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.
**Figure S6 Distribution of transmembrane (TM) domains across Odorant Receptor (OR) sequences.** All ORs showing $dS/dD>1$ 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.