

## Supplementary Material

**File S1.** A list of all amino acid sequences used for the evolutionary and phylogenetic analysis of *G. morsitans* tetraspanins: The list contains seventeen, thirty-seven, and sixteen protein sequences from the genomes of *Glossina morsitans* (Gm), *Drosophila melanogaster* (Dm), and *Musca domestica* (Md), respectively.

>GmTsp1

MGCATITIKYLLYVFNTLWAIIGILLIILGGFGWDAMPRNYAIGVISLGGVILLIAFFGC  
MGAARESARSLWTHAITMLVMIVLVVVMICFNTRDVFKKYALQEVNDFWQKEITQPGSMD  
NMQIVYACCGRDSAEDYVNIGRSPSSCKDSNCINPLNVYITGCITKVEAAFADEVLT  
TQICEWCLLGVSLVILLLATALAIHYTNQKRRFGY

>GmTsp42E1

MGCAATTVKISSIILNLIMAIFAICAIIWISFNPDYIQEQLAIIVYIACSLIVFFAFLGC  
FAAVRESMCLMATCAVFLLLAILQIVFTSNDISEGGMRNFGSIVNEAWESNSMDEIQIE  
HECCGKTSANDYVVLKPIPIISCYVDQDYTKVSNLFTEGCSSKLQTYEDEWHCSIIISW  
ILIAFELLAFLAVFLVINFRNTQRRMRF

>GmTsp42Ei

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LVTAIFGFIAALRESKRKLIYVPILVMLILTQLVMTSMASHGTRDGLSGSIRQGFEEELW  
SSEIQAPGALAHYEDWLHCCGVNNTDDYRRIQHEIPKTCCHKRDCSQMENLYQDGCMAKF  
EEYLSDKTLAFSIVNCLLIIVEVISAVLGWLMISKLKNEFRRTNARWL

>GmTsp42Ed

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IWDQRHTDQKVM DALQISFKCCGKNGFTDYTLAGEAIPPS CCEVSATSCTAIEAISRP GC  
VRAFTNFWENSMNIIRYAGLG VAGVELVAFIFGCCLANQMRNKHRRSHY

>GmTsp2

MNCQTTFYNIIVLNIINTVLSLLGVGLIALSVYELNISTPGTFEHI AVIIQIFIGSFLILT  
SFLGCFGACRESLGLIWSYGLCVVFLTFQIYILVVAHTTDYKR NATDDL IKLWQNY PVN  
VERIAEVEQNYCCGKNSTQDYISMKGFIPTSCYQNYERIDSKRYTKSCLEAVQENAAKS  
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>GmTsp3

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AFIGCGGALNGSLKLLSLYIFVLLMLMIGHVWKLWRYDESRIRNSVEVMITYTWIEELVE  
RGKMDALQYSYHCCGKRGYS DYTALSLKIPNSCYQVEKNNKKT FYPYGEGLSAVS NAYL  
DIYRAEKWFHVSLIGVEFFGIVLTVTLICNL TADTLRYSY

>GmTsp4

MGYDCGVWIGKYVLCIFNFLFFVLGTIVLGIGIWLAVDKASLIALLKM VENEHINQFTQP  
QVIEQLAYVLIAIGGVMFLMSFMGYCGAIRESKCLLT TYGTFMILLLIAEIVAGGLAAFY  
KDTARNETKTFLQSTITKYYTSREHTDAVTLMNQMMSTFACCGVNDYRDFDMSTAWAAN  
KGNRTVPEVCCILKDVKLMVPRDEDCVTNPTEGNSFFKRGCYEVFTEWIVTNRELLVAVL  
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>GmTsp5

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VLLVTSMTICVLSFVGCVGASKEVKCLLLTYFIIIVVLIFVTMLIGGILGFVFRERVQQT M  
RQKLRSSMSLYGSRDVTESWDQTQERLQCCGVDSWHDWNRLIPESCCQEIFGGQRKECT  
LIPAVTNLYSQGCLYVTTSFMRDHA AVIGGT AIAVAIIMIFGMIFSCLLFTMIE

## File S1. Cont.

&gt;GmTsp6

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 NVFYNIPESCCKDELKENVCMSRKLKFGGTFNPAIHQQGCVDKLIELIYENWVLLFGVT  
 AGVILLELLALTFSLSLCCAVRNHQYKA

&gt;GmTsp7

MGNAGYTCIRRTFCWLNITLWLCSCAFLGAGVWLRLSYEGYATLLPHHAVLSADSMFLGI  
 GVVGFVISFLGCCGAWVQSKCLLVLYFMLIVLLFVSEFLIGSLAFIFRGGFGRTLANELR  
 FGIENHYNVSDRGSIIAPSVATIWDNIQISFECCGVSTYEDWYDVQSWSGKRWPESCK  
 SLYENRGILTEGSGDSITKIDCGRSENPSLWPKGCADSLQTWLNQQLDVIGAVGLGIAF  
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&gt;GmTsp8

