Evolution of the *Tbx6/16* sub-family genes in vertebrates: insights from zebrafish

Supplementary Materials I

Daegwon Ahn, Kwan-Hee You, and Cheol-Hee Kim

Figure S1. Amino acid sequences of the T-box genes used in the phylogenetic analysis (in Figure 1 & Figure S3)

1) Human T-box genes with Genbank (mRNA) accession numbers

```
>TBX1  NM_080646 (variant A)
              MHFSTVTRDMEAFTASSLSSLGAAGGFPGAASPGADPYGPREPP
PPPPRYDPCAAAAPGAPGPPPPPHAYPFAPAAGAATSAAAEPEGPGASCAAAAKAPVK
KNAKVAGVSVQLEMKALWDEFNQLGTEMIVTKAGRRMFPTFQVKLFGMDPMADYMLLM
DFVPVDDKRYRYAFHSSSWLVAGKADPATPGRVHYHPDSPAKGAQWMKQIVSFDKLKL
TNNLLDDNGHIILNSMHRYQPRFHVVYVDPRKDSEKYAEENFKTFVFEETRFTAVTAY
QNHRITQLKIASNPFAKGFRDCDPEDWPRNHRPGALPLMSAFARSRNPVASPTQPSGT
EKGGHVLKDKEVKAETSRNTPEREVELLRDAGGCVNLGLPCPAECQPFNTQGLVAGRT
AGDRLC

>TBX2  NM_005994
              MREPALAASAMAYHPFHAPRPADFPMSAFLAAAQPSFFPALALP
PGALAKPLPDPGLAGAAAAAAAAAAAAAEAGLHVSALGPHPPAAHLRSLKSLEPEDEVE
DDPKVTLEAKELWDQFHKLGTEMVITKSGRRMFPPFKVRVSGLDKKAKYILLMDIVAA
DDCRYKFHNSRWMVAGKADPEMPKRMYIHPDSPATGEQWMAKPVAFHKLKLTNNISDK
HGFTILNSMHKYQPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKI
DNNPFAKGFRDTGNGRREKRKQLTLPSLRLYEEHCKPERDGAESDASSCDPPPAREPP
TSPGAAPSPLRLHRARAEEKSCAADSDPEPERLSEERAGAPLGRSPAPDSASPTRLTE
PERARERRSPERGKEPAESGGDGPFGLRSLEKERAEARRKDEGRKEAAEGKEQGLAPL
VVQTDSASPLGAGHLPGLAFSSHLHGQQFFGPLGAGQPLFLHPGQFTMGPGAFSAMGM
GHLLASVAGGGNGGGGGPGTAAGLDAGGLGPAASAASTAAPFPFHLSQHMLASQGIPM
PTFGGLFPYPYTYMAAAAAAAASALPATSAAAAAAAAAGSLSRSPFLGSARPRLRFSPY
QIPVTIPPSTSLLTTGLASEGSKAAGGNSREPSPLPELALRKVGAPSRGALSPSGSAK
EAANELQSIQRLVSGLESQRALSPGRESPK

>TBX3  NM_005996 (variant 1)
              MSLSMRDPVIPGTSMAYHPFLPHRAPDFAMSAVLGHQPPFFPAL
TLPPNGAAALSLPGALAKPIMDQLVGAAETGIPFSSLGPQAHLRPLKTMEPEEEVEDD
PKVHLEAKELWDQFHKRGTEMVITKSGRRMFPPFKVRCSGLDKKAKYILLMDIIAADD
CRYKFHNSRWMVAGKADPEMPKRMYIHPDSPATGEQWMSKVVTFHKLKLTNNISDKHG
FTILNSMHKYQPRFHIVRANDILKLPYSTFRTYLFPETEFIAVTAYQNDKITQLKIDN
NPFAKGFRDTGNGRREKRKQLTLQSMRVFDERHKKENGTSDESSSEQAAFNCFAQASS
PAASTVGTSNLKDLCPSEGESDAEAESKEEHGPEACDAAKISTTTSEEPCRDKGSPAV
KAHLFAAERPRDSGRLDKASPDSRHSPATISSSTRGLGAEERRSPVREGTAPAKVEEA
RALPGKEAFAPLTVQTDAAAAHLAQGPLPGLGFAPGLAGQQFFNGHPLFLHPSQFAMG
GAFSSMAAAGMGPLLATVSGASTGVSGLDSTAMASAAAAQGLSGASAATLPFHLQQHV
LASQGLAMSPFGSLFPYPYTYMAAAAAAASSAAASSSVHRHPFLNLNTMRPRLRYSPYS
IPVPVPDGSSLLTTALPSMAAAAGPLDGKVAALAASPASVAVDSGSELNSRSSTLSSS
SMSLSPKLCAEKEAATSELQSIQRLVSGLEAKPDRSRSASP

>TBX4  NM_018488
              MLQDKGLSESEEAFRAPGPALGEASAANAPEPALAAPGLSGAAL
GSPPGPGADVVAAAAAEQTIENIKVGLHEKELWKKFHEAGTEMIITKAGRRMFPSYKV
KVTGMNPKTKYILLIDIVPADDHRYKFCDNKWMVAGKAEPAMPGRLYVHPDSPATGAH
WMRQLVSFQKLKLTNNHLDPFGHIILNSMHKYQPRLHIVKADENNAFGSKNTAFCTHV
FPETSFISVTSYQNHKITQLKIENNPFAKGFRGSDDSDLRVARLQSKEYPVISKSIMR
QRLISPQLSATPDVGPLLGTHQALQHYQHENGAHSQLAEPQDLPLSTFPTQRDSSLFY
HCLKRRDGTRHLDLPCKRSYLEAPSSVGEDHYFRSPPPYDQQMLSPSYCSEVTPREAC
MYSGSGPEIAGVSGVDDLPPPPLSCNMWTSVSPYTSYSVQTMETVPYQPFPTHFTATT
MMPRLPTLSAQSSQPPGNAHFSVYNQLSQSQVRERGPSASFPRERGLPQGCERKPPSP
HLNAANEFLYSQTFSLSRESSLQYHSGMGTVENWTDG

>TBX5  NM_000192 (variant 1)
              MADADEGFGLAHTPLEPDAKDLPCDSKPESALGAPSKSPSSPQA
AFTQQGMEGIKVFLHERELWLKFHEVGTEMIITKAGRRMFPSYKVKVTGLNPKTKYIL
```

LMDIVPADDHRYKFADNKWSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKL
TNNHLDPFGHIILNSMHKYQPRLHIVKADENNGFGSKNTAFCTHVFPETAFIAVTSYQ
NHKITQLKIENNPFAKGFRGSDDMELHRMSRMQSKEYPVVPRSTVRQKVASNHSPFSS
ESRALSTSSNLGSQYQCENGVSGPSQDLLPPPNPYPLPQEHSQIYHCTKRKEEECSTT
DHPYKKPYMETSPSEEDSFYRSSYPQQQGLGASYRTESAQRQACMYASSAPPSEPVPS
LEDISCNTWPSMPSYSSCTVTTVQPMDRLPYQHFSAHFTSGPLVPRLAGMANHGSPQL
GEGMFQHQTSVAHQPVVRQCGPQTGLQSPGTLQPPEFLYSHGVPRTLSPHQYHSVHGV
GMVPEWSDNS

>TBX6 NM_004608
MYHPRELYPSLGAGYRLGPAQPGADSSFPPALAEGYRYPELDTP
KLDCFLSGMEAAPRTLAAHPPLPLLPPAMGTEPAPSAPEALHSLPGVSLSLENRELWK
EFSSVGTEMIITKAGRRMFPACRVSVTGLDPEARYLFLLDVIPVDGARYRWQGRRWEP
SGKAEPRLPDRVYIHPDSPATGAHWMRQPVSFHRVKLTNSTLDPHGHLILHSMHKYQP
RIHLVRAAQLCSQHWGGMASFRFPETTFISVTAYQNPQITQLKIAANPFAKGFRENGR
NCKRERDARVKRKLRGPEPAATEAYGSGDTPGGPCDSTLGGDIRESDPEQAPAPGEAT
AAPAPLCGGPSAEAYLLHPAAFHGAPSHLPTRSPSFPEAPDSGRSAPYSAAFLELPHG
SGGSGYPAAPPAVPFAPHFLQGGPFPLPYTAPGGYLDVGSKPMY

>TBX10 NM_005995
MAAFLSAGLGILAPSETYPLPTTSSGWEPRLGSPFPSGPCTSST
GAQAVAEPTGQGPKNPRVSRVTVQLEMKPLWEEFNQLGTEMIVTKAGRRMFPPFQVKI
LGMDSLADYALLMDFIPLDDKRYRYAFHSSAWLVAGKADPATPGRVHFHPDSPAKGAQ
WMRQIVSFDKLKLTNNLLDDNGHIILNSMHRYQPRFHVVFVDPRKDSERYAQENFKSF
IFTETQFTAVTAYQNHRITQLKIASNPFAKGFRESDLDSWPVAPRPLLSVPARSHSSL
SPCVLKGATDREKDPNKASASTSKTPAWLHHQLLPPPEVLLAPATYRPVTYQSLYSGA
PSHLGIPRTRPAPYPLPNIRADRDQGGLPLPAGLGLLSPTVVCLGPGQDSQ

>TBX15 NM_152380
MSSMEEIQVELQCADLWKRFHDIGTEMIITKAGRRMFPAMRVKI
TGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSPVPPRVYIHPDSLASGDT
WMRQVVSFDKLKLTNNELDDQGHIILHSMHKYQPRVHVIRKDFSSDLSPTKPVPVGDG
VKTFNFPETVFTTVTAYQNQQITRLKIDRNPFAKGFRDSGRNRTGLEAIMETYAFWRP
PVRTLTFEDFTTMQKQQGGSTGTSPTTSSTGTPSPSASSHLLSPSCSPPTFHLAPNTF
NVGCRESQLCNLNLSDYPPCARSNMAALQSYPGLSDSGYNRLQSGTTSATQPSETFMP
QRTPSLISGIPTPPSLPGNSKMEAYGGQLGSFPTSQFQYVMQAGNAASSSSSPHMFGG
SHMQQSSYNAFSLHNPYNLYGYNFPTSPRLAASPEKLSASQSTLLCSSPSNGAFGERQ
YLPSGMEHSMHMISPSPNNQQATNTCDGRQYGAVPGSSSQMSVHMV

>TBX18 NM_001080508
MAEKRRGSPCSMLSLKAHAFSVEALIGAEKQQQLQKKRRKLGAE
EAAGAVDDGGCSRGGGAGEKGSSEGDEGAALPPPAGATSGPARSGADLERGAAGGCED
GFQQGASPLASPGGSPKGSPARSLARPGTPLPSPQAPRVDLQGAELWKRFHEIGTEMI
ITKAGRRMFPAMRVKISGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSPV
PPRVYIHPDSPASGETWMRQVISFDKLKLTNNELDDQGHIILHSMHKYQPRVHVIRKD
CGDDLSPIKPVPSGEGVKAFSFPETVFTTVTAYQNQQITRLKIDRNPFAKGFRDSGRN
RMGLEALVESYAFWRPSLRTLTFEDIPGIPKQGNASSSTLLQGTGNGVPATHPHLLSG
SSCSSPAFHLGPNTSQLCSLAPADYSACARSGLTLNRYSTSLAETYNRLTNQAGETFA
PPRTPSYVGVSSSTSVNMSMGGTDGDTFSCPQTSLSMQISGMSPQLQYIMPSPSSNAF
ATNQTHQGSYNTFRLHSPCALYGYNFSTSPKLAASPEKIVSSQGSFLGSSPSGTMTDR
QMLPPVEGVHLLSSGGQQSFFDSRTLGSLTLSSSQVSAHMV

>TBX19 NM_005149
MAMSELGTRKPSDGTVSHLLNVVESELQAGREKGDPTEKQLQII
LEDAPLWQRFKEVTNEMIVTKNGRRMFPVLKISVTGLDPNAMYSLLLDFVPTDSHRWK
YVNGEWVPAGKPEVSSHSCVYIHPDSPNFGAHWMKAPISFSKVKLTNKLNGGGQIMLN
SLHKYEPQVHIVRVGSAHRMVTNCSFPETQFIAVTAYQNEEITALKIKYNPFAKAFLD
AKERNHLRDVPEAISESQHVTYSHLGGWIFSNPDGVCTAGNSNYQYAAPLPLPAPHTH
HGCEHYSGLRGHRQAPYPSAYMHRNHSPSVNLIESSSNNLQVFSGPDSWTSLSSTPHA
SILSVPHTNGPINPGPSPYPCLWTISNGAGGPSGPGPEVHASTPGAFLLGNPAVTSPP
SVLSTQAPTSAGVEVLGEPSLTSIAVSTWTAVASHPFAGWGGPGAGGHHSPSSLDG

>TBX20 NM_001077653
MEFTASPKPQLSSRANAFSIAALMSSGGSKEKEATENTIKPLEQ
FVEKSSCAQPLGELTSLDAHGEFGGGSGSSPSSSSLCTEPLIPTTPIIPSEEMAKIAC
SLETKELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRY
RYAYHRSSWLVAGKADPPLPARLYVHPDSPFTGEQLLKQMVSFEKVKLTNNELDQHGH
IILNSMHKYQPRVHIIKKKDHTASLLNLKSEEFRTFIFPETVFTAVTAYQNQLITKLK
IDSNPFAKGFRDSSRLTDIERESVESLIQKHSYARSPIRTYGGEEDVLGDESQTTPNR
GSAFTTSDNLSLSSWVSSSSSFPGFQHPQSLTALGTSTASIATPIPHPIQGSLPPYSR
LGMPLTPSAIASSMQGSGPTFPSFHMPRYHHYFQQGPYAAIQGLRHSSAVMTPFV

>TBX21 NM_013351
MGIVEPGCGDMLTGTEPMPGSDEGRAPGADPQHRYFYPEPGAQD
ADERRGGGSLGSPYPGGALVPAPPSRFLGAYAYPPRPQAAGFPGAGESFPPPADAEGY
QPGEGYAAPDPRAGLYPGPREDYALPAGLEVSGKLRVALNNHLLWSKFNQHQTEMIIT
KQGRRMFPFLSFTVAGLEPTSHYRMFVDVVLVDQHHWRYQSGKWVQCGKAEGSMPGNR
LYVHPDSPNTGAHWMRQEVSFGKLKLTNNKGASNNVTQMIVLQSLHKYQPRLHIVEVN
DGEPEAACNASNTHIFTFQETQFIAVTAYQNAEITQLKIDNNPFAKGFRENFESMYTS
VDTSIPSPPGPNCQFLGGDHYSPLLPNQYPVPSRFYPDLPGQAKDVVPQAYWLGAPRD
HSYEAEFRAVSMKPAFLPSAPGPTMSYYRGQEVLAPGAGWPVAPQYPPKMGPASWFRP
MRTLPMEPGPGGSEGRGPEDQGPPLVWTEIAPIRPESSDSGLGEGDSKRRRVSPYPSS
GDSSSPAGAPSPFDKEAEGQFYNYFPN

>TBX22 NM_001109878 (variant 1)
MALSSRARAFSVEALVGRPSKRKLQDPIQAEQPELREKKGGEEE
EERRSSAAGKSEPLEKQPKTEPSTSASSGCGSDSGYGNSSESLEEKDIQMELQGSELW
KRFHDIGTEMIITKAGRRMFPSVRVKVKGLDPGKQYHVAIDVVPVDSKRYRYVYHSSQ
WMVAGNTDHLCIIPRFYVHPDSPCSGETWMRQIISFDRMKLTNNEMDDKGHIILQSMH
KYKPRVHVIEQGSSVDLSQIQSLPTEGVKTFSFKETEFTTVTAYQNQQITKLKIERNP
FAKGFRDTGRNRGVLDGLLETYPWRPSFTLDFKTFGADTQSGSSGSSPVTSSGGAPSP
LNSLLSPLCFSPMFHLPTSSLGMPCPEAYLPNVNLPLCYKICPTNFWQQQPLVLPAPE
RLASSNSSQSLAPLMMEVPMLSSLGVTNSKSGSSEDSSDQYLQAPNSTNQMLYGLQSP
GNIFLPNSITPEALSCSFHPSYDFYRYNFSMPSRLISGSNHLKVNDDSQVSFGEGKCN
HVHWYPAINHYL

