

Each taxon name includes the number of the TPM paralog within a given species (if any) followed by the number of the MATE exon, e. g. Tru119d corresponds to the MATE exon 9d of the TPM1.1 of *Takifugu rubripes*. Species are abbreviated as follows: Aga, *Anopheles gambiae*; Ame, *Apis mellifera*; Bf, *Branchiostoma floridae*; Bma, *Brugia malayi*; Cbr, *Caenorhabditis briggsae*; Cca, *Capitella capitata*; Cel, *Caenorhabditis elegans*; Cin, *Ciona intestinalis*; Dme, *Drosophila melanogaster*; Dpu, *Daphnia pulex*; Hro, *Helobdella robusta*; Lgi, *Lottia gigantea*; Mbr, *Monosiga brevicollis*; Mmu, *Mus musculus*; Nve, *Nematostella vectensis*; Sko, *Saccoglossus kowalevskii*; Spu, *Strongylocentrotus purpuratus*; Tad, *Trichoplax adhaerens*; Tca, *Tribolium castaneum*; Tru, *Takifugu rubripes*; and Xtr, *Xenopus tropicalis*.

Exon 1

```
#NEXUS
[ Title ]
begin data;
  dimensions ntax=75 nchar=55;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Mbe1B -----MAM--EKIKAKMLALREEADANA EKVEQLEEKLRANERASA
Tad11B -----M--EAVKKK MAGLRKEAEDALQRAEQCEDQLRDTVQREEE
Nve11B -----M--ETIKKKMATLRQTLDEAEARA AKAEDELKNANDRADS
Spu11B -----M--EAI RKKMASLRSLDESLEKKLELEKLRDRDRADA
Spu21B -----MSQL--SNIKERLGLIQSDIDTSNGAI RELQTELEEH SQRAED
Sko1B -----M--ESIRKKVAALRAEAEAAQDRSEELERSLKDESARAEA
Bfl1B -----M--EAIKKKMQTLKSEAEQASERADFLEKMKVDERERADT
Bfl21B -----M--EAVKKKLANLRQEAELAKEKCEEAENARKEAEDRAEQ
Cin41B -----M--DKIKGKISCMISELDNKEEAIEKLTEDLRLADIKRRC
Cin51B -----M--ESIKKKISNLKNELDAKQDKIDELTDKLIKIEEELRA
Cin61B -----M--ENIKMKIAKLKAESDEKENQICDLS DQLKKVTEERKQ
Tru111B ----MAG----VTSL--EAVKRRIRVLQEKTDAAEERA EKQLQRELLAHKKEREQ
Tru121B ----MAA----VSSL--EAVKKKIKSLQE QADVAEDRAASLQRDLNKETRAREA
Xtr11B ----MAG----ITSL--EAVKRRIKCLQDQADAAEERA EKLRERDMERKQREA
Mmu1B ----MAG----SSSL--EAVRRKIRSLQE QADAAEERAGSLQRELDQERKLRER
Xtr31B ----MAG----VNSL--EAVKKKI QALQQQADDAEERA QLLQRELDSEERMRDK
Mmu31B ----MAG----TTTI--EAVKRRIQV LQQQADDAEERAERLQREVEGERRAREQ
Tru411B ----MAS----VNSL--DAVRRKI QTLQQQADDAEDRAQVLRQLDSERELREK
Tru421B ----M--EMVKKKI QTLQQQVDEAEERELAIQRELDSELELELREK
Xtr31B ----MSGG--GMSSI--EAVKRRIQV LQQQADEAE EKSERLRCRDLEGEKRARET
Mmu41B ----MAG----LNSL--EAVKRRIQAL QQQQADDAEDRAQGLQRELDGERERREK
TruX1B ----MSG----SISV--DAVKKKIKV LQDQVEEAMERAERLQKEVEKERRTREE
Dpu1B ----MSS----QGTL--DVLKKKMRQTKEEAEKY QEEAEYRKKLQIEIRRRRE
Tca1B ----MTTNI---QQGSL--DVLKKKMRQTKEEMERYKDECEEY NKRLHAECMRREE
Ame11B ----MSTQV---QGTL--DVLKKKMRQTKEEMEKYKDECEEY QKRLQVEVIRREE
Aga1B ----MAANV--QQSGNLL--DVLKKKMRQTKEEMEKYKDECEEFHKKLQNEVMRREE
Dme1B ----MTTSI---PQGTLL--DVLKKKMRQTKEEMEKYKDECEEFHKKRLQLEVVRRRE
Bma1B ----MSKPEKAGAQQTSL--DVLKKKMRQAREEAEAAKDEADEVKRLLEERKKRED
Cel1B ----MSKVNKEG AQQTSL--DVLKKKMRQAREEAEAAKDEADEVKRQLEEERKKRED
Cbr1B ----MSKVNKEG AQQTSL--DVLKKKMRQAREEAEAAKDEADEVKRQLEEERKKRED
Lgi1B ----MS--VLGNNNPSGVL--GNIKTKMAGLKTQI DDLSEENTRLRRDLGDKDSRINE
Cca1B ----MS-----GSAL--NVLKGKMQNLREAEKYKDQFDEKCRELTTEEQSRSE
Hro81B MFKVNNSNHNGGALVVS SLKQKMQTLREELERYK DLYDDKCREVNRERSLRND
Hro71B MATPTASS----GGAL--TSLMKMQSLRDEM DKTLDLYDAKCNELDLEKGLRAK
Spu11A -----M--ETIKKKMLSLKSEKEVA IDAKEVAEADLRTSKEREEQ
Sko1A -----M--EVVKKKMQSLRMEKEAALDLR DQAEQEMRNAIERAEK
Bfl1A -----M--DAIKKKMLMLKNDKENALDRAEQAE QAMKDAQEKNVK
Cin11A -----M--EAIKKKMTMLKLDKENA IDRAEQAETDKKSAEDKATG
Cin21A -----M--EAIKKKMTMLKLDKENALDRAEQAE IDRKSAESKAKE
Cin31A -----M--ESIHKHMEGLIKDKDEAIEKAI SLENEKRQMEDNAKE
Tru111A -----M--DAIKKKMQMLKLDKENALDRAEQAE TDKKAEDRSKQ
Tru121A -----M--DAIKKKMQMLKLDKENAM DRAEQAESDKKAAEDRSKQ
Xtr11A -----M--DAIKKKMQMLKLDKENALDRAEQAE ADKKGAEKSKQ
Mmu11A -----M--DAIKKKMQMLKLDKENALDRAEQAE ADKKAEDRSKQ
Tru21A -----M--EAIKKKMQMLKLDKENA IDRAEQAEGDKKQAE DKCKQ
Xtr21A -----M--DAIKKKMQMLKLDKENA IDRAEQAEGDKKQAE DRCKQ
Mmu21A -----M--DAIKKKMQMLKLDKENA IDRAEQAEDKKQAE DRCKQ
Tru31A -----M--EAVKKKMLMLKLDKENALDRAEQAE ADKKAEDRSKQ
Xtr31A -----M--EAIKKKMQMLKLDKENA IDRAEQAEADKKAEDKCKQ
Mmu31A -----M--EAIKKKMQMLKLDKENA IDRAEQAEAEQKQAE ERSKQ
Tru411A -----M--EAIKKKMQMLKLDKENA IDRAEQAETDKKAAEDKCKQ
Tru421A -----M--DAIKKKMQMLKLDKENA IDRAEQSESDQKS AEKCKQ
Xtr31A -----M--EAIKKKMQMLKLDKENAL DRAEQAEAEQKQVEEKSKQ
Dpu1A -----M--DAIKKKMQAMKAEKNAMDRAD TCEQQSRDANLRAEK
Tca1A -----M--DAIKKKMQAMKLEKDNALDRAI FNEQQAKDANLRAEK
Ame11A -----M--DAIKKKMQGMKLEKDNAMDRALL CEQQARDANARA EK
```

```

AgalA -----M--DAIKKKMQAMKLEKDNALDRALLCEQQARDANLRAEK
Dme1A -----M--DAIKKKMQAMKVVDKDGALERALVCEQFARDANTRAEK
Tca21A -----M--DAIKKKMQAMKLEKDNAQDKADAMEGQAKDANLRVEK
Ame21A -----M--DAIKKKMQAMKLEKDNAMDKADACEAQAKEANMRADK
Ame31A -----M--EAIKKKIAALKQEMDAANEKVEANEAKARSENFRADK
Ame41A -----M--NAIKKRLQMLKIEKDLAMDKADLCDQQAQAKEANRREEK
Aga21A -----M--DAIKKKMQAMKIEKDNAQDKADTCENQAQAKEANLRADK
Dme21A -----M--DAIKKKMQAMKLEKDNAIDKADTCENQAQKANDSRADK
Bma1A -----M--DAIKKKMQAMKIEKDNALDRADAAEEKVRQMTDKLER
CellA -----M--DAIKKKMQAMKIEKDNALDRADAAEEKVRQITEKLER
Cbr1A -----M--DAIKKKMQAMKIEKDNALDRADAAEEKVRQITEKLER
Lgi1A -----M--DAIKKKMLAMKMEKENALDRAEQLEQKLRDTEEQKSK
Cca1A -----M--DAIKKKMQAMKLEKESALDKADQLEQKLTQKETNEK
Hro11A -----M--ETIKKKMQAMRLERENAILKAQTLEEKVAEQKGINER
Hro21A -----M--DAIKKKMQVMKTEKDKALVRADQLEEKVSEQKALNEK
Hro31A -----M--EAIKKKKMQAMKLEKENAFDKAEQLEQKLAQKTVHEK
Hro41A -----M--NAIKKKVHTMKTLLKDSAGDEVELLEQKLLKYKAIGEK
Hro51A -----M--DAIKKKMQAMKLEKETAFDKCDQLEQKLAQKVVYEK
Hro61A -----M--TAIKKKMHGMKTLKESVDFEVDQLDQKLLQKAIYEK
;
end;
Exon2

#NEXUS
[ Title ]
begin data;
  dimensions ntax=44 nchar=42;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Spul2  LNDTIKERDDRIKQVELELDSTTDKLSQAAFDAAEAQGV
Sko2   GDEENKELMKKMRNLELELDTTQDKLSQAEKLLDAAEKTA
Bfl2   LEDEINDLNKKIRMEVELELDKAQESLKDQTELEAATKKAAD
Cin12  LEEELQGLQKRLKATEDELDTSQEKLRTAIENLENAEKKAAD
Cin22  LEEQLLGLGKRVKATEDELESAQEKLRLANEDLEKAEKKAAD
Cin32  LEEETSQITKKIVSLEDELQVMEQHRLSIEKLDVAEKVATD
Tru112a LEDELRELEKKLRVTEDEDRDRVTEEFQTAEEKLLTAAEVATK
Xtr12a LEEEIAQLEKQLRVTEDETRDKIMDDFHHAESLAAEEKATK
Mmu12a LEEEDIAAKEKLLRASEDERDRVLEELHKAEDSLAADETA
Tru112b LEDDLVALQKKLKGTEDELDFSEALKDAQEKLELAEKKATD
Tru122b LEDDLVALQKKLKGTEDELDFSEALKDAQEKLELAEKKATD
Xtr12b LEDELVALQKKLKGTEDELDFSEALKDAQEKLELAEKKATD
Mmu12b LEDELVSLQKKLKGTEDELDFSEALKDAQEKLELAEKKATD
Tru22  LEEELGLQKKLKGVEDELDFSEALKDAQEKLEQAEKKAAD
Xtr22  IEEEVMAQKKTKSTEDVEKYSSEVKEAQEKLEMAEKKATD
Mmu22  LEEEQALQKKLKGTEDEVEKYSSEVKDAQEKLEQAEKKATD
Tru32  HEDELLQMKKLLKGTEDELDFSEALKDAQEKLEVAEKKAAD
Xtr32  VEDELVALQKKLKGTEDELDFSEALKDAQEKLEQADKKATD
Mmu32  LEDELATMQKKLKGTEDELDFSEALKDAQEKLELAEKKAAD
Tru412 LEEELLDLQKKMKQTEDELDFSEGLKDAQEKLELSEKTAAD
Tru422 IEDELLALQKKLKFTEDEVDFKYSSEALKDAQDKLEMESEKAGD
Xtr32  LEDELGLQKKLKGTEDELDFSEALKDAQEKLEVAEKKAAD
Dpu2   SEEEVRAQKKMQQLENDLQQAQENLLAANSKLEEKDKALQ
Ame2   AEEEARALQKKIQTIENELDQTEALMQVNAKLEEKDKALQ
Tca2   LEEEARLQKKIQTIENELDQTEQLTQVNGKLEEKALQ
Aga2   AEEEARQLQKKIQAIENLDVTEQETLMQVNTKLEEKALQ
Dme2   AEEEARQLQKKIQTVENELDQTEALTLVTKLEEKKALQ
Ame22  VNEEVGELQKKLAQVEGDLEANKQNLQANKDLEEKKALTN
Ame32  LNDDVRDLAKKLTQLERDYEVAKANLEQSTADLEQCEKSWK
Ame42  LRDEVRELAKKLVQMERDLELSKAQLEKSNRDLQKERVYIV
Tca22  LNEELRELQKKLSQVEGDLTTTKNSLEQANKDLEEKKALTN
Aga22  IMEEVADLTKRLEQVTDHEKFKASLEQATKDSSEKDKLLTS
Dme22  LNEEVRDLEKKFVQVEIDLVTAKEQLEKANTELEEKLLTA
Bma2   IEEELRDTQKKMQTENDLKAQEDLAVANTNLEEKEKQVQ
Cbr2   VEEELRDTQKKMTQTGDDLKAQEDLSAATSKLEEKEKTVQ
Cel2   VEEELRDTQKKMTQTGDDLKAQEDLSAATSKLEEKEKTVQ
Lgi2   IEEDLNTLQKKYANLENDFDTANESLAEANTKLEEVSEKANE
Cca2   QEEEIQNQKRI SALEGLDQAQTQLEEATQKLENTEKQLGN
Hro12  QEEDIQTLQKTI AQLESELDEAQTHTLAEANTKLESTEKQLTN
Hro22  QEEEIQNQKQIQQLEGLDQAQTQLAEATSKLESTEKQLGN
Hro32  SSEEISNLQKRIVQLESDEHTRVQLKQTEKLETVHNSLAS
Hro42  SSEEISNLQKRIVQLESDEHTRVQLKQTEKLETVHNSLAS
Hro52  SAEIITNLQKRIVQLEADTEAAKASLDEQNQKLEAVSNDLTA
Hro62  QDEEILQLNKRIVQIQTDLGVVQQAQEAATEKLDATTKQLTT
;
end;

