

Figure S1. Phylogenetic tree and subgroup classification of NPF proteins in *A. thaliana*, *Gossypium hirsutum*, *G. raimondii* and *G. arboreum*. The numbers at nodes of the phylogenetic tree indicate the bootstrap values expressing branching probability per 1000 replicates; the bootstrap values of the confidence levels are shown as percentages.

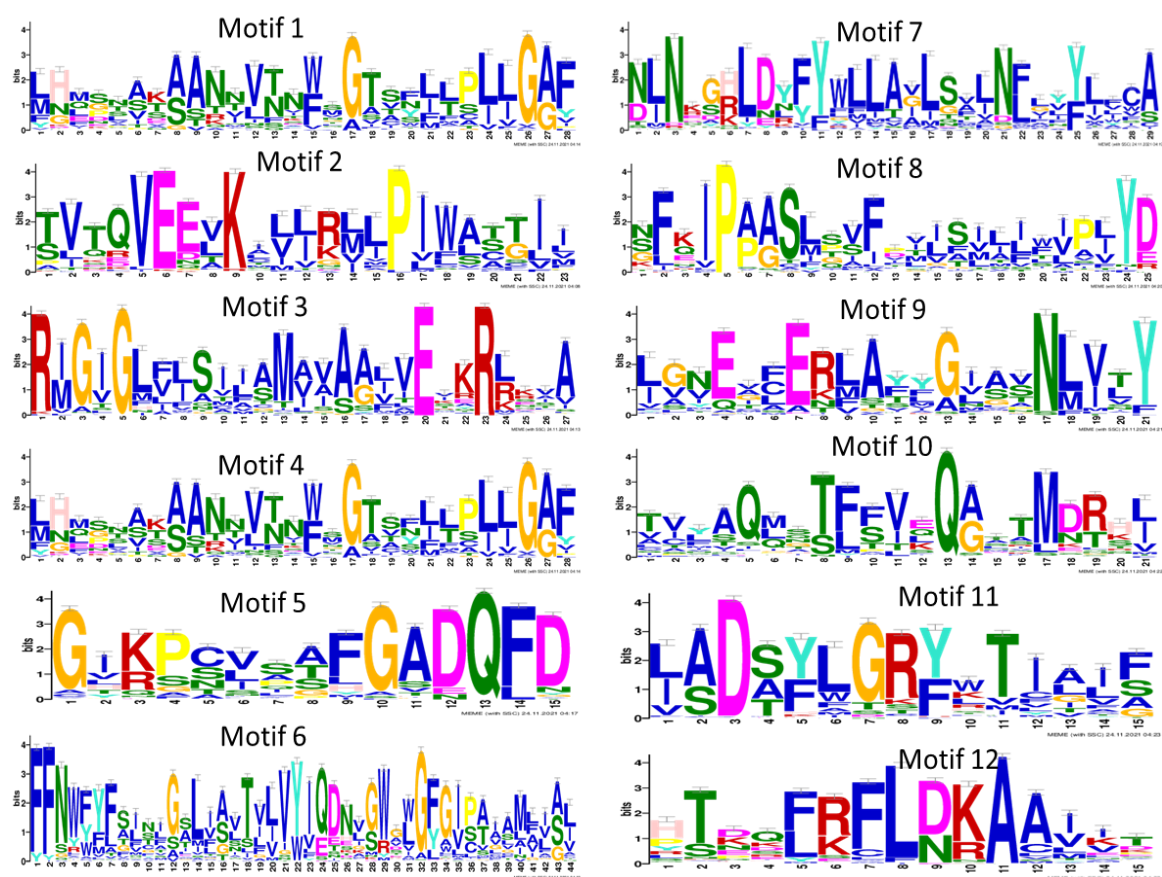


Figure S2. Sequence logo of the *GhNPFs* conserved-domain.

