

**Table 1 supplementary. Position for GPI**

| name           | pos | %   | Protein sequence  |
|----------------|-----|-----|---|
| IGLON5-ANOLIS  | 308 | 100 | MSCPLLGLGALLCRMGMALHQLLVRGVDFNQPADNYTVCQGDNATLSCYIDQQVTRVAWLNRSNIL<br>YAGNDKWSIDSRVELLTYTPSEFSIMITHVDVYDEGLYTCSFQTQDKPHTSQVYLIVHVPARIVNISSAVT<br>VNEGSNVNLLCLAMGKPEPTVTWRQLKDGFTSEGEFLEITEINRQQAGEYECITANGVSTPDSKRVLITV<br>NYPPTITDVKDSRPMGKTALLRCEAMAVPPAEFQWFKDDKQLVGGDLGLQIQNERTRSILLFPNVTTR<br>HYGNYTCLASNNGSFNVSLRRLRPGSLEN <b>MAAASMASPLFLGLLSSAFVTLFR</b> I  |
| IGLON5-FROG    | 308 | 100 | MKAPLQRVSLASLGVMLAQVLFVQCTEFVPPADNYTVSQGDNATLSCLDIDKVTVAWLNRSNILYA<br>GKDKWSIDSRVQLLTNTKSEYIVITHVDVADEGLYTCSFQTEDKPHTSQVYLIVQVPAKIVNISSVTV<br>NEGSNVNLQCLAVGKPEPTITWQQLSEGFSEGELEITEINRQQAGDYECVTSNGVSVPTDKKQVITVN<br>YPPYITDVKNAQSPVGRPATLRCKAMAVPPAEFEWYKDEKRLISGTEGLSIKTESSWSVIVFSNVTSRH<br>YGNYTCLASNKLGFSNSSLRLKPGDPLN <b>QGATHMVSPLLLGLLSSTLIPLLR</b> TV  |
| IGLON5-GORILLA | 295 | 100 | MPPPAPGARLRLLAAAALAGLAVISRGLLSQSLEFNSPADNYTVCEGDNATLSCFIDEHVTRVAWLNR<br>NILYAGNDRWTS DPRVRLINTPEEFSILITEVGLGDEGLYTCSFQTRHQPYTTQVYLIVHVPARIVNISSP<br>VTVNEGNNVNLCLAVGRPEPTVTWRQLRDGFTSEGEILEISDIQRGQAGEYECVTHNGVNSAPDSRRV<br>LVTVNYPTITDVTSARTALGRAALLRCEAMAVPPADFWYKDDRLLSSGTAEGKLVQTERTRSMMLF<br>ANVSARHYGNYTCR <b>PGSLENSAPRPPGLLALLSALGWLWWRM</b>  |
| IGLON5-HUMAN   | 311 | 100 | MPPPAPGARLRLLAAAALAGLAVISRGLLSQSLEFNSPADNYTVCEGDNATLSCFIDEHVTRVAWLNR<br>NILYAGNDRWTS DPRVRLINTPEEFSILITEVGLGDEGLYTCSFQTRHQPYTTQVYLIVHVPARIVNISSP<br>VTVNEGNNVNLCLAVGRPEPTVTWRQLRDGFTSEGEILEISDIQRGQAGEYECVTHNGVNSAPDSRRV<br>LVTVNYPTITDVTSARTALGRAALLRCEAMAVPPADFWYKDDRLLSSGTAEGKLVQTERTRSMMLF<br>ANVSARHYGNYTCRAANRLGASSASMRLLR <b>PGSLENSAPRPPGLLALLSALGWLWWRM</b>                                      |
| LACHSEIN-DROS  | 335 | 100 | MWRPSISNCVWSTLLLAIFVQQTLAQRTPPTISYITQEIQKIDIGGTVEFDCSVQYAKEYNVLFKTDSDPVF<br>LSTGSTLVIKDSRFLRYDPNSSTYKLQIKDIQETDAGTYTCQVISTVHKVSAEVKLSVRRPPVISDNST<br>QSVVASEGSEVQMECYASGYPTTITWRRENNAILPTDSATYVGNLRIKSVKKEDEGRGTYCVADNGV<br>SKGDRRNINVEVEFAPVITVPRRLGQALQYDMDLECHIEAYPPAIVWTKDDIQLANNQHSISHFATA<br>DEYTDSTLRVITVEKRQYGDYVCKATNRFGEAEARVNLFEIIPVCPACGQAY <b>IGAEDVSATS</b> FALVG<br><b>ILAALLFAR</b>       |
| LSAMP-GALLUS   | 313 | 100 | MVARAQPDQRKQLPLVLLRLLCCLPTGLPVRSVDFTRGTDNITVRQGDTAILRCFVEDRSSKVAWLNRSG<br>IIFAGEDKWSLDPRVELEKRSPLYSLRIQKVDVYDEGSYTCVQTHHPKTSQVYLIVQVPPKISNISSDI<br>TVNEGSNVTLVCMANGRPEPVITWRHLTPTGKEFEGEYEELEILGITREQSGKYECKAANEVASADVQK<br>VRVTVNYPTITITESKSNEATTGRQALLRCEASAVPTDFEYRDDTRINSANGLEIKSTGSQSLLMVAN<br>VTEEHYGNITCVAANKLGVTNASLYLRPGTGR <b>VDNGSVSLAVPLWLLAASLLCCLSKC</b>                                    |
