

Supplementary material

Dataset S1. Annotated amino acid sequences of *Glossina morsitans morsitans* ORs and GRs.

>GmmOR1|Orco GMOY005610 (TMP007718) scf-648683 14760:27560 reverse

MFKQTMANDLQPGKYVGLVADLMPNIKLMKFSGLFMHAFTSGSAVGKKIYSSIHLLALILL
QFLSILINMALNADEVNELSGNTITVLFTHSITKFIYLACSQKNFYRTISIWNVNTHP
LFAESDARYHSIALAKMRKLFFLVMLTTVTSIAIAWITLFFGESVKFAVDKENNSTMTVE
IPRLPIKSFYPWDASSGISYIVSFIYQAYFILFALSHANLCDVLFCSWLIFACEQLQHLK
SIMKPLMELSASLDTFRPDSGALFRSLSAHKAELIENEEKEPPPSNGLDLSGIYSSKAD
WGAQFRAPSTLQTFNNNNPNGLTKKQEMMVRSIAIKYWVERHKHVVRLVAAIGDTYGVALL
LHMLTATIKLTLLAYQATKITGVNVYALGVVGYLGYSLAQVFHFCIFGNRLIEESSVME
AAYSCHWYDGSSEAKTFVQIVCQQCQKAMSISGAKFFT VSLDLFASQWSHISWCWCNLNE
VIASFAIKFSSSSSLRPSLITKRNHGECISKISYLVYLYFV

>GmmOR2 GMOY005796 (TMP007907) scf-648756 29714:32260 reverse

MEYRAHLETNTAFRYHWLVWQLTGIIQPRYFSTSLYRLYTVLVNIVLTVLFLPLTFVINVF
FSKNLQQLCENLIITLCDITANLKFLNVFLVRKELQQIKIILECLDKRLNTEEEYRQLKR
AIRTAQLSFCIFLVISTTGTTLSLFMVLYSEERSLLFPAWYGLDWQKNDLAYAVCFTYQL
VALVVQAIQNVANDSYPPAYLIILTSHMRNLELRVRSVGLSPANNKENMFLSEKEQQLDF
KKFNDCIEDFIQINRLYDLIQKILSKACLAQFICTALVQC VVGLHILYLLDESDDYGAQI
LSFIFFLAVTMEVFIICYFGHYMSAQSALIDAFYECGWIPQTLAFRRNLIITLMRTQRY
AILYAGSYIPVDLPTFLLLMKYAYSTFTLLLRFK

>GmmOR3 GMOY004772 (TMP006862) scf-648228 109437:110684 reverse

MVVTKIHTWKAFEYHWRLWTFGLKPPRNSVWFKPYVAYAILLNISVTFPPCTLIINL
ILAKNMNEVCENLYHTITDVVCNIKFLNMFLVRKLLQINQILKRLDMRAQTLEEITELQ
RGVNSARNCFKIVGRFFCVALITSQLVAYLSPERILMYPWFWDWRASKMNFYAHSYQ
LYGLTLQTAQNLGSDTYPQAYLVVLIGHIKALSLRIKALGSEVTPFSTSDDEFKKNENH
LYRELVDCIIDHETINDLFRIVQQGISSTCLAQFFCTGLAQCTMGVYTFYVGLDYSKLPN
LIAYFSAVTAEIFILCYYGDLFCQANEKLINSIYSCNWVDPHRFLLQRSQKINTVMAGNI
IPVSLSTFVTVKTESYRLHLHFKSHIM

>GmmOR4 TMP_Or4 scf-642438 111181:112437 forward

MFLDTLQFFRNWLSWRLLGIVLPKGEQNHKLIKYLLWSTIVNVVATFLFPLHLLLGIFQ
EQPQSTRFESVAICVTSIATSLKFIIYARKLQHVKQMGKLFQRDLARISNDNERQFYQKH
IRRNVIQITMFIVVYISVGITVTVAFIFSQERRLFYPGWLPFDWHRSIKYMAALGFQL
ISIFFQILQNFANDCFTPALCLLSGHIELLYMRVANIGYVNRVAYQQNRNRELNECVL
DQKHLYQLFDVIQSIISWPMFLQFLASTVNMCMAMVTLLFFVTDILERIYYVYFAAMCL
QIFPTCYYGSDFEIKFERLHYAVFSSNWTEGTQCFKRHMMLFTERALRETRAMAGGVFRI
HLDTFFATIKGAYSLFAVVITMKN

>GmmOR5a GMOY012018-PA (TMP002414) scf-639717 1: 6297 MW: 51399.66

SELDKRVSTADECDYFIRQHQRKANSIAKIFFFVYLG TNSFAFMGAIVDQRLMAPAWFPF
DWKSSSTLYWSALLYQFIGLNMLIMQNLVNDTVGPMSLCLLSGHVHLLAMRVARIGYNKR
KSQKYHEDELKLCIEDHQKLLKAFTLLESSMSWLQFILFFTSGLNTCLGVNFLFYSRIL
YDYIYYGCFLALGVEVFPCYFYGSVLLLEEFKHLPPYAIFSSNWVEQSRNYRQNTTIFLEM
ALKSVTMLAGGIVETNLDSFFAIYKAAYS LFTVILTMKIGYNKRKSQKYHEDELKLCIED
HQKLLKAFTLLESSMSWLQFILFFTGGLNTCLGVNFLFYSRILYDYIYYGCFLLAIGME
VFPCYFYGSVLLLEEFKHLPPYAIFSSNWVEQSRNYRQNTTIFLEMALKSVTMLAGGIVEIN
LDSFFAIYKAAYS LFTVILTMK

>GmmOr5b GMOY012018-PA (TMP002414) scf-639717 - 1: 6297 MW: 35691.12

SELDKRVSTADECDYFIRQHQRKANSIAKIFFFVYLG TNSFAFMGAIVDQRLMAPAWFPF

DWKSSSTLYWSALLYQFIGLNMLIMQNLVNDTVGPMSLCLLSGHVHLLAMRVARIGYNKR
KSQKYHEDELKLCIEDHQKLLKIGYNKRKSQKYHEDELKLCIEDHQKLLKAFTLLESSMS
WLQFILFFTGGLNTCLGVVNFLFYSRILYDYIYYGCFLLAIGMEVPCYFYGSVLEEFK
HLPYAISSNWVEQSRNYRQNTTIFLEMALKSVTMLAGGIVEINLDSFFAIYKAAYSLFT
VILTMK

>GmmOr5c GMOY012018-PC (TMP002414) scf-639717 - 5069: 6297 MW: 33056.258
MKIEWWSKLDSTVAYGRFWSFCRILGVADFRYKALSQFYVICLTLFVTVYCPHLLIGLL
MLTDAGDFFKNFSMTLTSVCSLKYFFLRLNLNKIHQLIKIYSELDKRVSTADECDYLIG
YNKRKSQKYHEDELKLCIEDHQKLLKAFTLLESSMSWLQFILFFTGGLNTCLGVVNFLFY
SRILYDYIYYGCFLLAIGMEVPCYFYGSVLEEFKHLPYAISSNWVEQSRNYRQNTTI
FLEMALKSVTMLAGGIVEINLDSFFAIYKAAYSLFTVILTMK

