Comparative morphological and transcriptomic analyses reveal chemosensory genes in the poultry red mite, *Dermanyssus gallinae*

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Supplementary Materials-2

Table S1. Summary of the transcriptome sequencing data from *D. gallinae* samples.

Sample	Total raw reads (Million)	Total clean reads (Million)	Total Mapping (%)
F1 (Forelegs)	24.02	23.53	72.51
F2 (Forelegs)	21.73	21.49	68.43
F3 (Forelegs)	21.73	21.29	67.16
H1 (Hindlegs)	21.74	21.47	69.06
H2 (Hindlegs)	21.75	21.51	65.82
H3 (Hindlegs)	21.72	21.30	73.56

Table S2. Protein sequences of IRs used to construct phylogenetic tree.

>TuIr25a ; XP_015792522.1 ionotropic receptor 25a-like [Tetranychus urticae]
MIVINLLFLTLLINVQYCLTYYLNDFIIGVVTGPNGGFVERSFNAALEQLNLTSITISETKWIRGS
NNTAVSDICDSLVTRSHQYPSLIFDFTPQSVDNENGQFSTAIKKYSRLSGTPTVSTSLSLGATKNP
WNRLNSIENNYLIHLYRPGDVIPMIIQDIITLYNITEAVILHDQSFILDHKLTGLLDKSTVDYDVK
RLDADTLEDTMNELKASKVHNYFVLAKIANIDRILEMASSLGMFRFADSWFMITKGRGQIKCD
NCTHGSILLYQPSRVKSIEYDHSPGLNNISKEKRIDAFFIYDLVRLTLMSVDEMVKTNVWPINLT
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VMAERESIVDFTVPYYDLVGISILMKKTTTPSHMFKFLTVLTNEVWLSVLVCYLATCAAMFIID
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MALDENLDKKERGKLTVWDYPLTQKYSNILKQIEMTGMPKTFEEGVARVKKSKNSAEGFALL
ADATKIRYAAMTNCDLQQVGNEFSRKPIALAVQENSPLKDKLSSAILKLLNLRKLESLKEKWW
SNNPEKADCEDPKKASDGISIRNIGGVFIVISVGVVLACITLIWEHCIVKKFRKSSAKVSNVFRQ
EIGKKESSKL YNFPMPYNPKMKEKI

>GoIr25a; XP_003743738.1 ionotropic receptor 25a [Galendromus occidentalis]
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IELTNVELDHKKLCSMIMEKKPSLVINTVRTPGSNYYKLTMTIKEVLKNLGMPTLDLSYGISDE
YSMSGWSTKKGDQGNYLIHVTPPGDSYTQAVRELSLKMDLATAGILYDKTVLIDHKYARLLEN
VPTRHIMREVGESAADFWNKTQVIQSTDVSNYFVVGSISHLSNALEVAKKYDLRQRHHCWVL
VTKQEGEPSCDGCTNLEALFVHPVKVDDTRVGKEGPYGADKLDGLFYEEISEYTVKRIFATEK
YSKEPIVATCPGVGSARPNNNLYAALNSAKLKGIYGDVVFDMKVGYQQIRMKVEHLNFTTAK
NRDTQDKGYFTYQGDANVAVWKEGQSSLEQYGAVTFYKVVTIVQPPFVYRNNETKKFRGYCI

DLIDEIKKILKFEYEIYEVADSHFGSKNKEGTWSGLIGDLVQKKADIALGPIAVMAERETVVDFT
VPYYDLVGLSILMKKPEVKPSLFKFLTVLETNVWGCILAAYFFTSFLMFIFDRLSPYSYRNNKE
KYKDDDEKREFTLKECLWFCMTSLTPQGGGEAPRNLSGRLVAATWWLFGFIIIASYTANLAAFL
TVSRLESPIESLDDLSKQYKVKYAPQKDTTASTYFQRMANIEEKFYEIWKNMSLDDSLTDDQR
AELAVWDYPVSDKFTKIWWTMQEANLPESFEAGVQRVKDSLTSEGFAFIADATQIKYATMTNC
DLTQIGSEFSRKPLALAVQQNSPLRDQLSSAILKLLNQRRLESLKETWWNQNSEKKECDEEGK
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>TmIr25a; Tropilaelaps mercedesae IR25a mRNA for ionotropic receptor, complete cds (LC438511.1) Honey bee parasitic mites
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GWNKNTENERSYLIHVTPPGDSYTQAVRELSIRMDLATAGILYDKSVIIDHKYARLLENVPTRHI
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DDDEKREFTLKECLWFCMTSLTPQGGGEAPRNLSGRLVAATWWLFGFIIIASYTANLAAFLTVS
RLESPIESLDDLSKQYKVKYAPQADTTASTYFFRMANIEEKFYEIWKNMSLDDSLTDDQRAELA
VWDYPVSDKYTKIWWTMQEADLPKTFEEGVARVKNSQGGDGFAFIADATQIKYATMTNCDLT
QIGSEFSRKPLALAVQQNSPLRDQLSSAILKLLNQRKLESLKETWWNQNPEKKNCDDEGKNND
GISIKNIGGVFIVIFIGVVMACITLVFEYFWYKNKKPRSKVVSVKDHMPQKK

>TmIr93a IR93a Tropilaelaps mercedesae IR93a mRNA for ionotropic receptor, complete cds (LC438512.1) Honey bee parasitic mites
MWPRLIFFASLAAGWRTRAEEIKAVVLPDSQIVVDEQDVRDFIFNRTGEYNATVGAAGYYISFL
ATNIMSVSELNERVNPESESNINLNLLVIALDCDDTYKAMDVQMKKFPTSMLIALNRPYCPRFD
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GVRSNDEVNSAASIAFWEYCPPSALADGNCGLNSESMKRILDSYRNNDNKKVDREFIIIGDEEL
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KIRNPFDTVDSLLNSHMSWGAFRGQAVIEILKLQQQGPLTKLSMKLTHIETAHEGWALKEVAD
GNMALIGSEVTLYHYIGKQFIATGQCDYAVAKEEIIREIKVLAVRPGFPFLARFNTLLTRMVETGL
VIRWKKKYWPKENECTVESKPQAGDIRRITIAHMEGSFWVLGAGFLISFLLLGVELLRKRRELR
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SGFPNRTDLIPYNYP ARRY

>DgalIR1 DgIr763lcl|ORF2; GAIF01020763.1 TSA: Dermanyssus gallinae isotig25947 transcribed RNA sequence

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>DgalIR2 DgIr194lcl|ORF3; GAIF01026194.1 GAIF01026194.1|TSA: Dermanyssus gallinae isotig14279 transcribed RNA sequence

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>DgalIR3 DgIr4048lcl|ORF3; GAIF01024048.1 GAIF01024048.1|TSA: Dermanyssus gallinae isotig18401 transcribed RNA sequence

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>DgalIR4 DgIr3943lcl|ORF12; GAIF01033943.1 GAIF01033943.1|TSA: Dermanyssus gallinae isotig11463 transcribed RNA sequence

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>DgalIR5 DgIr780lcl|ORF3; GAIF01028780.1 GAIF01028780.1|TSA: Dermanyssus gallinae isotig14118 transcribed RNA sequence

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>DgalIR8 DgIr541 lcl|ORF2; GAIF01006541.1 GAIF01006541.1|TSA: Dermanyssus gallinae isotig08537 transcribed RNA sequence MNGLGAPVLALALLGVAVADIKIGGLFEAGEDIVEMAFNSAVERINSHGLAEKGERYTPTSDRLLTRVEHIERADSFQASRKVCTLLEEGVAAVFGPQSTDASFAVRSACETLDVPHIETHWDYRSRTTNHSLNLYPHPSALGKAYLDFIKYKDWKNFAILYEENDALVRLQEILKDATLMKENRVTVRQFEIGTEYRKTLKDIGKTGIKNIVLDVPIKNLYTVLKHAQQVDMMSEYHNYFITSLDAHTIDTEDFQYGGTNISAFRLIDFSSKEIDEVARDWIQRRHRFSSKKSSSVQSSFNTGDQDFYKNLTTKVALMYDAVRLFATALKDLHPDSGPKIQVAPLSCEREHKWSQGNAFVKYMRMINIKGLTGNIRFNKDGHRTDMRLTVLDMAHSGWREASEWTMLGCISVTANYTRE
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>DgalIR10 DgIr982 lcl|ORF1; GAIF01026982.1 GAIF01026982.1|TSA: Dermanyssus gallinae isotig09650 transcribed RNA sequence MAVDKVNRDMGLLSATRFQAKVFRVRSRDSFSAARHVCELARHKVAAFVGPRSPSVKELVKASAYRLNVPHISTDPELHERR
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HQ
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>DmelIR64a MHWWLLVFLPLSCQGLPEHELLELELDYGLAEPQRTSLLQSSLILQFSQDYKHIPRITYFTCQKP HLQTPNQIPNAAEHRDAFAAKNFQLIKSLYESELFVRIVLLDVLAQSPTSGRPNRPGNGPTGGFS QTPSQAQSNSEWLEGVLRMEALRQIAVVDLACGAVSRRFLELASAKMLYSEKFHWLLIEDFAW HGRTQTAEGSGKRDDGEMEEEEPPGQQIQATDDEDLPSIESFLGGMNLYMNTELTLAKRMSEA AHYTLFDVWNPGLNYGGHVNLTEIGSFTPTEGIQLHTWFRTTSTVRRRMDMQHARVRCMVV VTNKNMTGTLMYYLTHTMSGHIDTMNRFNFNLLMAVRDMFNWTFVLSRTTSWGYVKNGRF DGMIGALIRNETDIGGAPIFYWLERHKWIDVAGRSWSSRPCFIFRHPRSTQKDRIVFLQPFTNDV WILIVGCGVLTVFILWFLTTIEWKLVPHDGSALIKPKGGAPPRHHYQQQQQQEQVEAPVRPITA VSVVVSKEKVEEKQEEYEDSTPIDAGTLWQRCYQKLNKYIKDRKAKQKKAPERVGLFLESVL FFVGIICQQGLGFSTSFVSGRCIVITSLLFSFCIYQFYSASIVGTLLMEKPKTIKTLSDLVHSSLKV GMEDILYNRDYFLHTKDPVSMELYAKKITSVPTTKENEADEDEPVDPNPVSTDPAKSYRDIVHS HETGAHAKDNAASNWLDPETGLLRHLGFAFHVDVAAAYKIIAETFSEQDICDLTEVSMFPPQK TVSIMQKNSPMRKVISYGLRRVTETGILTYHFNVWHSRKPPCVKKIETSDLHVDMDTVSSALLI LLFSYAITLMILGTEILYSKWHNRIQLKWVGAT
>DmelIR67b MELLYLNTLQSLSLLEGNRLVQTVQELNNIYQTELNVFLEFGNGADILESAQGTFVPTLWIKNP QNQKVMKGNFTSCTLTILYLEDEHLDRGLYYLANWLWEYHHLEVLIFFNGGSYDKLIQIFSRCF NEGFVNVLVMLPGSDELYTFMPYQDLKILNLKSIKEFYSLSRKKMDLNGYNITSGLVIAGAPR WFSFRDRQNRLILTGYMLRMIVDFTNHFNGSVRLMNVLTVNDGLELLANRTIDFFPFLIRPLKS FSMSNILYLENCGLIVPTSRPLPNWVYLLRPYAFDTWIAWLIMLIYCSLALRILSKGQISISAAFL KVLRLVMYLSGSRDMGTRPTTRRLFLFVILTTSGFILTNLYVAQLSSNSAAGLYEKQINTWEDL DKSDSIWPLIDVDIKTMEKLIPDRTKLLKKIVPTLEADVDTYRRNLNTSCIHSGFFDRIDFALYQ QKFLRFPIFRKFPHLLYQQPLQISAAFGRPYLQLFNWFVRKIFESGIYLKMKDDAYRHGIQSGLL NLAFRDRHLEVKSNDVEYYYLIAGLWFGGLTLATVCFLLELLIGYAKIKVTISCKMNIM
>DmelIR67c MFCWLIFLNIILLSDRSESWSAREVIHQFNHDQQLQLNIYLDCNDVELQIGQEVSNLFVNSTAD

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FELSQQRYLRVPIFKILKEVYDQRPVFVALRHGLPYVELFNNYLRRIFESGIWIKLQEDSFLEGIA
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>DmelIR68a
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STGATENRQFFLEANDEVARKVGEKMEVFGYSDDLTSRIAKGQCAYYDNEFYLRYLRVADESG
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>DmelIR68b
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S

>DmelIR75a
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>DmelIR75b

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>DmelIR75d MKVQVAHWLPLIFFLLVSGTPRVAGSWRSEYSRQDPDPKTRWGNQLPDMLVAYYRHHGVHSL MLVVCHTDIADFRLWKLWQHFNLNNFYVQVSTESSLRDLQHVDALDEHKDAPPPKSFHANNS THWETSFLLPALPYKMGILLLEFSSECALNLLRWSAASEHNYFTTNRFWLLLTEDPGDIDLLED PEIFIPPDSELRVLHYENVGNFSCSLIDLYKVAAWKPLKRTLVGHNIRNSRHVIHALQHFGSAITY RQDLEGIVFNSAIVIAFPDLFTNIEDLSLRHIDTISKVNHRLMLELANRLNMSYNTYQTVNYGW RQPNGSFDGLMGRFQRYELDLAQLAIFMRLDRIALVDFVAETYRVRAGIMFRQPPLSAVANIFA MPFENDVWVSILMLLIITTVVLVLELFFSPHNHDMSYMDTLNFVWGAMCQQGFYVEVRNRSA RIIVFTTFVAALFLFTSFSANIVALLQSPSDAIQSLSDLGQSPLEIGVQDTQYNKIYFTESTDPVTK NLYHKKIASKGENIYMRPLLGMEKMRTGLFAYQVELQAGYQIVSDTFSEPEKCGLMELEPFQL PMLAIPTRKNFPYKELIRRQLRWQREVSLVNREERKWIPQKPKCEGGVGGFVSIGITECRYALGI FGCGAAVSFVLFLFEFIFRHFKQVYRIIKGYREVQR
>DmelIR76a MENLLVESYYFSTVLSFFAQQFFADSHATCIFWHPAFDFRLETVHPMPLIIMDWHRWANRSDQD VYDYKIKEDEFEGKGIPYNDWTLRLTVAIERSHCETFIAFQEQIPEFARYFYHASIYSIWRSLRNR FMFVYTKEFEDKKDSYLSGYIFQDQPNILVITSQYLNSSTFEIKTNRFVGPRNFNKNPEPVEFYIL QRFDAKGTKATWETQSAMSSKMRNLKGREVVIGIFDYKPFMLLDYEKPPLYYDRFMNTTDVT IDGTDIQLMLIFCELYNCTIQVDTSEPYDWGDIYLNASGYGLVGMILDRRNDYGVGGMYLWYE AYEYMDMTHFLGRSGVTCLVPAPNRLISWTLLLRPFQFVLWMCVMLCLLLESLALGITRRWEH SSVAAGNSWISSLRFGCISTLKLFVNQSTNYVTSSYALRTVLVASYMIDIILTTVYSGGLAAILTLP TLEEAADSRQRLFDHKLIWTGTSQAWITTIDERSADPVLLGLMEHYRVYDANLISAFSHTEQM GFVVERLQFGHLGNTELIENDALKRLKLMVDDIYFAFTVAFVPRLWPHLNAYNDFILAWHSSG

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>DmelIR84a MIKLQVKVISWPLIILTAFLRVLQIESINTNFLELAAFEDFLRSEHLSHVLVVRGDDADGDWKIECHQKLLANYRVQFYRPEMSANFEDLMFYGSPRTAVLVLNSEHVLVRRQVFGVASEAGYFNNSLAWFILGSGRESLPVEQLIDQLLSGYRMGIDADITVALRGPDNASMLFYDVYRISRQANTPLIIEKKGLWTHSGGYQKFGNFKNTWVIRRRNFLNVTLIGSTVLTEKPPGFGDMEYLADDKQLQQLDPMQRKTYQLFQLVERMFNLSLAISLTDKWGELLDNGSWSGVMGQVTSREADFAVCPIRFVLDRQPYVQYSAVLHTQNIHFLFRHPRRSHIKNIFFEPLSNQVWWCVLALVTGSTILLLFHVRLERMLSNMENRFSFVWFTMLETYLQQGPANEIFRLFSTRLLISLSCIFSFMLMQFYGAFIVGSLLSESARSIVNLQALYDSNLAIGMENISYNFPIFTNTSNQLVRDVYVKKICKSGEHNIMSLQQGAERIIQGRFAFHTAIDRMYRLLLELQMDEAEFCDLQEVMFNLPYDSGSVPKGSPWREHLAHALLHFRATGLLQYNDKKWMVRRPDCSLFKTSQAEVDLEHFAPALFALALAMVASALVFLLELFLHWLPDFRRRLGTMST
>DmelIR85a MSIQWLKHILLLAILVNLAGTRENHIPLDLKKSSIVMVKMSQILCKARIKVLFVYFENQTSHEHTGQILKEVTKCDISNQNTPLEAVKDDGILMYMVMITTNISQPLELSLIRKKSAAKHRSHVFLLVRDADTVSDAWMRASFRQFWKIWLLNIVILYWRDGRLNAYRYNPFMDNYLIPVDNKPNEVPTLEQLFPKTIPNMQRKPLRMCIYKDDVRAIFWRQGTILGTDGLLAAYVAERLNATMMITRPHSYNNHNLSSDICFLEVAKEYVDVAMNIRFLVPDTFRKQAESTVSHTRDDLCVIVPKAKTAPTFWNIFRSFGSLVWALILVSVLVANVFCYILKSEVGRVPMQLFAGALTMPMTQIPPNHSIRLFLIFWLYFGLLICSAFKGNLTSMMVFQPYLPDINQLGALARSHYHIIIRPRHVKHIQHFLTLGHKHESRIREQMLEVSDTQMYEMMRNNDIRFAYLEKYHIARFQVNSRVHMHLGRPLFHLMNSCLVPFHAVYIVPYGSPYLGFLDSLIRSSHEFGFERYWDRIMNSAFIKSGVKVVNRRRGSGNDEPVVLKLQHFHAVFALWLVGIGMACIVLAWEHLTHNYNLAVTKRRD
>DmelIR92a MLLQPLVMHLSQLLRIIVGQYFAEFPSILIVYNNSASTTPLQLEYLSALELVLRELSKPIRLQWINVAFLKDLNDLEDQVMGALNSSVTEGFITILSQTHHFIHARYYATRNANVRLKDKRYLFLCEDESPAELLCMDILQFYPHHLMVRPGTETAPTGPTGPHPDPRRGGGASVSTKNKDDGEGGAGNKTTSPYRDINFELWTQKFVGAVGNLDALLLDAFLPNETFANRVELYPNKLLNLQRRSLLVGSITYVPYTITNYVPAGQGDVDPIHPQWPNRSLTFDGAEANVMKTFCQVHNCHLRVEAYGADNWGGIYDNESSDGMLGDIYEQRVEMAIGCIYNWYDGITETSHTIARSSVTILGPAPAPLPSWRTNIMPFNNRAWLVLISTLVICGTFLYFMKYVSYRLRYSGTQVKFHHSRKLEKSMLDIFALFIQQPSAPLSFDRFAPRFFLATILCATITLENIYSGQLKSMLTFPFYSAPVDTIEKWAQSGWKWSAPSIIWVHTVQSSDLETEQILARNFEVHDYSYLSNVSFMPNYGFGIERLSSGSLSVGDYVSTEALENRIVLHDDLYFDYTRAVSIRGWILMPELNKHIRTCQETGLYFHWELEFIDKYMDKKKQEVLMDLANGHKVKGAPQALDVRNIAGALFVLAFGVAFAGCALVAELLIHRMDLSK
>DmelIR93a MNPGEMRPSACLLLLAGLQLSILVPTEANDFSSFLSANASLAVVVDHEYMTVHGENILAHFEKILSDVIRENLRNGGINVKYFSWNAVRLKKDFLAAITVTDCENTWNFYKNTQETSILLIAITDSDCPRLPLNRALMVPIVENGDEFPQLILDAKVQQILNWKTAVVFVDQTILEENALLVKSIVHESITNHITPISLILYEINDSLRGQQKRVALRQALSQFAPKKHEEMRQQFLVISAFHEDIIEIAETLNMFHVGNQWMIFVLDMVARDFDAGTVTINLDEGANIAFALNETDPNCQDSLNCTISEISLALVNAISKITVEEESIYGEISDEEWEAIRFTKQEKQAEILEYMKEFLKTNAKCSSCARWRVETAITWGKSQENRK

