

Supplementary Figure 2
(Top) The dendrogram tree presents the result of hierarchical clustering, and each node of the tree represent a single RNA-Seq sample. The Euclidian distance was used to calculate dissimilarity between two samples for the clustering.

(Bottom) Heatmap indicates correlations of RNA-Seq samples. Each cell shows a correlation between corresponded samples which identifiers are annotated at the corresponded row and column. An isolated rectangular box means the corresponded samples belong to the same cluster. The hierarchical clustering was used to determine the clusters.