```

Exon3

#NEXUS

[Title]

begin data;

dimensions ntax=56 nchar=44;

format missing=? gap=- matchchar=. datatype=protein interleave=yes;

matrix

[!Domain=Data;]

Mbe3 AEAANDAKRKLTLTEDDLKAEERLQSMQTRRLRDAEQEAEDAS
TadI3 VKEKIDELNKEIEETEQQLLDDRESKLAETLKTLLAEETKTDEHE
NveI3 AETEVAAALTKQLQLEDDDLAAESKLADTQGQLTEAEKQADESE
Spu13 AEAQVKNLNSKLIILEEDNGKQEEALSDDRRLRLETIEVEADENL
Spu23 FEEQAKTLNMKCRDLEDVMSDREDELQRKLLKIDEIEAESDENS
Sko3 AEAQVSSLQRRLLDEELERAQERYQVAADKLADIEKAADESE
Bfl13 AEAQVSSLNRRRIQLVEEELDRAQERLNSTVEKLTDESEKAADESE
Bfl23 AENDIESLRRKMLLEADLDTAETSLKETNERNOELESRLDEAE
Cin13 AEQEVASLNRRITLVEEELDRAQERLTISLSKLEAEKAADESE
Cin23 AEEVSAALNRRICLVEEELDQAQERLTISLQKLEAEKAADESE
Cin33 SELEVNAQTRRMQLLEEEEMQVTERLDEAVAKLEVAEKAAESES
Cin43 VEEENINLKHQLNAKENFICKLEPLLEDETVRKLASFEEERESANE
Cin53 AEDQNQDLERKRLRVEGDLDRADEKLTIAKAQLSLEQQSDDGS
Cin63 FEEVNRSLSNKISTNDTDIERLELQNEELKRSNAERELDEVQ
Tru113 AEAQVSSLNRRRIQLVEEELDRAQERLGTALTKLEAEKAADESE
Tru123 AEGDVASLNRRRIQLVEEELDRAQERLATALTKLEAEKAADESE
Xtr13 AEGDVASLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Mmu13 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Tru23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Xtr23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Mmu23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Tru33 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Xtr33 AEGEVAALNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Mmu33 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Tru413 AEGEVAALNRRRIQLVEEELDRAQERLAVLQKLEAEKAADESE
Tru423 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Xtr33 AEAQVSSLNRRRIQLVEEELDRAQERLSTALQKLEAEKAADESE
Mmu43 AEGDAAALNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
TruX3 AEMEVTTLSNRLQNEEDTLDRTOERLADALRKKVEEVEKVADESE
Dpu3 AEGEVAALNRRRIQLVEEELDRAQERLNTATTKLEAEKAADESE
Ame3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Tca3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Aga3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Dme3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Ame23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Tca23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Aga23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Ame33 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Ame43 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Dme23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Bma3a AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Bma3b AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Cbr3a AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Cbr3b AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Cel3a AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Cel3b AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Lgi3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Cca3 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro13 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro23 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro33 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro43 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro53 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro83 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro73 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
Hro63 AEAQVSSLNRRRIQLVEEELDRAQERLATALQKLEAEKAADESE
;

end;

Exon4.1

#NEXUS

[Title ex4a]

begin data;

dimensions ntax=70 nchar=15;

format missing=? gap=- matchchar=. datatype=protein interleave=yes;

matrix

```
[!Domain=Data;]
Mbe4 KLRLEATQDNDFGK
TadI41 ARAVLESRTNTSNTK
NveI41 ARKVLENRGASDEER
Spu141 ARKVLETRSASDDDK
Spu241 FSRVLKMENTNTDR
Sko41 ARKVLENRGLSDDDR
Bfl141a ARKVLENRGAADDDR
Bfl141b ARKVLENRQGADEDK
Bfl1241 SRQALEHRSTEDDK
Cin14 GRKVLENRSLKDEER
Cin24 GRKVLENRALKDEEK
Cin34 GRKVIEGRSFKDEET
Cin441 IIQKLESDYETSVIK
Cin54 AYKSLNEFNSSVNK
Cin64 ELKKLQSEHTASAER
Tru114 GMKVLENRAMKDEEK
Tru124 GMKVLENRAMKDEEK
Xtr14 GMKVLENRALKDEEK
Mmu14 GMKVIESRAQKDEEK
Tru24 GMKVLENRASKDEEK
Xtr24 GMKVLENRATKDEEK
Mmu24 GMKVLENRAMKDEEK
Tru34 GMKVLENRALKDEEK
Xtr34 GMKVLENRAMKDEEK
Mmu34 GMKVLENRALKDEEK
Tru414 GMKVLENRAMKDEEK
Tru424 GMKVLENRAMKDEEK
Xtr34 GMKVLENRALKDEEK
Mmu44 GMKVLENRAMKDEEK
TruX4 GMKVLENRAQKDEEK
Dpu4a IRKALENRTNMEDDR
Dpu4b MRKVLENRSLSDEER
Ame4a IRKALENRTNMEDDR
Ame4b ARKILENRS LADEER
Tca4a IRKALENRTNMEDDR
Tca4b QRKVLENRSLADEER
Aga4a IRKALENRTNMEDDR
Aga4b ARKVLENRALADEER
Dme4a IRKALENRTNMEDDK
Dme4b ARKILENRS LADEER
Ame24 MCKVLENRAQQDEER
Ame34 MCKVLEDRSRLDEER
Ame44 ICKVLENRSKQDEER
Tca24 MCKVLENRSQQDEER
Aga24 MCKVLENRSQQDEER
Dme24 MCKVLENRSQQDEER
Bma4a ARKSMETRSQQDEER
Bma4b ARKALENRIDVDHDR
Bma4c VRKVMENRSFQDEER
Cbr4a ARKSMETRSQQDEER
Cbr4b SRKALSNQIELDDDR
Cbr4c VRKVMENRSLQDEER
Cel4a ARKSMETRSQQDEER
Cel4b SRRALSNQIDMDDDR
Cel4c VRKVMENRSLQDEER
Lgi4a QKRTVENKLAAAEK
Lgi4b GRKVLESRSLSDDER
Lgi4c GRKVLENRSQGDEER
Cca4a QRVVLDLRRRTANEDR
Cca4b ARLALDSRSLATDDC
Cca4c NRKALESRSLADDER
Cca4d GRKVLENRNITDEER
Hro14 ARKSLESRS LADDER
Hro24 NRKSLETNSLMNDR
Hro34 GIKVLENRFTLEDEK
Hro44 GIKVLENRFTLEDEK
Hro54 GIKVLENKMI TEEER
Hro84 LKISNECFKNLDDEK
Hro74 ARKALESRQNMDDDK
Hro64 GRKVLENRIAIDEER
;
end;
Exon4.2
```

```
#NEXUS
[ Title ex4b]
```

```
begin data;
  dimensions ntax=70 nchar=24;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
Mbe4 AEALEDKYKDLKRQFDDVERSHAE
TadI42 LEELEQLNETLAAREEAETKYKE
NveI42 LASLERQYNDALERTEEAEKQYEE
Spu142 IIDLEQRMKENASRIEELDRHSE
Spu242 IKDLETMMDQQTADIERLDKVNNSD
Sko42a ILDLERLVNESRSMAEEADHKFEE
Sko42b ITELENLVKTTRQMAEDADVKYEE
Bfl142 MELLDMLREAKMIAEEADRKYEE
Bfl242 SSQMETDLKLAKEAKEEMELKYEE
Cin14 LEVQEIQLTEAKNIAEDADRKYVE
Cin24 LEAQEVSLNEAKSVAEDADKKYEE
Cin34 LELQEIQLRDAKZIAEDADRKYEE
Cin442 CEKLEDQLKEIRFTSEETGRKYEE
Cin54 YEAHLDDLRSKMLAEEMSRKYEE
Cin64 CDDLTEELKLRKMDLDEVVTNYDD
Tru114 MELQEIQLKEAKHIAEEADRKYEE
Tru124 MELQEIQLKEAKHIAEEADRKYEE
Xtr14 MELQEIQLKEAKHIAEEADRKYEE
Mmu14 MEIQEIQLKEAKHIAEDADRKYEE
Tru24 MEIQEMQLKEAKHIAEEADRKYEE
Xtr24 MVDQEQQLREAKNIAEESDRKYEE
Mmu24 MELQEMQLKEAKHIAEDSDRKYEE
Tru34 MELQEIQLKEAKHIAEDSDRKYEE
Xtr34 MEIQELQLKEAKHIAEEADRKYEE
Mmu34 MELQEIQLKEAKHIAEEADRKYEE
Tru414 MEIQEMQLKEAKHIAEEADRKYEE
Tru424 MEIQELQLKEAKHIAEEADRKCDE
Xtr34 MELQEIQLKEAKHIAEEADRKYEE
Mmu44 MEILEMQLKEAKHITDEADRKYEE
TruX4 LELLEYQLNEAKKIAEEADLKYEE
Dpu4a VAI LEAQVAQAKLIAEEADKKYEE
Dpu4b MDALENQLKEARFLAEEADKKYDE
Ame4a VSLLEQQLAQAKLIAEEADKKYEE
Ame4b MDALENQLKEARFLAEEADKKYDE
Tca4a VGI LETQLSQAKLIAEEADKKYEE
Tca4b MDALENQLKEARFLAEEADKKYDE
Aga4a VGILEAQLAQAKLIAEEADKKYEE
Aga4b MDALENQLKEARFMAEEADKKYDE
Dme4a VALLENQLAQAKLIAEEADKKYEE
Dme4b MDALENQLKEARFLAEEADKKYDE
Ame24 MDQLTNQLKEARLLAEDADGKSDE
Ame34 MEKLMQELKDARLIAEDADAKSEE
Ame44 MDQLMTQLKEARLIAEDADTKSDE
Tca24 MDQLTNQLKEARLLAEDADNKSDE
Aga24 MDQLSNQLKEARMLAEDADTKSDE
Dme24 MDQLTNQLKEARMLAEDADTKSDE
Bma4a ANVLEIQVDEAKMIADEADRKYEE
Bma4b CGELEQKLREAQALLAETENKSDE
Bma4c ANTVESQLKEAQLLAEEADRKYDE
Cbr4a ANFLETQVDEAKVIAEDADRKYEE
Cbr4b CAELERKLRECQSILHETENKAAE
Cbr4c ANTVEAQLKEAQLLAEEADRKYDE
Cel4a ANFLETQVDEAKVIAEDADRKYEE
Cel4b CSDLERKLRECQSILHETENKAAE
Cel4c ANTVEAQLKEAQLLAEEADRKYDE
Lgi4a LDEYETALKTAQAHATDTETRFEE
Lgi4b IDQLEAQLKEAKYIAEDAERKYDE
Lgi4c IELEKQFEEAKVIAEDVDRKYDE
Cca4a IAELEEALKAAQFCESETENKYQE
Cca4b ISVLESKLRDVTVSASESANKYDE
Cca4c LTFLEAQLKEAKFIAEDADRKYDE
Cca4d IVQVERELEETIILGEEADRKFEE
Hro14 LTFLETQLKEAKYISEDAGRKFDE
Hro24 ITFLEEQLKEAKYIAEDAGSKLEE
Hro34 IQQLEHEIEDVILVGEDSDRRYEE
Hro44 IQQLEHEIEDVILVGEDSDRRYEE
Hro54 IQQLEKELEETIMAGEDSDRRFEE
Hro84 ISSLEDQIRTLRLAADTAEKKYDE
Hro74 MLKLEQWLKESKASCEDAEKKYED
Hro64 MVILEKELEVITILFGEDADRKYEE
;
```

```

end;
Exon5

#NEXUS
[ Title ex5]
begin data;
  dimensions ntax=60 nchar=23;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Mbe5   ATRKLQLTEDDLEKAEERAEEVAE
TadI5  ISEKLEELEKELEEEEEKADTAE
NveI5  ISERLQELENELEEAQKADAAE
Spu15  SQRKLQMTQQLEVAEAKNTECE
Spu25  LQSKCQQMEDKLEDAEDNSIRLK
Sko5   VARKLVVTEAELERAEERAEEVAE
Bfl15  VARKLVITEGDLERAEERADLAE
Bfl25  VSRKLVMAEQQLDNMEDKYKEAE
Cin15  VARKLVMVEAELEERGEERAELAE
Cin25  VARKLVNVESDLERGEERAELAE
Cin35  VGRKLRMVENDLERVLDRAEIYE
Cin45  ATRRLTFMDTELEKSEQRIEKAE
Cin55  VARRLVLMDSLEKAEERCSVSE
Cin65  AMRRIKVL DGNCRLLDDKVQALE
Tru115 VARKLVIIEGDLERTEERAELAE
Tru125 VARKLVIIESDLERTEERAELSE
Xtr15  VARKLVIIEGDLERAEERAELSE
Mmu15  VARKLVIIESDLERAEERAELSE
Tru25  VARKLVILEGDLERSEERAEEVAE
Xtr25  VARKLVVLEGDLEERSEERAEEVAE
Mmu25  VARKLVILEGELERSEERAEEVAE
Tru35  VARKLVIVEAELEERTEERAELAE
Xtr35  VARKLVILEGELERAEERAEEVSE
Mmu35  VARKLVIIEGDLERTEERAELAE
Tru415 VARKLVILEGELERAEERAELSE
Tru425 VTRKLLVLEGELERAEERAEEVSE
Xtr35  VARKLVIIEGDLERTEERAELAE
Mmu45  VARKLVILEGELKRAEERAEEVSE
TruX5  NARKLTRVEGELEERAEDRAAKSE
Dpu5a  VARKLAMVEADLERAEERAETGGE
Dpu5b  VARKLVMLEADLERAEERAEEQGE
Ame5a  VARKLAMVEADLERAEERAEEAGE
Ame5b  VARKLVMMEQDLERAEKAEELSE
Tca5a  VARKLAMVEADLERAEERAEEAGE
Tca5b  VARKLVLMQDLERAEERAEEQSE
Aga5a  VARKLAMVEADLERAEERAEEAGE
Aga5b  VARKLVLMQDLERSEEEKVEMNE
Dme5a  VARKLAMVEADLERAEERAEEQGE
Dme5b  VARKLVLMQDLERSEEEKVELSE
Ame25  VSRKLAFVEDELEVAEDRVKSGE
Ame35  ISKKLALVEEELEGAEEERVKTSE
Ame45  ISRKLAFVEDELEAAEERVKSSE
Tca25  VSRKLAFVEDELEVAEDRVKGGD
Aga25  VSRKLAFVEDELEVAEDRVKSGE
Dme25  VSRKLAFVEDELEVAEDRVRSGE
Bma5   VARKLAMVEADLERAEERAEEAGE
Cbr5   VARKLAMVEADLERAEERAEEAGE
Cel5   VARKLAMVEADLERAEERAEEAGE
Lgi5a  AARKLAITEVDLERAEATREAAE
Lgi5b  SVRKLVVNDSDLERVEERAELYE
Cca5a  AARKLAITEVDLERAEARLEAAE
Cca5b  VVRKLLMTDSVLEKAEERAEEKAE
Hro15  AARKLAI AEVDLNKSEARLEAAE
Hro25  AARKLAI AEGTLESFESRLDASE
Hro35  VSRKLLMTEANLTRAEEAGLETAD
Hro45  VSRKLLMTEANLTRAEEAGLETAD
Hro55  IFKKLATTMELTRAEEASYEAAD
Hro85  AVRHLHMLELELGKSEERCELAE
Hro75  VSRKLTICETELDRAEERAIAAE
Hro65  TARKLAITEVDLERSEGRVALAE
;
end;
Exon6

#NEXUS
[ Title ex6]

