

**Description of additional supplementary files for
“Genome assembly of a moth-like butterfly (*Macrosoma leucophasiata*) reveals convergent
adaptation of visual genes to nocturnality”**

List of supplementary data with brief description of each file:

- 1. Supplementary Data 1_hifiasm_QUAST_report.pdf**
Genome assembly features of the raw assembly generated by Hifiasm
- 2. Supplementary Data 2_final-masked-assembly_QUAST_report.pdf**
Genome assembly features of the final soft-masked genome assembly
- 3. Supplementary Data 3_Mleu_augustus.aa**
Augustus gene model predicted from BRAKER3 EP+ pipeline
- 4. Supplementary Data 4_Mleu_eggnog_annotations.tsv**
Functional annotation using EggNOG-mapper based on the Augustus gene model
- 5. Supplementary Data 5_HOGs_of_20_species.tsv**
All the gene families (HOGs) reported from OrthoFinder
- 6. Supplementary Data 6_Mleu_rapid_evolved_genes.tsv**
The list of HOGs identified to be undergoing rapid gene size expansion and contraction from CAFE results
- 7. Supplementary Data 7_unfiltered_phototransduction-related_orthologs.tsv**
List of raw phototransduction-related orthologs and the gene copy number by blasting the sequence of putative phototransduction-related genes published in Macias-Munoz et al., 2019
- 8. Supplementary Data 8_filtered_phototransduction-related_orthologs.tsv**
List of phototransduction-related orthologs and the gene copy number after removing the HOGs containing no gene annotated with phototransduction-related function.
- 9. Supplementary Data 9_corrected_phototransduction-related_orthologs.tsv**
List of phototransduction-related orthologs and the gene copy number after correcting the false gene duplications.
- 10. Supplementary Data 10_all_gene_family_trees.pdf**
Images of the gene family trees (trees of clustered HOGs grouped by annotated family name)
- 11. Supplementary Data 11_opsin_gene_trees.pdf**
Images of the opsin gene trees.
- 12. Supplementary Data 12_MEME-HyPhy-Opsins-summary.xlsx**
Tabular summary of the MEME results with reported p-values and LRT statistics. The significantly selected sites are highlighted with yellow.
- 13. Supplementary Data 13_Reconciled-gene-trees_ThirdKind.pdf**
Gene tree reconciliations obtained from GeneRax and visualized on the ThirdKind platform using PhyloXML files obtained from GeneRax, to interpret duplications and transfers.
- 14. Supplementary Data 14_Euglenozoa_from_Macrosoma.fasta.gz**
Assembled contigs that blast to Euglenozoa from *Macrosoma leucophasiata* genome.
- 15. Supplementary Information.docx**
All the in-text citations referring to 'Supplementary Figure' and 'Supplementary Table' in the main text are included here.