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Supplemental information

Lung transcriptome of nonhuman primates exposed to total- and partial-body irradiation

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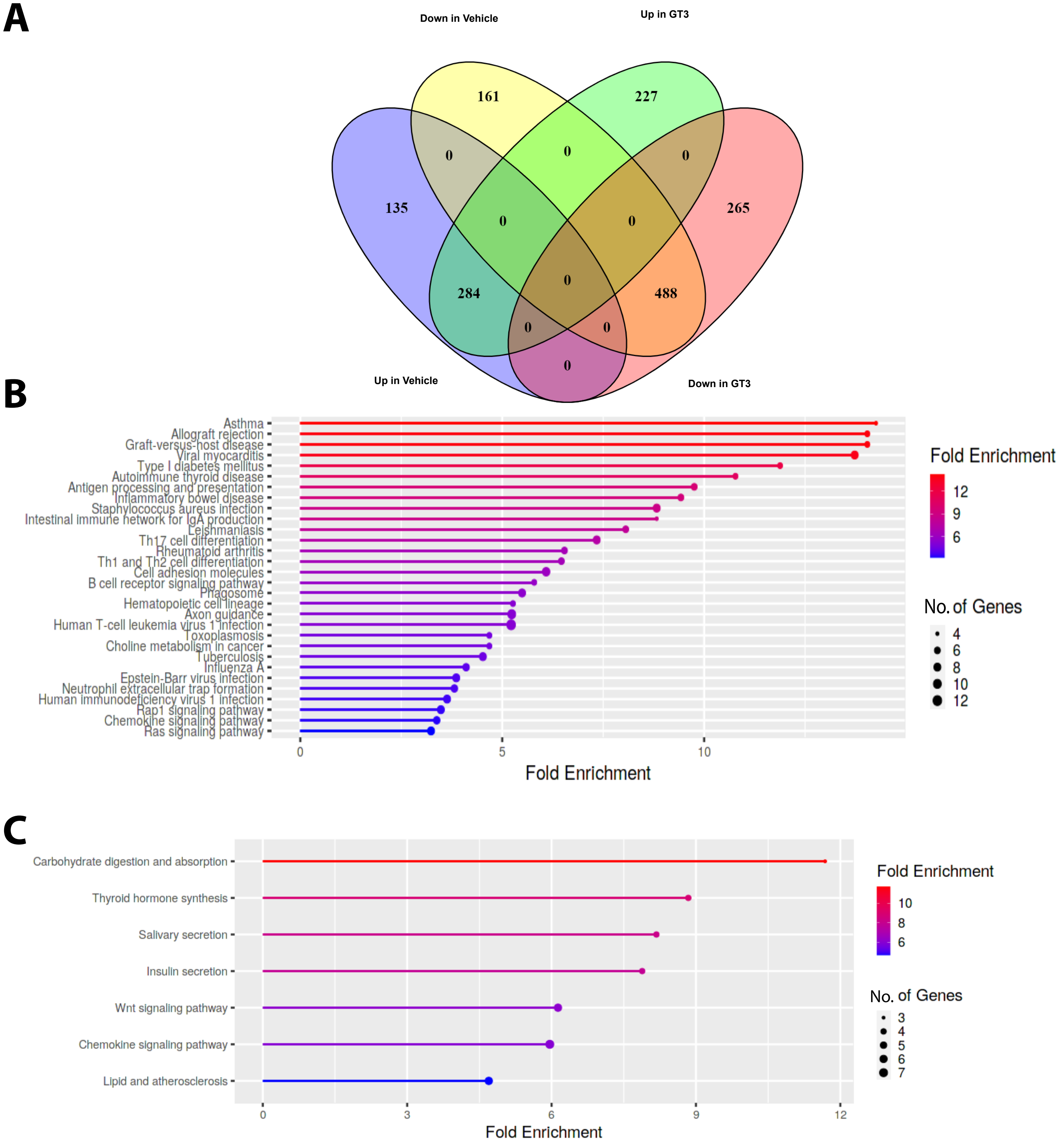


Figure S1: A. Common enriched IPA pathways identified in TBI-GT3 vs. Controls and TBI-Veh vs. Controls. Pathways differentially upregulated and downregulated are represented in this Venn diagram. **B.** KEGG enrichment analysis of the comparison TBI-GT3 vs. Controls and TBI-Veh vs. Controls. Only genes downregulated exclusively in TBI-GT3 compared to controls (n=265 in Supplementary Figure 1A) is included in this analysis. Top 20 enriched KEGG pathways are represented in this figure. The Y-axis lists pathways in order of the enrichment of FDR. The X-axis shows the FDR values for the enrichment of KEGG pathways. The color chart shows fold enrichment for each enriched pathway and the size of dots corresponds to the number of genes assigned to each pathway. **C.** KEGG enrichment analysis of the comparison TBI-GT3 vs. Controls and TBI-Veh vs. Controls. Only unique genes downregulated in irradiated (TBI-Veh, n=161 in Supplementary Figure 1A) is included in this analysis.