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 WIKDQATEGLRAFIHYREDPDQQLIDWIQEDWLQCCGIEGPKDWSNNYFNCSSGAIG  
 SREACGVPFSCRRRPQELIKNKQCGYDVRKEGYVSDRHTFYDYDWKPVDRHIYERGCLR  
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&gt;GmTsp9

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 NVGYQDWSKNEYFNCSSPSVEKCGVPYSCCINATDISSGLVNIMCGYGVQEHVAAAASKR  
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&gt;GmTsp10

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 GISNEINNYNFSNSTNNDNRDNLIDIVQKNLQCCGNESFTDWPQDAIPKSCFKNFKDYS  
 VPDIKNIYETGCAYKLKNVINKNFTAIGVTTSTIALFPFFGAVLSFGLSLMYNKGGYEMI  
 V

&gt;GmTsp42Eg

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&gt;GmTsp39D

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 MRDYNDRDDYRDAWSLLQSELECCGTGYPSEDWEAVYHNTTLHASCPIIVLNEADKCTTA  
 HASPDGCLNKLIHILDSNALVLAVVLGVASIQLLTILFACCLCRSFCRSYQTV

&gt;GmTsp11

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 DSFVEFLDKFSRTKVDNLHLWNRMQSQLQCCGVDPGLDYRRSLPWSCSRPEHAYESAC  
 DTHYKRGCLAVVSEQIKHRLITAFSAIIAIFQSLGLFCAVHLTILFGKSDNGYDNNKL  
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## File S1. Cont.

&gt;GmTsp29Fb

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CGSFSPDNLMHCEMTYESGCLERMDFIISQSTMLIATGATTVAFVQLLGSICAFMLAKTL  
RRNKSIREARRWQLQQLSLGVLISGGKMVPPSPNSPMTGYTQLEKAEKSENDPITYTPNSP  
SVN

&gt;DmTsp66E

MVFDCGVWCAKYLLCIFNFIFFVLGTIIFGVGLWLAVDKHSLIALLLKLVESERIEQFTQPQAIEQLAYVL  
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LGENVDATSLMWNQLMGNFGCCGINDYHDFDASPAWVNGKGNRTIPDACCILKDVAKLVPRDEDCTTNPS  
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&gt;DmTsp42Eh

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LHCCGRNSAEDYLHLEKMPPSPCCLNRDCTKHLNLFMTGCEVKFKEYVGAKTANFHSLSWFLVIFEFAGS  
VTTCYLVDSIRNHRDRIRFYN

&gt;DmTsp42Ea

MSCGISMVKYILFIFNLLCSICGILLIVFGALLFSKVRNMDDFAEALRTQQVPVTMIILGTIILLISWFG  
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CCLANSIRNYRRRAEY

&gt;DmTsp97E

MCGGFTCSKNALIALNILYVMIGFLLIGVGVYARAASIVTNLPVGGILACGVILICISMLGLAGAVKHH  
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&gt;DmTsp74F

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WDLTQERLQCCGVDTWHDWNRYGPVPESCCQELFGGQRKECTIFPTITNLYNQGCLYVTTNFIRDHAIVI  
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&gt;DmTsp68C

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&gt;DmTsp47F

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&gt;DmTsp42Eb

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## File S1. Cont.

&gt;DmTsp29Fb

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 VDFMQSMLECCGVNEPEDWKDYL SANVNFTLGVDVVVPNSCCGNQPTSLNDSTQMTCMETYDYGCFRKM  
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 VTGYQQLDNGEQGSHEPYTTPQSPSVN

&gt;DmTsp96F

MGLNGCCSCVKYLMVLINILFWLIGLTIVVTSVWMLTDPTFMLSMTQNYNHYHIALYVFLAIGILITLGA  
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 FDTLQKNLKCCGADGPGDWATSRFNNVDRTNIVEIAVSSMNVFYNIPESCKDNLKDNECELSRRLKFGG  
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&gt;DmTsp86D

MSNHRYHQGGNYMHPRISTYPHHFSYVSSCVKYMIFLLNFLFWLFGGLLLAIGVYAFMDKLMGNGWLRL  
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 FLEYQFTDKIIHSYRDDSDLQNFIDFAQQEFNCCGLSNAGYQDWSKNEYFNCSSPSVERCGVPYSCCINA  
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 GQIDLQKSRWS

&gt;DmTsp66A

MVDNEETGCLQRLLSVGKLQICKFIIYFVWLVNFI FSCADIYIYYFILKEHMPWCDC LFRSYMIIALTVN  
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 CGVLGPDDYKLGDLNIPKSCYKNGSERDEDLYRSGCSTRSIKPASPIIHVISFVIQYVLVICIEVFLIIL  
 LRSKSQPTSMWSERVTERFGSVKK