>TBR1 NM_006593
MQLEHCLSPSIMLSKKFLNVSSSYPHSGGSELVLHDHPIISTTD
NLERSSPLKKITRGMTNQSDTDNFPDSKDSPGDVQRSKLSPVLDGVSELRHSFDGSAA
DRYLLSQSSQPQSAATAPSAMFPYPGQHGPAHPAFSIGSPSRYMAHHPVITNGAYNSL
LSNSSPQGYPTAGYPYPQQYGHSYQGAPFYQFSSTQPGLVPGKAQVYLCNRPLWLKFH
RHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWRFQGGKWVPCGK
ADTNVQGNRVYMHPDSPNTGAHWMRQEISFGKLKLTNNKGASNNNGQMVVLQSLHKYQ
PRLHVVEVNEDGTEDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDHNPFAKGFR
DNYDTIYTGCDMDRLTPSPNDSPRSQIVPGARYAMAGSFLQDQFVSNYAKARFHPGAG
AGPGPGTDRSVPHTNGLLSPQQAEDPGAPSPQRWFVTPANNRLDFAASAYDTATDFAG
NAATLLSYAAAGVKALPLQAAGCTGRPLGYYADPSGWGARSPPQYCGTKSGSVLPCWP
NSAAAAARMAGANPYLGEEAEGLAAERSPLPPGAAEDAKPKDLSDSSWIETPSSIKSI
DSSDSGIYEQAKRRRISPADTPVSESSSPLKSEVLAQRDCEKNCAKDISGYYGFYSHS

>T NM_003181
MSSPGTESAGKSLQYRVDHLLSAVENELQAGSEKGDPTERELRV
GLEESELWLRFKELTNEMIVTKNGRRMFPVLKVNVSGLDPNAMYSFLLDFVAADNHRW
KYVNGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKAPVSFSKVKLTNKLNGGGQIML
NSLHKYEPRIHIVRVGGPQRMITSHCFPETQFIAVTAYQNEEITALKIKYNPFAKAFL
DAKERSDHKEMMEEPGDSQQPGYSQWGWLLPGTSTLCPPANPHPQFGGALSLPSTHSC
DRYPTLRSHRSSPYPSPYAHRNNSPTYSDNSPACLSMLQSHDNWSSLGMPAHPSMLPV
SHNASPPTSSSQYPSLWSVSNGAVTPGSQAAAVSNGLGAQFFRGSPAHYTPLTHPVSA
PSSSGSPLYEGAAAATDIVDSQYDAAAQGRLIASWTPVSPPSM

>EOMES NM_005442
MQLGEQLLVSSVNLPGAHFYPLESARGGSGGSAGHLPSAAPSPQ
KLDLDKASKKFSGSLSCEAVSGEPAAASAGAPAAMLSDTDAGDAFASAAAVAKPGPPD
GRKGSPCGEEELPSAAAAAAAAAAAAAATARYSMDSLSSERYYLQSPGPQGSELAAPC

SLFPYQAAAGAPHGPVYPAPNGARYPYGSMLPPGGFPAAVCPPGRAQFGPGAGAGSGA
GGSSGGGGGPGTYQYSQGAPLYGPYPGAAAAGSCGGLGGLGVPGSGFRAHVYLCNRPL
WLKFHRHQTEMIITKQGRRMFPFLSFNINGLNPTAHYNVFVEVVLADPNHWRFQGGKW
VTCGKADNNMQGNKMYVHPESPNTGSHWMRQEISFGKLKLTNNKGANNNNTQMIVLQS
LHKYQPRLHIVEVTEDGVEDLNEPSKTQTFTFSETQFIAVTAYQNTDITQLKIDHNPF
AKGFRDNYDSSHQIVPGGRYGVQSFFPEPFVNTLPQARYYNGERTVPQTNGLLSPQQS
EEVANPPQRWLVTPVQQPGTNKLDISSYESEYTSSTLLPYGIKSLPLQTSHALGYYPD
PTFPAMAGWGGRGSYQRKMAAGLPWTSRTSPTVFSEDQLSKEKVKEEIGSSWIETPPS
IKSLDSNDSGVYTSACKRRRLSPSNSSNENSPSIKCEDINAEEYSKDTSKGMGGYYAF
YTTP

>MGA NM_001164273 (variant 1)
MEEKQQIILANQDGGTVAGAAPTFFVILKQPGNGKTDQGILVTN
QDACALASSVSSPVKSKGKICLPADCTVGGITVTLDNNSMWNEFYHRSTEMILTKQGR
RMFPYCRYWITGLDSNLKYILVMDISPVDNHRYKWNGRWWEPSGKAEPHVLGRVFIHP
ESPSTGHYWMHQPVSFYKLKLTNNTLDQEGHIILHSMHRYLPRLHLVPAEKAVEVIQL
NGPGVHTFTFPQTEFFAVTAYQNIQITQLKIDYNPFAKGFRDDGLNNKPQRDGKQKNS
SDQEGNNISSSSGHRVRLTEGQGSEIQPGDLDPLSRGHETSGKGLEKTSLNIKRDFLG
FMDTDSALSEVPQLKQEISECLIASSFEDDSRVASPLDQNGSFNVVIKEEPLDDYDYE
LGECPEGVTVKQEETDEETDVYSNSDDDPILEKQLKRHNKVDNPEADHLSSKWLPSSP
SGVAKAKMFKLDTGKMPVVYLEPCAVTRSTVKISELPDNMLSTSRKDKSSMLAELEYL
PTYIENSNETAFCLGKESENGLRKHSPDLRVVQKYPLLKEPQWKYPDISDSISTERIL
DDSKDSVGDSLSGKEDLGRKRTTMLKIATAAKVVNANQNASPNVPGKRGRPRKLKLCK
AGRPPKNTGKSLISTKNTPVSPGSTFPDVKPDLEDVDGVLFVSFESKEALDIHAVDGT
TEESSSLQASTTNDSGYRARISQLEKELIEDLKTLRHKQVIHPGLQEVGLKLNSVDPT
MSIDLKYLGVQLPLAPATSFPFWNLTGTNPASPDAGFPFVSRTGKTNDFTKIKGWRGK
FHSASASRNEGGNSESSLKNRSAFCSDKLDEYLENEGKLMETSMGFSSNAPTSPVVYQ
LPTKSTSYVRTLDSVLKKQSTISPSTSYSLKPHSVPPVSRKAKSQNRQATFSGRTKSS
YKSILPYPVSPKQKYSHVILGDKVTKNSSGIISENQANNFVVPTLDENIFPKQISLRQ
AQQQQQQQQGSRPPGLSKSQVKLMDLEDCALWEGKPRTYITEERADVSLTTLLTAQAS
LKTKPIHTIIRKRAPPCNNDFCRLGCVCSSLALEKRQPAHCRRPDCMFGCTCLKRKVV
LVKGGSKTKHFQRKAAHRDPVFYDTLGEEAREEEEGIREEEEQLKEKKKRKKLEYTIC
ETEPEQPVRHYPLWVKVEGEVDPEPVYIPTPSVIEPMKPLLLPQPEVLSPTVKGKLLT
GIKSPRSYTPKPNPVIREEDKDPVYLYFESMMTCARVRVYERKKEDQRQPSSSSSPSP
SFQQQTSCHSSPENHNNAKEPDSEQQPLKQLTCDLEDDSDKLQEKSWKSSCNEGESSS
TSYMHQRSPGGPTKLIEIISDCNWEEDRNKILSILSQHINSNMPQSLKVGSFIIELAS
QRKSRGEKNPPVYSSRVKISMPSCQDQDDMAEKSGSETPDGPLSPGKMEDISPVQTDA
LDSVRERLHGGKGLPFYAGLSPAGKLVAYKRKPSSSTSGLIQVASNAKVAASRKPRTL
LPSTSNSKMASSSGTATNRPGKNLKAFVPAKRPIAARPSPGGVFTQFVMSKVGALQQK
IPGVSTPQTLAGTQKFSIRPSPVMVVTPVVSSEPVQVCSPVTAAVTTTTPQVFLENTT
AVTPMTAISDVETKETTYSSGATTTGVVEVSETNTSTSVTSTQSTATVNLTKTTGITT
PVASVAFPKSLVASPSTITLPVASTASTSLVVVTAAASSSMVTTPTSSLGSVPIILSG
INGSPPVSQRPENAAQIPVATPQVSPNTVKRAGPRLLLIPVQQGSPTLRPVSNTQLQG
HRMVLQPVRSPSGMNLFRHPNGQIVQLLPLHQLRGSNTQPNLQPVMFRNPGSVMGIRL
PAPSKPSETPPSSTSSSAFSVMNPVIQAVGSSSAVNVITQAPSLLSSGASFVSQAGTL
TLRISPPEPQSFASKTGSETKITYSSGGQPVGTASLIPLQSGSFALLQLPGQKPVPSS
ILQHVASLQMKRESQNPDQKDETNSIKREQETKKVLQSEGEAVDPEANVIKQNSGAAT
SEETLNDSLEDRGDHLDEECLPEEGCATVKPSEHSCITGSHTDQDYKDVNEEYGARNR
KSSKEKVAVLEVRTISEKASNKTVQNLSKVQHQKLGDVKVEQQKGFDNPEENSSEFPV
TFKEESKFELSGSKVMEQQSNLQPEAKEKECGDSLEKDRERWRKHLKGPLTRKCVGAS
QECKKEADEQLIKETKTCQENSDVFQQEQGISDLLGKSGITEDARVLKTECDSWSRIS
NPSAFSIVPRRAAKSSRGNGHFQGHLLLPGEQIQPKQEKKGGRSSADFTVLDLEEDDE
DDNEKTDDSIDEIVDVVSDYQSEEVDDVEKNNCVEYIEDDEEHVDIETVEELSEEINV
AHLKTTAAHTQSFKQPSCTHISADEKAAERSRKAPPIPLKLKPDYWSDKLQKEAEAFA
YYRRTHTANERRRRGEMRDLFEKLKITLGLLHSSKVSKSLILTRAFSEIQGLTDQADK
LIGQKNLLTRKRNILIRKVSSLSGKTEEVVLKKLEYIYAKQQALEAQKRKKKMGSDEF
DISPRISKQQEGSSASSVDLGQMFINNRRGKPLILSRKKDQATENTSPLNTPHTSANL
VMTPQGQLLTLKGPLFSGPVVAVSPDLLESDLKPQVAGSAVALPENDDLFMMPRIVNV
TSLATEGGLVDMGGSKYPHEVPDSKPSDHLKDTVRNEDNSLEDKGRISSRGNRDGRVT
LGPTQVFLANKDSGYPQIVDVSNMQKAQEFLPKKISGDMRGIQYKWKESESRGERVKS
KDSSFHKLKMKDLKDSSIEMELRKVTSAIEEAALDSSELLTNMEDEDDTDETLTSLLN
EIAFLNQQLNDDSVGLAELPSSMDTEFPGDARRAFISKVPPGSRATFQVEHLGTGLKE

LPDVQGESDSISPLLLHLEDDDFSENEKQLAEPASEPDVLKIVIDSEIKDSLLSNKKA
IDGGKNTSGLPAEPESVSSPPTLHMKTGLENSNSTDTLWRPMPKLAPLGLKVANPSSD
ADGQSLKVMPCLAPIAAKVGSVGHKMNLTGNDQEGRESKVMPTLAPVVAKLGNSGASP
SSAGK

2) Opossum (Monodelphis domestica) T-box gene with Genbank (mRNA) accession number

>Tbx16 XM_001377868

MAPRGTPAPGPHSPISASLEDVDLWTEFYRVGTEMVITKSGRRM
FPQCKIRLSGLVPYLKYVVLADFVSVDNFRYKWAKDQWEVAGKAEPQLPGRSYIHPDS
PAYGSHWMKEPVSFHKMKLTNNTLDQHGHIILHSMHRYQPRFLVAQADDLFNVCWNLF
QVFSFPQTVFISVTAYQNEQITKLKIDNNPFAKGFREQGRKPRRFSPGRGLTKERLRE
LVSSPEPERSGLTKEDAADQAEARGGSGPVSSSRFSPLWGPRELNQTEGPPGEAAGTS
PGPYPVYRVRVSEPGRPQITPGRNSEVRAGSGFGPGGSQAPTERLLHTSTPAEGP

3) Zebrafish T-box genes with Genbank (mRNA) accession numbers

>tbx1 NM_183339

MISAISSPWLTQLSHFCDVAAFTTSSLSSLNTPGSYHLSPSPGD
PYSHHESQFEPCPAAQHAYNYSGSNSAQAPAQGDSGTSNCSSSSSSSTPNKTLVKKNP
KVANINVQLEMKALWDEFNQLGTEMIVTKAGRRMFPTFQVKIFGMDPMADYMLLMDFL
PVDDKRYRYAFHSSSWLVAGKADPATPGRVHYHPDSPAKGAQWMKQIVSFDKLKLTNN
LLDDNGHIILNSMHRYQPRFHVVYVDPRKDSEKYAEENYKTFVFEETRFTAVTAYQNH
RITQLKIASNPFAKGFRDCDPEDWPRNHRPGSLQIMSAFARTRNPMSSPPQQNGTEKE
DSRREYDRDPSGNPLHSDPTHQLMSRVLSPALPVLGGLHAVPLTAGPRSPPHELRLDG
HPQPPDTLHHHPYKYPATYEHYLGAKTRPSPYPSPSIRGHGYHPHMNPTTANMYSATS
APTNYDYGPR

>tbx2a NM_001102384

MRDPVFTANAMAYHPFHAHRPADFPMSAFLAAAQPSFFPALTLP
PGLSKPLADHALSGAAEAGLHAALGHHHQAAHLRSFKGLEPEEDVEDDPKVTLEAKEL
WDQFHKIGTEMVITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYKFHNSRW
MVAGKADPEMPKRMYIHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFTILNSMHKY
QPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDNNPFAKGFRDT
GNGRREKRKQLAMPSMRMYDDQCKVDRDGGDSDDSSCEQTTGRDSVHSPTGPATSPLK
FTRSREDKNFNESDNELDQHDDGMIRVSSPEQRPQSPFSPRCEDRVKDRLNLEKKGDY
SDSRKENDSAFSIRHLDKDKLDARNVKDQDSSKKEADSVGMSTVKDGFSPLMVQTENP
SHFSASHLQSLALSGLHNQHFFNPLSSGQSLLFHPGQFAMTPSAFSTMGMGHLLASMS
GASGLENGSLSSQSTSSPNPFPFHLSQHMLASQGISMPTFGGLLPYPYTYMAAAAAAA
SALPAGSAASSLSRNPFLNNTRPRLRFSPYQIPMSFSQSSGLLTTGIPSTMSAESESS
KSGSRESSPMSEHHSHKTGNGQNTGSPKSSGKDSINELQNIQRLVSGLEKHRDASPRS
VSPK

>tbx2b NM_131051

MRDPVFTGTAMAYHPFHAHRPTDFPMSAFLAAAQPSFFPALTLP
PGALTKPIPDHTLAGAAEAGLHPALSHHHQAAHLRSLKSLEPEEEVEDDPKVTLEAKD
LWDQFHKLGTEMVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYKFHNSR
WMVAGKADPEMPKRMYIHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFTILNSMHK
YQPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDNNPFAKGFRD
TGNGRREKRKQLTLPSLRMYEDQCKVDRDGADSDASSSEPTTGRDAGHSPGPVSSPLR
FNRGSRDDKTCTDSEHEMDHQNDRCGGSSSPAPKPSSPFRSRSEDWGREKPIAEKKDD
YPDSRKTSDSIFSIRNLEKDKLESRSRKDTDSSKKDTENSGISGSKDSFSPLMVQTES
PSHFGAGHLQSLALSGLHSQQFFNPLNTGQPLLFHPGQFAMAPGAFSAMGMGHLLASV
SGAGGLENGSLSAQGTGSTPSPFPFHLSQHMLASQGIPMPTFGGLFPYPYTYMAAAAA
AASALPASSSTASSLSRNPFLSSSTRPRLRFNPYQLPVSIPQSTNLLTTGLPSGLNPS
SESSKCGSREASPVPDHKSGASQRNGSPKTTMKESINELQNIQRLVSGLESQRETSSP
RDSPK