```

```
begin data;
  dimensions ntax=68 nchar=25;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
```

```
Mbe6      KVRELERELDATANELRSREISEEQ
TadI6     RATQLENDLILTTNKKSMSEVMMK
NveI6     RVKELEEEVTLVGNLRSLEISEGK
Spu16     KLAQLTDEITTLRNNCKSLEAQDRE
Spu26     TLDDRQEELITQLRNSYKSLQATDKK
Sko6      KGSDLLEELKIVATNLKSLEVSEEK
Bfl16a    QRAELEEEIKTLVNNVKSLEAAVEK
Bfl16b    KARELEDELKTTTGQLKSMEAQATK
Bfl16c    KAAELEEEELKNVTNQLKSLEAAADK
Bfl126    ASEGVRGVTDHRRPGQVLGVQPEQ
Cin16     KATELEEEELKIVANNLKSLEASAEK
Cin26     KATELEEEELKTAANLKSLEAAAEK
Cin36     KVKKADDQLKSLNENLRSLEKISAD
Cin46     KYKEVSSNLHLSLQCIKKYESMNEK
Cin56     KNAELIESNKELSSLKSYEAMESS
Cin66     EAKQLRESGQDMGILKALEAKETT
Tru116a   EARRLDDELFRAMEQSMKSI SCSAMQ
Tru116b   KCAELEEEELKTVTNNLKSLEAQAEK
Tru126    KCSELEEEELKTVQNNLKSLEAQAEK
Xtr16a    RYRQLDDQLRIMDQTLKTLMAAEEK
Xtr16b    KCAELEEEELKTVTNNLKSLEAQAEK
Mmu16a    QVRQLEEQLRIMDQTLKALMAAEDK
Mmu16b    KCAELEEEELKTVTNNLKSLEAQAEK
Tru26     KSGDLEEEELKNVTNLKSLEAQAEK
Xtr26a    RLRQLEEEELRTMDQNLKSLIAAEEE
Xtr26b    KCGDLEEEELKNVTNLKSLEAQADK
Mmu26a    RARQLEEEELRTMDQALKSLIASEEE
Mmu26b    KCGDLEEEELKIVTNLKSLEAQADK
Tru36     KCAELEEEELKNVTNLKSLEAQAEK
Xtr36     KCSDLLEEEELKNVTNLKSLEAQSEK
Mmu36a    RCREMDEQIRLMDQNLKCLSAAEK
Mmu36b    KCSELEEEELKNVTNLKSLEAQAEK
Tru416    KASDLEEEELKNVTNLKSLEAQAEK
Tru426    KCGDLEEEELKNVTNLKSLEAQSEK
Xtr36a    RCRDLEEQIRMLDHSCLKLNATEEK
Xtr36b    KCAELEEEELKNVTNLKSLEAQAEK
Mmu46     KCGDLEEEELKNVTNLKSLEAASEK
TruX6     KCRILEEEELKSVFSTSRSLAQVEK
Dpu6      KIVELEEEELRVVGNLKSLEVSEEK
Ame6      KIVELEEEELRVVGNLKSLEVSEEK
Tca6      KIVELEEEELRVVGNLKSLEVSEEK
Aga6      KIVELEEEELRVVGNLKSLEVSEEK
Dme6      KIVELEEEELRVVGNLKSLEVSEEK
Ame26     KIMELEEEELKVVGNLKSLEVSEEK
Ame36     KIEREDELFI VQNI VKSLEVSEEK
Ame46     KIMEREDELFI VGNILKSLEVSEEK
Tca26     KIMELEEEELKVVGNLKSLEVSEEK
Aga26     KIMELEEEELKVVGNLKSLEVSEDK
Dme26     KIMELEEEELKVVGNLKSLEVSEEK
Bma6a     K TREMERELVAVGMNLKTLEVHEER
Bma6b     KIVELEEEELRVVGNLKSLEVSEEK
Cbr6a     KIVELEEEELRVVGNLKSLELSEEK
Cbr6b     KIVELEEEELRVVGNLKSLEVSEEK
Cel6a     KIVELEEEELRVVGNLKSLELSEEK
Cel6b     KIVELEEEELRVVGNLKSLEVSEEK
Lgi6a     KTKLLEDEVSTLTNNLRSLEINLEK
Lgi6b     KIYELDEELHVVGNLKYTYTVKVSE
Lgi6c     KILELEEEELKVVGNMKSLEISEQE
Cca6a     QVRQLEEEELHIVSNLKSFEINEDK
Cca6b     KIVELEEEELKVVGNMKSLEISEQE
Hro16     KITVLEEEELKIIGNMKALEIAEQE
Hro26     KITELEDELKEVGNMKTLEQSEQE
Hro36     KILELEEEELRVVTNNKKSLEIFQQE
Hro46     KILELEEEELRVVTNNKKSLEIFQQE
Hro56     KVVELEEEELHVVTNNMKSLEITEQE
Hro86     KARQLDNNLHILTSNLRSLSEISEQT
Hro76     RVKTLDTTEVHLISTTLKSLEISESK
Hro66     KILELEDELKVVGNNFKSLEIVQQE
```

```
;
end;
Exon7
```

```

#NEXUS
[ Title ex7]
begin data;
  dimensions ntax=62 nchar=21;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Mbe7 AQIAEEGSTERMRELKRDHDN
TadI7 AQEREEVAKAKLAEMEEKCAE
NveI7 ASEREDTYENQIRELETKLQD
Spu17 STEREKYEASIKQLRDGLDE
Spu27 MCELDLHFETDCRDKKKLLDE
Sko7 ASEREFNYEEKIKQLEASLKE
Bfl17 ASEKEEAYEEQVRDL SAKLKE
Bfl27 GEDEENSLQSRRELQDTQRE
Cin17 YAAKEGIFEEEEIKT LSDKLKD
Cin27 YSAKEKSYEEEEIKCLSDK LKD
Cin37 NSEKEDNFEKEIHL L TENLKN
Cin47 LKEKEIQTEDQLCT LQKRLYE
Cin57 FSSKETQADDRIRVLKST LLE
Cin67 YGNNEIQ AEDQIRSLKMALEE
Tru117 YSQKEDK YEEEEIKVLT DKLKE
Tru127 YSQKEDK YEEEEIKVLT DKLKE
Xtr17 YSQKEDK YEEEEIKVLT DKLKE
Mmu17 YSQKEDK YEEEEIKVLS DKLKE
Tru27 YSQKEDK YEEEEIRVL TDKLKE
Xtr27 YASKEDK YEDEIKLLSEK LKE
Mmu27 YSTKEDK YEEEEIKLLEE K LKE
Tru37 YSQKEDK YEEEEIKVLT DKLKE
Xtr37 YSEKEDK YEEEEIKILT DKLKE
Mmu37 YSQKEDK YEEEEIKILT DKLKE
Tru417 YSEKEDK YEEEEIKILT DKLKE
Tru427 YSEKEDK YEEEEIKIMNDR LKE
Xtr37 YSKKEDK YEEEEIKILT DKLKE
Mmu47 YSEKEDK YEEEEIKLLS DKLKE
TruX7 YSVKEDK YEEEEIRNL TDKVKK
Dpu7a ANQREEAYKEQIKL TTRMKQ
Dpu7b ATAREESYELQIKL TSSRLKE
Ame7a ANQREEEYKNQIKL TTSRLKE
Ame7b ATQREETFVGVQVIL DSQ LKE
Tca7a ANQREEEYKNQIKNL TTRLKE
Tca7b ATLKEEEYSVTLKQVEQRLAE
Tca7c AAVTREHSEDKIRAMS DKLRE
Aga7a ANQREEEYKNQIKL TTRLKE
Aga7b ATQREESYGGQVRVLDQRLKE
Dme7a ANQREEEYKNQIKL TNLRLKE
Dme7b ATQKEETFETQIKVLDHSLKE
Ame27 ANQRVEEFKRQLKTL TVKLKE
Ame37 ANARVEDFKIQLKQLK KKLRE
Ame47 ANQRVEEFKTLKDLKVK LKT
Tca27 ANQRVEEFKKQLKTL TVKLKE
Aga27 ANQRVEEFKRQLKSLT IKLKE
Dme27 ANQRVEEFKREMKTL SIKLKE
Bma7a ALQRENSFSDHIQSLQNRIKE
Bma7b ALQREDSYEEQIRTVSARLKE
Cbr7a ALEKEDIFAEQIRQLDFRLKE
Cbr7b ALQREDSYEEQIRTVSSRLKE
Cel7a ALEKEDIFAEQIRQLDFRLKE
Cel7b ALQREDSYEEQIRTVSSRLKE
Lgi7 ASQREDSYEETIRDL TNRLKE
Cca7 ASQREDSYEESIRDLTARLKD
Hro17 CIQREDSYEETIRDLTQRLKE
Hro27 ALQREDSYEETIRDLTVRLKD
Hro37 AEMKEDAYEETIRLLNDKLEI
Hro47 AEMKEDAYEETIRLLNDKLEI
Hro57 FYQREEEYEEERIAALTEGLKN
Hro87 LASKEDSYTSTIADLRRSLKE
Hro77 ASKEDTYEGTIKELT SRLKE
Hro67 FLVRQETYELTIQNLTDSLKD
;
end;
Exon8

#NEXUS
[ Title ex8]