&gt;DmTsp42Er

MGWSPLMIRYLAFLFNFLCAVLGIATIVNVNIAIDQIAPKDQLILGLYIAVGSIVFLLSFFGCFGAIKES  
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 DAYITVPSSCYDQNDTPYRDGCLAKMETQYEELLKGPKIVGWMLMVIEIGAF TFSTIMGVSLRNELR RSA  
 Y

&gt;DmTsp42Eq

MSCGTKALKVSSFVLDFLCCVLAALTIAACSYALIAFSHSV AIRVPSILGIVLGGLLFFSTIFGCIAALR  
 ESIRMTWIYAAILLALVFSQITVILAQPINYELLANETIYDAWQGQLYHSDRMSYFEIKYHCCGQTGPAN  
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 NAERRRLYR

&gt;DmTsp42Ep

MNGCYNTIKYTGLLSNLLYMLLGIGVMSGAGLGLQMAEPNTPEHTYFVKSLVLGGSICMIVMFGCYGMVA  
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 ADDYKRLHLLVPASCYQAAVN DTAQQIYPSGCLET LNRSQRYIQHRDKLYMWAIVGLEIFILLQTVALSV  
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&gt;DmTsp42Eo

MPTVRVCLQWTSVVFSTLT LIVGVLAALAGVYELDKFNEGSAEHTEKFVQLGMAGALILAGLVGCLGAIF  
 GSIKVMVNLILL LALIASHIWKVSHYNETKQLDATEVYVMDLWMKELVHHGAMQDLQQEYECCGDKGFS  
 DYTSLNMKVPRSCFHTKDG IHALYPYGE GCM AAVKRAYLQIYRYEKWVHCGLIGYEVVGIILGITLCCQL  
 TNKTRRYTY

&gt;DmTsp42En

MDCRTSFLKAVLIVLVNLLSLIGVT LIALSVYELNSSTPGTFEHIAIVVQIFVGTFFVLT SFLGCFATAR  
 VSLGLVWSYVICLLILLCLQIYIIAAAHSTDYVERSKKDFLATWADQRTNVERISLLEQKYSCCGQLGAH  
 DYILMGRGIPLSCYK DQERREYS LFSGGCLQAVQA HATDNVAIGLI IKWLLLLVEFAALGAATHLGITVR  
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## File S1. Cont.

&gt;DmTsp42El

MGCATGTIKYSLFLFNALWAILGILVLIFGGLGWGAMPDAYAIGILILGGTILVISLFGCCGAVRESPRM  
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KFWNNTVPSSCKDDSCVNPLNLYVRGCLIKVEEAFDEATTLGYLEWGLLGFNAILLLAILAIHYTN  
RRRRYNY

&gt;DmTsp42Ek

MGCTSGCVKCFNLNTLNALSGLSLIAIATLALSKAPIAYILFLYGLGGIIFVSAVLGCCGICMENVCN  
TATYGFLLLAQLIISLLGIFRFKFTTEYIEKFAAEVQMKWDEELVEPGAMDIYQTVYECCGRDSPDDYV  
AIGRQTLPPSCYPQEDPQMPHYLAGCVQKSSNFVVLFSYAHDTNWIALGITILMMIAAFYLVGRFRKQR  
VRYTY

&gt;DmTsp42Ej

MEKSFPITPWKYGLLVTCILIVTCNVFFFSCGVTTWGSASVSYGSYGSALCGGAVFGVAFGLMYVALKVS  
YKYSIYYLICSGLVIAALGSYLF T T T AMREQLMGRFEERMRLFERKTHSDDKMQPVHSLFGCCGIEGPQ  
DYLQEEHGALPSSCCYAFDCSKPAHVYEEGCSTKAVATLRMQAELNYSCMAIIALEFLGLFTAYHLGKA  
RKYAKTKIKDEETPIND

&gt;DmTsp42Ei

MGLGATTVKHVLNLFVFSVLGLALIAFGIFFLISAAENAVSIGKNVAGGLIIALGVVILIIAIFGCLA  
AIHEAPVRLLIYVGAVVLLILAQLIFLGMSSHGTDGSGSINEGFDRLWESERNQTGALSYYESWLQCC  
GVNSEDYWIHHGIPSSCCPESKCMDTPSRVFKTGCKAAFKYLDKLLVFKIVCWLLVIGEAVGAVFG  
WLLYSSVKNQSRNNNAVWM

&gt;DmTsp42Eg

MACSTNVLKGFAFWDIILALFGLVVLIGLVHIIYKFEHFNTAAFVIIAVGVVVVLTALFGALGAARESS  
ATSKVFVVILIVLVILEVLAVGFLWFQTSLINVDKTFDKLWNDQPVPIKPGNQSQIASLERWLDCCGN  
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RRSKYYQK