>tbx3a (currently tbx3) NM_001101670

MRDPVIQGSSMAYHPFLPHRGPEFAMSAMLGHQPPFFPALALPP
NGSLSLPGALGKPIMEQLMGAAETGLHFSSLGHQAAHLRPLKTLEPEEEVEDDPKVHL

EAKELWELFHKRGTEMVITKSGRRMFPPFKVRCTGLDKKAKYILLMDIVAADDCRYKF
HNSRWMVAGKADPEMPKRMYIHPDSPATGEQWMSKVVNFHKLKLTNNISDKHGFTILN
SMHKYQPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDHNPFAK
GFRDTGNGRREKRKQLALQSMRSYEEQQKKENGTSDDSSGEQASFKCFRQASSPAVST
AGHNHLKDFCDSDEDSDEEDKDANAKEGPDSSKISTTTEDSKDQDAGLGKSVFGESDS
SSGRRSEKTRADSRSPITLISSTTRSGEELKSPVREPAKTTDDCRTVSKENYMPLTVQ
TDGAAHLNQNHLHNFGFPPGLAGQQFFNHLGGAHPFLLHPSQFNMGGAFSNMAAGMGP
ILAAVSSGGVGSLDGSSLPSPSQSLTGAPMPFHLQQHVLASQGLAMSPFGGLFPYPYT
YMAAAAAASSAASSSVHRHPFLSAVRPRLRYSPYSLPSVPDSTLLTTAMQPMASSGLE
VKGDGMNTSPASAALDSEVTSRSSGSVSLSPKTCTEKDSSSELQSIQRLVSGLEPKPD
RARSVSP

>tbx3b (new) XM_002662004
MAYHHFIPASPTDFTISPMLGQQAQFFPVGYGHQQFANALQSSI
RLALKESAAPALLSGRTRDPVQTPEDEPVVHLEGNELWGQFHKVGTEMVITKSGRRMF
PAFKVRCSGFDRKARYILLMDIVASDDYRYKFHNCRWMVAGKADPEMPKRMYIHPDSP
STGEQWMSKAVTFHKLKLTNNISDKHGFTILNSMHKYQPRFHIVRANDVLKLPYSTFK
TYVFPETEFIAVTAYQNEKITQLKIDNNPFAKGFRETGNGRREKRKQMLHQRCEVEPK
KASVLTDDSSFDQISSNYLIQENTNESDIDGFGDEKESNEVESIQSISQDEQNSREIS
TTVQESKDDPNEEIGDRNPEINSKKQHSVEQPAHLPLDKKHAEQQKFAADVTDASQKD
SLARHFYFPTPGLINSLRLPSHVLSNLCQFNYVGTLPLLASEATGSWIPRRSNEGEGQ
GYTTSVSSSQQRLTGMQDLPPNFQQHRMTSQGVLVSAQGNIFPYPQDYMTTSAGSSSA
ASYQVHRQPFFNISYRPQCRPYPVPVWVHGRKIPQTTSVLIPYGETDINEHASIATPG
STLFGLKANKDQNTRCQDL

>tbx4 NM_130914
MLQEKASVVADEGMTVAQSGGRPELASDSSHLGLPTTPSNPQNN
EPDQSIENIKVVLHDRELWKKLHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILL
TDIVPADDHRYKFCDNKWMVAGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKLT
NNHLDPFGHIILNSMHKYQPRLHIVKADENNAFGSKNTAYCTHVFHETAFISVTSYQN
HKITQLKIENNPFAKGFRGSDEGDLRVSRLQGKDYPVISKNMVRQRLISSHGHLSGKL
SAGVLSSHPQVLSHYQYDSGVPLPNSDSQEALSNSFTSSREPSLLYHCFKHRDNPRHL
ELGCKRPYLDTTSSAVSEEHYFRSPPSYDSPLLSHPYCNEALGSREACMYGGLEGEGG
GAVGTDDLPAPSLNCNMWASVQPYPRYGMQTVEAMQYQPFTAHFNSTASAASMVSHHS
PSMQRPHPTPPDLVTFTTQRVLPPTPSSASTSPSGSGHHDRAHSSLFHRKAGSPLRSQ
RDFTGYSTHSPTSTREPAYQYQTGLSSVGPHWTDS

>tbx5a NM_130915
MADSEDTFRLQNSPSDSEPKDLQNEGKSDKQNAAVSKSPSSQTT
YIQQGMEGIKVYLHERELWTKFHEVGTEMIITKAGRRMFPSFKVKVTGLNPKTKYILL
MDVVPADDHRYKFADNKWSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKLT
NNHLDPFGHIILNSMHKYQPRIHIVKADENNGFGSKNTAFCTHVFPETAFIAVTSYQN
HKITQLKIENNPFAKGFRGSDDMELHRMSRMQSTKEYPVVPRSTVRQRVGSSQSPFSG
DVQGLSATGAISSQYSCENSVSSTSQDLLPQSSSYHEHTQDYHCIKRKVEDECPAGEH
PYKKPYVESSSSEDDHYYRPLSYSQSLGLSGGAPYRPESSQRQACMYASAPQPPEPVP
SLEDISWPGVPPYSVPQMERLPYQHHFSAHFASRQMPEAHGMYASSVSHQCSPSGGIQ
SPSAGLQGNEYLYAHGLQHTVPASVPHRAQRQHHA

>tbx5b NM_001198771
MANPMFESLRACSGGNSPAMDFERDKDSGHHGRNKTGSPPLQTQ
LSQQSMEGIKVYLHEKDLWAKFHDVTTEMIITKAGRRMFPSYKVKVTGLNPKAKYILL
MDIISADEHRYKFADNKWSISGKAEPAIPGRLYVHPDSPASGAHWMRQLVSFQKLKLT
NNHLDPFGHIILNSMHKYQPRLHIVKADERNSFGSSNTSFCTHSFAETTFIAVTSYQN
HTITQLKIENNPFAKGFRGNDDIELHRMSRTPSKEYPLVPRSTARQRAAPPSPDCLSR
SEYTVTQKPSPGFTCSDTSGDQSLTETPSIHDPTYPLFSYQLSPDVAPSSMDTTQHQP
CMYGGSQVGMEELRWASYSDSTTYQSFSSAKEMSGTFVPPADLSQELYPQYTCEVGVQ
SHCMMTDFSLYACNRSFSQNQQPNNWCGGS

>tbx6 NM_131052
MNHLANNYGYYPQDCRTQYSRMNSAEAELTSLPVHVSLQDRELW
DKFSSIGTEMLITKSGRRMFPSCKVTVTGLNPKVKYVVIMDMVPFDNHKYKWNKDCWE
VNGSSDPHLPNRFFIHPDSPAPGQKWMQYPISFHKLKLTNNTLNSNGLVVLHSMHKYQ

PRLHIVQSPDPCTPHNPGAYLRFTFPEAAFIAVTAYQNQEITKLKIDNNPFAKGFRDN
GLNRKRFRDKGTQEMQDTDRQVKLDLTANECAAGMSQMVEDVDVSVSSSVDCRDTQNS
SSVSLNPFISAFTNPSSAGGAAAHQTHTLLSLSNRHFSSPRESNLNSVCAALPVSQLS
TGHTSFSRLNPQETHHNSRPKIQLQPPHPSLQCHDLDVRLPLPPKLSRVQLSESALRN
LEMSPLSDCANPRPLTNILNRSCFRASTPSGKLLPNPPQPEQFLRGSEREIYPAVQEY
TDQQFTLNSQTEHRPHMRPLTEY

>tbx10 (new) XM_002664501 with a modification
Note: Genbank entry for this gene has a slight mis-prediction of
exon 4 (noted during the comparison with other fish sequences),
which is corrected in this version.
MVLKVQSSAGAETPRHRSAGGFSCPQPDDVSGRSCSKAPEVSSV
RVQLEMQSLWRQFDQLGTEMIVTKAGRRMFPTFQVHISGMDPAAEYVLLMDFIPVDDK
RYRYAFHSSSWLVAGRGDVAAPGRVHFHPDSPARGAQWIKQTVSFDRLKLTNNLLDDN
GHMILNSMHRYQPRLHVVLVDRSRNSQRFAHRNFCTFSFPETRFIAVTAYQNHRITQL
KIACNPFAKGFRTADPEHRADLNRAASMGPTDPPALGLPWAEAASRSRECQRHSDTHL
QPAVAGSVMDVASHTHLYTPAPVFFSLPGQWDVLTRAERDLTG

>tbx15 NM_153664
MSDRRRSAAALSSRAHAFSVEALIGTNKKRKLRGWEEKELELSM
ESLASNGQLGDGEDPANCLDIDPDSEASPGSDGEGLAERTSCSFGSPADLTSAACDPS
PSASMEEIQVELQCADLWKRFHDIGTEMIITKAGRRMFPAMRVKIVGLDPHQQYYIAM
DIVPVDNKRYRYVYHSSKWMVAGNADSPVPPRVYIHPDSLASGDTWMRQVVSFDKLKL
TNNELDDQGHIILHSMHKYQPRVHVIRKDFSSELSPTKPVPTGEGVKTFSFPETVFTT
ATAYQNQQITRLKIDRNPFAKGFRDSGRNSPPYRTGLEAIMETYAFWRPPVRTLTFED
FTNMQKQQGGSTGTSPTTSSTGTPSPSGATHLLSPSCSPPTFHLAPNTFNVGCRESRL
CNLGLSEYPVCARSNMAALQGYGGLADGSYGRLQTTGGAVASAQASESFLPQRTSSLI
AAGMQGGAHGSLATGNSGSGSGGGKMDAYGSQLASFPASQLQYVMQAGASSASGSSAS
SGSSSSSAHMFSGSHHHVQQSTYNAFSLHNPYNLYGYNFPASPRLAASPEKPQGGLLC
SSSSAGAFAERQYLSNGGMDSMHMIGNPTGSQQGAGSCDGRQYGSSSQMSMHMV

>tbx16 NM_131058
MQAIRDLKHNFSLPPPPSMPGAGDSYHQGNIRMTLEDPELWRSF
HEIGTEMIITKPGRRMFPHCKISLSGLVPYAKYILLVDMVPEDGLRYKWNKDKWEVAG
KAEPQPPYRTYLHPDSPAPGSHWMKQPVSFLKLKLTNNALDQHGHIILHSMHRYHPRF
HIVQADDLYSVRWSVFQTFTFPETSFTAVTAYQNTKITKLKIDHNPFAKGFRDEGTNS
KRRANRNLPDPERVAKKMSKDSEHGSPQDVQPSSCEALDDEHAGRKELEVKAERYSPW
GGACDRDSGHALRPESPLGSDHRDVYSSEQLVPGQNTYQPYRFHEYGKSPSPSSSSSV
GGSSACGSAGRPSFESRVLDVATVPDTDSSSKPSSAPEFSLPPHPSAGHQEYAGVLNM
AITQAKPGMLGTHPLYSHYSTEQSLGQWSGAAASQYPPPPPPHHHLPTEYSSQAVHHG
YHHGNVGDWSQYPLFSYSCW

>tbx18 NM_153665
MAEKRRSPCTMSLKAHAFSVEALIGTEKKRKLEEEDSENCFEEI
NEVPRMTESPQPSTGRTCPSTRSCEIDCTSDESPEPEDVLLDSPQPASQGAQVLVQSA
TSSGEEMRVDLQGSDLWKRFHEIGTEMIITKAGRRMFPAMRVKIAGLDPHQQYYIAMD
IVPVDNKRYRYVYHSSKWMVAGNADSPVPPRVYIHPDSPASGETWMRQVISFDKLKLT
NNELDDQGHIILHSMHKYQPRVHVIRKECGEELSPVKAVPTGDGVKAFSFTETVFTTV
TAYQNQQITRLKIDRNPFAKGFRDSGRNRMGLEALVESYAFWRPSLRTLTFEDILGIT
KQGAAGSHGVVGSSAHLLSSSSCPSPTFHLGSGAGPVCDYSTCSRTSHPLHRYGPSLS
ADSYSRLTSPTADAFSTSRSSTYVSGTESEAFSCTQTGLPIQIHSMPSTTSQLQYLMP
GHAHNAFSTNQSTQGSYNGFRLHNPYGLYGYNFSTSPRLATSPEKAAATQTSFLGSSP
SGTLTDRQVLSTMDGLHMLSSSQQNLFDSRTLGLTSSSSQVTAHMA

>tbx19 (new) XM_003198759
MKVEEDLRSGGTVSSGRGGNDCCITRLLSVVESELQAGREKGDP
TEKQLKVSLEDAELWRKFKEVTNEMIVTKNGRRMFPVLKVSVTGLDPNAMYSFLLDFT
PADGHRWKYVNGEWVPAGKPEPHSHSCVYIHPDSPNFGAHWMKAPVSFNKVKLTNKLN
GGGQIMLNSLHKYEPQIHIVRVGGSHRMVTNISFTDTQFIAVTAYQNEEITALKIKHN
PFAKAFLDAKERSHPKNHLEPPVENQHMGIPHCGWFISNPDSLCSASGGNFPYPGGLP
LTHHHHGYKHYPSLHGHRAAPYPSPYLPRHHHRGHNTVSLSDNLSPGVQMFSGHESWT
GVSPPGPAAMLSMQPAPNSPGASSQYPCLWTVSSCTVSSSPPGGVVSLTHGQDEPADG

ASTSASPCSLLQAHGPTGSDGSVDPANHSRVGGMSWASVTTHSF

>tbx20 NM_131506
MEYTSSPKPQLSSRANAFSIAALMSSGKTKDKESEENTIKPLEQ
FVEKSSCHPNLGDLPPLETHSDFSSGGGTGSGAPLCTEPLIPTTPGVPSEEKAKISCS
LETKELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVPMDIVPVDNKRYR
YAYHRSSWLVAGKADPPLPARLYVHPDSPFTGEQLSKQMVSFEKVKLTNNELDQHGHI
ILNSMHKYQPRVHIIKKKDHTASLLNLKSEEFRTFVFTETVFTCRTAYQNQLITRLKI
DSNPFAKGFRDSSRLTDIERESVESLIHKHSYARSPIRTYAGDEETLGEEGHSAHSRG
SAFTASDNLSLSSWVTTTSGFSGFQHPQSLSAIDTSTASLASPLPHPIQGSLPPYSRL
GMPLTPSALASSMQATGPTFPSFHMPRYHHYFQQGPYAAIQGLRHSSTVMTPFV

>tbx21 NM_001170599
MGGIGRNFYLNMLNGTDAQSFAKDAELSSHLHRHRDLSDFKMGI
QDTRFYYQDSIPNGQESLTLPFHAEHHQSAGAQTGRFYAPAPLGSCHFTSRSGTGHTY
VPAGADAYSSANGKDVYPSSADGYTASFQHGFPRAPMYSLPGLQVSGKTQVLLNNYPL
WAKFHKYQTEMIITKQGRRMFPFLSFNITSLDPSAHYNIYVDVVLADQHHWRYQGGKW
VQCGKAEGNMPGNRMYMHPDSPNTGTHWMRQEVSFGKLKLTNNKGSSNNVAQMIVLQS
LHKYQPRLHIVEVKEDGTEDPFLTSKTQTFVFPETQFIAVTAYQNADITQLKIDHNPF
AKGFRDNYDTLYAPPDPDRLTPSPTESQQLLSGSCYPHQPYLSDQYMSPLPQSRFYSR
EPVSMTQPCPKDPTSSPHSRWYLSSQQAVPPNRLDFSAYETEYTSNSLYKPFPLQSSP
HHPLSYYSENPFTSGAVSSANPGAWTASGRPSPQYLNHPHHSKPTSSLSWFRAVPSPA
ASSSPTATNSRFHASPSLLEPQRQPLLQDKSKESTEDTWIEAPSVKSVDSADSGLFEG
GESKKRRVSPYTSSTENSPPNRSAETCEKDNCSDAGYYGFYTH

>tbx22 NM_001164461
MACEDLRKSAKERKPAGAEAVRKVRVDLQGSDLWKRFHEIGTEM
IITKVGRRMFPSIRVKVHNLDPLQQYSIAMDIMPMDSKKYRYVYHSSQWVIAGNTDHS
CIPPHLYVHPDSPCSGENWMRQVISFDRVKLTNNELDDRGHIILKSMHKYRPRIHVIL
HCPPECLSKRLLSLPADGVFTFSFPETQFTTVTAYQNQQITKLKIDRNPFAKGFRERN
GAVLDGILESYSWHSPFNGFKSLAMELQGRCFGSSASGITPSVSSAQAVHPTAFSSPQ
CCKILPSSCFLAYRAYCSICLNNYTGLRPMLDLPLLTSLPVKKGDRCRSHWLYNSAGT
SMHPIHNTLSGWASENENTASAFMSPHSYSFPISHRFSTDTHHLKLAHSESTVLQMPM
ISSIGYSP

