# SUPPORTING INFORMATION LEGENDS

**Supplemental Figure S1: Coverage maps of features for chromosomes 1-6.** For features other than nucleosome occupancy likelihoods, scales represent the percentage of nucleotides annotated as the feature. For nucleosome occupancy likelihoods, the scale represents the estimated likelihood of occupancy where positive values predict the presence of a nucleosome and negative values predict the absence of a nucleosome.

**Supplemental Figure S2: Coverage maps of features for chromosomes 7-10.** For features other than nucleosome occupancy likelihoods, scales represent the percentage of nucleotides annotated as the feature. For nucleosome occupancy likelihoods, the scale represents the estimated likelihood of occupancy where positive values predict the presence of a nucleosome and negative values predict the absence of a nucleosome.

**Supplemental Figure S3: Length of coding sequence increases between gene annotations 1.4 and 3.1.** A) Scatterplot and b) density plot of CDS lengths of 23,135 matched gene model pairs between v1.4 and v3.1 illustrate that 7,646 v3.1 models have longer CDS lengths with an average increase in length of 400.5 bp.

**Supplemental Figure S4: Multiple sequence alignment of nine STA1 and nine STA2 sequences corresponding to 3 monomers from each of 3 arrays on different chromosome arms.** Nucleotide sequences, including the consensus sequence for STA1 and STA2, is contained in Supplemental File S2.

**Supplemental Figure S5: Gene expression correlations for all samples and replicates.**

**Supplemental Figure S6: Loadings for first three principal components of each gene.** Genes in blue represent the 2,500 genes with the greatest sum magnitude of loadings for PC1, PC2, and PC3.

**Supplemental Table S1: Presence and absence of telomere repeat and STA repeats in the sorghum genome.**

**Supplemental Table S2: Tissue samples present in the Sorghum Transcriptome Atlas.** Tissue samples in the gene atlas were collected as part of either a tissue by development timecourse or a nitrogen source study. This table represents an abridged version of the complete table, which can be found in Supplemental File S2.

**Supplemental Table S3: Genes annotated as having protein kinase activity responsible for ontological enrichment in the 2,500 genes with large principal component loadings.** These genes represent kinases with expression values that vary across the sampled tissues and may play a role in specifying or maintaining tissue identity. This table represents an abridged version of the complete table, which can be found in Supplemental File S3.

**Supplemental File S1: Supplemental Methods**

**Supplemental File S2: STA sequence**

**Supplemental File S3: Transcriptome Atlas ID Mapping**

**Supplemental File S4: Ontological Enrichments**

**Supplemental File S5: Whole Genome Sequence Accessions**