| LSAMP-GORILLA  | 330 | 100 | MVRRVQPDQRKQLPLVLLRLLCCLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNR<br>GIIFAGHDKWSLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCVQTHHPKTSQVYLIVQVPPKISNISS<br>DVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEYEELEILGITREQSGKYECKAANEVSSADV<br>KQVKVTVNYPTITITESKSNEATTGRQASLKCEASAVPAPDFEYRDDTRINSANGLEIKSTEGQSSLTVT<br>NVTEEHYGNITCVAANKLGVTNASLVLFKRVLPVPHPIQEIGTTVHFKQK <b>GPSVVRGINGSISLAVPLW</b><br><b>LLAASLLCCLSKC</b>   |
| LSAMP-RATTUS   | 330 | 100 | MVGRVQPDQRKQLPLVLLRLLCCLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNR<br>GIIFAGHDKWSLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCVQTHHPKTSQVYLIVQVPPKISNISS<br>DVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEYEELEILGITREQSGKYECKAANEVSSADV<br>KQVKVTVNYPTITITESKSNEATTGRQASLKCEASAVPAPDFEYRDDTRINSANGLEIKSTEGQSSLTVT<br>NVTEEHYGNITCVAANKLGVTNASLVLFKRVLPVPHPIQEIGTTVHFKQK <b>GPSVVRGINGSISLAVPL</b><br><b>WLLAASLFCLLSCC</b>   |
| LSAMP-FROG     | 341 | 100 | MVGRSQADRNLPLLLRLLCCLPTGLPVRSVDFNRSTNITVRQGDTAILRCFVEDRSSRVAWLNRSGI<br>IFAGDDKWSLDPRVELEKRSLLLEYSLRIQKVDVYDEGYPYTCVQTKQHTKTTQVYLIVQVPPKISNISADI<br>TVNEGSNVTLMCIA YGRPEPMITWRHLTPTAGTSPARDFEYEELEIQGITREQSGRYECKAANEVASA<br>DVKQVRVTVNYPTITITESKSNEATTGKQAILRCEASAVPAPDFEYKDDTRINSAQGLEIRNTGSRSVLM<br>VANVTEEHYGNITCVAANKLGITNTSLYLYKRVSPKPMASERGSNVHYQYKGP <b>PTIDSATSLAASL</b><br><b>WLMANLLFCLFCTC</b> |
| NEGR1-MUS      | 301 | 100 | MVLLAQGACCSNQWLAAVLLSLCCLPAGQSVDFPWA AVDNMLVRKGD TAVLR CYLEDGASKGAW<br>LNRSSIIFAGGDKWSVDPVRSISTLNKRDYSLQIQNVDTDDGPYTCVQTHHPKTSQVYLIVQVPPKI<br>YDISNDMTINEGTNVTLTCLATGKPEPVISWRHISPSAKPFENGQYLDIYGITRDQAGEYECSAENDVSFP   |

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|                  |     |          | DVKKVRVIVNFAPTIQEIKSGTVPGRSGLIRCEGAGVPPPAFEWYKGEKRLFNGQQGIIIQNFSTRSILTV<br>TNVTQEHEFGNYTCVAANKLGT <b>TNASLPLNQSSIPWQVFFMLKVSFLLVCIL</b>   |
| NTM-<br>CIONA    | 336 | 100      | MKWELLFGICVTVFVLTNANFIAPLNKNTVQGEDIVISCKISAGASYVKRSWTHKSTVIFANGNKL<br>KDPRTLLSNEHNEYTMQVKNVNTNDEGFYTCSLYLNLTYKSTMHLTVNVPQLTDVSEDKTVDEHDQ<br>VILRCIAFGKQPRTWRHLVPSADGVRATSKFLPLGVSVKRGSAGIYECTADNGVSSPVTSRILSVNYPP<br>EIDETLSPTTVLAPKGQTFYIECVTSFGPDPTFQWIMPDKTFKKQFSNERFNVLTTEKINTISKIFYFSP<br>QLSDYGNVTCIASNQMGVNTTIALSRKIVPPTRPPGDLFNRKWTGDGKGGRN <b>NSPLAKTLLSNHILIV<br/>IVTSVLAFL</b>   |
| NTM-<br>RATTUS   | 344 | 100      | MGVCGYFLPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA<br>WLNRSSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVSP<br>KIVEISSDISINEGNNISLTCIATGRPEPTVWRHISPKAVGFVSEDEYLEIQGITREQSGEYECASNDVAA<br>PVVRRVKVTVNYPYISEAKGTGVPVQKGLQCEASAVPSAEFQWFKDDKRLVEGKKGKVENRPL<br>SRLTFFNVSEHDYGNVTCVANKLGHNTASIMLFELNEPTSSTLLQEVKTTALTPWKGPVAVSEV <b>NGT<br/>SRRAGCIWLLPLLVLHLLK</b>   |