>tbx24 NM_153666
MLGVEMYPGLALGPQRLSDCYYRDRDVPLYPSTCEMAARALPPA
LLKPHGNIDSPAAPQDSVRMELENAGLWKQFSTVGTEMIVTKKGRRMFPQLRVKLSGL
NPSLRYILLLDIVPVDSSRYRFQDNSWQVVGGAEARLPDRVFIHPDSPATGEHWQNRT
ISFHRAKLTNNTLDAQGYIILHSLHRYQPRVHVIEARDVLMWGRTQHSFTFPETQFIT
VTAYQNNKITELKINSNPFAKGFRENGMNCKKQREARLKRKITSSQEECLDIESCDPC
DSTELLPQSVDLPSSALSIMNTALPITDSGFHTEVSSHPDQTDSDQTLVLEQAFLTSE
MPSSMESQQQTTSENNVNNALMDETGQMMDLSGYTSSFPTPQLSSHTSVPQSSSMYSV
VSTTQSSDLELPQASSISSPHSMPAYSSIPSAEYPGVNSSTAMPASTTSLSDSYSSIS
HSTSSHLLQSSSYHSLLPTDQSQDNLSPHTPTNPPFQSIPACQGTRLTIDSGQNQVDD
GGLSSANATTPAVPNPTQTAFPFPPVQPNNDPDPTSPSCQSLPQSALPYQQVSQCNQI
PTPSDPNTTPTAFPFPPSEQSTPNSIMVSSNPNTTAFPFPPVQQQLNLSTSGPSSFPV
SQSSGLNAIPNPVHPTTGSFSFPSTNAIHQGPMQSVPNTLHPSTAYTFPSSLPKHTGP
LPNPAPTSYPFPTPIPPGPHPLQSLTLPSSCSISNTSQIQSTFPQSYHNPSFSHIPPQ
MANHSQITSQSFPPLQSSSAPQLLSQSSTHPQCPPPSNAYPAVAPTEIGTFPQLNSAT
PYLPDVVLHPSILPSLDPSLSSSAPPSLYNPFPSYSLRLCQDPRSSLHLPLRHIYRQP
QHAHGQGSYFDLGGRTVF

>tbr1a (new) XM_688029
MHLQQQLISPANKPVSLDNGFPHIIMTAAAGVERVSSSCSSGDA
HEPPLKRPRSPSPNARETQDNGESENKPESSDPRTDFASEMFSYAGQHVVPALSGHYM
SPQPVISSGLYSGMSYSYPQPYEQTYANAAVYSFPAVSGKAQVYLCNRALWFKFHRHQ
TEMIITKQGRRMFPCLTFNVSGLDPAGHYNIAVDVILADPNHWRFQGGKWVPCGKADT
NVTGNRVYTHPDSPNTGAHWMRQEISFGKLKLTNNKGASSNNTQMIVLQSLHKYQPRV
HVIEISKNEDEDTSDPDGVQTFTFPETQFISVTAYQNTDITQLKIDHNPFAKGFRDNY
DTKYSMDNTDRLTPSDSPHSQLLPSSRYAMPSALFQEQFVDSYTKSCFTTGTPERGLE
FTNSIMTSNQTQESSVTSGQRWFVSSPSVPSYEADVDTAALLSYTTAGVKNLPFTSTG

GSSNSLDYYTSTAGWDSRGSLENGSKTISNLSGWVLDATLERSMQPNYLPDDRELMER
SSLGVSAELRGKDVVDSTWTDTQSSIKSVDSSDLRILEEAPKDDLSIRPDSEDQAAED
VQNRARNGIKESGFFHFDA

>tbr1b NM_001115090
MQLERCISPALARSKKCMIVGSGYPNAQASELALQDYPIISIGD
NLERSSPLKKNSAGMTNQSEADNFADSKDSSGDVQRGKLSPDLDGVADSRHTFDGSAG
ERYLLSQSSQVQPSPTTMFPYPSQHGPTHPAFSIASPSRYMAHHPVITNGAYNSLLSN
SSPQGYATAGYPYAQQYGHAYQGTAFYQFSSAQAGLVPGKAQVYLCNRALWLKFHRHQ
TEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWRFQGGKWVPCGKADT
NVTGNRVYMHPDSPNTGAHWMRQEISFGKLKLTNNKGATNNTGQMVVLQSLHKYQPRL
HVVQVNEDGTEDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDHNPFAKGFRDNY
DTVYTGCDIDRLTPSPGDSPRSQIMPSARYAMTGSFLQDQFVSSYAKSRFHPGVGGAP
GTDRSVPLSNSLLSPQQTEETTVASPQRWFVTPANNRLDFAASAYDAAAAADFAGNAA
TLLSYAAAGVKALPLPGAGCSNRPLGYYGEPPGWGTRTPPQYCSKSSSVLSCWPSNSV
GSRTTASSYLVPGLEDGDPIAPERSPLGGADESKPKDLSESSWIETPSSIKSIDSSDS
GIFEQAKRRRISPSATPVSETSSPLKSEMLTPRECEKNCSKDIGYYSFYPHS

>ntl-a NM_131162
MSASSPDQRLDHLLSAVESEFQKGSEKGDASERDIKLSLEDAEL
WTKFKELTNEMIVTKTGRRMFPVLRASVTGLDPNAMYSVLLDFVAADNNRWKYVNGEW
VPGGKPEPQSPSCVYIHPDSPNFGAHWMKAPVSFSKVKLSNKLNGGGQIMLNSLHKYE
PRIHIVKVGGIQKMISSQSFPETQFIAVTAYQNEEITALKIKHNPFAKAFLDAKERSD
HKEVPDHSTDNQQSGYSQLGGWFLPSNGPMGPSSSPPQFNGAPVHSSGSYCERYSSLR
NHRAAPYPSHYSHRSTTTNNYMDNSSGSLASHDSWSALQIPNSSGMGTLAHTTNTTSN
TSQYPSLWSVAGTTLTPSGSASGSITGGLTSQFLRGSSMSYSGLTSSLPVSSPSSMYD
PGLSEVGVGDAQFESSIARLTASWAPVAQSY

>ntl-b XM_001343597
MDSGDCPEKNIQFRVDHLLTAVENELQAGSEKGDPTERELKVAL
DENELWQKFKALTNEMIVTKNGRRMFPVLKVNISGLDPNAMYSFLLDFVPADNHRWKY
VNGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKSCVSFSKVKLTNKLNGGGQIMLNS
LHKYEPRIHIVRVGGPQRMITTHAFPETQFIAVTAYQNEEITSLKIKYNPFAKAFLDT
KERSDHKEIIEDVSESQQSGYSQLSSWFLPSAGSLCPSANPHAQLNSALSLSTSHGCE
RYSTLRGHRSAPYPSTYAHRTASPTGYSDSSSCLSMLPSHDNWSSLQMSSHSSVLPMG
HSSGPNSNTSQYTSLWSVGNSSQSGSMSSSLGSQFLRGSAGHYSSLAHPLTAPSSGSP
LYDTAASEASEYDTAAHTRLPTAWTHVAPPSL

>eom-a NM_131679
MQLESILPGASVNLPKTFYNLSSSSESTNNSPGSTQIDFQDMDR
TDSEQSSGAKKFLMDDADSESFTGTKAAAAATAAPDARKSSPVIGADDELSSTRRYNI
DDLGTDRYFISSSQPSSDVANPCSLFPYGGQTGSVYSGSNGSRYSSSLHYGSVLPPAG
FSSAVCASRSQFGGGYQFGQGPGCLYPSYPGPGSSLSSMPIPGSGSAARAQVYLCNRP
LWLKFHRHQTEMIITKQGRRMFPFLSFNITGLNLTAHYNVFVEIVLADPNHWRFQGGK
WVTCGKADNNMQGNKVYVHPESPNTGAHWMRQEISFGKLKLTNNKGANNNNTQMIVLQ
SLHKYQPRLHIVEVTEDGVEDMSSEAKTQTFTFPENQFIAVTAYQNTDITQLKIDHNP
FAKGFRDNYDSMYTAPESDRLTPSPTDSPRSHQIVPGARYAMQPFFQDQFVNNLPQNH
RFYGSERAVPQTNGLLSPQSEDSAAGSASAQRWFVGPVQQSGATTKLDLSYDSEYSAS
SLLPYGIKPLPLQSPHALGYYPDSAFASMAAGWSSRSSYQRKMTTGLPWSPRPSPPAY
TDDLLSSKDKLQDENSTAAPTAASTGPWMEAPPVLKSVDSGDTSGYSMACKRRRVSPG
GSSTDASPTIKCEDLSSEEYNKESHKAMGYYAFYTSP

>eom-b NM_001083575
MPGEGSSSGSALSSHPEAEEEKVSPVVCGDDLSSRYLLDGLSSS
RYFMQTQDSPSPCSLFPYSGQTGAVYAGSDGSRYSASLHYGSVLPSAGFCQSLCAGRG
DFSPGYHQFGHAAGNGYSPYQGSGSGAVALPSAALRAQVYLCNRPLWLKFHRHQTEMI
ITKQGRRMFPFLSFNMTGLSLSAHYNVFVEIVLADPNHWRFQGGKWVTCGKADNNMQG
NKIYMHPESPNTGAHWMRQEISFGKLKLTNNKGANINTSQMIVLQSLHKYQPRLHIVE
VSDDRSERDSNTQIFSFPENQFIAVTAYQNTDITQLKIDHNPFAKGFRDNYDSMYTLP
DRERLTPSPADSPRAQQMVPNARYAVQPFLQEQFSSLTQRSVTQPSSVEDPAQRWLIS
QNSSKLELTAYEGEYSSSLLPYSFKSLPLQSYYPDTAFSWGTRVSAGSSFPRKLPSGL
PWSPRPSPTDFSEDPEKAREENSPFCWMEKPSDAAEPSIYSVVCSKRRRLSGDAPPGK

TEEQNFHKDSPSAAKAIGYYAFYTSS

>mga-a (currently mga) NM_001170739
MADTEKQGAMVLHEEGVTAPTLAPPTTTPPSIFVVLKQLQSSDS
GNDKANLMAISEANKMGKSSIGTTVAGIQPTSSTFADTNSTTPSENLPADARCRGITV
TLDNNNMWNEFHRCKTEMILTKQGRRMFPYCRFRLSGMEPFQNYVLAMDIKPADNCRY
KWSGKGWEPNGKAEPHISRLFVHPESPASGLHWMQYPVSFYRLKLCNTLDQEGHIILH
SMHRYLPQIHIIPADKVSKDILILDRPNVVTLSFAQTEFFAVTAYQNLCITQLKIDYN
PFAKGFREDAVNARSSKAKNGLSTDETESELKLSKEMTTLNNLKTLFMKRKASVKVNV
NQNVPNPTNGENKVVNGAAPAVDTNVQSLCNKKRPSSSAFSDFIKGAHVKVKRLSLEN
INKTGGATEPSTACTSKQKEAADISSITENSLQVDQKDGNGAGDVLRCESTDTSLKTG
VLKANEIKKEIDEHSADKNTLKSSDQNLSCSDEKKMETVSSLSTEAKPDAQMKKTLPH
KRPERVPLPLLAKFLKQRRPILPKPVSHSSLSDSEKSCEPAQTSESSSVLMSFIPCVT
TNLDSQPAVTSLSQTVTSSTTDANNMTSLSTTLSYSSTTVPLIPSETQLCDRFSASPV
GSDPFSAPNTTSPSKPNSNPALDISNNTDAIFTPDHDNTLRSQSDISSDSTCDVVHDS
CPPTVNTDTVETPVVPSPTSVFDVPSSTDNDMNSYQDINSMPDVAEGDSISDCLLDSS
TGSCPEFFSEEIPQNTLFTNEESLSLPLDDASSPAFSLPSPAPSSPDPFPPSLFCDRS
VPPRKALDSFPERLLDCTAASARDPFPLGFFNDGREPPRQIFDLPERPLIGTVASRES
LSSSVNNGPEHPMETGDLFSQSHCPDRANSLNDLESAASCETAVSDNSISKPTKPSPH
GSSCKKYKGKQKKVGTLKLGEDSEVFDGPVPVPLQPSLEDVEGQLFVSFMSKKALRIH
LGDDDDDKPETAQENTDNPDGNNEEKIEKKIEGLEKVLLHDLKFMKNRQVIHPVLQEV
GLKLNLLDVTLEIDLQYLGVQLPIPPPALSPEETSSQAQFVSRTGKTSDFTQIKGWRD
KFAPSASLSEGVSSTDAGQSNLSAFCSDMLDEYLASEGKLIDERAASLSQADCTPVAY
QLPTKSTSYVRTLDSVLKKQVPAILTPTTNKVKPTFKSKVENKSKKPLKPGKGKQTKP
VISDAEPLCTKKPQQNKKYKSRKEFKSPEKPDVAEVPASNTTPMAEDSGSTSSTCAGG
RSPGLPKTLVKLLDVEDGAVWEGRHRSYITEERAAIALATLVTAEGASTGSADAIRII
RRRAPPCLNVFCRLGCVCASLVHLRRHHHCGKPQCMLGCSCLRRKVVALKTPKQEEGT
ADDSDPQGMSEENKAKWRKKNKMRKTYVLTDPELAPEPAKRVSTLWDRTRGNFDKEVL
YCPPPPRSPQPQLLSQELQHDLESFLSPSKQKRVEERNLSTSEDNIEINLTCARSRPF
HSNCHDKPKADDNKHHISQVSTPDIEEGELVPLNLSGPAKRLEMMSERTWTSIDMRNN
VMRIVCEHMAQDRLNQPFWMGKYFIKPVSKTLEKEENGSVEIYKVIISQPVEKKTENE
KITQKEEELEKHVKTSEVKGLPFLSKCCPAGLLKAEKKSPDAPGQIMVNGKHYPQAKL
ELGHMGALHPANRLAAYITGRICPTVSAITKPPVTTVPSSTLTTVSKVTCTPASTTTS
VSKSLGGSTLTTTTSASSPGLTSPAKKTVYITVASRNTGLSNSGTQIKKIVSPTGPPQ
TSGQKMLLQVVKTADGNTLYRNPNGQLMQLVPLSQIKALKPNLLSQGQPTIIRLPAPP
TVSMNKPQGGSATIVTSSIPTTQTLAKPSGTVPVSTSSSMGGKLISPPSSKSVSLSSL
PSTLKVVQGFLGQSGTCTLRILPPTTSTSSTVLSQSGLTLLKSASSMPPTQDSSNSET
NVSFSSQSTEKTVVQVLKQSTIDPAKQNSSDNANVKEKHFNKAPDPEEKEIGSDSTEL
TDDSDLYSDDDQEDASCMSASDREEKIEDTDGMDSEKKGYAEMVVDIETIEESAEQNR
IAKFRASALRRNQYRRNQKRIHDEMLEVRVQKVRKERKRRQTLXECFIKLQGTLGMSS
KKFEVSRMRILTKANKEVEYLVKLEDYLVEKKAKLQFKKERYIQTLSQLCDKSTESIG
LKLNEIISKQKALEAQSKTKETHPKPIQAKSKAKPKPKSKPKSKVVDVCDKPKGLAVQ
NKVNDVSKVTYSPSKPIDLSIKKQKSPEMTESVPKSTPSVSVPADLDGNKNTLNVLDT
NTVTTTSTPIQPSFNSTLVMKPVSIPSPIKHPPITRERMRPNILSRASSQAMQGSPVK
ESLLTNVCIPQVLPLMNTMVPCNPIITINNSLQPIGITSVGQQSSTPGVASVSIVPTI
SHPLRVENTLPMLHPQFIKITNSPVNINTKVDSASLPNISNVISLAENLVVPRKVVED
KPVFQAQPTSVDNQQNSSNDKIPDLEQKTDEAPSTNVPKQSVVEDQKGASVPKSNPEV
PENKSPDDSDDPEDENLLSLLDELVLLSQQLTNEDEDERIAVPGDVQSCSDKPEDQEP
ADDRALSPLFLTLDEDLMSPDSKDEIDIPPKVDDLVKVIFGSDSPSVSSESGVAQSTN
ASSPHASTCNATGDGLTPPPLLHMKAAYEAASRQSANEGTSVTWRPMPKLVPLGLKAQ
DAGKVINPSIPNLDSSEQDTPQM

