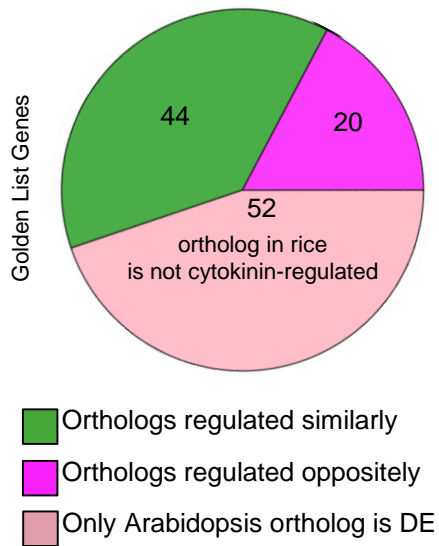
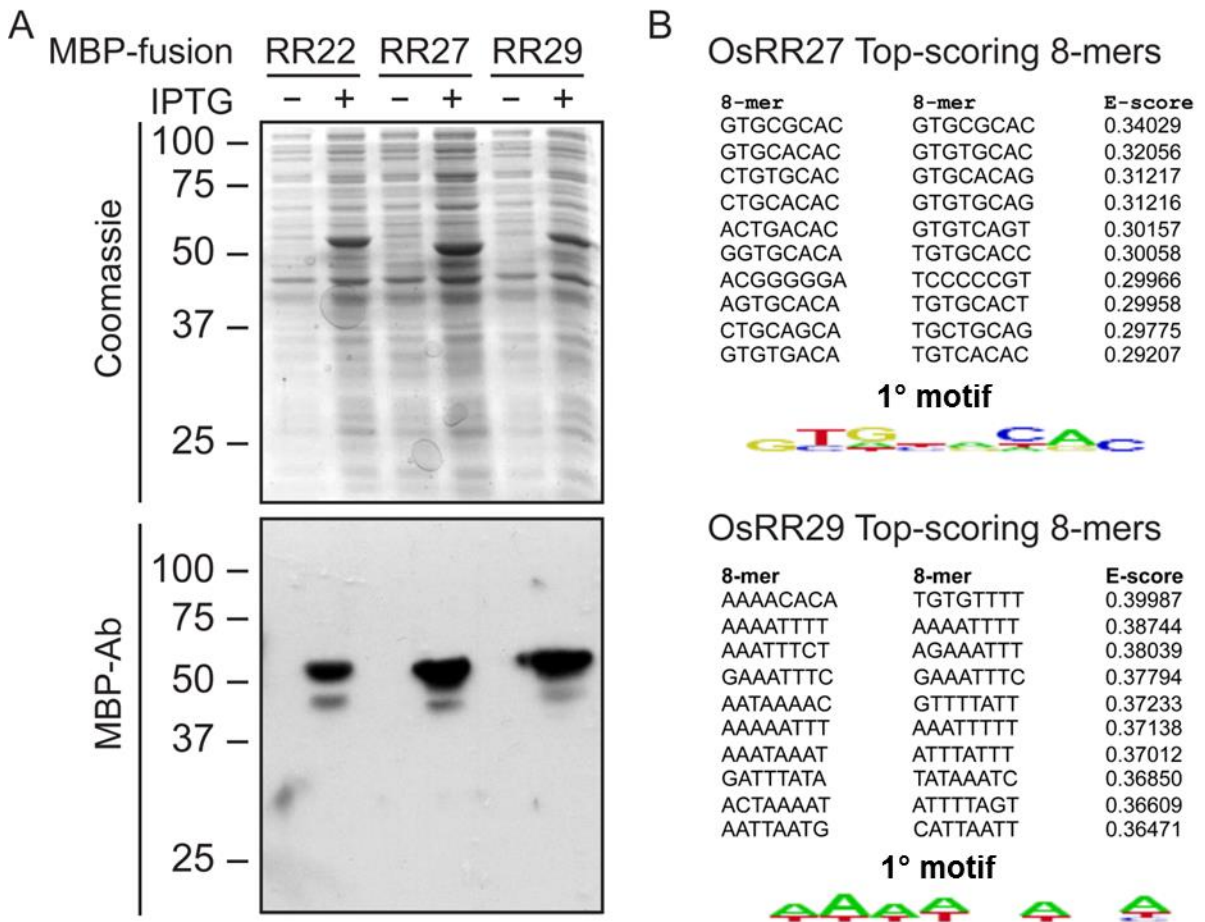


**Figure S1.** Regulation of genes involved in cytokinin (A) biosynthesis, (B) signaling, (C) response, and (D) degradation. Log<sub>2</sub>-fold change in the BA-treated samples relative to the mock control samples are indicated. Only genes that are differentially expressed between the control and cytokinin-treated samples are shown. Green boxes indicate genes differentially regulated in shoots; blue boxes in roots.

