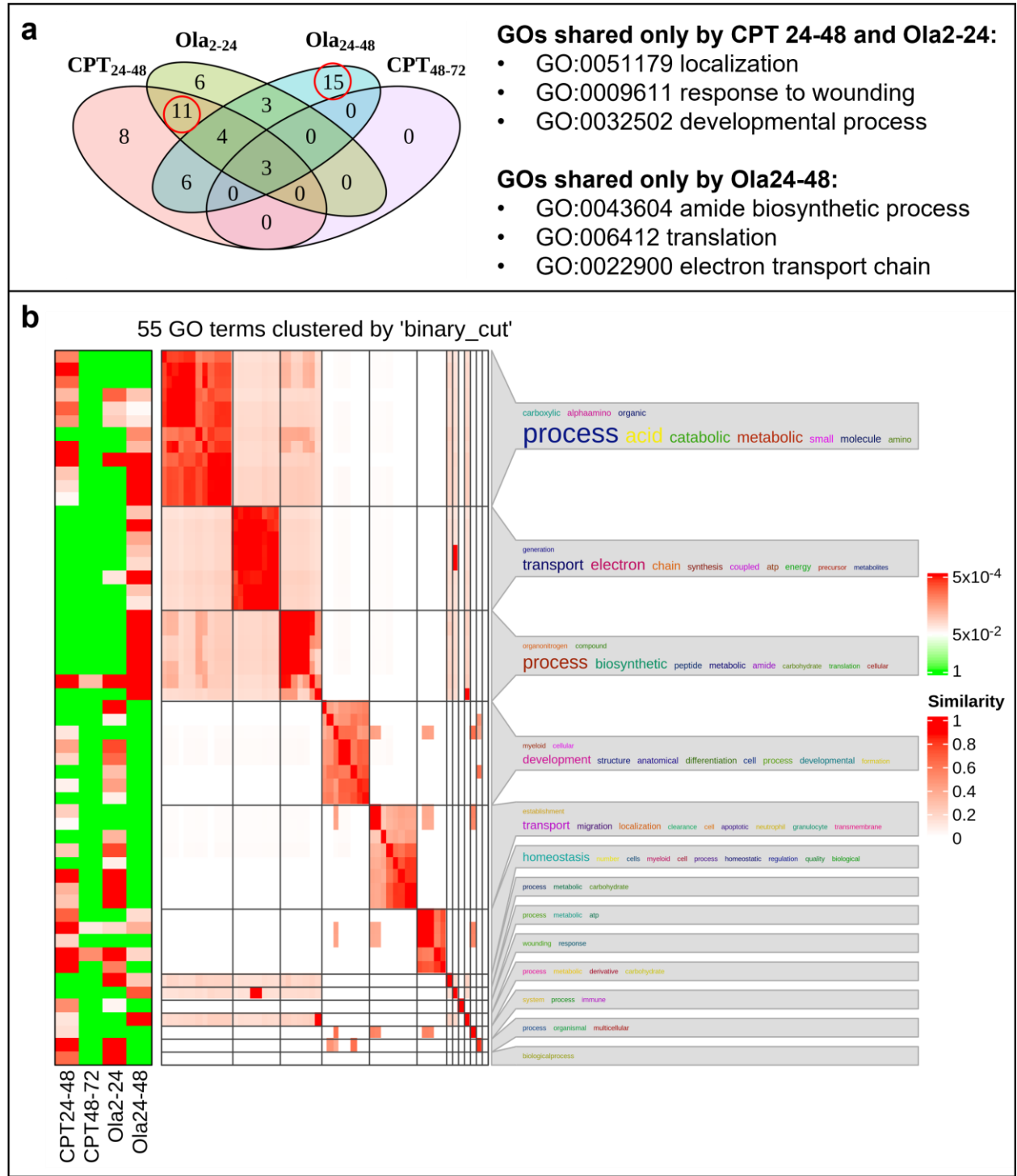
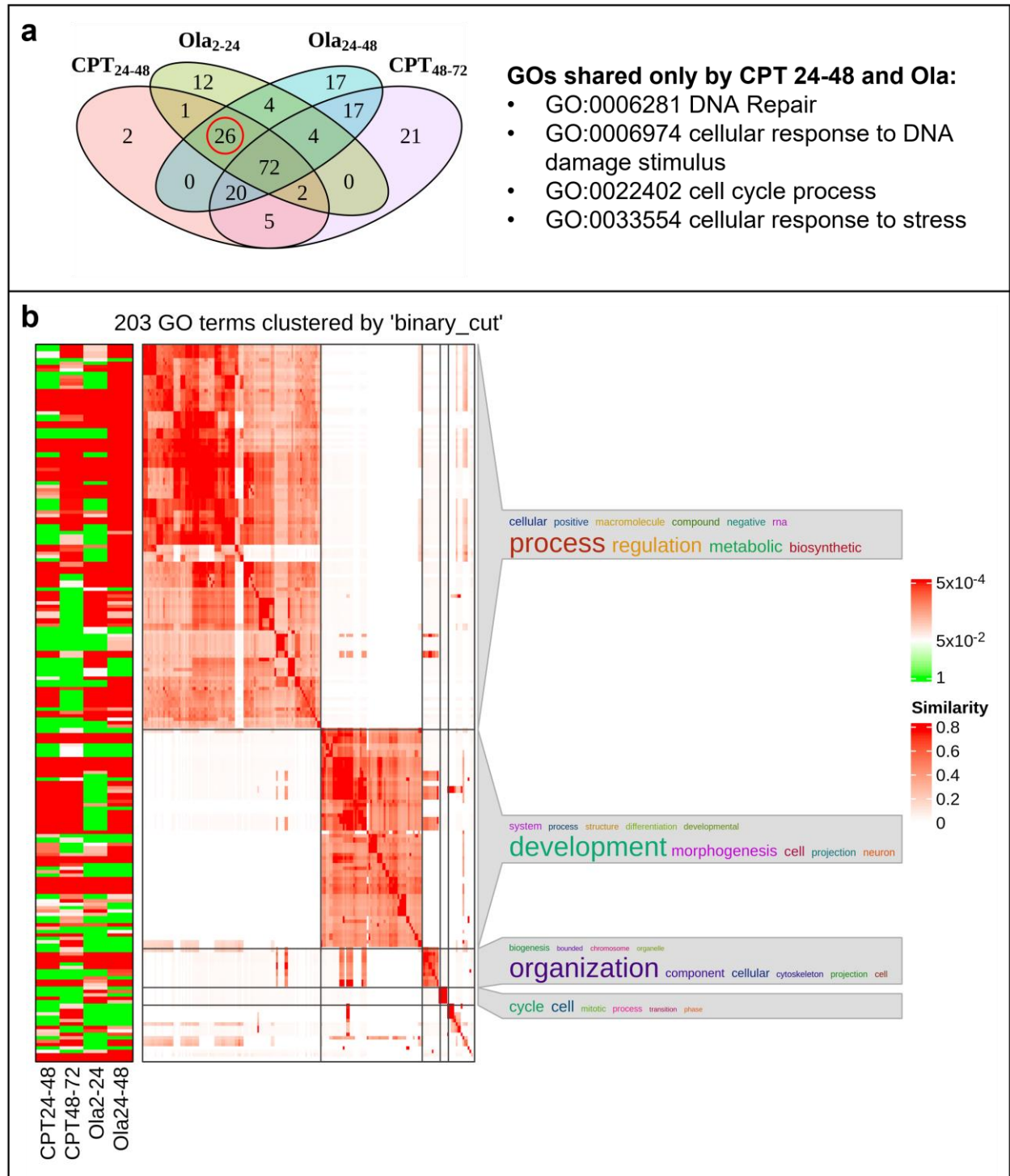


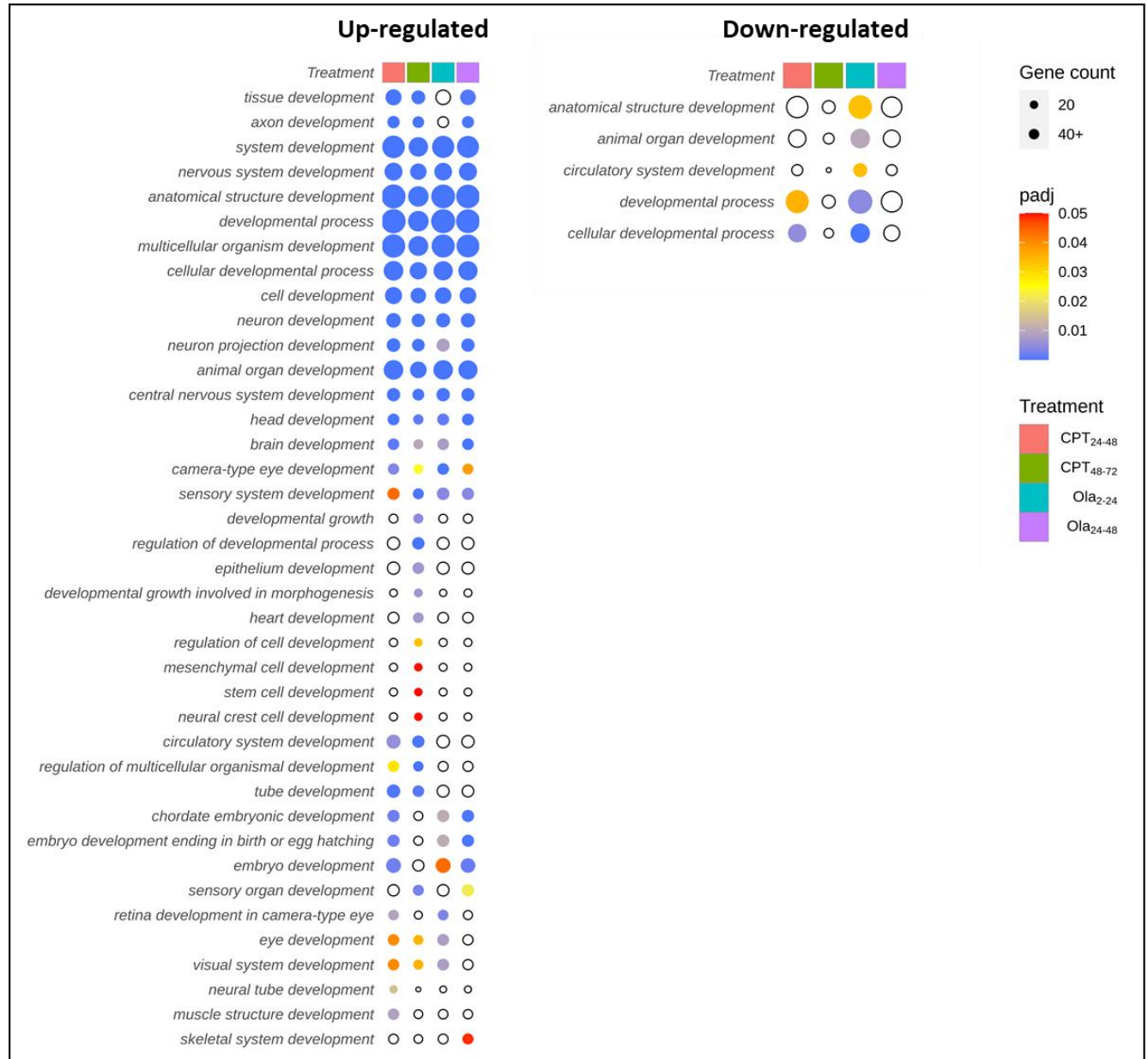
Supplementary Figure 1. Summary of significantly ($\text{padj} < 0.05$) enrichment Gene Ontology (GO) terms associated with the down-regulated differentially expressed genes. **(a)** Overlap of the enriched GO terms between each treatment condition. Shown is a subset of the list of Biological Processes shared by some of the treatment groups. **(b)** Summarized GO terms. Left most heatmap represents the padj values for the enriched GO terms. Second heatmap shows the similarity matrix of the GO terms.