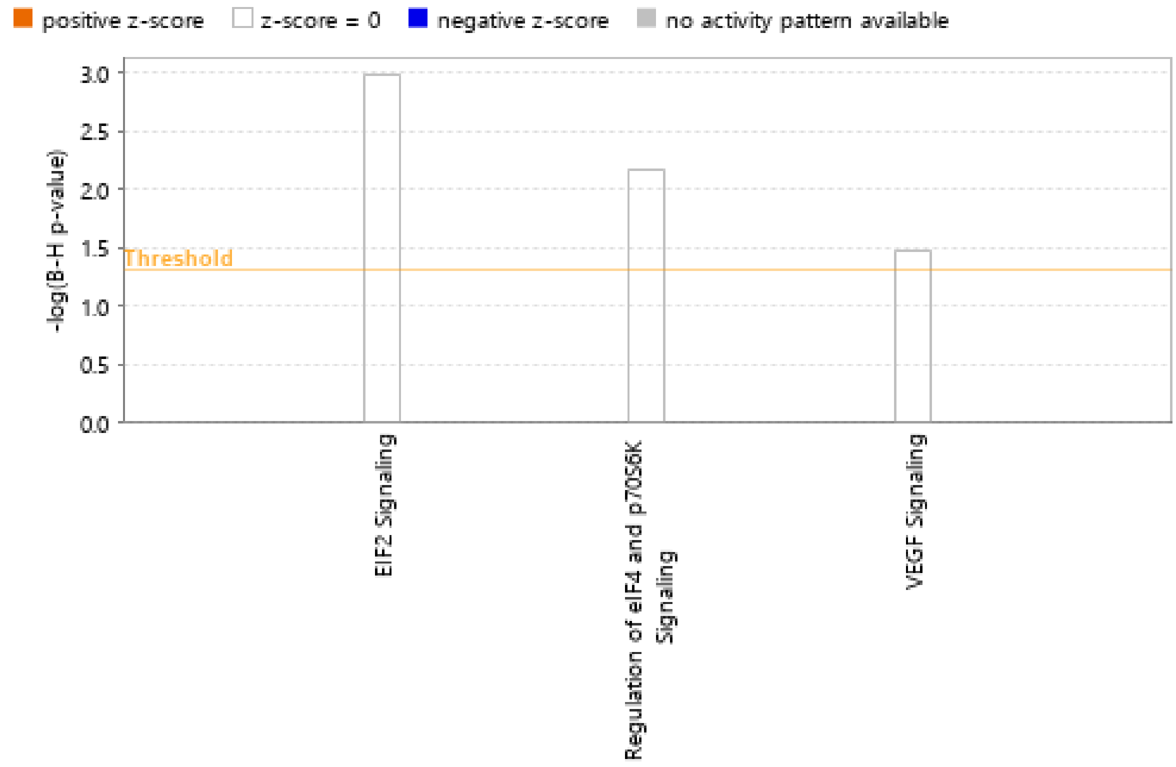


Figure S2: IPA enrichment analysis of the genes differentially expressed in the TBI-Veh and TBI-GT3 comparison. The Y-axis gives the negative logarithm function of Benjamini-Hochberg (B-H) false discovery rate p-value. White bars represent a z-score of 0, which is represented in this figure.

