

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

Supplementary Materials I

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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)
MHFSTVTRDMEAFATASSLSSLGAAGGFPGAASPGADPYGPREPP
PPPPRYDPCAAAAPGAPGPPPPHAYPFAPAAGAATSAAAEEGPGASCAAAAKAPVK
KNAKVAGVSVQLEMKALWDEFNQLGTEMIVTKAGRRMFPTFQVKLFGMDPMDYMLLM
DFVPVDDKRYRYAFHSSSWLVAGKADPATPGRVHYHPDSPAKGAQWMKQIVSFDKLKL
TNNLLDDNGHIIILNSMHRYQPRFHVVYVDPKRDSEKYAEENFKTFVFEETRFTAVTAY
QNHRTIQLKIASNPFAGFRDCDPEDWPRNHRPGALPLMSAFARSNPVASPTQPSGT
EKGGHVLKDKVEKAETSRNTPEREVELLRDAGGCVNGLPCPAECQPFNTQGLVAGRT
AGDRLC

>TBX2 NM_005994
MREPALAASAMAYHFFHAPRPADFMSAFLAAQPSFFPALALP
PGALAKPLPDPGLAGAAAAAEEAGLHVSAALGPHPPAAHLRSLKSLPEPEDEVE
DDPKVTLEAKELWDQFHKLGTEMVITKSGRRMFPPFKVRVSGLDKKAKYILLMDIVAA
DDCRYKFHNSRWMVAGKADPEMPKRMYPHPDSPATGEQWMAKPVAFHKLKLTNNISDK
HGFTIILNSMHKYQPRFHIVRANDILKLPYSTFRITYVPETDFIAVTAYQNDKITQLKI
DNNPFAKGFRDGTNGRREKRKQLTLPRLRYEEHCKPERDGAESDASSCDPPPAREPP
TSPGAAPSPLRLHRAAEKSCAADSDPEPERLSEERAGAPLGRSPAPDSASPTRLTE
PERARERRSPERGKEPAESGGDGPFGRLSLEKERAEEARRKDEGRKEAAEGKEQGLAPL
VVQTDASAPLGAGHLPLGLAFSSHLHGQQFFGPLGAGQPLFLHPGQFTMGPGAFSAMGM
GHLLASVAGGGNGGGGGPGTAAGLDAGGLGPAASAASTAAPFFPHLSQHMLASQGIPM
PTFGGLFPYPITYMAAAAAAASALPATSAAAAAAAGLSRSPLGSRPRLRFSPY
QIPVTIPPSTSLTTGLASEGSKAAGGNSREPSLPPELALRKVGAPSRGALSPSGSAK
EAANELQSIQRLVSGLESQRALSPGRESK

>TBX3 NM_005996 (variant 1)
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CRYKFHNSRWMVAGKADPEMPKRMYPHPDSPATGEQWMSKVVTFHKLKLTTNNISDKHG
FTIILNSMHKYQPRFHIVRANDILKLPYSTFRITYLPETEFIAVTAYQNDKITQLKIDN
NPFAGFRDGTNGRREKRKQLTLQSMRVFDERHKKENGTSDESSEQAAFNCFAQASS
PAASTVGTSNLKDLCPSEGESDAEAEESKEEHGPEACDAAKISTTTSEPCRDKGSPAV
KAHLFAAERPRDSGRDLKASPDSPSRHSPATISSSTRGLGAEERRSPVREGTAPAKVEEA
RALPGKEAFAPLTVQTDAAAHLAQGPLPGLGFAPGLAGQQFFNGHPLFLHPSQFAMG
GAFSSMAAAGPLLATVSGASTGVSGLDSTAMASAAAAQGLSGASAATLPFHLQQHV
LASQGLAMSPFGSLFPYPITYMAAAAAASSAAASSSVHRHPFLNLNTMRPRLRYSPPYS
IPVPVPDGSLLTTALPSMAAAAGPLDGKVAALAASPASVAVDSGSELNSRSSTLSSS
SMSLSPKLCAEKEAATSELQSIQRLVSGLEAKPDRSRASAP

>TBX4 NM_018488
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FPETSFISVTSYQNHKITQLKIENNPFAGFRGSDSDLRVARLQSKYEPVVISKIMR
QRLISPLSATPDVGPLLGTHQALQHYQHENGASQLAEPQDLPLSTFPTQRDSSLFY
HCLKRRDGTNRHLDLPCKRSYLEAPSSVGEDHYFRSPPPYDQQMLSPSYCSEVTPREAC
MYSGSGPEIAGVSGVDDLPPPLSCNMWTSVSPYTSYSVQTMETVPYQFPPTHFTATT
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>TBX5 NM_000192 (variant 1)
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LMDIVPADDHRYKFADNKWSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKL
TNNHLDPFPGHIIILNSMHKYQPRLHIVKADENNGFGSKNTAFCTHVFPETAFIAVTSYQ
NHKITQLKIENNPFPAKGFRGSDDMELHRMSRMSKEYPVVPRSTVRQKVASNHSPFSS
ESRALSTSSNLGSQYQCENGVSQDGLLPPNPYPLPQEHSSQIYHCTKRKEEECSTT
DHPYKKPYMETSPSEEDSFYRSSYPQQQGLGASYRTESAQRQACMYASSAPPSEPVPS
LEDISCNTWPSMPSYSSCTVTTVQPMDRLPYQHFSAHFTSGPLVPRLAGMANHGSPQL
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GMVPEWSDNS

>TBX6 NM_004608

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EFSSVGTEMIITKAGRRMFACRVSVTGLDPEARYLFLLDVIPVDGARYRWQGRWEP
SGKAEPRLPDRVYIHPDSPATGAHWMRQPVSFHRVKLTNSTLDPHGHLILHSMHKYQF
RIHLVRAAQLCSQHWGGMASFRFPETTFISVTAYQNQITQLKIAANPFAKGFRENGR
NCKRERDARVKRKLRGPEPAATEAYGSGDTPGGPCDSTLGGDIRESDEQAPAPGEAT
AAPAPLCGGPSAEAYLLHPAAFHGAPSHLPTRSPSFPEAPDSGRSAPYSAAFLELPHG
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>TBX10 NM_005995

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LGMDSLADYALLMDFIPLDDKRYRYAFHSSAWLVAGKADPATPGRVHFHPDSPAKGAQ
WMRQIVSFDKLLTNNLLDDNGHIIILNSMHRYQPRFHVVVVDPRKDSERYAQENFKSF
IFTETQFTAVTAYQNHRIITQLKIASNPFPAKGFRESLDLSDWPVAPRPLLSVPARSHSSL
SPCVLKGATDREKDPNKASASTSKTPAWLHHQLLPPPEVLLAPATYRPVTYQSLYSGA
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>TBX15 NM_152380

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WMRQVVVSFQKLLTNNELDDQGHIIILHSMHKYQPRVHVIRKDFSSDLSPTKPVVGDG
VKTNFNPETVFTTVTAYQNQQITRLKIDRNPFPAKGFDRSGNRNRTGLEAIMETYAFWRP
PVRTLTFEDFTTMQKQGGSTGTSTSTSTGTPSPSASSHLLSPSCSPPTFHLAPNTF
NVGCRESQLCNLNLSDYPPCARSNMAALQSYPLSDSGYNRLQSGTTSATQPSSETFMP
QRTPSLISGIPTPSPPLPGNSKMEAYGGQLGSFPTSQFYVMQAGNAASSSSSPHMFEGG
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>TBX18 NM_001080508

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GFQQGASPLASPGGSPKGSPARSLARPGTLPSPQAPRVDLQGAELWKRFEIGTEMI
ITKAGRRMFAMRVKISGLDPHQYYIAMDIVPDNKRIRYVYHSSKWMVAGNADSPV
PPRVYIHPDSPASGETWMRQVISFDKLLTNNELDDQGHIIILHSMHKYQPRVHVIRKD
CGDDLSPKIPVPSGEGVKAFFPETVFTTVTAYQNQQITRLKIDRNPFPAKGFDRSGRN
RMGLEALVESYAFWRPSLRTLTFEDIPGIPKQGNASSSTLLQGTGNGVPATHPHLLSG
SSCSPAFHGLPNTSQLCSLAPADYSACARSGTLNRYSTSLAETYNRLTNQAGETFA
PPRTPSYVGVSSSTSVNMSMGDTGDTFSCPQTSLSMQISGMSPQLQYIMPSPSSNAF
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>TBX19 NM_005149

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LEDAPLWQRFKEVTNEMIVTKNGRRMFVVLKISVTGLDPNAMYSLLLDFVPTDSHRWK
YVNGEWWPAGKPEVSSHSCVYIHPDSPNFGAHWMKAPISFSKVKLTKNLGGGQIMLN
SLHKYEPQVHIVRVGSAHRMVTNCSFPETQFIAVTAYQNEEITALKIKYNPFAKAFLD
AKERNHLRDVPEAISESQHVITYSHLGGWIFSNPDGVCTAGNSNYQYAAPLPLPAPHTH
HGCEHYSGLRGHRQAPYPSPAYMHRNHSPSVNLISSNNLQVFSGPDSTLSSTPHA
SILSVPHNTGPIPGPSPYPCLTWISNGAGGSPGPGPEVHASTPGAFLGPNPAVTSPP
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>TBX20 NM_001077653

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SLETKELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRY
RYAYHRSSWL VAGKADPPLPARLYVHPDSPFTGEQLLKQMVSEKVKLTNNELDQHGHI
IILNSMHKYQPRVHI IKKKDHTASLLNLKSEEFRTFIFPETVFTAVTAYQNQLITKLK
IDSNPFAKGF RDSSRLTDIERESVESLIQKHSYARSPIRTYGGEEDVLGDESQTTPNR
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>TBX21 NM_013351

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KQGRRMFPFLSFTVAGLEPTSHYRMFVDVVLVDQHHWRYQSGKWVQCGKAEGSMGPNR
LYVHPDSPNTGAHWMRQEVSFGLKLTNNKGASNNVTQMIVLQSLHKYQPRLHIVEVN
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VDT SIPSPPGPNCQFLGGDHYSPLLPNQYPVPSRFY PDLPGQAKDVVPQAYWLGAPRD
HSYEA EFRAVSMKPAFLPSAPGPTMSYYRGQEV LAPGAGWPVAPQYPPKMGPASWFRP
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GDSSSPAGAPSPFDKEAEGQFYNYFPN

>TBX22 NM_001109878 (variant 1)

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WMVAGNTDHL CII PRFYVHPDSPCSGETWMRQIIISFDRMKL TNNEMDDKGHIILQSMH
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LNSLLSPLCFSPMFHLPTSSLGMPCEAYLPNVNLPLCYKICPTNFWQQQPLVLPAPPE
RLASSNSSQSLAPLMMEVPM LSSLGVTNSKSGSSEDSSDQYLQAPNSTNQMLYGLQSP
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HVHWYPAINHYL

>TBR1 NM_006593

MQLEHCLSPSIMLSKKFLNVSSSYPHSGGSELVLHDHPIISTTD
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DRYLLSQSSQPQSAATAPSAMFPYPGQHGAHPAFSIGSPSRYMAHHPVITNGAYNSL
LSNSSPQGYPTAGYPYPQYGHSYQGAPFYQFSS TQPLGVPGKAQVYLCNRPLWLKFH
RHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNIFVDVILADPNHWR FQGGKWVPCGK
ADTNVQGNRVYMH PDSPNTGAHWMRQEISFGK LKLTNNKGASNNNGQMVVLQSLHKYQ
PRLHVVEVNEDGTEDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDHNPFAKGR
DNYDTIYTGCDMDRLTPSPNDSPRSQIVPGARYAMAGSFLQDQFVSNYAKARFHPGAG
AGPGPGTDRSVPH TNGLLSPQQAEDPGAPSPQRWFVTPANNRLDFAASAYDTATDFAG
NAATLLSYAAAGVKALPLQAAGCTGRPLGYADPSGWGARSP PQYCGTKSGSVLPCWP
NSAAAAARMAGANPYLGEEAEGLAAERSPLPPGAEDAKPKDLS DSSWIETPSSI KSI
DSSDSGIYEQA KRRRISPADTPVSESSSPLKSEVLAQRDCEKNCAKDISGYYG FYSHS

>T NM_003181

MSSPGTESAGKSLQYRVDHLLSAVENELQAGSEKGDPTERELRV
GLEESELWLRFKELTNEMIVTKNGRRMFV LKVNVSGLDPNAMYSFLLD FVAADNHRW
KYVNGEWPVGGKPEPQAPSCVYIHPDSPNFGAHWMKAPVSFSKV KLTNKLNGGGQIML
NSLHKYEPRIHIVRGGPQRMITSHCFPETQFIAVTAYQNEEITALKIKYNPFAKAF L
DAKERSD HKEMMEEPGDSQQPGYSQGWLLPGTSTLCPPANPH PQFGGALS LPS THSC
DRYPTLRSHRSSPYSPYAHRRNSPTYSDNSPACL SMLQSHDNWSSLGMPAHP SMLPV
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>EOMES NM_005442

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SLFPYQAAAGAPHGPVYPAPNGARYPYGSM LPPGGFFAAVCPPGRAQFGPGAGAGSGA
GGSSGGGGPGTYQYSQGAPLYGPYPGAAAAGSCGGLGGLGVPGSGFRAHVYLCNRPL
WLKFHRHQTEMIITKQGRMF PFLSFNINGLNPTAHYNVFVEVVLADPNHWRFGQGW
VTCGKADNNMQGNKMYVHPESPNTGSHWMRQEISFGKLKLTNNKGANNNTQMIVLQS
LHKYQPRHLHIVEVTEDEGVEDLNEPSKTQTFTFSETQFIAVTAYQNTDITQLKIDHNPF
AKGFRDNYDSSHQIVPGGRYGVQSFFPEPFVNTLPQARYYNGERTVPQTNGLLSPQQS
EEVANPPQRWLVPVQQPGTNKLDISSYESEYTSSTLLPYGIKSLPLQTSHALGYYPD
PTFPAMAGWGGGRSYQRKMAAGLPWTSRTSPTVFSQDLSKEKVKEEIGSSWIETPPS
IKSLDSNDSGVYTSACKRRRLSPSNSSNENSPSIKCEDINAEYSKDTSKGMGGYYAF
YTPP

