SUPPLEMENTARY MATERIAL

Chapter 1:

A.

```
#NEXUS
Begin data;
    Dimensions ntax=166 nchar=260;
    Format datatype=protein gap=- missing=X matchchar=. interleave;
    Matrix
AcaGbY       ---------------------------------------------------------MTDLDRRHIREIWTA-AFENPEENGRLVIIRFFSDYPASKQYF
AcaMb        -------------------------------------------------------MELSDQEWQKVIDIWGK-VEPEIPAYGQVVILRLFEQHPETQEKF
AplGbE       -------------------------------------------------------MPFSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYF
CanMb        -----------------------------------------------------------MADFDMVLKCWGP-VEADHATHGSLVLTRLFTEHPETLKLF
CauMb1       -----------------------------------------------------------MADHELVLKCWGV-VEADFEGTGGEVLTRLFKQHPETQKLF
CauMb2       -----------------------------------------------------------MADYERFLKCWGA-VEADYTGNGGEVLTRLFKAHPDTQKLF
CcaMb1       -----------------------------------------------------------MADHELVLKCWGG-VEADFEGTGGEVLTRLFKQHPETQKLF
CcaMb2       -----------------------------------------------------------MADYERFLKCWGA-IEADYAGHGGEVLTRLFKEHPDTLKLF
CcrMb        -------------------------------------------------------MGLSDGEWQLVLNIWGK-VEADIPGHGQEVLIRLFKNHPETLEKF
CmiGbY       ------------------------------------------------------MTGITEADKENIHFIWEK-LYENPEENGKTIVLRMFTDYPETKMYF
CpiCygb      ME-----------------KVQGEMEIERW----------------------ERSEELSDAEKKVIQETWSR-VYMNCEDVGVSILIRFFVKFPSAKQYF
CpiGbE       -------------------------------------------------------MAFSEAEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYF
CpiGbX       MGCALSGSGI---------APGKTISESKRSPSSENLAAPKAGPEHGGDGLGAGPFPLADAQKERIQESWRI-LHDNIARVGIIVFIRLFETHPECKDVF
CpiGbY       ------------------------------------------------------MALLTDADKKNIQHIWAK-LFENPEENGKTIVIKLFKDYPETKAYF
CpiHbaA      -------------------------------------------------------MVLNAGDKANVKAVWNK-VAAHVEEYGAETLERMFTVYPQTKTYF
CpiHbaD      --------------------------------------------------------MLNHDEKQLIKHAWEK-VLGHQEDFGAEALERMFAVYPQTKTYF
CpiHbB1      ------------------------------------------------------MVHWTAEEKQLITNLWGK-V--NVAECGSEALARLLIVYPWTQRFF
CpiHbB2      ------------------------------------------------------MVHWTADEKQLITSLWGK-V--NVEECGSEALARLLIVYPWTQRFF
CpiHbG       ------------------------------------------------------MVHWTAEEKQLITSLWGK-V--NAEECGGEALARLLIVYPWTQRFF
CpiHbZ       -------------------------------------------------------MTLTQAEKAAVVAIWGK-IAAQADALGTESLERLFSSFPQTKTYF
CpiMb        -------------------------------------------------------MGLSDDEWHHVLGIWAK-VEPDLSAHGQEVIIRLFQVHPETQERF
CpiNgb       ------------------------MESGR----------------------------LSSTQQALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLF
CraMb        -----------------------------------------------------------MADFDMVLKCWGP-MEADHATHGSLVLTRLFTEHPETLKLF
CycrMb       -------------------------------------------------------MGLSDGEWHLVLNVWGK-VETDLAGHGQEVLIRLFKSHPETLEKF
DreCygb1     ME--------------------GDGGVQLT----------------------QSPDSLTEEDVCVIQDTWKP-VYAERDNAGVAVLVRFFTNFPSAKQYF
DreCygb2     ME-----------------KEREDEETEGR----------------------ERPEPLTDVERGIIKDTWAR-VYASCEDVGVTILIRFFVNFPSAKQYF
DreGbX       MGCAISGSGLT--------AGAPEIRPGEE----------------------ETPAGLTTNHIRLIKESWRL-IQEDIAKVGIIMFVRLFETHPECKDVF
DreHbAa      -------------------------------------------------------MSLSDTDKAVVKAIWAK-ISPKADEIGAEALARMLTVYPQTKTYF
DreHbAe      -------------------------------------------------------MSLSAKDKAAVKTLWAK-IAGKADDIGHDALSRMLIVYPQTKTYF
DreHbAx      --------------------------------------------------------MPSSAEKELIAEIWDQ-MTPVAEEIGSEALLRMFTTFPQTKTYF
DreHbBa      ------------------------------------------------------MVEWTDAERTAILGLWGK-L--NIDEIGPQALSRCLIVYPWTQRYF
DreHbBe      ------------------------------------------------------MVVWTDFEKATIQDIFAK-A--DYDVIGPQALARCLIVYPWTQRYF
DreMb        -----------------------------------------------------------MADHDLVLKCWGA-VEADYAANGGEVLNRLFKEYPDTLKLF
DreNgb       ------------------------------------------------------MEKLSEKDKGLIRDSWES-LGKNKVPHGIVLFTRLFELDPALLTLF
EpeMb        -----------------------------------------------------------MADLDAVLKCWGA-VEADFNTVGGLVLARLFKDHPETQKLF
TruMb        -----------------------------------------------------------MADFETVLKFWGP-VEADYGAHGGIVLTRLFTENPETQKLF
GgaCygb      ME-----------------KVQGEMEIERW----------------------ERSEEISDAEKKVIQETWSR-VYANCEDVGVSILIRFFVNFPSAKQYF
GgaGbE       -------------------------------------------------------MSFSEAEVQSARGAWEK-MYVDAEDNGTAVLVRMFTEHPDTKSYF
GgaHbA       -------------------------------------------------------MVLSAADKNNVKGIFTK-IAGHAEEYGAETLERMFTTYPPTKTYF
GgaHbAD      -------------------------------------------------------MMLTAEDKKLIQQAWEK-AASHQEEFGAEALTRMFTTYPQTKTYF
GgaHbG       ------------------------------------------------------MVHWTAEEKQLITGLWGK-V--NVAECGAEALARLLIVYPWTQRFF
GgaMb        -------------------------------------------------------MGLSDQEWQQVLTIWGK-VEADIAGHGHEVLMRLFHDHPETLDRF
GgaNgb       ------------------------MESGM----------------------------LSRTQQALIRESWRR-VSGSPVQHGVVLFSRLFDLDPDLLPLF
GgiMb        -----------------------------------------------------------MADFDMVLKCWGP-VEADYTTHGSLVLTRLFTEHPETLKLF
HsaCYGB      ME-----------------KVPGEMEIERR----------------------ERSEELSEAERKAVQAMWAR-LYANCEDVGVAILVRFFVNFPSAKQYF
HsaHBA       -------------------------------------------------------MVLSPADKTNVKAAWGK-VGAHAGEYGAEALERMFLSFPTTKTYF
HsaHBB       ------------------------------------------------------MVHLTPEEKSAVTALWGK-V--NVDEVGGEALGRLLVVYPWTQRFF
HsaHBD       ------------------------------------------------------MVHLTPEEKTAVNALWGK-V--NVDAVGGEALGRLLVVYPWTQRFF
HsaHBE       ------------------------------------------------------MVHFTAEEKAAVTSLWSK-M--NVEEAGGEALGRLLVVYPWTQRFF
HsaHBG       ------------------------------------------------------MGHFTEEDKATITSLWGK-V--NVEDAGGETLGRLLVVYPWTQRFF
HsaHBZ       --------------------------------------------------------SLTKTERTIIVSMWAK-ISTQADTIGTETLERLFLSHPQTKTYF
HsaMB        -------------------------------------------------------MGLSDGEWQLVLNVWGK-VEADIPGHGQEVLIRLFKGHPETLEKF
HsaNGB       ---------------------------------------------------------MERPEPELIRQSWRA-VSRSPLEHGTVLFARLFALEPDLLPLF
IpuGbX       MGCAISGLGL---------APKNTTEAASE----------------------DDAPHLTSEHIAMIKESWKV-IQEDIAKVGIIVFVRLFETHPECKDVF
LchCygb      ME-----------------KVQGEMEMDRW----------------------ERSDQLSDTEVESIRQIWSN-VYTNCENVGVLVLIRFFVNFPSAKQYF
LchGbE       -------------------------------------------------------MALSDAEVQTARDVWGQ-IYANAEENGTIILVRMFTEHPDTKSYF
LchGbX1      MGCVFSGSGI---------APSKSTPDING----SEAESRLSEELKSGSGQNSDALLLSEPQKELIQESWRI-LHQDITRLGIIMFIRLFETHPECKDVF
LchGbX2      MGCAISGLSWRA---VKGPGEEAKGKEGEA----------------------EALPAISQLQIHLIQESWKL-IQEDIAKVGIIMFVRLFETHPECKDVF
LchGbY       ------------------------------------------------------MAALTEADKQNIRGIWKT-VFENAEENGRTIVIRLFEKYPETKVYF
LchHbA1      --------------------------------------------------------MLSANDKTLISSTWNK-VAANAEDIGAEALERLFLAHPQTKIYF
LchHbA2      -------------------------------------------------------MGLTAADKTLIKSIWGK-VEKETEAIGVEALVRLFKCFPQSKVYF
LchHbB1      ------------------------------------------------------MVHWTETERATIETVYQK-L--HLDEVGREALTRLFIVYPWTTRYF
LchHbB2      ------------------------------------------------------MVTWTAEERKAITSVWSK-V--NPEEVGHEALIRLFIVYPWTQRYF
LchMb        -------------------------------------------------------MALSEAEWGLILKVWGK-AEPEAASNGKSVLLRMFQEHPDTQQHF
LchNgb       ------------------------MEKHN----------------------------FSVRSKELIRESWDR-LGKNKLPHGTVMFTRLFELDPDLMHLF
LplaHbA      ------------------------MPIVDS----------------------GSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFF
LplaHbB      ------------------------MPIVDS----------------------GSVPALTAAEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQEFF
MangMb       -------------------------------------------------------MGLSDGEWHLVLNIWGK-VETDLAGHGQEVLIRLFRSHPETLEKF
MbiMb        -------------------------------------------------------MGLSEAEWQLVLHVWAK-VEADLSGHGQEILIRLFKGHPETLEKF
MgaGbE       -------------------------------------------------------MSFSEAEVQSARGAWEK-IYVDAEDNGTAVLIRMFTEHPDTKSYF
MglaHb2      ---------------------------MSA----------------------HGIARTTEGERAAVRASWAV-LMKDYEHAGVQILDKFFKANPAAKPFF
MmuMb        -------------------------------------------------------MGLSDGEWQLVLNVWGK-VEADLAGHGQEVLIGLFKTHPETLDKF
MniMb        -----------------------------------------------------------MADFEMVLKHWGP-VEADYATHGNLVLTRLFTEHPETQKLF
NcoMb        -----------------------------------------------------------MADFDMVLKCWGP-MEADYATHGGLVLTRLFTEHPETLKLF
OanGbY       ------------------------------------------------------MVQVTDVEKANIQSIWSK-MMENLEKNGIDIFTRLFREYPETKKYF
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OanHbW       ------------------------------------------------------MVNWTSEEKHAIVSIWGK-V--DIEETGANALSRLLVVYPWTQRYF
OanMb        -------------------------------------------------------MGLSDGEWQLVLKVWGK-VEGDLPGHGQEVLIRLFKTHPETLEKF
OanNgb       ------------------------MENGR----------------------------LSGPEQELIRESWRS-VNSNPLEHGMILFTRLFDLEPDLLPLF
OlaCygb1     ME-------------------RKQGEVDHL----------------------ERSRPLTDKERVMIQDSWAK-VYQNCDDAGVAILVRLFVNFPSSKQYF
OlaCygb2     MSCRESPPPPSPPPQML--GVQRGECEDRP----------------------ERAEPLSDAEMEIIQHTWGH-VYKNCEDVGVSVLIRFFVNFPSAKQYF
OlaHbA       -------------------------------------------------------MSLSAKDKAAVKAFWAK-VSGQADAIGSDALSRMLVVYPQTKTYF
OlaHbB       ------------------------------------------------------MVEWTEQERSIITNIFGN-L--DYEDVGSKALSRCLIVYPWTQRYF
OlaMb        -----------------------------------------------------------MADYDMVLKHWGP-VEADYNTHGNLVLTRLFHEYPETQKLF
OlaNgb       ------------------------------------------------------MEKLSGKDKELIRGSWES-LGKNKVPHGVIMFSRLFELDPALLSLF
PanGbE       ----------------------------------------------------------------------------------------MFKEHPHTLSYF
PanGbX       MGCALSR------------AGATDNSTTDVNEILEEMGPDTVIGSRTQSEVVSDLSTLAESQKELIQESWKI-LHQDIARLGVIVFIRLFETHPECKDVF
PanGbY       ------------------------------------------------------MCSLSTTDIKNIRDIWSI-VCQNPEENGRTVVIRLFLDYPQTRTYF
PanHba1      -------------------------------------------------------MPLSKAEKTILLAVWER-ISPYIEEFGAQALTRMFRCFPETKIYF
PanHba2      -------------------------------------------------------MTLTAAEKSCLASTFEK-IAPKAEQYGSELFQRMFLGFPQTRTYF
PanHba3      -------------------------------------------------------MTFTREDEVHIGEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYF
PanHba4      -------------------------------------------------------MTFTHEDEVHIAEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYF
PanHbb1      ------------------------------------------------------MVHWTSEEEFAITSIWGN-V--DVHEEGHDTLTRLMVVYPWTKKYF
PanHbb2      ------------------------------------------------------MVLWDAAEKKVIASVWAK-V--DIEADGFQALLRTLHVYPWTKRYF
PanHbb3      ------------------------------------------------------MVNWKANERQAVTSVWAS-I--DAAGHGQETLERLLHVYPWSRRYF
PanHbb4      ------------------------------------------------------MVNLEAAEKQTITSFWAS-V--DPAAQGENALQRLLYCYPWSRRYF
PanHbb5      ------------------------------------------------------MVHWDATEKQTITSFWGK-V--DLAADGEHSLQRLLYVYPWCRRYF
PanMb1       ------------------------------------------------------MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYF
PanMb2       -------------------------------------------------------MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLF
PanMb3       --------------------------------------------------------MASAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHF
PanMb4       ------------------------------------------------------MAGLSEVQWNELLAFWDKYVAPSSSEHGKHILIRMFQTEKATQTLF
PanMb5       ------------------------------------------------------MAGLSDAQWNDLLAFFDKFIAPNSAEHGKHILIRMFDSDRATQSLF
PanMb6a      ------------------------------------------------------MACPAK--------FWEENVVPDAAEHGKNILIRLYKEDPAALGFF
PanMb6b      ------------------------------------------------------MACPAK--------FWEENVVPDAAEHGKNILIRLYKEDPAAQGFF
PanMb7       ------------------------------------------------------MAGLSEAQWNELLAFWDKYVAPSSSEHGKHILIRMFDADKATQALF
PcaMb        -------------------------------------------------------MVLSEGEWQLVLHVWAK-VEADVAGHGQDILIRLFKSHPETLEKF
PgeMb        -----------------------------------------------------------MADFDMVLKCWGL-VEADYATYGSLVLTRLFTEHPETLKLF
PmaaHb1      ------------------------MPIVDS----------------------GSVPALTAAEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQAFF
PmaaHb10     ------------------------MPIVDS----------------------GSVGALSASEKAAVAGSWKA-VYANYEAAGKAVLIKFFTSNPGVQDFF
PmaaHb11     ------------------------MPIVDS----------------------GSAGALSAAEKAIITDSWKV-VYADYEAAGKAILIKFFTSNPGVQDFF
PmaaHb12     ------------------------MPIVDS----------------------GSVGEFSAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFSDNPGVQDFF
PmaaHb13     ------------------------MPIVDS----------------------GSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFF
PmaaHb14     ------------------------MPIVDS----------------------GSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFF
PmaaHb2a     ------------------------MPIVDT----------------------GSVAPLSAAEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFF
PmaaHb3      ------------------------MPIVDS----------------------GSVAPLSAAEKTKIRSAWAP-VYSNYETTGVDILVKFFTSTPAAQEFF
PmaaHb5a     ------------------------MPIVDT----------------------GSVAPLSAAEKTKIRSAWAP-VYSTYETSGVDILVKFFTSTPAAQEFF
PmaaHb5b     ------------------------MPIVDS----------------------GSVAPLSAAEKTKIRSAWAP-VYSTYETSGVDILVKFFTSNPAAQEFF
PmaaHb6      M-----------------------GALQDS----------------------GIVSSFKEDEKAALRESWDI-FNNSHQDAGVKILARFIINNPEAKKFF
PmaaHb7      ------------------------MPIEDT----------------------GSKPDFSDEEKKAIKDSWSG-VYSEYESASSEILIKFFVDNPSAQDFF
PmaaHb8      ------------------------MPIVDS----------------------GSVAPLSAAEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFF
PmaaHb9      ------------------------MPIVDS----------------------GSVGALSGAEKAAIADSWKA-VYSNYEEAGKAILIKFFTSNPGVQDFF
PmaaMb1      ------------------------MSIADS----------------------GSAPALSGDEKSAVRDTWKV-VYPHAEDHGTTILIKFLTENADAKKFF
PmaaMb2      M-----------------------SAIVDS----------------------GSAPALSGDEKAAIKSTWPS-VFAKAEDVGAEMLSRFISSNADVKKYF
PmaCygb      ME----------------------------------------------------QGWLSEEEIEALQDIWEK-VFKSAEDVGVILLVRLFTGHPASKQYF
PmaGbX1      MGCTVSTDER---------TGAQSSSQGQSQASRKQQQPEQQRAAGEGHQPPGPPQAPSESQRRLVRDSWLA-LQCDIARVGVIMFVRLFETHPECKDVF
PsiCygb      ME-----------------KVQGEMEIERW----------------------ERSEELSDAEKKVIQETWSR-VYTNCEDVGVSILIRFFVQFPSAKQYF
PsiGbE       -------------------------------------------------------MAFSEAEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYF
PsiGbX       MGCALSGSGS---------APGKRSSEAEQ----KDRAAWKAGPVRGGEGLEAGPFPPAGAQKERIQESWRI-LHDSIARVGIIVFIRLFETHPECKDAF
PsiGbY       ------------------------------------------------------MALLTDADKKSIHHIWSK-LFENPEENGKIIVIRLFKDYPETKAYF
PsiHbaA      -------------------------------------------------------MVLTACDKTNVKAVWTK-VSGHLEDYGAETLERMFATYPSTKTYF
PsiHbaD      --------------------------------------------------------MLTADEKQLVLHAWDK-VQGHQEDFGAEALERMFTTYPSTKTYF
PsiHbB       ------------------------------------------------------MVHWTAEEKQFITSLWGK-V--DVAECGGEALARLLIVYPWTQRFF
PsiHbG       ------------------------------------------------------MVHWTPEEKQMITSLWAK-V--NVAECGGEALARMMIVYPWTQRFF
PsiHbZ       -------------------------------------------------------MTLTQAEKAAVVAIWEK-VATHANAIGAESLERLFSGFPQTKTYF
PsiMb        -------------------------------------------------------MGLSDNEWQHVLGIWAK-VESDIPAHGQEVMIRLFQVHPETQSLF
PsiNgb       ------------------------MESGR----------------------------LSSTEKALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLF
RnoCygb      ME-----------------KVPGDMEIERR----------------------ERNEELSEAERKAVQATWAR-LYANCEDVGVAILVRFFVNFPSAKQYF
RnoMb        -------------------------------------------------------MGLSDGEWQMVLNIWGK-VEGDLAGHGQEVLISLFKAHPETLEKF
SchMb        -----------------------------------------------------------MADFDAVLKFWGP-VEADYTSHGGLVLTRLFKEHPETQKLF
SjaMb        -----------------------------------------------------------MADFDAVLKFWGP-VEADYDKIGNMVLTRLFTEHPDTQKLF
TalaMb       -----------------------------------------------------------MADFDAVLKCWGP-VEADYTTIGGLVLTRLFKEHPDTQKLF
TalbMb       -----------------------------------------------------------MADFDAVLKCWGP-VEADYTTMGGLVLTRLFKEHPETQKLF
TguCygb      ME-----------------KVQGEMEIERW----------------------ERSEEISDAEKKVIQEIWSR-VYANCEDVGVSILIRFFVNFPSAKQYF
TguGbE       -------------------------------------------------------MSLSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYF
TguHbA       -------------------------------------------------------MVLSAGDKSNVKAVFGK-IGGQADEYGADALERMFATYPQTKTYF
TguHbAD      --------------------------------------------------------MLTGEDKKLLQQTWGK-LGGAEEEVGADALWRMFHSYPPTKTYF
TguHbE       ------------------------------------------------------MVNWTAEEKQLVTTLWGR-V--NVDECGAEALARLLVAYPWTQRFF
TguMb        -------------------------------------------------------MGLSDQEWQQVLTVWGK-VESDLAGHGHQILMRLFQDHPETLDRF
TguNgb       ------------------------MESGM---------------------------RLSGGQRALIRESWQR-VSGSPVQHGLVLFTRLFDLDPDLLPLF
TniCygb1     ME-----------------RMQRDGEVDHV----------------------EQPGPLTEKEKVMIQDSWAK-VFQSCDDAGVAILVRFFVNFPSSKQFF
TniGbX       MGCAISSLGAKA-----EFGDRSAEEEDAAAA-------------------AAAVVYPREDQIQMIKDSWKV-IRDDIAKVGIIMFVRLFETHPECKDVF
TniMb        -----------------------------------------------------------MGDFDMVLKFWGP-VEADYSAHGGMVLTRLFTENPETQQLF
TniNgb       ------------------------------------------------------MEKLSSKDKELIRGSWDS-LGKNKVPHGVILFSRLFELDPELLNLF
TruCygb1     ME-----------------RMQGDGELDHV----------------------ERPSPLTDKEKVMIQDSWAV-VFQSCDDAGVAILVRLFVSFPSSKQLF
TruCygb2     MSHRESPPAPPPPPQLLGGQRRDVEGEDGP----------------------ERAKPLSDTEREMIQDTWGH-IYKNCEDVGVSVLIRFFVNFPSAKRYF
TruNgb       ------------------------------------------------------MEKLSSKDKELIRGSWDS-LGKNKVPHGVIMFSRLFELDPELLSLF
TthMb        -----------------------------------------------------------MADFDAVLKCWGP-VEADYTTIGGLVLTRLFKEHPETQKLF
XlaGbY       ------------------------------------------------------MADLTAADIENINEIWCK-IYANPEESGKTVVIRLFTTYPQTKVYF
XlaHbA1      --------------------------------------------------------TLTDSDKAAVIALWGK-IAPQANAIGAEALERLFLSYPQTKTYF
XlaHbAT5     -------------------------------------------------------MTFSSAEKAAIASLWGK-VSGHTDEIGAEALERLFLSYPQTKTYF
XtrCygb      ME-----------------KVQGENDMERW----------------------ERLEEITESERGVIKETWAR-VYANCEDVGVSILIRFFVNFPSAKQHF
XtrGbX       MGCILSSLGW---------QWRDSLDHTETSP-------------------LLPTLNLSEQQQQLLVESWRL-IQHDIAKVGVILFVRLFETHPECKDVF
XtrGbY       ------------------------------------------------------MADLTGADIENINEVWSK-IYANPEESGRTVVISLFLTYPQTKIYF
XtrHbA1      -------------------------------------------------------MHLTADDKKHIKAIWPS-VAAHGDKYGGEALHRMFMCAPKTKTYF
XtrHbB1      ------------------------------------------------------MVNLTAKERQLITGTWSK-I--CAKTLGKQALGSMLYTYPWTQRYF
XtrHbB2      ------------------------------------------------------MVHWTAEEKATIASVWGK-V--DIEQDGHDALSRLLVVYPWTQRYF
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XtrNgb          ------------------------MEKDQ----------------------------LSGPQKELIRESWQT-VSQDQLHHGTVLFSRLFELEPELVFLF
AcaGbY          ----KTVP------TDGDLKAHPQVAFHGRRIMVAFSQVIENMENWNQACVLLERLVNNHKNIHQ-V-PSGMFQLLFQAMLCTFDDLLGRT-FTP-EKRV
AcaMb           DKF-KNLK------SLDEMKNSEDLKKHGTIVLTALGKILKQKRQ---HEAELAPLAQSHATKHK-I-PVKYLEFISEVIVGVIAEKRSAD-FGA-ESQA
AplGbE          THF-KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-V-DPKNFRIICDIILQMMEEKFGG------DCKA
CanMb           PKF-AGI-------AHGDLAGDAGVSAHGATVLKKLGDLLKARGG---HAALLKPLSSSHATKHK-I-PIINFTLIAEVIGKVMEEKAGLD---A-AGQT
CauMb1          PKF-VGI-------AQSDLAGNAAVNAHGATVLKKLGELLKARGD---HAAILKPLATTHANKHK-I-ALNNFRLITEVLVKVMAEKAGLD---A-AGQT
CauMb2          PKF-KGI-------SQSELAGNALVAAHGATVLKKLGELLRAKGD---HAAILHPMATTHANKHK-I-TLNNFRLITEVLVEVMKEKAGLD---S-AGQG
CcaMb1          PKF-VGI-------AQSDLAGNAAVKAHGATVLKSWASCLKARGD---HAAILKPLATTHANTHK-I-ALNNFRLITEVLVKVMAEKAGLD---A-GGQS
CcaMb2          PKF-KGI-------PQSELAGDTLVASHGATVLKKLGELLRAKGD---HAAILQPLATTHANKHK-I-ALNNFRLITEVLVKVMAEKAGLD---T-AGQG
CcrMb           DKF-KSLK------SEGEMKASEDLKKHGATVLTALGGILKKKGQ---HAAELQPLAQSHANKHK-I-PVKYLEFISEAIIQVLQSKHSGD-FGA-DTKE
CmiGbY          QHF-KNIS------TLEEMKKSPQIKRHGKIVMSALNKLIANLDNGEELSSLLAKMAERHINVHK-V-DLHNFQIIFNIIIAILEETFGNA-FTP-EIRG
CpiCygb         SQF-KHME------DPLEMERTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-V-EPVYFKFFTGVMLEVIAEEYAND-FTP-EVQR
CpiGbE          THF-KGMG------TAEEMEQSDQVRSHGKRVLTTINDLVQHLDSTDAFLGIVNPLGKKHAMQLK-V-DPKNFRIICDIILQLMEEKYGG------DCKA
CpiGbX          FLF-RDIE------DLEQLKMNKELRAHGLRVMSFIEKSVARLDQEDKLEQLAFELGRSH-YRYN-A-PPKYYEYVGIQFISTVQPILKER-WTP-EVEE
CpiGbY          ----KNIP------TEGNLQEDPLVRFHGRRVMVALNQVVENLDNWKQACRILDRLADKHKNVHQ-V-PAVNFQSMFQVILNVCKDVLGNE-FST-EVSL
CpiHbaA         PHF--DLH------H-----GSAQIRTHGKKVLTALGEAVNHIDD---LASALSKLSDIHAQTLR-V-DPVNFKFLNHCFLVVVAIHQPSV-LTP-EVHV
CpiHbaD         PHF--DLH------H-----DSEQIRHHGKKVVTALGDAVRHMDN---LSEALSELSNLHAYNLR-V-DPVNFKLLSHCFQVVLAVHLADE-YTP-QVHV
CpiHbB1         SSF-GNLS------SPTAIIGNPKVRAHGKKVLTSFGEAVKNLDN---IKATYAKLSELHCDKLH-V-DPENFRLLGDILVIVLAAHFGRE-FTP-ACQA
CpiHbB2         STF-GNLS------NAEAILHNPHVHAHGKKVLTSFGEAVKNLDH---IKQTFATLSKLHCEKLH-V-DPENFKLLGNVLIIVLASHFTKE-FTP-ACQA
CpiHbG          SSF-GNLS------SPTAITGNPKVRAHGKKVLTSFGEAVKNLDN---IKATYAKLSELHCNKLH-V-DPENFRLLGDILVIVLASHFGRE-FTP-ACQA
CpiHbZ          PHF--DLS------Q-----GSAQLHGHGSKVLGAIGEAVKNIDN---ITGALATLSELHAYILR-V-DPVNFKLLSHCILCSVAAHFPND-FTP-EVHA
CpiMb           AKF-KNLK------TIDELKSSEEVKKHGTTVLTALGRILKLKNN---HEPELKPLAESHATKHK-I-PVKYLEFICEIIVKVIAEKHPSD-FGA-DSQA
CpiNgb          QYNCKKFS------SPQECLSSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLSNLGKKH-QTVG-V-KVDSFSAVGESLLFMLEKCLGTA-FSP-DVRE
CraMb           PKF-AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVIGKVMEEKAGLD---A-AGQT
CycrMb          DKF-KHLK------SEDDMRRSEDLRKHGNTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAIIHVLHSKHPAE-FGA-DAQA
DreCygb1        EHF-RELQ------DPAEMQQNAQLKKHGQRVLNALNTLVENLRDADKLNTIFNQMGKSHALRHK-V-DPVYFKILAGVILEVLVEAFPQC-FSPAEVQS
DreCygb2        SQF-QDME------DPEEMEKSSQLRKHARRVMNAINTVVENLHDPEKVSSVLVLVGKAHAFKYK-V-EPIYFKILSGVILEILAEEFGEC-FTP-EVQT
DreGbX          FLF-RDVE------DLERLRTSRELRAHGLRVMSFIEKSVARLDQLERLETLALELGKSH-YRYN-A-PPKYYGYVGAEFICAVRPILKDR-WTP-ELEE
DreHbAa         SHW-ADLS------P-----GSGPVKKHGKTIMGAVGEAISKIDD---LVGGLAALSELHAFKLR-V-DPANFKILSHNVIVVIAMLFPAD-FTP-EVHV
DreHbAe         SHW-KDLS------P-----GSAPVRKHGKTVMGGVAEAVSKIDD---LNAGLLNLSELHAFQLR-V-DPANFKILSHNILVVLATLFPAD-FTP-EAHV
DreHbAx         SHL--NIS------A-----NSEHLRSHGKKIVEALAEGAKNVST---LTTTLAPLSRFHAYQLR-I-HPTNFKLFNHCILVTLACRMGDD-FTP-VVHA
DreHbBa         ATF-GNLS------SPAAIMGNPKVAAHGRTVMGGLERAIKNMDN---VKNTYAALSVMHSEKLH-V-DPDNFRLLADCITVCAAMKFGQAGFNA-DVQE
DreHbBe         AKF-GNLY------NAAAILGNPMVAAHGKTVLKGLELAVKNMDN---IKATYADLSVLHSEKLH-V-DPDNFRLLADCLTIVVAAQMGAG-FTP-EVQA
DreMb           PKF-SGI-------SQGDLAGSPAVAAHGATVLKKLGELLKAKGD---HAALLKPLANTHANIHK-V-ALNNFRLITEVLVKVMAEKAGLD---A-AGQG
DreNgb          SYS-TNCG------DAPECLSSPEFLEHVTKVMLVIDAAVSHLDDLHTLEDFLLNLGRKH-QAVG-V-NTQSFALVGESLLYMLQSSLGPA-YTT-SLRQ
EpeMb           PKF-AGI-------T-GDIAGNAAVAAHGATVLKKLGELLKAKGN---HAAIIKPLANSHAKQHK-I-PINNFKLITEALAHVLHEKAGLD---A-AGQT
TruMb           PKF-AGI-------TQSDLAGNAAVSAHGATVLKKLGELLKAKGN---HAALLQPLANTHATKHK-I-PINNFKLIAEVIGKVMEEKAGLD---A-AGQQ
GgaCygb         SQF-KHMD------DTLEMERSLQLRKHAQRVMGAINTVVENLDDPEKVSSVLALVGKAHALKHK-V-EPVYFKKLTGVMLEVIAEAYGND-FTP-EAHG
GgaGbE          THF-KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-I-DPKNFRIICDIILQLMEEKFGG------DCKA
GgaHbA          PHF--DLS------H-----GSAQIKGHGKKVVAALIEAANHIDD---IAGTLSKLSDLHAHKLR-V-DPVNFKLLGQCFLVVVAIHHPAA-LTP-EVHA
GgaHbAD         PHF--DLS------P-----GSDQVRGHGKKVLGALGNAVKNVDN---LSQAMAELSNLHAYNLR-V-DPVNFKLLSQCIQVVLAVHMGKD-YTP-EVHA
GgaHbG          ASF-GNLS------SPTAILGNPMVRAHGKKVLSSFGDAVKNLDN---IKNTFSQLSELHCDKLH-V-DPENFRLLGDILIIVLAAHFSKD-FTP-ECQA
GgaMb           DKF-KGLK------TPDQMKGSEDLKKHGATVLTQLGKILKQKGN---HESELKPLAQTHATKHK-I-PVKYLEFISEVIIKVIAEKHAAD-FGA-DSQA
GgaNgb          QYNCKRFA------SPQECLAAPEFLDHIRKVMLVIDAAVSHLEDLPCLEEYLCNLGKKH-QAVG-V-KVESFSTVGESLLYMLEKCLGAA-FSP-DVRE
GgiMb           PKF-AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVIGKVMEEKAGLD---A-AGQT
HsaCYGB         SQF-KHME------DPLEMERSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-V-EPVYFKILSGVILEVVAEEFASD-FPP-ETQR
HsaHBA          PHF--DLS------H-----GSAQVKGHGKKVADALTNAVAHVDD---MPNALSALSDLHAHKLR-V-DPVNFKLLSHCLLVTLAAHLPAE-FTP-AVHA
HsaHBB          ESF-GDLS------TPDAVMGNPKVKAHGKKVLGAFSDGLAHLDN---LKGTFATLSELHCDKLH-V-DPENFRLLGNVLVCVLAHHFGKE-FTP-PVQA
HsaHBD          ESF-GDLS------SPDAVMGNPKVKAHGKKVLGAFSDGLAHLDN---LKGTFSQLSELHCDKLH-V-DPENFRLLGNVLVCVLARNFGKE-FTP-QMQA
HsaHBE          DSF-GNLS------SPSAILGNPKVKAHGKKVLTSFGDAIKNMDN---LKPAFAKLSELHCDKLH-V-DPENFKLLGNVMVIILATHFGKE-FTP-EVQA
HsaHBG          DSF-GNLS------SASAIMGNPKVKAHGKKVLTSLGDAIKHLDD---LKGTFAQLSELHCDKLH-V-DPENFKLLGNVLVTVLAIHFGKE-FTP-EVQA
HsaHBZ          PHF--DLH------P-----GSAQLRAHGSKVVAAVGDAVKSIDD---IGGALSKLSELHAYILR-V-DPVNFKLLSHCLLVTLAARFPAD-FTA-EAHA
HsaMB           DKF-KHLK------SEDEMKASEDLKKHGATVLTALGGILKKKGH---HEAEIKPLAQSHATKHK-I-PVKYLEFISECIIQVLQSKHPGD-FGA-DAQG
HsaNGB          QYNCRQFS------SPEDCLSSPEFLDHIRKVMLVIDAAVTNVEDLSSLEEYLASLGRKH-RAVG-V-KLSSFSTVGESLLYMLEKCLGPA-FTP-ATRA
IpuGbX          FLF-RDVE------DLERLRTSKELRAHGLRVMSFIEKSVARLDQLERLDSLAVELGRSH-YRYY-A-PPKYYGYVGTEFICAVRPILKEK-WTP-ELEK
LchCygb         SQF-RHLE------DPLDMERSVQLRKHARRVMGAINTVVENVED-QDIASVLAPVGKAHALKHK-V-EPVYFKILSGVILEILAEEYAQH-FTP-EVQK
LchGbE          GNF-KGMG------SAAEMEQSAQVRTHGKKIFSALNDMIQHLDSTDALLGVVNPLGKKHATQLK-V-DPKNFKIICNILLQVLDEKFGG------DARA
LchGbX1         FLF-RDID------DFHQLKMSKELQAHGLRVMSFIEKSVARLEQKDKLEQIAFELGRSH-CRYN-A-PPKYYQYVGVQFISVVKPILKEA-WTP-EVEE
LchGbX2         FLF-RDVD------DLQRLRTSKELRAHGLRVMSFVEKSVARLEHSERLEQLALELGKSH-YRYN-A-PPKYYQYVGIEFVCAVQPILKER-WTP-EVEE
LchGbY          KNF-KNIS------TMEEMQKNEQIRIHGLRVMNSLNQVIQNIDNLNEVYSILTHLAKRHQYVHR-V-DVHNFKLIFGVIIKILKEALGAT-FTE-EICT
LchHbA1         SHM--DLS------P-----GSSMLRAHGKKVMGTIEGSIKSIDK---LATVLSRLSDMHAYNFM-V-DPVNFKLLSQCILVALATQLMAD-FTP-EAQC
LchHbA2         DHF-TDLS------P-----SSQKLHAHAKVVLGALTKAVNHLDN---ITDTLHDISLVHAKKLL-V-DPVNFELLGHCLEVALAAHFATD-FTP-EVHL
LchHbB1         KSF-GDLS------SSKAIASNPKVTEHGLKVMNKLTEAIHNLDH---IKDLFHKLSEKHFHELH-V-DPQNFKLLSKCLIIVLATKLGKQ-LTP-DVQA
LchHbB2         STF-GSLS------SSTVIARNFKVQQHAAKVINALTEAIRNIDN---LKASFSDLSKLHFQKLH-V-DPENFKLLGKTLIITLSEKLGSE-FSP-QIQA
LchMb           PKF-KHM-------TYQELQSSEELKTHGDTVLSKLGCLLKLKGN---HAGDLHPLAQTHATKHK-I-PLHNFEIISEIIVKILAEKYPGD-FGA-DGQA
LchNgb          NYN-SSFP------SQAGCLTSPEFIDHIHKVMMVVDAAVNSLDNLLSLEDYLINLGKKH-QAAG-V-KMESFQVVGESLLYMLEHGLDSA-FSV-EVRH
LplaHbA         PKF-KGLD------SADQLKKSPAVRWHAERIINAVNDAVVAMDDPAKQSLQLKELSQKHAHELN-V-DPKYFKVLAGVISDAVVK-------SG-DAKA
LplaHbB         PKF-QGLT------SADQLKKSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLNELSSKHAKSFQ-V-DPQYFKVLAAVIVDTVL-----------PGDA
MangMb          DKF-KHLK------SEDDMRRSEDLRKHGNTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAIIQVLHNKHPGE-FGA-DTQA
MbiMb           DKF-KHLK------SEAEMKASEDLKKHGHTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISDAIIHVLHSKHPSD-FGA-DAQG
MgaGbE          THF-KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-I-DPKNFRIICDIILQLMEEKFGG------DCKT
MglaHb2         TKM-KDLH------TLEDLASSADARWHVERIIQAVNFAVINIEDREKLSNKFVKLSQDHIEEFH-VTDPQYFMILSQTILDEVEKRNG-G-LSG-EGKS
MmuMb           DKF-KNLK------SEEDMKGSEDLKKHGCTVLTALGTILKKKGQ---HAAEIQPLAQSHATKHK-I-PVKYLEFISEIIIEVLKKRHSGD-FGA-DAQG
MniMb           PKF-AGI-------AKADMAGNAAISAHGATVLKKLGELLKAKGS---HAAIIKPMANSHATKHK-I-PIKNFELISEVIGKVMHEKAGLD---A-AGQK
NcoMb           PKF-AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVIGKVMEEKAGLD---A-AGQT
OanGbY          ----KNIP------LEGNLQEDPLLRSHGRRVMVALNRIIQNLDNWKQVCKILNPLAEKHKIIHS-V-DVENFQFMLKCVGDVCQDYLGPC-YTP-EIAE
OanHbW          SAF-GNLS------SPTAIVGNPRVRAHGKKVLTSFGEAVKDLDH---VKSNFAKLSQLHSEKLH-V-DPENFRLLGDNLIIVLAATLGKD-FTP-EAQA
OanMb           DKF-KGLK------TEDEMKASADLKKHGGTVLTALGNILKKKGQ---HEAELKPLAQSHATKHK-I-SIKFLEYISEAIIHVLQSKHSAD-FGA-DAQA
OanNgb          QYNCRQFS------SPRDCLASPEFLDHIRKVMLVIDAAVIHLDDLSSLEEYLTNLGRKH-KAIG-V-KLSSFSTVGESLLFMLDKCLGPA-FSP-ATRE
OlaCygb1        SQF-KHIE------DAEELEKSSQLRKHARRVMNAINTLVESLDNSDKVSSVLNAVGKAHAIRHK-V-DPVYFKILSGVILEVLGEAYPQV-MTA-EVAS
OlaCygb2        SQF-QDMQ------DPEEMEKSSQLRQHARRVMNAIN-VVENLQDPEKVSSVLALVGKAHAVKHK-V-EPIYFKILSGVMLSVLSEDFPEF-FTA-EVQL
OlaHbA          AHW-KDLS------P-----GSAPVKKHGKTVMGGIADAVGKIDD---ISSGLLNLSELHAFTLR-V-DPTNFKILSHNILVVMAIMFPQD-FTP-EVHV
OlaHbB          ASF-GNLY------NAEAIKTNPNIAAHGTKVLHGLDRAVKNMDN---IKATYAELSVLHSEKLH-V-DPDNFKLLADCLTIVIAAKLGSA-FSP-EIQA
OlaMb           PKF-AGI-------AKGDMAGNAALSAHGATVLKKLGELLKARGN---HGAILKPLANSHATKHK-I-PINNFRLITEVIGKVMAEKAGLD---A-AGQQ
OlaNgb          NYN-TNCG------STQDCLSSPEFLDHVTKVMLVIDAAVNHLDDLHSLEDFLLNLGRKH-QAVG-V-STQSFAVVGESLLYMLQCSLGQA-YTA-ALSQ
PanGbE          TNF-KELQSTAGTASVTELEGLSEVRTHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-V-DVKEFEILCAILLELMAEKCGE------DAKT
PanGbX          FMF-RDID------DIQQLQLSRELQAHGLRVMSFIEKSVARLQQEDKLQQLAFELGRCH-CRYN-A-LPKYFEYVAFQFMTAVKPILKEK-WTS-EVDD
PanGbY          KNF-KNID------TEEGIKESRQVRQHGRRVVMLLSKVIECLEDWDKTSTLLSELADRHQQHHK-V-EVVNFKFLFAALNSVYIDVFGPT-FTP-DIEA
PanHba1         HEK--NID------P-----GSSYVRNQGGKIVTAIGTAVQNADN---IQEALADLCCLHAYRIR-V-DPVNFQYFSKCFLTVLAVHLQDD-FTA-DVHV
PanHba2         AHV--DTS------A-----NSPQLSAHGAKIIASLGKAIKNVDN---MSAALSDLSDLHAQSIR-V-DPSNFKYISHCLLVLLAAHLKAD-FTP-QVQI
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PanHba3        QKF-GDYK------A-----SSDKVIQHGKKVVDALVQASQHLHD---LESQLHPLSVKHATELM-V-DPVNFEHLSHCIHVTIAAHHGEK-YTA-EMHR
PanHba4        QKF-GDYK------A-----SSDKVIQHGKKVVDALVQASQHLHD---LESHLHPLSEKHARELM-V-DPVNFEHLSHCIHVTIAAHHGEK-YTA-EMHR
PanHbb1        SSF-GNLS------TTSTIASNDRVQAHGAKVLTAIGDALVDLPN---IKQNLTDLSRLHSEILH-V-DPENFRLLGQCLVIVLAAKFGAEKFNA-DVQA
PanHbb2        SHF-GAMS------TLKDIESNPKVRAHGRKVMAAVGDAISHMDN---IKGHLSQLSQLHSDKLH-V-DPANFELLGNNIVIVLAAKFGADAFTP-EVQA
PanHbb3        GKF-GDLS------TFSAIRQNPHVRTHGAKVLGAVVECLNHMDD---IKGHLAQLSILHSDTLH-V-DPANFTLLGNCFLIVLAKSVGAG-FTP-DVHA
PanHbb4        AKF-GDLS------TISAIRKNSHVRAHGHKVLSAVGDCIPHLGD---IKGHLAQLSKLHCETLH-V-DPANFCLLGKIIVVVLASHFGAK-FTP-EVQA
PanHbb5        HKF-GDLS------TISAIRKNSHVRAHGHKVLSALGDCVPHLGD---IKGHLAQLSKLHCETLH-V-DPANFCLLGQIITIVLASRFGAA-FTP-EVQA
PanMb1         PKF-RHLT------TEAEMRSNEDIRKHGNTVFTALGKLVKLKGN---VEGDLRSMADSHANKHK-I-HLENFDIISKVIDNYFHESFPGD-YGA-DVQD
PanMb2         DKF-RHLG------SEAEMRSCADLQKHGNTVFTALGKTLKLKGH---HDADLRPMAESHSHKHK-I-PVENFTLICSIIDKYLHESF-SD-YTG-DTRE
PanMb3         PKF-KDLA------SEAEMRGSDGLKNHGETVFTALGKALQQRDG---IANELRPLAVTHSQNHK-I-PLEEFENICEVIDVYLAEIC-PD-YAG-ETRT
PanMb4         SKF-KDI-------PTSDLAVNADVKKHGGVVVDFLGKLLKLKGQ---NDSQLHTMAESHKNKHK-I-PLDYFQVISSVIDVYVNENLPEE-Y-A-PVRQ
PanMb5         PKF-KDA-------PAADLPKNADVKKHGGVVVDFLGKLLKQKGH---NESMLHTMAETHKNKHK-V-LPDYFQLISSVIDVYVHENLPAE-Y-A-PVRD
PanMb6a        PKY-KDI-------PVSELGNNADVKEQGAVVVKALGELLKLKGQ---HESQLHAMAESHKNTYK-I-PVEYFPKIFKITDAYLQEKVGAA-Y-A-AIQA
PanMb6b        SKY-KDT-------PVSELGNNADVKEQGAVVVKALGELLKLKGQ---HESQLHAMAESHKNTYK-I-PVEYFPKIFKITDAYLHEKVGAV-Y-A-AIQA
PanMb7         SKY-KDI-------PTSDLAANADVKKHGGVVVDFLGKLLKLKGQ---NDSQLHTMAESHKNKHR-I-PLDYFQLISTVIDVYVYENLPGE-Y-G-PVRE
PcaMb          DRF-KHLK------TEAEMKASEDLKKHGVTVLTALGAILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAIIHVLHSRHPGD-FGA-DAQG
PgeMb          PKF-AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGG---HAALLKPLSSSHATKHK-I-PIINFKLIAEVIGKVMEEKAGLD---A-AGQT
PmaaHb1        PKF-QGLT------SADQLKKSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLRELSGKHAKSFQ-V-DPQYFKVLAAVIVDTVL----------PGDA
PmaaHb10       PKF-KGLD------SADKLSKSPAVRWHAERIINAVNDSVVALDDPEKQSLKLKALSQKHAYEFH-V-DSQYFKVLSATILEQVDDANG-G-LSA-EGKS
PmaaHb11       PKF-KGLD------SADQLSKSAAVRWHAERIINAVNDAVVALDDPEKQSLKLKALSKKHAQEFN-V-DPQYFKVLSANVLEQVAAANG-G-LSA-EAQG
PmaaHb12       PKF-KGLD------SADQLKKSPAVRWHAERIINAVNDAVVALDDPPKLSLKLKALSKKHAQELN-V-DPQYFKVLAGVISDAVAK-------SG-DEKA
PmaaHb13       PKF-KGLD------SADQLKKSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-V-DPSYFKVLAGVISDAVAK-------SG-DAKA
PmaaHb14       PKF-KGLD------SADKLKKSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-V-DPSYFKVLAGVISDAVAK-------SG-DAKA
PmaaHb2a       PKF-KGLT------TADQLKKSADVRWHAERIINAVNDAVVSMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVIADTVA----------AGDA
PmaaHb3        PKF-KGLT------TADQLKKSADVRWHAERIINAVNDAVVSMDDTEKMSMKLGDLSGKHAKSFQ-V-DPQYFKVLAAVIADTVA----------AGDA
PmaaHb5a       PKF-KGLT------TADQLKKSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVIADTVA----------AGDA
PmaaHb5b       PKF-KGLT------TADQLKKSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVIADTVA----------AGDA
PmaaHb6        PKF-KGLN------TAEELQNSAEVRIHGDKILAAVQQAVLDLDDPDKQKNKLKDLSKSHAQQFN-V-EPAYFKTFAEVILKYVTETCGKS-FTS-EMRT
PmaaHb7        PKF-KDLD------SEEKLKNSTAVRWHAERIINAVNDVIWLLDEPEKNAKNLKELSEKHAVQLN-V-DAKFFKVLAELILDKVAEKSGDS-FSD-SARS
PmaaHb8        PKF-KGMT------TADQLKKSADVRWHAERIINAVNDAVTSMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVIADTVA----------AGDA
PmaaHb9        PKF-KGLD------SADQLSKSAAVRWHAERIINAVNDAVVALDDPEKLSLKLKALSKKHAQEFN-V-DPQYFKVLAVNIVEGVSSANG-G-LGA-EAQA
PmaaMb1        PKF-QALK------TADEMKSSPVLRDHAKRIMNSINDMVVALDDTNAQNAQMNGLSKKHANDFK-V-DPKYFKVISNVILSVIAEGLGAQ-FND-AAKN
PmaaMb2        PKF-KDIS------SQAELKSSAKVRDHAKRIMAFINDLVDNIDNAGAQTAKLHSLSAEHAEKFK-V-DPQYFKVISNVLLDILGETFGAS-FSG-ATRS
PmaCygb        PMF-KDLE------TADDLKASAKLRWHAGRVMGSLDKAVRSLRKPEELIKILRAVGLSHARKATPV-DVKYYHILGGIIMDVLLETFKDE-LSP-TARS
PmaGbX1        YQF-RDCE------DLQKLKMNKQLQAHGLRVMSFIEKSVARLEQECVLEQLIVEMGRKH-YKYN-A-SPKYYSFVGIEFIATVQPFLQEK-WTN-EVED
PsiCygb        SQF-KHME------DPLEMERTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-V-EPVYFKFFTGVMLEVIAEEYAND-FTP-EVQR
PsiGbE         THF-KGMG------TAEEMEQSDQIRSHGKKVLTAINDLVQHLDSTDAFLGIVNPLGKKHATQLK-I-DPKNFRVICDIILQLMEEKYGG------DCKA
PsiGbX         FLF-RDIE------DLQQLKMSKELQAHGLRVMSFIEKSVARLDQEDKLEHLAFELGRNH-YRYS-A-PPKYYEYVGVQFISAVQPILKER-WTP-ELQE
PsiGbY         ----KSIP------TEGNLQEDPQIRYHGRRVMVALNQVIENLDNWKQACRILEHVAEKHKNTHH-V-PAANFQSMFQVILSVCKELMGNE-FSS-EVSS
PsiHbaA        AHF--DLH------H-----GSSQVRTQGKKVLSALGDAVAHVDD---LPSALSRLSDLHAKNLR-V-DPVNFKLLSHCFLVVVALHHPSL-FTP-EVHV
PsiHbaD        PHF--DLH------H-----DSEQVRHHGKKVVTALGNAVHHMDT---LSKTLSDLSDLHAYNLR-V-DPVNFKLLSHCFQVVLAVHLRDE-YTP-QLHV
PsiHbB         SSF-GNLS------SPTAILGNPKVRAHGKKVLTSFGEAVKNLDS---VKATYAKLSELHCNKLH-V-DPENFRLLGDILVIVLASHFGKE-FTP-ACQA
PsiHbG         STF-GNLS------NPQAIQHNPKVLEHGKKVLTSFGNAVKDLDH---IKETFAHLSELHCEKLH-V-DPENFKLLGNVLVIVLAAHIRKD-FPP-ACQA
PsiHbZ         PHF--DLS------Q-----GSAQLHGHGSKVLSAIGEATKNIDN---ITGALATLSELHAYILR-V-DPVNFKLLSHCILCSLAAHFPND-FTP-EVHA
PsiMb          AKF-KNLK------TADEMKSSDELKKHGITVLTALGRILKQKNN---HEQELKPLAESHATKHK-I-PVKYLEFICEIIVKVIAEKHPAD-FGA-DSQA
PsiNgb         QYNCRQFS------SPLECLSSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLTNLGKKH-QAVG-V-KVDSFSAVGESLLFMLEKCLSTA-FSS-DVRE
RnoCygb        SQF-KHME------DPLEMERSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-V-EPMYFKILSGVILDVIAEEFAND-FPV-ETQK
RnoMb          DKF-KNLK------SEEEMKSSEDLKKHGCTVLTALGTILKKKGQ---HAAEIQPLAQSHATKHK-I-PVKYLEFISEVIIQVLKKRYSGD-FGA-DAQG
SchMb          PKF-TGI-------AQADMAGNAAISAHGATVLKKLGELLKAKGN---HAAILKPMANSHATKHK-I-PINNFKLISEIIVKVMQEKAGMD---A-GGQQ
SjaMb          PKF-AGI-------GLGDMAGNAAISAHGATVLKKLAEVLKAKGN---HAGIIKPLANSHATKHK-I-AINNFKLITEIIVKVMQEKAGLD---A-GGQT
TalaMb         PKF-AGI-------AQADLAGNAAISAHGATVLKKLGELLKAKGS---HASILKPMANSHATKHK-I-PINNFKLISEVLVKVMQEKAGLD---A-GGQT
TalbMb         PKF-AGI-------AQADIAGNAAISAHGATVLKKLGELLKAKGS---HAAILKPLANSHATKHK-I-PINNFKLISEVLVKVMHEKAGLD---A-GGQT
TguCygb        SQF-KHME------DPLEMERSLQLRKHARRVMGAINTVVENLNDSEKVSSVLALVGKAHALKHK-V-EPIYFKKLTGVMLEVIAEEYPND-FTP-EAHG
TguGbE         PHF-KGMD------SAEEMKQSDQVRGHGKKVFGAINDMVQHLDNSEAFLGIVTPLGKKHATQLK-I-DPKNFRIICDIILQLMEEKFGG------DCKA
TguHbA         PHF--DLG------K-----GSAQVKGHGKKVAAALVEAANNVDD---LAGALSKLSDLHAQKLR-V-DPVNFKLLGQCFLVVVATRNPSL-LTP-EVHA
TguHbAD        PHF--DMS------Q-----GSDQVRGHGKKVMAALSNAVKNLDN---LSQALSELSNLHAYNLR-V-DPVNFKFLSQCLQVTLATRLGKE-YSP-EVHS
TguHbE         VSF-GNMS------SPTAVLGNPMVRAHGKKVLTSFGEAVRNMDS---VKKCFAQLSKLHCEKLH-V-DPENFRLLGDVLVVVLASHFGKE-FTP-ACQA
TguMb          EKF-KGLK------TPDAMKGSEDLKKHGVTVLTQLGKILKAKGN---HEAELKPLAQTHATKHK-I-PVKYLEFISEVIIKVLAEKHAAD-FGA-DAQA
TguNgb         QYNCKQFA------SPHECLSAPEFLDHIRKVMLVIDAAVSHLENLSCLEEYLCNLGKKH-QAVG-V-KVESFSTVGESLLYMREEKPGAA-FSP-EVQG
TniCygb1       KDF-KHME------EPEEMQQSVQLRKHAHRVMTALNTLVESLDNSDRVASVLKSVGRAHALKHN-V-DPKYFKILSGVILEVLGEAFTEI-ITA-EVAS
TniGbX         FLF-RDVE------DLERLRSSRELRAHGLRVMSFIEKSVARLDQQDRLEALAVELGKSH-YHYN-A-PPKYYSYVGAEFICAVQPILKER-FTS-ELEE
TniMb          PKF-VGI-------AQSELAGNAAVSAHGATVLKKLGELLKAKGN---HAAILQPLANSHATKHK-I-PIKNFKLIAEVIGKVMAEKAGLD---T-AGQQ
TniNgb         HYT-TNCG------STQDCLSSPEFLEHVTKVMLVIDAAVSHLDDLHSLEDFLLNLGRKH-QAVG-V-KPQSFAMVGESLLYMLQCSLGQA-YTA-SLRQ
TruCygb1       KDF-KDIE------EPEEMQRSIQLRKHAHRVMTTINTLVENLDDADAMASALKSVGRAHALRHK-V-DPKYFKILSGVILEVLGEAFTEI-ITA-EVAS
TruCygb2       SQF-QDME------DPEEMERSSQLRHHACRVMNAINTVVENLHDPEKVSSVLALVGKAHAIKHK-V-EPMYFKILCGVMLEVLCEAFPEF-FTA-DVRM
TruNgb         HYT-TNCG------STQDCLSSPEFLEHVTKVMLVIDAAVSHLDDLHSLEDFLLNLGRKH-QAVG-V-NPQSFATVGESLLYMLQCSLGQA-YTA-SLRQ
TthMb          PKF-AGI-------AQADIAGNAAVSAHGATVLKKLGELLKAKGS---HAAILKPLANSHATKHK-I-PINNFKLISEVLVKVMHEKAGLD---A-GGQT
XlaGbY         KNL-KNIA------TLEEMQVNPGIRAHGKRVMGALNQVIQNLNDWEVVSSALTHLAQRHQDVHK-V-GVNNFQLLFLVILTIFKEALGAD-FTP-EHCK
XlaHbA1        SHF--DLS------H-----GSADLANHGGKVVNALGEAAKHIND---LDAALSTLSDLHAYNLR-V-DPGNFKLLSHTIQVTLAIHFHKE-FDA-ATQA
XlaHbAT5       SHF--DLS------H-----GSKDLRSHGGKVVKAIGNAATHIDD---IPHALSALSDLHAFKLK-V-DPGNFKLLSHAIQVTLAIHFPAE-FNA-DAQA
XtrCygb        SQF-KHME------DPLEMEGSVQLRKHARRVMGAVNSVVENLGDPEKITTVLSIVGKSHALKHK-V-DPVYFKILTGVMLEVIAEEYAKD-FTP-DVQL
XtrGbX         FLF-RDVD------DLQALRANKDLRAHGLRVLSFVEKSVARIADCARLEELALELGRSH-YRYN-A-PPRYYQYVGTEFISAVCPMLHDK-WTA-EVEE
XtrGbY         KNL-KNIS------TLQEMQDNAGIRAHGKRVMGALNHVIENLKDWDAVCSALSHLAKRHQDVHK-V-EVNNFELLFLVIISVFKEALGSG-FTP-EQSK
XtrHbA1        PDF--DFS------E-----HSKHILAHGKKVSDALNEACNHLDN---IAGCLSKLSDLHAYDLR-V-DPGNFPLLAHQILVVVAIHFPKQ-FDP-ATHK
XtrHbB1        SSF-GNLS------SIEAIFHNAAVATHGEKVLTSIGEAIKHMDD---IKGYYAQLSKYHSETLH-V-DPYNFKRFCSCTIISMAQTLQED-FTP-ELQA
XtrHbB2       SSF-GNLS------NVSAVSGNVKVKAHGNKVLSAVGSAIQHLDD---VKSHLKGLSKSHAEDLH-V-DPENFKRLADVLVIVLAAKLGSA-FTP-QVQA
XtrNgb        QYNSSHFS------KVQDCLSSAEFTEHIRKVMTVIDAAVSSLDCLSSLDEYLTSLGRKH-RAVG-V-KLESFNTVGESLLFALESCLGDA-FTS-DTRE
AcaGbY         SWEKFFQVIQEEVEAAYDR---------------------------------------
AcaMb          AMRKALELFRNDMDRKYKELGFQ-GE--------------------------------
AplGbE         SFEKVTNEICTHLNNVYKEAGW------------------------------------
CanMb          ALRNVMAIIITDMEADYKELGFT-E---------------------------------
CauMb1         ALRKVMEAVIGDIDTYYKEFGFA-G---------------------------------
CauMb2         ALKRIMDCIIHDIDRYYKEIGFA-G---------------------------------
CcaMb1         ALRRVMDVVIGDIDTYYKEIGFA-G---------------------------------
CcaMb2         ALKRVMDCIIRDIDRYYKEIGFA-G---------------------------------
CcrMb          AMKKALELFRNDMAAKYKELGFQ-G---------------------------------
CmiGbY         TWTKLFGVIYACLESHYKDAGFY-P---------------------------------
CpiCygb        AWTKVKSLIYTHVTAAYKEVGWV-QYPNSTM---------------------------
CpiGbE         SFEKVTNEICTRLNNAYKEAGW------------------------------------
CpiGbX         AWQVGSSSAVGPLPCCRWQRSRP----------------------RLGGLDP---FILP
```

```
CpiGbY       SWEKLFGLLSEQINASYVSTSKS-------------------------------------
CpiHbaA      SLDKFLSAVGTVLTSKYR------------------------------------------
CpiHbaD      AYDKFLAAVSAVLAEKYR------------------------------------------
CpiHbB1      AWQKLVRVVAHALSYKYH------------------------------------------
CpiHbB2      AWQKLVSAVAHALALGYH------------------------------------------
CpiHbG       AWQKLAGVVAHALAHEYH------------------------------------------
CpiHbZ       AWDKFLSQISSVLTEKYR------------------------------------------
CpiMb        AMRKALELFRNDMASKYKEFGFQ-G-----------------------------------
CpiNgb       AWTRLYGSVVKAMSSGWDARKEG-E-----------------------------------
CraMb        ALRNVMAIIITDMEADYKELGFT-E-----------------------------------
CycrMb       AMKKALELFRNDIAAKYKELGFH-G-----------------------------------
DreCygb1     SWSKLMGILYWQMNRVYAEVGWE----NSKK-----------------------------
DreCygb2     SWSKLMAALYWHITGAYTEVGWV-KLSSSAV-----------------------------
DreGbX       AWKTLFQYVTSIMREGFLEEERN-KRSNTQTSSRERPDKRSTAI----------------
DreHbAa      SVDKFFNNLALALSEKYR------------------------------------------
DreHbAe      AMDKFLSALALAMSEKYR------------------------------------------
DreHbAx      AIDKFLSAFSAVLAEKFR------------------------------------------
DreHbBa      AWQKFLAVVVSALCRQYH------------------------------------------
DreHbBe      AFQKFIAVAVSALGRQYH------------------------------------------
DreMb        ALRRVMDAVIGDIGGYYKEIGFA-G-----------------------------------
DreNgb       AWLTMYSIVVSAMTRGWAKNGEH-KSN---------------------------------
EpeMb        ALRNVMGIVIADLEANYKELGFT-G-----------------------------------
TruMb        ALKNVMATIIADIDVTYKDLGFS-------------------------------------
GgaCygb      AWTKMRTLIYTHVTAAYKEAGWV-SYPSATL-----------------------------
GgaGbE       SFEKVTNEICTHLTNIYKEAGW--------------------------------------
GgaHbA       SLDKFLCAVGTVLTAKYR------------------------------------------
GgaHbAD      AFDKFLSAVSAVLAEKYR------------------------------------------
GgaHbG       AWQKLVRVVAHALARKYH------------------------------------------
GgaMb        AMKKALELFRNDMASKYKEFGFQ-G-----------------------------------
GgaNgb       AWIELYSAVVKAMQRGWEVLPEG-D-----------------------------------
GgiMb        ALRNVMAVIIADMEADYKELGFT-E-----------------------------------
HsaCYGB      AWAKLRGLIYSHVTAAYKEVGWV-QQVPNATTPPATLPSSG------------------P
HsaHBA       SLDKFLASVSTVLTSKYR------------------------------------------
HsaHBB       AYQKVVAGVANALAHKYH------------------------------------------
HsaHBD       AYQKVVAGVANALAHKYH------------------------------------------
HsaHBE       AWQKLVSAVAIALAHKYH------------------------------------------
HsaHBG       SWQKMVTGVASALSSRYH------------------------------------------
HsaHBZ       AWDKFLSVVSSVLTEKYR------------------------------------------
HsaMB        AMNKALELFRKDMASNYKELGFQ-G-----------------------------------
HsaNGB       AWSQLYGAVVQAMSRGWDGE----------------------------------------
IpuGbX       AWKTLFQYVTWLMRRGYNEEEEEAKRNNTVGSSRERPRQRNTAL----------------
LchCygb      AWTKLMSIICCHVTATYKEVGWG-QLSNSTM-----------------------------
LchGbE       GFEKVTDVLCTHLNHAYKEAGW--------------------------------------
LchGbX1      AWQILFKYLTAVMKKGYYVEEKK-ININNALYTKIPNALSSNPVQNNL------------
LchGbX2      AWQTLFKYVTEVMKRGYLQEEKI-KRTMETVEPKQASRRANNAI----------------
LchGbY       SWQKMLSFTYDYLVSCYHKSSGP-------------------------------------
LchHbA1      AWDKFLALISEILFSKYR------------------------------------------
LchHbA2      AIDKFLYEVEKALFETYR------------------------------------------
LchHbB1      TWEKLLSVVVAALSREYH------------------------------------------
LchHbB2      AWEKFMALVIDSLSRQYN------------------------------------------
LchMb        ALKKALSMIIQDMGGMYKEFGFK-G-----------------------------------
LchNgb       AWIALYSFVVETMARGWGANGEN-KLN---------------------------------
LplaHbA      AVDKLLSQVVILLKSAY-------------------------------------------
LplaHbB      GLEKLMSMICILLRSSY-------------------------------------------
MangMb       AMKKALELFRNDIATKYKELGFH-G-----------------------------------
MbiMb        AMTKALELFRKDIAAKYKELGFH-G-----------------------------------
MgaGbE       SFEKVTNEICTHLTNIYKEAGW--------------------------------------
MglaHb2      GWHKVMTIICKMLKSKY-------------------------------------------
MmuMb        AMSKALELFRNDIAAKYKELGFQ-G-----------------------------------
MniMb        ALKNVMTTIIADIEANYKELGFT-G-----------------------------------
NcoMb        ALRNVMAVIIADMEADYKELGFT-E-----------------------------------
OanGbY       SFQKLQSSLYDQVVITYLHSGSD-------------------------------------
OanHbW       AWQKLVGVVASALSSQYH------------------------------------------
OanMb        AMGKALELFRNDMAAKYKEFGFQ-G-----------------------------------
OanNgb       AWTRLYTAVVHAMSRGWGGE----------------------------------------
OlaCygb1     AWTNLLAILCCSIKAVYEELGWP-HLSNSTS-----------------------------
OlaCygb2     VWTKLMAAVYWHVTGAYTEVGWL-QVSSSAV-----------------------------
OlaHbA       ALDKFLAAVSLALSEKYR------------------------------------------
OlaHbB       TFQKFLAVVVSALGRQYH------------------------------------------
OlaMb        ALRSVMAGIIAEIEADYKELGFA-G-----------------------------------
OlaNgb       AWLNMYSIVVAAMSRGWAKNGED-KAD---------------------------------
PanGbE       DFKKVTDVVCEQIKSTY-------------------------------------------
PanGbX       AWKALFKYLISLMKKGFQEEEKT-HLINKSTYPKKQLISKMNFVKNNV------------
PanGbY       SWQKFYSLTYQQLEKCYSTCPSS-------------------------------------
PanHba1      VWDKFMCMLSCILAVKYR------------------------------------------
PanHba2      AWDKFLAAVSAVLTEKYR------------------------------------------
PanHba3      SADKFFERVSSQLVSLYR------------------------------------------
PanHba4      SFDKGLECVSSELVSLYR------------------------------------------
PanHbb1      AWQKLMGVIAAGLSKQYH------------------------------------------
PanHbb2      TFQKLVAVISSALTREYH------------------------------------------
PanHbb3      ACHKLMVEIADGLSRQYH------------------------------------------
PanHbb4      AFQKLVAEVAAGLSRKYH------------------------------------------
PanHbb5      CFEKLVGVTAAGLSSQYH------------------------------------------
PanMb1       YMKATLALIVQTLTKLYKELGK--------------------------------------
PanMb2       SLKSALGGVCHSLEKLYKEV----------------------------------------
PanMb3       SVKAVLDVFSQSMTTLYGEV----------------------------------------
PanMb4       SMKSALNQIANGLKDNYAKV----------------------------------------
PanMb5       AMNAALKQIANTLKSNYAKV----------------------------------------
PanMb6a      AMNVAFDQIADGLKTQYQTV----------------------------------------
PanMb6b      AMNVAFDQIADGLKTQYQTV----------------------------------------
```

```
PanMb7        SLKAALSQIANGLKANYAKV----------------------------------------
PcaMb         AMNKALELFRKDIAAKYKELGYQ-G-----------------------------------
PgeMb         ALRNVMAVIIADMEADYKELGFT-E-----------------------------------
PmaaHb1       GLEKLMSMICILLRSSY-------------------------------------------
PmaaHb10      GWEKLLSSICIHLKSAY-------------------------------------------
PmaaHb11      AWEKLLSIISILLKSQY-------------------------------------------
PmaaHb12      AVDKFLSQVVILLKFAY-------------------------------------------
PmaaHb13      AVDKFLSQVVILLKSAY-------------------------------------------
PmaaHb14      AVDKFLSQVVILLKSAY-------------------------------------------
PmaaHb2a      GFEKLMSMICILLRSAY-------------------------------------------
PmaaHb3       GFEKLMSMICILLRSAY-------------------------------------------
PmaaHb5a      GFEKLMSMICILLRSAY-------------------------------------------
PmaaHb5b      GFEKLMSMICILLRSAY-------------------------------------------
PmaaHb6       SWSKLLSLIIIELQSAY-------------------------------------------
PmaaHb7       AWEKLLTYICISLKVAY-------------------------------------------
PmaaHb8       GFEKLMSMICILLRSAY-------------------------------------------
PmaaHb9       AWEKFLSQVSILLKSQY-------------------------------------------
PmaaMb1       GWSKLLTTTCIGLKSAF-------------------------------------------
PmaaMb2       AWIKLLSIICIGLRSAF-------------------------------------------
PmaCygb       AWTKLLGTLCTEFENAYREEGVL-EQAAA-------------------------------
PmaGbX1       AWQCLFRYIAAVMKRGYLEEEAASNGVNTANYDRGQGNHGATAM----------------
PsiCygb       AWTKLKSLIYTHVTATYKEAD---REPSK-------------------------------
PsiGbE        SFEKVTNEICTRLNNAY-------------------------------------------
PsiGbX        AWQVGSGSAETSPSPG------------------------------------PLWFFIRP
PsiGbY        AWEKLFRLLFEQINTSYANASKS-------------------------------------
PsiHbaA       SLDKFMCAVSAVLTSKYR------------------------------------------
PsiHbaD       AFDKFMEAVCNVLTEKYR------------------------------------------
PsiHbB        AWQKLVGVVAHALAHQYH------------------------------------------
PsiHbG        AWHKLVAAVAHALALRYH------------------------------------------
PsiHbZ        ALDKFLSQISSVLTEKYR------------------------------------------
PsiMb         EMRKALELFRNSMASKYKEFGFQ-G-----------------------------------
PsiNgb        AWTKLYGAVVKAMSRGWDARKEG-E-----------------------------------
RnoCygb       AWTKLRGLIYSHVTAAYKEVGWV-QQVPNTTTLPATLPSSG------------------P
RnoMb         AMSKALELFRNDIAAKYKELGFQ-G-----------------------------------
SchMb         ALRNVMAAVIADLEANYKELGFS-G-----------------------------------
SjaMb         ALRNVMGVFIADMDANYKELGFS-G-----------------------------------
TalaMb        ALRNVMGIIIADLEANYKELGFT-G-----------------------------------
TalbMb        ALRNVMGIIIADLEANYKELGFS-G-----------------------------------
TguCygb       AWTKMKTLIYTHVTAAYKEVGWA-QYPTATL-----------------------------
TguGbE        SFEKVTNEICTHLNNIYKEEGW--------------------------------------
TguHbA        SLDKFLCAVGTVLTAKYR------------------------------------------
TguHbAD       AVDKFMSAVASVLAEKYR------------------------------------------
TguHbE        AWQKLVRVVAHALAHEYH------------------------------------------
TguMb         AMKKALELFRNDMATKYKEFGFQ-G-----------------------------------
TguNgb        GWSKLYNAVVKAMQRGWETLPEG-D-----------------------------------
TniCygb1      AWTKLLANMCCGIAAVYKEAGWT-ELSSSVE-----------------------------
TniGbX        AWKTLFQYVTGLMRKGHQEEGSR--QRHLALPPKDGPEKRTSAL----------------
TniMb         ALRNIMATIIADIDATYKELGFS-------------------------------------
TniNgb        AWLNMYSVVVASMSRGWAKNGED-KAD---------------------------------
TruCygb1      AWTKLLANMCCAVAAVYEEAGWT-KLSSSAE-----------------------------
TruCygb2      VWAKLMAAVYWHVTGAYTDVGWL-QVSSSAV-----------------------------
TruNgb        AWLNMYSVVVAAMSRGWAKNGED-KAD---------------------------------
TthMb         ALRNVMGIIIADLEANYKELGFS-G-----------------------------------
XlaGbY        SWEKLFSITYNFLDSCYTKSDS--------------------------------------
XlaHbA1       AWDKFLAEVATVLTSKYR------------------------------------------
XlaHbAT5      AWDKFLAVVSAVLVSKYR------------------------------------------
XtrCygb       AWNKLRSHLYSHVLSAYKEAGWT-QYPSNSV-----------------------------
XtrGbX        AWKGLFAYICTVMERGYQEEERR-HSDGRSLIDGLQGNKGLI------------------
XtrGbY        SWEKLFSITYKYLESCYANTDS--------------------------------------
XtrHbA1       ALDKFLVSVSNVLTSKYR------------------------------------------
XtrHbB1       AFEKLFAAIADALGKGYH------------------------------------------
XtrHbB2      VWEKLNATLVAALSHGYF------------------------------------------
XtrNgb        AWSLLYANVVQSMSRGWHRDSQE-QREGI-------------------------------
; end; begin mrbayes;
prset
aamodel=fixed(GTR);
prset aarevmatpr=fixed
(4.1586,2.708,3.8656,24.35,10.1598,9.4882,20.2114,3.5106,1.4657,3.8675,5.2486,10.9961,2.4819,11.5206,46.2446,20.9301,1.7679,
2
.142,24.925,7.3554,1.2126,5.2294,3.5606,27.4689,3.8171,23.7387,1.2423,2.9529,61.886,4.7361,0.5158,3.2531,8.395,5.6641,5.8071
,
3.0761,1.6717,49.6584,5.1728,5.2994,16.589,14.064,44.1125,1.8734,0.6694,20.9847,3.6294,0.8758,1.5827,39.2126,19.572,0.4439,5
.
9873,0.8187,0.612,51.2992,5.1201,8.2657,9.0697,0.1046,0.1475,2.7681,0.2499,0.1704,3.8588,12.1332,4.1661,0.2924,1.3217,0.3714
,
0.0342,0.8297,5.5689,6.2662,3.1366,5.811,0.1298,8.7426,10.8123,0.7374,27.2397,11.1863,6.5557,11.402,19.1672,40.3888,3.4127,4
.
1467,0.433,0.6816,17.6791,1.6996,0.184,4.103,5.9867,5.9141,0.7616,1.1743,2.3971,2.6214,47.0891,0.7127,5.698,31.6401,16.3622,
0
.3508,6.1073,11.9723,10.5666,2.3107,2.5174,2.0576,3.0472,0.0852,0.433,2.9019,1.3651,0.8764,1.9268,17.0218,1.2701,2.6266,0.53
4
9,0.7503,1.0652,3.5836,6.8211,4.3286,6.6732,4.9779,9.685,5.7157,5.8408,51.9152,1.1643,40.5499,1.5561,41.8074,10.8855,0.7658,
0
.6271,10.1128,1.0923,2.2747,104.177,1.3451,61.7519,25.3635,2.4365,1.7833,2.9635,6.0617,2.9314,16.6574,6.4234,0.234,3.8184,7.
3
241,11.1216,0.4882,1.2907,1.8118,17.5976,0.9768,3.3942,19.7646,6.8105,4.7085,18.5746,0.9241,3.5396,1.6142,24.0373,76.3432,6.
4
046,13.0905,5.5905,0.9306,0.8767,2.9006,63.3164,2.4345,3.9184,0.9623,1.3776,2.405,21.4061,30.8333,1.8539,2.439);
prset
```

```
statefreqpr=fixed(0.079066,0.055941,0.041977,0.053052,0.012937,0.071586,0.040767,0.057337,0.022355,0.062157,0.099081,0.0646,
0
.022951,0.042302,0.04404,0.061197,0.053287,0.012066,0.034155,0.069147);
lset rates=gamma;
mcmc ngen=5000000 printfreq=1000 samplefreq=1000 nchains=4 savebrlens=yes;
End;
```