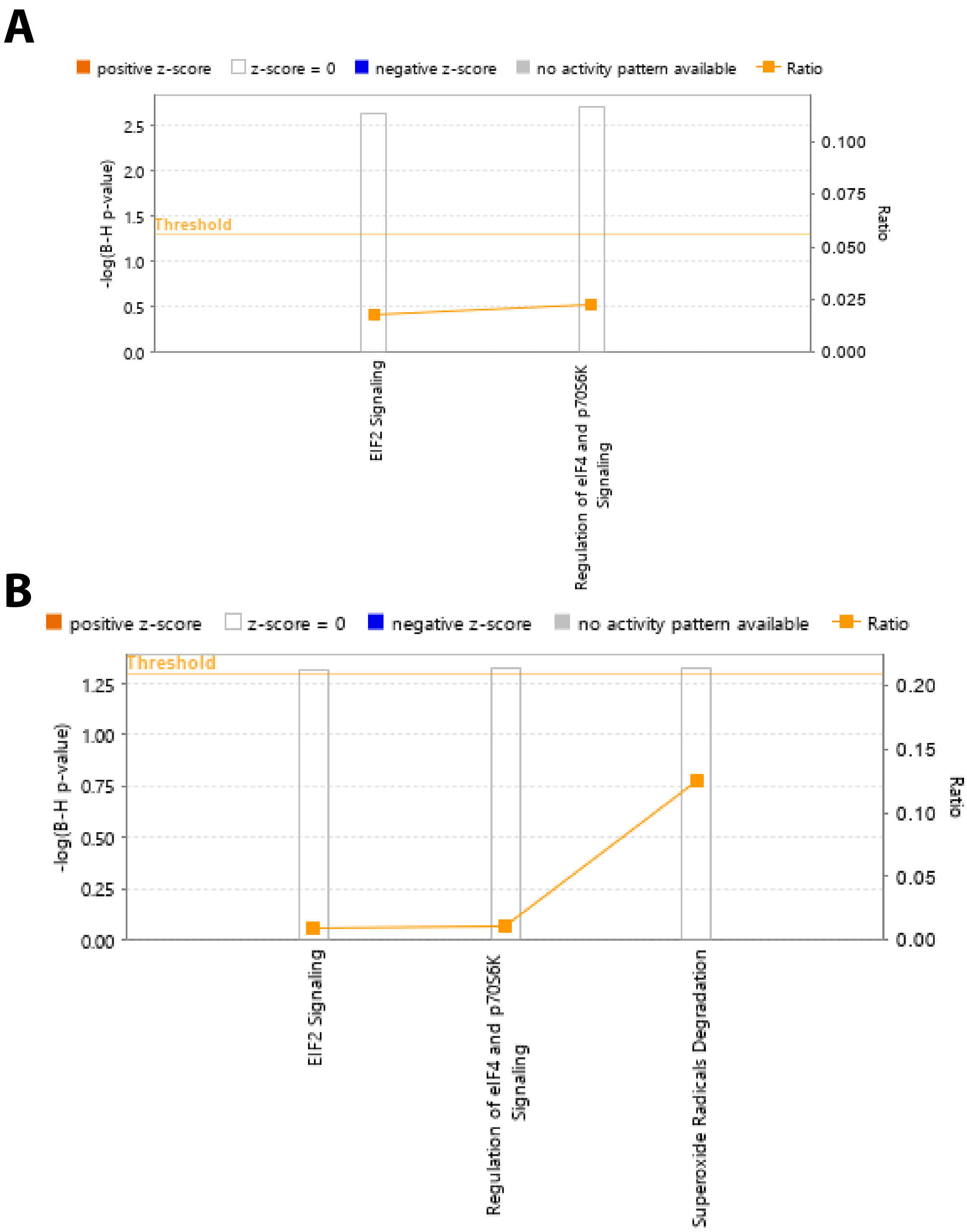


Figure S3: A. IPA analysis of enriched pathways among PBI-M-Veh vs. PBI-F-Veh comparison. **B.** IPA analysis of enriched pathways among PBI-M-GT3 vs. PBI-F-GT3 comparison. The Y-axis gives the negative logarithm function of Benjamini-Hochberg (B-H) false discovery rate p-value. White bars represent a z-score of 0, which is represented in this figure.

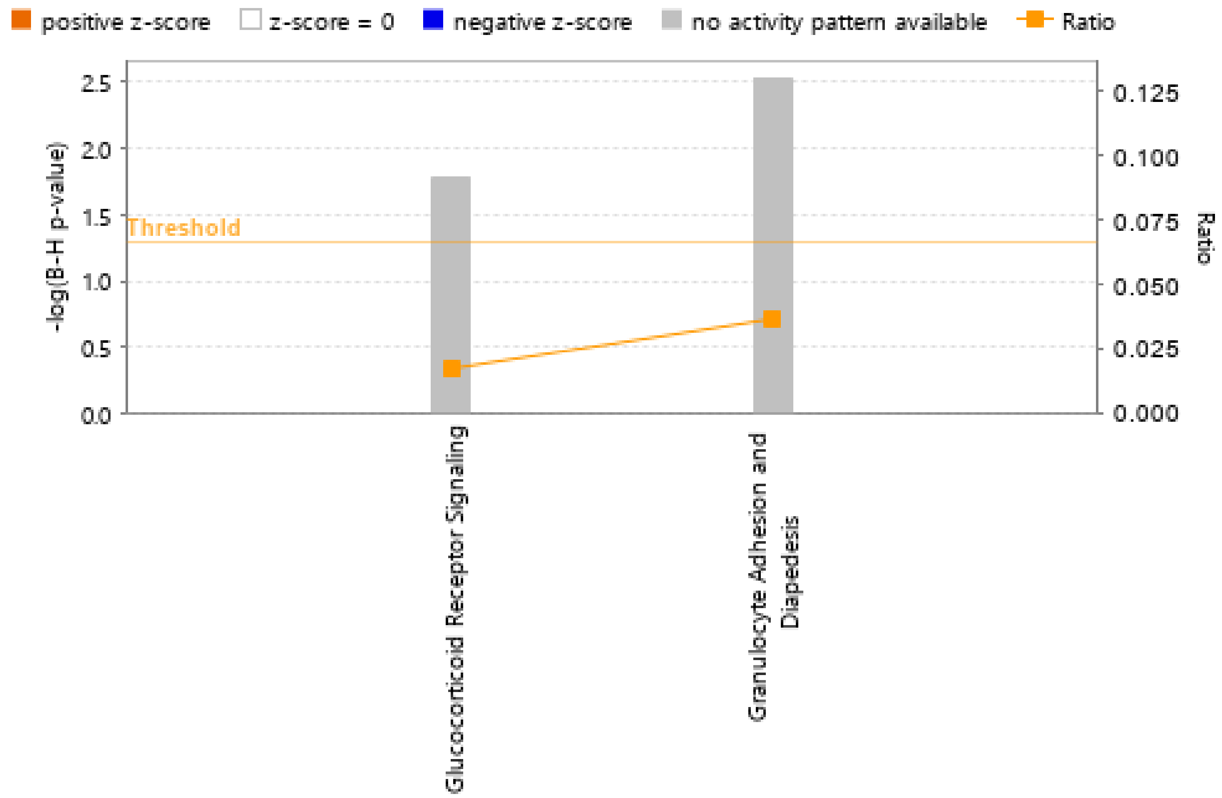


Figure S4: IPA analysis of enriched pathways among PBI-Veh at day 4 vs. PBI-GT3 at day 4 comparison. The Y-axis gives the negative logarithm function of Benjamini-Hochberg (B-H) false discovery rate p-value. White bars represent a z-score of 0, which is represented in this figure.

