

## Figure S2:

### Multiple sequence alignment using MUSCLE version 3.7.

```
lbra|LbrM18_V2.1630      MSQRRVEAVRVRPNTELCRNSCVSL-SHATHHISLQDNSGVNALAGRRSYKEDFLFDEH
lmex|LmxM18.1600        MSQRRVEAVRVRPDTESRHNSCVSL-NHATRRI TAQDDIGANVLGRRSYKEDFLFDEH
linf|LinJ18_V3.1590    MSQRRVEAVRVRPDTESRHNSCVSL-NHATRHI SAQDDTGANALTGRRSYKEDFLFDEH
lmaj|LmjF18.1600       MSQRRVEAVRVRPDTESRHNSCVSL-NHATRHI STQDDTGANALVGRRFYKEDFLFDEH
tcru|Tc00.1047053507625.180 -MGRRVQLVIRLRPGEQGA--SCVSV-GVNKKEITVVDLSGTHASSTPREFHVDQVVQED
tviv|TvY486_1012140    -MDRRVQVVVRTRPSEGQ--SCVSI-SSEGKEVVVSDVGAVYGNVCVPRSFYVDCSVYAN
tcon|TcIL3000.10.10660 -----
tbrg|Tbg972.10.14990   -MGRRTHVAVRLRPSEGSP--TCVDVKDDKGKEVVVADMSGIYAI S I P H I F R V D Q V L D E R
tbru|Tb927.10.12440   -----MSGIYAI S I P H I F R V D Q V L D E R
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```
lbra|LbrM18_V2.1630      VSNRAVFEKLVLRMLAATPEHPD TLCFLAYGHTSSGKTYTIGGSEKEP GILALC VEELL
lmex|LmxM18.1600        VSNRAVFEELVLRQKRAATPEHPD TLCFLAYGHTSSGKTYTIAGSEQEP GILALC VEELL
linf|LinJ18_V3.1590    VSNRAVFEELVLRQKRAATPEHPD TLCFLAYGHTSSGKTYTIAGSEQEP GILALC VEELL
lmaj|LmjF18.1600       VSNRAVFEELVLRQKRAATPEHPD TLCFLAYGHTSSGKTYTIAGSEQEP GILALC VEELL
tcru|Tc00.1047053507625.180 CGNEELFRSLVLRIRSSA-DEPDTSCFLAYGHTSSGKTHSIAGTDEKPGLLT LSAEALL
tviv|TvY486_1012140    CTNEKLFEFVLNDRIRTSV-DSPDTSCFLAYGHTNSGKTHTIAGCRREPGL LSLAARKVL
tcon|TcIL3000.10.10660 -----
tbrg|Tbg972.10.14990   CSNEELFEKLVYDRILSSA-EQPD TSCFLAYGHTNSGKTHTIAGGRREAGLL S LAARAVL
tbru|Tb927.10.12440   CSNEELFEKLVYDRILSSA-EQPD TSCFLAYGHTNSGKTHTIAGGRREAGLL S LAARAVL
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lbra|LbrM18_V2.1630      RGEVVEVAMLEVYLESVNDLLAHGEP RHIRRRQGPLGPVIVVEGLTTC SLTSVQQWNAV
lmex|LmxM18.1600        RGEVVEVAMLEVYLESVNDLLAHGEP RHIRRRQGM RGPVIVVEGLTTC SLTSVQQWNAV
linf|LinJ18_V3.1590    RGEVVEVAMLEVYLESVNDLLAHGEP RHIRRRQGM QGPVIVVEGLTTC SLTSVQQWNAV
lmaj|LmjF18.1600       RGEVVEVAMLEVYLESVNDLLAHGEP RHIRRRQGM QGPVIVVEGLTTC SLTSVQQWNAV
tcru|Tc00.1047053507625.180 HTYGVAEVAMLEVYGESVHDLLAQGERRMIRRRAGPDGTVIMVENLTSC SLTSMEEWKAL
tviv|TvY486_1012140    ETHGVLEVMLEVYGESVHDLLARGEKRFIRRRSSPEGVVIVVENLTCC SLSTLQEW EAV
tcon|TcIL3000.10.10660 -----
tbrg|Tbg972.10.14990   DMYGYLEVAMIEVYGENVHDLLAQGERRLIRRRAGPDGVAI IVEDLTTC SLSTLQEW EAV
tbru|Tb927.10.12440   DMYGYLEVAMIEVYGENVHDLLAQGERRLIRRRAGPDGVAI IVEDLTTC SLSTLQEW EAV
```

```
lbra|LbrM18_V2.1630      AAYSMSSRRTAPTERNPRSSRSHAI FTIKSRGVRLCFV DLAGSERQTVFSPQLNKESISI
lmex|LmxM18.1600        AAYGMSSRRTAPTERNRSSRSHAI FTIKSRGVRLCFV DLAGSERQTVFSPQLNKESISI
linf|LinJ18_V3.1590    AAYGMSSRRTAPTERNPRSSRSHAI FTIKSRGVRLCFV DLAGSERQTVFSPQLNKESISI
lmaj|LmjF18.1600       AAYGMNSRRTAPTERNPRSSRSHAI FTIKSRGVRLCFV DLAGSERQTVFSPQLNKESISI
tcru|Tc00.1047053507625.180 SEFGMLARRTAPTERNRSSRSHAI FTIKTRGMRLCLV DLAGSERQTTYS PQLNKESIAI
tviv|TvY486_1012140    SAYGMGTRRTAPTDRNSRSSRSHAI FTIKSHGVRLCMV DLAGSERQTTYS PQLNKESIAI
tcon|TcIL3000.10.10660 -----
tbrg|Tbg972.10.14990   SAFGMETRRTAPTERNRSSRSHAL FTIKSRGLRLCMV DLAGSERQTTYS PQLNSESIAI
tbru|Tb927.10.12440   SAFGMETRRTAPTERNRSSRSHAL FTIKSRGLRLCMV DLAGSERQTTYS PQLNSESIAI
```

```
lbra|LbrM18_V2.1630      NKSLRSLSTVLEALS NQRVTQD GARPYVNF RD T T L T V L L Q R Y L T G S S M T F L A C V H P S A D
lmex|LmxM18.1600        NKSLRSLSTVLEALS NQRVAQD GTRSYVNF RD T T L T V L L Q R Y L T G A S M T F L A C V H P S A D
linf|LinJ18_V3.1590    NKSLRSLSTVLEALS NQRVAQD GTRSYVNF RD T T L T V L L Q R Y L T G A S M T F L A C V H P S A D
lmaj|LmjF18.1600       NKSLRSLSTVLEALS NQKVAQD GTRSYVNF RD T T L T V L L Q R Y L T G A S M T F L A C V H P S A D
```

tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

NKSLRSLSTVLEALSSARMKSDGSTS YVNFRTTTLTVLLQRYLSGASMTVFLACIHPDTA  
NKSLRSLSTVLEALSTTRKRS DGTCSYVNFRTTTLTVLLQRYLCGSSMTVFLACIHPDVQ  
-----STVLEALSTMRRKPDGTSSYVNFRTTTLTVLLQRYLCGASMTVFLACIHPDVQ  
NKSLRSLSTVLEALSTIRRRPDGSSSYVNFRTTTLTVLLQRYLCGASMTVFLACIHPDVQ  
NKSLRSLSTVLEALSTIRRRPDGSSSYVNFRTTTLTVLLQRYLCGASMTVFLACIHPDVQ  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

YYQETLSTLRYTQRLKRI RTRVTKVDEVE-WSEMKTSEHQVLLDELTRLREQM-----  
YYQETLSTLRYTQRLKRI RCTITKDEGE-WSGLKVSEHQVLLDELTRLREQM-----  
YYQETLSTLRYTQRLKRI RTRVTKVDEGE-WSGMRVSEHQVLLDELNRLREQM-----  
YYQETLSTLRYTQRLKRI RTRVTKADEGE-WSGMRVSEHQVLLDELSRLREQV-----  
FYYETMSTMRYTQRLKCI NTKNAPKPNEDMSLFLQGENQKLEELMILRRI VGRQHEQR  
FIQETLSTMRYTQRLKRI KTKGRPKCDDLSLFRPSNQTNLLEELMMLRRI V-----  
FVQETMSTLRYTQRLKRI KTKSAPQKPSDDSSLFHPKEHQDLLEELALLRKIVN-----  
FVQETMSTMRYTQRLKHI KTKPPPQKPNDDSSLFHPKEHKNLLEELSALRKIVG-----  
FVQETMSTMRYTQRLKHI KTKPPPQKPNDDSSLFHPKEHKNLLEELLALRKIVG-----  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