B.

```
>AcaGbY
---------------------------------------------------------MTD
LDRRHIREIWTA-AFENPEENGRLVIIRFFSDYPASKQYF----KTVP------TDGDLK
AHPQVAFHGRRIMVAFSQVIENMENWNQACVLLERLVNNHKNIHQ-V-PSGMFQLLFQAM
LCTFDDLLGRT-FTP-EKRVSWEKFFQVIQEEVEAAYDR---------------------
--------------------
>AcaMb
-------------------------------------------------------MELSD
QEWQKVIDIWGK-VEPEIPAYGQVVILRLFEQHPETQEKFDKF-KNLK------SLDEMK
NSEDLKKHGTIVLTALGKILKQKRQ---HEAELAPLAQSHATKHK-I-PVKYLEFISEVI
VGVIAEKRSAD-FGA-ESQAAMRKALELFRNDMDRKYKELGFQ-GE--------------
--------------------
>AplGbE
-------------------------------------------------------MPFSE
AEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF-KGMD------SAEEMK
QSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-V-DPKNFRIICDII
LQMMEEKFGG------DCKASFEKVTNEICTHLNNVYKEAGW------------------
--------------------
>CanMb
-----------------------------------------------------------M
ADFDMVLKCWGP-VEADHATHGSLVLTRLFTEHPETLKLFPKF-AGI-------AHGDLA
GDAGVSAHGATVLKKLGDLLKARGG---HAALLKPLSSSHATKHK-I-PIINFTLIAEVI
GKVMEEKAGLD---A-AGQTALRNVMAIIITDMEADYKELGFT-E---------------
--------------------
>CauMb1
-----------------------------------------------------------M
ADHELVLKCWGV-VEADFEGTGGEVLTRLFKQHPETQKLFPKF-VGI-------AQSDLA
GNAAVNAHGATVLKKLGELLKARGD---HAAILKPLATTHANKHK-I-ALNNFRLITEVL
VKVMAEKAGLD---A-AGQTALRKVMEAVIGDIDTYYKEFGFA-G---------------
--------------------
>CauMb2
-----------------------------------------------------------M
ADYERFLKCWGA-VEADYTGNGGEVLTRLFKAHPDTQKLFPKF-KGI-------SQSELA
GNALVAAHGATVLKKLGELLRAKGD---HAAILHPMATTHANKHK-I-TLNNFRLITEVL
VEVMKEKAGLD---S-AGQGALKRIMDCIIHDIDRYYKEIGFA-G---------------
--------------------
>CcaMb1
-----------------------------------------------------------M
ADHELVLKCWGG-VEADFEGTGGEVLTRLFKQHPETQKLFPKF-VGI-------AQSDLA
GNAAVKAHGATVLKSWASCLKARGD---HAAILKPLATTHANTHK-I-ALNNFRLITEVL
VKVMAEKAGLD---A-GGQSALRRVMDVVIGDIDTYYKEIGFA-G---------------
--------------------
>CcaMb2
-----------------------------------------------------------M
ADYERFLKCWGA-IEADYAGHGGEVLTRLFKEHPDTLKLFPKF-KGI-------PQSELA
GDTLVASHGATVLKKLGELLRAKGD---HAAILQPLATTHANKHK-I-ALNNFRLITEVL
VKVMAEKAGLD---T-AGQGALKRVMDCIIRDIDRYYKEIGFA-G---------------
--------------------
>CcrMb
-------------------------------------------------------MGLSD
GEWQLVLNIWGK-VEADIPGHGQEVLIRLFKNHPETLEKFDKF-KSLK------SEGEMK
ASEDLKKHGATVLTALGGILKKKGQ---HAAELQPLAQSHANKHK-I-PVKYLEFISEAI
IQVLQSKHSGD-FGA-DTKEAMKKALELFRNDMAAKYKELGFQ-G---------------
--------------------
>CmiGbY
------------------------------------------------------MTGITE
ADKENIHFIWEK-LYENPEENGKTIVLRMFTDYPETKMYFQHF-KNIS------TLEEMK
KSPQIKRHGKIVMSALNKLIANLDNGEELSSLLAKMAERHINVHK-V-DLHNFQIIFNII
IAILEETFGNA-FTP-EIRGTWTKLFGVIYACLESHYKDAGFY-P---------------
--------------------
>CpiCygb
ME---------------KVQGEMEIERW------------------------ERSEELSD
AEKKVIQETWSR-VYMNCEDVGVSILIRFFVKFPSAKQYFSQF-KHME------DPLEME
RTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-V-EPVYFKFFTGVM
LEVIAEEYAND-FTP-EVQRAWTKVKSLIYTHVTAAYKEVGWV-QYPNSTM---------
```

```
--------------------
>CpiGbE
-------------------------------------------------------MAFSE
AEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYFTHF-KGMG------TAEEME
QSDQVRSHGKRVLTTINDLVQHLDSTDAFLGIVNPLGKKHAMQLK-V-DPKNFRIICDII
LQLMEEKYGG------DCKASFEKVTNEICTRLNNAYKEAGW------------------
--------------------
>CpiGbX
MGCALSGSGI---------APGKTISESKRSPSSENLAAPKAGPEHGGDGLGAGPFPLAD
AQKERIQESWRI-LHDNIARVGIIVFIRLFETHPECKDVFFLF-RDIE------DLEQLK
MNKELRAHGLRVMSFIEKSVARLDQEDKLEQLAFELGRSH-YRYN-A-PPKYYEYVGIQF
ISTVQPILKER-WTP-EVEEAWQVGSSSAVGPLPCCRWQRSRP-----------------
------RLGGLDP---FILP
>CpiGbY
------------------------------------------------------MALLTD
ADKKNIQHIWAK-LFENPEENGKTIVIKLFKDYPETKAYF----KNIP------TEGNLQ
EDPLVRFHGRRVMVALNQVVENLDNWKQACRILDRLADKHKNVHQ-V-PAVNFQSMFQVI
LNVCKDVLGNE-FST-EVSLSWEKLFGLLSEQINASYVSTSKS-----------------
--------------------
>CpiHbaA
-------------------------------------------------------MVLNA
GDKANVKAVWNK-VAAHVEEYGAETLERMFTVYPQTKTYFPHF--DLH------H-----
GSAQIRTHGKKVLTALGEAVNHIDD---LASALSKLSDIHAQTLR-V-DPVNFKFLNHCF
LVVVAIHQPSV-LTP-EVHVSLDKFLSAVGTVLTSKYR----------------------
--------------------
>CpiHbaD
--------------------------------------------------------MLNH
DEKQLIKHAWEK-VLGHQEDFGAEALERMFAVYPQTKTYFPHF--DLH------H-----
DSEQIRHHGKKVVTALGDAVRHMDN---LSEALSELSNLHAYNLR-V-DPVNFKLLSHCF
QVVLAVHLADE-YTP-QVHVAYDKFLAAVSAVLAEKYR----------------------
--------------------
>CpiHbB1
------------------------------------------------------MVHWTA
EEKQLITNLWGK-V--NVAECGSEALARLLIVYPWTQRFFSSF-GNLS------SPTAII
GNPKVRAHGKKVLTSFGEAVKNLDN---IKATYAKLSELHCDKLH-V-DPENFRLLGDIL
VIVLAAHFGRE-FTP-ACQAAWQKLVRVVAHALSYKYH----------------------
--------------------
>CpiHbB2
------------------------------------------------------MVHWTA
DEKQLITSLWGK-V--NVEECGSEALARLLIVYPWTQRFFSTF-GNLS------NAEAIL
HNPHVHAHGKKVLTSFGEAVKNLDH---IKQTFATLSKLHCEKLH-V-DPENFKLLGNVL
IIVLASHFTKE-FTP-ACQAAWQKLVSAVAHALALGYH----------------------
--------------------
>CpiHbG
------------------------------------------------------MVHWTA
EEKQLITSLWGK-V--NAEECGGEALARLLIVYPWTQRFFSSF-GNLS------SPTAIT
GNPKVRAHGKKVLTSFGEAVKNLDN---IKATYAKLSELHCNKLH-V-DPENFRLLGDIL
VIVLASHFGRE-FTP-ACQAAWQKLAGVVAHALAHEYH----------------------
--------------------
>CpiHbZ
-------------------------------------------------------MTLTQ
AEKAAVVAIWGK-IAAQADALGTESLERLFSSFPQTKTYFPHF--DLS------Q-----
GSAQLHGHGSKVLGAIGEAVKNIDN---ITGALATLSELHAYILR-V-DPVNFKLLSHCI
LCSVAAHFPND-FTP-EVHAAWDKFLSQISSVLTEKYR----------------------
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>CpiMb
-------------------------------------------------------MGLSD
DEWHHVLGIWAK-VEPDLSAHGQEVIIRLFQVHPETQERFAKF-KNLK------TIDELK
SSEEVKKHGTTVLTALGRILKLKNN---HEPELKPLAESHATKHK-I-PVKYLEFICEII
VKVIAEKHPSD-FGA-DSQAAMRKALELFRNDMASKYKEFGFQ-G---------------
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>CpiNgb
------------------------MESGR----------------------------LSS
TQQALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLFQYNCKKFS------SPQECL
SSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLSNLGKKH-QTVG-V-KVDSFSAVGESL
LFMLEKCLGTA-FSP-DVREAWTRLYGSVVKAMSSGWDARKEG-E---------------
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>CraMb
-----------------------------------------------------------M
ADFDMVLKCWGP-MEADHATHGSLVLTRLFTEHPETLKLFPKF-AGI-------AHGDLA
GDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVI
GKVMEEKAGLD---A-AGQTALRNVMAIIITDMEADYKELGFT-E---------------
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>CycrMb
-------------------------------------------------------MGLSD
GEWHLVLNVWGK-VETDLAGHGQEVLIRLFKSHPETLEKFDKF-KHLK------SEDDMR
RSEDLRKHGNTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAI
IHVLHSKHPAE-FGA-DAQAAMKKALELFRNDIAAKYKELGFH-G---------------
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>DreCygb1
ME--------------------GDGGVQLT----------------------QSPDSLTE
EDVCVIQDTWKP-VYAERDNAGVAVLVRFFTNFPSAKQYFEHF-RELQ------DPAEMQ
QNAQLKKHGQRVLNALNTLVENLRDADKLNTIFNQMGKSHALRHK-V-DPVYFKILAGVI
LEVLVEAFPQC-FSPAEVQSSWSKLMGILYWQMNRVYAEVGWE----NSKK---------
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>DreCygb2
ME-----------------KEREDEETEGR----------------------ERPEPLTD
VERGIIKDTWAR-VYASCEDVGVTILIRFFVNFPSAKQYFSQF-QDME------DPEEME
KSSQLRKHARRVMNAINTVVENLHDPEKVSSVLVLVGKAHAFKYK-V-EPIYFKILSGVI
LEILAEEFGEC-FTP-EVQTSWSKLMAALYWHITGAYTEVGWV-KLSSSAV---------
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>DreGbX
MGCAISGSGLT--------AGAPEIRPGEE----------------------ETPAGLTT
NHIRLIKESWRL-IQEDIAKVGIIMFVRLFETHPECKDVFFLF-RDVE------DLERLR
TSRELRAHGLRVMSFIEKSVARLDQLERLETLALELGKSH-YRYN-A-PPKYYGYVGAEF
ICAVRPILKDR-WTP-ELEEAWKTLFQYVTSIMREGFLEEERN-KRSNTQTSSRERPDKR
STAI----------------
>DreHbAa
-------------------------------------------------------MSLSD
TDKAVVKAIWAK-ISPKADEIGAEALARMLTVYPQTKTYFSHW-ADLS------P-----
GSGPVKKHGKTIMGAVGEAISKIDD---LVGGLAALSELHAFKLR-V-DPANFKILSHNV
IVVIAMLFPAD-FTP-EVHVSVDKFFNNLALALSEKYR----------------------
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>DreHbAe
-------------------------------------------------------MSLSA
KDKAAVKTLWAK-IAGKADDIGHDALSRMLIVYPQTKTYFSHW-KDLS------P-----
GSAPVRKHGKTVMGGVAEAVSKIDD---LNAGLLNLSELHAFQLR-V-DPANFKILSHNI
LVVLATLFPAD-FTP-EAHVAMDKFLSALALAMSEKYR----------------------
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>DreHbAx
--------------------------------------------------------MPSS
AEKELIAEIWDQ-MTPVAEEIGSEALLRMFTTFPQTKTYFSHL--NIS------A-----
NSEHLRSHGKKIVEALAEGAKNVST---LTTTLAPLSRFHAYQLR-I-HPTNFKLFNHCI
LVTLACRMGDD-FTP-VVHAAIDKFLSAFSAVLAEKFR----------------------
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>DreHbBa
------------------------------------------------------MVEWTD
AERTAILGLWGK-L--NIDEIGPQALSRCLIVYPWTQRYFATF-GNLS------SPAAIM
GNPKVAAHGRTVMGGLERAIKNMDN---VKNTYAALSVMHSEKLH-V-DPDNFRLLADCI
TVCAAMKFGQAGFNA-DVQEAWQKFLAVVVSALCRQYH----------------------
--------------------
>DreHbBe
------------------------------------------------------MVVWTD
FEKATIQDIFAK-A--DYDVIGPQALARCLIVYPWTQRYFAKF-GNLY------NAAAIL
GNPMVAAHGKTVLKGLELAVKNMDN---IKATYADLSVLHSEKLH-V-DPDNFRLLADCL
TIVVAAQMGAG-FTP-EVQAAFQKFIAVAVSALGRQYH----------------------
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>DreMb
-----------------------------------------------------------M
ADHDLVLKCWGA-VEADYAANGGEVLNRLFKEYPDTLKLFPKF-SGI-------SQGDLA
GSPAVAAHGATVLKKLGELLKAKGD---HAALLKPLANTHANIHK-V-ALNNFRLITEVL
VKVMAEKAGLD---A-AGQGALRRVMDAVIGDIGGYYKEIGFA-G---------------
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>DreNgb
------------------------------------------------------MEKLSE
KDKGLIRDSWES-LGKNKVPHGIVLFTRLFELDPALLTLFSYS-TNCG------DAPECL
SSPEFLEHVTKVMLVIDAAVSHLDDLHTLEDFLLNLGRKH-QAVG-V-NTQSFALVGESL
LYMLQSSLGPA-YTT-SLRQAWLTMYSIVVSAMTRGWAKNGEH-KSN-------------
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>EpeMb
-----------------------------------------------------------M
ADLDAVLKCWGA-VEADFNTVGGLVLARLFKDHPETQKLFPKF-AGI-------T-GDIA
GNAAVAAHGATVLKKLGELLKAKGN---HAAIIKPLANSHAKQHK-I-PINNFKLITEAL
AHVLHEKAGLD---A-AGQTALRNVMGIVIADLEANYKELGFT-G---------------
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>GgaCygb
ME---------------KVQGEMEIERW------------------------ERSEEISD
AEKKVIQETWSR-VYANCEDVGVSILIRFFVNFPSAKQYFSQF-KHMD------DTLEME
RSLQLRKHAQRVMGAINTVVENLDDPEKVSSVLALVGKAHALKHK-V-EPVYFKKLTGVM
LEVIAEAYGND-FTP-EAHGAWTKMRTLIYTHVTAAYKEAGWV-SYPSATL---------
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>GgaGbE
-------------------------------------------------------MSFSE
AEVQSARGAWEK-MYVDAEDNGTAVLVRMFTEHPDTKSYFTHF-KGMD------SAEEMK
QSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-I-DPKNFRIICDII
LQLMEEKFGG------DCKASFEKVTNEICTHLTNIYKEAGW------------------
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>GgaHbA
-------------------------------------------------------MVLSA
ADKNNVKGIFTK-IAGHAEEYGAETLERMFTTYPPTKTYFPHF--DLS------H-----
GSAQIKGHGKKVVAALIEAANHIDD---IAGTLSKLSDLHAHKLR-V-DPVNFKLLGQCF
LVVVAIHHPAA-LTP-EVHASLDKFLCAVGTVLTAKYR----------------------
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>GgaHbAD
-------------------------------------------------------MMLTA
EDKKLIQQAWEK-AASHQEEFGAEALTRMFTTYPQTKTYFPHF--DLS------P-----
GSDQVRGHGKKVLGALGNAVKNVDN---LSQAMAELSNLHAYNLR-V-DPVNFKLLSQCI
QVVLAVHMGKD-YTP-EVHAAFDKFLSAVSAVLAEKYR----------------------
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>GgaHbG
------------------------------------------------------MVHWTA
EEKQLITGLWGK-V--NVAECGAEALARLLIVYPWTQRFFASF-GNLS------SPTAIL
GNPMVRAHGKKVLSSFGDAVKNLDN---IKNTFSQLSELHCDKLH-V-DPENFRLLGDIL
IIVLAAHFSKD-FTP-ECQAAWQKLVRVVAHALARKYH----------------------
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>GgaMb
-------------------------------------------------------MGLSD
QEWQQVLTIWGK-VEADIAGHGHEVLMRLFHDHPETLDRFDKF-KGLK------TPDQMK
GSEDLKKHGATVLTQLGKILKQKGN---HESELKPLAQTHATKHK-I-PVKYLEFISEVI
IKVIAEKHAAD-FGA-DSQAAMKKALELFRNDMASKYKEFGFQ-G---------------
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>GgaNgb
------------------------MESGM----------------------------LSR
TQQALIRESWRR-VSGSPVQHGVVLFSRLFDLDPDLLPLFQYNCKRFA------SPQECL
AAPEFLDHIRKVMLVIDAAVSHLEDLPCLEEYLCNLGKKH-QAVG-V-KVESFSTVGESL
LYMLEKCLGAA-FSP-DVREAWIELYSAVVKAMQRGWEVLPEG-D---------------
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>GgiMb
-----------------------------------------------------------M
ADFDMVLKCWGP-VEADYTTHGSLVLTRLFTEHPETLKLFPKF-AGI-------AHGDLA
GDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVI
GKVMEEKAGLD---A-AGQTALRNVMAVIIADMEADYKELGFT-E---------------
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>HsaCYGB
ME---------------KVPGEMEIERR------------------------ERSEELSE
AERKAVQAMWAR-LYANCEDVGVAILVRFFVNFPSAKQYFSQF-KHME------DPLEME
RSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-V-EPVYFKILSGVI
LEVVAEEFASD-FPP-ETQRAWAKLRGLIYSHVTAAYKEVGWV-QQVPNATTPPATLPSS
G------------------P
>HsaHBA
-------------------------------------------------------MVLSP
ADKTNVKAAWGK-VGAHAGEYGAEALERMFLSFPTTKTYFPHF--DLS------H-----
GSAQVKGHGKKVADALTNAVAHVDD---MPNALSALSDLHAHKLR-V-DPVNFKLLSHCL
LVTLAAHLPAE-FTP-AVHASLDKFLASVSTVLTSKYR----------------------
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>HsaHBB
------------------------------------------------------MVHLTP
EEKSAVTALWGK-V--NVDEVGGEALGRLLVVYPWTQRFFESF-GDLS------TPDAVM
GNPKVKAHGKKVLGAFSDGLAHLDN---LKGTFATLSELHCDKLH-V-DPENFRLLGNVL
VCVLAHHFGKE-FTP-PVQAAYQKVVAGVANALAHKYH----------------------
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>HsaHBD
------------------------------------------------------MVHLTP
EEKTAVNALWGK-V--NVDAVGGEALGRLLVVYPWTQRFFESF-GDLS------SPDAVM
GNPKVKAHGKKVLGAFSDGLAHLDN---LKGTFSQLSELHCDKLH-V-DPENFRLLGNVL
VCVLARNFGKE-FTP-QMQAAYQKVVAGVANALAHKYH----------------------
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>HsaHBE
------------------------------------------------------MVHFTA
EEKAAVTSLWSK-M--NVEEAGGEALGRLLVVYPWTQRFFDSF-GNLS------SPSAIL
GNPKVKAHGKKVLTSFGDAIKNMDN---LKPAFAKLSELHCDKLH-V-DPENFKLLGNVM
VIILATHFGKE-FTP-EVQAAWQKLVSAVAIALAHKYH----------------------
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>HsaHBG
------------------------------------------------------MGHFTE
EDKATITSLWGK-V--NVEDAGGETLGRLLVVYPWTQRFFDSF-GNLS------SASAIM
GNPKVKAHGKKVLTSLGDAIKHLDD---LKGTFAQLSELHCDKLH-V-DPENFKLLGNVL
VTVLAIHFGKE-FTP-EVQASWQKMVTGVASALSSRYH----------------------
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>HsaHBZ
--------------------------------------------------------SLTK
TERTIIVSMWAK-ISTQADTIGTETLERLFLSHPQTKTYFPHF--DLH------P-----
GSAQLRAHGSKVVAAVGDAVKSIDD---IGGALSKLSELHAYILR-V-DPVNFKLLSHCL
LVTLAARFPAD-FTA-EAHAAWDKFLSVVSSVLTEKYR----------------------
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>HsaMB
-------------------------------------------------------MGLSD
GEWQLVLNVWGK-VEADIPGHGQEVLIRLFKGHPETLEKFDKF-KHLK------SEDEMK
ASEDLKKHGATVLTALGGILKKKGH---HEAEIKPLAQSHATKHK-I-PVKYLEFISECI
IQVLQSKHPGD-FGA-DAQGAMNKALELFRKDMASNYKELGFQ-G---------------
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>HsaNGB
---------------------------------------------------------MER
PEPELIRQSWRA-VSRSPLEHGTVLFARLFALEPDLLPLFQYNCRQFS------SPEDCL
SSPEFLDHIRKVMLVIDAAVTNVEDLSSLEEYLASLGRKH-RAVG-V-KLSSFSTVGESL
LYMLEKCLGPA-FTP-ATRAAWSQLYGAVVQAMSRGWDGE--------------------
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>IpuGbX
MGCAISGLGL---------APKNTTEAASE----------------------DDAPHLTS
EHIAMIKESWKV-IQEDIAKVGIIVFVRLFETHPECKDVFFLF-RDVE------DLERLR
TSKELRAHGLRVMSFIEKSVARLDQLERLDSLAVELGRSH-YRYY-A-PPKYYGYVGTEF
ICAVRPILKEK-WTP-ELEKAWKTLFQYVTWLMRRGYNEEEEEAKRNNTVGSSRERPRQR
NTAL----------------
>LchCygb
ME-----------------KVQGEMEMDRW----------------------ERSDQLSD
TEVESIRQIWSN-VYTNCENVGVLVLIRFFVNFPSAKQYFSQF-RHLE------DPLDME
RSVQLRKHARRVMGAINTVVENVED-QDIASVLAPVGKAHALKHK-V-EPVYFKILSGVI
LEILAEEYAQH-FTP-EVQKAWTKLMSIICCHVTATYKEVGWG-QLSNSTM---------
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>LchGbE
-------------------------------------------------------MALSD
AEVQTARDVWGQ-IYANAEENGTIILVRMFTEHPDTKSYFGNF-KGMG------SAAEME
QSAQVRTHGKKIFSALNDMIQHLDSTDALLGVVNPLGKKHATQLK-V-DPKNFKIICNIL
LQVLDEKFGG------DARAGFEKVTDVLCTHLNHAYKEAGW------------------
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>LchGbX1
MGCVFSGSGI---------APSKSTPDING----SEAESRLSEELKSGSGQNSDALLLSE
PQKELIQESWRI-LHQDITRLGIIMFIRLFETHPECKDVFFLF-RDID------DFHQLK
MSKELQAHGLRVMSFIEKSVARLEQKDKLEQIAFELGRSH-CRYN-A-PPKYYQYVGVQF
ISVVKPILKEA-WTP-EVEEAWQILFKYLTAVMKKGYYVEEKK-ININNALYTKIPNALS
SNPVQNNL------------
>LchGbX2
MGCAISGLSWRA---VKGPGEEAKGKEGEA----------------------EALPAISQ
LQIHLIQESWKL-IQEDIAKVGIIMFVRLFETHPECKDVFFLF-RDVD------DLQRLR
TSKELRAHGLRVMSFVEKSVARLEHSERLEQLALELGKSH-YRYN-A-PPKYYQYVGIEF
VCAVQPILKER-WTP-EVEEAWQTLFKYVTEVMKRGYLQEEKI-KRTMETVEPKQASRRA
NNAI----------------
>LchGbY
------------------------------------------------------MAALTE
ADKQNIRGIWKT-VFENAEENGRTIVIRLFEKYPETKVYFKNF-KNIS------TMEEMQ
KNEQIRIHGLRVMNSLNQVIQNIDNLNEVYSILTHLAKRHQYVHR-V-DVHNFKLIFGVI
IKILKEALGAT-FTE-EICTSWQKMLSFTYDYLVSCYHKSSGP-----------------
--------------------
>LchHbA1
--------------------------------------------------------MLSA
NDKTLISSTWNK-VAANAEDIGAEALERLFLAHPQTKIYFSHM--DLS------P-----
GSSMLRAHGKKVMGTIEGSIKSIDK---LATVLSRLSDMHAYNFM-V-DPVNFKLLSQCI
LVALATQLMAD-FTP-EAQCAWDKFLALISEILFSKYR----------------------
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>LchHbA2
-------------------------------------------------------MGLTA
ADKTLIKSIWGK-VEKETEAIGVEALVRLFKCFPQSKVYFDHF-TDLS------P-----
SSQKLHAHAKVVLGALTKAVNHLDN---ITDTLHDISLVHAKKLL-V-DPVNFELLGHCL
EVALAAHFATD-FTP-EVHLAIDKFLYEVEKALFETYR----------------------
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>LchHbB1
------------------------------------------------------MVHWTE
TERATIETVYQK-L--HLDEVGREALTRLFIVYPWTTRYFKSF-GDLS------SSKAIA
SNPKVTEHGLKVMNKLTEAIHNLDH---IKDLFHKLSEKHFHELH-V-DPQNFKLLSKCL
IIVLATKLGKQ-LTP-DVQATWEKLLSVVVAALSREYH----------------------
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>LchHbB2
------------------------------------------------------MVTWTA
EERKAITSVWSK-V--NPEEVGHEALIRLFIVYPWTQRYFSTF-GSLS------SSTVIA
RNFKVQQHAAKVINALTEAIRNIDN---LKASFSDLSKLHFQKLH-V-DPENFKLLGKTL
IITLSEKLGSE-FSP-QIQAAWEKFMALVIDSLSRQYN----------------------
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>LchMb
-------------------------------------------------------MALSE
AEWGLILKVWGK-AEPEAASNGKSVLLRMFQEHPDTQQHFPKF-KHM-------TYQELQ
SSEELKTHGDTVLSKLGCLLKLKGN---HAGDLHPLAQTHATKHK-I-PLHNFEIISEII
VKILAEKYPGD-FGA-DGQAALKKALSMIIQDMGGMYKEFGFK-G---------------
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>LchNgb -------------------
-----MEKHN-----------------
-----------FSV
RSKELIRESWDR-LGKNKLPHGTVMFTRLFELDPDLMHLFNYN-SSFP------SQAGCL
TSPEFIDHIHKVMMVVDAAVNSLDNLLSLEDYLINLGKKH-QAAG-V-KMESFQVVGESL
LYMLEHGLDSA-FSV-EVRHAWIALYSFVVETMARGWGANGEN-KLN-------------
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>LplaHbA
------------------------MPIVDS----------------------GSVGAISA
AEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF-KGLD------SADQLK
KSPAVRWHAERIINAVNDAVVAMDDPAKQSLQLKELSQKHAHELN-V-DPKYFKVLAGVI
SDAVVK-------SG-DAKAAVDKLLSQVVILLKSAY-----------------------
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>LplaHbB
------------------------MPIVDS----------------------GSVPALTA
AEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQEFFPKF-QGLT------SADQLK
KSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLNELSSKHAKSFQ-V-DPQYFKVLAAVI
VDTVL-----------PGDAGLEKLMSMICILLRSSY-----------------------
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>MangMb
-------------------------------------------------------MGLSD
GEWHLVLNIWGK-VETDLAGHGQEVLIRLFRSHPETLEKFDKF-KHLK------SEDDMR
RSEDLRKHGNTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAI
IQVLHNKHPGE-FGA-DTQAAMKKALELFRNDIATKYKELGFH-G---------------
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-------------------------------------------------------MGLSE
AEWQLVLHVWAK-VEADLSGHGQEILIRLFKGHPETLEKFDKF-KHLK------SEAEMK
ASEDLKKHGHTVLTALGGILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISDAI
IHVLHSKHPSD-FGA-DAQGAMTKALELFRKDIAAKYKELGFH-G---------------
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>MgaGbE
-------------------------------------------------------MSFSE
AEVQSARGAWEK-IYVDAEDNGTAVLIRMFTEHPDTKSYFTHF-KGMD------SAEEMK
QSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-I-DPKNFRIICDII
LQLMEEKFGG------DCKTSFEKVTNEICTHLTNIYKEAGW------------------
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>MglaHb2
---------------------------MSA----------------------HGIARTTE
GERAAVRASWAV-LMKDYEHAGVQILDKFFKANPAAKPFFTKM-KDLH------TLEDLA
SSADARWHVERIIQAVNFAVINIEDREKLSNKFVKLSQDHIEEFH-VTDPQYFMILSQTI
LDEVEKRNG-G-LSG-EGKSGWHKVMTIICKMLKSKY-----------------------
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>MmuMb
-------------------------------------------------------MGLSD
GEWQLVLNVWGK-VEADLAGHGQEVLIGLFKTHPETLDKFDKF-KNLK------SEEDMK
GSEDLKKHGCTVLTALGTILKKKGQ---HAAEIQPLAQSHATKHK-I-PVKYLEFISEII
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IEVLKKRHSGD-FGA-DAQGAMSKALELFRNDIAAKYKELGFQ-G---------------
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-----------------------------------------------------------M
ADFEMVLKHWGP-VEADYATHGNLVLTRLFTEHPETQKLFPKF-AGI-------AKADMA
GNAAISAHGATVLKKLGELLKAKGS---HAAIIKPMANSHATKHK-I-PIKNFELISEVI
GKVMHEKAGLD---A-AGQKALKNVMTTIIADIEANYKELGFT-G---------------
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>NcoMb
-----------------------------------------------------------M
ADFDMVLKCWGP-MEADYATHGGLVLTRLFTEHPETLKLFPKF-AGI-------AHGDLA
GDAGVSAHGATVLNKLGDLLKARGA---HAALLKPLSSSHATKHK-I-PIINFKLIAEVI
GKVMEEKAGLD---A-AGQTALRNVMAVIIADMEADYKELGFT-E---------------
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>OanGbY
------------------------------------------------------MVQVTD
VEKANIQSIWSK-MMENLEKNGIDIFTRLFREYPETKKYF----KNIP------LEGNLQ
EDPLLRSHGRRVMVALNRIIQNLDNWKQVCKILNPLAEKHKIIHS-V-DVENFQFMLKCV
GDVCQDYLGPC-YTP-EIAESFQKLQSSLYDQVVITYLHSGSD-----------------
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>OanHbW
------------------------------------------------------MVNWTS
EEKHAIVSIWGK-V--DIEETGANALSRLLVVYPWTQRYFSAF-GNLS------SPTAIV
GNPRVRAHGKKVLTSFGEAVKDLDH---VKSNFAKLSQLHSEKLH-V-DPENFRLLGDNL
IIVLAATLGKD-FTP-EAQAAWQKLVGVVASALSSQYH----------------------
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>OanMb
-------------------------------------------------------MGLSD
GEWQLVLKVWGK-VEGDLPGHGQEVLIRLFKTHPETLEKFDKF-KGLK------TEDEMK
ASADLKKHGGTVLTALGNILKKKGQ---HEAELKPLAQSHATKHK-I-SIKFLEYISEAI
IHVLQSKHSAD-FGA-DAQAAMGKALELFRNDMAAKYKEFGFQ-G---------------
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>OanNgb
------------------------MENGR----------------------------LSG
PEQELIRESWRS-VNSNPLEHGMILFTRLFDLEPDLLPLFQYNCRQFS------SPRDCL
ASPEFLDHIRKVMLVIDAAVIHLDDLSSLEEYLTNLGRKH-KAIG-V-KLSSFSTVGESL
LFMLDKCLGPA-FSP-ATREAWTRLYTAVVHAMSRGWGGE--------------------
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>OlaCygb1
ME-------------------RKQGEVDHL----------------------ERSRPLTD
KERVMIQDSWAK-VYQNCDDAGVAILVRLFVNFPSSKQYFSQF-KHIE------DAEELE
KSSQLRKHARRVMNAINTLVESLDNSDKVSSVLNAVGKAHAIRHK-V-DPVYFKILSGVI
LEVLGEAYPQV-MTA-EVASAWTNLLAILCCSIKAVYEELGWP-HLSNSTS---------
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>OlaCygb2
MSCRESPPPPSPPPQML--GVQRGECEDRP----------------------ERAEPLSD
AEMEIIQHTWGH-VYKNCEDVGVSVLIRFFVNFPSAKQYFSQF-QDMQ------DPEEME
KSSQLRQHARRVMNAIN-VVENLQDPEKVSSVLALVGKAHAVKHK-V-EPIYFKILSGVM
LSVLSEDFPEF-FTA-EVQLVWTKLMAAVYWHVTGAYTEVGWL-QVSSSAV---------
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>OlaHbA
-------------------------------------------------------MSLSA
KDKAAVKAFWAK-VSGQADAIGSDALSRMLVVYPQTKTYFAHW-KDLS------P-----
GSAPVKKHGKTVMGGIADAVGKIDD---ISSGLLNLSELHAFTLR-V-DPTNFKILSHNI
LVVMAIMFPQD-FTP-EVHVALDKFLAAVSLALSEKYR----------------------
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>OlaHbB
------------------------------------------------------MVEWTE
QERSIITNIFGN-L--DYEDVGSKALSRCLIVYPWTQRYFASF-GNLY------NAEAIK
TNPNIAAHGTKVLHGLDRAVKNMDN---IKATYAELSVLHSEKLH-V-DPDNFKLLADCL
TIVIAAKLGSA-FSP-EIQATFQKFLAVVVSALGRQYH----------------------
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>OlaMb
-----------------------------------------------------------M
ADYDMVLKHWGP-VEADYNTHGNLVLTRLFHEYPETQKLFPKF-AGI-------AKGDMA
GNAALSAHGATVLKKLGELLKARGN---HGAILKPLANSHATKHK-I-PINNFRLITEVI
GKVMAEKAGLD---A-AGQQALRSVMAGIIAEIEADYKELGFA-G---------------
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>OlaNgb
------------------------------------------------------MEKLSG
KDKELIRGSWES-LGKNKVPHGVIMFSRLFELDPALLSLFNYN-TNCG------STQDCL
SSPEFLDHVTKVMLVIDAAVNHLDDLHSLEDFLLNLGRKH-QAVG-V-STQSFAVVGESL
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LYMLQCSLGQA-YTA-ALSQAWLNMYSIVVAAMSRGWAKNGED-KAD-------------
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>PanGbE
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GLSEVRTHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-V-DVKEFEILCAIL
LELMAEKCGE------DAKTDFKKVTDVVCEQIKSTY-----------------------
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>PanGbX
MGCALSR------------AGATDNSTTDVNEILEEMGPDTVIGSRTQSEVVSDLSTLAE
SQKELIQESWKI-LHQDIARLGVIVFIRLFETHPECKDVFFMF-RDID------DIQQLQ
LSRELQAHGLRVMSFIEKSVARLQQEDKLQQLAFELGRCH-CRYN-A-LPKYFEYVAFQF
MTAVKPILKEK-WTS-EVDDAWKALFKYLISLMKKGFQEEEKT-HLINKSTYPKKQLISK
MNFVKNNV------------
>PanGbY
------------------------------------------------------MCSLST
TDIKNIRDIWSI-VCQNPEENGRTVVIRLFLDYPQTRTYFKNF-KNID------TEEGIK
ESRQVRQHGRRVVMLLSKVIECLEDWDKTSTLLSELADRHQQHHK-V-EVVNFKFLFAAL
NSVYIDVFGPT-FTP-DIEASWQKFYSLTYQQLEKCYSTCPSS-----------------
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>PanHba1
-------------------------------------------------------MPLSK
AEKTILLAVWER-ISPYIEEFGAQALTRMFRCFPETKIYFHEK--NID------P-----
GSSYVRNQGGKIVTAIGTAVQNADN---IQEALADLCCLHAYRIR-V-DPVNFQYFSKCF
LTVLAVHLQDD-FTA-DVHVVWDKFMCMLSCILAVKYR----------------------
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>PanHba2
-------------------------------------------------------MTLTA
AEKSCLASTFEK-IAPKAEQYGSELFQRMFLGFPQTRTYFAHV--DTS------A-----
NSPQLSAHGAKIIASLGKAIKNVDN---MSAALSDLSDLHAQSIR-V-DPSNFKYISHCL
LVLLAAHLKAD-FTP-QVQIAWDKFLAAVSAVLTEKYR----------------------
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>PanHba3
-------------------------------------------------------MTFTR
EDEVHIGEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYFQKF-GDYK------A-----
SSDKVIQHGKKVVDALVQASQHLHD---LESQLHPLSVKHATELM-V-DPVNFEHLSHCI
HVTIAAHHGEK-YTA-EMHRSADKFFERVSSQLVSLYR----------------------
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>PanHba4
-------------------------------------------------------MTFTH
EDEVHIAEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYFQKF-GDYK------A-----
SSDKVIQHGKKVVDALVQASQHLHD---LESHLHPLSEKHARELM-V-DPVNFEHLSHCI
HVTIAAHHGEK-YTA-EMHRSFDKGLECVSSELVSLYR----------------------
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>PanHbb1
------------------------------------------------------MVHWTS
EEEFAITSIWGN-V--DVHEEGHDTLTRLMVVYPWTKKYFSSF-GNLS------TTSTIA
SNDRVQAHGAKVLTAIGDALVDLPN---IKQNLTDLSRLHSEILH-V-DPENFRLLGQCL
VIVLAAKFGAEKFNA-DVQAAWQKLMGVIAAGLSKQYH----------------------
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>PanHbb2
------------------------------------------------------MVLWDA
AEKKVIASVWAK-V--DIEADGFQALLRTLHVYPWTKRYFSHF-GAMS------TLKDIE
SNPKVRAHGRKVMAAVGDAISHMDN---IKGHLSQLSQLHSDKLH-V-DPANFELLGNNI
VIVLAAKFGADAFTP-EVQATFQKLVAVISSALTREYH----------------------
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>PanHbb3
------------------------------------------------------MVNWKA
NERQAVTSVWAS-I--DAAGHGQETLERLLHVYPWSRRYFGKF-GDLS------TFSAIR
QNPHVRTHGAKVLGAVVECLNHMDD---IKGHLAQLSILHSDTLH-V-DPANFTLLGNCF
LIVLAKSVGAG-FTP-DVHAACHKLMVEIADGLSRQYH----------------------
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>PanHbb4
------------------------------------------------------MVNLEA
AEKQTITSFWAS-V--DPAAQGENALQRLLYCYPWSRRYFAKF-GDLS------TISAIR
KNSHVRAHGHKVLSAVGDCIPHLGD---IKGHLAQLSKLHCETLH-V-DPANFCLLGKII
VVVLASHFGAK-FTP-EVQAAFQKLVAEVAAGLSRKYH----------------------
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>PanHbb5
------------------------------------------------------MVHWDA
TEKQTITSFWGK-V--DLAADGEHSLQRLLYVYPWCRRYFHKF-GDLS------TISAIR
KNSHVRAHGHKVLSALGDCVPHLGD---IKGHLAQLSKLHCETLH-V-DPANFCLLGQII
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TIVLASRFGAA-FTP-EVQACFEKLVGVTAAGLSSQYH----------------------
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>PanMb1
------------------------------------------------------MASLSD
AQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKF-RHLT------TEAEMR
SNEDIRKHGNTVFTALGKLVKLKGN---VEGDLRSMADSHANKHK-I-HLENFDIISKVI
DNYFHESFPGD-YGA-DVQDYMKATLALIVQTLTKLYKELGK------------------
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>PanMb2
-------------------------------------------------------MTLSE
AQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKF-RHLG------SEAEMR
SCADLQKHGNTVFTALGKTLKLKGH---HDADLRPMAESHSHKHK-I-PVENFTLICSII
DKYLHESF-SD-YTG-DTRESLKSALGGVCHSLEKLYKEV--------------------
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>PanMb3
--------------------------------------------------------MASA
AQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKF-KDLA------SEAEMR
GSDGLKNHGETVFTALGKALQQRDG---IANELRPLAVTHSQNHK-I-PLEEFENICEVI
DVYLAEIC-PD-YAG-ETRTSVKAVLDVFSQSMTTLYGEV--------------------
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>PanMb4
------------------------------------------------------MAGLSE
VQWNELLAFWDKYVAPSSSEHGKHILIRMFQTEKATQTLFSKF-KDI-------PTSDLA
VNADVKKHGGVVVDFLGKLLKLKGQ---NDSQLHTMAESHKNKHK-I-PLDYFQVISSVI
DVYVNENLPEE-Y-A-PVRQSMKSALNQIANGLKDNYAKV--------------------
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>PanMb5
------------------------------------------------------MAGLSD
AQWNDLLAFFDKFIAPNSAEHGKHILIRMFDSDRATQSLFPKF-KDA-------PAADLP
KNADVKKHGGVVVDFLGKLLKQKGH---NESMLHTMAETHKNKHK-V-LPDYFQLISSVI
DVYVHENLPAE-Y-A-PVRDAMNAALKQIANTLKSNYAKV--------------------
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>PanMb6a
------------------------------------------------------MACPAK
--------FWEENVVPDAAEHGKNILIRLYKEDPAALGFFPKY-KDI-------PVSELG
NNADVKEQGAVVVKALGELLKLKGQ---HESQLHAMAESHKNTYK-I-PVEYFPKIFKIT
DAYLQEKVGAA-Y-A-AIQAAMNVAFDQIADGLKTQYQTV--------------------
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>PanMb6b
------------------------------------------------------MACPAK
--------FWEENVVPDAAEHGKNILIRLYKEDPAAQGFFSKY-KDT-------PVSELG
NNADVKEQGAVVVKALGELLKLKGQ---HESQLHAMAESHKNTYK-I-PVEYFPKIFKIT
DAYLHEKVGAV-Y-A-AIQAAMNVAFDQIADGLKTQYQTV--------------------
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>PanMb7
------------------------------------------------------MAGLSE
AQWNELLAFWDKYVAPSSSEHGKHILIRMFDADKATQALFSKY-KDI-------PTSDLA
ANADVKKHGGVVVDFLGKLLKLKGQ---NDSQLHTMAESHKNKHR-I-PLDYFQLISTVI
DVYVYENLPGE-Y-G-PVRESLKAALSQIANGLKANYAKV--------------------
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>PcaMb
-------------------------------------------------------MVLSE
GEWQLVLHVWAK-VEADVAGHGQDILIRLFKSHPETLEKFDRF-KHLK------TEAEMK
ASEDLKKHGVTVLTALGAILKKKGH---HEAELKPLAQSHATKHK-I-PIKYLEFISEAI
IHVLHSRHPGD-FGA-DAQGAMNKALELFRKDIAAKYKELGYQ-G---------------
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>PgeMb
-----------------------------------------------------------M
ADFDMVLKCWGL-VEADYATYGSLVLTRLFTEHPETLKLFPKF-AGI-------AHGDLA
GDAGVSAHGATVLNKLGDLLKARGG---HAALLKPLSSSHATKHK-I-PIINFKLIAEVI
GKVMEEKAGLD---A-AGQTALRNVMAVIIADMEADYKELGFT-E---------------
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>PmaaHb1
------------------------MPIVDS----------------------GSVPALTA
AEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQAFFPKF-QGLT------SADQLK
KSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLRELSGKHAKSFQ-V-DPQYFKVLAAVI
VDTVL-----------PGDAGLEKLMSMICILLRSSY-----------------------
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>PmaaHb10
------------------------MPIVDS----------------------GSVGALSA
SEKAAVAGSWKA-VYANYEAAGKAVLIKFFTSNPGVQDFFPKF-KGLD------SADKLS
KSPAVRWHAERIINAVNDSVVALDDPEKQSLKLKALSQKHAYEFH-V-DSQYFKVLSATI
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LEQVDDANG-G-LSA-EGKSGWEKLLSSICIHLKSAY-----------------------
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>PmaaHb11
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AEKAIITDSWKV-VYADYEAAGKAILIKFFTSNPGVQDFFPKF-KGLD------SADQLS
KSAAVRWHAERIINAVNDAVVALDDPEKQSLKLKALSKKHAQEFN-V-DPQYFKVLSANV
LEQVAAANG-G-LSA-EAQGAWEKLLSIISILLKSQY-----------------------
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>PmaaHb12
------------------------MPIVDS----------------------GSVGEFSA
AEKSLIVSAWAP-VYAKYEEAGVDILVKFFSDNPGVQDFFPKF-KGLD------SADQLK
KSPAVRWHAERIINAVNDAVVALDDPPKLSLKLKALSKKHAQELN-V-DPQYFKVLAGVI
SDAVAK-------SG-DEKAAVDKFLSQVVILLKFAY-----------------------
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>PmaaHb13
------------------------MPIVDS----------------------GSVGAISA
AEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF-KGLD------SADQLK
KSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-V-DPSYFKVLAGVI
SDAVAK-------SG-DAKAAVDKFLSQVVILLKSAY-----------------------
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>PmaaHb14
------------------------MPIVDS----------------------GSVGAISA
AEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF-KGLD------SADKLK
KSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-V-DPSYFKVLAGVI
SDAVAK-------SG-DAKAAVDKFLSQVVILLKSAY-----------------------
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>PmaaHb2a
------------------------MPIVDT----------------------GSVAPLSA
AEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFFPKF-KGLT------TADQLK
KSADVRWHAERIINAVNDAVVSMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVI
ADTVA-----------AGDAGFEKLMSMICILLRSAY-----------------------
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>PmaaHb3
------------------------MPIVDS----------------------GSVAPLSA
AEKTKIRSAWAP-VYSNYETTGVDILVKFFTSTPAAQEFFPKF-KGLT------TADQLK
KSADVRWHAERIINAVNDAVVSMDDTEKMSMKLGDLSGKHAKSFQ-V-DPQYFKVLAAVI
ADTVA-----------AGDAGFEKLMSMICILLRSAY-----------------------
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>PmaaHb5a
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AEKTKIRSAWAP-VYSTYETSGVDILVKFFTSTPAAQEFFPKF-KGLT------TADQLK
KSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVI
ADTVA-----------AGDAGFEKLMSMICILLRSAY-----------------------
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>PmaaHb5b
------------------------MPIVDS----------------------GSVAPLSA
AEKTKIRSAWAP-VYSTYETSGVDILVKFFTSNPAAQEFFPKF-KGLT------TADQLK
KSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVI
ADTVA-----------AGDAGFEKLMSMICILLRSAY-----------------------
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>PmaaHb6
M-----------------------GALQDS----------------------GIVSSFKE
DEKAALRESWDI-FNNSHQDAGVKILARFIINNPEAKKFFPKF-KGLN------TAEELQ
NSAEVRIHGDKILAAVQQAVLDLDDPDKQKNKLKDLSKSHAQQFN-V-EPAYFKTFAEVI
LKYVTETCGKS-FTS-EMRTSWSKLLSLIIIELQSAY-----------------------
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>PmaaHb7
------------------------MPIEDT----------------------GSKPDFSD
EEKKAIKDSWSG-VYSEYESASSEILIKFFVDNPSAQDFFPKF-KDLD------SEEKLK
NSTAVRWHAERIINAVNDVIWLLDEPEKNAKNLKELSEKHAVQLN-V-DAKFFKVLAELI
LDKVAEKSGDS-FSD-SARSAWEKLLTYICISLKVAY-----------------------
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>PmaaHb8
------------------------MPIVDS----------------------GSVAPLSA
AEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFFPKF-KGMT------TADQLK
KSADVRWHAERIINAVNDAVTSMDDTEKMSMKLRDLSGKHAKSFQ-V-DPQYFKVLAAVI
ADTVA-----------AGDAGFEKLMSMICILLRSAY-----------------------
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>PmaaHb9
------------------------MPIVDS----------------------GSVGALSG
AEKAAIADSWKA-VYSNYEEAGKAILIKFFTSNPGVQDFFPKF-KGLD------SADQLS
KSAAVRWHAERIINAVNDAVVALDDPEKLSLKLKALSKKHAQEFN-V-DPQYFKVLAVNI
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VEGVSSANG-G-LGA-EAQAAWEKFLSQVSILLKSQY-----------------------
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SSPVLRDHAKRIMNSINDMVVALDDTNAQNAQMNGLSKKHANDFK-V-DPKYFKVISNVI
LSVIAEGLGAQ-FND-AAKNGWSKLLTTTCIGLKSAF-----------------------
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>PmaaMb2
M-----------------------SAIVDS----------------------GSAPALSG
DEKAAIKSTWPS-VFAKAEDVGAEMLSRFISSNADVKKYFPKF-KDIS------SQAELK
SSAKVRDHAKRIMAFINDLVDNIDNAGAQTAKLHSLSAEHAEKFK-V-DPQYFKVISNVL
LDILGETFGAS-FSG-ATRSAWIKLLSIICIGLRSAF-----------------------
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ME----------------------------------------------------QGWLSE
EEIEALQDIWEK-VFKSAEDVGVILLVRLFTGHPASKQYFPMF-KDLE------TADDLK
ASAKLRWHAGRVMGSLDKAVRSLRKPEELIKILRAVGLSHARKATPV-DVKYYHILGGII
MDVLLETFKDE-LSP-TARSAWTKLLGTLCTEFENAYREEGVL-EQAAA-----------
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>PmaGbX1
MGCTVSTDER---------TGAQSSSQGQSQASRKQQQPEQQRAAGEGHQPPGPPQAPSE
SQRRLVRDSWLA-LQCDIARVGVIMFVRLFETHPECKDVFYQF-RDCE------DLQKLK
MNKQLQAHGLRVMSFIEKSVARLEQECVLEQLIVEMGRKH-YKYN-A-SPKYYSFVGIEF
IATVQPFLQEK-WTN-EVEDAWQCLFRYIAAVMKRGYLEEEAASNGVNTANYDRGQGNHG
ATAM----------------
>PsiCygb
ME-----------------KVQGEMEIERW----------------------ERSEELSD
AEKKVIQETWSR-VYTNCEDVGVSILIRFFVQFPSAKQYFSQF-KHME------DPLEME
RTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-V-EPVYFKFFTGVM
LEVIAEEYAND-FTP-EVQRAWTKLKSLIYTHVTATYKEAD---REPSK-----------
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>PsiGbE
-------------------------------------------------------MAFSE
AEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYFTHF-KGMG------TAEEME
QSDQIRSHGKKVLTAINDLVQHLDSTDAFLGIVNPLGKKHATQLK-I-DPKNFRVICDII
LQLMEEKYGG------DCKASFEKVTNEICTRLNNAY-----------------------
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>PsiGbX
MGCALSGSGS---------APGKRSSEAEQ----KDRAAWKAGPVRGGEGLEAGPFPPAG
AQKERIQESWRI-LHDSIARVGIIVFIRLFETHPECKDAFFLF-RDIE------DLQQLK
MSKELQAHGLRVMSFIEKSVARLDQEDKLEHLAFELGRNH-YRYS-A-PPKYYEYVGVQF
ISAVQPILKER-WTP-ELQEAWQVGSGSAETSPSPG------------------------
------------PLWFFIRP
>PsiGbY
------------------------------------------------------MALLTD
ADKKSIHHIWSK-LFENPEENGKIIVIRLFKDYPETKAYF----KSIP------TEGNLQ
EDPQIRYHGRRVMVALNQVIENLDNWKQACRILEHVAEKHKNTHH-V-PAANFQSMFQVI
LSVCKELMGNE-FSS-EVSSAWEKLFRLLFEQINTSYANASKS-----------------
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>PsiHbaA
-------------------------------------------------------MVLTA
CDKTNVKAVWTK-VSGHLEDYGAETLERMFATYPSTKTYFAHF--DLH------H-----
GSSQVRTQGKKVLSALGDAVAHVDD---LPSALSRLSDLHAKNLR-V-DPVNFKLLSHCF
LVVVALHHPSL-FTP-EVHVSLDKFMCAVSAVLTSKYR----------------------
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>PsiHbaD
--------------------------------------------------------MLTA
DEKQLVLHAWDK-VQGHQEDFGAEALERMFTTYPSTKTYFPHF--DLH------H-----
DSEQVRHHGKKVVTALGNAVHHMDT---LSKTLSDLSDLHAYNLR-V-DPVNFKLLSHCF
QVVLAVHLRDE-YTP-QLHVAFDKFMEAVCNVLTEKYR----------------------
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>PsiHbB
------------------------------------------------------MVHWTA
EEKQFITSLWGK-V--DVAECGGEALARLLIVYPWTQRFFSSF-GNLS------SPTAIL
GNPKVRAHGKKVLTSFGEAVKNLDS---VKATYAKLSELHCNKLH-V-DPENFRLLGDIL
VIVLASHFGKE-FTP-ACQAAWQKLVGVVAHALAHQYH----------------------
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>PsiHbG
------------------------------------------------------MVHWTP
EEKQMITSLWAK-V--NVAECGGEALARMMIVYPWTQRFFSTF-GNLS------NPQAIQ
HNPKVLEHGKKVLTSFGNAVKDLDH---IKETFAHLSELHCEKLH-V-DPENFKLLGNVL
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VIVLAAHIRKD-FPP-ACQAAWHKLVAAVAHALALRYH----------------------
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>PsiHbZ
-------------------------------------------------------MTLTQ
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GSAQLHGHGSKVLSAIGEATKNIDN---ITGALATLSELHAYILR-V-DPVNFKLLSHCI
LCSLAAHFPND-FTP-EVHAALDKFLSQISSVLTEKYR----------------------
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>PsiMb
-------------------------------------------------------MGLSD
NEWQHVLGIWAK-VESDIPAHGQEVMIRLFQVHPETQSLFAKF-KNLK------TADEMK
SSDELKKHGITVLTALGRILKQKNN---HEQELKPLAESHATKHK-I-PVKYLEFICEII
VKVIAEKHPAD-FGA-DSQAEMRKALELFRNSMASKYKEFGFQ-G---------------
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>PsiNgb
------------------------MESGR----------------------------LSS
TEKALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLFQYNCRQFS------SPLECL
SSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLTNLGKKH-QAVG-V-KVDSFSAVGESL
LFMLEKCLSTA-FSS-DVREAWTKLYGAVVKAMSRGWDARKEG-E---------------
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ME-----------------KVPGDMEIERR----------------------ERNEELSE
AERKAVQATWAR-LYANCEDVGVAILVRFFVNFPSAKQYFSQF-KHME------DPLEME
RSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-V-EPMYFKILSGVI
LDVIAEEFAND-FPV-ETQKAWTKLRGLIYSHVTAAYKEVGWV-QQVPNTTTLPATLPSS
G------------------P
>RnoMb
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GEWQMVLNIWGK-VEGDLAGHGQEVLISLFKAHPETLEKFDKF-KNLK------SEEEMK
SSEDLKKHGCTVLTALGTILKKKGQ---HAAEIQPLAQSHATKHK-I-PVKYLEFISEVI
IQVLKKRYSGD-FGA-DAQGAMSKALELFRNDIAAKYKELGFQ-G---------------
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-----------------------------------------------------------M
ADFDAVLKFWGP-VEADYTSHGGLVLTRLFKEHPETQKLFPKF-TGI-------AQADMA
GNAAISAHGATVLKKLGELLKAKGN---HAAILKPMANSHATKHK-I-PINNFKLISEII
VKVMQEKAGMD---A-GGQQALRNVMAAVIADLEANYKELGFS-G---------------
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>SjaMb
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ADFDAVLKFWGP-VEADYDKIGNMVLTRLFTEHPDTQKLFPKF-AGI-------GLGDMA
GNAAISAHGATVLKKLAEVLKAKGN---HAGIIKPLANSHATKHK-I-AINNFKLITEII
VKVMQEKAGLD---A-GGQTALRNVMGVFIADMDANYKELGFS-G---------------
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>TalaMb
-----------------------------------------------------------M
ADFDAVLKCWGP-VEADYTTIGGLVLTRLFKEHPDTQKLFPKF-AGI-------AQADLA
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VKVMQEKAGLD---A-GGQTALRNVMGIIIADLEANYKELGFT-G---------------
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>TalbMb
-----------------------------------------------------------M
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GNAAISAHGATVLKKLGELLKAKGS---HAAILKPLANSHATKHK-I-PINNFKLISEVL
VKVMHEKAGLD---A-GGQTALRNVMGIIIADLEANYKELGFS-G---------------
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>TguCygb ME-----------------
KVQGEMEIERW-----------------
-----ERSEEISD
AEKKVIQEIWSR-VYANCEDVGVSILIRFFVNFPSAKQYFSQF-KHME------DPLEME
RSLQLRKHARRVMGAINTVVENLNDSEKVSSVLALVGKAHALKHK-V-EPIYFKKLTGVM
LEVIAEEYPND-FTP-EAHGAWTKMKTLIYTHVTAAYKEVGWA-QYPTATL---------
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>TguGbE
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QSDQVRGHGKKVFGAINDMVQHLDNSEAFLGIVTPLGKKHATQLK-I-DPKNFRIICDII
LQLMEEKFGG------DCKASFEKVTNEICTHLNNIYKEEGW------------------
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GDKSNVKAVFGK-IGGQADEYGADALERMFATYPQTKTYFPHF--DLG------K-----
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GSAQVKGHGKKVAAALVEAANNVDD---LAGALSKLSDLHAQKLR-V-DPVNFKLLGQCF
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QVTLATRLGKE-YSP-EVHSAVDKFMSAVASVLAEKYR----------------------
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GNPMVRAHGKKVLTSFGEAVRNMDS---VKKCFAQLSKLHCEKLH-V-DPENFRLLGDVL
VVVLASHFGKE-FTP-ACQAAWQKLVRVVAHALAHEYH----------------------
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GSEDLKKHGVTVLTQLGKILKAKGN---HEAELKPLAQTHATKHK-I-PVKYLEFISEVI
IKVLAEKHAAD-FGA-DAQAAMKKALELFRNDMATKYKEFGFQ-G---------------
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SAPEFLDHIRKVMLVIDAAVSHLENLSCLEEYLCNLGKKH-QAVG-V-KVESFSTVGESL
LYMREEKPGAA-FSP-EVQGGWSKLYNAVVKAMQRGWETLPEG-D---------------
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ME-----------------RMQRDGEVDHV----------------------EQPGPLTE
KEKVMIQDSWAK-VFQSCDDAGVAILVRFFVNFPSSKQFFKDF-KHME------EPEEMQ
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LEVLGEAFTEI-ITA-EVASAWTKLLANMCCGIAAVYKEAGWT-ELSSSVE---------
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DQIQMIKDSWKV-IRDDIAKVGIIMFVRLFETHPECKDVFFLF-RDVE------DLERLR
SSRELRAHGLRVMSFIEKSVARLDQQDRLEALAVELGKSH-YHYN-A-PPKYYSYVGAEF
ICAVQPILKER-FTS-ELEEAWKTLFQYVTGLMRKGHQEEGSR--QRHLALPPKDGPEKR
TSAL----------------
>TniMb
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GDFDMVLKFWGP-VEADYSAHGGMVLTRLFTENPETQQLFPKF-VGI-------AQSELA
GNAAVSAHGATVLKKLGELLKAKGN---HAAILQPLANSHATKHK-I-PIKNFKLIAEVI
GKVMAEKAGLD---T-AGQQALRNIMATIIADIDATYKELGFS-----------------
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>TniNgb
------------------------------------------------------MEKLSS
KDKELIRGSWDS-LGKNKVPHGVILFSRLFELDPELLNLFHYT-TNCG------STQDCL
SSPEFLEHVTKVMLVIDAAVSHLDDLHSLEDFLLNLGRKH-QAVG-V-KPQSFAMVGESL
LYMLQCSLGQA-YTA-SLRQAWLNMYSVVVASMSRGWAKNGED-KAD-------------
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>TruCygb1
ME-----------------RMQGDGELDHV----------------------ERPSPLTD
KEKVMIQDSWAV-VFQSCDDAGVAILVRLFVSFPSSKQLFKDF-KDIE------EPEEMQ
RSIQLRKHAHRVMTTINTLVENLDDADAMASALKSVGRAHALRHK-V-DPKYFKILSGVI
LEVLGEAFTEI-ITA-EVASAWTKLLANMCCAVAAVYEEAGWT-KLSSSAE---------
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>TruCygb2
MSHRESPPAPPPPPPQLLGGQRRDVEGEDGP---------------------ERAKPLSD
TEREMIQDTWGH-IYKNCEDVGVSVLIRFFVNFPSAKRYFSQF-QDME------DPEEME
RSSQLRHHACRVMNAINTVVENLHDPEKVSSVLALVGKAHAIKHK-V-EPMYFKILCGVM
LEVLCEAFPEF-FTA-DVRMVWAKLMAAVYWHVTGAYTDVGWL-QVSSSAV---------
--------------------
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```

Supplementary Figure SII.1. Multiple sequence alignment of selected vertebrate globin proteins. The alignment is provided in the Nexus format (A), with the MrBayes block, and in FASTA format (B). See Supplementary table S2 for the abbreviations.

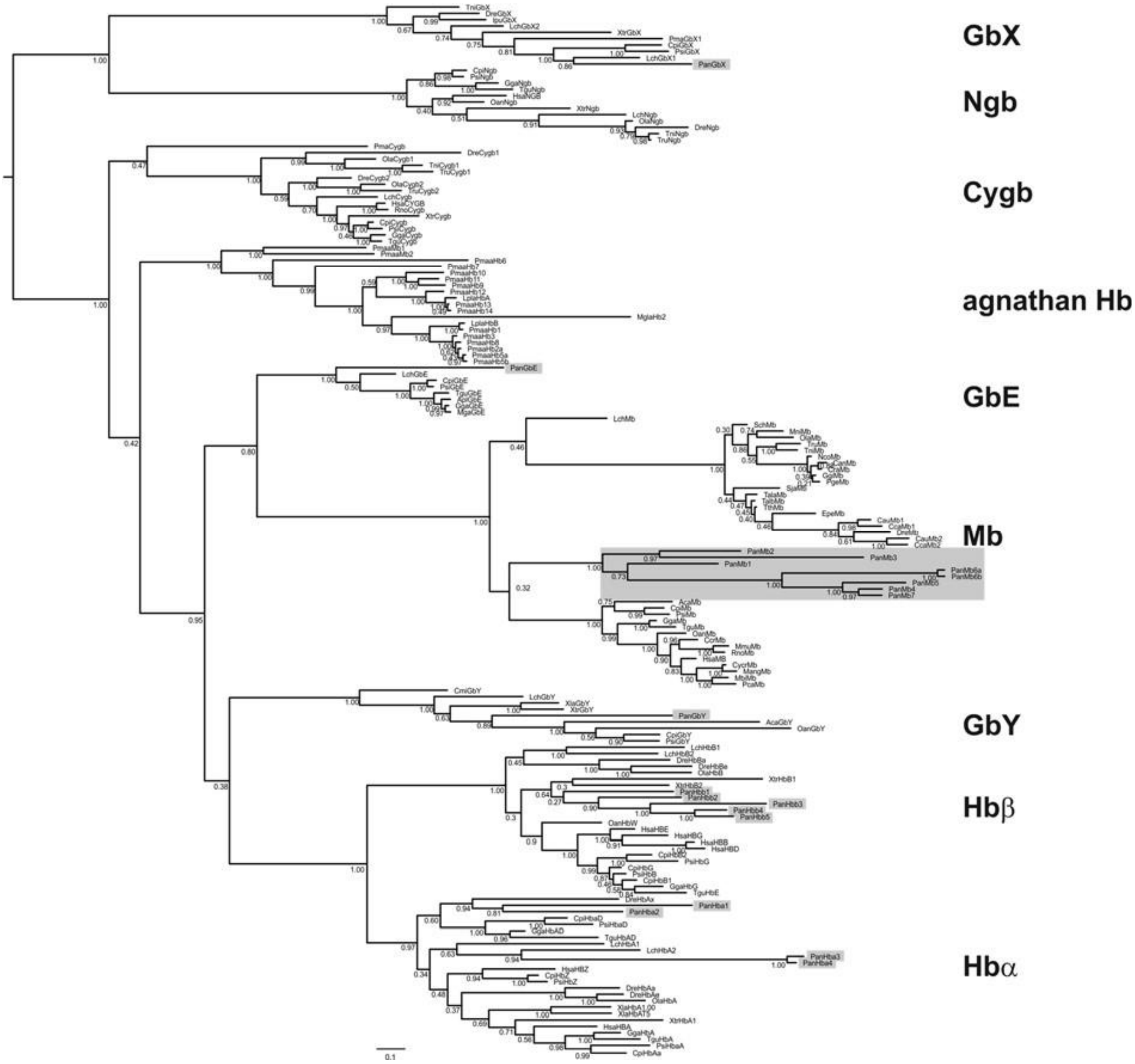

Figure SII.2. Bayesian phylogeny of vertebrate globins. The LG model of amino acid evolution was employed. The numbers at the nodes are posterior probabilities. The bar represents 0.1 PAM distance. Lungfish globins are shaded in grey. See supplementary table S2 for the abbreviations.

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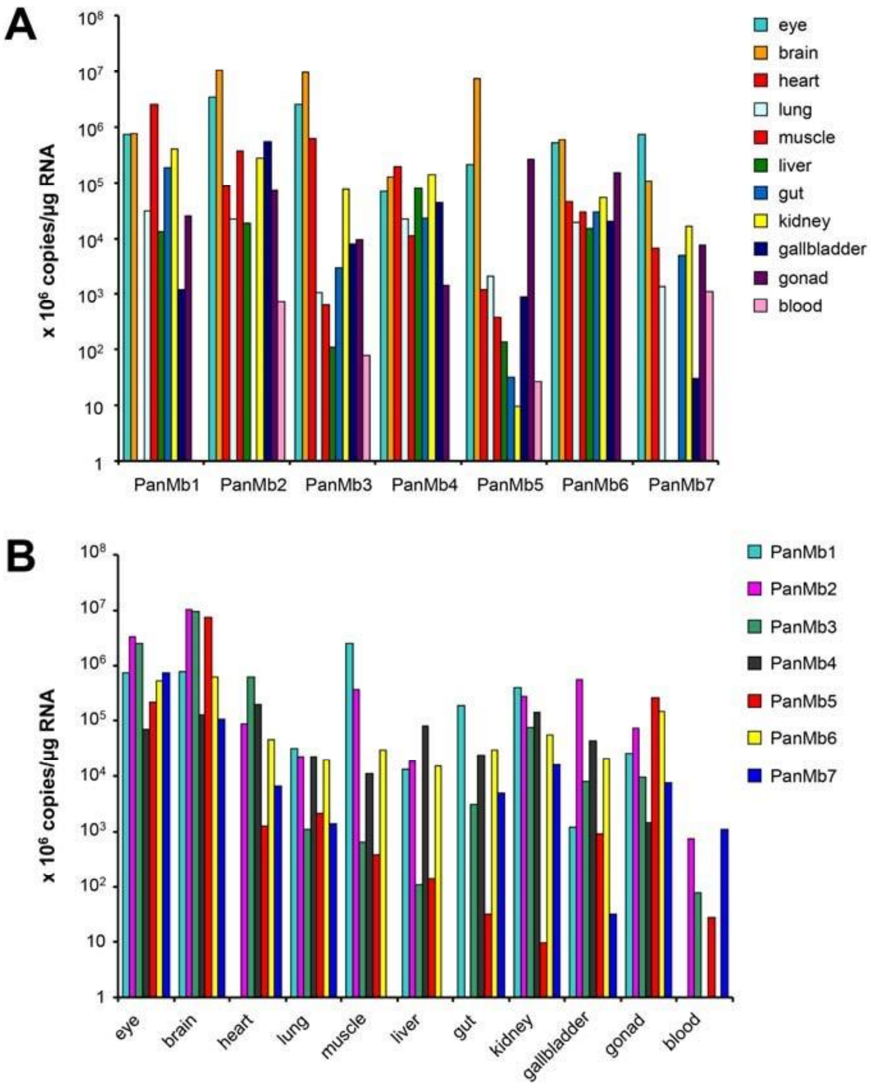
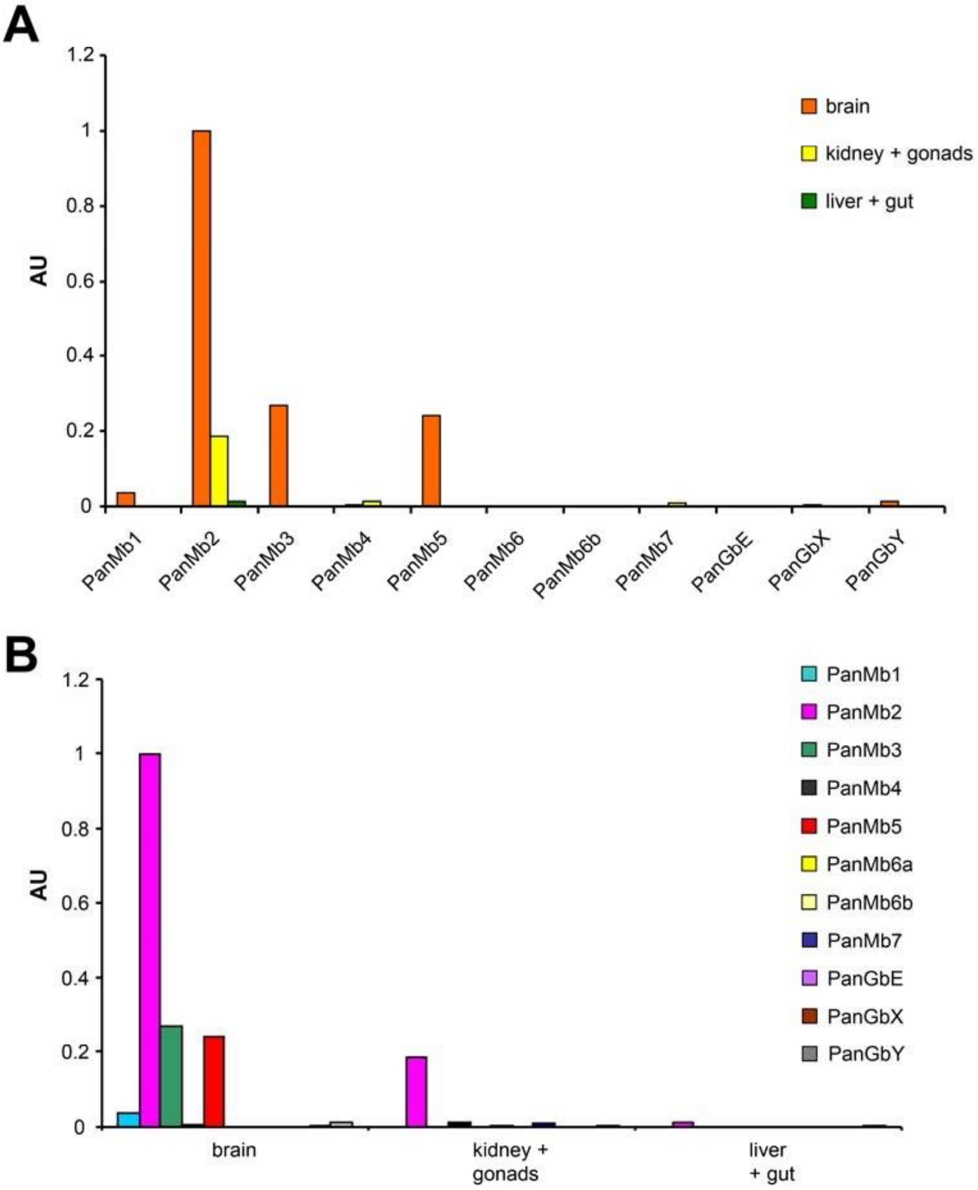
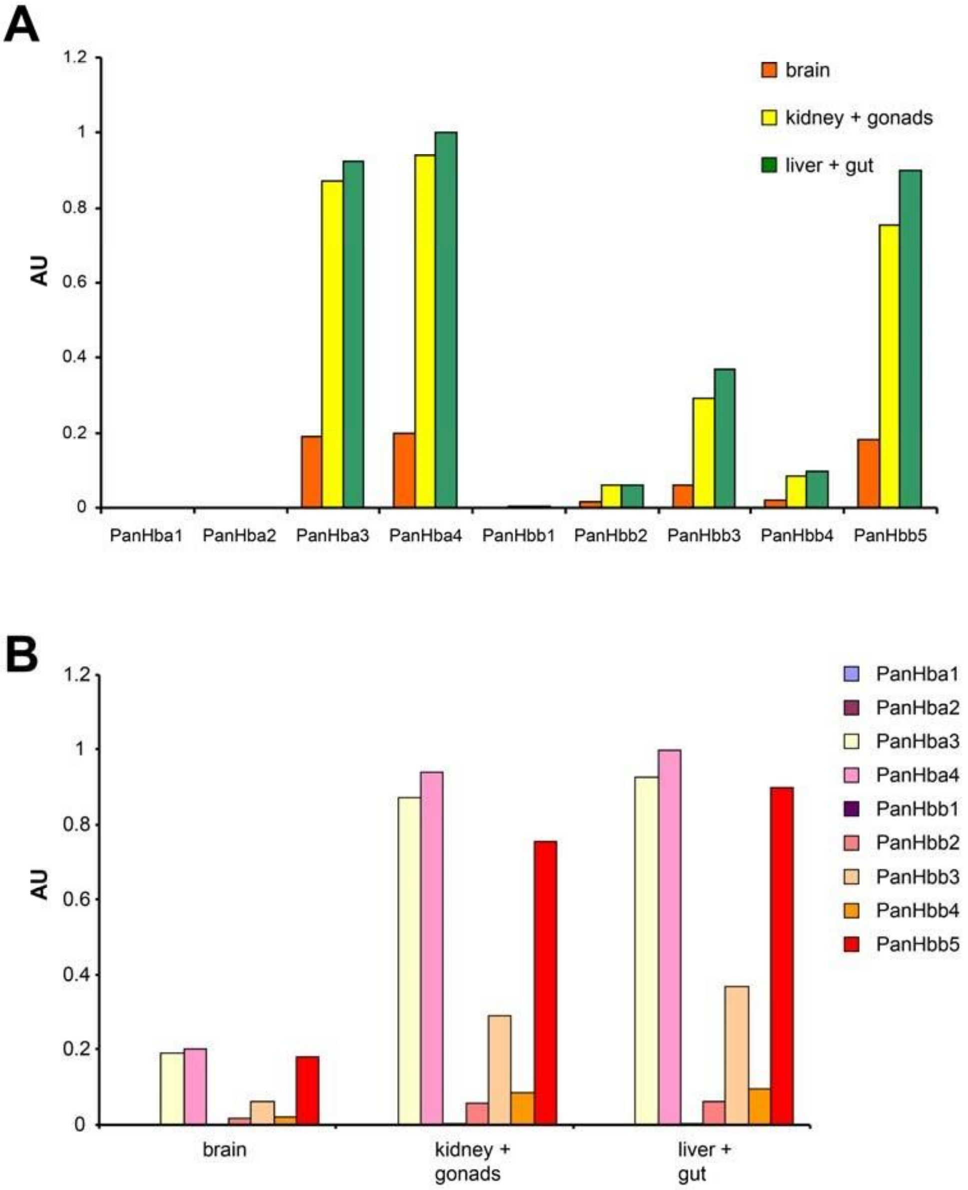
Supplementary Figure SII.3. Multiple sequence alignment Mb cDNA. The alignment is provided in the Nexus (A) and FASTA format (B). See supplementary table S2 for the abbreviations.



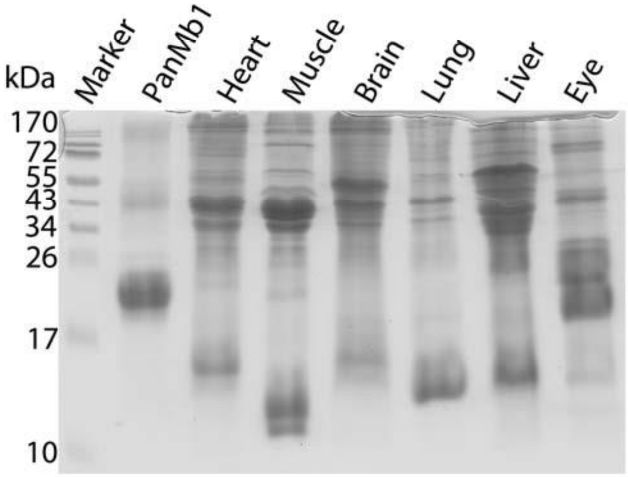
Supplementary Figure SII.4. – Expression of *Mb* mRNA in selected *P. annectens* tissue samples (log-scale data), as estimated by qRT-PCR. (A) PanMb2, 3 and 5 showed the highest expression levels, mainly in the brain. (B) The brain expresses most of the *P. annectens* Mbs. The copy numbers are given in Supporting Information table S4. The expression levels of all globins, as estimated by RNA-seq in brain, liver + gut, and kidney + gonads are given in supplementary fig. S5.



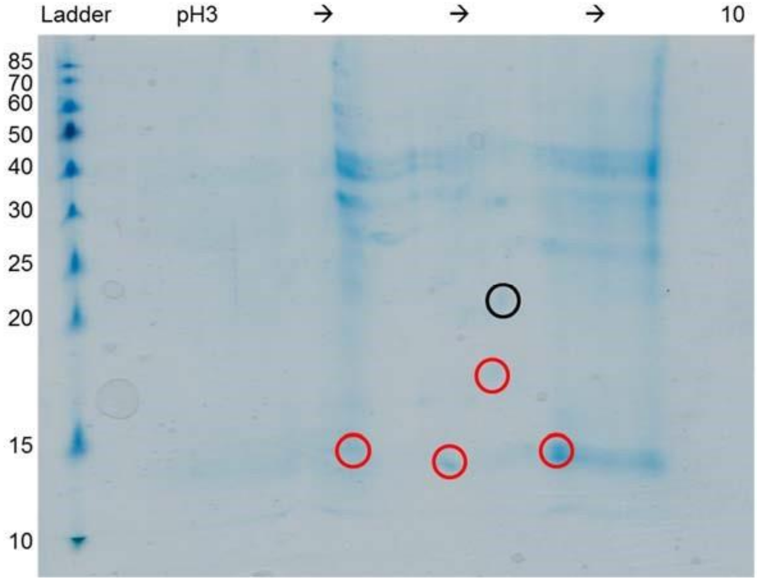
Supplementary Figure SII.5. – Expression levels of *Mb* genes, *GbE*, *GbX* and *GbY* in selected *P. annectens* tissue samples estimated by RNA-seq. Transcript numbers were calculated as arbitrary units (AU) values from the Illumina reads deposited at SRA (see also Supplementary table S5).



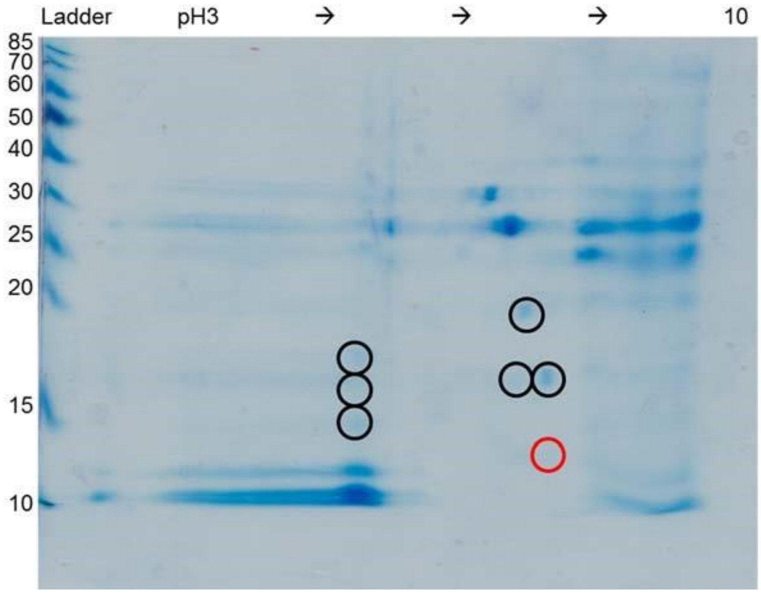
Supplementary Figure SII.6. – Expression levels of Hb chains in selected *P. annectens* tissue samples estimated by RNA-seq. Transcript numbers were calculated as arbitrary units (AU) values from the Illumina reads deposited at SRA (see also supplementary table S5).



Supplementary Figure SII.7. – SDS gel electrophoresis of 150 µg total protein from *P. annectans* from heart, muscle, brain, lung, liver, and eye samples. The recombinant expressed PanMb1 represents the benchmark of a lungfish myoglobin.



Supplementary Figure SII.8 - 2D gel electrophoresis of 250µg total protein from *P. annectans* brain. Red circles = spots in with PanMbs were identified, black circle = spots without PanMb.



Supplementary Figure SII.9 - 2D gel electrophoresis of 250µg total protein from *P. annectans* muscle. Red circles = spots in with PanMbs were identified, black circle = spots without PanMb.

Supplementary Table SII.1. Globin cDNA (left) and amino acid (right) sequences of *P. annectens*, as derived from the transcriptomes deposited at SRA with the accession numbers SRX152529 - SRX152531.

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AATCAGAGTAGATCCAGTTAATTTCCAGTATTTC
TCCAAATGTTTTTTAACTGTTTTGGCTGTTCACC
TGCAAGATGACTTTACAGCAGATGTTCATGTCGT
TTGGGATAAATTTATGTGCATGCTTTCCTGTATC
CTGGCTGTAAAATACCGATAA

MPLSKAEKTILLAVWERISPYIEEFG
AQALTRMFRCFPETKIYFHEKNIDPG
SSYVRNQGGKIVTAIGTAVQNADNIQ
EALADLCCLHAYRIRVDPVNFQYFSK
CFLTVLAVHLQDDFTADVHVVWDKFM
CMLSCILAVKYR

PanHba2
ATGACTCTGACAGCAGCTGAAAAGTCATGCCTTG
CTTCTACTTTTGAAAAGATTGCTCCTAAGGCGGA
GCAATATGGTTCTGAACTATTCCAGAGAATGTTT
TTAGGTTTTCCACAGACACGGACTTACTTTGCCC
ATGTAGACACCAGTGCTAACTCTCCTCAGCTCAG
TGCTCATGGTGCTAAAATCATTGCTTCTCTTGGC
AAAGCCATCAAGAATGTCGATAACATGTCAGCTG
CTCTGTCAGACCTCAGCGACCTGCATGCCCAGAG
CATCAGGGTTGATCCTAGCAACTTTAAGTACATC
TCCCATTGTCTCTTGGTTCTCCTGGCTGCTCACC
TCAAAGCTGACTTCACCCCTCAAGTACAGATCGC
ATGGGACAAATTTTTGGCAGCTGTTTCTGCTGTG
TTGACCGAGAAGTACAGATAA

MTLTAAEKSCLASTFEKIAPKAEQYG
SELFQRMFLGFPQTRTYFAHVDTSAN
SPQLSAHGAKIIASLGKAIKNVDNMS
AALSDLSDLHAQSIRVDPSNFKYISH
CLLVLLAAHLKADFTPQVQIAWDKFL
AAVSAVLTEKYR

PanHba3
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GCGAGGCCTGCAAATTACTCACTCAAATTCCAAA
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GCCTTCCCTGGTACAAAGTCCTACTTCCAGAAAT
TTGGTGATTACAAAGCAAGTAGTGACAAAGTGAT
TCAACATGGTAAGAAGGTGGTTGATGCCCTTGTA
CAAGCTTCGCAACATTTACATGACCTGGAAAGTC
AGTTGCATCCTTTAAGTGTAAAGCATGCCACGGA
ACTCATGGTGGACCCTGTCAACTTTGAACACTTG
TCTCACTGCATCCATGTTACTATTGCTGCCCATC
ATGGAGAAAAATACACAGCTGAGATGCATCGTTC
TGCAGACAAGTTCTTTGAGCGTGTGTCTTCGCAG
CTCGTCTCCCTGTACCGTTAA

MTFTREDEVHIGEACKLLTQIPNAGG
EALARMFAAFPGTKSYFQKFGDYKAS
SDKVIQHGKKVVDALVQASQHLHDLE
SQLHPLSVKHATELMVDPVNFEHLSH
CIHVTIAAHHGEKYTAEMHRSADKFF
ERVSSQLVSLYR

PanHba4
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CCGAGGCCTGCAAATTACTCACTCAAATTCCAAA
TGCAGGAGGAGAAGCCTTAGCAAGAATGTTTGCA
GCCTTCCCTGGTACAAAGTCCTACTTCCAGAAAT
TTGGTGATTACAAAGCAAGTAGTGACAAAGTGAT
TCAACATGGTAAGAAGGTGGTTGATGCCCTTGTA
CAAGCTTCGCAACATTTACATGACCTGGAAAGTC
ACTTGCATCCTTTAAGTGAAAAGCATGCCAGGGA
ACTCATGGTGGACCCTGTCAACTTTGAACACTTG
TCTCACTGCATCCATGTTACTATTGCTGCCCATC
ATGGAGAAAAATACACAGCTGAGATGCATCGTTC
TTTTGACAAGGGCCTTGAGTGTGTGTCTTCGGAG
CTCGTCTCCCTGTACCGTTAA

MTFTHEDEVHIAEACKLLTQIPNAGG
EALARMFAAFPGTKSYFQKFGDYKAS
SDKVIQHGKKVVDALVQASQHLHDLK
SHLHPLSEKHARELMVDPVNFEHLSH
CIHVTIAAHHGEKYTAEMHRSFDKGL
ECVSSELVSLYR

PanHbb1
ATGGTTCATTGGACAAGTGAGGAAGAATTTGCCA
TTACTTCTATATGGGGGAATGTGGACGTTCACGA
GGAAGGGCATGACACTTTGACAAGGCTCATGGTC
GTATATCCTTGGACAAAGAAGTACTTTTCTTCAT
TTGGAAACCTGAGCACTACAAGTACTATAGCATC
AAATGACCGGGTGCAGGCCCACGGTGCGAAAGTC
TTGACTGCTATTGGTGATGCGCTCGTAGATCTGC
CCAACATCAAACAGAATCTGACAGATCTCAGTCG
TCTCCATTCAGAAATACTCCATGTAGATCCAGAA
AATTTTAGGCTTCTTGGGCAGTGTTTAGTTATTG
TACTGGCAGCCAAATTCGGAGCTGAGAAGTTCAA
TGCTGATGTTCAAGCCGCCTGGCAGAAACTAATG
GGTGTCATTGCAGCGGGTCTTTCCAAGCAGTATC ATTAA

MVHWTSEEEFAITSIWGNVDVHEEGH
DTLTRLMVVYPWTKKYFSSFGNLSTT
STIASNDRVQAHGAKVLTAIGDALVD
LPNIKQNLTDLSRLHSEILHVDPENF
RLLGQCLVIVLAAKFGAEKFNADVQA
AWQKLMGVIAAGLSKQYH

PanHbb2
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TCGCCTCTGTCTGGGCAAAAGTGGACATTGAAGC
TGATGGCTTTCAGGCTTTGCTAAGGACTCTGCAT
GTGTATCCCTGGACTAAGAGATACTTCAGCCATT
TTGGTGCCATGTCTACACTCAAAGATATCGAATC
AAACCCAAAAGTTCGAGCTCATGGCAGAAAAGTA
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ATAACATCAAGGGTCATCTTTCACAACTGAGCCA
GCTGCACTCAGATAAACTCCATGTGGATCCAGCT
AACTTTGAGCTTCTTGGAAACAATATTGTGATTG
TGCTGGCAGCCAAATTTGGTGCTGATGCATTTAC
TCCTGAAGTCCAGGCTACTTTCCAAAAACTGGTG
GCTGTCATTTCATCTGCTCTAACCAGAGAATACC
ACTAG

MVLWDAAEKKVIASVWAKVDIEADGF
QALLRTLHVYPWTKRYFSHFGAMSTL
KDIESNPKVRAHGRKVMAAVGDAISH
MDNIKGHLSQLSQLHSDKLHVDPANF
ELLGNNIVIVLAAKFGADAFTPEVQA
TFQKLVAVISSALTREYH

PanHbb3
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TCACTTCTGTCTGGGCAAGCATTGACGCTGCAGG
TCATGGCCAAGAGACTTTGGAAAGGCTCCTGCAT
GTCTATCCCTGGTCTCGCAGATACTTTGGTAAAT
TTGGTGACCTATCTACTTTTAGTGCCATTAGACA
AAACCCCCATGTGAGAACTCATGGCGCGAAAGTG
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ATGACATCAAGGGTCATCTTGCCCAACTCAGCAT
TCTGCACTCTGATACACTCCATGTGGATCCAGCA
AACTTCACACTTCTGGGAAACTGTTTTTTAATTG
TCCTGGCCAAATCTGTCGGTGCCGGGTTCACTCC
TGATGTACATGCTGCCTGCCATAAACTAATGGTT
GAGATTGCTGATGGCCTGTCCAGACAGTACCACT
AA

MVNWKANERQAVTSVWASIDAAGHGQ
ETLERLLHVYPWSRRYFGKFGDLSTF
SAIRQNPHVRTHGAKVLGAVVECLNH
MDDIKGHLAQLSILHSDTLHVDPANF
TLLGNCFLIVLAKSVGAGFTPDVHAA
CHKLMVEIADGLSRQYH

PanHbb4
ATGACTTTCACTCATGAAGATGAGGTCCACATCG
CCGAGGCCTGCAAATTACTCACTCAAATTCCAAA
TGCAGGAGGAGAAGCCTTAGCAAGAATGTTTGCA
GCCTTCCCTGGTACAAAGTCCTACTTCCAGAAAT
TTGGTGATTACAAAGCAAGTAGTGACAAAGTGAT
TCAACATGGTAAGAAGGTGGTTGATGCCCTTGTA
CAAGCTTCGCAACATTTACATGACCTGGAAAGTC
ACTTGCATCCTTTAAGTGAAAAGCATGCCAGGGA
ACTCATGGTGGACCCTGTCAACTTTGAACACTTG
TCTCACTGCATCCATGTTACTATTGCTGCCCATC
ATGGAGAAAAATACACAGCTGAGATGCATCGTTC
TTTTGACAAGGGCCTTGAGTGTGTGTCTTCGGAG
CTCGTCTCCCTGTACCGTTAA

MVNLEAAEKQTITSFWASVDPAAQGE
NALQRLLYCYPWSRRYFAKFGDLSTI
SAIRKNSHVRAHGHKVLSAVGDCIGH
LGDIKGHLAQLSKLHCETLHVDPANF
CLLG

PanHbb5
ATGGTTCACTGGGATGCCACTGAGAAACAAACCA

MVHWDATEKQTITSFWGKVDLAADGE
HSLQRLLYVYPWCRRYFHKFGDLSTI
SAIRKNSHVRAHGHKVLSALGDCVPH
LGDIKGHLAQLSKLHCETLHVDPANF
CLLGQIITIVLASRFGAAFTPEVQAC
FEKLVGVTAAGLSSQYH

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        TCACCTCTTTTTGGGGAAAGGTTGACCTAGCAGC
        TGATGGAGAACATTCTTTGCAAAGGCTCCTATAC
        GTCTATCCCTGGTGTAGAAGATACTTCCATAAAT
        TTGGTGACTTGAGTACTATTAGTGCCATCCGAAA
        AAACTCCCATGTGCGAGCTCATGGTCATAAAGTG
        CTGAGTGCTCTTGGTGACTGCGTACCCCACTTGG
        GTGACATCAAAGGTCATCTTGCCCAACTCAGCAA
        GCTGCATTGTGAGACACTCCATGTGGATCCAGCA
        AATTTCTGTCTTCTGGGACAAATTATCACGATTG
        TCCTGGCCAGCCGTTTTGGTGCTGCATTCACTCC
        TGAAGTCCAGGCCTGCTTTGAGAAACTGGTCGGT
        GTGACTGCTGCTGGACTGTCCAGTCAGTACCATT
        AA

PanMb1  ATGGCATCACTATCAGATGCACAATGGAAAAAGC MASLSDAQWKKLQEFWVKNVEPNLTK
        TTCAGGAGTTCTGGGTAAAGAATGTCGAACCCAA HGQEVLVRMFVNHKSTLEYFPKFRHL
        CCTTACAAAACATGGCCAGGAGGTTTTAGTTCGC TTEAEMRSNEDIRKHGNTVFTALGKL
        ATGTTTGTGAATCATAAATCAACACTGGAGTACT VKLKGNVEGDLRSMADSHANKHKIHL
        TTCCTAAGTTTCGTCACCTTACTACTGAAGCAGA ENFDIISKVIDNYFHESFPGDYGADV
        GATGAGAAGCAATGAAGATATCCGAAAACATGGC QDYMKATLALIVQTLTKLYKELGK
        AATACTGTCTTTACTGCCTTGGGAAAACTGGTGA
        AGCTGAAAGGCAATGTTGAAGGAGACTTACGTTC
        AATGGCTGACTCACATGCCAACAAGCATAAGATA
        CACCTTGAAAACTTTGATATTATATCGAAAGTCA
        TCGACAATTACTTCCATGAATCATTCCCAGGAGA
        TTATGGAGCAGATGTCCAGGACTATATGAAGGCA
        ACACTTGCACTGATTGTCCAAACTTTGACTAAGC
        TGTACAAGGAACTAGGAAAATAA

PanMb2  ATGACACTCTCAGAAGCACAATGGAACAATGTCC MTLSEAQWNNVLAFWAKHIENDPTKH
        TGGCATTCTGGGCAAAACATATTGAGAATGATCC GHEVLIRLFLESKAAQNLFDKFRHLG
        TACAAAACATGGCCATGAGGTTTTAATTCGCTTG SEAEMRSCADLQKHGNTVFTALGKTL
        TTTTTGGAAAGTAAGGCGGCCCAAAACCTCTTTG KLKGHHDADLRPMAESHSHKHKIPVE
        ATAAATTCAGGCATTTAGGTTCAGAAGCAGAGAT NFTLICSIIDKYLHESFSDYTGDTRE
        GAGAAGTTGTGCCGACCTACAGAAACATGGCAAC SLKSALGGVCHSLEKLYKEV
        ACTGTCTTCACTGCCTTGGGAAAAACCCTGAAGC
        TGAAGGGCCACCATGATGCTGACCTTCGCCCAAT
        GGCCGAGTCACATTCTCACAAGCACAAGATCCCA
        GTGGAGAACTTCACGCTCATCTGCAGTATCATCG
        ACAAGTACCTGCATGAGTCATTCTCGGATTATAC
        AGGAGATACTAGAGAATCCCTCAAATCTGCTCTT
        GGTGGTGTTTGCCACAGTCTGGAAAAACTGTACA
        AAGAAGTGTAA
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PanMb3	ATGGCATCAGCTGCACAGTGGGATACTACCTTGA AATTCTGGGAAGCACATGTTGCGGGTGACCTTAA GAAACATGGTCATGAAGCTTTAGTTCGCTTGTTC TTGAAAAATAAAGATAGCCAAAAGCACTTTCCCA AATTCAAAGACCTTGCCAGTGAAGCAGAGATGAG AGGCTCTGATGGGCTTAAAAACCATGGAGAGACT GTGTTTACCGCATTAGGAAAAGCCCTGCAGCAGA GAGATGGCATTGCAAATGAACTACGTCCACTTGC AGTGACCCATTCCCAAAATCATAAAATCCCTCTG GAAGAATTTGAAAACATCTGCGAAGTCATTGATG TTTATTTGGCCGAGATATGTCCAGACTATGCAGG AGAGACACGTACATCTGTGAAGGCAGTGTTGGAT GTTTTTTCCCAAAGCATGACAACGCTGTATGGAG AAGTGTAA	MASAAQWDTTLKFWEAHVAGDLKKHG HEALVRLFLKNKDSQKHFPKFKDLAS EAEMRGSDGLKNHGETVFTALGKALQ QRDGIANELRPLAVTHSQNHKIPLEE FENICEVIDVYLAEICPDYAGETRTS VKAVLDVFSQSMTTLYGEV
PanMb4	ATGGCAGGACTTTCAGAAGTACAGTGGAATGAAC TATTGGCTTTTTGGGACAAATATGTTGCTCCAAG TTCTTCAGAACATGGTAAACACATTTTAATTCGC ATGTTTCAGACAGAAAAGGCAACTCAGACCCTCT TCTCAAAGTTCAAGGATATCCCTACTTCAGACCT AGCAGTCAATGCTGACGTGAAGAAACATGGCGGT GTTGTTGTTGATTTTTTGGGAAAGCTGCTGAAAC TGAAGGGCCAGAATGATAGCCAGCTACACACTAT GGCCGAATCTCATAAGAACAAGCACAAGATTCCA CTGGATTACTTTCAAGTAATTTCTTCTGTCATTG ACGTGTATGTGAATGAAAACCTGCCAGAAGAGTA TGCACCTGTCCGGCAATCCATGAAATCCGCACTC AACCAGATCGCCAATGGCCTAAAAGACAATTATG CCAAAGTATAA	MAGLSEVQWNELLAFWDKYVAPSSSE HGKHILIRMFQTEKATQTLFSKFKDI PTSDLAVNADVKKHGGVVVDFLGKLL KLKGQNDSQLHTMAESHKNKHKIPLD YFQVISSVIDVYVNENLPEEYAPVRQ SMKSALNQIANGLKDNYAKV
PanMb5	ATGGCTGGACTTTCAGATGCACAATGGAATGACC TCTTGGCTTTCTTTGACAAATTCATTGCCCCTAA TTCTGCAGAACATGGCAAACACATTTTAATTCGC ATGTTTGACAGTGACAGAGCAACTCAGAGCTTGT TTCCAAAGTTTAAGGATGCCCCTGCTGCAGACTT GCCAAAGAATGCTGATGTGAAGAAACACGGTGGT GTTGTTGTTGATTTCTTGGGAAAACTGCTGAAAC AAAAAGGTCATAATGAAAGCATGTTGCACACTAT GGCTGAGACCCATAAGAACAAGCACAAGGTTTTA CCAGATTATTTTCAACTGATTTCCTCTGTCATTG ATGTATACGTCCATGAAAATTTGCCAGCAGAGTA TGCACCTGTCCGGGATGCTATGAACGCAGCTCTG AAGCAGATTGCCAATACTTTGAAAAGCAACTACG CCAAAGTATAA	MAGLSDAQWNDLLAFFDKFIAPNSAE HGKHILIRMFDSDRATQSLFPKFKDA PAADLPKNADVKKHGGVVVDFLGKLL KQKGHNESMLHTMAETHKNKHKVLPD YFQLISSVIDVYVHENLPAEYAPVRD AMNAALKQIANTLKSNYAKV

PanMb6a	ATGGCATGCCCGGCTAAATTTTGGGAGGAAAATG TTGTGCCTGATGCTGCAGAACATGGCAAAAATAT TTTGATTCGGTTGTACAAGGAGGACCCTGCGGCT CTGGGCTTTTTCCCCAAGTATAAGGACATTCCTG TGTCTGAGCTGGGTAACAATGCTGATGTGAAAGA ACAGGGTGCTGTTGTAGTCAAAGCCTTGGGAGAG CTGCTGAAGCTGAAGGGCCAGCATGAAAGTCAGT TACACGCAATGGCTGAGTCTCATAAGAACACCTA CAAAATCCCAGTGGAATATTTTCCTAAAATTTTC AAGATTACAGATGCATATTTACAAGAAAAAGTGG GAGCAGCATATGCAGCTATCCAGGCTGCCATGAA TGTAGCGTTTGACCAGATTGCCGATGGACTGAAA ACCCAGTACCAAACTGTCTAA	MACPAKFWEENVVPDAAEHGKNILIR LYKEDPAALGFFPKYKDIPVSELGNN ADVKEQGAVVVKALGELLKLKGQHES QLHAMAESHKNTYKIPVEYFPKIFKI TDAYLQEKVGAAYAAIQAAMNVAFDQ IADGLKTQYQTV
PanMb6b	ATGGCATGCCCGGCTAAATTTTGGGAGGAAAATG TTGTGCCCGATGCTGCAGAACATGGCAAAAATAT TTTGATTCGGTTGTACAAGGAGGACCCTGCAGCT CAGGGCTTTTTCTCTAAGTATAAGGACACTCCTG TGTCTGAGCTGGGTAACAATGCTGATGTGAAAGA ACAGGGTGCTGTTGTAGTCAAAGCCTTGGGAGAG CTGCTGAAGCTGAAGGGACAGCATGAAAGTCAGT TACATGCAATGGCTGAGTCTCATAAGAACACCTA CAAAATCCCAGTGGAATATTTTCCTAAAATTTTC AAGATTACAGATGCATATTTACATGAAAAAGTGG GAGCAGTGTATGCAGCTATCCAGGCTGCCATGAA TGTAGCGTTTGACCAGATTGCCGATGGACTGAAA ACCCAGTACCAAACTGTCTAA	MACPAKFWEENVVPDAAEHGKNILIR LYKEDPAAQGFFSKYKDIPVSELGNN ADVKEQGAVVVKALGELLKLKGQHES QLHAMAESHKNTYKIPVEYFPKIFKI TDAYLHEKVGAVYAAIQAAMNVAFDQ IADGLKTQYQTV
PanMb7	ATGGCAGGACTTTCAGAAGCACAGTGGAATGAAC TCTTGGCCTTTTGGGACAAATATGTTGCCCCGAG TTCTTCAGAGCATGGCAAACACATTTTAATTCGC ATGTTTGATGCAGACAAAGCAACTCAGGCCCTCT TCTCAAAGTACAAAGATATCCCTACTTCAGACCT AGCAGCCAATGCTGATGTGAAGAAACATGGTGGT GTTGTTGTCGATTTCTTGGGGAAGCTGCTGAAAC TGAAGGGTCAGAATGATAGTCAGCTACACACTAT GGCTGAATCTCATAAGAACAAGCATCGGATTCCA CTGGATTACTTTCAACTAATTTCTACTGTCATTG ATGTGTACGTGTATGAAAACCTGCCAGGAGAGTA TGGACCTGTCCGGGAATCCTTGAAAGCAGCTCTG AGCCAGATTGCCAATGGCCTAAAAGCCAATTATG CCAAAGTATAA	MAGLSEAQWNELLAFWDKYVAPSSSE HGKHILIRMFDADKATQALFSKYKDI PTSDLAANADVKKHGGVVVDFLGKLL KLKGQNDSQLHTMAESHKNKHRIPLD YFQLISTVIDVYVYENLPGEYGPVRE SLKAALSQIANGLKANYA

Supplementary Table SII.2. –List of globin sequences used in this study. The EMBL/GenBank accession numbers of the nucleotides are given, if available. Some genes are indicated by the ENSEMBL identifier. Asterisks denote protein accession numbers.

Abbreviation	**Species**	**common name**	**Accession number**
AcaGbY	*Anolis carolinensis*	green anole	NW_003341080
AcaMb	*Anolis carolinensis*	green anole	XM_003220932
AplGbE	*Anas platyrhynchos*	mallard	XM_005012200
CanMb	*Cryodraco antarcticus*	long-fingered icefish	U71056
CauMb1	*Carassius auratus*	goldfish	AM747267
CauMb2	*Carassius auratus*	goldfish	AM747268
CcaMb1	*Cyprinus carpio*	common carp	KC342292
CcaMb2	*Cyprinus carpio*	common carp	DQ338464
CcrMb	*Condylura cristata*	star-nosed mole	NM_001287785
CmiGbY	*Callorhinchus milii*	elephant shark	NM_001292790
CpiCygb	*Chrysemys picta bellii*	Western painted turtle	XM_005297540
CpiGbE	*Chrysemys picta bellii*	Western painted turtle	XM_005293060
CpiGbX	*Chrysemys picta bellii*	Western painted turtle	XM_005293187
CpiGbY	*Chrysemys picta bellii*	Western painted turtle	XM_005306194
CpiHbaA	*Chrysemys picta bellii*	Western painted turtle	XM_005306158
CpiHbaD	*Chrysemys picta bellii*	Western painted turtle	XM_005306157
CpiHbB1	*Chrysemys picta bellii*	Western painted turtle	XM_005290010
CpiHbB2	*Chrysemys picta bellii*	Western painted turtle	XM_005290009
CpiHbG	*Chrysemys picta bellii*	Western painted turtle	XM_005290008
CpiHbZ	*Chrysemys picta bellii*	Western painted turtle	XM_005306148
CpiMb	*Chrysemys picta bellii*	Western painted turtle	XM_005300826
CpiNgb	*Chrysemys picta bellii*	Western painted turtle	XM_005301643
CraMb	*Chionodraco rastrospinosus*	ocellated icefish	U70871
CycrMb	*Cystophora cristata*	hooded seal	KC524751
DreCygb1	*Danio rerio*	zebrafish	BC165894
DreCygb2	*Danio rerio*	zebrafish	AJ635229
DreGbX	*Danio rerio*	zebrafish	AJ635194
DreHbAa	*Danio rerio*	zebrafish	AY325264
DreHbAe	*Danio rerio*	zebrafish	BC164447
DreHbAx	*Danio rerio*	zebrafish	AL915033
DreHbBa	*Danio rerio*	zebrafish	BC164283
DreHbBe	*Danio rerio*	zebrafish	NM_001097585
DreMb	*Danio rerio*	zebrafish	AY337025
DreNgb	*Danio rerio*	zebrafish	BC059416
EpeMb	*Euthynnus pelamis*	skipjack tuna	AF291837
GgaCygb	*Gallus gallus*	chicken	NM_001008789
GgaGbE	*Gallus gallus*	chicken	NM_001008786
GgaHbA	*Gallus gallus*	chicken	NM_001004376

GgaHbAD	*Gallus gallus*	chicken	CR338842
GgaHbG	*Gallus gallus*	chicken	M73995
GgaMb	*Gallus gallus*	chicken	XM_003202347
GgaNgb	*Gallus gallus*	chicken	NM_001031551
GgiMb	*Gobionotothen*	humped rockcod	U71057
	gibberifron		
HsaCYGB	*Homo sapiens*	man	AJ315162
HsaHBA	*Homo sapiens*	man	AF105974
HsaHBB	*Homo sapiens*	man	NM_000518
HsaHBD	*Homo sapiens*	man	NM_000519
HsaHBE	*Homo sapiens*	man	NM_005330
HsaHBG	*Homo sapiens*	man	NM_000559
HsaHBZ	*Homo sapiens*	man	M24173
HsaMB	*Homo sapiens*	man	NM_203377
HsaNGB	*Homo sapiens*	man	AB463927
IpuGbX	*Ictalurus punctatus*	channel catfish	CK416201
LchCygb	*Latimeria chalumnae*	coelacanth	XM_005993205
LchGbE	*Latimeria chalumnae*	coelacanth	XM_006011781
LchGbX1	*Latimeria chalumnae*	coelacanth	XM_005987904
LchGbX2	*Latimeria chalumnae*	coelacanth	XM_006012915
LchGbY	*Latimeria chalumnae*	coelacanth	XM_005990799
LchHbA1	*Latimeria chalumnae*	coelacanth	XM_006011045
LchHbA2	*Latimeria chalumnae*	coelacanth	XM_006011046
LchHbB1	*Latimeria chalumnae*	coelacanth	XM_006011047
LchHbB2	*Latimeria chalumnae*	coelacanth	XM_006011048
LchMb	*Latimeria chalumna*	coelacanth	XM_006011146
LchNgb	*Latimeria chalumnae*	coelacanth	XM_005986619
LplaHbA	*Lampetra zanandreai*	Po brook lamprey	Z24746
LplaHbB	*Lampetra zanandreai*	Po brook lamprey	Z24747
MangMb	*Mirounga angustirostris*	Northern elephant seal	KC524754
MbiMb	*Mesoplodon bidens*	Sowerby's beaked whale	KC524765
MgaGbE	*Meleagris gallopavo*	turkey	XM_003202331
MglaHb2	*Myxine glutinosa*	Atlantic hagfish	AF157494
MmuMb	*Mus musculus*	mouse	AK137456
MniMb	*Makaira nigricans*	Atlantic blue marlin	AF291833
NcoMb	*Notothenia coriiceps*	black rockcod	NM_001303294
OanGbY	*Ornithorhynchus anatinus*	platypus	genome
OanHbW	*Ornithorhynchus anatinus*	platypus	genome
OanMb	*Ornithorhynchus anatinus*	platypus	XM_001513063
OanNgb	*Ornithorhynchus anatinus*	platypus	XM_001508367
OlaCygb1	*Oryzias latipes*	medaka	NM_001104767

OlaCygb2	*Oryzias latipes*	medaka	NM_001104768
OlaHbA	*Oryzias latipes*	medaka	BAC20295
OlaHbB	*Oryzias latipes*	medaka	AB080120
OlaMb	*Oryzias latipes*	medaka	BJ883657
OlaNgb	*Oryzias latipes*	medaka	DK002855
PanGbE	*Protopterus annectens*	West African lungfish	transcriptome
PanGbX	*Protopterus annectens*	West African lungfish	transcriptome
PanGbY	*Protopterus annectens*	West African lungfish	transcriptome
PanHba1	*Protopterus annectens*	West African lungfish	transcriptome
PanHba2	*Protopterus annectens*	West African lungfish	transcriptome
PanHba3	*Protopterus annectens*	West African lungfish	transcriptome
PanHba4	*Protopterus annectens*	West African lungfish	transcriptome
PanHbb1	*Protopterus annectens*	West African lungfish	transcriptome
PanHbb2	*Protopterus annectens*	West African lungfish	transcriptome
PanHbb3	*Protopterus annectens*	West African lungfish	transcriptome
PanHbb4	*Protopterus annectens*	West African lungfish	transcriptome
PanHbb5	*Protopterus annectens*	West African lungfish	transcriptome
PanMb1	*Protopterus annectens*	West African lungfish	LT604990
PanMb2	*Protopterus annectens*	West African lungfish	LT604991
PanMb3	*Protopterus annectens*	West African lungfish	LT604992
PanMb4	*Protopterus annectens*	West African lungfish	LT604993
PanMb5	*Protopterus annectens*	West African lungfish	LT604994
PanMb6a	*Protopterus annectens*	West African lungfish	LT604995
PanMb6b	*Protopterus annectens*	West African lungfish	LT604996
PanMb7	*Protopterus annectens*	West African lungfish	LT604997
PcaMb	Physeter catodon	sperm whale	NM_001290722
PgeMb	Pseudochaenichthys georgianus	South Georgia icefish	U71055
PmaaHb1	*Petromyzon marinus*	sea lamprey	P09967*
PmaaHb10	*Petromyzon marinus*	sea lamprey	FD718926
PmaaHb11	*Petromyzon marinus*	sea lamprey	ENSPMAG00000001592
PmaaHb12	*Petromyzon marinus*	sea lamprey	Genome
PmaaHb13	*Petromyzon marinus*	sea lamprey	Genome
PmaaHb14	*Petromyzon marinus*	sea lamprey	Genome
PmaaHb2a	*Petromyzon marinus*	sea lamprey	Q9I9I3*
PmaaHb3	*Petromyzon marinus*	sea lamprey	P09968*
PmaaHb5a	*Petromyzon marinus*	sea lamprey	P02208*
PmaaHb5b	*Petromyzon marinus*	sea lamprey	ENSPMAG00000005354
PmaaHb6	*Petromyzon marinus*	sea lamprey	EG333697
PmaaHb7	*Petromyzon marinus*	sea lamprey	EE278870
PmaaHb8	*Petromyzon marinus*	sea lamprey	ENSPMAG00000005367
PmaaHb9	*Petromyzon marinus*	sea lamprey	ENSPMAG00000008540

PmaaMb1	*Petromyzon marinus*	sea lamprey	ENSPMAG00000006056
PmaaMb2	*Petromyzon marinus*	sea lamprey	EG021442
PmaCygb	*Petromyzon marinus*	sea lamprey	genome
PmaGbX1	*Petromyzon marinus*	sea lamprey	ENSPMAG00000007241
PsiCygb	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006136486
PsiGbE	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006127809
PsiGbX	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006131430
PsiGbY	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006124603
PsiHbaA	*Pelodiscus sinensis*	Chinese softshell turtle	ENSPSIG00000011874
PsiHbaD	*Pelodiscus sinensis*	Chinese softshell turtle	ENSPSIG00000012157
PsiHbB	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006130979
PsiHbG	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006130980
PsiHbZ	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006124534
PsiMb	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006137956
PsiNgb	*Pelodiscus sinensis*	Chinese softshell turtle	XM_006117796
RnoCygb	*Rattus norvegicus*	rat	NM_130744
RnoMb	*Rattus norvegicus*	Norway rat	AF197916
SchMb	*Sarda chiliensis*	Pacific bonito	AF291834
SjaMb	*Scomber japonicus*	chub mackerel	AF291835
TalaMb	*Thunnus alalunga*	albacore	AF291832
TalbMb	*Thunnus albacares*	yellowfin tuna	AF291838
TguCygb	*Taeniopygia guttata*	zebra finch	XM_002195407
TguGbE	*Taeniopygia guttata*	zebra finch	XM_002196350
TguHbA	*Taeniopygia guttata*	zebra finch	DQ216719
TguHbAD	*Taeniopygia guttata*	zebra finch	DQ213486
TguHbE	*Taeniopygia guttata*	zebra finch	NM_001245112
TguMb	*Taeniopygia guttata*	zebra finch	XM_002199380
TguNgb	*Taeniopygia guttata*	zebra finch	XM_003962460
TniCygb1	*Tetraodon nigroviridis*	spotted green pufferfish	AJ635230
TniGbX	*Tetraodon nigroviridis*	spotted green pufferfish	AJ635193

TniMb	*Tetraodon nigroviridis*	spotted green pufferfish	CR660178
TniNgb	*Tetraodon nigroviridis*	spotted green pufferfish	AJ315609
TruCygb1	*Takifugu rubripes*	torafugu	XM_003964492
TruCygb2	*Takifugu rubripes*	torafugu	AJ635231
TruMb	*Takifugu rubripes*	torafugu	XM_003976046
TruNgb	*Takifugu rubripes*	torafugu	genome
TthMb	*Thunnus thynnus orientalis*	Pacific bluefin tuna	AF291836
XlaGbY	*Xenopus laevis*	African clawed frog	NM_001095686
XlaHbA1	*Xenopus laevis*	African clawed frog	X02796
XlaHbAT5	*Xenopus laevis*	African clawed frog	X02798
XtrCygb	*Xenopus tropicalis*	Western clawed frog	AJ635232
XtrGbX	*Xenopus tropicalis*	Western clawed frog	NM_001011196
XtrGbY	*Xenopus tropicalis*	Western clawed frog	XM_002941194
XtrHbA1	*Xenopus tropicalis*	Western clawed frog	BC088005
XtrHbB1	*Xenopus tropicalis*	Western clawed frog	NM_203528
XtrHbB2	*Xenopus tropicalis*	Western clawed frog	NM_001016495
XtrNgb	*Xenopus tropicalis*	Western clawed frog	NM_001030351

Supplementary Table SII.3. – Relative rate tests.

			nucleotide		**amino acids**	
taxon 1	**taxon 2**	**outgroup**	χ^2	**P**	χ^2	**P**
PanMb1	HsaMb	DreMb	13.90	0.00019	7.81	0.00519
PanMb2	HsaMb	DreMb	9.97	0.00159	3.67	0.05551
PanMb3	HsaMb	DreMb	9.19	0.00244	1.80	0.17971
PanMb4	HsaMb	DreMb	15.45	0.00008	9.38	0.00219
PanMb5	HsaMb	DreMb	15.90	0.00007	7.08	0.00780
PanMb6a	HsaMb	DreMb	3.67	0.05551	1.88	0.16991
PanMb6b	HsaMb	DreMb	4.24	0.03959	3.43	0.06408
PanMb7	HsaMb	DreMb	17.94	0.00002	8.32	0.00392
PcaMb	HsaMb	DreMb	0.03	0.86180	2.27	0.13167
CcrMb	HsaMb	DreMb	2.78	0.09558	0.14	0.70546
RnoMb	HsaMb	DreMb	1.52	0.21704	0.40	0.52709
MmuMb	HsaMb	DreMb	3.93	0.04743	0.11	0.73888
GgaMb	HsaMb	DreMb	0.47	0.49130	1.14	0.28505
AcaMb	HsaMb	DreMb	1.49	0.22162	1.80	0.17971
LchMb	HsaMb	DreMb	2.13	0.14413	3.10	0.07817
PanMb1	RnoMb	TniMb	13.50	0.00024	6.40	0.01141
PanMb2	RnoMb	TniMb	11.84	0.00058	2.78	0.09558
PanMb3	RnoMb	TniMb	12.78	0.00035	7.05	0.00793
PanMb4	RnoMb	TniMb	13.41	0.00025	4.92	0.02650
PanMb5	RnoMb	TniMb	21.89	0.00000	9.98	0.00158
PanMb6a	RnoMb	TniMb	7.83	0.00513	1.53	0.21637
PanMb6b	RnoMb	TniMb	8.14	0.00433	1.92	0.16552
PanMb7	RnoMb	TniMb	14.96	0.00011	4.74	0.02946
PcaMb	RnoMb	TniMb	5.33	0.02092	1.33	0.24821
CcrMb	RnoMb	TniMb	0.02	0.88864	0.00	1.00000
HsaMb	RnoMb	TniMb	0.02	0.88150	0.40	0.52709
MmuMb	RnoMb	TniMb	0.60	0.43858	0.20	0.65472
GgaMb	RnoMb	TniMb	0.01	0.91153	0.05	0.82726

AcaMb	RnoMb	TniMb	0.17	0.67666	0.43	0.51269
LchMb	RnoMb	TniMb	0.96	0.32680	0.42	0.51641
PanMb1	LchMb	DreMb	26.17	0.00000	20.63	0.00001
PanMb2	LchMb	DreMb	20.21	0.00001	12.10	0.00050
PanMb3	LchMb	DreMb	20.25	0.00001	9.09	0.00257
PanMb4	LchMb	DreMb	28.97	0.00000	21.33	0.00000
PanMb5	LchMb	DreMb	27.26	0.00000	20.45	0.00001
PanMb6a	LchMb	DreMb	10.31	0.00132	8.33	0.00389
PanMb6b	LchMb	DreMb	11.27	0.00079	11.26	0.00079
PanMb7	LchMb	DreMb	31.39	0.00000	20.48	0.00001
PcaMb	LchMb	DreMb	2.39	0.12224	6.40	0.01141

CcrMb	LchMb	DreMb	0.31	0.58071	2.63	0.10476
RnoMb	LchMb	DreMb	0.58	0.44560	4.33	0.03737
MmuMb	LchMb	DreMb	0.08	0.77584	2.50	0.11385
GgaMb	LchMb	DreMb	0.91	0.34036	9.68	0.00186
AcaMb	LchMb	DreMb	6.23	0.01255	8.26	0.00406

Supplementary Table SII.4. mRNA copy numbers in lungfish tissues, as estimated by qRTPCR. The numbers are mRNA copies per µg total RNA.

	PanMb1	**PanMb2**	**PanMb3**	**PanMb4**	**PanMb5**	**PanMb6**	**PanMb7**
eye	724,685.3	3,375,105.7	2,563,646.6	70,829.4	212,796.7	530,476.2	730,838.7
brain	779,068.3	10,207,574.4	9,593,941.3	126,916.0	7,495,733.1	603,517.1	106,803.7
heart	0.0	86,255.1	613,323.3	193,640.6	1,225.9	45,186.6	6,606.9
lung	31,572.2	22,392.5	1,064.6	22,411.6	2,094.6	19,500.2	1,346.6
muscle	2,494,792.8	369,707.4	642.0	11,113.3	379.4	29,242.6	0.0
liver	13,000.6	18,376.5	109.3	80,860.4	133.7	15,183.5	0.0
gut	188,371.0	0.0	3,014.0	23,423.6	32.0	29,331.8	4,845.9
kidney	397,481.4	269,509.4	76,722.5	141,143.0	9.5	54,749.1	16,168.2
gallbladder	1,194.4	551,991.6	8,007.0	43,855.7	903.0	20,399.3	31.1
gonad	25,238.6	71,587.2	9,359.3	1,453.2	262,225.7	151,171.1	7,694.2
blood	0.0	730.4	78.5	0.0	27.2	0.0	1,089.4

Supplementary Table SII.5. Illumina read numbers in the transcriptomes from different lungfish tissues used for expression estimation by RNA-seq.

gene	brain	liver + gut	kidney + gonads
PanMb1	567	5.5	18
PanMb2	15480	293.5	3284.5
PanMb3	4209	0	17
PanMb4	102.5	3.5	233
PanMb5	3747	0	15
PanMb6a	0	0	26.5
PanMb6b	0.5	0	9.5
PanMb7	3.5	0	173.5
PanGbE	3	12.5	4
PanGbX	45	15	16
PanGbY	203.5	55	26.5
PanHba1	2.5	11.5	7.5
PanHba2	1	9.5	11
PanHba3	1711	13776	8994.5
PanHba4	1806	14890.5	9680.5
PanHbb1	7.5	65.5	32.5
PanHbb2	134	897.5	585.5
PanHbb3	542	5321.5	2895
PanHbb4	240.5	1883.5	1172.5
PanHbb5	1577.5	12950.5	7528

Supporting Information Table SII.6. –Peptide sequences found with mass spectroscopy in the myoglobin amino acid sequences from the *P. annectens*. A. Mb peptide sequences detected in the bands from brain, heart, liver and muscle samples. B. Mb peptide sequences detected in the spots from 2D gel electrophoresis of brain and muscle samples. Peptides identified by mass spectrometry are underlined.

A	**PanMb1**	**PanMb2**	**PanMb3**	**PanMb5**
brain	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV	MASAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKFKDLASEAEMRGSDGLKNHGETVFTALGKALQQRDGIANELRPLAVTHSQNHKIPLEEFENICEVIDVYLAEICPDYAGETRTSVKAVLDVFSQSMTTLYGEV	MAGLSDAQWNDLLAFFDKFIAPNSAEHGKHILIRMFDSDRATQSLFPKFKDAPAADLPKNADVKKHGGVVVDFLGKLLKQKGHNESMLHTMAETHKNKHKVLPDYFQLISSVIDVYVHENLPAEYAPVRDAMNAALKQIANTLKSNYAKV
eye	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV	MASAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKFKDLASEAEMRGSDGLKNHGETVFTALGKALQQRDGIANELRPLAVTHSQNHKIPLEEFENICEVIDVYLAEICPDYAGETRTSVKAVLDVFSQSMTTLYGEV	
heart	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV	MASAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKFKDLASEAEMRGSDGLKNHGETVFTALGKALQQRDGIANELRPLAVTHSQNHKIPLEEFENICEVIDVYLAEICPDYAGETRTSVKAVLDVFSQSMTTLYGEV	
muscle	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV		
liver	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV		
lung	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVR	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRL		

	MFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	FLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV		

B	**PanMb1**	**PanMb2**	**PanMb3**	**PanMb5**
brain	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV	MASAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKFKDLASEAEMRGSDGLKNHGETVFTALGKALQQRDGIANELRPLAVTHSQNHKIPLEEFENICEVIDVYLAEICPDYAGETRTSVKAVLDVFSQSMTTLYGEV	MAGLSDAQWNDLLAFFDKFIAPNSAEHGKHILIRMFDSDRATQSLFPKFKDAPAADLPKNADVKKHGGVVVDFLGKLLKQKGHNESMLHTMAETHKNKHKVLPDYFQLISSVIDVYVHENLPAEYAPVRDAMNAALKQIANTLKSNYAKV
muscle	MASLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKFRHLTTEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVEGDLRSMADSHANKHKIHLENFDIISKVIDNYFHESFPGDYGADVQDYMKATLALIVQTLTKLYKELGK	MTLSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKFRHLGSEAEMRSCADLQKHGNTVFTALGKTLKLKGHHDADLRPMAESHSHKHKIPVENFTLICSIIDKYLHESFSDYTGDTRESLKSALGGVCHSLEKLYKEV		

Supplementary Table SII.7. Original data of the cell culture experiments. HN33 cells were kept at 1% O_2 for 24 h. Control cells were kept at normoxia. The numbers give the fluorescence and absorbance values for the WST-1, the CellTiter-Glo® and the DCFH-DA tests.

	WST-1		**CellTiter-Glo®**		**DCFH-DA**	
	control	**24 h 1% O_2**	**control**	**24 h 1% O_2**	**control**	**24 h 1% O_2**
pcDNA	1.53033	0.28667	72722.00	34031.33	2059742.33	2783222.67
	1.56767	0.33233	72077.00	34985.00	1794558.67	2896840.00
	1.56067	0.28800	72077.00	33780.00	1802887.67	2881685.33
PanMb1	0.78267	0.50833	80410.00	28940.00	769372.67	541857.67
	0.77067	0.43100	79478.67	28786.33	756095.67	527755.00
	0.79833	0.49767	82013.00	29086.00	855283.33	516205.67
PanMb2	0.96367	0.48100	74411.67	28915.00	611255.00	388535.00
	0.93167	0.49433	74164.33	28719.33	586519.33	267797.00
	0.97067	0.47833	72757.67	28452.67	610708.67	373136.00
PanMb3	1.32833	0.32667	83825.00	45498.67	788881.67	482003.67
	1.40133	0.32500	83876.00	47011.67	825849.67	388626.67
	1.36333	0.32167	84668.33	50212.33	869837.33	464420.00
PanMb4	1.58400	0.40133	90757.00	32530.00	2738203.00	2631968.67
	1.62600	0.40767	90467.67	32686.00	2581700.00	2802125.00
	1.63633	0.41000	90120.67	32702.33	2964634.67	2796925.67
PanMb5	1.31167	0.42100	85712.67	32768.33	537292.00	264435.00
	1.47000	0.41900	87232.00	32293.67	419166.00	209270.67
	1.34100	0.40967	85530.00	32364.67	725609.00	245649.00
PanMb6a	1.31700	0.30367	75329.67	42195.00	1055382.67	513445.00
	1.41600	0.30833	76854.33	44076.00	1105534.33	506538.33
	1.35433	0.30267	75763.67	44233.67	1069829.67	466717.67

Supplementary Table SII.8. Oligonucleotide primers used for the generation of the standard plasmids (A) and for qRT-PCR expression analysis (B) of the seven *PanMb* in the different tissues.

A. Primers for standard plasmids	sequence 5'-3'	expected fragment length
Pan_Mb1_For	GCCGAATTCGTTATGGCATCACTATCAGAT	486
Pan_Mb1_Rev	GGTCTCGAGTTATTTTCCTAGTTCCTTGTA	
Pan_Mb2n_For	GCCGAATTCACCATGACACTCTCAGAA	474
Pan_Mb2_Rev	GGTCTCGAGTTACACTTCTTTGTACAG	
Pan_Mb3_For	GCCGAATTCGTTATGGCATCAGCTGC	471
Pan_Mb3_Rev	GGTCTCGAGTTACACTTCTCCATACAGC	
Pan_Mb4_For_2	GCCGAATTCACTATGGCAGGACTTTCAG	474
Pan_Mb4_Rev_2	CGGCTCGAGTTATACTTTGGCATAATTG	
Pan_Mb5_For	GCCGAATTCACTATGGCTGGACTTTCAG	474
Pan_Mb5_Rev	CGGCTCGAGTTATACTTTGGCGTAGTTG	
Pan_Mb6_For	CGTGAATTCGCTATGGCATGCCCGGCTAA	450
Pan_Mb6_Rev	CGGCTCGAGTTAGACAGTTTGGTACTGGGTTT	

B. Primers for qRT-PCR analysis	sequence 5'-3'	expected fragment length
Pan_Mb1_qPCR_For	ACTGAAGCAGAGATGAGAAGCA	119
Pan_Mb1_qPCR_Rev	GCCATTGAACGCAAGTCTCC	
Pan_Mb2_qPCR_For_2	CCAGTGGAGAACTTCACGCT	117
Pan_Mb2_qPCR_Rev_2	GCAAACACCACCAAGAGCAG	
Pan_Mb3_qPCR_For	GGCCGAGATATGTCCAGACT	100
Pan_Mb3_qPCR_Rev	CACTTCTCCATACAGCGTTGTC	
Pan_Mb4_qPCR_For_2	CAGACAGAAAAGGCAACTCAGAC	207
Pan_Mb4_qPCR_Rev_2	GTAATCCAGTGGAATCTTGTGC	
Pan_Mb5_qPCR_For	GCACACTATGGCTGAGACCC	120
Pan_Mb5_qPCR_Rev	ACAGGTGCATACTCTGCTGG	
Pan_Mb6_qPCR_For	AGGGCCAGCATGAAAGTCAG	137
Pan_Mb6_qPCR_Rev	TGCATATGCTGCTCCCACTT	
Pan_Mb7_qPCR_For_2	TGCAGACAAAGCAACTCAGGC	205
Pan_Mb7_qPCR_Rev_2	GTAATCCAGTGGAATCCGATG	

Chapter2:

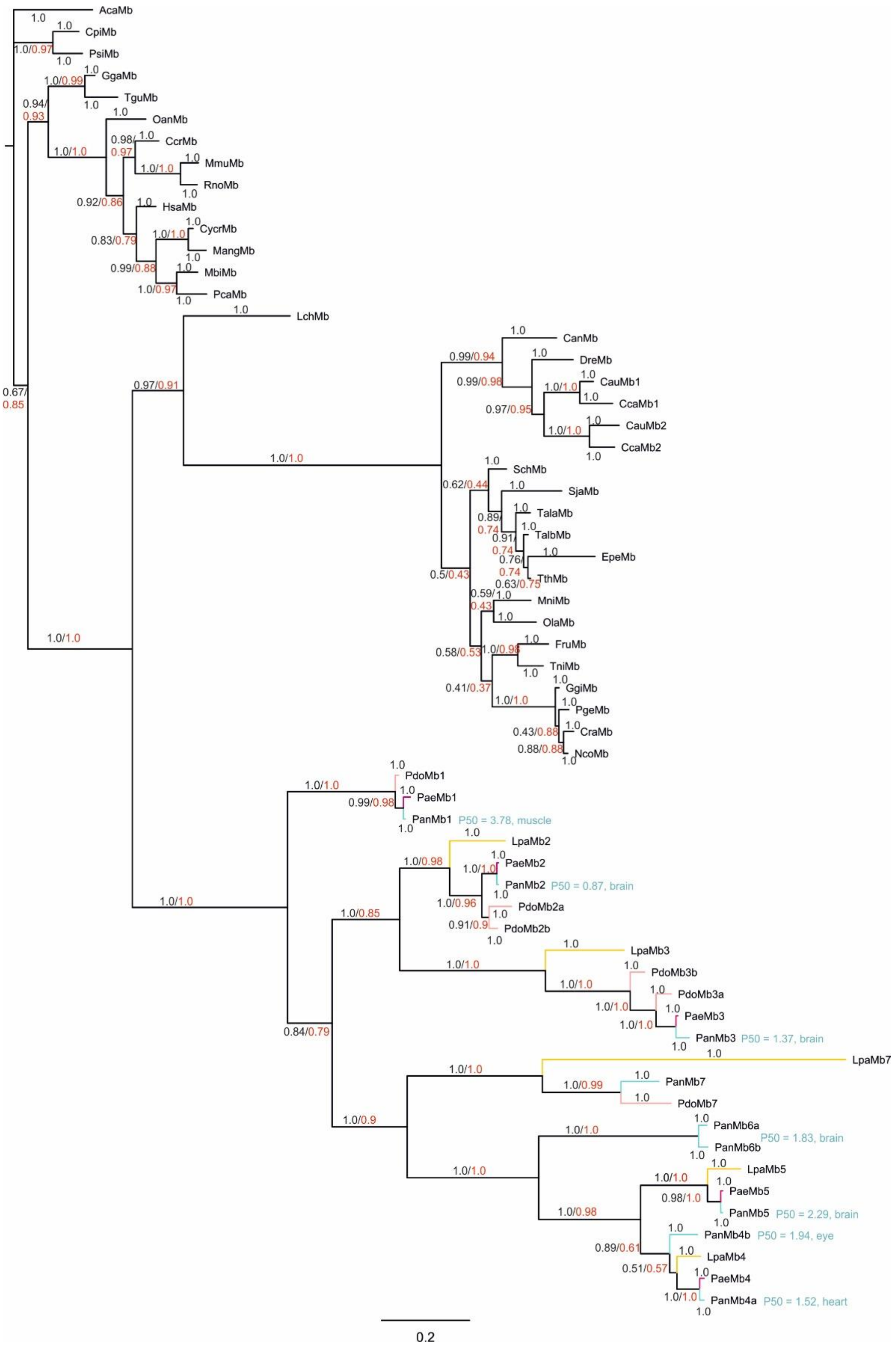

Figure SIII.1. Bayesian phylogenetic tree of vertebrate Mbs. Tree reconstruction was carried out with the amino acid sequences assuming the JTT model of protein evolution [61]. The bar represents 0.2 substitutions per site. The numbers at the nodes are the Bayesian posterior probabilities **(black)** and the **ultrafast bootstrap support (red)**. For the abbreviations and accession numbers, see Table S1. For the PanMbs, the P_{50}-values (in Torr) and the main expression sites are given. **(blue: *P. annectens* Mbs; pink: *P. aethiopicus* Mbs; light red: *P. dolloi* Mbs; yellow: *L. paradoxa* Mbs)**

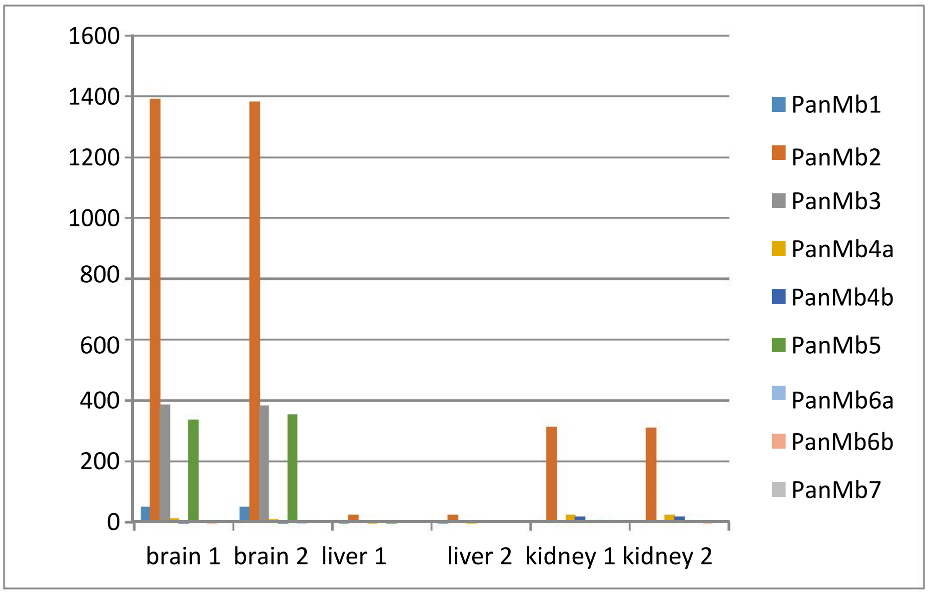

Figure SIII.2. Expression of the Mb genes in selected *P. annectens* tissues. mRNA levels were estimated by RNA-Seq and are displayed as RPKM values. Transcriptome accession numbers are given in Table S1. The copy numbers are given in Table S3.

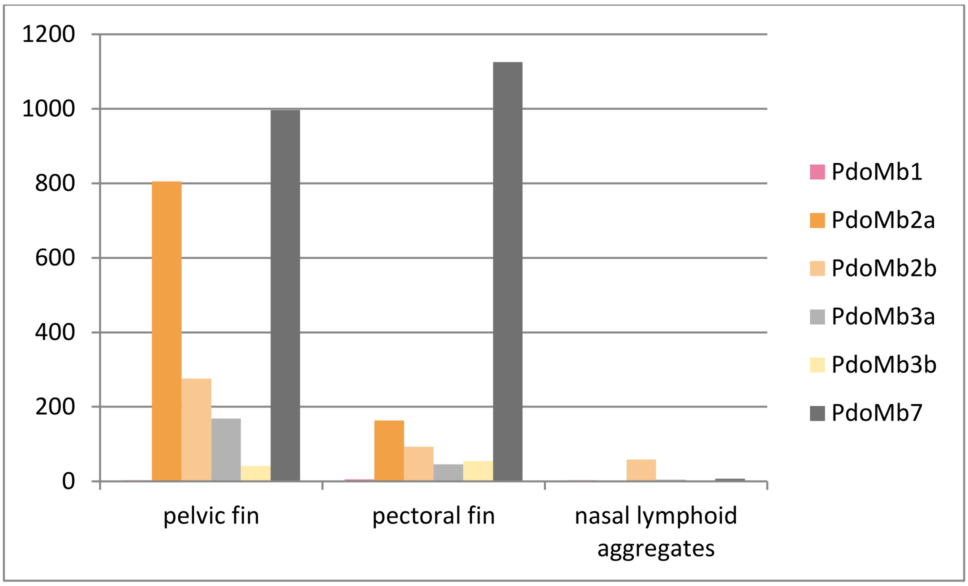

Figure SIII.3. Expression of the Mb genes in selected *P. dolloi* tissues. mRNA levels were estimated by RNA-Seq and are displayed as RPKM values. Transcriptome accession numbers are given in Table S1. The copy numbers are given in Table S4.

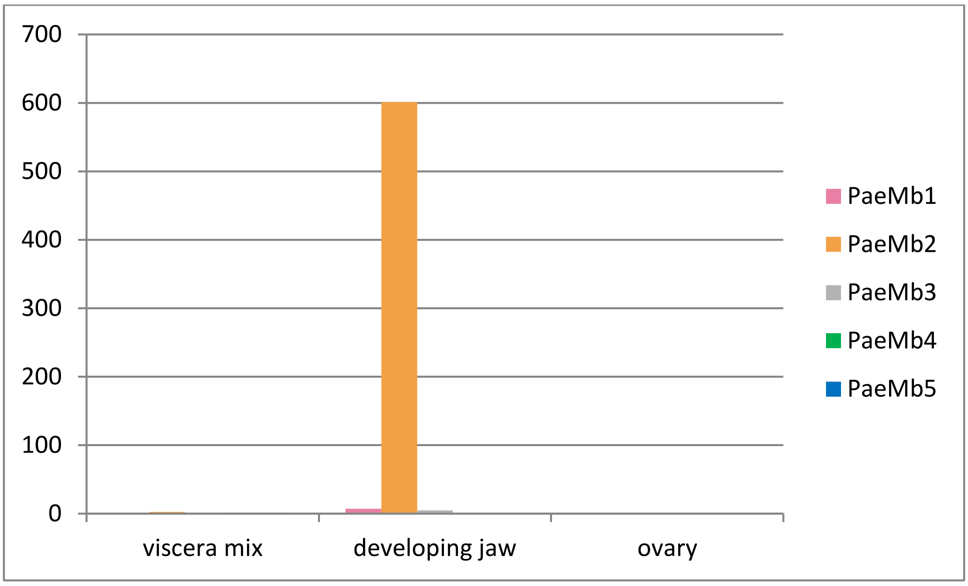

Figure SIII.4. Expression of the Mb genes in selected *P. aethiopicus* tissues. mRNA levels were estimated by RNA-Seq and are displayed as RPKM values. Transcriptome accession numbers are given in Table S1. The copy numbers are given in Table S5.

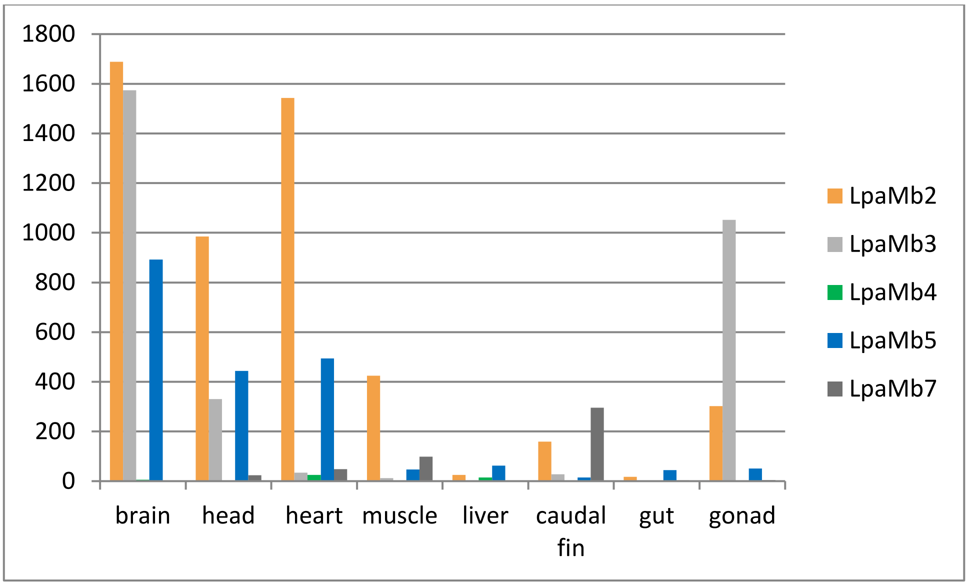

Figure SIII.5. Expression of the Mb genes in selected *L. paradoxa* tissues. mRNA levels were estimated by RNA-Seq and are displayed as RPKM values. Transcriptome accession numbers are given in Table S1. The copy numbers are given in Table S6.

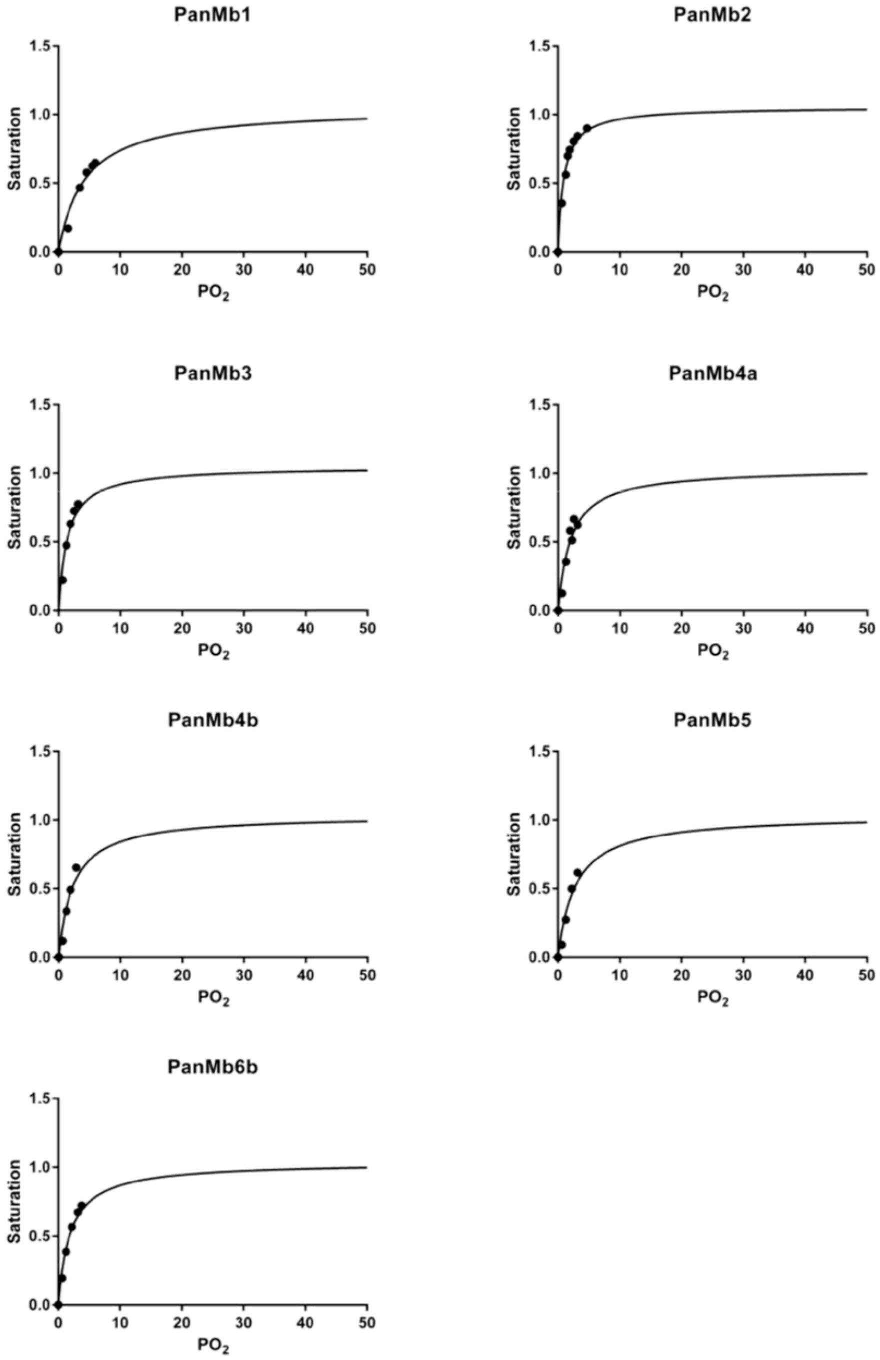

Figure SIII.6. O_2 equilibrium curves of recombinant expressed PanMbs. Measurements were done at pH 7.2, 20°C. Fitting of saturation data is indicated (continuous line).

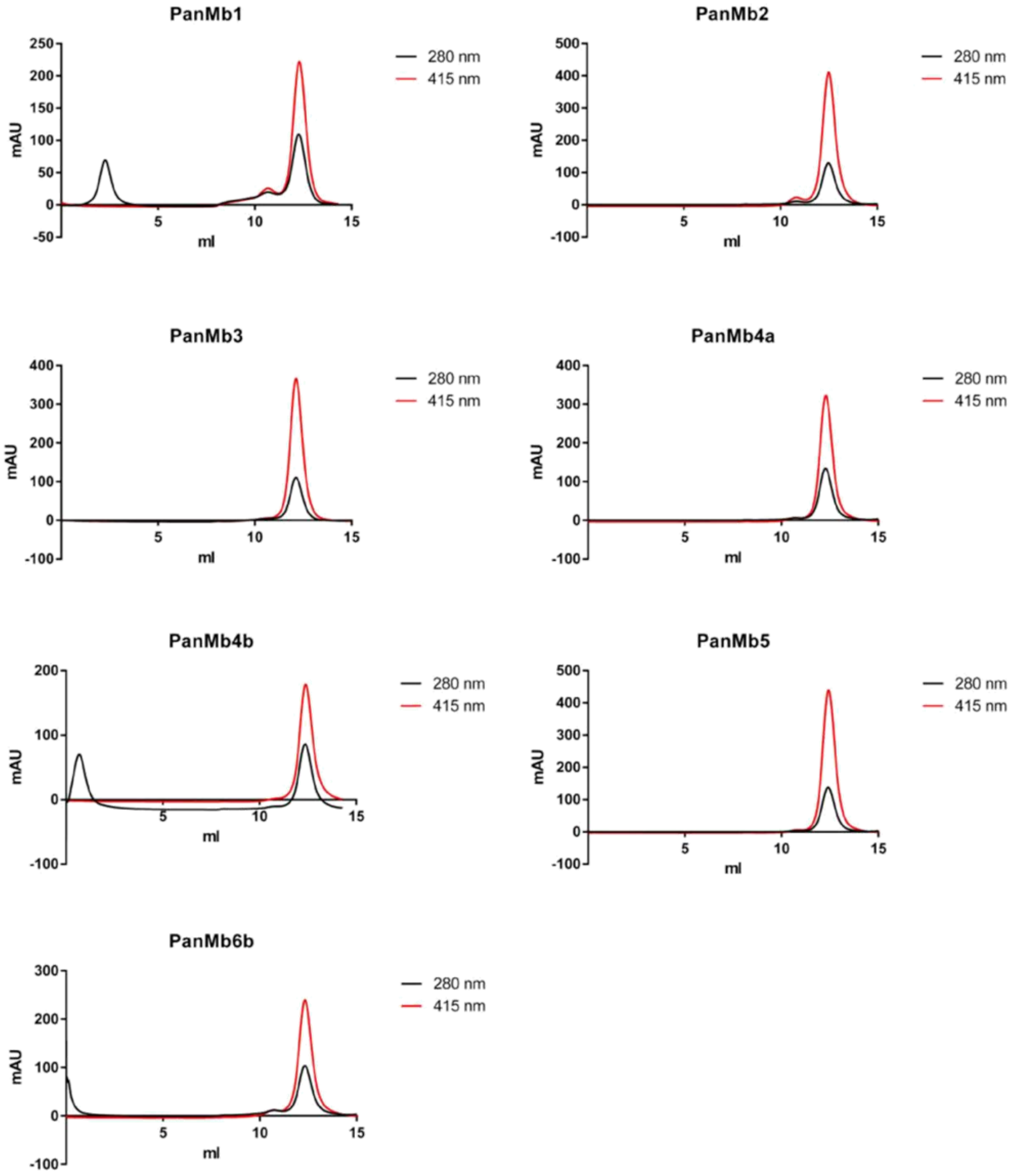

Fig. SIII.7. FPLC diagrams of recombinant PanMbs. Protein absorbance was measured at 280 nm, heme-specific absorbance at 415 nm.

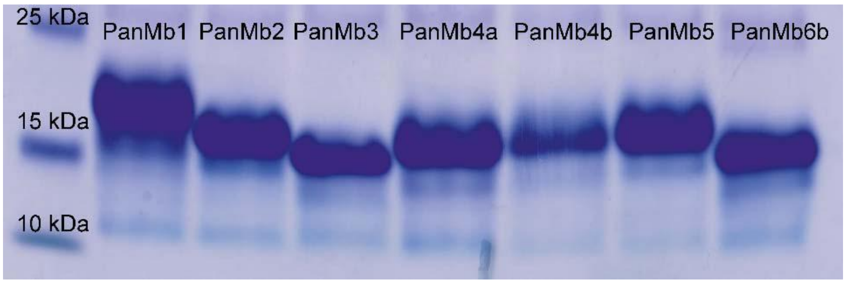

Fig. SIII.8. SDS-PAGE gel electrophoresis of recombinantly expressed *P. annectens* Mb1-6 proteins.

Table SIII.1. List of lungfish SRA data sets used in this study.

Run	Study	BioProject	BioSample	Experiment	Instrument	sex	tissue	species
SRR3632086	SRP076182	PRJNA317232	SAMN04601251	SRX1823854	Illumina HiSeq 2000	n.d.	muscle	*Lepidosiren paradoxa*
SRR3632085	SRP076182	PRJNA317232	SAMN04601250	SRX1823853	Illumina HiSeq 2000	n.d.	gut	*Lepidosiren paradoxa*
SRR3632084	SRP076182	PRJNA317232	SAMN04601249	SRX1823852	Illumina HiSeq 2000	n.d.	heart	*Lepidosiren paradoxa*
SRR3632083	SRP076182	PRJNA317232	SAMN04601248	SRX1823851	Illumina HiSeq 2000	n.d.	head	*Lepidosiren paradoxa*
SRR3632082	SRP076182	PRJNA317232	SAMN04601247	SRX1823850	Illumina HiSeq 2000	n.d.	brain	*Lepidosiren paradoxa*
SRR3632081	SRP076182	PRJNA317232	SAMN04601246	SRX1823849	Illumina HiSeq 2000	n.d.	gonad	*Lepidosiren paradoxa*
SRR3632080	SRP076182	PRJNA317232	SAMN04601245	SRX1823848	Illumina HiSeq 2000	n.d.	liver	*Lepidosiren paradoxa*
SRR3632079	SRP076182	PRJNA317232	SAMN04601244	SRX1823847	Illumina HiSeq 2000	n.d.	caudal fin	*Lepidosiren paradoxa*
SRR2895276	SRP065764	PRJNA301089	SAMN04235701	SRX1411327	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895273	SRP065764	PRJNA301089	SAMN04235701	SRX1411326	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895270	SRP065764	PRJNA301089	SAMN04235701	SRX1411325	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895265	SRP065764	PRJNA301089	SAMN04235701	SRX1411324	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895261	SRP065764	PRJNA301089	SAMN04235701	SRX1411322	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895255	SRP065764	PRJNA301089	SAMN04235701	SRX1411321	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895254	SRP065764	PRJNA301089	SAMN04235701	SRX1411314	Illumina HiSeq 2500	n.d.	blastema	*Lepidosiren paradoxa*
SRR1693787	SRP050575	PRJNA269317	SAMN03253061	SRX796494	Illumina HiSeq 2000	n.d.	kidney,lung,brain, spleen,heart,liver	*Lepidosiren paradoxa*
SRR505726	SRP013624	PRJNA164839	SAMN01041868	SRX152530	Illumina HiSeq 2000	n.d.	brain	*Protopterus annectens*
SRR505725	SRP013624	PRJNA164839	SAMN01041868	SRX152530	Illumina HiSeq 2000	n.d.	brain	*Protopterus annectens*
SRR505724	SRP013624	PRJNA164839	SAMN01041869	SRX152529	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR505723	SRP013624	PRJNA164839	SAMN01041870	SRX152531	Illumina HiSeq 2000	n.d.	kidney	*Protopterus annectens*
SRR505722	SRP013624	PRJNA164839	SAMN01041870	SRX152531	Illumina HiSeq 2000	n.d.	kidney	*Protopterus annectens*
SRR505721	SRP013624	PRJNA164839	SAMN01041869	SRX152529	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR2028027	SRP057960	PRJNA282925	SAMN03580842	SRX1016237	Illumina HiSeq 2000	male	gonad	*Protopterus annectens*
SRR2028021	SRP057960	PRJNA282925	SAMN03580841	SRX1016236	Illumina HiSeq 2000	female	liver	*Protopterus annectens*
SRR2028020	SRP057960	PRJNA282925	SAMN03580839	SRX1016234	Illumina HiSeq 2000	female	brain	*Protopterus annectens*
SRR2028017	SRP057960	PRJNA282925	SAMN03580843	SRX1016238	Illumina HiSeq 2000	male	gonad	*Protopterus annectens*
SRR2028000	SRP057960	PRJNA282925	SAMN03580840	SRX1016235	Illumina HiSeq 2000	male	liver	*Protopterus annectens*
SRR2027980	SRP057960	PRJNA282925	SAMN03580844	SRX1016241	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*

SRR2027979	SRP057960	PRJNA282925	SAMN03580844	SRX1016240	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*
SRR2027978	SRP057960	PRJNA282925	SAMN03580844	SRX1016239	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*
SRR2027914	SRP057960	PRJNA282925	SAMN03580838	SRX1016233	Illumina HiSeq 2000	male	brain	*Protopterus annectens*
SRR1685666	SRP044127	PRJNA254214	SAMN02902907	SRX790602	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR5114770	SRP095206	PRJNA357627	SAMN06146196	SRX2426781	Illumina HiSeq 1500	n.d.	developing jaw/ mandible	*Protopterus aethiopicus*
SRR5997828	SRP116672	PRJNA398732	SAMN07519109	SRX3153334	Illumina HiSeq 2000	n.d.	viscera mixture	*Protopterus aethiopicus*
SRR7240708	SRP044127	PRJNA473927	SAMN09288591	SRX4146489	Illumina NextSeq 500	female	ovary	*Protopterus aethiopicus*
SRR1823814	SRP055746	PRJNA276927	SAMN03382550	SRX895335	Illumina HiSeq 2000	n.d.	pelvic fin	*Protopterus dolloi*
SRR1823842	SRP055746	PRJNA276927	SAMN03382549	SRX895362	Illumina HiSeq 2000	n.d.	pectoral fin	*Protopterus dolloi*
SRR7879313	SRP159187	PRJNA486850	SAMN09984819	SRX4717958	Illumina NextSeq 500	n.d.	Nasal lymphoid aggregates	*Protopterus dolloi*

Table SIII.2. List of Mb sequences used in this study.

Abbreviation	**Species**	**common name**	**accession no.**
AcaMb	*Anolis carolinensis*	green anole	XM_003220932
CanMb	*Cryodraco antarcticus*	long-fingered icefish	U71056
CauMb1	*Carassius auratus*	goldfish	AM747267
CauMb2	*Carassius auratus*	goldfish	AM747268
CcaMb1	*Cyprinus carpio*	common carp	KC342292
CcaMb2	*Cyprinus carpio*	common carp	DQ338464
CcrMb	*Condylura cristata*	star-nosed mole	NM_001287785
CpiMb	*Chrysemys picta bellii*	Western painted turtle	XM_005300826
CraMb	*Chionodraco rastrospinosus*	ocellated icefish	U70871
CycrMb	*Cystophora cristata*	hooded seal	KC524751
DreMb	*Danio rerio*	zebrafish	AY337025
EpeMb	*Euthynnus pelamis*	skipjack tuna	AF291837
FruMb	*Takifugu rubripes*	Japanese pufferfish	
GgaMb	*Gallus gallus*	chicken	XM_003202347
GgiMb	*Gobionotothen gibberifron*	humped rockcod	U71057
HsaMb	*Homo sapiens*	man	NM_203377
LchMb	*Latimeria chalumna*	coelacanth	XM_006011146
LpaMb2	*Lepidosiren paradoxa*	South American lungfish	this study
LpaMb3	*Lepidosiren paradoxa*	South American lungfish	this study
LpaMb4	*Lepidosiren paradoxa*	South American lungfish	this study

LpaMb5	*Lepidosiren paradoxa*	South American lungfish	this study
LpaMb7	*Lepidosiren paradoxa*	South American lungfish	this study
MangMb	*Mirounga angustirostris*	Northern elephant seal	KC524754
MbiMb	*Mesoplodon bidens*	Sowerby's beaked whale	KC524765
MmuMb	*Mus musculus*	mouse	AK137456
MniMb	*Makaira nigricans*	Atlantic blue marlin	AF291833
NcoMb	*Notothenia coriiceps*	black rockcod	NM_001303294
OanMb	*Ornithorhynchus anatinus*	platypus	XM_001513063
OlaMb	*Oryzias latipes*	medaka	BJ883657
PaeMb1	*Protopterus aethiopicus*	Marbled lungfish	this study
PaeMb2	*Protopterus aethiopicus*	Marbled lungfish	this study
PaeMb3	*Protopterus aethiopicus*	Marbled lungfish	this study
PaeMb4	*Protopterus aethiopicus*	Marbled lungfish	this study
PaeMb5	*Protopterus aethiopicus*	Marbled lungfish	this study
PanMb1	*Protopterus annectens*	West African lungfish	LT604990
PanMb2	*Protopterus annectens*	West African lungfish	LT604991
PanMb3	*Protopterus annectens*	West African lungfish	LT604992
PanMb4a	*Protopterus annectens*	West African lungfish	LT604993
PanMb4b	*Protopterus annectens*	West African lungfish	LT604997
PanMb5	*Protopterus annectens*	West African lungfish	LT604994
PanMb6a	*Protopterus annectens*	West African lungfish	LT604995
PanMb6b	*Protopterus annectens*	West African lungfish	LT604996
PanMb7	*Protopterus annectens*	West African lungfish	this study
PcaMb	*Physeter catodon*	sperm whale	NM_001290722
PdoMb1	*Protopterus dolloi*	Slender lungfish	this study
PdoMb2a	*Protopterus dolloi*	Slender lungfish	this study

PdoMb2b	*Protopterus dolloi*	Slender lungfish	this study
PdoMb3a	*Protopterus dolloi*	Slender lungfish	this study
PdoMb3b	*Protopterus dolloi*	Slender lungfish	this study
PdoMb7	*Protopterus dolloi*	Slender lungfish	this study
PgeMb	*Pseudochaenichthys georgianus*	South Georgia icefish	U71055
PsiMb	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006137956
RnoMb	*Rattus norvegicus*	Norway rat	AF197916
SchMb	*Sarda chiliensis*	Pacific bonito	AF291834
SjaMb	*Scomber japonicus*	chub mackerel	AF291835
TalaMb	*Thunnus alalunga*	albacore	AF291832
TalbMb	*Thunnus albacares*	yellowfin tuna	AF291838
TguMb	*Taeniopygia guttata*	zebra finch	XM_002199380
TniMb	*Tetraodon nigroviridis*	spotted green pufferfish	CR660178
TthMb	*Thunnus thynnus orientalis*	Pacific bluefin tuna	AF291836

Table SIII.3. RPKM of *Mb* genes in the transcriptomes of *P. annectens* tissues used for expression estimation by RNA-Seq.

	SRR505725 brain 1	SRR505726 brain 2	SRR505721 liver 1	SRR505724 liver 2	SRR505722 kidney 1	SRR505723 kidney 2
PanMb1	50.65	50.66	0.50	0.43	1.85	1.38
PanMb2	1391.06	1381.08	24.61	23.93	312.91	310.25
PanMb3	384.82	382.17	0.00	0.00	1.81	1.52
PanMb4a	10.06	8.84	0.52	0.17	21.67	23.69
PanMb4b	0.47	0.37	0.00	0.00	17.37	16.23
PanMb5	335.26	352.76	0.09	0.00	1.60	1.71
PanMb6a	0.00	0.49	0.00	0.00	4.53	3.19
PanMb6b	0.30	0.00	0.00	0.00	1.79	0.96
PanMb7	0.00	0.00	0.00	0.00	0.00	0.00

Table SIII.4. RPKM of *Mb* genes in the transcriptomes of *P. dolloi* tissues used for expression estimation by RNA-Seq.

	SRR1823814 pelvic fin	SRR1823842 pectoral fin	SRR7879313 nasal lymphoid aggregates
PdoMb1	2.52	5.26	2.69
PdoMb2a	805.14	163.23	0.38
PdoMb2b	276.24	92.70	58.59
PdoMb3a	168.31	45.55	4.47
PdoMb3b	41.19	54.55	0.00
PdoMb7	996.86	1125.65	6.88

Table SIII.5. RPKM of *Mb* genes in the transcriptomes of *P. aethiopicuss* tissues used for expression estimation by RNA-Seq.

	SRR5997828	SRR5114770	SRR7240708
	viscera mix	developing jaw	ovary
PaeMb1	0.00	7.16	0.00
PaeMb2	2.43	601.44	0.00
PaeMb3	0.00	4.95	0.04
PaeMb4	1.27	0.30	0.00
PaeMb5	0.87	0.19	0.03

Table SIII.6. RPKM of *Mb* genes in the transcriptomes of *L. paradoxa* tissues used for expression estimation by RNA-Seq.

	SRR3632082	SRR3632083	SRR3632084	SRR3632086	SRR3632080	SRR3632079	SRR3632085	SRR3632081
	brain	head	heart	muscle	liver	caudal fin	gut	gonad
LpaMb2	1688.21	985.24	1542.81	424.27	24.54	159.67	17.59	302.31
LpaMb3	1573.33	330.14	34.50	12.30	2.02	28.08	0.00	1052.40
LpaMb4	5.90	1.95	25.12	0.33	14.95	0.00	0.37	0.68
LpaMb5	892.49	444.12	494.21	47.21	63.14	14.66	44.70	51.03
LpaMb7	1.58	24.14	48.28	98.73	0.00	295.88	3.62	4.50

Table SIII.7. Overview of nitrite reductase observed rates (min-1 and s-1) and of second order rate constants (M-1 s-1) of PanMbs. Conditions: 0.1 mM nitrite, pH 7.2, 20 °C.

Nitrite-Reductase-Rate			(nitrite)
	k (min-1)	k (sec -1)	M-1 s-1
PanMb1	0.16	0.003	26.95
PanMb2	0.08	0.001	13.78
PanMb3	0.25	0.004	42.13
PanMb4a	0.14	0.002	22.91
PanMb4b	0.20	0.003	33.63
PanMb5	0.06	0.001	10.26
PanMb6b	0.00	0.000	0.00

Chapter 3:

a. Sequences of *Lepidosiren paradoxa*

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c. Sequences of *Protopterus aethiopicus*

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Supplemental Information Fig. IV.1. Nucleotide sequences obtained in this study.

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AIGDALVDMPNIKHNLTDLSRLHSEILHVDPENFRLLGKCLLIVLAAKFGAKKFNVDVHAAWKKLMEIIA
AGLSKQYH
>LpaHbB2
MVHWEDAEKQYIVSVFSKIDVDHVGANTLERVLIAFPWTKRYFSSFGDLS
>SPGAIKHNNKVIAHGRKVLAAIIECTRHFGNIKGHLANLSHLHSEKLHVD
>PHNFRVLGQCLRIELAAALGFKEFTPERNAYFQKFMDVISHSLGREYH"
>LpaHbB3
MVHWESNERQTLSSVWAKIDSEVIGGEALARLFIVYPWSQRYFSKFGDLSTHDAISHNPKVKAHGKKVLA
AVGDCLKHLDNIKGHLTEHSHHHYNALHVDPANFTLLAYCLDIVLARHFGYKVFTPEVQGTFQKFMREVT
GGLSTEYS
>LpaMb2
MTLSDAQWNNVLGFWTKHIEGDLANIGHEVLIRLFLQSKAAQNLFEKFKHLSSEAEMRGCADLQKHGNTV
FTALGKTLKLKGHHDAELRPMAESHSKKHKIPVENFTLICNVIDKYFHEKYPDYAGELRESFKQATLGVA
HTLEKLYKEV
>LpaMb3a
```

```
MASDAQWNVALDFWEKNIASDPKKHGHAVLIGLFKKSKDSQVHFPKFKDLASEAEMKSSEGLQKHGETVF
TALGKALAQKDGIANELRPLAETHVKEHKIPVEEFSKICDVISDYCAIEFKDYTGDTCTAFKAVLSVVVQ
TMNNLYKEV
>LpaMb3b
MVKASNSQYECLYAFLMQSIGEDPAAFGHESLISFFKEDEENKQYFPKFKHLANEAEMRNCAELKQHGKT
VATTFADLVKKKGDHDKDINKLAFSHVHEHGVPVGKFKEIFVHMKKKLSPKPGYTPEIDASFDAVTDSIY
NCLEENYKKVKK
>LpaMb5
MAGLSDAQWNDLLGFFDKFIAPNSAEHGKHILIRMFERDRATQSVFPKFKDVSPSDLPKNADVKKHGGVV
VDFLGKLLKQKGHNESMLHTMAETHKNTHKVSPDYFQLISSVMDVYIHENLPGEYAPVRDAMNAALKQIA
STLKSNYSKV
>LpaMb7
MTSLSEAQWNELLAFWDKYVAPSSLEHGKHILIRMFQTDKATQALFSKFKDIPTSDLAINDDVKKHGGVV
VDFLGKLLKLKGQNDSMLHTMAQSHKNKHKIPLDYFQLISSVIDVYVHENLPGEYAPVRESMKAALSQIA
NGLKDNYTKV
```