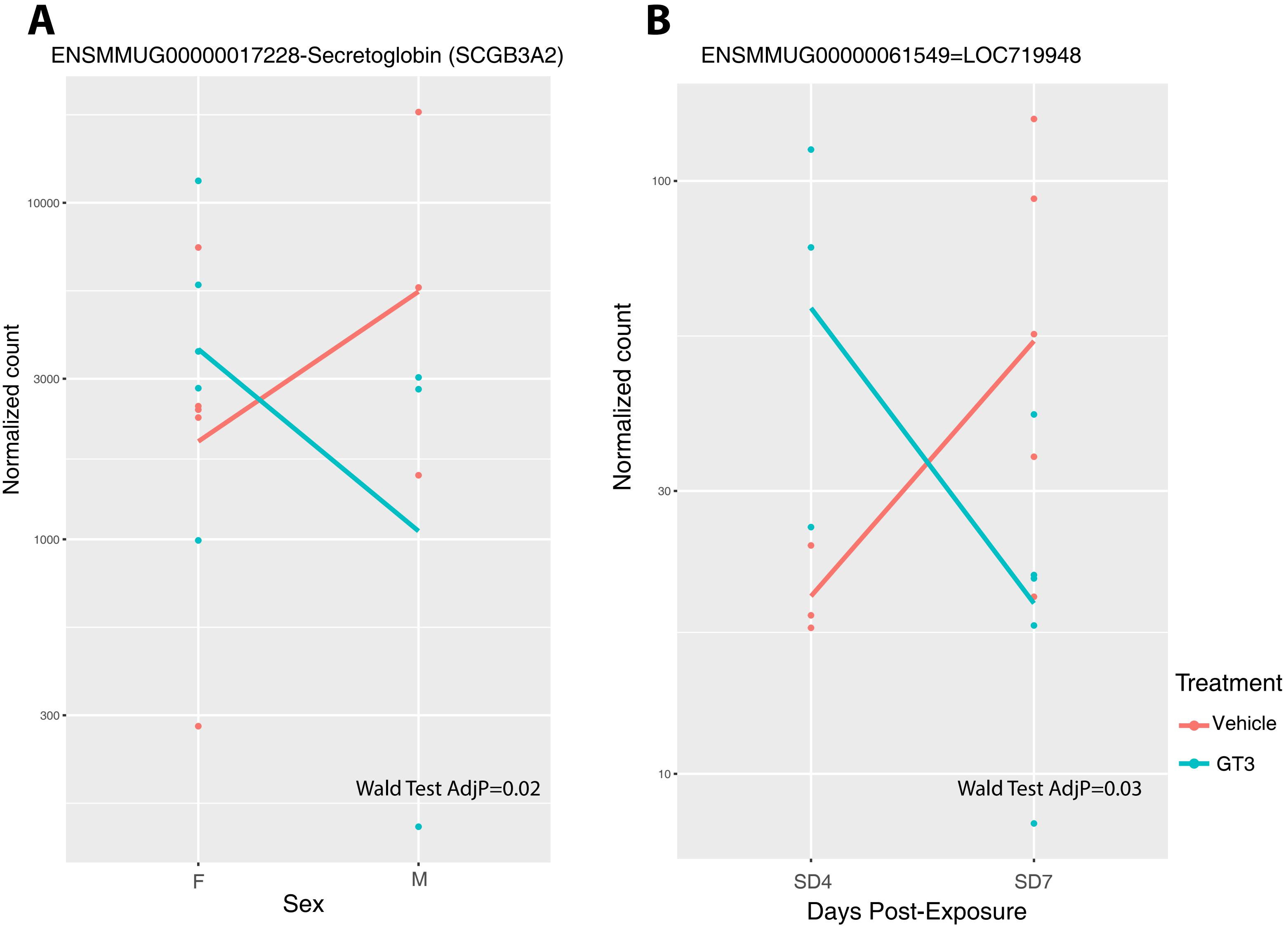


Figure S5: A. Secretoglobin was differentially expressed in male and female NHPs exposed to vehicle or GT3. In females, gene expression was higher after GT3 treatment, but in males, expression was higher in vehicle. X-axis represents male and female NHPs and Y-axis represents normalized gene counts. **B.** ENSMMUG00000061549 was differentially expressed in NHPs exposed to vehicle or GT3 at day 4 or day 7. At day4, gene expression was higher after GT3 treatment, but at day 7, expression was higher in vehicle. X-axis represents male and female NHPs and Y-axis represents normalized gene counts.