>mga-b (new)
Note: The full-length sequence of this gene is not known.
This clone is a composite sequence made from the following
three sequences from Ensembl & Genbank databases:

XM_002667174
ENSDART00000125698
XM_002661949

MFEHPAAMEITAEGMLGNHDTVKCTNPADSGAL

VSTEGRPSRVIEATLENESVWSRFHSLGTEMLLTPQGRRMFPCCRFRLRGLDPDLQYFLL
MDIAPLDDLRHRFNGEAWEPDGPGEAHLQSPVCFHPDSPAVGQHWMDSPVSFYTVKLTHD
SCEREGVLLQPMHRYQPRLYVAPVSACLERAVPLKSPNVHMFTFPKTEFYAVTSYQNPQI
TRLKIDCNPFMLAFREDETSARLIQNKLKLALTPARTHTAKYTADNHTTSDGEQHLRKSC
RLIVNLNVRCVCFMTCRLHSELKHSHTEKSFVRFSKHEGIDSNDSRTIFLKSAKTKVNTA
NNDSSSDGEQYLSQQDSIRLTVRFSSLKQQKLNKHQLINENKLENNSMTNIYKRNKYLLI
QLSNIYSTFRSNSSSTTLIIIIINQYKLLPKTYFLKSKCYIYLTSSLKNKAKSNNDKTYN
GNNLNTLITTFLCCGTVNHQQPHDFICVAFKFVLLLKIKNIFDFNSKVNANCLSPNKISV
NQHFNTKAGNKLSSKPKFLKTFEVFNLNSQKEKNLRSDEDLTFKLSMCSKAGRRPLSRGQ
RVVLRRPRPMKRGKKARAKWWTRVKNVQALLDHRKRMQSISTHTDVCMQPDLEDVEGVLF
VSFTAKEALDVHVGNMRSSVGSSSPPPPSPSISPSSHTQQLSACVTDPPVTEADRISELE
LALLQDLKEKKNRQILHPALQKAESGFVSRTGKTNDLTRIKGWMEKFSLRSTSGTANSSA
FCSEMLDEYLESEGQRISERAEVFSSSDPSPVVYQLPVRSSSYVRTLDSVLQMRTSPSAA
ATAPQQPSRRVAKRMRISPVRVVSRPVALPQPAVYSAGVGRVRSRRGRKRRRPHISFNRD
AVDGAQPSCTEKHTQLRTLEEQALTHGQIHTFISTERARVSLSALLTAQSVLVETPQWST
HIADDGACAKLFCRLGCVCDSLSRESAGSTHCRRVECMFSCTCFKHKILLIRSADHSQSV
RSLQTLHPDPEGRPAPAARVTRLWERSAEESDPEPMSTPKPAGALRPAPRTHTHTHTYTL
TPRGRPPANRPPNAQVPMEKDPVYLYLESMMTCARVREYNSNPPPQVHILPAKKSSDEAL
SDTSLLNPSKRPHAAQSPDKPEPTKVLEIISGCNWESQRSRVLKELFQRVQTNTLPSVLS
LDDYTVKLLSEHLKKDGPRSMITYKVCVSLSDKEKSAQKECVQKECVEKERVQKERGKEP
ALKPVPLLCGVMTAGHLKAQRRAPDLHCPIQVNGRTYAQAKLTLGRMGSLHPANRLAAYV
TGRIKSFVPSRTRTTAASRRSKYTATRANHSTDVFKKPATQRLSIPRPPGGIRFPKVRRI
LNALAPPLSAADRVVPASALPPGQQVVLQPVAGMSGVNMCQFNGQMIQLVPVSAAAPMQI
QTSTTHSSGGASQEPQSSLQLPANTALPFIIPRIHSVPGRNGFTFASAAAPGVQNNLLNK
TGTFSFRICPPSAESQSPAPTGAPQGSVTASTLILPGGYKLIKLINPAEKPDQNNPAEEP
DQTIPAEEPDQNKPTEKPDQNNPTKYPDQNNPTEKPAQNNPAEKPDQNNPTDKPDQNKPT
EKPAQNNPAEKPDQNNPTEYPDQNNPTEEPAQNNPAEKPDQNNPTEKPDQGNPTEEPDQD
NPTEEPDQTIPAEEPAQNNPTEKPDQDNPGKKPDQDNPTEEPDQNNPTEEPDHNNPAEKP
DQDNPTEKPDHNNPAEKPDQDNPTEKPDHNNTEPDQTIPAEEPDQTNPTEKPDQDNPTEE
PDQDNPTEEPDQTIPAEEPDQNNPGKKPDQDNPTEKPDQNNPAEKPDQNNPAMEPDQDNP
TEKLEQNNPAEKPDQDNPAMEPDKNNPAEKPDQNNPAEKPDQNNPAEKPDQNNPTEKLEQ
NKPTEKPDQDNPTEEPDQNNPAEKPDQNNPAERVENSQSSVCVKVEPAEAEEDITTQSAH
KPPALIKTEPEHIQIPQLTNDGGTAKFTIKIEDAEADESVPQQQSRRKEEPFQFGGFSFE
GLTNSAFSRLSFAVPSPPAEPGEPDGSVQKSLDWLWRGRADVDTHAELSEKPQQNGTLMY
SSDGCTTEDSMEQLSEGEVDIETFEENDQIISRLREKARRKIQSRVPPPPPRSRQLKVKP
VKSCTAHPVRLMSDLLLYRRTRRLNQPIREKRRQLELLQSERTLRRTMCVREQSISTEEL
LHQACELITSLEDHSRFLIEEKRALMRQHSHYQTLICISQASGRFLHDSHIGPSGSCCIM
PEHDHCTVNDDDDEDDMSD

4) Amphioxus T-box genes with Genbank (mRNA) accession numbers

>Amphi-Tbx1/10 XM_002611831
MEANSPLSPKANAFSIASLISASEQGGLLMSDLHGKDQGLDDGQ
DWGMQYSSIPREMEASCMLSNQRMPGHQLAHMTEHPSAFGVTQARGEAYDIPGMDSCR
NGGGLPNGNENNNLLNDGVKDERKQNPKVANVKVMLEMKALWDEFHELGTEMIVTKAG
RRMFPTFQVKMFGLEPMSDYILLMDFVPVDDKRYRYAFHSSSWLVAGKADPDMPRRIH
VHPDSPAKGAQWMKQIVSFDKLKLTNNLLDDNGHIILNSMHRYQPRFHVVYIDGKKGD
SDTVHENYKTFIFPETKFTAVTAYQNHRITQLKIASNPFAKGFRDCDPDDWRTLTFHG
RNESDSVVEVLTQIPPSQRPRNHHRPSSLQLVGVTRTRTVGQMNTSQDQERRDRQEDT
SQQCQSSPIVSRVLSPNLAGGGMHVNLQRPEQTALAHTSLPDNSYKYHYNGYMAAKTR
PTPYPLPSMRPTGYHPVNNSLYAPCTRSSPYDLD

>Amphi-Tbx2/3 XM_002598876
MAYHPFLAASKALDFPMPSFLAQPGLFPGMPLLPSGAHGLGMPK
LSDPSPGQTPADVSKALGGAGSVLRPIPQQQDDDSEDPQVELEYKDLWDQFHTYGTEM
VITKSGRRMFPSFKVKVSGLDKRAKYIFLMDIVAADDCRYKFHNSRWMVAGKADPEMP
KRMYIHPDSPATGEHWMSKTVSFHKLKLTNNISDKHGFTILNSMHKYQPRFHIVKTND
IMKLPYCHFRTYVFRETAFIAVTAYQNEKITQLKIDHNPFAKGFRDTGAGRRGEKRKH
LHTFGHQHPGFLEEGHSSDLETVDCGDTVTEKEPRLESRPPLSPKEPASPVVEGSPSV
GANYRTEPGSRPFATCSGDEGSEQQERPASLHTHKGNCTETNKSAQECHRRDAPPHCG
NEIRPGTAALREGEERGAHGGGGASDKENGEHHHNEKTESQQQQQREKNLEKKAVHHN
NKESSSEKSESNNNNKLPTSSSLPSPLSAMNPGSSHMGRIHPSQLQGLASMYPYQLLS

GGHGLPNRPPFLFHPSQLAMSGGGMPQFPMNPFLAFPVPHSGMNGATQPLSSPTHPLL
ASQGYPFFGMSPQGYTALLDGSIFNPGFSFPQAAELHKRAMAGARHPLRFSPYPLSAT
STTMVTTGSPVVCPGIPSRTDASSSSDAPRESPSSSSSPGVRKNTSPKRASSPPTRTS
VSAPEVSSELQNIQKLVSGLEKQQEQLAVETLTKLTEQSKLQ

>Amphi-Tbx4/5 EU084005/XM_002598875
MSGDLKESVGDERPRQREPDRKDDGPPGADDRTDGVPEGLEDVK
VELQDAGLWQRFHKAGTEMIITKAGRRMFPSIKVKVTGLQPKTKYIFVMDIVAVDSHR
YKFNESKWSVAGKAEPAMPGRVFVHPDSPATGTHWMKQVVCFQKLKLTNNYMDTFGHI
MLNSMHKYQPRLHIVQASENNKFELKKTCFRTFIFPETEFMAVTSYQNHQITQLKIEH
NPFAKGFRGGDDTEFSRSARKSINYPVIPRSNPVQASLLPRGRPNNNYACSSNMAADT
CPSLSSNHYQQTTAGYNTVPIGSSIQMTTQENSGGCMQNSFSGGTDLGPLPKRACREE
DRLLSDNSVATSTLTTWSNPQILPNMENLQPLNRETCMFANSATGDTTSSLLAAPQPL
DPLSTAFNNNQNFSSVPFSSSGTGFVSANGGMNFLPSCSYAQMPQQGLGMNGTPFLHE
VSRNVGCPSMQIPQ

>Amphi-Tbx6/16 XM_002611967
MMYESEDVLTQRARAFSINNMLTGSPHAFPFPGFPMAQAAPAPP
PDPCAFSDRFATDFHMTADHKTQRLGLGHLPAPQNFPPPSALKDMKVTLEQKDLWDSF
HDIGTEMIITKAGRRMFPTYKASISGLDPNAKYILLMDIVPMDDNRYKYHNSEWVVSG
KAEPLMPGRLYIHPDSPATGTQWMKQSVTFHKLKLTNNAMDQQGHIILNSMHKYQPRL
HIVQANDVYSLRWNSFSTFAFPETSFIAVTAYQNEKITQLKIDNNPFAKGFRDNGGNR
RERAIVSTKRSADAAGEPGDSVSNKRPCTGGEQPERNNRPPSCDCSGVGEESDVPRGP
SQYNPPAQADDLNPCGNPLTIVTDDIATDFAKERSPGVPHALGGQGSAALPTRDQAAL
GSCQGEDMRCQTRTACAQDPRDLLASPDSADYHQQYHPGGYSGQAAGDPTDSTVVPLG
YGTGPSFQELSVQTDLGTAADMASACKNDAVGLNAPGTAVLPSYPAVSSFHTGLPVSN
PPLYASGGTPPQRSYDVYPTGLFAAPTAYEPLDYATTCKMAGFSRMQMSVAPAPHLSH
FPTSSATSMPVNFHGMFNTHPMPAAYPGHAGKFAA

>Amphi-Tbx15/18/22 XM_002599011
MAEKRKSAPVTLSSRAHAFSVEALLGPRVKKQRTAQFHSSREDA
PEDNVLENFSTSDGRQEDRAAEQSSSALGSIQALQSRLAYPLPQPDGPDQVRVELQGK
DLWSRFHDIGTEMIITKAGRRMFPAIRTKVTGLDPKAQYIVIMDIVPVDNKRYRYVYH
SSKWMCAGSADAPPPPRVYVHPDSPASGEAWMRQTVSFDKLKLTNNENDEQGYIILHS
MHKYQPRVHIIKKTAHTDLTNKTSISPSDKAQTFAFPETVFTTVTAYQNQQITRLKID
RNPFAKGFRDSGRNRSGLECIMDSYALWHNPAGRPLTYGQYTSMKSQEEEKLMSGMLQ
PPSPPTAFYLAPNTFNVGCREGQACLTPERYQEPSQRTSINKENVFSADLPSDSPRLA
HPQCSATGSMCRHPLMPESPALPHPDDYVRQTATQPPSIPYQYLPSSPHFSQTTLSPT
QHSPLLGAPYPSPRNCSAGSSPHSYLPISPSTSGTSSCPTTSHLSPTFCTSATFPHPY
FNNLQVLPTSALPTSALPTSALPTSAPSGYSYLHGQYRLAVHRIPSPQASLV

>Amphi-Tbx20 jgi|Brafl1|221929|e_gw.90.81.1
Note: The Genbank entry for Amphi-Tbx20 (XM_002612304) has
a possible error in exon prediction such that the first 19
amino acids of the T-domain are missing. This entry is from
the JGI website, which sports the full-length T-domain for
this gene.
MECNASPKPQLSSRANAFSIAAIMSSSCSTKKDSPEQAIKPLENFVEKSGCAQPLCGE
ASSAETTTDGGRAGRESSAAESRQESASTEPAPSDGSHLQNKEGSPELKNVQCKLESK
ELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIIPVDNKRYRYAYH
RSSWLVAGKADPPQPARLYVHPDSPFTGEQLQKQIVSFEKLKLTNNELDQHGHIILNS
MHRYQPRVHIIKKKEHTASLLNLNSEEFKTFVFQECMFTAVTAYQNQLITKLKIDSNP
FAKGFRDSSRLTDIERESVETMLKEHRYARSPIRAYAEEEPPRKSPRLSSSSSSGGLT
SPSTSVGGWPSPSFTPLPHYPHSSHPIPITPHPINPSVTATTSSLTSPLPHPLPHTLG
FGALGIPGLPHPTSALPAPIPMLSAPSPFHPLHIQRYPYFPQTAYSSVHTLRHYV

>Amphi-Eomes/Tbr1/Tbx21 XM_002589046
MDAADVDDTAVGTDSFQPPGLSMPYGMSGGYTPPDSNSSRSSPG
DGVDAELSRYNSQVPPDYPLGHYPGATNPENAYSITSMTPSPHPYTNGYDQPQMYGQQ
PPGYFAPIESGPPQPPNGQYQHGYNGNYPYPGGGSMYGYPPGPPPTPAKLSVFLTNRD
LWVKFHQHETEMIITKQGRRMFPVLQFAISGLDPHAQYNVFVDMVLADVNHWKFQNGK
WVPCGRADTNPQGSRVYVHPESPNSGAHWMKQEVVFSKLKLTNNKGADNGHVVLNSMH

KYQPRLHIIEVSNRAGGGERVLQSHSFPETQFIAVTAYQNTDITQLKIDYNPFAKGFR
DNYDGPTNIRPNGFDGRSAGMEPGMHPSLGGPLPLMPPIYPVGPPMPAHNRGIHLPYD
MRSHSSGGSSSSPGSPEMQPKDLELKETASDLPGSAQNGQSNATPEKQASPTRVNNSN
LLLTTTAPYTVNSSGQPHYSMAMTMHSRGMPPRNGGLPQNGQVSENGNMAPNGHISQN
GQSQGEEARPEWRSPSKTRPSGDEDDNRDAAAKRLRTEELPPYHDATPGNNYDVYDDQ
PGDGTSSFGQQQDHMQYHRYNGYYSANPEDYGHYYDRNAMQYGYYGNQGYQASAHAQF
VDSEKFAHAHYNGAYHQAQYNGGYMPTSTASAETATGHY

>Amphi-Bra1 XM_002590345
MSSAETMKQPTAASPDQFSVSHLLSAVESEISAGSEKGDPTERD
LKITLEEKPLWDKFNALTNEMIVTKNGRRMFPVLKVNVSGLDPNAMYSFLLDFTAADN
HRWKYVNGEWVPGGKPEPSVPSCVYIHPDSPNFGAHWMKSPVSFSKVKLTNKLNGGGQ
QIMLNSLHKYEPRLHIIKVGGPDNQRMVSTHTFPETQFIAVTAYQNEEITALKIKYNP
FAKAFLDAKERSDGKDGMEDLQDQPQYSQLGGWFLPGTGPICPPPNPHQFAPSLGLPS
HGCDRYSTLRNHRSAPYPHPYQRSSPPTNYGHDTAASLPMMPTHDNWSGLPVSTHNML
SMSAMPHTTTSTHAQYPNLWSVSNNNLTPTTHAQTHMSGTMGTGLPHQFLRTTAPAPY
HSIPTCTVPTTASSSPVYHDSHEVSSTDSGYGHSTTPPAPQTRITSNNWSPMTPPSL