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>DmelIR94a MALPKQLKFINIFLVLLIIYGSSDGTENQHEIFLNRLLQAVHNERSVETLFLLHHSNLANCSLQD WNPPRIPTIRSNELTVFNVEKTFNHNALALVCLMKNSYREILNTLAKSFDCMRQERIILMIHRKS DSKFIEDITHEVKNLQFLHLIVLIVQEKYNGQVFASTLRLQSFPEPHFKRIRNVFAIQRIFYRPINF HGKVLNAIPNDIPILFVALNEMFTEYARRYNSTLRIQNRTIKEDIEITEDNYDIDMKIQLHNSQNF LHHMNIAMDIGSNSLIILVPCATELRGLDIFKELGVRTLTWLALLFYIIFVLVEMLFVFISNRFNG RNFTMRYTNPLINLRAVRAILGQTSPISNRYSLSIQHFFVFMSLFGTLFGGFFDCKLRSFLTKRPY YSQIENFSELRKSGVTVVVDHTTRQFIEQEINANFFRDEVPNVRTTTIQELINHVYSYDRKFAFV ANSIPWRTFREEMKSINQKILCDSKNLTILENVPLTFSIRRNAIFSHHLRNFIINAADSGMITCWF KMAGKVIRKHIKTTLRESEQQPSHLPLSFDHFKWLWAVLCIAYVMSFMVFVMEILWSKYQRRT RSVSIV
>DmelIR94b MSLIFNLLFILILSQAVSQETEFLQLKYLNNIVRSMIKLHKMETLVIVKHHLDNNCSLQNWNAH GMGIIRTNDQGKLIMKDTFNSRTLAIICIGQNSHITLLRNVFETFGKVQQKKIILWTQMELKEKF FQEISKKSRDLKLLNLLVLKAVTKDKLLIYRLNPFPSPHFKRIENIWTPNDTLFMDTKFNFHGMT AVVKHDYNWTIQMGNIRKFPISRIEDKEVIEFALKYNLTLQFFNDVERFDIELRKRIILKSNSTQP IDSGIPMVFSSLLIVVPCGNYLSIQDVIKVSGIEKWIFYIILVYVIFVLIEITFLGVTILISRQSRHQM IPNTLVNLCAFRAILGLPFPETRRTSLSLRQLFLAIALFGMIFSIFINCKLSSMLTNPCPRPQVNNF EELKTSGLTVVMDHDAENFIEKEIGVDFFNQYMPRKVTLTFTERAKLLFSLKGNHAFTLFSESF AIIESYQRSKGLRAHCTSEDLIVAERVPRIYILENNSILDRPLRRFIRQMQESGITNHWLKNIPSSL EKNLMQITIPYDRERVHPLSIEHLTWLWCILILGYSISMIVFFVEMSLKRRKKNLENRAPNICIC
>DmelIR94c MSKVFKLLVLPLIYLSLTKGSKNPQLKFLRELINVIEEGREIRTIMVIKHSRDEYCHLDQWNPRG SPILRTNEMGSIRISGYFNDQAVILACMGENSDYGLLKSLANAMDNMRQERIILWSEREPTKML MDYISQQADRYNFAQIIIVTMNEDVDAVPSLHQLNPYPTPRFRQITNISNIRRTSFFGCGLSFQGK TAILKESVVSNIRFKVWSPSGPIPLSELKDYEIVQFAVKYNLSLKLYDQNESKSDHFDIQLGPLFI TKDFPTQMAFVSPNTACSLIVIVPCSPKWRFMDVLHKLGVLKLIGCLLIAYAVFVLIETLILWLT HRISGREVRLTSLNQLLNPRAFRGILGLPFPEFRRSSISLRQLFLVISVFGLVYSNFVSCTLSALLT KPAQNPQVRNFKELRDSGLITIMDKYTHSFIEKHIDPEFFDHVLPHYLILQKKEALRMIWNFND SYSYVMYTTTWKSLNTVQKSFDERVFCESESLTIAWNLPRMYVLGNNSVLKWMLSRYITYMP QTGIPDSWTEQLPKVLKLLYNVTSPRRIKEGAVPLSIQHLSWIWHLLFIGESIATLVFIVEILLQKS NQHTSNMRERSSEDDDFV
>DmelIR94d MGQLHLLLVALVLLSPGGDSFYHSLIHHLNRELKIEYVLLLGNFDTTWLDILWQLPVSVLQIKE HSRETYSLLENPSHNVLTIAFVNDSPEDILEILYRNLRMLNTQPVLLVIRKSTIRVNSLLEWCWH HQLLKVVAIAQDFMESLIVYSYNPFPVLQFIERRLDNSTVIFEKRLENLHGYEVPIALGGSSPRLI

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>DmelIR94f
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>Vd22269 MSGVVAPVLALALLGVAVADIKIGGLFETGEDIVEMAFNSAVERINSHGLAEPGERYTPTSDRLL TRVEHIERADSFQASRKVCTLLEEGVAAVFGPQSTDASFAVRSACETLDVPHIETHWDYRSRTT NHSLNLYPHPSALGKAYLDFIKYKDWKNFAILYEENDALVRLQEILKDATLMKENRVTVRQFEI GTEYRKTLKDIGKTGIKNIVLDVPIRSLYTVLKHAQQVDMMSEYHNYFITSLDAHTIDTEDFQY GGTNISAFRLIDFSSKEIDEVARDWIQRRHRFSSKKSSSVQSNFNTGAQDFYKNLTTKVALMYD AVRLFATALKDLHPDSGPKIQVAPLSCEREHKWSQGNAFVKYMRMINIKGLTGNIRFNKDGHR TDMRLTVLDMAHSGWREAGEWTMHGGISITANYTRELEEARLSLLNKTLVVTTILQPPYVMY KENWRDNGLTGNDKYEGYCIDLLDAIASSEHFDNNMKYVIREVADNSYGRKDADGRWNGMI GELLSGKADLAVADLTITFVREEAVDFTMPFMTLGISILYKKTAKPPPGLFSFLDPLSLEVWIYM MTAFLGVSLFLFVLARFSPYEWVNPHPCEGNPEELDNQFTIWNTLWFTIGCLMQQGCDVTPRA LSTRVAAGMWWFFTLIMVSSYTANLAAFLTVERLVSPIESVEDLAKQTTIQYGCLRSGSTQSFF KDSQFPTYAKMWHVMQSQRPTVFAESNQKGIDRVLRGKYAYLMESTSIEYNIERNCDLTQIGS LLDNKGYGIATPPGSPYRTMLSQAILRLQENGDLHVLKERWWKKKRISKKCPKDIINKGTSAM TVASVGGVFIVLLVGSCVAIISAIVEFVWRAKKIVPEERDPVCVELCRELKFTLTCGSKKTPDTPS LG
>Vd22292 MHNIMTVVQKALKALEQIEAMRRRVKTSVHYPTIFECRSGRAGANLLLSLLVVPGVFASSVPT VTADLHSNGNSASVLDPEIISKAVLDADLSVNAINLAAEELPRVYNVGAVLSHPEGIAYFEEAIL DAMATYNIDLVAKSVHMSLNPIRMAENVCEQLISQQVYAVVISSPLKGELSPAAVSYTCGFYSIP VIGISSRHSSLSDKNLHRTFLRTVPPYSHQADVWMKLLRHLGYQSVVFVHSSDNDGRATLGRF HSVAAQHKNAVHIEHVIEFESGVSETDLTAALRNASRRHCRVYYVLYADTSEASKVFDVVKKLD MTTSGYVWIVSEQALKAPNCPDGVLGLELVNAVDERAHIRDSVNLIALALKKLQKDSKVAAP QLNCSNLEHNWDAGLKLVSILKEQVLESGENGHVKFDQRGDRLNSDYDIFNIQRDKESYLVK VGEYMYSEYDMEMELKINLNAVSWPGKATEKPLGFVIPKHLRVATLAERPFVWSRKVNSSTEC SSVEILCPWYNRTADTGHDEAFCCSGYCMDLLHFLASKLNFTFDLYLVEDGQYGNLDSNVEG KRVWTGLIGDLVRKKADMVVAPLTITPERSMEVDFTKPFKYQGITILAKKQDKSSTLASFLQPF QKSLWILVVVSVHVVALGLYLLDRFSPFGNYRVLPSERDEDGLNLSSALWFAWGVLLNSGMAE GTPRSFSGRVLGMVWAGFAMIVVASYTANLAAFLVLEKPESSLAGINDPRLRNPSENFTYATVR GSAVDTYFKRQVELQNMYRIMEGKNFDTVDHGIHALMNGNIDAFIWDSSRLEYEAARHCELL TAGEQFGRSGYGVALQRNSFWVDKVTLALLEMHESGFMEQLDSLWIHNGGRRCESKLERTPA TLGLTNMAGVFILVGAGIFGGLVLIIIEINYKRYLAKQKRRMQIARKAAAKWRGIVERRRSLRR PSHHRIMLPSNIQQLPVLIGSLASGMPSAQTVVPAHSGASKHENLGHQGLSRLKSASTSIKSSHE TRSDLADLPPPPPPPARVQATPGTRMNASTRYLLGAQENKPVSFDINV
>Vd370 MGYRSGSRHLAGVTTLSVLFLCGWMNTTGAVPARVHKDVGTIGIIVEDQDLAKHFLYIASKLV DSNLKAVSKVIQNDDILEAIQSMCALMESDVNVVFGPTSPVSSLHVSSMARHFDLPHIEFRWDP SLIDDEHSLNLFPDPVQIAEAQTALMEYWKWRDIALIYESDDDIIEMRRLLQELQEDGITVNYF KKDKGETFRTLLRQIKERDIRNVVVDLEQKAEREKDKEGKIESFLKQAMQVAMLNENYNYFF LSLDFHVAKLNDFMHSRANITALRLVDMKHHIADDLLRGQDSPQDNKKGSASGRHNQQKAA MARARRDRNDRRLLKRDEHNGEADEEEEADEDASFPPGLETEVALIYDAIMLFKLGVKDLVN

KKSSYTKALPTAKCNGRKSLDSEHLGTELTKTMLRRTFEGATGRVNFNEKGIREDFVLFVTELGTDGLEEIGIWSKSSGLNITNDENEFELSKEEKTKIDDIHLRIVTVMIPPWIMKDEKLSTEDRPRYKGFLIDLLEDMKKRSPRPLDYELYTSPDGSYGVETRYENGTITWNGMIGELVKEKANVAIADLIVSDERLRAVDFTLPFMTAQLVAVVKAPVPRKPGGVWSFFLPLTREVWMYTVVAGLLTALIMYMCARFCLSEYVNTGDGVNGPAEEVDNQLGIVSCLLFVFTTLLHQRMHLDPNATATRVLAGFWYFFTFVILAIIVGNLCESVLYEDEDFSKLETIQGLLRIRGMKFTCIEHGATCRTLMTSHAPVLWEINKRMFKDETPKVKNMTHALAKISQDEHLAFIMEYASAKYLVASSCDLVMTKPFANHASYGIALNKKNPGKTNRLLSEIVLNLQAKGILQEREERWWKTKRFCDVDNDGDFDDVDDGDDDSINEQKVELRTLSPGDLSGAFILLFLGLCFALLINIGEVIVEHLTREKRDTYFNMITVVDHIRFAFKMQTNQVDLSETSLPRNHWKDQLQKRRENRTRENGQKSNDPTSPRKTDSLSSKIPQYQ
>Vd52944 MTWLCAVLASVTVVSISFSTGVHGGTYKIAGVFSAETGQVESKVFARAVDRVNTDNREFPEVQMQAIPIMLKEGQTWENYQELCRQFESGVVAIVGAESSVEDSLISSVSSAVRIPHIRTGFNRELEDPDDLSLGLAPSPSDLAEVVRELILHMGWNHIVYIYDTSTGLLRMNELEEDPEFKGRRLVPIDLSVDANPWDNIIKLSIRHVVVDIESKSVHQVLKEISMSGLSQDYYSFIMPNSDIRLPENSTQRTFFIDADVYTFSLVDPDNREMHWIYRMLEMNSSENEPNLPFIYDSVLQIGHTLNNLTKLQRPIRSSPGNCTLKVAFKDGRKLYDSIRESTKFEGVTGFVEFDDKGARKVKHVHVKLLKDGKLTKVADWRPLDGLTFIKELDPKGEPDEALEHDEGLNNRALVVTTILLPPFLMRDDSPHLKGNERYSGFIVDLLEKLARLLKFQYLIKEVEDGAYGTYNATTNSYNGMIGEILLGKADIAVAPFTINAERYQILDFSFPFLEAGLGLLARREVDPLEHNFLSPFSAIMWFSLFGTMMFATFVITFIARLSPREWSSVTDTVIETHFTVGNCFWYLYSTLMFQRFQHRPNSLGVIVAFFAWFIFCLAIMVSYGTVLGDFIIKYNERPALSKIDDLRSENNRVKFSAIKTGSTMRFFEETEYPNYKQLYAKLDKDAAVRNLSEAIQRVKNEDFALFLETPYIEYFVGHDCSLQQVEGTVGSVSYGIAMSQGSSLQKYLSAGVLSLRREGSLQSMRAKWWNEQHAGRHCPDHLHIVRPTPFTVRFGRVNMLFVFLLGGIILSVAITIYNYVRKQMTIEDKNEFRYFLPTLIREVETLFRKRPVPTNPSPEPTAA
>Vd17150 (25a, MF069507.1) MEILLRVVYELLVTLYFVENGLGQTLNIAVIVEKKFELARQAVEAGLQRAKNDGKTIHWQFVVMDADDELKDLCDIIMENQPSLVINTVRTPGSNYYKLTKEIKQTVRNLAIPTLDLSYGSTDEYQMSGWNGKKPEENDYLIHVTPPGDSYTQAVRELSIKMDLATAGILYDKSVIIDHKYARLLENVPTRHIMRQVSESSADFVNKTKVIQSTDVSNYFVVGTISHLSNALHSAQENDWKPRHHCWVLITKQEGEPVCEDCMNHEVLFVHPADKEGKRIGIDGAYGSEKLDGLFYEEITYYMITRIFADNKYSKQPIRASCREKPATRDDYNLLNALESSKLSTRYGDIYFTDAGNKPGYQAINMKVAHFNYTASKTRQDNEKGFYVYGGDAKAAMWTKADQTALEQFGSVTFYKVVTLIQPPFVYKGNGSGPEFYGYCIDLIDEIKKILKFEYNIYAVEDKHFGSKDKETGLWNGLIGELVKKKAEIALGPIAVMAERETVVDFTVPYYDLVGLSILMKKPEIKPSLFKFLTVLETNVWGCILAAYFFTSFLMFVFDRLSPYSYRNNKEKYKDDDEKREFTLKECLWFCMTSLTPQGGGEAPRNLSGRLVAATWWLFGFIIIASYTANLAAFLTVSRLESPIESLDDLSKQYKVKYAPQGQTTASTYFHRMANIEEKFYEIWKNMSLDDTLTDDQRAELAVWDYPVSDKYTKIWWTMQEASLPLTFEEGVARVKNSQGSDGFAFIADATQIKYATMTNCDLTQIGSEFSRKPLALAVQQNSPLRDQLSSAILKLLNQRKLESLKEAWWNGNPEKKNCDDEGKNNDGISIKNIGGVFIVIFIGVVMACITLVFEYFWYKNKKPRSKVVSVKDHMPQKK
>Vd18850 MAVKSMEYQINRVTTVHHRYEANIPADQQWGVIFPNGSATGMIGMLTRNESDWAANAFGQTLDRHRVVTLSSEFMVQDLSILAGRTFGFQDNYFGLFGAFESNVWTCLLMATLVMPVILVLSRLLERNEGNVNRTLFSRMLVLYGRNLMSVVRTILFESIEDRDLPKGNSGRILIGLWLTSIYLTMSIFQGT