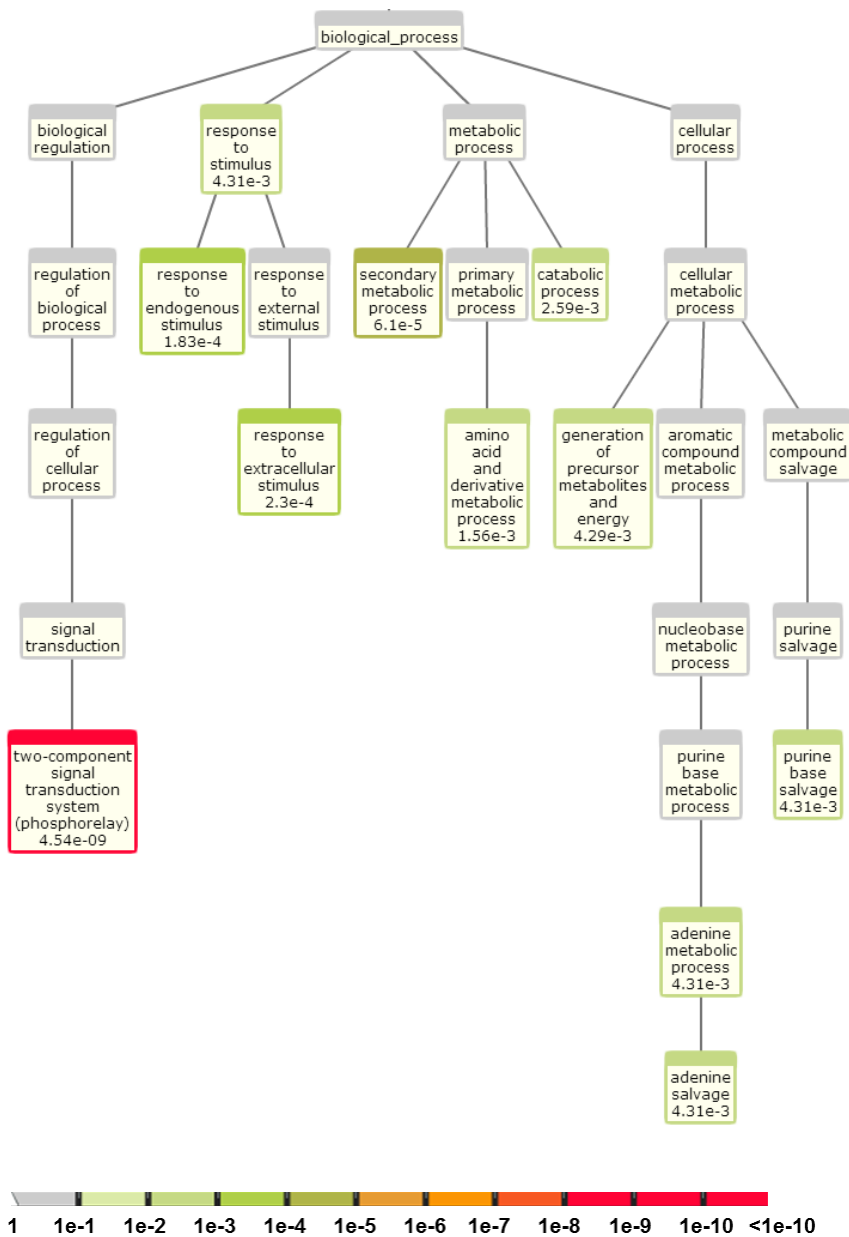


**Figure S2. Cytokinin regulation of orthologous genes in rice and Arabidopsis.**

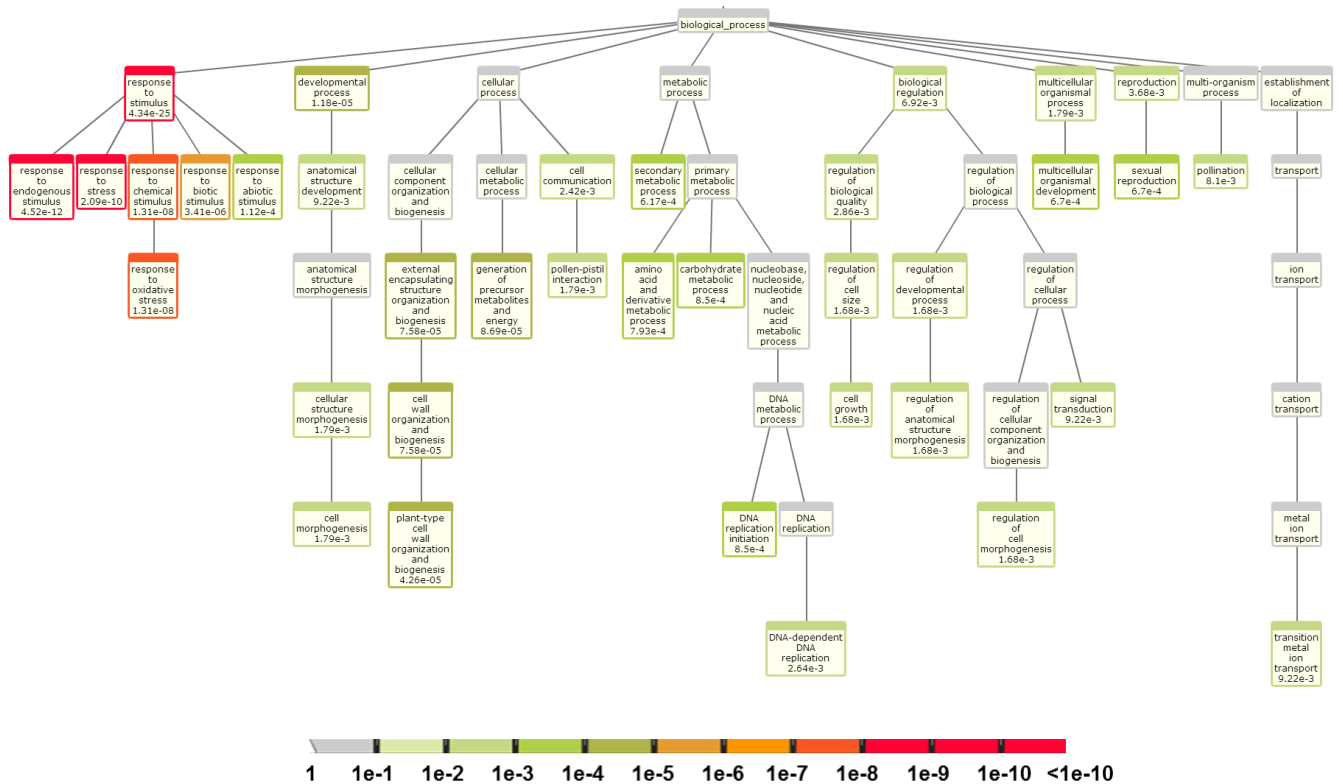
Comparison of the regulation of the rice orthologs of the robustly cytokinin-regulated genes (aka the “golden list”) in Arabidopsis discovered in a meta-analysis of Arabidopsis transcriptome studies [36].



**Figure S3. Characterization of rice type-B RRs through use of protein binding microarrays.** (A) Expression of the DNA-binding domains for RR22, RR27, and RR29 as fusions to maltose binding protein (MBP) in *E. coli*. A Coomassie Blue-stained gel of total bacterial protein is shown before (-) and after (+) IPTG induction of the fusion proteins (top panel) as well as immunoblot analysis for the fusion proteins with an anti-MBP antibody (lower panel). The fusion proteins are predicted to have molecular masses of 50.7 kDa (MBP-RR22), 49.4 kDa (MBP-RR27), and 50.5 kDa (MBP-RR29). (B) OsRR27 and OsRR29 do not display preferential binding to any particular DNA motif.