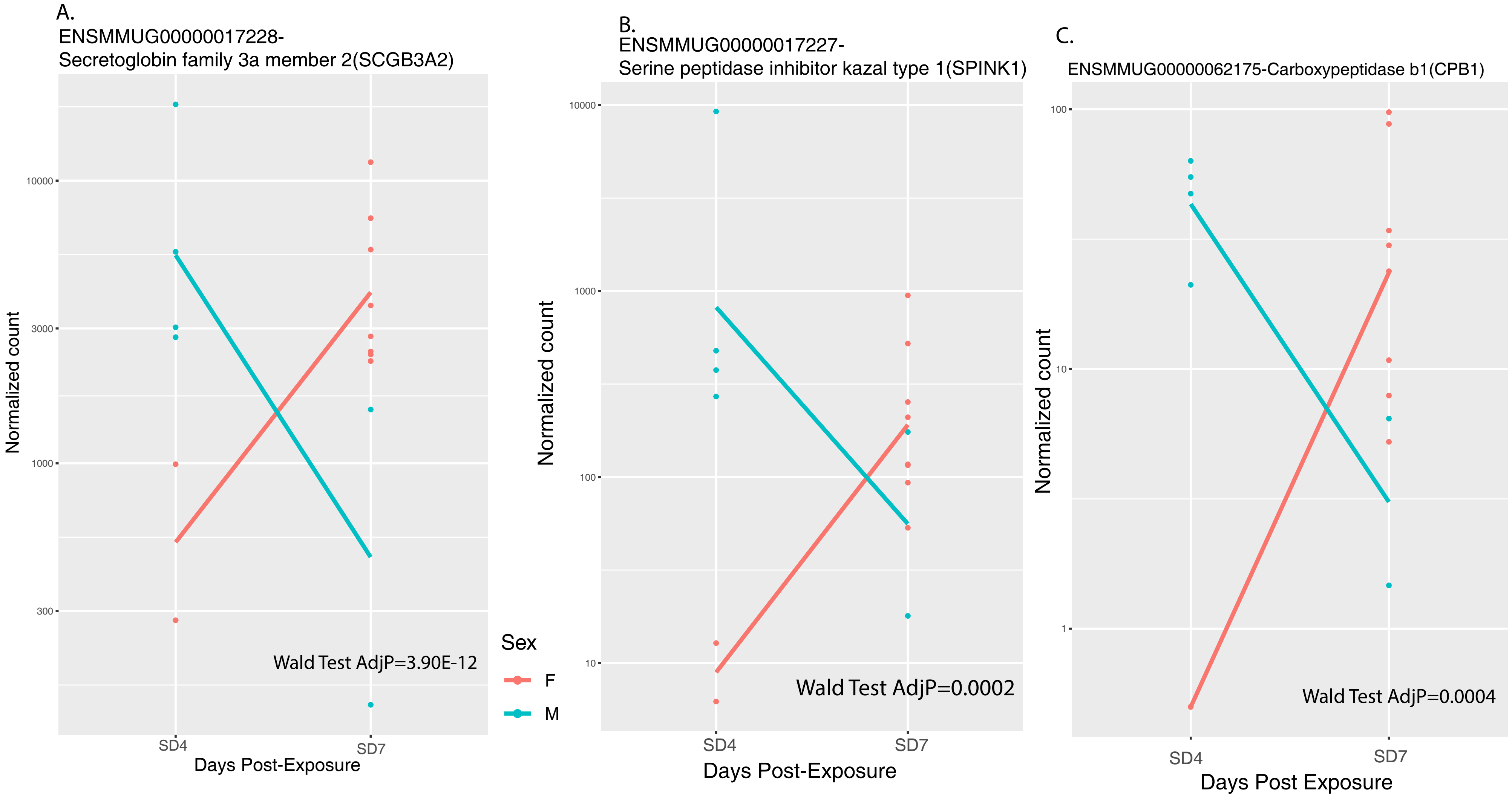


Figure S6: Secretoglobin,SPINK1, and CPB1 was differentially expressed in male and female GT3 treated NHPs at day 4 and day 7. At day 4, gene expression was higher in males after GT3 treatment, but at day 7, expression was higher in vehicle. X-axis represents days post-irradiation and Y-axis represents normalized gene counts.