b. Sequences of *Protopterus annectens*

```
>PanGbE1a
MALAADDIQKAKSVWEKFYVNAEDNGAIVLSRMFKEHPHTVSYFTNFKELQSIAGTASAAKLEGLSEVRT
HGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELKVDVKEFEILCGILLDLMAEKCGEDTKTDFKKV
TDVVCEQIKSTY
>PanGbE1b
MALAADDIQKAKSVWEKFYVNAEDNGAIVLSRMFKEHPHTVSYFTNFKELQSIAGTASAAKLEGLSEVRA
HGKKVLSALNDMVSQVDNMDALKAIIEPLGKKHAVELKVDVKEFEILCGILLDLMAEKCGEDTKTDFKKV
TDVVCEQIKSTY
>PanGbE2a
MALSAEDTQTAGAVWEKIYADVEDNGAVVLSRMFKEHHHTVSYFKNFTQLQSVAETASAEEIAALAEVRA
HGKKVFLALNDMVPHLNNVDALKETIAPLAKKHATELKIDVKDFEIIFDNLLALIGEKQGADAKTAFKKV
TDLIYEEIKAAY
>PanGbE2b
MALSAEDTQTASAVWEKIYADVEDNGAVVLSRMFKENPHTVSYFKNFTQLQSIAETASAEEIAALAEVRA
HGKKVFSALNDMVSHLTNVDALKETINPLAKKHAAELKVDVKDFRIIFENLLDLIGEKQGADAKTAFKKV
TDLIYEEIKAAY
>PanGbE2c
MALSAEDTQTAGAVWEKIYADVEDNGAVVLSRMFKEHHHTVSYFKNFTQLQSVAETASAEEIAALAEVRA
HGKKVFLALNDMVPHLTNVDALKETIAPLAKKHAAELKVDVKDFRIIFENLLDLIGEKQGADAKTAFKKV
TDLIYEEIKAAY
```

