

Figure S1: Title Text

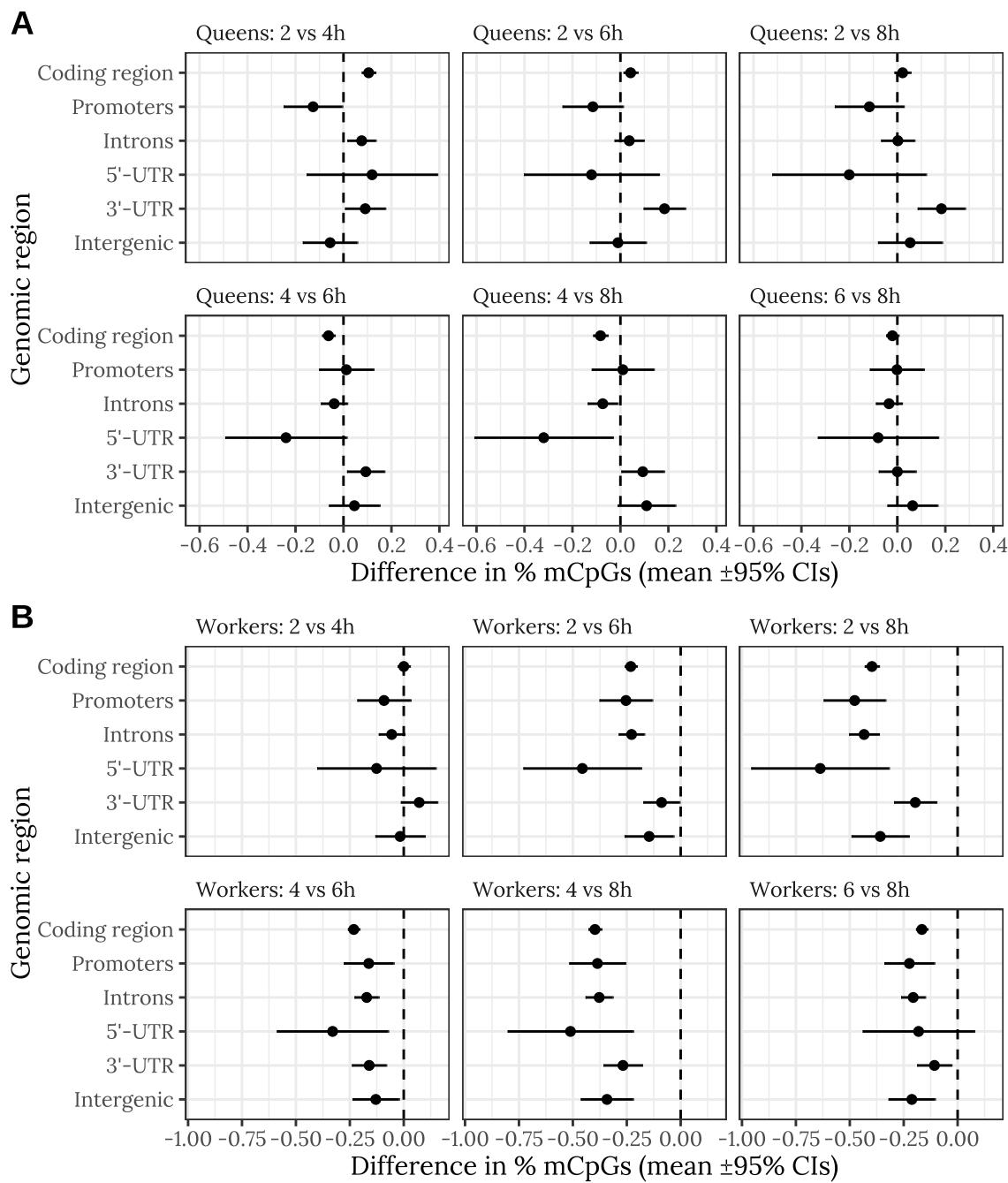


Figure S2: Similar heatmap to Figure 1C, except showing all CpG sites with at least 2.7% methylated sequencing reads ($n = 110,626$ sites).