>MGA NM_001164273 (variant 1)

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ESPSTGHYWMHQPVSYFYKLKLTNNTL DQEGHII LHSMHRYL PRLHLVPAEKAVEVIQL
NGPGVHTFTFPQTEFFAVTAYQNIQITQLKIDYNPFAKGFRDDGLNNKFPQRDGKQKNS
SDQEGNNISSSSGHRVRLTEGQSGEIQPGDLDP LSRGHETSGKGLEKTS LNKRDFLG
FMDTDSALSEVPQLKQEISECLIASSFEDDSRVASPLDQNGSFNVV IKEEPLDDYDYE
LGECPEGVTVKQEETDEETDVYSNSDDDP ILEKQLKRHNKVDNPEADHLS SKWLPSSP
SGVAKAKMFKLDTGKMPVVYLEPCAVTRSTVKISELPDNMLSTSRKDKSSMLAELEYL
PTYIENSNETAFCLGKESENGLRKHSPDLRVVQKYPLLKEPQWKYPDISDSISTERIL
DDSKDSVGDLSL GKEDLGRKRTTMLKIATAAKVVNANQNASPNVPGKRGRPRK LKCK
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TESSSLQASTTNDSGYRARI SLEKELIEDLKT LRHKQVIHPGLQEVGLKLNSVDPT
MSIDLKYLGVQLPLAPATSFPFWNLGTGNPASPDAGFPFVSRTGKTNDFTKIKGWRGK
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AQOQQOQQOQGSRPGLSKSQVKLMDLED CALWEGKPRTYITEERADVSLTLLTAQAS
LKTKEIHTIIRKRAPP CNNDFCRLGCVCS SLALEKRQPAHCRRPDCMFGCTCLKRKV
LVKGGSKTKHFQRKAHRDPVFYDTLGEEAREEEEEGIREEEQLKEKKRKKLEYTIC
ETEPEQPVRHYPLWVKVEGEVDPEPVYIPTPSVIEPMKPLLLPQPEVLSPTVKGKLLT
GIKSPRSYTPKPNPVIREEDKDPVYLYFESMMTCARVRVYERKKEDQRQPSSSSSPSP
SFQOQTSCHSSPENHNNAKEPDSEQQPLKQLTCDLEDDSDKLQEKSWKSSCNEGESSS
TSYMHQRSPGGPTKLIBIISDCNWEEDRNKILSILSQHINSNMPQSLKVG SFIIELAS
QRKSRGEKNPPVYSSRVKISMPSQCDQDDMAEKSGSETPDGPLSPGKMEDISPQVTD
LDSVRERLHGGKGLPFYAGLS PAGKLVA YKRKPSSSTSGLIQVASNAKVAASRKPRTL
LPSTNSKMASSSGTATNRP GKNLKA FVPAKRPIAARSPGGVFTQFVMSKVGALQOQK
IPGVSTPQTLAGTKFSIRPSPVMVPTPVVSSEPVQVCSPVTAAVTTTTPQVFLENTT
AVTPMTAISDVETKETTYSSGATTTGVVEVSETNTSTSVTSTQSTATVNLTKTTGITT
PVASVAFPKSLVASPSTITLPVASTASTSLVVVTAASSSMVTPTSSLGSVP IILSG
INGSPVVSQRPENAAQIPVATPQVSPNTVKRAGPRLLLLIPVQQGSPTLRPVSN TQLQG
HRMVLQFVRSPSGMNLFRHPNGQIVQLLPLHQLRGSNTQPNLQPV MFRNPGSVMGIRL
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TLRISPPEPQSFASKTGSETKITYSSGGQPVGTASLIPLQSGSFALLQLPGQKVPVPS
ILQHVASLQMKRESQNP DQKDETN SIKREQETKKVLQSEGEAVDPEANVIKQNSGAAT
SEETLNDLSLEDGRDHLDEECLPEEGCATVKPSEHSCITGSHTDQDYKDVNEEYGARNR
KSSKEKVAVLEVRTISEKASNKT VQNL SKVQHQLGDKVKEQQKGFDNPEENSSEFPV
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QECKKEADEQLIKETKTQENSDVFQOQEGISDL LGKSGITEDARVLKTECD SWSRIS
NPSAFSIVPRAAKSRNGHFQGHLLLPGEQIQPKQEKKGGRSSADFTVLDLEEDDE
DDNEKTDDSIDEIVVSDYQSEEVDDVEKNNCVEYIEDDEEHVDIETVEELSEEINV
AHLKTTAAHTQSFQKPSCTHISADEKAAERSRKAPPIPLKLPDYWSDKLQKEAEFA
YYRRHTANERRRRGEMRDLFEKLKITLGLLHSSKVS KSLILTRAFSEIQGLTDQADK
LIGQKNLLTRKRNILIRKVSSLSGKTEEVVLKKLEYIYAKQQA LEAQKRKKMG SDEF
DISPRISKQOEGSSASSVDLGQMFINNRRGKPLILSRKKDQATENTSPLNTPHTS ANL
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KDS SFHKLKMKDLKDSSIEMELRKVTS AIEEAALDSSELLTNMEDEDDTDETLTSLN
EIAFLNQQLNDDSVGLAELPSSMDTEFPGDARRAFISKVPPGSRATFQVEHLGTGLKE

LPDVQGESDSISPLLLHLEDDDFSENEKQLAEPASEPDVLKIVIDSEIKDSLLSNKKA
IDGGKNTSGLPAEPESVSSPPTLHMKTGLENSNSTDTLWRPMPKLAPLGLKVANPSSD
ADGQSLKVMPC LAPIAAKVGSVGHKMNL TGNDQEGRESKVMPTLAPVVAKLGN SGASP
SSAGK

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

>**Tbx16** XM_001377868

MAPRGTPAPGPHSPISASLEDVDLWTEFYRVGTEMVITKSGRRM
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PAYGSHWMKEPVSFHKMKLTNNLTLDQHGHIILHSMHRYQPRFLVAQADDLFNVWCNLF
QVFSFPQTVFISVTAYQNEQITKLIDNNPFAKGFREQGRKPRRFSPPGRGLTKERLRE
LVSSPEPERSGLTKEDAADQAEARGGSGPVSSSRFSPLWGPRELNQTEGPPGEAAGTS
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3) **Zebrafish T-box genes** with Genbank (mRNA) accession numbers

>**tbx1** NM_183339

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PYSHHESQFEPCPAAQHAYNYSGSNSAQAPAQGDSGTSNCSSSSSSSTPNKTLVKKNP
KVANINVQLEMKALWDEFNQLGTEMIIVTKAGRRMFTFQVKIFGMDPMADYMLLMDFL
PVDDKRYRYAFHSSSWLVAGKADPATPGRVHYHPDSPAKGAQWMKQIVSFDKCLKLTNN
LLDDNGHIILNSMHRYQPRFHVVYVDPRKDSEKYAEENYKTFVFEETRFTAVTAYQNH
RITQLKIASNPFAKGFRCDDPEDWPRNHRPGSLQIMSAFARTRNPMSSPPQNGTEKE
DSRREYDRDPGSGNPLHSDPTHQLMSRVLSPALPVLGGLHAVPLTAGPRSPPHELRLDG
HPQPPDTLHHHPYKYPATYEHYLGAKTRPSPYSPSIRGHGYHPHMNPTTANMYSATS
APTNYDYGPR

>**tbx2a** NM_001102384

MRDPVFTANAMAYHFFHAHRPADFPMSAFLAAQAQPSFFPALTLP
PGLSKPLADHALSGAAEAGLHAALGHHHQAHLRSFKGLEPEEVEDDDPKVTLEAKEL
WDQFHKIGTEMVITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYKFHNSRW
MVAGKADPEMPKRMYPHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFTILNSMHKY
QPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDNNPFAKGFRTD
GNGRREKRKQLAMP SMRMYDDQCKVDRDGGSDSDSCEQT TGRDSVHSPTGPAT SPLK
FTRSREDKNFNESDNELDQHDGDMIRVSSPEQRQPSPFSPRCEDRVKDRNLNLEKKGDY
SDSRKENDSAF SIRHLDDKDKLDARNVKDQDSSKKEADSVGMSTVKDGFSPLMVQ TENP
SHFSASHLQSLALSGLHSHFFNPLSSGQSLLFHPGQFAMTPSAFSTMGMGHL LASMS
GASGLENGSLSSQSTSSPNPFFHLSQHMLASQGISMPFTFGGLLPYPYTYMAAAAAA
SALPAGSAASSLSRNPFLNNT RPRLRFSYPYQIPMSFSQSSGLLTGIPSTMSAESESS
KSGSRESSPMSEHSHKGTNGQNTGSPKSSGKDSINELQNIQRLVSGLEKHRDASPRS
VSPK

>**tbx2b** NM_131051

MRDPVFTGTAMAYHFFHAHRPTDFPMSAFLAAQAQPSFFPALTLP
PGALT KPIPDHTLAGAAEAGLHPALSHHHQAHLRSLKSLEPEEEVEDDDPKVTLEAKD
LWDQFHKLGTEMVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYKFHNSR
WMVAGKADPEMPKRMYPHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFTILNSMHK
YQPRFHIVRANDILKLPYSTFRTYVFPETDFIAVTAYQNDKITQLKIDNNPFAKGFRTD
TGNGRREKRKQLTLP SLRMYEDQCKVDRDGDSDASSEPTTGRDAGHSPPGVSSPLR
FNRGSRDDKTCTDSEHEMDHQNDRCGSSSPAPKPSPSPFRSRSEDWGREKPIAEKKDD
YPDSRKTSDSIFSIRNLEKDKLESRSRKDTDSSKKDTENSGISGSKDSFSPLMVQTES
PSHFAGHLQSLALSGLHSHQFFNPLNTGQPLL FHPGQFAMAPGAFSAMGMGHL LASV
SGAGGLENGSLSAQGTGSTPSPFFHLSQHMLASQGI PMPTFGGLFPYPYTYMAAAAA
AASALPASSSTASSLSRNPFLSSSTRPRLRFNPYQLPVSI PQSTNLLTTGLPSGLNPS
SESSKCGSREASVPVDHKNHGASQRNGSPKTTMKESINELQNIQRLVSGLESQRETSSP
RDSPK

>**tbx3a** (currently tbx3) NM_001101670

MRDPVIQSSMAYHFFLPHRGPEFAMSAMLGHQPPFFPALALPP
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EAKELWELFHKRGTEMVITKSGRRMFPPFKVRCTGLDKKAKYIILLMDIVAADDCRYKF
HNSRWMVAGKADPEMPKRMYPHPDSPAETGEQWMSKVNFHKLKLTNNISDKHGFTILN
SMHKYQPRFHVIRANDILKLPYSTFRITYVFPETDFIAVTAYQNDKITQLKIDHNPFAK
GFRDTGNRREKRKQLALQSMRSYEEQQKKENGTSDDSSGEQASFKCFRQASSPAVST
AGHNHLKDFCDSDEDSDEEDKDANAKEGPDSSKISTTTEDSKDQDAGLGKSVFGESDS
SSGRRSEKTRADSRSPITLISSTTRSGEELKSPVREPAKTTDDCRTVSKENYMLTVQ
TDGAHLNQNHLNFGFPPLAGQQFFNHLGGAHPFLHPSQFNMGGAFSNMAAGMGP
ILAAVSSGGVGLDGSLLPSPSQTGTGAPMPFHLQQHVLASQGLAMSPFGGLFPYPYT
YMAAAAAASSAASSSVHRHPFLSAVRPRLRSPYSLPSVPDSTLLTTAMQPMASGLE
VKGDGMNTSPASAAALDSEVTSRSSGSVLSPKTCTEKDSSSELQSIQRLVSGLEPKPD
RARSVSP

>tbx3b (new) XM_002662004

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PAFKVRCSGFDRKARYIILLMDIVASDDYRYKFHNCRWMVAGKADPEMPKRMYPHPDSP
STGEQWMSKAVTFHKLKLTNNISDKHGFTILNSMHKYQPRFHVIRANDVLKLPYSTFK
TYVFPETEFIAVTAYQNEKITQLKIDNNPFAKGFRETGNRREKRKQMLHQRCEVEPK
KASVLTDDSSFDQISSNYLIQENTNESDIDGFGDEKESNEVESIQSISQDEQNSREIS
TTVQESKDDPNEEIGDRNPEINSKKQHSVEQPAHLPLDKKHAEQQKFAADVTASQKD
SLARHFYFPTPGLINSRLPSHVLNLCQFNIVGTLPLLASEATGSWIPRRSNEGEGQ
GYTTSVSSSQRLTGMQDLPPNFQQRMTSQGVLSAQGNIFPYPQDYMTTSAGSSSA
ASYQVHRQPPFNISYRQCRPYVPVWVHGRKIPQTTSVLIPYGETDINEHASIATPG
STLFLGLKANKDQNTRCQDL

>tbx4 NM_130914

MLQEKASVVADEGMTVAQSGGRPELASDSSHLGLPTTPSNPQNN
EPDQSIENIKVVLHRELWKKLHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILL
TDIVPADDHRYKFCDNKWMVAGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKLT
NNHLDPFPGHIIILNSMHKYQPRHLIVKADENNAFGSKNTAYCTHVHETAFISVTSYQN
HKITQLKIENNPFAKGFGRGSDGDLRVSRLQGDYFVISKNMVRQRLISSHGHLGKGL
SAGVLSHPQVLSHYQYDSGVPLPNSDSQEALNSFTSSREPSLLYHCFKHRDNPRL
ELGCKRPYLDTTSSAVSEEHYFRSPPSYDSSLSSHYPYCNEALGSREACMYGGLEGE
GAVGTDDLPAAPSLNLCNMWASVQPYPRYGMQTVEMQYQFPTAHFNSTASAAMVSHHS
PSMQRPHTPPDLVTFTTQVRPLPPTPSSASTSPSGSGHHDRHSSLFHRKAGSPLRSQ
RDFGTGYSTHSPTSTREPAYQYQTLGLSSVGPWHTDS