c. Sequences of *Protopterus aethiopicus*

```
>PaeGbE1a
MALAADDIQKVKSVWEKFYVNAEDNGAIVLSRMFKEHPHTVSYFTNFKELQSIAGTASAAKLEGLSEVRA
HGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELKVDVKEFEILCGILLDLMAEKCGEDTKTDFKKV
TDVVCEQIKSTY
>PaeGbE1b
MALAADDIQKARGVWEKFYVNAEDNGAIVLSRMFKEHPHTLSYFTNFKELQSTAGTASVTELEGLSEVRT
HGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELKVDVKEFEILCAILLELMAEKCGEDAKTDFKKV
TDVVCEQIKSTY
>PaeGbE1c
MALVADDIQKAKSVWEKFYVNAEDNGAIVLSRMFKEHPHTVSYFTNFKELQSIAGTASAAKLEGLSEVRA
HGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELKVDVKEFEILCGILLDLMAEKYGEDTKTDFKKV
TDVVCEQIKSTY
>PaeGbE2a
MALSAEDTQTAGAVWEKIYADVEDNGAVVLSRMFKEHHHTVSYFKNFTQLQSVAETASAEEIAALAEVRA
HGKKVFLALNDMVPHLSNVDALKETIAPLAKKHATELKVDVKDFEIIFDNLLALIGEKQGADAKTAFKKV
TDLIYEEIKAAY
>PaeGbE2b
MALSAEDIQTVSAIWEKIYADVEDNGADVLSRMFKEHHHTVNYFKNFTQLQSVAETASAVDIAALAEVRA
HGKKVFSALHDMVPHLTNVDALKETINPLAKKHAAELKVDVKDFRILFENLLDLIGEKQGADAKTAFKKV
TDLIYEEIKAAY
```

```
>PaeGbE2c
MALSAEDAKTASAVWEKIYTDVEDNGAVVLSRMFKEHHHTVSYFKNFTQLQSVAETASAQEIAALAEVRT
HGKKVFSALNDMVSHLTNVDALKGTIAPLAKKHATELKVDVKDFVIIFENLLDLIGEKQGGDAKEAFKKV
TDVMYEEIKAAY
>PaeGbE2d
MAFSAEDAKTASAVWEKIYADVEDNGAIVLSRMFKENPHTVSYFKNFTQLQSIPETASAEEIAALAEVRG
HGKKVFSALNDLVSHLTNVDSLKATIVPLAKKHATELKVDVKDFGIIFENLLHLIGQKQGGDAKEAFEKV
TNLIYEEIKAAY
```