MKASLLISSGSSRIDSMRDLVVRKQVVPIIWRGTAYHKLFQRADMDIYQTVYSRAMEKNGILP GNQLYTNENFMNVLQGRAVIINEQSSIMYNLGRSCDALRGHPGEFYFAKEPVYTHGLSMSLRK TLHPMLKRVINKTIRELQETGNIRKWLNIAMADFFTCEIVNGAPTQEEPTVYTLGLSKLKGPLII YGMGAVATLITLCAELAWESKCFCFIWQNGKLIA
>Vd19098 MTEVTSREGRVVNVNGTLVELLKELARKLNFTYTFIMPPEPVPGLKQSDGRWSGLIGLLVRQEI DLALYDFTPTPDRQQAVNFTVAFDESPYKFLVPKPQPNYKYLFLDPFTWDTWLAVLGTVLIIGPI LWCVHINSKFYDYYDMRDGKGLFKLANCEWYCFGAIIQQGGIHLPDAISGRILVGFWWLFVIV TLTTYSGNLVADLTFPKIRNPYDTVSSLLNSDITWGAFKGHAVIEILKLQQQGLLTQLSAKLAHI ETAHESWALKEVADGKMALIGSEVTLFHYIGKQFIATNLCQYAVAKKEIIRQVKVLAVRPGFPFL ARFNTLLTRIVETGLIIRWKKKYWPKENECTVDSKPQAGDIRRITIAHMEGSFWILGVGFLVSFT LLALEIFRKRRELRDPNGGRPQRIGPRDFKDNLFRKTNYSDKDHYNTDYGAQVGGAGPGAGK GGQSGYGFEPSNTPFRGYSGFPNRTDLIPYN YPARRY
>Vd22240 TDDFWQSIRFRDAGSSLNVTAFRLVDSELPHVMRFHKKMMQNPNYRDSFKNQGTESYLFLDA VTALLTNYDRALQDKPTLLEAYLPQEDGSKGTVGFNCMDQSRFFEHGKDLASLLKQIKLPEGQ TGTVEFLADGSRLQPTIAVIHSSHVGHVKLGSWSPKKGLMLTDKPEALPQIKAPGAITPNKEISV GGILSPPYLMLKRGSDADFTGLIPELLEALANVMPFSYKIHAVPRGQAGARTDNNASWTGLISE VINKKVEIAIADIPLTADRQQHVEYTQPFLMDDLSVVVSRKSQAGRPSLSICFITIFSWQLWLCIL GVFFTFVLLAYLLNRLVSPQEEADSFGRTLWLSAGSFLCRSPGPEGRCRASRLLLLFWWFFLAM VTVLYVSAFVAIVQTVVFGYGPDVFTMRKFVQDAASGTVDIGYVRDVVPGKVLK
>Isc000549 MAHSFFNKTLLDDFVESVLFWYPYDPHAAFSETPQGIKVTTGLLGDIIRELSHSMKFNETPQGI KVTTGLLGDIIRELSNSMKFNYTVSFTPERTLGIRHPNGSWTGLIGSLQRDEGDFALGLMIPTNS RNAIARPTTEVYIDEITIFAGRTHSKSMNVFSYVWVCVVIAMFTLAFLSTGFDYFYEHTVRNRK SFSERFFTHLWEYFENLLGKGSSVESDWHATRLLSGFWWIGVTVLVFAFAGQMRACLMVKSQ EAMIRNVDDLARRSNVKPYTLSGSILTTILRNSKKPSYTKVFQRIVKGRGQTELHQIYGPKILKE VVQGKSVVIADRGSFTYKVARTCRNYTDGEFYIAAEPILNFRFVMYLSATMDPRTQWEINRRL VWLRENGIVGKWIKMLGDWEHCRQESSRVTLSFEDTYAIFVMWALLIAASLVAFGCEKLHHA CAAAKERPSQRPGPILGWGVTTVSRKRPKVAKPFQAYNFKV
>Isc005598 ILRRLCEDLLPDDVVAVLYLTNSAVFGSNAASVQYVLQLLGYLGVPVIAWNADNIGLDQRVSQ ARVLQLAPSVVHQVAAIFAILERYAWYQFAVVTTQLGGHEDFVRAKNEHIYSFSVLDVYTLRG HTRQEFRSQLEPVATGEARVLLLFASKEDSREVFAAVGQLGMTSKNYVWIVTQSVIGAHPGLAP QEYPAGLLGIHYNTSLAKLHDEIERAVLVLGHGLELFVNEPANANLSLNPGLRCYEVGRAHWS QGDHFFRYLRNVSIEAKGSPNIEFLPDGTLKYVELDIVNLNKDGYWDRIGGWTQKGIDIKDIV WPGNELVPPRGVPEKFNLKVTFMEERPFLNIGQPDNETGECESGRAVKCRVVPEAMLQGINDT AARKNSTYYKCCLGFCIDLLQKFAQDLGFTYDIHRVEDGTWGVKDNGTWNGLIAELLDKKAD IVVTSIKINSDRQMAVDFTVPFLETGIAIVVAKRTGIISPKAFLEPFDTVSWLLILLVSIQVAAFSIF VFEWMSPSGYDMRITPPREISLFAEHRFSLFRTYWLVWAILFGAAVNVDCPRGYTARFMSNVW AMFAVVFLAIYTANLAAFMITREEYYNLAGIEDNRLQNPQQTDPPFRFGTIPRGNTEAVLKQNK PQLYAYMRPFNRSTVTEGIRDVKRGELDAFVYDATVLDYLVGQDDECRLLTVGSWYAMTGYG FALPKKSKYLAMFNRQMVEYRERGDLERLQRFWLQGACKPDKPKRNASNPLDVNQFMSAFL

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>Isc007957 (XP_029841705.1 ionotropic receptor 93a [Ixodes scapularis]) MNNKNMMTFHREFVSVVTQPIDDDFQKLVVGFPDGANVLAAYPEIADNDCPVEPGCQLPLAM ETVAKTIGDKLEKGTYRTTEFFTTKFIFSNTSKSLLLASGKCGQCARFIIRSVAKVQGIQEFLKIG EWTPAVGLKMTHKQFFPGIMGNLGGIRLTIGVINDPPMSVVEMSPDRKTVKNVTGTMADMVE ALAKGLNFTYTWKVPKEEIPGSKENGNWNGLIGMLATGEADLGAYGFSVTKERSEVVNFTSA YDESPYKILVPKPRANYKYLFLDPFTWDTWVAVLVSLVLIGPILWGIHCASPFYDYHGLRDNKG LFLLQNCEWYCFGAIIQQGGIHLPEAISGRILVGFWWLFVIVTLTTYSGNLVADLTFPKIRNPVDS VENLVAHRGYMRWGAFKGQAVFELLKSQEQGPLKVLSDRMNVFEPNHEMWVLDQVRLGYM ALIGSEVNMFHYLGRELNRTGECDFAVARGEVIRDVKSLAVAPNFAFLERLNNEPDHDGRPPPR RLKRLVESGLVMRWKKKYWPQDNECTVESKPQAGDIRKITLRHMTGSFWVLGVGFFSSFAAL FVEFVRRKRELTAPPTHKPPTVIHTKSPFFTRTEYSGKDTLTTDRFATDYGGRGPRDNAGFAFSP PNSPFRYNGYPNNRSDLIPYNYPARS
>Isc008225 (IR25a) MQPPFIVRKNASNGENQFEGYCIDLINAIKEILKFEYVITEVKDKMFGSIDKNTKQWNGMIREL VDKNADIALGPISVMAERETVVDFTVPYYDLVGISILMKKPEVNFLMYLFDRLSPYSYRNNKE KYKDDEEKRDFNLKECLWFCMTSLTPQGGGEAPRNLSGRLVAATWWLFGFIIIASYTANLAAFL TVSRLDSPIESLDDLAKQYKIKYAPQKDTSSMTYFERMAYIEEKFYE
>Isc008266 MGTPEVLCLLLLGCLAAHADIKIGGIFETGDDVLEMAFSSAVDRVNTMGLAEPGTQFVAAGSR LLARVEHIERLDSFQASRKVCSLLEEGVAAVFGPQSGEASAAVRSACDVLDVPHIETHWDYRA RPDNHSVNLFPHPAALGKAYLDFIKHKDWRTFAILYEENDALIRLQEILKDPLMRERKVVVRQF ESGVEYRKILKDVGKSGIKNIVLDVPTERIHTALKHAQQVDMMSEYHNYFITSLDAHTVDMED FQYGGTNISGFRLVDVNAKEFDEVARDWLTRRLRFSKKGEKEENFYRTKVALMYDAVRLFATA LRDLQPDNGPKIQVRPLSCETEEPWAQGNSFVKYMRMINVQGLTGNIRFNPNGHRTDMRLAIL EITHNGLREAGEWTMHGGINITTNYSRQLEEARLHLMNKTLIVTTLVQAPYTMLKENHAELEG NAKYEGYCIDLLEEISKLPDISLKYKIREVADKAHGRRDDKNEWNGMIGELLHGKADLAIADL TITYVREEVVDFTMPFMNLGISILYRKADKKPPWLFSFLAPLSLEVWIYMSTAFLGVSLFLFVVA RFSPYEWVNPHPCDPNPTELENRFTIWNTLWFTIGCLMQQGCDVTPRALSTRVAAGMWWFFT LIMVSSYTANLAAFLTVERLVSPIESVEDLAKQTTIQYGSLQSGSTQSFFKESEFPTYKKMWHV MQAARPSVFTESNQKGIERVRRGKYAYLMESTSIEYAIERNCDLTQIGSLLDNKGYGIATPPGSP YRTMLSQAILQLQESGTLHVLKERWWKKRHIVKKCPKEEASASKGTSALGLANVGGVFVVLL TGSCIACITAIFEFIWRSRKAVPEEREPVCMELCRELKFTLTCGGKKPVQNKSEDRQPPGENGLP FMPLTGYNAVVSKDTFS
>Isc009282 MAPGSRPRMRASGRRSAPQWARSHRSHGAFRAAPRPVAGAMARLAPPVLVAWLLLVPAVLLV AVDSTPALLAALPPRSAPQLARALRRALARWGAGPGDASATSWVVAAFSAVPDTRAALSALCT ALEGHAPLLVVMPVLAYTGGYLDRAAQEASPLYLSLDPGLPELTEALFGLLSQNRWYHFVLVT DESAASSMLAQRLGSLCHGVPWRPMLRLALPGPTQPLLGPLAKITASQARIVLLFVEAPMVRA VLDAARTLGLLAGDHLWLFVERDDPNPASPHPCGGDVEGSALKGCPLGALSLQLRQSHVERT DAPRLLAGLLHDGLSRWGPIEYPLALRNASGAPTPSCWEEPSARREMFSQRLHGYLRAAAAD AVQSQRFPPPVFDILNLVPAEGGAQWRSVGNVTKGSAVLDAVLWPSTGEPTLMGPRPFGQPRFR VVTAYAAPFVMAATRLRNGSCLTGVPCLQVSTAISDELAALFAHYHRTGGHTRHPGYNVTCCA

GIAIDLLKSLARDLSFDFDLYLVADGSFGTDRGGRWGGITADLISGAAHVAATAYSVTSSRSRRVDFSVPFFHSGVSCLAYAVKRDVPLSAFLVPFSVPLWLAIFLSLKVTALAAALYEWFSPFGLNPWGRQRTRNFSLASALWVMWSLLFSHLVAFKAPKSWPNKVLINLWGCFSVIFLASYTANIAAHFAGLFFQMQVHDFHDTSVPEGYVFAENKRLWEHIQRFGVASLEQGLESLRLGTLDVLIGDTAVLNYYRANEPSCRLRLLGDSIFDDAYAVGMARGFPLTAAVSELILRYNAVGYLDQLHGKWYGRAHCLQDGLLQRLDKPMPLGVRAVAGLFIMLLVGLLAGSLVLILEHLVFRYALPGLRARSKQCFWKSPNLMFFSQKLYRFINTVELVSPHHSAKEIVSNLREGQIASLFQKSVKRKIKEEARRRKSKSQFFEMIQEIRRVVRQQQTERDEESPTSPHEGPFSATSSIGPLLVREPSPPSGSSSSSAPTSSWVHGALLSVSLEELPSVAPPACRRRRSHSLGDLSHMRPAWQPRRAPPSCASDLDDVRLRALSREQLLHRWRDSERRLLNLLREALREKQALERKLAFLHSALRNKPP
>Isc010976 GASFSFRRLLKKQKLLRGETGRVRFDDRGDRLDSDYDILNVVRGNHAPVGQYWSMSMELDLELDRVVWPGNRTETPLGYVIPKHLKVATIAERPFVWVRPVPDESDCLPSEIFCPWTNSSDGIAYPFCCEGYCMDLLQSLSQKLNFTYTLYQVQDGQYGTFDFVNGSTHKRWSGMVGDLVRGVADMIIAPLTITPERSMEIEFTKPFKYQGITILAKKANKSSTLASFLQPFQKTLWILVMVSVHVVALALYLLDRFSPFGRYKLPNSDATEEDALNLSSAIWFAWGVLLNSGIAEGTPRSFSGRVLGMVWAGFAMIVVASYTANLAAFLVLEKPESSLSGINDPRVGGVFSEYFTRVSSPGDETTRGRPQREMALASATRILPHTKTFSSGGAPNIVNDLQLDAFIWDSSRLEFEAAQHCELVTAGEQFGRSGYGIGLQRNSFWVDKVTLTLLEMHESESPLSVSFIILSSRQGEDTVLPRAWLGPFISAGVFILVGAGIVGGIGLIVIEIVYKKHQTRKQRRLELARHAADKWRGAVEVSQHTPTLFPTMRHRGVQLVAPSAVPLTLSGLPQNGANIHQGLNSHWNDGHRSLLHHK
>Isc012402 GGIFESGSQKAQLSFRYAIDQINKDISILPRTELMPIIHEVKQKDSFTASKALCTFFKQRVSAIIGPTSEAVTSFTKSACTNLNVPHLQTSWEPKSNRNPYTLNLFPDPEVFGKAYLDLIINKKWKSFTVLYEHQDSLILLKDVINSSLAQNHSVSLVQVNPKLSFKKMLKDIGYQKQFNIILDVKTESLPLLFRQAMEVNMMTYYHNYIITSLDLHTLDLREFVGLQANITAFRLVDPSRPEVMNVLRDIKIGSALWRYGADNHTSPAHIDTDTALTFDAVALLANGLHNADRVLQTLDLQSLNCEHPKPWRHGSSLLDAMKMITIRGLTGDVRLEEKGVREEFTLDVLELKARGLKQVATWHPRTGLSYFANYTLSEKEFTDELEGFTLKVTTVETKPYTMVYPDSENKTGNDRFYGYAIDLIAMLAKEIGFKHEFYLTEDGKYGSPQPNKEWNGMIKELLDRKADAAIVDLTITYERESAVDFTIPFMNTGISILFKKAEKSDPSLFSFLYPFSVDVWLYMLTAYLGVSLLMFIMGRFTPYEWVSPHPCVPEEGDLQNQFNLPNSFWFTTGAIMQQGSEIAPIAISTRIASSMWWFFSLIMISSYTANLAAFLTAQRMTAPIENANDLAKQTKIVYGCKEEGSTCLFFKNSDDPLMKRMWTTMLAARPKAFADSNEKAVERVKKGNYAFLMESSSIEYVVERDCNLTQIGGLLDSKGYGIATPPGDNL
>Isc1653 CW012407-PA conserved hypothetical protein|protein_coding|DS907449:516555:547561:-1|gene:ISCW012407 ,>EEC16531.1 conserved hypothetical protein [Ixodes scapularis] MGHPPYVIAKSSGRFIGVAAVNGTSELRLTGFAIELLDILARALGFDYNVRVSGEDYGSLSPNGTWTGLVRQVYEREADLGVGDISITRERLEYVDFTAPFMQNGIGILYRNVDRQFEEIPHFLRPWTSELWLYVLTAVLATSLLFSFLSRLSSAEWVCKRRAGPSCRKLAGKEHLKNRFTLINSFWFVLASLLQQGTDMFPRYELQLLLFFVELAKLT
>Isc015703 MNSSVLPHLIVAFPDSPPFMTPKYRNGKLYLDGIFGHILQAVAQFVPFSYELVYDRKRTYGVRLPNGTFNGIMGLLQSGEADLAAAPLIVRQDRAEAINFTPVIYTTYLSLLAVAGEPTANAFSYILAFD

WQVWAILFVSIPILSALLAAIETRRARNKHKYLREFHDNFWDLLRTISYEGLDAAIRTTPGRLM
MATWWLTVLVLTNAFAGHMKACMSIKTEPPRFSSIDDVVLHPKIRPMIWKDTGYEFYIRTSEKE
SLRMLSRMAQKHGGFVPLSEMQSPAAVAQVYSGRAVYVNDRDSMLYLLSKQCGRTGSLYVAP
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>Isc016542
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>Isc017534
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STLEELSMQNKVKFGTLRTGGVQEYFEESQYRTNKLIWEAMKTERHVLVGTRQEGVGRVRSS
DGKYVFFTESLFADYVNGRRPCDTKVIGEVFATQYFGLAVTPGSPLREKLNEAIVNMTESGEID
EMKAKWWASECDAPPPDEPMRLELFLHIIFYLACLLIVGIAVALLELLVRGCNKWRFSRLRAVS
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>Isc017535
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VVDHLAWDTFVYVYDSDNGPSKLQRLLSHQFKNSVSMRYAKRISNSSDANDFLRLLETTDRES
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PQELGEIITRNLREVRPKDTEVDVCSCNFVLLVPSIVLQTLLCFYVLLQRSFQGLTGSIRFTSDGC
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QRVPDAQDRMGNDRYDGYCKDLIDALARELDIKYELRAAEETVYGRRDHKVRGGWTGLIGE
VLRKASQNAQSPSTATVINAERKEAVDFSQPFMTTGIAALMLKPSDLPGRGMFTFLAPFSLELW

IFFVSSFGLVFVIMFFVSFFTTRVSSTKPGMEHSACGTIYKSLCYSLEAFTPHYIDSYYARPYEVLRSTGSYRRRYPIFPTLSRSISGRVIGNIWWLFIVFVFSAYTASMVPFLSKESRIRPIRSVEDLPLQSQVDYGFSRQSMAKKYFENPNLNSTAHRRMWEVMNSKPDVFKNSNAEGVDAVRSSKGNYVFFMEANAVFVNTQRPCDTMQLGGTFGVRSFAVAVPKGSSLRKHLDEAIAHLSETGELDKLKKKWWTQKSYCQYPERKKDETVMPLDNFVFFILGGGVALGILVGLIEFI
>Isc022877 MAAKYRNTTLRLSNVGWYPYVFTVNQPDGTFRLKGITGSMIDYILASMGIKYQLVDPSDHKWGNLEPDGSWSGMIGQINRNEADLALGPFVLTEREAMVANPSPPYTDEDMIILSGVAKEHKSNVYGYISAFDLHVWMVLLCFLGFVATVAVVAEYLLSNPEMSIRQRRQRLTRIFWTFVASVFLESSTFNFTSHSQRLLFGFWFLMIVVLMNTFVSYMESALMLKEETDRVETIEQLALHPDIQPMVFEAAGFLQVIREAEGQAFQKVLRMMEEYDHEEEVHGEELFTPPYLSMVLKRKAVFLMERISLLARVSQHCYDVELKGQGLFHLGRKRILQIKMVFYVRKTMDPVLQASATPPQEEIFKRVRWIMDSGLNLHWHEDLIPDPGPCWTKFHPDHLHDYASLNYQDFAVIFYLLLCSHGLAFCGYLSELVLFHWCCLKSRSRIGPNSYLN
>Isc023268 LYQVVFQAAIDIVNEDSSVNLEPDILPVVDILPEDDSYEAVRDACRLLEQGVAAIFGPMSGVSSVHVSSVCDSLNVPHLETRWDPFMEDSDDSINIFPHPNVLAEAYTALMKYWEWSALAILYDEDDAIVQLKDLLQELREDGIEVSYFFRNSSDSFRDVLKKIKEAEYVNIFVAIEDEDLEVFLKQAMQIEMLGEEYNYLFMSLDFHVADLSDFIYAKANITALRIVDVEDPVADIFQKKIDENLLRTLSLATLRLTIVKHFVAKKKYLELRQVIGTKSRHSMSSEVLATPAITYGIYNAHFPQVAFDGLTGTVKFDEHGFRKDFQLYVTELGTDGLEEIGTWSPTSGLNITKDEEEKGDDVVLRVVVISVSFVLHKPFVIVNNDEDGSPKFSGFCVDLLQELSAMLDFKYELHASYDGRYGSLQEDGQWNGMVGELTNGNADLAMADLTITEQRERVVDFTLPFMSTGLAIVTKKGEPMRPGGIWSFFLPLTREVWVYVILATTCTIFVMYIGARLSFREWTLVEDGKGEECMENRFNLFNCFLFVVTTLLHQRITLDPRAPATRVLAGFWYFFTFIILAIIVSNLCESILWEDDGPDYDTAQELLRARGFTYVVVHHGSSQKFLQDSKVPLHQRISSLVERNYRNLPTSVGDGLQRVKDEDKVAFVMETASAAYATQEDCNFSRTDPFVFHSAYGFATPRDSPYRSKLSEGILKLQENGRLQWIQQRWWNPKR
>Isc023274 CNLISSGVAAIFGPNDPMIGAHIQSLSDSLDIPHIESRLDLEPDAKDCSVNLHPDPHITGKSMRDLVDYLNWTRIAVLYQDDISLISLQELVRPFPPKNVQYLFRRAENFTATLMDIKSRGIYSMIIDVRPENLTAFLRAILQIQMNDYKYHYHFATYDIEAYNLEDFQYNFVNITAYRMVDSDNQTVRHIMKDMEKFQPFGQNILNRTNVIITEPALMFDAVYAFAHGLNDLQRSTTLRPANVSCEDEVSWTEGTSLFNLISMVDFYGLTGNIRFNEGNRTSLKLDLLKLRQNFLEKVGEWSTNDGLNITNHNAFHDFGTSNITLRVTTIESRPYVMMKDNKNLTGNDRFDGFCIDLLRTIADLLGFNYELYLVPDKKFGVENTSTGEWNGMVREIIDKNADLAVAPMTINYARESVIDFTKPFMNLGIGILFMLPSGMPVKLFSFMSPLDVDIWLYVLAAYILVSFTMFIVARSDGAKTSRTKKSRRYTEPQTRVLLYNLNIFFKLSCQKQLQSCDLNPKAMSTRIVGTIWWFFTLILISSYTANLAAFLTVERMITPIESVEDLAEQSKIAYGTLDSGSTMTFFRDSKIETYQKMWRYMENRPTVFVSTYEDGARVLQGNYAFLMESTMLDFMVQRDCNLTQVGGLLDSKGYGIATPMGSPWRDKISLAILDLQEKGVIQMLYNKWWKSPGLTCNRDDKNKEGKANALGLANIGGVFVVLLCGLAVAIVTAVMEFCINSRKHAQTDRQSLCSEMAEELRFAVRCRASRQRPALRRQCSKCIPGTTYVPSAMDLPQENGIMQMLE

Table S3. Protein sequences of OBP used to construct phylogenetic tree.