>tbx5a NM_130915

MADSEDTFRLQNSPSPDSEPKDLQNEGKSDKQNAAVSKSPSSQTT
YIQQMGEGIKVYLHERELWTKFHEVGTEMIITKAGRRMFPSFKVKVTGLNPKTKYILL
MDVVPADDHRYKFADNKWSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKLKLT
NNHLDPFPGHIIILNSMHKYQPRIHIVKADENNGFGSKNTAFCTHVFPETAFIAVTSYQN
HKITQLKIENNPFAKGFGRGSDDMELHRMSRMQSTKEYPVVPRSTVRQVRGSSQSPFSG
DVQGLSATGAISSQYSCENSVSSTSQDLLPQSSSYHEHTQDYHCIRKKEVEDECPAGEH
PYKKPYVESSSEDDHYRPLSYQSLSGLSGGAPYRPESSQRQACMYASAPQPEPVP
SLEDISWPGVPPYVFPQMERLPYQHHSFSAHFASRQMPPEAHGMYASSVSHQCSPSGGIQ
SPSAGLQGNEYLYAHGLQHTVPASVPHRAQRQHHA

>tbx5b NM_001198771

MANPMFESLRACSGGNSPAMDFERDKDSGHHGRNKTGSPPLQTQ
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MDIISADEHRYKFADNKWSISGKAEPALPGRLYVHPDSPASGAHWMRQLVSFQKLKLT
NNHLDPFPGHIIILNSMHKYQPRHLIVKADERNSTFGSSNTSFCTHSFAETTFIAVTSYQN
HTITQLKIENNPFAKGFGRNDDIELHRMSRTPSKEYPLVPRSTARQRAAPPSPDCLSR
SEYTVTQKPSPGFTCSDTSGDQSLTETPSIHDPYPLFSYQLSPDVAPSSMDTTQHQP
CMYGGSQVGMEELRWASYSSTTYQSFSSAKEMSGTFVPPADLSQELYPQYTCEVGQV
SHCMMTDFSLYACNRSFSQNNQPPNNWCGGS

>tbx6 NM_131052

MNHLANNYGYYPQDCRTQYSRMNSAEAEELTSPLVHVSQDRELW
DKFSSIGTEMLITKSGRRMFPSCKVTVTGLNPKVKYVIMDMVPFDNHKYKWNKDCWE
VNGSSDPHLNRRFFIHPDSPAPGQKWMQYPISFHKLKLTNNTLNSNGLVVLHSMHKYQ

PRLHIVQSPDPCTPHNPGAYLRFTTFPEAAFIAVTAYQNQEITKCLKIDNNPFAKGFRDN
GLNRKRFRDKGTQEMQDTRQVKLDTANECAAGMSQMVEDVDVSVSSSVDCRDTQNS
SSVSLNPFISAFTNPSSAGGAAHQTHTLTSLSNRHFSSPRESNLNSVCAALPVSQLS
TGHTSFSRLNPQETHHNSRPKIQLQPPHPSLQCHDLDPVRLPLPPKLSRVQLSESALRN
LEMSPLSDCANPRPLTNILNRSCFRASFTPSGKLLPNPPQPEQFLRGSEREIYPVQVEY
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.

MVLKVQSSAGAETPRHRSAGGFSCPQDDVSGRSCSKAPEVSSV
RVQLEMQSLWRQFDQLGTEMIVTKAGRRMFPTFQVHISGMDPAEYVLLMDFIPVDDK
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GHMILNSMHRYQPRHLVVLVDRSRNSQRFARNFCTFSFPETRFIAVTAYQNHRTQL
KIACNPFAGKFRADPEHRADLNRAASMGPTDPPALGLPWAEAAASRSRECRHSDTHL
QPAVAGSVMDVASHTHLYTPAPVFFSLPGQWDVLTRAERDLTG

>tbx15 NM_153664

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PSASMEEIQVELQCADLWKRFDIGTEMIITKAGRRMFAMRVKIVGLDPHQYYIAM
DIVPVDNKRYRYVYHSSKMMVAGNADSPVPPRVYIHPDSLASGDTWMRQVVSFCLKL
TNNELDDQGHIIILHSMHKYQPRVHVIRKDFSSSELSPTKPVPTGEGVKTFSPETVFTT
ATAYQNQQITRLKIDRNPFAGKFRDSGRNSPPYRTGLEAIMETYAFWRPPVRTLTFED
FTNMQKQQGGSTGTSTSTSTGTPSPSGATHLLSPSCSPPTFHLAPNTFNVGCRSRL
CNLGLSEYPVCARSNMAALQGYGGLADGSYGRQLTTGGAVASQAASESFLPQRTSSLI
AAGMQGGAHGSLATGNSGSGSGGKMDAYGSQLASFASQLQYVMQAGASSASGSSAS
SGSSSSSAHMFSGSHHVQQSTYNAFSLHNPYNLYGYNFPASPRLAASPEKPQGGLLC
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>tbx16 NM_131058

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KAEPQPPYRTYLHPDSPAPGSHWMKQPVSFLLKLTNNALDQHGHIILHSMHRYHPRF
HIVQADDLYSVRWSVFQTFTFPETSFATAVTAYQNTKITKCLKIDHNPFAKGRDEGTNS
KRRANRNLDPDERVAKKMSKDSEHSGSPQDVQPSSCEALDDEHAGRKELEVKAERYSPW
GGACDRDSGHALRPESPLGSDHRDVYSSEQLVPGQNTYQPYRFHEYGKSPSPSSSSSV
GGSSACGSAGRPSFESRVLDVATVPDTSSSKPSAPEFSLPPHPSAGHQEYAGVLNM
AITQAKPGMLGTHPLYSHYSTEQSLGQWSGAAASQYPPPPPHHLPTEYSSQAVHHG
YHHGNVGDWSQYPLFSYSCW

>tbx18 NM_153665

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TSSGEEMRVDLQGSGLWKRFEIGTEMIITKAGRRMFAMRVKIAGLDPHQYYIAM
IVPVDNKRYRYVYHSSKMMVAGNADSPVPPRVYIHPDSPASGETWMRQVISFCLKL
TNNELDDQGHIIILHSMHKYQPRVHVIRKECGEELSPVKAVPTGDGVKAFTETVFTTV
TAYQNQQITRLKIDRNPFAGKFRDSGRNRMGLEALVESYAFWRPSLRTLTFEDILGIT
KQGAAGSHGVVGSSAHLSSSSSCPSPTFHLGSGAGPVCDYSTCSRTSHPLHRYGPSLS
ADSYSRLTSPTADAFSTSRSTYVSGTESEAFSCTQTGLPIQIHSMPSTTSQLQYLMP
GHAHNAFSTNQSTQGSYNGFRLHNPYGLYGNFSTSPRLATSPEKAAATQTSFLGSSP
SGTLTDRQVLSTMDGLHMLSSSQNLFDSTLGLTSSSSQVTAHMA

>tbx19 (new) XM_003198759

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PADGHRWKYVNGEWPAGKPEPHSHSCVYIHPDSPNFGAHWMKAPVSFNKVLTNKL
GGGQIMLNSLHKYEPQIHIVRVGGSHRMVTNISFTDTQFIAVTAYQNEEITALKIKHN
PFAKAFLDAKERSHPKNHLEPPVENQHMGIPHCGWFI SNPDSLCSASGGNFYPGGLP
LTHHHHGYKHYPSLHGHAAPYPSPYLPRHHHRGHNTVSLSDNLSPGVQMFSGHESWT
GVSPPGAAMLSMQPAPNSPGASSQYPCLTWTVSSCTVSSSPGGVVSLTHGQDEPADG

ASTSASPCSLQAHGPTGSDGSVDPANHSRVGGMSWASVTTHSF

>tbx20 NM_131506

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LETKELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVPMDIVPVDNKRYR
YAYHRSSWLVLGAKADPPLPARLYVHPDSPFTGEQLSKQMVSEKVKLTNNELDQHGHI
ILNSMHKYQPRVHIIKKKDHTASLLNLKSEEFRTFVFTETVFTCTAYQNQLITRLKI
DSNPFAGKFRDSSRLTDIERESVESLIHKHSYARSPIRTYAGDEETLGEEGSAHSRG
SAFTASDNLSSLSSWVTTTSGFSGFQHPQSLSAIDTSTASLASPLPHPIQGSLPPYSRL
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>tbx21 NM_001170599

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VPAGADAYSSANGKDVPSSADGYTASFQHGFPRAPMYSLPGLQVSGKTQVLLNNYPL
WAKFHKYQTEMIITKQGRRMFPFLSFNITSLDPSAHYNIYVDVVLADQHHWRYQGGKW
VQCGKAEGNMPGNRMYPHDPSPNTGTHWMRQEVSFGLKLTNNKGSSNNVAQMIVLQ
LHKYQPRLHIVEVKEDGTEDPFLTQTFVFPETQFIAVTAYQNADITQLKIDHNP
AKGFRDNYDTLYAPPDPDLRLTPSPTESQQLLSGSCYPHPYLSQYMSPLPQSRFYR
EPVSMTPQPCPKDPTSSPHSRWYLSQAVPPNRLDFSAYETEYTSNSLYKFPPLQSSP
HHPLSYSENPFSTGAVSSANPGAWTASGRPSPQYLNHPHHSKPTSSLSWFRVPSPA
ASSSPATNSRFHASPSLLEPQRQPLLQDKSKESTEDTWIEAPSVKSVDSADSGLFEG
GESKKRRVSPYTSSTENSPPNRSATCEKDNCS DAGYYGFYTH

>tbx22 NM_001164461

MACEDLRKSAKERKPAGAEAVRKVRVDLQGS DLWKR FHEIGTEM
IITKVGRRMFPSIRVKVHNLDPQQYSIAMDIMPMDSKKYRYVYHSSQWVIAGNTDHS
CIPPHLYVHPDSPSCGENWMRQVISFDRVKLTNNELDDRGHIILKSMHKYRPRIHVIL
HCPPECLSKRLLSLPADGVFTFSFPETQFTTVTAYQNQQITKLKIDRNPFAKGFERN
GAVLDGILESYSWHSFPNGFKSLAMELQGRFCGSSASGITPSVSSAQAVHPTAFSSPQ
CKLILPSSCFLAYRAYCSICLNNTGLRPMDLPLLTSLPVKKGDRCRSHWLYNSAGT
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ISSIGYSP

>tbx24 NM_153666

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NPSLRYILLLDIVPVDDSSRYRFQDNSWQVVGGAEARLPDRVFIHPDSPATGEHWQNR
ISFHRAKLTNNTLDAQGYIILHSLHRYQPRVHVIEARDVLMWGRTQHSFTFPETQFIT
VTAYQNNKITEKINSNPFAGKGFRENGMNCKKQREARLKRKITSSQEECLDIESCDPC
DSTELLPQSVLDLPSSALSIMNTALPITDSGFHTEVSSHDPQTDSDQTLVLEQAFLTSE
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VSTTQSSDLELPQASSISSPHSMPAYSSIPSAEYPGVNSSTAMPASTTSLSDSYSSIS
HSTSSHLLQSSSYHSLLPDQSQDNLSPHPTPTNPPFQSI PACQGTRLTIDSGQNQVDD
GGLSSANATTPAVPNPTQTAFPPVPQPNNDPDPTSPSCQSLPQSALPYQQVVSQCNI
PTPSPDNTTPTAFPPFPSEQSTPNSIMVSSNPNTTAFPPVPVQQQLNLSTSGPSSFPV
SQSSGLNAIPNPVHPTTGSFSFPSTNAIHQGPMSVPNTLHPSTAYTFPSSLPKHTGP
LPNPAPTSYFPPTPIPPGPHPLQSLTLSSCSISNTSQIQSTFPQSYHNPSFSHIPQ
MANHSQITSQSFPPLQSSSAPQLLSQSSTHPQCPPPSNAYPAVAPTEIGTFPQLNSAT
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>tbria (new) XM_688029

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TEMIITKQGRRMFCLTFNVSGLDPA GHYNI AVDVILADPNHWRFGGKWPVPCGKADT
NVTGNRVYTHPDS PNTGAHWMRQEISFGKLKLTNNKGASSNNTQMIVLQSLHKYQPRV
HVIEISKNEDEDTSDPDGVQTFTFPETQFISVTAYQNTDITQLKIDHNPFAKGFERN
DTKYSMDNTDRLTSPDSPHSQLLPSSRYAMP S ALFQE QFVDSYTKSCFTTGTPERGLE
FTNSIMTSNQTQESSVTSGQRWFVSSPSVPSYEADVDTAALLSYTTAGVKNL PFTSTG

GSSNSLDYYTSTAGWDSRGSLENGSKTISNLSGWVLDATLERSMQPNYLPDDRELMER
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VQNRARNGIKESGFFHFDA

>tblb NM_001115090

MLERCISPALARSKKCMIVGSGYPNAQASELALQDYPIISIGD
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SSPQGYATAGYPYAQQYGHAYQGTAFYQFSSAQAGLVPGKAQVYLCNRALWLKFHRHQ
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NVTGNRVYMHDPSPNTGAHWMRQEISFGKLKLTNNKGATNNTGQMVVLQSLHXYQPRL
HVQVNEDEGTEDTSQPGRVQTFTFPETQFIAVTAYQNTDITQLKIDHNPFAKGFRDNY
DTVYTGCDIDRLTPSPGDSPRSQIMPSARYAMTGSFLQDQFVSSYAKSRFHPGVGGAP
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TLLSYAAAGVKALPLPGAGCSNRPLGYYGEPGWGTRTPPQYCSKSSSVLSCWPSNSV
GSRTTASSYLVPGLDGDPIAPERSPLGGADESKPKDLSSESWIETPSSIKSIDSSDS
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>ntl-a NM_131162

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VPGGKPEPQSPSCVYIHPDSPNFGAHWMKAPVSFSKVKLSNKLNGGGQIMLNSLHXYE
PRIHIVKVGGIQKMISSQSFPETQFIAVTAYQNEEITALKIKHNPFAKAFLDAKERSD
HKEVPDHSTDNQSGYSQLGGWFLPSNGPMGPSSSPQFNGAPVHSSGSYCYERYSSLR
NHRAAPYP SHYSHRSTTTNNYMDNSSGSLASHDSWALQIPNSSGMGTLAHTTNTSN
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>ntl-b XM_001343597