&gt;DmTsp42Ef

MASTSSVKLIVYALDVLCTLLALVLISFGIYVAVSYNLNEIGQLTAYGYVGLGAAALLVVLWGYSAWRE  
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QDYIVNERLPPETCFRNHDKSKPENLIHTGCRVEFENYWQHLTKIFNILALVLIGFELLSVISCRCLNS  
IRNDARRSYF

&gt;DmTsp42Ee

MDCGTSVMKYILFIFNTIVSVIGILGIVYGVILILKSIGVVEVNGQVGFPIQALMPIILISLGSIVVFISF  
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SLHCCGSSSALDYIGKGLVPPSCCSGSLIPTNYYPGCRGKFVELMTTGSDNAKYVGIGLIGIELIGFI  
FACCLANNVRNYKRRNAY

&gt;DmTsp42Ed

MDCGGVFVKYVLFIFNILFVICGILLITFGSIMVSTIKDFSGVGETFTANSVAIIILVLGCVVFLVAFMG  
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CCGLNGFADYGITYPASCCDSPSNGTCALTQVMTRSSCLKAVDSFWDNTVSIICYAGLGTAVELVAFIF  
ACCLANQTRNSQRRQNY

&gt;DmTsp42Ec

MGCLSGIVNFILYIVNIVFLIVGILLIVLGSIMLSDLSRFDVAGSGTDPNTIPICVTVLGGILFVVSFFG  
CYGIFRQSVCMGTGAYTSMVFVLFILQLVLTWCWFVNRS AFLGDMSNLVNLWDSDHYTAMGVLEETFGCC  
GDTSYTNYNIGLSVPGTCCGYLDRQATCNTPSVYQSRPGCSAKFEFWDNMDIIRWSGLGLCIFDLVV  
FLIAGALTNCMRSQNAGRQVYA

&gt;DmTsp42A

MANPFRWCRVSHDCVFQINVVLVVVGVIFFLLDVLSHLYLKAVMFPGRLYPVALRPWLFVWRALTMVAYI  
LNAVLGIIHMARQPTVLKYAGYMLVGSVLLYTISIGVTRFMYRKRFEFFAEMLVLMQWVRDRLGKVEVEF  
ECCGRSSVVDYQTASSNRTWPIGSCCGKQNGCTGCTAKLSQYLWTIEMDVARDNIIVSVLLFVAMIVMVLH  
FKDVQSLDDTSDVDESSELVDDSDAKE

## File S1. Cont.

&gt;DmTsp39D

MASGGLTCVKYLTFECNLLFALTGLLIFLVGGMVQLNYAHYSNFVSDHVWTAPIILMIVGAAVAVICFLG  
CCGALKESSMILSFALLAVVIFLFEIGLGLAGYVKHTGLHQIMESQFNSTMQHYKERADYRDAWTLTQT  
ELDCCGINGPNWETVYRNSTLPAACCSVINLSEAKECTNTHATQHGCLQKLEILDSKTLILASVVLGV  
AGIQMLTILFACCLYRSFRRSYDHV

&gt;DmTsp33B

MRQPFRRASVYLHLLLITEAVIGLLILVVTAYYHTVLTGYLSDIECRLVYGYLFGIYVFGAQVVVTFCLCS  
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LLWDGLQWHKECCGVHGYKDWMAEWMPPRENNCTSMVLAPFACCKRSCDSCFNNFLPSEGQSIGGNSRQ  
PPFALTVD SINANGCLPAFVSAVWNCFYILMALWVLALKFLIVLCCMTKFIVHRQNEGDGCDNVGLTDDD  
GHPLVVVKYPCNVRCVTIAEDDLVSDNVPDINYCNCCTEMDDEPCGY

&gt;DmTsp29Fa

MSLLTGSANVKYTLFGFNLI FLITGIILIAVGAGVGAVYTGYKFLAGKFFSIPTFLIVIGSFIIIIISF  
FGCWGALKENYCLVLSFSVMLAIIFILELAAGISGYVLRNDASDLIKTSLTYSLNEYNSINPNATTKLWD  
DIQDEFECGVTSYNDWITAFPNGDLPISCCNVHVGAVGTFTCNNAQSSVADRHKVGCLDGFSGYISAHA  
VSLGAAGVVIAILQFFGVIFACYIAREIKIRNGITGFM

&gt;DmTsp26A

MPAAVRKFRRETSEISCLKYLLFASNVILWLSALLVLSVGIWAWSEKGMFRNIARLHFIALDPAFVLII  
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EDADQQNLIDWIQEDWLQCCGIDGPKDWDSNNYFNCSSIAIGSREACGVFPSCRRRPQEVINKKQCGYD  
VRKEGYPVDRNIHERGCLRAGEDWLEAHLISVAIGCVALLVLQILGICFAQNLADIYTQKSKWH

