



**Figure S4.** ML phylogeny of *L. japonicus*, *M. truncatula*, *C. arvense*, *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 maximum likelihood method. ScHsf1 and the Hsfs of *C. reinhardtii*, *S. moellendorffii* and *P. patens* were used as outgroup. In the MJ tree, the defined ortholog clades were largely consistent with the results of the NJ tree in Figure 1.