-----ASENASKLV EAAHQRI--AELESTL---AKQGRSPCGAVGASPLLSPPRELNA  
-----VSENA TKLVEATHRRRI--AELEHTL---AKQGG LHDGAAGASAPLSAPREMNA  
-----VSENVTKLVEATHRRRI--AELEHTL---AKQGG SHDGAAGASAPLSAPREMNA  
-----VSENTTKLVEATHRRRI--AELEHTL---AQGG LHDGAAGASAPLSAPREVSA  
EEYHYNDEFKRVSEETVIGRLPKDHCSDSL---FQNHESALQESSPMI SASIVGHRQRL  
-----EKQYASLLRS SKHPGASPDCECDGRLDYVSTTANPPQKESAGSSNLGSLNRRRKL  
---QSSCGEFS PQNDEALAA SVCRRHFD PST---PQRETGPETENNDQCNS SGLRHKQRL  
---INPCAGVAAGNDDTLKTKLYQDNCAPPA---PPQDAAPRVEG PDRSERSIMRHKQRL  
---INPCAGVAAGNDDTLKTKLYQDNCAPPA---PPQDAAPRVEG PDRSERSIMRHKQRL  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

SRARDTRRVAGWLLSRVLGELPELNVGYDAYFDAYFPPSVQVIGYVSTMASLVPRIPGD-  
RRVRDTRRVAGWLLSRVLGDLPELNVGYDAYFDAYFPPSVQVIGYVSAMASLVPRTAGD-  
RRARDTRRVAGWLLSRVLGDLPELNVGYDDYFDAYFPPSVQVIGYVSAMASLVPRIASD-  
RRARDTRRVAGWLLSRVLGDLPELNVGYDAYFDAYFPPSVQVIGYVSAMASLVPRTAGD-  
LRYKDAMRVAGWLLSRILSELPELSVGFDDYFDYLP SQVQVVG YISLMTCMAPRDVNEA  
LRSKDTRRVAGWLLSRILGKLPALSVGFDDYFDPFINDGVQVVG YVSLMACLPDRDAGDA  
IRSKDIRRVAGWLVSR TGLMPLHLSVRFDDYFDDFLPCEVQVVG YVSLMACLPDCKA EA  
LRSKDIRRVAGWLVSR TSLMLPQLSVGFDDYFDDYLPGEIQVVG YVSLMACLPDCKTEA  
LRSKDIRRVAGWLVSR TSLMLPQLSVGFDDYFDDYLPGEIQVVG FVSLMACLPDCKTEA  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

-DPLAFLDVGD LAMGLSMLDAGVPPFVRLHLSRCGDPSGWE GYEWDS SHDVVYVLAFFEY  
-DPLAFLDVGD LAMGLSMLDAGVPPFVRLHKSVCSDLSN WAGCEW DGTQSVVYVLTFFEY  
-DPLAFLDVGD LAMGLSMLDAGVPPVRLHKSVCSDPSSWEGCEW DGTQNMVYVLAFFEY  
-DPLAFLDVGD LAMGLSMLDAGVPPFVRLHKSVCSDPSSWEGCEW DGAQNVVYVLAFFEY  
MGGLAFLDVGD I AMGLSMLDAGIPACVGLHRLTCGESNTWEAHE YDGVNR-VFVLAFFEI  
TGTLAFLDVGD LVMGF SMLDAGIPACVGLHRLNCGSSSWAHE YSEVDK-VFVLAFFEY  
SHSLAFLDVGD PALGLSMLDAGIPACVGLHRLDCKGIRYWEVHE YDETN S-VFLAFFRV  
LNLAFLDVGD P SIGLSMLDAGIPACVGLHKLSCKEVHSWEVHE YNETNN-IFLLAFFKV  
LNLAFLDVGD P SIGLSMLDAGIPACVGLHKLSCKEVHSWEVHE YNETNN-IFLLAFFKV  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590

