



Figure S2. Principal components analyses performed on each of the *Strongyloides* species. The RNA-seq datasets reveal patterns of similarity between life stages and biological samples. For each species dataset, filtered and normalized abundance data were used to construct principal components (PCs) via the stats R package v3.6.3. Samples are plotted across the first two PCs. Color indicates life stage. For *S. ratti* and *S. venezuelensis*, icons representing technical replicates are superimposed due to high similarities between replicates. For all species, visibly repeated icons thus represent biological replicates. See Figure S3 for additional plots related to similarities between biological and technical replicates. Numerical values in the axis labels indicate percent of total variance explained by the indicated PC.