Accession number	organism	Abbriviated name
XP_022672530.1	*Varroa destructor*	Vd1
XP_022666940.1	*Varroa destructor*	Vd2
XP_022645714.1	*Varroa destructor*	Vd3
XP_022653293.1	*Varroa destructor*	Vd4
XP_022653281.1	*Varroa destructor*	Vd5
JZ172282.1	*Amblyomma americanum*	Aam
OQR79252.1	*Tropilaelaps mercedesae*	Tp1
OQR73552.1	*Tropilaelaps mercedesae*	Tp2
OQR80083.1	*Tropilaelaps mercedesae*	Tp3
OQR74725.1	*Tropilaelaps mercedesae*	Tp4
EEC12103.1	*Ixodes scapularis*	Ix1
XP_002399632.1	*Ixodes scapularis*	Ix2
XP_002433530.1	*Ixodes scapularis*	Ix3
KFM70022.1	*Stegodyphus mimosarum*	Sm1
KFM79180.1	*Stegodyphus mimosarum*	Sm2
XP_025016893.1	*Tetranychus urticae*	Tu1
XP_015782945.1	*Tetranychus urticae*	Tu2
XP_015791022.1	*Tetranychus urticae*	Tu3
XP_015794342.1	*Tetranychus urticae*	Tu4
KPM10930.1	*Sarcoptes scabiei*	Sc1
KPM10909.1	*Sarcoptes scabiei*	Sc2
OXU16759.1	*Trichomalopsis sarcophagae*	Ts1
OXU23289.1	*Trichomalopsis sarcophagae*	Ts2
EAT43854.1	*Aedes aegypti*	Aa1
EAT36416.1	*Aedes aegypti*	Aa2
XP_019538846.2	*Aedes albopictus*	Aal
KPI92605.1	*Papilio xuthus*	Px
OXA59970.1	*Folsomia candida*	Fc

XP_002039957.1	*Drosophila sechellia*	Ds
XP_017053738.1	*Drosophila ficusphila*	Df
OTF72123.1	*Euroglyphus maynei*	Em
ODM87445.1	*Orchesella cincta*	Oc
XP_002066115.1	*Drosophila willistoni*	Dw

>DgalOBP1 (GAIF01000051.1 lcl|ORF1)

MKAIVLVALAAVIYVVSGDTATGDHNEDTSKFGKWRSCIAEKLPADKKPVFDGCATKPGGTD
QSKFRRGLGCVLESYGLTKDQEVDLKKMGSTAASVSSPELKKAFQECPKDEKNSAEDRTIKC
VIDHLETQCKVEQ

>DgalOBP2 (GAIF01009917.1 lcl|ORF5)

MKAIVLVALAAVIYVVSADTATGDHNEDTSKFGKWRSCIAEKLPADKKPVFDGCATKPGGTD
QSKFRRGLGCVLESYGLTKDHKVDLKKMGSTAASVSSPELKKAFQECPKDEKNSAEDRTIKC
VIDHLETQCKVEQ

>DgalOBP3 (GAIF01034646.1 lcl|ORF7)

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DMSKFRRGLECVLDSYGVVKDHRVNLQKMSRTAPTVRSAELKKAFQECPRDDKNVSLDRSIK
CVIDHLETSCPLDKNRG

>DgalOBP4 (GAIF01001373.1 lcl|ORF7)

MKTLIFGFVVVFAYLAAGDTATGDHQPDTNQFGRWRSCLTSKLPADKQATMQGCVSRPGGT
DMSKFRRGLECVLDSYGVVKDHRVNLQKMSRTAPTVRSAELKKAFQECPRDDKNVSLDRSIK
CVIDHLETSCPLEKNRG

>DgalOBP5 (GAIF01024919.1lcl|ORF6)

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CVIDHGDVLSARKEPRLSLLNPTRRQWAGKTAKRGRKKQEEARSPHRGTWH

>Vd1
MKVFVIIALVGMAKAAPQAPASATPAKVPVIEWGKCEQLKPSESERTSKAAVVDKCLQSLPLP
DPEKATQQEIDKHRESVTTCALKAEGWFDDEGVYKFDRARNEIKNKKLDSEVEEAVLLKHDA
CQKEATEKHDDYINQVQLYQACMDYNISQICGIKVMV

>Vd2

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>Vd3 MKTFIGLVLVGMAMAAPPASGGPEAGKPPTIEWGKCSQLKPSDSERMTKAAVVEKCVQSLPLPEAGKASQAEIEKHREDVTTCALKAEGWFDDKGVYKFDRARDEIKNKKLASDIETPVLEKHAECQKEAGEKHTSDYIKQVQLYQACMDFNISQICGIKVVS
>Vd4 MNAAVYIVTAMLACCCSADTASGDHASDTSQFGKWRTCLADKLPAKKREVFDECFIKPGGTDMNKFRRGLNCVLTSDGLLKNHKVDLKKMSMTAASAGSPELKKAYENCPKDDKNTSEDRSIKCLIDHLEVDCKLASK
>Vd5 MYENRLLHLNGICGGGIQADRCEPAYLPDTVVRIIVKMKTLVVALLASTACLTAADTATGDHQPDSNQFGRWRTCLKSKIPENKQPGMEACINKPGGTDMSKFRRGLGCVLESYGIVNNHRVDLTKMRSSASLVTSPELKKAFMECPKDDKNSSLDRSIKCVIDHLETSCSAVKAQG
>Aam JZ172282.1 Amblyomma americanum cDNA, mRNA sequenceMVAFKAALLLCVLVLPAAYCQSAAEPPRPDINWGKCPQLQPSKEERQQKALVIDTCLEKVPLPDVEHANETVIQQHREDVTTCALHSEGWFNKNGQYRFDRARTEILNKKLAADVEPKVLAKHDECKKEAEEKFAHQFVAQVQLYQACMDYHISQICGIQIQGAQGGAAAPAHG
>Tp1 MKTLVIALIAGTACLAAADIATGDHQPDTNQFGQWRTCLKSKIPQDKQATMDNCVKKPGGTDMAKFRRGISCVLESYGVVNGHRVDLRKMGSTASSVRSPELKKAFQECPKDDKNASLDRSIKCVIDHLETSCPLVKAQG
>Tp2 MKVFVVMALMGMAMAAPQAPAAPTSAKAPVIEWGKCDQLKPSENERTSKAAVVDKCLQSLPLPDPEKATQQEIDKHRESVTTCALKAEGWFDDKGVYKFDRARNEIKNKKLDGEIEAAVLVKHDACQKEATEKHEDYINQVQLYQACMDYNISQICGIKVMV
>Tp3 VEQFFTSNWGECEPLKNPLVLPEISDGSTWERCRAHIPLTPEQVEEALPNLSRCMLKVIGWVRPNGNMNLTKYMDYLSQAGLDEKTLELTKIAHEKCSQRALSDGAGNYKEQDKIYVECIFRHFDKTCPPNFQAAVKQGYIVGITQISFVPRYDDVEMEVDSDADAEDPNGAYPGPGADDANASSGGSSNNNNKDDSNNNNKADSNGDAQ
>Tp4 MSKVLTLYTNGFNVHKLGALLVSMAYSFSPTEDRPVIEQCLGQHDNETVMELIKCYMEKMNIMGGGNMCEVKKLKDLLASKMTAAPPVATAVLQKYAECICQNSGAEGMVCVQQKTMDYAKTFCSAIVGDD
>Ix1 MWTSAGKSALVTLGVLLAVGVGLGDAGPVDPKKTDKPEKQTIHEFFSSNWGACEPLKNPLVIPEMSNPTTWVKCQKHLPEHPQDIEEYLPRLSRCMLKSTGWVRSNGNMNLSKYLQYLSLLGLDDETMNGTREAHKGCIAKAYKEKDYKTQDKVYVECIFKFFTKSCSANFQGAVKEGYIVGITQLSFMPRMGPLEVVDDVEAEVSEDDAPQDVLPVTNSTSTS
>Ix2MVAFKVSVAVLLCVGSAFAIPAGGKDLDAAAQTQAGVPPRPQINWGKCPQLQPSENERQQ

KALVIDQCLDKVPLPDVDTANDTVIQQHRQDVTTCALKTEGWFNSNGQYRFDRARTEILNKKLAKDVEPQVLSKHDECKKEAEEKFAKNFVAQVQLYQACMDYHISQICGIQIAQAAEAHPQGAQQG
>Ix3 MKILLITVVVCVFAATDASRRSTRRQQFTDWRNCMVEQLPSEKKPIYDACYNRSRGTDMHKFREGLKCVLTDYNLLNGTKIDLAAMTTRASSVSGKLGQAFTDCPKDDHNRNAAKGVKCIIDRLETDCPVPTGSTAH
>Sm1 MLLSVLLTLFGVGVILAAPPTTVQPQNEASLESQNYPVPQIDWGKCPQLKPTEADKEQKRLVIQKCLDQNPPPALETVTDPKQIDDHRELVTTCALKTEGWFNEDGSYKFNRAKTEIESKKLDSQVEKNISKRHQECQDEAVKRFPGGYIQQVQLYQACMDYHIAEICEIELIPPPGGFPIEEFGDYDESPLQPEQPEKSQETTTQPQAQPASAK
>Sm2 MKCFVLAVLCFAAVAIAQEVPQVNWGKCPELEPTAEEQKSKGEVIQQCLEKNPPPAEGASLTQEQIDAHRETITTCALKTEGWFGADNKYNYQRARKEIQSKNLKPEAEILAKHDECSKEAKENFPDNNIPQVQLYQACMDFHITKICEIKITPPATEAPAAASA
>Tu2 MINSLSHSVSLCLIVLVVNSSNCAPQATPNRQGGFSGQLQGPPQPPQINWGKCPQLEPVESDKKAKADIISSCLKSIALPENMTQETVEKHRTEVARCALNAENWFTEDGKYRYDKAESEIKAKKLSQEVEPQILRQHGECRKEAEGQFPSGIAQIQLYQACMDYHISQICGITIVGPSSPQ
>Tu3 MILITLCLVVLAINSSYGQPQRFLAPQPTSDQLEGSPQGGFPGQPQGPPQPPQINWGKCPQLEPKESDKKAKADIISSCIKSIPLPENVTQESIEKHRTEVAICALNAENWFSADMKYRYDKAESEIRAKKLVSDVEPLVLRQHGECRKEAEGQFPSGIAQVQLYQACMDYHISQICGITIVGASSPQ
>Tu4 MNYLSLCVFIIFFLTIGFSESARLPRSTSSPATSSSTTTTSSTVNNKKNEENQPSTSSASSSAGSATGGPTINWGRCPQLEPTNEEKIKKAAVITKCLESTPVPVNITRETVELHREQVAACALRMEGWFNGQGLYRFDKAENEIKAKKLTREVEEKVLSFHRQCKDEAEEKYPVSSNQLIAQIQLYQACMDYFISEVCGIEVQIAGSEGSSE
>Sc1 MMAIHQLFLTTVASLWSVMLMTAVVALPQPLNTSTNNKPADSISTASSSSIDSNVPLMASASSPSGQNLRSSSQQPMLLTLEQQQELLDQLAQLQRQTQQLLAAQQSLAAVAAAAAVNGNNNGVSIGTPLDGNSNNDAGSHSPITSGSIQYHRQQNQQQTHPTTQQLNNPTSNQQSAAIRNDNIDQGSLEQSQSKSNQLNQMINNAQNSQSQSMSGLPQSPQINWGKCPELEPSEQEKLAKANVITKCLETTPLPANITRESVEQHREQIAGCALRSEGWFTPNGGYDFSKAEKEIRNKHLQADLENQVLNYHGQCRVESEEKYPTSNSSIIAQIQLYQACMDYFISDVCGIEVNDTDSPQF
>Tu1 MKNLQSITILCLIFGFIVSTVYSQPLGSSDSNPDTQDTKEASTSVNDKSSDQEGSSESDEDAPTPVAGPHRPPTINWGKCPQLEPKEAEKKQKADIIRTCLKSITLPENITQESVEKHRTEVAKCALNAENWFAEDGSYRYDKAESEIKNKKLQPEIEPQIVNQHSECRKEAEEQFPSGIAQIQLYQACMDYHISMICGIQIVGTGYSQ
>Sc2 MIANMNLYALAIILLLAHLCDAQSTEKLDKSKLKQQQQLPQRPKIDWGKCPQLEPSEKDIKSKSNILQRCLKENPPPNQDSITPELIIGHQKNVTECALKIENWFDKKGDYKFEKAEKEIKNKKLSSE

MQKALVGSHQDCAEVSKTQKKQSKTPMDVVEQVQIYQGCMDAHITQHCQIKIGA
>Ts1 MSSNLKMINMIGSWILNVTSSNKSRYWKNKYEACFDYKEGSVIICGQYLISMSRHLIITLTLFSAVFVVKSLSPEEREARDKCLKENGFSREPDFIGNDAVDMRTKCYAACALRGYGIMNEDGSIDINKILEHISDTKNKDIDVKKSLIIPCAEKKGETDCDTGYLITNCVVLASLSQEDIDARNKCLKEHGFTIEPKYVSAYKTIDTRAKCYASCLMRETGVIKEDGSIDLNKVLEKISDPENKTLDEDVKKSFIPCTEKKGDNDCDTVHQILTCIVATISILKESMKIV
>Ts2 MLANTARLNAFAMCMLQQFNVMDSNGMVNPDVMSYSIISTVPNATAGISQQCISKRGIDAVNTARMIMNCYLRANQMVLALSRRDRTYIIRINYITVACPVLAYLQASFSPLIENDFHAYEADCGAKSGASDESIEAARRARQLPQSPQMNAFALCMMQKYKVMAADGSVNPDVRSYGIITDGPDNTWRVSEHCRDLDGNSSGETARMIMNCYLDNNQLVMGLTPRVSA
>Aa1 MQVLNFLCLVLLCLVLEKVAVAEECIKFEDHKDEILNCCKYQPPYPKDDVKECVQEAQGKSGGDKHEFFACLLECYLPKIGIINGDSIDEDKISEHLQSLDENARDILLAAYKECDESTTGTTRAQCSSYALDLETCVLQKLDQQCPDEFYNPSEICDKLKSGVEICH
>Aa2 MKATVTSVLVLLAISHATLADPAAPDNVPASCLNKNFNVDPFECCKTPKLLDEGTVKECVHSFPPPQNAQDEIKPDCMSECVMNSTRIFDRRQNVNDAKAMETFLEKLNGKSVWAEIVQKAVKQCLDDADNRKEEFSRDMKALQQKFPKERICSPAAGFIMECVHVSVYKNCPASIFKDNLAGCPAIKKHLNVDNCPFYTIFPEKKAPKPVKRH
>Aal MKAIVASVLVLLALSHTTRADASAPDDVPATCLNKNFNVDPFECCKTPKLLDETVVKQCVKSYPPPQDVKDEIKPDCMSECVMNSTQIFDRRQNVNDAKAMETFLEKLNGKSVWADIVQKAVMQCLDDADNRKEEFNRDMKALQQRFPKERICSPAAGFIMECVHVVVYKNCPASVFKDSLTGCPAIKKHLNVDNCPFYTIFPEKKGNKAKKH
>Px MSKLYCVFLFLGLAVSLRHVRALSQEDIAAIKTGLRPLIAECGKEFGVDEADIKKAKESGKIESLDPCLFACIGKKMGMINDKGEFDVEKSSETVKKFVTDKDEQKQILEIIEKCSSVNDEAVSDDKGCDRAVLLHKCMEPYKDQGNSLGDLQKSYADLVIECAKEFPITTEDIAQLQNKQLPDKESVKCLFACAYKKAGMMDDEGKMSVEGALEVINKYLADDPDTMKKAIDFTNACSTVNDAEVSDGTKGCDRAALMFRCSIDKADEFDINL
>Fc MQPTLHFVLLCTIGVLHFQDGVFAAEEKPCNAVVADLTKKQLGGISACTKALKFKDAKEKAKKTTCIMKCVLKKEALLDEKGQLTLEQFDKFLAKHFPDSMTEKANSTFRPCVDGALKGMDDTEEFCKDYDPMIKCLLSTFPNESDKSCKQIMADMTKRQLSGITKCIKGMKFKNGKEKAAKMNCIMKCAMENEGLVSKTGDISREQIDEILIREFPSSLLERANATFQPCVEKYAGTMDANPETDPLCATYDPVIKCLISALPNLCPPA
>Df MLRTGILIFVVLSQFLEGPLAIRIHCRHTERIHEENIHHCCKHPDGHNDVTEMCAKQTNFKLPNPNEEAIEDVTVDQAMVGTCWAKCVFDHYNLMENNTLDMAKVRHYYKRYHKIDPEYETEMLNAYESCHSKSEDATEQFLSLPIVRAFATSKFCKPTSSIIMSCVIYHFFHNCPKNRWSNTTECVETLAFAKKCKDVLTTM
>Em