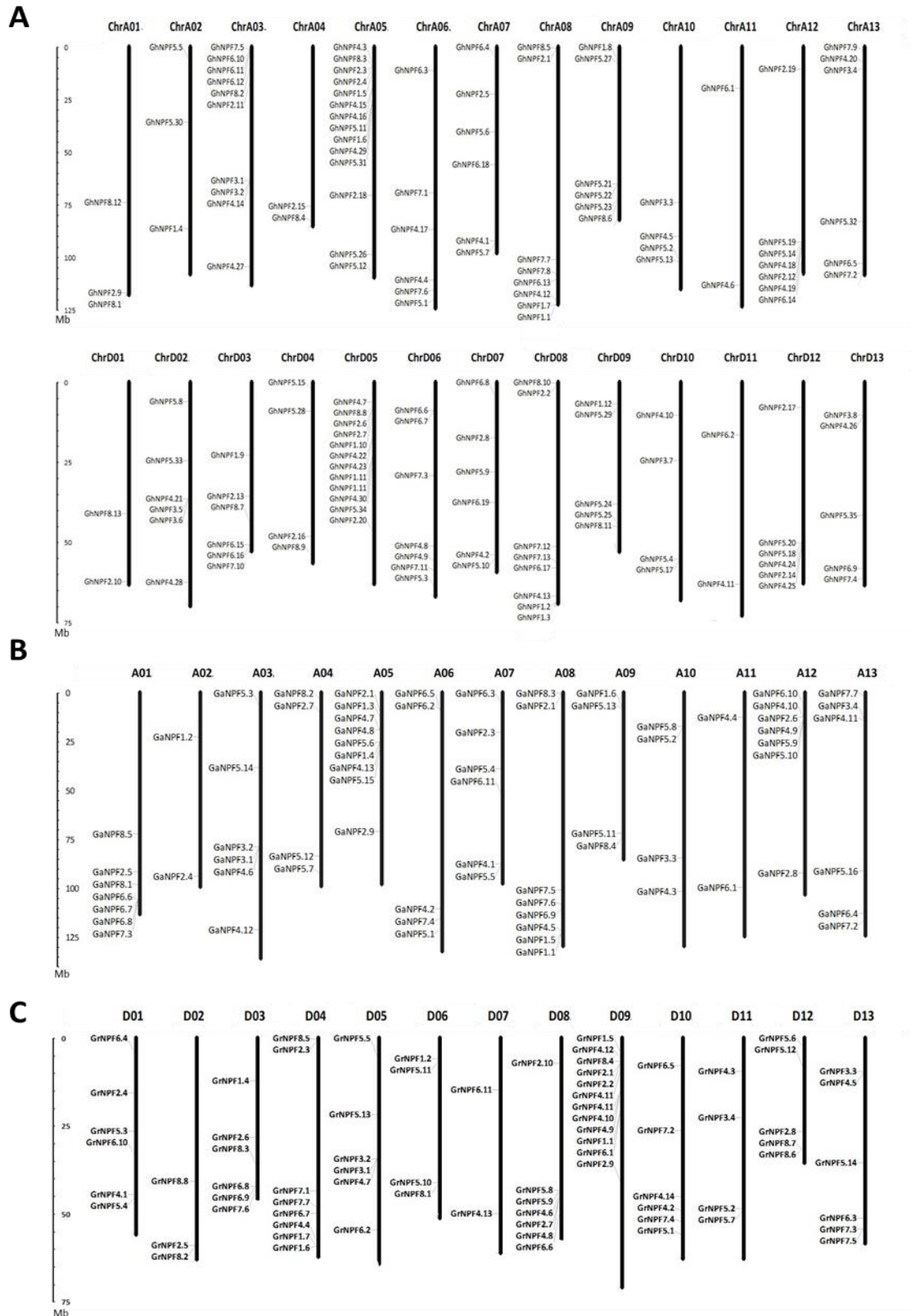


Figure S3. Chromosome distribution of *NPF* genes in *G. hirsutum* (A), *G. raimondii* (B) and *G. arboreum* (C). Scale on left is in Mb. Chromosome numbers are indicated on top of bar.

