substrate affinity of the enzyme accompanied by a low v_{max} value representing a slow conversion of sucrose would be a basic working model (Figure 4.2). Additionally, a higher cold sensitivity of the enzyme can intensify the described biochemical parameters leading to even less sucrose conversion into the reducing sugars glucose and fructose and a better potato chips quality.

Biochemical analysis of the *Pain-1* alleles was performed at 30°C and at 4°C. The analysis at 4°C was carried out to study possible differences of enzyme kinetics due to allelic amino acid composition in response to cold storage conditions. It was previously reported that cold storage influences transcriptional changes regarding vacuolar invertases (ZRENNER ET AL., 1996; ZHOU ET AL., 2004; BAGNARESI ET AL., 2008), but no study investigated the effect of low temperatures on the enzyme activity itself. The 30°C assay of *Pain-1* alleles showed that substrate affinity ranged between 15mM of the allele *Pain_P40N2* and 23mM of the allele *Pain_SN* (section 3.1.2.3, Table 3.1.15). Maximal velocities of the alleles varied between 2mmol*h^{-1}*mg protein^{-1} in the case of the allele *Pain_TN2* and 12mmol*h^{-1}*mg protein^{-1} for the allele *Pain_DA*. The enzymatic characteristics of the analyzed alleles from the cultivar 'Satina' showed no significant differences. In the K_m and v_{max} values of the cultivar 'Diana' differences were displayed in respect to the allele *Pain_DN2*. *Pain_DN2* showed the highest substrate affinity with a K_m of approximately 16mM, and the slowest substrate conversion with a v_{max} of around 6mmol*h^{-1}*mg protein^{-1}. The other two analyzed alleles *Pain_DA* and *Pain_DN1* displayed substrate affinities of approximately 20mM and maximal velocities of around 12mmol*h^{-1}*mg protein^{-1}. Comparison of the associated *Pain-1* alleles *Pain_SA* and

Pain_DA, which are not identical at amino acid level, revealed no significant differences regarding the enzyme's affinity to sucrose, but showed strong differences in the rate of sucrose conversion. The allele *Pain_DA* converts sucrose approximately 2.5 times faster than the allele *Pain_SA*.

Looking at the other analyzed *Pain-1* alleles, the two 'Theresa' alleles showed similar enzymatic characteristics and did not differ significantly. K_m values varied from 20 to 21mM and v_{max} values ranged from 2 to 3mmol*h^{-1}*mg $protein^{-1}$. Biochemical analysis of the alleles from the diploid potato genotypes P18 and P40 did not display any significant K_m and v_{max} differences. K_m- and v_{max} values of *Pain_P18N1* and *Pain_P18N2* ranged from 17 to 20mM and 3 to 5.5mmol*h^{-1}*mg $protein^{-1}$, respectively. The alleles *Pain_P40N1* and *Pain_P40N2* displayed substrate affinities between 15 and 17mM and v_{max} values between 6 and 7mmol*h^{-1}*mg $protein^{-1}$.

The biochemical analysis of the enzymatic characteristics of the *Pain-1* alleles at 4°C showed a dramatic increase in the enzyme's affinity to sucrose (section 3.1.2.3, Table 3.1.15). It is accepted that the rate of chemical reaction decreases approximately twofold for each 10°C decrease in temperature (AVERY, 1974). The K_m values decreased approximately 5.5 times compared to K_m values measured at 30°C. Also the maximal velocities of the alleles were affected at 4°C. By trend v_{max} values were around 2mmol*h^{-1}*mg $protein^{-}$1. The 4°C invertase assay showed the effect of low temperatures towards the vacuolar invertase alleles of potato. In the cold, the alleles showed a higher affinity to sucrose and in agreement a slower maximal velocity due to a stronger binding of the substrate and the general effect of low temperature to slow down enzymatic reaction rates. In contrast, the sucrose affinity of the yeast wild type strain *FY 1679*, used as reference, was not that much affected in the cold. The K_m values remained stable at approximately 22mM. Differences were detected in the rate of sucrose conversion. Yeast invertase slowed down from approximately 24mmol*h^{-1}*mg $protein^{-1}$ to 7.5mmol*h^{-1}*mg $protein^{-1}$ indicating a decrease of around threefold.

In conclusion, the associated *Pain-1* alleles *Pain_SA* and *Pain_DA*, which showed in 3D-analysis a charge effect of the sucrose binding site, which might lead to reduced conversion of sucrose, did not display strong physiological differences compared to the other alleles of the corresponding genotypes. The ideal biochemical characteristics outlined in Figure 4.2 for superior allelic invertases associated with superior chips quality were not clearly recognized for vacuolar invertase alleles.

The 30°C assay of *invGE* alleles (section 3.2.2.3, Table 3.2.13) showed that the two associated *invGE* alleles *E_SA* and *E_TA*, which are not amino acid identical but are

characterized by the associated SNP 1103*, displayed similar K_m values of approximately 20mM. From the tetraploid cultivar 'Satina' three alleles *E_SA*, *E_SN1*, and *E_SN3* were analyzed. Regarding the enzyme affinity, *E_SN3* displayed the lowest sucrose affinity with a K_m value of approximately 24mM, whilst the allele *E_SN1* showed the highest substrate affinity with a K_m value of around 17mM. The K_m value of the associated allele *E_SA* of 20mM was in between and was significantly different from *E_SN3*.

From the tetraploid cultivar 'Theresa' two alleles *E_TA* and *E_TN1* were analyzed. Neither the K_m values nor the v_{max} values of these alleles differed significantly from each other.

Compared to the other *invGE* alleles, the associated alleles *E_SA* and *E_TA* did not show strong K_m and v_{max} differences. The lowest K_m value was approximately 17mM (*E_SN1*), the highest K_m value was 24mM in the case of the allele *E_P18N1*.

It could be shown by 3D-analysis that the charge of the putative sucrose binding site of the associated *invGE* alleles did not display any differences like observed for associated *Pain-1* alleles. This is in agreement with determined K_m values, which did not show strong physiological differences. Biochemical parameters of *invGE* alleles did not indicate the presence of obvious superior invertase alleles according to the assumption concerning K_m and v_{max} characteristics mentioned above (Figure 4.2).

Biochemical analysis of *invGF* alleles showed that substrate affinities ranged from approximately 12mM in case of *F_SN2* and 21mM for the allele *F_P40N1* (section 3.2.2.3, Table 3.2.15). The alleles *F_SN4* and *F_DN1*, which clustered phenetically together (section 3.2.1.2.8, Figure 3.2.11) as observed for the associated *invGE* alleles *E_SA*, *E_DA*, and *E_TA*, displayed K_m values of 18mM and 13mM, respectively. Within the tested 'Satina' *invGF* alleles *F_SN4* revealed the lowest sucrose affinity, which differs significantly from *F_SN1* and *F_SN2*.

The 'Diana' allele *F_DN1*, which is not identical at amino acid level to *F_SN4* but belongs to the same outlaying group, displayed a K_m value of 13mM. These differences between *F_SN4* and *F_DN1* were significant, whilst the differences within the tested 'Diana' alleles were similar and not significant.

The allele *F_SN4*, which is considered as a representative of the associated SSCP fragment *invGf-4d*, showed among the tested 'Satina' alleles the lowest sucrose affinity. 3D structural analysis of this allele showed that a charge change of the putative sucrose binding site occurred due to the allelic amino acid composition. The electrostatic potential of the site switched from positive to negative, possibly leading to less sucrose conversion reflected by a high K_m value as detected for the allele *F_SN4*. To what extend this allele might contribute to

potato chips quality remains unclear since *invGF* is expressed in flowers and leaves and to date no transcripts in tubers were detected.
Comparing the measured K_m values of vacuolar and cell wall-bound invertase isoforms revealed overall similar enzymatic characteristics. Nevertheless, there are K_m and v_{max} values of single *Pain-1*, *invGE*, or *invGF* alleles, which are distinct from the average alleles. Even though the biochemical analysis of *Pain-1*, *invGE*, or *invGF* alleles in the heterologous system yeast revealed only slight allelic differences regarding substrate affinity and substrate conversion, no statement can be made concerning the *in vivo* situation in potato.

The measured invertase affinities towards the substrate sucrose are in general agreement with previously detected K_m values. FRIDMAN ET AL. (2004) measured substrate affinities between approximately 5 and 12mM for a functional cell wall-bound tomato invertase isoform expressed in yeast. The *Arabidopsis* soluble invertase *INV2* displayed a K_m of 12mM (TANG ET AL., 1996). The substrate affinity for a soluble acid invertase from *Triticum aestivum* was set at 19.6mM (KRISHNAN ET AL., 1985).
Convincing evidence that the invertase assay is suitable for the detection of the corresponding enzyme activities is the fact that, concerning the yeast wild type invertase, a sucrose affinity of approximately 22mM was measured. GASCON ET AL. (1968) determined the K_m value of yeast invertase at 25mM, which is nearly identical to the K_m value detected in this study.
Documented K_m values for plant invertases as described above from the BRENDA database (http://www.brenda-enzymes.org) were similar to the measured values in this study.

4.4 Potato invertase isoforms and corresponding alleles display a large structural and functional variation and are interesting candidate genes in the trait potato chips quality

The identification of alleles of five different potato invertase genes revealed high allelic diversity within the selected six genotypes. However, there are certain alleles identified shared by more than one genotype, representing basic invertase alleles. It is remarkable that invertase alleles identical at amino acid level displayed synonymous polymorphisms in their nucleotide sequences. These 'silent' SNPs not leading to any amino acid exchanges might influence mRNA secondary structure, stability, translational efficiency, and protein folding leading to altered enzyme activity. Possible effects of synonymous SNPs were not subject of this study but the further investigation of these SNPs will clarify if there is a connection between the latter and the trait potato chips quality.

3D-modelling of the alleles gave first insights in possible structural and charge effects regarding amino acid differences between the alleles. It was found that alleles associated with superior potato chips quality showed charge changes in the putative sucrose binding site leading to a putative lower conversion of sucrose into the reducing sugars glucose and fructose. As these reducing sugars are known to interfere with potato chips quality, lower conversion would imply a better chips phenotype. To test, whether allele specific amino acid differences lead to altered enzyme properties, invertase assays were performed in the heterologous system yeast. Determining the enzyme's affinity to sucrose (K_m) and the maximal rate of substrate conversion (v_{max}) showed that vacuolar and cell wall-bound invertase alleles displayed no differences that could explain the effect on chips quality. The observed differences might reflect the slight differences present *in vivo* since natural occurring alleles were analyzed and no mutant, wild accession, or other impaired alleles were tested like done for tomato (FRIDMAN ET AL., 2004). Genotype dependent alleles were detected, which displayed extreme values regarding their K_m and v_{max} values. The associated alleles were similar to not associated ones, indicating that K_m and v_{max} values do not seem to be relevant for possible reduced sucrose conversion into the sugars glucose and fructose and, therefore, better chips quality. Convincing evidence that the heterologous system yeast was suitable for assaying potato invertase activity was the analysis of two nucleotide variants of the *Pain-1* allele *Pain_SN* (section 3.1.2.3, Tables 3.1.20 and 3.1.21). The variability ranged from one to three nucleotide differences. It was shown that all nucleotide versions displayed similar K_m and v_{max} values, showing that a codon usage independent comparison of different alleles was possible.

Additionally, expression analysis revealed genotype dependent transcription patterns of invertase alleles. Associated alleles showed transcriptional changes for *Pain_SA* and *Pain_P18N1* compared to their genomic distribution. The latter is amino acid identical to *Pain_DA*, which showed no specific expression pattern. The transcript levels of associated *invGE* and the putative associated *invGF* alleles in leaves and flowers, respectively, were similar to their genomic dosages.

Invertase is functional as a complex of allelic subunits, thus it might be possible that allelic structural differences on the enzyme's surface, charge differences of the molecule as well as changed ratios of subunits due to transcriptional and translational regulation, lead to altered enzyme complexes less functional than in other genotypes with an inferior potato chips quality phenotype.

Another regulation of invertase activity is inhibition mediated by the endogenous invertase inhibitor (SCHWIMMER ET AL., 1961; PRESSEY, 1967; EWING AND MCADOO, 1971; WEIL ET AL., 1994; HEIBGES ET AL., 2003) or inhibition from a potato lectin (ISLA ET AL., 1991). The invertase inhibitor forms a non-dissociable complex with the enzyme, whilst the lectin is a dissociable inhibitor. Assuming allelic variants of invertase inhibitors acting differentially on allelic subunits of a putative invertase enzyme complex might lead to altered invertase activity. Also the potato lectin might act dependent on the allelic composition of an invertase complex in different ways to modulate invertase activity.

Association analysis of *Pain-1* allelic fragments revealed LD with allelic fragments of two other genes on chromosome III (LI ET AL., 2008). The first gene of this associated haplotype block located 6cM in the distal of *Pain-1* is the plastidic L-type α-Glucan phosphorylase (*Stp*23). The metabolic role of *Stp*23 is the phosphoric degradation of starch. The second gene within the associated block is soluble starch synthase I (*Sss*I) 14cM in the proximal of *Pain-1*. *Sss*I plays a role in starch synthesis by connecting ADP-glucose to form linear amylose chains. It is possible that alleles of the other two associated genes might be responsible for or contribute to the studied trait potato chips quality. Also additive effects of alleles of all three loci *Pain-1, Stp*23, and *Sss*I might be reasonable by their role in the carbohydrate metabolism leading to superior chips quality (OMHOLT ET AL., 2000; BIRCHLER ET AL., 2001).

In conclusion, the data presented in this study do not allow to a definite statement about the functional role of invertases on potato chips quality. However, it was shown that tremendous allelic variation of potato invertases exists, which leads to variation of transcript levels and biochemical parameters.

4.5 Future perspectives about the investigation of potato invertases and their natural variation

The results obtained in this thesis revealed important aspects about the diversity of invertase alleles and their regulation at transcriptional and biochemical level.

Considering the information available through this study, the question of 'associated' and 'not associated' alleles has to be addressed in a new manner. In the course of the work, no consistent functional characteristics of alleles statistically associated with better potato chips quality were determined. The nomenclature of association was based on the SSCP analysis by LI ET AL. (2005, 2008). Having now allele specific SNPs in hands, new alleles not detected so far by SSCP analysis but associated with superior chips quality can be analyzed in a larger population that allows screening for their impact on this trait. Being aware of allelic variability found in this study, new and up to now unidentified invertase alleles not detectable by SSCP analysis can be assessed by PCR based cloning. In consequence deeper biochemical and molecular characterization could enrich the understanding of allelic impact on potato chips quality.

Furthermore, allelic sequence variation strongly implies possible variations in regulatory domains like promoter sequences, enhancer-, and signalling domains. Additional studies of allelic promoter sequences and their influence on transcript levels might be useful to elucidate regulatory mechanisms of specific invertase alleles and identifying eQTLs as well as determining their impact on potato and the quantitative trait chips quality.

Another interesting aspect to follow is how invertase complexes might be build in potato, to what extend allelic monomers are involved in proper complex formation, how allelic monomer abundance due to transcriptional and translational regulations might influence enzyme complexes and, therefore, enzymatic activity.

The information gained by these additional approaches could help to draw a more detailed picture how invertases are regulated and to what extend allelic differences might contribute to a superior potato chips quality.

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Appendix

A2 Map of the yeast expression vector 112 A1 NE.

A3 Description of the amino acid exchanges using the alignment program Multalin version 5.4.1 (http://bioinfo.genetoul.fr).

A3.1.1 Alignment of full-length amino acid sequences of *Pain-1* 'Satina' alleles.

A3.1.2 Alignment of full-length amino acid sequences of *Pain-1* 'Diana' alleles.

A3.1.3 Alignment of full-length amino acid sequences of *Pain-1* 'Theresa' alleles.

A3.1.4 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_SA*.

A3.1.5 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_SN*.

A3.1.6 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_DA*.

A3.1.7 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_DN1*.

A3.1.8 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_DN2*.

A3.1.9 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_TN1*.

A3.1.10 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_TN2*.

A3.1.11 Alignment of full-length *Pain-1* nucleotide sequences obtained from all tetraploid genotypes.

A3.1.12 Alignment of full-length amino acid sequences of *Pain-1* P18 alleles.

A3.1.13 Alignment of full-length amino acid sequences of *Pain-1* P40 alleles.

A3.1.14 Alignment of full-length amino acid sequences of *Pain-1* P54 alleles.

A3.1.15 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_P18N1*.

A3.1.16 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_P18N2*.

A3.1.17 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_P40N1*.

A3.1.18 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_P40N2*.

A3.1.19 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_P54N*.

A3.1.20 Alignment of full-length *Pain-1* nucleotide sequences obtained from all diploid genotypes.

A3.1.21 Alignment of full-length *Pain-1* nucleotide sequences obtained from all tetraploid and diploid genotypes.

A3.1.22 Full-length alignment of nucleotide sequences of *Pain-1* alleles from 'Satina', 'Diana', and 'Theresa' to identify allele specific SNPs for assigning cloned alleles to associated SSCP fragments.

A3.1.23 Amino acid alignment of *Pain-1* BAC insert sequences and the P40 alleles *Pain_P40N1* and *Pain_P40N2*.

A3.1.24 Alignment of the genomic *Pain-1* BAC insert sequence with the *Pain-1* cDNA sequence to identify the exon- and intron structure of the *Pain-1* gene.

A3.1.25 Alignment of full-length nucleotide sequences from SNPs variants of the *Pain-1* allele *Pain_SN*.

A3.2 Exception of alleles, from which only one full-length sequence was obtained.

A3.2.1 Alignment of full-length amino acid sequences of *invGE* 'Satina' alleles.

A3.2.2 Alignment of full-length amino acid sequences of *invGE* 'Diana' alleles.

A3.2.3 Alignment of full-length amino acid sequences of *invGE* 'Theresa' alleles.

A3.2.4 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_SA*.

A3.2.5 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_SN1*.

A3.2.6 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_SN3*.

A3.2.7 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_DA*.

A3.2.8 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_DN1*.

A3.2.9 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_TA*.

A3.2.10 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_TN1*.

A3.2.11 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_TN2*.

A3.2.12 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_TN3*.

A3.2.13 Alignment of full-length *invGE* nucleotide sequences obtained from all tetraploid genotypes.

A3.2.14 Alignment of full-length amino acid sequences of *invGE* P18 alleles.

A3.2.15 Alignment of full-length amino acid sequences of *invGE* P40 alleles.

A3.2.16 Alignment of full-length amino acid sequences of *invGE* P54 alleles.

A3.2.17 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P18N1*.

A3.2.18 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P18N2*.

A3.2.19 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P40N1*.

A3.2.20 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P40N2*.

A3.2.21 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P54N1*

A3.2.22 Alignment of full-length nucleotide sequences from SNPs variants of the *invGE* allele *E_P54N2*.

A3.2.23 Alignment of full-length *invGE* nucleotide sequences obtained from all diploid genotypes.

A3.2.24 Alignment of full-length *invGE* nucleotide sequences obtained from all tetraploid and diploid genotypes.

A3.2.25 Alignment of full-length amino acid sequences of *invGF* 'Satina' alleles.

A3.2.26 Alignment of full-length amino acid sequences of *invGF* 'Diana' alleles.

A3.2.27 Alignment of full-length amino acid sequences of *invGF* 'Theresa' alleles.

A3.2.28 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_SN1*.

A3.2.29 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_SN2*.

A3.2.30 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_SN3*.

A3.2.31 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_SN4*.

A3.2.32 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_DN2*.

A3.2.33 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_TN1*.

A3.2.34 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_TN2*.

A3.2.35 Alignment of full-length *invGF* nucleotide sequences obtained from all tetraploid genotypes.

A3.2.36 Alignment of full-length amino acid sequences of *invGF* P18 alleles.

A3.2.37 Alignment of full-length amino acid sequences of *invGF* P40 alleles.

A3.2.38 Alignment of full-length amino acid sequences of *invGF* P54 alleles.

A3.2.39 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_P18N*.

A3.2.40 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_P40N2*.

A3.2.41 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_P54N1*.

A3.2.42 Alignment of full-length nucleotide sequences from SNPs variants of the *invGF* allele *F_P54N2*.

A3.2.43 Alignment of full-length *invGF* nucleotide sequences obtained from all diploid genotypes.

A3.2.44 Alignment of full-length *invGF* nucleotide sequences obtained from all tetraploid and diploid genotypes.

A3.2.45 Alignment of full-length amino acid sequences of the *invGE* allele *E_SA* and *invGF* allele *F_SN4*.

A3.3 Exception of alleles, from which only one full-length sequence was obtained.

A3.3.1 Alignment of full-length amino acid sequences of *pCD111* ‘Satina’ alleles.

A3.3.2 Alignment of full-length amino acid sequences of *pCD111* ‘Theresa’ alleles

A3.3.3 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD111* allele *CD111_S1*.

A3.3.4 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD111* allele *CD111_S2*.

A3.3.5 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD111* allele *CD111_T2*.

A3.3.6 Alignment of full-length *pCD111* nucleotide sequences obtained from all tetraploid genotypes.

A3.3.7 Alignment of full-length amino acid sequences of *pCD111* P54 alleles.

A3.3.8 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD111* allele *CD111_P54_1*.

A3.3.9 Alignment of full-length *pCD111* nucleotide sequences obtained from all diploid genotypes.

A3.3.10 Alignment of full-length *pCD111* nucleotide sequences obtained from all tetraploid and diploid genotypes.

A3.3.11 Alignment of full-length amino acid sequences of *pCD141* 'Satina' alleles.

A3.3.12 Alignment of full-length amino acid sequences of *pCD141* 'Diana' alleles.

A3.3.13 Alignment of full-length amino acid sequences of *pCD141* 'Theresa' alleles.

A3.3.14 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_S2*.

A3.3.15 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_S3*.

A3.3.16 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_D1*.

A3.3.17 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_T1*.

A3.3.18 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_T2*.

A3.3.19 Alignment of full-length *pCD141* nucleotide sequences obtained from all tetraploid genotypes.

A3.3.20 Alignment of full-length amino acid sequences of *pCD141* P18 alleles.

A3.3.21 Alignment of full-length amino acid sequences of *pCD141* P40 alleles.

A3.3.22 Alignment of full-length amino acid sequences of *pCD141* P54 alleles.

A3.3.23 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_P18_1*.

A3.3.24 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_P18_2*.

A3.3.25 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_P40_1*.

A3.3.26 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_P54_1*.

A3.3.27 Alignment of full-length nucleotide sequences from SNPs variants of the *pCD141* allele *CD141_P54_2*.

A3.3.28 Alignment of full-length *pCD141* nucleotide sequences obtained from all diploid genotypes.

A3.3.29 Alignment of full-length *pCD141* nucleotide sequences obtained from all tetraploid and diploid genotypes.

A3.3.30 Amino acid alignment of the *pCD111* BAC insert sequence and the P40 allele *CD111_P40_1*.

A3.3.31 Amino acid alignment of the *pCD141* BAC insert sequence and the P40 allele *CD141_P40_1*.

A3.3.32 Alignment of the genomic *pCD111* BAC insert sequence with the P40 *pCD111* cDNA sequence to identify the exon- and intron structure of the *pCD111* gene.

A3.3.33 Alignment of the genomic *pCD141* BAC insert sequence with the P40 *pCD141* cDNA sequence to identify the exon- and intron structure of the *pCD141* gene.

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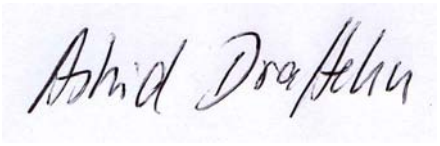
ERKLÄRUNG

Köln, 2009

Ich versichere, dass ich die von mir vorgelegte Dissertation selbständig angefertigt, die benutzten Quellen und Hilfsmittel vollständig angegeben und die Stellen der Arbeit – einschließlich Tabellen, Karten und Abbildungen – die anderen Werken im Wortlaut oder dem Sinn nach entnommen sind, in jedem Einzelfall als Entlehnung kenntlich gemacht habe; dass diese Dissertation noch keiner anderen Fakultät oder Universität zur Prüfung vorgelegen hat; dass sie noch nicht veröffentlicht worden ist sowie, dass ich eine solche Veröffentlichung vor Abschluss des Promotionsverfahrens nicht vornehmen werde.

Die Bestimmungen dieser Promotionsordnung sind mir bekannt. Die von mir vorgelegte Dissertation ist von PD Dr. Christiane Gebhardt betreut worden.



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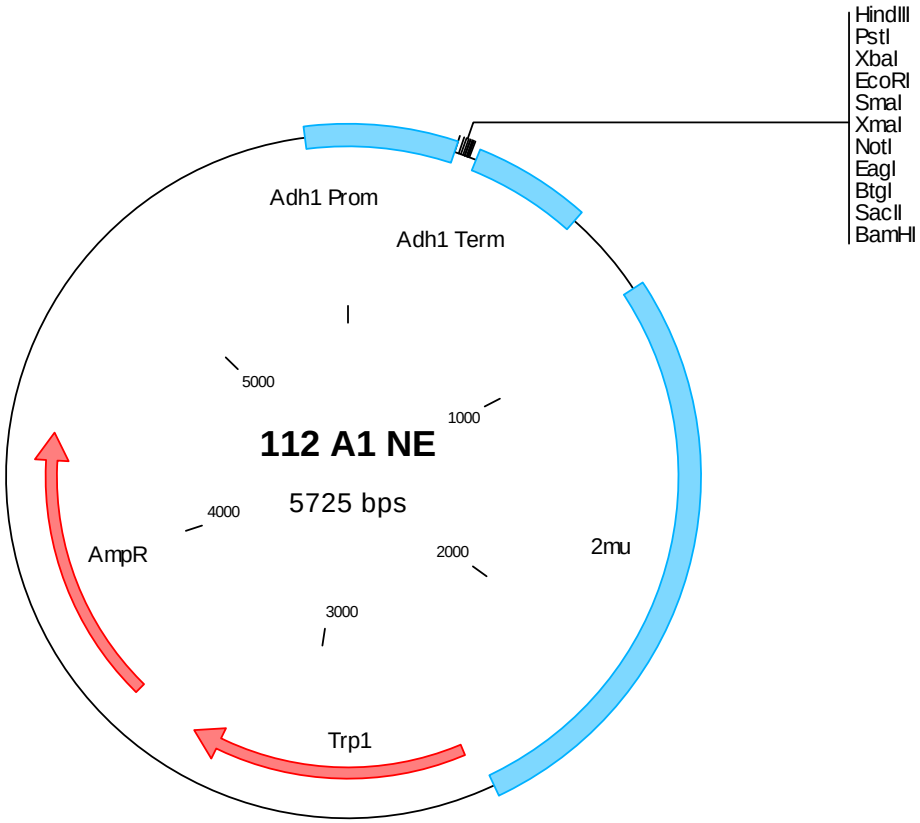
11/2003	Verteidigung Diplomarbeit

Appendix A2

Map of the yeast expression vector 112 A1 NE.



Appendix A3

For aligning the amino acid and nucleotide sequences of the obtained alleles the following software was used:

Multalin version 5.4.1 (http://bioinfo.genetoul.fr)
Copyright I.N.R.A. France 1989, 1991, 1994, 1996
Multiple sequence alignment with hierarchical clustering
F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Different matrixes were used for comparing the allelic sequences.
For all alignments except A3.1.24, A3.2.45, A3.3.32, and A3.3.33 the following parameters were used:

Symbol comparison table: **blosum62**
Gap weight: 12
Gap length weight: 2
Consensus levels: high=90% low=50%
Consensus symbols:
! is anyone of IV
$ is anyone of LM
% is anyone of FY
# is anyone of NDQEBZ

For aligning the sequences of A3.1.24, A3.2.45, A3.3.32, and A3.3.33 the following matrix was used:

Symbol comparison table: **dayhoff**
Gap weight: 5
Gap length weight: 0
Consensus levels: high=90% low=50%
Consensus symbols:
$ is anyone of LM
% is anyone of FY
# is anyone of BDENQZ

```
                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SN1        MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SN2        MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SN3        MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SN4        MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SA         MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SA1        MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SA3        MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_SA2        MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSDAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Consensus       MATQYHSSYDlENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWS#AMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_SN1        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_SN2        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_SN3        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_SN4        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_SA         WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
Pain_SA1        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
Pain_SA3        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWPL
Pain_SA2        WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAIVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
Consensus       WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAmVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIG!KDFRDPTTAWTGPQNGQWlL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SN1        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SN2        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SN3        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SN4        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SA         TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SA1        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SA3        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_SA2        TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Consensus       TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_SN1        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_SN2        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_SN3        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_SN4        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVAVIADQTLSELT
Pain_SA         WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Pain_SA1        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Pain_SA3        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Pain_SA2        WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Consensus       WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVvVIADQtLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_SN1        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_SN2        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_SN3        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_SN4        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_SA         PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_SA1        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_SA3        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_SA2        PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Consensus       PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGsSVTASVKIWSLESANIqSFPLQDL
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      Pain_DA   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Pain_DA2   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Pain_DA1   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Pain_DN2   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_1   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_3   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_6   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_2   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_4   MATQYHSSYDPENSAPHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN2_5   MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Pain_DN1   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN1_2   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN1_4   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN1_1   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN1_3   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Pain_DN1_5   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Consensus   MATQYHSSYDpENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASH!SYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      Pain_DA   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
     Pain_DA2   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
     Pain_DA1   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
     Pain_DN2   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_1   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_3   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_6   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_2   WYHFFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_4   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVMVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN2_5   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
     Pain_DN1   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN1_2   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN1_4   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN1_1   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN1_3   WYHLFYQYNPDSAIWGNXTWGHAVSRDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Pain_DN1_5   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIDVKDFRDPTTAWTGPQNGQWLL
     Consensus   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIg!KDFRDPTTAWTGPQNGQWLL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      Pain_DA   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Pain_DA2   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Pain_DA1   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMRECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Pain_DN2   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_1   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_3   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_6   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_2   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_4   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN2_5   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Pain_DN1   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN1_2   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN1_4   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN1_1   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASRTFYDPKKQRRVLWG
   Pain_DN1_3   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIELKLDYGKYYASKTFYDPKKQRRVLWG
   Pain_DN1_5   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Consensus   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDnPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      Pain_DA   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
     Pain_DA2   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
     Pain_DA1   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
     Pain_DN2   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_1   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_3   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_6   WIGETDSESADLQKGWASVQSVPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_2   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPSVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_4   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN2_5   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQLPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
     Pain_DN1   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN1_2   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN1_4   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN1_1   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN1_3   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Pain_DN1_5   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELPHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
     Consensus   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRaGDPIVKQVNLQPGSIELlHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQtLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      Pain_DA   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
     Pain_DA2   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
     Pain_DA1   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
     Pain_DN2   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_1   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_3   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_6   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_2   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_4   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNTTGASVTASVKIWSLESANIRSFPLQDL
   Pain_DN2_5   PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
     Pain_DN1   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
   Pain_DN1_2   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
   Pain_DN1_4   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
   Pain_DN1_1   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
   Pain_DN1_3   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
   Pain_DN1_5   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVGSFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
     Consensus   PVYF%ISKGADGRAETHFCADQTRSSEAPGVAKqVYGSSVPVLDGEKHSMRLLVDHSIVeSFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGaSVTASVKIWSLESANIrSFPLQDL
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_TN1      MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN1_1    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN1_2    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN1_3    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN2      MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN2_1    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN2_2    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_TN2_3    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
   Consensus    MATQYHSSYDpENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_TN1      WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN1_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN1_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN1_3    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN2      WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN2_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN2_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_TN2_3    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
   Consensus    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_TN1      TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN1_1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN1_2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN1_3    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN2      TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN2_1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN2_2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSHNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_TN2_3    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDKPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
   Consensus    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSyNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDkPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_TN1      WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN1_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN1_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN1_3    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN2      WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN2_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALRGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN2_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_TN2_3    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVDFSCSTSGGAASRGILGPFGVVVIADQTLSELT
   Consensus    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALqGIIEADHVgFSCSTSGGAASRGILGPFGVVVIADQTLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_TN1      PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_TN1_1    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_TN1_2    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_TN1_3    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSLRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_TN2      PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
  Pain_TN2_1    PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
  Pain_TN2_2    PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
  Pain_TN2_3    PVYFFISKGADGRAETHFCADQTRSSEAPGVAKRVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
   Consensus    PVYF%ISKGADGRAETHFCADQTRSSEAPGVAKrVYGSSVPVLDGEKHS$RLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGaSVTASVKIWSLESANIrSFPLQDL
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                1    10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SA1        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SA3        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SA2        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SA1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SA3        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SA2        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SA1        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SA3        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SA2        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCGATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCaATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SA1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SA3        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SA2        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATTGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATgGTTCCTGATCAATGGT

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SA1        ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SA3        ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SA2        ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SA1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SA3        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCCTTTA
Pain_SA2        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCtTTTA

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SA1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SA3        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SA2        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911   920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SA1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SA3        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SA2        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SA1        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SA3        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SA2        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SA1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SA3        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SA2        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SA1        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SA3        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SA2        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_SA1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_SA3        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_SA2        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SA1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SA3        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SA2        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SA1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SA3        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SA2        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SA         CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_SA1        CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_SA3        CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_SA2        CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN2        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGACCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN1        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN3        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN4        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGAtCAACCcGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN2        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN3        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN4        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN2        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN1        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN3        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN4        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN2        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN3        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN4        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN2        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN1        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN3        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN4        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN2        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN3        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN4        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN2        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN3        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN4        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN2        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN3        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN4        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN2        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN1        GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN3        GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN4        GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAAtAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN2        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN3        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN4        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN2        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN1        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAGCCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN3        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN4        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAaCCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN2        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN3        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN4        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGCTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGtTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN2        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN3        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN4        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN2        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN3        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN4        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN2        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN1        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN3        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN4        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DA2        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DA1        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DA2        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DA1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DA2        TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DA1        TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DA2        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DA1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DA2        ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DA1        ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DA2        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DA1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCGCTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DA2        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DA1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGAGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCaCTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGtGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DA2        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DA1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DA2        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DA1        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DA2        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DA1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DA2        TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DA1        TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_DA2        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_DA1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Pain_DA2        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Pain_DA1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DA2        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DA1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_DA2        CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_DA1        CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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                1    10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DN1_4      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DN1_3      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DN1_1      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DN1_2      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DN1_5      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCcGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DN1_4      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DN1_3      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DN1_1      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DN1_2      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DN1_5      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DN1_4      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DN1_3      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DN1_1      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DN1_2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_DN1_5      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DN1_4      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DN1_3      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATANCACATGGGGCCATGCCGTATCCAGGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DN1_1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DN1_2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_DN1_5      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATAtCACATGGGGCCATGCCGTATCCAaGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DN1_4      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DN1_3      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DN1_1      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DN1_2      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_DN1_5      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DN1_4      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DN1_3      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DN1_1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DN1_2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_DN1_5      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGATGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGgTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DN1_4      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DN1_3      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DN1_1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DN1_2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_DN1_5      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DN1_4      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DN1_3      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DN1_1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DN1_2      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_DN1_5      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DN1_4      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DN1_3      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGAGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DN1_1      GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAGGACATTTTACGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DN1_2      GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_DN1_5      GACTAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACaAAGAAtAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGgGTTGAAGCTGGATTATGGGAAATATTATGCATCAAaGACATTTTAtGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATCCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DN1_4      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DN1_3      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DN1_1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DN1_2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_DN1_5      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATtCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DN1_4      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DN1_3      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DN1_1      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DN1_2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_DN1_5      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACCCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACtCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_DN1_4      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_DN1_3      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_DN1_1      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_DN1_2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_DN1_5      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_DN1_4      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_DN1_3      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_DN1_1      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_DN1_2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_DN1_5      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DN1_4      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DN1_3      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DN1_1      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DN1_2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_DN1_5      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGGGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGaGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DN1        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DN1_4      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DN1_3      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DN1_1      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DN1_2      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DN1_5      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
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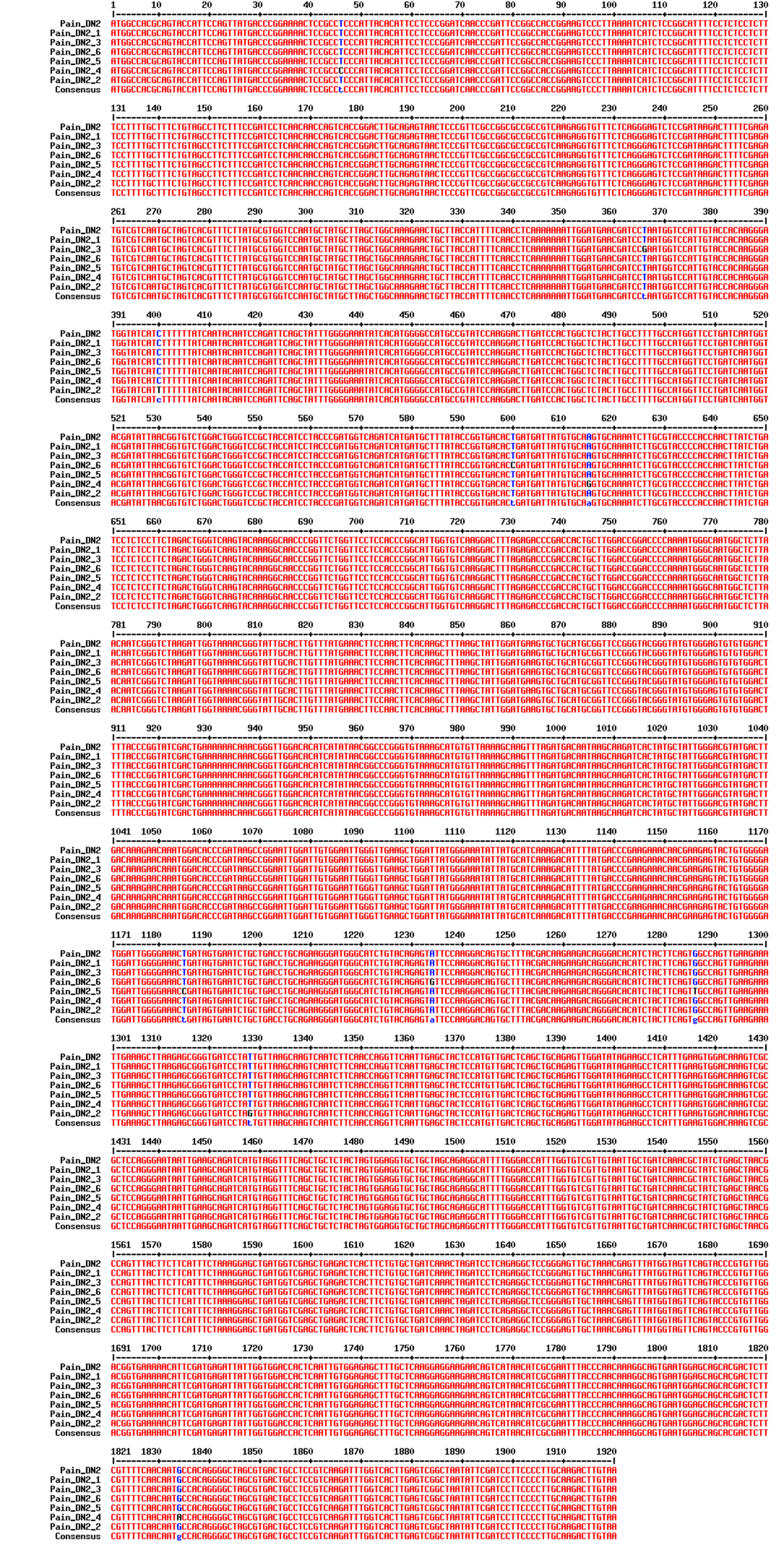

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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN1_1      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN1_2      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN1_3      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCtGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN1_1      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN1_2      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN1_3      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN1_1      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN1_2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN1_3      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN1_1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN1_2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN1_3      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN1_1      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN1_2      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN1_3      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_TN1_1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_TN1_2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_TN1_3      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN1_1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN1_2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN1_3      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN1_1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN1_2      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN1_3      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN1_1      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN1_2      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN1_3      GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAAcAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN1_1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN1_2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN1_3      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN1_1      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN1_2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN1_3      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTCAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTtAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN1_1      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN1_2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN1_3      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN1_1      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN1_2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN1_3      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN1_1      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN1_2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN1_3      ACGGTGAAAAACATTCGTTGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCGGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGaTGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCaGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN1        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN1_1      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN1_2      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN1_3      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN2_1      ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN2_2      ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN2_3      ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN2_1      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN2_2      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN2_3      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAgTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN2_1      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN2_2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN2_3      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN2_1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN2_2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN2_3      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN2_1      ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN2_2      ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN2_3      ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA
Pain_TN2_1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA
Pain_TN2_2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA
Pain_TN2_3      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCTGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCcGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN2_1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN2_2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN2_3      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN2_1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN2_2      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCACATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN2_3      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCAtATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN2_1      GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN2_2      GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN2_3      GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN2_1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN2_2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN2_3      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN2_1      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN2_2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN2_3      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN2_1      GCTCCGGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN2_2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN2_3      GCTCCAGGGAATAATTGAAGCAGATCATGTAGATTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCaGGGAATAATTGAAGCAGATCATGTAGgTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN2_1      CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN2_2      CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN2_3      CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN2_1      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN2_2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN2_3      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_TN2        CGTTTTCAATAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN2_1      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN2_2      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN2_3      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAAcAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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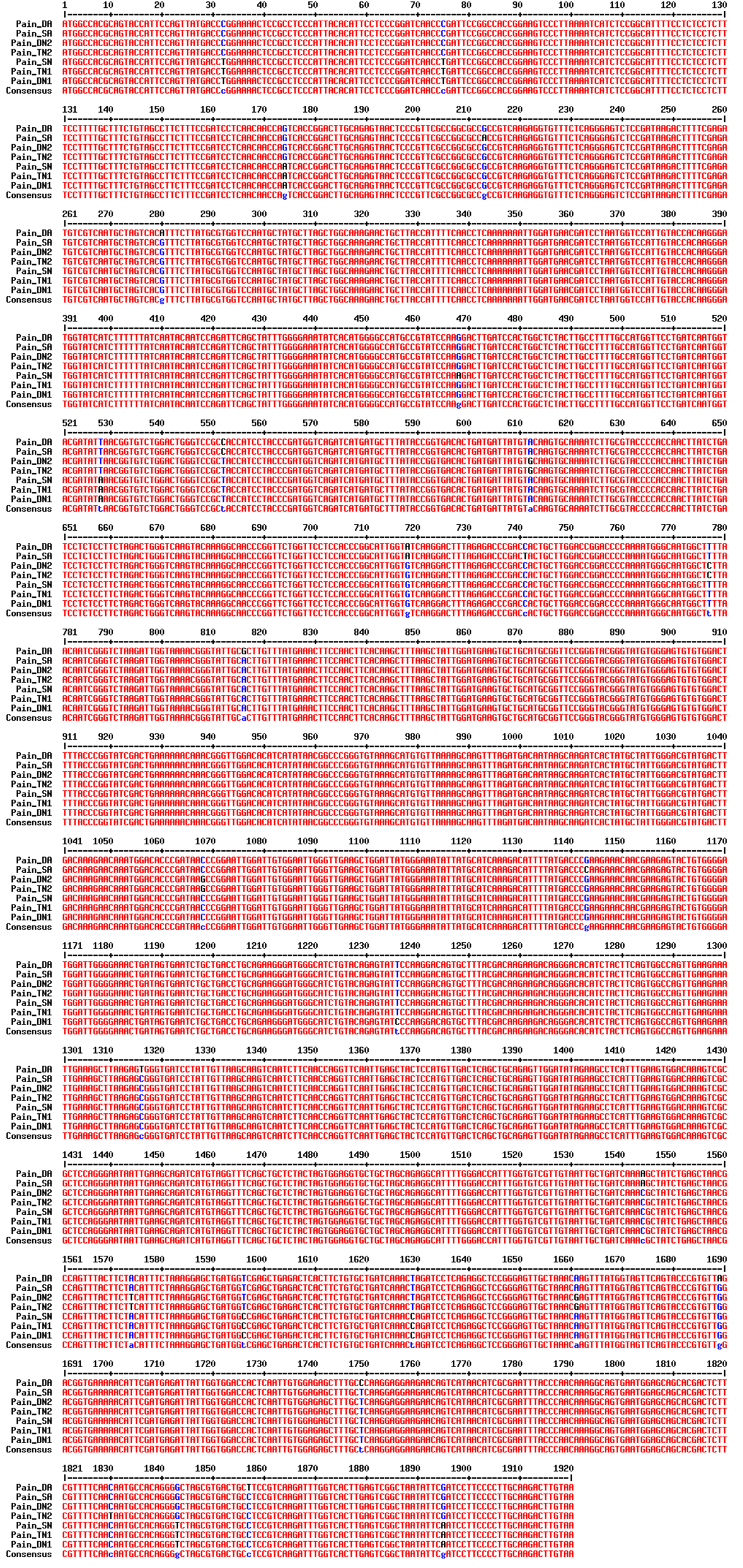

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P18N1    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P18N1_1    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P18N1_2    MATQYHSSYDPENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILSNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHISYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P18N2    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P18N2_1    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P18N2_3    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P18N2_2    MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
      Consensus MATQYHSSYDlENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILnNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASH!SYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P18N1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
Pain_P18N1_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
Pain_P18N1_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGIKDFRDPTTAWTGPQNGQWLL
  Pain_P18N2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P18N2_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P18N2_3    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P18N2_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVRYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
      Consensus WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVkYKGNPVLVPPPGIG!KDFRDPTTAWTGPQNGQWLL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P18N1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P18N1_1    TIGSKIGKTGIALVYETSNFTNFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKRVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P18N1_2    TIGSTIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P18N2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P18N2_1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P18N2_3    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTHDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P18N2_2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
      Consensus TIGSkIGKTGIALVYETSNFTsFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKhVLKASLDDNKQDHYAIGTyDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P18N1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Pain_P18N1_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
Pain_P18N1_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRVGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQKLSELT
  Pain_P18N2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P18N2_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P18N2_3    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P18N2_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
      Consensus WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRaGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQtLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P18N1    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P18N1_1    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P18N1_2    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
  Pain_P18N2    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_P18N2_1    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_P18N2_3    PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Pain_P18N2_2    PVYSYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
      Consensus PVYfYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGsSVTASVKIWSLESANIqSFPLQDL
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N1_1    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N1_2    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N1_4    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N1_3    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P40N2    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSLKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNARSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N2_1    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSLKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNARSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N2_2    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSLKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNARSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
     Consensus    MATQYHSSYDPENSASHYTFLPDQHDSGHRKSiKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAhSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N1_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N1_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N1_4    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N1_3    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P40N2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N2_1    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N2_2    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
     Consensus    WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N1_1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N1_2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N1_4    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N1_3    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P40N2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N2_1    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N2_2    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
     Consensus    TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P40N1_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P40N1_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P40N1_4    WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P40N1_3    WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_P40N2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGIVVIADQTLSELT
Pain_P40N2_1    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGIVVIADQTLSELT
Pain_P40N2_2    WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGIVVIADQTLSELT
     Consensus    WIGETDSESADLQKGWASVQSIPRTVLYDKKTrTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFG!VVIADQTLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N1_1    PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N1_2    PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N1_4    PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N1_3    PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPALDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
  Pain_P40N2    PVYFYISKGADGRAETHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N2_1    PVYFYISKGADGRAETHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N2_2    PVYFYISKGADGRAETHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
     Consensus    PVYFYISKGADGRA#THFCADQTRSSVAPGVAKQVYGSSVPvLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P54N_1   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P54N_2   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P54N_4   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P54N_5   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
  Pain_P54N_3   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
    Consensus   MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P54N_1   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P54N_2   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P54N_4   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNSSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P54N_5   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
  Pain_P54N_3   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
    Consensus   WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNlSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P54N_1   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P54N_2   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P54N_4   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P54N_5   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
  Pain_P54N_3   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
    Consensus   TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGTASRGILGPFGVVVIADQTLSELT
  Pain_P54N_1   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGTASRGILGPFGVVVIADQTLSELT
  Pain_P54N_2   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_P54N_4   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_P54N_5   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
  Pain_P54N_3   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
    Consensus   WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGaASRGILGPFGVVVIADQTLSELT

                521     530       540       550       560       570       580       590       600       610       620       630       639
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_P54N_1   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_P54N_2   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_P54N_4   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_P54N_5   PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVCGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
  Pain_P54N_3   PVYFYISKGADGRAETHFCADQTRSSEAPGAAKQVYSSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
    Consensus   PVYFYISKGADGRAETHFCADQTRSSEAPGvAKQVygSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N1_2    ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N1_1    ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N1_2    TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAGCAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N1_1    TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAaCAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N1_2    TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N1_1    TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N1_2    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N1_1    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N1_2    ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N1_1    ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
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                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N1_2    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N1_1    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N1_2    ACAATCGGGTCTACGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N1_1    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAACTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAaGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAgCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N1_2    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N1_1    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCGTGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCaTGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N1_2    GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N1_1    GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N1_2    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N1_1    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAAAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAgAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N1_2    TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N1_1    TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_P18N1_2    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_P18N1_1    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Pain_P18N1_2    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Pain_P18N1_1    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG

                1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N1      ACGGTGAGAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N1_2    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N1_1    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAaAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920
                |----+----|----+----|----+----|----+----|----+----|----+
Pain_P18N1      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N1_2    CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N1_1    CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N2_1    ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N2_3    ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N2_2    ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N2_1    TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N2_3    TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N2_2    TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N2_1    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N2_3    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N2_2    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N2_1    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N2_3    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N2_2    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N2_1    ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N2_3    ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N2_2    ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAAGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N2_1    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N2_3    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N2_2    TCCTCTCCTTCTAGACTGGGTCAGGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAaGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAgGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N2_1    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N2_3    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N2_2    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N2_1    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N2_3    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGCATGACTT
Pain_P18N2_2    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGtATGACTT

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N2_1    GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N2_3    GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N2_2    GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N2_1    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N2_3    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N2_2    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N2_1    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N2_3    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N2_2    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P18N2_1    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P18N2_3    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P18N2_2    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P18N2_1    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P18N2_3    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P18N2_2    CCAGTTTACTCCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTtCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N2_1    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N2_3    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N2_2    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920
                |----+----|----+----|----+----|----+----|----+----|----+----|
Pain_P18N2      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N2_1    CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N2_3    CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N2_2    CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
  Pain_P40N1_2  ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
  Pain_P40N1_4  ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
  Pain_P40N1_3  ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
  Pain_P40N1_1  ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
        Consensus  ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P40N1_2  TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P40N1_4  TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P40N1_3  TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P40N1_1  TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
        Consensus  TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P40N1_2  TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P40N1_4  TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P40N1_3  TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P40N1_1  TGTCGTCAATGCTAGTCATGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
        Consensus  TGTCGTCAATGCTAGTCAcGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P40N1_2  TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P40N1_4  TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P40N1_3  TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P40N1_1  TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
        Consensus  TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
  Pain_P40N1_2  ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
  Pain_P40N1_4  ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
  Pain_P40N1_3  ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
  Pain_P40N1_1  ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
        Consensus  ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P40N1_2  TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P40N1_4  TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P40N1_3  TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P40N1_1  TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
        Consensus  TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P40N1_2  ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P40N1_4  ACGATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P40N1_3  ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P40N1_1  ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
        Consensus  ACaATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911   920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P40N1_2  TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P40N1_4  TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P40N1_3  TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P40N1_1  TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
        Consensus  TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
  Pain_P40N1_2  GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
  Pain_P40N1_4  GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
  Pain_P40N1_3  GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
  Pain_P40N1_1  GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
        Consensus  GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P40N1_2  TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P40N1_4  TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P40N1_3  TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P40N1_1  TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
        Consensus  TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P40N1_2  TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P40N1_4  TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P40N1_3  TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P40N1_1  TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
        Consensus  TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P40N1_2  GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P40N1_4  GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P40N1_3  GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P40N1_1  GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
        Consensus  GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P40N1_2  CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P40N1_4  CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P40N1_3  CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGCGTTGG
  Pain_P40N1_1  CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
        Consensus  CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGtGTTGG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P40N1_2  ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P40N1_4  ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P40N1_3  ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P40N1_1  ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
        Consensus  ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P40N1    CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P40N1_2  CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P40N1_4  CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P40N1_3  CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P40N1_1  CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
        Consensus  CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
Pain_P40N2_1    ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
Pain_P40N2_2    ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
Consensus       ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P40N2_1    TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P40N2_2    TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAACGGTCCATTGTACCACAAGGGA
Pain_P40N2_1    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAACGGTCCATTGTACCACAAGGGA
Pain_P40N2_2    TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAACGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAACGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P40N2_1    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P40N2_2    TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      ACGATATTAACGGGGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
Pain_P40N2_1    ACGATATTAACGGGGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
Pain_P40N2_2    ACGATATTAACGGGGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
Consensus       ACGATATTAACGGGGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P40N2_1    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P40N2_2    TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCAAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P40N2_1    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCAAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P40N2_2    ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCAAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCAAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TTTACCCGGTATCGACCGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P40N2_1    TTTACCCGGTATCGACCGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P40N2_2    TTTACCCGGTATCGACCGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACCGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P40N2_1    GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P40N2_2    GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P40N2_1    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P40N2_2    TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCGATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P40N2_1    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCGATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P40N2_2    TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCGATTGAGCTACTCCATGTTGACTCAGCNGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCGATTGAGCTACTCCATGTTGACTCAGCtGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTATCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P40N2_1    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTATCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P40N2_2    GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTATCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTATCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCGGTGTTGG
Pain_P40N2_1    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCGGTGTTGG
Pain_P40N2_2    CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCGGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCGGTGTTGG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P40N2_1    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P40N2_2    ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N2      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P40N2_1    CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P40N2_2    CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
  Pain_P54N_2   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
  Pain_P54N_1   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
  Pain_P54N_3   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
  Pain_P54N_4   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
  Pain_P54N_5   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
    Consensus   ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCtGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P54N_2   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P54N_1   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P54N_3   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P54N_4   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
  Pain_P54N_5   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
    Consensus   TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P54N_2   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P54N_1   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P54N_3   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P54N_4   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
  Pain_P54N_5   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
    Consensus   TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P54N_2   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P54N_1   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P54N_3   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P54N_4   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
  Pain_P54N_5   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
    Consensus   TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
  Pain_P54N_2   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
  Pain_P54N_1   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
  Pain_P54N_3   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
  Pain_P54N_4   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTCATCTGA
  Pain_P54N_5   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
    Consensus   ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTtATCTGA

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P54N_2   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P54N_1   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P54N_3   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P54N_4   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
  Pain_P54N_5   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
    Consensus   TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P54N_2   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P54N_1   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P54N_3   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P54N_4   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
  Pain_P54N_5   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
    Consensus   ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911   920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P54N_2   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P54N_1   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P54N_3   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P54N_4   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
  Pain_P54N_5   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
    Consensus   TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
  Pain_P54N_2   GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
  Pain_P54N_1   GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGCGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
  Pain_P54N_3   GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
  Pain_P54N_4   GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
  Pain_P54N_5   GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
    Consensus   GACAAAGAAcAAATGGACACCCGATAACCCGGAATTGGATTGtGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P54N_2   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P54N_1   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P54N_3   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P54N_4   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
  Pain_P54N_5   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
    Consensus   TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P54N_2   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P54N_1   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P54N_3   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P54N_4   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
  Pain_P54N_5   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
    Consensus   TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P54N_2   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P54N_1   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTACTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P54N_3   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P54N_4   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
  Pain_P54N_5   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
    Consensus   GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTgCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P54N_2   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P54N_1   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P54N_3   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGCTGCTAAACAAGTTTATAGTAGTTCAGTACCCGTGTTGG
  Pain_P54N_4   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
  Pain_P54N_5   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTGTGGTAGTTCAGTACCCGTGTTGG
    Consensus   CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGtTGCTAAACAAGTTTaTgGTAGTTCAGTACCCGTGTTGG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P54N_2   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P54N_1   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P54N_3   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P54N_4   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
  Pain_P54N_5   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
    Consensus   ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  Pain_P54N     CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P54N_2   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P54N_1   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P54N_3   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P54N_4   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
  Pain_P54N_5   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
    Consensus   CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCATTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
Pain_P40N2      ATGGCCACGCAGTACCACTCAAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACACGATTCCGGCCACCGGAAATCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTC
Pain_P18N2      ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P54N       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_P18N1      ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCAtTCcAGTTATGACCcGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACccGATTCCGGCCACCGGAAgTCCcTTAAAATCATCTCCGGCATTTTCCTCTCCTCTt

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCATTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P40N2      TCCTTTTGCTTTCTTTAGTCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAAAGTAACGCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N2      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P54N       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_P18N1      TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTgTAGcCTTCTTTCCGATCCTCAACAACCAgTCACCGGACTTGCAgAGTAACtCCCgTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P40N2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAACGGTCCATTGTACCACAAGGGA
Pain_P18N2      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P54N       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_P18N1      TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACgTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAAtGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P40N2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N2      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P54N       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_P18N1      TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
Pain_P40N2      ACGATATTAACGGGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACTGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCGCCAACTTATCTGA
Pain_P18N2      ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P54N       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_P18N1      ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATtAACGGtGTCTGGACTGGGTCCGCtACCATCCTACCCGATGGTCAGATCATGATGCTTTATACcGGTGACACTGATGATTATGTaCAAGTGCAAAATCTTGCGTACCCCaCCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P40N2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N2      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAAGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P54N       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_P18N1      TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTgTCAAgGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAACTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P40N2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCAAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N2      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P54N       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_P18N1      ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCcAACTTCACAAGCTTTAAgCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P40N2      TTTACCCGGTATCGACCGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N2      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P54N       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_P18N1      TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACtGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTGCTGTGGGGA
Pain_P40N2      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N2      GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P54N       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_P18N1      GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAAcAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTaCTGTGGGGA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAAGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P40N2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N2      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P54N       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_P18N1      TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAgGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P40N2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGCCAATCTTCAACCAGGTTCGATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N2      TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P54N       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_P18N1      TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGcGGGTGATCCTATTGTTAAGCAAGtCAATCTTCAACCAGGTTCaATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P40N2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTATCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P18N2      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P54N       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_P18N1      GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTgTCGTTGTAATTGCTGATCAAAcGCTATCTGAGCTAACG

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTCAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P40N2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGTGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCGGTGTTGG
Pain_P18N2      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P54N       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_P18N1      CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGtCGAGCTgAGACTCACTTCTGTGCTGATCAAACtAGATCCTCAGaGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCcGTGTTgG

                1691  1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCACGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P40N2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N2      ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P54N       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_P18N1      ACGGTGAGAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAaAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCtCAAGGAGGAAGAACAGTCATAACATCgCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821  1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_P40N1      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P40N2      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N2      CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_P54N       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_P18N1      CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGgCTAGCGTGACTGCcTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCgATCCTTCCCCTTGCAAGACTTGTAA
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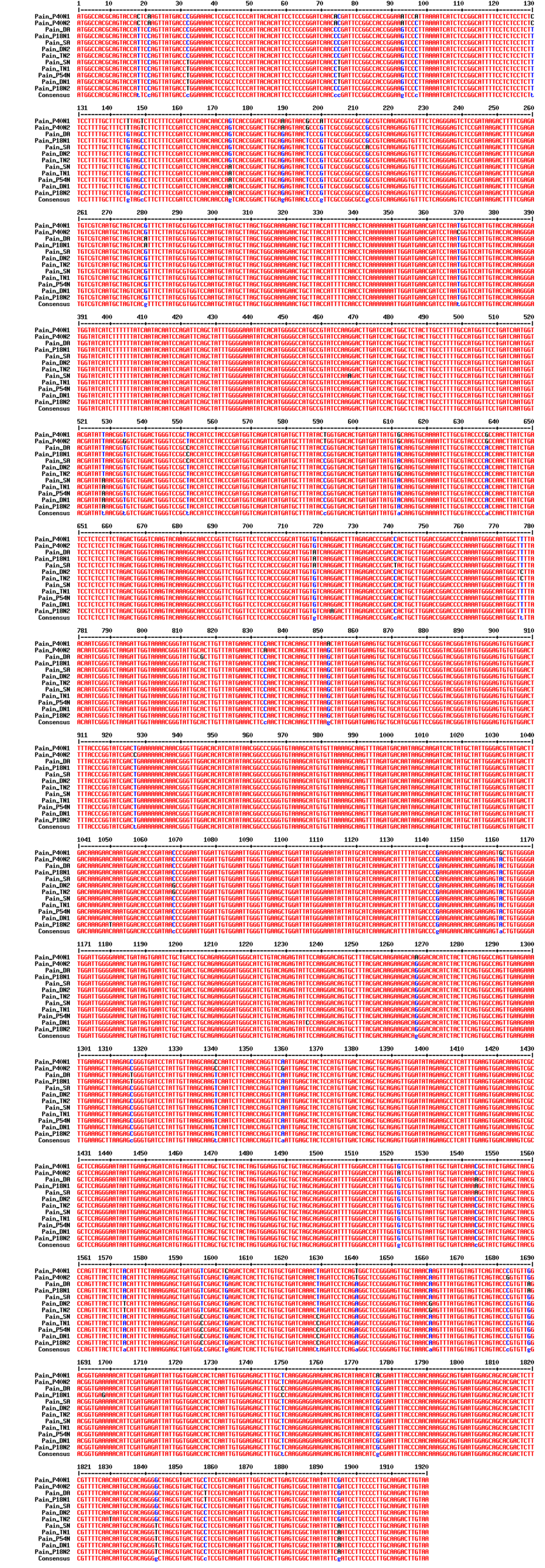

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SA         ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN2        ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_TN1        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCcGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCcGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SA         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCACCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN2        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_TN1        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAgTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCgCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGTCGTCAATGCTAGTCACATTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SA         TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN2        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_TN1        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACgTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SA         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN2        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_TN1        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SA         ACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN2        ACGATATTAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTGCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_TN1        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATtAACGGTGTCTGGACTGGGTCCGCtACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTaCAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SA         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTATCAAGGACTTTAGAGACCCGACTACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_TN2        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTCTTA
Pain_TN1        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTgTCAAGGACTTTAGAGACCCGACcACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTtTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCGCTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SA         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN2        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_TN1        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCaCTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SA         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN2        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_TN1        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SA         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCCAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN2        GACAAAGAACAAATGGACACCCGATAAGCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_TN1        GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAACAAATGGACACCCGATAAcCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCgAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SA         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN2        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_TN1        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         TTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SA         TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN2        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_TN1        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGcGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_SA         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACG
Pain_TN2        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_TN1        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAcGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAG
Pain_SA         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN2        CCAGTTTACTTCTTCATTTCTAAAGGAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAGATCCTCAGAGGCTCCGGGAGTTGCTAAACGAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_TN1        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTaCATTTCTAAAGGAGCTGATGGtCGAGCTGAGACTCACTTCTGTGCTGATCAAACtAGATCCTCAGAGGCTCCGGGAGTTGCTAAACaAGTTTATGGTAGTTCAGTACCCGTGTTgG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCCCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SA         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN2        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_TN1        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCtCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_DA         CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_SA         CGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN2        CGTTTTCAATAATGCCACAGGGGCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Pain_TN1        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAAcAATGCCACAGGGgCTAGCGTGACTGCcTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCgATCCTTCCCCTTGCAAGACTTGTAA
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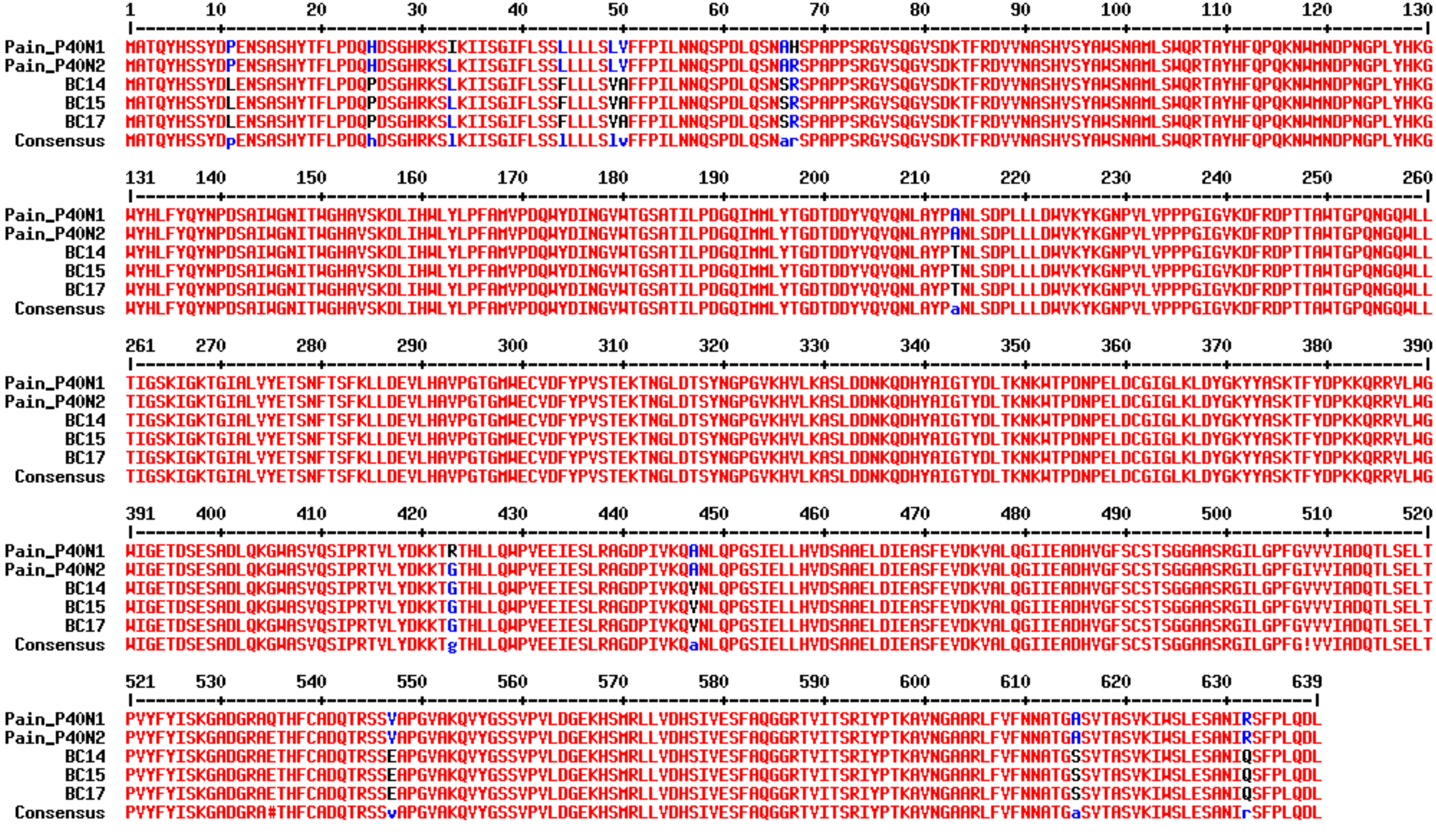
1 10 20 30 40 50 60 70 80 90 100 110 120 130
Pain_P40N1 MATQYHSSYDPENSASHYTFLPDQHDSGHRKSIKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNAHSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Pain_P40N2 MATQYHSSYDPENSASHYTFLPDQHDSGHRKSLKIISGIFLSSLLLLSLVFFPILNNQSPDLQSNARSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
BC14 MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
BC15 MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
BC17 MATQYHSSYDLENSASHYTFLPDQPDSGHRKSLKIISGIFLSSFLLLSVAFFPILNNQSPDLQSNSRSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
Consensus MATQYHSSYDpENSASHYTFLPDQhDSGHRKSlKIISGIFLSSlLLLSlvFFPILNNQSPDLQSNarSPAPPSRGVSQGVSDKTFRDVVNASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPNGPLYHKG
131 140 150 160 170 180 190 200 210 220 230 240 250 260
Pain_P40N1 WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Pain_P40N2 WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
BC14 WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
BC15 WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
BC17 WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPTNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
Consensus WYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGSATILPDGQIMMLYTGDTDDYVQVQNLAYPaNLSDPLLLDWVKYKGNPVLVPPPGIGVKDFRDPTTAWTGPQNGQWLL
261 270 280 290 300 310 320 330 340 350 360 370 380 390
Pain_P40N1 TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Pain_P40N2 TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
BC14 TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
BC15 TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
BC17 TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
Consensus TIGSKIGKTGIALVYETSNFTSFKLLDEVLHAVPGTGMWECVDFYPVSTEKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLTKNKWTPDNPELDCGIGLKLDYGKYYASKTFYDPKKQRRVLWG
391 400 410 420 430 440 450 460 470 480 490 500 510 520
Pain_P40N1 WIGETDSESADLQKGWASVQSIPRTVLYDKKTRTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Pain_P40N2 WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQANLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGIVVIADQTLSELT
BC14 WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
BC15 WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
BC17 WIGETDSESADLQKGWASVQSIPRTVLYDKKTGTHLLQWPVEEIESLRAGDPIVKQVNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFGVVVIADQTLSELT
Consensus WIGETDSESADLQKGWASVQSIPRTVLYDKKTgTHLLQWPVEEIESLRAGDPIVKQaNLQPGSIELLHVDSAAELDIEASFEVDKVALQGIIEADHVGFSCSTSGGAASRGILGPFG!VVIADQTLSELT
521 530 540 550 560 570 580 590 600 610 620 630 639
Pain_P40N1 PVYFYISKGADGRAQTHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
Pain_P40N2 PVYFYISKGADGRAETHFCADQTRSSVAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGASVTASVKIWSLESANIRSFPLQDL
BC14 PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
BC15 PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
BC17 PVYFYISKGADGRAETHFCADQTRSSEAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGSSVTASVKIWSLESANIQSFPLQDL
Consensus PVYFYISKGADGRA#THFCADQTRSSvAPGVAKQVYGSSVPVLDGEKHSMRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGAARLFVFNNATGaSVTASVKIWSLESANIrSFPLQDL

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          1    10   20   30   40   50   60   70   80   90   100  110  120  130
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      ATGGCCACCCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_DA   ATGGCCACGCAGTACCATTCCAGTTATGACCCGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus ATGGCCACcCAGTACCATTCCAGTTATGACCcGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

          131  140  150  160  170  180  190  200  210  220  230  240  250  260
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TCCTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_DA   TCCTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAGTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus TCCTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAaTCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

          261  270  280  290  300  310  320  330  340  350  360  370  380  390
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGGTAATTAACTTTCTTATTTTGACTTTTCT
Pain_DA   TGTCGTCAATGCTAGTCACATTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACG----------------------------
Consensus TGTCGTCAATGCTAGTCACaTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACG----------

          391  400  410  420  430  440  450  460  470  480  490  500  510  520
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GTAATTTCCTATTTATTTGATCTTAGAATTGAAAAAAATTATAAATACTTATACCGTTTTTTTTTTCTTAATGATATTTATGGCTATTGATCTGTTGGGGTATCTTTTGGATTCTGATTGGATGCTATT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          521  530  540  550  560  570  580  590  600  610  620  630  640  650
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      CTGCAGATCCTAATGGTGAGTTCAAAGTTAATTATCATCACTATTTTCTGTTAGTATTTAATTAATTATATTCTTTAACCATGAAATAAAACTTAAAGGCAGTAAAATTCTCTCATGAGGTAATTATGG
Pain_DA   -------ATCCTAATGGT----------------------------------------------------------------------------------------------------------
Consensus ......ATCCTAATGGT..........................................................................................................

          651  660  670  680  690  700  710  720  730  740  750  760  770  780
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TTTTAATTGAATTAAGCCTATAAGTGGCAAACAATCCATGTATGAGCAAATCATTAATTCGGGTATGTCATCTCGGTTAATCCTTTACCTTTTACTCAAAAGGAACTATTACTCCGTCCAAAATAATTG
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          781  790  800  810  820  830  840  850  860  870  880  890  900  910
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      ATGTTTCACATAATCAATGTGATGTTTAATTTTTTTTTTCAAATTACCCTTGGTATATACCTAATCCCTATAATGATTATGCCAAATCTAATATGAAAAGAAAATCATAATTACAGATATTTAGTCAC
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          911  920  930  940  950  960  970  980  990  1000 1010 1020 1030 1040
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      AATTAATTCATGTTAAAATATCAATAATTTTGGATTGGAGGTAGTACTAATTAGGAAAATAATTAAGTTAAATCATTTTCACTAAACATTGTTTAGACTAAGGATGAAATAGGGGAGGAATCAATTATCT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TATTTTTGTAAATGGATAAGTATTTTGAAATAACAAATTTTAAGAAAACACGACAAGTCAAATAGAGTAGGATTGATGGAGTGTATTCTAACCTTTCTAGATATTCATAAAAATTGGTTGAATTTTTTTT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      AATAAACACGACAAGTTGATGGATTAGGCTTGTTGTTCCAATATAATTGGGATTAACATGAGATCGTGTGGCAGCAAAGTTTTTGGTTTTGGGTAATTTTCCAATAAAAATTAAACACATGATTGGCCA
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GTTTTATACAAGTTTGGAAATCAATCACGTTATGTGGGTCATACTTTTTTGTAGTAATGTAATAATTCCATTAGTTGGCCCCCCATCCAAATTATTTGTCCATCTTTCCACTTGGTCATTTTCTCTCTT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TTATTTTTTTGAAATGGAGTAGGTTATCTTGTGCCGCTTAGAAGCAATTACTATTACCATTTCGAAGTCATAAAAAAATCAATATATATTATAAGGATAAAAATATATAACATAAATTTCATGAGTTTAT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TTATTTAAAATTTAGGGGAGGAGGACATAACATAGTAACATATCACTAGTAAAATTTGTTTAAGTAGCTTGTTGAAGATAATCTTAATTATTCAAAGGTCAAAAATAATAACTCATGGCGAAATTTTCAA
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TAAAAGAACGTTATCTTTTTGCCGCAAAAAGCATAGCAATTTTGGTACGGAACATATTGAGATTTCGTAGAGTATTTTACAATTCAAATTGCATAGAAAAGTCTTACCTAATGCAAGTAAAATACATAAT
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          1821 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TACTTTGAAATTTCTACTAACGTGAATAAATTGGTCAACAGGTCCATTGTACCACAAGGGATGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCC
Pain_DA   ----------------------------------------CCATTGTACCACAAGGGATGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGCCATGCC
Consensus .....................................CCATTGTACCACAAGGGATGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGCCATGCC

          1951 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGTACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATA
Pain_DA   GTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGTACGATATTAACGGTGTCTGGACTGGGTCCGCCACCATCCTACCCGATGGTCAGATCATGATGCTTTATA
Consensus GTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGTACGATATaAACGGTGTCTGGACTGGGTCCGCcACCATCCTACCCGATGGTCAGATCATGATGCTTTATA

          2081 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      CCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGATCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGT
Pain_DA   CCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGATCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTAT
Consensus CCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGATCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTaT

          2211 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      CAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTAACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTT
Pain_DA   CAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTAACAATCGGGTCTAAGATTGGTAAAACGGGTATTGGCGCTTGTTTATGAAACTTCCAACTTCACAAGCTTT
Consensus CAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTAACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCaCTTGTTTATGAAACTTCCAACTTCACAAGCTTT

          2341 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      AAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACTTTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATG
Pain_DA   AAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACTTTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATG
Consensus AAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACTTTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATG

          2471 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTTGACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGG
Pain_DA   TGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTTGACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGG
Consensus TGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTTGACAAAGAACaAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGG

          2601 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGATGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGGTATGGACT
Pain_DA   GAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGATGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAG---------
Consensus GAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGATGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAG.........

          2731 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TCGATTAACACATTGTTTTGTTGTTTAGTTTGCACCATACACAATAATCGTGCGAAATTATATCTATCAGTAGGGAAATTTCTTATTTAGAAAAAAGTTGTATATAATCAATGCATTTGTTGGTGAAGTGA
Pain_DA   ----------------------------------------------------------------------------------------------------------------------------
Consensus ..........................................................................................................................

          2861 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      ATTGGAATTTTTGTTGAAGTATATTCTCAATTATATATGAAACATCTCTAATAATTTTGTAATACGAATAATAACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCA
Pain_DA   ----------------------------------------------------------------AGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCA
Consensus ..............................................................AGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCA

          2991 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GTGGCCAGTTGAAGAAATTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGGTTTGTTGCGCGACTTTGTTT
Pain_DA   GTGGCCAGTTGAAGAAATTGAAAGCTTAAGAGTGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAG----------------------
Consensus GTGGCCAGTTGAAGAAATTGAAAGCTTAAGAGcGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAG......................

          3121 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      AAAATTACAAACTTTATACTTATACGCGCTTAATCTGCAGTCTTAAAACTTGTTGGCTATTGTGCAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGCGCTCCAGGGAATAATTGAAGCAGAT
Pain_DA   ----------------------------------------------------TTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGCGCTCCAGGGAATAATTGAAGCAGAT
Consensus ..................................................TTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGCGCTCCAGGGAATAATTGAAGCAGAT

          3251 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      CATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACGCCAGTTTACTTCTACATTTCTAAAG
Pain_DA   CATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAAGCTATCTGAGCTAACGCCAGTTTACTTCTACATTTCTAAAG
Consensus CATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAAaGCTATCTGAGCTAACGCCAGTTTACTTCTACATTTCTAAAG

          3381 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGGTTTGCTTCTATTTTCTCTATCTGGCACAATTAATTTGTCATAATAGTCCTTGTAAAATGGAGATGGATAAAAGTAGCGCGTTA
Pain_DA   GAGCTGATGGTCGAGCTGAGACTCACTTCTGTGCTGATCAAACTAG-----------------------------------------------------------------------------
Consensus GAGCTGATGGcCGAGCTGAGACTCACTTCTGTGCTGATCAAACcAG.....................................................................

          3511 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      TGATCTGATATATGCAGATCCTCAGAGGCTCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGGACGGTGAAAAACATTCGATGAGATTATTGGTAAGTGATGATGATTCCCTTATTT
Pain_DA   ----------------ATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTAGACGGTGAAAAACATTCGATGAGATTATTGGT----------------------
Consensus ................ATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTaGACGGTGAAAAACATTCGATGAGATTATTGGT......................

          3641 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      ACCTTTGTTTATATCAAGCTTATATTCAGTTCTTGTAGTCTAGTTGGTTCACTATAAAAAAAGTACTTGGCAGTTGCATTTGAGTAAAAGTTTTATAAACTGAATTTTAGGTGGACCACTCAATTGTGGA
Pain_DA   ----------------------------------------------------------------------------------------------------GGACCACTCAATTGTGGA
Consensus ..........................................................................................GGACCACTCAATTGTGGA

          3771 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900
          |----+----+----+----+----+----+----+----+----+----+----+----+----|
BC14      GAGCTTTGCTCAAGGAGGAAGGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTTCGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATT
Pain_DA   GAGCTTTGCCCAAGGAGGAAGGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTTCGTTTTCAACAATGCCACAGGGGCTAGCGTGACTGCTTCCGTCAAGATT
Consensus GAGCTTTGCcCAAGGAGGAAGGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTTCGTTTTCAACAATGCCACAGGGgCTAGCGTGACTGCcTCCGTCAAGATT

          3901 3910 3920 3930 3940 3951
          |----+----+----+----+----+---|
BC14      TGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_DA   TGGTCACTTGAGTCGGCTAATATTCGATCCTTCCCCTTGCAAGACTTGTAA
Consensus TGGTCACTTGAGTCGGCTAATATTCaATCCTTCCCCTTGCAAGACTTGTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN**       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGACCAACCTGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Pain_SN*        ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGATCAACCCGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT
Consensus       ATGGCCACGCAGTACCATTCCAGTTATGACCTGGAAAACTCCGCCTCCCATTACACATTCCTCCCGGAtCAACCtGATTCCGGCCACCGGAAGTCCCTTAAAATCATCTCCGGCATTTTCCTCTCCTCTT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN**       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Pain_SN*        TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA
Consensus       TCCTTTTGCTTTCTGTAGCCTTCTTTCCGATCCTCAACAACCAATCACCGGACTTGCAGAGTAACTCCCGTTCGCCGGCGCCGCCGTCAAGAGGTGTTTCTCAGGGAGTCTCCGATAAGACTTTTCGAGA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN**       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Pain_SN*        TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA
Consensus       TGTCGTCAATGCTAGTCACGTTTCTTATGCGTGGTCCAATGCTATGCTTAGCTGGCAAAGAACTGCTTACCATTTTCAACCTCAAAAAAATTGGATGAACGATCCTAATGGTCCATTGTACCACAAGGGA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN**       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Pain_SN*        TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT
Consensus       TGGTATCATCTTTTTTATCAATACAATCCAGATTCAGCTATTTGGGGAAATATCACATGGGGCCATGCCGTATCCAAGGACTTGATCCACTGGCTCTACTTGCCTTTTGCCATGGTTCCTGATCAATGGT

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN**       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Pain_SN*        ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA
Consensus       ACGATATAAACGGTGTCTGGACTGGGTCCGCTACCATCCTACCCGATGGTCAGATCATGATGCTTTATACCGGTGACACTGATGATTATGTACAAGTGCAAAATCTTGCGTACCCCACCAACTTATCTGA

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN**       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Pain_SN*        TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA
Consensus       TCCTCTCCTTCTAGACTGGGTCAAGTACAAAGGCAACCCGGTTCTGGTTCCTCCACCCGGCATTGGTGTCAAGGACTTTAGAGACCCGACCACTGCTTGGACCGGACCCCAAAATGGGCAATGGCTTTTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN**       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Pain_SN*        ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT
Consensus       ACAATCGGGTCTAAGATTGGTAAAACGGGTATTGCACTTGTTTATGAAACTTCCAACTTCACAAGCTTTAAGCTATTGGATGAAGTGCTGCATGCGGTTCCGGGTACGGGTATGTGGGAGTGTGTGGACT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN**       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Pain_SN*        TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT
Consensus       TTTACCCGGTATCGACTGAAAAAACAAACGGGTTGGACACATCATATAACGGCCCGGGTGTAAAGCATGTGTTAAAAGCAAGTTTAGATGACAATAAGCAAGATCACTATGCTATTGGGACGTATGACTT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN**       GACAAAGAACAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Pain_SN*        GACAAAGAATAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA
Consensus       GACAAAGAAcAAATGGACACCCGATAACCCGGAATTGGATTGTGGAATTGGGTTGAAGCTGGATTATGGGAAATATTATGCATCAAAGACATTTTATGACCCGAAGAAACAACGAAGAGTACTGTGGGGA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN**       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Pain_SN*        TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA
Consensus       TGGATTGGGGAAACTGATAGTGAATCTGCTGACCTGCAGAAGGGATGGGCATCTGTACAGAGTATTCCAAGGACAGTGCTTTACGACAAGAAGACAGGGACACATCTACTTCAGTGGCCAGTTGAAGAAA

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN**       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAACCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Pain_SN*        TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAGCCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC
Consensus       TTGAAAGCTTAAGAGCGGGTGATCCTATTGTTAAGCAAGTCAATCTTCAaCCAGGTTCAATTGAGCTACTCCATGTTGACTCAGCTGCAGAGTTGGATATAGAAGCCTCATTTGAAGTGGACAAAGTCGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN**       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Pain_SN*        GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG
Consensus       GCTCCAGGGAATAATTGAAGCAGATCATGTAGGTTTCAGCTGCTCTACTAGTGGAGGTGCTGCTAGCAGAGGCATTTTGGGACCATTTGGTGTCGTTGTAATTGCTGATCAAACGCTATCTGAGCTAACG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN**       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Pain_SN*        CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG
Consensus       CCAGTTTACTTCTACATTTCTAAAGGAGCTGATGGCCGAGCTGAGACTCACTTCTGTGCTGATCAAACCAGATCCTCAGAGGCTCCGGGAGTTGCTAAACAAGTTTATGGTAGTTCAGTACCCGTGTTGG

                1691    1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800      1810      1820
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN**       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Pain_SN*        ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT
Consensus       ACGGTGAAAAACATTCGATGAGATTATTGGTGGACCACTCAATTGTGGAGAGCTTTGCTCAAGGAGGAAGAACAGTCATAACATCGCGAATTTACCCAACAAAGGCAGTGAATGGAGCAGCACGACTCTT

                1821    1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
                |-------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
Pain_SN         CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN**       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Pain_SN*        CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
Consensus       CGTTTTCAACAATGCCACAGGGTCTAGCGTGACTGCCTCCGTCAAGATTTGGTCACTTGAGTCGGCTAATATTCAATCCTTCCCCTTGCAAGACTTGTAA
```

