**README: Supplementary Information Differential Expression Analyses**

**Supplementary Table A:** Summary statistics of raw and preprocessed RNA-seq reads, alignment percentage of preprocessed reads to the reference transcriptome and percentage of reads of pseudoalignment

**Supplementary Table B:** Differential Gene Expression results for all comparisons of control samples vs experiment samples for *S. mediterranea* including logFC, logCPM, p-value and FDR corrected p-value as long as the expression of each sample per gene

**Supplementary Table C:** Differential Gene Expression results for all comparisons of control samples vs experiment samples for *O. nungara* including logFC, logCPM, p-value and FDR corrected p-value as long as the expression of each sample per gene

**Supplementary Data A:** Density plots of log2FPKM for all samples of *S. mediterranea* and *O. nungara*

**Supplementary Data B:** Volcano plots for all comparisons of *S. mediterranea*. Red dots indicate the statistically significant genes

**Supplementary Data C:** Volcano plots for all comparisons of *O. nungara*. Red dots indicate the statistically significant genes

**Supplementary Data D:** Heatmaps of Differentially Expressed Genes for all comparisons of *S. mediterranea*. Rows indicate genes and columns indicate sample information. Yellow indicates upregulation and purple downregulation.

**Supplementary Data E:** Heatmaps of Differentially Expressed Genes for all comparisons of *O. nungara.* Rows indicate genes and columns indicate sample information. Yellow indicates upregulation and purple downregulation.