



Figure S3. Benchmarking of selected differential expression analyses. For *S. stercoralis*, *S. ratti*, and *S. venezuelensis*, the figure shows a comparison of genes included in the *Strongyloides* RNA-seq Browser to previously published analyses (Hunt *et al* 2016, 2018). **A)** Number of genes included in the app dataset versus published analyses. In all cases, the number of genes included in the *Strongyloides* RNA-seq Browser is greater than the number of genes included in published analyses in which the same raw data were analyzed using different pipelines. **B-D)** Violin plots of log₂ counts per million (CPM) expression for genes found in both the *Strongyloides* RNA-seq Browser and published analyses (colors) and genes included in the app but not in published analyses (grey). Overall, genes that are excluded from published analyses have lower expression levels within samples than genes that overlap. Color hue indicates developmental life stage. Dots indicate median values.