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VNGEWPVGGKPEPQAPSCVYIHPDSPNFGAHWMKSCVFSKVKLTNKLNGGGQIMLNS
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KERSDHKEIIEDVSESQQSGYSQLSSWFLPSAGSLCPSANPHAQLNSALSLSLSTSHGCE
RYSTLRGHRSA PYPSTYAHRTASPTGYSDSSSCLSMPLSHDNWSSLQMSHSSVLP MG
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>eom-a NM_131679

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FSSAVCASRSQFGGGYQFGQGPGLYPSYPGPGSSLSMPIPGSGSAAARQVYLCNRP
LWLKFHRHQTEMIITKQGRRMFPFLSFNITGLNLTAHYNVFEIVLADPNHWRFGGK
WVTGKADNNMQGNKVYVHPESPNTGAHWMRQEISFGKLKLTNNKGANNNTQMIVLQ
SLHXYQPRLHIVEVTEDEGDVEDMSSEAKTQTFTFPENQFIAVTAYQNTDITQLKIDHNP
FAKGFRDNYDSMYTAPESDRLTPSPTDSPRSHQIVPGARYAMQPFQDQFVNNLPQNH
RFYGSERAVPQTNGLLSPQSEDS AAGSASAQRWFGVPVQQSGATTKLDLSYDSEYSAS
SLLPYGIKPLPLQSPHALGYYPDSAFASMAAGWSSRSSYQRKMTTGLPWSRPSPPAY
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>eom-b NM_001083575

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DFSPGYHQFGHAAGNGYSPYQSGSGAVALPSAALRAQVYLCNRPLWLKFHRHQTEMI
ITKQGRRMFPFLSFNMTGLSLSAHYNVFEIVLADPNHWRFGGKWPVTCGKADNNMQG
NKIYMHPESPNTGAHWMRQEISFGKLKLTNNKGANINTSQMIVLQSLHXYQPRLHIVE
VSDDRSERDSNTQIFSFENQFIAVTAYQNTDITQLKIDHNPFAKGFRDNYDSMYTLP
DRERLTPSPADSPRAQQMVPNARYAVQPFLEQFSSLTQRSVTQPSSVEDPAQRWLIS
QNSSKLELTAYEGEYSSSLLPYSFKSLPLQSYYPDTAFSWGTRVSAGSSFPRKLPSGL
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TEEQNFHKDSPSAAKAIGYYAFYTSS

>mga-a (currently mga) NM_001170739
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KWSGKGWEPNGKAEPHISRLFVHPESPASGLHWMQYPVSFYRLKLCNTLDQEGHIIH
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PFAKGFREDAVNARSSKAKNGLSTDETESELKLSKEMTTLNNLKTLMKRKASVKVNV
NQNVPNPTNGENKVVNGAAPVDNTNVQSLCNKKRPSSSAFSDFIKGAHVKKVRLSLEN
INKTGGAETPSTACTSKQKEAADISSITENSLQVDQKDGNGAGDVLRCSTDTSLKTG
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KRPERVPLPLLAHLKQRRPILPKPVSHSSSLDSEKSCEPAQTSESSSVLMSFIPCVT
TNLDSQPAVTSLSQTVTSSTTDANNMTSLSTTSLYSSTTVPLIPSETQLCDRFSASPV
GSDPFSAPNTTSPSKPNSNPALDISNNTDAIFTDPHDNTLRSQSDISSDSTCDVVHDS
CPPTVNTDVTETPVVPSPTS VFDVPSSTDNDMNSYQDINSMPDVAEGDISDCLLDSS
TGSCPEFFSEEIPQNTLFTNEESLSLPLDDASSPAFSLPSPAPSSPDPFPPSLFCDRS
VPPRKALDSFPERLLDCTAASARDPFLGFFNDGREPPRQIFDLPERPLIGTVASRES
LSSSVNNGPEHPMETGDLFSQSHCPDRANSLNDLESAASCETAVSDNSISKPTKPSPH
GSSCKKYKGKQKVGTLKLGEDSEVFDGPVPVPLQPSLEDVEGQLFVSFMSKKALRIH
LGDDDDDKPETAQENTDNP DGNNEEKIEKKIEGLEKVLLHDLKFMKNRQVIHPVLQEV
GLKLNLLDVTLEIDLQYLGVLPIPPALSP EETSSQAQFVSRTGKTSDFITQIKWRD
KFAPSASLSEGVSTSDAGQSNLSAFCSMDLDEYLASEGKLIDERAASLSQADCTPVAY
QLPTKSTSYVRTLDSVLKKQVPAILTPTTNKVKPTFKSKVENKSKKPLKPGKGKQTKP
VISDAEPLCTKKPQQNKKYKSRKEFKSPEKPDVAEVPASNTTPMAEDSGSTSSTCAGG
RSPGLPKTLVKLLDVEDGAVWEGRHRYSYTEERAAIALATLVTAEGASTGSADAIRII
RRRAPCLNVFCRLGCVCASLVHLRRHHHC GKPCMLGCSCLRKVVALKTPKQEEGT
ADDSDPQGMSEENKAKWRKKNMKRTYVLTDP ELAPEPAKRVSTLWDRTRGNFDKEVL
YCPPPRSPQPQLLSQELQHDLESFLSPSKQKRVEERNLSTSEDNIEINLTCARSRPF
HSNCHDKPKADDNKHHSIQVSTPDIEEGELVPLNLSGPAKRLEMMSERTWTSIDMRNN
VMRIVCEHMAQDRNLQPFWMGKYFIKPVSKTLEKEENG SVEIYKVIISQPV EKKTENE
KITQKEEELEKHVKTSEVKG LPLFLSKCCPAGLLKAEKKSPDAPGQIMVNGKHYPQAKL
ELGHMGALHPANRLAAYITGRICPTVSAITKPPVTTVPSSLTTLTVSKVTCTPASTTS
VSKSLGGSTLTSTTSASSPGLTSPAKKTVYITVASRNTGLSNSGTQIKKIVSPTGPPQ
TSGQKMLLQVVKTAGNTLYRNPNGQLMQLVPLSQIKALKPNLLSQGQPTIIRLPAPP
TVSMNKPQGGSATIVTSSIPTTQTLAKPSGTVPVSTSSSMGGKLISPPSSKSVLSL
PSTLVVQGFGLQSGTCTLRILPPTTSTSTVLSQSGLTLLKSASSMPPTQDSSNSET
NVSFSSQSTTEKTVVQLKQSTIDPAKQNSSDNANVKEKHFNKAPDPEEKEIGSDSTEL
TDDSDLYSDDQEDASCMSASDREEKIEDTDGMDSEKKGYAEMVVDIETIEESAEQNR
IAKFRASALRRNQYRRNQKRIHDEMLEVRVQKVRKERKRRQTLXECFIKLQGTLMSS
KKFEVSRMRILTKANKEVEYLVKLEDYLVEKKAKLQFKKERYIQTLSQLCDKSTESIG
LKLNEIISKQKALEAQSKTKETHPKPIQAKSKAKPKPSKPSKVVDVCDKPKGLAVQ
NKVNDVSKVTYSPSKPIDLSIKKQKSP EMTESVPKSTPSVSPADLDGNKNTLNVLDT
NTVTTTSTPIQPSFNSTLVMKPVSIPIKHPPITRERM RPNIILSRASSQAMQGSVPK
ESLLTNVCIPQVLPLMNTMVP CNPIITINNSLQPIGITSVVGQSSSTPGVASVSIVPTI
SHPLRVENTLPLHLPQFIKITNSPVNINTKVDSASLPNISNVISLAENLVVPRKVVED
KPVFQAQPTSVDNQQNSSNDKIPDLEQKTDEAPSTNVPKQSVVEDQKGASVPKSNPEV
PENKSPDDSDDPEDENLLSLLDELVLLSQQLTNEDEDERIAVPGDVQSCSDKPEDQEP
ADDRALSPLFLTLEDLMSPD SKDEIDIPKVDDL VKVIFGSDSPSVSSESGVAQSTN
ASSPHASTCNATGDGLTPPPLLHMKAA YEASRQSANEGTSVTWRPMPKLVPLGLKAQ
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
MDIAPLDDLHRHFNGEAWE PDGPGEAHLQSPVCFHPDSPA VGQHWMDSPVSFYTVKLTHD
SCEREGVLLQPMHRYQPRLYVAPVSACLERAVPLKSPNVHMF TFPKTEFYAVTSYQNPQI
TRLKIDCNPFMLAFREDETSARLIQNKLKALTPARTHTAKYTADNHTTSDGEQHLRKSC
RLIVNLNVRCVCFMTCRLHSELKHSHTKESFVRFKHEGIDSNDSTIFLKSATKVNTA
NNDSSSDGEQYLSQQDSIRLTVRFS SLKQQKLNKHQLINENKLENNSM TNIYKR NKYLLI
QLSNIYSTFRSNSSTTLIIIIINQYKLLPKTYFLKSKCYIYLTSSLKNKAKSNNDKTYN
GNNLNTLITTFCCGTVNHQQPHDFICVAFKFVLLLKIKNIFD FNSKVNANCLSPNKISV
NQHFNTKAGNKLSSKPKFLKTFEVFNLSQKEKNLRSDEDLTFKLSMCSKAGRRPLSRGQ
RVVLRPRPRPMKRGKKARAKWTRVKNVQALLDHRKRMQSISTHTDVCMPDLEDVEGVLF
VSFTAKEALDVHVGNMRS SVGSSSPPPSPSISPSSHTQQLSACVTDPPVTEADRISELE
LALLQDLKESKRNRI LHPALQKAESGFVSR TGKTNDLTRIKGWMEKFSLRSTSGTANSSA
FCSEMLDEYLESEGGQRISERA E VFS SSSDPSPVVYQLPVRSSSYVRTLDSVLQMRTPSAA
ATAPQQPSRRVAKRMRI SPVRVVS RPVALPQPAVYSAGVGRVRSRRGRKRRRPHISFNRD
AVDGAQPSCTEKHTQLRTLEE QAL THGQIHTFISTERARVSL SALLTAQSVLVETPQWST
HIADDGACAKLFCRLGCVCDLSRESAGSTHCRVCEMFSCTCFKHKILLIRSADHSQSV
RSLQTLHPDPEGRPAPAARVTRLWERSAEESDPEPMSTPKPAGALRPAPRTHTHTHYTL
TPRGRPPANRPNAQVPM EKDPVYLYLESMMTCARVREYNSNPPQVHILPAKKSSDEAL
SDTSLNPSKRPHAAQSPDKPEPTKVL EII SGCNWESQSRSVLKELFQRVQNTNLP SVLS
LDDYTVKLLSEHLKKDGRSMITYKVCVSLSDKEKSAQKECVQKECVEKERVQKERGKEP
ALKPVPLLCGVM TAGHLKAQRRAPDLHCPIQVNGRTYAQAKLT LGRMGSLHPANRLAAYV
TGRIKSFVPSRTRTTAASRRSKYTATRANHSTDVFKK PATQRLSIPRPPGGIRFPKVRRI
LNALAPPLSAA DRVVPASALPPGQQVVLQPVAGMSGVNMCQFNGQM IQLVPVSAAPMQI
QTSTTHSSGGASQEPQSSQLPANTALPFIIPRIHSVPGRNGFTFASAAAPGVQNNLLNK
TGTFSEFRICPPSAESQSPAPTGA PQGSVTASTLILPGGYKLIKLINPAEKPDQNNPAEEP
DQTI PAEEP DQNKPT EKPDQNNPTKYPDQNNPTEKPAQNNPAEKPDQNNPTDKPDQNKPT
EKPAQNNPAEKPDQNNPTEYPDQNNPTEEPAQNNPAEKPDQNNPTEKPDQGNPTEEPDQD
NPTEEPDQTI PAEEPAQNNPTEKPDQDNPGKKPDQDNPT EEPDQNNPTEEPDHNNPAEK
DQDNPT EKPDHNNPAEKPDQDNPT EKPDHNNTEPDQTI PAEEPDQTNPT EKPDQDNPT EE
PDQDNPT EEPDQTI PAEEPDQNNPGKKPDQDNPT EKPDQNNPAEKPDQNNPAMEPDQDN
TEKLEQNNPAEKPDQDNPAMEPDKNPAEKPDQNNPAEKPDQNNPAEKPDQNNPTEKLEQ
NKPT EKPDQDNPT EEPDQNNPAEKPDQNNPAERVENSSQSSVCVKVEPAEAEEDITQSAH
KPPALIKTEPEHIQIPQLTNDGGTAKFTIKIEDAEADESV PQQQSRRKEEPFQFGGFSFE
GLTNSAFSRLSFAVSPPAEPGEPDGSVQKSLDWLWRGRADV DTHAELSEKPPQNGTLMY
SSDGCTTEDSMEQLSEGEVDIETFEENDQII SRLREKARRKIQSRVPPPPPSRQLKV K
VKSC TAHPVRLMSDLLLYRRTRRLNQPIREKRRQLELLQSERTLRRTMCMVREQSISTEEL
LHQACELITSLEDHSRFLIEEKRALMRQHSHYQTLICISQASGRFLHDSHIGPSGCCIM
PEHDHCTVNDDDDDDMSD

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

>**Amphi-Tbx1/10** XM_002611831
MEANSPLSPKANAFS IASLISASEQGGLMSDLHGKDQGLDDGQ
DWGMQYSSIPREMEASCMLSNQRM PGHQLAHMTEHPSAFGVTQARGEAYDIPGMDSCR
NGGGLPNGNENNNLLNDGVKDERKQNP KVANVKVLMEMKALWDEFHELGT EMIVTKAG
RRMFPTFQVKMFGLEPMSDYILLMDFVPVDDKRYRYAFHSSSWLVAGKADPDMPRRIH
VHPDSPAKGAQWMKQIVSFDKLLKTNNLLDDNGHII LNSMHRYQPRFHV VYIDGKKGD
SDTVHENYKTFIFPETKFTAVTAYQNH RITQLKIASNPF AKGFRDCPD DDWRTLT FHG
RNESDSVVEVL TQIPPSQRPRNHHRPSSLQLVGVT RTRTVGQMNTSQDQERRDRQEDT
SQQCQSSPIVSRVLS PNLAGGGMHVNLQRPEQTALAH TSLPDNSYKYHYNGYMAAKTR
PTPYPLPSMRPTGYHPVNNSLYAPCTRSSPYDLD