| OPCML-<br>GALLUS | 312 | 100      | MYHPACWIVFTATTALLFIPGVPVRSGDATFPKAMDNVTVRQGESATLRCTVDDRRVAVWLNRSSTIL<br>YAGNDKWSIDNRVILSNTKTQYSIKIHNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVPPQIVNISSDIT<br>VNEGSSVTLMLCLAFGRPEPTVWRHLSGKQGFVSEDEYLEITGITREQSGEYECASVNDVAVPDVRKV<br>KVTNYPYISNAKNTGASVQKGLQCEASAVPSAEFQWFKEDTRLANGLEGVRIESKGRSLTFFN<br>VSEKDYGNVTCVATNKLGNNTASIIYGPVAVHD <b>SGNAASRAAAGLCLWATLLARLLDF</b>   |
| CEPU1-<br>ANOLIS | 482 | 99.<br>9 | MFLVHLGTDGHDLANVDMSYGRLRLAKGSTLPSLEPSSSTGQHLVDADDMEVMEAIRMWKPSLPQ<br>LFTMNGQILTSVIFTMNVSWSGEKFREEVADSLCLSAFAASFQSKGGIRPESKPSFLLLTALWRGKRCL<br>LEGKARLWTGGEGEEGEGEHPADLEHEWTSGEDAHPALLGRLGRDGLRPLPRCIVDNRVTRVA<br>WLNRSSTILYAGNDKWCLDPRVELIANTKTHYAIRINDVDVYDEGPYTCVQTDNHPKTSRVHLIVQVPP<br>KIVEISSDISINEGNNISLTCIATGRPDPTITWRHISPKAVGFVSEDEYLEITGITREQSGEYECASNDVAT<br>PVVRRVKVTVNYPYISDNTKGTGVPVQKGLQCEASAVPSAEFQWYKDDKRLTEGQKGLKVENKAFF<br>SRLTFFNVSEQDYGNVTCVAYNQLGNTNASIILYEISEPTSSTLFQETTAVQTPWKGPVAVHDGN <b>SGGS<br/>RAVCVWLLPFLHLLK</b> |
| IGLON5-<br>DANIO | 307 | 99.<br>9 | MSCAMLRHALALLLALLWKGPSGAQAEEFGLHPDNITVLEGESVVLRCIDEEVTHKAWLNRSNIF<br>GTDKWSLDSRVSLNNNSDFSIRIERVMVADEGPYTCVQARNKPRTAHVYLIVQVPARIVNISQDKSV<br>NEGEDVNLFCVAVGRPEPTITWKDFKYGLLNEGEFLEITEIKRHAEDFECITNNGVAPPDTRKVKVTVN<br>YPIITDVKNMPAQVGKTAILRCEAMAVPTASFEWYRDDRRPVESDNTLKIKNEKTRSLLLFTNVTEKH<br>FGNYTCFASNRLGASNAMLLFRPGAVY <b>GAAASLNGRLSGVGLWFCLSSISVLMKV</b>  |
| IGLON5-<br>MUS   | 314 | 99.<br>9 | MPPPAPGARLRLAAAALAGLAVISRGLLSQSLEFSSPADNYTVCEGDNATLSCFIDEHVTRVAWLNRS<br>NILYAGNDRWTS DPRVRLINTPEEFILITQVGLGDEGLYTCVQTRHQPYYTQVYLIVVHPARIVNISSP<br>VAVNEGNNVLLCLAVGRPEPTVWRQLRDGFTSEGEILEISDIQRGQAGEYECVTHNGVNSAPDSRRV<br>LVTNYPPTITDVTSARTALGRAALLRCEAMAVPPADQWYKDDRLSSGSAEGLKVQTERTRSMMLF<br>ANVSARHYGNVTCRAANRLGASSAMRLLRPG <b>LENSAPRPPGPLTLLSALSWLWWRM</b>  |
| LSAMP-<br>ANOLIS | 287 | 99.<br>9 | MEKIPKISSFILCRCFIEDKSSKVAWLNRSIIIFAGQDKWSDPRVELQQLSLEYSRLIQKVDVYDEGSY<br>TCSVQTLHHPKTSQVYLIVQVPPKISNISSDVTVNEGSNVTLCMANGRPEPVITWRHLTPTGREFEGEE<br>EFLEILGITREQSGKYECKAANEVSTADVQVVRVTVNYPPTITESKSNESATGRPVSLKCAASAVPTPDF<br>EWYRDDARINNANGLEIRSTGSQFLTVANVTEHYGNVTCVATNKLGITNASLFLYKILPTLPNPFPG<br>PGTGM <b>AGNGSMCLAVPLWLLAASLLCLLSC</b>   |
