Supplementary Figures

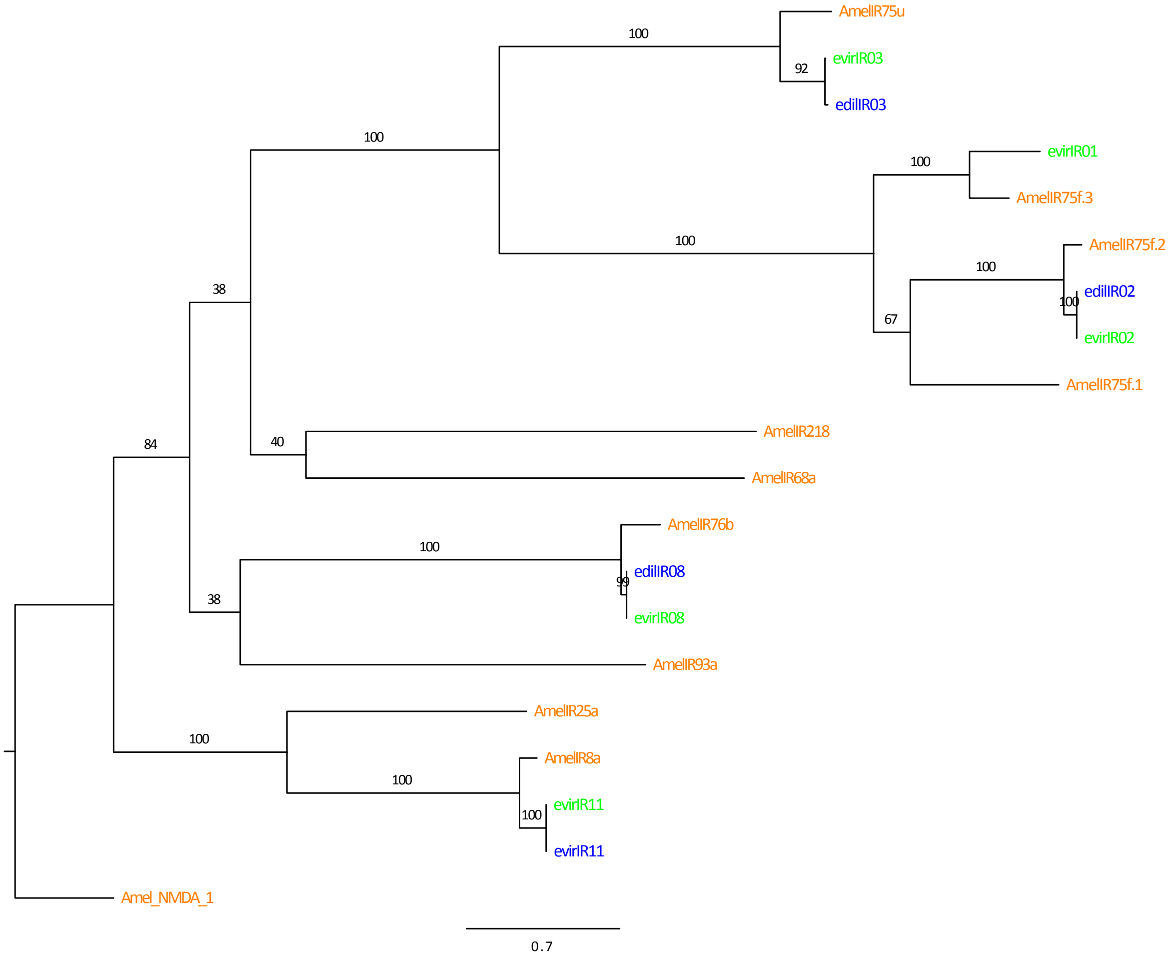

Figure S1. Phylogenetic relationships of the 4 candidate *Euglossa dilemma* (blue) and 5 *Euglossa viridissima* (green) Ionotropic Receptors to *Apis mellifera* (orange). This maximum likelihood tree was rooted by *A. mellifera* NMDA1. Numbers above branches show bootstrap-supports based on 1000 replicates.