>**Amphi-Tbx2/3** XM_002598876
MAYHPFLAASKALDFPMPSFLAQ PGLFPGMPLLP SGAGHLGMPK
LSDPSPGQTPADVSKALGGAGSVLRPI PQQQDDSDPQVELEYKDLWDQFHTYGT EM
VITKSGRRMFPSFKVKVSGLDKRAKYIFLMDIVAADD CRYKFHNSRWMVAGKADPEMP
KRM YIHPDSPATGEHWSKTVSFHKLKL TNNISDKHGFTI LNSMHKYQPRFHI VKTND
IMKLPHYCHFRTYVFRETA FIAVTAYQNEKITQLKIDHNPF AKGFRD TGAGRRGEK RKH
LHTFGHQHPGFLEE GHSSDLETVD CGDTVTEKEPRLSRPPLSPKEPASPVVEGSPSV
GANYRTEPGSRPFATCSGDEGSEQQERPASLH THKGNCTETNKS AQECHRRDAPPHCG
NEIRPGTAALREGEERGAHGGGGASDKENGEHHHNEKTESQQQQQREKNLEKKAVHHN
NKESSEKSESNNNNKLPTSSSLSPLSAMNPGSSHMGR IHPSQLQGLASMPYPYQLLS

GGHGLPNRPFFLFHPSQLAMSGGGMPQFPMNPFLAFFVPHSGMNGATQPLSSPTHPLL
ASQGYFFFGMSPQGYTALLDGSIFNPGFSFPQAAELHKRAMAGARHPLRFSPYPLSAT
STTMVTTGSPVVCPIPSRTDASSSSDAPRESPSSSSSPGVRKNTSPKRASSPPTRTS
VSAPEVSSSELQNIQKLVSGLEKQQEQQLAVETLTKLTEQSKLQ

>Amphi-Tbx4/5 EU084005/XM_002598875
MSGDLKESVGDERPRQREPD RKDDGPPGADDRTDGVPEGLEDVK
VELQDAGLWQRFHKAGTEMIITKAGRRMFPSIKVKVTGLQPKTKYIFVMDIVAVDSHR
YKFNESKWSVAGKAEPAMPGRVVFVHPDSPATGTHWMKQVVCFQKLKLTNNYMDTFGHI
MLNSMHKYQPRLHIVQASENNKFELKKTCTFRTFIFPETEFMAVTSYQNHQITQLKIEH
NPPFAKGFRGGDDTEFSRSARKSINYPVIPSNNPVQASLLPRGRPNNNYACSSNMAADT
CPSLSSNHYQQTAGYNTVPIGSSIQMTTQENSGGCMQNSFSGGTDLGPLPKRACREE
DRLLSDNSVATSTLTWSNPQILPNMENLQPLNRETCTMFANSATGDTTSSLLAAPQPL
DPLSTAFNNNQNFSSVPFSSSGTGFSVANGGMNFLPSCSYAQMPPQGLGMNGTPFLHE
VSRNVGCPMQIPQ

>Amphi-Tbx6/16 XM_002611967
MMYESEDVLTQARAFSINNMLTGSPHAFPPGFFPMAQAAPAPP
PDPCAFSDRFATDFHMTADHKTQRLGLGLHLPAPQNFPPPSALKDMKVTLEQKDLWDSF
HDIGTEMIITKAGRRMFPTYKASISGLDPNAKYILLMDIVPMDDNRYKYHNSEWVVS
KAEPMLPGRLYIHPDSPATGTQWMKQSVTFHKLKLTNNAMDDQGHIIILNSMHKYQPRL
HIVQANDVYSLRWNSFTFAFPETSFIAVTAYQNEKITQLKIDNNPFAKGFRDNGGNR
RERAIVSTKRSADAAGEPGDSVSNKRPCTGGEQPERNNRPPSCDCSGVGEESDVPRGP
SQYNPPAQADDLNP CGNPLTIVTDDIATDFAKERSPGVPHALGGQGSAAALPTRDQAAL
GSCQGEDMRCQTRTACAQDPRDLLASPDADYHQYHPGGYSGQAAGDPTDSTVVPLG
YGTGPSFQELSVQTDLGTAADMASACKNDVGLNAPGTAVLPSYPAVSSFHTGLPVS
NPLYASGGTTPPQRSYDVYPTGLFAAPTAYEPLDYATTCKMAGFSRMQMSVAPAPHL
SHFPTSSATSMFPVNFHGMFNTHPMPAAYPGHAGKFAA

>Amphi-Tbx15/18/22 XM_002599011
MAEKRKSAPVTLSSRAHAFSVEALLGPRVKKQRTAQFHSSREDA
PEDNVLENFSTSDGRQEDRAAEQSSSALGSIQALQSRLAYPLPQPDGPDQVRVELQ
GKDLWSRFHDIGTEMIITKAGRRMFPAIRTKVTGLDPKAQYIVIMDIVPVDNKRYRYVYH
SSKWMCAGSADAPPPRVYVHPDSPASGEAWMRQTVSFDKCLKLTNNENDEQGYIILHS
MHKYQPRVHIIKKTAHTDLTNKTSISPSDKAQTFAPFETVFTTVTAYQNQQITRLKID
RNPFAKGFRDGRNRSGLCEIMDSYALWHPNAGRPLTYGQYTSMKSQEEEEKLMSGMLQ
PPSPPTAFYLA PNFTFNVGCREGQACLTPEYQEPSQRTSINKENVSADLPSPD
SPRLAHPQCSATGSMCRHPLMPESPALPHPDYVRQTATQPPSIPYQYLPSSPHFSQTTLSPT
QHSPLLGA PYPSPRNCSAGSSPHSYLPISPSSTSGTSSCPTTSHLSPTFTSATFPHPY
FNNLQVLPTSALPTSALPTSALPTSAPSGSYLHGQYRLAVHRIPSPQASLV

>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
ASSAETTTDGGRAGRESSAAESRQESASTEPAPSDGSHLQNKESPELKNVQCKLESK
ELWDKFHELGTEMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIIPVDNKRYRYAYH
RSSWLIVAGKADPPQPARLYVHPDSPFTGEQLQKQIVSFEKLKLTNNELDQHGHIILNS
MHRYQPRVHIIKKKEHTASLLNLNSEEKTFVVFQECMFTAVTAYQNQLITKLKIDSNP
FAKGFRDSSRLTDIERESVETMLKEHRYARSPIRAYAEPEPRKSPRLSSSSSSGGLT
SPSTSVGGWPSPSFTPLPHYPHSSHPIPIPHPINPSVTATTSSLTSPHPLPHTLG
FGALGIPGLPHPTSALPAPIMLSAPSPFHPLHIQRYPYFPQTAYSSVHTLRHYV

>Amphi-Eomes/Tbx1/Tbx21 XM_002589046
MDAADVDDTAVGTD SFQPPGLSMPYGMSSGYTPPDSNSSRSSPG
DGVD AELSRYSQVPPDYPLGHYPGATNPENAYSITSMTSPSPHYTNGYDQPPQMYGQQ
PPGYFAPIESGPPQPPNGQYQHGYNGNYPYPGGGSMYGYPPGPPPTPAKLSVFLTNRD
LWVKFHQHETEMIIITKQGRRMFPVLQFAISGLDPHAQYNVFDVMVLADVNHWKFQNGK
WVPCGRADTNPQGSRVYVHPESPNSGAHWMKQEVVFSKLKLTNNKGADNGHVVLNSMH

KYQPRLHIIIEVSNRAGGGERVLSHSPFETQFIAVTAYQNTDITQLKIDYNPFAGKFR
DNYDGPTNIRPNGFDRSAGMEPGMHPSLGGPLPLMPPIYPVGPPMPAHNRGIHLPYD
MRSHSSGGSSSSPGSPMQPKDLELKETASDLPGSAQNGQSNATPEKQASPTRVNSN
LLLTTPAYTVNSSGQPHYSMATMHSRGMPPRNGGLPQNGQVSENGNMAPNGHISQN
GQSQGEARPEWRSPSKTRPSPGDEDDNRDAAAKRLRTEELPPYHDATPGNNYDVYDDQ
PGDGTSSFGQQDHMQYHRYNGYYSANPEDYGHYYDRNAMQYGYGNQGYQASAHQF
VDSEKFAHAHYNGAYHQAQYNGGYMPTSTASAETATGHY

>Amphi-Bra1 XM_002590345
MSSAETMKQPTAASPDQFSVSHLLSAVESEISAGSEKGDPTERD
LKITLEEKPLWDKFNALTNEMIVTKNGRRMFVVKVNVSGLDPNAMYSFLLDFTAADN
HRWKYVNGEWPVGGKPEPSVPSCVYIHPDSPNFGAHWMKSPVSFSKVKLTNKLNGGGQ
QIMLNSLHKYEPRLHIKVGGPDPNQRMVSTHTFPETQFIAVTAYQNEEITALKIKYNP
FAKAFLDAKERSDGKDGMEDLQDQPQYSQLGGWFLPGTGPICPPPNPHQFAPSLGLPS
HGCDRYSTLRNHRSAFYHPYQRSSPPTNYGHDTAASLPMMPHDNWSGLPVSTHNML
SMSAMPHTTTSTHAQYPNLWSVSNNLTPTTHAQTHMSGTMGTGLPHQFLRTTAPAPY
HSIPTCTVPTTASSSPVYHDSHEVSSTDSDGYGHSTTPPAPQTRITSNNWSPMTPPSL

>Amphi-Bra2 XM_002590344
MKQTPDQFSVSHLLSAVESEISAGSEKGDPTERDLKVTLGEKPL
WEKFKSLTNEMIVTKSGRRMFVVKVNVSGLDPNAMYSFLLDFTAADNHRWKYVNGEW
VPGGKPEPSVPSCVYIHPDSPNFGAHWMKSPVSFSKVKLTNKLNGGGQQIMLNSLHKY
EPRIHIVKVGGPDPNQRTLSTHTFAETQFIAVTAYQNEELTALKIKHNPFAKAFLDAKE
RNDTKSGHDDLTDQQPQFSQLGGWFLPGTGPICPPPNPHQFAPSLGLPSHGCDRYSTL
RNHRSAFYHPYQRSSPPTNYGHDTAASLPMMPHDNWSGLPVSTHNMLSMSAMPHTT
TSTHAQYPNLWSVSNNLTPTTHAQTHMSGTMGTGLPHQFLRTTAPAPYHSIPTCTVP
TTASSSPVYHDSHEVSSTDSDGYGHSTTPPAPQTRITSNNWSPMTMPSM

>Amphi-Tbx6d1 (new) XM_002588055
MSLSEKAQAFSIDSLAADPKTSEDGNEELSPMCDIVPSCGVS
STGLNSDNFALHRSLGPPWGHGSLQSTGAAERDGLQGNMFPLTGEADRSPPPAATPR
DVSSQEYGLPIAKTTHGVTVSLEKAGLWRQFQECGTEMILNRAGRMRFPVMTITGL
DPSATYRVYMDVVPADGYRHKFTKTAWVATGPAEFSISNPPYEHPNSPASGAGWMGT
VSFAKAKITNNNDSEGNFLLHSMHKYQTKIIISRQETDKKARSCLGDHTHTFQFEET
AFVAVTAYQNRVTRLKIKNNPFAKAFRSDVMALVTFHLFHQGSWRAPDSLQEVTPV
PTKRSMGIEVVAEHFVVTLLF

