

Additional file 1. Statistical details of the RNA sequencing analysis.

1) Removal of genes with low expression. A gene was considered to have low expression if: (1) its expression level was 0 across all samples, or (2) its mean expression level was lower than the 10th quantile of the distribution of mean expression levels of all genes across all samples.

2) Removal of genes with low coefficient of variation (CV). CV of gene i was defined as:

$$CV_i = \frac{\sigma_i}{\bar{x}_i}$$

where $\bar{x}_i$ is the mean of the expression of gene i and σ_i is its standard deviation. A gene i was removed from the analysis if CV_i was lower than the 25th quantile of the distribution of the CV of all genes across all samples.