>Amphi-Bra2 XM_002590344
MKQTPDQFSVSHLLSAVESEISAGSEKGDPTERDLKVTLGEKPL
WEKFKSLTNEMIVTKSGRRMFPVLKVNVSGLDPNAMYSFLLDFTAADNHRWKYVNGEW
VPGGKPEPSVPSCVYIHPDSPNFGAHWMKSPVSFSKVKLTNKLNGGGQQIMLNSLHKY
EPRIHIVKVGGPDNQRTLSTHTFAETQFIAVTAYQNEELTALKIKHNPFAKAFLDAKE
RNDTKSGHDDLTDQQPQFSQLGGWFLPGTGPICPPPNPHQFAPSLGLPSHGCDRYSTL
RNHRSAPYPHPYQRSSPPTNYGHDTAASLPMMPTHDNWSGLPVSTHNMLSMSAMPHTT
TSTHAQYPNLWSVSNNNLTPTTHAQTHMSGTMGTGLPHQFLRTTAPAPYHSIPTCTVP
TTASSSPVYHDSHEVSSTDSGYGHSTTPPAPQTRITSNNWSPMTMPSM

>Amphi-Tbx6d1 (new) XM_002588055
MSLSEKAQAFSIDSLLAADPDKTSEDGNEELSPMCDIVPSCGVS
STGLNSDNFALHRSLGPPWGHDGSLQSTGAAERDGLQGNMFPLTGEADRSPPPAATPR
DVSSQEYGLPIAKTTHGVTVSLEKAGLWRQFQECGTEMILNRAGRRMFPPVMVTITGL
DPSATYRVYMDVVPADGYRHKFTKTAWVATGPAEFSISNPPYEHPNSPASGAGWMGTV
VSFAKAKITNNNDSVEGNFLLHSMHKYQTKIIISRQETDKKARSCLGDHTHTFQFEET
AFVAVTAYQNHRVTRLKIKNNPFAKAFRDSDVMALVTFHLFHQGSWRAPDSLQEVTPV
PTKRSMGIEVVAEHFVVTLLF

>Amphi-Tbx6d2 (new) jgi|Brafl1|86982|fgenesh2_pg.scaffold_157000034
Note: The Genbank entry for this gene (XM_002611966) has a
spurious exon in the T-box region. This entry is from JGI
website and does not contain the spurious exon.
MPCDQRSVLRETQRQCMYQKAASACSGMPTRPKVELEAENRKLWELFHQAGTEMIINTKG
RCMFPTLTLNLTGLKPERRYYILVKMILTDESLYGYRNNQWVVVNGDAKPSVADSVYVHP
KCPEYGAKLMERPLAFPALKLSSRMHDGKNMVQLRSMHKYQPVVQVVEADNTTDLAVAPS
WQFSFPVTEFMAVSSYYSDKIRKLKVDNNKFAKNLRNLESVDRRERSQGQVPAVPRMVRP
PAQKSPPPITCVLPPTTCGNSTQTASPTAADTHVSPKQGQLVSRVQPRCIQQEMLGELYN
PAEMEKLRATTTMQAPMACTTAALHTQQISDIPLTQPLQPTALAYMRHFPGVPATFTPTS
NDVVNPIAVRTKAQLKAYPTHMGYFPLPPGMVL

Figure S2. Alignment of the amino acid sequences of the T-domains used in the phylogenetic analysis (in Figure 1 & Figure S3). Sequences in masked regions (grey) cannot be reliably aligned and therefore were excluded from the analysis. Human and zebrafish gene names are written in all upper case (human) or in all lower case (zebrafish) letters. Mdom: *Monodelphis domestica* (grey short-tailed opossum). Amphi: *Branchiostoma floridae* (amphioxus). Sequences are given in an interleaved format.

```
TBX1                LWDEFNQLGTEMIVTKAGRRMFPTFQVKLFGMDPMADYMLLMDFVPVDDKRYRYAFHSSS
tbx1                LWDEFNQLGTEMIVTKAGRRMFPTFQVKIFGMDPMADYMLLMDFLPVDDKRYRYAFHSSS
TBX10               LWEEFNQLGTEMIVTKAGRRMFPPFQVKILGMDSLADYALLMDFIPLDDKRYRYAFHSSA
tbx10               LWRQFDQLGTEMIVTKAGRRMFPTFQVHISGMDPAAEYVLLMDFIPVDDKRYRYAFHSSS
Amphi-Tbx1/10       LWDEFHELGTEMIVTKAGRRMFPTFQVKMFGLEPMSDYILLMDFVPVDDKRYRYAFHSSS
TBX15               LWKRFHDIGTEMIITKAGRRMFPAMRVKITGLDPHQQYYIAMDIVPVDNKRYRYVYHSSK
tbx15               LWKRFHDIGTEMIITKAGRRMFPAMRVKIVGLDPHQQYYIAMDIVPVDNKRYRYVYHSSK
TBX18               LWKRFHEIGTEMIITKAGRRMFPAMRVKISGLDPHQQYYIAMDIVPVDNKRYRYVYHSSK
tbx18               LWKRFHEIGTEMIITKAGRRMFPAMRVKIAGLDPHQQYYIAMDIVPVDNKRYRYVYHSSK
TBX22               LWKRFHDIGTEMIITKAGRRMFPSVRVKVKGLDPGKQYHVAIDVVPVDSKRYRYVYHSSQ
tbx22               LWKRFHEIGTEMIITKVGRRMFPSIRVKVHNLDPLQQYSIAMDIMPMDSKKYRYVYHSSQ
Amphi-Tbx15/18/22   LWSRFHDIGTEMIITKAGRRMFPAIRTKVTGLDPKAQYIVIMDIVPVDNKRYRYVYHSSK
TBX20               LWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRYRYAYHRSS
tbx20               LWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVPMDIVPVDNKRYRYAYHRSS
Amphi-Tbx20         LWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIIPVDNKRYRYAYHRSS
TBX2                LWDQFHKLGTEMVITKSGRRMFPPFKVRVSGLDKKAKYILLMDIVAADDCRYK--FHNSR
tbx2a               LWDQFHKIGTEMVITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYK--FHNSR
tbx2b               LWDQFHKLGTEMVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYK--FHNSR
TBX3                LWDQFHKRGTEMVITKSGRRMFPPFKVRCSGLDKKAKYILLMDIIAADDCRYK--FHNSR
tbx3a               LWELFHKRGTEMVITKSGRRMFPPFKVRCTGLDKKAKYILLMDIVAADDCRYK--FHNSR
tbx3b               LWGQFHKVGTEMVITKSGRRMFPAFKVRCSGFDRKARYILLMDIVASDDYRYK--FHNCR
Amphi-Tbx2/3        LWDQFHTYGTEMVITKSGRRMFPSFKVKVSGLDKRAKYIFLMDIVAADDCRYK--FHNSR
TBX4                LWKKFHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLIDIVPADDHRYK--FCDNK
tbx4                LWKKLHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLTDIVPADDHRYK--FCDNK
TBX5                LWLKFHEVGTEMIITKAGRRMFPSYKVKVTGLNPKTKYILLMDIVPADDHRYK--FADNK
tbx5a               LWTKFHEVGTEMIITKAGRRMFPSFKVKVTGLNPKTKYILLMDVVPADDHRYK--FADNK
tbx5b               LWAKFHDVTTEMIITKAGRRMFPSYKVKVTGLNPKAKYILLMDIISADEHRYK--FADNK
Amphi-Tbx4/5        LWQRFHKAGTEMIITKAGRRMFPSIKVKVTGLQPKTKYIFVMDIVAVDSHRYK--FNESK
TBX6                LWKEFSSVGTEMIITKAGRRMFPACRVSVTGLDPEARYLFLLDVIPVDGARYR--WQGRR
tbx24               LWKQFSTVGTEMIVTKKGRRMFPQLRVKLSGLNPSLRYILLLDIVPVDSSRYR--FQDNS
Mdom-Tbx16          LWTEFYRVGTEMVITKSGRRMFPQCKIRLSGLVPYLKYVVLADFVSVDNFRYK--WAKDQ
tbx6                LWDKFSSIGTEMLITKSGRRMFPSCKVTVTGLNPKVKYVVIMDMVPFDNHKYK--WNKDC
tbx16               LWRSFHEIGTEMIITKPGRRMFPHCKISLSGLVPYAKYILLVDMVPEDGLRYK--WNKDK
MGA                 MWNEFYHRSTEMILTKQGRRMFPYCRYWITGLDSNLKYILVMDISPVDNHRYK--WNGRW
mga-a               MWNEFHRCKTEMILTKQGRRMFPYCRFRLSGMEPFQNYVLAMDIKPADNCRYK--WSGKG
mga-b               VWSRFHSLGTEMLLTPQGRRMFPCCRFRLRGLDPDLQYFLLMDIAPLDDLRHR--FNGEA
Amphi-Tbx6/16       LWDSFHDIGTEMIITKAGRRMFPTYKASISGLDPNAKYILLMDIVPMDDNRYK--YHNSE
TBX19               LWQRFKEVTNEMIVTKNGRRMFPVLKISVTGLDPNAMYSLLLDFVPTDSHRWK--YVNGE
tbx19               LWRKFKEVTNEMIVTKNGRRMFPVLKVSVTGLDPNAMYSFLLDFTPADGHRWK--YVNGE
T                   LWLRFKELTNEMIVTKNGRRMFPVLKVNVSGLDPNAMYSFLLDFVAADNHRWK--YVNGE
ntl-a               LWTKFKELTNEMIVTKTGRRMFPVLRASVTGLDPNAMYSVLLDFVAADNNRWK--YVNGE
ntl-b               LWQKFKALTNEMIVTKNGRRMFPVLKVNISGLDPNAMYSFLLDFVPADNHRWK--YVNGE
Amphi-Bra1          LWDKFNALTNEMIVTKNGRRMFPVLKVNVSGLDPNAMYSFLLDFTAADNHRWK--YVNGE
Amphi-Bra2          LWEKFKSLTNEMIVTKSGRRMFPVLKVNVSGLDPNAMYSFLLDFTAADNHRWK--YVNGE
EOMES               LWLKFHRHQTEMIITKQGRRMFPFLSFNINGLNPTAHYNVFVEVVLADPNHWR--FQGGK
eom-a               LWLKFHRHQTEMIITKQGRRMFPFLSFNITGLNLTAHYNVFVEIVLADPNHWR--FQGGK
eom-b               LWLKFHRHQTEMIITKQGRRMFPFLSFNMTGLSLSAHYNVFVEIVLADPNHWR--FQGGK
TBR1                LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGK
tbr1a               LWFKFHRHQTEMIITKQGRRMFPCLTFNVSGLDPAGHYNIAVDVILADPNHWR--FQGGK
tbr1b               LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGK
TBX21               LWSKFNQHQTEMIITKQGRRMFPFLSFTVAGLEPTSHYRMFVDVVLVDQHHWR--YQSGK
tbx21               LWAKFHKYQTEMIITKQGRRMFPFLSFNITSLDPSAHYNIYVDVVLADQHHWR--YQGGK
Amphi-Eom/Tbr1/Tbx21LWVKFHQHETEMIITKQGRRMFPVLQFAISGLDPHAQYNVFVDMVLADVNHWK--FQNGK
Amphi-Tbx6d1        LWRQFQECGTEMILNRAGRRMFPPVMVTITGLDPSATYRVYMDVVPADGYRHK--FTKTA
Amphi-Tbx6d2        LWELFHQAGTEMIINTKGRCMFPTLTLNLTGLKPERRYYILVKMILTDESLYG--YRNNQ
```

```
TBX1                WLVA-GKADPA-TP-GRVHYHPDSPAKGAQWMKQIVSFDKLKLTNN---LLDDNGHIILN
tbx1                WLVA-GKADPA-TP-GRVHYHPDSPAKGAQWMKQIVSFDKLKLTNN---LLDDNGHIILN
TBX10               WLVA-GKADPA-TP-GRVHFHPDSPAKGAQWMRQIVSFDKLKLTNN---LLDDNGHIILN
tbx10               WLVA-GRGDVA-AP-GRVHFHPDSPARGAQWIKQTVSFDRLKLTNN---LLDDNGHMILN
Amphi-Tbx1/10       WLVA-GKADPD-MP-RRIHVHPDSPAKGAQWMKQIVSFDKLKLTNN---LLDDNGHIILN
TBX15               WMVA-GNADSP-VP-PRVYIHPDSLASGDTWMRQVVSFDKLKLTNN---ELDDQGHIILH
tbx15               WMVA-GNADSP-VP-PRVYIHPDSLASGDTWMRQVVSFDKLKLTNN---ELDDQGHIILH
TBX18               WMVA-GNADSP-VP-PRVYIHPDSPASGETWMRQVISFDKLKLTNN---ELDDQGHIILH
tbx18               WMVA-GNADSP-VP-PRVYIHPDSPASGETWMRQVISFDKLKLTNN---ELDDQGHIILH
TBX22               WMVA-GNTDHLCII-PRFYVHPDSPCSGETWMRQIISFDRMKLTNN---EMDDKGHIILQ
tbx22               WVIA-GNTDHSCIP-PHLYVHPDSPCSGENWMRQVISFDRVKLTNN---ELDDRGHIILK
Amphi-Tbx15/18/22   WMCA-GSADAP-PP-PRVYVHPDSPASGEAWMRQTVSFDKLKLTNN---ENDEQGYIILH
TBX20               WLVA-GKADPP-LP-ARLYVHPDSPFTGEQLLKQMVSFEKVKLTNN---ELDQHGHIILN
tbx20               WLVA-GKADPP-LP-ARLYVHPDSPFTGEQLSKQMVSFEKVKLTNN---ELDQHGHIILN
Amphi-Tbx20         WLVA-GKADPP-QP-ARLYVHPDSPFTGEQLQKQIVSFEKLKLTNN---ELDQHGHIILN
TBX2                WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
tbx2a               WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
tbx2b               WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
TBX3                WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMSKVVTFHKLKLTNN---ISDKHGFTILN
tbx3a               WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMSKVVNFHKLKLTNN---ISDKHGFTILN
tbx3b               WMVA-GKADPE-MP-KRMYIHPDSPSTGEQWMSKAVTFHKLKLTNN---ISDKHGFTILN
Amphi-Tbx2/3        WMVA-GKADPE-MP-KRMYIHPDSPATGEHWMSKTVSFHKLKLTNN---ISDKHGFTILN
TBX4                WMVA-GKAEPA-MP-GRLYVHPDSPATGAHWMRQLVSFQKLKLTNN---HLDPFGHIILN
tbx4                WMVA-GKAEPA-MP-GRLYVHPDSPATGAHWMRQLVSFQKLKLTNN---HLDPFGHIILN
TBX5                WSVT-GKAEPA-MP-GRLYVHPDSPATGAHWMRQLVSFQKLKLTNN---HLDPFGHIILN
tbx5a               WSVT-GKAEPA-MP-GRLYVHPDSPATGAHWMRQLVSFQKLKLTNN---HLDPFGHIILN
tbx5b               WSIS-GKAEPA-IP-GRLYVHPDSPASGAHWMRQLVSFQKLKLTNN---HLDPFGHIILN
Amphi-Tbx4/5        WSVA-GKAEPA-MP-GRVFVHPDSPATGTHWMKQVVCFQKLKLTNN---YMDTFGHIMLN
TBX6                WEPS-GKAEPR-LP-DRVYIHPDSPATGAHWMRQPVSFHRVKLTNS---TLDPHGHLILH
tbx24               WQVV-GGAEAR-LP-DRVFIHPDSPATGEHWQNRTISFHRAKLTNN---TLDAQGYIILH
Mdom-Tbx16          WEVA-GKAEPQ-LP-GRSYIHPDSPAYGSHWMKEPVSFHKMKLTNN---TLDQHGHIILH
tbx6                WEVN-GSSDPH-LP-NRFFIHPDSPAPGQKWMQYPISFHKLKLTNN---TLNSNGLVVLH
tbx16               WEVA-GKAEPQ-PP-YRTYLHPDSPAPGSHWMKQPVSFLKLKLTNN---ALDQHGHIILH
MGA                 WEPS-GKAEPH-VL-GRVFIHPESPSTGHYWMHQPVSFYKLKLTNN---TLDQEGHIILH
mga-a               WEPN-GKAEPH-I--SRLFVHPESPASGLHWMQYPVSFYRLKLCNT----LDQEGHIILH
mga-b               WEPD-GPGEAH-LQ-SPVCFHPDSPAVGQHWMDSPVSFYTVKLTHD---SCEREG-VLLQ
Amphi-Tbx6/16       WVVS-GKAEPL-MP-GRLYIHPDSPATGTQWMKQSVTFHKLKLTNN---AMDQQGHIILN
TBX19               WVPA-GKPEVS-SH-SCVYIHPDSPNFGAHWMKAPISFSKVKLTNK---LNGGGQ-IMLN
tbx19               WVPA-GKPEPH-SH-SCVYIHPDSPNFGAHWMKAPVSFNKVKLTNK---LNGGGQ-IMLN
T                   WVPG-GKPEPQ-AP-SCVYIHPDSPNFGAHWMKAPVSFSKVKLTNK---LNGGGQ-IMLN
ntl-a               WVPG-GKPEPQ-SP-SCVYIHPDSPNFGAHWMKAPVSFSKVKLSNK---LNGGGQ-IMLN
ntl-b               WVPG-GKPEPQ-AP-SCVYIHPDSPNFGAHWMKSCVSFSKVKLTNK---LNGGGQ-IMLN
Amphi-Bra1          WVPG-GKPEPS-VP-SCVYIHPDSPNFGAHWMKSPVSFSKVKLTNK---LNGGGQQIMLN
Amphi-Bra2          WVPG-GKPEPS-VP-SCVYIHPDSPNFGAHWMKSPVSFSKVKLTNK---LNGGGQQIMLN
EOMES               WVTC-GKADNN-MQGNKMYVHPESPNTGSHWMRQEISFGKLKLTNNKGANNNNTQMIVLQ
eom-a               WVTC-GKADNN-MQGNKVYVHPESPNTGAHWMRQEISFGKLKLTNNKGANNNNTQMIVLQ
eom-b               WVTC-GKADNN-MQGNKIYMHPESPNTGAHWMRQEISFGKLKLTNNKGANINTSQMIVLQ
TBR1                WVPC-GKADTN-VQGNRVYMHPDSPNTGAHWMRQEISFGKLKLTNNKGASNNNGQMVVLQ
tbr1a               WVPC-GKADTN-VTGNRVYTHPDSPNTGAHWMRQEISFGKLKLTNNKGASSNNTQMIVLQ
tbr1b               WVPC-GKADTN-VTGNRVYMHPDSPNTGAHWMRQEISFGKLKLTNNKGATNNTGQMVVLQ
TBX21               WVQC-GKAEGS-MPGNRLYVHPDSPNTGAHWMRQEVSFGKLKLTNNKGASNNVTQMIVLQ
tbx21               WVQC-GKAEGN-MPGNRMYMHPDSPNTGTHWMRQEVSFGKLKLTNNKGSSNNVAQMIVLQ
Amphi-Eom/Tbr1/Tbx21WVPC-GRADTN-PQGSRVYVHPESPNSGAHWMKQEVVFSKLKLTNNKGA--DNG-HVVLN
Amphi-Tbx6d1        WVAT-GPAEFS-IS-NPPYEHPNSPASGAGWMGTVVSFAKAKITNN---NDSVEGNFLLH
Amphi-Tbx6d2        WVVVNGDAKPS-VA-DSVYVHPKCPEYGAKLMERPLAFPALKLSSR---MHDGKNMVQLR
```

```
TBX1                 SMHRYQPRFHVVYVDPRKD----SEKYAEENFKTFVFEETRFTAVTAYQNHRITQLKIAS
tbx1                 SMHRYQPRFHVVYVDPRKD----SEKYAEENYKTFVFEETRFTAVTAYQNHRITQLKIAS
TBX10                SMHRYQPRFHVVFVDPRKD----SERYAQENFKSFIFTETQFTAVTAYQNHRITQLKIAS
tbx10                SMHRYQPRLHVVLVDRSRN----SQRFAHRNFCTFSFPETRFIAVTAYQNHRITQLKIAC
Amphi-Tbx1/10        SMHRYQPRFHVVYIDGKKG----DSDTVHENYKTFIFPETKFTAVTAYQNHRITQLKIAS
TBX15                SMHKYQPRVHVIRKDFSSDLSPTKPVPVGDGVKTFNFPETVFTTVTAYQNQQITRLKIDR
tbx15                SMHKYQPRVHVIRKDFSSELSPTKPVPTGEGVKTFSFPETVFTTATAYQNQQITRLKIDR
TBX18                SMHKYQPRVHVIRKDCGDDLSPIKPVPSGEGVKAFSFPETVFTTVTAYQNQQITRLKIDR
tbx18                SMHKYQPRVHVIRKECGEELSPVKAVPTGDGVKAFSFTETVFTTVTAYQNQQITRLKIDR
TBX22                SMHKYKPRVHVIEQGSSVDLSQ-IQSLPTEGVKTFSFKETEFTTVTAYQNQQITKLKIER
tbx22                SMHKYRPRIHVILHCPPECLSKRLLSLPADGVFTFSFPETQFTTVTAYQNQQITKLKIDR
Amphi-Tbx15/18/22    SMHKYQPRVHIIKKTAHTDLTNKTSISPSDKAQTFAFPETVFTTVTAYQNQQITRLKIDR
TBX20                SMHKYQPRVHIIKKKDHTA---SLLNLKSEEFRTFIFPETVFTAVTAYQNQLITKLKIDS
tbx20                SMHKYQPRVHIIKKKDHTA---SLLNLKSEEFRTFVFTETVFTCRTAYQNQLITRLKIDS
Amphi-Tbx20          SMHRYQPRVHIIKKKEHTA---SLLNLNSEEFKTFVFQECMFTAVTAYQNQLITKLKIDS
TBX2                 SMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDN
tbx2a                SMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDN
tbx2b                SMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDN
TBX3                 SMHKYQPRFHIVRANDILK-------LPYSTFRTYLFPETEFIAVTAYQNDKITQLKIDN
tbx3a                SMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDH
tbx3b                SMHKYQPRFHIVRANDVLK-------LPYSTFKTYVFPETEFIAVTAYQNEKITQLKIDN
Amphi-Tbx2/3         SMHKYQPRFHIVKTNDIMK-------LPYCHFRTYVFRETAFIAVTAYQNEKITQLKIDH
TBX4                 SMHKYQPRLHIVKADENNA-----FGSKNTAFCTHVFPETSFISVTSYQNHKITQLKIEN
tbx4                 SMHKYQPRLHIVKADENNA-----FGSKNTAYCTHVFHETAFISVTSYQNHKITQLKIEN
TBX5                 SMHKYQPRLHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTSYQNHKITQLKIEN
tbx5a                SMHKYQPRIHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTSYQNHKITQLKIEN
tbx5b                SMHKYQPRLHIVKADERNS-----FGSSNTSFCTHSFAETTFIAVTSYQNHTITQLKIEN
Amphi-Tbx4/5         SMHKYQPRLHIVQASENNK-----FELKKTCFRTFIFPETEFMAVTSYQNHQITQLKIEH
TBX6                 SMHKYQPRIHLVRAAQLCS-------QHWGGMASFRFPETTFISVTAYQNPQITQLKIAA
tbx24                SLHRYQPRVHVIEARDVLM--------WGRTQHSFTFPETQFITVTAYQNNKITELKINS
Mdom-Tbx16           SMHRYQPRFLVAQADDLFN-------VCWNLFQVFSFPQTVFISVTAYQNEQITKLKIDN
tbx6                 SMHKYQPRLHIVQSPDPCT------PHNPGAYLRFTFPEAAFIAVTAYQNQEITKLKIDN
tbx16                SMHRYHPRFHIVQADDLYS-------VRWSVFQTFTFPETSFTAVTAYQNTKITKLKIDH
MGA                  SMHRYLPRLHLVPAEKAVE----VIQLNGPGVHTFTFPQTEFFAVTAYQNIQITQLKIDY
mga-a                SMHRYLPQIHIIPADKVSK---DILILDRPNVVTLSFAQTEFFAVTAYQNLCITQLKIDY
mga-b                PMHRYQPRLYVAPVSACLE---RAVPLKSPNVHMFTFPKTEFYAVTSYQNPQITRLKIDC
Amphi-Tbx6/16        SMHKYQPRLHIVQANDVYS-------LRWNSFSTFAFPETSFIAVTAYQNEKITQLKIDN
TBX19                SLHKYEPQVHIVRVGSAHR-----------MVTNCSFPETQFIAVTAYQNEEITALKIKY
tbx19                SLHKYEPQIHIVRVGGSHR-----------MVTNISFTDTQFIAVTAYQNEEITALKIKH
T                    SLHKYEPRIHIVRVGGPQR-----------MITSHCFPETQFIAVTAYQNEEITALKIKY
ntl-a                SLHKYEPRIHIVKVGGIQK-----------MISSQSFPETQFIAVTAYQNEEITALKIKH
ntl-b                SLHKYEPRIHIVRVGGPQR-----------MITTHAFPETQFIAVTAYQNEEITSLKIKY
Amphi-Bra1           SLHKYEPRLHIIKVGGPDN---------QRMVSTHTFPETQFIAVTAYQNEEITALKIKY
Amphi-Bra2           SLHKYEPRIHIVKVGGPDN---------QRTLSTHTFAETQFIAVTAYQNEELTALKIKH
EOMES                SLHKYQPRLHIVEVTEDGV----EDLNEPSKTQTFTFSETQFIAVTAYQNTDITQLKIDH
eom-a                SLHKYQPRLHIVEVTEDGV----EDMSSEAKTQTFTFPENQFIAVTAYQNTDITQLKIDH
eom-b                SLHKYQPRLHIVEVSDDRS-------ERDSNTQIFSFPENQFIAVTAYQNTDITQLKIDH
TBR1                 SLHKYQPRLHVVEVNEDGT----EDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDH
tbr1a                SLHKYQPRVHVIEISKNED----EDTSDPDGVQTFTFPETQFISVTAYQNTDITQLKIDH
tbr1b                SLHKYQPRLHVVQVNEDGT----EDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDH
TBX21                SLHKYQPRLHIVEVNDGEP----EAACNASNTHIFTFQETQFIAVTAYQNAEITQLKIDN
tbx21                SLHKYQPRLHIVEVKEDGT----EDPFLTSKTQTFVFPETQFIAVTAYQNADITQLKIDH
Amphi-Eom/Tbr1/Tbx21SMHKYQPRLHIIEVSNRAG-------GGERVLQSHSFPETQFIAVTAYQNTDITQLKIDY
Amphi-Tbx6d1         SMHKYQTKIIISRQETDKK----ARSCLGDHTHTFQFEETAFVAVTAYQNHRVTRLKIKN
Amphi-Tbx6d2         SMHKYQPVVQVVEADNTTD-------LAVAPSWQFSFPVTEFMAVSSYYSDKIRKLKVDN
```