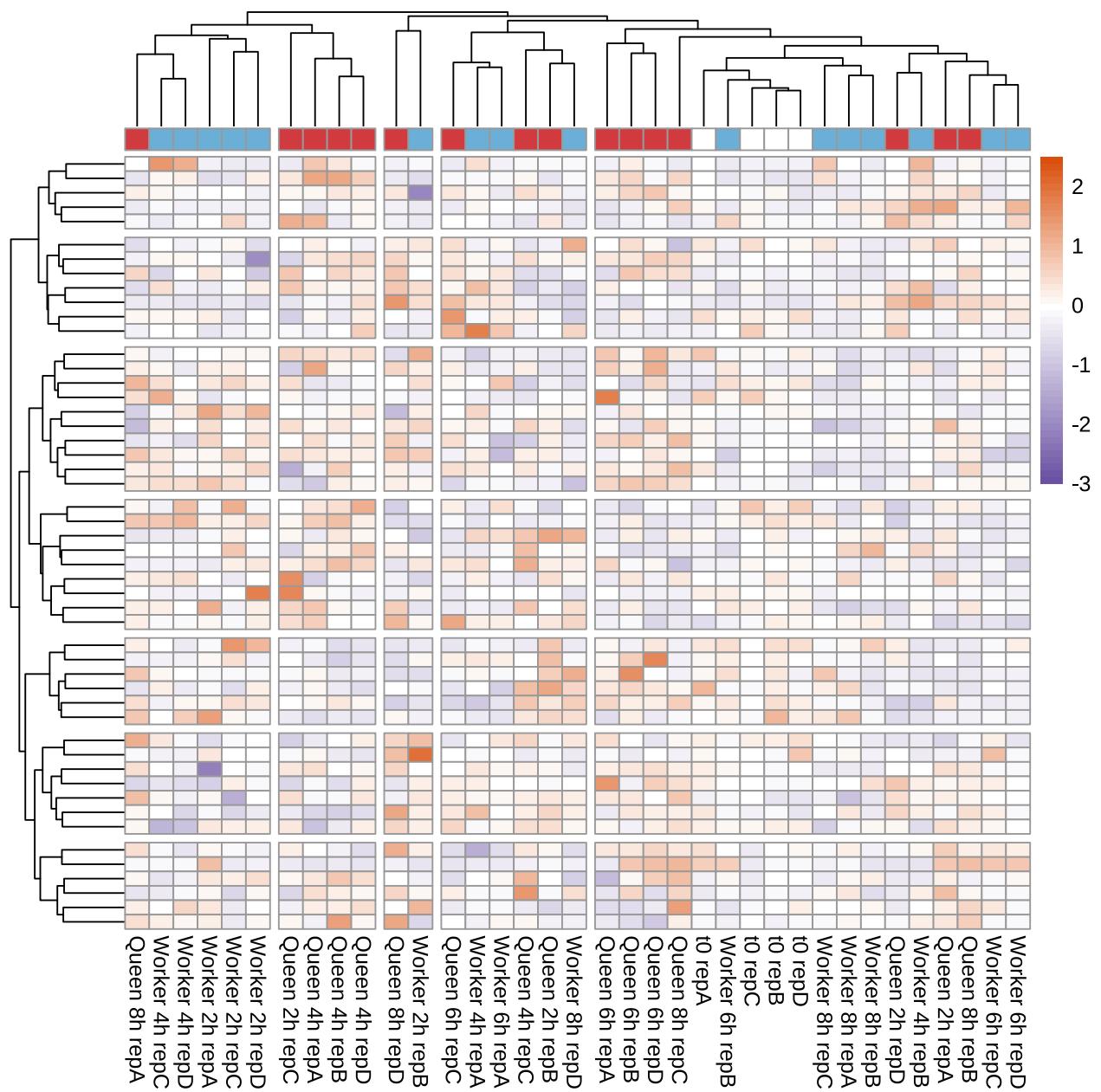


Figure S3: GO and KEGG terms that are enriched among genes showing QDL- or WDL-biased methylation (as measured by the difference in mean % CpG methylation for all sites in the introns, exons, and promoters of the gene; red: QDL-biased, blue: WDL-biased). Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations.

