**Figure Legends**

Fig.1 An unrooted Maximum-Likelihood tree showing the hylogeny and classification of 670 HSFs sequences from 44 species representing seven main taxa including chlorophyta, bryophyta, peridophyta, gymnospermae, basal angiosperms, eudicots and monocots. The information of species and sequences accession numbers used for the tree are listed in Additional files 1. HSFA, HSFB and HSFC are clustered into three main clades. The clade of subfamilies HSFA2-7, HSFA8 and HSFA9, HSFB2-5, and HSFC1 and HSFC2, were shown over relevant branches with different colors. The three groups HSFA, HSFB, and HSFC were highlighted with shades of different colors. The scale bar represents amino acid substitutions per site.

Fig. 2 [A] Synteny analysis between the subfamilies HSFA2, HSFA6, HSFA7, HSFA9 of seven representative plant species (*Amborella trichopoda, Liriodendron chinense, Arabidopsis thaliana, Solanum lycopersicum, Oryza sativa, Sorghum bicolor, Zea mays*). [B] Synteny analysis between the subfamilies HSFB1, HSFB2, HSFB4, HSFB5 of seven representative plant species (*Selaginella moellendorffii, Amborella trichopoda, Liriodendron chinense, Arabidopsis thaliana, Solanum lycopersicum, Oryza sativa, Zea mays*). [C] Synteny analysis between the subfamilies HSFA1, HSFA4, HSFA5 of eight representative plant species (*Ginkgo biloba, Amborella trichopoda, Liriodendron chinense, Arabidopsis thaliana, Solanum lycopersicum, Oryza sativa, Sorghum bicolor, Zea mays*).

Black, and blue lines indicate orthologous, and paralogous gene pairs respectively. The different colored circle represent HSF genes from different subfamilies. The name of the genes is inside the circle.

Fig. 3 A dated phylogenetic reconstruction for the subfamilies HSFA2 and HSFA9. Red ovals indicate gene duplication events. The divergence time of HSFA2 and HSFA9 are marked with red.

Fig 4. A dated phylogenetic reconstruction were done for the subfamilies HSFC1 and HSFc2. Red ovals indicate gene duplication events. The divergence time of HSFC1 and HSFc2 are marked with red.

Fig.S1 A detailed Maximum-Likelihood tree of HSFs constructed with the program RaxML. The classifications are based on HSFs annotations identified using the HEATSTER website ([https://applbio.biologie.uni-frankfurt.de/HSF/heatster/](https://applbio.biologie.uni-frankfurt.de/hsf/heatster/)). The detail information of sequences was provided in Additional file1.

Fig S2. A Maximum-Likelihood phylogenetic reconstruction for the group HSFA and HSFC. The branch and the genes’ name of distinct clusters of HSFA3, HSFA4, HSFA5, HSFA8, and HSFA9 were color coded. In the others, only the gene names were colored. The relevant support values are shown. The scale bar represents amino acid substitutions per site.

Fig S3. A Maximum-Likelihood phylogenetic reconstruction for the HSFB group. The branch and the genes’ name of distinct clusters of HSFB2, HSFB3, HSFB5 were color coded. In the others, only the gene names were colored. The relevant support values are shown. The scale bar represents amino acid substitutions per site.

Additional file 1: List of the accession number of HSF sequences used for the phylogenetic analysis.