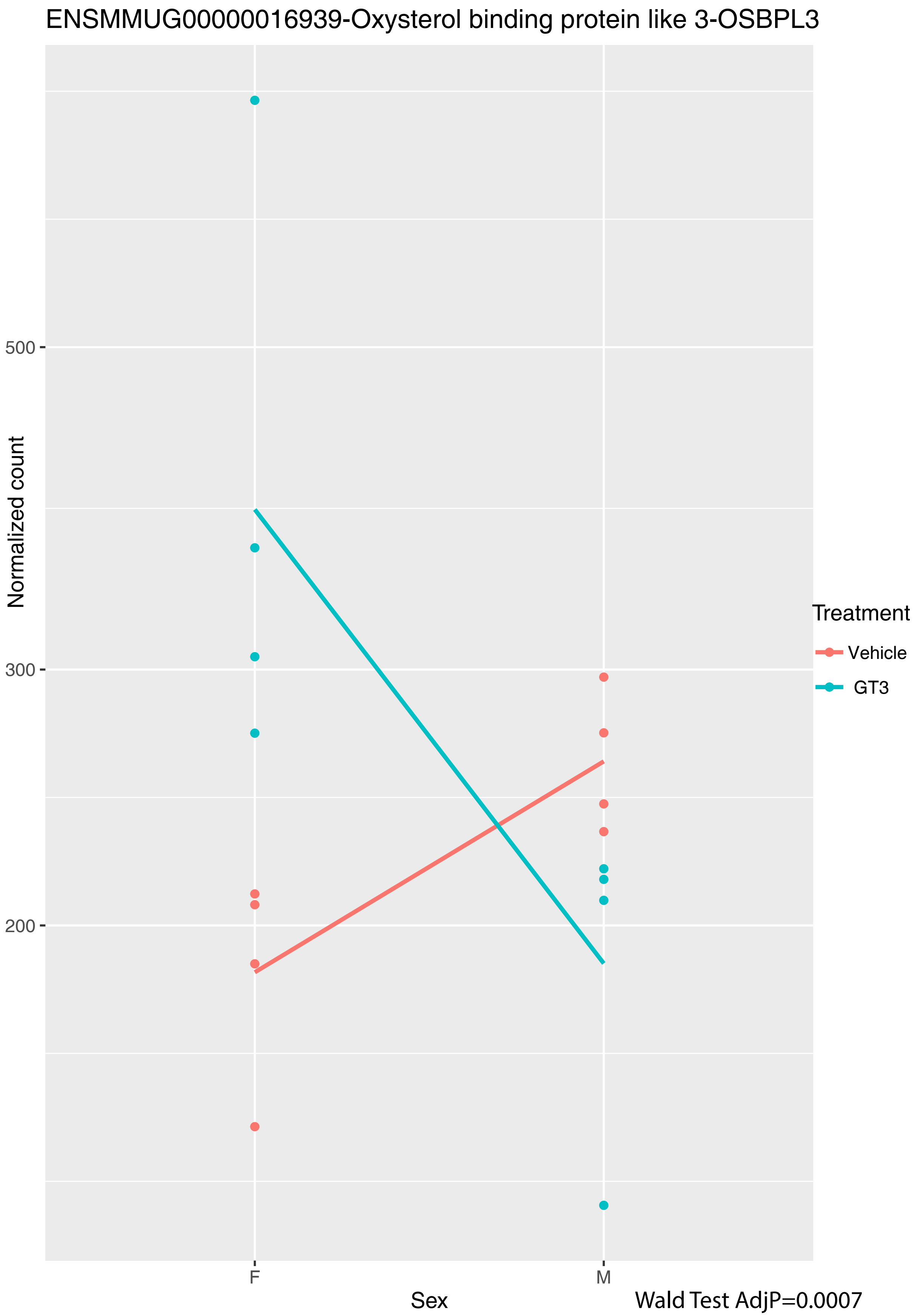
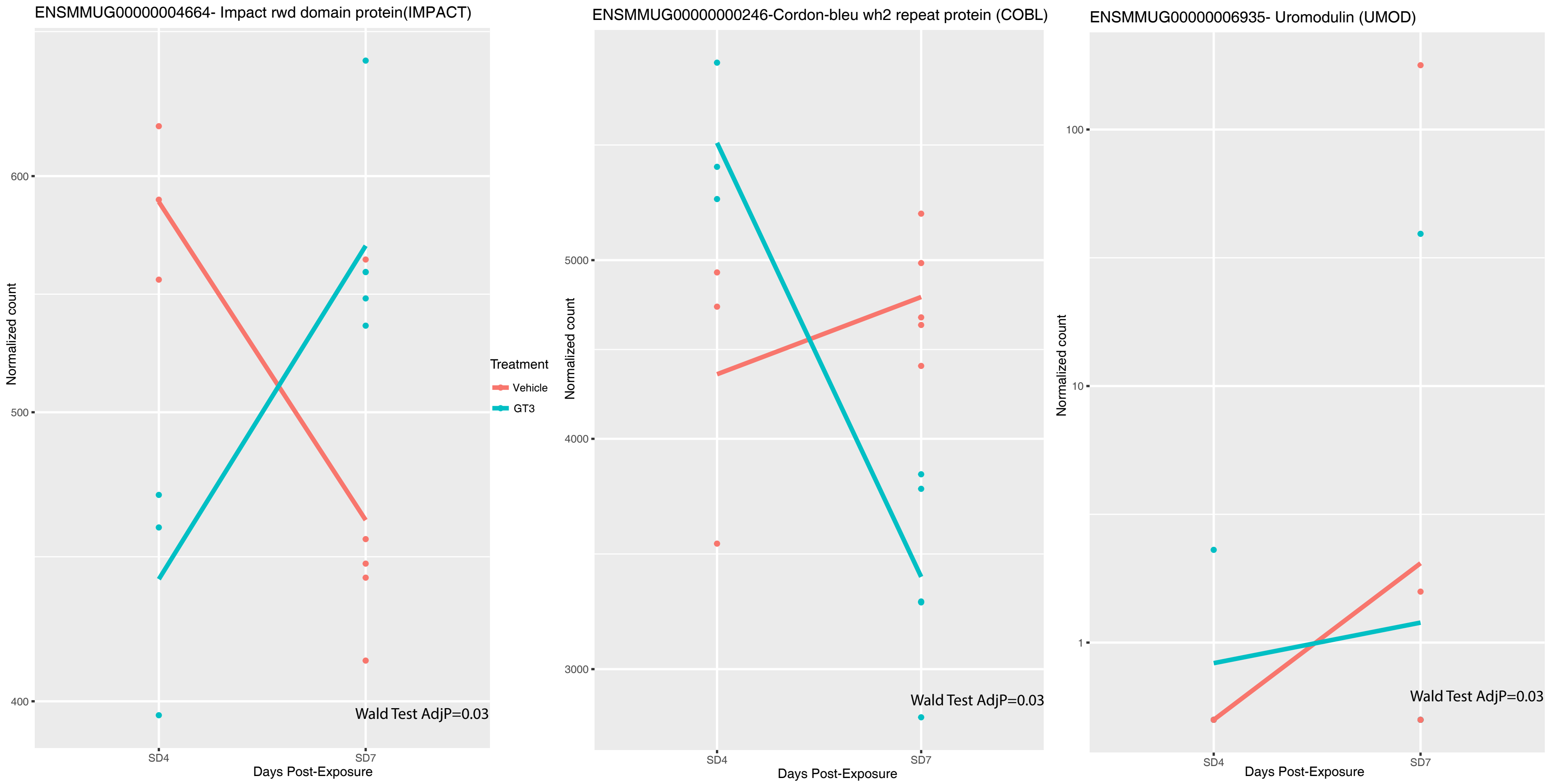