Supplemental Information Fig. IV.2. Amino acid sequences obtained in this study. The GbE peptide sequences identified by mass spectrometry in the ovaries of *L. paradoxa* and *P. aethiopicus* are underlined.

```
#NEXUS
Begin data;
    Dimensions ntax=192 nchar=256;
    Format datatype=protein gap=- missing=X matchchar=. interleave;
    Matrix
AcaGbY       ------------------------------------------------------MTDLDRRHIREIWTA-AFENPEENGRLVIIRFFSDYPASKQYF---
AcaMb        ME----------------------------------------------------LSDQEWQKVIDIWGK-VEPEIPAYGQVVILRLFEQHPETQEKFDKF
AplGbE       MP----------------------------------------------------FSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF
CanMb        MA--------------------------------------------------------DFDMVLKCWGP-VEADHATHGSLVLTRLFTEHPETLKLFPKF
CauMb1       MA--------------------------------------------------------DHELVLKCWGV-VEADFEGTGGEVLTRLFKQHPETQKLFPKF
CauMb2       MA--------------------------------------------------------DYERFLKCWGA-VEADYTGNGGEVLTRLFKAHPDTQKLFPKF
CcaMb1       MA--------------------------------------------------------DHELVLKCWGG-VEADFEGTGGEVLTRLFKQHPETQKLFPKF
CcaMb2       MA--------------------------------------------------------DYERFLKCWGA-IEADYAGHGGEVLTRLFKEHPDTLKLFPKF
CcrMb        MG----------------------------------------------------LSDGEWQLVLNIWGK-VEADIPGHGQEVLIRLFKNHPETLEKFDKF
CliGbE       MS----------------------------------------------------FSEAEVQGARGAWEK-MYADAEDNGTTVLVRMFTEHPDTKSYFTHF
CmiGbY       MT---------------------------------------------------GITEADKENIHFIWEK-LYENPEENGKTIVLRMFTDYPETKMYFQHF
CmyGbE       MA----------------------------------------------------FSEAEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYFTHF
CpiCygb      ME------------------------------------KVQGEMEIERWERSEELSDAEKKVIQETWSR-VYMNCEDVGVSILIRFFVKFPSAKQYFSQF
CpiGbE       MA----------------------------------------------------FSEAEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYFTHF
CpiGbX       MGCALSGS------GIAPGKTISESKRSPSSENLAAPKAGPEHGGDGLGAGPFPLADAQKERIQESWRI-LHDNIARVGIIVFIRLFETHPECKDVFFLF
CpiGbY       MA---------------------------------------------------LLTDADKKNIQHIWAK-LFENPEENGKTIVIKLFKDYPETKAYF---
CpiHbA       MV----------------------------------------------------LNAGDKANVKAVWNK-VAAHVEEYGAETLERMFTVYPQTKTYFPHF
CpiHbaA      MV----------------------------------------------------LNAGDKANVKAVWNK-VAAHVEEYGAETLERMFTVYPQTKTYFPHF
CpiHbaD      -M----------------------------------------------------LNHDEKQLIKHAWEK-VLGHQEDFGAEALERMFAVYPQTKTYFPHF
CpiHbB1      MV---------------------------------------------------HWTAEEKQLITNLWGK-V--NVAECGSEALARLLIVYPWTQRFFSSF
CpiHbB2      MV---------------------------------------------------HWTADEKQLITSLWGK-V--NVEECGSEALARLLIVYPWTQRFFSTF
CpiHbG       MV---------------------------------------------------HWTAEEKQLITSLWGK-V--NAEECGGEALARLLIVYPWTQRFFSSF
CpiHbZ       MT----------------------------------------------------LTQAEKAAVVAIWGK-IAAQADALGTESLERLFSSFPQTKTYFPHF
CpiMb        MG----------------------------------------------------LSDDEWHHVLGIWAK-VEPDLSAHGQEVIIRLFQVHPETQERFAKF
CpiNgb       ME-----------SGR--------------------------------------LSSTQQALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLFQYN
CraMb        MA--------------------------------------------------------DFDMVLKCWGP-MEADHATHGSLVLTRLFTEHPETLKLFPKF
CycrMb       MG----------------------------------------------------LSDGEWHLVLNVWGK-VETDLAGHGQEVLIRLFKSHPETLEKFDKF
DreCygb1     ME---------------------------------------GDGGVQLTQSPDSLTEEDVCVIQDTWKP-VYAERDNAGVAVLVRFFTNFPSAKQYFEHF
DreCygb2     ME------------------------------------KEREDEETEGRERPEPLTDVERGIIKDTWAR-VYASCEDVGVTILIRFFVNFPSAKQYFSQF
DreGbX       MGCAISGS------GL---------------------TAGAPEIRPGEEETPAGLTTNHIRLIKESWRL-IQEDIAKVGIIMFVRLFETHPECKDVFFLF
DreHbAa      MS----------------------------------------------------LSDTDKAVVKAIWAK-ISPKADEIGAEALARMLTVYPQTKTYFSHW
DreHbAe      MS----------------------------------------------------LSAKDKAAVKTLWAK-IAGKADDIGHDALSRMLIVYPQTKTYFSHW
DreHbAx      MP-----------------------------------------------------SSAEKELIAEIWDQ-MTPVAEEIGSEALLRMFTTFPQTKTYFSHL
DreHbBa      MV---------------------------------------------------EWTDAERTAILGLWGK-L--NIDEIGPQALSRCLIVYPWTQRYFATF
DreHbBe      MV---------------------------------------------------VWTDFEKATIQDIFAK-A--DYDVIGPQALARCLIVYPWTQRYFAKF
DreMb        MA--------------------------------------------------------DHDLVLKCWGA-VEADYAANGGEVLNRLFKEYPDTLKLFPKF
DreNgb       ME---------------------------------------------------KLSEKDKGLIRDSWES-LGKNKVPHGIVLFTRLFELDPALLTLFSYS
EpeMb        MA--------------------------------------------------------DLDAVLKCWGA-VEADFNTVGGLVLARLFKDHPETQKLFPKF
FalGbE       MS----------------------------------------------------LSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF
FpeGbE       MS----------------------------------------------------FSEAEVQSARGAWEK-IYVDAEDNGTTVLVRMFTEHPDTKSYFTHF
FruMb        MA--------------------------------------------------------DFETVLKFWGP-VEADYGAHGGIVLTRLFTENPETQKLFPKF
GfoGbE       MS----------------------------------------------------LSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF
GgaCygb      ME------------------------------------KVQGEMEIERWERSEEISDAEKKVIQETWSR-VYANCEDVGVSILIRFFVNFPSAKQYFSQF
GgaGbE       MS----------------------------------------------------FSEAEVQSARGAWEK-MYVDAEDNGTAVLVRMFTEHPDTKSYFTHF
GgaHbA       MV----------------------------------------------------LSAADKNNVKGIFTK-IAGHAEEYGAETLERMFTTYPPTKTYFPHF
GgaHbAD      MM----------------------------------------------------LTAEDKKLIQQAWEK-AASHQEEFGAEALTRMFTTYPQTKTYFPHF
GgaHbG       MV---------------------------------------------------HWTAEEKQLITGLWGK-V--NVAECGAEALARLLIVYPWTQRFFASF
GgaMb        MG----------------------------------------------------LSDQEWQQVLTIWGK-VEADIAGHGHEVLMRLFHDHPETLDRFDKF
GgaNgb       ME-----------SGM--------------------------------------LSRTQQALIRESWRR-VSGSPVQHGVVLFSRLFDLDPDLLPLFQYN
GgiMb        MA--------------------------------------------------------DFDMVLKCWGP-VEADYTTHGSLVLTRLFTEHPETLKLFPKF
HsaCYGB      ME------------------------------------KVPGEMEIERRERSEELSEAERKAVQAMWAR-LYANCEDVGVAILVRFFVNFPSAKQYFSQF
HsaHBA       MV----------------------------------------------------LSPADKTNVKAAWGK-VGAHAGEYGAEALERMFLSFPTTKTYFPHF
HsaHBB       MV---------------------------------------------------HLTPEEKSAVTALWGK-V--NVDEVGGEALGRLLVVYPWTQRFFESF
HsaHBD       MV---------------------------------------------------HLTPEEKTAVNALWGK-V--NVDAVGGEALGRLLVVYPWTQRFFESF
HsaHBE       MV---------------------------------------------------HFTAEEKAAVTSLWSK-M--NVEEAGGEALGRLLVVYPWTQRFFDSF
HsaHBG       MG---------------------------------------------------HFTEEDKATITSLWGK-V--NVEDAGGETLGRLLVVYPWTQRFFDSF
HsaHBZ       -S----------------------------------------------------LTKTERTIIVSMWAK-ISTQADTIGTETLERLFLSHPQTKTYFPHF
HsaMB        MG----------------------------------------------------LSDGEWQLVLNVWGK-VEADIPGHGQEVLIRLFKGHPETLEKFDKF
HsaNGB       ------------------------------------------------------MERPEPELIRQSWRA-VSRSPLEHGTVLFARLFALEPDLLPLFQYN
IpuGbX       MGCAISGL------GL----------------------APKNTTEAASEDDAPHLTSEHIAMIKESWKV-IQEDIAKVGIIVFVRLFETHPECKDVFFLF
LchCygb      ME------------------------------------KVQGEMEMDRWERSDQLSDTEVESIRQIWSN-VYTNCENVGVLVLIRFFVNFPSAKQYFSQF
LchGbE       MA----------------------------------------------------LSDAEVQTARDVWGQ-IYANAEENGTIILVRMFTEHPDTKSYFGNF
LchGbX1      MGCVFSGS------GIAPSKSTPDINGS----EAESRLSEELKSGSGQNSDALLLSEPQKELIQESWRI-LHQDITRLGIIMFIRLFETHPECKDVFFLF
LchGbX2      MGCAISGLSWRAVKGP----------------------GEEAKGKEGEAEALPAISQLQIHLIQESWKL-IQEDIAKVGIIMFVRLFETHPECKDVFFLF
LchGbY       MA---------------------------------------------------ALTEADKQNIRGIWKT-VFENAEENGRTIVIRLFEKYPETKVYFKNF
LchHbA1      M-----------------------------------------------------LSANDKTLISSTWNK-VAANAEDIGAEALERLFLAHPQTKIYFSHM
LchHbA2      MG----------------------------------------------------LTAADKTLIKSIWGK-VEKETEAIGVEALVRLFKCFPQSKVYFDHF
LchHbB1      MV---------------------------------------------------HWTETERATIETVYQK-L--HLDEVGREALTRLFIVYPWTTRYFKSF
LchHbB2      MV---------------------------------------------------TWTAEERKAITSVWSK-V--NPEEVGHEALIRLFIVYPWTQRYFSTF
LchMb        MA----------------------------------------------------LSEAEWGLILKVWGK-AEPEAASNGKSVLLRMFQEHPDTQQHFPKF
LchNgb       ME-----------KHN--------------------------------------FSVRSKELIRESWDR-LGKNKLPHGTVMFTRLFELDPDLMHLFNYN
LpaGbE1      MA----------------------------------------------------MSADDIQKGRSAWEK-FYANAEDNGAVVLSRMFKEHPHTVSYFKNF
LpaGbE2a     MA----------------------------------------------------LSAEDIQMVSGVWSK-IFADAESNGAVVLSRMFKEYPHTVKYFKNF
LpaGbE2b     MA----------------------------------------------------LSAEEIQNATGVWSK-IFADAESNGSVVLSRMFKEYPHTVKYFKNF
LpaGbE2c     MA----------------------------------------------------FSAEDIQTATDVWDK-IFVNAEENGAIVLSRMFKEHSHTVSHFKNF
LpaGbE2d     MA----------------------------------------------------LSAEDIQTATGVWDK-IFVNAEENGAIVLSRMFKEHSHTVSHFKNF
LpaGbE2e     MA----------------------------------------------------LSAEDIQTAIGVWDK-IVVNAEEHGAIVLSRMFKEHSHTVSHFKNF
LplaHbA      MP-------------------------------------------IVDSGSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF
LplaHbB      MP-------------------------------------------IVDSGSVPALTAAEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQEFFPKF
MangMb       MG----------------------------------------------------LSDGEWHLVLNIWGK-VETDLAGHGQEVLIRLFRSHPETLEKFDKF
MbiMb        MG----------------------------------------------------LSEAEWQLVLHVWAK-VEADLSGHGQEILIRLFKGHPETLEKFDKF
MgaGbE       MS----------------------------------------------------FSEAEVQSARGAWEK-IYVDAEDNGTAVLIRMFTEHPDTKSYFTHF
MglaHb2      MS----------------------------------------------AHGIARTTEGERAAVRASWAV-LMKDYEHAGVQILDKFFKANPAAKPFFTKM
MmuMb        MG----------------------------------------------------LSDGEWQLVLNVWGK-VEADLAGHGQEVLIGLFKTHPETLDKFDKF
MniMb        MA--------------------------------------------------------DFEMVLKHWGP-VEADYATHGNLVLTRLFTEHPETQKLFPKF
MunGbE       MS----------------------------------------------------FSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFSHF
NcoMb        MA--------------------------------------------------------DFDMVLKCWGP-MEADYATHGGLVLTRLFTEHPETLKLFPKF
OanGbY       MV---------------------------------------------------QVTDVEKANIQSIWSK-MMENLEKNGIDIFTRLFREYPETKKYF---
OanHbW       MV---------------------------------------------------NWTSEEKHAIVSIWGK-V--DIEETGANALSRLLVVYPWTQRYFSAF
OanMb        MG----------------------------------------------------LSDGEWQLVLKVWGK-VEGDLPGHGQEVLIRLFKTHPETLEKFDKF
OanNgb       ME-----------NGR--------------------------------------LSGPEQELIRESWRS-VNSNPLEHGMILFTRLFDLEPDLLPLFQYN
OlaCygb1     ME------------------------------------RKQ--GEVDHLERSRPLTDKERVMIQDSWAK-VYQNCDDAGVAILVRLFVNFPSSKQYFSQF
OlaCygb2     MSCRESPPPPSPPPQML---------------------GVQRGECEDRPERAEPLSDAEMEIIQHTWGH-VYKNCEDVGVSVLIRFFVNFPSAKQYFSQF
```