```



```
begin data;
  dimensions ntax=56 nchar=23;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
```

```
Mbe8 LSRELEEARRRVKELEIENDQME
TadI8 AEQEVDRDAEDSVTQLEKTLDERE
NveI8 AEEAEKAEQKVQLEAQAEAME
Spu18 ASNRAEGAEGQVKSLOHQVDSLE
Spu28 TSCRAEDAETSVTQLRKRVDLE
Sko8 AETRAEFAERSNQKLERQVDDLE
Bfl18a AETRAEFAERTVAKLEKNVDDLE
Bfl18b AETRAEFAERSVAKLEKNIDDLE
Bfl128 TETRAEAAAERKIQLMETEISKLE
Cin18 SETRAEFAEKSVVKLEKNIDELE
Cin28 SENRAEFAEKSVVQLERSIDDLE
Cin38 AETRAEFAERTVDKLEKTIDYLE
Cin48 SENLRAIAENSLNLAQQVGVLE
Cin58 TEAAREAAEKSVSIMNLRMENME
Cin68 SECRRALENEAKKYQADIEKLE
Tru118 AETRAEFAERTVAKLEKTIDDLE
Tru128 AETRAEFAERSVAKLEKTIDDLE
Xtr18 AETRAEFAERTVAKLEKTIDDLE
Mmu18 AETRAEFAERSVTKLEKSIDDLE
Tru28 AETRAEFAERSVAKLEKTIDDLE
Xtr28 TDGRVEFAEKSVVKLEKTIDDLE
Mmu28 AETRAEFAERSVAKLEKTIDDLE
Tru38 AETRAEFAERSVAKLEKTIDDLE
Xtr38 AETRAEFAERSVAKLEKTIDDLE
Mmu38 AETRAEFAERSVAKLEKTIDDLE
Tru418 AETRAEFAERTVTKLEKSIDDLE
Tru428 AENRAEFAERTVAKLEKTIDDLE
Xtr38 AETRAEFAERSVAKLEKTIDDLE
Mmu48 AETRAEFAERTVSKLEKTIDDLE
TruX8 AESRAEEAERSRDNCERTINNLE
Dpu8 AEARAEFAERSVQKLQKEVDRLE
Ame8 AEARAEFAERSVQKLQKEVDRLE
Tca8 AEARAEFAERSVQKLQKEVDRLE
Aga8 AEARAEFAERSVQKLQKEVDRLE
Dme8 AEARAEFAERSVQKLQKEVDRLE
Ame28 AEARAEFAEKTVKKLQKEVDRLE
Tca28 AEARAEYAEKTVKKLQKEVDRLE
Aga28 AETRAENAENKVKLQKEVDRLE
Ame38 AEKRAIHAERTVKKLLKEVDMKE
Ame48 AEKRAIIAEKVMKMSKELDARE
Dme28 AEQRAEHAEKQVKKLQKEVDRLE
Bma8 AETRAEFAERSVQKLQKEVDRLE
Cbr8 AETRAEFAERSVQKLQKEVDRLE
Cel8 AETRAEFAERSVQKLQKEVDRLE
Lgi8a AENRATEAERTVSKLQKEVDRLE
Lgi8b VELRAETAGRELSRLHIQFEKVE
Cca8a AENRASEAERTVSKLQKEVDRLE
Cca8b TENTNEMMQRELHITRLELDKKE
Hro18 AENRAADAERSVSKLQKEIDRLE
Hro28 TENKASEAERTVSKLQKEIDRLE
Hro38 AEQRCAEAENNIQKLQREIDKLE
Hro48 AEQRCAEAENNIQKLQREIDKLE
Hro58 AEQRCAEAENNYVQLLQKEVDKLE
Hro88 SEMCIDVLKRELKSKQQEELDKSE
Hro78 AEGKSAEMERNAGKLQREVDRL
Hro68 AENRAILAERAVTMLQKEVDRLE
```

```
;
end;
Exon9
```

```
#NEXUS
```

```
[ Title ex92]
```

```
begin data;
  dimensions ntax=87 nchar=27;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
```

```
Mbe9 DLEKTTEAYKKVKAEEETLSELSDI-
TadI9 ELQEEKENLKKAEELANAMAELQSI-
NveI9 ELEKAKEQYKVKKEELDSTLAESEM-
```

Spu19a EVQVTKEEHRKVQMDLDSCLTELGDLD-
Spu19b ELVQEKEKSRGMNDEMDCRCLQELNMDI
Spu29 ELQEWQSKKHTCQGELNQLISEINEM-
Sko9 ELFSEKEKNKSMADQLDQTLQDLHAM-
Bfl19a ELYAEKLFKFGISEELDHTLNDLSTF-
Bfl19b QLYAEKLYKYGISEELDQTLNDLTAL-
Bfl19c SLYDAKERYKNVSEELDQTLSELSTY-
Bfl19d SLYAEKEKYRGVSEELDQALNELHNM-
Bfl19e QLFTEKEKHKMVCDELDQTLNDLNAL-
Bfl19f ELFEQKEKYKRVSEELDKTFLSDLSSM-
Bfl129 QLEEVKKEYQGAKADLDAALNELNEM-
Cin19 SLYAEKCKIKAISEMDVTLQGIGDL-
Cin29 ELYKQKMLRNFNEEMWFDLRNM----
Cin39 QLYTEKLAYKYGISEKLDKTLSDMITLN
Cin59 EIAYLHSEVDKAKKMYTEAVNELNEL-
Cin69 DLDKEMAEKEEAKAELDRVLSSELGEM-
Cin79 ELEAAETKAEDAKKQLEETMAELSDI-
Tru119a ELYSQKLYKAISEELDHALNDMTSM-
Tru119d KLSQAKEENLDMHQMDQTLMELNNL-
Tru129a ELYAQKLYKAISEELDHALNDMTSM-
Xtr19a ELYAQKLYKAISEELDHALNDMTSM-
Xtr19d KVTHAKEENLNMHQMLDQTLLELNMM-
Mmu19a ELYAQKLYKAISEELDHALNDMTSM-
Mmu19c QLYHQLEQNRRLTNEKLKALNED----
Mmu19d KVAHAKEENLSMHQMLDQTLLELNMM-
Tru29a EVYAQKLGKALSEELDHALNDMTTL-
Tru29d KLAQAKEENLDMHQVLDQTLLELNNL-
Xtr29a EVYSQKMRYKAISEELDNALNDITSL-
Xtr29d NLSAAKESIELNQTLQTLLELNMM-
Mmu29a EVYAQKMYKAISEELDNALNDITSL-
Mmu29d TLASAKEENVEIHQTLQTLLELNNL-
Tru39a ELYAQKLYKAISEELDHALNDMTSM-
Xtr39a ELYAQKLYKAISEELDHALNDMTSL-
Xtr39d KLATAKEENLGMHQVLDQTLQELGSL-
Mmu39a ELYAQKLYKAISEELDHALNDMTSM-
Mmu39d KLKCTKEEHLCTQRMLDQTLLELNEM-
Tru419a ELYAQKLYKAISEELDHALNDMTSL-
Tru419d KLSAKEENLGMHQVLDQTLLELNNSL-
Tru429a ELYNQKLYKAISEELDHALNDLNTL-
Tru429d ELAIAKEKNVELHQALDQTMHELNNL-
Xtr39a ELYAQKLYKAISEELDHALNDMTSM-
Xtr39d KLRLTKDENAKMOTMLDQTLQQLNSL-
Mmu49 KLAQAKEENVGLHQTLQTLNELNCI-
TruX9 AVSKAQEENVKINATLEQTLHDLNLF-
Dpu9a DMLAQKEKNKLLQEEMESTLQDIQNM-
Dpu9b ELVHEKEKYKSI TDDLDQTFSELSAY-
Dpu9c ELVHEKEKYKSI ADEMDDTFVELAGY-
Ame9a DLAAEREKNKLLQEEMEATLHDIQNM-
Ame9b EMVAEKEKYKEIGDGLDQAFQELYGV-
Ame9c ELVHEKEKYKYICDDLDTFTELETKN
Ame9d VVVNERCKYKAI ADEMDDQTFADLAGY-
Tca9a DLLAEKEKNKLLSDEMEATLHDIQNM-
Tca9b ELVAEKERYKEIGDDLDTAFVELIL--
Tca9c ELVDEKTKYKAI ADEMDDQTMADLAGY-
Aga9a ELIVEKLYAEIGDDLDFAFVDLIPG-
Aga9b ELVMEKEKYREIGDDLDTAFVELILKE
Dme9a DLLNVRGKNKLLQEEMEATLHDIQNM-
Dme9b DLVLEKERYKDIGDDLDTAFVELILKE
Ame29a VLHQQKEKRKTICEELDKTFSELSGY-
Ame29b ELGINKDRYKSLADEMDSTFAELAGY-
Ame39 ELREEKEKYKAVCDDMDATFAEMTGY-
Ame49 FLFREKEKYKYICDDMDSTFAELTGY-
Tca29 ELGINKDRYKSLADEMDSTFAELAGY-
Aga29 KLMNEKEKYKAI CDDLDSTFAELTGY-
Dme29a RLFNEKEKYKAI CDDLDQTFFAELTGY-
Dme29b ELGINKDRYKSLADEMDSTFAELAGY-
Cbr9a ELLLEKERVNRNLTTEEIEQTVQEIQGS-
Cbr9b DRDAEIRKARQLQDELDMVQELNSV-
Cbr9c ELVHEKERYKTI SEELDSTFQELSGY-
Cel9a ELLLEKERVNRNLTTEEIEQTVQEIQGS-
Cel9b LRDAEVLKARQLQDELDMVQELNSV-
Cel9c ELVHEKERYKTI SEELDSTFQELSGY-
Lgi9a ELDMEREKSKSLQRELESTMEELHDI-
Lgi9b ELLAEKEKYKAI SDELDSTFAELAGY-
Cca9a QLCDARMQYKSLREEMDATLVDIQSM-
Cca9b ELLSEKEKYKTI SEELDTTFAELAGF-
Hro19 ELLLEKEKYRTI SEELDGTFFSELATF-

```
Hro29  ELLAEKEKYKDISEELDGTFSSELASF-
Hro39  ELIAEKEKCKVINRELDATFAELTGF-
Hro49  ELIAEKEKCKVINRELDATFAELTGF-
Hro59  ELAAEKEKCKTIDSELNATFAELTGF-
Hro89  NFNEMREYKYLRDELDSYKELNSL-
Hro79  ELLLSREENKKLREEFDAAFQEIQNI-
Hro69  ELTSEKDKFRLVLGELDSTITELTGF-
;
end;
Externalization in lophotrochozoans.
```

Exon1

```
#NEXUS
[ Title 1lofo]
begin data;
  dimensions ntax=12 nchar=55;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Lgi1B  -MS--VLGNNNPSGVL--GNIKTKMAGLKTQIDDLSEENTRLRRDLGDKDSRINE
Cca1B  -MS-----GSAL--NVLKGMQNLREEAKEYKDQFDEKCRELTEEQSRSE
Hro81B MFKVNSSNHNGGGALVVSSLKQMQTLREELERYKDLYDDKCREVNRERSLRND
Hro71B MATPTASS----GGAL--TSLKMKQSLRDEMKTkdLYDAKCNELDLEKGLRAK
Lgi1   -----M--DAIKKKMLAMKMEKENALDRAEQLEQKLRDTEEQKSK
Cca1   -----M--DAIKKKMQAMKLEKESALDKAQLEQKLTQKETNEK
Hro11  -----M--ETIKKKMQAMRLERENAILKAQTLEEKVVAEQKGINER
Hro21  -----M--DAIKKKMQVMKTEKDQALVRADQLEEKVSEQKALNEK
Hro31  -----M--EAIKKKMQAMKLEKENAFDKAEQLEQKLAEQKTVHEK
Hro41  -----M--NAIKKKVHTMKTlKDSAGDEVELLEQKLEKLEYKAIgek
Hro51  -----M--DAIKKKMQAMKLEKETAFDKCDQLEQKLAEQKVVEK
Hro61  -----M--TAIKKKMHGMKTLKESVFDEVDQLDQKLEQKAIYek
;
end;
```

Exons 3 and 7 (constitutive)

```
#NEXUS
[ Title 37lofo]
begin data;
  dimensions ntax=10 nchar=65;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
Lgi    LETEAAGFTRRITLLEEDLERSEERLTSAQSKLEEASKAADESEASQREDSYEETIRDLTNRLKE
Cca    AEGEVQALTRRIRLLEEDYEQTENRLQNASEKLEEASKAADESEASQREDSYEESIRDLTARLKD
Hro1   AEGEVGGLTRRISLLEVDYEQTAVRLSTASEKLEASKVAEEAECIQREDSYEETIRDLTQRLKE
Hro2   AESDVGALTRRIQLLEVDYEQTASRLIASEKLEASKHAESEALQREDSYEETIRDLTVRLKD
Hro3   AETEVQTLAKKVGKLEEDFENTESRLKAANEKLEEAATKAADESEAEKEDAYEETIRLLNDKLEI
Hro43  AETEVQTLAKKVGKLEEDFENTESRLKAANEKLEEAATKAADESEAEKEDAYEETIRLLNDKLEI
Hro53  AEAEVQNLTKTVRNLEEKFDTENRLKQTSEKLELASKAADESEFYQREEEYEERIAALTEGLKN
Hro83  AESQVMALTRRVELLEDERDEMRRYSSVLNKLNDASKVVDFELASKEDSYTSTIADLRRSLKE
Hro73  AEEDLSTLTKKRLLEEDYEHlQTQLQSTNEKILELSKTSDENEASKKEDTYEGTIKELTSRLKE
Hro63  AEAEVMSLQKTVRSLEEDYESTENRLLQTTTKLEQAAKSFEESEDFLVRQETYEELTIQNLTDSLKD
;
end;
```