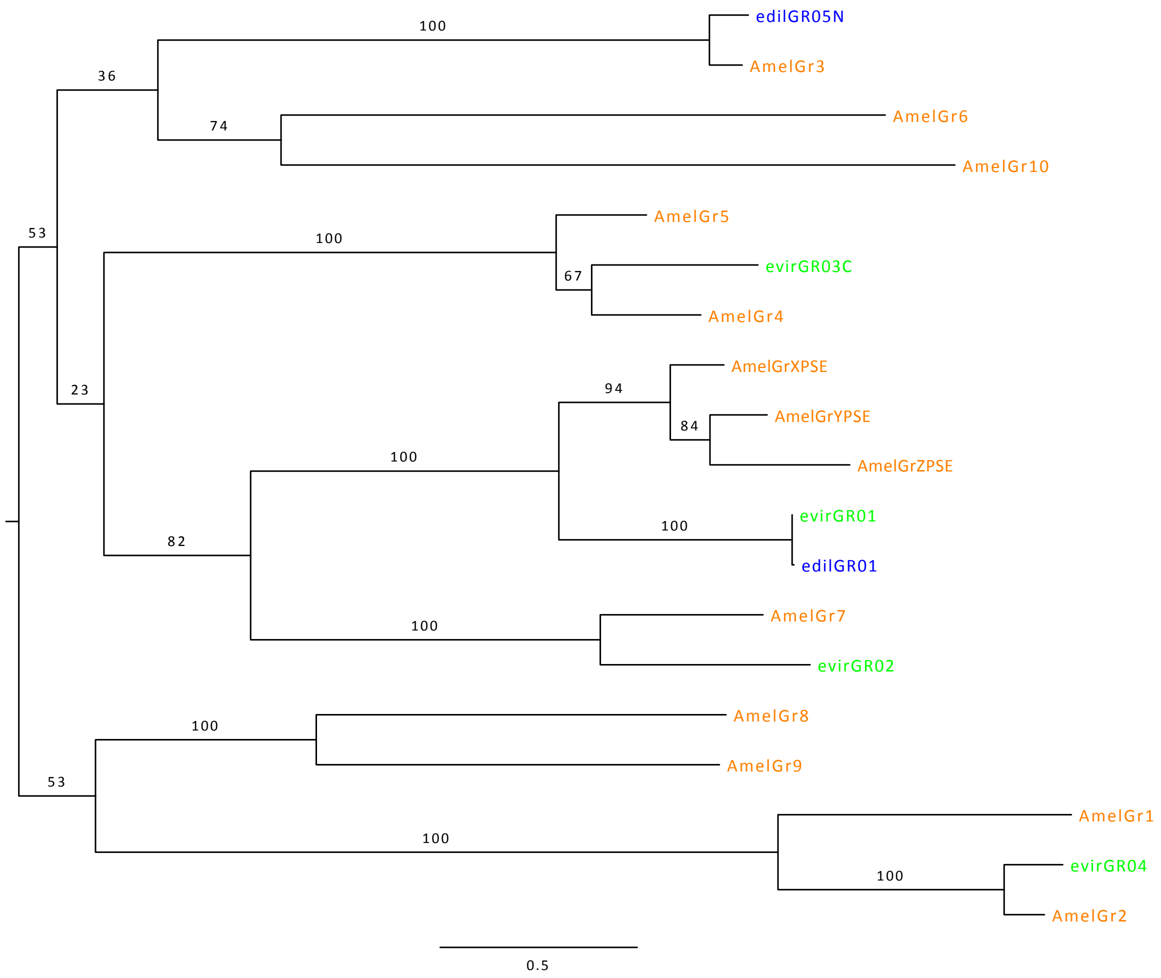

Figure S2. Phylogenetic relationships of the 2 candidate *E. dilemma* (blue) and 4 *E. viridissima* (green) Gustatory Receptors to *A. mellifera* (orange). This maximum likelihood tree was rooted at the midpoint in absence of a suitable outgroup. Numbers above branches show bootstrap-supports based on 1000 replicates. Symbols after the GR descriptors: C: C-terminus is missing, N: N-terminus is missing, PSE: pseudogene (after Robertson and Wanner 2006).

