***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Not applicable. Our analyses require a single genome per hexapod order.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Not applicable. Our analyses require a single genome per hexapod order. Multiple lineages provide support as ‘pseudo-replicates’.

**Statistical reporting**

* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Our analysis requires presence-absence data. No statistical tests are necessary to support our central hypotheses about the origins of the OR family in insects.

Our phylogenetic tree showing the detailed relationships of the OR proteins in insects is based on 1000 bootstrap replications.

(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.)

**Group allocation**

* 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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Not applicable. Our analysis is descriptive and not experimental.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
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Please indicate the figures or tables for which source data files have been provided:

In the Supplementary file we provide all of the protein sequences from the new OR gene models we have built in several insect genome sequences. We also provide a more detailed version of the phylogenetic tree shown in the main text. We have submitted the firebrat *Thermobia domestica* genome assembly to the DRYAD database, with doi:10.5061/dryad.p2t8170. All new OR protein sequences and the alignment used for the phylogenetic analysis have also been placed in the DRYAD database at the same doi. All raw sequence files have been submitted to the Short Read Archive at the National Center for Biotechnology Information as BioProject PRJNA474784.