HPTAMSA-----GMEEALQCCGGYVTSAPLLPIATVLCVAESATRRVKEEVLQRLVDL  
HPTAMSSA-AEDAAGME EALPCCGGYVTSAPLLPIATVLCVAAS TTRRVKEEVLQRLVDL  
HPTAMSSATAGDAAGME EALPCCGGYVTSAPLLPIATVLCVAAS TTRRVKEEVLQRLVDL

lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

HPTAMSPA-AGDAAGMEEALTCGGYVTSAPLLPIATVLCVAASTTRRVKEEVLQRLVDL  
NEHLVEIM-----GDTHDAFECGGLLTLEPLVPLAIVLCTPLDSSDELKENVLQHLVTL  
NEHLVESM-----NGTGEALECCDGLTLEPLVPLALVLCPTPDASDELKESVLQHLITL  
GEGLEVEPM-----DVSGNPFECGGVLTLEPLVPLALVFGTSRDTCEHVKENVLQHLITL  
DEQLVEPL-----GASGSPFACCGLLTLEPLMPLALVFGAPLNAPNEVKENVLQHLVTL  
DEQLVEPL-----GASGSPFACCGLLTLEPLMPLALVFGAPLNAPNEVKENVLQHLVTL  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

QCEQHEAVMEQANAGARTPSLSSSLSSSRQST---LPSGTELLDASLVH--SVGGAEGDN  
QCEQHEAVAEQAKAGARTPSLSSSMLSSRQDG---FPSDAALLDASEMR--NISEAESDD  
QCEQHEAVAEQAKTGARSPSLSSMTLSSRQAG---FPSAASLLDASDMR--NVSEAESDD  
QCEQHEAVAEQAKTRARTPSLSSSMLLSRQDG---FPSEASLLDTSDMR--NVSEAESHD  
QGEQDGAL--ESSIGSSSLSQLTPMHTGIDGAMENPKLSLLKAMTQWRDDYVKEVTSSS  
QSDQEETS--NCFPVNSASMLQVMSDLHPVDVVVKYPEEEQSKILPDCQ--HGFTQDPDE  
QTEQGHVTEGNAATQTSRSLYEQGSASCENS---RCGCRALVDTSETT--YSSGVDEET  
QSEQHQPPAGASNDTASQSVHKKSNDSHGVSVP---FFNSEVLDALSDYS--YHYEVGEDS  
QSEQHQPPAGASNDTASQSVHKKSNDSHGVSVP---FFNSEVLDALSDYS--YHYEVGEDS  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

DASAISSAANGNAL-LGKEVHNQAADTPCIVAPLKEEDSSTNNSNSHSCDSRKEARAEI-  
TASASTDSTSGGAF-LAQEVRRQAADTSHIVTPFQEEEECSASGGR-SCDSREEARAEV-  
DASASTGSTSGGAL-LALEARCQAADTPHIATPFQ-EEEGSASGGC-SCDSCEEARAAM-  
DASASTGSTSGGAL-LALELRRQTADTSHIVTPFQEEEEGSASDGR-SCDSREARAEM-  
DTESFSAAP-----LAEIEERQTLNKLQVCSFPQ-ESASVNSGEAFSNEKTTIIHLDH-  
TTDSIASVMETLKR-EVRHSFRDPLNQSHLSTEKA--QHCETPDIGSLCRNRPFLVTA-  
EFESIVTIHGTEPPSVLKEGSPQSSTHTPGRSPHSREQSDEVHNPR-RAQFFGGKRSDA-  
LIGSPVG--PQRKA-LTDHNEGQNGDGFRSQISWESVQFQEDLTEMVCCRAVGSADIDEA  
LIGSPVG--PQRKA-LTDHNEGQNGDGFRSQISWESVQFQEDLTEMVCCRAVGSADIDEA  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