Exons 4, 5, 6 and 9 (MATEs)

```
#NEXUS
[ Title lofo4569]
begin data;
  dimensions ntax=17 nchar=114;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix

[!Domain=Data;]
LgiS4A5B6A9A  QKRTVENKLAEEKLEDEYETALKTAQAHATDTETRFEEsvRKLvVNDSDLERVEERAELYERKTKLLEDEVTSLTNNLR
CcaS4A5B6A9A  QRvVLDrrTANEDRIAELLEEALKAQFCESETENKYQEVVRKLLMTDSVLEKAEERAeKAESQVRQLEEEELHIVSNNLK
CcaS4B5B6A9A  ARlALDSRLSATDDCISVLESKLRDVTVSASESANKYDEVVRKLLMTDSVLEKAEERAeKAESQVRQLEEEELHIVSNNLK
HroTPM8       LKISNECFKNLDDEKISSLEDQIRTLRLAADTAEKKYDEAVRHLMLELELGKSEERCELAESKARQLDNNLHlITSNLR
HroTPM7       ARKALeSRQNMDEKMLKLEQWLKESKASCEDAEKKYEDVSRKLTICETELDRAEERAIAAETRVKTLDTevHLlSTTLK
CcaL4C5A6B9B  NRKALeSRSLADDERLTFLAQlKEAKFIAEDADRKYDEAARKLAITEVDLERAeARLEAAEAKIVELEEEELKVVGNMNMK
CcaL4D5A6B9B  GRKVLENRNITDEERIVQVERELEETILLGEEADRKFEEAARKLAITEVDLERAeARLEAAEAKIVELEEEELKVVGNMNMK
LgiL4B5A6B9B  GRKVLeSRSLSDDERIDQLEAQlKEAKYIAEDAERKYDEAARKLAITEVDLERAeARLEAAEAKIYELDEELHVVGNMNMK
```

LgiL4C5A6B9B GRKVLNRSQGDEERIELEKQFEEAKVIAEDVDRKYDEAARKLAITEVDLERAETRLEAAEAKIYELDEELHVVGNNLK
LgiL4B5A6C9B GRKVLRSLSDDERIDQLEAQLKEAKYIAEDAERKYDEAARKLAITEVDLERAETRLEAAEAKILELEELKVVGNMNMK
LgiL4C5A6C9B GRKVLNRSQGDEERIELEKQFEEAKVIAEDVDRKYDEAARKLAITEVDLERAETRLEAAEAKILELEELKVVGNMNMK
HroTPM1 ARKSLESRLADDERLTFLFLETQLKEAKYISEDAGRKFDEAARKLAIAEVDLNKSEARLEAAEQKITVLEELKIIGNMNMK
HroTPM2 NRKSLETNSLMNDERITFLEEQLKEAKYIAEDAGSKLEEAARKLAIAEGTLESFESRDLASESKI TELEDELKEVGNMNMK
HroTPM3 GIKVLENRFTLEDEKIQQLEHEIEDVILVGEDSDRRYEEVSRKLLMTEANLTRAEGLETADAKILELEELRVVTNNKK
HroTPM4 GIKVLEARITYDEERIAQIETELEVIILFGEDADRKYEETARKLAITEVDLSRSESRVQIAEARGMELEEEYKVVSNMNMK
HroTPM5 GIKVLENKMITTEERIQQLEKELEETIMAGEDSDRRFEEIFKKLATDMEMLTRAEEASYEADAKVVELEELHVVTNNMNMK
HroTPM6 GRKVLNRIAIDEERMVILEKELEVTILFGEDADRKYEETARKLAITEVDLERSEGRVALAEAKIIELEDELKVVGNMNMK

LgiS4A5B6A9A SLEINLEKELDMEREKSKSLQRELESTMEELHDI
CcaS4A5B6A9A SFEINEDKQLCDARMQYKSLREEMDATLVDIQSM
CcaS4B5B6A9A SFEINEDKQLCDARMQYKSLREEMDATLVDIQSM
HroTPM8 SLEISEQTNFNEMREEYKYLRDELDSYKELNSL
HroTPM7 SLEISEKELLLSREENKKLREEFDAAFQEIQNI
CcaL4C5A6B9B SLEISEQEELLSEKEKYKTISEELDTTFAELAGF
CcaL4D5A6B9B SLEISEQEELLSEKEKYKTISEELDTTFAELAGF
LgiL4B5A6B9B TYTVKVSEELLAEKEKYKAI SDELSTFAELAGY
LgiL4C5A6B9B TYTVKVSEELLAEKEKYKAI SDELSTFAELAGY
LgiL4B5A6C9B SLEISEQEELLAEKEKYKAI SDELSTFAELAGY
LgiL4C5A6C9B SLEISEQEELLAEKEKYKAI SDELSTFAELAGY
HroTPM1 ALEIAEQEELLLEKEKYRTISEELDGTFSSELATF
HroTPM2 TLEQSEQEELLAEKEKYKDISEELDGTFSSELASF
HroTPM3 SLEIFQQEELIAEKEKCKVINRELDATFAELTGF
HroTPM4 SLEIFQIEELAAEKDKFRLVANELDFTFTELTAFA
HroTPM5 SLEITEQEELAAEKEKCKTIDSELNATFAELTGF
HroTPM6 SLEIVQQEELTSEKDKFRLVGLGELDSTITELTGF

;
end;
Exon4 (Protostomes)

#NEXUS
[Title 4 proto]
begin data;
dimensions ntax=40 nchar=39;
format missing=? gap=- matchchar=. datatype=protein interleave=yes;
matrix

[!Domain=Data;]
Dpu4a IRKALENRTNMEDDRVAILEAQVAQAKLIAEEADKKYEE
Dpu4b MRKVLNRSLSDEERMDALENQLKEARFLAEADKKYDE
Ame4a IRKALENRTNMEDDRVSLLEQQLAQAKLIAEEADKKYEE
Ame4b ARKILENRSRLADEERMDALENQLKEARFLAEADKKYDE
Tca4a IRKALENRTNMEDDRVGILETQLSQAQLIAEEADKKYEE
Tca4b QRKVLNRSRLADEERMDALENQLKEARFLAEADKKYDE
Aga4a IRKALENRTNMEDDRVGI LEAQLAQAKLIAEEADKKYEE
Aga4b ARKVLNRRALADEERMDALENQLKEARFMAEEADKKYDE
Dme4a IRKALENRTNMEDDKVALLNQLAQAKLIAEEADKKYEE
Dme4b ARKILENRRALADEERMDALENQLKEARFLAEADKKYDE
Ame24 MCKVLNRSQQDEERMDQLTNQLKEARLLAEDADGKSDE
Ame34 MCKVLEDRSRLDEERMEKLMQELKDARLIAEDADAKSEE
Ame44 ICKVLNRSKQDEERMDQLMTQLKEARLIAEDADTKSDE
Tca24 MCKVLNRSQQDEERMDQLTNQLKEARLLAEDADNKSDE
Aga24 MCKVLNRSQQDEERMDQLSNQLKEARMLAEDADTKSDE
Dme24 MCKVLNRSQQDEERMDQLTNQLKEARMLAEDADTKSDE
Bma4a ARKSMETRSQQDEERANVLEIQVDEAKMIADEADRKYEE
Bma4b ARKALENRIDVDHRCGELEQKLREAQALLAETENKSDE
Bma4c VRKVMENRSFQDEERANTVESQLKEAQLLAEADKKYDE
Cbr4a ARKSMETRSQQDEERANFLETQVDEAKVIAEDADRKYEE
Cbr4b SRKALSNQIELDDDRCAELERKLRQCQSILHETENKAAE
Cbr4c VRKVMENRSIQDEERANTVEAQLKEAQLLAEADKKYDE
Cel4a ARKSMETRSQQDEERANFLETQVDEAKVIAEDADRKYEE
Cel4b SRRALSNQIDMDDDRCSDLERKLRQCQSILHETENKAAE
Cel4c VRKVMENRSIQDEERANTVEAQLKEAQLLAEADKKYDE
Lgi4a QKRTVENKLAEEKLDYEYETALKTAQAHATDTETRFEE
Lgi4b GRKVLRSLSDDERIDQLEAQLKEAKYIAEDAERKYDE
Lgi4c GRKVLNRSQGDEERIELEKQFEEAKVIAEDVDRKYDE
Cca4a QRVVLDRRRTANEDRIAEELEALKAAQFCESETENKYQE
Cca4b ARLALDSRLSATDDCISVLESKLRDVTVSASESANKYDE
Cca4c NRKALRSRLADDERLTFLAQLKEAKFIAEDADRKYDE
Cca4d GRKVLNRRNITDEERIVQVERELEETILLGEEADKKFEE
Hro14 ARKSLESRLADDERLTFLFLETQLKEAKYISEDAGRKFDE
Hro24 NRKSLETNSLMNDERITFLEEQLKEAKYIAEDAGSKLEE
Hro34 GIKVLENRFTLEDEKIQQLEHEIEDVILVGEDSDRRYEE
Hro44 GIKVLENRFTLEDEKIQQLEHEIEDVILVGEDSDRRYEE
Hro54 GIKVLENKMITTEERIQQLEKELEETIMAGEDSDRRFEE
Hro84 LKISNECFKNLDDKISSLEDQIRTLRLAADTAEKKYDE

```
Hro74 ARKALESRQNMDDKMLKLEQWLKESKASCEDAEKKYED
Hro64 GRKVLENRIAIDEERMVILEKELEVITLFGEDADRKYEE
;
end;
Externalization in insects (exons 4, 5 and 7)
```

```
#NEXUS
[ Title ins457]
begin data;
  dimensions ntax=16 nchar=83;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
DpuS4a5b7b IRKALENRTNMEMDDRVAILEAQVAQAKLIAEEADKKYEEVARKLVLMLEADLERAEERAEQGEATAREESYELQIKTLLSSRLKE
TcaS4a5b7b IRKALENRTNMEMDDRVGILETQLSQAQAKLIAEEADKKYEEVARKLVLMLEADLERAEERAEQSEATLKEEEYSVTLKQVEQRLAE
AmeS4a5b7b IRKALENRTNMEMDDRVSLLEQQLAQAKLIAEEADKKYEEVARKLVLMLEADLERAEERAEQSEATQREETFVGVQVKILDSQLKE
AgaS4a5b7b IRKALENRTNMEMDDRVGILEAQLAQAKLIAEEADKKYEEVARKLVLMLEADLERSEEEKVEMNEATQREESYGGQVRVLDQRLKE
DmeS4a5b7b IRKALENRTNMEMDDKVALLENQLAQAKLIAEEADKKYEEVARKLVLMLEADLERSEEEKVELSEATQKEETFQIKVLDHSLKE
DpuL4b5a7a MRKVLENRSLSEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAEERAEETGEANQREEEAYKEQIKTLLTRMKQ
TcaL4b5a7a QRKVLENRSLADEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAEERAEAGEANQREEEYKNQIKNLTTRLKE
AmeL4b5a7a ARKILLENRSLADEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAEERAEAGEANQREEEYKNQIKTLLSRLKE
AgaL4b5a7a IRKALENRLADEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAEERAEAGEANQREEEYKNQIKTLLSRLKE
DmeL4b5a7a ARKILLENRALADEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAEERAEQGEANQREEEYKNQIKTLLNTRLKE
TcaTPM2 MCKVLENRSQQDEERMDQLTNQLKEARLLAEDADNKSDEVSRKLAFFVEDELEVAEDRVKGGDANQVRVEEFKQKLTITVKKLE
AmeTPM2 MCKVLENRAQQDEERMDQLTNQLKEARLLAEDADGKSDEVSRKLAFFVEDELEVAEDRVKSGEANQVRVEEFKQKLTITVKKLE
AmeTPM3 MCKVLEDRSRLDEERMEKLMQELKDARLIAEEDADAKSEIISKLLALVEEELGAEERVKTSEANARVEDFKIQLKQLKXKLE
AmeTPM4 ICKVLENRSKQDEERMDQLMTQLKEARLIAEDADTKSDEISRKLAFFVEDELEAAEERVKSSSEANQVRVEEFKQKLDLKVKKLT
AgaTPM2 MCKVLENRSQQDEERMDQLSNQLKEARMLAEDADTKSDEVSRKLAFFVEDELEVAEDRVKSGEANQVRVEEFKQKLSLTIKLE
DmeTPM2 MCKVLENRSQQDEERMDQLTNQLKEARMLAEDADTKSDEVSRKLAFFVEDELEVAEDRVRSGEANQVRVEEFKREMKTSLIKLE
;
end;
General tree
```