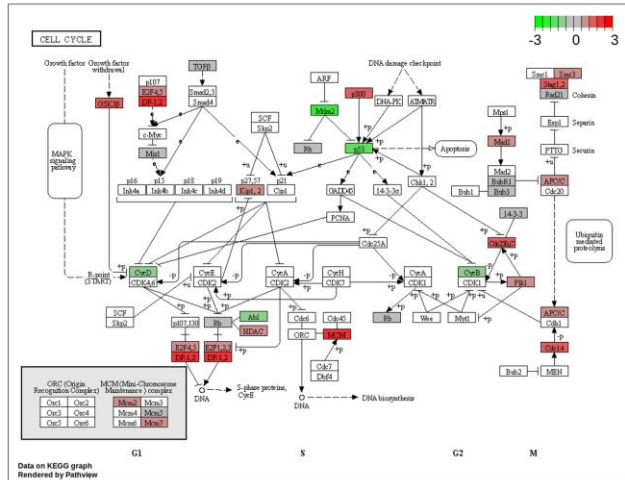
Supplementary Figure 2. Summary of significantly ($\text{padj} < 0.05$) enrichment Gene Ontology (GO) terms associated with the up-regulated differentially expressed genes. **(a)** Overlap of the enriched GO terms between each treatment condition. Shown is a subset of the list of Biological Processes shared by CPT 24-48 and the Ola treatment groups related to DNA damage response. **(b)** Summarized GO terms. Left most heatmap represents the padj values for the enriched GO terms. Second heatmap shows the similarity matrix of the GO terms.



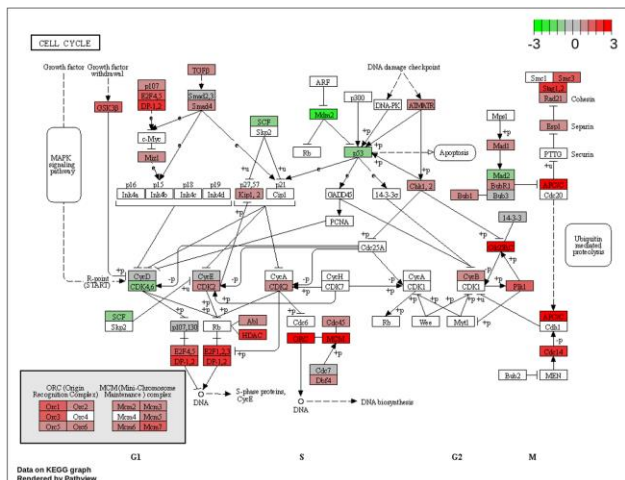
Supplementary Figure 3. List of significantly enriched Gene Ontology terms associated with Developmental Biological Processes that were either up-regulated or down-regulated within the treated samples versus the control. Color scale represents the adjust p-values less than 0.05, with empty circles showing those greater than 0.05. The size of the circle represents the number of significantly differentially expressed genes that are part of the given GO term.