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OlaHbA       MS----------------------------------------------------LSAKDKAAVKAFWAK-VSGQADAIGSDALSRMLVVYPQTKTYFAHW
OlaHbB       MV---------------------------------------------------EWTEQERSIITNIFGN-L--DYEDVGSKALSRCLIVYPWTQRYFASF
OlaMb        MA--------------------------------------------------------DYDMVLKHWGP-VEADYNTHGNLVLTRLFHEYPETQKLFPKF
OlaNgb       ME---------------------------------------------------KLSGKDKELIRGSWES-LGKNKVPHGVIMFSRLFELDPALLSLFNYN
PaeGbE1a     MA----------------------------------------------------LAADDIQKVKSVWEK-FYVNAEDNGAIVLSRMFKEHPHTVSYFTNF
PaeGbE1b     MA----------------------------------------------------LAADDIQKARGVWEK-FYVNAEDNGAIVLSRMFKEHPHTLSYFTNF
PaeGbE1c     MA----------------------------------------------------LVADDIQKAKSVWEK-FYVNAEDNGAIVLSRMFKEHPHTVSYFTNF
PaeGbE2a     MA----------------------------------------------------LSAEDTQTAGAVWEK-IYADVEDNGAVVLSRMFKEHHHTVSYFKNF
PaeGbE2b     MA----------------------------------------------------LSAEDIQTVSAIWEK-IYADVEDNGADVLSRMFKEHHHTVNYFKNF
PaeGbE2c     MA----------------------------------------------------LSAEDAKTASAVWEK-IYTDVEDNGAVVLSRMFKEHHHTVSYFKNF
PaeGbE2d     MA----------------------------------------------------FSAEDAKTASAVWEK-IYADVEDNGAIVLSRMFKENPHTVSYFKNF
PanGbE1a     MA----------------------------------------------------LAADDIQKAKSVWEK-FYVNAEDNGAIVLSRMFKEHPHTVSYFTNF
PanGbE1b     MA----------------------------------------------------LAADDIQKAKSVWEK-FYVNAEDNGAIVLSRMFKEHPHTVSYFTNF
PanGbE2a     MA----------------------------------------------------LSAEDTQTAGAVWEK-IYADVEDNGAVVLSRMFKEHHHTVSYFKNF
PanGbE2b     MA----------------------------------------------------LSAEDTQTASAVWEK-IYADVEDNGAVVLSRMFKENPHTVSYFKNF
PanGbE2c     MA----------------------------------------------------LSAEDTQTAGAVWEK-IYADVEDNGAVVLSRMFKEHHHTVSYFKNF
PanGbX       MGCALSR---------AGATDNSTTDVNEILEEMGPDTVIGSRTQSEVVSDLSTLAESQKELIQESWKI-LHQDIARLGVIVFIRLFETHPECKDVFFMF
PanGbY       MC---------------------------------------------------SLSTTDIKNIRDIWSI-VCQNPEENGRTVVIRLFLDYPQTRTYFKNF
PanHba1      MP----------------------------------------------------LSKAEKTILLAVWER-ISPYIEEFGAQALTRMFRCFPETKIYFHEK
PanHba2      MT----------------------------------------------------LTAAEKSCLASTFEK-IAPKAEQYGSELFQRMFLGFPQTRTYFAHV
PanHba3      MT----------------------------------------------------FTREDEVHIGEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYFQKF
PanHba4      MT----------------------------------------------------FTHEDEVHIAEAC-K-LLTQIPNAGGEALARMFAAFPGTKSYFQKF
PanHbb1      MV---------------------------------------------------HWTSEEEFAITSIWGN-V--DVHEEGHDTLTRLMVVYPWTKKYFSSF
PanHbb2      MV---------------------------------------------------LWDAAEKKVIASVWAK-V--DIEADGFQALLRTLHVYPWTKRYFSHF
PanHbb3      MV---------------------------------------------------NWKANERQAVTSVWAS-I--DAAGHGQETLERLLHVYPWSRRYFGKF
PanHbb4      MV---------------------------------------------------NLEAAEKQTITSFWAS-V--DPAAQGENALQRLLYCYPWSRRYFAKF
PanHbb5      MV---------------------------------------------------HWDATEKQTITSFWGK-V--DLAADGEHSLQRLLYVYPWCRRYFHKF
PanMb1       MA---------------------------------------------------SLSDAQWKKLQEFWVKNVEPNLTKHGQEVLVRMFVNHKSTLEYFPKF
PanMb2       MT----------------------------------------------------LSEAQWNNVLAFWAKHIENDPTKHGHEVLIRLFLESKAAQNLFDKF
PanMb3       MA-----------------------------------------------------SAAQWDTTLKFWEAHVAGDLKKHGHEALVRLFLKNKDSQKHFPKF
PanMb4       MA---------------------------------------------------GLSEVQWNELLAFWDKYVAPSSSEHGKHILIRMFQTEKATQTLFSKF
PanMb5       MA---------------------------------------------------GLSDAQWNDLLAFFDKFIAPNSAEHGKHILIRMFDSDRATQSLFPKF
PanMb6a      MACP-----------------------------------------------------------AKFWEENVVPDAAEHGKNILIRLYKEDPAALGFFPKY
PanMb6b      MACP-----------------------------------------------------------AKFWEENVVPDAAEHGKNILIRLYKEDPAAQGFFSKY
PanMb7       MA---------------------------------------------------GLSEAQWNELLAFWDKYVAPSSSEHGKHILIRMFDADKATQALFSKY
PcaMb        MV----------------------------------------------------LSEGEWQLVLHVWAK-VEADVAGHGQDILIRLFKSHPETLEKFDRF
PgeMb        MA--------------------------------------------------------DFDMVLKCWGL-VEADYATYGSLVLTRLFTEHPETLKLFPKF
PhuGbE       MS----------------------------------------------------LSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF
PmaaHb1      MP-------------------------------------------IVDSGSVPALTAAEKATIRTAWAP-VYAKYQSTGVDILIKFFTSNPAAQAFFPKF
PmaaHb10     MP-------------------------------------------IVDSGSVGALSASEKAAVAGSWKA-VYANYEAAGKAVLIKFFTSNPGVQDFFPKF
PmaaHb11     MP-------------------------------------------IVDSGSAGALSAAEKAIITDSWKV-VYADYEAAGKAILIKFFTSNPGVQDFFPKF
PmaaHb12     MP-------------------------------------------IVDSGSVGEFSAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFSDNPGVQDFFPKF
PmaaHb13     MP-------------------------------------------IVDSGSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF
PmaaHb14     MP-------------------------------------------IVDSGSVGAISAAEKSLIVSAWAP-VYAKYEEAGVDILVKFFAANPEAQAFFPKF
PmaaHb2a     MP-------------------------------------------IVDTGSVAPLSAAEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFFPKF
PmaaHb3      MP-------------------------------------------IVDSGSVAPLSAAEKTKIRSAWAP-VYSNYETTGVDILVKFFTSTPAAQEFFPKF
PmaaHb5a     MP-------------------------------------------IVDTGSVAPLSAAEKTKIRSAWAP-VYSTYETSGVDILVKFFTSTPAAQEFFPKF
PmaaHb5b     MP-------------------------------------------IVDSGSVAPLSAAEKTKIRSAWAP-VYSTYETSGVDILVKFFTSNPAAQEFFPKF
PmaaHb6      MG------------------------------------------ALQDSGIVSSFKEDEKAALRESWDI-FNNSHQDAGVKILARFIINNPEAKKFFPKF
PmaaHb7      MP-------------------------------------------IEDTGSKPDFSDEEKKAIKDSWSG-VYSEYESASSEILIKFFVDNPSAQDFFPKF
PmaaHb8      MP-------------------------------------------IVDSGSVAPLSAAEKTKIRSAWAP-VYSNYETSGVDILVKFFTSTPAAQEFFPKF
PmaaHb9      MP-------------------------------------------IVDSGSVGALSGAEKAAIADSWKA-VYSNYEEAGKAILIKFFTSNPGVQDFFPKF
PmaaMb1      MS-------------------------------------------IADSGSAPALSGDEKSAVRDTWKV-VYPHAEDHGTTILIKFLTENADAKKFFPKF
PmaaMb2      MS------------------------------------------AIVDSGSAPALSGDEKAAIKSTWPS-VFAKAEDVGAEMLSRFISSNADVKKYFPKF
PmaCygb      ME-------------------------------------------------QGWLSEEEIEALQDIWEK-VFKSAEDVGVILLVRLFTGHPASKQYFPMF
PmaGbX1      MGCTVSTD------ERTGAQSSSQGQSQASRKQQQPEQQRAAGEGHQPPGPPQAPSESQRRLVRDSWLA-LQCDIARVGVIMFVRLFETHPECKDVFYQF
PsiCygb      ME------------------------------------KVQGEMEIERWERSEELSDAEKKVIQETWSR-VYTNCEDVGVSILIRFFVQFPSAKQYFSQF
PsiGbE       MA----------------------------------------------------FSEAEVQRARGAWEK-MYANAEDNGTTVLVRMFTEHPDTKSYFTHF
PsiGbX       MGCALSGS------GSAPGKRSSEAEQ----KDRAAWKAGPVRGGEGLEAGPFPPAGAQKERIQESWRI-LHDSIARVGIIVFIRLFETHPECKDAFFLF
PsiGbY       MA---------------------------------------------------LLTDADKKSIHHIWSK-LFENPEENGKIIVIRLFKDYPETKAYF---
PsiHbaA      MV----------------------------------------------------LTACDKTNVKAVWTK-VSGHLEDYGAETLERMFATYPSTKTYFAHF
PsiHbaD      -M----------------------------------------------------LTADEKQLVLHAWDK-VQGHQEDFGAEALERMFTTYPSTKTYFPHF
PsiHbB       MV---------------------------------------------------HWTAEEKQFITSLWGK-V--DVAECGGEALARLLIVYPWTQRFFSSF
PsiHbG       MV---------------------------------------------------HWTPEEKQMITSLWAK-V--NVAECGGEALARMMIVYPWTQRFFSTF
PsiHbZ       MT----------------------------------------------------LTQAEKAAVVAIWEK-VATHANAIGAESLERLFSGFPQTKTYFPHF
PsiMb        MG----------------------------------------------------LSDNEWQHVLGIWAK-VESDIPAHGQEVMIRLFQVHPETQSLFAKF
PsiNgb       ME-----------SGR--------------------------------------LSSTEKALIRESWQK-VSSNLLQHGIVLFTRLFDLDPDLLPLFQYN
RnoCygb      ME------------------------------------KVPGDMEIERRERNEELSEAERKAVQATWAR-LYANCEDVGVAILVRFFVNFPSAKQYFSQF
RnoMb        MG----------------------------------------------------LSDGEWQMVLNIWGK-VEGDLAGHGQEVLISLFKAHPETLEKFDKF
SchMb        MA--------------------------------------------------------DFDAVLKFWGP-VEADYTSHGGLVLTRLFKEHPETQKLFPKF
SjaMb        MA--------------------------------------------------------DFDAVLKFWGP-VEADYDKIGNMVLTRLFTEHPDTQKLFPKF
TalaMb       MA--------------------------------------------------------DFDAVLKCWGP-VEADYTTIGGLVLTRLFKEHPDTQKLFPKF
TalbMb       MA--------------------------------------------------------DFDAVLKCWGP-VEADYTTMGGLVLTRLFKEHPETQKLFPKF
TguCygb      ME------------------------------------KVQGEMEIERWERSEEISDAEKKVIQEIWSR-VYANCEDVGVSILIRFFVNFPSAKQYFSQF
TguGbE       MS----------------------------------------------------LSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFPHF
TguHbA       MV----------------------------------------------------LSAGDKSNVKAVFGK-IGGQADEYGADALERMFATYPQTKTYFPHF
TguHbAD      -M----------------------------------------------------LTGEDKKLLQQTWGK-LGGAEEEVGADALWRMFHSYPPTKTYFPHF
TguHbE       MV---------------------------------------------------NWTAEEKQLVTTLWGR-V--NVDECGAEALARLLVAYPWTQRFFVSF
TguMb        MG----------------------------------------------------LSDQEWQQVLTVWGK-VESDLAGHGHQILMRLFQDHPETLDRFEKF
TguNgb       ME-----------SGM-------------------------------------RLSGGQRALIRESWQR-VSGSPVQHGLVLFTRLFDLDPDLLPLFQYN
TniCygb1     ME------------------------------------RMQRDGEVDHVEQPGPLTEKEKVMIQDSWAK-VFQSCDDAGVAILVRFFVNFPSSKQFFKDF
TniGbX       MGCAISSL------GA---------------KAEFGDRSAEEEDAAAAAAAVVYPREDQIQMIKDSWKV-IRDDIAKVGIIMFVRLFETHPECKDVFFLF
TniMb        MG--------------------------------------------------------DFDMVLKFWGP-VEADYSAHGGMVLTRLFTENPETQQLFPKF
TniNgb       ME---------------------------------------------------KLSSKDKELIRGSWDS-LGKNKVPHGVILFSRLFELDPELLNLFHYT
TruCygb1     ME------------------------------------RMQGDGELDHVERPSPLTDKEKVMIQDSWAV-VFQSCDDAGVAILVRLFVSFPSSKQLFKDF
TruCygb2     MSHRESPPAPPPPPQLLGG-------------------QRRDVEGEDGPERAKPLSDTEREMIQDTWGH-IYKNCEDVGVSVLIRFFVNFPSAKRYFSQF
TruNgb       ME---------------------------------------------------KLSSKDKELIRGSWDS-LGKNKVPHGVIMFSRLFELDPELLSLFHYT
TthMb        MA--------------------------------------------------------DFDAVLKCWGP-VEADYTTIGGLVLTRLFKEHPETQKLFPKF
XlaGbY       MA---------------------------------------------------DLTAADIENINEIWCK-IYANPEESGKTVVIRLFTTYPQTKVYFKNL
XlaHbA1      -T----------------------------------------------------LTDSDKAAVIALWGK-IAPQANAIGAEALERLFLSYPQTKTYFSHF
XlaHbAT5     MT----------------------------------------------------FSSAEKAAIASLWGK-VSGHTDEIGAEALERLFLSYPQTKTYFSHF
XtrCygb      ME------------------------------------KVQGENDMERWERLEEITESERGVIKETWAR-VYANCEDVGVSILIRFFVNFPSAKQHFSQF
XtrGbX       MGCILSSL------GWQWRDSLDHTETSP-------------------LLPTLNLSEQQQQLLVESWRL-IQHDIAKVGVILFVRLFETHPECKDVFFLF
XtrGbY       MA---------------------------------------------------DLTGADIENINEVWSK-IYANPEESGRTVVISLFLTYPQTKIYFKNL
XtrHbA1      MH----------------------------------------------------LTADDKKHIKAIWPS-VAAHGDKYGGEALHRMFMCAPKTKTYFPDF
XtrHbB1      MV---------------------------------------------------NLTAKERQLITGTWSK-I--CAKTLGKQALGSMLYTYPWTQRYFSSF
XtrHbB2      MV---------------------------------------------------HWTAEEKATIASVWGK-V--DIEQDGHDALSRLLVVYPWTQRYFSSF
XtrNgb       ME-----------KDQ--------------------------------------LSGPQKELIRESWQT-VSQDQLHHGTVLFSRLFELEPELVFLFQYN
ZalGbE       MS----------------------------------------------------LSEAEVQSARGAWEK-IYVDAEDNGTAVLVRMFTEHPDTKSYFTHF