Figure S7: OSBPL3 gene expression was higher in females after GT3 treatment, whereas this gene had higher expression in vehicle treated males. X-axis represents the two sexes and Y-axis represents normalized gene counts.

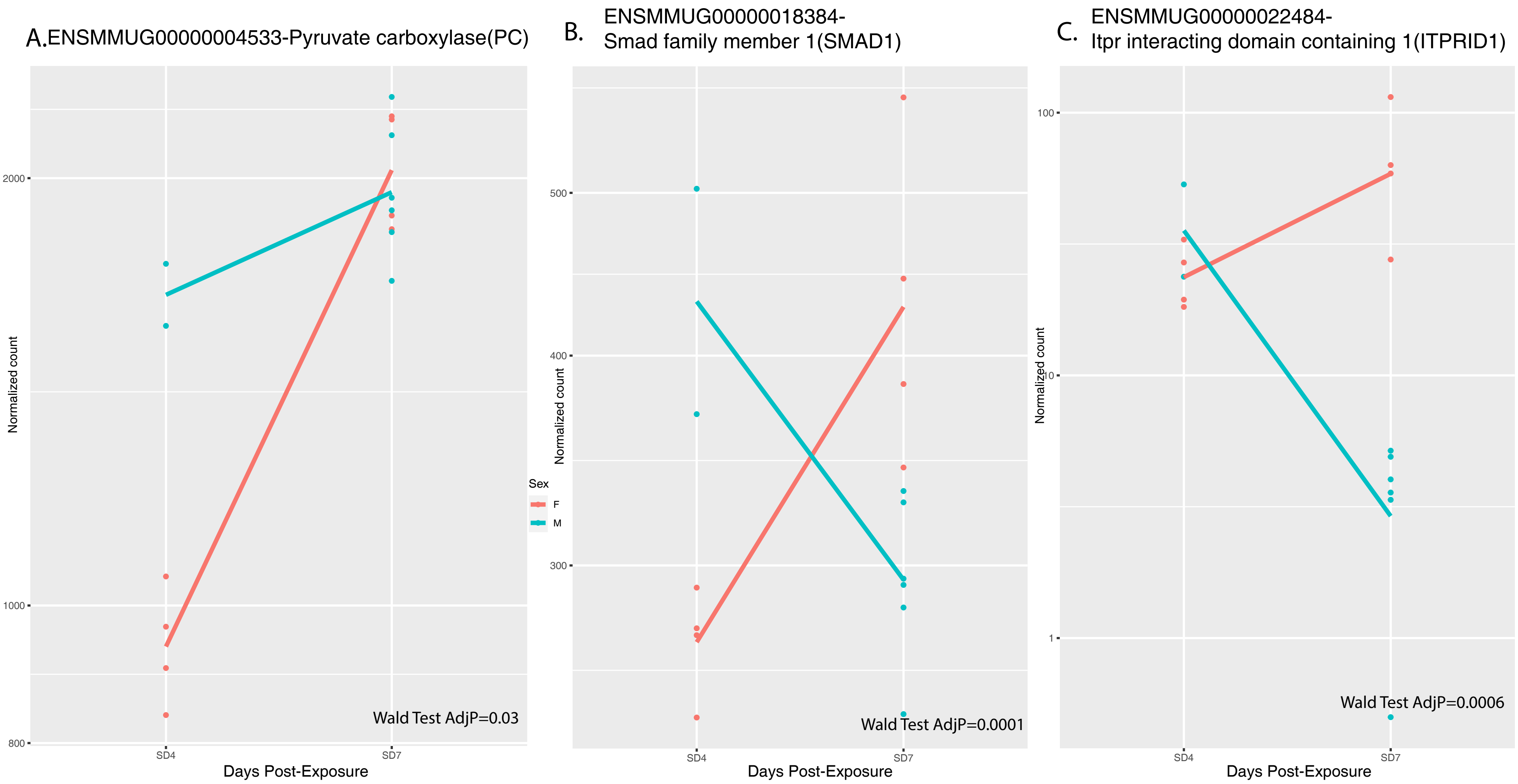


ENSMMUG00000004664- Impact rwd domain protein(IMPACT)

ENSMMUG00000000246-Cordon-bleu wh2 repeat protein (COBL)

ENSMMUG00000006935- Uromodulin (UMOD)

Figure S8: Gene expression differences across day 4 and day 7 of vehicle treated and GT3 NHPs. X-axis represents days post-irradiation and Y-axis represents normalized gene counts.


