Supplemental Tables

**Table S1** Sample information for RNAseq experiments.

**Table S2** Percentage of the genomes from six grasses genomes in categories classified by annotation.

**Table S3** The full list of the number of orthologs shared by different combinations of species. Note “0” means the species contained no genes in clusters with that pattern and “1” means that species contained genes in clusters with that pattern.

**Table S4** Gene Ontology enrichment for five clusters in the leaf and crown under cold, freezing, and recovery conditions.

**Table S5** Gene Ontology enrichment for five clusters of genes differentially expressed in shoots subjected to abiotic stresses.

**Table S6** All of the candidate transcription factors in *B. sylvaticum.*

Supplemental figures

**Figure S1** Upset plot of showing orthologs shared by all combinations of six grass species. Note some of these were shown in figure 6.

**Figure S2** RNAseq experimental designs. (a) Leaf and crown under cold, freezing, and recovery; (b) Shoot treated under drought, heat, and salt stresses along five timepoints.

**Figure S3** Expression analysis using k-means clustering. (a) The cluster associated with freezing response (Cluster 3) based on K-mean clustering analysis. The clustering analysis utilized normalized counts for 3,296 DEGs with variance >1.5 and mean expression abundance >4. (b) Gene Ontology enrichment for the genes in Cluster 3. Only GO terms with FDR <0.05 are plotted. (c) Gene family enrichment for genes from Cluster 3. (d) The cluster associated with response to recovery from freezing (Cluster 5) based on K-mean clustering. (e) Gene Ontology enrichment for the genes in Cluster 5. Only GO terms with FDR <0.05 were plotted. (f) Gene family enrichment for genes from Cluster 5.

**Figure S4** (a) The cluster associated with heat response (Cluster 1) based on K-mean clustering analysis. The clustering analysis utilized normalized counts for 1,911 DEGs with variance >1.5 and mean expression abundance >4. (b) Gene Ontology enrichment for the gene in Cluster 1. Only the GO terms with FDR <0.05 are plotted. (c) Gene family enrichment for genes from Cluster 1. (d) The cluster associated with heat response (Cluster 1) based on K-mean clustering analysis (details in Methods). The clustering analysis utilized normalized counts for 1911 DEGs with variance >1.5 and mean expression abundance >4. (e) Gene Ontology enrichment for the genes in Cluster 1. Only the GO terms with FDR <0.05 are plotted. (f) Gene family enrichment for genes from Cluster 1.

Supplemental dataset

**File S1** Database of orthologs identified from *Brachypodium sylvaticum, Brachypodium distachyon*, *Brachypodium stacei*, *Oryza sativa*, *Panticum hallii*, and *Sorghum bicolor*.

**File S2** Normalized counts of all genes differentially expressed in the freezing experiment.

**File S3** Normalized count of 17,184 differentially expressed genes in the abiotic stress time-course experiment.

**File S4** The phylostrata for 36,927 protein-coding genes of *B. sylvaticum.*