QLPRAPKINWGRCPQLEPTQRDIEAKSSILQECLRQNPPPQSESITQEQIIQREYKYEKAEKEIKNKNLAKEMEKVLLESHKQCSQIAKDRKQAVKNLSNVEQVQIYQGCMDAHITQNCQIQISAV
>Oc MMKLCLLVTACILAVISVQAQDLKSCRAVFSEQNRKQLTWINGCVKQLGYKSAREKTQKSTCVWKCVLDNFNMLNADGNMDVNQYNHHLQEEWPAHMLDRANSTFQPCLKIGSETTQDEFCKGYDPLIKCMTRNFANLCKGIK
>Dw MSASHLLILTCCLVLAQNVRGQTQINCQRPPQLVDPSLCCRDGGRDQITEQCAQKIVGSAANGPPSIETATCLAECILTTSNYITEPQKINATNIRNNLSAKFSDKEYVEAMSMAFTKCEPQAQQRLAVIQQQQRQQPKCSPFSAILLGCTYMEYFKNCPANRWTQSTECALAKTFVTQCGLGA

Table S4. Protein sequences of OBP used to construct motif analysis

Accession number	E-value	organism	Abbriviated name
XP_022672530.1	6e-116	Varroa destructor	Vd1
XP_022666940.1	3e-173	Varroa destructor	Vd2
XP_022645714.1	5e-117	Varroa destructor	Vd3
XP_022653293.1	7e-97	Varroa destructor	Vd4
XP_022653281.1	2e-129	Varroa destructor	Vd5
JZ172282.1		Amblyomma americanum	Aam
OQR79252.1	2e-99	Tropilaelaps mercedesae	Tp1
OQR73552.1	8e-117	Tropilaelaps mercedesae	Tp2
OQR80083.1	3e-156	Tropilaelaps mercedesae	Tp3
EEC12103.1	3e-167	Ixodes scapularis	Ix1
XP_002399632.1	1e-135	Ixodes scapularis	Ix2
XP_002433530.1	2e-98	Ixodes scapularis	Ix3
KFM70022.1	2e-156	Stegodyphus mimosarum	Sm1
KFM79180.1	2e-117	Stegodyphus mimosarum	Sm2
XP_025016893.1	2e-131	Tetranychus urticae	Tu1
XP_015782945.1	2e-125	Tetranychus urticae	Tu2
XP_015791022.1	1e-135	Tetranychus urticae	Tu3
XP_015794342.1	2e-155	Tetranychus urticae	Tu4
KPM10930.1	0.0	Sarcoptes scabiei	Sc1
KPM10909.1	9e-130	Sarcoptes scabiei	Sc2
OXU23289.1	4e-169	Trichomalopsis sarcophagae	Ts2
XP_017053738.1	1e-151	Drosophila ficusphila	Df
OTF72123.1	5e-85	Euroglyphus maynei	Em
XP_002066115.1	2e-132	Drosophila willistoni	Dw

>DgalOBP1 (GAIF01000051.1 lcl|ORF1)

MKAIVLVALAAVIYVVSGDTATGDHNEDTSKFGKWRSCIAEKLPADKKPVFDGCATKPGGTD QSKFRRGLGCVLESYGLTKDQEVDLKKMGSTAASVSSPELKKAFQECPKDEKNSAEDRTIKC VIDHLETQCKVEQ
>DgalOBP2 (GAIF01009917.1 lcl|ORF5) MKAIVLVALAAVIYVVSADTATGDHNEDTSKFGKWRSCIAEKLPADKKPVFDGCATKPGGTD QSKFRRGLGCVLESYGLTKDHKVDLKKMGSTAASVSSPELKKAFQECPKDEKNSAEDRTIKC VIDHLETQCKVEQ
>DgalOBP3 (GAIF01034646.1 lcl|ORF7) MKTLIFGFVVVFAYLAAGDTATGDHQPDTNQFGRWRSCLTSKLPADKQATMQGCVSRPGGT DMSKFRRGLECVLDSYGVVKDHRVNLQKMSRTAPTVRSAELKKAFQECPRDDKNVSLDRSIK CVIDHLETSCPLDKNRG
>DgalOBP4 (GAIF01001373.1lcl|ORF7) MKTLIFGFVVVFAYLAAGDTATGDHQPDTNQFGRWRSCLTSKLPADKQATMQGCVSRPGGT DMSKFRRGLECVLDSYGVVKDHRVNLQKMSRTAPTVRSAELKKAFQECPRDDKNVSLDRSIK CVIDHLETSCPLEKNRG
>DgalOBP5 (GAIF01024919.1lcl|ORF6) MKTLIFGFVVVFAYLAAGDTATGDHQPDTNQFGRWRSCLTSKLPADKQATMQGCVSRPGGT DMSKFRRGLECVLDSYGVVKDHRVNLQKMSRTAPTVRSAELKKAFQECPRDDKNVSLDRSIK CVIDHGDVLSARKEPRLSLLNPTRRQWAGKTAKRGRKKQEEARSPHRGTWH
>Vd1 MKVFVIIALVGMAKAAPQAPASATPAKVPVIEWGKCEQLKPSESERTSKAAVVDKCLQSLPLPD PEKATQQEIDKHRESVTTCALKAEGWFDDEGVYKFDRARNEIKNKKLDSEVEEAVLLKHDAC QKEATEKHDDYINQVQLYQACMDYNISQICGIKVMV
>Vd2 MHRSFVLQCCGLLFIVGLALAGPLAKDKSERITPKQTVEEFFTSNWGECEPLKNPLVLPEISDAA TWERCRVHIPLSPDQVEEALPNLSRCMLKVIGWVRANGNMNLTKYMDYLSQAGLDDKTLELT KTAHEKCSQRALSDGSGDYKEQDKIYVECIFRHFDKTCPPNFQAAVKQGYIVGITQISFVPRYD EVEVESDTDAETEGQAGPSVADATGEAAANDNANGSGGPQ
>Vd3 MKTFIGLVLVGMAMAAPPASGGPEAGKPPTIEWGKCSQLKPSDSERMTKAAVVEKCVQSLPLP EAGKASQAEIEKHREDVTTCALKAEGWFDDKGVYKFDRARDEIKNKKLASDIETPVLEKHAE CQKEAGEKHTSDYIKQVQLYQACMDFNISQICGIKVVS
>Vd4 MNAAVYIVTAMLACCCSADTASGDHASDTSQFGKWRTCLADKLPAKKREVFDECFIKPGGTD MNKFRRGLNCVLTSDGLLKNHKVDLKKMSMTAASAGSPELKKAYENCPKDDKNTSEDRSIKC

LIDHLEVDCKLASK
>Vd5 MKTLVVALLASTACLTAADTATGDHQPDSNQFGRWRTCLKSKIPENKQPGMEACINKPGGTDMSKFRRGLGCVLESYGIVNNHRVDLTKMRSSASLVTSPELKKAFMECPKDDKNSSLDRSIKCVIDHLETSCSAVKAQG
>Tp1 MKTLVIALIAGTACLAAADIATGDHQPDTNQFGQWRTCLKSKIPQDKQATMDNCVKKPGGTDMAKFRRGISCVLESYGVVNGHRVDLRKMGSTASSVRSPELKKAFQECPKDDKNASLDRSIKCVIDHLETSCPLVKAQG
>Tp2 MKVFVVMALMGMAMAAPQAPAAPTSAKAPVIEWGKCDQLKPSENERTSKAAVVDKCLQSLPLPDPEKATQQEIDKHRESVTTCALKAEGWFDDKGVYKFDRARNEIKNKKLDGEIEAAVLVKHDACQKEATEKHEDYINQVQLYQACMDYNISQICGIKVMV
>Tp3 VEQFFTSNWGECEPLKNPLVLPEISDGSTWERCRAHIPLTPEQVEEALPNLSRCMLKVIGWVRPNGNMNLTKYMDYLSQAGLDEKTLELTKIAHEKCSQRALSDGAGNYKEQDKIYVECIFRHFDKTCPPNFQAAVKQGYIVGITQISFVPRYDDVEMEVDSDADAEDPNGAYPGPGADDANASSGGSSNNNNKDDSNNNNKADSNGDAQ
>Ix1 MWTSAGKSALVTLGVLLAVGVGLGDAGPVDPKKTDKPEKQTIHEFFSSNWGACEPLKNPLVIPEMSNPTTWVKCQKHLPEHPQDIEEYLPRLSRCMLKSTGWVRSNGNMNLSKYLQYLSLLGLDDETMNGTREAHKGCIAKAYKEKDYKTQDKVYVECIFKFFTKSCSANFQGAVKEGYIVGITQLSFMPRMGPLEVVDDVEAEVSEDDAPQDVLPVTNSTSTS
>Ix2 MVAFKVSVAVLLCVGSAFAIPAGGKDLDAAAQTQAGVPPRPQINWGKCPQLQPSENERQQKALVIDQCLDKVPLPDVDTANDTVIQQHRQDVTTCALKTEGWFNSNGQYRFDRARTEILNKKLAKDVEPQVLSKHDECKKEAEEKFAKNFVAQVQLYQACMDYHISQICGIQIAQAAEAHPQGAQQG
>Ix3 MKILLITVVVCVFAATDASRRSTRRQQFTDWRNCMVEQLPSEKKPIYDACYNRSRGTDMHKFREGLKCVLTDYNLLNGTKIDLAAMTTRASSVSGKLGQAFTDCPKDDHNRNAAKGVKCIIDRLETDCPVPTGSTAH
>Sm1 MLLSVLLTLFGVGVILAAPPTTVQPQNEASLESQNYPVPQIDWGKCPQLKPTEADKEQKRLVIQKCLDQNPPPALETVTDPKQIDDHRELVTTCALKTEGWFNEDGSYKFNRAKTEIESKKLDSQVEKNISKRHQECQDEAVKRFPGGYIQQVQLYQACMDYHIAEICEIELIPPPGGFPIEEFGDYDESPLQPEQPEKSQETTTQPQAQPASAK
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>Tu1

MKNLQSITILCLIFGFIVSTVYSQPLGSSDSNPDTQDTKEASTSVNDKSSDQEGSSESDEDAPTPVAGPHRPPTINWGKCPQLEPKEAEKKQKADIIRTCLKSITLPENITQESVEKHRTEVAKCALNAENWFAEDGSYRYDKAESEIKNKKLQPEIEPQIVNQHSECRKEAEEQFPSGIAQIQLYQACMDYHISMICGIQIVGTGYSQ
>Tu2 MINSLSHSVSLCLIVLVVNSSNCAPQATPNRQGGFSGQLQGPPQPPQINWGKCPQLEPVESDKKAKADIISSCLKSIALPENMTQETVEKHRTEVARCALNAENWFTEDGKYRYDKAESEIKAKKLSQEVEPQILRQHGECRKEAEGQFPSGIAQIQLYQACMDYHISQICGITIVGPSSPQ
>Tu3 MILITLCLVVLAINSSYGQPQRFLAPQPTSDQLEGSPQGGFPGQPQGPPQPPQINWGKCPQLEPKESDKKAKADIISSCIKSIPLPENVTQESIEKHRTEVAICALNAENWFSADMKYRYDKAESEIRAKKLVSDVEPLVLRQHGECRKEAEGQFPSGIAQVQLYQACMDYHISQICGITIVGASSPQ
>Tu4 MNYLSLCVFIIFFLTIGFSESARLPRSTSSPATSSSTTTTSSTVNNKKNEENQPSTSSASSSAGSATGGPTINWGRCPQLEPTNEEKIKKAAVITKCLESTPVPVNITRETVELHREQVAACALRMEGWFNGQGLYRFDKAENEIKAKKLTREVEEKVLSFHRQCKDEAEEKYPVSSNQLIAQIQLYQACMDYFISEVCGIEVQIAGSEGSSE
>Sc1 MMAIHQLFLTTVASLWSVMLMTAVVALPQPLNTSTNNKPADSISTASSSSIDSNVPLMASASSPSGQNLRSSSQQPMLLTLEQQQELLDQLAQLQRQTQQLLAAQQSLAAVAAAAAVNGNNNGVSIGTPLDGNSNNDAGSHSPITSGSIQYHRQQNQQQTHPTTQQLNNPTSNQQSAAIRNDNIDQGSLEQSQSKSNQLNQMINNAQNSQSQSMSGLPQSPQINWGKCPELEPSEQEKLAKANVITKCLETTPLPANITRESVEQHREQIAGCALRSEGWFTPNGGYDFSKAEKEIRNKHLQADLENQVLNYHGQCRVESEEKYPTSNSSIIAQIQLYQACMDYFISDVCGIEVNDTDSPQF
>Sc2 MIANMNLYALAIILLLAHLCDAQSTEKLDKSKLKQQQQLPQRPKIDWGKCPQLEPSEKDIKSKSNILQRCLKENPPPNQDSITPELIIGHQKNVTECALKIENWFDKKGDYKFEKAEKEIKNKKLSSEMQKALVGSHQDCAEVSKTQKKQSKTPMDVVEQVQIYQGCMDAHITQHCQIKIGA
>Ts2 MLANTARLNAFAMCMLQQFNVMDSNGMVNPDVMSYSIISTVPNATAGISQQCISKRGIDAVNTARMIMNCYLRANQMVLALSRRDRTYIIRINYITVACPVLAYLQASFSPLIENDFHAYEADCGAKSGASDESIEAARRARQLPQSPQMNAFALCMMQKYKVMAADGSVNPDVRSYGIITDGPDNTWRVSEHCRDLDGNSSGETARMIMNCYLDNNQLVMGLTPRVSA
>Df MLRTGILIFVVLSQFLEGPLAIRIHCRHTERIHEENIHHCCKHPDGHNDVTEMCAKQTNFKLPNPNEEAIEDVTVDQAMVGTCWAKCVFDHYNLMENNTLDMAKVRHYYKRYHKIDPEYETEMLNAYESCHSKSEDATEQFLSLPIVRAFATSKFCKPTSSIIMSCVIYHFFHNCPKNRWSNTTECVETLAFAKKCKDVLTTM
>Em QLPRAPKINWGRCPQLEPTQRDIEAKSSILQECLRQNPPPQSESITQEQIIQREYKYEKAEKEIKNKNLAKEMEKVLLESHKQCSQIAKDRKQAVKNLSNVEQVQIYQGCMDAHITQNCQIQISAV
>Dw MSASHLLILTCCLVLAQNVRGQTQINCQRPPQLVDPSLCCRDGGRDQITEQCAQKIVGSAANGPPSIETATCLAECILTTSNYITEPQKINATNIRNNLSAKFSDKEYVEAMSMAFTKCEPQAQQRLAVI

QQQQRQQPKCSPFSAILLGCTYMEYFKNCPANRWTQSTECALAKTFVTQCGLGA

Table S5. Protein sequences of NPC2 used to construct phylogenetic tree.

Accession number	organism	Abbreviated name
XP_022652195.1	*Varroa destructor*	Vd1
XP_022649311.1		Vd2
XP_022654520.1		Vd3
XP_022654596.1		Vd4
gi_283753684		Vd5
NP_608637.1	*Drosophila melanogaster*	Dm1
NP_650331.1		Dm2
AAN71436.1		Dm3
ADL59625.1		Dm4
NP_001247376.1		Dm5
AEN25572.1		Dm6
OQR69913.1	*Tropilaelaps mercedesae*	Tm1
OQR78448.1		Tm2
OQR69614.1		Tm3
OQR72593.1		Tm4
OQR76180.1		Tm5
OQR69865.1		Tm6
EEC00381.1	*Ixodes scapularis*	Isc1
EEC07080.1		Isc2
EEC07323.1		Isc3
EEC03680.1		Isc4
XP_002435260.1		Isc5
EEC08723.1		Isc6
EEC06676.1		Isc7
EEC13424.1		Isc8
EEC13423.1		Isc9
EEC18444.1		Isc10
EEC16220.1		Isc11

>DgalNPC2-1 GAIF01015586.1 lcl|ORF7 MANNFFFLIVASLALTAYAGELVQINNPVQCDGLTTIKAVYVEDCTNGEMCDLVKGHNYSLKIT YTAPKDVQTAKALVTGVIGGAELPFPGLQRYVCKTPGNEDFCPQVKGKDYTVSMVLPIMSLFP KLETTATVRFIDDDAKSEAEEKLGCFQLPIRLVDDPNAPKQPTRVDNEDDDE
>DgalNPC2-2 GAIF01031731.1 lcl|ORF2

MANNFFFLIVASLALTAYAGELVQINNPVQCDGLTTIKAVYVEDCTNGEMCDLVKGHNYSLKIT YTAPKDVQTAKALVTGVIGGAELPFPGLQRYVCKTPGNEDFCPQVKGKDYTVSMVLPIMSLFP KLETTATVRFIDDDAKSEAEEKLGCFQLPIRLVDDPTPLSSRRALTTKTTMSNERQRDDAT
>DgalNPC2-3 GAIF01008081.1 lcl|ORF7 MANNFFFLIVASLALTAYAGELVQINNPVQCDGLTTIKAVYVEDCTNGEMCDLVKGHNYSLKIT YTAPKDVQTAKALVTGVIGGAELPFPGLQRYVCKTPGNEDFCPQVKGKDYTVSMVLPIMSLFP KLETTATVRFIDDDAKSEAEEKLGCFQLPIRLVDDPTPLSSRRALTTKTTMSNTSARDDAT
>DgalNPC2-4 GAIF01004272.1 lcl|ORF7 MISQRIVVLPLIVAVLAVAVHGSPYKLCKTPSIGTVVKVVIEGCSDDVQSCVLRKGTEAKLSLTFI PNVDVKSLVAKAYGLIAGVPVPYPLKNSDACKDSGLSCPLKKDPKVTYKQAFDVMKEFPSMS LTVKWVLRDEQNAHIVCPDTCQTGVVARREFWTVWTQVVSSRPLRKGCVAVGDKNVAFRPV YFAVKLQ
>DgalNPC2-5 GAIF01014813.1 lcl|ORF6 MPRFTATTAAAVVIAAIVLLSASPSVLGQREITFTPCDDPGKGIVKRVTATPCDTDPCELKKGSM TSFNFEFIADQNTTSITLDARVRVLGIFIPVPFIETDMCRVIDCPVVKGQEIVGQFNATVPRVPVKS SVIRVKVIGDEGMSCCISYKVVLK
>DgalNPC2-6 GAIF01031088.1 lcl|ORF3 MAPKRGLRRVAAVPAERALATIVVLAAVCVAIVRGSPFKSCGGSAKITAVDIENCPSSAKSCTVH KGAAFKVQVTFKPAKDAVNATLHKAVIINNVTKKLTPCVSVCNAGLKCPLHKNVPATLQYTGH VPKDSPKGKLFGQLSLTDSAGSLILCAQSPIEVA
>Vd1 XP_022652195.1 epididymal secretory protein E1-like [Varroa destructor] MKTFLVIFALAAIAIASPFTSCNHSQGTIRTVEISGCKDTDPYCVLYKGTNVNLSITFVPASDASR VTVEVYGLISGFGIPYPLPNSNACARGLICPLKNGETATYKHSFPVRNGFPSIALDVIWTLFDER KNRIICARFPVVIQ
>Vd2 XP_022649311.1 epididymal secretory protein E1-like [Varroa destructor] MLRFVMLAAIASAAYAGELYKVQNVQQCDGLSTIKSVEVENCTKEDLCELIRGHNHLLRVTYV PPRSAQVVKVLITGFVGEAELPFPGFKRYVCKTPGNENFCPQTAGQEYTTTMVLPILSVFPNIET TAFVRFIDDDAKSEAEEKLGCFSMKIRLIDDPNASTEPANVDNQEDDE
>Vd3 XP_022654520.1 uncharacterized protein LOC111247622 [Varroa destructor] MTSVTQSALIILVVVTTWPWASFARKVQYQECNPKRNIKMMDVDNCDVQPCRVFHRTTIKMT TQLSSPINSSSAEWEIRAFVNGRPYGHPEPVSDACLFVNSTSPNAFSSSHRTPLNSDQFKSGPST AYRQKSFLPMCPLFAGKIYRFSNVFYVHDQFPKVATTIQYLLRGDNDEMIACARLHILMSS
>Vd4 XP_022654596.1 epididymal secretory protein E1-like isoform X1 [Varroa destructor] MMLLDLFTVVFAVMLMMNENNAKQLDSYVNCGGTGHIENITVVPCESEPCEFAKGSKVNVH FIGSFSHDANSVRVQPSVIVDKMNVTLTGVDQELCGKHVQCPIKANELRDAEIEIPIFNVYPNIK TEVVFMIFSENVLQFCVRTKIIISDKK
>Vd5 gi_283753684 MWLYVWVTVAALATVGNGSIFQSCEKIETKGTILTLDIEGCPNTENVCVLKRGVDTKIALTFTP EVEMNNITVKVFGVIENIPVPYPIPHSNACIKSGLECPLEKGVPATYTQTFPVPKVFPSIFLIIKWT FVDSFNNELICALIPTRLQ

