



Fig. S2 (a) Annotated GO terms and KEGG pathway enrichment analysis of 7794 DEGs in *A. annua* scion (b) Annotated GO terms among 50 mobile *N. benthamiana* genes detected in *A. annua* scion. Red, blue, and green color represents biological process, cellular component, molecular function, respectively. The ordinate showed the Go serial number and function. The horizontal ordinate represents the number of genes in each Go term category. GO enrichment bar plot in upper left corner inflected the number and distribution of genes with significant differences located in biological process, cellular component and molecular function. The top25, top15, top 10 were orderly chosen for drawing the part of GO bar plot. In upper right corner, the x-coordinate rich factor means the number of differential genes or total number located in corresponding GO, ordinate is the GO functional annotation. Similarly, the KEGG photos in the bottom part included KEGG difference analysis of the system level (left) and the number of DEGs in top20 of KEGG pathway (right).