>GmmOr5d |GMOY012018-PD (TMP002414) scf-639717 - 1: 902 MW: 31461.035
SELDKRVSTADECDYFIRQHQRKANS AIKIFFFVYLGTSFAFMGAIVDQRLMAPAWFPF
DWKSSSTLYWSALLYQFIGLNMLIMQNLVNDTVGPMSLCLLSGHVHLLAMRVARIGYNKR
KSQKYHEDELKLCIEDHQKLLNSMSWLQFILFFTSGLNTCLGVVNFLFYSRILYDYIYYG
CFLALGVEVPCYFYGSVLEEFKHLPYAISSNWVEQSRNYRQNTTIFLEMALKSVTM
LAGGIVETNLSFFAIYKAAYSLFTVILTMKIGYNKRKSQKYHEDELKLCIEDHQKLLKY
LKYSYI

>GmmOR6 GMOY009475 (TMP011670) scf-651846 662444:668878 reverse
MLLALSRGVGVKTQSSQASEYLFNVINFLAQDFHRKWTFGFFFQSFVANGTVVLFMPILF
NLSYLNDSMQFDLGQLFTSVQAANICAIPKIFITMQLYMKNLHRINEMLNILDGRCKHP
EEFSKLRHCAITGNRIYVGAIIVYFSYSISTCMGFMLTGQAAYNIYIPGINWRNSLFEFV
IQGLVEFASMNLICLHQTVDYSYSGIYLYIIRIHIQILNERVKRLGSLNKNNEKQSYEEL
IQSILDHKLILREGMALKSSRDNQYPLVAAISPMSLTIFVQFAITAAMLATTMINISFF
SNVVGRIASIFYIILVFAQSSLCYQATCLVSDADELPVSIFHCQWVEQGYRFRKMIIYF
MVNTQKPITFTAGKLFVNMASVLSNY

>GmmOR7 TMP_Or7-RA scf-651846 655714:658243 reverse
MESVIPNTVEDQOSGERHSINKGRFDSQLNINVTNNAFDRNARTMHGTMFLFNGFRF
LGVYMPEKNRLFYLIWSFLINSTVTVYLPVAFILSFVKISGDDLQIGNLLTSAQVAINVV
GCSVKIILMGFLLPKLLSTEKFLNRLDERCRTAEEELASINKFTKQGNRFVVLFSVAYWSY
STSTCISAVAFGRPLPNIYNPFDDHHQSIGHFILSVLMEMTLVNIACFQQVVDSDSYAVIY
VNILRTHVDLLLKRIKRLGLTVSMSHEQTYEELKLCIIDHKYIIQFTITATILGTTLINI
LLFATNFASIVASCFYVLAVVVEIFPLCYTQYLMDESNLLAEVVFHSNWMEQNLPYQKM
LIFFMQRSQRVMEFTAGKLPITLNSFLSVSES

>GmmOR8 TMP_Or8-RA scf-651846 - 655986:662305 reverse
MLVDTVADYKSPISSFEATTYLFRIYRVLGINKPQRHKNLYIFYTIILNGVVNLFQPIAF
TMNYFTNELVSKLGSLLTSIEIVINVYGCTAKFIIIWLLPRSNATVQLLKKLDERCQAP
DELELLKSIKFGRLVVVVLAVSYLSYSVSQFICSLIAGHPYGLYIPYINWKRSFWEFL
VASSIEFLLMNVSCIVQASNDAYPIIYNILRTHIKILLKRLNRLGTGADKSQDEHLEEL
KLCIKDHKNLNRFAAFSLFETIAPIISTTVFVQFMITAAIALTINMLFFTTNISAVA
NSCVYIADLVLEIFPICYYANCLIDDNDLLSMEIFHSAWPEQNKIYRKMLIVFMQRSQQS
MSLTAGKMF PINLNTFINLQYRFIYNFYNNICAIYNNCHHIGYDSY

>GmmOR9 TMP_Or9-RA scf-652157 136730:138889 reverse
MLTFRKFFKMAHFRGDGPPPCTRDAVLYLFRGITIIGLLTPASNKKCFYVWSLFINSLVT
LYMPVGFLLSFIMRLSSFSPSEFFTSLQISINCVGASLKLFFVSLMYKRLIKATKYMDRL
DKRPIDEQGEFTLRQAVAFSNCSSLLFTLLYLSYSSSTFLSSVINRRPPYQIYNPVIEWR
NSTRNFIIQSAIEYVMIDVHCYQQALLDAYPVIYIMIRAHHLHLSRRISQLGKDDKLLK
NQRYEELVQCVDLHKNIMQLYNLFSFVISGTMFVQFLIIGILGVTTIHIVLFANFFAIV
ASLFYVASILAETFPESYLANSLMDDSDLSLAIFHSGWFNEEPYKQVVVFFLQHTQKT

LVLTAMKIFPITMNSNINVVVKFAFSVYTLISQMDLRQKLDKDSVAGQEA

>GmmOR10 TMP_Or10 scf-644232 131824:133273 forward

MDGREHCRYLKTIFYKHQCWVFRFLFGLWKLSDMTRSHQLLHALYFNILTIVVLSLDASC
IMQLVIKAGDLNEVIEVFSIFATALAVLAKFLSIKMKNHLYRQWCEIVESSTFRPNNERE
IQLFQQSERLARLIRNAYCVLSLIALNMLIFIVDDRGLPLSVYSPFDMNRKWGYLSTYGY
QYIAASICCYLNI AFDSL SASFLIHLKGQMDILCDRLKNFGKYSECNNDHKITEELKNCI
KYYEEILKVAHLIEDLISLPISIQIICSVLVMVANFFGMAFLAEPGDYAYFFKMLIYQLC
MLSQIYILCYFPNEVTDRSQTISRSLYSAEWFWSQMNRKLTLLMMDRFDVPIRFRSIIP
TYSFNLA AFTSVFTTKRQQNNILLCFIKKHEQLKYFSANLKLKRNLRRTTKSLIGPKSNN
RETSTADVKERN SWTEDELDEYS

>GmmOR11 GMOY0110761 (TMP012981) scf-652156 1267206:1269387 reverse

MDNSAESVKMLYSKQILIFRLVSIWDLAANAGYYKRLAFAVYFWIVAIFLVALFALLII
QIFCDINNISEVIRVMFN LASLTVLGKFLTVMKMNRSFQQFDLLHSTEYLPRDLKEDK
LFKRALQLSKTVLKVYGGMSLISINTTFLIQFAKDTTELPLPIYEPIDATVPWKYFIMYF
YEYLGFGLCVMNIAYDSLGAFFIHIKQVDILSKRLEEIGHKSSSKQNHSHINEELKA
CAIYYDRILELTHMMEDLMCLPLSIQILFTLTSEKLSLAIYRAGWVDWNEKNRKLALQMM
GRDLPIRIKTINRCYSFNLA AFTSIVNSSYSYFALLKNFN

>GmmOR12 GMOY009271 (TMP011461) scf-651831 454103:455258 reverse

MLHVPITFTFTTLMWLKVIFSSNLNDVTDVLHMAFTETGLVIKILSAWR FARLLQFVFLE
WQTNNLFSLSANEQLIWN DQFKSFITAFVYMSCSLSVVIFSFISVPLMKTYR LPAFW
TPAGWEQSSYFWYICFYDFIGITFTCISNCTVDMYFCYLLKHITVCLRMISVRLVKLGY
SEDVTKNLKEITFHNLKRM SRHCEKVISYPILGQILFSSMVLCF SIYRLQAISFIETP
FDFLSVFQYMWVMAAQIYLPCHYCNELTLQSGALHTAIYNCNWIAMTAAERKTILLFMLY
IKRPIILKAGHFFEIGLPIFTKTMNNAYSLLALVLNMSDS