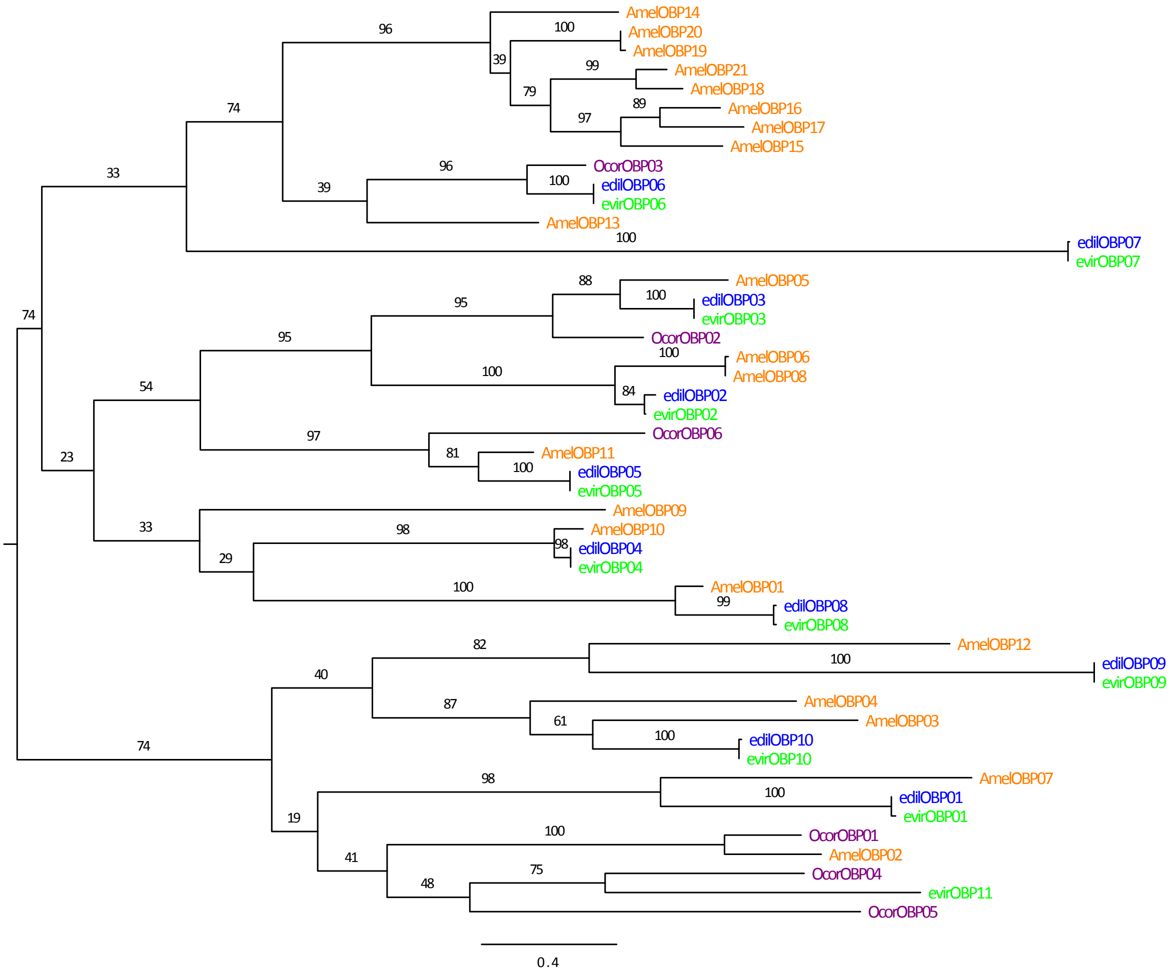

Figure S3. Phylogenetic relationships of the 10 candidate *E. dilemma* (blue) and 11 *E. viridissima* (green) Odorant Binding Proteins to *A. mellifera* (orange) and *Osmia cornuta* (purple). This maximum likelihood tree was rooted at midpoint in absence of a suitable outgroup. Numbers above branches show bootstrap-supports based on 1000 replicates.