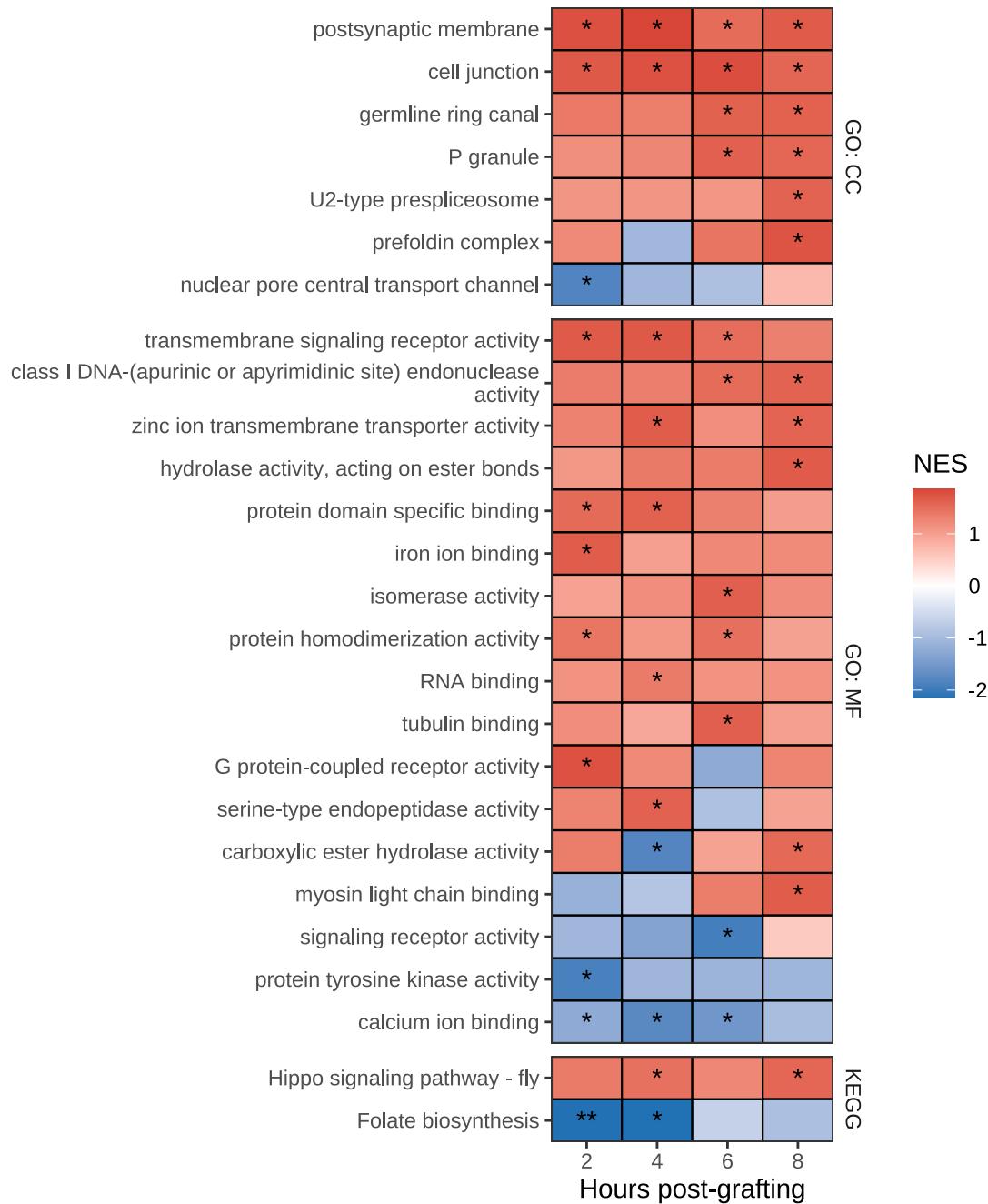


Figure S4: GO and KEGG terms that are enriched among genes showing QDL- or WDL-biased methylation (as measured by the difference in mean % CpG methylation for all sites in the introns, exons, and promoters of the gene; red: QDL-biased, blue: WDL-biased). Results are from Kolmogorov-Smirnov enrichment tests using the standard *A. mellifera* GO and KEGG annotations.