>GmmOR13 GMOY003312 (TMP005369) scf-645812 24048:26362 reverse

MIDL FERQRFLRVMGHNFVRDRSQQSRRWHNTRCTYKYILCLFLV VSAQVPMINYTIYY
LDHVELATASLSICFTNILT TVKIITFLLYKWEFAALMEKMEEMYEVRKAETKAKLKR
NDYAGDLTRMYWNSCCCTGAYFMTTPILKIIWSKLQGM DVPEL PMPMRFSDFESTPGY
EFCYIYTGLTTLVVIAYAV AIDGLFIGFTINLKAHFIALQSIHETNNFLKSESELQRDLS
ACIGYHNKILSLAFKLRDIYRPIIFAQFLMTSLQVCVIVYQMVTVSASQYINAQHIFLKN
CLFLCSILLQLFIYCYGGEILKLESLRVGVSVEISHWYNLKP SHRRILCLLMLRSQREAI
IKAGFYEASLANFTAILKAAMSYITLIQSIE

>GmmOR14 GMOY001365 (TMP003388) scf-641298 67504:69789 forward

MFFKQWLPKADDALPSVNGLSRHFTVQQYTFAAIGLDPKSLQRPIFNKMLALVPMLGLFS
LVIPMIGYASLYKSDILKVTDALSPVWEGLLALAKFFYFIWNRQKVIQLLRKIWIKNLEV
SSNPEELTIIAEANHRDYLFSLTFCINVITGVLALAAPLIATFYTLQGEKFLNVLEPP
LKATYPDFHTPNGLIALYVWDSL FVYFIIFGNLSIDGIFSWFTCNIAAHFRILRLRLKY
AGQENGGNITKTTVNGCIDLHRQTIELAEFNKIFRVNVFIKFTISCLQIACLAFLVRG
KEKVDQIFHFSFLTSVTLQFLLYCYGGQKIKDEVIMS NYGL

>GmmOR15 TMP_Or15-RA scf-651027 85495:88783 forward

MLLHTLQLKRYFWVTRRSFN LIGIDITALDYHDIVKYPMRCFLFTAFAAVLAWAMTIHVY
EYRDDFG EFADTSGMLLQTIIALWKT LVFLFKRKEICDLMQNVWQCININVPQEFHIILK
FNSQNFTISALYMLVLSSTVFGSFLVPLIYMFEFYRKNGEKIWLPPQKGGYFWDYSNAIG
YSVLYICHLLGIFFVAAFSIGVDTLCPWLVSNI VVQYHVMYYRLRDIAELS YEISTEKLN
AKIIECVKCHRQVLNLSNQL ENFFAEIIFIKFVISGLLICS LAFRLVRAEGQFYILLYQL
VFLT TVSTQLLMYCYSGQR LKNESQVASEIYSIFEW SHLSRNSQKLLLFAMMRSQRECH
LTGAFFMVDLSL FVWVRERERDVCMYVKQK KKKKKR TNIFNFWFCLKKKS YHFVLLLVHVF
LCYLLKVLRTGGSLIAMLKTLDEKQV

>GmmOR16 TMP_Or16-RA scf-649095 5203:6553 reverse

MPDKKCAKFLSIQQRNLAVLGFDLNAAERRYLVKPLKLLFVLSCNFYWTYGLMNFAYN
IENFDEITGSLSVFNQDILLFFKMFIFFAKADKYLNLIKSMNKLADKAKNQEYDEWSEN
RLAELIAKVYSYTCRVAVAFSATVPLIYSVYVITYTAGELKLLKLPVKARFTLDGKLSYFAC
NYITFVIHLNSMASLTVGLDSLYFWFIYNISAHFRILRKKLEIMAVNLKTNLQYSIQDDL
GAIVVYHLEVIRFIKSMNEIFGEILWAEVTMSCLQMCFATHALMSDVDVSNAPFNIVVVF
AVIIQLAIYCFGGKIREESISLCSDVYLLFPWHKMSMHQRRLMMLPLLRAQKEAYLKGL
FFQVDRNLFFVFSKRIRSVTLIPVGFA

>GmmOR17 GMOY005386 (TMP007492) scf-648564 107291:115929 forward
MSFRLGNVSNLNRKIIIVAYGLIETHLFKYHESNIPKICLNDLIRAITIHEMDYKFKKLE
PHNYIKNGSDELNHIIVWLMKAYS DNILNSVETGLKDKCLEMILVATMWKIKQSLMNHFP
SDPRKGQIGSIELNLWLAQMSGVSVMLRQNSSDINIFILY TALITILVTFVYTACEFY
DLALNWDYDLNLTQNSCISLTHLAGLAKIINALYKLDIQQVLDKLYGLRITYTISKEQR
QTFLDGELENKLLLSVYVAIVATTGLLGMFVFLSIQVLLHPVKMAGKTFPYRAVPSWV
PFPLQLLYMSLSVLIFAMQIVADYLNINLLNQLRYQLNILNLAFDKLSFEKEQKNPAPH
SRRLNAIIEHHCLLKEVCQDIESIFSVSILLQFFTSLIIFAMTGFQATVQSDASNEAILI
YFYCGCICCELFYCCFGNAVTEQSKTLPIRSFNSSWYDYDGPYRKSLLVFLTNAQQPFV
FTAGRFDLSLPSFLGILSKSYSYIALLRQLYGPLNLGAQAPGTVVFMFLAAFPSSIM
S

>GmmOR18 TMP_Or18-RA:CDS scf-648792 266134:274630 forward
MAANLREELERSRLSHQKILKPLKVISLAVGVDIRQPTRFWNPVKILAIALIVNGFVGF
ADYNFIRNNLNESINVYADSLISMQIISNIKLIHLILKQHEFYKVIKMAENSEILLNL
REFELTTNEHKNLMQKIKDILKESWQDIHRQLSFFIYSCCAIVGWYWIVALAQNIHDLYK
RSEHFTVTTTHPVKYPVWINKGPKFIIDPLQYINSAACNHISGFGAVCYDGIYVVLVHC
AALVHVLRLVLEHSTTNEIPQARRVQYLLGCIRFYQKIFEFYSSIDGLFRIVNLIQYCN
AIIICMIIFQASIGLEAEASLVVKMFLYLLAIGFQNMICYNGEKLITQNSLPIAWYSC
CWYNESAEFKFLVRMILRTNRALYMKMSDFSTMSLMTMLTVIISDKLLFFFTLEKRQCG
SMKAYAVQL

>GmmOR19 GMOY012322 (TMP008029) scf-648792 271039:283655 forward
MSNMLIEVLKNEQKCNKTLKNLYKISFMTGVNIKYKTDKDPVKLVNLFITISLMGLC
AQYCLVWHNRHESFVESADAICTANQAWISIFKMIYLVFVQHKFYDLLHAATDGNLLYDL
GIFDLAINCKEQLLKEIKDILRDSWLDIRRLNFFIFSCMMACGFYMFSCFLVNYYYMHI
NPQNFTLQLRAVCFDGIIVVVVHCSALFQILHQLLQHATDEDIPRSERVYLLCCVQLH
DRIYNYAKINSMYKNPSLAQCLLSMLVLCVVMFMANVGLEEDITLFFKMLCFLMAAGFQ
IVIICYNGQKIITQSGMSPSSWYNCSWYNESPQFKYIINMMVLRANRTLYLQVSGFTTMS
HMTLLSIVQTSGSYFLLLRNLSGMD