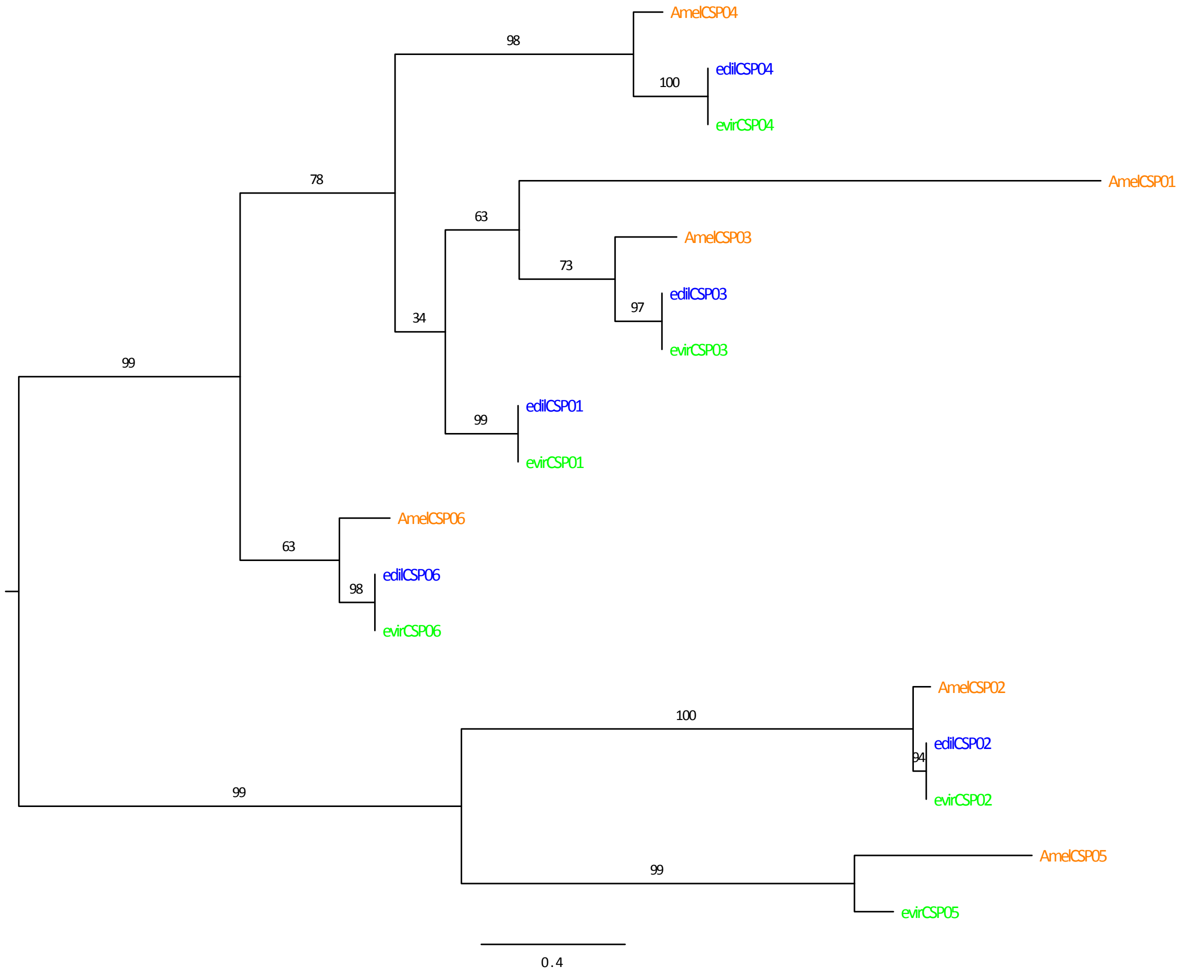

Figure S4 Phylogenetic relationships of the 5 candidate *E. dilemma* (blue) and 6 *E. viridissima* (green) Chemosensory Proteins to *A. mellifera* (orange) The maximum likelihood tree was rooted at midpoint in absence of a suitable outgroup. Numbers above branches show bootstrap-supports based on 1000 replicates.