&gt;DmTsp5D

MGNAGYTCIRRTFCWLNIILWLCSCAFLGAGLWLRLSYAGYATLLPQHAGLSADTIFMGIGGTGFVVSFF  
GCCGAWVQSRCLLVLYFMLIVMLFMSEFLVGSIAFLFRGGLGRTLANELRFGIERHYNSSDRGSLVAPSV  
ASIWDSVQQSFECCGVSSYEDWYDIQSWPGRRWVPESCCRTLYDQRQVLTEGSGDGMMRPDCGRSENPSL  
WWDKGCAHSLQSWFTGQLNVVGAVGLGIAFVQLFGLITSMLLFCTVKHKRASDTYKSYSPSIDPQTRTSS  
WED

&gt;DmTsp3A

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DKWEDANGSVRLNFYDVFLNISLVMILAGTVIFLVFSFGCVGALRENTFLLKFYSMCLLLFFLLEMAIA  
IVCFVCPQYMNTFLEKQFTHKIIHSYRDDPDQNFIDFAQQEFKCCGLSNSGYQDWSKNEYFNCSSPSVE  
KCGVPYSCCINATDISSGLVNIMCGYGVQNAVPPEATKLIWTSGCIEIVRVWAEHNLVYIAGNALGIALI  
QLLVIYLAKTLEGQIELQKSRWLA

&gt;DmTsp2A

MGIGYGASDEQLEKQIGCVKYTLFCFNIVAWMISTALFALT VWLRAEPGFNDWLRILEAQSFYIGVYVLI  
GISIVMMAVSFLGCLSALMENTLALFVFGTQVFGFIAIVAGSAVLLQFSTINSSLQPLLNVSLRGRFVAT  
SEYTYSNYVL TMIQENIGCCGATGPWDYLDLRQPLPSSCRD TVSGNAFFNGCVDEL TWFFEGKTGWIVAL  
AMTLGLLNVICAVMSFVLVQAVKKEEEQASNYRR

&gt;DmTM4SF

MALPKKIKCFKYLVSYSVVLALTGAAQIFLGTSLLWGHSVYYGIVQNKLWAPAAILLCLGPVTFILCWM  
GCQATNQRKRCLLGMFAALLVACICVQFIICGWSLAMRENLP TSVEIFIDDSFVEFLDKFSRTKVDNLHL  
WNRMQSQLQCCGVDGPLDYRRSLPWSCCSRPEHAYESACDTHYKRGCLAVVSEQIRNRLLITAFGAII  
AIFQSLGIFCAVHLTILFGKNDNTHPMNMNRKKKQQQFLPLTIQDKRHMPSPINLSPSAPGQRVLTAL  
PSAMHK

&gt;Dmlbm

MGCATTSVKIASIVLNAVLGFLAAGAIGWIAYNADTETEEFVIAAYIACSLILVFALLGIFAAIRESVVL  
TATSAVFLILAILQIVSTCLFLHEFDVKSGRDMVEVAWQANNMDSLQKHECCGQSSAQDYIHL SLLIP  
PSCYADLQQTPDHLYLDGCIEKVQSFYESDKLRFIIVSWVLVAFELICFALAVFLAISFNKQRRMEF

## File S1. Cont.

&gt;DmCG30160

MNCLSAMFKYLLYLLNLVFAVGILLIVVGSIMLSTMGNTAFDGGVNTQTIPICIIIVIGSVTFVVAFFG  
CCGTIRENACCTTIYAICMLILFGLQLALSIWIFAANDKFLSSMGKAVDKAWDENNAAQGYPM DALQLAF  
SCCGNTGYQQYETVPSSCCGYKDR TKVCEAEIYSQRP GCRQEFVDFWASNTDLIRWSSLI ALFELGIFI  
MSCCLASAMRKR

&gt;Md - T1P8U3

MGLNGCCSCVKFLMVLFNILFWVIGLAIVIASAWLLTDPTFVLSMTQSYNHYYIALYVFL  
GIGVLITIGAFFGCCGVLKESQCLLVSFVCVILVVMVAQIAAGAWAFHNKDKLDDIVRAS  
VKYSVQEEYGQSSMSRTVTFDTIQKNL KCCGADGPADWATSRFNNVDR TNIVDIAISSM  
NVFYNIPESCKDELKENVCMSRKLKFGGTINPAIHQQGCVDK LIEVIYENWVLLFGIT  
GGIVLLELLALTLSLSLCCAVRSQQYKA