>GmmOR20-pseu scf-652157 - 1785914: 1788436 MW: 36658.492
MVLISEMSYVIMATMTEHFVKVIVNLSYIRVGVETKTRRLYKFPKRNTNQKAYQVML
YPRNYRRTTMFYTFIHESLILTQFAYKNDKLDSSILKLSVERGPTSFICTAKFSWTHWH
VATISQWFAFAPDSFTTDYAFSRIKENLIPDGHYERHKNTLKDIIRYPQSLRLSPFTCI
TEWHHIVSVAKFSRQTNDSSHITMFASLCVINLKSTVQSIIYRKINYSIGNFFQPNVFQ
TSKLIKLLLFPGCCLVQMFLIWASFQFHLSADIRYKMLLVVLEHFQKPPVLKATSLLD
FTFFLLMQFF

>GmmOR21 GMOY011399 (TMP013635) scf-652170 3479799:3481562 reverse
MASNDYHGGKANILYSIRDSERLDNLFILMIKYLKLTGQIPLDLSSYIPTFLSPIERWFS
RLYGFLVLFVSLHVALFLAKNTFDILETGELEQITDSLVLTMIIYLFASFSSAYWMFRQKR
LMELFQQINQLHRHSLAGVTFVSYRCSYNLAHKAVKYWNLWCIIGVFWALAPLCMGSH
TLPLPCWYPPDALLPFIYELVYITQFWAQFNMGLLFGNGSALFVAIIIVLGQFDVLYCS
LKNLDSHALLMSGQTLKAIKDSQSLQDDNEREVNQYLYSTEYLSLENLSQQILKKGDKS
FKRRLHEALIECVHLHQFILKACDTLEELFNPFLIKSLQVTFQLCLLVFVGVGERSTV

RIVNFLQYLCLTLVEFFLFAYFGEMLRHRSVRVGDALWRSRWWLNAHLIKRDVFIFLINS
ERAVKITAGKLTMDLDRLSVVTQAFSFLTLLQNMAEKQENEVA

>GmmOr22-pseu scf-641538 58384:59452 MW: 35047.4

MTIKIMQSFLFPMVLTIGYEFVHAKPTSKWLLCLKRVLTHFYCSSYSIKQMYDIARNGM
PNVPLFLRLTSSLMYTISGDVKLLNFVIHLKQSKAMFKRFQYIYPQSLEEPHSYQVNQHF
WSSWDYGILYFYLLSTFFIIVSPVTNSSIVISLSSAESWMVWRFMLRRSLYDGYGHGSRI
IDIYSLSTHSCRTILCGLLLWSATDYFGNCYNLLTTYFKFFFQSKNIGNSAYNHRWYIA
SSSYKKSILILIRAQKEADLNANSMQTISFEAFKILLYRYWVRFIALLLYLELC

>GmmOR23 TMP_Or23-RA scf-652170 23283182:23286809 forward

MHLRTIEDVPLYQTSLRIMKFWFSLLDQDNWRRYVCLIPYVIINTTQFLDIYHSEESIDAI
VRNAYIAVLFNTILRAVLLCINRLDYEFMDNIRLLYIDLMDSEDNVIRALVRDRTTIAA
KYIAKINLLMGVCSCVGFVTYPIFATSRVLPFGMYVPGIDKHESPFYEIFFVLQVIITPM
GCCMYIPFTNIIAVFILFGILMCKVMQHKLKQLHNIIEDEKAREVIIWCIKYQLGLINYVK
TINELTTYTYLVEFLAFLGAMLCAMFLLLIIVGPNGDYRHLHIHDILTECYYSLFVAEAA
DSDWDFDNVTTQKILHLLILRAQKPCAILVGNIPMNLEMLQSLNNTTYSYFTLLKRLYG

>GmmOR24 GMOY010839 (TMP013060) scf-652157 888049:890329 reverse

MKLYKFEDFVRLANLFYTSLGIOPYALGQSTKWQIFCRYLIFSFIINLSSMVVCEVTYV
FLAFRNDNNFLEATMIMSYIGFVLVGFKMLSIWRQSLTTFVQELLRIFPQTPEQQRL
YNLDIYVRQSTRVTVCFSLYMLLIWTYNLFAILQYVIYERWLMWRVVGKQLPYTMYILW
DWHHDWSYPLYALECIAAGFTSAAGQISCDLLCAFATQLIMHYDYVSRSLAMYEYVCMRQ
KFREPRKAMAEDMKFLTNIAYHANVLSLSELMNEVFGVALFFNFMASSFVICFVGFQMT
MGADPDTLFLKFLFLFTSASQVYLISHYGQQLIDAQWYNADIGYKKMLVLIARAQKPVE
LQATKFLVLSRGTMTDVSVIKKYQKYFD

>GmmOR25 GMOY012357 (TMP008534) scf-649009 35111:37791 forward

MSADQSTSTNFNSFVKGPKNMFKLLGIKQKQGNLISTMYTSFVVISATIVAILQLCHI
LTSDTSDPHRVQNVVYITYFTVGLGKILNILYRRSILIECLSELEGIYDPKEMERKYSLQ
HYLKRYKRAEYFFWNFAMFLISVYNIETIVRSLLQLYLKGRYGYLLVRIYAPFPYDGLK
LVYLCYFALGSITGAWIAIIIAADLYLLGCVLQLCLHFELLTKQLMELDTRILTESEAI
KRLNAIAKYQSELIRLSRKVNRTFSGSMIVSLTAASFIIICFLFQLLGDVQLVDIAMVLI
LLNESKQVLLICYCGDKLLNSSQRFNESLYMHNWVDGVSRYQHLLFMLLYARNPIMLN
LLDITDITLVTLKEVLVVKTLGKRI

>GmmOR26 TMP_Or26-RA scf-652170 7565092:7567386 forward

MLTVREVTSPFRFYNFVGIKLFQWDDNDTLTKREKYTLLVTLIIFVMNFVCKFSCFVLR
KYEDAQELTKLISYFGFACNGVFKMLSVWIGRKTTHAVIKDLAKNFPRTASECHEYKFYE
QYAFKLRHMYLLSLIHWSIAITFMLFPVQSFIEYLVNFNDNGKFIYRFPYIMYIPFDHH
TPAGFIFAYITQLIGGITHSYFCGSDCLLATVHLVNMQFVSLAVRIKKFKPQTYEKDL
KQLRKILKLHISAHQNAKLVNDVFSISIFLNYLISIAVLVMIGVQVISGSEFWEFKFGV
FLIASASQVYYVCLYGSLLLDYEWYFADNRYQRMVILAIARSQRPAHLTAYKFFMISMES
FANVRLNHLTRNCFVLMTTSYQFFTLKARMEEQN

>GmmOR27 GMOY008038 (TMP010200) scf-650866 8500:9930 reverse

MDEEVIVTIKEFFDIPLKFCLTLGIRLYKWSETERTTILQVCLLSNLLLHTSVYPPFLVI
YQIKIDPNDLLGRTSSLAISLFCVNAVSKILFVARHYKDLRKIIHKLIKYFPPTSSGGQKN
FNLHYEFKTMRRVSSIMLWTHLITAVLFDFTPPITFGIEMNSGGKKEFNFILPYGIWYP
WDHEDSAIMFVFTYMTQLLGSYVAVVSFVVPDLLLISVVALANMNFYISKLIREFHPTG
TNEDFKSLGQILHYHDDILNMIDEVNDVFSFSVLLSFFGFGGLLCLVAFNAVVGSSMLDI
FSQTLFILSILLIMYYLSAYGTEMIRLVNNGNGNEIEMKFKTRQKQTIFQSTDVSVALTDH
PWYDGSIHQRMLPFIARAQRPAQLLGYKFFVVSMEFQSLMTTSYQLFTLIKARYDED