-----GSAEV-RHNLGECTAPSRPSVSPPREGKAE-----  
-----RSKAVHRHLPGELTSPSRSSVPPRARKAE-----  
-----RSAEVHRHLGELTSPSRPSAPPPRARNAE-----  
-----RSAEMHRHLPGELTSLSRPSVPPRACKAE-----  
--KLHAIYASSSSSFSESSSDSSVILGSKLSLLS PAVADEGQCQEIS-----RTHM  
-----PLLSFSSSLSSSFSTAPSTLPQVGANTQEGLTSPSPVPRDEAMEQNSYAESNEEQ  
----SDVLSSLSVSSSNEEGQRDLVSPGLTEERVACTTSGSTQDQS-----PQST  
DDPEPSSLSPPSTFCGEEKELNPVPLPNSVAVRAVSCDIDPEKGEQS-----PQSV  
DDPEPSSLSPPSTFCGEEKELNPVPLPNSVAVRAVSCDIDPEKGEQS-----PQSV  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600  
linf|LinJ18\_V3.1590  
lmaj|LmjF18.1600  
tcru|Tc00.1047053507625.180  
tviv|TvY486\_1012140  
tcon|TcIL3000.10.10660  
tbrg|Tbg972.10.14990  
tbru|Tb927.10.12440

-----ETKAAEGSTTAAVSPQASPT--  
-----EPAQVRGGTAAAVASSQLMPAT--  
-----ESAKVRGCTAAAVSSPLLMPAT--  
-----EPSQVRGGSAAAVSSPPLMPAS--  
SSECPSETECDAEKGVGMPQSIDREVHGANQVGVSVSPADVHVDMYRNPYLPHAPQTN--  
HEGTMDDTIGVELFQSDSATKSSFVLDHGGEDAARAPCATEVGSVVELPGGTLPAS--  
GEQIITDRDTCMDGNTS-GDPAFRARWLDGNTTSLDEIEQAASNVLDPVPPSPQHT--  
GEQIITDSADQCDVETLDDQPQLRAGGDESEISFK-EVELTVGTTANTSSSPGLLESQAK  
GEQIITDSADQCDVETLDDQPQLRAGGDESEISFK-EVELTVGTTANTSSSPGLLESQPK  
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lbra|LbrM18\_V2.1630  
lmex|LmxM18.1600

-----RRLFSQP-----RPS-----GTALALLPDAVSPGCTSKRRH  
-----CKSLSPW-----RTS-----GTS LAPLPADALPPGHTSKRRH

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linf|LinJ18_V3.1590      -----CKSFSP-----RPS-----GTSSAPLPPADEFPFGHTSKRRN
lmaj|LmjF18.1600        -----CKSFSA-----RTS-----GTSSAPLPPADELPPARTSKRRN
tcru|Tc00.1047053507625.180  -----CYSIEEFPAYAVIARERSKSDKKDDCAECSATASVSPPEKERIYEKNEKKKKK
tviv|TvY486_1012140      -----DQTILPA-----ETVSENTAPHNGPSSVDAPVKQEFEMSTGKKRKN
tcon|TcIL3000.10.10660     -----ASRFTVL-----HDRECTDRTQEGAASDAGAPSGKPSGGKGNNGD
tbrg|Tbg972.10.14990     SSHILVACEEENRL-----DCPRGEILELSGTLASESPEAHK-GKGKTKREN
tbru|Tb927.10.12440     SSHILVACEEENRL-----DCPRGEILELSGTLASESPEVHK-GKGKTKREN

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lbra|LbrM18_V2.1630      R--TAREGKAVKMQTCQGCSAA
lmex|LmxM18.1600        R--ATGEGKTVHMQSCQGCRCM
linf|LinJ18_V3.1590      R--TAGEGKTVKMQSCQGCRCM
lmaj|LmjF18.1600        R--IAGEGKTVNMQSCQGCSSM
tcru|Tc00.1047053507625.180  K--NLHRKRKPVVLQGCHNCVVL
tviv|TvY486_1012140      R-----RSREFVAHGCHGCTVA
tcon|TcIL3000.10.10660     DGVDShrkrepvsegchlcVml
tbrg|Tbg972.10.14990     R--DNHRDRDPVKQGCHYCVIL
tbru|Tb927.10.12440     R--DNHRDRDPVKQGCHYCVIM

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