Replicate 1

```
#NEXUS
[ Title gen1]
begin data;
  dimensions ntax=61 nchar=203;
  format missing=? gap=- matchchar=. datatype=protein interleave=yes;
  matrix
```

```
[!Domain=Data;]
MbeTPM ABAEANDAKRKLTLTEDDLKAEERLQSMQTRLRDAEQEAEADASKLQRLEATQDNDFGKAAELEDKYKDLKRQFDDVERS
TadTPM2 AEQELASLIRKRTLLESDDLNRTEERLSEAESRLNSASTSNLDLEERKRLEDVDYADDERIDQIESDLKAAKLSTEEAERQ
TadTPM1 VKEKIDELNKEIEETEQQDDRESKLAETLKTLLAEATKTDHEEARAVLESRTNNTKLEELERQLNETLAAREEAETK
HmaTPMB AAEVASYLRKIQLLEKDYNEVVSRCFALEKLAITQDKGMSVEARKQLEENENEGDEKIQRLLEEVEKAKRLLLEENETK
HmaTPMIA VEEKLEELIKLKTITIEDKLDEADEREKLLKLSLAAEAKNQDEGLVKRELEHRGNAGSSQLQRLERELSELLAKNEKVTA
HmaTPMIB SEEEVDRLQKELNNLDELESSESKLNLTIKRLHEAEKQAESEARVLESRGQTDEKLSKLQSELDVMSKNSDVENR
HmaTPMDIC ABEVTELTKELENDLEDQLDASESKMSTLQEKLAEEAKLHEEHDDARRILENRRSGDGGRIQLQDELDELTLNLNKVVET
PcaTPM1 TEQTADLQKTLADLEDELDAESRLTSLTEKYNEEKKAEEGRAHKELENRGQTDYSRLNRLLETALAEITEQNEVVVEK
NveTPM10 DKNESATLRRSCSLTEHQLDKTEDILDQKLERLVLMLHKKTEQDIMLVLEDRELEVDNSLDRLEPSAKAAIQRQHDAMR
NveTPM97 HESDLSMQKRINLLSEDLKTELEAYEKKARLDSLEEKQESDGVVRELESVELEGERLAELEEKTKAEAVATVNOQEH
NveTPM1 AETEVAAALTKQLQLEDLDAESKLADTQGGQTEAEKQADESEARKVLENRGASDEERLASLERQYNDALERTEEAEKQ
SpuTPM1 AAEAVNLNRRILILEEDNGQEEALSDFTRRLETTIEVEADENLARKVLETRASDDDKIIDLQRMKENASRIEELDRL
SpuTPM FEEQAKTLNMKCRDLEDVMSDREDELQRKLIKIDEIEAESDENSFSRVLMKRENTNTDRIKDLETMMDQQTADIERLDKV
SkoTPM AAEVSSLQRRLQLLDEELERAQERYQVAADKLADIEKAADESEARKVLENRGLSDDDRILDRLVNESRSMAEADHK
BflTPM1 AAEAVASLNRRIQLVVEEELDRAQERLNSTVEKLTDSKAADESEARKVLENRGADEDRMELLDMLQREAKMIAEEADRK
BflTPM2 AENDIESLRRKMLLEADLDTAETSLEKTEENRQLESLDEAESAQALEHRSTTEDDKSSQMETDLKLAKAEKEMELK
CinTPM1 AEQEVASLNRRITLVEEELDRAQERLTIISLKLLEEAKEAADADESEGRKVIENRSLKDEERLEVQEIQLTEAKNIAEDADRK
CinTPM2 AEEVVSALNRRICLVEEELDQAQERLTIISLKLLEEAKEAADADESEGRKVIENRSLKDEERLEVQEIQLTEAKNIAEDADRK
CinTPM3 SELEVNAQTRRMQLLEEMQVRTERLDEAVAKLEVAEKAEESEGRKVIENRSLKDEERLEVQEIQLTEAKNIAEDADRK
CinTPM4 VEEENINLKHQLNAKENFIGKLEPLLEDVTRKLSAEEERANEIQQLESYETSIVIKCEKLEDQLKEIRFISEETGRK
CinTPM5 AEDQNQDLERKLRLVLEGLDRADEKLTIAKQLSSLEQQSDGGSAYKSLNEFNSSVKNYEAHLDDLDRSKMLAEEMSRK
CinTPM6 FEEVNSLSNKI STNDTIERLELQNEELKRRSENAERELDEVQELKQLQSEHTASAECCDLTEELKLRKMDLDEVTTN
TruTPM11 AAEAVASLNRRIQLVVEEELDRAQERLGTALTKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
TruTPM12 AEGDVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
TruTPM2 AAEAVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
TruTPM3 AAEAVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEDSDRK
TruTPM41 AEGEVAALNRRIQLVVEEELDRAQERLAVLQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
TruTPM42 AAEVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
TruTPMX AEMEVTLSNRLQNEEDTLDRTOERLADALRKVEEVEKVADESEGMKVIENRAQKDEEKLELLEYQLNEAKHIAEEADLK
XtrTPM1 AEGDVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
XtrTPM2 AAEVASLNRRIQLVVEEELDRAQERLATALQKLEETEKADESEGMKVIENRATKDEEKMVDQEQQLREAKNIAEESDRK
XtrTPM4 AEGEVAALNRRIQLVVEEELDRAQERLATALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
XtrTPM3 AAEVASLNRRIQLVVEEELDRAQERLSTALQKLEEAKEAADADESEGMKVIENRAMKDEEKMEIQEIQLKEAKHIAEEADRK
```

MmuTPM1 AEADVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEKADESEGKVIIESRAQKDEEKMEIQEIQLKEAKHIAEDDRK
MmuTPM2 AEADVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEKADESEGKVIENRAMKDEEKMEIQEMQLKEAKHIAEDSDRK
MmuTPM3 AEAEVASLNRRIQLVVEEELDRAQERLATALQKLEEAKEKADESEGKVIENRALKDEEKMEIQEIQLKEAKHIAEEDDRK
MmuTPM4 AEGDAAALNRRIQLVVEEELDRAQERLATALQKLEEAKEKADESEGKVIENRAMKDEEKMEILEMQLKEAKHITDEADRK
DpuTPM AEGEVAGLNRRVQLLEEDLERSEERLNTATTKLAEEASHSADESEIRKALENRTNMEDDRVAILEAQVQAQAKLIAEEDDK
AmeTPM1 AESEVAALNRRIQLVVEEEDLERSEERLATATAKLAEEASQAADSEIRKALENRTNMEDDRVSLLEQQLAQAKLIAEEDDK
AmeTPM2 AESEVAALNRRVQLLEEDLERSEERLNTATAKLAEEASQAADSESMCKVLENRSQQDEERMDQLTNQLKEARLLAEDADGK
AmeTPM3 AEQDRTTTLTKRVQIEIATLTKKEELRLTAQTKLGRASELADARMCKVLEDRSRLDEERMEKLMQELKCDARLIAEDADAK
AmeTPM4 TQSELAVLNRRMQCCIQNLEKSEERRLTAQAKLAQAMETAEDAKICKVLENRSKQDEERMDQLMTQLKEARLIAEDADTK
TcaTPM1 AESEVAALNRRIQLVVEEEDLERSEERLATATAKLAEEASQAADSEIRKALENRTNMEDDRVGILETQLSQAQAKLIAEEDDK
TcaTPM2 AEAEMASLNRRVQLLEEDLERSEERLATATTKLAEEASQAADSESMCKVLENRSQQDEERMDQLTNQLKEARLLAEDADNK
AgaTPM1 AESEVAALNRRIQLVVEEEDLERSEERLASATAKLEASQAADSEIRKALENRTNMEDDRVGILEAQLAQAKLIAEEDDK
AgaTPM2 TEANVAALTRKVQVVEEDLEKSEERSAALSLLLEATQASADENNMCKVLENRSQQDEERMDQLSNQLKEARMLAEDADTK
DmeTPM AESEVAALNRRIQLVVEEEDLERSEERLGSATAKLEASQAADSEIRKALENRTNMEDDKVALLENQLAQAKLIAEEDDK
DmeTPM2 TESEVATLNRRVQLLEEDLERSEERLSTAQKLEEAQAADSESMCKVLENRSQQDEERMDQLTNQLKEARLLAEDADNK
BmaTPM AEAEEVAALNRRMTLLEEEELERAEERLKIATDKLEEATHADESEVRKVMENRSFQDEERANTVESQLKEAQLLAEEDDRK
CelTPM AEAEEVASLNRRMTLLEEEELERAEERLKIATEKLEEAETHNVDESEVRKVMENRSQDEERANTVEAQLKEAQLLAEEDDRK
CbrTPM AEAEEVASLNRRMTLLEEEELERAEERLKIATEKLEEAETHNVDESEVRKVMENRSQDEERANTVEAQLKEAQLLAEEDDRK
LgiTPM LETEAAGFTRRITLLEEDLERSEERLSTAQKLEEAQAADSESMCKVLENRSQQDEERMDQLTNQLKEARLLAEDADNK
CcaTPM AEGEVQALTRRIRLLEEDYEQTENRLQNASEKLEEAQAADSEENRKALESRSLADDERLTFLEAQLKEAKFIAEDADRK
HroTPM1 AEGEVGGLTRRISLLEVDYEQTAVRLSTASEKLEEAQAADSEENRKALESRSLADDERLTFLETQLKEAKYIASEDAGRK
HroTPM2 AESDVGALTRRISLLEVDYEQTASRLIEASEKLEEAQAADSEENRKSLETNSLMNDERITFLEEQLKEAKYIASEDAGSK
HroTPM3 AETEVTLAKKVKLEEDFENTESRLKAANEKLEEAQAADSESEGIKVENRFTLEDEKIQQLEHEIEDVILVGEDSDRR
HroTPM4 AETEVTLAKKVKLEEDFENTESRLKAANEKLEEAQAADSESEGIKVENRFTLEDEKIQQLEHEIEDVILVGEDSDRR
HroTPM5 AEAEEVQNLTKTVRNLEEKFDENRQLKQTSKLEELASQAADSESEGIKVENRFTLEDEKIQQLEHEIEDVILVGEDSDRR
HroTPM6 AEAEMVSLGKTVRSLEEDYESTENRLLQTTTLEKLEEAQAADSESDGRKVENRIADIEERMVILEKELEVTILFGEDADRK
HroTPM8 AESQVMALTRRVELEEDEREMDRRYSSVTLNKLEEAQAADSESEGIKVENRFTLEDEKIQQLEHEIEDVILVGEDADRK
HroTPM7 AEEDLSTLTKKRLLEEDYEHIQTQLQSTNEKILELSKTSDENARKALESQRNMDEKMLKLEQWLKESKASCEDAEKK

MbeTPM HAAEATRKQLTEDDLEKAEERAEVAEKVRELERELDATANELRSREISSEQAQIAEEGSTERMRELKRDHNLRSRELEEA
TadTPM2 FEEAEKRLRVLEGDHQRRAIEKASSDKITNLEGELQGVNENLKEADDAERIANDQEEDYQAKIKALEERLLAADVRLEEA
TadTPM1 YKEISEKLEEELEKELEEEEEKADTAERATQLENDLILTTNNKKSMEVSMMAQEREEVAKAKLAEMEEKCAEEAQEVDA
HmaTPM2 SNESERRRVVFRDIERTAAKADSLERIQVLEQETIDNATISLKELEAREGESSQREYNAEQIVMLEGKYKEAEVRAEAA
HmaTPM1A LEKVTKIEIADLETQDIEEERCADLDRVRELEPEMIVIGNMLRSMKINESKATVRMESSEKLEKMHVYKLEIEERVART
HmaTPM1B YEQIAKEIKLEKMEEDNRCRTAAEKVLEERREVIQVNTLRTMEVNETQASEREDKDFSTRNLNDLTKYNDLAKQKY
HmaTPM1C FNELTQILAEADKLEQDEEERDIADKVKLELEVEVTQVGNLRSMEINEGQASVRTECGDTKISEMEAKYQEMEARAEF
PcaTPM1 LSELSSQLEENERILDEEEERCATADQVKELEVDVQVGNQLRSMEINEEKASKSNDQSANLEDTIEKYNTIKDRADDA
NveTPM10 CMEVQRRLTLTTSELHKIRARQREKEEVRENERLKVGGRSIQQLVISEEKYCDKEDFRHRIRLLKANLAATILRAEES
NveTPM97 NTEINQKIVVTELELTKVNERLALTIERLEATIEEBSTMASLEQKQTDASQWEIEVEEKIIRFLNKLKLEVLVRAEDA
NveTPM1 YEEISERLQLELENEEEAEQKADAAERVKELEEEVTLVGNLRSLEITSEKASEREDTYENQIRELETQLQDAEERAEKA
SpuTPM1 HSESQRKLQMTQQLEVAEAKNTECEKLAQLTDEITLRLNCKSLEAQDRESTEREKYEASIKQLRDGLDEASNRAEGA
SpuTPM NSDLQSKCQQMEDKLEDAEDNSIRLKTLDLDRQEEITQLRNSYKSLQATDKMCELDLHFETDCRDKLLDETSCEAEDA
SpuTPM FEEVARKLVTEAELEERAERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
BflTPM1 YEEVARKLVITEGDLERAERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
BflTPM2 YEEVSRKLVMAEQQLDNMEDKYKAEASEGVGRGVTDHRRPGQVLGVQPEQGEDEENSLQSRVRELQDTQRETETRAEAA
CinTPM1 YVEVARKLVMAEQQLDNMEDKYKAEASEGVGRGVTDHRRPGQVLGVQPEQGEDEENSLQSRVRELQDTQRETETRAEAA
CinTPM2 YVEVARKLVNVEDLGERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
CinTPM3 YEEVGRKLRMVENDLERVLDRAEEYKVKKADLQKLSNLNLSLEKISADNSEKEDNFEKEIHLTLNKLKLEAETRAEFA
CinTPM4 YEEATRRLTFMDTELEKSEQRIEKAEKYKEVSNLHLSLQCIKKYSESMNEKLEKEIQTEDQLCTLQKRLYESENLRITA
CinTPM5 YEEVARRLVLMDSLEKAEERCSVSEKNAELIESNKBLSLLKSYEAMESSFSKETQADDRIRVLKSTLLETAAREAAA
CinTPM6 YDDAMRRIKVLDDNCRLLDDKQVQALEEAKQLRESGDMDGILKALEAKETTYGNIEQAEDQIRSLKMALESECRREAL
TruTPM11 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPM12 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPM2 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPM3 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPM41 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPM42 CDEVTRKLLVLEGELEERAERAEVSEKCGDLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TruTPMX YEENARKLTRVEGELEERAERAEVSEKCGDLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
XtrTPM1 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
XtrTPM2 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
XtrTPM4 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
XtrTPM3 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
MmuTPM1 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
MmuTPM2 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
MmuTPM3 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
MmuTPM4 YEEVARKLVITEGDLERTEERAELAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
DpuTPM YEEVARKLAMVEADLERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AmeTPM1 YEEVARKLAMVEADLERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AmeTPM2 SDEVSRLAFVEDELEVAEDRVKSGEKIMELEELKVVGNLSKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AmeTPM3 SEEISKKLALVEEELGAEERVKTSSEKIMEREDLFTVQNIKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AmeTPM4 SDEISRLAFVEDELEVAEDRVKSGEKIMELEELKVVGNLSKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TcaTPM1 YEEVARKLAMVEADLERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
TcaTPM2 SDEVSRLAFVEDELEVAEDRVKGGDKIMELEELKVVGNLSKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AgaTPM1 YEEVARKLAMVEADLERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
AgaTPM2 SDEVSRLAFVEDELEVAEDRVKSGEKIMELEELKVVGNLSKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
DmeTPM YEEVARKLAMVEADLERAEERAEVAEKGSDBLEELKIVATNLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEFA
DmeTPM2 SDEVSRLAFVEDELEVAEDRVRSSEKIMELEELKVVGNLSKLSLEVSEKASEREFNYEIKIQLEASLKEAETRAEHA