>Amphi-Tbx6d2 (new) jgi|Brafl1|86982|fgenes2_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
RCMFPTLTNLTLGLKPERRYIILVKMILTDESLYGRNNQWVVVNGDAKPSVADSIVVHP
KCPEYGAKLMERPLAFAFKLSSRMHDGKNMVQLRSMHKYQPVVQVVEADNTTDLAVAPS
WQFSFPVTEFMAVSSYSYDKIRKLKVDNNKFAKNLRNLESVDRRERSQGVPAVPRMVRP
PAQKSPPPITCVLPPTTCGNSTQTASPTAADTHVSPKQGLVSRVQPRCIQQEMLGELYN
PAEMEKLRAATTTMQAPMACTTAALHTQQISDIPLTQPLQPTALAYMRHFPVGPATFTPTS
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	LWDEFNQLGTEMIIVTKAGRRMFPTFQVKLFGMDPMADYMLLMDFVPVDDKRYR	YAFHSSS
tbx1	LWDEFNQLGTEMIIVTKAGRRMFPTFQVKIFGMDPMADYMLLMDFLPVDDKRYR	YAFHSSS
TBX10	LWEEFNQLGTEMIIVTKAGRRMFPTFQVKILGMDSLADYALLMDFIPLDDKRYR	YAFHSSA
tbx10	LWRQFDQLGTEMIIVTKAGRRMFPTFQVHISGMDPAEYVLLMDFIPVDDKRYR	YAFHSSS
Amphi-Tbx1/10	LWDEFHELGTETMIITKAGRRMFPTFQVKMFGLPMSDYILLMDFVPVDDKRYR	YAFHSSS
TBX15	LWKRFDHIGTEMIITKAGRRMFAMRVKITGLDPHQYYIAMDIVPVDNKRYR	YVYHSSK
tbx15	LWKRFDHIGTEMIITKAGRRMFAMRVKIVGLDPHQYYIAMDIVPVDNKRYR	YVYHSSK
TBX18	LWKRFEHIGTEMIITKAGRRMFAMRVKISGLDPHQYYIAMDIVPVDNKRYR	YVYHSSK
tbx18	LWKRFEHIGTEMIITKAGRRMFAMRVKIAGLDPHQYYIAMDIVPVDNKRYR	YVYHSSK
TBX22	LWKRFDHIGTEMIITKAGRRMFPSVRVKVGLDPGQYHVAIDVVPVDSKRYR	YVYHSSQ
tbx22	LWKRFEHIGTEMIITKVGRRMFPSIRVKVHNLDPLQQYSIAMDIMPMSKKYR	YVYHSSQ
Amphi-Tbx15/18/22	LWSRFHDIGTEMIITKAGRRMFPARTKVTGLDPKAYIVIMDIPVDNKRYR	YVYHSSK
TBX20	LWDKFHELGTETMIITKSGRRMFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRYR	YAYHRSS
tbx20	LWDKFHELGTETMIITKSGRRMFPTIRVSFSGVDPDAKYIVPMDIVPVDNKRYR	YAYHRSS
Amphi-Tbx20	LWDKFHELGTETMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIIPVDNKRYR	YAYHRSS
TBX2	LWDQFHKLGTEMIITKSGRRMFPPFKVRVSGLDKKAKYILLMDIVAADDCRYK	--FHNSR
tbx2a	LWDQFHKIGTEMIITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYK	--FHNSR
tbx2b	LWDQFHKLGTEMIITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYK	--FHNSR
TBX3	LWDQFHKRGTEMIITKSGRRMFPPFKVRCGLDKKAKYILLMDIIAADDCRYK	--FHNSR
tbx3a	LWELFHKRGTEMIITKSGRRMFPPFKVRCTGLDKKAKYILLMDIVAADDCRYK	--FHNSR
tbx3b	LWGQFHKVGTEMIITKSGRRMFPFKVRCSGFDRKARYILLMDIVASDDYRYK	--FHNCR
Amphi-Tbx2/3	LWDQFHTYGTETMIITKSGRRMFPSFKVKVSGLDKRAKYIFLMDIVAADDCRYK	--FHNSR
TBX4	LWKKFHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLIDIVPADDHRYK	--FCDNK
tbx4	LWKKLHEAGTEMIITKAGRRMFPSYKVKVTGMNPKTKYILLTDIVPADDHRYK	--FCDNK
TBX5	LWLKFHEVGTEMIITKAGRRMFPSYKVKVTGLNPKTKYILLMDIVPADDHRYK	--FADNK
tbx5a	LWTKFHEVGTEMIITKAGRRMFPSFKVKVTGLNPKTKYILLMDVVPADDHRYK	--FADNK
tbx5b	LWAKFHDVTETMIITKAGRRMFPSYKVKVTGLNPKAKYILLMDIISADEHRYK	--FADNK
Amphi-Tbx4/5	LWQRFHKAGTEMIITKAGRRMFPSIKVKVTGLQPKTKYIFVMDIVAVDSHRYK	--FNESK
TBX6	LWKEFSSVGTEMIITKAGRRMFACRVSVTGLDPEARYLFLLDVIVPDGARYR	--WQGRR
tbx24	LWKQFSTVGTEMIIVTKGRRMFPLRVKLSGLNPSLRYILLLDIVPVDSSRYR	--FQDNS
Mdom-Tbx16	LWTEFYRVGTETMIITKSGRRMFQCKIRLSGLVPYLYKVVVLADFVSVDNFYK	--WAKDQ
tbx6	LWDKFSSIGTEMLITKSGRRMFPSCKVTVTGLNPKVKYVIMDMVPFDNHKYY	--WNKDC
tbx16	LWRSFHEIGTEMIITKPGRRMFPHCKISLSGLVPYAKYILLVDMVPEDGLRYK	--WNKDK
MGA	MWNEFYHRSTEMILTKQGRRMFPYCRYWITGLDSNLKYILVMDISPVDNHRYK	--WNGRW
mga-a	MWNEFHRCKTEMIITKQGRRMFPYCRFRLSGMEPFQNYVLAMDIKPADNCRYK	--WSGKG
mga-b	VWSRFHSLGTEMLTPQGRRMFPCCRFLRGLDPLQYFLLMDIAPLDDLHRH	--FNGEA
Amphi-Tbx6/16	LWDSFHDIGTEMIITKAGRRMFPTYKASISGLDPNAKYILLMDIVPMDDNRYK	--YHNSE
TBX19	LWQRFKEVTNEMIVTKNGRRMFVPLKISVTGLDPNAMYSLLLDVFPTDSHRWK	--YVNGE
tbx19	LWRKFKEVTNEMIVTKNGRRMFVPLKVSVTGLDPNAMYSFLLDFTPADGHRWK	--YVNGE
T	LWLRFKELTNEMIVTKNGRRMFVPLKVNVSGLDPNAMYSFLLDFVAADNHRWK	--YVNGE
ntl-a	LWTKFKELTNEMIVTKTGRRMFPVLRASVTGLDPNAMYSVLLDFVAADNHRWK	--YVNGE
ntl-b	LWQKFKALTNEMIVTKNGRRMFVPLKVNISGLDPNAMYSFLLDFVPADNHRWK	--YVNGE
Amphi-Bra1	LWDKFNALTNEMIVTKNGRRMFVPLKVNVSGLDPNAMYSFLLDFTAADNHRWK	--YVNGE
Amphi-Bra2	LWEKFKSLTNEMIVTKSGRRMFVPLKVNVSGLDPNAMYSFLLDFTAADNHRWK	--YVNGE
EOMES	LWLKFHRHQTEMIITKQGRRMFPFLSFNINGLNPTAHYNVFEVVLADPNHWR	--FQGGK
eom-a	LWLKFHRHQTEMIITKQGRRMFPFLSFNITGLNLTAHYNVFEIVLADPNHWR	--FQGGK
eom-b	LWLKFHRHQTEMIITKQGRRMFPFLSFNMTGLSLSAHYNVFEIVLADPNHWR	--FQGGK
TBR1	LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNI FVDVILADPNHWR	--FQGGK
tbr1a	LWFKFHRHQTEMIITKQGRRMFPCLTFNVSGLDPAHYNIAVDVILADPNHWR	--FQGGK
tbr1b	LWLKFHRHQTEMIITKQGRRMFPFLSFNISGLDPTAHYNI FVDVILADPNHWR	--FQGGK
TBX21	LWSKFNQHQTEMIITKQGRRMFPFLSFTVAGLEPTSHYRMFVDVVLVDQHHWR	--YQSGK
tbx21	LWAKFHKYQTEMIITKQGRRMFPFLSFNITSLDPSAHYNI YVDVVLADQHHWR	--YQGGK
Amphi-Eom/Tbr1/Tbx21	LWVKFHQHETEMITKQGRRMFPVLQFAISGLDPAQYNVFDVMDVADVNHWK	--FQNGK
Amphi-Tbx6d1	LWRQFQECGTEMIILNRAGRRMFPPVMVTITGLDPSATYRVYMDVVPADGYRHK	--FTKTA
Amphi-Tbx6d2	LWELFHQAGTEMIINTKGRCMFPTLTNLNLTGLKPERRYIILVKMILTDESLYG	--YRNNQ

TBX1	WLVA-GKADPA-TP-GRVHYHPDSPAKGAQWMKQIVSFDKCLKLTNN---LLDDNGHIILN
tbx1	WLVA-GKADPA-TP-GRVHYHPDSPAKGAQWMKQIVSFDKCLKLTNN---LLDDNGHIILN
TBX10	WLVA-GKADPA-TP-GRVHFHPDSPAKGAQWMRQIVSFDKCLKLTNN---LLDDNGHIILN
tbx10	WLVA-GRGDVA-AP-GRVHFHPDSPARGAQWIKQTVSFDRLKLTNN---LLDDNGHMIILN
Amphi-Tbx1/10	WLVA-GKADPD-MP-RRIHVHPDSPAKGAQWMKQIVSFDKCLKLTNN---LLDDNGHIILN
TBX15	WMVA-GNADSP-VP-PRVYIHPDSLASGDTWMRQVVSFDKCLKLTNN---ELDDQGHIIILH
tbx15	WMVA-GNADSP-LP-ARLYVHPDSLASGDTWMRQVVSFDKCLKLTNN---ELDDQGHIIILH
TBX18	WMVA-GNADSP-VP-PRVYIHPDSPASGETWMRQVISFDKCLKLTNN---ELDDQGHIIILH
tbx18	WMVA-GNADSP-VP-PRVYIHPDSPASGETWMRQVISFDKCLKLTNN---ELDDQGHIIILH
TBX22	WMVA-GNTDHLICII-PRFYVHPDSPCSGETWMRQIISFDRMKLTNN---EMDDKGHIILQ
tbx22	WVIA-GNTDHSCIP-PHLYVHPDSPCSGENWMRQVISFDRVKLTNN---ELDDRGHIIILK
Amphi-Tbx15/18/22	WMCA-GSADAP-PP-PRVYVHPDSPASGEAWMRQTVSFDKCLKLTNN---ENDEQGYIILH
TBX20	WLVA-GKADPP-LP-ARLYVHPDSPFTGEQLLKQMVSEKVKLTNN---ELDQHGHIILN
tbx20	WLVA-GKADPP-LP-ARLYVHPDSPFTGEQLSKQMVSEKVKLTNN---ELDQHGHIILN
Amphi-Tbx20	WLVA-GKADPP-QP-ARLYVHPDSPFTGEQLQKQIVSEKCLKLTNN---ELDQHGHIILN
TBX2	WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
tbx2a	WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
tbx2b	WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMAKPVAFHKLKLTNN---ISDKHGFTILN
TBX3	WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMSKVTFHKLKLTNN---ISDKHGFTILN
tbx3a	WMVA-GKADPE-MP-KRMYIHPDSPATGEQWMSKVNFHKLKLTNN---ISDKHGFTILN
tbx3b	WMVA-GKADPE-MP-KRMYIHPDSPSTGEQWMSKAVTFHKLKLTNN---ISDKHGFTILN
Amphi-Tbx2/3	WMVA-GKADPE-MP-KRMYIHPDSPATGEHWMKTVSFHKLKLTNN---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-GRVHVHPDSPATGTHWMKQVVCFQKLKLTNN---YMDTFGHIMLN
TBX6	WEPS-GKAEPR-LP-DRVYIHPDSPATGAHWMRQPVSFHRVKLTNS---TLDPHGHLILH
tbx24	WQVV-GGAEAR-LP-DRVFIHPDSPATGEHWQNRTISFHRAKLTNN---TLDAQGYIILH
Mdom-Tbx16	WEVA-GKAEPQ-LP-GRSYIHPDSPAYGSHWMKEPVSFHKMKLTNN---TLDQHGHIILH
tbx6	WEVN-GSSDPH-LP-NRFFIHPDSPAPGQKWMQYPISFHKKLKLTNN---TLNSNGIVVLH
tbx16	WEVA-GKAEPQ-PP-YRTYLHPDSPAPGSHWMKQPVSFCLKLTNN---ALDQHGHIILH
MGA	WEPS-GKAEPH-VL-GRVFIHPDSPSTGHYWMHQPVSFYKCLKLTNN---TLDQEGHIILH
mga-a	WEPN-GKAEPH-I--SRLFVHPESPASGLHWMQYPVSFYRLKLCNT---LDQEGHIILH
mga-b	WEPD-GPGEAH-LQ-SFVCFHPDSPAVGQHWMDSPVSFYTVKLTHD---SCEREG-VLLQ
Amphi-Tbx6/16	WVVS-GKAEPL-MP-GRLYIHPDSPATGTQWMKQSVTFHKLKLTNN---AMDQQGHIILN
TBX19	WVPA-GKPEVS-SH-SCVYIHPDSPNFGAHWMKAPISFSKVKLTKN---LNGGGQ-IMLN
tbx19	WVPA-GKPEPH-SH-SCVYIHPDSPNFGAHWMKAPVSFKNVKLTNK---LNGGGQ-IMLN
T	WVPG-GKPEPQ-AP-SCVYIHPDSPNFGAHWMKAPVSFSKVKLTKN---LNGGGQ-IMLN
ntl-a	WVPG-GKPEPQ-SP-SCVYIHPDSPNFGAHWMKAPVSFSKVLSNK---LNGGGQ-IMLN
ntl-b	WVPG-GKPEPQ-AP-SCVYIHPDSPNFGAHWMKSCVSFSKVKLTKN---LNGGGQ-IMLN
Amphi-Bra1	WVPG-GKPEPS-VP-SCVYIHPDSPNFGAHWMKSPVSFSKVKLTKN---LNGGGQ-IMLN
Amphi-Bra2	WVPG-GKPEPS-VP-SCVYIHPDSPNFGAHWMKSPVSFSKVKLTKN---LNGGGQ-IMLN
EOMES	WVTC-GKADNN-MQGNKMYVHPESPNTGSHWMRQEISFGKLKLTNNKGANNNTQMIVLQ
eom-a	WVTC-GKADNN-MQGNKVYVHPESPNTGAHWMRQEISFGKLKLTNNKGANNNTQMIVLQ
eom-b	WVTC-GKADNN-MQGNKIYMHPEPNTGAHWMRQEISFGKLKLTNNKGANINTSQMIVLQ
TBR1	WVPC-GKADTN-VQGNRVYMHDPSPNTGAHWMRQEISFGKLKLTNNKGASNNNGQMVVLQ
tbr1a	WVPC-GKADTN-VTGNRVYTHDPSPNTGAHWMRQEISFGKLKLTNNKGASNNNTQMIVLQ
tbr1b	WVPC-GKADTN-VTGNRVYMHDPSPNTGAHWMRQEISFGKLKLTNNKGATNNTQMIVLQ
TBX21	WVQC-GKAEGS-MPGNRLYVHPDSPNTGAHWMRQEVSFGLKLTNNKGASNNVTQMIVLQ
tbx21	WVQC-GKAEGN-MPGNRMVYMHDPSPNTGTHWMRQEVSFGLKLTNNKGSSNNVAQMIVLQ
Amphi-Eom/Tbr1/Tbx21	WVPC-GRADTN-PQGSRVYVHPESPNSGAHWMKQEVVFSKLKLTNNKGA--DNG-HVVLN
Amphi-Tbx6d1	WVAT-GPAEFS-IS-NEPYEHPNSPASGAGWMGTVVSFAKAITNN---NDSVEGNFLLH
Amphi-Tbx6d2	WVVVN-GDAKPS-VA-DSVYVHPKCPYEGAKLMERPLAFPAKLSSR---MHDGKNMVQLR