AcaGbY       -KTVP------TDGDLKAHPQVAFHGRRIMVAFSQVIENMENWNQACVLLERLVNNHKNIHQ-VPSGMFQLLFQAMLCTFDDLLGRT-FTP-EKRVSWEK
AcaMb        -KNLK------SLDEMKNSEDLKKHGTIVLTALGKILKQKRQHE---AELAPLAQSHATKHK-IPVKYLEFISEVIVGVIAEKRSAD-FGA-ESQAAMRK
AplGbE       -KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-VDPKNFRIICDIILQMMEEKFGG------DCKASFEK
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CanMb           -AGI-------AHGDLAGDAGVSAHGATVLKKLGDLLKARGGHA---ALLKPLSSSHATKHK-IPIINFTLIAEVIGKVMEEKAGLD---A-AGQTALRN
CauMb1          -VGI-------AQSDLAGNAAVNAHGATVLKKLGELLKARGDHA---AILKPLATTHANKHK-IALNNFRLITEVLVKVMAEKAGLD---A-AGQTALRK
CauMb2          -KGI-------SQSELAGNALVAAHGATVLKKLGELLRAKGDHA---AILHPMATTHANKHK-ITLNNFRLITEVLVEVMKEKAGLD---S-AGQGALKR
CcaMb1          -VGI-------AQSDLAGNAAVKAHGATVLKSWASCLKARGDHA---AILKPLATTHANTHK-IALNNFRLITEVLVKVMAEKAGLD---A-GGQSALRR
CcaMb2          -KGI-------PQSELAGDTLVASHGATVLKKLGELLRAKGDHA---AILQPLATTHANKHK-IALNNFRLITEVLVKVMAEKAGLD---T-AGQGALKR
CcrMb           -KSLK------SEGEMKASEDLKKHGATVLTALGGILKKKGQHA---AELQPLAQSHANKHK-IPVKYLEFISEAIIQVLQSKHSGD-FGA-DTKEAMKK
CliGbE          -KGMD------SAEEMKQSDQVRGHGKKVFTAINDMVQHLDNSEAFLGIVNPLGKKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKSSFEK
CmiGbY          -KNIS------TLEEMKKSPQIKRHGKIVMSALNKLIANLDNGEELSSLLAKMAERHINVHK-VDLHNFQIIFNIIIAILEETFGNA-FTP-EIRGTWTK
CmyGbE          -KGMG------TAEEMEQSDQVRSHGKRVLTTINDLVQHLDSTDAFLGIVNPLGKKHAMQLK-VDPKNFRIICDIILQLMEEKYGG------DCKASFEK
CpiCygb         -KHME------DPLEMERTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-VEPVYFKFFTGVMLEVIAEEYAND-FTP-EVQRAWTK
CpiGbE          -KGMG------TAEEMEQSDQVRSHGKRVLTTINDLVQHLDSTDAFLGIVNPLGKKHAMQLK-VDPKNFRIICDIILQLMEEKYGG------DCKASFEK
CpiGbX          -RDIE------DLEQLKMNKELRAHGLRVMSFIEKSVARLDQEDKLEQLAFELGRSH-YRYN-APPKYYEYVGIQFISTVQPILKER-WTP-EVEEAWQV
CpiGbY          -KNIP------TEGNLQEDPLVRFHGRRVMVALNQVVENLDNWKQACRILDRLADKHKNVHQ-VPAVNFQSMFQVILNVCKDVLGNE-FST-EVSLSWEK
CpiHbA          --DLH------H-----GSAQIRTHGKKVLTALGEAVNHIDDLA---SALSKLSDIHAQTLR-VDPVNFKFLNHCFLVVVAIHQPSV-LTP-EVHVSLDK
CpiHbaA         --DLH------H-----GSAQIRTHGKKVLTALGEAVNHIDDLA---SALSKLSDIHAQTLR-VDPVNFKFLNHCFLVVVAIHQPSV-LTP-EVHVSLDK
CpiHbaD         --DLH------H-----DSEQIRHHGKKVVTALGDAVRHMDNLS---EALSELSNLHAYNLR-VDPVNFKLLSHCFQVVLAVHLADE-YTP-QVHVAYDK
CpiHbB1         -GNLS------SPTAIIGNPKVRAHGKKVLTSFGEAVKNLDNIK---ATYAKLSELHCDKLH-VDPENFRLLGDILVIVLAAHFGRE-FTP-ACQAAWQK
CpiHbB2         -GNLS------NAEAILHNPHVHAHGKKVLTSFGEAVKNLDHIK---QTFATLSKLHCEKLH-VDPENFKLLGNVLIIVLASHFTKE-FTP-ACQAAWQK
CpiHbG          -GNLS------SPTAITGNPKVRAHGKKVLTSFGEAVKNLDNIK---ATYAKLSELHCNKLH-VDPENFRLLGDILVIVLASHFGRE-FTP-ACQAAWQK
CpiHbZ          --DLS------Q-----GSAQLHGHGSKVLGAIGEAVKNIDNIT---GALATLSELHAYILR-VDPVNFKLLSHCILCSVAAHFPND-FTP-EVHAAWDK
CpiMb           -KNLK------TIDELKSSEEVKKHGTTVLTALGRILKLKNNHE---PELKPLAESHATKHK-IPVKYLEFICEIIVKVIAEKHPSD-FGA-DSQAAMRK
CpiNgb          CKKFS------SPQECLSSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLSNLGKKH-QTVG-VKVDSFSAVGESLLFMLEKCLGTA-FSP-DVREAWTR
CraMb           -AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGAHA---ALLKPLSSSHATKHK-IPIINFKLIAEVIGKVMEEKAGLD---A-AGQTALRN
CycrMb          -KHLK------SEDDMRRSEDLRKHGNTVLTALGGILKKKGHHE---AELKPLAQSHATKHK-IPIKYLEFISEAIIHVLHSKHPAE-FGA-DAQAAMKK
DreCygb1        -RELQ------DPAEMQQNAQLKKHGQRVLNALNTLVENLRDADKLNTIFNQMGKSHALRHK-VDPVYFKILAGVILEVLVEAFPQC-FSPAEVQSSWSK
DreCygb2        -QDME------DPEEMEKSSQLRKHARRVMNAINTVVENLHDPEKVSSVLVLVGKAHAFKYK-VEPIYFKILSGVILEILAEEFGEC-FTP-EVQTSWSK
DreGbX          -RDVE------DLERLRTSRELRAHGLRVMSFIEKSVARLDQLERLETLALELGKSH-YRYN-APPKYYGYVGAEFICAVRPILKDR-WTP-ELEEAWKT
DreHbAa         -ADLS------P-----GSGPVKKHGKTIMGAVGEAISKIDDLV---GGLAALSELHAFKLR-VDPANFKILSHNVIVVIAMLFPAD-FTP-EVHVSVDK
DreHbAe         -KDLS------P-----GSAPVRKHGKTVMGGVAEAVSKIDDLN---AGLLNLSELHAFQLR-VDPANFKILSHNILVVLATLFPAD-FTP-EAHVAMDK
DreHbAx         --NIS------A-----NSEHLRSHGKKIVEALAEGAKNVSTLT---TTLAPLSRFHAYQLR-IHPTNFKLFNHCILVTLACRMGDD-FTP-VVHAAIDK
DreHbBa         -GNLS------SPAAIMGNPKVAAHGRTVMGGLERAIKNMDNVK---NTYAALSVMHSEKLH-VDPDNFRLLADCITVCAAMKFGQAGFNA-DVQEAWQK
DreHbBe         -GNLY------NAAAILGNPMVAAHGKTVLKGLELAVKNMDNIK---ATYADLSVLHSEKLH-VDPDNFRLLADCLTIVVAAQMGAG-FTP-EVQAAFQK
DreMb           -SGI-------SQGDLAGSPAVAAHGATVLKKLGELLKAKGDHA---ALLKPLANTHANIHK-VALNNFRLITEVLVKVMAEKAGLD---A-AGQGALRR
DreNgb          -TNCG------DAPECLSSPEFLEHVTKVMLVIDAAVSHLDDLHTLEDFLLNLGRKH-QAVG-VNTQSFALVGESLLYMLQSSLGPA-YTT-SLRQAWLT
EpeMb           -AGI-------T-GDIAGNAAVAAHGATVLKKLGELLKAKGNHA---AIIKPLANSHAKQHK-IPINNFKLITEALAHVLHEKAGLD---A-AGQTALRN
FalGbE          -KGMD------SAEEMKQSDQVRGHGKKVFGAINDMVQHLDNSEAFLGILTPLGKKHASQLK-IDPKNFRIICDIILQLMEEKFGG------DCKASFEK
FpeGbE          -KGMD------SAEEMKQSDQVRGHGKKVFSAINDMVQHLDNSEAFLGIVNPLGKKHATQLK-IDPKNFRILCDIILQLMEEKFGG------DCKASFEK
FruMb           -AGI-------TQSDLAGNAAVSAHGATVLKKLGELLKAKGNHA---ALLQPLANTHATKHK-IPINNFKLIAEVIGKVMEEKAGLD---A-AGQQALKN
GfoGbE          -KGMD------SAEEMKQSDQVRGHGKKVFSAINDMVQHLDNSEAFLGIVTPLGKKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKASFEK
GgaCygb         -KHMD------DTLEMERSLQLRKHAQRVMGAINTVVENLDDPEKVSSVLALVGKAHALKHK-VEPVYFKKLTGVMLEVIAEAYGND-FTP-EAHGAWTK
GgaGbE          -KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKASFEK
GgaHbA          --DLS------H-----GSAQIKGHGKKVVAALIEAANHIDDIA---GTLSKLSDLHAHKLR-VDPVNFKLLGQCFLVVVAIHHPAA-LTP-EVHASLDK
GgaHbAD         --DLS------P-----GSDQVRGHGKKVLGALGNAVKNVDNLS---QAMAELSNLHAYNLR-VDPVNFKLLSQCIQVVLAVHMGKD-YTP-EVHAAFDK
GgaHbG          -GNLS------SPTAILGNPMVRAHGKKVLSSFGDAVKNLDNIK---NTFSQLSELHCDKLH-VDPENFRLLGDILIIVLAAHFSKD-FTP-ECQAAWQK
GgaMb           -KGLK------TPDQMKGSEDLKKHGATVLTQLGKILKQKGNHE---SELKPLAQTHATKHK-IPVKYLEFISEVIIKVIAEKHAAD-FGA-DSQAAMKK
GgaNgb          CKRFA------SPQECLAAPEFLDHIRKVMLVIDAAVSHLEDLPCLEEYLCNLGKKH-QAVG-VKVESFSTVGESLLYMLEKCLGAA-FSP-DVREAWIE
GgiMb           -AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGAHA---ALLKPLSSSHATKHK-IPIINFKLIAEVIGKVMEEKAGLD---A-AGQTALRN
HsaCYGB         -KHME------DPLEMERSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-VEPVYFKILSGVILEVVAEEFASD-FPP-ETQRAWAK
HsaHBA          --DLS------H-----GSAQVKGHGKKVADALTNAVAHVDDMP---NALSALSDLHAHKLR-VDPVNFKLLSHCLLVTLAAHLPAE-FTP-AVHASLDK
HsaHBB          -GDLS------TPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLK---GTFATLSELHCDKLH-VDPENFRLLGNVLVCVLAHHFGKE-FTP-PVQAAYQK
HsaHBD          -GDLS------SPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLK---GTFSQLSELHCDKLH-VDPENFRLLGNVLVCVLARNFGKE-FTP-QMQAAYQK
HsaHBE          -GNLS------SPSAILGNPKVKAHGKKVLTSFGDAIKNMDNLK---PAFAKLSELHCDKLH-VDPENFKLLGNVMVIILATHFGKE-FTP-EVQAAWQK
HsaHBG          -GNLS------SASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLK---GTFAQLSELHCDKLH-VDPENFKLLGNVLVTVLAIHFGKE-FTP-EVQASWQK
HsaHBZ          --DLH------P-----GSAQLRAHGSKVVAAVGDAVKSIDDIG---GALSKLSELHAYILR-VDPVNFKLLSHCLLVTLAARFPAD-FTA-EAHAAWDK
HsaMB           -KHLK------SEDEMKASEDLKKHGATVLTALGGILKKKGHHE---AEIKPLAQSHATKHK-IPVKYLEFISECIIQVLQSKHPGD-FGA-DAQGAMNK
HsaNGB          CRQFS------SPEDCLSSPEFLDHIRKVMLVIDAAVTNVEDLSSLEEYLASLGRKH-RAVG-VKLSSFSTVGESLLYMLEKCLGPA-FTP-ATRAAWSQ
IpuGbX          -RDVE------DLERLRTSKELRAHGLRVMSFIEKSVARLDQLERLDSLAVELGRSH-YRYY-APPKYYGYVGTEFICAVRPILKEK-WTP-ELEKAWKT
LchCygb         -RHLE------DPLDMERSVQLRKHARRVMGAINTVVENVEDQD-IASVLAPVGKAHALKHK-VEPVYFKILSGVILEILAEEYAQH-FTP-EVQKAWTK
LchGbE          -KGMG------SAAEMEQSAQVRTHGKKIFSALNDMIQHLDSTDALLGVVNPLGKKHATQLK-VDPKNFKIICNILLQVLDEKFGG------DARAGFEK
LchGbX1         -RDID------DFHQLKMSKELQAHGLRVMSFIEKSVARLEQKDKLEQIAFELGRSH-CRYN-APPKYYQYVGVQFISVVKPILKEA-WTP-EVEEAWQI
LchGbX2         -RDVD------DLQRLRTSKELRAHGLRVMSFVEKSVARLEHSERLEQLALELGKSH-YRYN-APPKYYQYVGIEFVCAVQPILKER-WTP-EVEEAWQT
LchGbY          -KNIS------TMEEMQKNEQIRIHGLRVMNSLNQVIQNIDNLNEVYSILTHLAKRHQYVHR-VDVHNFKLIFGVIIKILKEALGAT-FTE-EICTSWQK
LchHbA1         --DLS------P-----GSSMLRAHGKKVMGTIEGSIKSIDKLA---TVLSRLSDMHAYNFM-VDPVNFKLLSQCILVALATQLMAD-FTP-EAQCAWDK
LchHbA2         -TDLS------P-----SSQKLHAHAKVVLGALTKAVNHLDNIT---DTLHDISLVHAKKLL-VDPVNFELLGHCLEVALAAHFATD-FTP-EVHLAIDK
LchHbB1         -GDLS------SSKAIASNPKVTEHGLKVMNKLTEAIHNLDHIK---DLFHKLSEKHFHELH-VDPQNFKLLSKCLIIVLATKLGKQ-LTP-DVQATWEK
LchHbB2         -GSLS------SSTVIARNFKVQQHAAKVINALTEAIRNIDNLK---ASFSDLSKLHFQKLH-VDPENFKLLGKTLIITLSEKLGSE-FSP-QIQAAWEK
LchMb           -KHM-------TYQELQSSEELKTHGDTVLSKLGCLLKLKGNHA---GDLHPLAQTHATKHK-IPLHNFEIISEIIVKILAEKYPGD-FGA-DGQAALKK
LchNgb          -SSFP------SQAGCLTSPEFIDHIHKVMMVVDAAVNSLDNLLSLEDYLINLGKKH-QAAG-VKMESFQVVGESLLYMLEHGLDSA-FSV-EVRHAWIA
LpaGbE1         -KELQSMAEKASSVELQGLSEVRGHGKKVLSALNDMVQYLDNMDSLKKVTEPLGKKHAVELQ-VDVKDFDIIFTILLDLLGEKCGG------DAKTDLKK
LpaGbE2a        -PELQSIAETASAADIAGLAEVRGHAKTVLTAFNDMVQHLENIDTLKETATPLAKKHSEELK-VDVKDFKILCDNLVDLVGEKQDE------DAKTTFKK
LpaGbE2b        -PELQSVGETASAAEIAGLAEVQGHAKTVFTAFNDMVQHLENIDALKETATPLAKKHSEELK-VDVKDFKILCDNLVDLVGEKQDE------DAKSTFKK
LpaGbE2c        -TELQSIAETGSAAEIAALAEVQGHGKKVFTALNDLVLKVDNADALKEAVAPLAKKHAEELK-VDVKDLGVLCEILIDLVGEKQG-------DAKTAFKK
LpaGbE2d        -TELQSIAETASAAEIAALAEVQGHGKKVFTALNDLVLHVDNADALNKIAAPLAKKHAEELK-VDVKDLGVLCEILIDLVGEKQGE------DAKTAFKK
LpaGbE2e        -TELQSIAEIASAAEIAGLAEVRGHGKKVFTALNDLVLHVDNADALNKIAAPLAKKHAEELK-VCVKDLGVLCEILIDLVGEKQG-------DAKTAFKK
LplaHbA         -KGLD------SADQLKKSPAVRWHAERIINAVNDAVVAMDDPAKQSLQLKELSQKHAHELN-VDPKYFKVLAGVISDAVVK-------SG-DAKAAVDK
LplaHbB         -QGLT------SADQLKKSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLNELSSKHAKSFQ-VDPQYFKVLAAVIVDTVL-----------PGDAGLEK
MangMb          -KHLK------SEDDMRRSEDLRKHGNTVLTALGGILKKKGHHE---AELKPLAQSHATKHK-IPIKYLEFISEAIIQVLHNKHPGE-FGA-DTQAAMKK
MbiMb           -KHLK------SEAEMKASEDLKKHGHTVLTALGGILKKKGHHE---AELKPLAQSHATKHK-IPIKYLEFISDAIIHVLHSKHPSD-FGA-DAQGAMTK
MgaGbE          -KGMD------SAEEMKQSDQVRGHGKRVFTAINDMVQHLDNTEAFLGILNPLGQKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKTSFEK
MglaHb2         -KDLH------TLEDLASSADARWHVERIIQAVNFAVINIEDREKLSNKFVKLSQDHIEEFHVTDPQYFMILSQTILDEVEKRNGG--LSG-EGKSGWHK
MmuMb           -KNLK------SEEDMKGSEDLKKHGCTVLTALGTILKKKGQHA---AEIQPLAQSHATKHK-IPVKYLEFISEIIIEVLKKRHSGD-FGA-DAQGAMSK
MniMb           -AGI-------AKADMAGNAAISAHGATVLKKLGELLKAKGSHA---AIIKPMANSHATKHK-IPIKNFELISEVIGKVMHEKAGLD---A-AGQKALKN
MunGbE          -KGMD------SAEEMKQSDQIRGHGKRVFTAINDMVQHLDNSEAFLGIVNPLGKKHATQLK-IDPKNFRVICDIILQLMEEKFGG------DCKASFEK
NcoMb           -AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGAHA---ALLKPLSSSHATKHK-IPIINFKLIAEVIGKVMEEKAGLD---A-AGQTALRN
OanGbY          -KNIP------LEGNLQEDPLLRSHGRRVMVALNRIIQNLDNWKQVCKILNPLAEKHKIIHS-VDVENFQFMLKCVGDVCQDYLGPC-YTP-EIAESFQK
OanHbW          -GNLS------SPTAIVGNPRVRAHGKKVLTSFGEAVKDLDHVK---SNFAKLSQLHSEKLH-VDPENFRLLGDNLIIVLAATLGKD-FTP-EAQAAWQK
OanMb           -KGLK------TEDEMKASADLKKHGGTVLTALGNILKKKGQHE---AELKPLAQSHATKHK-ISIKFLEYISEAIIHVLQSKHSAD-FGA-DAQAAMGK
OanNgb          CRQFS------SPRDCLASPEFLDHIRKVMLVIDAAVIHLDDLSSLEEYLTNLGRKH-KAIG-VKLSSFSTVGESLLFMLDKCLGPA-FSP-ATREAWTR
OlaCygb1        -KHIE------DAEELEKSSQLRKHARRVMNAINTLVESLDNSDKVSSVLNAVGKAHAIRHK-VDPVYFKILSGVILEVLGEAYPQV-MTA-EVASAWTN
OlaCygb2        -QDMQ------DPEEMEKSSQLRQHARRVMNAIN-VVENLQDPEKVSSVLALVGKAHAVKHK-VEPIYFKILSGVMLSVLSEDFPEF-FTA-EVQLVWTK
OlaHbA          -KDLS------P-----GSAPVKKHGKTVMGGIADAVGKIDDIS---SGLLNLSELHAFTLR-VDPTNFKILSHNILVVMAIMFPQD-FTP-EVHVALDK
OlaHbB          -GNLY------NAEAIKTNPNIAAHGTKVLHGLDRAVKNMDNIK---ATYAELSVLHSEKLH-VDPDNFKLLADCLTIVIAAKLGSA-FSP-EIQATFQK
OlaMb           -AGI-------AKGDMAGNAALSAHGATVLKKLGELLKARGNHG---AILKPLANSHATKHK-IPINNFRLITEVIGKVMAEKAGLD---A-AGQQALRS
OlaNgb          -TNCG------STQDCLSSPEFLDHVTKVMLVIDAAVNHLDDLHSLEDFLLNLGRKH-QAVG-VSTQSFAVVGESLLYMLQCSLGQA-YTA-ALSQAWLN
PaeGbE1a        -KELQSIAGTASAAKLEGLSEVRAHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-VDVKEFEILCGILLDLMAEKCGE------DTKTDFKK
PaeGbE1b        -KELQSTAGTASVTELEGLSEVRTHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-VDVKEFEILCAILLELMAEKCGE------DAKTDFKK
PaeGbE1c        -KELQSIAGTASAAKLEGLSEVRAHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-VDVKEFEILCGILLDLMAEKYGE------DTKTDFKK
PaeGbE2a        -TQLQSVAETASAEEIAALAEVRAHGKKVFLALNDMVPHLSNVDALKETIAPLAKKHATELK-VDVKDFEIIFDNLLALIGEKQGA------DAKTAFKK
PaeGbE2b        -TQLQSVAETASAVDIAALAEVRAHGKKVFSALHDMVPHLTNVDALKETINPLAKKHAAELK-VDVKDFRILFENLLDLIGEKQGA------DAKTAFKK
PaeGbE2c        -TQLQSVAETASAQEIAALAEVRTHGKKVFSALNDMVSHLTNVDALKGTIAPLAKKHATELK-VDVKDFVIIFENLLDLIGEKQGG------DAKEAFKK
PaeGbE2d        -TQLQSIPETASAEEIAALAEVRGHGKKVFSALNDLVSHLTNVDSLKATIVPLAKKHATELK-VDVKDFGIIFENLLHLIGQKQGG------DAKEAFEK
PanGbE1a        -KELQSIAGTASAAKLEGLSEVRTHGKKVLSALNDMVQQVDNMDALKAIIEPLGKKHAVELK-VDVKEFEILCGILLDLMAEKCGE------DTKTDFKK
PanGbE1b        -KELQSIAGTASAAKLEGLSEVRAHGKKVLSALNDMVSQVDNMDALKAIIEPLGKKHAVELK-VDVKEFEILCGILLDLMAEKCGE------DTKTDFKK
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PanGbE2a     -TQLQSVAETASAEEIAALAEVRAHGKKVFLALNDMVPHLNNVDALKETIAPLAKKHATELK-IDVKDFEIIFDNLLALIGEKQGA------DAKTAFKK
PanGbE2b     -TQLQSIAETASAEEIAALAEVRAHGKKVFSALNDMVSHLTNVDALKETINPLAKKHAAELK-VDVKDFRIIFENLLDLIGEKQGA------DAKTAFKK
PanGbE2c     -TQLQSVAETASAEEIAALAEVRAHGKKVFLALNDMVPHLTNVDALKETIAPLAKKHAAELK-VDVKDFRIIFENLLDLIGEKQGA------DAKTAFKK
PanGbX       -RDID------DIQQLQLSRELQAHGLRVMSFIEKSVARLQQEDKLQQLAFELGRCH-CRYN-ALPKYFEYVAFQFMTAVKPILKEK-WTS-EVDDAWKA
PanGbY       -KNID------TEEGIKESRQVRQHGRRVVMLLSKVIECLEDWDKTSTLLSELADRHQQHHK-VEVVNFKFLFAALNSVYIDVFGPT-FTP-DIEASWQK
PanHba1      --NID------P-----GSSYVRNQGGKIVTAIGTAVQNADNIQ---EALADLCCLHAYRIR-VDPVNFQYFSKCFLTVLAVHLQDD-FTA-DVHVVWDK
PanHba2      --DTS------A-----NSPQLSAHGAKIIASLGKAIKNVDNMS---AALSDLSDLHAQSIR-VDPSNFKYISHCLLVLLAAHLKAD-FTP-QVQIAWDK
PanHba3      -GDYK------A-----SSDKVIQHGKKVVDALVQASQHLHDLE---SQLHPLSVKHATELM-VDPVNFEHLSHCIHVTIAAHHGEK-YTA-EMHRSADK
PanHba4      -GDYK------A-----SSDKVIQHGKKVVDALVQASQHLHDLE---SHLHPLSEKHARELM-VDPVNFEHLSHCIHVTIAAHHGEK-YTA-EMHRSFDK
PanHbb1      -GNLS------TTSTIASNDRVQAHGAKVLTAIGDALVDLPNIK---QNLTDLSRLHSEILH-VDPENFRLLGQCLVIVLAAKFGAEKFNA-DVQAAWQK
PanHbb2      -GAMS------TLKDIESNPKVRAHGRKVMAAVGDAISHMDNIK---GHLSQLSQLHSDKLH-VDPANFELLGNNIVIVLAAKFGADAFTP-EVQATFQK
PanHbb3      -GDLS------TFSAIRQNPHVRTHGAKVLGAVVECLNHMDDIK---GHLAQLSILHSDTLH-VDPANFTLLGNCFLIVLAKSVGAG-FTP-DVHAACHK
PanHbb4      -GDLS------TISAIRKNSHVRAHGHKVLSAVGDCIPHLGDIK---GHLAQLSKLHCETLH-VDPANFCLLGKIIVVVLASHFGAK-FTP-EVQAAFQK
PanHbb5      -GDLS------TISAIRKNSHVRAHGHKVLSALGDCVPHLGDIK---GHLAQLSKLHCETLH-VDPANFCLLGQIITIVLASRFGAA-FTP-EVQACFEK
PanMb1       -RHLT------TEAEMRSNEDIRKHGNTVFTALGKLVKLKGNVE---GDLRSMADSHANKHK-IHLENFDIISKVIDNYFHESFPGD-YGA-DVQDYMKA
PanMb2       -RHLG------SEAEMRSCADLQKHGNTVFTALGKTLKLKGHHD---ADLRPMAESHSHKHK-IPVENFTLICSIIDKYLHESF-SD-YTG-DTRESLKS
PanMb3       -KDLA------SEAEMRGSDGLKNHGETVFTALGKALQQRDGIA---NELRPLAVTHSQNHK-IPLEEFENICEVIDVYLAEICPD--YAG-ETRTSVKA
PanMb4       -KDI-------PTSDLAVNADVKKHGGVVVDFLGKLLKLKGQND---SQLHTMAESHKNKHK-IPLDYFQVISSVIDVYVNENLPEE-YAP--VRQSMKS
PanMb5       -KDA-------PAADLPKNADVKKHGGVVVDFLGKLLKQKGHNE---SMLHTMAETHKNKHK-VLPDYFQLISSVIDVYVHENLPAE-YAP--VRDAMNA
PanMb6a      -KDI-------PVSELGNNADVKEQGAVVVKALGELLKLKGQHE---SQLHAMAESHKNTYK-IPVEYFPKIFKITDAYLQEKVGAA-YAA--IQAAMNV
PanMb6b      -KDT-------PVSELGNNADVKEQGAVVVKALGELLKLKGQHE---SQLHAMAESHKNTYK-IPVEYFPKIFKITDAYLHEKVGAV-YAA--IQAAMNV
PanMb7       -KDI-------PTSDLAANADVKKHGGVVVDFLGKLLKLKGQND---SQLHTMAESHKNKHR-IPLDYFQLISTVIDVYVYENLPGE-YGP--VRESLKA
PcaMb        -KHLK------TEAEMKASEDLKKHGVTVLTALGAILKKKGHHE---AELKPLAQSHATKHK-IPIKYLEFISEAIIHVLHSRHPGD-FGA-DAQGAMNK
PgeMb        -AGI-------AHGDLAGDAGVSAHGATVLNKLGDLLKARGGHA---ALLKPLSSSHATKHK-IPIINFKLIAEVIGKVMEEKAGLD---A-AGQTALRN
PhuGbE       -KGMD------SAEEMKQSDQVRGHGKKVFSAINDMVQHLGNSEAFLGIVTPLGKKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DSKASFEK
PmaaHb1      -QGLT------SADQLKKSMDVRWHAERIINAVNDAVVAMDDTEKMSLKLRELSGKHAKSFQ-VDPQYFKVLAAVIVDTVL-----------PGDAGLEK
PmaaHb10     -KGLD------SADKLSKSPAVRWHAERIINAVNDSVVALDDPEKQSLKLKALSQKHAYEFH-VDSQYFKVLSATILEQVDDANGG--LSA-EGKSGWEK
PmaaHb11     -KGLD------SADQLSKSAAVRWHAERIINAVNDAVVALDDPEKQSLKLKALSKKHAQEFN-VDPQYFKVLSANVLEQVAAANGG--LSA-EAQGAWEK
PmaaHb12     -KGLD------SADQLKKSPAVRWHAERIINAVNDAVVALDDPPKLSLKLKALSKKHAQELN-VDPQYFKVLAGVISDAVAK-------SG-DEKAAVDK
PmaaHb13     -KGLD------SADQLKKSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-VDPSYFKVLAGVISDAVAK-------SG-DAKAAVDK
PmaaHb14     -KGLD------SADKLKKSPAVRWHAERIINAVNDAVVALDDPAKQSLQLKALSQKHAHELN-VDPSYFKVLAGVISDAVAK-------SG-DAKAAVDK
PmaaHb2a     -KGLT------TADQLKKSADVRWHAERIINAVNDAVVSMDDTEKMSMKLRDLSGKHAKSFQ-VDPQYFKVLAAVIADTVA-----------AGDAGFEK
PmaaHb3      -KGLT------TADQLKKSADVRWHAERIINAVNDAVVSMDDTEKMSMKLGDLSGKHAKSFQ-VDPQYFKVLAAVIADTVA-----------AGDAGFEK
PmaaHb5a     -KGLT------TADQLKKSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-VDPQYFKVLAAVIADTVA-----------AGDAGFEK
PmaaHb5b     -KGLT------TADQLKKSADVRWHAERIINAVNDAVASMDDTEKMSMKLRDLSGKHAKSFQ-VDPQYFKVLAAVIADTVA-----------AGDAGFEK
PmaaHb6      -KGLN------TAEELQNSAEVRIHGDKILAAVQQAVLDLDDPDKQKNKLKDLSKSHAQQFN-VEPAYFKTFAEVILKYVTETCGKS-FTS-EMRTSWSK
PmaaHb7      -KDLD------SEEKLKNSTAVRWHAERIINAVNDVIWLLDEPEKNAKNLKELSEKHAVQLN-VDAKFFKVLAELILDKVAEKSGDS-FSD-SARSAWEK
PmaaHb8      -KGMT------TADQLKKSADVRWHAERIINAVNDAVTSMDDTEKMSMKLRDLSGKHAKSFQ-VDPQYFKVLAAVIADTVA-----------AGDAGFEK
PmaaHb9      -KGLD------SADQLSKSAAVRWHAERIINAVNDAVVALDDPEKLSLKLKALSKKHAQEFN-VDPQYFKVLAVNIVEGVSSANGG--LGA-EAQAAWEK
PmaaMb1      -QALK------TADEMKSSPVLRDHAKRIMNSINDMVVALDDTNAQNAQMNGLSKKHANDFK-VDPKYFKVISNVILSVIAEGLGAQ-FND-AAKNGWSK
PmaaMb2      -KDIS------SQAELKSSAKVRDHAKRIMAFINDLVDNIDNAGAQTAKLHSLSAEHAEKFK-VDPQYFKVISNVLLDILGETFGAS-FSG-ATRSAWIK
PmaCygb      -KDLE------TADDLKASAKLRWHAGRVMGSLDKAVRSLRKPEELIKILRAVGLSHARKATPVDVKYYHILGGIIMDVLLETFKDE-LSP-TARSAWTK
PmaGbX1      -RDCE------DLQKLKMNKQLQAHGLRVMSFIEKSVARLEQECVLEQLIVEMGRKH-YKYN-ASPKYYSFVGIEFIATVQPFLQEK-WTN-EVEDAWQC
PsiCygb      -KHME------DPLEMERTPQLRKHARRVMGAVNTVVENINDSEKVSSVLALVGKAHALKHK-VEPVYFKFFTGVMLEVIAEEYAND-FTP-EVQRAWTK
PsiGbE       -KGMG------TAEEMEQSDQIRSHGKKVLTAINDLVQHLDSTDAFLGIVNPLGKKHATQLK-IDPKNFRVICDIILQLMEEKYGG------DCKASFEK
PsiGbX       -RDIE------DLQQLKMSKELQAHGLRVMSFIEKSVARLDQEDKLEHLAFELGRNH-YRYS-APPKYYEYVGVQFISAVQPILKER-WTP-ELQEAWQV
PsiGbY       -KSIP------TEGNLQEDPQIRYHGRRVMVALNQVIENLDNWKQACRILEHVAEKHKNTHH-VPAANFQSMFQVILSVCKELMGNE-FSS-EVSSAWEK
PsiHbaA      --DLH------H-----GSSQVRTQGKKVLSALGDAVAHVDDLP---SALSRLSDLHAKNLR-VDPVNFKLLSHCFLVVVALHHPSL-FTP-EVHVSLDK
PsiHbaD      --DLH------H-----DSEQVRHHGKKVVTALGNAVHHMDTLS---KTLSDLSDLHAYNLR-VDPVNFKLLSHCFQVVLAVHLRDE-YTP-QLHVAFDK
PsiHbB       -GNLS------SPTAILGNPKVRAHGKKVLTSFGEAVKNLDSVK---ATYAKLSELHCNKLH-VDPENFRLLGDILVIVLASHFGKE-FTP-ACQAAWQK
PsiHbG       -GNLS------NPQAIQHNPKVLEHGKKVLTSFGNAVKDLDHIK---ETFAHLSELHCEKLH-VDPENFKLLGNVLVIVLAAHIRKD-FPP-ACQAAWHK
PsiHbZ       --DLS------Q-----GSAQLHGHGSKVLSAIGEATKNIDNIT---GALATLSELHAYILR-VDPVNFKLLSHCILCSLAAHFPND-FTP-EVHAALDK
PsiMb        -KNLK------TADEMKSSDELKKHGITVLTALGRILKQKNNHE---QELKPLAESHATKHK-IPVKYLEFICEIIVKVIAEKHPAD-FGA-DSQAEMRK
PsiNgb       CRQFS------SPLECLSSPEFLDHIRKVMLVIDAAVTHLENLSSLEEYLTNLGKKH-QAVG-VKVDSFSAVGESLLFMLEKCLSTA-FSS-DVREAWTK
RnoCygb      -KHME------DPLEMERSPQLRKHACRVMGALNTVVENLHDPDKVSSVLALVGKAHALKHK-VEPMYFKILSGVILDVIAEEFAND-FPV-ETQKAWTK
RnoMb        -KNLK------SEEEMKSSEDLKKHGCTVLTALGTILKKKGQHA---AEIQPLAQSHATKHK-IPVKYLEFISEVIIQVLKKRYSGD-FGA-DAQGAMSK
SchMb        -TGI-------AQADMAGNAAISAHGATVLKKLGELLKAKGNHA---AILKPMANSHATKHK-IPINNFKLISEIIVKVMQEKAGMD---A-GGQQALRN
SjaMb        -AGI-------GLGDMAGNAAISAHGATVLKKLAEVLKAKGNHA---GIIKPLANSHATKHK-IAINNFKLITEIIVKVMQEKAGLD---A-GGQTALRN
TalaMb       -AGI-------AQADLAGNAAISAHGATVLKKLGELLKAKGSHA---SILKPMANSHATKHK-IPINNFKLISEVLVKVMQEKAGLD---A-GGQTALRN
TalbMb       -AGI-------AQADIAGNAAISAHGATVLKKLGELLKAKGSHA---AILKPLANSHATKHK-IPINNFKLISEVLVKVMHEKAGLD---A-GGQTALRN
TguCygb      -KHME------DPLEMERSLQLRKHARRVMGAINTVVENLNDSEKVSSVLALVGKAHALKHK-VEPIYFKKLTGVMLEVIAEEYPND-FTP-EAHGAWTK
TguGbE       -KGMD------SAEEMKQSDQVRGHGKKVFGAINDMVQHLDNSEAFLGIVTPLGKKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKASFEK
TguHbA       --DLG------K-----GSAQVKGHGKKVAAALVEAANNVDDLA---GALSKLSDLHAQKLR-VDPVNFKLLGQCFLVVVATRNPSL-LTP-EVHASLDK
TguHbAD      --DMS------Q-----GSDQVRGHGKKVMAALSNAVKNLDNLS---QALSELSNLHAYNLR-VDPVNFKFLSQCLQVTLATRLGKE-YSP-EVHSAVDK
TguHbE       -GNMS------SPTAVLGNPMVRAHGKKVLTSFGEAVRNMDSVK---KCFAQLSKLHCEKLH-VDPENFRLLGDVLVVVLASHFGKE-FTP-ACQAAWQK
TguMb        -KGLK------TPDAMKGSEDLKKHGVTVLTQLGKILKAKGNHE---AELKPLAQTHATKHK-IPVKYLEFISEVIIKVLAEKHAAD-FGA-DAQAAMKK
TguNgb       CKQFA------SPHECLSAPEFLDHIRKVMLVIDAAVSHLENLSCLEEYLCNLGKKH-QAVG-VKVESFSTVGESLLYMREEKPGAA-FSP-EVQGGWSK
TniCygb1     -KHME------EPEEMQQSVQLRKHAHRVMTALNTLVESLDNSDRVASVLKSVGRAHALKHN-VDPKYFKILSGVILEVLGEAFTEI-ITA-EVASAWTK
TniGbX       -RDVE------DLERLRSSRELRAHGLRVMSFIEKSVARLDQQDRLEALAVELGKSH-YHYN-APPKYYSYVGAEFICAVQPILKER-FTS-ELEEAWKT
TniMb        -VGI-------AQSELAGNAAVSAHGATVLKKLGELLKAKGNHA---AILQPLANSHATKHK-IPIKNFKLIAEVIGKVMAEKAGLD---T-AGQQALRN
TniNgb       -TNCG------STQDCLSSPEFLEHVTKVMLVIDAAVSHLDDLHSLEDFLLNLGRKH-QAVG-VKPQSFAMVGESLLYMLQCSLGQA-YTA-SLRQAWLN
TruCygb1     -KDIE------EPEEMQRSIQLRKHAHRVMTTINTLVENLDDADAMASALKSVGRAHALRHK-VDPKYFKILSGVILEVLGEAFTEI-ITA-EVASAWTK
TruCygb2     -QDME------DPEEMERSSQLRHHACRVMNAINTVVENLHDPEKVSSVLALVGKAHAIKHK-VEPMYFKILCGVMLEVLCEAFPEF-FTA-DVRMVWAK
TruNgb       -TNCG------STQDCLSSPEFLEHVTKVMLVIDAAVSHLDDLHSLEDFLLNLGRKH-QAVG-VNPQSFATVGESLLYMLQCSLGQA-YTA-SLRQAWLN
TthMb        -AGI-------AQADIAGNAAVSAHGATVLKKLGELLKAKGSHA---AILKPLANSHATKHK-IPINNFKLISEVLVKVMHEKAGLD---A-GGQTALRN
XlaGbY       -KNIA------TLEEMQVNPGIRAHGKRVMGALNQVIQNLNDWEVVSSALTHLAQRHQDVHK-VGVNNFQLLFLVILTIFKEALGAD-FTP-EHCKSWEK
XlaHbA1      --DLS------H-----GSADLANHGGKVVNALGEAAKHINDLD---AALSTLSDLHAYNLR-VDPGNFKLLSHTIQVTLAIHFHKE-FDA-ATQAAWDK
XlaHbAT5     --DLS------H-----GSKDLRSHGGKVVKAIGNAATHIDDIP---HALSALSDLHAFKLK-VDPGNFKLLSHAIQVTLAIHFPAE-FNA-DAQAAWDK
XtrCygb      -KHME------DPLEMEGSVQLRKHARRVMGAVNSVVENLGDPEKITTVLSIVGKSHALKHK-VDPVYFKILTGVMLEVIAEEYAKD-FTP-DVQLAWNK
XtrGbX       -RDVD------DLQALRANKDLRAHGLRVLSFVEKSVARIADCARLEELALELGRSH-YRYN-APPRYYQYVGTEFISAVCPMLHDK-WTA-EVEEAWKG
XtrGbY       -KNIS------TLQEMQDNAGIRAHGKRVMGALNHVIENLKDWDAVCSALSHLAKRHQDVHK-VEVNNFELLFLVIISVFKEALGSG-FTP-EQSKSWEK
XtrHbA1      --DFS------E-----HSKHILAHGKKVSDALNEACNHLDNIA---GCLSKLSDLHAYDLR-VDPGNFPLLAHQILVVVAIHFPKQ-FDP-ATHKALDK
XtrHbB1      -GNLS------SIEAIFHNAAVATHGEKVLTSIGEAIKHMDDIK---GYYAQLSKYHSETLH-VDPYNFKRFCSCTIISMAQTLQED-FTP-ELQAAFEK
XtrHbB2      -GNLS------NVSAVSGNVKVKAHGNKVLSAVGSAIQHLDDVK---SHLKGLSKSHAEDLH-VDPENFKRLADVLVIVLAAKLGSA-FTP-QVQAVWEK
XtrNgb       SSHFS------KVQDCLSSAEFTEHIRKVMTVIDAAVSSLDCLSSLDEYLTSLGRKH-RAVG-VKLESFNTVGESLLFALESCLGDA-FTS-DTREAWSL
ZalGbE       -KGMD------SAEDMKQSDQVRGHGKKVFSAINDMVQHLDNSEAFLGIVTPLGKKHATQLK-IDPKNFRIICDIILQLMEEKFGG------DCKASFEK

AcaGbY       FFQVIQEEVEAAYDR-----------------------------------------
AcaMb        ALELFRNDMDRKYKELGFQGE-----------------------------------
AplGbE       VTNEICTHLNNVYKEAGW--------------------------------------
CanMb        VMAIIITDMEADYKELGFTE------------------------------------
CauMb1       VMEAVIGDIDTYYKEFGFAG------------------------------------
CauMb2       IMDCIIHDIDRYYKEIGFAG------------------------------------
CcaMb1       VMDVVIGDIDTYYKEIGFAG------------------------------------
CcaMb2       VMDCIIRDIDRYYKEIGFAG------------------------------------
CcrMb        ALELFRNDMAAKYKELGFQG------------------------------------
CliGbE       VTNEICSHLNNVYKEAGW--------------------------------------
CmiGbY       LFGVIYACLESHYKDAGFY-P-----------------------------------
CmyGbE       VTNEICTRLNNAYKEAGW--------------------------------------
CpiCygb      VKSLIYTHVTAAYKEVGWV-QYPNSTM-----------------------------
CpiGbE       VTNEICTRLNNAYKEAGW--------------------------------------
CpiGbX       GSSSAVGPLPCCRWQRSRP-----------------------RLGGLDP---FILP
CpiGbY       LFGLLSEQINASYVSTSKS-------------------------------------
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CpiHbA        FLSAVGTVLTSKYR------------------------------------------
CpiHbaA       FLSAVGTVLTSKYR------------------------------------------
CpiHbaD       FLAAVSAVLAEKYR------------------------------------------
CpiHbB1       LVRVVAHALSYKYH------------------------------------------
CpiHbB2       LVSAVAHALALGYH------------------------------------------
CpiHbG        LAGVVAHALAHEYH------------------------------------------
CpiHbZ        FLSQISSVLTEKYR------------------------------------------
CpiMb         ALELFRNDMASKYKEFGFQG------------------------------------
CpiNgb        LYGSVVKAMSSGWDARKEG-E-----------------------------------
CraMb         VMAIIITDMEADYKELGFTE------------------------------------
CycrMb        ALELFRNDIAAKYKELGFHG------------------------------------
DreCygb1      LMGILYWQMNRVYAEVGWE----NSKK-----------------------------
DreCygb2      LMAALYWHITGAYTEVGWV-KLSSSAV-----------------------------
DreGbX        LFQYVTSIMREGFLEEERN-KRSNTQTSSRERPDKRSTAI----------------
DreHbAa       FFNNLALALSEKYR------------------------------------------
DreHbAe       FLSALALAMSEKYR------------------------------------------
DreHbAx       FLSAFSAVLAEKFR------------------------------------------
DreHbBa       FLAVVVSALCRQYH------------------------------------------
DreHbBe       FIAVAVSALGRQYH------------------------------------------
DreMb         VMDAVIGDIGGYYKEIGFAG------------------------------------
DreNgb        MYSIVVSAMTRGWAKNGEH-KSN---------------------------------
EpeMb         VMGIVIADLEANYKELGFTG------------------------------------
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FpeGbE        VTNEICTHLNNVYKEAGW--------------------------------------
FruMb         VMATIIADIDVTYKDLGFS-------------------------------------
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GgaNgb        LYSAVVKAMQRGWEVLPEG-D-----------------------------------
GgiMb         VMAVIIADMEADYKELGFTE------------------------------------
HsaCYGB       LRGLIYSHVTAAYKEVGWV-QQVPNATTPPATLPSSG------------------P
HsaHBA        FLASVSTVLTSKYR------------------------------------------
HsaHBB        VVAGVANALAHKYH------------------------------------------
HsaHBD        VVAGVANALAHKYH------------------------------------------
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HsaHBG        MVTGVASALSSRYH------------------------------------------
HsaHBZ        FLSVVSSVLTEKYR------------------------------------------
HsaMB         ALELFRKDMASNYKELGFQG------------------------------------
HsaNGB        LYGAVVQAMSRGWDGE----------------------------------------
IpuGbX        LFQYVTWLMRRGYNEEEEEAKRNNTVGSSRERPRQRNTAL----------------
LchCygb       LMSIICCHVTATYKEVGWG-QLSNSTM-----------------------------
LchGbE        VTDVLCTHLNHAYKEAGW--------------------------------------
LchGbX1       LFKYLTAVMKKGYYVEEKK-ININNALYTKIPNALSSNPVQNNL------------
LchGbX2       LFKYVTEVMKRGYLQEEKI-KRTMETVEPKQASRRANNAI----------------
LchGbY        MLSFTYDYLVSCYHKSSGP-------------------------------------
LchHbA1       FLALISEILFSKYR------------------------------------------
LchHbA2       FLYEVEKALFETYR------------------------------------------
LchHbB1       LLSVVVAALSREYH------------------------------------------
LchHbB2       FMALVIDSLSRQYN------------------------------------------
LchMb         ALSMIIQDMGGMYKEFGFKG------------------------------------
LchNgb        LYSFVVETMARGWGANGEN-KLN---------------------------------
LpaGbE1       VTDLLYEEIKSTY-------------------------------------------
LpaGbE2a      AVDVIYENISAAY-------------------------------------------
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LpaGbE2e      VMDVIYENIKAAY-------------------------------------------
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MangMb        ALELFRNDIATKYKELGFHG------------------------------------
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MniMb         VMTTIIADIEANYKELGFTG------------------------------------
MunGbE        VTNEICTHLNNAYKEAGW--------------------------------------
NcoMb         VMAVIIADMEADYKELGFTE------------------------------------
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OanHbW        LVGVVASALSSQYH------------------------------------------
OanMb         ALELFRNDMAAKYKEFGFQG------------------------------------
OanNgb        LYTAVVHAMSRGWGGE----------------------------------------
OlaCygb1      LLAILCCSIKAVYEELGWP-HLSNSTS-----------------------------
OlaCygb2      LMAAVYWHVTGAYTEVGWL-QVSSSAV-----------------------------
OlaHbA        FLAAVSLALSEKYR------------------------------------------
OlaHbB        FLAVVVSALGRQYH------------------------------------------
OlaMb         VMAGIIAEIEADYKELGFAG------------------------------------
OlaNgb        MYSIVVAAMSRGWAKNGED-KAD---------------------------------
PaeGbE1a      VTDVVCEQIKSTY-------------------------------------------
PaeGbE1b      VTDVVCEQIKSTY-------------------------------------------
PaeGbE1c      VTDVVCEQIKSTY-------------------------------------------
PaeGbE2a      VTDLIYEEIKAAY-------------------------------------------
PaeGbE2b      VTDLIYEEIKAAY-------------------------------------------
PaeGbE2c      VTDVMYEEIKAAY-------------------------------------------
PaeGbE2d      VTNLIYEEIKAAY-------------------------------------------
PanGbE1a      VTDVVCEQIKSTY-------------------------------------------
PanGbE1b      VTDVVCEQIKSTY-------------------------------------------
PanGbE2a      VTDLIYEEIKAAY-------------------------------------------
PanGbE2b      VTDLIYEEIKAAY-------------------------------------------
PanGbE2c      VTDLIYEEIKAAY-------------------------------------------
PanGbX        LFKYLISLMKKGFQEEEKT-HLINKSTYPKKQLISKMNFVKNNV------------
PanGbY        FYSLTYQQLEKCYSTCPSS-------------------------------------
PanHba1       FMCMLSCILAVKYR------------------------------------------
PanHba2       FLAAVSAVLTEKYR------------------------------------------
PanHba3       FFERVSSQLVSLYR------------------------------------------
PanHba4       GLECVSSELVSLYR------------------------------------------
PanHbb1       LMGVIAAGLSKQYH------------------------------------------
PanHbb2       LVAVISSALTREYH------------------------------------------
PanHbb3       LMVEIADGLSRQYH------------------------------------------
PanHbb4       LVAEVAAGLSRKYH------------------------------------------
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PanMb1       TLALIVQTLTKLYKELGK--------------------------------------
PanMb2       ALGGVCHSLEKLYKEV----------------------------------------
PanMb3       VLDVFSQSMTTLYGEV----------------------------------------
PanMb4       ALNQIANGLKDNYAKV----------------------------------------
PanMb5       ALKQIANTLKSNYAKV----------------------------------------
PanMb6a      AFDQIADGLKTQYQTV----------------------------------------
PanMb6b      AFDQIADGLKTQYQTV----------------------------------------
PanMb7       ALSQIANGLKANYAKV----------------------------------------
PcaMb        ALELFRKDIAAKYKELGYQG------------------------------------
PgeMb        VMAVIIADMEADYKELGFTE------------------------------------
PhuGbE       VTNEICTHLNNIYKEEGW--------------------------------------
PmaaHb1      LMSMICILLRSSY-------------------------------------------
PmaaHb10     LLSSICIHLKSAY-------------------------------------------
PmaaHb11     LLSIISILLKSQY-------------------------------------------
PmaaHb12     FLSQVVILLKFAY-------------------------------------------
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PmaaHb5a     LMSMICILLRSAY-------------------------------------------
PmaaHb5b     LMSMICILLRSAY-------------------------------------------
PmaaHb6      LLSLIIIELQSAY-------------------------------------------
PmaaHb7      LLTYICISLKVAY-------------------------------------------
PmaaHb8      LMSMICILLRSAY-------------------------------------------
PmaaHb9      FLSQVSILLKSQY-------------------------------------------
PmaaMb1      LLTTTCIGLKSAF-------------------------------------------
PmaaMb2      LLSIICIGLRSAF-------------------------------------------
PmaCygb      LLGTLCTEFENAYREEGVL-EQAAA-------------------------------
PmaGbX1      LFRYIAAVMKRGYLEEEAASNGVNTANYDRGQGNHGATAM----------------
PsiCygb      LKSLIYTHVTATYKEAD---REPSK-------------------------------
PsiGbE       VTNEICTRLNNAYKEAGW--------------------------------------
PsiGbX       GSGSAETSPSPG------------------------------------PLWFFIRP
PsiGbY       LFRLLFEQINTSYANASKS-------------------------------------
PsiHbaA      FMCAVSAVLTSKYR------------------------------------------
PsiHbaD      FMEAVCNVLTEKYR------------------------------------------
PsiHbB       LVGVVAHALAHQYH------------------------------------------
PsiHbG       LVAAVAHALALRYH------------------------------------------
PsiHbZ       FLSQISSVLTEKYR------------------------------------------
PsiMb        ALELFRNSMASKYKEFGFQG------------------------------------
PsiNgb       LYGAVVKAMSRGWDARKEG-E-----------------------------------
RnoCygb      LRGLIYSHVTAAYKEVGWV-QQVPNTTTLPATLPSSG------------------P
RnoMb        ALELFRNDIAAKYKELGFQG------------------------------------
SchMb        VMAAVIADLEANYKELGFSG------------------------------------
SjaMb        VMGVFIADMDANYKELGFSG------------------------------------
TalaMb       VMGIIIADLEANYKELGFTG------------------------------------
TalbMb       VMGIIIADLEANYKELGFSG------------------------------------
TguCygb      MKTLIYTHVTAAYKEVGWA-QYPTATL-----------------------------
TguGbE       VTNEICTHLNNIYKEEGW--------------------------------------
TguHbA       FLCAVGTVLTAKYR------------------------------------------
TguHbAD      FMSAVASVLAEKYR------------------------------------------
TguHbE       LVRVVAHALAHEYH------------------------------------------
TguMb        ALELFRNDMATKYKEFGFQG------------------------------------
TguNgb       LYNAVVKAMQRGWETLPEG-D-----------------------------------
TniCygb1     LLANMCCGIAAVYKEAGWT-ELSSSVE-----------------------------
TniGbX       LFQYVTGLMRKGHQEEGSR--QRHLALPPKDGPEKRTSAL----------------
TniMb        IMATIIADIDATYKELGFS-------------------------------------
TniNgb       MYSVVVASMSRGWAKNGED-KAD---------------------------------
TruCygb1     LLANMCCAVAAVYEEAGWT-KLSSSAE-----------------------------
TruCygb2     LMAAVYWHVTGAYTDVGWL-QVSSSAV-----------------------------
TruNgb       MYSVVVAAMSRGWAKNGED-KAD---------------------------------
TthMb        VMGIIIADLEANYKELGFSG------------------------------------
XlaGbY       LFSITYNFLDSCYTKSDS--------------------------------------
XlaHbA1      FLAEVATVLTSKYR------------------------------------------
XlaHbAT5     FLAVVSAVLVSKYR------------------------------------------
XtrCygb      LRSHLYSHVLSAYKEAGWT-QYPSNSV-----------------------------
XtrGbX       LFAYICTVMERGYQEEERR-HSDGRSLIDGLQGNKGLI------------------
XtrGbY       LFSITYKYLESCYANTDS--------------------------------------
XtrHbA1      FLVSVSNVLTSKYR------------------------------------------
XtrHbB1      LFAAIADALGKGYH------------------------------------------
XtrHbB2      LNATLVAALSHGYF------------------------------------------
XtrNgb       LYANVVQSMSRGWHRDSQE-QREGI-------------------------------
ZalGbE       VTNEICTYLNNIYKEEGW--------------------------------------

;

End;

begin mrbayes;

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7519,25.3635,2.4365,1.7833,2.9635,6.0617,2.9314,16.6574,6.4234,0.234,3.8184,7.3241,11.1216,0.4882,1.2907,1.8118,17.597
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lset rates=gamma;
mcmc ngen=5000000 printfreq=1000 samplefreq=1000 nchains=4 savebrlens=yes;
End;
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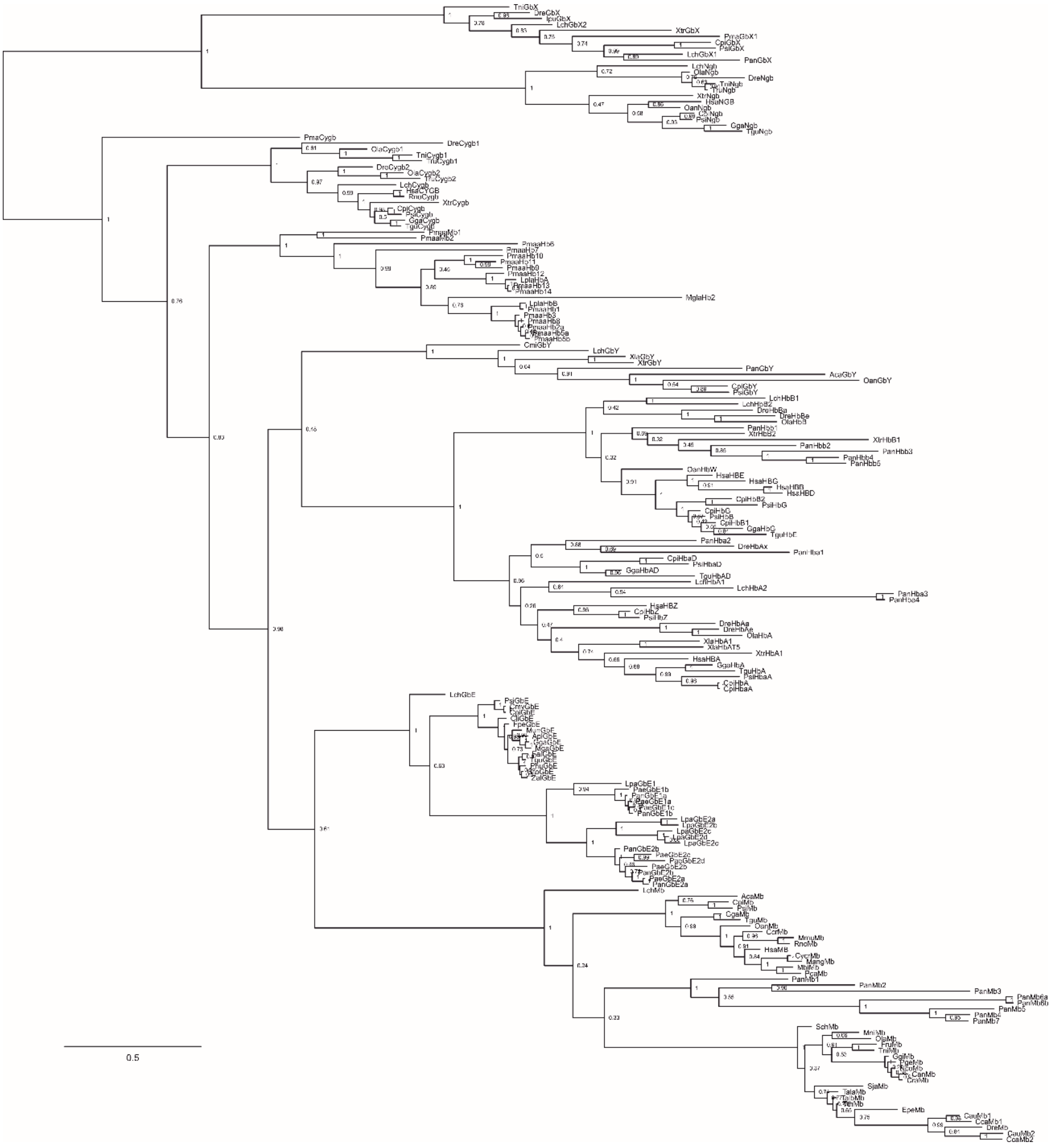
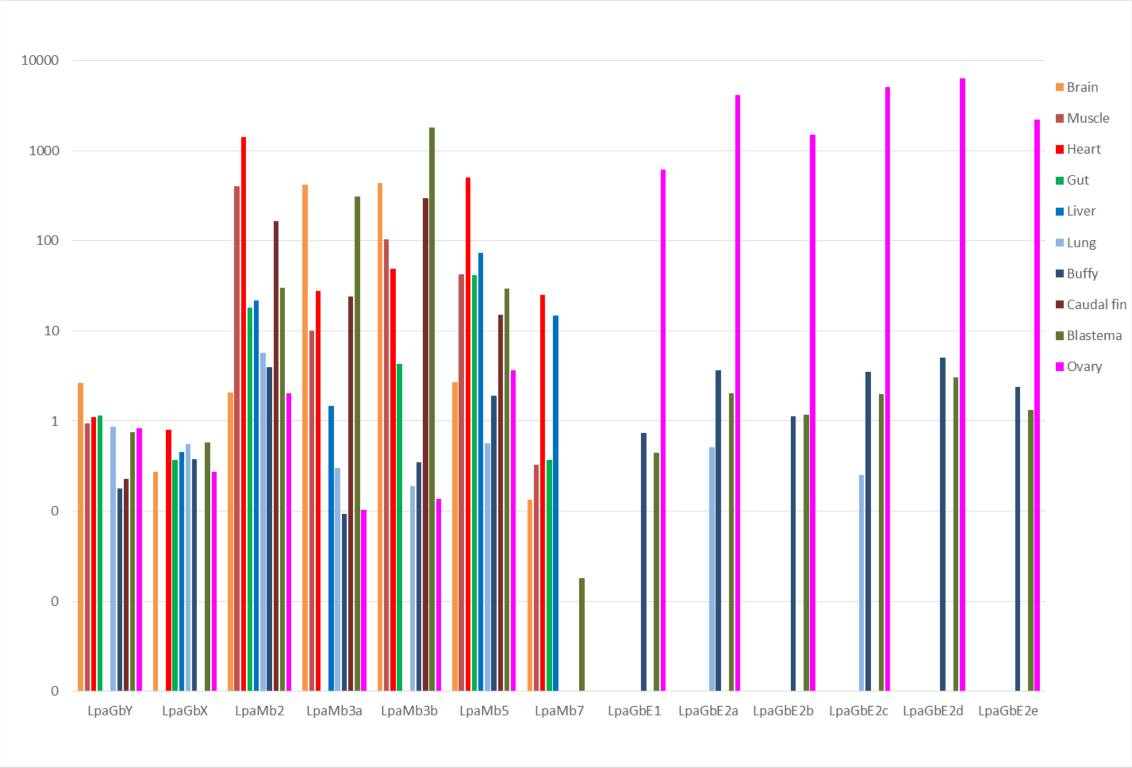
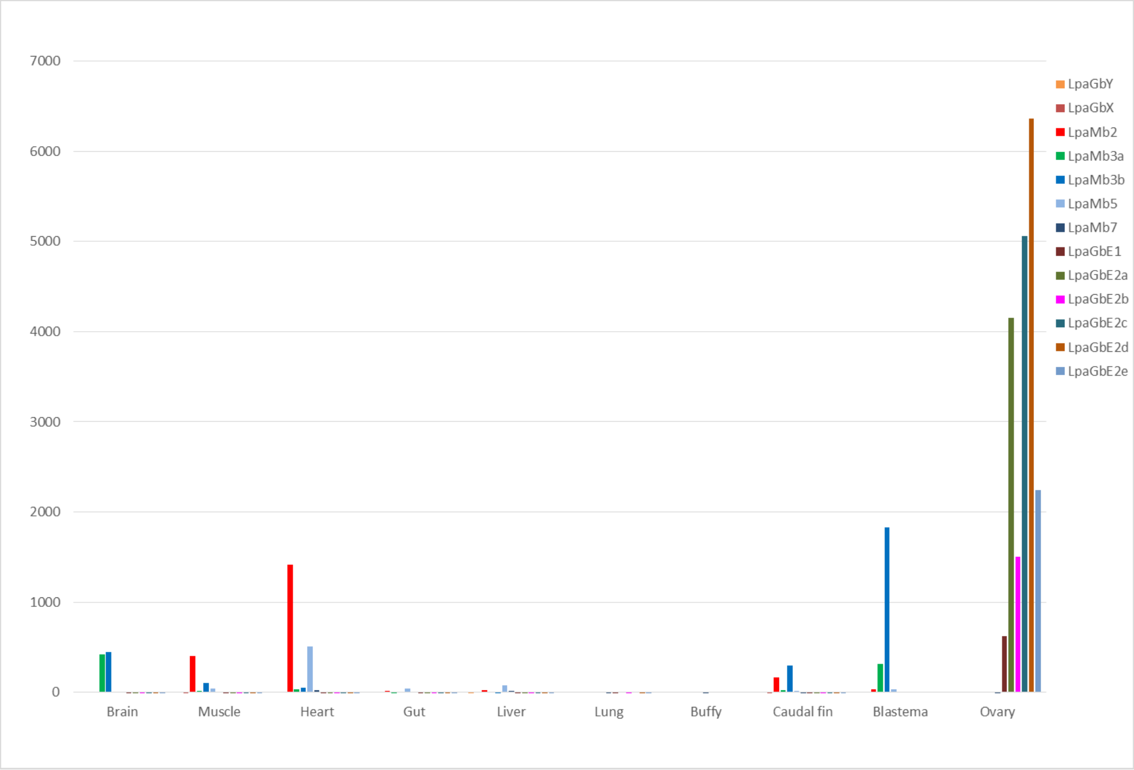
Supplemental Information Fig. IV.3. Multiple sequence alignment (Nexus-format) of the globin sequences used for phylogenetic studies.