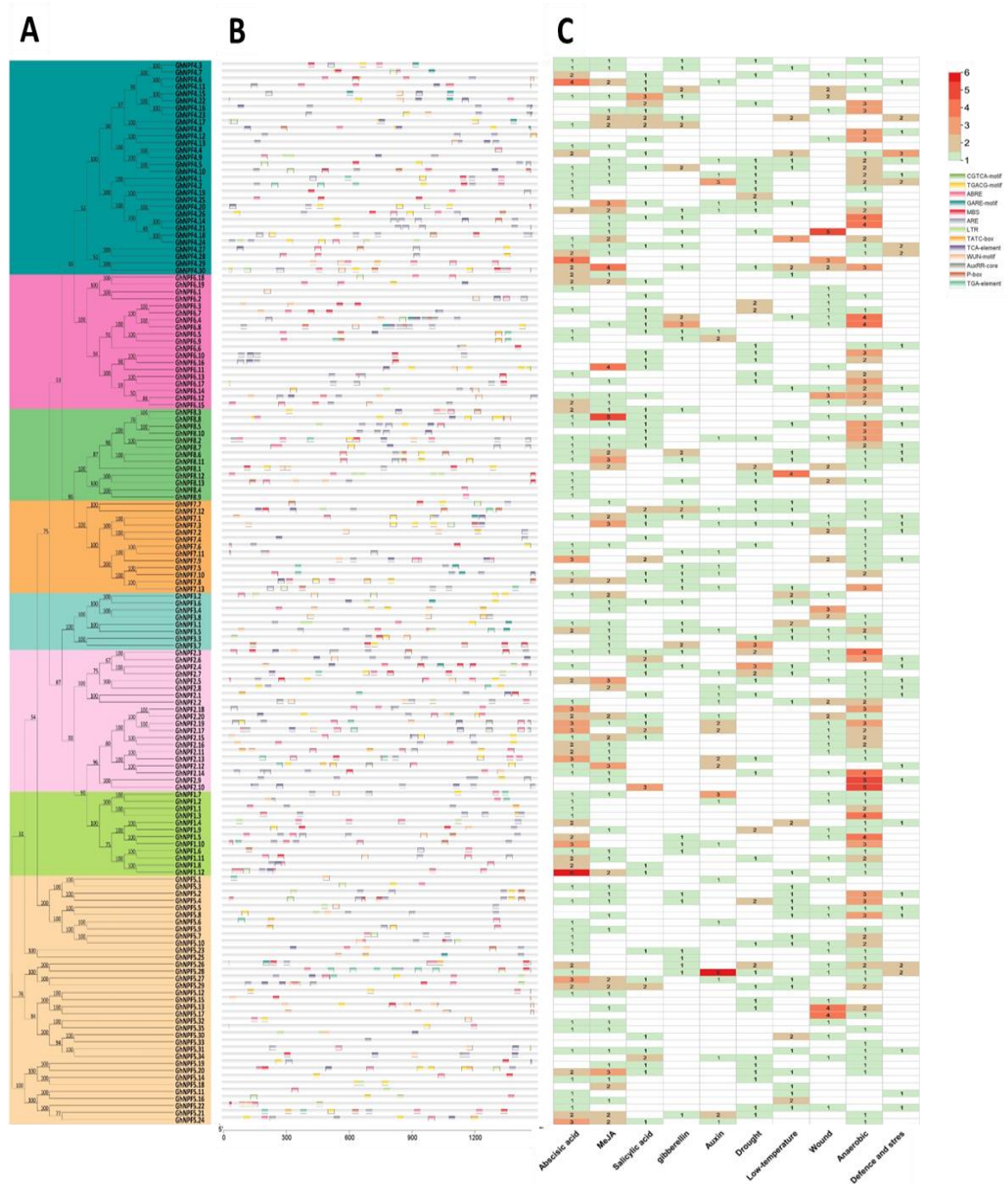


Figure S4. Analysis of cis-elements in *GhNPF* promoters. (A) Phylogenetic tree of *GhNPF*s. (B) Cis-elements in promoters of *GhNPF* gene family members. (C) Frequency of cis-elements in the promoter region of *GhNPF* genes. The number in colored box represents the number of cis-acting elements.