BmaTPM YDEVARKLAMVEADLERAEERAEAGEKTREMERELVAVGMNLKTLVHEERALQRENSFSDHIQSLQNRRIKEAETRAEFA
CelTPM YDEVARKLAMVEADLERAEERAEAGEKIVELEELRVVGNLKSLELSEEKALEKEDIFAEQIRQLDFRLKEAETRAEFA
CbrTPM YDEVARKLAMVEADLERAEERAEAGEKIVELEELRVVGNLKSLELSEEKALEKEDIFAEQIRQLDFRLKEAETRAEFA
LgiTPM YDEAARKLAI TEVDLERAETRLEAAEKTKLLEDEVTSLTNNLRSLEINLEKASQREDSYEETIRDLTNRLKEAENRATEA
CcaTPM YDEAARKLAI TEVDLERAEARLEAAEQVRQLEEBELHIVSNLKSFEINEDKASQREDSYEESIRDLTARLKDAENRASEA
HroTPM1 FDEAARKLAI AEVDLNLKSEARLEAAEKITVLEELKII GNNMKALEIAEQECIQREDSYEETIRDLTQRLKEAENRAADA
HroTPM2 LEEAARKLAI AEGTLESFESRLDASEKI TELEDELKEVGNMKTLEQSEQEQALQREDSYEETIRDLTVRLKDTENKASEA
HroTPM3 YEEVSRKLLMTEANLTRAEEAGLETADKILELEELRVVTTNNKKSLEIFQQEAEEMKEDAYEETIRLLNDKLEIAEQRCAEA
HroTPM4 YEEVSRKLLMTEANLTRAEEAGLETADKILELEELRVVTTNNKKSLEIFQQEAEEMKEDAYEETIRLLNDKLEIAEQRCAEA
HroTPM5 FEEIFKKLATDMELTRAEEASYEAADKVVELEELHVTTNNMKSLEITEQEFYQREEEYEERIAALTEGLKNAEQRCADA
HroTPM6 YEETARKLAI TEVDLERSERVALAEKII ELEDELKVVGNNFKSLEIVQQEFLVRQETYEELTQNLTDLSKDAENRAILA
HroTPM8 YDEAVRHLHMLELELGKSEERCALAEKARQLDNNLHILTSNLSLEISEQTLASKEDSYTSTIADLRSLKESEMCI DVL
HroTPM7 YEDVSRKLLTICETELDRAEERAIAAERVKTLTDEVHLISTTLKSLEISESKASKKEDTYEGTIKELTSRLKEAEGKSAEM

MbeTPM RRRVKELEIENDQMEDLEKTT EAYKKVKALEETLSELSDI--
TadTPM2 DRRKGQLNRQLGEINLLDEKRRKCEAVKDELDSILEELNEA--
TadTPM1 EDSVTQLEKTLDEREELQEEKENLKKAAEELANAMAELOSI--
HmaTPMB ERNCCVLERNIKELEEIEKVKKLTIDIENIADMDVGEDDD--
HmaTPMIA AAREDELELKMTELEVLQAAKDEYTRAKAELDATIQELSEL--
HmaTPMIB EAQVKTLETTLAKLEQLKVEKDMYNRVKNLDRLLAEIQQMNV
HmaTPMDIC BEKAKRLERRQEELDELQLEKDFNQTKTEFDALCAHINEM--
PcaTPM1 EARSRDLEAELENECDELAALAAEAYGQSKADMDELLELASM--
NveTPM10 ERRCMRLERENDMVEETRAYKKNYDMMQKELHDTLNDIECV--
NveTPM97 ERRCGPLERLLEDEQSQIDDFRNKRRDVEKEMEDMVGLVDESID
NveTPM1 EQKVQLELAQAEEAMELEKAKEQYKVEEELDSTLAELESEM--
SpuTPM1 EGQVKSLSHQVDSLEELVQEKEKSRGMNDEMDCRCLQELNMDI--
SpuTPM ETSVTQLRKRVDLELELQEWQSKKHTCQGELNQLISEINEM--
SkoTPM ERSNQKLERQVDDLEELFSEKEKNKSMADELDQTLQDLHAM--
BflTPM1 ERTVAKLEKNVDDLESLYAEKEKYRGVSEELDQALNELHNM--
BflTPM2 ERKIQLMETEISKLEQLEEVKEKYQGAKADLDAALNELNEM--
CinTPM1 EKSVVKLEKNI DELESLYAEKCKIKAI SEDMDVTLQIGDL--
CinTPM2 EKSVVQLERSIDLEELYKQKQLRNFNEEMWFDLRNM----
CinTPM3 ERTVDKLEKTI DYLEQLYTEKLAYKGI SEKLDKTLSDMITLN--
CinTPM4 ENSLNNLAQQVGVLEELYEVKMKV-----
CinTPM5 EKSVS IMNLRMENMEEIAYLHSEVDKAKKMYTEAVNELNEL--
CinTPM6 ENEAKKYQADIEKLELDKEMAEKEEAKAELDRVLSSELGEM--
TruTPM11 ERTVAKLEKTI DDLEKLSQAKEENLDMHQMDQTLMELENNL--
TruTPM12 ERSVAKLEKTI DDLEELYAQKLYKAI SEELDHALNDMTSM--
TruTPM2 ERSVAKLEKTI DDLEKLAQAKEENLDMHQVLDQTLLELNNL--
TruTPM3 ERSVAKLEKTI DDLEELYAQKLYKAI SEELDHALNDMTSM--
TruTPM41 ERTVTKLEKSI DDLEKLSAKEENLGMHQVLDQTLLELNSL--
TruTPM42 ERTVAKLEKTI DDLEELAI AKEKNVLEHQAALDQTMHELENNL--
TruTPMX ERSRDNCERTINNLEAVSKAQEENVKINATLEQTLHDLNFL--
XtrTPM1 ERTVAKLEKTI DDLEKVT HAKEENLNMHQMLDQTLLELNNM--
XtrTPM2 EKSVVKLEKTI DDLENLSAAKEESI ELNQLDQTLLELNNM--
XtrTPM3 ERSVAKLEKTI DDLEKLATAKEENLGMHQVLDQTLQELGSL--
XtrTPM4 ERSVAKLEKTI DDLEKRLR LTKDENAKMQTMLDQTLQQLNSL--
MmuTPM1 ERSVTKLEKSI DDLEKVAHAKEENLSMHQMLDQTLLELNNM--
MmuTPM2 ERSVAKLEKTI DDLETLASAKEENVEIHQTLDQTLLELNNL--
MmuTPM3 ERSVAKLEKTI DDLEKLC TKEEHLCTQRMLDQTLLELNNM--
MmuTPM4 ERTVSKLEKTI DDLEKLAQAKEENGLHQTLDQTLNELNCI--
DpuTPM ERSVQKLQKEVDRLEDMLAQKEKKNLLQEEMESTLQDIQNM--
AmeTPM1 ERSVQKLQKEVDRLEVVVNERCKYKAI ADEMMDQTFADLAGY--
AmeTPM2 EKTVKKLQKEVDRLEELGINKDRYKSLADEMDSTFAELAGY--
AmeTPM3 ERTVKKLLKEVDMKEELREEKEKYKAVCDDMDATFAEMTGY--
AmeTPM4 EKVMKMF SKELDAREFLFREKEKYKYICDDMDSTFAELTGY--
TcaTPM1 ERSVQKLQKEVDRLEDLAEKEKKNLLSDEMEATLHDIQNM--
TcaTPM2 EKTVKKLQKEVDRLEELGINKDRYKSLADEMDSTFAELAGY--
AgaTPM1 ERSVQKLQKEVDRLEELIVEKLYAEIGDDLDFAFVDLIPG--
AgaTPM2 EKNVKKLQKEVDRLEKLMNEKEKYKAI CDDLDSTFAELTGY--
DmeTPM ERSVQKLQKEVDRLEDLVLEKERYKDIGDDLDFAFVELILKE--
DmeTPM2 EKQVKRLQKEVDRLEELGINKDRYKSLADEMDSTFAELAGY--
BmaTPM ERSVQKLQKEVDRLE-----
CelTPM ERSVQKLQKEVDRLEELLLLEKERVRLNLTTEEIEQTVQEIQGS--
CbrTPM ERSVQKLQKEVDRLEELLLLEKERVRLNLTTEEIEQTVQEIQGS--
LgiTPM ERTVSKLQKEVDRLEELLAEEKEKYKAI SDELSTFAELAGY--
CcaTPM ERTVSKLQKEVDRLEELLLSEKEKYKTI SEELDSTFAELAGF--
HroTPM1 ERSVSKLQKEIDRLEELLLLEKEKYRTI SEELDSTFAELATF--
HroTPM2 ERTVSKLQKEIDRLEELLAEEKEKYKDI SEELDSTFSELASF--
HroTPM3 ENNIQKLQREIDKLEELIAEKEKCKVINRELDATFAELTGF--
HroTPM4 ENNIQKLQREIDKLEELIAEKEKCKVINRELDATFAELTGF--
HroTPM5 ENYVQLLQKEVDKLEELAAEKEKCKTIDSELNATFAELTGF--
HroTPM6 ERAVTMLQKEVDRLEELTSEKDFRVLVGLGELDSTITELTGF--
HroTPM8 KRELKSKQQLDSENFNEMREEYKYLRDELDCYKELNSL--
HroTPM7 ERNAGKLQREVDRLEELLLSREENKLLREEDAAEQEIQNI--

;
end;