| LSAMP-<br>DANIO  | 308 | 99.<br>9 | MSCLWIHSVFIPGFLLFGFEGFPVISVESQRSTDNITRQGDVVIRCYVDDKVSVAWLNRSNIIFAGED<br>KWSLDPRVELVTQGLEYSRLIQKVDVDEGPYTCVQTRHQPYYTQVYLIVQVPAIYKVEDITVNEG<br>SNVALTCLANGRPDAITWRLLNPSAEALDVGEYLEISGVRSQAGRYECKASNDVSTPDVKYVNVVV<br>NYPYIKDVRSETAVGQAGVLHCEASAVPQEFVWYRDERLSSQSLTIQVSGSRTVLLVANVTEED<br>YGNVTCVATNRLGVHNASVFLYKPGMGR <b>DINSAGCICQSLWLLLCVSSALLQC</b>  |
| NEGR1-<br>DANIO  | 331 | 99.<br>9 | MDIMIAVQDACVSGQWLTAIILSLCCFLPCLPAGQTVDYTTSSVSVSRQGDALLRCYLLDGISKGA<br>WLNRSIIYAGNDKWSGDPRVSVISNVGDKHEYSLQIQKVDVDEGVYTCVQTRHQPYYTQVYLIVQVPAIYK<br>PKIYDISSDITVNEGSNVSILCAASGKPEPKISWRHISPSARKYESGEYLNITGISRDQAGDYECGAENDIA<br>SPDTKTVRVTNFPFAIHEMKSHGVRPGQVALLRCEAAA VSPVFEWYKGEKINMGQIVINNLSRS<br>VLTVKNMTQDRYGNVTCVAVNRLGTANASVPLNPIIEPTTSAVSSPAS <b>NPAMYGSTGGAEVLLACWY<br/>LILALSSLVTVY</b>  |
| NEGR1-<br>RATTUS | 325 | 99.<br>9 | MVLLAQGACCSNQWLAAVLLSLCCLPAGQSVDFPWA AVDNMLVRKGDVAVLRCYLEDGASKGAW<br>LNRSSIIIFAGGDKWSVDPVRSISTLNKRDYSLQIQNVVDVDDGPYTCVQTRHQPYYTQVYLIVQVPAIYK<br>YDISNDMTINEGTVTLTCLATGKPEPAISWRHISPSAKPFENGQYLDIYGITRDQAGEYECASNDVSP<br>DVKKVRVVNFAPTIQEIKSGTVPGRSGLIRCEGAGVPPPAFEWYKGEKRLFNGQQGIIIQNFSTRSILTV  |

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|               |     |      | VTNVTQEHFGNYTCVAANKLGTNASLPLNPPSTAQYGITGSACDLFSCWSLALTLSSVISIFYLKNAILO  |
| NTM-HUMAN     | 344 | 99.9 | MKTIQPKMHNSISWAIFTGLAALCLFQGVVRSQDATFPKAMDNTVTRQGESATLRCTIDNRVTRVAW<br>LNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVSPKI<br>VEISSDISINEGNNISLTCIATGRPEPTVTRWRHISPKAVGFVSEDEYLEIQGITREQSGDYECASNDVAAP<br>VRRVKVTVNYPPISEAKGTGVPVQKGTQCEASAVPSAEFQWYKDDKRLIEGKKGKVENRPFSL<br>KLIFNVSEHDYGNITCVASNKLGHNTASIMLFELNEPTSSTLLQEVKTTALTPWKGPVAVSEVSNNGTS<br>RRAGCVWLLPLLVLHLLKLF      |
| NTM-MUS       | 344 | 99.9 | MKTIQAKMHNSISWAIFTGLAALCLFQGVVRSQDATFPKAMDNTVTRQGESATLRCTIDNRVTRVAW<br>LNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVSPKI<br>VEISSDISINEGNNISLTCIATGRPEPTVTRWRHISPKAVGFVSEDEYLEIQGITREQSGEYECASNDVAAPV<br>VRRVKVTVNYPPISEAKGTGVPVQKGTQCEASAVPSAEFQWYKDDKRLIEGKKGKVENRPFSLK<br>LTFNVSEHDYGNITCVASNKLGHNTASIMLFELNEPTSSTLLQEVKTTALTPWKGPVAVSEVSNNGTSR<br>RAGCIWLLPLLVLHLLKLF     |
| NTM-FROG      | 345 | 99.9 | MDMQLQARMLHSVPVWIFSGMAVLCCLLQGVVRSQDAGFPKAMDNTVTRQGDSAILRCTVDNRVTR<br>VAWLNRSSTILYTGNDKWSIDPRVLLANTKSQYSIEIQNVVDIYDEGPYTCVQTDNHPKTSRVHLIVQV<br>PRIVDISSIAVNEGSNVSLICIANGRPEPVVNWRYLSPKARGFVSEDEYLEITGITREQSGIYECASNDVS<br>APDVRVKVTVNYPPIYILDAQNIGAPLGHGILQCEASAVPAADFFWYKEDKRLSDSWRGVVENRETI<br>SRVTFNVSEQDYGNITCMAKNLLGHSNASILFELFQSTSSPLLQEESTAALTPWKGPVAVHDGNSGST<br>QCSFCAPLILLILLPFSLLPPAQF |
| OPCML-DANIO   | 291 | 99.9 | MGVPARSGDSYLKDNITVTRQGDSAVLKCSVDNKVSRVAWLNRTTILFTGNEKWSLDPRVLLNTAVN<br>EYSIKILNVNLYDEGPYVCSILTNNKPESTKVHLIVQVPARIVNVSTDVSNVNEGSNVSLMCLAIGRPEPSIL<br>WKFRSSKGNRIVTEGEYVEMTGTIKDMSGSYDCITSNDISPPDVRTVQTVNYPVISRARSTGTAVGQK<br>GVLWCEASAVPLADFQWFKGERRILNGFNGVKIENKQKQSMLETFNVSEEDYGNITCVAINTLGITNAS<br>IILYGPVGAHVDVNAALSPTCSLLLLTLLTLLSLSKF  |
