Supplemental Figure 1 Coding sequence similarity among syntenic genes in sorghum, maize1, and maize2. Sequence similarity between annotated coding sequence for maize1 and maize2, maize1 and sorghum, and maize2 sorghum syntenic gene pairs. (Supports Figure 1)
Supplemental Figure 2 Representative sample of cold stressed seedling phenotypes. Phenotypes of a larger set of seedlings than could be displayed in Figure 2 under control conditions, after one day of cold treatment and after 14 days of cold treatment followed by 2 days recovery under greenhouse conditions. (Supports Figure 2)
Supplemental Figure 3 Individual examples of genes in each of six possible DRO/DEG classification categories. (A) Examples of maize/sorghum gene pairs which fall into each of the six combinations of DRO/DEG classification presented in Figure 5. (B): Number of genes classified as DROs and CROs within each of the DE0, DE1, and DE2 categories for maize1/sorghum gene pairs and maize2/sorghum gene pairs. (Supports Figure 5)
Supplemental Figure 4 Comparison of Ka/Ks ratio and expression level for genes grouped based on expression classification model. Distributions of Ka/Ks ratios and log2 transformed expression (control condition) for maize gene pairs categorized based on whether the additive or multiplicative model proved to be the better predictor of gene regulatory pattern for a given gene pair. (Supports Figure 5)
Supplemental Figure 5 Frequency of known CBF binding motifs within the 1 kb proximal promoters of maize and sorghum. Frequency of known CBF binding motifs within the 1 kb proximal promoters of maize and sorghum based on expression classification from the initial 2 time point cold stress analysis. **: p<0.01 as calculated based on Fisher Exact Test.
(Supports Figure 6)
Supplemental Figure 6. Relationship between gene pair expression pattern in maize and sorghum after subdividing genes based on Ka/Ks ratio and expression tertile.

Relationship between gene pair expression pattern in maize and sorghum at the 24 hours cold stress time point and chromatin accessibility estimated using data on MNase HS
using windows of 50bp. The set gene pairs overlapping between each possible tertile pairs between FPKM and Ka/Ks values from low to high were used for analysis. Results of Maize1/sorghum and maize2/sorghum have been merged. (Supports Figure7)