TBX1	SMHRYQPRFHVV	YVDPRKD----	SEKYAEENFKTFVFEETRFTAVTAYQNHRITQLKIAS	
tbx1	SMHRYQPRFHVV	YVDPRKD----	SEKYAEENYKTFVFEETRFTAVTAYQNHRITQLKIAS	
TBX10	SMHRYQPRFHVV	FVDPRKD----	SERYAQENFKSFIFTETQFTAVTAYQNHRITQLKIAS	
tbx10	SMHRYQPRLHV	LVDRSRN----	SQRFAHRNFCTFSFPETRFIAVTAYQNHRITQLKIAC	
Amphi-Tbx1/10	SMHRYQPRFHVV	YIDGKKG----	DSDTVHENYKTFIFPETKFTAVTAYQNHRITQLKIAS	
TBX15	SMHKYQPRVHVI	RKDFSSDLSPTKPV	PGDGVKTFNFPETVFTTAVTAYQNQQITRLKIDR	
tbx15	SMHKYQPRVHVI	RKDFSSDLSPTKPV	TGEGVKTFSFPETVFTTAVTAYQNQQITRLKIDR	
TBX18	SMHKYQPRVHVI	RKDCGDDLSP	IKPVPSGEGVKA	FSFPETVFTTAVTAYQNQQITRLKIDR
tbx18	SMHKYQPRVHVI	RKECGEELSP	VKAVPTGDGVKA	FSFTETVFTTAVTAYQNQQITRLKIDR
TBX22	SMHKYKPRVHVI	EQGSSVDLSQ-	IQSLPTEGVKTF	FSFKETEFTTAVTAYQNQQITKLKIER
tbx22	SMHKYRPRIHVI	LHCPPECLSK	RLLSLPADGVTF	FSFPETQFTTAVTAYQNQQITKLKIDR
Amphi-Tbx15/18/22	SMHKYQPRVHII	KKTAHTDLTNK	TISPSPDKAQTF	FAFPETVFTTAVTAYQNQQITRLKIDR
TBX20	SMHKYQPRVHII	KKKDHTA---	SLNLKSEEFRTF	IFPETVFTAVTAYQNQLITKLKIDS
tbx20	SMHKYQPRVHII	KKKDHTA---	SLNLKSEEFRTF	VFTETVFTCTRTAYQNQLITRLKIDS
Amphi-Tbx20	SMHRYQPRVHII	KKKEHTA---	SLNLNSEEFTF	VFVQECMFTAVTAYQNQLITKLKIDS
TBX2	SMHKYQPRFHIV	RANDILK-----	LPYSTFRTYVFP	ETDFIAVTAYQNDKITQLKIDN
tbx2a	SMHKYQPRFHIV	RANDILK-----	LPYSTFRTYVFP	ETDFIAVTAYQNDKITQLKIDN
tbx2b	SMHKYQPRFHIV	RANDILK-----	LPYSTFRTYVFP	ETDFIAVTAYQNDKITQLKIDN
TBX3	SMHKYQPRFHIV	RANDILK-----	LPYSTFRTYLFP	ETEFIAVTAYQNDKITQLKIDN
tbx3a	SMHKYQPRFHIV	RANDILK-----	LPYSTFRTYVFP	ETDFIAVTAYQNDKITQLKIDH
tbx3b	SMHKYQPRFHIV	RANDVLK-----	LPYSTFKTYVFP	ETEFIAVTAYQNEKITQLKIDN
Amphi-Tbx2/3	SMHKYQPRFHIV	KTNDIMK-----	LPYCHFRTYVFR	ETAFIAVTAYQNEKITQLKIDH
TBX4	SMHKYQPRLHIV	KADENNA-----	FGSKNTAFCTH	VFPETSFISVTSYQNHKITQLKIEN
tbx4	SMHKYQPRLHIV	KADENNA-----	FGSKNTAYCTH	VFHETAFISVTSYQNHKITQLKIEN
TBX5	SMHKYQPRLHIV	KADENNG-----	FGSKNTAFCTH	VFPETAFIAVTSYQNHKITQLKIEN
tbx5a	SMHKYQPRIHIV	KADENNG-----	FGSKNTAFCTH	VFPETAFIAVTSYQNHKITQLKIEN
tbx5b	SMHKYQPRLHIV	KADERN-----	FGSSNTSFC	THSFAETTFIAVTSYQNHKITQLKIEN
Amphi-Tbx4/5	SMHKYQPRLHIV	QASENNK-----	FELKKTCFRTF	IFPETEFMAVTSYQNHQITQLKIEH
TBX6	SMHKYQPRIHLV	RAAQLCS-----	QHWGGMASFR	FPETTFISVTAYQNPQITQLKIAA
tbx24	SLHRYQPRVHVI	EARDVLM-----	WGRTQHSFTFP	ETQFITVTAYQNNKITELKINS
Mdom-Tbx16	SMHRYQPRFLVA	QADDLFN-----	VCWNLFQVFS	FPQTVFISVTAYQNEQITQLKIDN
tbx6	SMHKYQPRLHIV	QSPDPCT-----	PHNPGAYLR	FTFPEAAFIATAYQNQEITKLKIDN
tbx16	SMHRYHPRFHIV	QADDLYS-----	VRWSVFQTF	TFPETSFTAVTAYQNTKITKLKIDH
MGA	SMHRYLPRHLV	PAEKAVE----	VIQLNGPGVHT	FTFPQTEFFAVTAYQNIQITQLKIDY
mga-a	SMHRYLPQIHII	PADKVSK---	DILILDRPNV	VTLSFAQTEFFAVTAYQNLCTQLKIDY
mga-b	PMHRYQPRLYV	APVSACLE---	RAVPLKSPNV	HMTFFPKTEFYAVTSYQNPQITRLKIDC
Amphi-Tbx6/16	SMHKYQPRLHIV	QANDVYS-----	LRWNSFSTFA	FPETSFIATAYQNEKITQLKIDN
TBX19	SLHKYEPQVHIV	RVGSAHR-----	MVTNCSFPET	QFIAVTAYQNEEITALKIKY
tbx19	SLHKYEPQIHIV	RVGGSHR-----	MVTNISFTDT	QFIAVTAYQNEEITALKIKH
T	SLHKYEPRIHIV	RVGGPQR-----	MITSHCFPET	QFIAVTAYQNEEITALKIKY
ntl-a	SLHKYEPRIHIV	KVGGIQK-----	MISSQSFPET	QFIAVTAYQNEEITALKIKH
ntl-b	SLHKYEPRIHIV	RVGGPQR-----	MITTHAFPET	QFIAVTAYQNEEITSLIKY
Amphi-Bra1	SLHKYEPRLHII	KVGGPDN-----	QRMVSTHTFP	ETQFIAVTAYQNEEITALKIKY
Amphi-Bra2	SLHKYEPRIHIV	KVGGPDN-----	QRTLSTHTFA	ETQFIAVTAYQNEELTALKIKH
EOMES	SLHKYQPRLHIV	EVTEDEGV----	EDLNESKQT	TFTFSETQFIAVTAYQNTDITQLKIDH
eom-a	SLHKYQPRLHIV	EVTEDEGV----	EDMSSEAKT	QTFTFPENQFIAVTAYQNTDITQLKIDH
eom-b	SLHKYQPRLHIV	EVSDRS-----	ERDSNTQIF	SFPENQFIAVTAYQNTDITQLKIDH
TBR1	SLHKYQPRLHV	EVNEDGT----	EDTSQPGRVQ	TFTFPETQFIAVTAYQNTDITQLKIDH
tbr1a	SLHKYQPRVHVI	EISKNE-----	EDTSDPDGVQ	TFTFPETQFISVTAYQNTDITQLKIDH
tbr1b	SLHKYQPRLHV	QVNEDEGT----	EDTSQPGRVQ	TFTFPETQFIAVTAYQNTDITQLKIDH
TBX21	SLHKYQPRLHIV	EVNDGEP----	EAACNASNTH	IFTFQETQFIAVTAYQNAEITQLKIDN
tbx21	SLHKYQPRLHIV	EVEDGEGT----	EDPFLTSKT	QTFVFPETQFIAVTAYQNADITQLKIDH
Amphi-Eom/Tbr1/Tbx21	SMHKYQPRLHII	EVSNRAG-----	GGERVLSHS	FPETQFIAVTAYQNTDITQLKIDY
Amphi-Tbx6d1	SMHKYQTKII	ISRQETDKK----	ARSCLGDHT	HTFQFEETAFAVTAYQNHRVTRLKIKN
Amphi-Tbx6d2	SMHKYQPVVQVV	EADNTTD-----	LAVAPSWQ	FSFPVTEFMAVSSYSDKIRKLKVDN

TBX1	NPFAKGFRD
tbx1	NPFAKGFRD
TBX10	NPFAKGFRE
tbx10	NPFAKGFRD
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.

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>TBX15      LWKRFHDIGTEMIITKAGRMFFPAMRVKITGLDPHQQYYIAMDIVPVDNKRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSLASGDTWMRQV
>tbx15      LWKRFHDIGTEMIITKAGRMFFPAMRVKITGLDPHQQYYIAMDIVPVDNKRYVYHSSKWMVAGNADSP-VP-PRVYIHPDSLASGDTWMRQV
>TBX18      LWKRFHEIGTEMIITKAGRMFFPAMRVKISGLDPHQQYYIAMDIVPVDNKRYVYHSSKWMVAGNADSP-VP-PRVYIHPDPASGETWMRQV
>tbx18      LWKRFHEIGTEMIITKAGRMFFPAMRVKISGLDPHQQYYIAMDIVPVDNKRYVYHSSKWMVAGNADSP-VP-PRVYIHPDPASGETWMRQV
>TBX22      LWKRFHDIGTEMIITKAGRMFFPSVRVKIGLDPGKQYHVAIDVVPVDSKRYVYHSSQWMVAGNTDHLCIIPR-FYVHPDPCSGETWMRQI
>tbx22      LWKRFYEIGTEMIITKVGRMFFPSVRVKHNLDPLQQYSIAMDIMPDSKRYVYHSSQWVIAGNTDHSCIP-PHLYVHPDPCSGENWMRQV

>TBX20      LWDKFHELGTEMITKSGRMFFPTIRVSFSGVDPEAKYIVLMDIVPVDNKRYAYHRSSWLVAGKADPP-LP-ARLYVHPDSPTGEQLLKQM
>tbx20      LWDKFHELGTEMITKSGRMFFPTIRVSFSGVDPDAKYIVLMDIVPVDNKRYAYHRSSWLVAGKADPP-LP-ARLYVHPDSPTGEQLLKQM

>TBX1       LWDEFNQLGTEMIVTKAGRMFFPTQVKIFGMDPADYMLLMDIFPVDDKRYAFHSSSWLVAGKADPA-TP-GRVYHHPDSPAKGAQWMQI
>tbx1       LWDEFNQLGTEMIVTKAGRMFFPTQVKIFGMDPADYMLLMDIFPVDDKRYAFHSSSWLVAGKADPA-TP-GRVYHHPDSPAKGAQWMQI
>TBX10      LWDEFNQLGTEMIVTKAGRMFFPQVKILGMDSLADYALLMDIFPLDDKRYAFHSSAWLVAGKADPA-TP-GRVYHHPDSPAKGAQWMQI
>tbx10      LWRQFDQLGTEMIVTKAGRMFFPTQVHISGMDPAEYVLLMDIFPVDDKRYAFHSSSWLVAGRGDVA-AP-GRVYHHPDSPARGAQWIKQT

>TBX2       LWDQFHKLGTEMITKSGRMFFPPFKVRVSGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>tbx2a      LWDQFHKIGTEMITKSGRMFFPPFKVRVNGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>tbx2b      LWDQFHKLGTEMITKSGRMFFPPFKVRINGLDKKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMAKP
>TBX3       LWDQFHKRGTEMITKSGRMFFPPFKVRCSGLDKAKYILLMDIIAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMSKV
>tbx3a      LWELFHKRGTEMITKSGRMFFPPFKVRCTGLDKAKYILLMDIVAADDCRYK--FHNSRWMVAGKADPE-MP-KRMYIHPDSPATGEQWMSKV
>tbx3b      LWGQFHKVGTEMITKSGRMFFPAFKVRCSGFDRKARYILLMDIVASDDYRYK--FHNCWMVAGKADPE-MP-KRMYIHPDSPTGEQWMSKA

>TBX4       LWKKFHEAGTEMIITKAGRMFFPSYKVKVTGMNPKTKYILLDIVPADDHRYK--FCDNKWMVAGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx4       LWKKFHEAGTEMIITKAGRMFFPSYKVKVTGMNPKTKYILLDIVPADDHRYK--FCDNKWMVAGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>TBX5       LWLKFHEVGTEMIITKAGRMFFPSYKVKVTGLNPKTKYILLMDIVPADDHRYK--FADNKWSVTGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx5a      LWLKFHEVGTEMIITKAGRMFFPSKVKVTGLNPKTKYILLMDIVPADDHRYK--FADNKWSVTGKAEPA-MP-GRLYVHPDSPATGAHWMRQL
>tbx5b      LWAKFHDVTTEMIITKAGRMFFPSYKVKVTGLNPKAKYILLMDIISADEHRYK--FADNKWSISGKAEPA-IP-GRLYVHPDSPASGAHWMRQL

