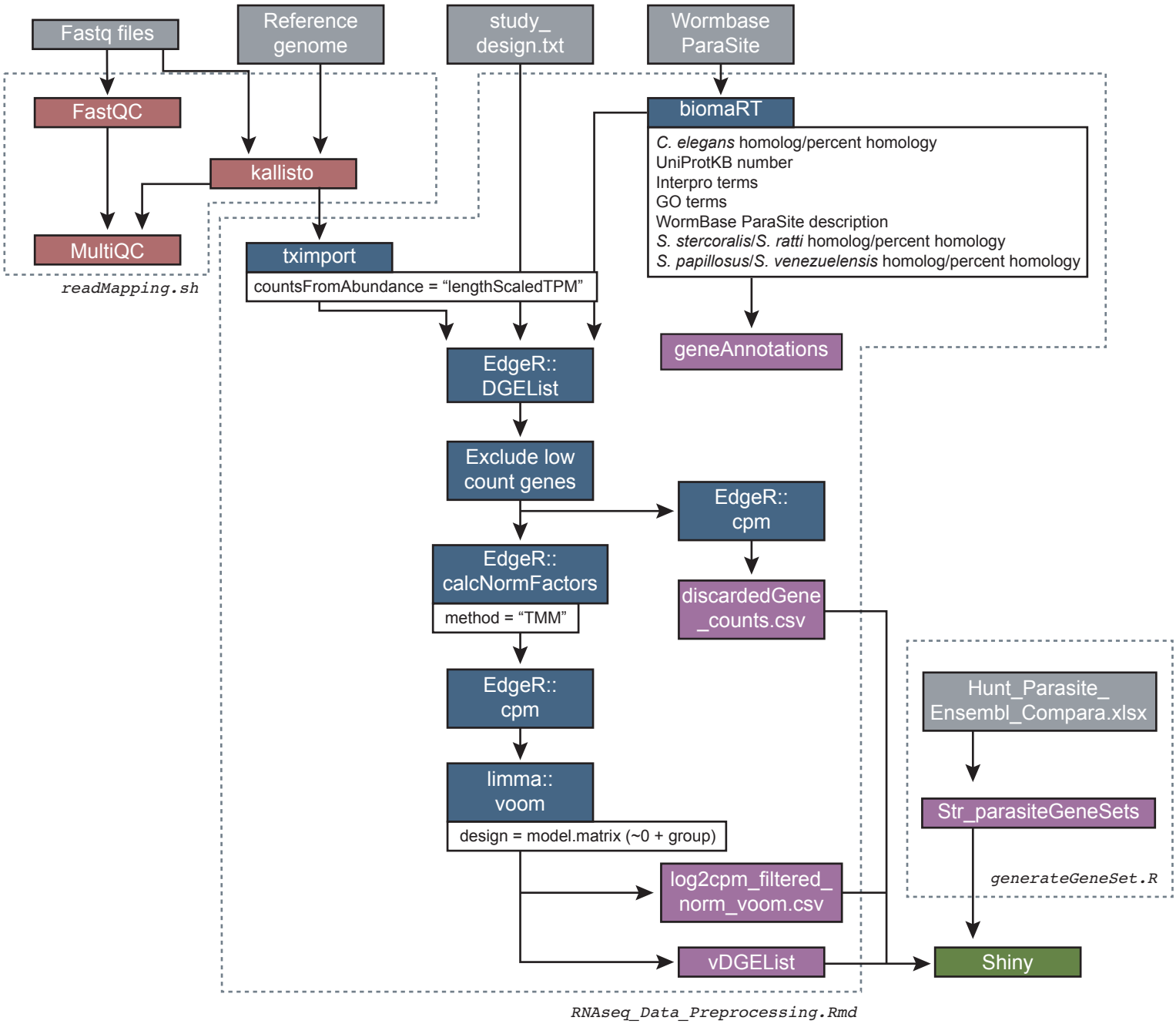

Figure S1. Detailed graphic view of the Strongyloides RNA-seq Browser preprocessing pipeline. Grey boxes are publicly available data sets or sources, red boxes are shell commands, blue boxes are commands run in R, white boxes are important code details, purple boxes are saved output files, and the green box represents the interactive web app elements generated using the Shiny package. Dashed lines show division of code elements into the named files. The preprocessing pipeline is divided between three code files: a shell script that performs the Kallisto alignment and quality control checks (*readMapping.sh*); an R script that extracts Strongyloides gene sets from a database of parasite Ensembl Compara protein families (*generateGeneSet.R*); and an R Markdown file that performs gene annotation and converts Kallisto-generated transcript abundance data to filtered and normalized $\log_2$ counts per million ($\log_2$CPM) data using the trimmed mean of M-values (TMM) method and a voom-based precision weights approach (*RNAseq_Data_Preprocessing.Rmd*). These steps produce multiple output files (purple boxes) that are imported into the Shiny-based interactive web app environment (green box). Pre-processing pipelines for each species are implemented in separate R Markdown files and may be viewed on GitHub.