| OPCML-FROG    | 317 | 99.9 | MARGVAAAHLVHHVCWMFGAALTVLLSITGVPVRSQDAGFPKAMDNTVTRQGDSAILRCTVDNRVTR<br>VAWLNRSSTILYTGNDKWSIDPRVLLANTKSQYSIEIQNVVDIYDEGPYTCVQTDNHPKTSRVHLIVQV<br>APQILNISSDITVNEGSTVALRCLATGRPEPAVTRWRHFTGKSHRFVSDDEYLEITGITRDQSGQYECASAN<br>DVSAPDIRKVRVTVNYPPIYISDTRNTGASLGQKILRCSASAVPLAEFQWYREETRLANGLDGVRIENK<br>DHMSILTFNVSEKDYGNITCVASNKLGNASVILYAGPGAHNRSSSASAAIAATCLWCSILYSLTTF                           |
| OPCML-GORILLA | 331 | 99.9 | MGVCGYFLPWKCLVSVSLRLLFLVPTGVPVRSQDATFPKAMDNTVTRQGESATLRCTIDDRVTRVA<br>WLNRSSTILYAGNDKWSIDPRVILLVNTPTQYSIMIQNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVPPQ<br>IMNISSDITVNEGSSVTLCLAIGRPEPTVTRWHLVKEGQGFVSEDEYLEISDIKRDQSGEYECALNDV<br>AAPDVRVKVITVNYPPYISKAKNTGVSQKILSCEASAVPMAEFQWFKETRLATGLDGMRIENK<br>RMSTLTFNVSEKDYGNITCVATNKLGNNTASITLYEISPSSAVAGPVIDGVNSASRALACLWLSGT<br>LLAHFFIKF                       |
| OPCML-HUMAN   | 331 | 99.9 | MGVCGYFLPWKCLVSVSLRLLFLVPTGVPVRSQDATFPKAMDNTVTRQGESATLRCTIDDRVTRVA<br>WLNRSSTILYAGNDKWSIDPRVILLVNTPTQYSIMIQNVVDVYDEGPYTCVQTDNHPKTSRVHLIVQVPPQ<br>IMNISSDITVNEGSSVTLCLAIGRPEPTVTRWHLVKEGQGFVSEDEYLEISDIKRDQSGEYECALNDV<br>AAPDVRVKVITVNYPPYISKAKNTGVSQKILSCEASAVPMAEFQWFKETRLATGLDGMRIENK<br>RMSTLTFNVSEKDYGNITCVATNKLGNNTASITLYEISPSSAVAGPVIDGVNSASRALACLWLSGT<br>LLAHFFIKF                       |
| IGLON5-RATTUS | 310 | 99.6 | IECLSQLALPQLSRLSNPLPSAGLLSQSLEFSSPADNYTVEGDNATLSCFIDEHVTRVAWLNRSNLYAG<br>NDRWTSVDRVLLINTPEEFSILITQVGLGDEGLYTCFQTRHQPYTTQVYLIVHVPARIVNISSPVAVNE<br>GGNVNLLCLAVGRPEPTVTRWRQLRDGFTSEGEILEISDIQRGQAGEYECVTHNGVNSAPDSRRVLTVN<br>YPTITDVTARTALGRAALLRCEAMAVPPADFQWYKDDRLLSSGSAEGLKVQTERTRSMILLFANVSA<br>RHYGNITCRAANRLGASSASMRLLRPGSLENSAPRPPGPLTLLSALSWLWWRM   |
| NTM-GORILLA   | 280 | 99.6 | MDNVTVTRQGESATLRCTIDNRVTRVAWLNRSSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVY<br>EGPYTCVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRWRHISPKAVGFVSE<br>DEYLEIQGITREQSGDYECASNDVAAPVRRVKVTVNYPPISEAKGTGVPVQKGTQCEASAVPSA<br>EFQWYKDDKRLIEGKKGKVENRPFSLKLIFNVSEHDYGNITCVASNKLGHNTASIMLFGPVAVSEVSN<br>NSTSRAGCVWLLPLLVLHLLKLF   |
| NEGR1-GALLUS  | 329 | 99.5 | MVPLVRGAGGSHQWLAAVLLGLCCLLPAGRLAAPPDGFPGAAADSLVVRKGDVAVLRCYLEDGASK<br>GAWLNRSIIIFAGSDKWSVDRVSIATANRREYSLQIQDQVVDVTDGDPYTCVQTDHTPRMQVHLTVQ<br>VSPKIFRISSDIVNEGSNVTLVCLATGKPEPISWRHISPAKPFESGQYLDIYGITRDQAGEYECASND<br>VSPVDVKKVKVTVNFAPTIQELKSSGVMGGNGLIRCEGAGVPAVFEWYRGERKLISGQQGITIKNYS<br>TRSLTNTVTEEHFGNYTCVAANKLGMTNASLPLNPPSTAQYGITGDAEVLFSWYLVTLSSLTISIFY<br>LKNILH                         |

