



Figure S6. Differential gene expression analyses of the *S. stercoralis* iL3 versus free-living female life stages. Both plots were generated by the *Strongyloides* RNA-seq Browser. **A)** Volcano plot displaying results of limma-voom differential gene expression to compare iL3 to free-living female (FLF) samples. Dots indicate the \log_2 fold-change (\log_2FC) value relative to the Benjamini-Hochberg-adjusted p -value for each gene. Positive \log_2FC values indicate enrichment in iL3s relative to free-living females; negative \log_2FC values indicated enrichment in free-living females relative to iL3s. Larger values on the y-axis indicate increasing statistical significance (*i.e.*, lower p -values). **B)** Bubble plot displaying results of gene set enrichment analysis (GSEA) of differential gene expression between iL3s and free-living females. Color scale represents the normalized enrichment score (NES), *i.e.*, the degree to which elements of the gene set are over-represented among genes displaying large magnitude gene expression changes between the life stages. Negative NES values (blue) indicate gene sets whose elements are over-represented in genes that are significantly upregulated in FLF samples. Positive NES values (red) indicate gene sets whose elements are over-represented in genes that are significantly upregulated in iL3s. Opacity reflects the estimated significance level of the enrichment score, adjusted for multiple hypothesis testing. The size of dots reflects the number of genes included in the gene set. Gene sets named *sgpf-1* to *sgpf-6* are novel *Strongyloides* genome project families (Hunt *et al* 2016).