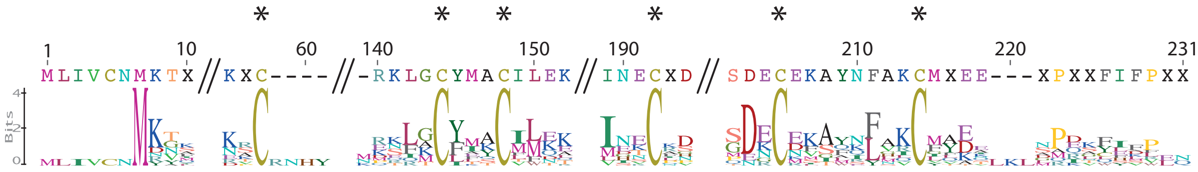

Figure S5 Sequence logo of the protein sequence alignment of all candidate *Euglossa* OBPs Relative sizes of letters indicate the frequency of an amino acid at the given site among the entire alignment. * indicates conserved cysteines present in all OBP sequences. Letters above the sequence logo represent the consensus sequence of the alignment at indicated positions.

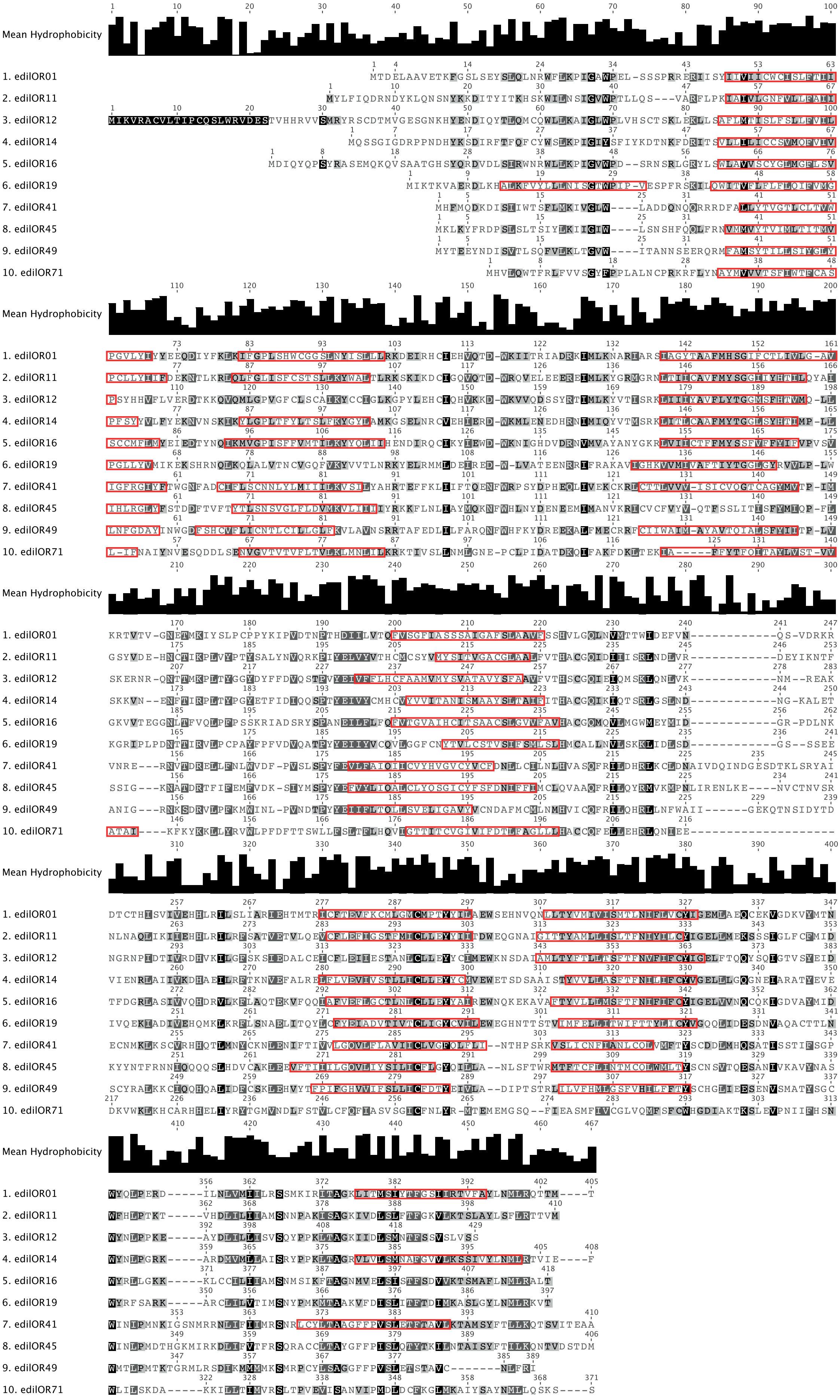
Mean Hydrophobicity
1. edilOR01 MTDELAAVETKFGSLSEYSLQLNRWFLKPIGAWPEL-SSSPRRERIISYIIVIICWCISLFTII
2. edilOR11 MYLFIQDRNDYKLQNSNYKKDITYITKHSKWILNSIGVWPTLLQS---VARFLPKIAIVLGNFVLLFAII
3. edilOR12 MIKVRACVLTIPCQSLWRVDESTVHHRVVSMRYRSCDTMVGESGNKHYENDIQYTLQMCQWLLKAIGLWPLVHSCTSKLEKLLSAFLMTISLFSLLFVLL
4. edilOR14 MQSSGIGDRPPNDHYKSDIRFTFQFCYWSLKPIGIYSFIYKDTNKFDRITSVLLILICCSVMQFVIV
5. edilOR16 MDIQYQPSYRASEMQKQVSAATGHSYQRDVDLSIRWNRWLLKPIGVWPD--SRNSRLGRYLSWLAVVSCYGLMGLSV
6. edilOR19 MIKTKVAERDLKHALKFVYLLLNISGTWPIP-VESPFRSKILQWITVFLFLFLQIFVMG
7. edilOR41 MHFMQDKDISLIWTSFLMKIVGLW----LADDQNQQRRRDFALLYTVGTLCLTVW
8. edilOR45 MKLKYFRDPSLSLTSIYLKIIGIW----LSNSHFQQLFRNVMMVYTVIMLTITMV
9. edilOR49 MYTEEYNDISVTLSQFVLKLTGVW----ITANNSEERQRMFAMSYTILLSIYGLY
10. edilOR71 MHVLQWTFRLFVVSGYFPPLALNCPRKRFLYNAYMVVVTSFIWTFCAS
Mean Hydrophobicity
1. edilOR01 PGVLYIYYEEQDIYFKLKIFGPLSHWCGGSLNYISLLRKDEIRHCIEHVQTD-WKIITRIADRKIMLKNARIARSIAGYTAAFMHSGIFCTLIVLG-AV
2. edilOR11 PCLLYIIFDEKNTLKRLQLFGLISFCSTSLLKYWALTLRKSKIKDCIGQVQTD-WRQVELEEREIMLKYGRMGRNLTIICAVFMYSGGIIYHTILQYAI