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| OPCML-RATTUS  | 322 | 99.4 | MGVCGYFLFPWKCLVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTIDDRVTRVA<br>WLNRSSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVDVYDEGPYTCVQTDNHPKTSRVHLIVQVPPQ<br>IMNISSDITVNEISSVTLCLAIGRPEPTVTRHLSVKEGQGFVSEDEYLEISDIKRDQSGEYECALNDVA<br>APDVRKVKITVNYPPYISKAKNTGVSQKILSCEASAVPMAEFQWFKEDTRLATGLDGVRIENKGR<br>STLTFNVESEKDYGNVTCVATNKLGNNTASITLYGPGAVIDGVNSASRALACLWLSGTTFFAHFFIKF  |
| NTM-GALLUS    | 330 | 99.2 | MAQAKMQHPVSWVIFAGMAALLLQGVVRSVGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVAW<br>LNRSSILYAGNDKWCLDPRVLLANTKTQYSIQIHDVDVYDEGPYTCVQTDNHPKTSRVHLIVQVSPK<br>ITETSSDISINEGGNVSLTLCIATGRPDPTITWRHISPKAVGFISEDEYLEITGITREQSGEYECASNDVAAP<br>VVQRKVKITVNYPPYISDAKSTGVPVQKILMCEASAVPSADFQWYKDDKRLAEGQKGLKVENKAFF<br>SRLTFNVESEKDYGNVTCVASNQLGNNTASMLYEETTTALTPWKGPVAVHDGNSGAWRRGSCAWLL<br>ALPLAQLARQF                                  |
| NEGR1-FROG    | 357 | 99.1 | MDMMLLVQGAACCSNQWLAADVLSLCLLPSCLPAGQSMDFQWPAVDNLVVRQGETAMLRCFLEEG<br>ASKGAWLNRSSIFAGGDKWSVDPVRSIATSSKQEYSLRIQKVDVSDDGYPYTCVQTEHSPRTLQVHLTV<br>HVSPIYDISSDMTVNEGTVSLICLATGKPEPISWRHISPSAKQFSGQYLDIYGITRDQAGDYECASAE<br>NDVSFPDVKKVKVTVNFAPITILEITPTGVSGLRGTGLRRCETAAVPAVFEWYKGEKLTNGQRGIRIQNY<br>NTRSILTVSNVTEEHFGNYTCVAVNKLGTNSASPLNQIIEPSTTSPVTSSAKYSVKHYARSSSDKPHYAA<br>PSTAQYGITGRAEILFSCWYLVLTSSSFTSIYLNKNAIQ |
| OPCML-ANOLIS  | 289 | 98.6 | MDNVTVKQGESATLRCTVDDRVTVAWLNRSSTILYAGNDKWSIDDRVILTNTKTQYSIMIHNDIYD<br>EGPYTCVQTDNHPKTSRVHLIVQVPPQIINITSIAVNEGSSVTLCLAFGRPEPTVTKHLSGKGGQFI<br>SDDEYLEITGITRDQSGEYECAAVNDVAAPDIRRVKVTVNYPPSISNPRNTGVSQKILRCEASAVP<br>AEFQWFKEDTRLANGLDGVRIENKGRMSTLTFNVESEKDYGNVTCVAINKLGNNTASIILYEISQPTALA<br>GPGAVIDGNSAASRAMACLWLSGTLFLYFLLKF  |
| NEGR1-GORILLA | 266 | 89.1 | CYLEDGASKGAWLNRSSIFAGGDKWSVDPVRSISTLNKRDSLQIQNVDTVDDGPYTCVQTHPTPT<br>MQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPISWRHISPSAKPFENGQYLDIYGITRDQA<br>GEYECSAENDVSFPDVKVKVVNFAPITIQEIKSGTVTPGRSGLIRCEGAGVPPPAFEWYKGEKLFNG<br>QQGIIIQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTNASLPLNPPSTAQYGITGSADVLFSCWYLVLT<br>LSSSFTSIFYLNKNAIQ   |
| OPCML-MUS     | 290 | 71.2 | MDNVTVRQGESATLRCTIDDRVTVAWLNRSSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVDVYDE<br>GPYTCVQTDNHPKTSRVHLIVQVPPQIMNISSDITVNEGSSVTLCLAIGRPEPTVTRHLSVKEGQGFV<br>SEDEYLEISDIKRDQSGEYECALNDVAAPDVRKVKITVNYPPYISKAKNTGVSQKILSCEASAVPM<br>AEFQWFKEDTRLATGLDGVRIENKGRISTLTFNVESEKDYGNVTCVATNKLGNNTASITLYEISSSAVA<br>GPGAVIDGNSASRALACLWLSGTTFFAHFFIKF  |
