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Analysis methods are provided for the phylogenetic trees in Figure 2C and Figure 2 – figure supplement 2.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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Supplementary files 1-7 are included with this submission. These data provide annotated sequences, alignments, code, and outputs of protein topology predictions. Outputs of *ab initio* modelling of insect chemosensory receptor homologs with trRosetta and RaptorX are provided in the Dryad repositoryreferred to in the text.