A. ENSMMUG00000004533-Pyruvate carboxylase(PC)

B. ENSMMUG00000018384-
Smad family member 1(SMAD1)

C. ENSMMUG00000022484-
Itpr interacting domain containing 1(ITPRID1)

Figure S9: Gene expression differences in male and female NHPs pretreated with GT3 and irradiated. X-axis represents days post-irradiation and Y-axis represents normalized gene counts.

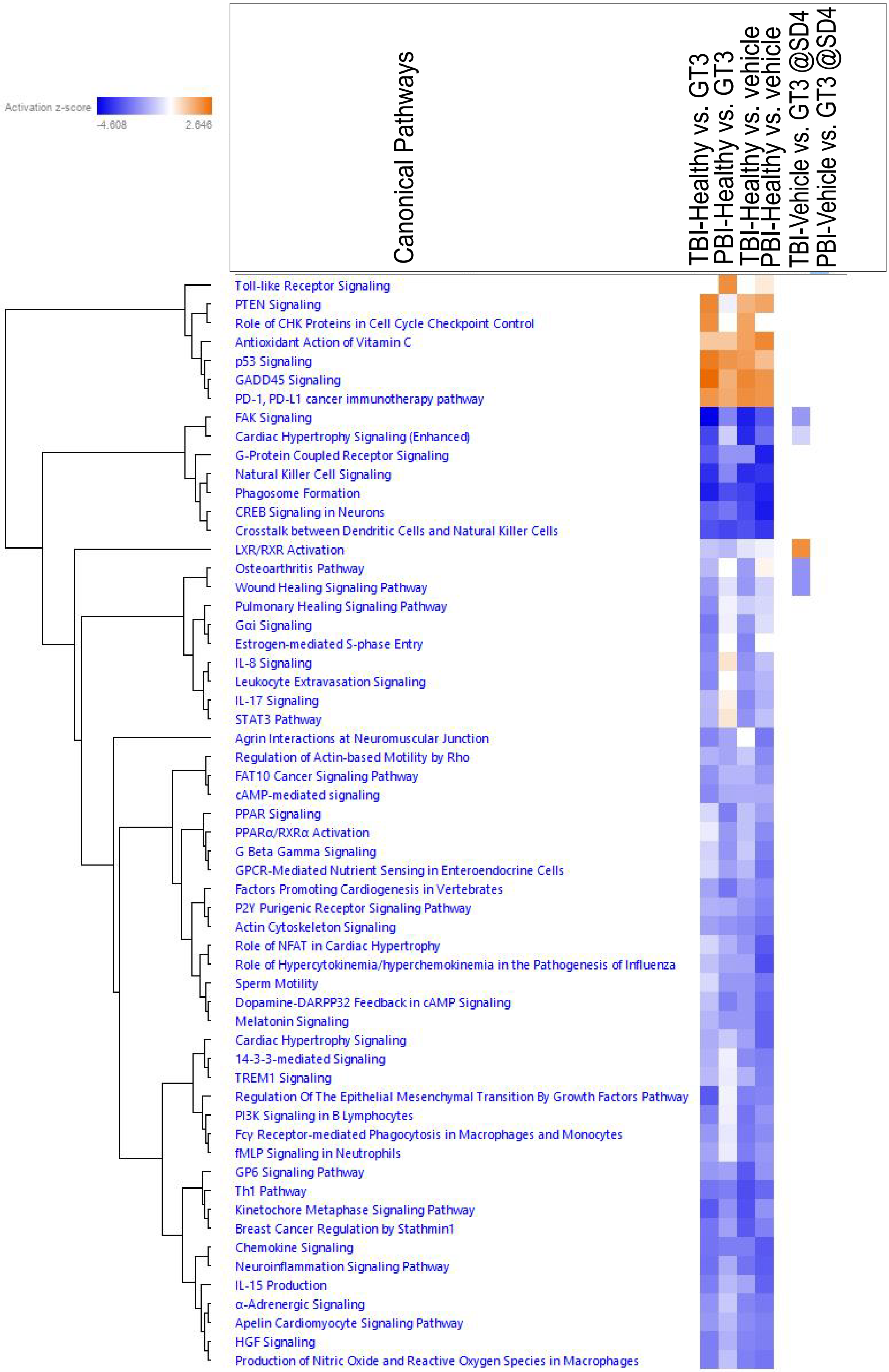


Figure S10: IPA comparison analysis across all comparisons. This analysis predicted pathways differentially regulated across different comparisons. Differentially activated pathways is represented in orange and repressed in blue. Hierarchical clustering was applied to both pathways.