| LSAMP-MUS     | 316 | 60.6 | MVGRVQPDRKQLPLVLLRLLCLLPTGLPVRVDFNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRS<br>GIIFAGHDKWLDPRVELEKRHALEYSLRIQKVDVYDEGSYTCVQTHPEPKTSQVYLIVQVPPKISNISS<br>DVTVNEGSNVTLCMANGRPEPVITWRHLTPLGREFEGEEYEILGITREQSGKYECKAANEVSSADV<br>KQVKVTVNYPTITESKSNEATTGRQASLKCEASAVPAPDFEYRDDTRINSANGLEIKSTEGQSSLTVT<br>NVTEEHYGNVTCVAAANKLGTNASLVLFKSKYAKTEPDSMQVIEFLHIDLKSIRHPLKVNPIQK  |
| NEGR1-HUMAN   | 297 | 42.5 | MDMMLLVQGACCSNQWLAADVLSLCLLPSCLPAGQSVDFPWAAVDNMMVVRGDTAVLRCYLEDG<br>ASKGAWLNRSSIFAGGDKWSVDPVRSISTLNKRDSLQIQNVDTVDDGPYTCVQTHPTPTMQVHLT<br>VQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPISWRHISPSAKPFENGQYLDIYGITRDQAGEYECSA<br>ENDVSFPDVKVKVVNFAPITIQEIKSGTVTPGRSGLIRCEGAGVPPPAFEWYKGEKLFNGQQGIIIQ<br>FSTRSILTVTNVTQEHFGNYTCVAANKLGTNASLPLNHKKEVSS   |
| NEGR1-ANOLIS  | 290 | 34.8 | MPWSVDFPGTAVDSLVRKGDVAVLRCLYLEDGASKGAWLNRSSIFAGGDKWSVDPVRSIATANKREY<br>SLQIQDQVSDDGYPYTCVQTHPTPTMQVYLVTKVSPKISHISNDIVVNEGSNVTLCIATGKPDPSIS<br>WRHISPSAKPFENGQYLDIYGITRDQAGEYECSAENDVSVPDVKKVKVTVNFSPITQEIKSSGVTGGPG<br>FIRCESAGVPSPAFEWYKGERRLINGQQGITIKSFSRSFLNFNNVTEEHFGNYTCIAANKLGTNASLLL<br>NPPSTTQLGITGGAEVLLSCWYLVLTSSYSIMYLNKNIILQ   |
| LSAMP-HUMAN   | 331 | 11   | MVRRVQPDRKQLPLVLLRLLCLLPTGLPVRVDFNRGTDNITVRQGDTAILRCVVEDKNSKVAWLNRS<br>GIIFAGHDKWLDPRVELEKRHSLEYSLRIQKVDVYDEGSYTCVQTHPEPKTSQVYLIVQVPPKISNISS<br>DVTVNEGSNVTLCMANGRPEPVITWRHLTPTGREFEGEEYEILGITREQSGKYECKAANEVSSADV<br>KQVKVTVNYPTITESKSNEATTGRQASLKCEASAVPAPDFEYRDDTRINSANGLEIKSTEGQSSLTVT<br>NVTEEHYGNVTCVAAANKLGTNASLVLFKRVLPITPHPIQEIGTTVHFKQKQVQSSIHLDTESNLFHLGVE<br>NLDLAC                                   |

**Table 2 supplementary. Functional Divergence Parameters –Test I**

|                       | IGLON<br>5/NEG<br>R1 | IGLON5/IN<br>VERTEBRA<br>TES | IGLON<br>5/LSA<br>MP | IGLON<br>5/OPC<br>ML-<br>NTM | NEGR1/IN<br>VERTEBR<br>ATES | NEGR<br>1/LSA<br>MP | NEGR1<br>/OPCM<br>L-NTM | INVERTEB<br>RATES/LS<br>AMP | INVERTEB<br>RATES/OPC<br>ML-NTM | LSAM<br>P/OPC<br>ML-<br>NTM |
|-----------------------|----------------------|------------------------------|----------------------|------------------------------|-----------------------------|---------------------|-------------------------|-----------------------------|---------------------------------|-----------------------------|
| MFE<br>Θ              | 0.44                 | 0.43                         | 0.46                 | 0.44                         | 0.11                        | 0.23                | 0.61                    | 0.10                        | 0.44                            | 0.35                        |