Appendix 3.2

A sequence was defined as an allele when it was found twice in two independent PCRs. Additionally, the consensus sequence of all alleles found in one genotype was used for allele definition when variable sequence polymorphisms occurred.

In the following Table, *invGE* and *invGF* alleles are listed, which do not correspond to this definition because only one full-length sequence was obtained. Nevertheless, several independent PCR amplifications gave rise to sequences that after partial sequencing indicated the existence of the alleles as mentioned above, clearly implying their existence. These additional sequences exhibited frame shifts or other modifications (e.g. missing or modified start and stop codons) and, therefore, were not completely sequenced. Furthermore, pyrosequencing analysis was carried out for allele specific SNPs demonstrating the presence of the latter SNPs in the corresponding genotype at genomic level.

Table A3.2.1: Overview of fully and partially sequenced *invGE* and *invGF* alleles.

Gene	Full-length allele	Additional partial sequences	Pyrosequencing assay
invGE	*E_SN2*	No additional sequences	Section 3.2.2.1.1, Figure 3.2.24
	E_DN2	No additional sequences	Section 3.2.2.1.1, Figure 3.2.24
invGF	*F_DN1*	2	Section 3.2.2.1.3, Figure 3.2.26
	F_TN2	2	Section 3.2.2.1.3, Figure 3.2.26
	F_P40N1	2	Section 3.2.2.1.4, Figure 3.2.27

```
                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SA3           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SA2           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SA1           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKGLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN1           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN1_1         MELFMKSSSLWGLEIYLFCLFTVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN2           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN3           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN3_1         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_SN3_2         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
Consensus       MELFMKSSSLWGLEIYLFCfFIVLSNINkVFaSHN!FLDLQSSSAISVKNVHRTgFHFQPPKhWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKdLINWIHLEPAIYPSKKFDKYGAWSGSA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_SA3           TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRGRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_SA2           TILPNNKPVIXYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_SA1           TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_SN1           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_SN1_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_SN2           TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_SN3           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_SN3_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_SN3_2         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus       TILPNNKP!ILYTGVVDSHDsQVQNYAIPANLSDPFLRKW!KPNNNPLI!PDNSINKTKFRDPTTAWMGqDGlWRIVIGSMRkHRGMALLYRSRDFIKW.KAQHPLHSSPHTGNWECPDFFPVSLkNTNG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_SA3           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNLYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_SA2           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_SA1           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_SN1           LDASYRGKKKVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_SN1_1         LDASYRGKKKVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_SN2           LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_SN3           LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_SN3_1         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_SN3_2         LDASYRGK-NVKHVLKNSLDVNRSDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
Consensus       LDASYRGK.nVKhVLKNSLDVNRf#YYTIGMYDTkKDRYIPDNNSIDGsKGLRLDYGNFYASKSFYDPmKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDpSGKQLIQWPIEELETLRKQKI.

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SA3           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SA2           QSNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SA1           QLNNKKLSKGEMFEVKGISASQSDIEVSFSLSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SN1           QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNEAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKILMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SN1_1         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNEAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKILMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SN2           QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_SN3           QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATVASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SN3_1         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATVASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_SN3_2         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATVASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
Consensus       QLNNKKLSKGEMFEVkGISASQaDIEVSFSfSSLNkAEQFDPkWADLYAQDVCAIKGSTIQGGLGPFGLaTlASKNLEEYTPVFFRVFKAQKNYK!LMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDmK

                521     530       540       550       560       570       580   586
                |--------+---------+---------+---------+---------+---------+-----|
E_SA            KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SA3           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SA2           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SA1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN1_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN2           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN3           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN3_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_SN3_2         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
Consensus       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIH#NAHLFVFNNGSETITIETLNAWSMDVPKMH
```

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DA2           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DA1           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DN1           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DN1_3         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DN1_2         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DN1_1         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_DN2           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
Consensus       MELFMKSSSLWGLEIYLFClFIVLSNINgVFaSHN!FLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_DA2           TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_DA1           TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKHRGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTNG
E_DN1           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_DN1_3         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_DN1_2         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_DN1_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_DN2           TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALVYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus       TILPNNKP!ILYTGVVDSHDsQVQNYAIPANLSDPFLRKW!KPNNNPLI!PDNSINKTKFRDPTTAWMGqDGlWRIVIGSMRkHRGMALlYRSRDFIKW.KAQHPLHSSPHTGNWECPDFFPVSLkNTNG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_DA2           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_DA1           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_DN1           LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_DN1_3         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_DN1_2         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_DN1_1         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_DN2           LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDLMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
Consensus       LDASYRGK.NVKyVLKNSLDVNRF#YYTIGMYDTkKDRYIPDNNSIDGsKGLRLDYGNFYASKSFYDpmKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDpSGKQLIQWPIEELETLRKQKIi

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_DA2           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_DA1           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQLGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_DN1           QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_DN1_3         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_DN1_2         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_DN1_1         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_DN2           QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
Consensus       QLNNKKLSKGEMFEVKGISASQaDIEVSFSFSSLNKAEQFDPkWADLYAQDVCAIKGSTIQgGLGPFGLaTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDtK

                521     530       540       550       560       570       580   586
                |--------+---------+---------+---------+---------+---------+-----|
E_DA            KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DA2           KLSLRGLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DA1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DN1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DN1_3         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DN1_2         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DN1_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_DN2           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
Consensus       KLSLRsLIDNSVVESFGAGGKTCITSRVYPTLAIH#NAHLFVFNNGSETITIETLNAWSMDVPKMH
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA            MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TA2           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TA3           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TA4           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TA5           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TA1           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTSFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLVNWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1           MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1_4         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1_1         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1_5         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1_3         MELFMKSSSLWGLEIYLFCFFTVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN1_2         MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN2           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN2_1         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN3_1         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N1         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN3           MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSPISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN3_2         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSPISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_TN3_3         MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSPISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
Consensus       MELFMKSSSLWGLEIYLFCfFIVLSNINkVFASHNIFLDLQSSSaISVKNVHRTgFHFQPPKyWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA            TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TA2           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TA3           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TA4           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TA5           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TA1           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN1           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN1_4         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN1_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN1_5         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN1_3         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDELWRIVIGSMRKHSGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN2           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN2_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN3_1         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N1         TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN3           TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN3_2         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_TN3_3         TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHrGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA            LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TA2           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TA3           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TA4           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TA5           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TA1           LDASYRGK-NVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKI-
E_TN1           LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN1_4         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN1_1         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN1_5         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN1_3         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN1_2         LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWAWINESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN2           LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_TN2_1         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRRQKII
E_TN3_1         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRRQKII
E_P18N1         LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_TN3           LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN3_2         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_TN3_3         LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
Consensus       LDASYRGK NVKyVLKNSLDVNRF#YYTIGMYDTkKDRYIPDNNSIDGsKGLRLDYGNFYASKSFYDPmKNRRIVWgWtNESDVLPDDEIKKGWAGIQAIPRKVWLDpSGKQLIQWPIEELETLRKQKI.

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA            QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TA2           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TA3           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TA4           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TA5           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TA1           QLNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1           QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1_4         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1_1         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1_5         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1_3         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN1_2         QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN2           QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_TN2_1         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_TN3_1         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N1         QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_TN3           QLNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFQVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_TN3_2         QLNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFQVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMR
E_TN3_3         QLNKKLSKGEMFEVKGTSASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFQVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMR
Consensus       QLNnKKLSKGEMFEVkGISASQaDIEVSFSFSSLNKAEQFDPkWADLYAQDVCAIKGSTIQGGLGPFGLaTLASKNLEEYTPVFFrVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDmk

                521     530       540       550       560       570       580    586
                |--------+---------+---------+---------+---------+---------+-----|
E_TA            KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TA2           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TA3           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TA4           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TA5           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TA1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN1           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH
E_TN1_4         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH
E_TN1_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH
E_TN1_5         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPRMH
E_TN1_3         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH
E_TN1_2         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETINAWSMDVPKMH
E_TN2           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN2_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN3_1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N1         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN3           KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN3_2         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_TN3_3         KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
Consensus       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIH#NAHLFVFNNGSETITIETlNAWSMDVPKMH
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
E_SA2           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
E_SA3           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
E_SA1           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SA2           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SA3           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SA1           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCCCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCtCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
E_SA2           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
E_SA3           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
E_SA1           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGGCTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
Consensus       AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGaCTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
E_SA2           ACTATTCTACCTAATAACAAGCCTGTTATTNTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
E_SA3           ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
E_SA1           ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
Consensus       ACTATTCTACCTAATAACAAGCCTGTTATTtTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SA2           ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SA3           ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SA1           ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
E_SA2           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
E_SA3           GGCATTATTGTATAGAGGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
E_SA1           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
Consensus       GGCATTATTGTATAGAaGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_SA2           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_SA3           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_SA1           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_SA2           CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_SA3           CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATCTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_SA1           CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATtTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_SA2           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATCG
E_SA3           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_SA1           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
Consensus       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATtG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_SA2           AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_SA3           AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCGTTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_SA1           AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTCTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
Consensus       AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCaTTTTCTtTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_SA2           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_SA3           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_SA1           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
Consensus       ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_SA2           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_SA3           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_SA1           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
Consensus       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SA            TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_SA2           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_SA3           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_SA1           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
Consensus       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG

                1691    1700      1710      1720      1730      1740      1750 1755
                |--------+---------+---------+---------+---------+---------+----|
E_SA            GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SA2           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SA3           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SA1           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_SN1_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTACAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTAcAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SN1_1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_SN1_1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_SN1_1         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SN1_1         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
E_SN1_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           TTAGATGCATCGTATCGCGGAAAAAAAAAAGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_SN1_1         TTAGATGCATCGTATCGCGGAAAAAAAAAAGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
Consensus       TTAGATGCATCGTATCGCGGAAAAAAAAAAGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_SN1_1         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
Consensus       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           CGATGAAATTAAGAAAGGATGGGCTGGTATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTGAGAAAGCAAAAGATTCAA
E_SN1_1         CGATGAAATTAAGAAAGGATGGGCTGGTATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTGAGAAAGCAAAAGATTCAA
Consensus       CGATGAAATTAAGAAAGGATGGGCTGGTATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTGAGAAAGCAAAAGATTCAA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACGAGGCCGAACAATTTGATCCTAAATGGG
E_SN1_1         TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACGAGGCCGAACAATTTGATCCTAAATGGG
Consensus       TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACGAGGCCGAACAATTTGATCCTAAATGGG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           CCGACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGGCCATTTGGGCTTGCGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
E_SN1_1         CCGACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGGCCATTTGGGCTTGCGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
Consensus       CCGACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGGCCATTTGGGCTTGCGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           TAAGGCTCAAAAGAATTATAAGATTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAG
E_SN1_1         TAAGGCTCAAAAGAATTATAAGATTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAG
Consensus       TAAGGCTCAAAAGAATTATAAGATTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN1           TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAACA
E_SN1_1         TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAACA
Consensus       TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAACA

                1691    1700      1710      1720      1730      1740      1750    1758
                |--------+---------+---------+---------+---------+---------+-------|
E_SN1           ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SN1_1         ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTCATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_SN3_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_SN3_2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTtATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SN3_1         GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_SN3_2         GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_SN3_1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_SN3_2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_SN3_1         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_SN3_2         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SN3_1         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_SN3_2         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_SN3_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_SN3_2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_SN3_1         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_SN3_2         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTCTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTtTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_SN3_1         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_SN3_2         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGCAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_SN3_1         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGCAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_SN3_2         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGCAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
Consensus       TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGCAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCTG
E_SN3_1         AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCTG
E_SN3_2         AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCTG
Consensus       AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCTG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACAGTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_SN3_1         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACAGTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_SN3_2         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACAGTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
Consensus       ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACAGTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_SN3_1         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGGTATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_SN3_2         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
Consensus       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGaTATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_SN3           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_SN3_1         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_SN3_2         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
Consensus       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG

                1691    1700      1710      1720      1730      1740      1750 1755
                |--------+---------+---------+---------+---------+---------+----|
E_SN3           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SN3_1         GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_SN3_2         GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
E_DA2           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
E_DA1           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGGTTCTCATAATGTTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_DA2           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_DA1           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
E_DA2           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
E_DA1           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC
Consensus       AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTACCCATCCAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCC

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
E_DA2           ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
E_DA1           ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA
Consensus       ACTATTCTACCTAATAACAAGCCTGTTATTTTATACACTGGAGTAGTAGATTCTCATGATACTCAAGTTCAAAACTATGCCATCCCAGCTAACTTGTCTGATCCGTTTCTTCGTAAATGGGTCAAACCCA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_DA2           ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_DA1           ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTATTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTGTAGATGGGGTTTGGAGGATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
E_DA2           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
E_DA1           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGTCAAAGCCCAACACCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAATAATACTAATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_DA2           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_DA1           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_DA2           CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_DA1           CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_DA2           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_DA1           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
Consensus       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_DA2           AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_DA1           AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
Consensus       AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_DA2           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_DA1           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAACTTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
Consensus       ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAggTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_DA2           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_DA1           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
Consensus       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_DA            TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_DA2           TCTCTTAGGGGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_DA1           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
Consensus       TCTCTTAGGaGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG

                1691    1700      1710      1720      1730      1740      1750 1755
                |--------+---------+---------+---------+---------+---------+----|
E_DA            GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_DA2           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_DA1           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_DN1_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_DN1_3         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_DN1_2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_DN1_1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_DN1_3         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_DN1_2         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_DN1_1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_DN1_3         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_DN1_2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_DN1_1         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_DN1_3         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_DN1_2         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_DN1_1         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_DN1_3         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_DN1_2         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_DN1_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_DN1_3         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_DN1_2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_DN1_1         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_DN1_3         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_DN1_2         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_DN1_1         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_DN1_3         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_DN1_2         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
E_DN1_1         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
E_DN1_3         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
E_DN1_2         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
Consensus       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
E_DN1_1         TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
E_DN1_3         TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
E_DN1_2         TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
Consensus       TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
E_DN1_1         CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
E_DN1_3         CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
E_DN1_2         CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
Consensus       CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
E_DN1_1         TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
E_DN1_3         TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
E_DN1_2         TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
Consensus       TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
E_DN1           TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
E_DN1_1         TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
E_DN1_3         TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
E_DN1_2         TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
Consensus       TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA

                1691 1700 1710 1720 1730 1740 1750 1758
                |----+----+----+----+----+----+----|
E_DN1           ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_DN1_1         ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_DN1_3         ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_DN1_2         ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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           1       10        20        30        40        50        60        70        80        90       100       110       120       130
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TA4      ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TA5      ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TA1      ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TA3      ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TA2      ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCCTCAA
Consensus  ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCtTCAA

           131     140       150       160       170       180       190       200       210       220       230       240       250       260
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TA4      GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TA5      GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TA1      GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TA3      GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TA2      GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus  GTGCAATTAGTGTCAAGAATGTTCATAGAACTAGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

           261     270       280       290       300       310       320       330       340       350       360       370       380       390
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TA4      AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TA5      AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TA1      AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGGTAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TA3      AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TA2      AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus  AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGaTAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

           391     400       410       420       430       440       450       460       470       480       490       500       510       520
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TA4      ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TA5      ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TA1      ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TA3      ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TA2      ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus  ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

           521     530       540       550       560       570       580       590       600       610       620       630       640       650
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TA4      ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TA5      ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TA1      ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TA3      ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TA2      ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus  ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

           651     660       670       680       690       700       710       720       730       740       750       760       770       780
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TA4      GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TA5      GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TA1      GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TA3      GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TA2      GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
Consensus  GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC

           781     790       800       810       820       830       840       850       860       870       880       890       900       910
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_TA4      TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_TA5      TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_TA1      TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_TA3      TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
E_TA2      TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT
Consensus  TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTACTACACTATTGGCATGTATGACACCAGAAAAGATAGGTACATTCCTGATAACAATT

           911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_TA4      CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_TA5      CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_TA1      CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_TA3      CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
E_TA2      CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA
Consensus  CTATCGATGGTTGTAAGGGATTGAGGCTTGATTATGGGAATTTCTATGCATCTAAATCATTTTATGATCCTACTAAGAATCGAAGAATTGTGTGGGGTTGGACCAATGAATCAGATGTTTTACCTGACGA

           1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_TA4      TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_TA5      TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_TA1      TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_TA3      TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
E_TA2      TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG
Consensus  TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGAAAAGTATGGCTCGATCATAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACCTTAAGAAAACAAAAGATCCAATTG

           1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_TA4      AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_TA5      AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_TA1      AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_TA3      AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
E_TA2      AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG
Consensus  AATAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGTCTGATATTGAAGTGTCATTTTCTTTTTCAAGTTTGAACAAAGCTGAACAATTTGATCCTAATTGGGCTG

           1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_TA4      ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_TA5      ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_TA1      ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_TA3      ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
E_TA2      ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA
Consensus  ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCAACATTAGCTTCTAAAAACTTGGAAGAATATACACCTGTTTTCTTTCGAGTGTTTAA

           1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TA4      GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TA5      GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TA1      GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TA3      GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TA2      GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
Consensus  GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

           1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
           |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TA       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_TA4      TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_TA5      TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_TA1      TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
E_TA3      TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCTCATTTATTTGTCTTCAATAATG
E_TA2      TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCACATTTATTTGTCTTCAATAATG
Consensus  TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGAGGAAAAACATGCATAACATCGAGGGTGTATCCAACATTAGCAATTCATGATAATGCaCATTTATTTGTCTTCAATAATG

           1691  1700      1710      1720      1730      1740      1750 1755
           |--------+---------+---------+---------+---------+---------+----|
E_TA       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TA4      GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TA5      GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TA1      GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TA3      GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TA2      GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus  GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN1_4         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN1_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN1_5         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN1_3         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTACAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN1_2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTAtAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
E_TN1_4         GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
E_TN1_1         GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
E_TN1_5         GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
E_TN1_3         GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
E_TN1_2         GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACGGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCAAATGCACCAATGTATTATAATGGAGTGTATCATTTATTCTATCAATACAATCCAAA

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN1_4         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN1_1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN1_5         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN1_3         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN1_2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN1_4         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN1_1         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN1_5         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN1_3         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN1_2         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCAGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
E_TN1_4         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
E_TN1_1         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
E_TN1_5         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
E_TN1_3         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
E_TN1_2         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGAGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT
Consensus       ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCTTGGATGGGCCAAGATGgGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGTGGGAT

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN1_4         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN1_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAGAATACTAATGGC
E_TN1_5         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN1_3         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN1_2         GGCATTACTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTAtTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAaAATACTAATGGC

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN1_4         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN1_1         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN1_5         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN1_3         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN1_2         TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGACGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGAtGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911   920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
E_TN1_4         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
E_TN1_1         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
E_TN1_5         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
E_TN1_3         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
E_TN1_2         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGCTTGGATAAATGAATCAGATGTTTTACCTGACGA

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN1_4         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN1_1         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN1_5         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN1_3         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN1_2         TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
Consensus       TGAAATTAAGAAAGGATGGGCAGGAATTCAAGCTATTCCACGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN1_4         AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN1_1         AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN1_5         AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN1_3         AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN1_2         AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
Consensus       AACAACAAGAAGTTAAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_TN1_4         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_TN1_1         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_TN1_5         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_TN1_3         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
E_TN1_2         ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
Consensus       ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN1_4         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN1_1         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN1_5         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN1_3         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN1_2         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
Consensus       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN1           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_TN1_4         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_TN1_1         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_TN1_5         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_TN1_3         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
E_TN1_2         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
Consensus       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG

                1691  1700      1710      1720      1730      1740      1750 1755
                |----------+---------+---------+---------+---------+---------+----|
E_TN1           GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN1_4         GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN1_1         GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN1_5         GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAGGATGCACTAA
E_TN1_3         GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN1_2         GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       GATCTGAGACAATCACAATTGAGACTATTAATGCTTGGAGCATGGATGTACCTAaGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN2_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TN2_1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN2_1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN2_1         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TN2_1         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_TN2_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
E_TN2_1         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
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                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_TN2_1         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
E_TN2_1         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAGGCAAAAGATTATTCAA
Consensus       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAaGCAAAAGATTATTCAA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
E_TN2_1         TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
Consensus       TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
E_TN2_1         CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
Consensus       CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
E_TN2_1         TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
Consensus       TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_TN2           TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
E_TN2_1         TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
Consensus       TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA

                1691    1700      1710      1720      1730      1740      1750    1758
                |--------+---------+---------+---------+---------+---------+-------|
E_TN2           ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN2_1         ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN3_1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN3_2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_TN3_3         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           GTCCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TN3_1         GTCCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TN3_2         GTCCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_TN3_3         GTCCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTCCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN3_1         AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN3_2         AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_TN3_3         AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGTAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           ACTATTCTACCAAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN3_1         ACTATTCTACCAAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN3_2         ACTATTCTACCAAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_TN3_3         ACTATTCTACCAAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCAAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGACCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TN3_1         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGACCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TN3_2         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGACCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_TN3_3         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGACCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
Consensus       ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCAAATTTCGTGACCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN3_1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN3_2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_TN3_3         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAATAATT
E_TN3_1         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAATAATT
E_TN3_2         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAATAATT
E_TN3_3         TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAATAATT
Consensus       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAATAATT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_TN3_1         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_TN3_2         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
E_TN3_3         CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
Consensus       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN3_1         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN3_2         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
E_TN3_3         TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
Consensus       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           AACAAGAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATTCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN3_1         AACAAGAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATTCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN3_2         AACAAGAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATTCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
E_TN3_3         AACAAGAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAACCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
Consensus       AACAAGAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAAtCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCAAGTGTTTAA
E_TN3_1         ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCAAGTGTTTAA
E_TN3_2         ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCAAGTGTTTAA
E_TN3_3         ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCAAGTGTTTAA
Consensus       ACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCAAGTGTTTAA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCGAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN3_1         GGCTCAAAAGGATTATAAGGTTCTCATGTGCTCAGATGCGAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
E_TN3_2         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCGAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAGGAAGTTA
E_TN3_3         GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCGAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAGGAAGTTA
Consensus       GGCTCAAAAGaATTATAAGGTTCTCATGTGCTCAGATGCGAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAaGAAGTTA

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
E_TN3           TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATAATG
E_TN3_1         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATAATG
E_TN3_2         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATAATG
E_TN3_3         TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATAATG
Consensus       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATAATG

                1691 1700 1710 1720 1730 1740 1750 1755
                |----+----|----+----|----+----|----+---|
E_TN3           GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN3_1         GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN3_2         GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_TN3_3         GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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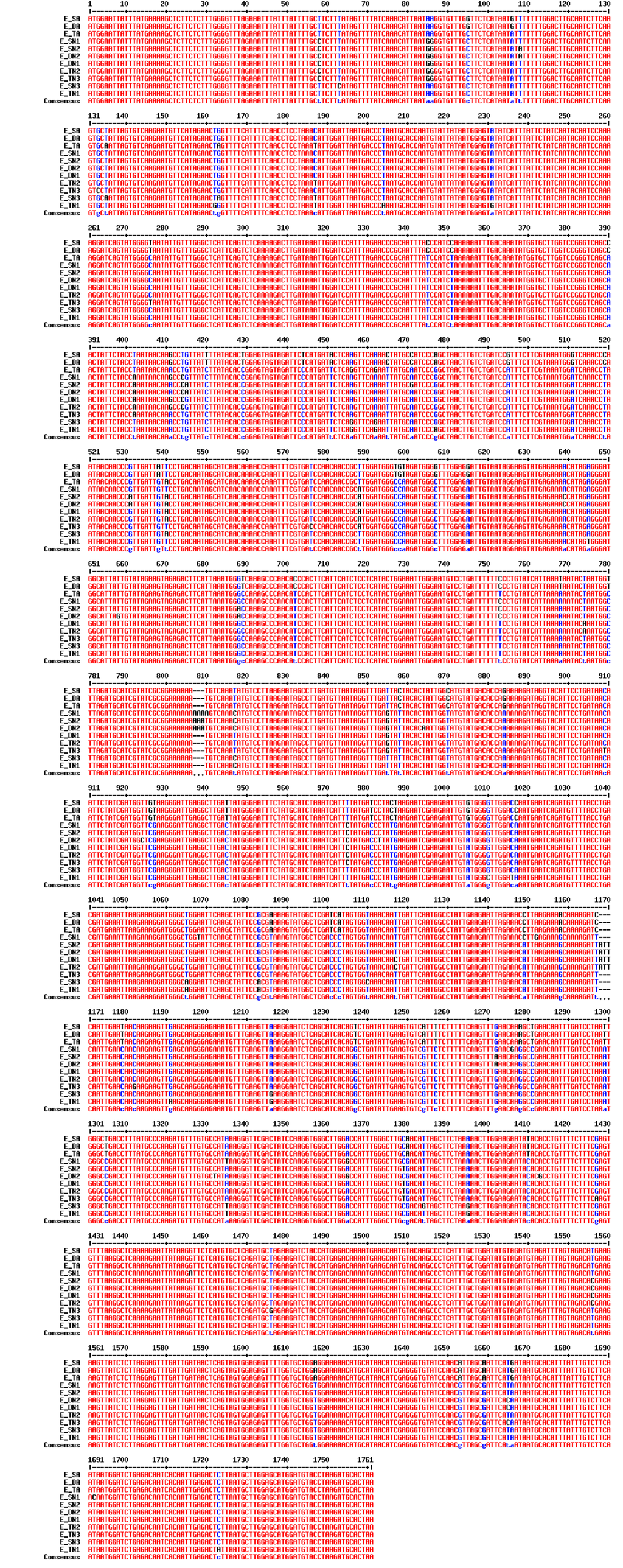

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N1_1       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N1_2       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N1_3       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
  E_P18N2       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N2_1       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N2_3       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPATYPSKKFDKYGAWSGSA
E_P18N2_2       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P18N2_4       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKYWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
Consensus       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKyWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAiYPSKKFDKYGAWSGSA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N1_1       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N1_2       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N1_3       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLRNTNG
  E_P18N2       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N2_1       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N2_3       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N2_2       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P18N2_4       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus       TILPNNKP!ILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRkHRGMALLYRSRDFIKWaKAQHPLHSSPHTGNWECPDFFPVSLKNTNG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P18N1_1       LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P18N2_1       LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P18N2_3       LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P18N2_2       LDASYRGK-NVKYVPKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKRGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P18N2_4       LDASYRGK-NVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
Consensus       LDASYRGK.NVKyVlKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKkGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N1_1       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N1_2       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N1_3       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTR
  E_P18N2       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N2_1       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N2_3       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N2_2       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P18N2_4       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQTEAMYKPSFAGYVDVDLVDTK
Consensus       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQnEAMYKPSFAGYVDVDLVDTK

                521     530       540       550       560       570       580   586
                |--------+---------+---------+---------+---------+---------+-----|
  E_P18N1       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N1_1       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N1_2       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N1_3       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
  E_P18N2       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N2_1       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N2_3       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N2_2       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P18N2_4       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIGTLNAWSMDVPKMH
Consensus       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIeTLNAWSMDVPKMH
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N1_1       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N1_2       MELFMKSSSLWGLEIYLFCLFIVLSNINGVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHSFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
  E_P40N2       MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N2_4       MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N2_2       MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N2_1       MELFIKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
E_P40N2_3       MELFMKSSSLWGLEIYLFCFFIVLSNINKVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
Consensus       MELFmKSSSLWGLEIYLFCfFIVLSNINkVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHlFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N1_1       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N1_2       TILPNNKPIILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRNHRGMALLYRSRDFIKWTKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
  E_P40N2       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIIIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N2_4       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIIIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N2_2       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIIIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N2_1       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIIIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P40N2_3       TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTESRDPTTAWMGQDGLWRIIIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus       TILPNNKP!ILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTefRDPTTAWMGQDGLWRI!IGSMRkHRGMALLYRSRDFIKWaKAQHPLHSSPHTGNWECPDFFPVSLKNTNG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P40N1_1       LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
E_P40N1_2       LDASYRGKKNVKHVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKII
  E_P40N2       LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_P40N2_4       LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_P40N2_2       LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIRWPIEELETLRKQKI-
E_P40N2_1       LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
E_P40N2_3       LDASYRGK-NVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-
Consensus       LDASYRGK.NVKHVLKNSLDVNRF#YYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIqWPIEELETLRKQKI.

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P40N1_1       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
E_P40N1_2       QLNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTK
  E_P40N2       QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLLCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_P40N2_4       QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLLCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_P40N2_2       QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLLCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_P40N2_1       QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLLCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
E_P40N2_3       QLNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLLCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMK
Consensus       QLNNKKLSKGEMFEVeGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLaTLASKNLEEYTPVFFRVFKAQKNYKVL$CSDARRSTMRQNEAMYKPSFAGYVDVDLVDmK

                521     530       540       550       560       570       580   586
                |--------+---------+---------+---------+---------+---------+-----|
  E_P40N1       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P40N1_1       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P40N1_2       KLSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
  E_P40N2       KLSLRSLIDNSVVESFGADGKTCITSRVYPTLAIHNNAHLFVFNNGSETIIIETLNAWSMDVPKMH
E_P40N2_4       KLSLRSLIDNSVVESFGADGKTCITSRVYPTLAIHNNAHLFVFNNGSETIIIETLNAWSMDVPKMH
E_P40N2_2       KLSLRSLIDNSVVESFGADGKTCITSRVYPTLAIHNNAHLFVFNNGSETIIIETLNAWSMDVPKMH
E_P40N2_1       KLSLRSLIDNSVVESFGADGKTCITSRVYPTLAIHNNAHLFVFNNGSETIIIETLNAWSMDVPKMH
E_P40N2_3       KLSLRSLIDNSVVESFGADGKTCITSRVYPTLAIHNNAHLFVFNNGSETIIIETLNAWSMDVPKMH
Consensus       KLSLRSLIDNSVVESFGAdGKTCITSRVYPTLAIHNNAHLFVFNNGSETIiIETLNAWSMDVPKMH
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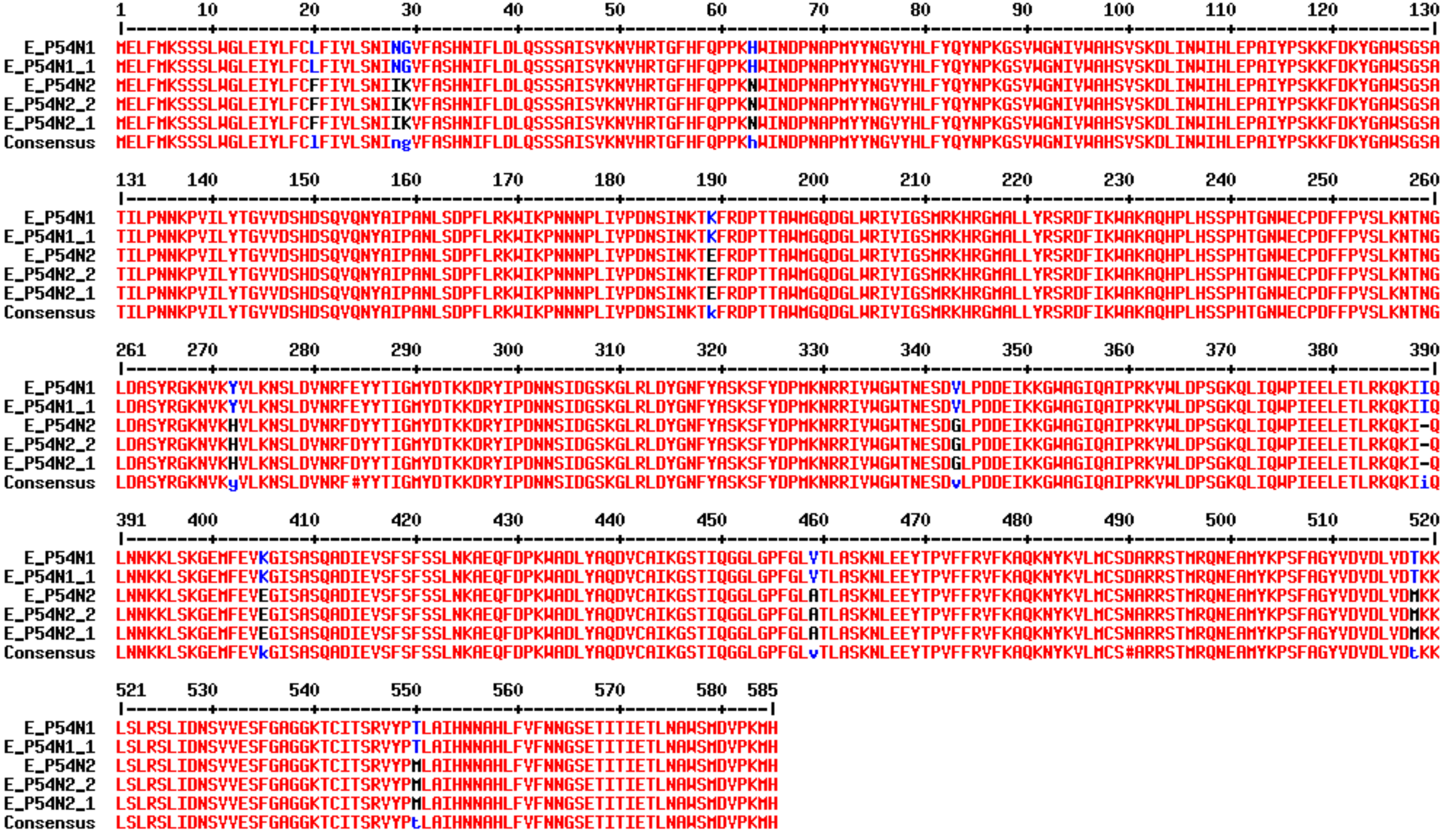
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Consensus MELFMKSSSLWGLEIYLFClFIVLSNIngVFASHNIFLDLQSSSAISVKNVHRTGFHFQPPKhWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
131 140 150 160 170 180 190 200 210 220 230 240 250 260
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E_P54N1_1 TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTKFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
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E_P54N2_2 TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
E_P54N2_1 TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTEFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
Consensus TILPNNKPVILYTGVVDSHDSQVQNYAIPANLSDPFLRKWIKPNNNPLIVPDNSINKTkFRDPTTAWMGQDGLWRIVIGSMRKHRGMALLYRSRDFIKWAKAQHPLHSSPHTGNWECPDFFPVSLKNTNG
261 270 280 290 300 310 320 330 340 350 360 370 380 390
E_P54N1 LDASYRGKNVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQ
E_P54N1_1 LDASYRGKNVKYVLKNSLDVNRFEYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIIQ
E_P54N2 LDASYRGKNVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDGLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-Q
E_P54N2_2 LDASYRGKNVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDGLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-Q
E_P54N2_1 LDASYRGKNVKHVLKNSLDVNRFDYYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDGLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKI-Q
Consensus LDASYRGKNVKgVLKNSLDVNRF#YYTIGMYDTKKDRYIPDNNSIDGSKGLRLDYGNFYASKSFYDPMKNRRIVWGWTNESDvLPDDEIKKGWAGIQAIPRKVWLDPSGKQLIQWPIEELETLRKQKIiQ
391 400 410 420 430 440 450 460 470 480 490 500 510 520
E_P54N1 LNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTKK
E_P54N1_1 LNNKKLSKGEMFEVKGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLVTLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDTKK
E_P54N2 LNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSNARRSTMRQNEAMYKPSFAGYVDVDLVDMKK
E_P54N2_2 LNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSNARRSTMRQNEAMYKPSFAGYVDVDLVDMKK
E_P54N2_1 LNNKKLSKGEMFEVEGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSNARRSTMRQNEAMYKPSFAGYVDVDLVDMKK
Consensus LNNKKLSKGEMFEVkGISASQADIEVSFSFSSLNKAEQFDPKWADLYAQDVCAIKGSTIQGGLGPFGLvTLASKNLEEYTPVFFRVFKAQKNYKVLMCS#ARRSTMRQNEAMYKPSFAGYVDVDLVDtKK
521 530 540 550 560 570 580 585
E_P54N1 LSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P54N1_1 LSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P54N2 LSLRSLIDNSVVESFGAGGKTCITSRVYPMLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P54N2_2 LSLRSLIDNSVVESFGAGGKTCITSRVYPMLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
E_P54N2_1 LSLRSLIDNSVVESFGAGGKTCITSRVYPMLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH
Consensus LSLRSLIDNSVVESFGAGGKTCITSRVYPtLAIHNNAHLFVFNNGSETITIETLNAWSMDVPKMH

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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
E_P18N1_1       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
E_P18N1_3       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
E_P18N1_2       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P18N1_1       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P18N1_3       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P18N1_2       GTGCCATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCtATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P18N1_1       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P18N1_3       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P18N1_2       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P18N1_1       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P18N1_3       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P18N1_2       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
E_P18N1_1       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
E_P18N1_3       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
E_P18N1_2       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
Consensus       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
E_P18N1_1       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
E_P18N1_3       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAGAAATACTAATGGC
E_P18N1_2       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCGTCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCaTCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAaAAATACTAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P18N1_1       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P18N1_3       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P18N1_2       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
Consensus       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P18N1_1       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P18N1_3       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P18N1_2       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
Consensus       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P18N1_1       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P18N1_3       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P18N1_2       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
Consensus       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
E_P18N1_1       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
E_P18N1_3       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
E_P18N1_2       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
Consensus       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P18N1_1       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P18N1_3       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P18N1_2       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
Consensus       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P18N1_1       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P18N1_3       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAGG
E_P18N1_2       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
Consensus       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAaG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P18N1       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P18N1_1       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P18N1_3       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P18N1_2       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
Consensus       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA

                1691    1700      1710      1720      1730      1740      1750      1761
                |--------+---------+---------+---------+---------+---------+---------+|
  E_P18N1       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P18N1_1       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P18N1_3       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P18N1_2       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P18N2_1     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P18N2_3     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P18N2_4     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P18N2_2     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  Consensus     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131 140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P18N2_1     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P18N2_3     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P18N2_4     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P18N2_2     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  Consensus     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261 270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P18N2_1     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P18N2_3     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAACTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P18N2_4     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P18N2_2     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  Consensus     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAAtTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391 400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P18N2_1     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P18N2_3     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P18N2_4     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P18N2_2     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  Consensus     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521 530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P18N2_1     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P18N2_3     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P18N2_4     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P18N2_2     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  Consensus     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651 660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  E_P18N2_1     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  E_P18N2_3     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  E_P18N2_4     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  E_P18N2_2     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  Consensus     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC

                781 790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P18N2_1     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P18N2_3     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P18N2_4     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P18N2_2     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCCTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  Consensus     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCtTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911 920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P18N2_1     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P18N2_3     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P18N2_4     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P18N2_2     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  Consensus     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  E_P18N2_1     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  E_P18N2_3     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  E_P18N2_4     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  E_P18N2_2     TGAAATTAAGAGAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  Consensus     TGAAATTAAGAaAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  E_P18N2_1     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  E_P18N2_3     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  E_P18N2_4     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  E_P18N2_2     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  Consensus     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  E_P18N2_1     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  E_P18N2_3     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  E_P18N2_4     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  E_P18N2_2     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  Consensus     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  E_P18N2_1     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  E_P18N2_3     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  E_P18N2_4     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAACTGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  E_P18N2_2     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  Consensus     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAaTGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P18N2       TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
  E_P18N2_1     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
  E_P18N2_3     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
  E_P18N2_4     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
  E_P18N2_2     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA
  Consensus     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATA

                1691 1700 1710 1720 1730 1740 1750 1758
                |----+----|----+----|----+----|----+---|
  E_P18N2       ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P18N2_1     ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P18N2_3     ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P18N2_4     ATGGATCTGAGACAATCACAATTGGGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P18N2_2     ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  Consensus     ATGGATCTGAGACAATCACAATTGaGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
  E_P40N1_1     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
  E_P40N1_2     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
  Consensus     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P40N1_1     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P40N1_2     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTCATTCTATCAATACAATCCAAA
  Consensus     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTtATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N1_1     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N1_2     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  Consensus     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N1_1     ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N1_2     ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  Consensus     ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
  E_P40N1_1     ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
  E_P40N1_2     ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
  Consensus     ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  E_P40N1_1     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  E_P40N1_2     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  Consensus     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
  E_P40N1_1     TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
  E_P40N1_2     TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
  Consensus     TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
  E_P40N1_1     ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
  E_P40N1_2     ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
  Consensus     ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
  E_P40N1_1     CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
  E_P40N1_2     CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
  Consensus     CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
  E_P40N1_1     CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
  E_P40N1_2     CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
  Consensus     CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
  E_P40N1_1     GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
  E_P40N1_2     GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
  Consensus     GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
  E_P40N1_1     GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
  E_P40N1_2     GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
  Consensus     GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P40N1       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
  E_P40N1_1     AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
  E_P40N1_2     AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
  Consensus     AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA

                1691    1700      1710      1720      1730      1740      1750      1761
                |--------+---------+---------+---------+---------+---------+---------+|
  E_P40N1       ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N1_1     ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N1_2     ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  Consensus     ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P40N2_4     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P40N2_2     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P40N2_1     ATGGAATTATTTATAAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P40N2_3     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  Consensus     ATGGAATTATTTATgAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
  E_P40N2_4     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
  E_P40N2_2     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
  E_P40N2_1     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
  E_P40N2_3     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
  Consensus     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N2_4     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N2_2     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N2_1     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P40N2_3     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  Consensus     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N2_4     ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N2_2     ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N2_1     ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P40N2_3     ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  Consensus     ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P40N2_4     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P40N2_2     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P40N2_1     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P40N2_3     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATCTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
  Consensus     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATtTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
  E_P40N2_4     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
  E_P40N2_2     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
  E_P40N2_1     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
  E_P40N2_3     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
  Consensus     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P40N2_4     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P40N2_2     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P40N2_1     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P40N2_3     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  Consensus     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P40N2_4     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P40N2_2     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P40N2_1     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P40N2_3     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  Consensus     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P40N2_4     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P40N2_2     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCGATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P40N2_1     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P40N2_3     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  Consensus     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCaATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P40N2_4     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P40N2_2     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P40N2_1     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P40N2_3     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  Consensus     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P40N2_4     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P40N2_2     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P40N2_1     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P40N2_3     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  Consensus     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P40N2_4     GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P40N2_2     GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P40N2_1     GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P40N2_3     GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  Consensus     GGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
  E_P40N2       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P40N2_4     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P40N2_2     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P40N2_1     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P40N2_3     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  Consensus     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG

                1691 1700 1710 1720 1730 1740 1750 1755
                |----+----|----+----|----+----|----+---|
  E_P40N2       GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N2_4     GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N2_2     GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N2_1     GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P40N2_3     GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  Consensus     GATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P54N1_1     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  Consensus     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P54N1_1     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  Consensus     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P54N1_1     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  Consensus     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P54N1_1     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  Consensus     ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  E_P54N1_1     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
  Consensus     ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  E_P54N1_1     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
  Consensus     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P54N1_1     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  Consensus     TTAGATGCATCGTATCGCGGAAAAAATGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  E_P54N1_1     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA
  Consensus     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  E_P54N1_1     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA
  Consensus     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATTCAA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  E_P54N1_1     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG
  Consensus     TTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAGTACACACCTGTTTTCTTTCGAGTGTT
  E_P54N1_1     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTT
  Consensus     CCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAaTACACACCTGTTTTCTTTCGAGTGTT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  E_P54N1_1     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG
  Consensus     TAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAGAAG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N1       TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
  E_P54N1_1     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA
  Consensus     TTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCAATA

                1691    1700      1710      1720      1730      1740      1750    1758
                |--------+---------+---------+---------+---------+---------+-------|
  E_P54N1       ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P54N1_1     ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  Consensus     ATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTATTAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P54N2_2     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTATTAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  E_P54N2_1     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTATTAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
  Consensus     ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTATTAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAAATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P54N2_2     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAAATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  E_P54N2_1     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAAATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
  Consensus     GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAAATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P54N2_2     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  E_P54N2_1     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
  Consensus     AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P54N2_2     ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  E_P54N2_1     ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
  Consensus     ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGGGGGAT
  E_P54N2_2     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGGGGGAT
  E_P54N2_1     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGGGGGAT
  Consensus     ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGGGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  E_P54N2_2     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  E_P54N2_1     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
  Consensus     GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P54N2_2     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  E_P54N2_1     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT
  Consensus     TTAGATGCATCGTATCGCGGAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACAATT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGGTTTACCTGACGA
  E_P54N2_2     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGGTTTACCTGACGA
  E_P54N2_1     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGGTTTACCTGACGA
  Consensus     CTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGGTTTACCTGACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P54N2_2     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  E_P54N2_1     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG
  Consensus     TGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTCAATTG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P54N2_2     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  E_P54N2_1     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG
  Consensus     AACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAATGGGCCG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P54N2_2     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  E_P54N2_1     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA
  Consensus     ACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGTGTTTAA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAAATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P54N2_2     GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAAATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGTTA
  E_P54N2_1     GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAAATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGCTA
  Consensus     GGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAAATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAGAAGtTA

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  E_P54N2       TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAATGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P54N2_2     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAATGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  E_P54N2_1     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAATGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG
  Consensus     TCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAATGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCAATAATG

                1691    1700      1710      1720      1730      1740      1750 1755
                |--------+---------+---------+---------+---------+---------+----|
  E_P54N2       GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P54N2_2     GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  E_P54N2_1     GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
  Consensus     GATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
E_P40N1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATATTTTTGGACTTGCAATCTTCAA
E_P18N2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_P54N1         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCCTCTTTATAGTTTTATCAAACATTAATGGGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_P40N2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTAATAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
E_P54N2         ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCTTCTTTATAGTTTTATCAAACATTATTAAGGTGTTTGCTTCTCATAATATTTTTTTGGACTTGCAATCTTCAA
Consensus       ATGGAATTATTTATGAAAAGCTCTTCTCTTTGGGGTTTAGAAATTTATTTATTTTGCctCTTTATAGTTTTATCAAACATTAatggGGTGTTTGCTTCTCATAATATtTTTTTGGACTTGCAATCTTCAA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P40N1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P18N2         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAATATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P54N1         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
E_P40N2         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAACATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAACCCAAA
E_P54N2         GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAAATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAATCCAAA
Consensus       GTGCTATTAGTGTCAAGAATGTTCATAGAACTGGTTTTCATTTTCAACCTCCTAAAcATTGGATTAATGACCCTAATGCACCAATGTATTATAATGGAGTATATCATTTATTCTATCAATACAAtCCAAA

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P40N1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P18N2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P54N1         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P40N2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
E_P54N2         AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA
Consensus       AGGATCAGTATGGGGCAATATTGTTTGGGCTCATTCAGTCTCAAAAGACTTGATAAATTGGATCCATTTAGAACCCGCAATTTATCCATCTAAAAAATTTGACAAATATGGTGCTTGGTCCGGGTCAGCA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P40N1         ACTATTCTACCAAATAACAAACCCATTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P18N2         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P54N1         ACTATTCTACCAAATAACAAGCCCGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAAGTTCAAAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P40N2         ACTATTCTACCTAATAACAAACCTGTTATCTTATATACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
E_P54N2         ACTATTCTACCTAATAACAAACCTGTTATCTTATACACCGGAGTAGTAGATTCCCATGATTCTCAGGTTCAGAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA
Consensus       ACTATTCTACCaAATAACAAaCCcgTTATCTTATAcACCGGAGTAGTAGATTCCCATGATTCTCAaGTTCAaAATTATGCAATCCCGGCTAACTTGTCTGATCCATTTCTTCGTAAATGGATCAAACCTA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
E_P40N1         ATAACAACCCATTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAACCATAGAGGGAT
E_P18N2         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_P54N1         ATAACAACCCGTTGATTGTACCTGACAATAGCATCAACAAAACCAAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGAGGGAT
E_P40N2         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTATAATAGGAAGTATGAGAAAACATAGAGGGAT
E_P54N2         ATAACAACCCGTTGATTGTTCCTGACAATAGCATCAACAAAACCGAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTGTAATAGGAAGTATGAGAAAACATAGGGGGAT
Consensus       ATAACAACCCgTTGATTGTaCCTGACAATAGCATCAACAAAACCaAATTTCGTGATCCAACAACCGCATGGATGGGCCAAGATGGGCTTTGGAGAATTgTAATAGGAAGTATGAGAAAaCATAGaGGGAT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
E_P40N1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGACCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
E_P18N2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_P54N1         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACAAATGGC
E_P40N2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTATCATTAAAAAATACTAATGGC
E_P54N2         GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGGCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTATCATTAAAAAATACTAATGGC
Consensus       GGCATTATTGTATAGAAGTAGAGACTTCATTAAATGGgCCAAAGCCCAACATCCACTTCATTCATCTCCTCATACTGGAAATTGGGAATGTCCTGATTTTTTcCCTGTATCATTAAAAAATACtAATGGC

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P40N1         TTAGATGCATCGTATCGCGGAAAAAAAAATGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P18N2         TTAGATGCATCGTATCGCGGAAAAAA---TGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P54N1         TTAGATGCATCGTATCGCGGAAAAAA---TGTCAAATATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAGTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P40N2         TTAGATGCATCGTATCGCGGAAAAAA---TGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
E_P54N2         TTAGATGCATCGTATCGCGGAAAAAA---TGTCAAACATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGATTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA
Consensus       TTAGATGCATCGTATCGCGGAAAAAA...TGTCAAAcATGTCCTTAAGAATAGCCTTGATGTTAATAGGTTTGAgTATTACACTATTGGTATGTATGACACCAAAAAAGATAGGTACATTCCTGATAACA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P40N1         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P18N2         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P54N1         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTCTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P40N2         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGTTTTACCTGA
E_P54N2         ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTTTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGGTTTACCTGA
Consensus       ATTCTATCGATGGTTCGAAGGGATTGAGGCTTGACTATGGGAATTTCTATGCATCTAAATCATTcTATGACCCTATGAAGAATCGAAGAATTGTATGGGGTTGGACAAATGAATCAGATGtTTTACCTGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P40N1         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P18N2         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P54N1         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAACTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTATT
E_P40N2         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGATCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATT---
E_P54N2         CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGACCCTAGTGGTAAACAATTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATT---
Consensus       CGATGAAATTAAGAAAGGATGGGCTGGAATTCAAGCTATTCCGCGTAAAGTATGGCTCGAcCCTAGTGGTAAACAAtTGATTCAATGGCCTATTGAAGAATTAGAAACATTAAGAAAGCAAAAGATTatt

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
E_P40N1         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTAAACAAGGCCGAACAATTTGATCCTAAAT
E_P18N2         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAAT
E_P54N1         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTAAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAAT
E_P40N2         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAAT
E_P54N2         CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTGAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTGAACAAGGCCGAACAATTTGATCCTAAAT
Consensus       CAATTGAACAACAAGAAGTTGAGCAAGGGAGAAATGTTTGAAGTTaAAGGAATCTCAGCATCACAGGCTGATATTGAAGTGTCGTTCTCTTTTTCAAGTTTgAACAAGGCCGAACAATTTGATCCTAAAT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P40N1         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P18N2         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P54N1         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATAAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGTGACATTAGCTTCTAAAACTTGGAAGAGTACACACCTGTTTTCTTTCGAGT
E_P40N2         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
E_P54N2         GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATTAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGCGACATTAGCTTCTAAGAACTTGGAAGAATACACACCTGTTTTCTTTCGAGT
Consensus       GGGCCGACCTTTATGCCCAAGATGTTTGTGCCATaAAGGGTTCGACTATCCAAGGTGGGCTTGGACCATTTGGGCTTGtGACATTAGCTTCTAAaAACTTGGAAGAaTACACACCTGTTTTCTTTCGAGT

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P40N1         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P18N2         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P54N1         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACACGAAG
E_P40N2         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCCTATGCTCAGATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAG
E_P54N2         GTTTAAGGCTCAAAAGAATTATAAGGTTCTCATGTGCTCAAATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACATGAAG
Consensus       GTTTAAGGCTCAAAAGAATTATAAGGTTCTCaTgTGCTCAgATGCTAGAAGATCTACCATGAGACAAAATGAAGCAATGTACAAGCCCTCATTTGCTGGATATGTAGATGTAGATTTAGTAGACAcGAAG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
E_P18N1         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P40N1         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P18N2         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P54N1         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCACAATAATGCACATTTATTTGTCTTCA
E_P40N2         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGATGGAAAAACATGCATAACATCGAGGGTGTATCCAACGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
E_P54N2         AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGGTGGAAAAACATGCATAACATCGAGGGTGTATCCAATGTTAGCGATTCATAATAATGCACATTTATTTGTCTTCA
Consensus       AAGTTATCTCTTAGGAGTTTGATTGATAACTCAGTAGTGGAGAGTTTTGGTGCTGgTGGAAAAACATGCATAACATCGAGGGTGTATCCAAcGTTAGCGATTCAtAATAATGCACATTTATTTGTCTTCA

