Figure S6. Gene families enriched in genes contributing to *S. stercoralis* PC1 and PC2 identity. Bubble plot displaying results of gene set enrichment analysis (GSEA) of genes contributing to the identity of principal components 1 and 2. Values used to rank genes for GSEA analysis are PC1 and PC2 scores; the two ranked lists were analyzed independently, then merged for plotting. Gene families used in GSEA analysis are from a parasite Ensembl Compara gene family database (Hunt *et al*, 2016). Color scale represents the normalized enrichment score (NES), which indicates the degree to which elements of the gene set are over-represented among genes displaying large contributions to PC1 or PC2 identity. Direction of the contribution to PC identity (negative versus positive PC score) is indicated by hue (blue versus red). For PC1, positive values (red hue) indicates gene sets that contribute to "larval" identity; negative values (blue hue) indicates gene sets that contribute to "adult" identity. For PC2, hue colors indicate "parasitic" (red) and "non-infectious" identities (blue). 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).