&gt;Md - T1PBG6

MGCATRTIKCVLLIFNTLWAI FGVLLLLLAGFGWDAMPQNYGIGI IALGCVILLTSLFGC  
FGSIRE SARSLWTYAVMLLIILVLT VVFI CLNTRDVFKNYAIQEVNQLWEQELIHPGAMD  
QKQLVYECCGKNPDDYLLAGRITPSSCKDSNCINPLNIHINGCLSKIEEAFSNEALTS  
QISEWLLGLNAV VLLMSIMLAIHYTNQRRRFNY

&gt;Md - T1PB83

MDCGTTFAKYVLFIFNAIVSILGILVIVFGVLILNSIGMIEVDGQTGFPPQAAMP IGMIT  
IGSIVVFISFLGCCGAIRE DVCMTMCYAVLMLILLIIQLIVVLLW TNQDKIETAMDNVI  
ESAWQSEVREAGVFEVVQKSLKCCGVNSAADYALNGRIPP KSCCPADETCIVINYYPGCK  
KEARKFITGSSEKAKYFGLGLIVVELVGFIFACCLANNVRNSKRRNAY

&gt;Md - T1PDV0

MACSTKTLKFFSIKWDVIYAILSI ALIVLGAFILIKFERFDTVGYTLVGMGSLVLLFTIV  
GIVGAARERSTLLKIFALIVVILAITHVII LGFFWIFQTSFLINADKAFDEIWRDQPTPI  
KPENGSHIANIERWLSCCGNSGSVDYHLPPHSCYDSKTDKLNTDGCRQKFVDFITESWTY  
LNIFVLVYVVIELICAIFAFVLANSIVNRWRRSKYYSK

&gt;Md - T1PAF0

MSCGMTMVKYTLFLFNILCSICGILLIVFGAMLFSNIHTVEDFAEAVKTQQVPLTMIVLG  
IVILLISFFGCCGAIRESYCMSMTYSILLFVLMIGQLVLVTYMWLQDKYLVIMGDVVEK  
AWQNRTRKSDYMDALQISMECCGRSGRADYHFQGYPPSCCKDVRQCNDSTAFNIGCKQA  
FVEFWDKNADIIKYAGLAIAAIEFAGFIFACCLANNIRNYKRRSGY

&gt;Md - T1P904

MGFSSRMDCCGQFVKYSLFVSNFVIFVGGATVFCLSLWTLVDRSFMNELLGTNLFSGAVY  
VLLVTSVAICLLSFLGCVGAGKEVKCLLLTYFIMVALVFVTMLIGGILGYVFRERVQQT  
MQEMRSSMALYGSRRDITIAWDQTQERLQCCGVDTWHDWNRFGPIPESCCQEIFGGQRKE  
CTIFPTITNLYNQGCLYVTSNFIRDHAAVIGGTSIGVAIVMIFGMIFSCLLFNMI E

&gt;Md - T1PJU0

MYISKRTYKIIIVIIINVICAILGSVLTWFGSWLYKSIDDEKFDHGEKLASIVIMTLGGVL  
IFTAIYGTLATVFELSNMLISFAVLLIALLMQIVLVSI SYTALNNGVSKRLEKGFDELW  
DPLHLKPSENLSFYEEWLQCCGKNSPEDYLLDKYPPTSCCKDHNCIKIHNLYKDG CADK  
YRDYVKS KVENFNILSWVIIATEFIGSIFSCLLIDSIRNYRDLRRFYS

&gt;Md - T1PCN8

MGCTSDCMKCILNIFNVLYGISGIVLIVFGVSLLQSANIVQLYII IAMGAINLIAAILGC  
CGICHEHVCM TATYSLFILSSLVGQIYNKIKPASTDEIKKIIRSTIKAVWDEELKTPGAM  
DSTQKSLKCCGLDGPTDYQRNGRFVLPASCYPDDVSTAGHAFFNVGCVTASENKVFS LAK  
YQTSSEWGVIAVTAVLFIFSIYLVFRFNSRNKRYRY

## File S1. Cont.

&gt;Md - T1PBY6

MGCATTTVKISSIAFNIIALFAIASIIVISFNPDSMREDIAIGAYIACSLIVFFAFLGC  
FAAIRESVCLTATCAVFLLVLAHVQIALTCVGMTDTGVRSVAVETVDKAWESNAMDAIQSE  
HECCGKISPNDYITLNKAIPISCYIDEDASKTSNLFEGCKDKLQRHYESEAYIFTVVS  
SLVAFVIIGFLLAVFLAISFRNTQRRMQF

&gt;Md - T1PF15

MKEYNPHTNDVTFMWYVQRTFTCCGVESYKDWNTVLNGSLPLSCCRNPVGHVGSFTCT  
MNNEDVNRYSLGCLSEFSNYIAAHAVSLGAAGVVIAIIQFFGVLFACYIAREIKIRNGIT  
GFMG

