Supplemental Figure and Table Captions

Supplemental Fig. S1. Comparison of ribonucleic acid sequencing (RNA-seq) read depth and number of expressed genes detected across a diverse set of tissues. Reads were mapped using Bowtie version 0.12.7 (Langmead et al., 2009) and TopHat version 1.2.0 (Trapnell et al., 2009). Fragments per kilobase pair of exon model per million fragments mapped (FPKM) values were calculated using Cufflinks version 0.9.3 (Trapnell et al., 2010), the version 2 (v2) pseudomolecules, and the v2 annotation. Genes were considered expressed if the 95% confidence interval lower boundary FPKM value was greater than zero. DAP, days after pollination.

Supplemental Fig. S2. Comparison between number of expressed genes detected and sampling depth. For all tissues 5, 10, and 15 million reads were randomly selected from the total pool of reads for all tissues, and for tissues with sufficient reads, 20 and 25 million reads were also selected. Reads were mapped using Bowtie version 0.12.7 (Langmead et al., 2009) and TopHat version 1.2.0 (Trapnell et al., 2009). Fragments per kilobase pair of exon model per million fragments mapped (FPKM) values were calculated using Cufflinks version 0.9.3 (Trapnell et al., 2010), the version 2 (v2) pseudomolecules, and the v2 annotation. Genes were considered expressed if the 95% confidence interval lower boundary FPKM value was greater than zero. DAP, days after pollination.

Supplemental Table S1. Raw expression values, gene family assignments, and network module information for version 2 (v2) annotated gene models. Fragments per kilobase pair of exon model per million fragments mapped (FPKM) values were calculated using Cufflinks version 0.9.3 (Trapnell et al., 2010), the maize v2 pseudomolecules, and the v2 annotation. Gene family assignments and gene family sizes were determined with the OrthoMCL algorithm (Li et al., 2003). Gene coexpression module assignments were determined using the weighted gene coexpression network analysis method (WGCNA) protocol (Langfelder and Horvath, 2007) after CV filtering. The included genes and their module assignments are indicated. DAP, days after pollination.

Supplemental Table S2. Expression of cloned genes with characterized expression patterns measured as fragments per kilobase pair of exon model per million fragments mapped (FPKM). The FPKM values were calculated using Cufflinks version 0.9.3 (Trapnell et al., 2010), the version 2 (v2) pseudomolecules, and the v2 annotation. DAP, days after pollination.

Supplemental Table S3. Expression values of genes with expression restricted to a single tissue as determined in this study. Expression was measured as fragments per kilobase pair of exon model per million fragments mapped (FPKM). The FPKM values were calculated using Cufflinks version 0.9.3 (Trapnell et al., 2010), the version 2 (v2) pseudomolecules, and the v2 annotation. Genes were classified as having expression restricted to a single tissue within this study if only one of the tissues in this study had a 95% confidence interval lower boundary FPKM value greater than zero. DAP, days after pollination.

Supplemental Table S4. Previously described maize genes assigned to gene coexpression modules. Two lists of previously characterized maize genes were obtained from (Schnable and Freeling, 2011) and from the Maize Genome Sequence Project (2011). The lists of known maize genes were cross-referenced with the genes assigned to each module.