



Supplemental Figure 3. Analysis of different samples global gene expression. (a) The principal component analysis (PCA) of the RNA-seq data of the 12 samples; (b) Total number of genes expressed at each developmental stage; (c) Percentage of gene numbers in different categories according to their expression levels in each tissue, based on FPKM values; (d) Gene ontology (GO) enrichment analysis of the all expression gene in four developmental stages.