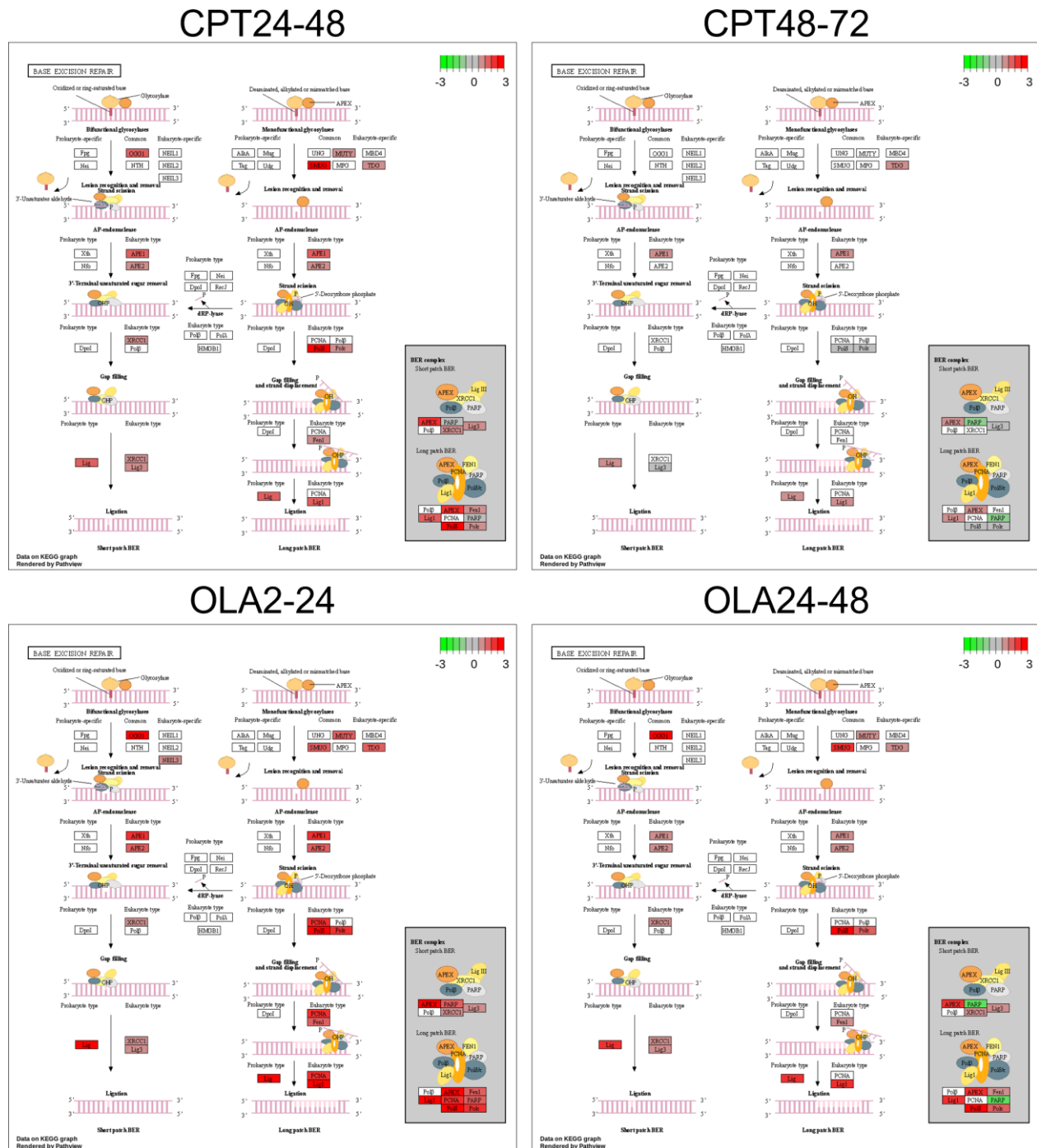
CPT48-72

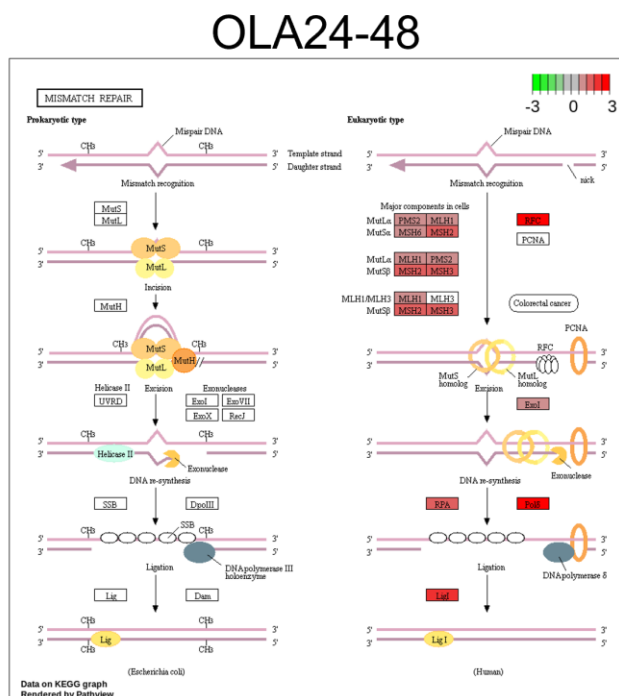


OLA24-48

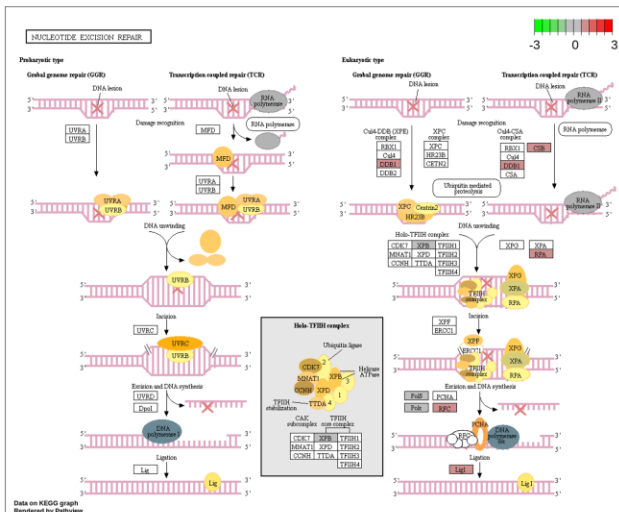


Supplementary Figure 5. Significantly ($p_{adj} < 0.1$) differentially expressed genes mapped to the KEGG pathway, base excision repair (hsa03410). Color scale represents the Log2 fold change between the treated and the control samples, capped at a maximum of 3 and minimum of -3.

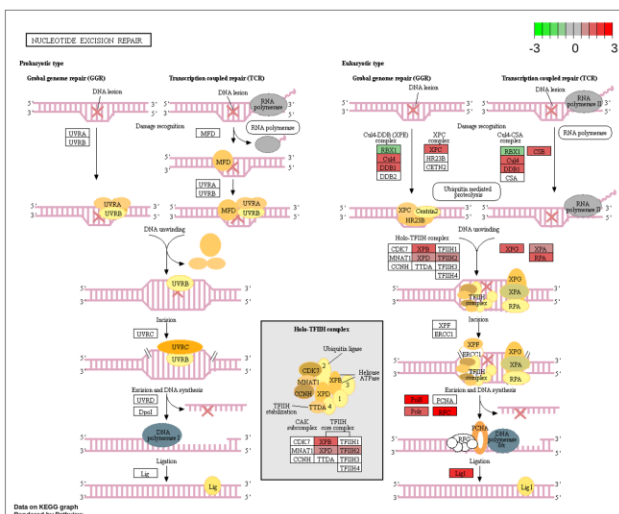


[illegible]

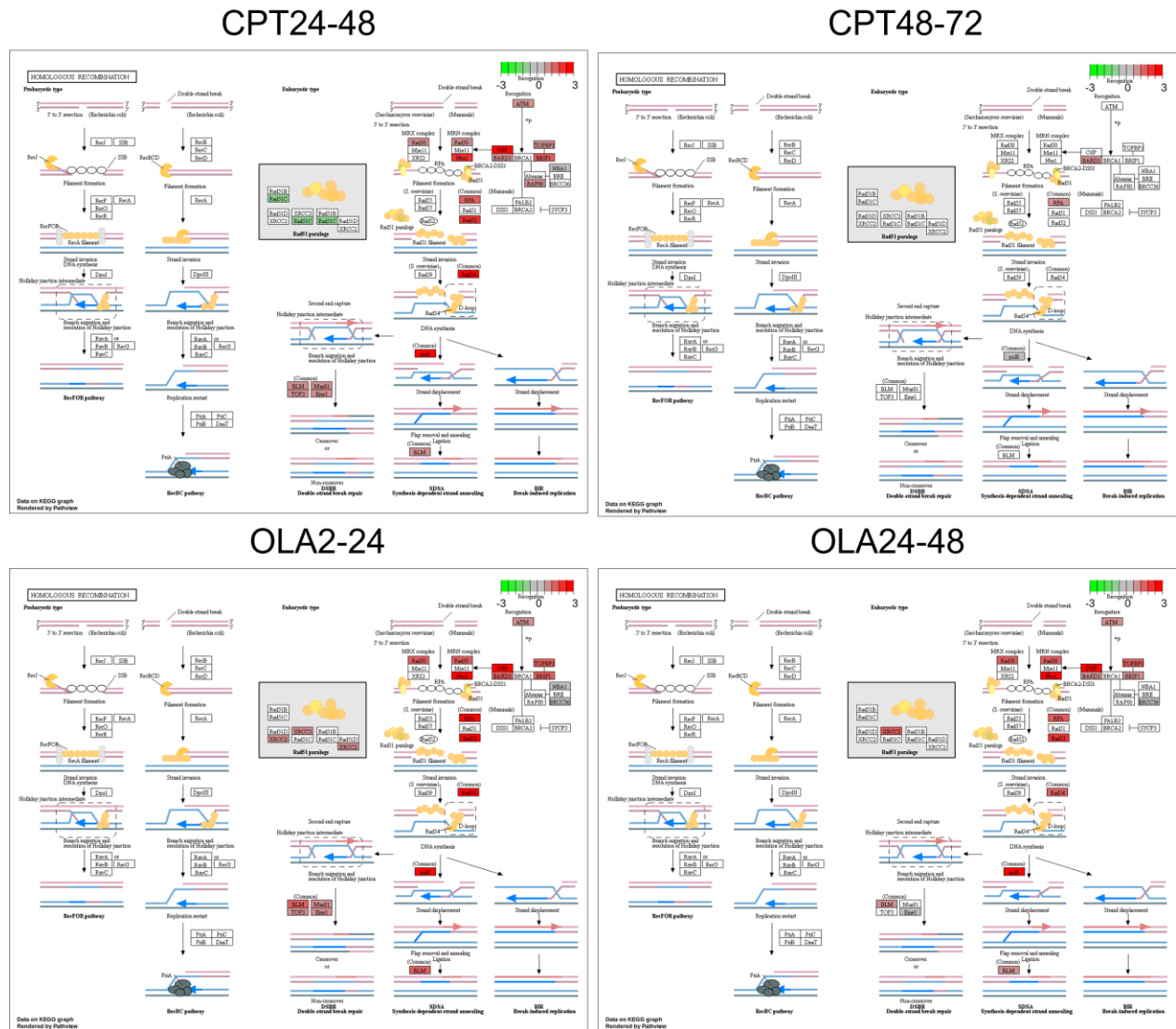
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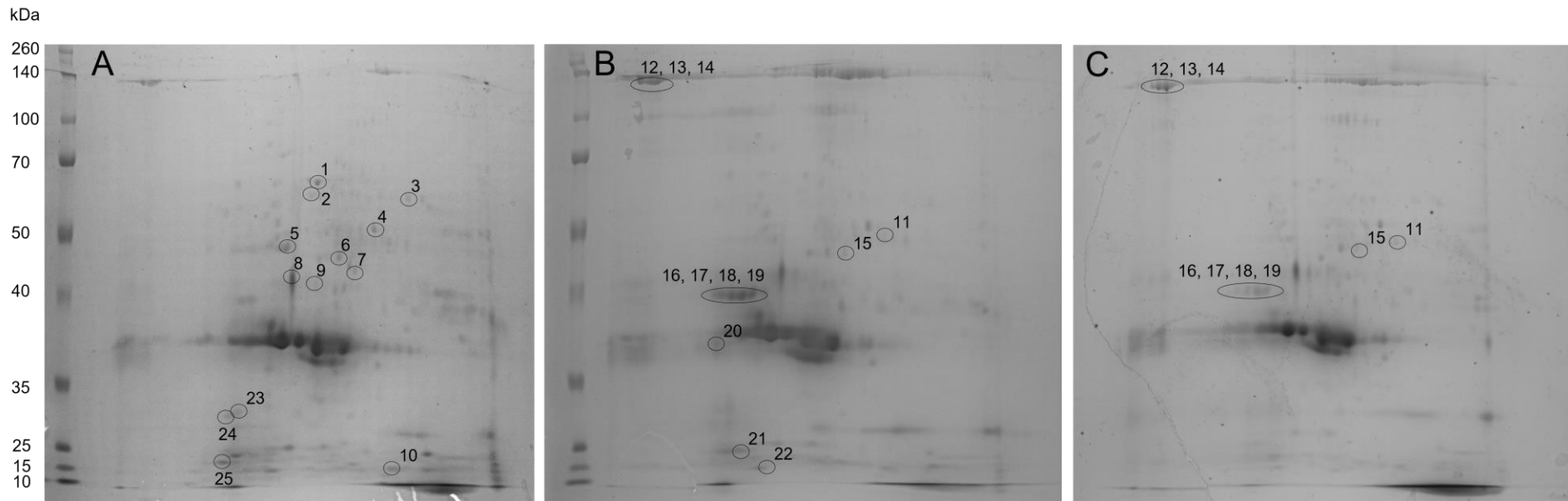
