Figure S1. RNA-seq pre-processing statistics. x-axis: RNA-seq pre-processing tools used in sequential order as FastQC, STAR and featureCounts (see details in Methods section). y-axis: Number of reads per library. Boxplots show read count statistics of every RNA-seq library (dots). The rows of the table shows library read statistics: n, number of samples/libraries; min/max, minimum/maximum number of reads across libraries; median/mean/iqr, median/mean/interquartile-range of all libraries.