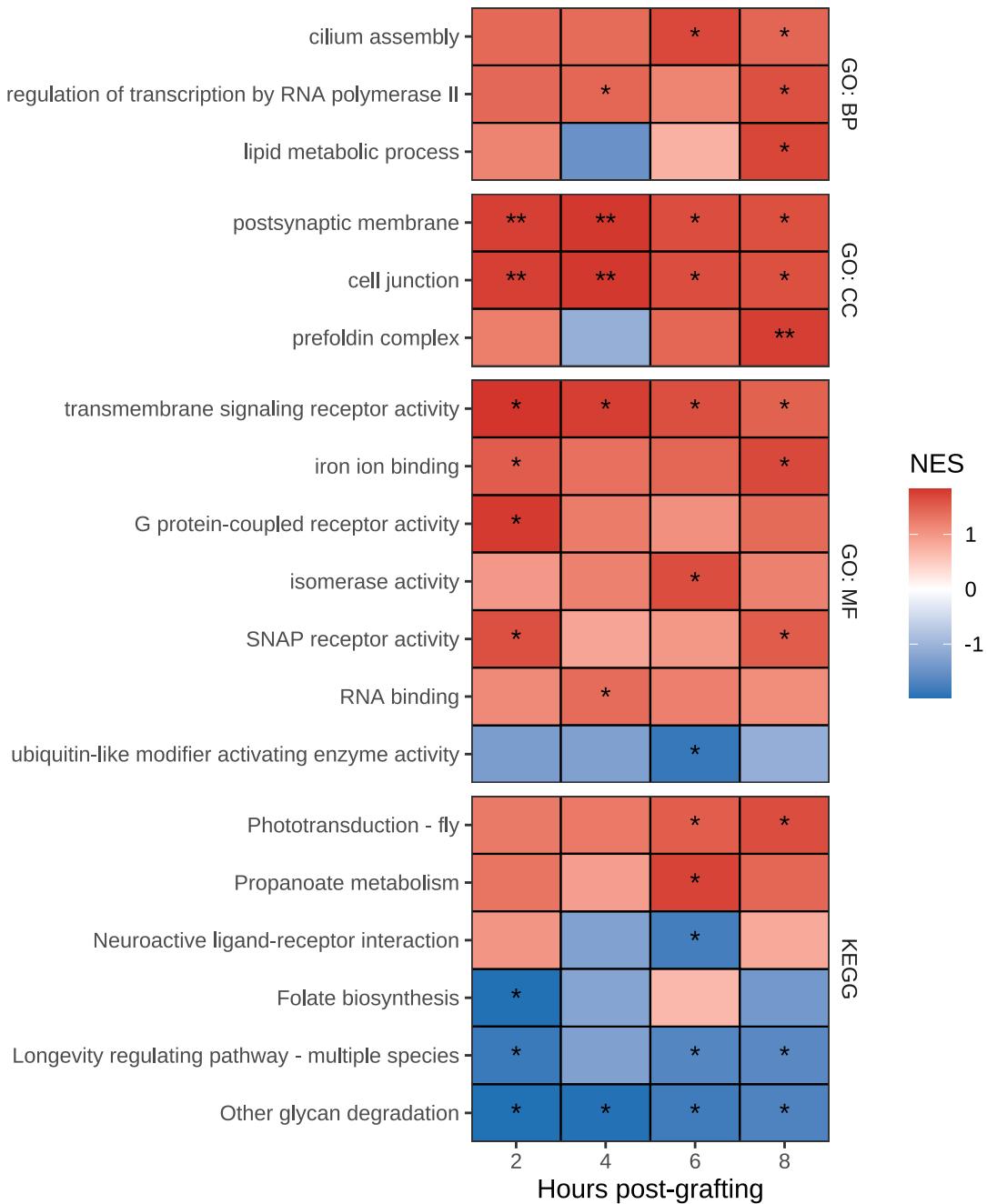


Figure S5: GO and KEGG terms that are enriched among genes showing temporally variable methylation within each treatment group (as measured by the difference in mean % CpG methylation between the 2h and 8h QDL or WDL samples for all sites in the introns, exons, and promoters of the gene). Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations. Orange indicates functional categories for which the relevant genes show increasing methylation over time, purple indicates decreasing methylation over time.