**Figure S4: GO categorization of genes induced by cytokinin in both the root and shoot** Using the VirtualPlant (<http://virtualplant.bio.nyu.edu>) tool for gene ontology (GO) term enrichment, analysis was performed on genes induced by cytokinin in both the root and shoot tissues of rice. All terms have p-value cutoff of < 0.01 and the p-value of the GO group is depicted by the color scale below.



**Figure S5: GO categorization of genes repressed by cytokinin in both the root and shoot** Using the VirtualPlant (<http://virtualplant.bio.nyu.edu>) tool for gene ontology (GO) term enrichment, analysis was performed on genes repressed by cytokinin in both the root and shoot tissues of rice. All terms have p-value cutoff of < 0.01 and the p-value of the GO group is depicted by the color scale below.

A

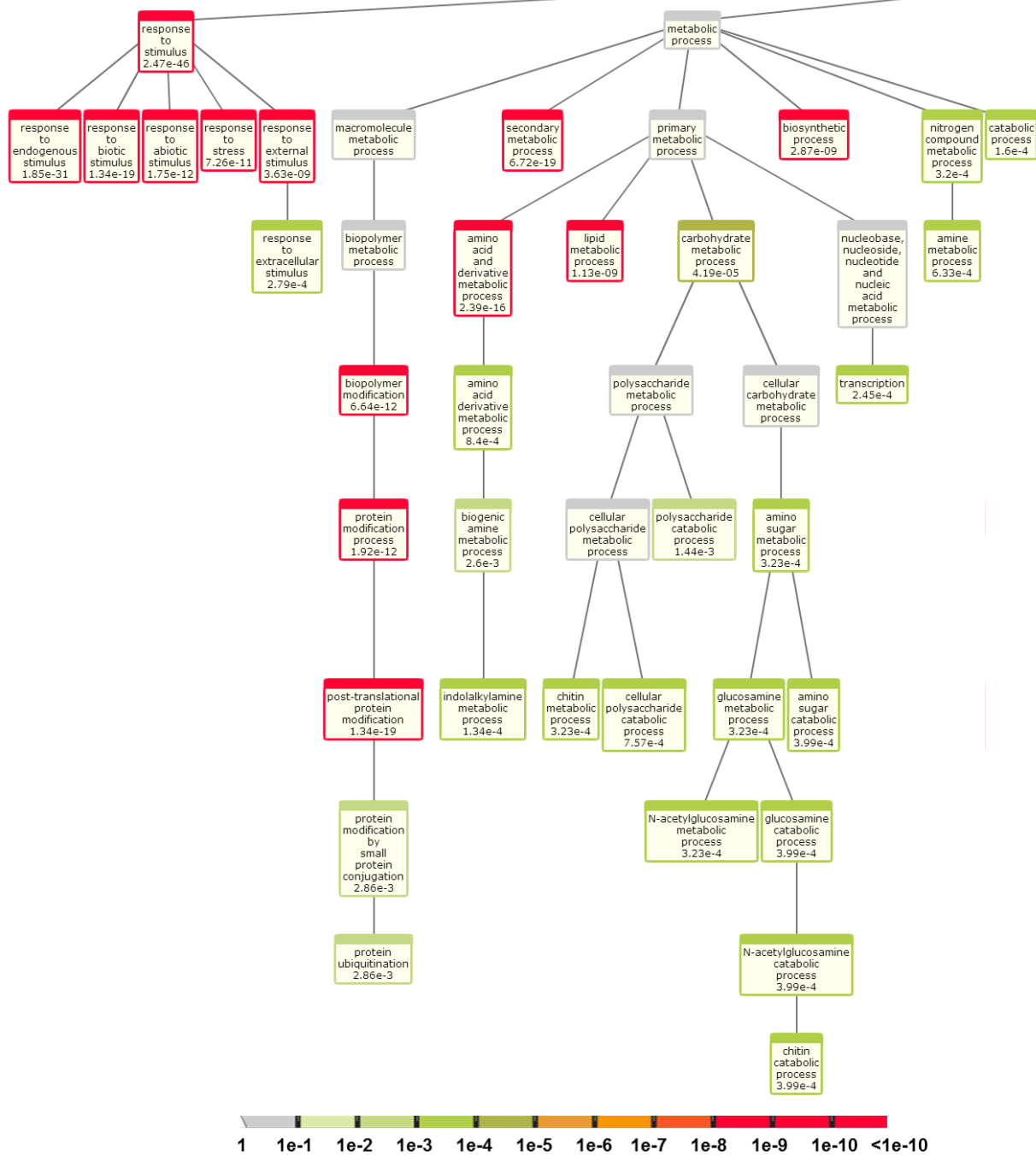
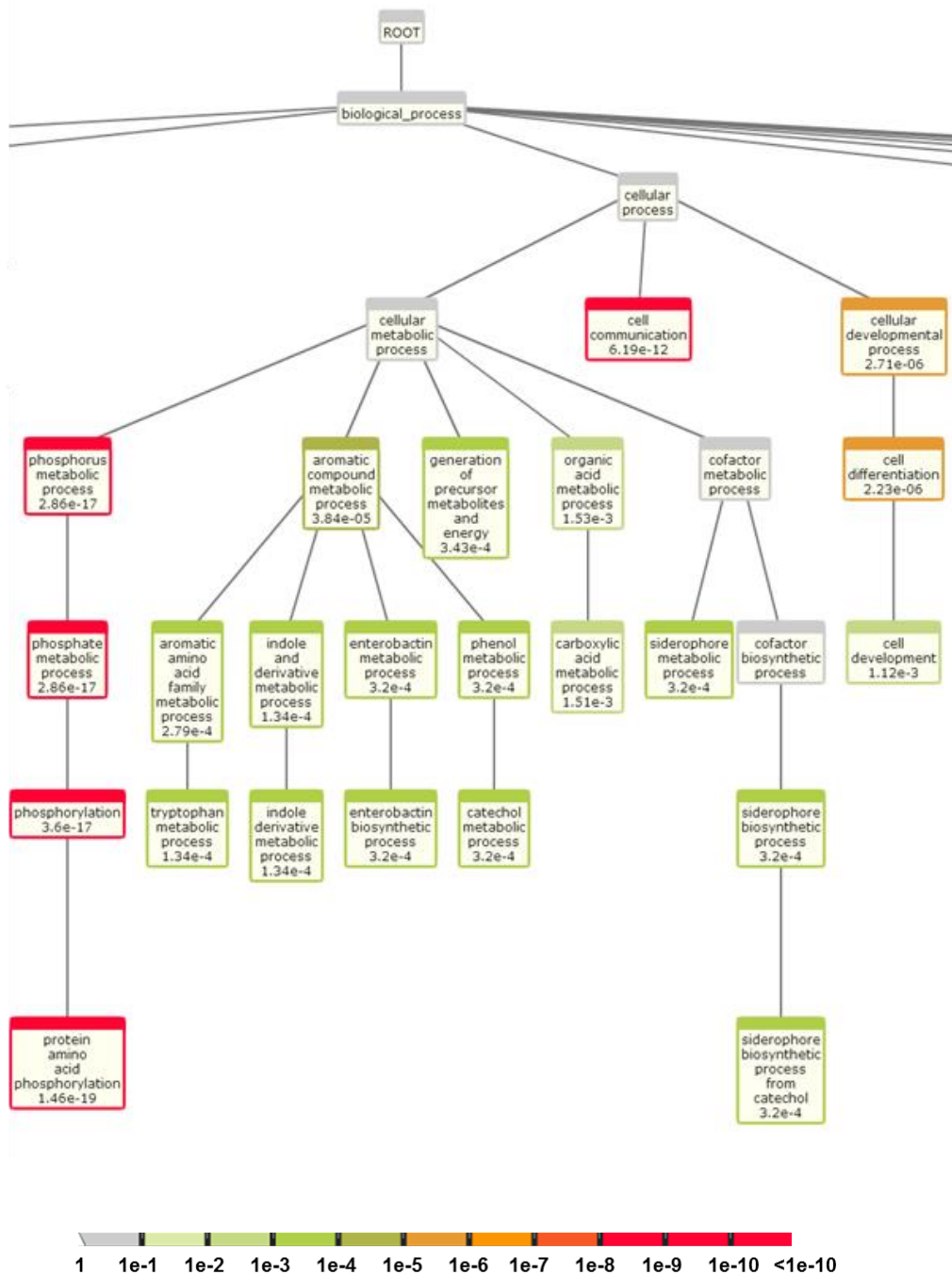
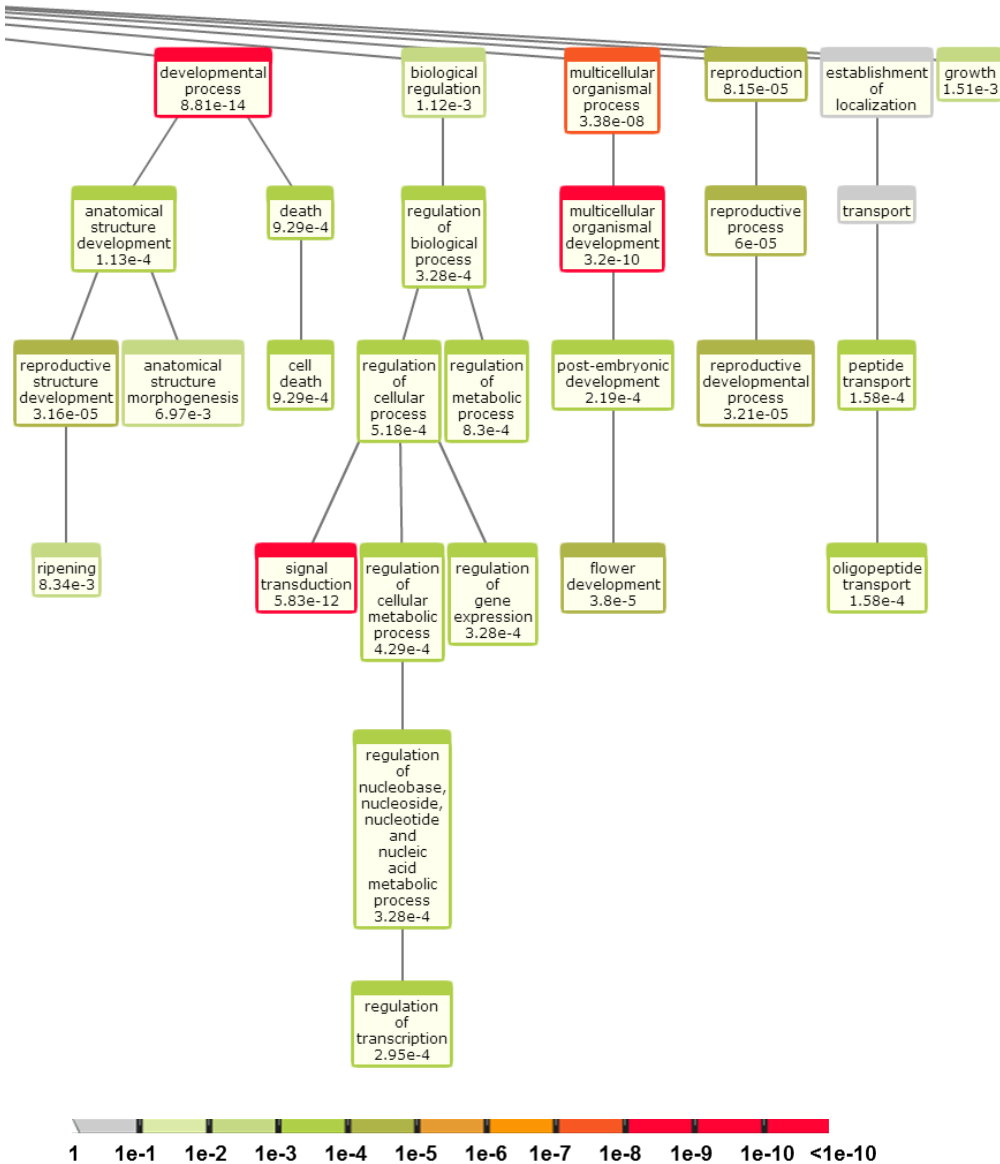