3. edilOR12 PSYHHVFLVERDTKKQVQMLGPVGFCLSCAIKYCCIGLKGPYLEHCIQHVKKD-WKVVQDSSYRTIMLKYVTISRKLIIIYAVFLYTGGMSFHTVMQ-LL
4. edilOR14 PFSYYVLFYEKNVNSKIKYLGPLTYFLTSLFKYGYLAMKGSELNRCVEHIERD-WKMLENEDHRNIMIQYVTMSRKLITLCAAFMYTGGLSYHTIMP-LL
5. edilOR16 SCCMFLMYEIEDTYNQIKMVGPISFFVMTILKYYQLIIHENDIRQCIKYIEWD-WKNIGHDVDRNVMVAYANYGKRLVIICTFFMYSSFVFFYIFVPVSV
6. edilOR19 PGLLYVMIKEKSHRNQLKQLALVTNCVGQFVKYVVVTLNRKYELRMMLDEIRED-W-LVATEENRRIFRAKAVIGHKVVMIVAFTIYTGGLGYRVVLP-LW
7. edilOR41 IGFRGIYFTWGNFADCIFLSCNNLYLMIIILKVSILYAHRTEFFKLIIFTQENFWRPSYDPHEQLIVEKCKRLCTTLVVV-ISICVQGTCAGYMVTP-IM
8. edilOR45 IHLRGLYFSTDDFTVFTYTLSNSVGLFLDVMKVLIIIIYRKKFLNLIAYMQKNFWHLNYDENEEMIMANVKRICVCFVYV-QTFSSLITISFYMIQP-FL
9. edilOR49 LNFGDAYINWGDFSHCVFLICNTLCILLGLFKVLAVNSRRTAFEDLILFARQNFWHFKYDREEKALFMECRRFCIIWAIM-AYAVTQIALSFYIITP-LV
10. edilOR71 L-IFNAIYNVESQDDLSENVGVTVTVFLTVLKLMNLILKRKTIVSLLNMLGNE-PCLPIDATDKQIFAKFDKLTEKIA-----FFYTFQITAYLVST-VV
Mean Hydrophobicity
1. edilOR01 KRTVTV-GNEYMKIYSLPCPPYKIPVDTNPTHDIILVTQFVSGFIASSSAIGAFSLAAVFSSHVLGQLNVMTTWIDEFVN------------QS-VDRKR
2. edilOR11 GSYVDE-HNCTIKPLVYPTYSALYNVQRKPIYELVYVTHCMCSYVMYSITVGACGLAALFVTHACGQIDIIISRLNDLVR------------DEYIKNTF
3. edilOR12 SKERNR-QNTTMKPLTYGGYDYFFDVQSTPVYEIVFFLHCFAAMVMYSVATAVYSFAAVFVTHSCGQIEIQMSKLQNLVK------------NM--REAK
4. edilOR14 SKKVN--ENFTIRPLTYPGYETFIDIQQSPTYEIVYCMHCVYVVITANISMAAYSLTAIFITHACGQIKIQTSRLGSLND------------NG-KALET
5. edilOR16 GKVVTEGGNLIFVQLPFPSSKRIADSRYSPANEILFLFQFVTGVAIHCITSAACSLGVFAVHACGQMQVLMGWMEYMID------------GR-PDLNK
6. edilOR19 KGRIPLPDNTIRVLPCPAYFPFVDVQATPYEIIYVCQVLGGFCNYTVLCSTVSIFSMLSLHMCALLNVLSKKLIDLSD------------GS--SSEE