| MFE<br>SE             | 0.127                | 0.179                        | 0.128                | 0.126                        | 0.170                       | 0.119               | 0.138                   | 0.168                       | 0.184                           | 0.126                       |
| MFE<br>RX             | 0.312                | 0.236                        | 0.301                | 0.315                        | 0.362                       | 0.418               | 0.214                   | 0.365                       | 0.228                           | 0.355                       |
| MFE<br>RMA<br>X       | 0.563                | 0.420                        | 0.566                | 0.567                        | 0.407                       | 0.54                | 0.550                   | 0.409                       | 0.410                           | 0.552                       |
| MFE<br>z <sub>S</sub> | -3.950               | -2.594                       | -4.148               | -3.977                       | -0.663                      | -2.146              | -5.034                  | -0.645                      | -2.544                          | -3.142                      |
| Θ <sub>ML</sub>       | 0.400                | 0.388                        | 0.332                | 0.1936                       | 0.013                       | 0.176               | 0.458                   | 0.035                       | 0.483                           | 0.188                       |
| α <sub>ML</sub>       | 0.671                | 1.765                        | 0.627                | 0.763                        | 2.026                       | 0.696               | 0.857                   | 2.132                       | 2.019                           | 0.822                       |
| Θ <sub>SE</sub>       | 0.1021               | 0.142                        | 0.091                | 0.066                        | 0.165                       | 0.110               | 0.099                   | 0.187                       | 0.150                           | 0.081                       |
| LRT<br>THE<br>TA      | 15.40                | 7.374                        | 13.13                | 8.417                        | 0.006                       | 2.538               | 21.242                  | 0.035                       | 10.35                           | 5.36                        |