TBX1	NPFAKGFRD
tbx1	NPFAKGFRD
TBX10	NPFAKGFRE
tbx10	NPFAKGFRT
Amphi-Tbx1/10	NPFAKGFRD
TBX15	NPFAKGFRD
tbx15	NPFAKGFRD
TBX18	NPFAKGFRD
tbx18	NPFAKGFRD
TBX22	NPFAKGFRD
tbx22	NPFAKGFRE
Amphi-Tbx15/18/22	NPFAKGFRD
TBX20	NPFAKGFRD
tbx20	NPFAKGFRD
Amphi-Tbx20	NPFAKGFRD
TBX2	NPFAKGFRD
tbx2a	NPFAKGFRD
tbx2b	NPFAKGFRD
TBX3	NPFAKGFRD
tbx3a	NPFAKGFRD
tbx3b	NPFAKGFRE
Amphi-Tbx2/3	NPFAKGFRD
TBX4	NPFAKGFRG
tbx4	NPFAKGFRG
TBX5	NPFAKGFRG
tbx5a	NPFAKGFRG
tbx5b	NPFAKGFRG
Amphi-Tbx4/5	NPFAKGFRG
TBX6	NPFAKGFRE
tbx24	NPFAKGFRE
Mdom-Tbx16	NPFAKGFRE
tbx6	NPFAKGFRD
tbx16	NPFAKGFRD
MGA	NPFAKGFRD
mga-a	NPFAKGFRE
mga-b	NPFMLAFRE
Amphi-Tbx6/16	NPFAKGFRD
TBX19	NPFAKAFLD
tbx19	NPFAKAFLD
T	NPFAKAFLD
ntl-a	NPFAKAFLD
ntl-b	NPFAKAFLD
Amphi-Bra1	NPFAKAFLD
Amphi-Bra2	NPFAKAFLD
EOMES	NPFAKGFRD
eom-a	NPFAKGFRD
eom-b	NPFAKGFRD
TBR1	NPFAKGFRD
tbr1a	NPFAKGFRD
tbr1b	NPFAKGFRD
TBX21	NPFAKGFRE
tbx21	NPFAKGFRD
Amphi-Eom/Tbr1/Tbx21	NPFAKGFRD
Amphi-Tbx6d1	NPFAKAFRD
Amphi-Tbx6d2	NKFAKNLRN