&gt;Md - T1PC83

MLIIILLFLSEFLIGSIAFVFRGGLKRTLANELRFGIEEHYNATDRGSIIAPSVAAIWDNV  
QMSFECCGVSSYEDWDYIKSWSGKRWVPESCCRPYENRGILIEGSGDSVLRVDCGRSEN  
PTLWWDKGCQSLQTLTDKLDVIGVVGLGIAFAQLFGLITSMLLCTVKHKKDSPTYKS  
YSPSIDPQTRPSSWED

&gt;Md - T1P9W2

MSNYRHHIGSGGYCGIEVRDMHPRISQNTYVSSCVKYMIFMLNFIWLFGLLLAIGLY  
AFKDKWESTGSRLESFYDVILNISLVLMIAGVVVFVVSFAGCLGALRENTCLLKFYSMC  
LLLFLLMEMAIAIMGFVFPQNMNSFLEETFTDKIIHSYRDDPDLQNFIDFAQQEFKCCGL  
SNAGYQDWSKNEYFNCSSPSVEKCGVPYSCCINATDISSGLVNIMCGYEVQAHSVAAASK  
RIWTSGCIEIVRVWAERNLYAIAAGIALGIALIQLFVIYLAKTLEGQIDLQKSRWSA

&gt;Md - T1P8S2

MATRDQLNSGMRCAYMLLIVSFMFAITAILLVMVGSTIQAIFGDFRQFVDDHFLSPPA  
LLIAIGFILLFVATLGAYGAIKESVMLINLYGVCLFLVFILEVSASIAAFVMQGVREML  
VRTMNESLANYESNEYIQAGVDFMQSGLECCGVDPDWINFIIQQSNSTDNRIDVPLSCC  
GMYSYDLESCEKQYENGCFGRMDFIISQSTMLIATGATTVAFVQLLALCAFMLAKTLRR  
NKSIREARRWQLQQLGVLISGGKMAPPMPMTGYTQLEKSERFYEQEPIAYTPNSPSV  
N

&gt;Md - T1PJ11

MLATSLFALT VWLRAEPGFNEWLILQAEAFYIGVYILIAISIIMMAVSFLGCLSALMEN  
TLALFVFIGTQIFGFLISIVGSALLMQYSTMHSSLQPLLQTSLSNFVSTSEQPYSSYVLN  
MIQENVGCCGASGPWDYLNLRQPLPSSCRDTSVGN AFFNGCVDEL TWFFEAKTSWIVAIA  
LGLAMLNVISAVMSLVLVQAVKKEEEVQAYRR

&gt;Md - T1PD63

MGSDCGVWFGKYVLCIFNFVFFILGTIVLGTGIWLAVDKSSLIALFKMVESEHINEFTQP  
QVIEQMAYVLIAIGGFMLMSFLGYCGAIRESRCLTTYGVFMILLIAEIVAGGLAAFY  
KETARNESKGLQSTITKYTSSEHTDAVTLMNQMMTTFGCCGVVDYRDFEQSPSWLTS  
KGNRTVPEACCRLKDIKNLIPEDFCVTNPSEANSFYMKGCYETFTDWIIHREIIIGVL  
AGAGIIHLLVIFLAFCLSKSFAKYHGMRL

&gt;Md - T1PC85

MASKSAVKRFIYIFDILCILLASVLIGFGAYVICTNETNEIGTMGAYGYIAIGVATFVVF  
IFLNVGAMRDNVCTVT FIVLMVLIIFAQGVVAFFMIAGRESVASNLANELDATWEKELK  
NHGAMSIYENWFDCCGRASPQDYIVAGRLPPPTCFVGHDISLPENLIESGCRIKFEDYWL  
ELLGIFNILACVLIGLELILSFIACCLCVSIRNERRRSYY



**File S2.** Analysis of selection pressures exerted on tetraspanins in *Glossina morsitans*, *Drosophila melanogaster* and *Musca domestica*: The analyses revealed that several sites are under positive selection based on statistical significance tests as assessed by various models such as MEME, SLAC, FEL, IFEL, REL and FUBAR (Tables S1 to S6, respectively).