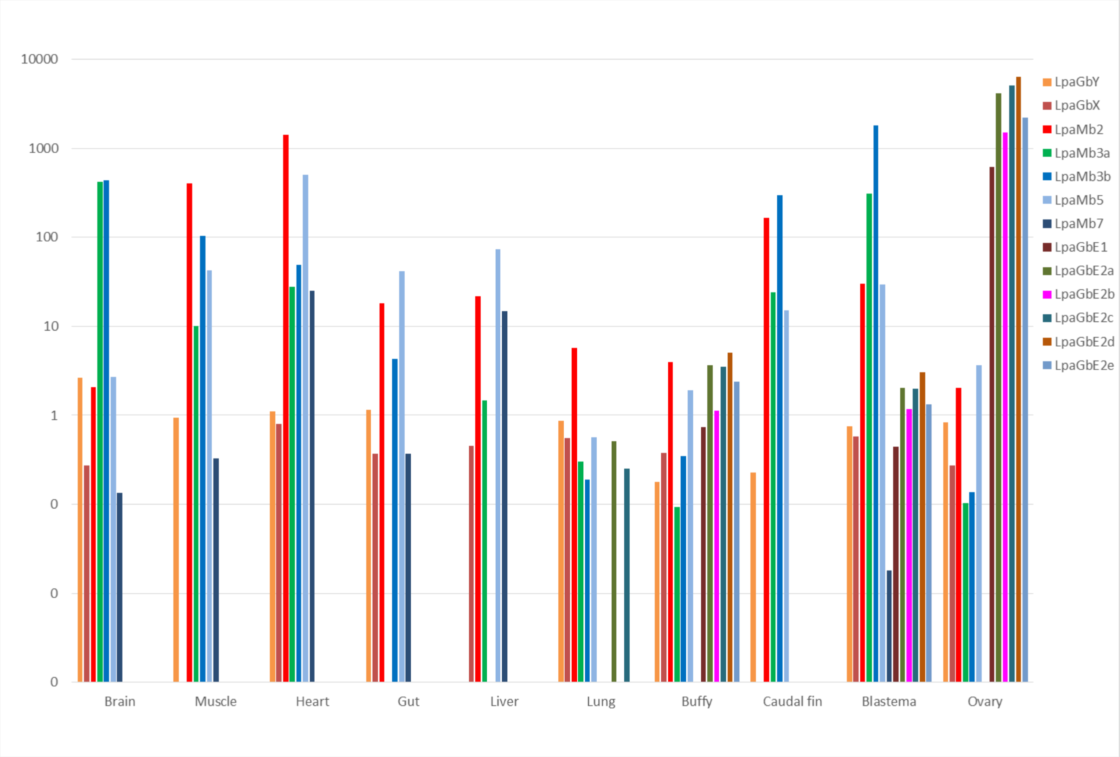
Supplemental Information Fig. IV.4. Bayesian phylogenetic tree of vertebrate globins. Tree reconstruction was carried out with the amino sequences assuming the LG model. The bar represents 0.1 PAM distance. The numbers at the nodes are posterior probabilities. For the abbreviations and accession numbers, see Supplemental Information Table 2.



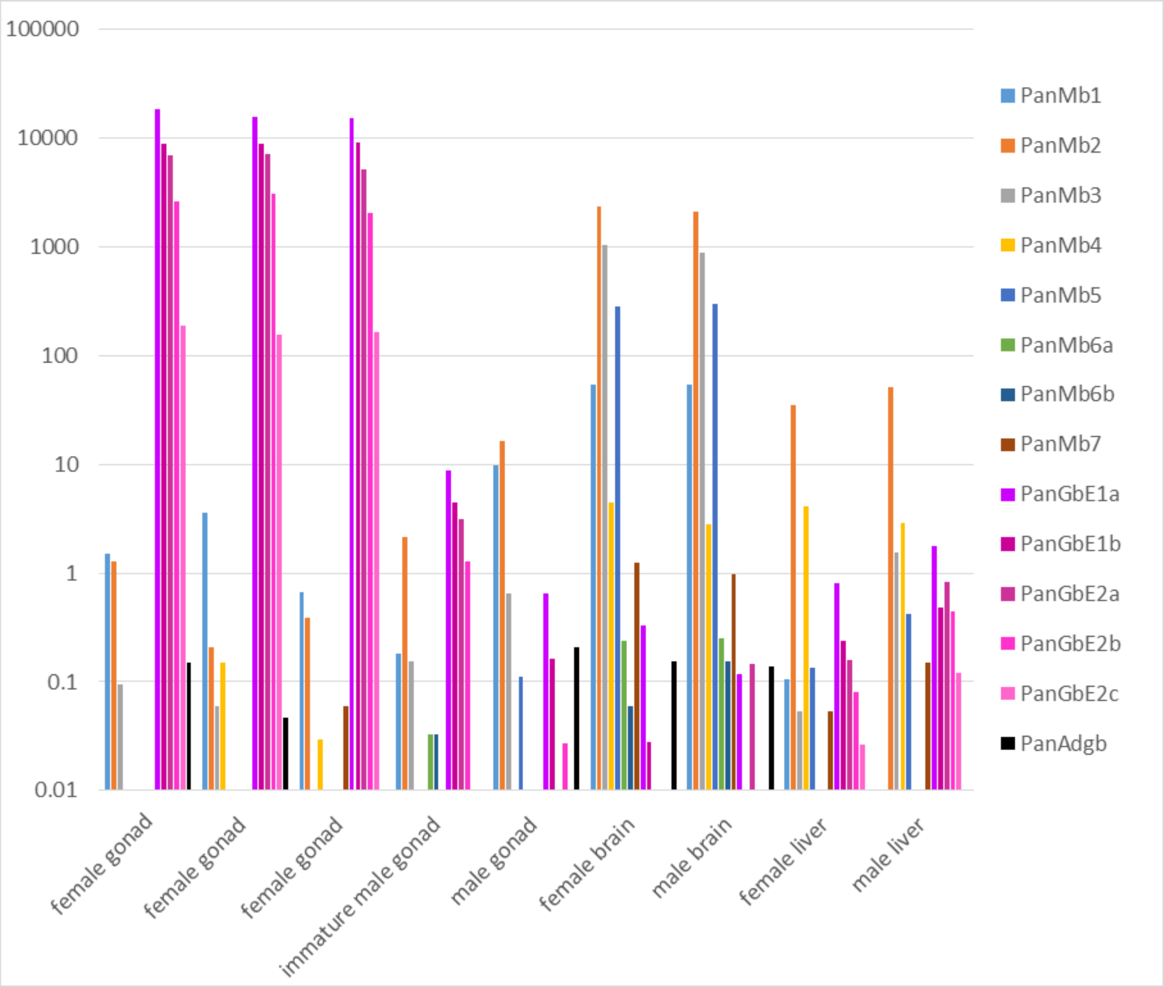
Supplemental Information Fig. IV.5. Expression of the *Mb* and *GbE* genes in selected *L. paradoxa* tissues, as estimated by RNA-Seq. The mRNA levels are displayed as RPKM in log-scale values. Transcriptome accession numbers are given in Supplemental Information Table 1, the copy numbers in Supplemental Information Table 3.



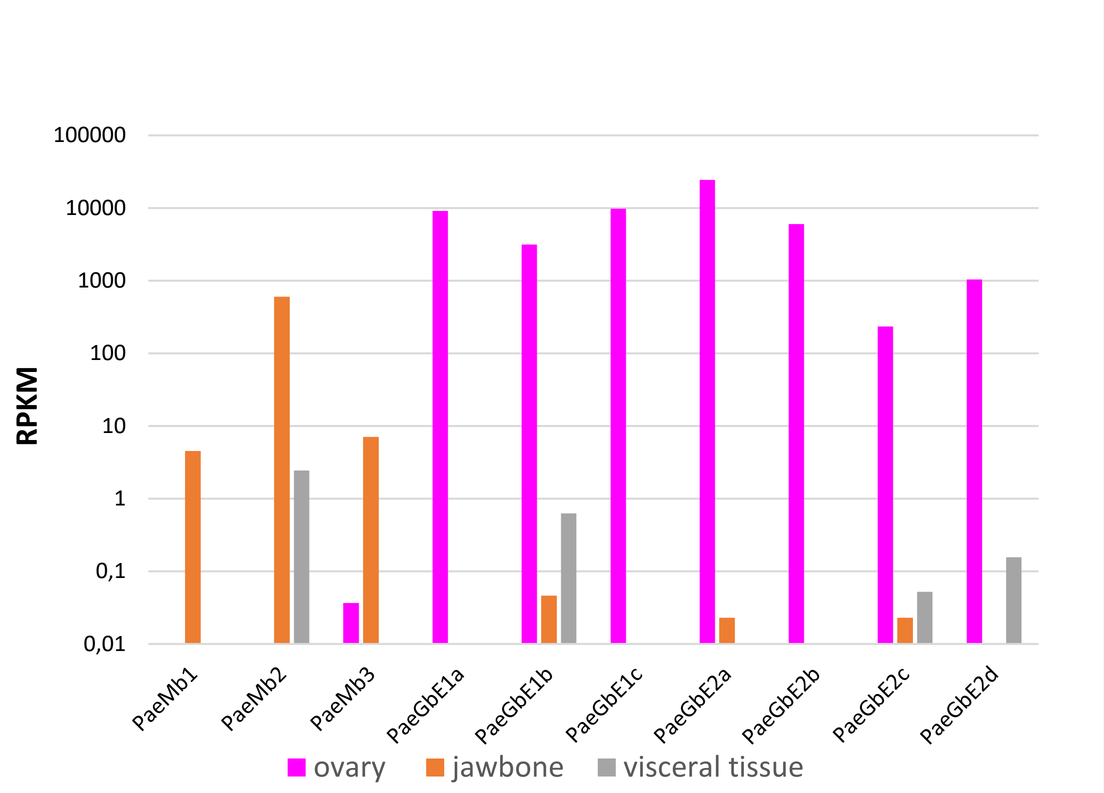
Supplemental Information Fig. IV.6. Tissue-specific expression of the *Mb* and *GbE* genes in *L. paradoxa*, as estimated by RNA-Seq. The mRNA levels are displayed as RPKM values. Transcriptome accession numbers are given in Supplemental Information Table 1, the copy numbers in Supplemental Information Table 3. Log-scale data are presented in Supplemental Information Fig. 7.



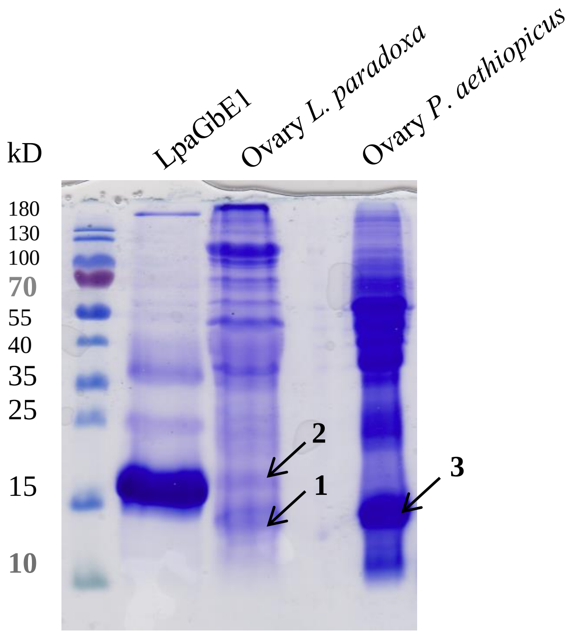
Supplemental Information Fig. IV.7. Tissue-specific expression of the *Mb* and *GbE* genes in *L. paradoxa*, as estimated by RNA-Seq. The mRNA levels are displayed as RPKM in log-scale values. Transcriptome accession numbers are given in Supplemental Information Table 1, the copy numbers in Supplemental Information Table 3.



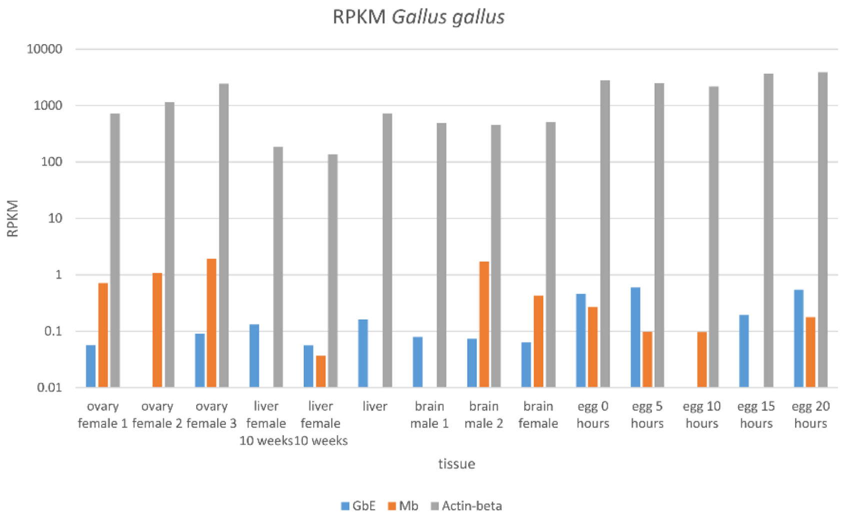
Supplemental Information Fig. IV.8. Expression of the *Mb* and *GbE* genes in selected *P. annectens* tissues, as estimated by RNA-Seq. The mRNA levels are displayed as RPKM values in log-scale. Transcriptome accession numbers are given in Table S1. Note the dominant expression of *GbE* in the ovary.



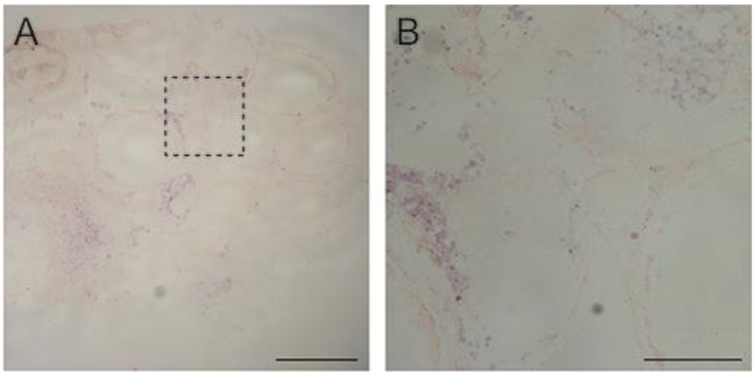
Supplemental Information Fig. IV.9. Expression of *Mb* and *GbE* genes in selected *P. aethiopicus* tissues, as estimated by RNA-Seq. The mRNA levels are displayed as log-scale RPKM values in log-scale. Transcriptome accession numbers are given in Supplemental Information Table 1.



Supplemental Information Fig. IV.10. SDS-PAGE gel electrophoresis of recombinantly expressed GbE1 of *L. paradoxa* (lane 1) and proteins from the ovaries of *L. paradoxa* (lane 2) and *P. aethiopicus* (lane 4). The numbers indicate the bands excised for mass spectrometry.



Supplemental Information Fig. IV.11. RNA-Seq of *Mb*, *GbE* and β-actin genes in chicken tissues. The mRNA levels are RPKM values in log-scale.



Supplemental Information Fig. IV.12. *In situ* hybridization of *GbE1* sense control probe. (A) sense probe showed no specific signal in *L. paradoxa* ovary sections. (B) zoom in of a region denoted in a dashed box in A. Scale bar: 2 mm (A) and 0.5 mm (B).

Supplemental Information Table IV.1. List of lungfish SRA data sets used in this study.

Run	Study	BioProject	BioSample	Experiment	Instrument	sex	tissue	species
SRR3632086	SRP076182	PRJNA317232	SAMN04601251	SRX1823854	Illumina HiSeq 2000	n.d.	muscle	*Lepidosiren paradoxa*
SRR3632085	SRP076182	PRJNA317232	SAMN04601250	SRX1823853	Illumina HiSeq 2000	n.d.	gut	*Lepidosiren paradoxa*
SRR3632084	SRP076182	PRJNA317232	SAMN04601249	SRX1823852	Illumina HiSeq 2000	n.d.	heart	*Lepidosiren paradoxa*
SRR3632083	SRP076182	PRJNA317232	SAMN04601248	SRX1823851	Illumina HiSeq 2000	n.d.	head	*Lepidosiren paradoxa*
SRR3632082	SRP076182	PRJNA317232	SAMN04601247	SRX1823850	Illumina HiSeq 2000	n.d.	brain	*Lepidosiren paradoxa*
SRR3632081	SRP076182	PRJNA317232	SAMN04601246	SRX1823849	Illumina HiSeq 2000	n.d.	gonad	*Lepidosiren paradoxa*
SRR3632080	SRP076182	PRJNA317232	SAMN04601245	SRX1823848	Illumina HiSeq 2000	n.d.	liver	*Lepidosiren paradoxa*
SRR3632079	SRP076182	PRJNA317232	SAMN04601244	SRX1823847	Illumina HiSeq 2000	n.d.	caudal fin	*Lepidosiren paradoxa*
SRR2895276	SRP065764	PRJNA301089	SAMN04235701	SRX1411327	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895273	SRP065764	PRJNA301089	SAMN04235701	SRX1411326	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895270	SRP065764	PRJNA301089	SAMN04235701	SRX1411325	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895265	SRP065764	PRJNA301089	SAMN04235701	SRX1411324	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895261	SRP065764	PRJNA301089	SAMN04235701	SRX1411322	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895255	SRP065764	PRJNA301089	SAMN04235701	SRX1411321	Illumina HiSeq 2000	n.d.	blastema	*Lepidosiren paradoxa*
SRR2895254	SRP065764	PRJNA301089	SAMN04235701	SRX1411314	Illumina HiSeq 2500	n.d.	blastema	*Lepidosiren paradoxa*
SRR1693787	SRP050575	PRJNA269317	SAMN03253061	SRX796494	Illumina HiSeq 2000	n.d.	kidney,lung,brain, spleen,heart,liver	*Lepidosiren paradoxa*
SRR7515656	SRP153183	PRJNA477294	SAMN04235701	SRX4385751	Illumina HiSeq 2500	female	ovary	*Lepidosiren paradoxa*
SRR8167646	SRP153183	PRJNA477294	SAMN04235701	SRX4988299	Illumina HiSeq 2500	n.d.	buffy	*Lepidosiren paradoxa*
SRR8167645	SRP153183	PRJNA477294	SAMN04235701	SRX4988300	Illumina HiSeq 2500	n.d.	brain	*Lepidosiren paradoxa*
SRR8167644	SRP153183	PRJNA477294	SAMN04235701	SRX4988301	Illumina HiSeq 2500	n.d.	lung	*Lepidosiren paradoxa*
SRR505726	SRP013624	PRJNA164839	SAMN01041868	SRX152530	Illumina HiSeq 2000	n.d.	brain	*Protopterus annectens*
SRR505725	SRP013624	PRJNA164839	SAMN01041868	SRX152530	Illumina HiSeq 2000	n.d.	brain	*Protopterus annectens*
SRR505724	SRP013624	PRJNA164839	SAMN01041869	SRX152529	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR505723	SRP013624	PRJNA164839	SAMN01041870	SRX152531	Illumina HiSeq 2000	n.d.	kidney	*Protopterus annectens*
SRR505722	SRP013624	PRJNA164839	SAMN01041870	SRX152531	Illumina HiSeq 2000	n.d.	kidney	*Protopterus annectens*
SRR505721	SRP013624	PRJNA164839	SAMN01041869	SRX152529	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR2028027	SRP057960	PRJNA282925	SAMN03580842	SRX1016237	Illumina HiSeq 2000	male	gonad	*Protopterus annectens*
SRR2028021	SRP057960	PRJNA282925	SAMN03580841	SRX1016236	Illumina HiSeq 2000	female	liver	*Protopterus annectens*
SRR2028020	SRP057960	PRJNA282925	SAMN03580839	SRX1016234	Illumina HiSeq 2000	female	brain	*Protopterus annectens*
SRR2028017	SRP057960	PRJNA282925	SAMN03580843	SRX1016238	Illumina HiSeq 2000	male	gonad	*Protopterus annectens*
SRR2028000	SRP057960	PRJNA282925	SAMN03580840	SRX1016235	Illumina HiSeq 2000	male	liver	*Protopterus annectens*

SRR2027980	SRP057960	PRJNA282925	SAMN03580844	SRX1016241	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*
SRR2027979	SRP057960	PRJNA282925	SAMN03580844	SRX1016240	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*
SRR2027978	SRP057960	PRJNA282925	SAMN03580844	SRX1016239	Illumina HiSeq 2000	female	gonad	*Protopterus annectens*
SRR2027914	SRP057960	PRJNA282925	SAMN03580838	SRX1016233	Illumina HiSeq 2000	male	brain	*Protopterus annectens*
SRR1685666	SRP044127	PRJNA254214	SAMN02902907	SRX790602	Illumina HiSeq 2000	n.d.	liver	*Protopterus annectens*
SRR5114770	SRP095206	PRJNA357627	SAMN06146196	SRX2426781	Illumina HiSeq 1500	n.d.	developing jaw/ mandible	*Protopterus aethiopicus*
SRR5997828	SRP116672	PRJNA398732	SAMN07519109	SRX3153334	Illumina HiSeq 2000	n.d.	viscera mixture	*Protopterus aethiopicus*
SRR7240708	SRP044127	PRJNA473927	SAMN09288591	SRX4146489	Illumina NextSeq 500	female	ovary	*Protopterus aethiopicus*
SRR4897316	SRP092419	PRJNA352091	SAMN05966305	SRX2318355	Illumina HiSeq 2500	female	ovary	*Gallus gallus*
SRR5412257	SRP102989	PRJNA381064	SAMN06679865	SRX2704305	Illumina HiSeq 2500	female	ovary	*Gallus gallus*
SRR5412258	SRP102989	PRJNA381064	SAMN06679864	SRX2704306	Illumina HiSeq 2500	female	ovary	*Gallus gallus*
SRR6756988	SRP133195	PRJNA434773	SAMN08574267	SRX3729595	Illumina HiSeq 4000	female	liver	*Gallus gallus*
SRR6756992	SRP133195	PRJNA434773	SAMN08574268	SRX3729591	Illumina HiSeq 4000	female	liver	*Gallus gallus*
SRR6844900	SRP135813	PRJNA438519	SAMN08719874	SRX3800311	HiSeq X Ten	n.d.	liver	*Gallus gallus*
SRR5412243	SRP102989	PRJNA381064	SAMN06679879	SRX2704291	Illumina HiSeq 2500	male	brain	*Gallus gallus*
SRR5412244	SRP102989	PRJNA381064	SAMN06679878	SRX2704292	Illumina HiSeq 2500	male	brain	*Gallus gallus*
SRR5412242	SRP102989	PRJNA381064	SAMN06679880	SRX2704290	Illumina HiSeq 2500	female	brain	*Gallus gallus*
ERR753794	ERP009492	PRJEB8414	SAMEA3235032	ERX697515	Illumina Genome Analyzer IIx	n.d.	egg 0 hours	*Gallus gallus*
ERR753795	ERP009492	PRJEB8414	SAMEA3235033	ERX697516	Illumina Genome Analyzer IIx	n.d.	egg 5 hours	*Gallus gallus*
ERR753791	ERP009492	PRJEB8414	SAMEA3235029	ERX697512	Illumina Genome Analyzer IIx	n.d.	egg 10 hours	*Gallus gallus*
ERR753792	ERP009492	PRJEB8414	SAMEA3235030	ERX697513	Illumina Genome Analyzer IIx	n.d.	egg 15 hours	*Gallus gallus*
ERR753793	ERP009492	PRJEB8414	SAMEA3235031	ERX697514	Illumina Genome Analyzer IIx	n.d.	egg 20 hours	*Gallus gallus*

Supplemental Information Table IV.2. List of globin sequences used in this study. The EMBL/GenBank accession numbers of the nucleotides are given, if available.

Abbreviation	**Species**	**common name**	**accession no.**
AcaGbY	*Anolis carolinensis*	anole lizard	NW_003341080
AcaMb	*Anolis carolinensis*	green anole	XM_003220932
AplGbE	*Anas platyrhynchos*	mallard	XM_005012200
CanMb	*Cryodraco antarcticus*	long-fingered icefish	U71056
CauMb1	*Carassius auratus*	goldfish	AM747267
CauMb2	*Carassius auratus*	goldfish	AM747268
CcaMb1	*Cyprinus carpio*	common carp	KC342292
CcaMb2	*Cyprinus carpio*	common carp	DQ338464
CcrMb	*Condylura cristata*	star-nosed mole	NM_001287785
CliGbE	*Columba livia*	common pigeon	XM_005507829
CmiGbY	*Callorhinchus milii*	elephant shark	NM_001292790
CmyGbE	*Chelonia mydas*	green sea turtle	XM_007064067
CpiCygb	*Chrysemys picta bellii*	Western painted turtle	XM_005297540
CpiGbE	*Chrysemys picta bellii*	Western painted turtle	XM_005293060
CpiGbX	*Chrysemys picta bellii*	Western painted turtle	XM_005293187
CpiGbY	*Chrysemys picta bellii*	Western painted turtle	XM_005306194
CpiHbaA	*Chrysemys picta bellii*	Western painted turtle	XM_005306158
CpiHbaD	*Chrysemys picta bellii*	Western painted turtle	XM_005306157
CpiHbB1	*Chrysemys picta bellii*	Western painted turtle	XM_005290010
CpiHbB2	*Chrysemys picta bellii*	Western painted turtle	XM_005290009
CpiHbG	*Chrysemys picta bellii*	Western painted turtle	XM_005290008
CpiHbZ	*Chrysemys picta bellii*	Western painted turtle	XM_005306148
CpiMb	*Chrysemys picta bellii*	Western painted turtle	XM_005300826
CpiNgb	*Chrysemys picta bellii*	Western painted turtle	XM_005301643
CraMb	*Chionodraco rastrospinosus*	ocellated icefish	U70871
CycrMb	*Cystophora cristata*	hooded seal	KC524751
DreCygb1	*Danio rerio*	zebrafish	BC165894
DreCygb2	*Danio rerio*	zebrafish	AJ635229

DreGbX	*Danio rerio*	zebrafish	AJ635194
DreHbAa	*Danio rerio*	zebrafish	AY325264
DreHbAe	*Danio rerio*	zebrafish	BC164447
DreHbAx	*Danio rerio*	zebrafish	AL915033
DreHbBa	*Danio rerio*	zebrafish	BC164283
DreHbBe	*Danio rerio*	zebrafish	NM_001097585
DreMb	*Danio rerio*	zebrafish	AY337025
DreNgb	*Danio rerio*	zebrafish	BC059416
EpeMb	*Euthynnus pelamis*	skipjack tuna	AF291837
FalGbE	*Ficedula albicollis*	collared flycatcher	XM_005039642
FpeGbE	*Falco peregrinus*	peregrine falcon	XM_005237389
GfoGbE	*Geospiza fortis*	medium ground-finch	XM_005421887
GgaCygb	*Gallus gallus*	chicken	NM_001008789
GgaGbE	*Gallus gallus*	chicken	NM_001008786
GgaHbA	*Gallus gallus*	chicken	NM_001004376
GgaHbAD	*Gallus gallus*	chicken	CR338842
GgaHbG	*Gallus gallus*	chicken	M73995
GgaMb	*Gallus gallus*	chicken	XM_003202347
GgaNgb	*Gallus gallus*	chicken	NM_001031551
GgiMb	*Gobionotothen gibberifron*	humped rockcod	U71057
HsaCYGB	*Homo sapiens*	man	AJ315162
HsaHBA	*Homo sapiens*	man	AF105974
HsaHBB	*Homo sapiens*	man	NM_000518
HsaHBD	*Homo sapiens*	man	NM_000519
HsaHBE	*Homo sapiens*	man	NM_005330
HsaHBG	*Homo sapiens*	man	NM_000559
HsaHBZ	*Homo sapiens*	man	M24173
HsaMB	*Homo sapiens*	man	NM_203377
HsaNGB	*Homo sapiens*	man	AB463927
IpuGbX	*Ictalurus punctatus*	channel catfish	CK416201
LchCygb	*Latimeria chalumnae*	coelacanth	XM_005993205
LchGbE	*Latimeria chalumnae*	coelacanth	XM_006011781

LchGbX1	*Latimeria chalumnae*	coelacanth	XM_005987904
LchGbX2	*Latimeria chalumnae*	coelacanth	XM_006012915
LchGbY	*Latimeria chalumnae*	coelacanth	XM_005990799
LchHbA1	*Latimeria chalumnae*	coelacanth	XM_006011045
LchHbA2	*Latimeria chalumnae*	coelacanth	XM_006011046
LchHbB1	*Latimeria chalumnae*	coelacanth	XM_006011047
LchHbB2	*Latimeria chalumnae*	coelacanth	XM_006011048
LchMb	*Latimeria chalumna*	coelacanth	XM_006011146
LchNgb	*Latimeria chalumnae*	coelacanth	XM_005986619
LpaGbE1	*Lepidosiren paradoxa*	South American lungfish	LR030441
LpaGbE2a	*Lepidosiren paradoxa*	South American lungfish	LR030442
LpaGbE2b	*Lepidosiren paradoxa*	South American lungfish	LR030443
LpaGbE2c	*Lepidosiren paradoxa*	South American lungfish	LR030444
LpaGbE2d	*Lepidosiren paradoxa*	South American lungfish	LR030445
LpaGbE2e	*Lepidosiren paradoxa*	South American lungfish	LR030446
LplaHbA	*Lampetra zanandreai*	Po brook lamprey	Z24746
LplaHbB	*Lampetra zanandreai*	Po brook lamprey	Z24747
MangMb	*Mirounga angustirostris*	Northern elephant seal	KC524754
MbiMb	*Mesoplodon bidens*	Sowerby's beaked whale	KC524765
MgaGbE	*Meleagris gallopavo*	turkey	XM_003202331
MglaHb2	*Myxine glutinosa*	Atlantic hagfish	AF157494
MmuMb	*Mus musculus*	mouse	AK137456
MniMb	*Makaira nigricans*	Atlantic blue marlin	AF291833
MunGbE	*Melopsittacus undulatus*	budgerigar	XM_005150295
NcoMb	*Notothenia coriiceps*	black rockcod	NM_001303294
OanGbY	*Ornithorhynchus anatinus*	platypus	genome
OanHbW	*Ornithorhynchus anatinus*	platypus	genome
OanMb	*Ornithorhynchus anatinus*	platypus	XM_001513063
OanNgb	*Ornithorhynchus anatinus*	platypus	XM_001508367
OlaCygb1	*Oryzias latipes*	medaka	NM_001104767
OlaCygb2	*Oryzias latipes*	medaka	NM_001104768
OlaHbA	*Oryzias latipes*	medaka	BAC20295

OlaHbB	*Oryzias latipes*	medaka	AB080120
OlaMb	*Oryzias latipes*	medaka	BJ883657
OlaNgb	*Oryzias latipes*	medaka	DK002855
PaeGbE1a	*Protopterus aethiopicus*	marbled lungfish	LR030452
PaeGbE1b	*Protopterus aethiopicus*	marbled lungfish	LR030453
PaeGbE1c	*Protopterus aethiopicus*	marbled lungfish	LR030454
PaeGbE2a	*Protopterus aethiopicus*	marbled lungfish	LR030455
PaeGbE2b	*Protopterus aethiopicus*	marbled lungfish	LR030456
PaeGbE2c	*Protopterus aethiopicus*	marbled lungfish	LR030457
PaeGbE2d	*Protopterus aethiopicus*	marbled lungfish	LR030458
PanGbE1a	*Protopterus annectens*	West African lungfish	LR030447
PanGbE1b	*Protopterus annectens*	West African lungfish	LR030448
PanGbE2a	*Protopterus annectens*	West African lungfish	LR030449
PanGbE2b	*Protopterus annectens*	West African lungfish	LR030450
PanGbE2c	*Protopterus annectens*	West African lungfish	LR030451
PanGbX	*Protopterus annectens*	West African lungfish	TBA
PanGbY	*Protopterus annectens*	West African lungfish	TBA
PanHba1	*Protopterus annectens*	West African lungfish	TBA
PanHba2	*Protopterus annectens*	West African lungfish	TBA
PanHba3	*Protopterus annectens*	West African lungfish	TBA
PanHba4	*Protopterus annectens*	West African lungfish	TBA
PanHbb1	*Protopterus annectens*	West African lungfish	TBA
PanHbb2	*Protopterus annectens*	West African lungfish	TBA
PanHbb3	*Protopterus annectens*	West African lungfish	TBA
PanHbb4	*Protopterus annectens*	West African lungfish	TBA
PanHbb5	*Protopterus annectens*	West African lungfish	TBA
PanMb1	*Protopterus annectens*	West African lungfish	LT604990
PanMb2	*Protopterus annectens*	West African lungfish	LT604991
PanMb3	*Protopterus annectens*	West African lungfish	LT604992
PanMb4	*Protopterus annectens*	West African lungfish	LT604993
PanMb5	*Protopterus annectens*	West African lungfish	LT604994
PanMb6a	*Protopterus annectens*	West African lungfish	LT604995

PanMb6b	*Protopterus annectens*	West African lungfish	LT604996
PanMb7	*Protopterus annectens*	West African lungfish	LT604997
PcaMb	*Physeter catodon*	sperm whale	NM_001290722
PgeMb	*Pseudochaenichthys georgianus*	South Georgia icefish	U71055
PhuGbE	*Pseudopodoces humilis*	Tibetan ground-tit	XM_014256596
PmaaHb1	*Petromyzon marinus*	sea lamprey	P09967
PmaaHb10	*Petromyzon marinus*	sea lamprey	FD718926
PmaaHb11	*Petromyzon marinus*	sea lamprey	ENSPMAG00000001592
PmaaHb12	*Petromyzon marinus*	sea lamprey	genome
PmaaHb13	*Petromyzon marinus*	sea lamprey	genome
PmaaHb14	*Petromyzon marinus*	sea lamprey	genome
PmaaHb2a	*Petromyzon marinus*	sea lamprey	Q9I9I3
PmaaHb3	*Petromyzon marinus*	sea lamprey	P09968
PmaaHb5a	*Petromyzon marinus*	sea lamprey	P02208
PmaaHb5b	*Petromyzon marinus*	sea lamprey	ENSPMAG00000005354
PmaaHb6	*Petromyzon marinus*	sea lamprey	EG333697
PmaaHb7	*Petromyzon marinus*	sea lamprey	EE278870
PmaaHb8	*Petromyzon marinus*	sea lamprey	ENSPMAG00000005367
PmaaHb9	*Petromyzon marinus*	sea lamprey	ENSPMAG00000008540
PmaaMb1	*Petromyzon marinus*	sea lamprey	ENSPMAG00000006056
PmaaMb2	*Petromyzon marinus*	sea lamprey	EG021442
PmaCygb	*Petromyzon marinus*	sea lamprey	genome
PmaGbX1	*Petromyzon marinus*	sea lamprey	ENSPMAG00000007241
PsiCygb	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006136486
PsiGbE	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006127809
PsiGbX	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006131430
PsiGbY	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006124603
PsiHbaA	*Pelodiscus sinensis*	Chinese soft-shelled turtle	ENSPSIG00000011874
PsiHbaD	*Pelodiscus sinensis*	Chinese soft-shelled turtle	ENSPSIG00000012157
PsiHbB	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006130979
PsiHbG	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006130980

PsiHbZ	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006124534
PsiMb	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006137956
PsiNgb	*Pelodiscus sinensis*	Chinese soft-shelled turtle	XM_006117796
RnoCygb	*Rattus norvegicus*	rat	NM_130744
RnoMb	*Rattus norvegicus*	Norway rat	AF197916
SchMb	*Sarda chiliensis*	Pacific bonito	AF291834
SjaMb	*Scomber japonicus*	chub mackerel	AF291835
TalaMb	*Thunnus alalunga*	albacore	AF291832
TalbMb	*Thunnus albacares*	yellowfin tuna	AF291838
TguCygb	*Taeniopygia guttata*	zebra finch	XM_002195407
TguGbE	*Taeniopygia guttata*	zebra finch	XM_002196350
TguHbA	*Taeniopygia guttata*	zebra finch	DQ216719
TguHbAD	*Taeniopygia guttata*	zebra finch	DQ213486
TguHbE	*Taeniopygia guttata*	zebra finch	NM_001245112
TguMb	*Taeniopygia guttata*	zebra finch	XM_002199380
TguNgb	*Taeniopygia guttata*	zebra finch	XM_003962460
TniCygb1	*Tetraodon nigroviridis*	green spotted puffer	AJ635230
TniGbX	*Tetraodon nigroviridis*	green spotted puffer	AJ635193
TniMb	*Tetraodon nigroviridis*	spotted green pufferfish	CR660178
TniNgb	*Tetraodon nigroviridis*	green spotted puffer	AJ315609
TruCygb1	*Takifugu rubripes*	torafugu	XM_003964492
TruCygb2	*Takifugu rubripes*	torafugu	AJ635231
TruMb	*Takifugu rubripes*	torafugu	XM_003976046
TruNgb	*Takifugu rubripes*	torafugu	genome
TthMb	*Thunnus thynnus orientalis*	Pacific bluefin tuna	AF291836
XlaGbY	*Xenopus laevis*	African clawed frog	NM_001095686
XlaHbA1	*Xenopus laevis*	African clawed frog	X02796
XlaHbAT5	*Xenopus laevis*	African clawed frog	X02798
XtrCygb	*Xenopus tropicalis*	Western clawed frog	AJ635232
XtrGbX	*Xenopus tropicalis*	Western clawed frog	NM_001011196
XtrGbY	*Xenopus tropicalis*	Western clawed frog	XM_002941194
XtrHbA1	*Xenopus tropicalis*	Western clawed frog	BC088005

XtrHbB1	*Xenopus tropicalis*	Western clawed frog	NM_203528
XtrHbB2	*Xenopus tropicalis*	Western clawed frog	NM_001016495
XtrNgb	*Xenopus tropicalis*	Western clawed frog	NM_001030351
ZalGbE	*Zonotrichia albicollis*	white-throated sparrow	XM_005488706

Supplemental Information Table IV.3. RPKM of *GbY*, *GbX*, *Mb* and *GbE* genes in the transcriptomes from different lungfish (*L. paradoxa*) tissues used for expression estimation by RNA-seq.

	SRR8167645	SRR3632086	SRR3632084	SRR3632085	SRR3632080	SRR8167644	SRR8167646	SRR3632079	SRR2895254	SRR7515656
	Brain	**Muscle**	**Heart**	**Gut**	**Liver**	**Lung**	**Buffy**	**Caudal fin**	**Blastema**	**Ovary**
LpaGbY	2.63	0.93	1.11	1.16	0.00	0.88	0.18	0.23	0.75	0.84
LpaGbX	0.27	0.00	0.79	0.37	0.45	0.56	0.37	0.00	0.57	0.27
LpaMb2	2.09	404.68	1412.10	17.99	21.92	5.69	3.99	166.20	30.26	2.03
LpaMb3a	419.21	10.15	27.73	0.00	1.47	0.30	0.09	24.21	310.19	0.10
LpaMb3b	442.74	104.72	48.89	4.29	0.00	0.19	0.35	299.39	1826.12	0.14
LpaMb5	2.70	42.23	503.26	41.82	73.22	0.56	1.90	15.00	29.38	3.64
LpaMb7	0.13	0.33	25.12	0.37	14.95	0.00	0.00	0.00	0.02	0.00
LpaGbE1	0.00	0.00	0.00	0.00	0.00	0.00	0.73	0.00	0.44	623.12
LpaGbE2a	0.00	0.00	0.00	0.00	0.00	0.51	3.70	0.00	2.04	4153.06
LpaGbE2b	0.00	0.00	0.00	0.00	0.00	0.00	1.13	0.00	1.18	1498.12
LpaGbE2c	0.00	0.00	0.00	0.00	0.00	0.25	3.49	0.00	2.01	5061.83
LpaGbE2d	0.00	0.00	0.00	0.00	0.00	0.00	5.07	0.00	3.05	6364.72
LpaGbE2e	0.00	0.00	0.00	0.00	0.00	0.00	2.40	0.00	1.32	2241.18

Supplemental Information Table IV.4. RPKM of *Mb*, *GbE* and *Adgb* genes in the transcriptomes from different lungfish (*P. annectens*) tissues used for expression estimation by RNA-seq.

	SRR2027978	SRR2027979	SRR2027980	SRR2028027	SRR2028017	SRR2028020	SRR2027914	SRR2028021	SRR2028000
	female gonad	**female gonad**	**female gonad**	**immature male gonad**	**male gonad**	**female brain**	**male brain**	**female liver**	**male liver**
PanMb1	1.51	3.58	0.67	0.18	9.78	53.59	54.25	0.10	0.00
PanMb2	1.27	0.21	0.39	2.15	16.46	2378.25	2106.90	34.89	51.16
PanMb3	0.10	0.06	0.00	0.15	0.64	1039.06	891.26	0.05	1.56
PanMb4	0.00	0.15	0.03	0.00	0.00	4.47	2.80	4.15	2.88
PanMb5	0.00	0.00	0.00	0.00	0.11	282.55	298.36	0.13	0.43
PanMb6a	0.00	0.00	0.00	0.03	0.00	0.24	0.25	0.00	0.00
PanMb6b	0.00	0.00	0.00	0.03	0.00	0.06	0.16	0.00	0.00
PanMb7	0.00	0.00	0.06	0.00	0.00	1.26	0.97	0.05	0.15
PanGbE1a	18509.96	15819.15	15249.05	8.83	0.66	0.33	0.12	0.80	1.80
PanGbE1b	8990.94	8922.64	9225.27	4.49	0.16	0.03	0.00	0.24	0.48
PanGbE2a	6927.00	7200.72	5242.37	3.09	0.00	0.00	0.15	0.16	0.84
PanGbE2b	2658.76	3124.96	2035.23	1.27	0.03	0.00	0.00	0.08	0.45
PanGbE5	187.95	156.17	163.98	0.00	0.00	0.00	0.00	0.03	0.12
PanAdgb	0.15	0.05	0.00	0.00	0.21	0.16	0.14	0.00	0.00

Supplemental Information Table IV.5. RPKM of *GbY*, *GbX*, *Mb*, *GbE* and *Hb* genes in the transcriptomes from different lungfish (*P. aethiopicus*) tissues used for expression estimation by RNA-seq.

	SRR7240708	SRR5114770	SRR5997828
	Ovary	**Jawbone**	**Viscera**
PaeGbY	0.10	6.79	0.20
PaeGbX	0.10	1.04	0.29
PaeMb1	0.00	4.54	0.00
PaeMb2	0.00	603.20	2.43
PaeMb3	0.04	7.11	0.00
PaeGbE1a	9138.16	0.00	0.00
PaeGbE1b	3126.12	0.05	0.63
PaeGbE1c	9759.73	0.00	0.00
PaeGbE2a	24330.54	0.02	0.00
PaeGbE2b	6036.05	0.00	0.00
PaeGbE2c	234.41	0.02	0.05
PaeGbE2d	1036.76	0.00	0.16
PaeHba	0.00	0.00	0.00
PaeHbb3	15.97	283.66	671.21
PaeHbb4	0.00	0.00	0.00
PaeHbb5	50.73	619.42	1132.24

Supplemental Information Table IV.6. RPKM of *GbE, Mb* and *β-actin* genes in the transcriptomes from different chicken (*Gallus gallus*) tissues used for expression estimation by RNA-seq.

	SRR5412257	SRR5412258	SRR4897316	SRR6756988	SRR6756992	SRR6844900	SRR5412243	SRR5412244	SRR5412242	ERR753794	ERR753795	ERR753791	ERR753792	ERR753793
	ovary female 1	**ovary female 2**	**ovary female 3**	**liver female 10 weeks**	**liver female 10 weeks**	**liver**	**brain male 1**	**brain male 2**	**brain female 2**	**egg 0 hours**	**egg 5 hours**	**egg 10 hours**	**egg 15 hours**	**egg 20 hours**
GgaGbE	0.06	0.00	0.09	0.13	0.06	0.16	0.08	0.07	0.06	0.46	0.60	0.00	0.19	0.55
GgaMb	0.72	1.09	1.92	0.00	0.04	0.00	0.00	1.73	0.43	0.27	0.10	0.10	0.00	0.18
Gga β-actin	727.04	1156.21	2447.47	184.04	137.77	733.95	490.71	453.66	514.02	2803.80	2493.15	2186.35	3643.92	3904.20