OLA24-48



Supplementary Figure 8. Significantly ($p_{adj} < 0.1$) differentially expressed genes mapped to the KEGG pathway, homologous recombination (hsa03440). Color scale represents the Log2 fold change between the treated and the control samples, capped at a maximum of 3 and minimum of -3.



Supplementary Figure 9. Two-dimensional gel electrophoresis (2D-PAGE) of sterlet embryo proteins following exposure to CPT. The separated proteins were stained with Coomassie Brilliant Blue R-250. **A)** 2D-PAGE of a control embryo; **B)** 2D-PAGE of an embryo exposed to CPT at 24-48 hours post-fertilization (hpf); **C)** 2D-PAGE of an embryo exposed to CPT at 48-72 hpf. The protein molecular weight marker is shown on the left. Circles indicate the positions of the spots that were differentially abundant between the control and treatment groups. The spots were cut out for identification by mass spectrometry. The images are of a single full gel representative of the experiment (N = 3-4).



Supplementary Figure 10. Two-dimensional gel electrophoresis (2D-PAGE) of sterlet embryo proteins following exposure to olaparib (Ola). The separated proteins were stained with Coomassie Brilliant Blue R-250. **A)** 2D-PAGE of a control embryo; **B)** 2D-PAGE of an embryo exposed to Ola at 2-24 hours post-fertilization (hpf); **C)** 2D-PAGE of an embryo exposed to Ola at 24-48 hpf. The protein molecular weight marker is shown on the left. Circles indicate the positions of the spots that were differentially abundant between the control and treatment groups. The spots were cut out for identification by mass spectrometry. The images are of a single full gel representative of the experiment (N = 3-4).