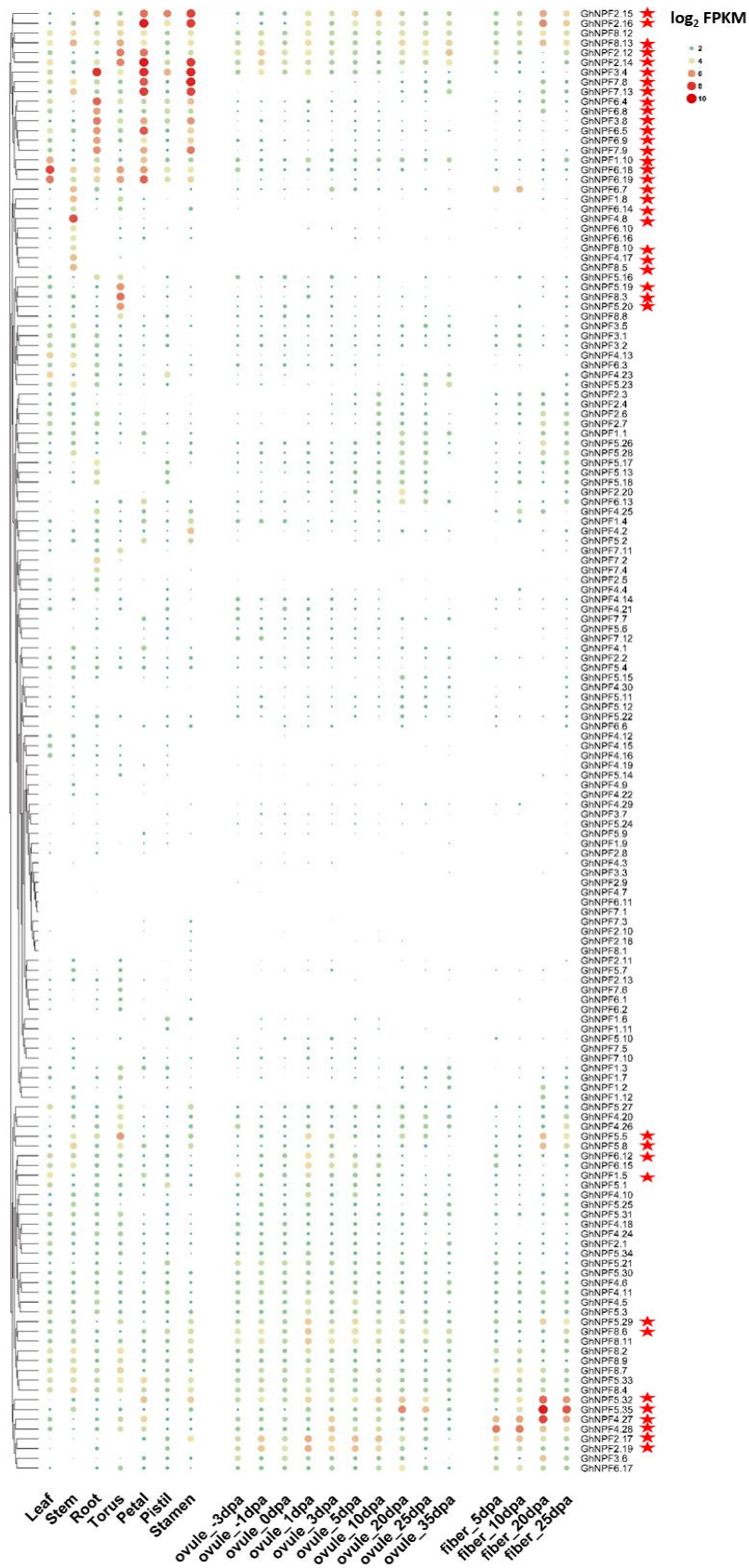


Figure S5. Expression patterns of *GhNPF* family genes in different tissues. The expression data were obtained from RNA-seq data and shown as \log_2 FPKM. Asterisks marked *GhNPF* genes selected for N deficiency treatment candidate genes.