                1691    1700      1710      1720      1730      1740      1750      1761
                |----------+---------+---------+---------+---------+---------+---------+|
E_P18N1         ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P40N1         ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P18N2         ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P54N1         ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P40N2         ATAATGGATCTGAGACAATCATAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
E_P54N2         ATAATGGATCTGAGACAATCACAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
Consensus       ATAATGGATCTGAGACAATCAcAATTGAGACTCTTAATGCTTGGAGCATGGATGTACCTAAGATGCACTAA
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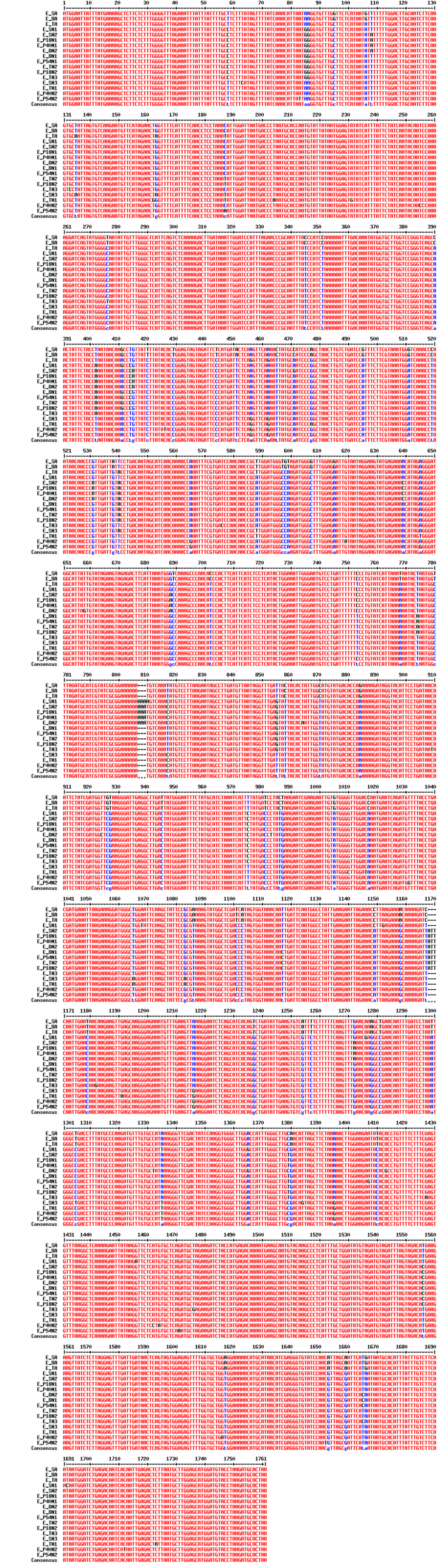

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      F_SN1     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN1_2     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN1_1     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
      F_SN2     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN2_1     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN2_2     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN2_3     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
      F_SN3     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN3_2     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN3_3     MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN3_1     MDYSSNSRRALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
      F_SN4     MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN4_2     MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN4_3     MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    F_SN4_1     MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
    Consensus     MDYSSNSRWALPVILVCFF!VLLSNNVVFASHKVFIHLQSQNAVNVqTVHRTGYHFQPEKHWINDPNAPMYFNG!YHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      F_SN1     LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN1_2     LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN1_1     LPGNKPVILYTGIVDANQTQVQNYANPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
      F_SN2     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN2_1     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN2_2     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN2_3     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
      F_SN3     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN3_2     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN3_3     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
    F_SN3_1     LPGNKPVILYTGIVDANQTQVQNYAIPANVSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
      F_SN4     LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
    F_SN4_2     LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
    F_SN4_3     LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
    F_SN4_1     LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
    Consensus     LPGNKPVILYTGIVDANQTQVQNYA!PAN.SDPYLREWIKPDNNPLIVADaSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGi

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      F_SN1     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
    F_SN1_2     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
    F_SN1_1     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
      F_SN2     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
    F_SN2_1     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
    F_SN2_2     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
    F_SN2_3     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLVQWPVEELETLRTQKVQLSNK
      F_SN3     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN3_2     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN3_3     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKSRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN3_1     DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
      F_SN4     DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN4_2     DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN4_3     DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    F_SN4_1     DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQLIQWPVEELETLRTQKVQLSNK
    Consensus     DQYGEEyKYVLKNSMDLTRFEYYTLGKYDTKKDRY!PDVGSIDSWKGLRFDYGNFYASKtFYDtSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKYWLDPSGKQL!QWPVEELETLRTQKVQLSNK

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
      F_SN1     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN1_2     KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN1_1     KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
      F_SN2     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN2_1     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN2_2     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN2_3     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
      F_SN3     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN3_2     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN3_3     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTEMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN3_1     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
      F_SN4     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN4_2     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN4_3     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    F_SN4_1     KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
    Consensus     KLNNGEKVEVTGITPAQADVEVtFSFASLDKAESFDsSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS

                521     530       540       550       560       570       581
                |--------+---------+---------+---------+---------+---------+|
      F_SN1     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN1_2     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDVWSMGKAKIQY
    F_SN1_1     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
      F_SN2     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN2_1     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN2_2     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN2_3     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
      F_SN3     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN3_2     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN3_3     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN3_1     LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
      F_SN4     LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
    F_SN4_2     LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDEWSMGKAKIQY
    F_SN4_3     LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQ
    F_SN4_1     LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKDH
    Consensus     LIDNSVIESFGAGGKTCITSRVYPTLAIN#KAHLFAFNNGTEPITIETLDaWSMGKakiqy
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN1           MDYSSNSRWTLPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_DN2           MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_DN2_1         MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
Consensus       MDYSSNSRWaLPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVqTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN1           LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
F_DN2           LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_DN2_1         LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
Consensus       LPGNKPVILYTGIVDANQTQVQNYA!PANlSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGi

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN1           DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNK
F_DN2           DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_DN2_1         DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
Consensus       DQYGEEyKYVLKNSMDLTRFEYYTLGKYDTKKDRY!PDVGSIDSWKGLRFDYGNFYASKtFYDtSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQL!QWPVEELETLRTQKVQLSNK

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN1           KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_DN2           KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_DN2_1         KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
Consensus       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS

                521     530       540       550       560       570       581
                |--------+---------+---------+---------+---------+---------+|
F_DN1           LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_DN2           LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_DN2_1         LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus       LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_TN1_1         MDYSSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_TN2           MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
Consensus       MDYSSNSRWALPVILVCFF!VLLSNNVVFASHKVFIHLQSQNAVNVhTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
F_TN1_1         LPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGQ
F_TN2           LPGNKPVILYTGIVDANQTQVQNYAVPANLSDPHLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
Consensus       LPGNKPVILYTGIVDANQTQVQNYAVPANiSDPyLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGq

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNK
F_TN1_1         DQYGEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNK
F_TN2           DQYGEEYKNVLKNGMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNK
Consensus       DQYGEEhKyVLKNsMDLTRFEYYTLGKYDTKKDRY!PDVGSIDSWKGLRFDYGNFYASKsFYDpSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQLSNK

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_TN1_1         KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYRVSFAGFVDVDLADKKLSLRS
F_TN2           KLNNGEKVEVTGITPAQADVEVTFSFASLDKAELFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
Consensus       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAEsFDpSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYkVSFAGFVDVDLADKKLSLRS

                521     530       540       550       560       570       581
                |--------+---------+---------+---------+---------+---------+|
F_TN1           LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_TN1_1         LIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_TN2           LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus       LIDNSVIESFGAGGKTCITSRVYPTLAIN#KAHLFAFNNGTEPITIETLDAWSMGKAKIQY
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          1       10        20        30        40        50        60        70        80        90       100       110       120       130
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAGTCTCAAAATGCTG
F_SN1_1   ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_SN1_2   ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
Consensus ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAatCTCAAAATGCTG

          131       140       150       160       170       180       190       200       210       220       230       240       250       260
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_SN1_1   TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_SN1_2   TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC

          261       270       280       290       300       310       320       330       340       350       360       370       380       390
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_SN1_1   AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_SN1_2   AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

          391       400       410       420       430       440       450       460       470       480       490       500       510       520
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_SN1_1   CTACCTGGCAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGAATCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_SN1_2   CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus CTACCTGGtAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGAtTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA

          521       530       540       550       560       570       580       590       600       610       620       630       640       650
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_SN1_1   ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_SN1_2   ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
Consensus ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC

          651       660       670       680       690       700       710       720       730       740       750       760       770       780
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN1_1   TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN1_2   TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

          781       790       800       810       820       830       840       850       860       870       880       890       900       910
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAGGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN1_1   GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN1_2   GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAgGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

          911       920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_SN1_1   GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_SN1_2   GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

          1041      1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN1_1   GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN1_2   GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGAtCCAAGTGGTAAACAATTGGTTCAaTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

          1171      1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_SN1_1   AAGTTGAACAATGGTGAAAAGGTTGAGGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_SN1_2   AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus AAgTTGAACAATGGTGAAAAGGTTGAaGTTACAGGAATCACACCTGCACAGGCgGATGTTGAAGTGAtATTTtCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

          1301      1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN1_1   CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN1_2   CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus CACAAGATGTTTGTGGACTtAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

          1431      1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN1_1   AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_SN1_2   AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
Consensus AAATTACAAGGTTCTCTTGTGcTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCtGACAAGAAATTGTCACTCAGAAGC

          1561      1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN1     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN1_1   TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_SN1_2   TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
Consensus TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCaTTCAACAACGGAACTGAGCCAA

          1691      1700      1710      1720      1730      1740  1746
          |--------+---------+---------+---------+---------+-----|
F_SN1     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN1_1   TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN1_2   TCACAATTGAGACTTTGGATGTATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus TCACAATTGAGACTTTGGATGcATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN2_1         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN2_3         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN2_2         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

                131 140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           TAAATGTTCACACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN2_1         TAAATGTTCACACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN2_3         TAAATGTTCACACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN2_2         TAAATGTTCACACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
Consensus       TAAATGTTCACACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC

                261 270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_SN2_1         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_SN2_3         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_SN2_2         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391 400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAATTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAACA
F_SN2_1         CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAATTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAACA
F_SN2_3         CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAATTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAACA
F_SN2_2         CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAATTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAATTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAACA

                521 530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           ATCCATTGATTGTAGCTGATGATAGTATCAACAAAACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN2_1         ATCCATTGATTGTAGCTGATGATAGTATCAACAAAACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN2_3         ATCCATTGATTGTAGCTGATGATAGTATCAACAAAACCAAATTTCGTGATCCAACTACTGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN2_2         ATCCATTGATTGTAGCTGATGATAGTATCAACAAAACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGATAGTATCAACAAAACCAAATTTCGTGATCCAACaACTGCaTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

                651 660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN2_1         AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN2_3         AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN2_2         AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA

                781 790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTATGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN2_1         GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTATGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN2_3         GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTATGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN2_2         GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTATGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTATGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

                911 920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN2_1         GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN2_3         GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN2_2         GTTGGAAGGGATTAAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCCGAAGATGATAATGC
Consensus       GTTGGAAGGGATTgAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCtGAAGATGATAATGC

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN2_1         GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAGGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN2_3         GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN2_2         GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAaGTATGGCTTGACCCAAGTGGTAAACAATTGGTTCAGTGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_SN2_1         AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_SN2_3         AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_SN2_2         AAATTGAACAATGGTGAAAAGGTTGAAGTTACGGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus       AAATTGAACAATGGTGAAAAGGTTGAAGTTACaGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN2_1         CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTGCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN2_3         CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN2_2         CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTaCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN2_1         AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN2_3         AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN2_2         AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN2           TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN2_1         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN2_3         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN2_2         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691 1700 1710 1720 1730 1740 1746
                |----+----+----+----+----+----|
F_SN2           TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN2_1         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN2_3         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN2_2         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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           1   10   20   30   40   50   60   70   80   90  100  110  120  130
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN3_1    ATGGATTATTCATCTAATTCTCGTAGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN3_2    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN3_3    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus  ATGGATTATTCATCTAATTCTCGTtGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

           131  140  150  160  170  180  190  200  210  220  230  240  250  260
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN3_1    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN3_2    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN3_3    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTTTACCATCTATTCTACCAATACAACCCAAACGGGTC
Consensus  TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTTTACCATCTATTCTACCAATACAACCCAAACGGGTC

           261  270  280  290  300  310  320  330  340  350  360  370  380  390
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGGTCTGCAACTATT
F_SN3_1    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGGTCTGCAACTATT
F_SN3_2    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGGTCTGCAACTATT
F_SN3_3    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGGTCTGCAACTATT
Consensus  AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTCGGTACGTGGTCTGGGTCTGCAACTATT

           391  400  410  420  430  440  450  460  470  480  490  500  510  520
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAATA
F_SN3_1    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAATA
F_SN3_2    CTACCTGGTAACAAGCCTGTTATTTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAATA
F_SN3_3    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAATA
Consensus  CTACCTGGTAACAAGCCTGTTATcTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACGTATCTGATCCTTATCTCCGTGAATGGATCAAGCCTGATAATA

           521  530  540  550  560  570  580  590  600  610  620  630  640  650
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN3_1    ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN3_2    ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN3_3    ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus  ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

           651  660  670  680  690  700  710  720  730  740  750  760  770  780
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      AATAATGTATAGAAGCAAAGATTTTATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN3_1    AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN3_2    AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_SN3_3    AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus  AATAATGTATAGAAGCAAAGATTTcATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA

           781  790  800  810  820  830  840  850  860  870  880  890  900  910
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCCATTGATA
F_SN3_1    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN3_2    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_SN3_3    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus  GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCtATTGATA

           911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN3_1    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN3_2    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
F_SN3_3    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAGCCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC
Consensus  GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAaCCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAAGATGATAATGC

           1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN3_1    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN3_2    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_SN3_3    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus  GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

           1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATTATGTATG
F_SN3_1    AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATTATGTATG
F_SN3_2    AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATTATGTATG
F_SN3_3    AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGAGATGTATG
Consensus  AAATTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGAtATGTATG

           1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN3_1    CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN3_2    CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN3_3    CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus  CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

           1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN3_1    AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN3_2    AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN3_3    AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
Consensus  AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC

           1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_SN3      TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN3_1    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN3_2    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN3_3    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus  TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

           1691 1700 1710 1720 1730 1740 1746
           |----+----+----+----+----+----+---|
F_SN3      TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN3_1    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN3_2    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN3_3    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus  TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN4_2         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN4_3         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_SN4_1         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN4_2         TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN4_3         TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
F_SN4_1         TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACACTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
Consensus       TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACAtTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
F_SN4_2         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
F_SN4_3         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
F_SN4_1         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
Consensus       AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
F_SN4_2         CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
F_SN4_3         CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
F_SN4_1         CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN4_2         ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN4_3         ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_SN4_1         ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
F_SN4_2         TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
F_SN4_3         TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
F_SN4_1         TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
Consensus       TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
F_SN4_2         GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
F_SN4_3         GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
F_SN4_1         GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
F_SN4_2         GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
F_SN4_3         GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
F_SN4_1         GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
Consensus       GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
F_SN4_2         TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
F_SN4_3         TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
F_SN4_1         TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
Consensus       TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
F_SN4_2         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
F_SN4_3         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
F_SN4_1         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAgGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN4_2         CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN4_3         CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_SN4_1         CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN4_2         AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN4_3         AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_SN4_1         AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_SN4           TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN4_2         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN4_3         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_SN4_1         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691    1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
F_SN4           TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN4_2         TCACAATTGAGACTTTGGATGAATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_SN4_3         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATAA
F_SN4_1         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGATCACTAG
Consensus       TCACAATTGAGACTTTGGATGcATGGAGTATGGGCAAAGcTaAgatacaata....
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_DN2_1         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCAcTTGCAATCTCAAAATGCTG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAATCCAAACGGGTC
F_DN2_1         TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTAcCATCTATTCTACCAATACAAcCCAAAcGGGTC

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           AGTATGGGGCAATATTGTGTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_DN2_1         AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAATATTGTgTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCaTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATTGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTTCGTGAATGGATCAAGCCTGATAACA
F_DN2_1         CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATTGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTTCGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATTGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTTCGTGAATGGATCAAGCCTGATAACA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_DN2_1         ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_DN2_1         TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCCGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAATTGGGAATGTCCcGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_DN2_1         GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
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                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_DN2_1         GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_DN2_1         GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
F_DN2_1         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_DN2_1         CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_DN2_1         AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGcTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_DN2           TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGAGTTTATCCAACACTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_DN2_1         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGAGTTTATCCAACACTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGAGTTTATCCAACACTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691    1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
F_DN2           TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_DN2_1         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTAA
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTaA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_TN1_1         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTGTAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCATAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
F_TN1_1         TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC
Consensus       TAAATGTTCACACTGTTCATAGAACTGGTTATCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAACCCAAACGGGTC

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
F_TN1_1         AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT
Consensus       AGTATGGGGCAACATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCTAAACCATTTGATCAATTTGGTACATGGTCTGGATCAGCAACTATT

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
F_TN1_1         CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAACCTGTTATCTTGTACACTGGAATAGTGGATGCTAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACATATCTGATCCTTATCTACGTGAATGGATCAAGCCTGATAACA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_TN1_1         ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCTTGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
F_TN1_1         TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA
Consensus       TATAATGTATAGAAGCAAAGACTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCCGTTGCATTGAAAGGAACTAATGGGCAA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
F_TN1_1         GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAACACAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACATACCAGATGTTGGTTCTATTGATA
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                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
F_TN1_1         GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC
Consensus       GTTGGAAGGGATTGAGATTCGACTATGGTAATTTCTATGCATCAAAGTCTTTCTATGATCCTAGCAAAAATCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAACGC

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
F_TN1_1         TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG
Consensus       TAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGCAACAAG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
F_TN1_1         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATCCTAGTTGGACTGATATGTATG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_TN1_1         CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAAGGTGCAGATGTTCAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_TN1_1         AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAGAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGCTCTGATGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAaAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN1           TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_TN1_1         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGACAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691    1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
F_TN1           TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_TN1_1         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_TN2_1         ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAATCCAAACGGGTC
F_TN2_1         TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAATCCAAACGGGTC
Consensus       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTATCATCTATTCTACCAATACAATCCAAACGGGTC

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           AGTATGGGGCAATATTGTGTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_TN2_1         AGTATGGGGCAATATTGTGTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAATATTGTGTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACTTATCTGATCCACATCTTCGTGAATGGATCAAGCCTGATAATA
F_TN2_1         CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACTTATCTGATCCATATCTTCGTGAATGGATCAAGCCTGATAATA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGGTTCCAGCTAACTTATCTGATCCAcATCTTCGTGAATGGATCAAGCCTGATAATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_TN2_1         ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGTATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           TATAATGTATAGGAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_TN2_1         TATAATGTATAGGAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       TATAATGTATAGGAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           GATCAATATGGTGAAGAATATAAAAATGTGCTTAAGAATGGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACGTACCAGATGTTGGTTCTATTGATA
F_TN2_1         GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACGTACCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAATATAAAaATGTGCTTAAGAATaGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTACGTACCAGATGTTGGTTCTATTGATA

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_TN2_1         GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           GAAAGGGTGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAG
F_TN2_1         GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAG
Consensus       GAAAGGaTGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACCCAAGTGGTAAACAATTGATTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAG

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTTATTTGATTCTAGTTGGACTGATATGTATG
F_TN2_1         AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTTATTTGATTCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTTATTTGATTCTAGTTGGACTGATATGTATG