7. edilOR41 VNRE---RNVTDREIILENLWVDF-PVSLSPYEEVLFAIQIICVYHVGVCYVCFDNLLCLLNLHVASQFRILDHRLKCLDNAIVDQINDGESDTKLSRYAI
8. edilOR45 SSIG---KNATDRTFIIFEMEVDK-SIYMSPYYEFVYLIQALCLYQSGICYFSFDNIFFLMCLQVAAQFRILQYRMVKMPNLIRENLKE----NVCTNVSR
9. edilOR49 ANIG---RNKSDRVIPFKMWINL-PVNDTPYYEIIFLTQLLSVELIGAVYVCNDAFMCLMHVICQFRILQHRLLNFWAII------GEKQTNSIDYTD
10. edilOR71 ATAI----KFKYKKLLYRVWLPFDFTTSWLLFSLTFLHQVIGTTITCVGIVIFDTLFAGLLLHACCQFELLEHRLQNIEE--------------------
Mean Hydrophobicity
1. edilOR01 DTCTHISVIVEHHLRILSLIARIEHTMTRICFTEVFKCMLGMCMPTYYILAEWSEHNVQNLLTYVMIVISMTLNIFLVCYIGEMLAEQCEKVGDKVYMTN
2. edilOR11 NLNAQLIKIIEHHLRILRFSATVETVLQEVCFLEFIGSTFMICLLEYYIITDWEQGNAIGITTYAMLLISLTFNIYILCYIGELLMEKSSSIGLFCFMID
3. edilOR12 NGRNPIDTIVRDHVKILGFSKSIEDALCEICFLEIIESTANICLLEYYCIMEWKNSDAIAMLTYFTLLTSFTFNVFIFCYIGELFTQQYSQIGTVSYEID
4. edilOR14 VIENRLAIIVKDHAEILRRTKNVEFALRELFLVEVIVSTLLICLLEYYCMVEWETSDSAAISTYVVLLASFTFNILLFCYVGELLGQGNEIARATYEVE
5. edilOR16 TFDGRLASIVVQHDRVLKFLAQTEKVFQQIAFVEFLGCTLNICLLEYYAIREWNQKEKAVAFTYVLLLMSFTFNIFIFCYIGELVVNQCQKIGDVAYMID
6. edilOR19 IVQEKIADIVEHQMKLKRFLSNAELITQYLCFYEIADVTIVTCLIGYCVILEWEGHNTTSTVIMFELLITWIFTTYLICYVGQQLIDESDNVAQACTTLN
7. edilOR41 ECNMKLKSCVRHHQTLMNYCKNLENIFTIVVLGQVLFLAVIICLVGFQLFLI--NTHPSRKVSLICNFHANLCQLVMFTYSCDDLMHQSATISSTIFSGP
8. edilOR45 KYYNTFRNNIQQQQSLHDVCAKLEEVFTIIILGQVLIYSILICFLGYQILLA--NLSFTWRMTFTCFLINTMCQLWMLTYSCNSVTQESANIVKAVYNAS
9. edilOR49 SCYRALKKCIQQHQALIDFCSKLEHVYTFPIFGHVVIFSLLICFDTYEIVLA--DIPTSTRLILVFHMIGSFVHILFFTYSCHGLIEESENVSMATYSGC