>Mdom-Tbx16 LWTEFYRVGTEMIVTKSGRMFFPQCKIRLSGLVPYLKYVVLADFVSVDNFRYK--WAKDQWEVAGKAEPQ-LP-GRSYIHPDSPAYGSHWMKEP
>tbx16      LWSRFHEIGTEMIITKPGRMFFPCHKISLSGLVPYAKYILLVDMVPEDGLRYK--WNKDKEVAGKAEPQ-PP-YRTYLHPDSPAPGSHWMQKP
>tbx6       LWDKFSSIGTEMITKSGRMFFPCKVTVTGLNPKYVYVIMDVPFDNHKYK--WNKDCWEVNGSSDPH-LP-NRFFIHPDSPAPGQWMQYP
>TBX6       LWKEFSSVGTEMIITKAGRMFFPACRVSVTGLDPEARYLFLLDVPVDGARYR--WQGRRWEPSGKAEPR-LP-DRVYIHPDSPATGAHWMRQP
>tbx24      LWKQFSTVGTEMITKKGRMFFPQLRVKLSGLNPSLRYILLLDIVPVDSSRYR--FQDNSWQVVGGAEAR-LP-DRVFIHPDSPATGEHWQNRT
>MGA        MWNEFYHRSTEMILTKQRRMFPYCRYWITGLDSNLKYILVMDISPDNHRYK--WNGRWEPSGKAEPH-VL-GRVFIHPESPSTGHYWMHQP
>mga-a      MWNEFHRCKTEMILTKQRRMFPYCRFLSGMEPFQNYVLAMDIKPADNCRYK--WSGKGWEPNGKAEPH-I--SRLFVHPESPASGLHWMQYP
>mga-b      VWSRFHSLGTEMLLTPQRRMFPCRFLRGLDPLQYFLMDIAPLDLLRH--FNGEAWEPDGPGEAH-LQ-SPVCFHPDSPAVGQHWMDSP

>EOMES      LWLKFHRHQTEMIITKQGRRMFFPLSFNINGLNPTAHYNVFVEVLADPNHWR--FQGGKWVTCGKADNN-MQGNKMYVHPESPNTGSHWMRQE
>eom-a      LWLKFHRHQTEMIITKQGRRMFFPLSFNITGLNLTAHYNVFVEIVLADPNHWR--FQGGKWVTCGKADNN-MQGNKVYVHPESPNTGAHWMRQE
>eom-b      LWLKFHRHQTEMIITKQGRRMFFPLSFNMTGLSLSAHYNVFVEIVLADPNHWR--FQGGKWVTCGKADNN-MQGNKIYMHPESPNTGAHWMRQE
>TBR1       LWLKFHRHQTEMIITKQGRRMFFPLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGKWVPCGKADTN-VQGNRVYMHPDSNTGAHWMRQE
>tbr1a      LWFKFHRHQTEMIITKQGRRMFFPCLTFNSGLDPAGHYNIAVDVLADPNHWR--FQGGKWVPCGKADTN-VTGNRVYTHPDSNTGAHWMRQE
>tbr1b      LWLKFHRHQTEMIITKQGRRMFFPLSFNISGLDPTAHYNIFVDVILADPNHWR--FQGGKWVPCGKADTN-VTGNRVYMHPDSNTGAHWMRQE
>TBX21      LWSKFNQHQTEMIITKQGRRMFFPLSFTVAGLEPTSHYRMFVDVVLVDQHHWR--YQSGKWVQCGKAEGS-MPGNRLYVHPDSPNTGAHWMRQE
>tbx21      LWAKFHKYQTEMIITKQGRRMFFPLSFNITSLDPSAHYNIYDVVVLADQHHWR--YQGGKWVQCGKAEGN-MPGNRMVHPDSNTGTHWMRQE

>TBX19      LWQRFKEVTNEMITKNGRMFFPVLKISVTGLDPNAMYSLLLDFVPTDSHRWK--YVNGEWVPAGKPEVS-SH-SCVYIHPDSPNFGAHWMKAP
>tbx19      LWRKFKEVTNEMITKNGRMFFPVLKSVTGLDPNAMYSFLLDFTPADGHRWK--YVNGEWVPAGKPEPH-SH-SCVYIHPDSPNFGAHWMKAP
>T          LWRKFKEVTNEMITKNGRMFFPVLKVNSGLDPNAMYSFLLDFVAADNHRWK--YVNGEWVPGGKPEPQ-AP-SCVYIHPDSPNFGAHWMKAP
>ntl1-a     LWTKFKELTNEMITKTGRMFPVLRASVTGLDPNAMYSVLLDFVAADNNRWK--YVNGEWVPGGKPEPQ-SP-SCVYIHPDSPNFGAHWMKAP
>ntl1-b     LWQKFKALTNEMITKNGRMFFPVLKVISGLDPNAMYSFLLDFPADNHRWK--YVNGEWVPGGKPEPQ-AP-SCVYIHPDSPNFGAHWMKSC
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>TBX15 VSFDKLKLTTNN---ELDDQGHIIILHSMHKYQPRVHVIRKDFSSDLSPTKPVVGDGVKTFNFPETVFTTVTAYQNQQ ITRCLKIDRNPPFAKGFRD
 >tbx15 VSFDKLKLTTNN---ELDDQGHIIILHSMHKYQPRVHVIRKDFSSDLSPTKPVVGDGVKTFNFPETVFTTVTAYQNQQ ITRCLKIDRNPPFAKGFRD
 >TBX18 ISFDKLKLTTNN---ELDDQGHIIILHSMHKYQPRVHVIRKDCGDDLSPIKPVPSGEGVKAFFSPETVFTTVTAYQNQQ ITRCLKIDRNPPFAKGFRD
 >tbx18 ISFDKLKLTTNN---ELDDQGHIIILHSMHKYQPRVHVIRKECGEELSPVKAAPTGDGVKAFFSETVFTTVTAYQNQQ ITRCLKIDRNPPFAKGFRD
 >TBX22 ISFDRMKLTTNN---EMDDKGHIIILQSMHKYQPRVHVIEQSSVDLSQ-IQSLPTEGVKTFSEKETEFTTVTAYQNQQ ITKLKIERNPPFAKGFRD
 >tbx22 ISFDRVKLTTNN---ELDDRGIILKSMHKYRPIRHHVILHCPPECLSKRLLSLPADGVFTFSFPETQFTTVTAYQNQQ ITKLKIERNPPFAKGFRD

 >TBX20 VSFEKVKLTTNN---ELDQGHIIILNSMHKYQPRVHIKKKDHTA---SLLNLKSEEFRTFIFPETVFTAVTAYQNQL ITKLKIDSNPPFAKGFRD
 >tbx20 VSFEKVKLTTNN---ELDQGHIIILNSMHKYQPRVHIKKKDHTA---SLLNLKSEEFRTFVFETVFTAVTAYQNQL ITRCLKIDSNPPFAKGFRD

 >TBX1 VSFDKLKLTTNN---LLDDNGHIIILNSMHRYQPRFHVVVDPRKD----SEKYAEENFKTFVFEETRFTAVTAYQNHR ITQLKIASNPPFAKGFRD
 >tbx1 VSFDKLKLTTNN---LLDDNGHIIILNSMHRYQPRFHVVVDPRKD----SEKYAEENFKTFVFEETRFTAVTAYQNHR ITQLKIASNPPFAKGFRD
 >TBX10 VSFDKLKLTTNN---LLDDNGHIIILNSMHRYQPRFHVVVDPRKD----SERVAQENFKSFIETETQFTAVTAYQNHR ITQLKIASNPPFAKGFRD
 >tbx10 VSFDRKLKLTTNN---LLDDNGHIIILNSMHRYQPRHLVVLVDRSRN----SQFAHRNFCTFSFPETRFIAVTAYQNHR ITQLKIACNPPFAKGFRD

 >TBX2 VAFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDILK-----LPYSTFRITYVFPETDFIAVTAYQNDK ITQLKIDNNPPFAKGFRD
 >tbx2a VAFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDILK-----LPYSTFRITYVFPETDFIAVTAYQNDK ITQLKIDNNPPFAKGFRD
 >tbx2b VAFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDILK-----LPYSTFRITYVFPETDFIAVTAYQNDK ITQLKIDNNPPFAKGFRD
 >TBX3 VTFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDILK-----LPYSTFRITYVFPETDFIAVTAYQNDK ITQLKIDNNPPFAKGFRD
 >tbx3a VNFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDILK-----LPYSTFRITYVFPETDFIAVTAYQNDK ITQLKIDNNPPFAKGFRD
 >tbx3b VTFHKLKLTTNN---ISDKHGFIIILNSMHKYQPRFHIVRANDVLK-----LPYSTFKITYVFPETDFIAVTAYQNEK ITQLKIDNNPPFAKGFRD

 >TBX4 VSFQKLKLTTNN---HLDPPFGHIIILNSMHKYQPRHLHIVKADENNA-----FGSKNTAFCTHVFPETSFISVTSYQNHK ITQLKIENNPPFAKGFRG
 >tbx4 VSFQKLKLTTNN---HLDPPFGHIIILNSMHKYQPRHLHIVKADENNA-----FGSKNTAYCTHVPHETAFISVTSYQNHK ITQLKIENNPPFAKGFRG
 >TBX5 VSFQKLKLTTNN---HLDPPFGHIIILNSMHKYQPRHLHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTAYQNHK ITQLKIENNPPFAKGFRG
 >tbx5a VSFQKLKLTTNN---HLDPPFGHIIILNSMHKYQPRIHIVKADENNG-----FGSKNTAFCTHVFPETAFIAVTAYQNHK ITQLKIENNPPFAKGFRG
 >tbx5b VSFQKLKLTTNN---HLDPPFGHIIILNSMHKYQPRHLHIVKADERN-----FGSSNTSFCTHSFAETTFIAVTAYQNH ITQLKIENNPPFAKGFRG

 >Mdom-Tbx16 VSFHKMKLTTNN---TLDQGHIIILNSMHRYQPRFLVAQADDLFN-----VCWNLFQVFSFPQTVFISVTAYQNEQ ITKLKIDNNPPFAKGFRD
 >tbx16 VSFKLKLKLTTNN---ALDQGHIIILNSMHRYQPRFHIVQADDLYS-----VRWSVFQTFTFPETSFTAVTAYQNTK ITKLKIDNNPPFAKGFRD
 >tbx6 VSFHKLKLTTNN---TLNSNGLVVLHSMHKYQPRHLHIVQSPDPCT-----PHNPGAYLRFTFPEAAFIATVAYQNQE ITKLKIDNNPPFAKGFRD
 >TBX6 VSFHRVKLTNS---TLDPHGHLIILHSMHKYQPRHLHIVRAAQLCS-----QHWGGMASFRFPETTFISVTAYQNQP ITQLKIAANPPFAKGFRD
 >tbx24 ISFHRAKLTTNN---TLDAQGYIIILHSLHRYQPRVHVIEARDVLM-----WGRTOHSFTFPETQFIVTAYQNNK ITTELKINSNPPFAKGFRD
 >MGA VSFYKLKLTTNN---TLDQEGHIIILNSMHRYLPRHLHIVPAEKAVE---VIQLNGPGVHTFTFPQTEFFAVTAYQNIQITQLKIDYNPPFAKGFRD
 >mga-a VSFYRLKLCNT---LDQEGHIIILNSMHRYLPQIHIIIPADKVS---DILILDRPNVVTLSFAQTEFFAVTAYQNL CITQLKIDYNPPFAKGFRD
 >mga-b VSFYTVKLTHD---SCEREG-VLLQPMHRYQPRLYVAPVSACLE---RAVPLKSPNVHMTFPKTEFYAVTSYQNPQITRLKIDCNPFMLAFRE

 >EOMES ISFGKLKLTTNNKGANNNTQMIVLQSLHKYQPRHLHIVEVTEDEGV---EDLNEPSKTQTFTFSETQFIAVTAYQNTD ITQLKIDHNPPFAKGFRD
 >eom-a ISFGKLKLTTNNKGANNNTQMIVLQSLHKYQPRHLHIVEVTEDEGV---EDMSSEAKTQTFTFPENQFIAVTAYQNTD ITQLKIDHNPPFAKGFRD
 >eom-b ISFGKLKLTTNNKGANNINTSQMIVLQSLHKYQPRHLHIVEVSDRS-----ERDSNTQIFSFPENQFIAVTAYQNTD ITQLKIDHNPPFAKGFRD
 >TBR1 ISFGKLKLTTNNKGASNNNQMVVLQSLHKYQPRHLHVVEVNEDEGT---EDTSQPGRVQTFTFPETQFIAVTAYQNTD ITQLKIDHNPPFAKGFRD
 >tbr1a ISFGKLKLTTNNKGASNNNTQMIVLQSLHKYQPRVHVIEISKNEDE---EDTSDPDGVQTFTFPETQFISVTAYQNTD ITQLKIDHNPPFAKGFRD
 >tbr1b ISFGKLKLTTNNKGATNNNTQMIVLQSLHKYQPRHLHVQVNEDEGT---EDTSQPGRVQTFTFPETQFIAVTAYQNTD ITQLKIDHNPPFAKGFRD
 >TBX21 VSFGLKLKLTTNNKGASNNVTQMIVLQSLHKYQPRHLHIVEVNDGEP---EAACNASNTHIFTFQETQFIAVTAYQNAE ITQLKIDNNPPFAKGFRD
 >tbx21 VSFGLKLKLTTNNKGSSNNVAQMIVLQSLHKYQPRHLHIVEVKEDEGT---EDPFLTSKTQTFVFPETQFIAVTAYQNAE ITQLKIDHNPPFAKGFRD

 >TBX19 ISFSKVKLTKN---LNGGGQ-IMLNSLHKYEPQVHIVRVGSAHR-----MVTNCSFPETQFIAVTAYQNEE ITALKIKYNPPFAKAFLD
 >tbx19 VSFNKVKLTKN---LNGGGQ-IMLNSLHKYEPQIHIVRVGSSHR-----MVTNISFTDTQFIAVTAYQNEE ITALKIKHNPPFAKAFLD
 >T VSFSKVKLTKN---LNGGGQ-IMLNSLHKYEPRIHIVRVGGPQR-----MITSHCFPETQFIAVTAYQNEE ITALKIKYNPPFAKAFLD
 >ntl-a VSFSKVKLSNK---LNGGGQ-IMLNSLHKYEPRIHIVKVGGIQK-----MISSQSFPETQFIAVTAYQNEE ITALKIKHNPPFAKAFLD
 >ntl-b VSFSKVKLTKN---LNGGGQ-IMLNSLHKYEPRIHIVRVGGPQR-----MITTHAFPETQFIAVTAYQNEE ITSLKIKYNPPFAKAFLD

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.