Replicate 2

#NEXUS

[Title gen2]

begin data;

dimensions ntax=61 nchar=203;

format missing=? gap=- matchchar=. datatype=protein interleave=yes;

matrix

[!Domain=Data;]

```
MbeTPM      AEAEANDAKRKLTLTEDDLKAEERLQSMQTRLRDAEQEAEDASKLQRLEATQDNDFGKAAEALEDKYKDLKRQFDDVERS
TadTPM2     AEQELASLIRRKTLLESDDLNRTEERLSEAESRLNSASTSNLDLEERKRLEDVDYADDERIDQIESDLKAAKLSTEEAERQ
TadTPM1     VKEKIDELNKEIEETEQQDDRESKLAETLTKTLEAETKTDEHEARAVLESRTNTSNTKLEELERQLNETLAAREEAETK
HmaTPMB     AESEVASYLRKIQLLEKDYNEVVSRCEALEEKLAITQDKGMSVEARKQLEENENEGDEKIQRLEEEVKEAKRLLLEENETK
HmaTPM1A    VEEKLEELIKLKTITIEDKLEADEREKLLKLSLAAEAQNQDEGLVKRELEHRGNAGSSQLQRLELERSELLAKNEKVTAKE
HmaTPM1B    SEEEVDRLQKELNNLDDELESSESCLNLTLIKRLHEAEKQAESEARRVLESRGQTDEKLSKLQSELDVMSKNSDVENR
HmaTPMDIC   AEERVTELTKELENDLEDQLDASESKMSTLQEKLAEEAKLHEEHDAARRILENRGRSDGGRI SRLQDELDELTLNLNKVVET
PcaTPM1     TEQTADQLKTLADLEDELDAESRLTSLTEKYNEEEKKAEDEGRAHKELENRGQTDYSRLNRLETLAEITEQNEVVVEK
NveTPM10    DKNESATLRRSCLTEHQLDKTEDILDQKLERLVLMLHKKTEQDIMLVKLEDRLEVDNSLDRLEPSAKAAIQRQHDAMER
NveTPM97    HESDLDSMQKRINLLSEDLDTLEAYEKKARLDSLEEKQESDGVVRELESVELEGDERLAELEEKTKREAVATVNVQKEHD
NveTPM1     AETEVAAALTKQLQLEEDDLDAESKLAETQGGQTEAEKQADESEARKVLENRGASDEERLASLERQYNDALERTEEAEKQ
SpuTPM1     AEAENVNLNSKLI LLEEDNGKQEALSDTRRRLETFIEVEADENLARKVLETRSASDDDKIIDLQRMKENASRIEELDRL
SpuTPM2     FEEQAKTLNMKCRDLEDVMSDREDELQRKLLKIDEIEAESDENSFSRVLMKRENTNTDRIKDLTMMDQQTADIERLDKV
SkoTPM      AEAEVSSLQRRQLLLEDEELERQERYQVAADKLADIEKAADESEARKVLENRGLSDDDRITELNVLKTRQMAEDADVKE
BflTPM1     AEAEVASLNRRIQLVVEEELDRAQERLNSTVEKLTDSDEKAADESEARKVLENRQGADEDKMELLDMLQREAKMIAEEADRK
BflTPM2     AENDIESLRRKMLLEADLTAETSLKETNEKNRLEDEAESRQALEHRSTDEDDKSSQMETDELDAKEAKEEMELK
CinTPM1     AEQEVASLNRRITLVEEELDRAQERLTI SLSKLEEAKEKAADESEGRKVIENRSLKDEERLEVEQEIQLTEAKNIAEDADRK
CinTPM2     AEEEVASLNRRICLVVEEELDQAQERLTI SLSKLEEAKEKAADESEGRKVIENRSLKDEERLEVEQEIQLTEAKNIAEDADRK
CinTPM3     SELEVNAQTRRMQLLEEEEMQVTERLDEAVAKLEVAEKAAEESSEGRKVIENRSLKDEERLEVEQEIQLTEAKNIAEDADRK
CinTPM4     VEEENINLKHQLNAKENFIGKLEPLLDLDTVRRKLETFIEVEADENLARKVLETRSASDDDKIIDLQRMKENASRIEELDRL
CinTPM5     AEDQNQDLERLRLVVEGLDRADEKLTIAKAQLSSLEQSDGSAKYLENEFNSSVKNYEAHLDDLDRSKMLAEEMSRK
CinTPM6     FEEVNRSLSNKISTNSTDIERLELQNEELKRSSENAERELDEVQELKQLQSEHTASAEERCDLLEELKLRKMDLDEVTTN
TruTPM11    AEAEVASLNRRIQLVVEEELDRAQERLGTALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPM12    AEGDVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPM2     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPM3     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPM41    AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPM42    AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
TruTPMX     AEMEVTTLSNRLQNEEDTLDRQERLADALRQVEEVEKVADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
XtrTPM1     AEGDVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
XtrTPM2     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
XtrTPM4     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
XtrTPM3     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
MmuTPM1     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
MmuTPM2     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
MmuTPM3     AEAEVASLNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
MmuTPM4     AEGDAAALNRRIQLVVEEELDRAQERLATALTKLEEAKEKAADESEGKVIENRAMKDEEKMEIQEIQLEKAKHIAEEADRK
DpuTPM      AEGEVAGLNRRVQLLEEDLERSEERLNTATTKLAEASHSADESEMRKVLNRSLSDEERMDALENQLKEARFLAEEDADRK
AmeTPM1     AESEVAALNRRIQLVVEEELDRAQERLATALTKLAEASQAADSEARKILENRSLSDEERMDALENQLKEARFLAEEDADRK
AmeTPM2     AESEVAALNRRIQLVVEEELDRAQERLATALTKLAEASQAADSEARKILENRSLSDEERMDALENQLKEARFLAEEDADRK
AmeTPM3     AEQDRTTLTTRVQIEIATLTTKKEELRLTAQTKLGEASELADDAARQSELEKMLVLEDRSRLDEERMEKMLQDLKADLADGK
AmeTPM4     TQSELAVLNRRKMQQCQLNLEKSEERRLTAQAKLAQAMETAEDAKICKVLENRSKQDEERMDQLMTQLKEARLIAEDADTK
TcaTPM1     AESEVAALNRRIQLVVEEELDRAQERLATALTKLAEASQAADSEARKILENRSLSDEERMDALENQLKEARFLAEEDADRK
TcaTPM2     AEAEMASLNRRKQVQIEEDLERSEERLNTATTKLAEASQAADSEMRKVLNRSLSQDEERMDQLTNQLKEARLIAEDADTK
AgaTPM1     AESEVAALNRRIQLVVEEELDRAQERLATALTKLAEASQAADSEARKILENRSLSDEERMDALENQLKEARFLAEEDADRK
AgaTPM2     TEANVAALTRKVVQVEEDLEKSEERSAALSLEATQADENNMCKVLENRSQDEERMDQLSNQLKEARMLAEDADTK
DmeTPM1     AESEVAALNRRIQLVVEEELDRAQERLATALTKLAEASQAADSEARKILENRSLSDEERMDALENQLKEARFLAEEDADRK
DmeTPM2     TESEVATQNRKVVQIEEDLEKSEERSSTAQKLEATQADENNMCKVLENRSQDEERMDQLTNQLKEARMLAEDADTK
BmaTPM      AEAEVASLNRRMTLLEEEELERAEERLKIATDKLEEAETHAADAESSEARKSMETRSQQDEERANVLEIQVDEAKMIAEDADRK
CelTPM      AEAEVASLNRRMTLLEEEELERAEERLKIATEKLEEAETHNVDESEARKSMETRSQQDEERANVLEIQVDEAKMIAEDADRK
CbrTPM      AEAEVASLNRRMTLLEEEELERAEERLKIATEKLEEAETHNVDESEARKSMETRSQQDEERANVLEIQVDEAKMIAEDADRK
LgiTPM      LETEAAGFTRRITLLEEDLERSEERLTSAQSKLEEAASKAADESEQRKRTVENKLAEEAEKLEDEYETALKTAQAHAHTDTETR
CcaTPM      AEGEVQALTRRIRLLEEDYEQTENRNLQNASEKLEEAASKAADESEGRKVLNRRNITDEERIVQVERLEETILLGEEADRK
HroTPM1     AEGEVGGLTRRISLLEVDYEQTAVRLSTASEKLEDEASKVAEEAEARKSLESRLADDERLTFLETQLKEAKYI SEDAGRK
HroTPM2     AESDVGALTRRIQLLEVDYEQTASRLBIASEKLEEAASKHAESENRKSLNLSLMDNERITFLEEQLKEAKYI TAEDAGSK
HroTPM3     AETEVQTLAKKVGKLEEDFENTESRLKAANEKLEEAATKAADESEGIKVLNRRFTLEDEKIQQLEHEIEDVILVGEDSDRR
HroTPM4     AETEVQTLAKKVGKLEEDFENTESRLKAANEKLEEAATKAADESEGIKVLNRRFTLEDEKIQQLEHEIEDVILVGEDSDRR
HroTPM5     AEAEVQNLTKTVRNLEEKFFEDTENRKLQTSKLELASKAADESEGIKVLNRRMITEEERIQQLEKELEETIMAGEDSDRR
HroTPM6     AEAEMVSLGKTVRSLEEDYEYESTENRLLQTTTKLEQAASKFEESDGRKVLNRRNIAIDDEERMVILEKLELVITLFGEDADRK
HroTPM7     AEDDLSTLTKKLRLLIEEDYEHIQTQLQSTNEKILELSKTSDENEARKALESRQNMDDKMLKLEQWLKESKASCEDAEKK
HroTPM8     AESQVMALTRRVELLEDERDEMRRYSVLLNKLNDASKVVDFELKISNECFKNLDDEKISSLEDQIRTLRLAADTAEEK
```

```
MbeTPM      HAEATRKLQLTEDDLEKAEERAEVAEKVRELERELDATANELRSREISEEQQAIAEEGSTERMRELKRHDNLSRELEEA
TadTPM2     FEEAERKLRVLEGDHQRATIEKASSDKITNLEGLQVGNENLKEADDAERIAANDQEEDYQAKIKALEERLLAADVRLEEA
TadTPM1     YKEISEKLEELKELEEEEEKADTAERATQLENDLILTTNNKSMKVEVMSMKAQEREEVAKLAEMEKCAEAEQEVDRDA
HmaTPMB     SNESERRRVVFRDIERTAAKADSLERIQVLQETIDNATISLKELEAREGESSQREYNAEQIVMLEGKYKEAEVRAEAN
```



```

CinTPM4  ENSLNNLAQQVGVLEELYEVKMKV-----
CinTPM5  EKSVSIMNLRMENMEEIAYLHSEVDKAKKMYTEAVNELNEL--
CinTPM6  ENEAKKYQADIEKLELDKEMAKEEAKAELDRVLSSELGEM--
TruTPM11 ERTVAKLEKTIDDLEELYSQKLYKKAISEELDHALNDMTSM--
TruTPM12 ERSVAKLEKTIDDLEELYAQKLYKKAISEELDHALNDMTSM--
TruTPM2  ERSVAKLEKTIDDLEEVYAQKLGKALSEELDLALNDMTTL--
TruTPM3  ERSVAKLEKTIDDLEELYAQKLYKKAISEELDLALNDMTSM--
TruTPM41 ERTVTKLEKSIDDLEELYAQKLYKKAISEELDHALNDMTSL--
TruTPM42 ERTVAKLEKTIDDLEELYNQKLYKKAISEELDHALNDLNTL--
TruTPMX  ERSRDCERTINNLEAVSKAQEENVKINATLEQTLHDLNFL--
XtrTPM1  ERTVAKLEKTIDDLEELYAQKLYKKAISEELDHALNDMTSM--
XtrTPM2  EKSVVKLEKTIDDLEEVYSQKMRYKKAISEELDNALNDITSL--
XtrTPM4  ERSVAKLEKTIDDLEELYAQKLYKKAISEELDHALNDMTSL--
XtrTPM3  ERSVAKLEKTIDDLEELYAQKLYKKAISEELDHALNDMTSM--
MmuTPM1  ERSVTKLEKSIDDLEELYAQKLYKKAISEELDHALNDMTSM--
MmuTPM2  ERSVAKLEKTIDDLEEVYAQKMYKKAISEELDNALNDITSL--
MmuTPM3  ERSVAKLEKTIDDLEELYAQKLYKKAISEELDHALNDMTSM--
MmuTPM4  ERTVSKLEKTIDDLEKLAQAKEENVGLHQTLTDLQTLNELNCI--
DpuTPM  ERTVAKLQKEVDRLEELVHEKEKYKAITDDLDQTFSELSAY--
AmeTPM1  ERSVQKLQKEVDRLEDLAAEREKNKLLQEEMEATLHDIQNM--
AmeTPM2  EKTVKKLQKEVDRLEVLHQKEKRKTICEELDKTFSELSGY--
AmeTPM3  ERTVKKLLKEVDMKEELREEKEKYKAVCDDMDATFAEMTGY--
AmeTPM4  EKMVKMFSKELDAREFLFREKEKYKICDDMDSTFAELTGY--
TcaTPM1  ERSVQKLQKEVDRLEELVAEKERYKEIGDDLDTAFVELIL---
TcaTPM2  EKTVKKLQKEVDRLEELGINKDRYKSLADEMDSTFAELAGY--
AgaTPM1  ERSVQKLQKEVDRLEELVMEKEKYREIGDDLDTAFVELILKE--
AgaTPM2  EKNVKKLQKEVDRLEKLMNEKEKYKAI CDDLDSTFAELTGY--
DmeTPM1  ERSVQKLQKEVDRLEDLLNVRGKNKLLQEEMEATLHDIQNM--
DmeTPM2  EKQVKRLQKEVDRLELRFNEKEKYKAI CDDLDQTFFAELTGY--
BmaTPM  ERSVQKLQKEVDRLE-----
CeltPM  ERSVQKLQKEVDRLELRDAEVLKARQLQDELDMVQELNSV--
CbrTPM  ERSVQKLQKEVDRLEDRDAEIRKARQLQDELDMVQELNSV--
LgitPM  GRELSRLHIQFEKVEELDMEREKSKSLQRELESTMEELHDI--
CcaTPM  QRELHITRLELDKKEQLCDARMQYKSLREEMDATLVDIQSM--
HroTPM1 ERSVSKLQKEIDRLEELLEKEKYRTISEELDGTFFSELATF--
HroTPM2 ERTVSKLQKEIDRLEELLAEEKEKYKDI SEELDGTFFSELASF--
HroTPM3 ENNIQKLQREIDKLEELIAEKEKCKVINRELDATFAELTGF--
HroTPM4 ENNIQKLQREIDKLEELIAEKEKCKVINRELDATFAELTGF--
HroTPM5 ENYVQLLQKEVDKLEELAAEKEKCKTIDSELNATFAELTGF--
HroTPM6 ERAVTMLQKEVDRLEELTSEKDKFRLVLGELDSTITELTGF--
HroTPM7 ERNAGKLQREVDRLEELLLSREENKLLREEFDAAFQEIQNI--
HroTPM8 KRELKSKQELDKSENFNEMREEYKYLRDEL DSCYKELNSL--
;
end;

```