



Figure S3. NJ phylogeny of *A. thaliana*, *O. sativa*, *Z. mays*, *L. japonicus*, *M. truncatula*, *C. arietinum*, *G. max*, *C. cajan* and *P. vulgaris* Hsf proteins. The conserved N-terminal parts of the proteins containing the DBD and the HR-A/B region were used for constructing the phylogenetic tree by neighbor-joining method. ScHsf1 was set as the outgroup. The legume Hsfs were grouped into three major classes, A, B and C. Class A and B were further divided into nine (A1–9) and five (B1–5) subgroups with high bootstrap values (>50).