



**Figure S1.** Expression levels of lipid related genes in soybean tissues. The heatmap showing tissue-specific expression profiles was generated using the log2-transformed (Fragments Per Kilobase of exon model per Million mapped fragments (FPKM) + 1) values of lipid related genes. High expression (FPKM > 50) is indicated with “\*\*”, while low expression (FPKM < 1) is indicated by “#”. Brackets on the top show the results of column cluster analysis. The heatmap above was generated on the basis of RNA-seq data from the website (<https://phytozome-next.jgi.doe.gov/>).