N

>GmmOr28-pseu scf-650866 82839: 84829 MW: 29955.6

MNGLNYSNVPLNIIEMSHLTKTQRVSTISLAFSITVIYLMVYSIPGITMNSVCILLHFWL
KCVCMMGGGEVGYLAVISFVNPDLLFISIVALAYMNFKHVSKLIQELRPEGTDEDLST
IHARYFNLSSVYIVQSIDNVLLVCAYGTEMIRLVNGNEIEMKFKTRQKQTFQSTDVSA
LTDYPWYDGSIIYQRMPLPFPIARAQRPAQLLGYKFFVVSMECFQSVSRYRHRLRFRYLF
YSLFIIPVATDNVLSIIRFD

>GmmOR29 TMP_Or29-RA scf-652141 245471:248227 reverse

MVRNSGAKPMVVLDFFKVPFLILQKFGVCVYRTSSKERLSVKEAISFAISMVQIGAYSIL
VPLFFIKTTPPTTAEFSDACIPLILFFTSIVRLTSILVNPKRIRTLVDIFQKYFPQNMEE
QKNFKVERNYKELIRVTKALAICLSLGCVLFSLAPLNFAMAYYTIGDEAKFDYRMPYPI
WYPFKVNTPGMYAIMCSTQAFAAFSCVCAYFLPNMVLITSMMLINMNFKHLAKTVRNLTP
TNTDDDMKNLSKILGHHQDTFLLVDVTNEIFNISVFISFFSSIALLCSIGMNVLGESQPY
HIIKQSLLLVTSFLDYTYTCKYADDMKTSVRNIWLNSVYRVLTLLVHFAARGANEVRIR
EHATRNYISKPKTKYSLDMSDALAEHPWYDGSVYYQRMLLFPMARAQRPAQLMAYKFFAV
SMESVLSVNTNIAYLTSI

>GmmOR30 TMP_Or30-RA scf-652141 215509:218352 reverse

MVRNSGAQVMVVLDFFEFPGFWMFEKFGVCLYRTSSKERLSLKEAISFAISMVQIGAYSIL
VPLFFIKTTPPTTAEFSDACIPLILFFTSIVRLTSILVNPKRIRTLVDIFQKYFPQNMEE
QKNFKVERNYKELIRVTKALAICLSLGCVLFSLAPLNFAMAYYTIDDEAKFDYRMPYPI
WYPFKVNTPGMYAIMCSTQAFAAFSCVCAYFLPNMVLITSMMLINMNFNLVDVTNEIFNI
SVFISFFSSIALLCSIGMNVLGESQPYHIIKQSLLLVSSLCDLYTYTCKYADDMKTSVRNI
WLNSVYRVLTLLVHFAARGANEVRIREHATRNYISKPKTKYVLTNSYQLLTLVKARFDV
E

>GmmOR31 TMP_Or31-RA scf-650238 26161:28277 reverse

MIPQFLRDDYPLEKHLFLIPKFALRLIGFYPESKLNTPLLCWAFFNFLLLGYSYAEFTY
GIHYLTIDMQTALDALCPVLSSIMSFIFFIWHRSEYKHLIEEVRRLTAAQSSRKNVH
IKRKFFTIATRLTALVLFDFGNTSTAYTVRLVISNTILYLNQQPMPIYPLTCILSHWHGY
ITVAGFVGADGFFLGFCFYFATLTKMLQQDLSDALAVNNCKSVNATMYLALLDKNSQAIR
CEADMVSNLTDIIRRHNEIAQLMKKFSSIMVGIVLSHFITSSLIIGTSFSGYAILVYIVH
TCAVIAEISLYCLGGTAVMECVIPSSTKSSPGIMPFQNTETTNLHTNFQNSSSSKRLAN
EELALQAYCSQWYDYSVRIQKMILLIMVRSQQTITVKVPFLTPALPMLAAVCIVIVYPAI
LRFAGSVITLTKTTI

>GmmOR32 GMOY005084 (TMP007180) scf-648410 219323:223133 reverse

MFNPVPANDKRFWPRQCVWLKLNKSWPLKSTKEFQSEFYTTENYSSFLYILWSWYVILS
VGVTIVYQTAFLITNFGDIMMTENCCTTFMGALNFVRLHMLRNQNFRRVIEQFVNNI
WINRREHHPQVAHECENRMSTFRIMTILLSCLIAMYCLLPLILFVDVGNAPKPFYK
MLFPYDAHNGWRYAFTYVFTSYAGICVVTTLFAEDSIFGFFITYTCGKFRILHQRIDNII
SDSIEVTSTRQNDNNVQRIFEKLLNEIAYDHNKLIERFSNRLEHFFNPILLVNFLISSVL
ICMVGFLVLTGQEMFIGDYVKFIVYISSLSQLYILCWNGDDLIQHVSRSSTETAKHLYGC
NWEGTTLNIRNAKKFKWHRAEEFHLTSIHPTNKEFRQNLQIMILCSQRPVKITALKFSI
LSLQSFTAVILSTSMSYFTLLQTVYNADQEEDHNIN

>GmmOR33 GMOY005479 (TMP007587) scf-648614 40250:49045 forward

MFEEIPLIYMNVKILKFWFLFEKNWRRYLCLPATTFLVFTQFVYMFKTKEGIDSIIRNS
YMLVLWFENTILRAYIMIYDNDKYQQVIHELVELFYDLKKSDDYVKDLLLEVNSKGIIMA
RGNLFLGLLTCIGFGVYPSLAVDRVLPFGSIIPGINEYSSPFYELWYIFEMCITPIGCCM
YIPYTSLIVSFILFGVMSKTLQHRLRTLHRIANQPKLIHAEIISCIKYQKRIINFIEAV
NGLCTFIFLLEFLAFGALLCALLFLLIIVNSSGQAIIVCAYIIMILAQISALYWYANELR
QENFAIAAAAYETDWFYDTIVQKDILLVILRAQKPCSVFIMFFKSYNEILFL

>GmmOR34 GMOY011902 (TMP014141) scf-652170 25006662:25007967 forward

MTIKIVQSLNQLKQFDDYIWFNPAVLKTIIGYEFHAKPTSKWLLCLKRALTLLEISAHFYC

SSYSIKQMYDIARNGMPNVPLFLRLTSSLMYTISGDVKLLNFVHLLKQSKTMFKRFQDIY
PQYFEEPHSYRVNQHFVPSWVNVILYFYLLSTFFIILLTVGYAEAHFFYLKCEDELPYSFD
HPMKLLLSLLFIAFYVWRFMLPRSLYDGYGHGSRIIDIYSLSTHSCRILCGLLLWSATD
YFGNCYNLLTTYVVKFFFQSKNIGNSAYNHRWYIASSSYKKSILILIRAQKEADLNANS
MQAISFEAFKIVLGAVYRAFAVFRMLK

>GmmOR35 TMP_Or35-RA scf-648722 141939:145983 reverse

MSSHSLKLEDNPMLEINVKVKYLSVIFPDREHAWRVYVFLPVCVMNIMQFVYLLRMWG
DLAPFILNTFFAAAIFDALLRTCLVIINRDKFEAFLELAEMYRDIEESKDDTYGRELLR
AATATVRKISIFNLTAFFDIIGALYPLLCEGRVHPFGVAIPGVDMTASPIYEIFYILQ
FPTPIILTMYMPFVSLFASFAIFAKTALKVLQHRMNSIFLYNYRTEEHQFAALTACITY
YSRIARVPIWGDYMFALAILHEYCKCSCCYCCLINFLILTKLYFKIDSSTQIVSIVMYIL
TMLYVLFYYWHANEVIMEVGHRLMFSNLRKRTTFYCCRVLKCLRQLMGYRGIIVVNAFI
MVGNVYPMTLATFQSLNNTSYTYFTMLRGLYG