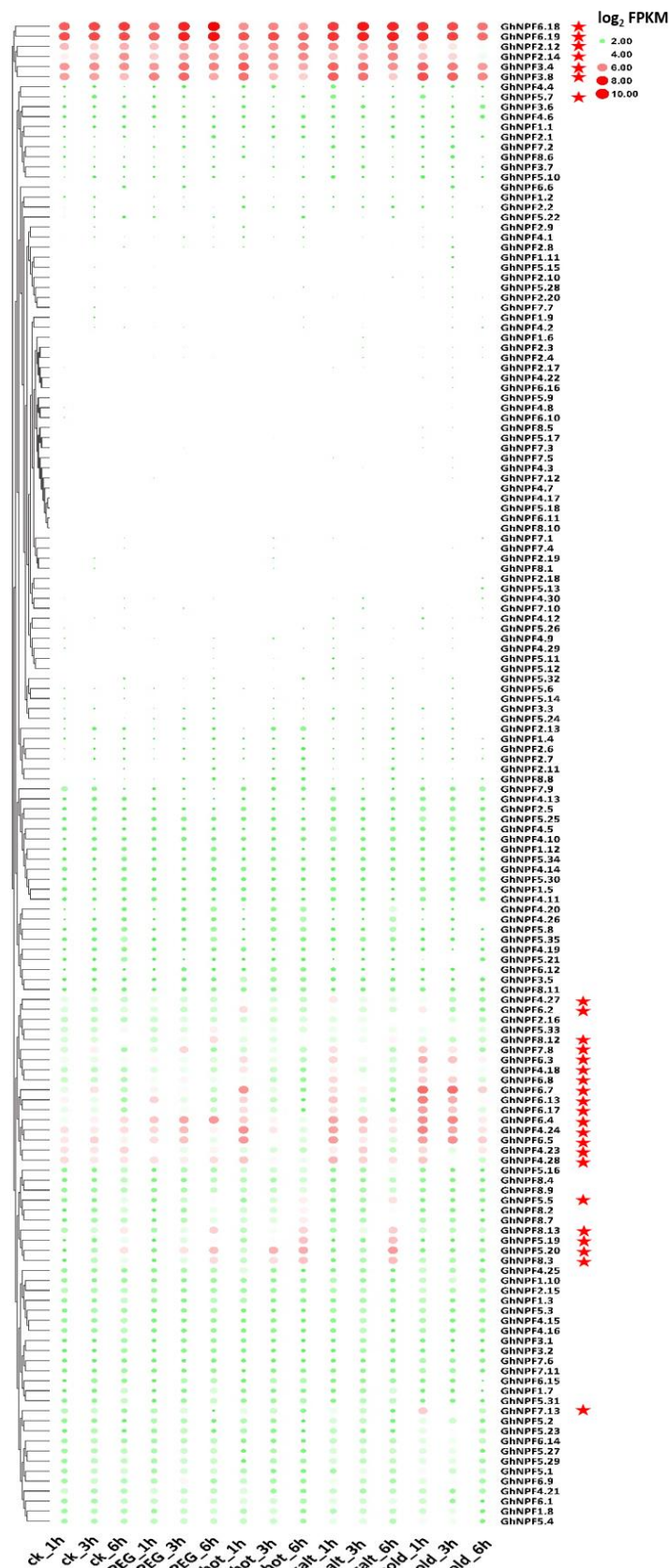


Figure S6. Differentially expression level of *GhNPF* gene family members under cold, hot, salt and PEG stress. The expression data were obtained from RNA-seq data and shown as \log_2 FPKM. Asterisks marked *GhNPF* genes selected for N deficiency treatment candidate genes.