**Table S1.** Codons under positive selection based on MEME analysis.

| <i>Codon</i> | $\alpha$ | $\beta^-$ | $Pr [\beta = \beta^-]$ | $\rho$ value |
|--------------|----------|-----------|------------------------|--------------|
| 7            | 0        | 0         | 0.680891               | 0.000419473  |
| 8            | 1.62595  | 0.89548   | 0.929245               | 0.0749407    |
| 10           | 0        | 0         | 0.621438               | 0.0000006    |
| 11           | 0.915328 | 0.90513   | 0.887747               | 0.0228057    |
| 12           | 0        | 0         | 0.967885               | 0.000061     |
| 13           | 0        | 0         | 0.925898               | 0.0537399    |
| 15           | 0        | 0         | 0.798366               | 0.000000022  |
| 16           | 0        | 0         | 0.944415               | 0.00271562   |
| 22           | 0        | 0         | 0.627583               | 0.000637962  |
| 25           | 0        | 0         | 0.673026               | 0.00850381   |
| 30           | 0.22188  | 0.22188   | 0.687667               | 0.0000029    |
| 33           | 0.112483 | 0.112483  | 0.707372               | 0.000007544  |
| 35           | 0        | 0         | 0.672794               | 0.00004139   |
| 37           | 0.521743 | 0         | 0.510877               | 0.0186541    |
| 38           | 0.119991 | 0.119991  | 0.715983               | 0.0000000149 |
| 39           | 0.00118  | 0.001178  | 0.625878               | 0.000346185  |
| 41           | 0.07541  | 0.07541   | 0.84294                | 0.0000000014 |
| 42           | 0.08907  | 0.08907   | 0.715871               | 0.0164398    |

**Table S2.** Codons under positive selection based on SLAC analysis.

| <i>Codon</i> | $dN/dS$ | <i>Normalized dN/dS</i> |
|--------------|---------|-------------------------|
| 3            | 12.7691 | 0.6068                  |
| 7            | 7.51301 | 0.3570                  |
| 9            | 5.82693 | 0.2769                  |
| 10           | 13.4225 | 0.6379                  |
| 11           | 16.4621 | 0.7823                  |
| 14           | 12.0891 | 0.5745                  |
| 17           | 11.6889 | 0.5555                  |
| 23           | 8.64387 | 0.4108                  |
| 26           | 8.54061 | 0.4059                  |
| 28           | 10.7545 | 0.5110                  |
| 32           | 14.9546 | 0.7106                  |
| 33           | 9.72562 | 0.4622                  |
| 37           | 9.21561 | 0.4379                  |
| 38           | 10.1208 | 0.4810                  |
| 40           | 10.2132 | 0.4854                  |
| 41           | 6.8901  | 0.3274                  |
| 42           | 5.82768 | 0.2769                  |

**Table S3.** Codons under positive selection based on FEL analysis.

| <i>Codon</i> | <i>dN/dS</i> | <i>Normalized dN/dS</i> |
|--------------|--------------|-------------------------|
| 7            | 3.435        | 0.0651972               |
| 10           | 10.715       | 0.0645841               |
| 15           | 3.179        | 0.0446692               |
| 22           | 4.311        | 0.0849642               |
| 39           | 5.425        | 0.0498576               |
| 41           | 14.162       | 0.0629439               |
| 42           | 3.133        | 0.0375647               |

**Table S4.** Codons under positive selection based on IFEL analysis.

| <i>Codon</i> | <i>dN/dS</i> | <i>Normalized dN/dS</i> |
|--------------|--------------|-------------------------|
| 7            | 4.547        | 0.1031                  |
| 10           | 9.872        | 0.0544                  |
| 15           | 4.709        | 0.0720                  |
| 22           | 4.292        | 0.0844                  |
| 25           | 2.949        | 0.0627                  |
| 39           | 6.271        | 0.0555                  |
| 41           | 14.444       | 0.0653                  |

**Table S5.** Codons under positive selection based on REL analysis.

| <i>Codon</i> | <i>Normalized E[dN-dS]</i> | <i>Posterior Probability</i> |
|--------------|----------------------------|------------------------------|
| 6            | 0.0134554                  | 0.993061                     |
| 10           | 0.551239                   | 0.998573                     |
| 11           | 0.643135                   | 1                            |
| 15           | 0.769529                   | 1                            |
| 16           | 0.55005                    | 1                            |
| 22           | 0.0236506                  | 0.992037                     |
| 25           | 0.545118                   | 0.999993                     |
| 31           | 0.546731                   | 0.999663                     |
| 38           | 0.545081                   | 1                            |
| 39           | 0.540439                   | 0.993907                     |
| 39           | 0.608109                   | 1                            |
| 40           | 0.540071                   | 0.997656                     |
| 41           | 0.732863                   | 1                            |
| 42           | 0.554127                   | 0.999987                     |

**Table S6.** Codons under positive selection based on FUBAR analysis.

| <i>Codon</i> | <i>B-<math>\alpha</math></i> | <i>Prob <math>\beta &gt; \alpha</math></i> |
|--------------|------------------------------|--------------------------------------------|
| 10           | 0.168443                     | 0.998531                                   |
| 15           | 0.110881                     | 0.965741                                   |
| 22           | 0.412523                     | 0.997355                                   |
| 38           | 0.425619                     | 0.998779                                   |
| 39           | 0.117648                     | 0.946172                                   |
| 40           | 0.290936                     | 0.945438                                   |
| 41           | 0.167577                     | 0.99861                                    |
| 42           | 0.0886742                    | 0.90174                                    |