>GmmOR36 TMP_Or36-RA scf-648722 191876:198790 reverse

MYYRLPLFSVNVKGWLYFGYIGKRNQGIKSLNALLTLAAEILLYIKTEDVSNVIRDI
FKTAILFNSLVRILYVMRREEDFIQFMKGIESWYQEFKDDNDHMLAILNRLPKYTKLVT
AFGLSFGSIGAVASTITALLWHTHIFPIYVPGFDAFQSPLYEIIINLWQSITMVSFVMSAY
ILFTNLFISWLIFGIGLLEILCKKFEQMSSANDAERLRNLKYLIRYHKRIIRYGELEDL
VALISMVELILFTVMLCVLLVFFLITENFVDQIATVIYIFSIFYVLFISYWHTNAFSAES
LKIPDAAYRIDWAESGPETRKCLLILISRSQTALQISESNRYT

>GmmOR37 TMP_Or37-RA scf-648373 4213:5709 reverse

MNLLYRPKLSDGKLVRLSWPIAMFRLTHIVCWPLEDDAPRWAYVFDRFCWFLAFIVFVLT
NDAELRYLRVNMQNLDELLNGVPTYLVLIEAHIRGFTLGyrkNKFKNLLRKFYTDIYVDE
RQHPSFYKKIQPRFWPLYVFSSMYVATLTNFIVTPLALLLTRGSRELTfKMIPLFDYRYF
PIYLPCLLSNIWVGFLVSLFSAEPNIGLVVLHLHSRYLIMNENLRKKTENLLKNPSNT
EIARRFRKIVVETIDENKRLNLFAQEIQNEFSFRIFILFSFAAMCLCAVASKVYMSISI
GRKSLSLNSIFFHFNDVSQNPLGSFAYIFWMFGKIQELMIIGDLGSTIATTDEVSTM
YYNSNWESVIARSSDCENVRLMKLLTMAIALNRKPFYLTGLNFFT VSLNTVIKILQGAG
SYFTCLISFR

>GmmOR38 TMP_Or38-RA scf-648495 88188:91340 forward

MIGILPREWSEEHVYYSLAHTLLIAMGSMFIVTVACDLYEARQNLTLLGDDIVVIIGGSL
IMLKIYFHGQHSSEIHPIVDKMNDLHKMFAEYNGRSRLTIKRLQCSFYLFVFAFSFYIF
LIVLFASAVMVPPLLTHHGLPYRAHFPILRWENSdqHPiGFVIAYIFQVIWTFHALLSIV
CMDLACGIFLQTALNLKILCIRLREISAQNVEERESLNELKSLIKIHQYIINLIEKINA
CYLNYVAQMGASTFMICLTAFEALLAQDRPMIAIKFEIYMLSAFLQLLYWCCAGNLVFF
ESLNVADAAYEIPLWYTRSKEFKMTVAFLIRRAQKPLQFRPSPLYGFNIKTFTSILSTSY
SYFALLCTMNK

>GmmOR39 GMOY004392 (TMP006475) scf-648080 333109:334447 forward

MHFYKIDEFFLILHPLQKYTRWIYDFRRRDSSVPFEFQSMTKLKISLAFVLFELICNFI
KFAIEIRADRLSEAKQIAAVTSIALLCMIRGISLYTDRNRMLAICNDLDKIFPNTFYLQR
RMRVQKLAFAFFKVRFRVLSYLYGLPAFASIPLIRYFLFYDRENGGRLLDEYHQHASWA
PFQLKQNNRAYPYVYVYETFLTILGFTCILTWDHIFTVTVSQLTMHFVFNTELESNVR
DTTRSMTSKFYWRRLKEIIVYHQHVYRLAKKLNFTNLTIFLTDIGCAGSICFHLYLIAN
SDSVLTIVTFFFPCFILIAFTFDYCCQGSRLAEASARLQTVLYNQEWYDASPTYRRLMLS
LLQYAHKPFTLNGFKLFDLMLHFQSIMTIAYRLFAFVQTQGK

>GmmOR40 GMOY012356 TMP_Or40-RA scf-649009 40802:42730 forward

MVEIKDLQIRPEVCQNPLIVHLLKSMMLYGFIVSTEQKHKRFSLRGAVFTISFVISCAL
IVSRGFESLAAGATSCATAFLYLSTISITIVNAFFQRARVVRMCTFLHDDINKLMELADER
EKKMFAATVKYLRVYTAILWTPSVFAGFIAYADCFYRTIFMPETVFNIPQVLRGEAEPIL