>Dm1 MLRYAVIACAALVVFAGALEFSDCGSKTGKFTRVAIEGCDTTKAECILKRNTTVSFSIDFALAEEATAVKTVVHGKVLGIEMPFPLANPDACVDSGLKCPLEKDESYRYTATLPVLRSYPKVSVLVKWELQDQDGADIICVEIPAKIQ
>Dm2 MKLSLGLFVIFAALIGFTSSTDVSQCPKSKSKALAAGDVSISNCPKSKCILKRNTEASIQMKIRPERDFQELTSDIQGIILDVPLPFPGYYGTSACPHIYDEAGEKKVGCPLKAGQVYTYKNSFKILPVYPTVSLEIHWGLGDKHGDAACFQIPAKIKA
>Dm3 MLRPSSLQAVAIAIVLISSSASAEVVNFEPCPDSVDTCTIQQVRVSPCPEALNNAACNIRRKHNSEMSFDFTPNFDADTLVASLGWAKSENVELPLLTLDSAACKYTPCPVRSGVKQTYTTLVPIEAKFPLSPYTIRWALKDPVSQKRCCFTIDIKVVR
>Dm4 MLRIVVTLALILATVNATNVQQCKNKPFPLDVNIKDCEEPPCVVVYKGTIAVMEVHFLGNNNNIKSITATTTAKVLGMNLPYALPDEVSDVCRNLLYGAICPIDKDEDVTYQFNFYVEPSFPEITADVTVTLNDAQNEPITCFVVSCKIRKGATAAQMDGYLLDWTNPL
>Dm5 MLRLSSLLPVAFALVLSSVSAEIVNFQTCEDSVDSCSISQVRVTPCPEANANAACHIRRRHRFTMSFDFTPHFDADTLVASLGWAKSENVELPLLTMDQEACKYTTCPVRSGVTQTYTNNMPADARFPLSPYTIRWALKDPVSQKRCCFTIDIKVVR
>Dm6 MSSFKKLSLCLVLSIMWTSVADSTPIRQCADSNYPQPLMVQIDDCDALPCDLWKGTEAKIDIQFVATRNTMKKLSAEVHLTSLGVTIPYDLEASRGNVCSNLLHGAYCPLDAGEDVTYQLLLPVTTNQPEVPTRLEVRLLDSDDENRVVSCFLADTRVKKPRSAV
>Tm1 MFCSIAYYVVSSVLIFVLADVYAGLNGSSPPPKPRPTVPENQEFYRTLANVTLDRYMDLISMPQVPSRYMRNDDDHPNKWIFEEDDDDYIRSYQVTSCPHERNPVVKYSNLRVHPDPLIFPGTIRITSDIQVLEDVTEPITVQVRMRRRMVYFWMDLPCVAAYGSCLYENICDTTIKCPIFYELLGLPCGCPIKKGNYRTHNKAYDVPDVLPTWLTSGDYQVILKASSNNRPLFCVRFKLSVEGPDDRNRLLSFLSKIR
>Tm2 MRTGVCQRQSTDGLSTIKSVAVENCKNSELCEWTKGRNHELKVTYTAPKNVETVKVLISGLVGGAELPFPGLKRYICKTPGNENFCPQTAGQEYTATITLPILSVFPKIETTAFVRFIDDDAKSEAEEKLGCFHMQIKLIDDPEAPKVERVDNQEDDE
>Tm3 MALNRFVVLIALVAVGYASPFKSCDSKDGSILSLDIEGCPDDNYECILHKGDDAKISITFTPNVNSNTVMAKAFGIIAGIPIPYAIPESNACLHGLVCPLKSGVVTKYSQTFPVQRTYPSLALEVKWMLIDDRGDAIVCAKIPVRLQ
>Tm4 MLRLSVIVFLAISAFGQQVVVPKKCAETGGGILKKLVVSPCTAEPCVMKKGRNATLTFEYIADQNSTTAVIDARVKAFGMKVPVPGIDTDLCKIISCPVKEGATYTAQITVPVPKIPIKK

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>Tm5 MVSFNVPAIALAVALTIHQEVDGQRKLKSYTDCGRDTNTVRVRPSVIFGKLNVTLPGVDS ELCGKHLKCPIKANELQDADIEVPVFKTYPS
>Tm6 MKRLGQTLLICGFLCAQIVHLQKKVINDMQICGGNGVVQLVIVEPCSNEPCMFQRPGQIK VHIEAGFDRPSETAKLSASAMVKSRNLTLPGVPNNLCRLTSCPLNGRGDIRNLSFTVPIK SFYPPGTYELSFVASGDDGMEICRRLNVTIITDQ
>Isc1 SPLHTTTDAMARHLLPGTLLLAALCGLTEAIKWTDCGSSEGQVASVSVTGCEHTDTCNLK KGTDVSLIIDFTSNVKSPTVQVKAYGVLEHVPIPFDVPQPDACQSGVTCPVQPAGKYNYR GSFPIKPMYPSISLDIKWELLDDKDQYLVCVLIPVKID
>Isc2 MAASLRLELLALVVTRLMAIFEASEFTVVDYTTCGGEALQVRVDPCEQLPCSFKKGRSVK IEMDFAASKNQSQVSVGIMGKAGGMLLPLPFNQKDGCKGSGLDCPLVAGRNYTVSRAVRV YRIYPKMEILAVFEIRGNDGEVLACVQFPVHIQ
>Isc3 MGEKPLFKQLFFTSQHHSSRDILTFIMAGSMVFFALCAFAFVSAATAADALSVVKVDQCT DGSTKNVKEVRMTHCESLPCNVKLADKPRFEVDFVAERDSNVMRVKVQGQIGALNPENFP GFKSDACSNMGVECPLVAGKQYTAKSQLTMSPTFPPTQAKAIFKGVDAGGELFCFTVPVE LKQ
>Isc4 MNRLCYAASLVLVSAALVSAEFDVVKHEKCGGEFGEVRIDPCPELPCIFKKGTPLKLQVDFVAA DSFKTLQMKLLGELSKGVWLPFPNFGRNACKKNGLTCPLESGKPYTLQSTLNVLSSFPTVRGS RGVYMKGDNQTIFCFLVPVKVSD
>Isc5 MQHHFEAALLVCVIALLGQCSAIWKSCNADNGQVLDMRVTPGGDREVYILRKGTNVTLNIEF WSSVDSGSAKVRAHGMVMGVPIPLKMPNEDACVDCGISCPMRNGEKYLYKQGFEVKASYPK MSATIKWALGDDNGGTVACVLIPVEIVD
>Isc6 MASSVVLALAVVVCAGFVVGDLVAFKDCGHGNVKSVNIVSCKKAPCKVKIGTRVVFEASFVA PFDVTSAFNDIGAYIERHRFRLPEPRVDACNGYLSPRCPMRKGQTYTYRYTMPVREIYPATPATI EYKLTNEEGRLIGCTSIPVQIFR
>Isc7 MPGAVIQSLIVTPCTSDPCVIPVGTQINITFEVESNQDSDRVLFDPRVTVLGVQLPIPGVEKDACR SGAVVCPVHKGKLFAGTISAYVYNFVPSLTVTTTWKMVGAQGIIACGATNVTIVRK
>Isc8 FLPTAGGDVTHVRVQPCTHEPCSIKRGETVLIEVPFRANQDSDKLATKISAQLEDLELPLPSLKK DGCREQGIRCPLEKNEKYVFTYSLLLIYLLFQLNTTAKLSLTGAKGVVFCVTFPVNLTD
>Isc9 MSIILFSTDQNSAKLSTKISAVIDNKNELVLPSVKRNTCRNQGIKCPLEQGTDYVFEYNLEIKPSF PTLDTTAKLNITGAEGPVFCVTFPIHLVE
>Isc10

MLSTRNMVLLAGSALALLLVVPACVRGQDAPGEPTFRNFYNCTWAKGDPGEQAQAYLGGCGSEEICPLYRGSEAKLELQFSPRSDTSGVFRRIFGLFDKVLVPYGREVNVCNSTTSIDDNVRCSEESHGLRQGRLYRHSGAFLVKPFFPKVQLNVTVYLYDKSPQKVPVACVQIPVQIKDKDRS
>Isc11 MRDSDVMRLKVQGQIGQLQPENFPGFKSDACSQMGVECPLVAGKQYTAKSQLTMSPTFPPTQAKAIFKGVDAAGELFCFTVPVELKQ

Table S6: Protein sequences of NPC2 used to construct motif analysis.

Accession number	E-value	organism	Abbreviated name
XP_022652195.1	2e-31	*Varroa destructor*	Vd1
XP_022649311.1	5e-128		Vd2
XP_022654520.1			Vd3
XP_022654596.1			Vd4
gi_283753684			Vd5
NP_608637.1	5e-104	*Drosophila melanogaster*	Dm1
NP_650331.1	2e-113		Dm2
AAN71436.1	2e-112		Dm3
ADL59625.1	6e-120		Dm4
NP_001247376.1	1e-112		Dm5
OQR69913.1	0.0	*Tropilaelaps mercedesae*	Tm1
OQR78448.1	6e-114		Tm2
OQR69614.1	1e-103		Tm3
OQR72593.1	4e-98		Tm4
OQR76180.1	8e-61		Tm5
EEC00381.1	5e-112	*Ixodes scapularis*	Isc1
EEC07080.1	2e-108		Isc2
EEC07323.1	4e-132		Isc3
EEC03680.1	9e-106		Isc4
XP_002435260.1	1e-108		Isc5
EEC08723.1	6e-106		Isc6
EEC06676.1	1e-82		Isc7
EEC13424.1	2e-85		Isc8
EEC13423.1	3e-63		Isc9
EEC18444.1	6e-134		Isc10
EEC16220.1	9e-57		Isc11

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>DgalNPC2-2 GAIF01031731.1 lcl|ORF2
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>DgalNPC2-3 GAIF01008081.1 lcl|ORF7
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>DgalNPC2-4 GAIF01004272.1 lcl|ORF7
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YFAVKLQ

>DgalNPC2-5 GAIF01014813.1 lcl|ORF6
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SVIRVKVIGDEGMSCCISYKVVLK

>DgalNPC2-6 GAIF01031088.1 lcl|ORF3
MAPKRGLRRVAAVPAERALATIVVLAAVCVAIVRGSPFKSCGGSAKITAVDIENCPSSAKSCTVH
KGAAFKVQVTFKPAKDAVNATLHKAVIINNVTKKLTPCVSVCNAGLKCPLHKNVPATLQYTGH
VPKDSPKGKLFGQLSLTDSAGSLILCAQSPIEVA

>Vd1 XP_022652195.1 epididymal secretory protein E1-like [Varroa destructor]
MKTFLVIFALAAIAIASPFTSCNHSQGTIRTVEISGCKDTDPYCVLYKGTNVNLSITFVPASDASR
VTVEVYGLISGFGIPYPLPNSNACARGLICPLKNGETATYKHSFPVRNGFPSIALDVIWTLFDER
KNRIICARFPVVIQ

>Vd2 XP_022649311.1 epididymal secretory protein E1-like [Varroa destructor]
MLRFVMLAAIASAAYAGELYKVQNVQQCDGLSTIKSVEVENCTKEDLCELIRGHNHLLRVTYV
PPRSAQVVKVLITGFVGEAELPFPGFKRYVCKTPGNENFCPQTAGQEYTTTMVLPILSVFPNIET
TAFVRFIDDDAKSEAEEKLGCFSMKIRLIDDPNASTEPANVDNQEDDE

>Vd3 XP_022654520.1 uncharacterized protein LOC111247622 [Varroa destructor]
MTSVTQSALIILVVVTTWPWASFARKVQYQECNPKRNIKMMDVDNCDVQPCRVFHRTTIKMT
TQLSSPINSSSAEWEIRAFVNGRPYGHPEPVSDACLFVNSTSPNAFSSSHRTPLNSDQFKSGPST
AYRQKSFLPMCPLFAGKIYRFSNVFYVHDQFPKVATTIQYLLRGDNDEMIACARLHILMSS

>Vd4 XP_022654596.1 epididymal secretory protein E1-like isoform X1 [Varroa destructor]
MMLLDLFTVVFAVMLMMNENNAKQLDSYVNCGGTGHIENITVVPCESEPCEFAKGSKVNVH
FIGSFSHDANSVRVQPSVIVDKMNVTLTGVDQELCGKHVQCPIKANELRDAEIEIPIFNVYPNIK

TEVVFMIFSENVLQFCVRTKIIISDKK
>Vd5 gi_283753684 MWLYVWVTVAALATVGNGSIFQSCEKIETKGTILTLDIEGCPNTENVCVLKRGVDTKIALTFTPEVEMNNITVKVFGVIENIPVPYPIPHSNACIKSGLECPLEKGVPATYTQTFPVPKVFPSIFLIIKWTFVDSFNNELICALIPTRLQ
>Dm1 MLRYAVIACAALVVFAGALEFSDCGSKTGKFTRVAIEGCDTTKAECILKRNTTVSFSIDFALAEEATAVKTVVHGKVLGIEMPFPLANPDACVDSGLKCPLEKDESYRYTATLPVLRSYPKVSVLVKWELQDQDGADIICVEIPAKIQ
>Dm2 MKLSLGLFVIFAALIGFTSSTDVSQCPKSKSKALAAGDVSISNCPKSKCILKRNTEASIQMKIRPERDFQELTSDIQGIILDVPLPFPGYYGTSACPHIYDEAGEKKVGCPLKAGQVYTYKNSFKILPVYPTVSLEIHWGLGDKHGDAACFQIPAKIKA
>Dm3 MLRPSSLQAVAIAIVLISSSASAEVVNFEPCPDSVDTCTIQQVRVSPCPEALNNAACNIRRKHNSEMSFDFTPNFDADTLVASLGWAKSENVELPLLTLDSAACKYTPCPVRSGVKQTYTTLVPIEAKFPLSPYTIRWALKDPVSQKRCCFTIDIKVVR
>Dm4 MLRIVVTLALILATVNATNVQQCKNKPFPLDVNIKDCEEPPCVVYKGTIAVMEVHFLGNNNNIKSITATTTAKVLGMNLPYALPDEVSDVCRNLLYGAICPIDKDEDVTYQFNFYVEPSFPEITADVTVTLNDAQNEPITCFVVSCKIRKGATAAQMDGYLLDWTNPL
>Dm5 MLRLSSLLPVAFALVLSSVSAEIVNFQTCEDSVDSCSISQVRVTPCPEANANAACHIRRRHRFTMSFDFTPHFDADTLVASLGWAKSENVELPLLTMDQEACKYTTCPVRSGVTQTYTNNMPADARFPLSPYTIRWALKDPVSQKRCCFTIDIKVVR
>Tm1 MFCSIAYYVVSSVLIFVLADVYAGLNGSSPPPKPRPTVPENQEFYRTLANVTLDRYMDLISMPQVPSRYMRNDDDHPNKWIFEEDDDDYIRSYQVTSCPHERNPVVKYSNLRVHPDPLIFPGTIRITSDIQVLEDVTEPITVQVRMRRRMVYFWMDLPCVAAYGSCLYENICDTTIKCPIFYELLGLPCGCPIKKGNYRTHNKAYDVPDVLPTWLTSGDYQVILKASSNNRPLFCVRFKLSVEGPDDRNRLLSFLSKIR
>Tm2 MRTGVCQRQSTDGLSTIKSVAVENCKNSELCEWTKGRNHELKVTYTAPKNVETVKVLISGLVGGAELPFPGLKRYICKTPGNENFCPQTAGQEYTATITLPILSVFPKIETTAFVRFIDDDAKSEAEEKLGCFHMQIKLIDDPEAPKVERVDNQEDDE
>Tm3 MALNRFVVLIALVAVGYASPFKSCDSKDGSILSLDIEGCPDDNYECILHKGDDAKISITFTPNVNSNTVMAKAFGIIAGIPIPYAIPESNACLHGLVCPLKSGVVTKYSQTFPVQRTYPSLALEVKWMLIDDRGDAIVCAKIPVRLQ
>Tm4 MLRLSVIVFLAISAFGQQVVVPKKCAETGGGILKKLVVSPCTAEPCVMKKGRNATLTFEYIADQNSTTAVIDARVKAFGMKVPVPGIDTDLCKIISCPVKEGATYTAQITVPVPKIPIKKTTLEVKIIGDKGLSSCFTHPLFLK
>Tm5

