



Figure S2. Detailed graphic view of the *Strongyloides* RNA-seq Browser codebase. Grey boxes are outputs from pre-processing pipelines, here used as inputs to the interactive Shiny program. Red boxes are interactive user inputs. Green boxes are output elements displayed within the browser; output values directly depend on inputs provided via red elements. Blue boxes are commands run in R, white boxes are code details. Purple boxes are downloadable output file options. Dashed lines show division of code elements into the named files. For file names, the “_gw” suffix indicates files specific for “Browse by Gene” mode, while the “_ls” suffix indicates files specific for “Browse by Life Stage” mode.