LFQLFPFGEVYDNFLVGYLGACYALFLGITIIPCWHTFITCLMKYIVIKFQIINKRLEAM
DISKLSPKFSLQPDMDNLNEKDLDNYWRLKMCFCVQEQTNIKW
>GmmOR41 GMOY006480 (TMP008603) scf-649048 4425:5787 reverse
MPCLDRFRKFIGAASLIARFCACDMFDETYTMFNPLFMVLLGFLAIYTVCFVYTIYDGFV
TNQDWTIILQCLTIGAMALQAISKYACYIHRRTLRKVVKYLDEIYGEYQDRGARYEYAL
KKSLLQKIMKCSKITGIIYFTSLAGLIVSFIYMLITGKRELTLIALIPGIDPKETVGYFI
HTGFHSAIISFAGVGFASEIVMFSIFLHVLLHRDILMEKFHDLNEATAKPDVPAARTRD
LLNDIIAWHQKYNLFVKYIEELFSGVIFVHVTTSCASICSTLFCIVLKVWPFAPVLLLLN
TSMYAYCGFGQLLATNDDVTRMIYEVCIWYRLEVKEQKMILLMLRKSQYAVELTVGKIM
PLNFNTALQLSKGIYTYLMVNLINLE
>GmmOR42 GMOY006479 (TMP008602) scf-649048 15:1464 reverse
MPPLDRFRKLKHLRVVRFACDMFDETYTMFNPFMVLLLLCLAIYTVCFINTIYDGFV
INNDWTIILQCLAVGAMAVQAISKYLCYSHRITLRKMVKHLDNIYEEYQSRGTRYEYAL
KKSLLQKIVKCLKVAGGIYFTTIVIGLIVLPIIYMLITGKRELSTALIPGIDPKETVGYFI
HTGFHSAIILFSGVGFASDTIMFSMLLHVLLHRDIMVAKFYDLNEITEQDDKSAERSRP
SLNDIIAWHQKYNLFMEYIEELFSGIIFVHITTSVCISCTLFCIVLKVWPFAPLLLISN
TSMYAYCGFGQLLATNDDVTRMIYEVCIWYRLEVKEQKMILLMLRKSQYAVELTVGKIM
PLNFNTALQLSKGIYTYLMVNLINLE
>GmmOR43 TMP_Or43-RA scf-651490 579:1910 forward
MSPLDHFRLKLLKHMVMVRFACDMFDETYNINPVMVLLCLAIYTACFINIYDGFV
INNDWTIVLQCLAVGSLAVQVIIIKIIYIYIYIYIYTYNIYMIKMKVHLDTIYDEYQSRG
TQYAYALKKSLLQKIVKCSKITGIIYFTSLAGLIVSFIYMLITGKRELTLALIPGIDPK
ETVGYFIHTGFHCAIILFSGVGFASDTIMFSMLLHVLLHRDIMVAKFHDLDNEITEQEDK
PAERSRPLLNDIIAWHQKYNLRTYAGGYENGRSQVFPCRFEYIEELFSGVIFVHVTTSC
ASICSTLFCIVLKVWPFAPVLLLLNTSMYGYCGFGQLLVANEDVTRMIYEVCIWYRLKV
KEQKMILLMLRKSQNAAKLTVGKIMPLNF
>GmmOR44 GMOY006265 (TMP008385) scf-648928 37939:39536 reverse
MEHELTCIQRFKIIVLRIKAKMCGCDILNPDYKMNFIWLLIVGVNGFFLCTIYTIYK
GMTIDHDWTVIPVCMCIIGSGIQLAKILLVLKYRKVIVEQQYFLENVYTVYQQKTERYR
HVLNRWLEYTVKTYRICASMYVFGVTIIIFPYIYWYIYGIRTMIMQFEIPFVDPNHTHG
YIIHTLYHFPMIAWGCLGHFMTDIYMFMFIINVPLKDLLEQKFLDLNEIILEETNESEKV
LPLLKDIQWHLKYNEFIAGVDKIYRTIIFIEITCGLSICCTIFSIVLDVWPAAYGYII
YLIFCLYSFCIMGTLIEISNDNVIEIYTISHWYKLLKLPKELILIMLIKSQKPIELTVG
QILPLSVSTALQVTKVVYVSYFLMLLLNLLDK
>GmmOR45 GMOY007896 (TMP010054) scf-650705 207676:209075 forward
MKLYSERYQEILNVSVTLKLCGINIFAKNFRMNLITWFIIGIIGLYFILFTYTVYVGIQ
NDWSIVLVKVTMSTTATQGLIKLQNFCLNPKTLRKLAEELLEVYLEYERRTNQKYPKYLQ
RSIALIKRINYAVLAFCLIALSTVIVWPLIFSYVKGEKLLVGSMPRIPCVDKNGWGFIIH
FALQSVMLIIGAYGNFAADSYCFLLAHTSLFKDLYCKFQDLNEILQQYPRNSLRSP
LQDILKWHQKHVLFETASSIYFWVILVQISTAVTGIVTTLVCQFLGIYPTAVGYLIYCA
VLFYIYCGIGNLYERVNEEVINIICDSLWYELTIDEQKLILFMLHKSQTVEGLTIGNLIP
LSLNTALKLTRFMYTLSTMMLLQFLD
>GmmOR46 GMOY003305 (TMP005362) scf-645804 155235:156578 reverse
MIVACVDHFRKLVRIFRCAGICGADFGDRNYPWNPLVFTLSSIVFFTCTVYTIYAG
LVYDNDWTVILQCLCLASSAFQGYDPKNRECSDDRYEARRFPLHNSYIACASAPLSIN
FGKRLFIMRFFIPGLDPNSTMGYFLHMLIQFMCIFFGAFGNFSGDMFFIVLVLHVPLLKD
IITEKLNELNRTQLKRNKLLKDTFEWHQRCNLFIEDISELYSEIIFIEIFLCCGLICCT
TFSIVLSLSAWPAAPAYLLFTLVAMYVYCVLGYTIEEASDTLLRNIYTECLWYELAVQQQ
QMILLMLIKAQSPVVLNIGKVMPLSLSSALQLTKAIYSFLMMLLNFLLE

>GmmGR1 GMOY007472 (TMP009619) scf-650411 214655:216066 MW: 48775.35
MAFWAAATGRTSPSKVVPVLNPNQKQFLQDEIRYREKMNILARTDAGNLTDDYVVRKQETI
DDPELLDKHDSFYHTTKSLLVLFQIMGVMPIHRSPKTNLPRTGYSWTSKQVMWACVVFA
IQTTLVVLVLRERVNKFVTNSDKRFDEAIYNVIFISLLFTNFFLPVSWRHGPQVAIFKN
MWTNYQLKFLKVTGTPIVFPNLYPLTWGLCIFSWLLSIVINLSQYFLQPDFELWYTLAYY
PIIAMLNCFCSLWYINCNAFGTASRALSDSLQTTKGDKPAQKLTEYRHLWVDLSHMMQQ
LGRAYSNMYGMYCLVFFFTTIVATYGSFSEIHDGATYKEVGLFVIVLYCMTLLYIICNE
AHYASQSVGLDFQTKLLNVNLTAVDSATQKEVEMFLVAIAKNPPIMNLDGYANINRELIT
SVGIT

>GmmGR2 GMOY011510 (TMP013746) scf-652170 18996209:18997720 MW: 49157.684
MDIITEKEFDSTLDSSVLTDDMEKLLKSEKRKKFIKNSNHNPDLMERLTMRAKRAKLSR
HGQTAELYDQFYRDHKLKLLKLVILGVMPLARQAGRVTFWSKSYQMYALVFYILTTLVV
LKVGSERIKLLHTTNEYDEYIYAIIIFILFLLPHFWIPYVGVGWVANQVAHYKSMWGTQVR
YYRVTGTTLVFPPLKIAIIIFIGCVLLSILFLFSLSQLDFFLLWHTTAYFHIITMINM
NAALFYINSKGTKIASKSLSDCFKDMRIECNYIMIKQYRLLWLNLSEILQALGNAYART
YCTYCLFMSINITIGSYGALSEILEFGFSYKVLGLVVTIYCASLLFIICDCAQSATSVM
AEGVQSTLLSLNLLQLDVQTQKEIDHFISAIELNPPVVNLRGYALINRELLTAVNFYLHY
IHAFI

>GmmGR3 TMP-Gr5 scf-652170 18992721:18996270 MW: 59057.336
MPSSINIYPLDNIFKMYSVLEEKVVAENINFDLLRSDLKVNKVDNINKHKINSMDLIV
QEKEYERFERSRLNSSDGDVEIHDQFYRDHKLKLLILFRVLAVMPILRSEPGRITFSWRS
IATVYAIIFWFFMTVVVIVGKERIHILQTTTQFDEYIYAIIFVIYLVPHFWIPVGVGWV
ATEVAKYKTSWGAFLRYFRVTGTSLQFPRLKSLIVVISVGCLLCAILFLLCFLLEGY
PLWHTLAYYHIITMINMNCALWYINSRAIKTASYSMALCFRKEVMKDCSASIISKYRFLW
LNLSELLQSLGNAYARTYSTLCIFIVNIVIAVYGAFAEIVDHHKHYTISYKEAGLIVDV
VYCCTLLFIFCDCHNATLGVAKGIQKTLLSINLLKADLEAKNEIDLFIVAIEMNPAIVS
LKGYYVTNRELLSGSISMITVYLLVLIQKFSLDKSTTNDKRNQFVLTFLFLETNDQLMLSF
VSLGNNISKLMKNTYGYINGKRIRLDSGFVCVNR

>GmmGR4 GMOY008001 (TMP010160) scf-650833 228463:237409 MW: 55967.164
MLNNYNRKKKHDTVFLNVKPAANGIGVRKYSNGILDRIDSGFGINYDNEKRASRHSVGTI
DSMNQQFVFNIFRNAPVKWFLSVIGVLPMPTRPGPSAKFTIGSLAFVYSILTFLLTL
YVVYVANNRIRIVTSLSGPFEEAVIAYLFLVNILPIFLIPLLWWETRKCICVLLNDWDDFE
ILYYQISGHSVPLHLRRTAVTVTVALPLLSVISVIITHVTMADFQLSQVIPYCILDNLTA
MLGAWWYLICEALSRTANILAEFQKALRHIGPAAMVADYRALWLRSLKLRDTGTATCY
TFTFLNVYLLFFIITLSIYGLMSQLSEGFGIKDIGLAITAVWNVCLLFFICDQAHYASFNV
RTNFQKKLLMVELNWMNSDAQTEINMFLRATERNPSNINCGFFNVNRNLFKGLLTTMVT
YLVVLLQFQISIPTEIHNTNVNMTLDDDDYDDDLLTNAIVTTTTTIAIKGRKDPGGGHG
IATVAISRSLFMRKL