Figure S4. Exon-intron structures of the T-box regions of vertebrate T-box genes included in the phylogenetic analysis (Figures 1 & S3). Sequences are organized by sub-family memberships and shown in an interleaved format. Alignment gaps are as in Fig. S2. Except for the *Mga* genes, which are intron-less in the T-box region (Hurlin et al. 1999), the T-domains of vertebrate T-box genes are encoded by 4 or 5 exons, which have diagnostic differences in their sizes and numbers as well as in the codon positions of exon- intron junctions (Wattler et al. 1998). The portions of T-domains encoded by different exons are shown in violet, cyan, blue, black, and green colors. The residues whose codons are split between neighboring exons are indicated by red and brown colors, in which the red color means that the codon is split between the 2nd & 3rd bases (e.g., AG-A) while the brown color indicates that the codon is split between the 1st & 2nd bases (e.g., A-GA). Note that, in terms of the exon-intron structure of the T-box regions, the *Tbx6/16* sub-family of vertebrate T-box genes can be sub-divided further into three groups of genes: 1) *Tbx16*-like genes containing 5-exon T-boxes; 2) *Tbx6*-like genes containing 4-exon T-boxes; and 3) *Mga*-like genes containing single-exon T-boxes.

```
>TBX15       LWKRFHDIGTEMIITKAGRRMFPAMRVKITGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSLASGDTWMRQV
>tbx15       LWKRFHDIGTEMIITKAGRRMFPAMRVKIVGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSLASGDTWMRQV
>TBX18       LWKRFHEIGTEMIITKAGRRMFPAMRVKISGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSPASGETWMRQV
>tbx18       LWKRFHEIGTEMIITKAGRRMFPAMRVKIAGLDPHQQYYIAMDIVPVDNKRYRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSPASGETWMRQV
>TBX22       LWKRFHDIGTEMIITKAGRRMFPSVRVKVKGLDPGKQYHVAIDVVPVDSKRYRYVYHSSQWMVAGNTDHLCII-PRFYVHPDSPCSGETWMRQI
>tbx22       LWKRFYEIGTEMIITKVGRRMFPSIRVKVHNLDPLQQYSIAMDIMPMDSKKYRYVYHSSQWVIAGNTDHSCIP-PHLYVHPDSPCSGENWMRQV

>TBX20       LWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRYRYAYHRSSWLVAGKADPP-LP-ARLYVHPDSPFTGEQLLKQM
>tbx20       LWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIVPVDNKRYRYAYHRSSWLVAGKADPP-LP-ARLYVHPDSPFTGEQLLKQM

>TBX1        LWDEFNQLGTEMIVTKAGRRMFPTFQVKLFGMDPMADYMLLMDFVPVDDKRYRYAFHSSSWLVAGKADPA-TP-GRVHYHPDSPAKGAQWMKQI
>tbx1        LWDEFNQLGTEMIVTKAGRRMFPTFQVKIFGMDPMADYMLLMDFLPVDDKRYRYAFHSSSWLVAGKADPA-TP-GRVHYHPDSPAKGAQWMKQI
>TBX10       LWEEFNQLGTEMIVTKAGRRMFPPFQVKILGMDSLADYALLMDFIPLDDKRYRYAFHSSAWLVAGKADPA-TP-GRVHFHPDSPAKGAQWMRQI
>tbx10       LWRQFDQLGTEMIVTKAGRRMFPTFQVHISGMDPAAEYVLLMDFIPVDDKRYRYAFHSSSWLVAGRGDVA-AP-GRVHFHPDSPARGAQWIKQT

>TBX2        LWDQFHKLGTEMVITKSGRRMFPPFKVRVSGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>tbx2a       LWDQFHKIGTEMVITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>tbx2b       LWDQFHKLGTEMVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>TBX3        LWDQFHKRGTEMVITKSGRRMFPPFKVRCSGLDKKAKYILLMDIIAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMSKV
>tbx3a       LWELFHKRGTEMVITKSGRRMFPPFKVRCTGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMSKV
>tbx3b       LWGQFHKVGTEMVITKSGRRMFPAFKVRCSGFDRKARYILLMDIVASDDYRYK--FHNCRWMVAGKADPE-MP-KRMYIHPDSPSTGEQWMSKA

>TBX4        LWKKFHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLIDIVPADDHRYK--FCDNKWMVAGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx4        LWKKFHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLTDIVPADDHRYK--FCDNKWMVAGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>TBX5        LWLKFHEVGTEMIITKAGRRMFPSYKVKVTGLNPKTKYILLMDIVPADDHRYK--FADNKWSVTGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx5a       LWTKFHEVGTEMIITKAGRRMFPSFKVKVTGLNPKTKYILLMDVVPADDHRYK--FADNKWSVTGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx5b       LWAKFHDVTTEMIITKAGRRMFPSYKVKVTGLNPKAKYILLMDIISADEHRYK--FADNKWSISGKAEPA-IP-GRLYVHPDSPASGAHWMRQL

>Mdom-Tbx16  LWTEFYRVGTEMVITKSGRRMFPQCKIRLSGLVPYLKYVVLADFVSVDNFRYK--WAKDQWEVAGKAEPQ-LP-GRSYIHPDSPAYGSHWMKEP
>tbx16       LWRSFHEIGTEMIITKPGRRMFPHCKISLSGLVPYAKYILLVDMVPEDGLRYK--WNKDKWEVAGKAEPQ-PP-YRTYLHPDSPAPGSHWMKQP
>tbx6        LWDKFSSIGTEMLITKSGRRMFPSCKVTVTGLNPKVKYVVIMDMVPFDNHKYK--WNKDCWEVNGSSDPH-LP-NRFFIHPDSPAPGQKWMQYP
>TBX6        LWKEFSSVGTEMIITKAGRRMFPACRVSVTGLDPEARYLFLLDVIPVDGARYR--WQGRRWEPSGKAEPR-LP-DRVYIHPDSPATGAHWMRQP
>tbx24       LWKQFSTVGTEMIVTKKGRRMFPQLRVKLSGLNPSLRYILLLDIVPVDSSRYR--FQDNSWQVVGGAEAR-LP-DRVFIHPDSPATGEHWQNRT
>MGA         MWNEFYHRSTEMILTKQGRRMFPYCRYWITGLDSNLKYILVMDISPVDNHRYK--WNGRWWEPSGKAEPH-VL-GRVFIHPESPSTGHYWMHQP
>mga-a       MWNEFHRCKTEMILTKQGRRMFPYCRFRLSGMEPFQNYVLAMDIKPADNCRYK--WSGKGWEPNGKAEPH-I--SRLFVHPESPASGLHWMQYP
>mga-b       VWSRFHSLGTEMLLTPQGRRMFPCCRFRLRGLDPDLQYFLLMDIAPLDDLRH R--FNGEAWEPDGPGEAH-LQ-SPVCFHPDSPAVGQHWMDSP

>EOMES       LWLKFHRHQTEMIITKQGRRMFPFLSFNINGLNPTAHYNVFVEVVLADPNHWR--FQGGKWVTCGKADNN-MQGNKMYVHPESPNTGSHWMRQE
>eom-a       LWLKFHRHQTEMIITKQGRRMFPFLSFNITGLNLTAHYNVFVEIVLADPNHWR--FQGGKWVTCGKADNN-MQGNKVYVHPESPNTGAHWMRQE
>eom-b       LWLKFHRHQTEMIITKQGRRMFPFLSFNMTGLSLSAHYNVFVEIVLADPNHWR--FQGGKWVTCGKADNN-MQGNKIYMHPESPNTGAHWMRQE
>TBR1        LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGKWVPCGKADTN-VQGNRVYMHPDSPNTGAHWMRQE
>tbr1a       LWFKFHRHQTEMIITKQGRRMFPCLTFNVSGLDPAGHYNIAVDVILADPNHWR--FQGGKWVPCGKADTN-VTGNRVYTHPDSPNTGAHWMRQE
>tbr1b       LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGKWVPCGKADTN-VTGNRVYMHPDSPNTGAHWMRQE
>TBX21       LWSKFNQHQTEMIITKQGRRMFPFLSFTVAGLEPTSHYRMFVDVVLVDQHHWR--YQSGKWVQCGKAEGS-MPGNRLYVHPDSPNTGAHWMRQE
>tbx21       LWAKFHKYQTEMIITKQGRRMFPFLSFNITSLDPSAHYNIYVDVVLADQHHWR--YQGGKWVQCGKAEGN-MPGNRMYMHPDSPNTGTHWMRQE

>TBX19       LWQRFKEVTNEMIVTKNGRRMFPVLKISVTGLDPNAMYSLLLDFVPTDSHRWK--YVNGEWVPAGKPEVS-SH-SCVYIHPDSPNFGAHWMKAP
>tbx19       LWRKFKEVTNEMIVTKNGRRMFPVLKVSVTGLDPNAMYSFLLDFTPADGHRWK--YVNGEWVPAGKPEPH-SH-SCVYIHPDSPNFGAHWMKAP
>T           LWLRFKELTNEMIVTKNGRRMFPVLKVNVSGLDPNAMYSFLLDFVAADNHRWK--YVNGEWVPGGKPEPQ-AP-SCVYIHPDSPNFGAHWMKAP
>ntl-a       LWTKFKELTNEMIVTKTGRRMFPVLRASVTGLDPNAMYSVLLDFVAADNNRWK--YVNGEWVPGGKPEPQ-SP-SCVYIHPDSPNFGAHWMKAP
>ntl-b       LWQKFKALTNEMIVTKNGRRMFPVLKVNISGLDPNAMYSFLLDFVPADNHRWK--YVNGEWVPGGKPEPQ-AP-SCVYIHPDSPNFGAHWMKSC
```

```
>TBX15       VSFDKLKLTNN---ELDDQGHIILHSMHKYQPRVHVIRKDFSSDLSPTKPVPVGDGVKTFNFPETVFTTVTAYQNQQ ITRLKIDRNPFAKGFRD
>tbx15       VSFDKLKLTNN---ELDDQGHIILHSMHKYQPRVHVIRKDFSSELSPTKPVPTGEGVKTFSFPETVFTTVTAYQNQQ ITRLKIDRNPFAKGFRD
>TBX18       ISFDKLKLTNN---ELDDQGHIILHSMHKYQPRVHVIRKDCGDDLSPIKPVPSGEGVKAFSFPETVFTTVTAYQNQQ ITRLKIDRNPFAKGFRD
>tbx18       ISFDKLKLTNN---ELDDQGHIILHSMHKYQPRVHVIRKECGEELSPVKAVPTGDGVKAFSFTETVFTTVTAYQNQQ ITRLKIDRNPFAKGFRD
>TBX22       ISFDRMKLTNN---EMDDKGHIILQSMHKYKPRVHVIEQGSSVDLSQ-IQSLPTEGVKTFSFKETEFTTVTAYQNQQ ITKLKIERNPFAKGFRD
>tbx22       ISFDRVKLTNN---ELDDRGHIILKSMHKYRPRIHVILHCPPECLSKRLLSLPADGVFTFSFPETQFTTVTAYQNQQ ITKLKIDRNPFAKGFRE

>TBX20       VSFEKVKLTNN---ELDQHGHIILNSMHKYQPRVHIIKKKDHTA---SLLNLKSEEFRTFIFPETVFTAVTAYQNQL ITKLKIDSNPFAKGFRD
>tbx20       VSFEKVKLTNN---ELDQHGHIILNSMHKYQPRVHIIKKKDHTA---SLLNLKSEEFRTFVFTETVFTAVTAYQNQL ITRLKIDSNPFAKGFRD

>TBX1        VSFDKLKLTNN---LLDDNGHIILNSMHRYQPRFHVVYVDPRKD----SEKYAEENFKTFVFEETRFTAVTAYQNHR ITQLKIASNPFAKGFRD
>tbx1        VSFDKLKLTNN---LLDDNGHIILNSMHRYQPRFHVVYVDPRKD----SEKYAEENYKTFVFEETRFTAVTAYQNHR ITQLKIASNPFAKGFRD
>TBX10       VSFDKLKLTNN---LLDDNGHIILNSMHRYQPRFHVVFVDPRKD----SERYAQENFKSFIFTETQFTAVTAYQNHR ITQLKIASNPFAKGFRE
>tbx10       VSFDRLKLTNN---LLDDNGHMILNSMHRYQPRLHVVLVDRSRN----SQRFAHRNFCTFSFPETRFIAVTAYQNHR ITQLKIACNPFAKGFRT

>TBX2        VAFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDK ITQLKIDNNPFAKGFRD
>tbx2a       VAFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDK ITQLKIDNNPFAKGFRD
>tbx2b       VAFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDK ITQLKIDNNPFAKGFRD
>TBX3        VTFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDILK-------LPYSTFRTYLFPETEFIAVTAYQNDK ITQLKIDNNPFAKGFRD
>tbx3a       VNFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDILK-------LPYSTFRTYVFPETDFIAVTAYQNDK ITQLKIDHNPFAKGFRD
>tbx3b       VTFHKLKLTNN---ISDKHGFTILNSMHKYQPRFHIVRANDVLK-------LPYSTFKTYVFPETEFIAVTAYQNEK ITQLKIDNNPFAKGFRE

>TBX4        VSFQKLKLTNN---HLDPFGHIILNSMHKYQPRLHIVKADENNA-----FGSKNTAFCTHVFPETSFISVTSYQNHK ITQLKIENNPFAKGFRG
>tbx4        VSFQKLKLTNN---HLDPFGHIILNSMHKYQPRLHIVKADENNA-----FGSKNTAYCTHVFHETAFISVTSYQNHK ITQLKIENNPFAKGFRG
>TBX5        VSFQKLKLTNN---HLDPFGHIILNSMHKYQPRLHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTSYQNHK ITQLKIENNPFAKGFRG
>tbx5a       VSFQKLKLTNN---HLDPFGHIILNSMHKYQPRIHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTSYQNHK ITQLKIENNPFAKGFRG
>tbx5b       VSFQKLKLTNN---HLDPFGHIILNSMHKYQPRLHIVKADERNS-----FGSSNTSFCTHSFAETTFIAVTSYQNHT ITQLKIENNPFAKGFRG

>Mdom-Tbx16  VSFHKMKLTNN---TLDQHGHIILHSMHRYQPRFLVAQADDLFN-------VCWNLFQVFSFPQTVFISVTAYQNEQ ITKLKIDNNPFAKGFRE
>tbx16       VSFLKLKLTNN---ALDQHGHIILHSMHRYHPRFHIVQADDLYS-------VRWSVFQTFTFPETSFTAVTAYQNTK ITKLKIDHNPFAKGFRD
>tbx6        ISFHKLKLTNN---TLNSNGLVVLHSMHKYQPRLHIVQSPDPCT------PHNPGAYLRFTFPEAAFIAVTAYQNQE ITKLKIDNNPFAKGFRD
>TBX6        VSFHRVKLTNS---TLDPHGHLILHSMHKYQPRIHLVRAAQLCS-------QHWGGMASFRFPETTFISVTAYQNPQ ITQLKIAANPFAKGFRE
>tbx24       ISFHRAKLTNN---TLDAQGYIILHSLHRYQPRVHVIEARDVLM--------WGRTQHSFTFPETQFITVTAYQNNK ITELKINSNPFAKGFRE
>MGA         VSFYKLKLTNN---TLDQEGHIILHSMHRYLPRLHLVPAEKAVE----VIQLNGPGVHTFTFPQTEFFAVTAYQNIQ ITQLKIDYNPFAKGFRD
>mga-a       VSFYRLKLCNT----LDQEGHIILHSMHRYLPQIHIIPADKVSK---DILILDRPNVVTLSFAQTEFFAVTAYQNLC ITQLKIDYNPFAKGFRE
>mga-b       VSFYTVKLTHD---SCEREG-VLLQPMHRYQPRLYVAPVSACLE---RAVPLKSPNVHMFTFPKTEFYAVTSYQNPQ ITRLKIDCNPFMLAFRE

>EOMES       ISFGKLKLTNNKGANNNNTQMIVLQSLHKYQPRLHIVEVTEDGV----EDLNEPSKTQTFTFSETQFIAVTAYQNTD ITQLKIDHNPFAKGFRD
>eom-a       ISFGKLKLTNNKGANNNNTQMIVLQSLHKYQPRLHIVEVTEDGV----EDMSSEAKTQTFTFPENQFIAVTAYQNTD ITQLKIDHNPFAKGFRD
>eom-b       ISFGKLKLTNNKGANINTSQMIVLQSLHKYQPRLHIVEVSDDRS-------ERDSNTQIFSFPENQFIAVTAYQNTD ITQLKIDHNPFAKGFRD
>TBR1        ISFGKLKLTNNKGASNNNGQMVVLQSLHKYQPRLHVVEVNEDGT----EDTSQPGRVQTFTFPETQFIAVTAYQNTD ITQLKIDHNPFAKGFRD
>tbr1a       ISFGKLKLTNNKGASSNNTQMIVLQSLHKYQPRVHVIEISKNED----EDTSDPDGVQTFTFPETQFISVTAYQNTD ITQLKIDHNPFAKGFRD
>tbr1b       ISFGKLKLTNNKGATNNTGQMVVLQSLHKYQPRLHVVQVNEDGT----EDTSQPGRVQTFTFPETQFIAVTAYQNTD ITQLKIDHNPFAKGFRD
>TBX21       VSFGKLKLTNNKGASNNVTQMIVLQSLHKYQPRLHIVEVNDGEP----EAACNASNTHIFTFQETQFIAVTAYQNAE ITQLKIDNNPFAKGFRE
>tbx21       VSFGKLKLTNNKGSSNNVAQMIVLQSLHKYQPRLHIVEVKEDGT----EDPFLTSKTQTFVFPETQFIAVTAYQNAD ITQLKIDHNPFAKGFRD

>TBX19       ISFSKVKLTNK---LNGGGQ-IMLNSLHKYEPQVHIVRVGSAHR-----------MVTNCSFPETQFIAVTAYQNEE ITALKIKYNPFAKAFLD
>tbx19       VSFNKVKLTNK---LNGGGQ-IMLNSLHKYEPQIHIVRVGGSHR-----------MVTNISFTDTQFIAVTAYQNEE ITALKIKHNPFAKAFLD
>T           VSFSKVKLTNK---LNGGGQ-IMLNSLHKYEPRIHIVRVGGPQR-----------MITSHCFPETQFIAVTAYQNEE ITALKIKYNPFAKAFLD
>ntl-a       VSFSKVKLSNK---LNGGGQ-IMLNSLHKYEPRIHIVKVGGIQK-----------MISSQSFPETQFIAVTAYQNEE ITALKIKHNPFAKAFLD
>ntl-b       VSFSKVKLTNK---LNGGGQ-IMLNSLHKYEPRIHIVRVGGPQR-----------MITTHAFPETQFIAVTAYQNEE ITSLKIKYNPFAKAFLD
```

Supplementary Materials References

Hurlin PJ, Steingrimsson E, Copeland NG, Jenkins NA, Eisenman RN. 1999. *Mga*, a dual-specificity transcription factor that interacts with *Max* and contains a T-domain DNA-binding motif. *EMBO J* 18: 7019-7028.

Wattler S, Russ A, Evans M, Nehls M. 1998. A combined analysis of genomic and primary protein structure defines the phylogenetic relationship of new members of the T-box family. *Genomics* 48: 24-33.