10. edilOR71 DKVWKLKHCARHHELIYRYTGMVNDLFSTVLCFQFIASVSGICFNLYR-MTEMEMGSQ--FIEASMFIVCGLVQMFSFCWHGDIAKTKSLEVPNIIFHSN
Mean Hydrophobicity
1. edilOR01 WYQLPERD-----ILNLVMIILRSMKIRITAGKLITMSIYTFGSIIRTVFAYLNMLRQTTM----T
2. edilOR11 WFHLPTKT-----VHDLILIIAMSNNPAKISAGKIVDLSLFTFGKVLKTSLAYLSFLRTTVM
3. edilOR12 WYNLPPKE-----AYDLILLISVSQYPPKLTAGKIIDLSMNTFSSVSLVSS
4. edilOR14 WYNLPGRK-----ARDMVMLLAISRYPPKLTAGRVLVLSMNAFGVVLKSSIVYLNMLRTVIE----F
5. edilOR16 WYRLLGKK-----KLCCILIIAMSNMSIKFTAGNMVELSISTFSDVVKTSMAFLNMLRALT
6. edilOR19 WYRFSARK-----ARCLILVTIMSNYPMKMTAAKVFDISLIFTTDIMKASLGYLNMLRKVT
7. edilOR41 WINIPMNKIGSNMRRNLIFIIMRSNRLCYLTAAGFFFVSLETFTAVLKTAMSYFTLLKQTSVITEAA
8. edilOR45 WINLPMDTHGKMIRKDLIFVTFRSQRACCLTAYGFFPISLQTYTKILNTAISYFTILKQNTVDSTDM
9. edilOR49 WMTLPMTKTGRMLRSDIKMMMMKSMRPCYLSAGGFFPVSLETSTAVC-------NLFRI
10. edilOR71 WLILSKDA-----KKILLTIMVRSLTPVEVISANVIPMDLDCFKGLMKAIYSAYNMLLQSKS----S

Figure S6 Distribution of transmembrane (TM) domains across Odorant Receptor (OR) sequences. All ORs showing d_N/d_S>1 represented by the *Euglossa dilemma* homologs (indicated by edilORXX) were aligned using MAFFT (see Materials and Methods) and consensus TM predictions were mapped onto the respective OR sequences (Red boxes; Supplementary Table S5). Amino acids are colored by the degree of conservation relative to amino acids at homologous sites in the alignment using a color gradient from white for unconserved to black for highly conserved residues. Mean hydrophobicity is indicated for each site in a barplot above the alignment. The Plot was generated in Geneious v5.4.6.