>GmmGR5 GMOY004207 (TMP006286) scf-647997 53981:55829 MW: 53912.25
MSQQHQQSCSYVLLHFSLFYLCFLGIYPQNLSAYRNKHSLEASKNGSFLVVIVMIWII
VCYNTFILSQSEGKDHREANHNALNFVIGIFLTQIKIIVMATDQLSSICNQGRLAEFYNR
VYSIDNRLIKEGCLLNGLSLALHCYVMVVLTFLEIIIIILTFVNLINYTQWVLMWIFS
CLPTLYDSLDKIWFTTSLHALRIRLSALNKTLTNLKGVKEKSIFKRFYEEECNELSLLKI
DYVNGLEYLKRNLNAGRNVKFNIRSFNIFEQKSFADKFINVEKVKERLTNICQLHD
EICELVQTLHKMWTCPILALMAYGFLIFTAQLYFMYCVTQKQIPILFRSAESLLISILF
LSYTGVKCIYPIFLSWKTVLEAKCTGIALHEYAINLNDKAVYEIVSVNHLSLKLNLHAFD
FANCGFLSLMRTLCLGLSGVITSYTIILLQFNFAAQQSKEADLMGME

>GmmGR6 GMOY011615 (TMP013853) scf-652170 14942509:14944789 MW: 50882.254

MTFWRDFIKPSDSYAAEQTLWTTFLMGLTPIRISSERNGERNIYISRAGYIISIVQVS
FFLYSFIYSFLMDESIVGYFFKTEISQVGDVQLKFIGMSGMLILFGVSLYKTNDLMELYH
VVAKIDNQFLGVGVEFNRYRFIMKFRHSLMFIISICSIYIGGSFWMLFHNNVWPTFQAIV
AFFVPHIFLLSVVTLNVAFIMRFTQHYDLINKVLKNLRHQWETRSIKTISHKQKSLQCLD
SFSMYTMVSKNPCDVVQESMEIHQLICEAASTANKYFTYQLLTIISIAFLIIVFDAYYVL
ETLLGKSKRETkFKTIEFVTFSCQMMMLYLVAIISIVEGSNRAIKKSEKTASIVHALLNK
AKTPDVKEKLQQFSMQLLHLKINFATAAGLFNIDRSLYFTISGALTTYLILLQFTTNSSP
PSSSDCTFNSPVTSPIPMNSTST

>GmmGR7 GMOY006209 (TMP008329) scf-648889 6876:8857 MW: 46324.344

MDVENQNNLPLARPAYRNRWRSLSAKGLYESLQPLFLLLYWHGLMVYSIKANADGKKEKEL
RHSLWSHLNVFFHLTYIVCYIMTVMNNFESVAGYFFQSKISRFGDFMQILSGFIGVTVI
YITAIIPKHYVQNCLQFIQEIDQCLLRVGVIMYSKILRYSCIFIVAMILIDILYTAASF
QILKSANEEPSLYLHITFILQHTVVLTAIAMFSCFTKLIARFTMLHKKSLQCFDSFSTQ
TVASKSPCEIVQESMEIHQLICEASSMANKYFSCQLLTIISTAFIIVFDAYYVLETLLG
KSRRESKFKTIEFVTFSCQMILYVIAIISVVEGSNRAIKKSEKTGSIVHALLNRAKTLD
VKEKLQQFSMQLLHVKINFATAAGLFNIDRSLYFTVMICETIH

>GmmGR8 TMP-Gr4 scf-651593 207733:209113 MW: 47166.812

MYIKVRSLKSQAVRKWSGKVKHQSIRQENDVILNDLRIIMFPLKIISLIPLYGSASSYEL
GPPTKILYTIVMRFLILVIPVYNLYNLYLNSTETSNEPEWIDSSLNFLNYIITISFCTR
HYQLLEKIINGLLKFYEEMKEYGKCVDVTEARFSITFTIIMTLQCCVVILKIVAIIDVPL
AFNISIESVLYAFQNIIVPDLYIIFISSLMRTIATQFSNLNNIATASTCGIYEGTIKNQIS
SNTLVLGFLQMYRKLRIHKFISDYCTFILLFYVGYAFFSITSKTYIYIFVWIISPQEIS
QSEVSLSFHILVMHMLLLILLCRCFNLVARKVFQTTNVKYVKIPRSKFKPGYMPYQGWIR
VLVVLTTLSCTPVPNWNFKICNRTLIFIYSRTLKQFGAEHPKRTGSL

>GmmGR9 GMOY011903 (TMP014142) scf-652170 23328288:23329768 MW: 39397.14

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ILVKASDNEIGQTVDSVQMVGIRMAHIASVLESIRKNDQKKFYDDVKEIDRIFESSLGI
TINNRIIKERLNELVAALDEVNLTAEPTPMRTRMAQNHSGHVFSKPRQQESNIENSP
LTKLVVIRNIYDRLHSQSVINHCFCGVSMLINVGNDFISITSNCYWIFINFKDFSSTVID
FLQIACSAIWSVPHLLNVLVLAIFICERTVHTSVDMALILHRINSNFNNDKYGSAVTQFSL
QLLHQKLSLTAAGFFTIDSTLLYTVIGATTTYLILIQFHLNEMKPNT

>GmmGR10 GMOY003231 (TMP005286) scf-645661 235649:237209 rev

MEFSNCDLLYDHISRLTLPSTVYHELMFASVMDKGLLILSWIYGVSPWNISRRSYCCNIL
DYGQMLMMLFFYLTCYALVNFDFGFIYQAPDCNGFCRLGNQLFLHLGCLLYLTTQLLAMK
SRKKFCKKFEQTLINMDRSLETCQLDERGEMSMKRNQSLHFLYKTAMTLGLLMLLIYEVR
QLTYFYGHWWFFVPLMVTTPYSAATVMLLQFAYYVYKISDRHQIINQFLEQINQDIVKTP
KEITPEIFNVESEIKITSSGNVQLNERHVKQTTTHREENDYNEDSMKFLESSTKRYATT
SLTKLFKMFDSVLSLSVLTNSEYGPHCVPYMSACFVITIFCIIFFQIKIYHVVGKSRLLD
YIVFIYFIWSFVTMLVTYIVLRLCCNASGEAKQTAVIVQEIMRKRPAFMFGVDGNYNEMK
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>GmmGR11 TMP-Gr3 scf-652146 202807:205545 MW: 52777.453

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HVLLIMLASYFGRKTFTFSLTFILDFDSKLLKHKIRMHYIDLKFLRNHLSLNF AFFLS
AVMLGFIQRRSLLGILTVNTSYTLPNVITQTSLIQYYALVYVVKRMQLLHQLIEQTFQ
QSLKGNIFNVQQLRVLRGLYADMDAYTKHLNDAFAVPLLLFFMASLKSLSFYIFTLYKW
IDQWTDLSYTVISYAIIEICWQFSRAFLILHFNQAIQNQRKQAAILFTSFSSVAERLEPT
IVLIISDQPFYCAIVYGSSELYLWNHTVKYACSDDGKRYILGKETMVCVVLQFQNNFPF
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>GmmGR12 TMP-Gr2 scf-650947 5268:6453 MW: 44579.047
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>GmmGR13 TMP-Gr1 scf-640662 25103:26585 MW: 53170.637
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