MVSFNVPAIALAVALTIHQEVDGQRKLKSYTDCGRDTNTVRVRPSVIFGKLNVTLPGVDSELCGKHLKCPIKANELQDADIEVPVFKTYPS
>Isc1 SPLHTTTDAMARHLLPGTLLLAALCGLTEAIKWTDCGSSEGQVASVSVTGCEHTDTCNLKKGTDVSLIIDFTSNVKSPTVQVKAYGVLEHVPIPFDVPQPDACQSGVTCPVQPAGKYNYRGSFPIKPMYPSISLDIKWELLDDKDQYLVCVLIPVKID
>Isc2 MAASLRLELLALVVTRLMAIFEASEFTVVDYTTCGGEALQVRVDPCEQLPCSFKKGRSVKIEMDFAASKNQSQVSVGIMGKAGGMLLPLPFNQKDGCKGSGLDCPLVAGRNYTVSRAVRVYRIYPKMEILAVFEIRGNDGEVLACVQFPVHIQ
>Isc3 MGEKPLFKQLFFTSQHHSSRDILTFIMAGSMVFFALCAFAFVSAATAADALSVVKVDQCTDGSTKNVKEVRMTHCESLPCNVKLADKPRFEVDFVAERDSNVMRVKVQGQIGALNPENFPGFKSDACSNMGVECPLVAGKQYTAKSQLTMSPTFPPTQAKAIFKGVDAGGELFCFTVPVELKQ
>Isc4 MNRLCYAASLVLVSAALVSAEFDVVKHEKCGGEFGEVRIDPCPELPCIFKKGTPLKLQVDFVAADSFKTLQMKLLGELSKGVWLPFPNFGRNACKKNGLTCPLESGKPYTLQSTLNVLSSFPTVRGSRGVYMKGDNQTIFCFLVPVKVSD
>Isc5 MQHHFEAALLVCVIALLGQCSAIWKSCNADNGQVLDMRVTPGGDREVYILRKGTNVTLNIEFWSSVDSGSAKVRAHGMVMGVPIPLKMPNEDACVDCGISCPMRNGEKYLYKQGFEVKASYPKMSATIKWALGDDNGGTVACVLIPVEIVD
>Isc6 MASSVVLALAVVVCAGFVVGDLVAFKDCGHGNVKSVNIVSCKKAPCKVKIGTRVVFEASFVAPFDVTSAFNDIGAYIERHRFRLPEPRVDACNGYLSPRCPMRKGQTYTYRYTMPVREIYPATPATIEYKLTNEEGRLIGCTSIPVQIFR
>Isc7 MPGAVIQSLIVTPCTSDPCVIPVGTQINITFEVESNQDSDRVLFDPRVTVLGVQLPIPGVEKDACRSGAVVCPVHKGKLFAGTISAYVYNFVPSLTVTTTWKMVGAQGIIACGATNVTIVRK
>Isc8 FLPTAGGDVTHVRVQPCTHEPCSIKRGETVLIEVPFRANQDSDKLATKISAQLEDLELPLPSLKKDGCREQGIRCPLEKNEKYVFTYSLLLIYLLFQLNTTAKLSLTGAKGVVFCVTFPVNLTD
>Isc9 MSIILFSTDQNSAKLSTKISAVIDNKNELVLPSVKRNTCRNQGIKCPLEQGTDYVFEYNLEIKPSFPTLDTTAKLNITGAEGPVFCVTFPIHLVE
>Isc10 MLSTRNMVLLAGSALALLLVVPACVRGQDAPGEPTFRNFYNCTWAKGDPGEQAQAYLGGCGSEEICPLYRGSEAKLELQFSPRSDTSGVFRRIFGLFDKVLVPYGREVNVCNSTTSIDDNVRCSEESHGLRQGRLYRHSGAFLVKPFFPKVQLNVTVYLYDKSPQKVPVACVQIPVQIKDKDRS
>Isc11 MRDSDVMRLKVQGQIGQLQPENFPGFKSDACSQMGVECPLVAGKQYTAKSQLTMSPTFPPTQAKAIFKGVDAAGELFCFTVPVELKQ

Table S7. Protein sequences of SNMP used to construct phylogenetic tree.

Long name	Organism	Abbriviated name
TRINITY_DN24266_c1_g1	*Varroa destructor*	Var24266
TRINITY_DN24854_c0_g1		Var24854
TRINITY_DN26930_c0_g1		Var26930
TRINITY_DN27012_c0_g1		Var27012
TRINITY_DN29484_c0_g1		Var29484
TRINITY_DN30020_c0_g1		Var30020
TRINITY_DN30199_c0_g1		Var30199
Q7KVF1	*Drosophila melanogaster*	DmQ7KVF1
Q9W0X0		DmQ9W0X0
A0A0B4LGP3		DmLGP3
CRQ		DmCRQ
Q9VM10		DmQ9VM10
PESTE		DmPESTE
A8JNI3		DmA8JNI3
R9PY22		DmR9PY22
SNMP2		DmSNMP2
Q961K6		DmQ961K6
Q8INY3		DmQ8INY3
Q9VLU7		DmQ9VLU7
H1UUH0		DmH1UUH0
Q9VJA7		DmQ9VJA7
M9MRL5		DmM9MRL5
A0A0B4KGL9		DmKGL9
Q8SYC3		DmQ8SYC3
Q9VET1		DmQ9VET1
Q9W0X1		DmQ9W0X1
A0A1V9XAB4	*Tropilaelaps mercedesae*	TrpXAB4
A0A1V9XVQ6		TrpXVQ6
A0A1V9X7A6		TrpX7A6
A0A1V9XVL0		TrpXVL0
A0A1V9XA72		TrpXA72
A0A1V9WZC0		TrpWZC0
A0A1V9XN95		TrpXN95
A0A1V9XQP1		TrpXQP1
A0A1V9XHA3		TrpXHA3
A0A1V9XPJ7		TrpXPJ7
A0A1V9XQK1		TrpXQK1
A0A1V9XQS8		TrpXQS8
B7PC41	*Ixodes scapularis*	IscPC41
B7Q461		IscQ461
B7QI62		IscQI62
B7PD82		IscPD82
B7Q458		IscQ458
B7P9A7		IscP9A7

>DgalSNMP-1 lcl|ORF3 GAIF01013616.1 GAIF01013616.1:1-930 + PF01130.21 0.5, 0.38, 0.36, 6.48, 32.29, 0.7 MEAISALNSEESKKGKFGLAIDKNETEPGIFNMYTGATGVTDLNRIYSVNNQHELSIWPTEHDN VCNQVDGTFGYLRPPMNETNEQVVFVPDMCRPITIHYQKDVTFHGIRLRRFTLTPENFFSSKQK PENFCYDSKMKMPSGVAEVGPCKQGAPILMSMPHFMHADPSFSEKVKGMTPDIEKHTFTMDH EPTTGMTVAVRGRLQANIAVRPVDLLGADDLPTVVMPLFWQDMYVEAGPGVVAFLKKVLG YPGLAKIGLVILLLVGLIVLFIGAGLLINYSRRVRQTG
>DgalSNMP-2 lcl|ORF1 GAIF01030464.1 GAIF01030464.1:1-1157 + PF01130.21 0.19, 0.2, 0.05, 1.96, 4.9, 0.1 MGVVSYTTFPSILEQQVNANLVIDPSNEVYESWKESPIPIYAKMYLFNYTNPNEVIEGERPKLQ QLGPFVYRERRHKVNITFNGNGTVSYRQVVSYEFLPHLSRGTLDDSLYTLNVPLIGTAYRNRK YLPDEQEPMAASMEEAFQMYNQSLIIHRKVRELLFEGYEDPMLRIAKTMGWSPFSRFGYQIGR NNSNDGLYTIFTGSNGMDKYGTVESWQGRQKVTGFRKFCNFVNGTSGEMWPPYTHTTHSHL NFFAPALCRSLRLDFLRNETVKGIRVRASRESVVTPAPSQSSKSLLAVRIAGHLRHFVSFHSKID
>DgalSNMP-3 GAIF01028952.1 GAIF01028952.1:1-882 + PF01130.21 lcl|ORF1 0, 0.2, 0, 0, 0, 0 MDFNGDRNLDYYMNSQCSVSGTNGQIFPSFYATPAQVTVFFPFLCKPWTLRSYKHFILQGDEEI VRFIADKATFLRESTSDKCVNWKPTGISGLFDASNCHLDNKVGNEFVNYFAPVLSWPHFLHAD VKLHDDVHGLRPESRKHEFFIDVHSRSGVTVDMRLRYQVNVRLYPSRIMEATIPKIMFPIYWQE IA
>DgalSNMP-4 lcl|ORF1 GAIF01014656.1 GAIF01014656.1:1-610 + PF01130.21 2.42, 3.98, 4.08, 5.09, 5.72, 2.98 MSKRYADYDLKMYTMPVVLSLPHFLHGDPLLLANISGLHPDEERHRFYIDVHAGSGLTVDMR FRFQVNMRLVPLETEQVPSIIFPIFWIEDANLPSDRNKLVHILRKSSVVRWSALAACLCLLATSA LMCGLLL
>DgalSNMP-5 Icl|ORF20 GAIF01027311.1 GAIF01027311.1:1-2641 + 7.55, 10.23, 6.79, 31.36, 42.21, 5.35 MLNDTDDGYLTVYAGIDDATRSRRNFIVQWRSRETIPYYSGRCNRLWGQTQSCSLHSVVHHLQ TLAYFWRLYVGPGHCASTAHVWKTALSSCALLVVSTYFHRRPAMMPLTASSWTAGRGACLMA PVNMAFPPSSACRISSTLRKNFFRMSMDFNPTSRSITFISTSTRC
>Var24266 MKLIRGKQKSAPFLNFLKMGVNAGRGAGVICVVVGAFLVVLGAAVLINFTATFQFILSRKVVL SSTAQGFPIWRDVSDHLDTKTAWYFFNLTNPEEFMQGTQPILQEVGPFWYKTILKKINIEFLDN KTVTFEEHREFEFDAENSVLPNTTRITMINVPVMSALQRLKPLGYFARLAVDPVIKAAIADQQL TANYSVAELTYDGVYNNLVALSKIKEGFLEAIFALNSKDNKKGKFGFGVDKHDPTTFNMFTGG TGVMDLNRIYSINHKHVLSMWPNIENTTCNIVDGTFGYLRPPMNESNEQKVYIPDMCRPVTIR YEKDVNTNGIRLRRFILGKENFYNREAEPANACYDEIYREPSGVAEAGPCKQGAPILLSMPHFM HADPSFSEKVIGMNADPERHTFIMDHEPMTGMTVTVRGRLQANFRVTQLDCLDGEKLPELLM PLFWQELYVEAGPGIVAFLHKVLSYPGLAKIALIIVLLLGIIISIIGAGFLMNHSRRTRQTEQLNPT KYHKMATQEATRKPELDQLV
>Var24854

MKSRGIAGLGISCAFFLVACLSLLAYLKIPSFLQLAVSRSGLSPGSFAADLFSAIPFDIRQNVYMFNITNSEDFFNGAKPRFKQLGPYIFRIGLRKQMTWSEGDLLTFRENRKFWFDADLSHGHLNDTVYTVDPIYAMAQEVIDELPEFLERLFRPLLKSRKVLFKHSVDELLYNGYSDSLAELAHLIKPNLPVIGGKIGYLRAFNDTDDGDITVFAGTNPFTKDKRNLITQWNHKKTIPYYGDGCNGIWGANAELFPSFLSSSPPAQIGVFLPLLCRPWSLHFNETRQENGIELARFATGLDIFSPSNSSQIEQCAQPAGWPRGVFDVRACQHSFPALISLPHFLHSDEKILDAVDGLTPNVTEHDFHLDIFPLLGIPVRPAIRAQINVRIWRHLDTSQSNNPPIVYPVLWQEIVLSESAISYLSTMIWYIILLPETTLRVILMLLTILSVSLAVSYAYTSFSKVSDEETESILASAEDSAASS

>Var26930

MCGGSFCQSELNKPGGHRSEASVGRCTPHLAVTCSLCIGLFFCVFGMVSYAAFGPILRQQVKANLIIDPSNEVYENWKETPVPIYVSMFLFNYTNPDDIILGAKPKLQQLGPFVYRERRQKVNITFNGNGTVSYRQLLSYEHLPELSASSLDVKLYTLNVPMIGAAYKNRKTPSNEEQPMASALEEMFSKMNQSLLIHRTVRELLFDGYEDQMLKLAKQWSWSPTTRFGYQIDRNNSNDGIYTVFTGENGMANYGTIESWQGRHRVIGFRKSCSFINGTTGEMWPPYTLTSKSSLLFFTSPLCRSLRLDFLRNEVVKGIQVLRYHLNERLFDYSIEENQCFCSKKKGKDPECFPNGVLDLNAPIVVSLPHLLYASPSITEAVEGLSPDPQLHEFFMDVEPSMGIPLRVSAKVQMNVIVDAFKYFKYFEMFETRKFLPTFWIETAAVVNDDFAFKIRLVVQDLGSYVSFASYAWVLIGLFIIMFTLGYVIAHTRRSRMGQPSPYGYSTIKMAEVVTGR

>Var27012

MILTGVPRWVAFIVFAASAVVFILGVVGYYMVPSIIGAKVSQQMRLVENGSTLKRWANVAVPIYFSAFMFNITNPEEFANGEKPQVQEIGPYVYLQKRRKLITHIDRDVVTYKDYKSYHFLPEYSIGTPDDRLYALNVPLVAMDKLIGSKLPGDLAKSLLQPILEGLLEKHNEKLVVQRNVSEMLFDGYAVPMMNELSKLAAAFMPDTKLPAISNFGLFYNKNNTADQWFTVGTGAGEYPFATILEWNNHTSLDFWSRDNCNKINGTDGGQFSPFVRTDQKLFVFATDLCRSIYFEYEKNTQVKGVDTKRFTVPDAIFASGKRQPENQCFCEAINRCHEGGVIPLSSCRKGAPVMLSAPHFYQGDAKLVQDVAGLRPQKKYHETYLDVQTMTGLVLRAAKRLQINIDLKQSDLLYPLANVSSRVMPIAWVEERMEATGPMTDGLKEKLIFPQKMGVLISTAAALGGAIGAIAAILVIVVRQAGTTRSAKLQPSK

>Var30020

MPRHVLTISPVKTVSAEIERDPLERYNAMTADLQNGKQKEKTKTPSKCCCCSYKVCSLLLFILSFIMTVTAVVLQSQFDAFFDRALKDQMHLGPSGLVFPAWRVSDLRMRMRVYFFNITNPVEVQLGDKPILNELGPYTWRIYMEKFDIKFHENSTLSYREKKWYQFLREESIGGYNDIITTVNVPYAAVAQRLKDGGTVAKSTATFTLNGLGQTVMHAKQVGELTFEGYPDFLILVANAVEAGKKEDSGFGTILGTGLRIFTNVLAAEPDVQGSFGYFVDRNNTDDGIVTIFTGEDNRQKINRVNVVNGHTELTTWPQHKCNKIKGTMGHLRPPMSSRENPLLIFVPDICRSLPLRYENVSVYEGLSTLRFVAGRETFNNSGPDPCFAGSRKFKSGVMDIGPCKKGAPLVISFPHYLFADEAHQNSVIGLNPRKEAHQFYLESDPLTGVTVSVRARFQVGVVMERVHGLGNLGTIFDGTIPLFWQELQLEALPPTVFQLSILRQLPIYAKQTALVLIGTAILISLIAVFLVYRYVHSTYVL

>Var29484

MKKSLKNELIGVLCHTEENGLFTMCSGGQRLSEQEVRSDQRYDSAPTGCSPLLRVIISLCIGLLFCILGVVSYTTFAPILEQQVKANLVIDPSNEVFESWQEPPITINVKMYLFNYTNPEKILAGLKPTVDELGPFVYRERRQKVNITFNGNGTVSYRQIVSYDFLPHLSVGNLDDELFTLNVPMIGSAYKNR

KALLNEESMMAHTIEELFEKHNQTFLIQRKVRELLFEGYQDPLLRVAKEMGWSSSTRFGYQVN RNNSDDGIYTIYTGEEGMENYGTVDSWDGKKRVLAFRRSCSFINGTTGFTISSMTEFIQSTRGK KGWRTTARWIAGTARKGYSLSALRYHLSQRLFDYSIKENQCFCTKKKGKDPECFPNGLLDLNR CQPDAPIVASLPHHLYAASSVSEAVDGLSPDPELHEFFMDVEPTMGIPLRVSARLQLNVIVDAFK YFKQFQVFKKRVFLPTFWTETTAMINDDIAFKIRLVTEDLANYVTFAALAWVLIGLIVIICTFGY VIAYTRRSVRLIQKIYVDYNSIWDISNPDPSFLKDRLVF
>Var30199 MGLKKSYVVLISASLLVSFLGCIGILTLHPLFQTLLSHRLPLKPGSESYNGWKKVPFPIYQRFYY FNVTNPDEFLNFGEKPVLEEVGPYTWRSEWVKEAVEWHANGTLQYRERKRFWFDREQSAGD QEDVIFTINTPLVAASQKIRNASPLIKLAFLIFLNAANETLFIRRSIRQLTYEGYPDVLAHISHVIDP NVPVKDGRFAYMSGKNDTDEGLFNVYTGSVDLRYFNRIDKWNGRTELPWWESGTPCAKLLG TNGELVHPIVSSDEHIYFFNPVFCKPWRLTRAPDVDSLGITLTRFVAGPEVLFNSSREPANRCFET PGKSLPSGGMDLSRCQFGLPLVLSYPHFYAADSKYLEKVEGLSPNQERHQFQIDIEPRLGITLGL SARAQINVKLERVDFLKYFRSVPELVFPVFWQDVVIEQTPAFADHIRVLLDRPLFYAQFAFRFMT MCGSLVALGAYIYVVILAKKESKKDRFGPLLDDEEINEDEHGEGDVAEDSASGQSQGH
>DmQ7KVF1 MNGPKHKFCTKLSSTYLRKWWITIVVAAALIIGGIVVACEFTVLIDAVVDRMVALRPGAK TFGWWAKPPVEPRISLYIYNVTNADDFLSNGSKAIVDEVGPYVYSETWEKVNIVENDNGT LSYNLRKIYSFREDLSVGPEDDVVIVPNIPMLSATSQSKHAARFLRLAMASIMDILKIKP FVQVSVGQLLWGYEDPLLKLAKDVVPKEQKLPYEEFGLLYGKNGTSSDRVTVNTGVDDIR RYGIIDNFNGRTHLPHWTTDACNTLAGTDGSIFPPHIDHDRILHVYDKDLCRLLPLVFEK EVMTSNEVPGYRFTPPEWVFADVDSHPDNMCFCPAGKPSCSPNGLFNVSLCQYDSPIMLS FPHFYLADESLRTQVEGISPPMKEKHQFFFDVQPKMGTTLRVRARIQINLAVSQVFDIKQ VANFPDIIFPILWFEEGIDNLPDEVTDLMRFAEQVPPKIRVALIVGLCALGVILLLLSTF CLIRNSHRQSTLHLEGSNYLATAQVDMNKKQNKDNQPARY
>DmQ9W0X0 MQLDDILHINNCKADCSSLSTTPNPKTDLVNMNGPKHKFCTKLSSTYLRKWWITIVVAAA LIIGGIVVACEFTVLIDAVVDRMVALRPGAKTFGWWAKPPVEPRISLYIYNVTNADDFLS NGSKAIVDEVGPYVYSETWEKVNIVENDNGTLSYNLRKIYSFREDLSVGPEDDVVIVPNI PMLSATSQSKHAARFLRLAMASIMDILKIKPFVQVSVGQLLWGYEDPLLKLAKDVVPKEQ KLPYEEFGLLYGKNGTSSDRVTVNTGVDDIRRYGIIDNFNGRTHLPHWTTDACNTLAGTD GSIFPPHIDHDRILHVYDKDLCRLLPLVFEKEVMTSNEVPGYRFTPPEWVFADVDSHPDN MCFCPAGKPSCSPNGLFNVSLCQYDSPIMLSFPHFYLADESLRTQVEGISPPMKEKHQFF FDVQPKMGTTLRVRARIQINLAVSQVFDIKQVANFPDIIFPILWFEEGIDNLPDEVTDLM RFAEQVPPKIRVALIVGLCALGVILLLLSTFCLIRNSHRQSTLHLEGSNYLATAQVDMNK KQNKDNQPARY
>DmLGP3 MQLDDILHRITIVVAAALIIGGIVVACEFTVLIDAVVDRMVALRPGAKTFGWWAKPPVEP RISLYIYNVTNADDFLSNGSKAIVDEVGPYVYSETWEKVNIVENDNGTLSYNLRKIYSFR