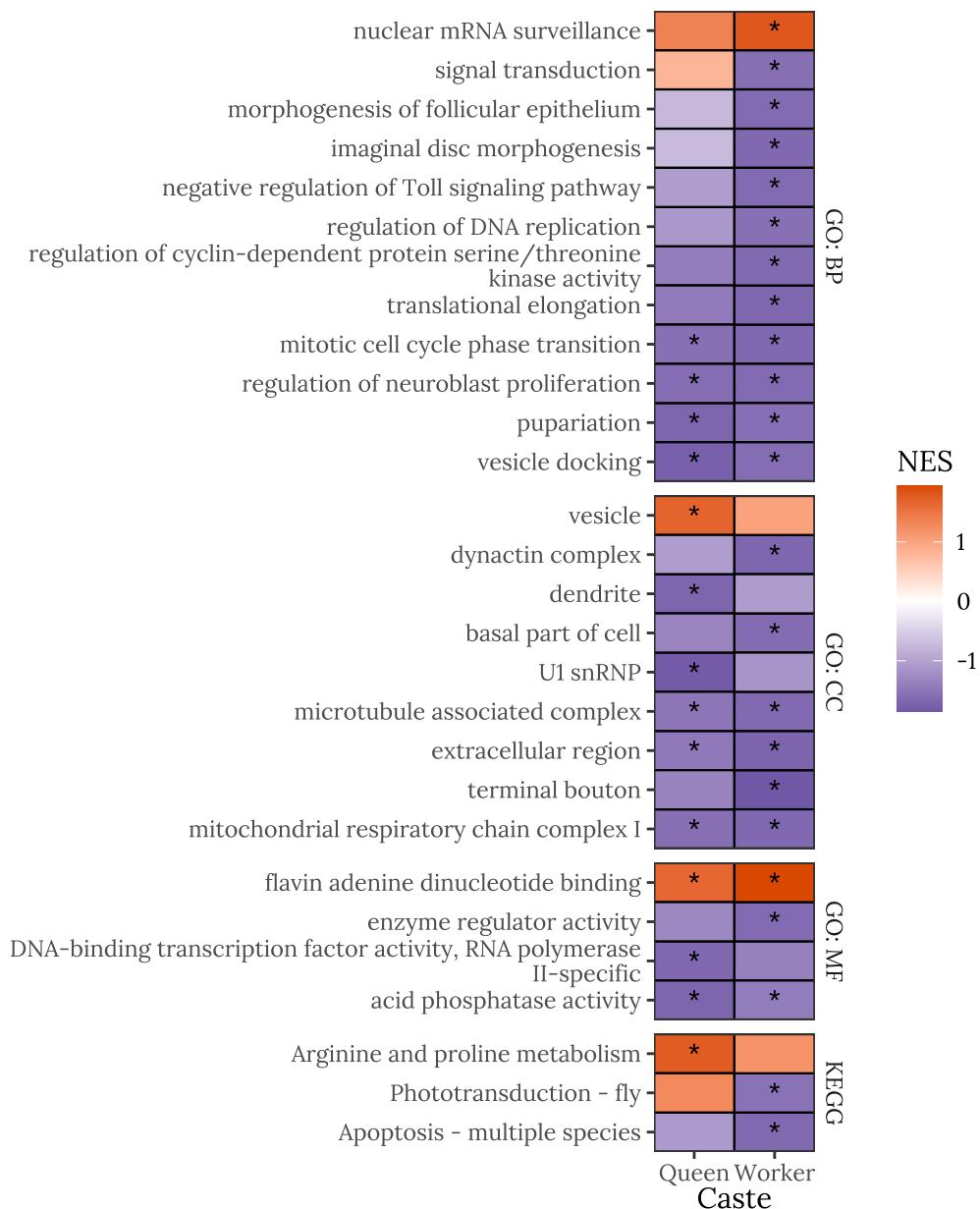


Figure S6: GO and KEGG terms that are enriched among genes showing temporally variable methylation within each treatment group (as measured by the difference in mean % CpG methylation between the 2h and 8h QDL or WDL samples for all sites in the introns, exons, and promoters of the gene). Results are from Kolmogorov-Smirnov enrichment tests using the standard *A. mellifera* GO and KEGG annotations. Orange indicates functional categories for which the relevant genes show increasing methylation over time, purple indicates decreasing methylation over time.

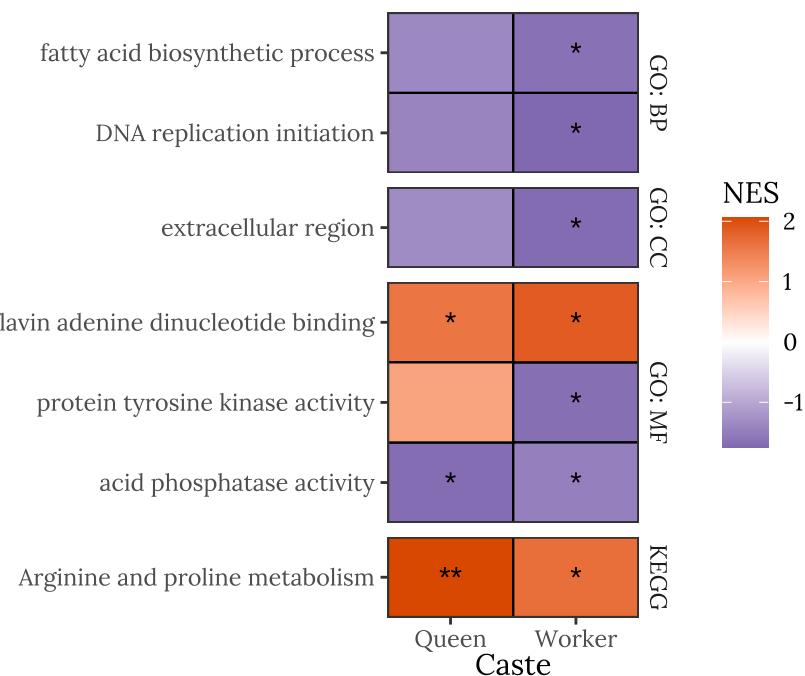


Figure S7: dfhsf

