

Descriptions of Additional Supplementary Files

File Name: Supplementary Data 1 – Description: Statistics of sequencing data

File Name: Supplementary Data 2 – Description: HiFi CCS reads from contaminating microorganisms

File Name: Supplementary Data 3 – Description: Statistical overview of genome assemblies with Hifiasm and HiCanu

File Name: Supplementary Data 4 – Description: BUSCO analysis (V5, diptera_odb10, N=3285) of *D.melanogaster* and *B.dorsalis* genome assemblies

File Name: Supplementary Data 5 – Description: Genes failed to be aligned to other *B.dorsalis* assembly

File Name: Supplementary Data 6 – Description: Repeat annotation

File Name: Supplementary Data 7 – Description: Gene annotation and statistics

File Name: Supplementary Data 8 – Description: Consensus sequences of centromeric satellite monomers

File Name: Supplementary Data 9 – Description: Telomere and centromeric regions in chromosome assemblies

File Name: Supplementary Data 10 – Description: Nuclear mitochondrial DNA segments in the nuclear genome

File Name: Supplementary Data 11 – Description: Differentially expressed genes (DEGs) between male and female in peripheral tissues. DEGs identified by DESeq2 (two-sided Wald test; BH FDR adjusted; significance at $p_{adj} < 0.05$)

File Name: Supplementary Data 12 – Description: Molecular interactions of *D.melanogaster* ATPsyn β in alliancegenome database

File Name: Supplementary Data 13 – Description: List of species and publicly available datasets used in comparative genomic analysis

File Name: Supplementary Data 14 – Description: Summary of OR subfamilies in *B.dorsalis*

File Name: Supplementary Data 15 – Description: Summary of mutant primers, PCR conditions and target sequences

File Name: Supplementary Data 16 – Description: Survival and mutagenesis of *B.dorsalis* after microinjection of CRISPR/Cas9 complex

File Name: Supplementary Data 17 – Description: Statistical analysis of EAG in BdorOR88a mutants and wild-type strains. The EAG responses (mean $\pm$ SEM) are not significantly different between BdorOR88a mutants and wild-type strains at various doses, with $P=0.7496$ (0.01 μ g), $P=0.0572$ (0.1 μ g), $P=0.7007$ (1 μ g), $P=0.547$ (10 μ g), $P=0.7266$ (100 μ g), $P=0.8321$ (1000 μ g). Statistical test was performed by two-side unpaired t-test (normally distributed data) or Mann Whitney U test (nonnormally distributed data).

File Name: Supplementary Data 18 – Description: Statistical analysis of behavioral responses in BdorOR88a mutants and wild-type strains. The behavioral responses (mean $\pm$ SEM) to ME are significantly different between BdorOR88a mutants and wild-type strains at most time points, with $P=0.0039$ (1 min), $P=0.0014$ (2 min), $P=0.0004$ (3 min), $P=0.0079$ (4 min), $P=0.0042$ (5 min), $P=0.0009$ (6 min), $P=0.0016$ (7 min), $P=0.000008$ (9 min), and $P=0.0079$ (10 min), except at 0 min and 8 min, where $P=0.3198$ and $P=0.0923$, respectively. Statistical test was performed by two-side unpaired t-test (normally distributed data) or Mann Whitney U test (nonnormally distributed data).

File Name: Supplementary Data 19 – Description: Sample collection for transcriptome study

File Name: Supplementary Data 20 – Description: Statistics of QC from RNA-seq

File Name: Supplementary Data 21 – Description: Statistics of QC from iso-seq

File Name: Supplementary Data 22 – Description: The orthogroup composition of OrthoFinder result

File Name: Supplementary Data 23 – Description: The genomic coordinate information used for the synteny analysis

File Name: Supplementary Data 24 – Description: Probes sequence for the centromere's validation

File Name: Supplementary Data 25 – Description: The alignment of sgRNA sequence to BdorOR88 target