EDLSVGPEDDVVIVPNIPMLSATSQSKHAARFLRLAMASIMDILKIKPFVQVSVGQLLWG YEDPLLKLAKDVVPKEQKLPYEEFGLLYGKNGTSSDRVTVNTGVDDIRRYGIIDNFNGRT HLPHWTTDACNTLAGTDGSIFPPHIDHDRILHVYDKDLCRLLPLVFEKEVMTSNEVPGYR FTPPEWVFADVDSHPDNMCFCPAGKPSCSPNGLFNVSLCQYDSPIMLSFPHFYLADESLR TQVEGISPPMKEKHQFFFDVQPKMGTTLRVRARIQINLAVSQVFDIKQVANFPDIIFPIL WFEEGIDNLPDEVTDLMRFAEQVPPKIRVALIVGLCALGVILLLLSTFCLIRNSHRQSTL HLEGSNYLATAQVDMNKKQNKDNQPARY
>DmCRQ MCCKCCGETQRKVWVFGLGSVFLLLGILIVVFWPGIADNLVEDGLTLKPGTDAYESWLEA PIPIYLSFYMFNWTNPEDIRNPDIKPNFVEMGPYTFLEKHKKENYTFYDNATVAYYERRT WFFDPERSNGTLDDMVTAAHAITATVADEMRDQRKIVKKIINFMLNHEGGKLYVTKPVGE WIFEGYQDNITDFLNLFNTTKIDIPYKRFGWLADRNESLTYDGLFTIHTGTDDISNLGRL THWNGKSETGFYEMPCGIVNGTTGDMFPPKMNVNDEITIFATDACRFMNLRPRGTYENHG LTATKWVGTEETLDSGENYPNQACFCDEARFDECPKTGVVECKACRDKAPIYSSFPHFYL ADQSYVDAVSGMKPEKEKHEFFLAVEPITGVPVQVHGRIQINMMIEPDDDFDIYRGVQKV LMPMFWFDQYAELSSELASKAKLAINLSSYGIIFGYSMIAFASVFLITGITLTVTKKWVR RTPEDEDILTN
>DmQ9VM10 MPTQNSAMWGQKSNRKLIIGIFGFCLGLFGILCGMFWVDLFDWIMHKEMALAPDTRVYEN WKSPPIDLSLDIYLYNWTNPEDFGNLSTKPILEQVGPYRFIERPDKVDIHWHPENASVTY RRRSLFYFDAAGSNGSLDDEITTLNAVALSAAATAKYWPPVKRSLVDVGLKMYGAEMSVQ KSIDELLFTGYNDAMIDVAMAMPIFGDEVKVPFDKFGWFYTRNGSADLTGVFNVFTGADQ LAKLGQMHSWNYQENTGFFDSYCGMTNGSAGEFQPQHLKPGDSVGLFTPDMCRTIPLDYV ETVDIEGLEGYKFSGGPRSVDNGTQYPENLCFCGGQCVPSGVMNISSCRFGSPVFMSYPH FFNADPYYPDQVEGLSPNQKDHEFYMVVQPSTGIPLEVAARFQVNMLVEPIQGISLYTGI PRIFFPLVWFEQKVRITPDMADQLKVLPIVMLSGHIFAGICLIVGITLLCWTPVQILLAS CRNRRYDLRTKTKTNGQYKSRSQFSSAEELKSKASTLVCEKSVKGSPDSSPLLEKGRKPT IIKSQTGESVATASTAISDNKQD
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YTPPIDQRNRSRRVEDESLIDHDSILTPSDIEDSFERPKSH
>TrpXPJ7 YPDSLAEIAHLIEPKLPIIDGKVGFLLGKNATNDGLYSVFSGANNHLDLLNVITEFQNST TIPYYDEPCNEIRGTNGELYPPFFDAPPESIEIFSPVMCRPWPLHRNGSTTVRGINSVVF SSGEDLFTKTNNETMDRCFEKMPYMNGVKGTFDASACQFGQPIVITLPHFFKADPELHKL VTGLEPDARKHDFSLSVFEFGIVTDLQVRLQVNIPVRVRPGANTGPLILYPIWWQELIFL EQDRNKLSDIIWDQAVRPKVLIQSFLIGLGLLLIATFIIVAITFYIIDRKGKTPDDDELL RDEERVERRFEVSDRLSR
>TrpXQK1 MELTPVRIAVFFSIALFVAICFGAYPLVPDVIRAIARTRLALVPGSATADQSKALPVNIT QRVYMFNITNYSAFMDKGAVPNVRQLGPYTFASEWVKNLSWNGDQLLFRENRTFYFLPDL SNGTLDDEIVTVDLVVVGAIQMVDKLPERIQKFIRPLLDLRPILCKHKVREFLYEG
>TrpXQS8 LQNLVIDPSNEVYESWQEPPIDIYVKLYLFNYTNPEKMQAGLKPKVEELGPFVYRWLPC
>IscPC41 MWPSVQKLPLVNGSEAFELWRDIPLPAFQRVYFFNLTNPYEFLQEGKKPKLQEVGPYTFG VSMVKTNIVWNPNHTVSYREVRTFHFDREKSVGGQDDVIVSINAPLVGAGALLKRANPAL RLVMAVVINKLNEQLIVNHTVGELLYDGYPDFLAAASHMLDPTIPTSDGKFGYMHGRNAT DDGLYTVYTGEDQMDLYNIITRWNGKENLTAWKGTCNMINGTSSFPQGSFKLVREGTDSL YGISAVRFRVDNRTFDNGTTYPPNACFDTKRTMASGAVDIGPCQHNLPAALSFPHFYLAD PSYSDKVEGMKPDPDRHSFTLDMEPDDDSSLLINDDKVDEPSDKENGIIHG
>IscQ461 MNCIKERISLCVISLLSVVLGMLTLLGFDNIFRLILNKVIRRISLCVISLLSVVLGMLTL LGFDNIFRLILNKEVSLAEHSRAFPMWRDVGHDTLVRFYFFNTTAQLLKEQNFIIRGIAS LTLSGLGQRIFISRTVGQLTFGGYPDILILLGSVVDSGRPRPGQPGFNIQDVFRNGYRAV TKVLGSLVDPNQQGTNGKFGYMINKNDTVDGEYTIFTGENDISQVNKVYEFNKQRSIPTE NMGYEDFMGLKVKRFVAGPLAFDSGQKFRENSCFAAGKELPEGGTDLGPCKQGAPLVLSF PHFLYADPAYLADVDGLHPDVTKHQFFFNSEPTLGVTVNVRGRIQYVEARGDTLKMLRTI VNLPEYVQWFSVGIIIVSSIALASTAFALFRPRTRRGDITKVRPINGASKAKYADTHCAD ILPNKVERIIQNGLERLPNTFGITAARNNFINELKSGNNNNPRRPSEPSAPPEVNIYKS
>IscQI62 SAAHTVRFDTEEFEFFKEAVSEIFVAKNSTFFVRRTMRELLFDGYDEPILTAAKSLGIEV PSTKFGWLLGKNGTDDGEYTIFTGSKGMHNYGEMDKYNGLRSIRLSYLGDVETRGVKLRR YWGEGRLFDYAEKDNRCFCTGACFPSGVLNISACQQGAPVAVSFPHFLYGDPSYQQAVEG IAPDPKRHQMYLDIEPLASADKGLLSKVRLVTEEIPQYVTVASFGAVIIGGIVLLATLVY AIRYTRRPKPVRPTYIPVTVLK
>IscPD82 MINGTDGGQFAPFVSKDSELYVFATDLCRSMRFNYERDTEVHGLKTMRFTPPATLFASAD EDENNRCFCTTSTCPKSGVVYVSTCQKGAPIVLSSPHFYLGDNEYVNGVAGLSPVKEQHE TFLDIHPLTGLVLRASKRLQINIDLKNYDKLHKVTVIPDHSHDVSNHLSDGSVE
>IscQ458 MWGGDECNLIRGTFGNVRPPMATTDEQRVFIPDIKRSVLLRYVHDSKVGSVHTRRFAVTP EVFASGKTRPENACYNKRTLPDGAADMGPVAKGAPVAVSLPHFLYGNQSEFGVEGLTPDE

DKHLLYVDSEPKKS
>IscP9A7 MAPVCLLQNLILEPGNEVYAHWQEVPIPIYIKYYFFNVTNPNEVLEQTEKPRLEELGLRE

Table S8. Protein sequences of GPCR used to construct phylogenetic tree.

>DgalGPCR1 D. gallinae-Rhodopsin MCRLSCTYINLFICASNFIVVALTMERFYAVAVPMKARTRGFSGRPNWSIGVCFFLAIVLYLPSV YNYRLMAIEHSIDESTTLPSFRCYVCQWSRFQEQQDGRVYVCIREIFSRVIPVFIVVILNVGMVIS LKHHQKSRAKLSECRASQAIASPDAADSDEDRLKRLLIVVMILFVVCNAPTVFRFLLMRSSGIN ELLPEIFVFCANLLALFNIACNFYVYCFCSTAVRTRVWELLFKVVPGYTTTTSTEKKHTLT
>G. occidentalis-Rhodopsin MNADNISAFFDDWASNFTDNTQSENVTVVPTVIRGSKQIADGICSHFFMGPRSRNVSPAIDWVR SIEFHILLPTIAVLGFVGNAINLIVLRSFTGRTFFYLFWLAVSDLGTMIFDSLFSLSFSIAPTNSLMA FLQCHMVPAGAGISLTCSNFIVVVLTVDRFRAVCYPIETRAKENNSRPRLKVLLCFVSALVVFGP NTYRRRVEAVVFDLGERSTMTTLCYVCQRRRFSNNTLITFYRILLAVFSKIIPVMIVATVNISIVV GLTRHQSERSANLHLGPLRQETAEDRLKKLILTITTIFVICLVPIAFRQLYYRQEPNTLGFAVFKA LSLVMIHLNTACNFYVYCFYSEAIRNQLRKISGHLLNTAKKNLTRTTTILSSTSPSTPSSPGTPDT AISFISFDPSVDSKL
>I. scapularis-secretin MAPTSRHKTCGNADPPRYRTAYACEGSQLHIACDDGHLVQLIRANYGRFSISICNEHGTLDWS VDCMSHRSFRDLPKGTPGGDLVPPLPGTVHAAAPPAVVQADNARTPPPPSPEHVLDIGFPFRTT TTEETTEAPSTEAATQEVSTSLDLLTDFCQPVTVREISWNWTRAGEVAVYPCPGGARGDARW QCGVNPVKWLSERPDLSGCNSFWVGDLERRIHDGVSVVNLASELAQKTRVKVLYGGDLLHT TSIVQQLLSKMEDKLDQALDSYQRQQVVEELMNYVVDFSSNLLEEHQRSSWGDLPPMEQRA AASSLLEGLERNAMLLVKSHSANMNYSRLQSNIMVAVRVLGLQSVTDLSFPDPKMVRGTPW ADLGDSIYLPYKTLLESARNGVVKVAFFSYRQMEAILSAPSPPGGDGVGGNMTRLVNSRVMA AALGRRRVLGLSQPVLVTLRHNKEENVSDPECVFWDFSKRDWSERGCWVESSNQTHTTCAC NHLTNFAVLMDVRAVQLSYSNEVALQVITYIGCFISIICMALTIITFHFFRSLESDRTVIHKNLCT CLLVAEIVFVAGITQTSQRVVCGVVAGLLHYFFLAAFLWMFVEGFQLYVMLIEVFDSEKSRLG WYYVLAYGAPAVVVTVAACVDPTSYGTERYCWLRADNYFILSFVGPVVAILLANLVFLSIAIY MMCRHASLASSVKNKEQSKMANLRIWIRSATVLVFLLGLTWAFGLLYLNAESVVMAYLFTFL NSLQGLFIFVFHCLRNDKVRKEYRQLVRQCPWAPPCVRREDKCPPAERPSYAHSNGTAHSAPS GAALSVRTSCTSTFAHPAPADHIYETIDQEDAFPLSATVGGGCARFVPIDPGECHIRSRSDASHQ SNSSLGCDRRPLIRQRIGGSALSDAGERPVDPALVMAVFDGDRVKCTLQGTAPGRLGGKALVT KHPCQPSAHLSTDC
>S. scabiei-secretin MRLPIVLSQYDTTLPTMSDPTNNDVSVHIPYKVLAQNANDQGQVKVIFLMYRRLSNLLRVRN PIYDFPIHLQQYAYKHSTNERSNDFEYPIYQYQRQQHQFHHPNPLFRSIPQPPINTIINSDIVGLIL PSDLQHSSYDRLPLPLNGMIELTFRHLRTENVTNGRCAYWDMKRIDEDTFGDWSTAGCETVS TNQTHTICRCNHLTNFAVLMDINNISFESNDELVLRLITRIGCSISIIALALTLLTLSVYRSLNSIR NSIHKHLCGCLLVAEVIFLLGIDETRMKLVCGLIAIALHYFFLASFLWMFFEGLQLYTMLVQVF

EHRHNRLTIYSLVAYGAPALLVIVAALVDPLSYGTSQHCWLRTDNHFIWSFLGPALAILLANILFLSLALSIMCRHTPSSIISTTTFAVHQKQQQQQHLKVYPSTLTPSPSYSITEHSRMHSIRFVNSKFIT
>V. jacobsoni-metabotropic MLFAIDRINEDETLLPGVRLGATILDTCSSDSYALNQSLEFIRASINTADPHNYYCHGGGNLTLKPEASAAISGVIGGSYSEVSLQVANLLRLFRIPQISPASTGTALSDKTRYDFFARTVPPDTFQALAMVAVVETFNWSYVSLVYSEGQYGESGQEQFTKEARHHNICIAISEKIPHSATEQQYLSALERLQQKPNAKVVVLFVRADHAEGVLRAAKELKRKYRDRLQSFDFYWIASDGWGARALSEDMQEAAEGAITIELESRRIEAFDRYMLDLTVENNERNPWFRDYWEALFECKIRNTSSEKEKLPQGISGSNSSLPSCSENLNISSTKDGYKQENKVQFVVDAVYAMAHAIDSVREKVCGAHGVCPRLKEVDGGLIYQALLNVSFVDLVNSTVRFDEKGDAQAPYIIYNYRRNYSSGELQYIQVGKWLGVEEGLELMAGDITFGRRETHDRVIPVSVCSAECGIGEVKKVQAGDHCCWICTRCEPHEFVVNESTCADCGPSRWPHPHKRSCFDLPVQHMQWNNLFSAVPIAVALLGIVLTCGTIAVFVRNNETPIVKASGRELSYMLLSGILICYLMTFVLLLKPTPVSCTAQRFGVGLGFSIIYGSLLTKTNRISRIFDSARRSARRPSFISPKSQMVITCMLISVQVMATLVWFVLEPPATRTEYPEGRRNQVILKCKIRDSSFLVSLVYNMFLITTCTVYAIKTRKIPENFNESKFIGFTMYTTCIIWLAFVPIYFGTGNNFQVQITTLCVSISLSAYVALFCLFSPKVYIILFHPDKNVRKLTMNSATYKKAPTSSTTGGGGGAGGGPPGHNLGSGHGTAVNNQPPTTCTTGTADSCVETVKLVPVATISQHTLQQTSPEMTVAQALRGAPPCSQPTQIEGGRCFQGANTGECVTSDQPRLPGQYSSASRATPSSSPPATGNKSPCDQGSTMMKAVDDRGGGDCDSMQSL
>G. occidentalis-metabotropic MARCPYLNSVPAALLLPGLLLVVVLVTEADTSHHHHRHLGFDEASLYGFDDFPPESRFHKTNNNYHQAPNHVNGVHDTYSTHNTGLNFSWPVKRVAHKKGEVMLGALMMVHERHANWTCGPIMPQGGIQALECMLFTIDYVNRQEWMPSNVSFGYYILDDCDSDTYGLEQAVDFIKGSIGRLHDNDDRITCSQKSSARGSSNSRPSSPATVDVISGVLGAASSVTSIQVANLLRLFRIPQISFFSTSPELSNKQRFEYFLRTVPSDRDQAAAMVELVKLLRWTYISIVYEESNYGIQAFSVLESLLGQQGICIAAKEKLTKDSGQANDKAYDYIVDKLKAKSRARGVIVFGSDQEVAHLMSAVARGNATGMFSWIGSDGWSARSLVSDGHEAQVEGTISVQPMAHPIPEFESYFRNLTAQGNKRNPWFIEYWEYTFKCRWPNETITPYNQAYNRTCSGHEKLSDNTQTGGFELERQLQFVSDAVLAFAYAVRDMHQQLCPGFSGLCRKMKPIEGSQLLSYLKRVTFDGLTSDEFRFAENTLDGPSRYNILHFKQTKPGTYDWVKIGEYRDGQLTLNQTELQFRLEERNTSAEDGSILTGTTPSPPISVCSLPCERGSAKKFLEGEKCCWQCMPCQKYEVLRTETECVECARGTLPDEDHQVCLEIPAQHVNPHSSWATGAMAFASAGSILTLCVIYVFVKYRDTPVVRASGRELSAVLLLGILFCYCVTFVLVQKPTDLFCGLQRTGVGLSFTIVYAAILTKSNRIARIFRAGKRTSRRPSFISPKSQLIICGILVCIQVLVTAVWLLFSPPKAVKHYPTREQSQLLCQASLGSSYVVSFAYPVMLVCVCTAYAVITRKIPEAFNESKYIGFTMYTTCIIWLSFIPLYLTTSSQLAIGVTVMCVSISLSATVTLVCMFAPKLCIILLHPEKNVRQPVGMIQNNRYGALRSMQRRHVECATQSDDLELGVTVMAKSAVSLASSCAATQTEEEGEEAEETDRLWRQNGIGGDVQL

Table S9. Primer sequences for quantitative RT–PCR.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')	length
DgalOBP1	TGCGTTCTTGAGAGCTATGG	TTCATCCTTCGGACACTCTG	126 bp
DgalOBP2	GGCTTTGGCTGCTGTAATCTA	GCAACTTCTCCGCGATACAA	110 bp
DgalGPCR1	TCTGCGCGAGCAACTTTA	AGACTCCGATGCTCCAATTC	120 bp
DgalNPC2-5	TATCGTCGTGCTACCTCTGAT	TCGTCAGAACAGCCTTCAATC	126 bp
Fun14-like (HKG)	TAA CTG GCT CAC CCG AAC TC	CTT TCT CCA CAG CCT TCC AG	208 bp