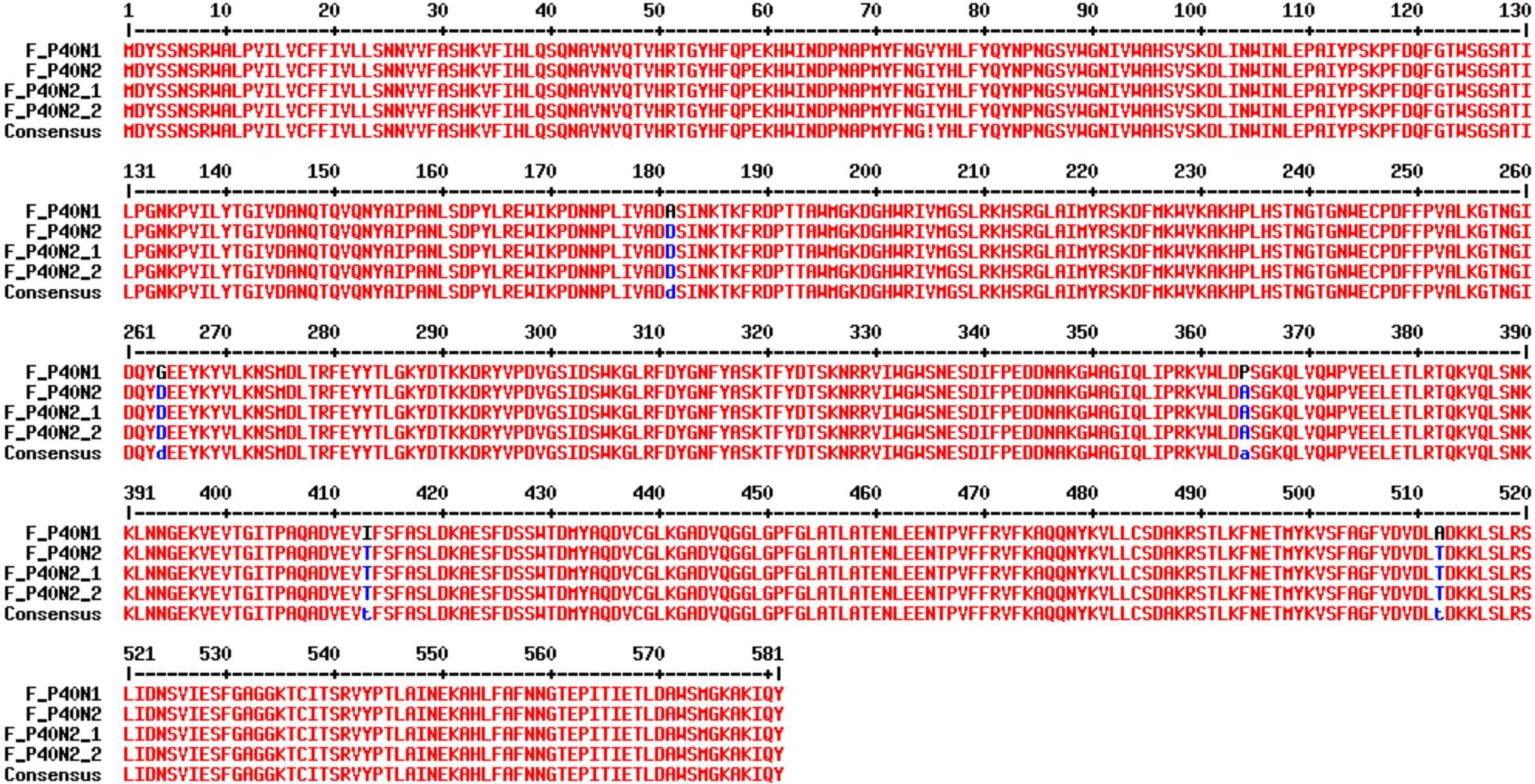
                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_TN2_1         CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
F_TN2_1         AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCAGACAAGAAATTGTCACTCAGAAGC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_TN2           TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTAGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_TN2_1         TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTAGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTAGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691    1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
F_TN2           TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTAA
F_TN2_1         TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAATCACTAG
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAacacaAG.............
```


1 10 20 30 40 50 60 70 80 90 100 110 120 130
F_P18N MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P18N_1 MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
Consensus MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
131 140 150 160 170 180 190 200 210 220 230 240 250 260
F_P18N LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P18N_1 LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
Consensus LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
261 270 280 290 300 310 320 330 340 350 360 370 380 390
F_P18N DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P18N_1 DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
Consensus DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
391 400 410 420 430 440 450 460 470 480 490 500 510 520
F_P18N KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P18N_1 KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
Consensus KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
521 530 540 550 560 570 581
F_P18N LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P18N_1 LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY


1 10 20 30 40 50 60 70 80 90 100 110 120 130
F_P40N1 MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P40N2 MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P40N2_1 MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P40N2_2 MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGIYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
Consensus MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNG!YHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
131 140 150 160 170 180 190 200 210 220 230 240 250 260
F_P40N1 LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P40N2 LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P40N2_1 LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P40N2_2 LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADDSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
Consensus LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADdSINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
261 270 280 290 300 310 320 330 340 350 360 370 380 390
F_P40N1 DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P40N2 DQYDEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDASGKQLVQWPVEELETLRTQKVQLSNK
F_P40N2_1 DQYDEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDASGKQLVQWPVEELETLRTQKVQLSNK
F_P40N2_2 DQYDEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDASGKQLVQWPVEELETLRTQKVQLSNK
Consensus DQYdEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDaSGKQLVQWPVEELETLRTQKVQLSNK
391 400 410 420 430 440 450 460 470 480 490 500 510 520
F_P40N1 KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P40N2 KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLTDKKLSLRS
F_P40N2_1 KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLTDKKLSLRS
F_P40N2_2 KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLTDKKLSLRS
Consensus KLNNGEKVEVTGITPAQADVEVtFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLtDKKLSLRS
521 530 540 550 560 570 581
F_P40N1 LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P40N2 LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P40N2_1 LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P40N2_2 LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N1_1       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N1_2       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMHFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N1_5       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQAVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N1_3       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
  F_P54N2       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N2_3       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N2_2       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N1_4       MDYSSNSRWALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
F_P54N2_1       MDYSSNSRRALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI
Consensus       MDYSSNSRwALPVILVCFFIVLLSNNVVFASHKVFIHLQSQNAVNVQTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSATI

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N1_1       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWIKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N1_2       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N1_5       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N1_3       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
  F_P54N2       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N2_3       LPGNRPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N2_2       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N1_4       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTARMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
F_P54N2_1       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI
Consensus       LPGNKPVILYTGIVDANQTQVQNYAIPANLSDPYLREWIKPDNNPLIVADASINKTKFRDPTTAwMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTNGI

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P54N1_1       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P54N1_2       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
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  F_P54N2       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P54N2_3       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
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F_P54N1_4       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
F_P54N2_1       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDILPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK
Consensus       DQYGEEYKYVLKNSMDLTRFEYYTLGKYDTKKDRYVPDVGSIDSWKGLRFDYGNFYASKTFYDTSKNRRVIWGWSNESDIfPEDDNAKGWAGIQLIPRKVWLDPSGKQLVQWPVEELETLRTQKVQLSNK

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N1_1       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N1_2       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N1_5       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N1_3       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
  F_P54N2       KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N2_3       KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N2_2       KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N1_4       KLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
F_P54N2_1       KLNNGEKVEVTGITPAQADVEVIFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS
Consensus       KLNNGEKVEVTGITPAQADVEVtFSFASLDKAESFDSSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLADKKLSLRS

                521     530       540       550       560       570       581
                |--------+---------+---------+---------+---------+---------+|
  F_P54N1       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N1_1       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N1_2       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N1_5       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N1_3       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIEALDAWSMGKAKIQY
  F_P54N2       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N2_3       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N2_2       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
F_P54N1_4       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETSDAWSMGKAKIQY
F_P54N2_1       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus       LIDNSVIESFGAGGKTCITSRVYPTLAINEKAHLFAFNNGTEPITIETlDAWSMGKAKIQY
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P18N_1        ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P18N_1        TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P18N_1        AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P18N_1        CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P18N_1        ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P18N_1        TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P18N_1        GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
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                911   920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P18N_1        GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P18N_1        GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P18N_1        AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAaGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P18N_1        CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P18N_1        AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
F_P18N          TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P18N_1        TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA

                1691  1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
F_P18N          TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P18N_1        TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_P40N2_2       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
F_P40N2_1       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_P40N2_2       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
F_P40N2_1       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAAcGGGTC

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTTGGTACGTGGTCTGGATCTGCAACTATT
F_P40N2_2       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTTGGTACGTGGTCTGGATCTGCAACTATT
F_P40N2_1       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCaTTTGATCAATTtGGTACGTGGTCTGGATCTGCAACTATT

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P40N2_2       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P40N2_1       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_P40N2_2       ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
F_P40N2_1       ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P40N2_2       AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P40N2_1       AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       GATCAATATGATGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P40N2_2       GATCAATATGATGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P40N2_1       GATCAATATGATGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGATGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       GTTGGAAGGGATTGAGATTCGATTATGGTAACTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P40N2_2       GTTGGAAGGGATTGAGATTCGATTATGGTAACTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P40N2_1       GTTGGAAGGGATTGAGATTCGATTATGGTAACTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus       GTTGGAAGGGATTGAGATTCGATTATGGTAACTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACGCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P40N2_2       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACGCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P40N2_1       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACGCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACGCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P40N2_2       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P40N2_1       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P40N2_2       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P40N2_1       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGACAGACAAGAAATTGTCACTCAGAAGC
F_P40N2_2       AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGACAGACAAGAAATTGTCACTCAGAAGC
F_P40N2_1       AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGACAGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGACAGACAAGAAATTGTCACTCAGAAGC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P40N2       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_P40N2_2       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
F_P40N2_1       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA

                1691    1700      1710      1720      1730      1740  1746
                |--------+---------+---------+---------+---------+-----|
  F_P40N2       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P40N2_2       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P40N2_1       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1_3       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1_5       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1_1       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1_2       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1_4       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTCTTTATTCATTTGCAATCTCAAAATGCTG
Consensus       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTtTTTATTCATTTGCAATCTCAAAATGCTG

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1_3       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1_5       TAAATGTTCAAGCTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1_1       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1_2       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGCATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1_4       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus       TAAATGTTCAAaCTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGtATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1_3       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1_5       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1_1       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1_2       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1_4       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1_3       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1_5       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1_1       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1_2       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1_4       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1_3       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1_5       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1_1       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1_2       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1_4       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCACGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
Consensus       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCAtGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1_3       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1_5       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1_1       TATAATGTATAGAAGCAAAGATTTCATGAAATGGATTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1_2       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1_4       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus       TATAATGTATAGAAGCAAAGATTTCATGAAATGGgTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1_3       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1_5       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1_1       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1_2       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1_4       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

                911   920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1_3       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1_5       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1_1       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1_2       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1_4       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1_3       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1_5       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1_1       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1_2       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1_4       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1_3       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1_5       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1_1       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1_2       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1_4       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1_3       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1_5       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1_1       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1_2       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1_4       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus       CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1_3       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1_5       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1_1       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1_2       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1_4       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
Consensus       AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  F_P54N1       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1_3       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1_5       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1_1       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1_2       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1_4       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
Consensus       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA

                1691  1700      1710      1720      1730      1740  1746
                |----------+---------+---------+---------+---------+-----|
  F_P54N1       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1_3       TCACAATTGAGGCTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1_5       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1_1       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1_2       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1_4       TCACAATTGAGACTTCGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus       TCACAATTGAGaCTTtGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N2_3     ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N2_1     ATGGATTATTCATCTAATTCTCGTAGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N2_2     ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
Consensus     ATGGATTATTCATCTAATTCTCGTtGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N2_3     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N2_1     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N2_2     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
Consensus     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N2_3     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N2_1     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N2_2     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
Consensus     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N2_3     CTACCTGGTAACAGGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N2_1     CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N2_2     CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGACCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus     CTACCTGGTAACAaGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGAtCCATATCTCCGTGAATGGATCAAGCCTGATAACA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N2_3     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N2_1     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N2_2     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
Consensus     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N2_3     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N2_1     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N2_2     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N2_3     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N2_1     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N2_2     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N2_3     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N2_1     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATACTCCCTGAGGATGATAATGC
F_P54N2_2     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATAtTCCCTGAGGATGATAATGC

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N2_3     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N2_1     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N2_2     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAGCCCAAAAGGTTCAATTGAGTAACAAA
Consensus     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAaCCCAAAAGGTTCAATTGAGTAACAAA

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N2_3     AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N2_1     AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N2_2     AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus     AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N2_3     CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N2_1     CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N2_2     CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAGAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus     CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAaAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N2_3     AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N2_1     AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N2_2     AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
Consensus     AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
  F_P54N2       TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_P54N2_3     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_P54N2_1     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_P54N2_2     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
Consensus     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA

                1691 1700 1710 1720 1730 1740 1746
                |----+----+----+----+----+----+---|
  F_P54N2       TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N2_3     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N2_1     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N2_2     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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           1   10   20   30   40   50   60   70   80   90  100  110  120  130
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N1    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P40N1    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P54N2    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCATTTGCAATCTCAAAATGCTG
F_P40N2    ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCACTTGCAATCTCAAAATGCTG
Consensus  ATGGATTATTCATCTAATTCTCGTTGGGCTTTGCCAGTTATCTTAGTTTGCTTTTTTATAGTTTTATTATCCAATAATGTTGTTTTTGCTTCTCACAAAGTTTTTATTCAtTTGCAATCTCAAAATGCTG

           131  140  150  160  170  180  190  200  210  220  230  240  250  260
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N1    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P40N1    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P54N2    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAGTCTACCATCTATTCTACCAATACAACCCAAATGGGTC
F_P40N2    TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAATTTACCATCTATTCTACCAATACAACCCAAACGGGTC
Consensus  TAAATGTTCAAACTGTTCATAGAACTGGTTACCATTTTCAGCCAGAAAAACATTGGATCAATGATCCCAATGCACCAATGTATTTCAATGGAgTcTACCATCTATTCTACCAATACAACCCAAAtGGGTC

           261  270  280  290  300  310  320  330  340  350  360  370  380  390
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N1    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P40N1    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P54N2    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCCTTTGATCAATTCGGTACGTGGTCTGGATCTGCAACTATT
F_P40N2    AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCATTTGATCAATTTGGTACGTGGTCTGGATCTGCAACTATT
Consensus  AGTATGGGGCAATATTGTTTGGGCTCATTCAGTTTCAAAGGACTTAATCAATTGGATCAATTTAGAACCCGCAATTTACCCATCCAAACCcTTTGATCAATTcGGTACGTGGTCTGGATCTGCAACTATT

           391  400  410  420  430  440  450  460  470  480  490  500  510  520
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N1    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P40N1    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P54N2    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
F_P40N2    CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA
Consensus  CTACCTGGTAACAAGCCTGTTATCTTGTACACTGGAATAGTAGATGCCAACCAAACTCAAGTTCAAAACTACGCGATTCCAGCTAACTTATCTGATCCATATCTCCGTGAATGGATCAAGCCTGATAACA

           521  530  540  550  560  570  580  590  600  610  620  630  640  650
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N1    ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P40N1    ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P54N2    ATCCATTGATTGTAGCTGATGCTAGCATCAACAAGACCAAATTTCGTGATCCAACAACCGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGGAAACATAGTAGGGGTTTAGC
F_P40N2    ATCCATTGATTGTAGCTGATGATAGTATCAACAAGACCAAATTTCGTGATCCAACAACTGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGAAAACATAGTAGGGGTTTAGC
Consensus  ATCCATTGATTGTAGCTGATGcTAGcATCAACAAGACCAAATTTCGTGATCCAACAACcGCATGGATGGGTAAAGATGGACATTGGAGAATTGTGATGGGAAGTTTGAGgAAACATAGTAGGGGTTTAGC

           651  660  670  680  690  700  710  720  730  740  750  760  770  780
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N1    TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P40N1    TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P54N2    TATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAATGGTACTGGAAACTGGGAATGTCCTGATTTTTTCCCTGTTGCATTGAAAGGAACTAATGGGATA
F_P40N2    AATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCTGTTGCATTGAAAGGAACTAATGGGATA
Consensus  tATAATGTATAGAAGCAAAGATTTCATGAAATGGGTTAAGGCTAAACACCCACTTCACTCAACTAAtGGTACTGGAAAcTGGGAATGTCCTGATTTTTTcCCTGTTGCATTGAAAGGAACTAATGGGATA

           781  790  800  810  820  830  840  850  860  870  880  890  900  910
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N1    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P40N1    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P54N2    GATCAATATGGTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
F_P40N2    GATCAATATGATGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA
Consensus  GATCAATATGgTGAAGAATATAAATATGTGCTTAAGAATAGTATGGATCTTACTCGATTTGAGTACTATACTCTTGGTAAGTACGATACAAAAAAAGATAGGTATGTTCCAGATGTTGGTTCTATTGATA

           911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N1    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P40N1    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P54N2    GTTGGAAGGGATTGAGATTCGATTATGGTAATTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
F_P40N2    GTTGGAAGGGATTGAGATTCGATTATGGTAACTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC
Consensus  GTTGGAAGGGATTGAGATTCGATTATGGTAAtTTCTATGCATCAAAGACTTTCTATGATACTAGCAAAAACCGAAGGGTTATTTGGGGTTGGTCTAATGAATCAGATATATTCCCTGAGGATGATAATGC

           1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N1    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P40N1    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P54N2    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGATCCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
F_P40N2    GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGACGCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA
Consensus  GAAAGGATGGGCTGGAATTCAATTGATCCCACGTAAAGTATGGCTTGAtcCAAGTGGTAAACAATTGGTTCAATGGCCTGTTGAAGAATTAGAAACCCTAAGAACCCAAAAGGTTCAATTGAGTAACAAA

           1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N1    AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCAGATGTTGAAGTGACATTTTCTTTTGCAAGTTTGGATAAGGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P40N1    AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P54N2    AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGAATCACACCTGCACAGGCGGATGTTGAAGTGATATTTTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
F_P40N2    AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGGATCACACCTGCACAGGCAGATGTTGAAGTGACATTCTCTTTTGCAAGTTTGGATAAAGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG
Consensus  AAGTTGAACAATGGTGAAAAGGTTGAAGTTACAGGaATCACACCTGCACAGGCaGATGTTGAAGTGAcATTtTCTTTTGCAAGTTTGGATAAaGCAGAGTCATTTGATTCTAGTTGGACTGATATGTATG

           1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTGGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P54N1    CACAAGATGTTTGTGGACTTAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
F_P40N2    CACAAGATGTTTGTGGACTCAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTAGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA
Consensus  CACAAGATGTTTGTGGACTcAAGGGTGCAGATGTACAAGGTGGGCTTGGGCCATTTGGTCTTGCTACATTGGCTACTGAAAACTTaGAAGAAAACACACCTGTTTTCTTCCGAGTTTTCAAAGCACAACA

           1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N1    AAATTACAAGGTTCTTTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P40N1    AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P54N2    AAATTACAAGGTTCTCTTGTGCTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGGCTGACAAGAAATTGTCACTCAGAAGC
F_P40N2    AAATTACAAGGTTCTCTTGTGTTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGACAGACAAGAAATTGTCACTCAGAAGC
Consensus  AAATTACAAGGTTCTcTTGTGcTCTGACGCTAAAAGGTCAACTCTTAAGTTCAATGAAACAATGTACAAAGTTTCATTTGCTGGATTTGTGGATGTTGATTTGgCtGACAAGAAATTGTCACTCAGAAGC

           1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
           |----+----+----+----+----+----+----+----+----+----+----+----+----|
F_P18N     TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P54N1    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAATGGAACTGAGCCAA
F_P40N1    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_P54N2    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCATTCAACAACGGAACTGAGCCAA
F_P40N2    TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCGTTCAACAACGGAACTGAGCCAA
Consensus  TTGATTGATAATTCAGTTATAGAAAGTTTTGGTGCTGGTGGAAAGACATGTATAACATCGAGGGTTTATCCAACATTGGCGATTAATGAGAAGGCACATTTATTTGCgTTCAACAAcGGAACTGAGCCAA

           1691 1700 1710 1720 1730 1740 1746
           |----+----+----+----+----+----|
F_P18N     TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N1    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P40N1    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P54N2    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
F_P40N2    TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
Consensus  TCACAATTGAGACTTTGGATGCATGGAGTATGGGCAAAGCTAAGATACAATATTGA
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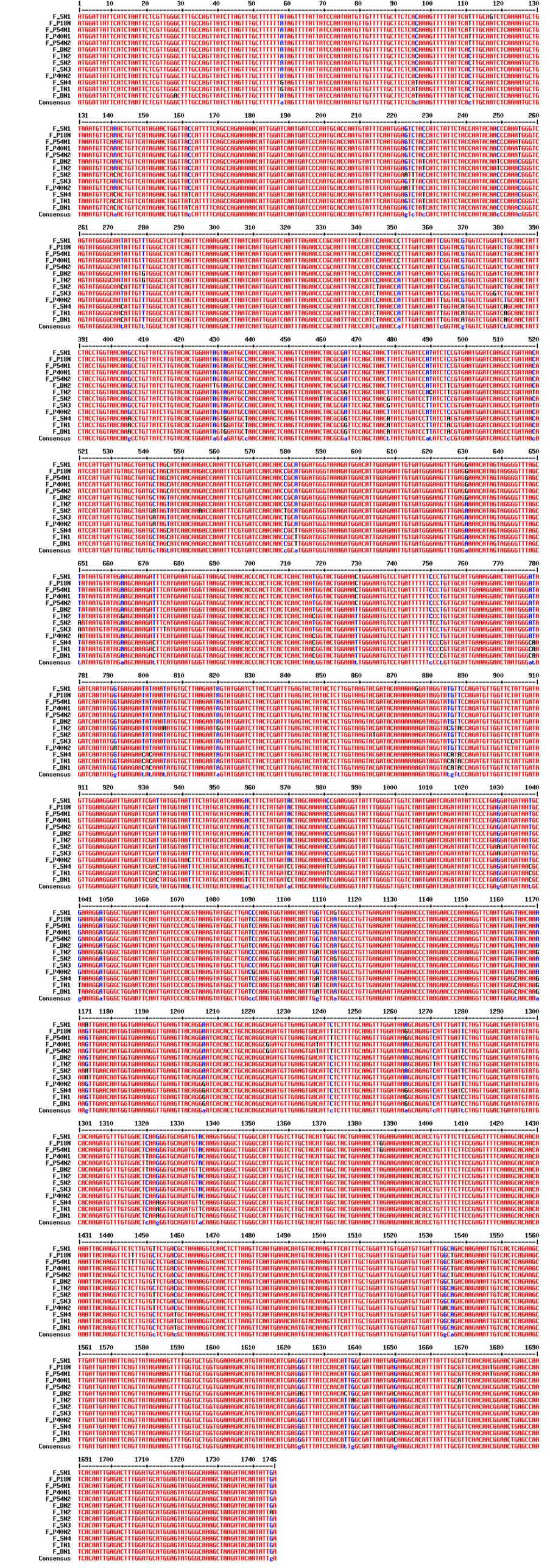
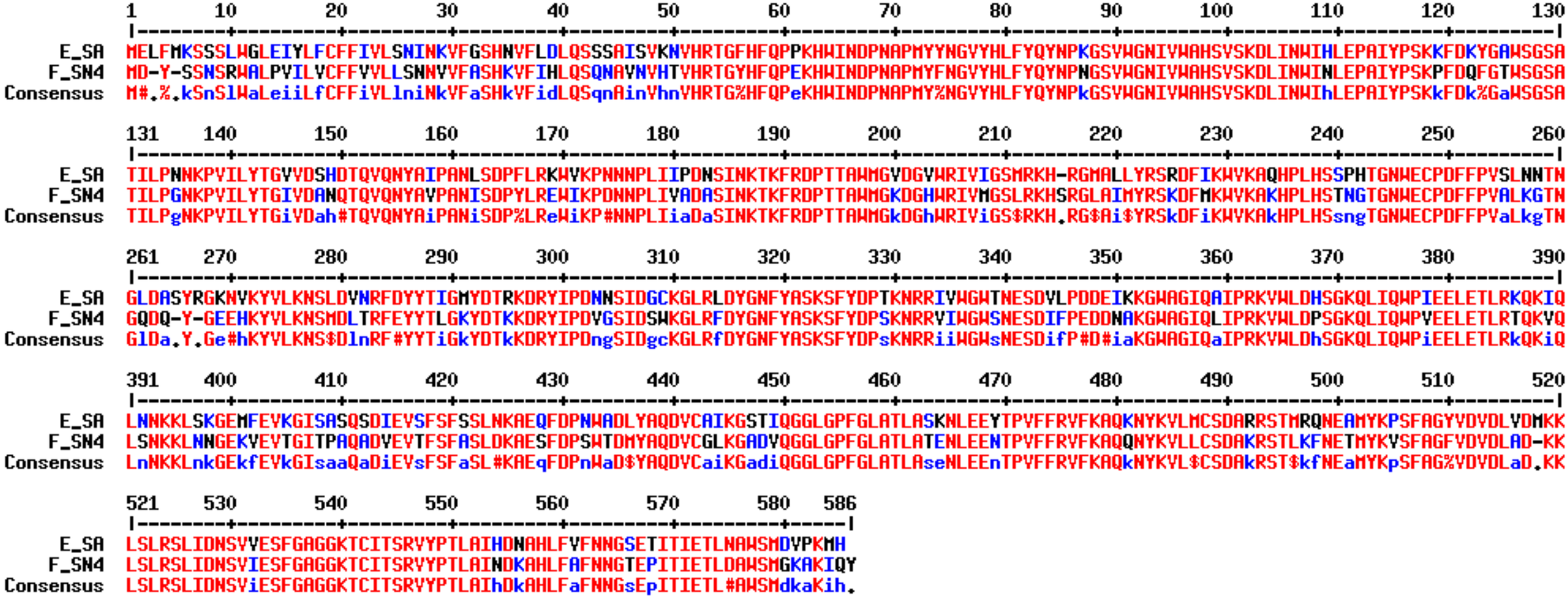



1 10 20 30 40 50 60 70 80 90 100 110 120 130
E_SA MELFMKSSSLWGLEIYLFCFFIVLSNINKVFGSHNVFLDLQSSSAISVKNVHRTGFHFQPPKHWINDPNAPMYYNGVYHLFYQYNPKGSVWGNIVWAHSVSKDLINWIHLEPAIYPSKKFDKYGAWSGSA
F_SN4 MD-Y-SSNSRWALPVILVCFFVVLLSNNVVFASHKVFIHLQSQNAVNVHTVHRTGYHFQPEKHWINDPNAPMYFNGVYHLFYQYNPNGSVWGNIVWAHSVSKDLINWINLEPAIYPSKPFDQFGTWSGSA
Consensus M#.%.kSnSlWaLeiiLfCFFiVLlniNkVFaSHkVFidLQSqnAinVhnVHRTG%HFQPeKHWINDPNAPMY%NGVYHLFYQYNPkGSVWGNIVWAHSVSKDLINWIhLEPAIYPSKkFDk%GaWSGSA
131 140 150 160 170 180 190 200 210 220 230 240 250 260
E_SA TILPNNKPVILYTGVVDSHDTQVQNYAIPANLSDPFLRKWVKPNNNPLIIPDNSINKTKFRDPTTAWMGVDGVWRIVIGSMRKH-RGMALLYRSRDFIKWVKAQHPLHSSPHTGNWECPDFFPVSLNNTN
F_SN4 TILPGNKPVILYTGIVDANQTQVQNYAVPANISDPYLREWIKPDNNPLIVADASINKTKFRDPTTAWMGKDGHWRIVMGSLRKHSRGLAIMYRSKDFMKWVKAKHPLHSTNGTGNWECPDFFPVALKGTN
Consensus TILPgNKPVILYTGiVDah#TQVQNYAiPANiSDP%LReWiKP#NNPLIiaDaSINKTKFRDPTTAWMGkDGhWRIViGS$RKH.RG$Ai$YRSkDFiKWVKAkHPLHSsngTGNWECPDFFPVaLkgTN
261 270 280 290 300 310 320 330 340 350 360 370 380 390
E_SA GLDASYRGKNVKYVLKNSLDVNRFDYYTIGMYDTRKDRYIPDNNSIDGCKGLRLDYGNFYASKSFYDPTKNRRIVWGWTNESDVLPDDEIKKGWAGIQAIPRKVWLDHSGKQLIQWPIEELETLRKQKIQ
F_SN4 GQDQ-Y-GEEHKYVLKNSMDLTRFEYYTLGKYDTKKDRYIPDVGSIDSWKGLRFDYGNFYASKSFYDPSKNRRVIWGWSNESDIFPEDDNAKGWAGIQLIPRKVWLDPSGKQLIQWPVEELETLRTQKVQ
Consensus GlDa.Y.Ge#hKYVLKNS$DlnRF#YYTiGkYDTkKDRYIPDngSIDgcKGLRfDYGNFYASKSFYDPsKNRRiiWGWsNESDifP#D#iaKGWAGIQaIPRKVWLDhSGKQLIQWPiEELETLRkQKiQ
391 400 410 420 430 440 450 460 470 480 490 500 510 520
E_SA LNNKKLSKGEMFEVKGISASQSDIEVSFSFSSLNKAEQFDPNWADLYAQDVCAIKGSTIQGGLGPFGLATLASKNLEEYTPVFFRVFKAQKNYKVLMCSDARRSTMRQNEAMYKPSFAGYVDVDLVDMKK
F_SN4 LSNKKLNNGEKVEVTGITPAQADVEVTFSFASLDKAESFDPSWTDMYAQDVCGLKGADVQGGLGPFGLATLATENLEENTPVFFRVFKAQQNYKVLLCSDAKRSTLKFNETMYKVSFAGFVDVDLAD-KK
Consensus LnNKKLnkGEkfEVkGIsaaQaDiEVsFSFaSL#KAEqFDPnWaD$YAQDVCaiKGadiQGGLGPFGLATLAseNLEEnTPVFFRVFKAQkNYKVL$CSDAkRST$kfNEaMYKpSFAG%VDVDLaD.KK
521 530 540 550 560 570 580 586
E_SA LSLRSLIDNSVVESFGAGGKTCITSRVYPTLAIHDNAHLFVFNNGSETITIETLNAWSMDVPKMH
F_SN4 LSLRSLIDNSVIESFGAGGKTCITSRVYPTLAINDKAHLFAFNNGTEPITIETLDAWSMGKAKIQY
Consensus LSLRSLIDNSViESFGAGGKTCITSRVYPTLAIhDkAHLFaFNNGsEpITIETL#AWSMdkaKih.

Appendix 3.3

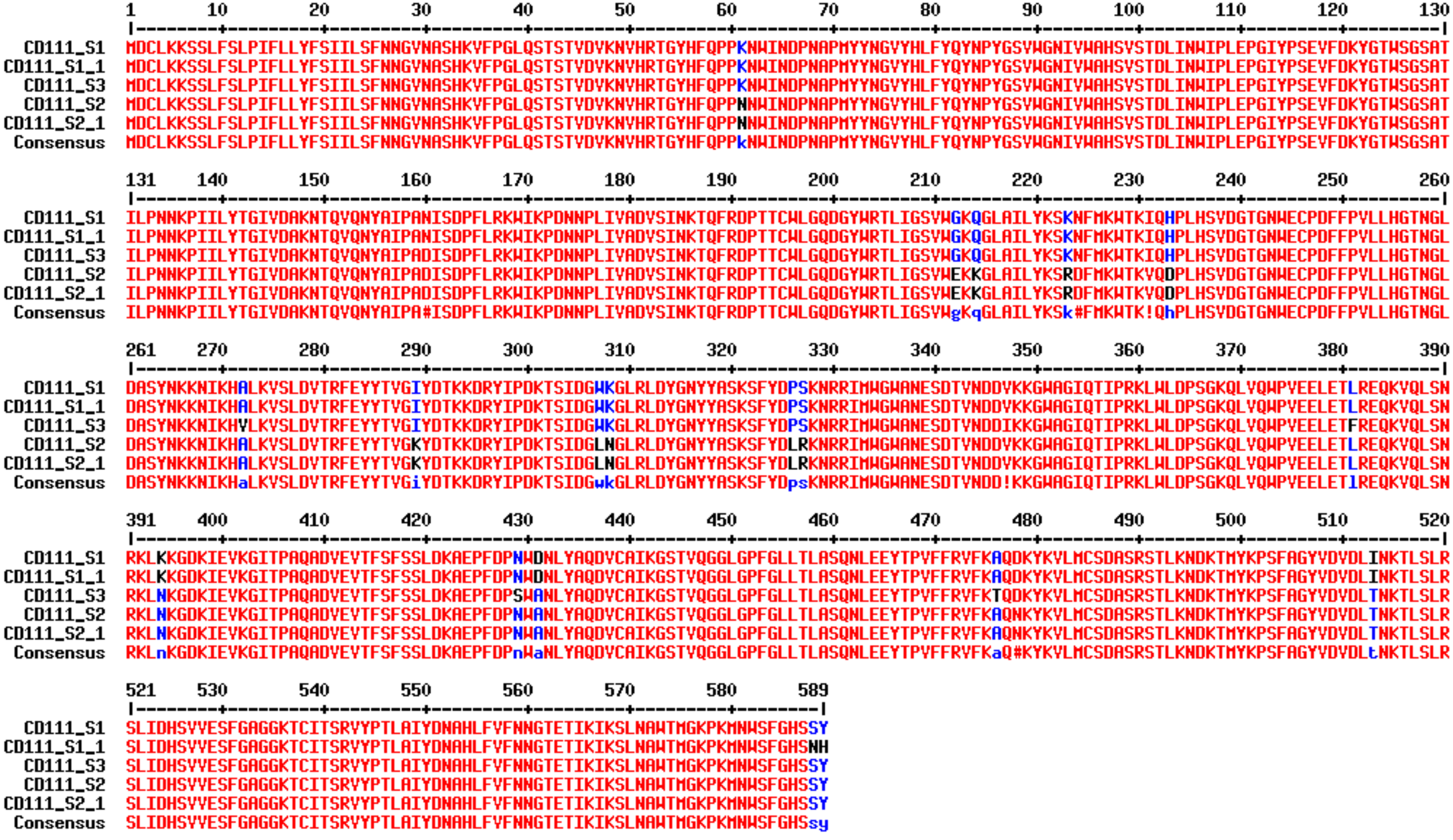
A sequence was defined as an allele when it was found twice in two independent PCRs. Additionally, the consensus sequence of all alleles found in one genotype was used for allele definition when variable sequence polymorphisms occurred.

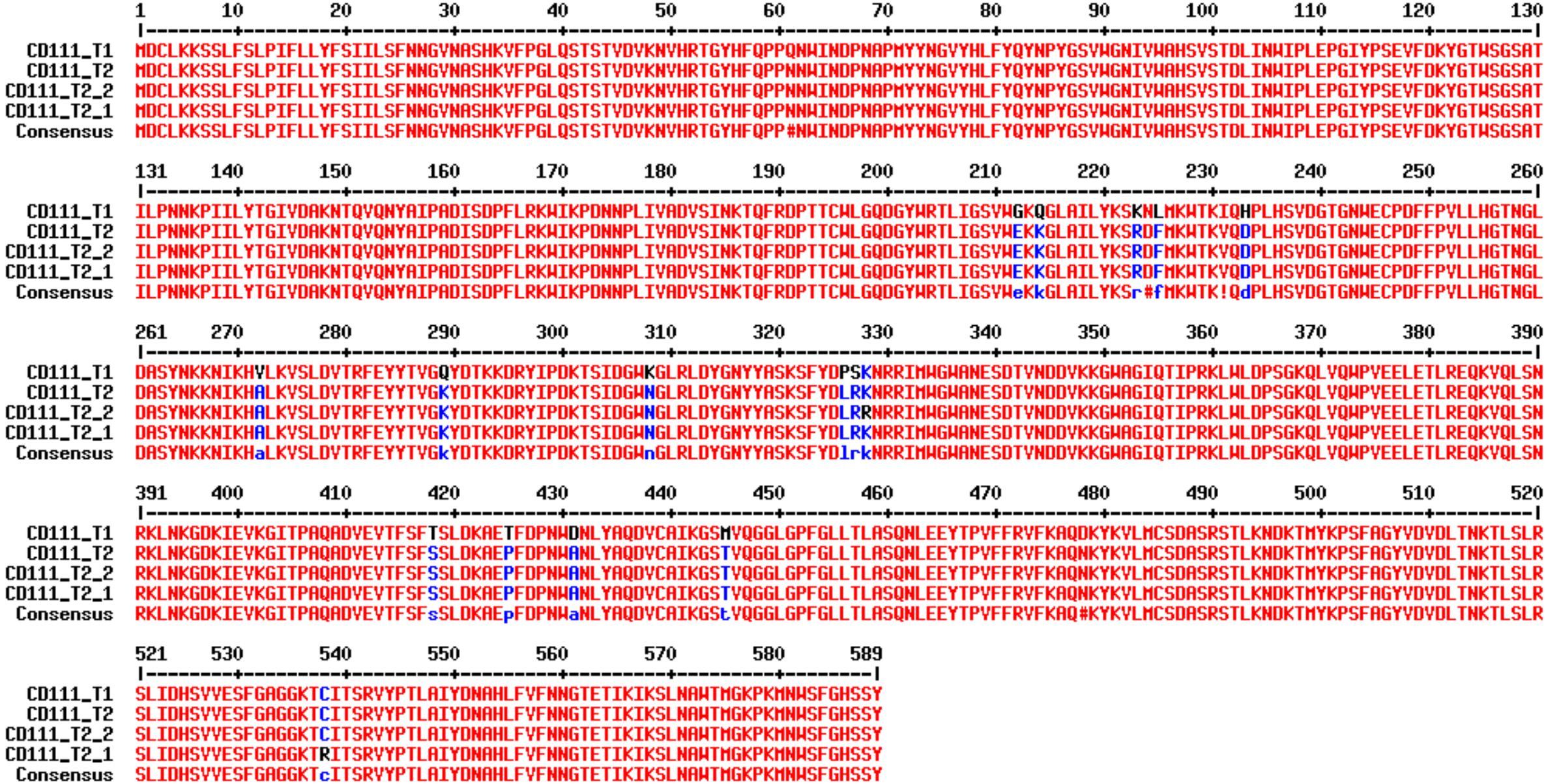
In the following Table, *pCD111* and *pCD141* alleles are listed, which do not correspond to this definition because only one full-length sequence was obtained. Nevertheless, for some of the listed alleles independent PCR amplifications gave rise to sequences that after partial sequencing indicated the existence of the alleles as mentioned above, clearly implying their existence. These additional sequences exhibited frame shifts or other modifications (e.g. missing or modified start and stop codons) and, therefore, were not completely sequenced.

Cloning of *pCD111* and *pCD141* alleles was carried out in addition to *Pain-1*, *invGE*, and *invGF* allele cloning, which were in the focus of the present study.

Table A3.3.1: Overview of fully and partially sequenced *pCD111* and *pCD141* alleles.

Gene	Full-length allele	Additional partial sequences
pCD111	*pCD111_S3*	No additional sequences
	pCD111_D1	No additional sequences
	pCD111_T1	No additional sequences
	pCD111_P40_1	2
	pCD111_P54_2	No additional sequences
pCD141	*pCD141_S1*	2
	pCD141_D2	No additional sequences
	pCD141_T3	No additional sequences


1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD111_S1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_S1_1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_S3 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_S2 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_S2_1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
Consensus MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPkNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD111_S1 ILPNNKPIILYTGIVDAKNTQVQNYAIPANISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_S1_1 ILPNNKPIILYTGIVDAKNTQVQNYAIPANISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_S3 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_S2 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_S2_1 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
Consensus ILPNNKPIILYTGIVDAKNTQVQNYAIPA#ISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWgKqGLAILYKSk#FMKWTK!QhPLHSVDGTGNWECPDFFPVLLHGTNGL
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD111_S1 DASYNKKNIKHALKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_S1_1 DASYNKKNIKHALKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_S3 DASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSN
CD111_S2 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGLNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_S2_1 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGLNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
Consensus DASYNKKNIKHaLKVSLDVTRFEYYTVGiYDTKKDRYIPDKTSIDGwkGLRLDYGNYYASKSFYDpsKNRRIMWGWANESDTVNDD!KKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETlREQKVQLSN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD111_S1 RKLKKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWDNLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLINKTLSLR
CD111_S1_1 RKLKKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWDNLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLINKTLSLR
CD111_S3 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPSWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_S2 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_S2_1 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
Consensus RKLnKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPnWaNLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKaQ#KYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLtNKTLSLR
521 530 540 550 560 570 580 589
CD111_S1 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_S1_1 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSNH
CD111_S3 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_S2 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_S2_1 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
Consensus SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSsy


1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD111_T1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPQNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_T2 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_T2_2 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_T2_1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
Consensus MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPP#NWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD111_T1 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNLMKWTKIQHPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_T2 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_T2_2 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_T2_1 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
Consensus ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWeKkGLAILYKSr#fMKWTK!QdPLHSVDGTGNWECPDFFPVLLHGTNGL
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD111_T1 DASYNKKNIKHVLKVSLDVTRFEYYTVGQYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_T2 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_T2_2 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFYDLRRNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_T2_1 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
Consensus DASYNKKNIKHaLKVSLDVTRFEYYTVGkYDTKKDRYIPDKTSIDGWnGLRLDYGNYYASKSFYDlrkNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD111_T1 RKLNKGDKIEVKGITPAQADVEVTFSFTSLDKAETFDPNWDNLYAQDVCAIKGSMVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_T2 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_T2_2 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_T2_1 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
Consensus RKLNKGDKIEVKGITPAQADVEVTFSFsSLDKAEpFDPNWaNLYAQDVCAIKGStVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQ#KYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
521 530 540 550 560 570 580 589
CD111_T1 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_T2 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_T2_2 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_T2_1 SLIDHSVVESFGAGGKTRITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
Consensus SLIDHSVVESFGAGGKTcITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_S1_1      ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_S1_1      CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_S1_1      ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCAACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_S1_1      ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCAACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCAACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_S1_1      ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
Consensus       ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_S1_1      AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
Consensus       AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_S1_1      GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        TCGATGGTTGGAAGGGATTGAGGCTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_S1_1      TCGATGGTTGGAAGGGATTGAGGCTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTGGAAGGGATTGAGGCTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CAAGAAAGGATGGGCAGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_S1_1      CAAGAAAGGATGGGCAGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCAGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CGCAAGTTAAAGAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTTTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGATAACCTTT
CD111_S1_1      CGCAAGTTAAAGAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTTTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGATAACCTTT
Consensus       CGCAAGTTAAAGAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTTTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGATAACCTTT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_S1_1      ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGGCCCA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAATAAACAAGACATTGTCTTTAAGG
CD111_S1_1      AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAATAAACAAGACATTGTCTTTAAGG
Consensus       AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAATAAACAAGACATTGTCTTTAAGG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACACCTATTTGTCTTTAATAATGGGACAGAGA
CD111_S1_1      AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACAcCTATTTGTCTTTAATAATGGGACAGAGA

                1691    1700      1710      1720      1730      1740      1750      1760      1770
                |--------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_S1_1      CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTAATCACTAG
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTaaTcAcTaa
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_S2_1      ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_S2_1      CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_S2_1      ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_S2_1      ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_S2_1      ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
Consensus       ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_S2_1      AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
Consensus       AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAGGATAGGTATATTCCCGATAAGACTTCTA
CD111_S2_1      GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAGGATAGGTATATTCCCGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAGGATAGGTATATTCCCGATAAGACTTCTA

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        TCGATGGTTTGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_S2_1      TCGATGGTTTGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTTGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_S2_1      CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_S2_1      CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
Consensus       CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_S2_1      ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_S2_1      AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
Consensus       AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_S2        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_S2_1      AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA

                1691 1700 1710 1720 1730 1740 1750 1760 1770
                |----+----|----+----|----+----|----+----|----+
CD111_S2        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_S2_1      CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        ATGGATTGTTTAAAAAAGTCCTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_T2_1      ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_T2_2      ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCtTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA

                131 140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_T2_1      CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_T2_2      CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261 270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_T2_1      ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAACCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_T2_2      ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAgCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA

                391 400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_T2_1      ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_T2_2      ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521 530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_T2_1      ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_T2_2      ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
Consensus       ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC

                651 660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_T2_1      AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_T2_2      AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
Consensus       AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA

                781 790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        GATGCCTCATACAACAAGAAGAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
CD111_T2_1      GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
CD111_T2_2      GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAaAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA

                911 920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_T2_1      TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_T2_2      TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAGAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAaAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_T2_1      CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_T2_2      CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_T2_1      CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_T2_2      CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
Consensus       CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_T2_1      ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_T2_2      ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_T2_1      AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_T2_2      AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
Consensus       AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD111_T2        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_T2_1      AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACACGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_T2_2      AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATTACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACAtGTATcACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA

                1691 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790
                |----+----|----+----|----+----|----+----|----+----|----+-|
CD111_T2        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_T2_1      CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGAAATCACTAGTGA
CD111_T2_2      CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA.............
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                1    10        20        30        40        50        60        70        80        90        100       110       120       130
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_T1        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_S3        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_D1        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_S2        ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_T2        ATGGATTGTTTAAAAAAGTCCTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCtTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_T1        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTCAAAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_S3        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCTCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_D1        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCTCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_S2        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_T2        CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTaAaAACTGGATCAATGATCCCAATGCcCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_T1        ATCAGTATGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_S3        ATCAGTATGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACGGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_D1        ATCAGTATGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACGGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_S2        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_T2        ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTtTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACcGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTtGACAAATATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCAACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_T1        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_S3        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_D1        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_S2        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_T2        ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCgACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_T1        ACAACCCATTAATTGTTGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_S3        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_D1        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_S2        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_T2        ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
Consensus       ACAACCCATTAATTGTcGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGgAAAAcAAGGATTGGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_T1        AATATTGTATAAAAGTAAAAATTTAATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_S3        AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_D1        AATATTGTATAAAAGTAAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_S2        AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_T2        AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTA
Consensus       AATATTGTATAAAAGTAaAaATTTcATGAAATGGACCAAGaTtCAAcATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTtCCAGTGTTATTGCATGGTACAAATGGATTg

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        GATGCCTCATACAACAAGAAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_T1        GATGCCTCATACAACAAGAAAAAATATTAAACATGTTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTCAATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_S3        GATGCCTCATACAACAAGAAAAAATATTAAACATGTTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_D1        GATGCCTCATACAACAAGAAAAAATATTAAACATGTTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_S2        GATGCCTCATACAACAAGAAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGGATAGGTATATTCCCGATAAGACTTCTA
CD111_T2        GATGCCTCATACAACAAGAAGAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAaAATATTAAACATGcTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACcGTTGGTaaATATGATACAAAAAAAaGATAGGTATATTCCaGATAAGACTTCTA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        TCGATGGTTGGAAGGGATTGAGGCTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_T1        TCGATGGTTGGAAGGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_S3        TCGATGGTTGGAAGGGATTGAGACTTGATTATGGTAATTATTATGCATCTAAATCATTCTACGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATAT
CD111_D1        TCGATGGTTGGAAGGGATTGAGACTTGATTATGGTAATTATTATGCATCTAAATCATTCTACGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATAT
CD111_S2        TCGATGGTTTGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_T2        TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTgGAAgGGATTGAGaCTTGAcTATGGTAATTATTATGCATCTAAATCATTCTAtGACCcTAGcAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATgT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CAAGAAAGGATGGGCAGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_T1        CAAGAAAGGATGGGCAGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_S3        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAACACAATTAGTCCAATGGCCTGTCGAAGAATTAGAAACTTTTAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_D1        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAACACAATTAGTCCAATGGCCTGTCGAAGAATTAGAAACTTTTAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_S2        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_T2        CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCgGGAATTCAAACTATTCCCCGCAAAtTATGGCTTGATCCTAGTGGAAAgCAATTgGTCCAATGGCCTGTCGAAGAATTAGAAACTcTaAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CGCAAGTTAAAGAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTTTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGATAACCTTT
CD111_T1        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTTTCATTTACAAGTTTGGATAAGGCAGAGACATTTGATCCCAATTGGGATAACCTTT
CD111_S3        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAGTTGGGCTAACCTTT
CD111_D1        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_S2        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_T2        CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
Consensus       CGCAAGTTAAAcAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTcTCATTTtCAAGTTTGGATAAGGCAGAGcCATTTGATCCCAaTTGGGcTAACCTTT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_T1        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAATGGTGCAAGGGGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_S3        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGACCCA
CD111_D1        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGACCCA
CD111_S2        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_T2        ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       ATGCTCAAGATGTATGCGCCATTAAAGGCTCAAcGGTGCAAGGtGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACgCCGGTATTTTTCAGAGTTTTTAAGgCCCA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAATAAACAAGACATTGTCTTTAAGG
CD111_T1        AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_S3        AGATAAATATAAGGTTCTCATGTGCTCTGATGCCTCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_D1        AGATAAATATAAGGTTCTCATGTGCTCTGATGCCTCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_S2        AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_T2        AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
Consensus       AgATAAATATAAGGTTCTCATGTGCTCTGATGCaTCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAAcAAACAAGACATTGTCTTTAAGG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |----------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACACCTATTTGTCTTTAATAATGGGACAGAGA
CD111_T1        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_S3        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_D1        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_S2        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_T2        AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACAtCTATTTGTCTTTAATAATGGGACAGAGA

                1691    1700      1710      1720      1730      1740      1750      1760      1770
                |----------+---------+---------+---------+---------+---------+---------+---------|
CD111_S1        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_T1        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_S3        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_D1        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_S2        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_T2        CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
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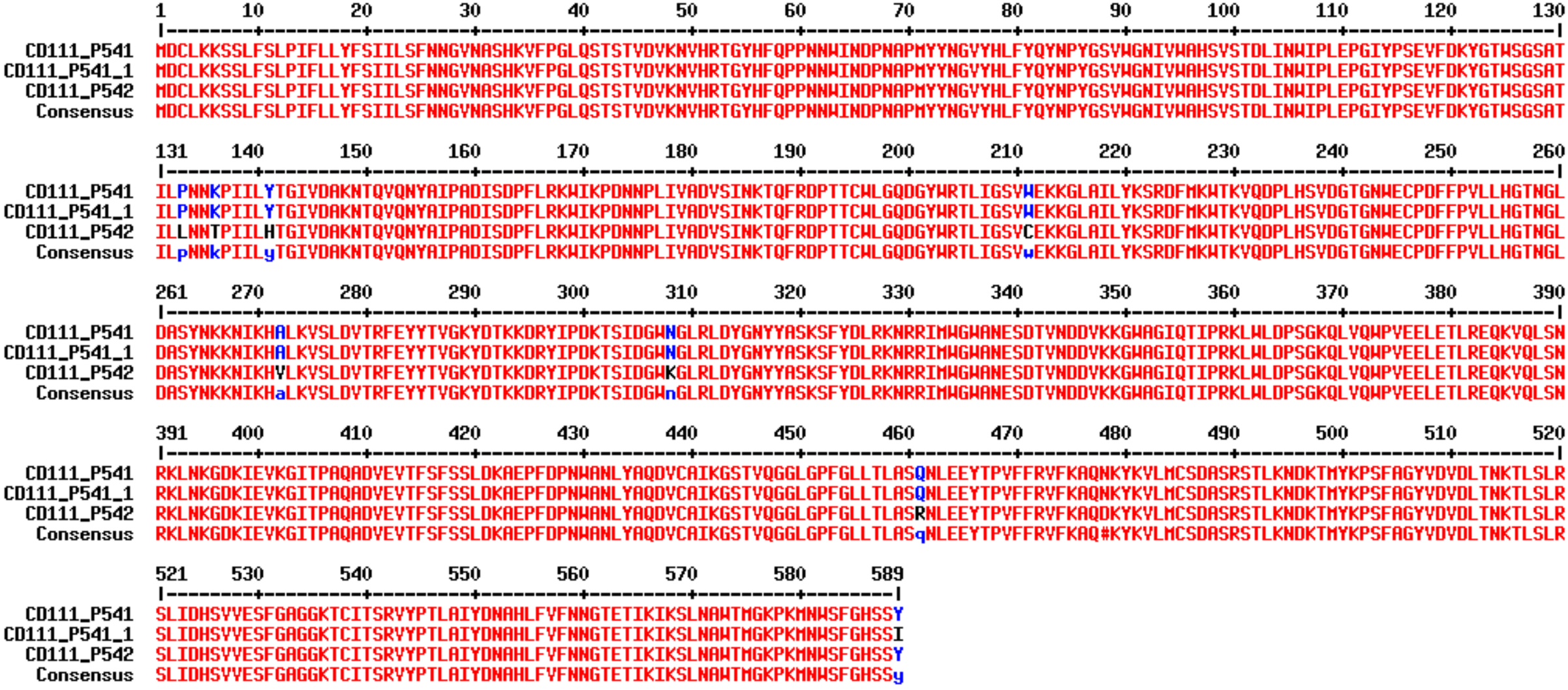
1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD111_P541 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_P541_1 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_P542 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
Consensus MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPNNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD111_P541 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_P541_1 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
CD111_P542 ILLNNTPIILHTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVCEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
Consensus ILpNNkPIILyTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVwEKKGLAILYKSRDFMKWTKVQDPLHSVDGTGNWECPDFFPVLLHGTNGL
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD111_P541 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_P541_1 DASYNKKNIKHALKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWNGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
CD111_P542 DASYNKKNIKHVLKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
Consensus DASYNKKNIKHaLKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWnGLRLDYGNYYASKSFYDLRKNRRIMWGWANESDTVNDDVKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETLREQKVQLSN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD111_P541 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_P541_1 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQNKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_P542 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASRNLEEYTPVFFRVFKAQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
Consensus RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASqNLEEYTPVFFRVFKAQ#KYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
521 530 540 550 560 570 580 589
CD111_P541 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
CD111_P541_1 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSI
CD111_P542 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSY
Consensus SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSy

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCTGGGTTGCAATCTACAAGCA
CD111_P541_1    ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCaGGGTTGCAATCTACAAGCA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_P541_1    CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_P541_1    ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_P541_1    ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACCCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_P541_1    ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
Consensus       ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      AATATTGTATAAAAGTAGAGATTTCATGAAGTGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_P541_1    AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
Consensus       AATATTGTATAAAAGTAGAGATTTCATGAAaTGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
CD111_P541_1    GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_P541_1    TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_P541_1    CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_P541_1    CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
Consensus       CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_P541_1    ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_P541_1    AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
Consensus       AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_P541_1    AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA

                1691    1700      1710      1720      1730      1740      1750      1760      1770
                |--------+---------+---------+---------+---------+---------+---------+---------|
CD111_P541      CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_P541_1    CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCAATCACT
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCaaacaca
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
CD111_P54_1     ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCTGGGTTGCAATCTACAAGCA
CD111_P54_2     ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCAGGGTTGCAATCTACAAGCA
Consensus       ATGGATTGTTTAAAAAAGTCTTCTCTTTTTTCTTTGCCAATTTTTTTGTTATATTTCTCCATAATTTTATCTTTCAACAATGGCGTTAATGCTTCACACAAAGTTTTTCCaGGGTTGCAATCTACAAGCA

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCCAATGCTCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_P54_1     CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
CD111_P54_2     CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAATAACTGGATCAATGATCCCAATGCCCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG
Consensus       CGGTTGATGTGAAAAATGTTCATAGAACTGGTTATCATTTTCAACCTCCTAAtAACTGGATCAATGATCCCAATGCcCCAATGTACTATAATGGTGTCTATCATCTATTCTACCAATACAATCCATATGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     ATCAGTATGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACGGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTTGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_P54_1     ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACCGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGACAAATATGGTACATGGTCCGGGTCAGCCACA
CD111_P54_2     ATCAGTTTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACGGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTCGATAAATATGGTACATGGTCCGGGTCAGCCACA
Consensus       ATCAGTtTGGGGAAATATTGTTTGGGCCCATTCAGTTTCAACgGACTTGATTAATTGGATCCCACTTGAGCCCGGAATCTATCCATCCGAAGTATTcGAcAAATATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     ATCTTACCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_P54_1     ATCTTACCAACAACAAGCCCATTATCCTCTACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
CD111_P54_2     ATCTTACTCAACAACACGCCCATTATCCTCCACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA
Consensus       ATCTTACcCAACAACAaGCCCATTATCCTCtACACCGGAATCGTCGATGCAAAAAATACCCAAGTCCAAAACTATGCAATCCCAGCCGACATATCCGATCCATTTCTTCGTAAATGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGGAAAACAAGGATTGGC
CD111_P54_1     ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGGGAAAAAAAAGGATTGGC
CD111_P54_2     ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGCGAAAAAAAAGGATTGGC
Consensus       ACAACCCATTAATTGTCGCTGACGTTAGCATTAACAAGACCCAATTCCGTGACCCAACCACATGTTGGTTGGGTCAGGATGGTTATTGGAGAACCTTGATAGGGAGTGTGTGgGaAAAAaAAGGATTGGC

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     AATATTGTATAAAAGTAAAATTTCATGAAATGGACCAAGATTCAACATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGCATGGTACAAATGGATTG
CD111_P54_1     AATATTGTATAAAAGTAGAGATTTCATGAAGTGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTA
CD111_P54_2     AATATTGTATAAAAGTAGAGATTTCATGAAATGGACCAAGGTCCAAGATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCCAGTGTTATTGCATGGTACAAATGGATTG
Consensus       AATATTGTATAAAAGTAgAgATTTCATGAAaTGGACCAAGgTcCAAgATCCACTTCATTCAGTTGACGGTACTGGAAATTGGGAATGTCCTGATTTTTTTcCCAGTGTTATTGCATGGTACAAATGGATTg

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     GATGCCTCATACAACAAGAAAAATATTAAACATGTTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACAGTTGGTATATATGATACAAAAAAAGATAGGTATATTCCAGATAAGACTTCTA
CD111_P54_1     GATGCCTCATACAACAAGAAAAATATTAAACATGCTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
CD111_P54_2     GATGCCTCATACAACAAGAAAAATATTAAACATGTTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACCGTTGGTAAATATGATACAAAAAAAGATAGGTATATTCCCGATAAGACTTCTA
Consensus       GATGCCTCATACAACAAGAAAAATATTAAACATGtTCTTAAAGTTAGTCTTGATGTTACGAGGTTTGAATACTATACcGTTGGTAaATATGATACAAAAAAAGATAGGTATATTCCcGATAAGACTTCTA

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     TCGATGGTTGGAAGGGATTGAGACTTGATTATGGTAATTATTATGCATCTAAATCATTCTACGACCCTAGCAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATAT
CD111_P54_1     TCGATGGTTGGAACGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
CD111_P54_2     TCGATGGTTGGAAGGGATTGAGACTTGACTATGGTAATTATTATGCATCTAAATCATTCTATGACCTTAGGAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATGT
Consensus       TCGATGGTTGGAAgGGATTGAGACTTGAcTATGGTAATTATTATGCATCTAAATCATTCTAtGACCtTAGgAAAAATCGAAGAATTATGTGGGGTTGGGCTAATGAATCAGATACTGTCAATGACGATgT

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAATTATGGCTTGATCCTAGTGGAAAACAATTAGTCCAATGGCCTGTCGAAGAATTAGAAACTTTTAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_P54_1     CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
CD111_P54_2     CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAACTATGGCTTGATCCTAGTGGAAAGCAATTGGTCCAATGGCCTGTCGAAGAATTAGAAACTCTAAGAGAGCAAAAGGTGCAATTAAGTAAT
Consensus       CAAGAAAGGATGGGCGGGAATTCAAACTATTCCCCGCAAAcTATGGCTTGATCCTAGTGGAAAgCAATTgGTCCAATGGCCTGTCGAAGAATTAGAAACTcTaAGAGAGCAAAAGGTGCAATTAAGTAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_P54_1     CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
CD111_P54_2     CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT
Consensus       CGCAAGTTAAACAAAGGAGATAAAATTGAAGTTAAAGGAATCACACCTGCACAGGCTGATGTTGAAGTGACATTCTCATTTTCAAGTTTGGATAAGGCAGAGCCATTTGATCCCAATTGGGCTAACCTTT

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACGCCGGTATTTTTCAGAGTTTTTAAGACCCA
CD111_P54_1     ATGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCAAAATTTGGAAGAATATACACCGGTATTTTTCAGAGTTTTTAAGGCCCA
CD111_P54_2     ACGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCGAAATTTGGAAGAATATACACCAGTATTTTTCAGAGTTTTTAAGGCCCA
Consensus       AtGCTCAAGATGTATGCGCCATTAAAGGCTCAACGGTGCAAGGTGGACTTGGGCCATTTGGGCTCTTAACTTTGGCTTCTCaAAATTTGGAAGAATATACaCCgGTATTTTTCAGAGTTTTTAAGgCCCA

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     AGATAAATATAAGGTTCTCATGTGCTCTGATGCCTCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_P54_1     AAATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
CD111_P54_2     AGATAAATATAAGGTTCTCATGTGCTCTGATGCATCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG
Consensus       AgATAAATATAAGGTTCTCATGTGCTCTGATGCaTCAAGATCAACCCTCAAGAATGATAAGACAATGTACAAGCCATCATTTGCTGGATATGTAGATGTAGATTTAACAAACAAGACATTGTCTTTAAGG

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_P54_1     AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
CD111_P54_2     AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA
Consensus       AGTTTGATTGATCACTCAGTAGTAGAAAGCTTTGGTGCCGGAGGAAAAACATGTATCACATCAAGGGTTTATCCGACATTAGCAATTTATGATAATGCACATCTATTTGTCTTTAATAATGGGACAGAGA

                1691    1700      1710      1720      1730      1740      1750      1760      1770
                |--------+---------+---------+---------+---------+---------+---------+---------|
CD111_P40_1     CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCGCTCTTCTTATTGA
CD111_P54_1     CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
CD111_P54_2     CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCACTCTTCTTATTGA
Consensus       CTATCAAAATTAAGTCATTGAATGCATGGACCATGGGTAAACCTAAGATGAATTGGTCATTTGGTCaCTCTTCTTATTGA
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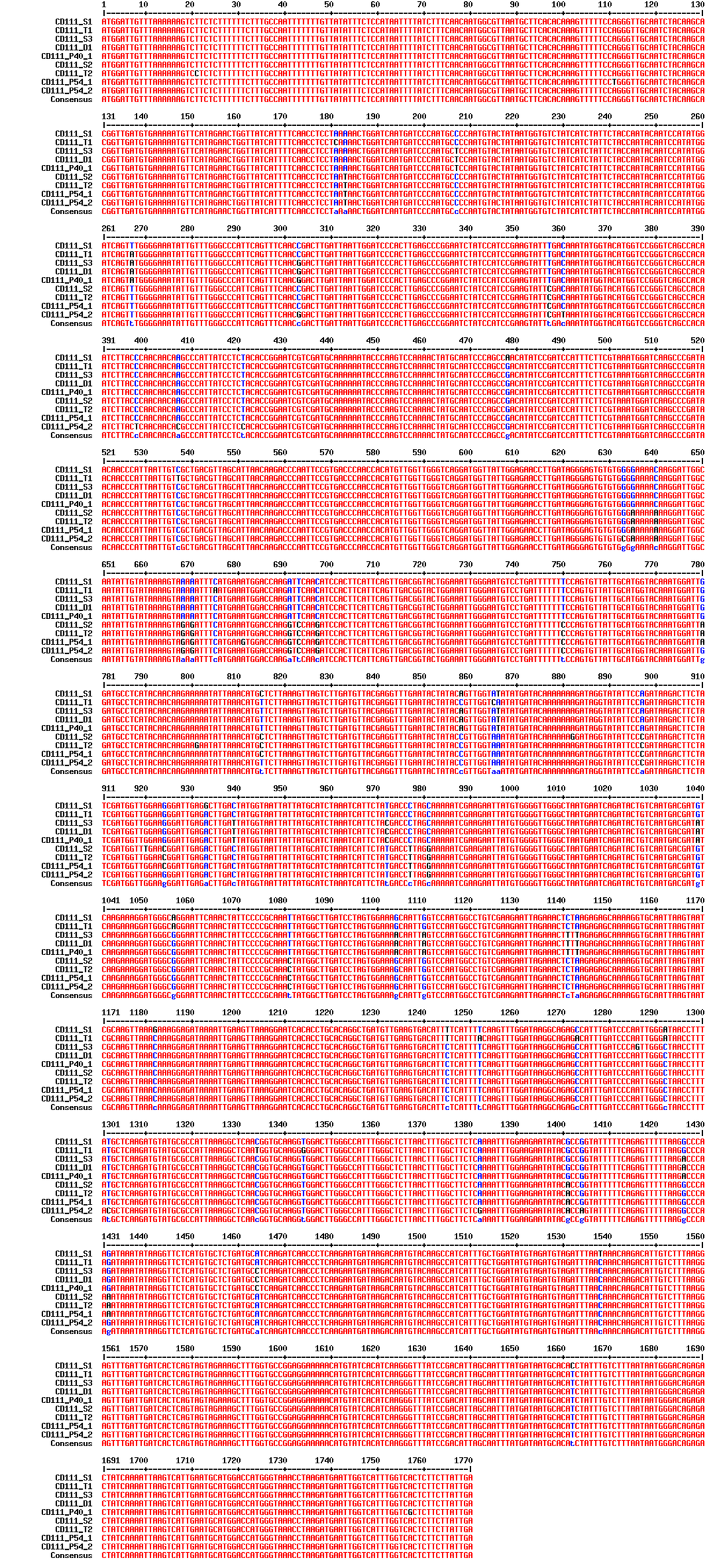

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_S1        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIIWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_S2        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_S2_1      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_S2_2      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_S3        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPSKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_S3_1      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPSKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus       MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDaSKVHRTGYHFQPpKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNI!WAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_S1        ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_S2        ILPGNKPVILYTGIVDANKTQVQNYAIPANISDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSDKDFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_S2_1      ILPGNKPVILYTGIVDANKTQVQNYAIPANISDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSDKDFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_S2_2      ILPGNKPVILYTGIVDANKTQVQNYAIPANISDPYLRKWIKPDNNPLIVADRTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSDKDFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_S3        ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDRNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_S3_1      ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDRNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus       ILPGNKPVILYTGIVDANKTQVQNYAIPANmSDPYLRKWIKPDNNPLIVADkTINKSQFRDPTTAWMGRDgNWRILVGSVRNHRGKVIMYKS#K#FMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNK#G

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_S1        LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKHFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTRDNDVRKGWAGVHPIPRKIWLDSSGKQLVQWPVQELETLRKKKVQLN
CD141_S2        LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_S2_1      LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_S2_2      LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_S3        LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_S3_1      LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus       LDTSYNGKDIKHVLKVSFDVTRFDHYT!GTYDTKKDKyFPDNTSIDGWKGLRLDYGNYYASKTFFDsGKNRRILLGWANESDTvDNDVRKGWAGVHPIPRKIWLDpSGKQLVQWPVQELETLRKKKVQLN

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_S1        NKKLNKGEKVEIKGITVAQADVEVIFSFASLEKAELFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_S2        NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_S2_1      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_S2_2      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_S3        NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_S3_1      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus       NKKLNKGEKVEIKGITVAQADVEVIFSFtSL#KAEpFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL

                521     530       540       550       560       570       58882
                |--------+---------+---------+---------+---------+---------+-|
CD141_S1        RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_S2        RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_S2_1      RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_S2_2      RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_S3        RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_S3_1      RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus       RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
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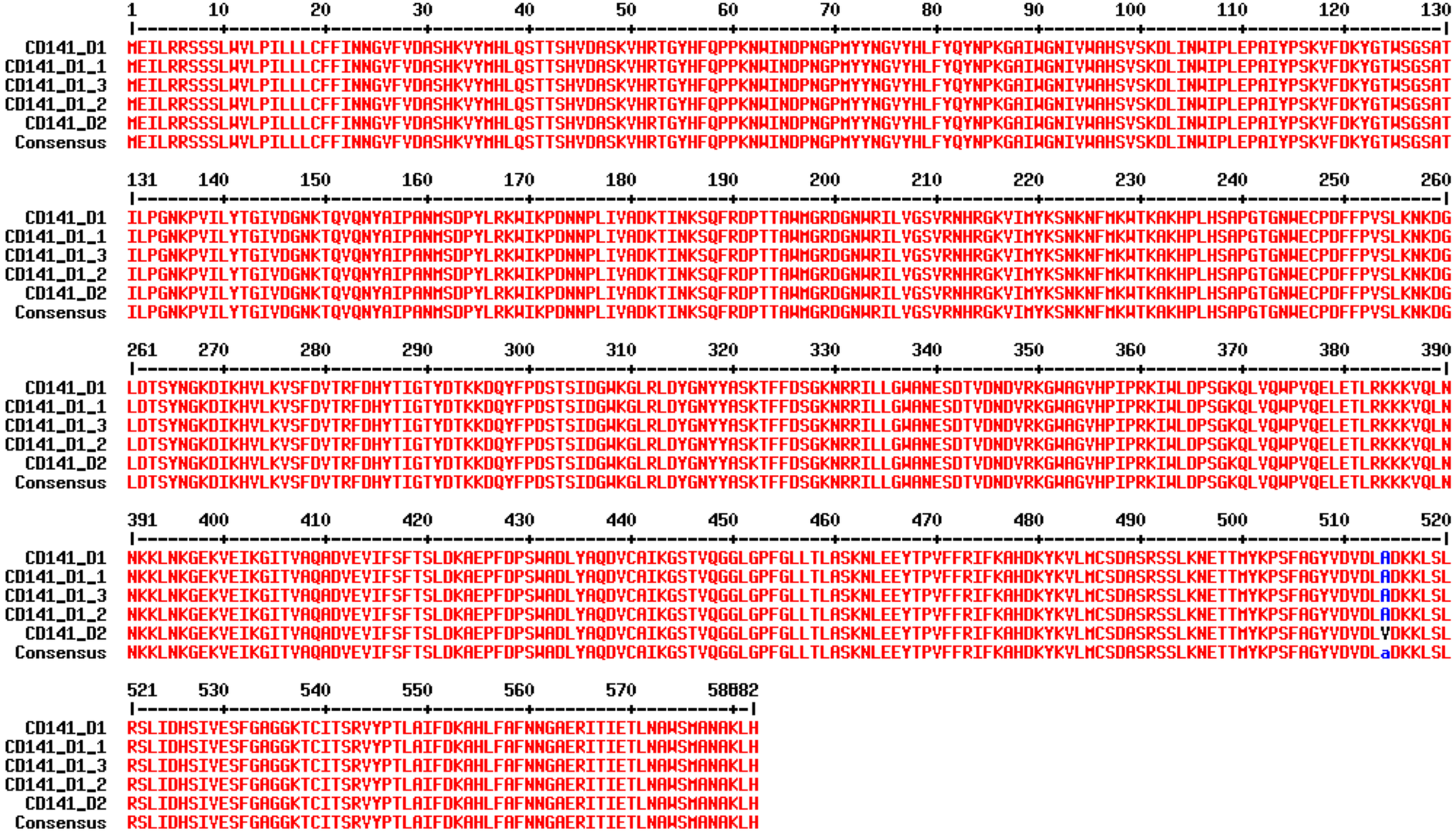
1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD141_D1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_D1_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_D1_3 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_D1_2 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_D2 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD141_D1 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_D1_1 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_D1_3 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_D1_2 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_D2 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD141_D1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_D1_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_D1_3 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_D1_2 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_D2 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD141_D1 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_D1_1 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_D1_3 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_D1_2 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_D2 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLVDKKLSL
Consensus NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLaDKKLSL
521 530 540 550 560 570 58882
CD141_D1 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_D1_1 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_D1_3 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_D1_2 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_D2 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_T1_2      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_T2        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_T2_1      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_T3        MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_T1_1      MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus       MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDvSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_T1_2      ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWGCPDFFPVSLKNKDG
CD141_T2        ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_T2_1      ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_T3        ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWVKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_T1_1      ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus       ILPGNKPVILYTGIVDaNKTQVQNYAIPANMSDPYLRKW!KPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWeCPDFFPVSLKNKDG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_T1_2      LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_T2        LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_T2_1      LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_T3        LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_T1_1      LDTSYNGKDIKHVLKVSCDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus       LDTSYNGKDIKHVLKVSfDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_T1_2      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_T2        NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_T2_1      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_T3        NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_T1_1      NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus       NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL

                521     530       540       550       560       570       58882
                |--------+---------+---------+---------+---------+---------+-|
CD141_T1        RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_T1_2      RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_T2        RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_T2_1      RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_T3        RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_T1_1      RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus       RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCATAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_S2_1      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_S2_2      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCAcAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_S2_1      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_S2_2      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_S2_1      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_S2_2      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAACTATGCAATCCCAGCTAACATATCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_S2_1      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAACTATGCAATCCCAGCTAACATATCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_S2_2      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAACTATGCAATCCCAGCTAACATATCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAACTATGCAATCCCAGCTAACATATCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_S2_1      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_S2_2      ACAATCCATTGATTGTTGCTGACAGAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAaAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        TATAATGTACAAAAGTGATAAGGACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCCGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_S2_1      TATAATGTACAAAAGTGATAAGGACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCCGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_S2_2      TATAATGTACAAAAGTGATAAGGACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCCGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTGATAAGGACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCCGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_S2_1      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_S2_2      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_S2_1      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_S2_2      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        TGTGAGGAAAGGATGGGCTGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_S2_1      TGTGAGGAAAGGATGGGCTGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_S2_2      TGTGAGGAAAGGATGGGCTGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCTGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_S2_1      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_S2_2      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_S2_1      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_S2_2      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_S2_1      TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_S2_2      TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
Consensus       TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S2        AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_S2_1      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_S2_2      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG

                1691 1700 1710 1720 1730 1740 1749
                |----+----|----+----|----+----|---|
CD141_S2        AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_S2_1      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_S2_2      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_S3_1      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

              131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTTCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_S3_1      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTTCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTTCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

              261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_S3_1      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

              391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_S3_1      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

              521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATAGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_S3_1      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATAGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATAGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT

              651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_S3_1      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT

              781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_S3_1      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
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                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACGGTTGATAACGA
CD141_S3_1      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACGGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACGGTTGATAACGA

             1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAACTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_S3_1      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAACTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAACTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

             1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_S3_1      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

             1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_S3_1      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC

             1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        TCAAGATAGATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_S3_1      TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
Consensus       TCAAGATAaATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT

             1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_S3        AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAATAACGGCGCGG
CD141_S3_1      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAATAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAATAACGGCGCGG

             1691 1700 1710 1720 1730 1740 1749
                |----+----|----+----|----+----|---|
CD141_S3        AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_S3_1      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_D1_2      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_D1_3      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_D1_1      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131 140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_D1_2      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_D1_3      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_D1_1      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261 270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_D1_2      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_D1_3      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_D1_1      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA

                391 400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_D1_2      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_D1_3      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_D1_1      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521 530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_D1_2      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_D1_3      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_D1_1      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT

                651 660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_D1_2      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_D1_3      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_D1_1      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT

                781 790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_D1_2      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_D1_3      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_D1_1      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
Consensus       TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT

                911 920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_D1_2      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_D1_3      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_D1_1      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_D1_2      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_D1_3      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_D1_1      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGACCCTAGTTGGGCTGATC
CD141_D1_2      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_D1_3      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_D1_1      AACAAAAAGTTGAACAAGGGAGAAAAGGTCGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAGAAAAGGTtGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGAtCCTAGTTGGGCTGATC

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_D1_2      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_D1_3      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_D1_1      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_D1_2      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_D1_3      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_D1_1      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
Consensus       TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----+----+----+----+----+----+----+----+----+----+----+----|
CD141_D1        AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_D1_2      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_D1_3      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_D1_1      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG

                1691 1700 1710 1720 1730 1740 1749
                |----+----+----+----+----+----+
CD141_D1        AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_D1_2      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_D1_3      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_D1_1      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1    10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_T1_2      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_T1_1      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGGGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_T1_2      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_T1_1      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGaGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_T1_2      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_T1_1      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACCGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_T1_2      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACCGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_T1_1      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACCGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACCGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_T1_2      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_T1_1      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_T1_2      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGGATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_T1_1      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGaATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_T1_2      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_T1_1      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTGTGATGTTACAAGGTTTGATCATTACACAATTGGCACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
Consensus       TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTtTGATGTTACAAGGTTTGATCATTACACAATTGGtACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_T1_2      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_T1_1      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_T1_2      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_T1_1      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_T1_2      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_T1_1      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_T1_2      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_T1_1      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_T1_2      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_T1_1      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
Consensus       TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T1        AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_T1_2      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_T1_1      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG

                1691    1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+---------|
CD141_T1        AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_T1_2      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_T1_1      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_T2_1      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_T2_1      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_T2_1      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_T2_1      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_T2_1      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_T2_1      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_T2_1      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
Consensus       TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_T2_1      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_T2_1      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_T2_1      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_T2_1      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_T2_1      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
Consensus       TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_T2        AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_T2_1      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG

                1691    1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+---------|
CD141_T2        AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_T2_1      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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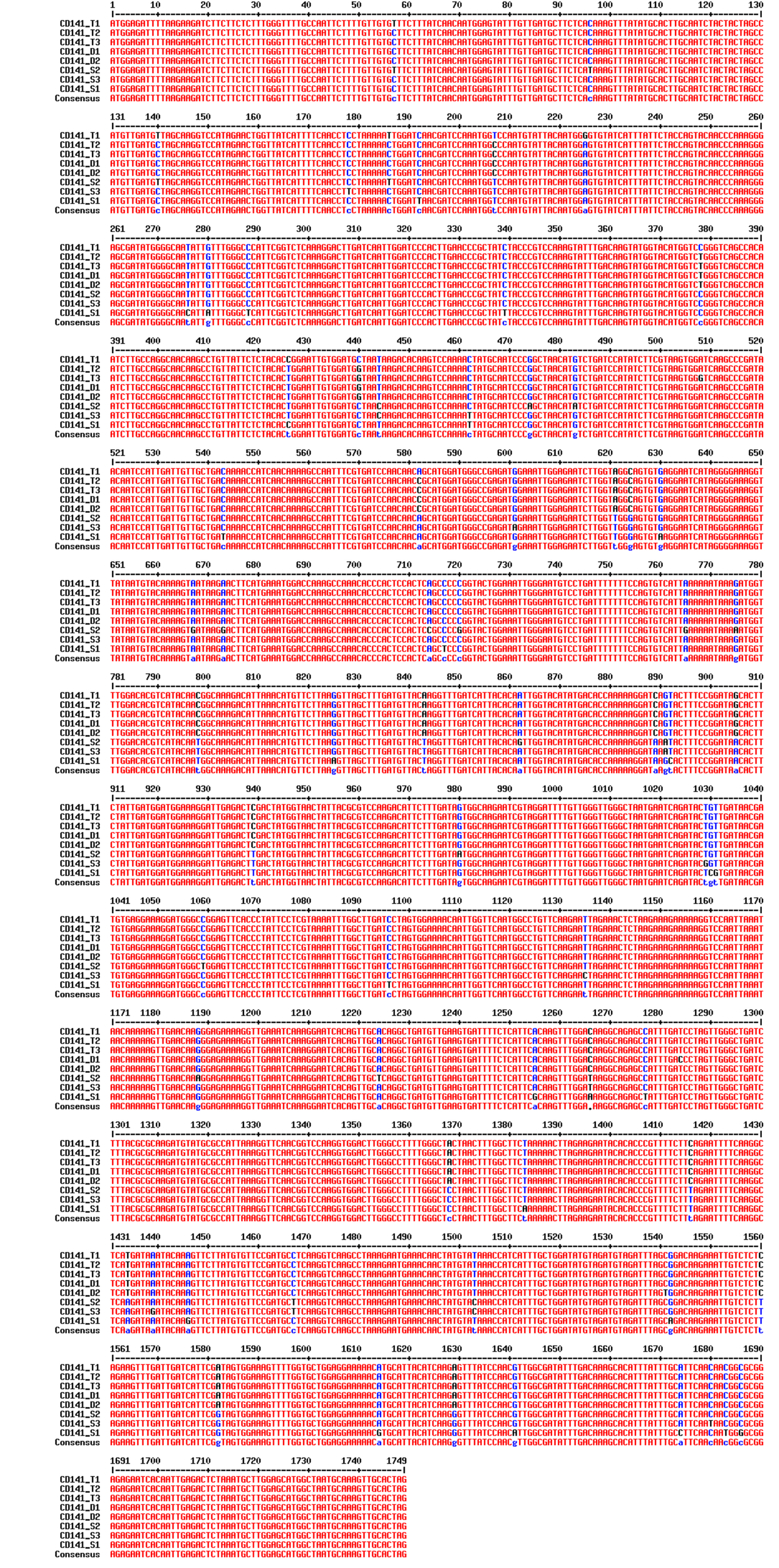
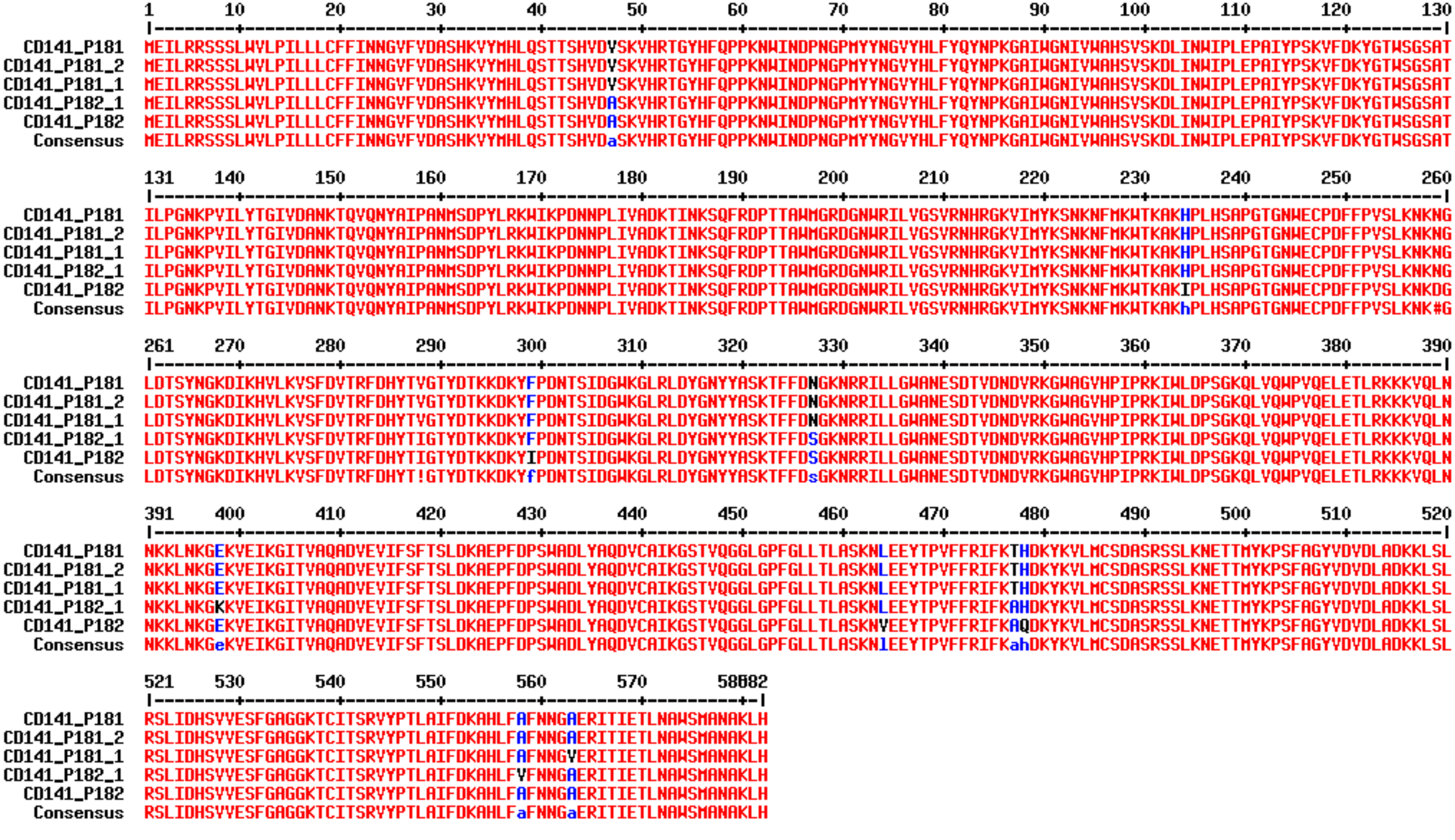
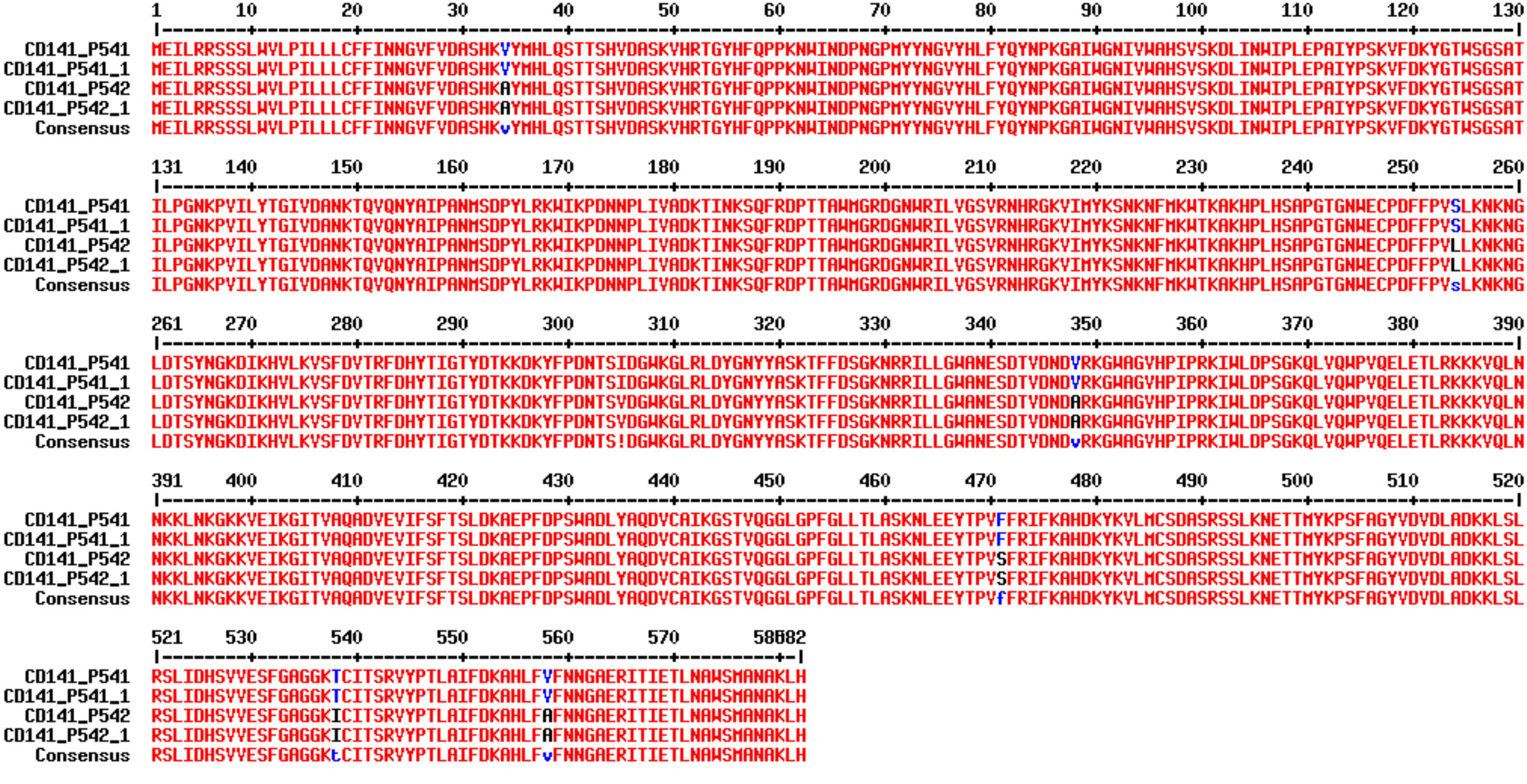



1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD141_P181 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P181_2 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P181_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDVSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P182_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P182 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDaSKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD141_P181 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P181_2 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P181_1 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P182_1 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P182 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKIPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKhPLHSAPGTGNWECPDFFPVSLKNK#G
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD141_P181 LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P181_2 LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P181_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTVGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDNGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P182_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P182 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYIPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus LDTSYNGKDIKHVLKVSFDVTRFDHYT!GTYDTKKDKYfPDNTSIDGWKGLRLDYGNYYASKTFFDsGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD141_P181 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKTHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P181_2 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKTHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P181_1 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKTHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P182_1 NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P182 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNVEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus NKKLNKGeKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNlEEYTPVFFRIFKahDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
521 530 540 550 560 570 58882
CD141_P181 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_P181_2 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_P181_1 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGVERITIETLNAWSMANAKLH
CD141_P182_1 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFVFNNGAERITIETLNAWSMANAKLH
CD141_P182 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFaFNNGaERITIETLNAWSMANAKLH


1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD141_P401 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P401_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD141_P401 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_P401_1 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD141_P401 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P401_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD141_P401 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P401_1 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
521 530 540 550 560 570 58882
CD141_P401 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_P401_1 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH


1 10 20 30 40 50 60 70 80 90 100 110 120 130
CD141_P541 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P541_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P542 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKAYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P542_1 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKAYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus MEILRRSSSLWVLPILLLCFFINNGVFVDASHKvYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
CD141_P541 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P541_1 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKNG
CD141_P542 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVLLKNKNG
CD141_P542_1 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVLLKNKNG
Consensus ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVsLKNKNG
261 270 280 290 300 310 320 330 340 350 360 370 380 390
CD141_P541 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P541_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P542 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSVDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDARKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
CD141_P542_1 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSVDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDARKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTS!DGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDvRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
CD141_P541 NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P541_1 NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P542 NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVSFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P542_1 NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVSFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus NKKLNKGKKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVfFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
521 530 540 550 560 570 58882
CD141_P541 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFVFNNGAERITIETLNAWSMANAKLH
CD141_P541_1 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFVFNNGAERITIETLNAWSMANAKLH
CD141_P542 RSLIDHSVVESFGAGGKICITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_P542_1 RSLIDHSVVESFGAGGKICITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus RSLIDHSVVESFGAGGKtCITSRVYPTLAIFDKAHLFvFNNGAERITIETLNAWSMANAKLH

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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P181_2    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P181_1    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P181_2    ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P181_1    ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P181_2    AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P181_1    AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGACA
CD141_P181_2    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGACA
CD141_P181_1    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGACA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGACA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P181_2    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P181_1    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P181_2    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCGGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P181_1    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCaGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      TTGGACACGTCATACAATGGCAAAGACGTTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P181_2    TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P181_1    TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACaTTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT

                911     920       930       940       950       960       970       980       990       1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P181_2    CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P181_1    CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACACTGAGAAAGAAAAAAGTCCAATTAAAT
CD141_P181_2    TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACACTGAGAAAGAAAAAAGTCCAATTAAAT
CD141_P181_1    TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACACTGAGAAAGAAAAAAGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACACTGAGAAAGAAAAAAGTCCAATTAAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P181_2    AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P181_1    AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGAC
CD141_P181_2    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGAC
CD141_P181_1    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGAC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGAC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      TCATGATAAATACAAGGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCAGACAAGAAATTGTCTCTT
CD141_P181_2    TCATGATAAATACAAGGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCAGACAAGAAATTGTCTCTT
CD141_P181_1    TCATGATAAATACAAGGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCAGACAAGAAATTGTCTCTT
Consensus       TCATGATAAATACAAGGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCAGACAAGAAATTGTCTCTT

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P181      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P181_2    AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P181_1    AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGTGG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGcGG

                1691    1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+---------|
CD141_P181      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P181_2    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P181_1    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P182_1    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131 140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P182_1    ATGTTGATGCTAGCAAGGTCCACAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCAcAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAAcGATCCAAATGGcCCAATGTATTACAATGGAGTGTAcCATTTATTCTACCAGTACAACCCAAAGGG

                261 270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P182_1    AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAAcATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391 400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P182_1    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAAcAAGACACAAGTCCAAAAcTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521 530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P182_1    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTaGGGAGTGTGAGGAATCATAGGGGAAAGGT

                651 660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAAATCCCACTCCACTCGGCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_P182_1    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAAaaCCCACTCCACTCaGCCCCcGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTaAAAAATAAAaATGGT

                781 790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAGTACATTCCGGATAACACTT
CD141_P182_1    TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAaTACaTTCCGGATAACACTT

                911 920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P182_1    CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P182_1    TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P182_1    AACAAAAAGTTGAACAAGGGAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAaGGAaAAAAGGTTGAAATCAAAGGAATCACAGTTGCaCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACGTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_P182_1    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACgTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P182_1    TCATGATAAATACAAGGTTCTTATGTGTTCTGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
Consensus       TCAaGATAAATACAAaGTTCTTATGTGTTCcGATGCcTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTAcAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P182      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P182_1    AGAAGTTTGATTGATCATTCGGTAGTCGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACATTGGCGATATTTGACAAAGCACATTTATTTGTGTTCAACAACGGCGCAG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTcGAAAGTTTTGGTGCcGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACaTTGGCGATATTTGACAAAGCACATTTATTTGcaTTCAACAACGGCGCaG

                1691 1700 1710 1720 1730 1740 1749
                |----+----|----+----|----+----|---|
CD141_P182      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P182_1    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P401_1    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P401_1    ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_P401_1    AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P401_1    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P401_1    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_P401_1    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_P401_1    TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
Consensus       TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT

                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P401_1    CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P401_1    TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P401_1    AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_P401_1    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_P401_1    TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
Consensus       TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P401      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P401_1    AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCcGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG

                1691    1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+---------|
CD141_P401      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P401_1    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAA
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAa
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                1       10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P541_1    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC

                131     140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      ATGTTGATGCTAGCAAGGTCCACAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P541_1    ATGTTGATGCTAGCAAGGTCCACAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCTAGCAAGGTCCACAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG

                261     270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P541_1    AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391     400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P541_1    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521     530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P541_1    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT

                651     660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P541_1    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT

                781     790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P541_1    TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
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                911     920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGCGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P541_1    CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGcGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041    1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P541_1    TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171    1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P541_1    AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301    1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_P541_1    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC

                1431    1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      TCATGATAAATACAAGGTTCTTATGTGTTCTGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P541_1    TCATGATAAATACAAGGTTCTTATGTGTTCTGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
Consensus       TCATGATAAATACAAGGTTCTTATGTGTTCTGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT

                1561    1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P541      AGAAGTTTGATTGATCATTCGGTAGTCGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACATTGGCGATATTTGACAAAGCACATTTATTTGTGTTCAACAACGGCGCAG
CD141_P541_1    AGAAGTTTGATTGATCATTCGGTAGTCGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACATTGGCGATATTTGACAAAGCACATTTATTTGTGTTCAACAACGGCGCAG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTCGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACATTGGCGATATTTGACAAAGCACATTTATTTGTGTTCAACAACGGCGCAG

                1691    1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+---------|
CD141_P541      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P541_1    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1    10        20        30        40        50        60        70        80        90       100       110       120       130
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGCTTATATGCACTTGCAATCTACTACTAGCC
CD141_P542_1    ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGCTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGCTTATATGCACTTGCAATCTACTACTAGCC

                131   140       150       160       170       180       190       200       210       220       230       240       250       260
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      ATGTTGATGCAAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P542_1    ATGTTGATGCAAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGCAAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG

                261   270       280       290       300       310       320       330       340       350       360       370       380       390
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P542_1    AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA

                391   400       410       420       430       440       450       460       470       480       490       500       510       520
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P542_1    ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA

                521   530       540       550       560       570       580       590       600       610       620       630       640       650
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGN
CD141_P542_1    ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGn

                651   660       670       680       690       700       710       720       730       740       750       760       770       780
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCTCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P542_1    TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTTATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCcCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTcATTGAAAAATAAAAATGGT

                781   790       800       810       820       830       840       850       860       870       880       890       900       910
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGGTCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P542_1    TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGaTCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT

                911   920       930       940       950       960       970       980       990      1000      1010      1020      1030      1040
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      CTGTTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P542_1    CTGTTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTGTTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041  1050      1060      1070      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P542_1    TGCGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
Consensus       TGcGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT

                1171  1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P542_1    AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301  1310      1320      1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCCGAATTTTCAAGGC
CD141_P542_1    TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTCCTTCCGAATTTTCAAGGC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTcCTTCCGAATTTTCAAGGC

                1431  1440      1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      TCATGATAAATACAAGGTTCTCATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P542_1    TCATGATAAATACAAGGTTCTCATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
Consensus       TCATGATAAATACAAGGTTCTCATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT

                1561  1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680      1690
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
CD141_P542      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAATATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAATGGCGCGG
CD141_P542_1    AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAATATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAATGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAATATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAATGGCGCGG

                1691  1700      1710      1720      1730      1740      1749
                |--------+---------+---------+---------+---------+--------|
CD141_P542      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P542_1    AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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                1   10   20   30   40   50   60   70   80   90  100  110  120  130
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGCTTATATGCACTTGCAATCTACTACTAGCC
CD141_P541      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P182      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P401      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGCTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
CD141_P181      ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGTTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGTTTATATGCACTTGCAATCTACTACTAGCC
Consensus       ATGGAGATTTTAAGAAGATCTTCTTCTCTTTGGGTTTTGCCAATTCTTTTGTTGTGcTTCTTTATCAACAATGGAGTATTTGTTGATGCTTCTCACAAAGtTTATATGCACTTGCAATCTACTACTAGCC

                131  140  150  160  170  180  190  200  210  220  230  240  250  260
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      ATGTTGATGCAAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P541      ATGTTGATGCTAGCAAGGTCCACAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAATGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P182      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGTCCAATGTATTACAATGGAGTGTACCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P401      ATGTTGATGCTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAACTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
CD141_P181      ATGTTGATGTTAGCAAGGTCCATAGAACTGGTTATCATTTTCAACCTCCTAAAAATTGGATCAACGATCCAAATGGCCCAATGTATTACAATGGAGTGTATCATTTATTCTACCAGTACAACCCAAAGGG
Consensus       ATGTTGATGctAGCAAGGTCCAtAGAACTGGTTATCATTTTCAACCTCCTAAAAAcTGGATCAAcGATCCAAATGGcCCAATGTATTACAATGGAGTGTAtCATTTATTCTACCAGTACAACCCAAAGGG

                261  270  280  290  300  310  320  330  340  350  360  370  380  390
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P541      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P182      AGCGATATGGGGCAACATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
CD141_P401      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCTGGGTCAGCCACA
CD141_P181      AGCGATATGGGGCAATATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCCGGGTCAGCCACA
Consensus       AGCGATATGGGGCAAtATTGTTTGGGCCCATTCGGTCTCAAAGGACTTGATCAATTGGATCCCACTTGAACCCGCTATCTACCCGTCCAAAGTATTTGACAAGTATGGTACATGGTCcGGGTCAGCCACA

                391  400  410  420  430  440  450  460  470  480  490  500  510  520
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P541      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P182      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P401      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGGTAATAAGACACAAGTCCAAAACTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGATA
CD141_P181      ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGCTAACAAGACACAAGTCCAAAATTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGACA
Consensus       ATCTTGCCAGGCAACAAGCCTGTTATTCTCTACACTGGAATTGTGGATGcTAAtAAGACACAAGTCCAAAAcTATGCAATCCCGGCTAACATGTCTGATCCATATCTTCGTAAGTGGATCAAGCCCGAtA

                521  530  540  550  560  570  580  590  600  610  620  630  640  650
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGN
CD141_P541      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P182      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCTTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGGAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P401      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACCGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTAGGCAGTGTGAGGAATCATAGGGGAAAGGT
CD141_P181      ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACAGCATGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTTGGGAGTGTGAGGAATCATAGGGGAAAGGT
Consensus       ACAATCCATTGATTGTTGCTGACAAAACCATCAACAAAAGCCAATTTCGTGATCCAACAACcGCtTGGATGGGCCGAGATGGAAATTGGAGAATCTTGGTtGGgAGTGTGAGGAATCATAGGGGAAAGGt

                651  660  670  680  690  700  710  720  730  740  750  760  770  780
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCTCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P541      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
CD141_P182      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAAATCCCACTCCACTCGGCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_P401      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTAAAAAATAAAGATGGT
CD141_P181      TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAACACCCACTCCACTCAGCCCCGGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTGAAAAATAAAAATGGT
Consensus       TATAATGTACAAAAGTAATAAGAACTTCATGAAATGGACCAAAGCCAAAcaCCCACTCCACTCaGCcCCgGGTACTGGAAATTGGGAATGTCCTGATTTTTTTCCAGTGTCATTgAAAAATAAAaATGGT

                781  790  800  810  820  830  840  850  860  870  880  890  900  910
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGGTCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P541      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
CD141_P182      TTGGACACGTCATACAATGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATAAGTACATTCCGGATAACACTT
CD141_P401      TTGGACACGTCATACAACGGCAAAGACATTAAACATGTTCTTAAGGTTAGCTTTGATGTTACAAGGTTTGATCATTACACAATTGGTACATATGACACCAAAAAGGATCAGTACTTTCCGGATAGCACTT
CD141_P181      TTGGACACGTCATACAATGGCAAAGACGTTAAACATGTTCTTAAGGTTAGCTTTGATGTTACTAGGTTTGATCATTACACAGTTGGTACATATGACACCAAAAAGGATAAATACTTTCCGGATAACACTT
Consensus       TTGGACACGTCATACAAtGGCAAAGACaTTAAACATGTTCTTAAGGTTAGCTTTGATGTTACaAGGTTTGaTCATTACACAaTTGGTACATATGACACCAAAAAGGATaAaTACtTTCCGGATAaCACTT

                911  920  930  940  950  960  970  980  990 1000 1010 1020 1030 1040
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      CTGTTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P541      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGCGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P182      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P401      CTATTGATGGATGGAAAGGATTGAGACTCGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAGTGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
CD141_P181      CTATTGATGGATGGAAAGGATTGAGACTTGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAATGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA
Consensus       CTaTTGATGGATGGAAAGGATTGAGACTtGACTATGGTAACTATTACGCGTCCAAGACATTCTTTGATAgtGGCAAGAATCGTAGGATTTTGTTGGGTTGGGCTAATGAATCAGATACTGTTGATAACGA

                1041 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P541      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P182      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P401      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACTCTAAGAAAGAAAAAGGTCCAATTAAAT
CD141_P181      TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACACTGAGAAAGAAAAAAGTCCAATTAAAT
Consensus       TGTGAGGAAAGGATGGGCCGGAGTTCACCCTATTCCTCGTAAAATTTGGCTTGATCCTAGTGGAAAACAATTGGTTCAATGGCCTGTTCAAGAATTAGAAACtCTaAGAAAGAAAAAgGTCCAATTAAAT

                1171 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P541      AACAAAAAGTTGAACAAGGGAAAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P182      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCTCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P401      AACAAAAAGTTGAACAAGGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGACAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
CD141_P181      AACAAAAAGTTGAACAAAGGAGAAAAGGTTGAAATCAAAGGAATCACAGTTGCACAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGATAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC
Consensus       AACAAAAAGTTGAACAAgGGAgAAAAGGTTGAAATCAAAGGAATCACAGTTGCaCAGGCTGATGTTGAAGTGATTTTCTCATTCACAAGTTTGGAtAAGGCAGAGCCATTTGATCCTAGTTGGGCTGATC

                1301 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCCGAATTTTCAAGGC
CD141_P541      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_P182      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTCCTAACTTTGGCTTCTAAAAACGTAGAAGAATACACACCCGTTTTCTTTAGAATTTTCAAGGC
CD141_P401      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGGC
CD141_P181      TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTACTAACTTTGGCTTCTAAAAACTTAGAAGAATACACACCCGTTTTCTTCAGAATTTTCAAGAC
Consensus       TTTACGCGCAAGATGTATGCGCCATTAAAGGTTCAACGGTCCAAGGTGGACTTGGGCCTTTTGGGCTcCTAACTTTGGCTTCTAAAAACtTAGAAGAATACACACCCGTTTTCTTcaGAATTTTCAAGgC

                1431 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      TCATGATAAATACAAGGTTCTCATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P541      TCATGATAAATACAAGGTTCTTATGTGTTCTGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P182      TCAAGATAAATACAAAGTTCTTATGTGTTCCGATGCTTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTACAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTT
CD141_P401      TCATGATAAATACAAAGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCGGACAAGAAATTGTCTCTC
CD141_P181      TCATGATAAATACAAGGTTCTTATGTGTTCCGATGCCTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTATAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCAGACAAGAAATTGTCTCTT
Consensus       TCAtGATAAATACAAgGTTCTtATGTGTTCcGATGCcTCAAGGTCAAGCCTAAAGAATGAAACAACTATGTAtAAACCATCATTTGCTGGATATGTAGATGTAGATTTAGCgGACAAGAAATTGTCTCTt

                1561 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690
                |----+----|----+----|----+----|----+----|----+----|----+----|----+----|
CD141_P542      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAATATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAATGGCGCGG
CD141_P541      AGAAGTTTGATTGATCATTCGGTAGTCGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACATTGGCGATATTTGACAAAGCACATTTATTTGTGTTCAACAACGGCGCAG
CD141_P182      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P401      AGAAGTTTGATTGATCATTCGATAGTGGAAAGTTTTGGTGCCGGAGGAAAAACATGCATTACATCAAGAGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
CD141_P181      AGAAGTTTGATTGATCATTCGGTAGTGGAAAGTTTTGGTGCTGGAGGAAAAACATGCATTACATCAAGGGTTTATCCAACGTTGGCGATATTTGACAAAGCACATTTATTTGCATTCAACAACGGCGCGG
Consensus       AGAAGTTTGATTGATCATTCGgTAGTgGAAAGTTTTGGTGCtGGAGGAAAAAcATGCATTACATCAAGgGTTTATCCAACgTTGGCGATATTTGACAAAGCACATTTATTTGcaTTCAACAAcGGCGCgG

                1691 1700 1710 1720 1730 1740 1749
                |----+----|----+----|----+----|---|
CD141_P542      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P541      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P182      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P401      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
CD141_P181      AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
Consensus       AGAGAATCACAATTGAGACTCTAAATGCTTGGAGCATGGCTAATGCAAAGTTGCACTAG
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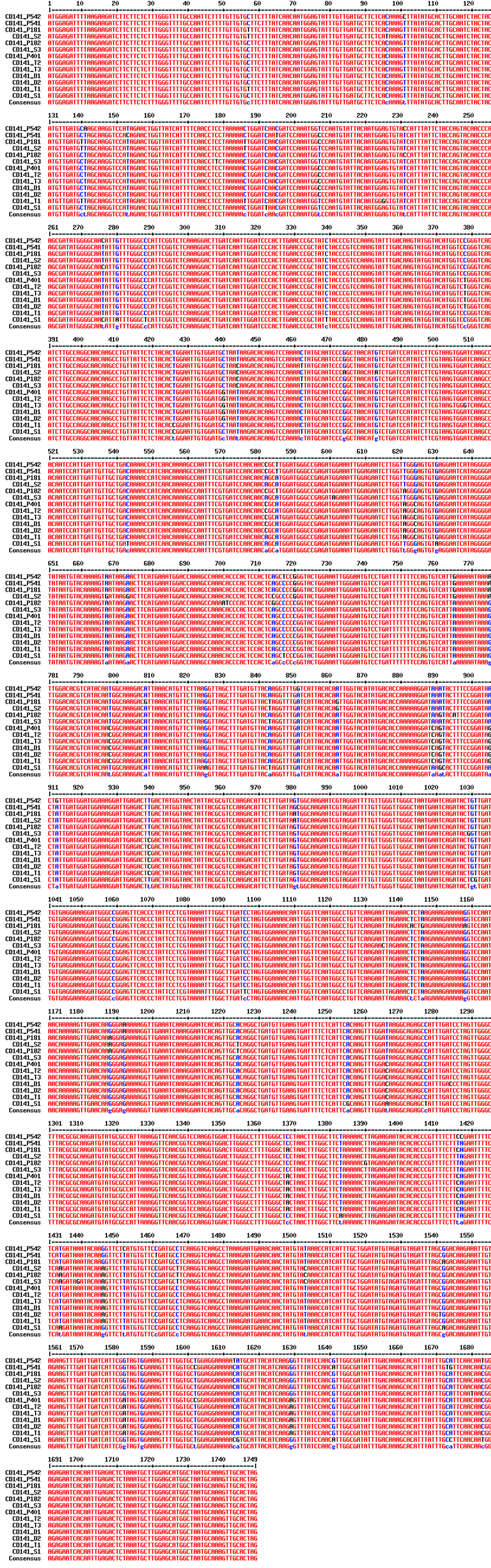

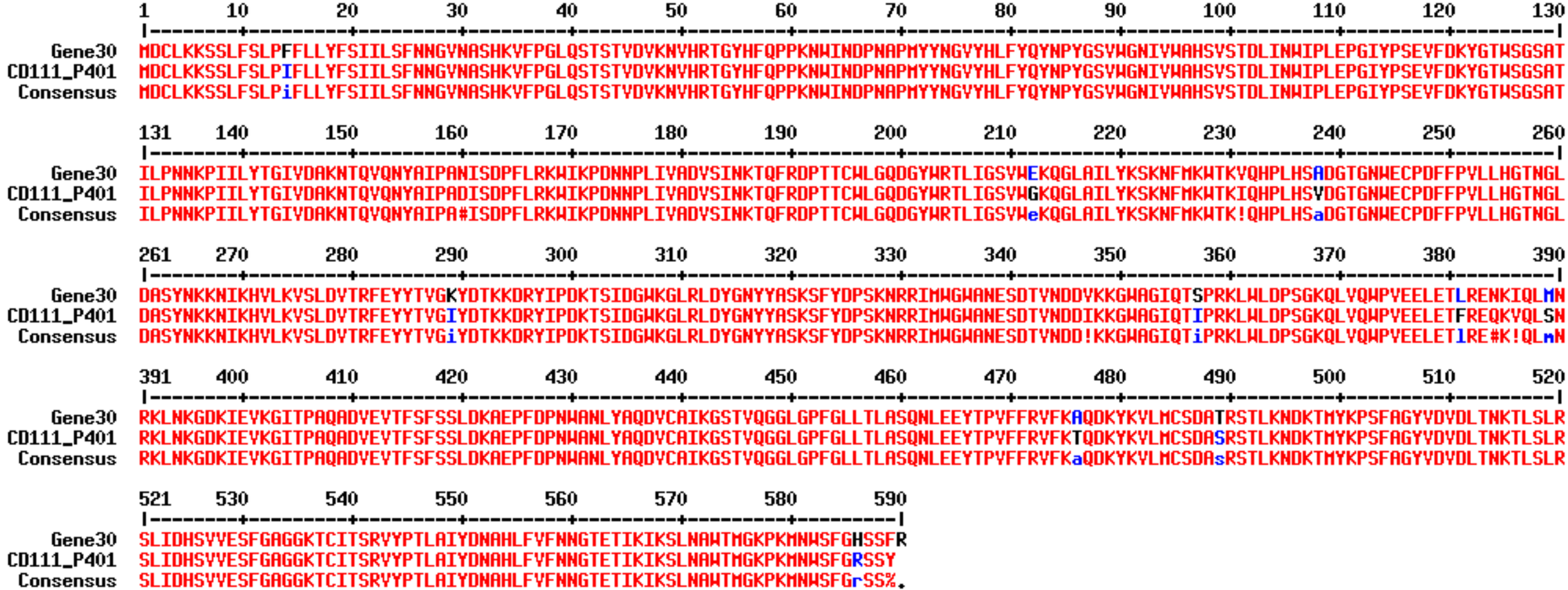
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Gene30 MDCLKKSSLFSLPFFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
CD111_P401 MDCLKKSSLFSLPIFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
Consensus MDCLKKSSLFSLPiFLLYFSIILSFNNGVNASHKVFPGLQSTSTVDVKNVHRTGYHFQPPKNWINDPNAPMYYNGVYHLFYQYNPYGSVWGNIVWAHSVSTDLINWIPLEPGIYPSEVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
Gene30 ILPNNKPIILYTGIVDAKNTQVQNYAIPANISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWEKQGLAILYKSKNFMKWTKVQHPLHSADGTGNWECPDFFPVLLHGTNGL
CD111_P401 ILPNNKPIILYTGIVDAKNTQVQNYAIPADISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWGKQGLAILYKSKNFMKWTKIQHPLHSVDGTGNWECPDFFPVLLHGTNGL
Consensus ILPNNKPIILYTGIVDAKNTQVQNYAIPA#ISDPFLRKWIKPDNNPLIVADVSINKTQFRDPTTCWLGQDGYWRTLIGSVWeKQGLAILYKSKNFMKWTK!QHPLHSaDGTGNWECPDFFPVLLHGTNGL
261 270 280 290 300 310 320 330 340 350 360 370 380 390
Gene30 DASYNKKNIKHVLKVSLDVTRFEYYTVGKYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDVKKGWAGIQTSPRKLWLDPSGKQLVQWPVEELETLRENKIQLMN
CD111_P401 DASYNKKNIKHVLKVSLDVTRFEYYTVGIYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDDIKKGWAGIQTIPRKLWLDPSGKQLVQWPVEELETFREQKVQLSN
Consensus DASYNKKNIKHVLKVSLDVTRFEYYTVGiYDTKKDRYIPDKTSIDGWKGLRLDYGNYYASKSFYDPSKNRRIMWGWANESDTVNDD!KKGWAGIQTiPRKLWLDPSGKQLVQWPVEELETlRE#K!QLmN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
Gene30 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKAQDKYKVLMCSDATRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
CD111_P401 RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKTQDKYKVLMCSDASRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
Consensus RKLNKGDKIEVKGITPAQADVEVTFSFSSLDKAEPFDPNWANLYAQDVCAIKGSTVQGGLGPFGLLTLASQNLEEYTPVFFRVFKaQDKYKVLMCSDAsRSTLKNDKTMYKPSFAGYVDVDLTNKTLSLR
521 530 540 550 560 570 580 590
Gene30 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGHSSFR
CD111_P401 SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGRSSY
Consensus SLIDHSVVESFGAGGKTCITSRVYPTLAIYDNAHLFVFNNGTETIKIKSLNAWTMGKPKMNWSFGrSS%.


1 10 20 30 40 50 60 70 80 90 100 110 120 130
Gene40 MEILRKSSSLWALPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIIWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
CD141_P401 MEILRRSSSLWVLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNIVWAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
Consensus MEILRrSSSLWaLPILLLCFFINNGVFVDASHKVYMHLQSTTSHVDASKVHRTGYHFQPPKNWINDPNGPMYYNGVYHLFYQYNPKGAIWGNI!WAHSVSKDLINWIPLEPAIYPSKVFDKYGTWSGSAT
131 140 150 160 170 180 190 200 210 220 230 240 250 260
Gene40 ILPGNKPVILYTGIVDANKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
CD141_P401 ILPGNKPVILYTGIVDGNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
Consensus ILPGNKPVILYTGIVDaNKTQVQNYAIPANMSDPYLRKWIKPDNNPLIVADKTINKSQFRDPTTAWMGRDGNWRILVGSVRNHRGKVIMYKSNKNFMKWTKAKHPLHSAPGTGNWECPDFFPVSLKNKDG
261 270 280 290 300 310 320 330 340 350 360 370 380 390
Gene40 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDKYFPDNTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTRDNDVRKGWAGVHPIPRKIWLDSSGKQLVQWPVQELETLRKKKVQLN
CD141_P401 LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDQYFPDSTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTVDNDVRKGWAGVHPIPRKIWLDPSGKQLVQWPVQELETLRKKKVQLN
Consensus LDTSYNGKDIKHVLKVSFDVTRFDHYTIGTYDTKKDqYFPDnTSIDGWKGLRLDYGNYYASKTFFDSGKNRRILLGWANESDTrDNDVRKGWAGVHPIPRKIWLDpSGKQLVQWPVQELETLRKKKVQLN
391 400 410 420 430 440 450 460 470 480 490 500 510 520
Gene40 NKKLNKGEKVEIKGITVAQADVEVIFSFASLEKAELFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAQDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
CD141_P401 NKKLNKGEKVEIKGITVAQADVEVIFSFTSLDKAEPFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAHDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
Consensus NKKLNKGEKVEIKGITVAQADVEVIFSFaSL#KAElFDPSWADLYAQDVCAIKGSTVQGGLGPFGLLTLASKNLEEYTPVFFRIFKAqDKYKVLMCSDASRSSLKNETTMYKPSFAGYVDVDLADKKLSL
521 530 540 550 560 570 58882
Gene40 RSLIDHSVVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
CD141_P401 RSLIDHSIVESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH
Consensus RSLIDHS!VESFGAGGKTCITSRVYPTLAIFDKAHLFAFNNGAERITIETLNAWSMANAKLH