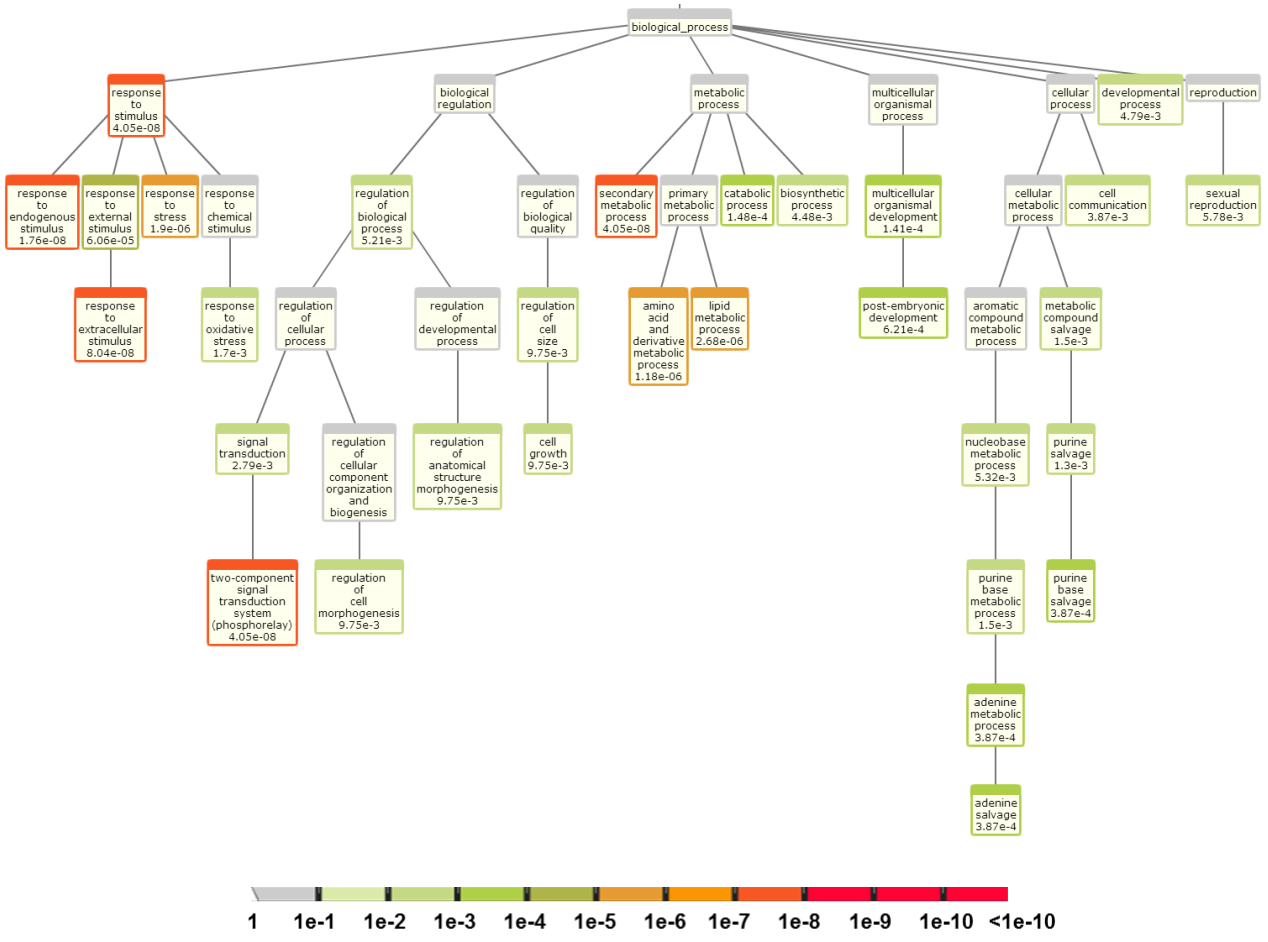
Figure S6a

**B****Figure S6b**

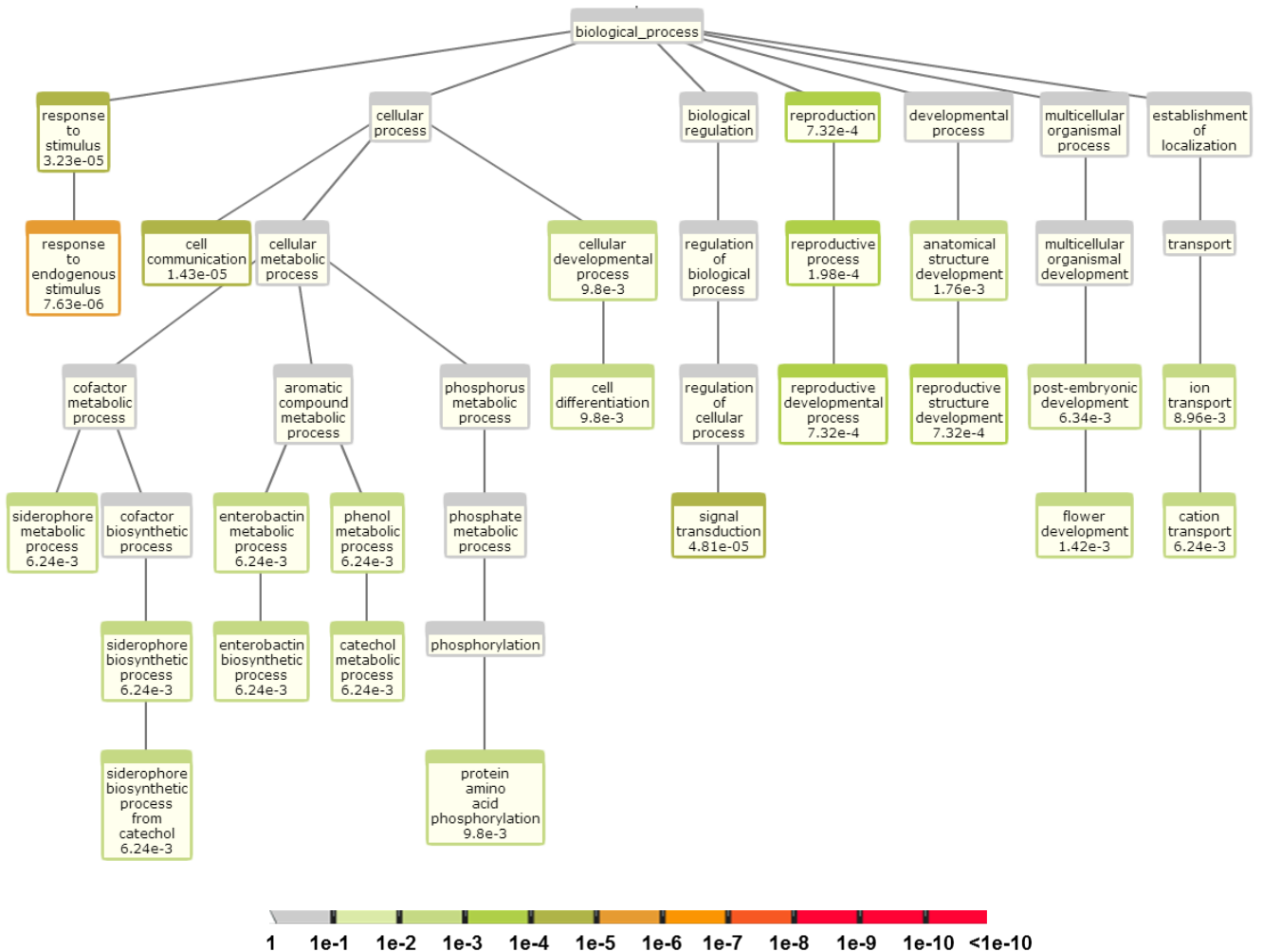
**C**

**Figure S6: GO categorization of genes induced by cytokinin in the root** Using the VirtualPlant (<http://virtualplant.bio.nyu.edu>) tool for gene ontology (GO) term enrichment, analysis was performed on genes induced by cytokinin in root tissues of rice. (A) The far left-hand side of the network, (B) the mid-section of the network and (C) the far right-hand side of the network. All terms have p-value cutoff of < 0.01 and the p-value of the GO group is depicted by the color scale below.

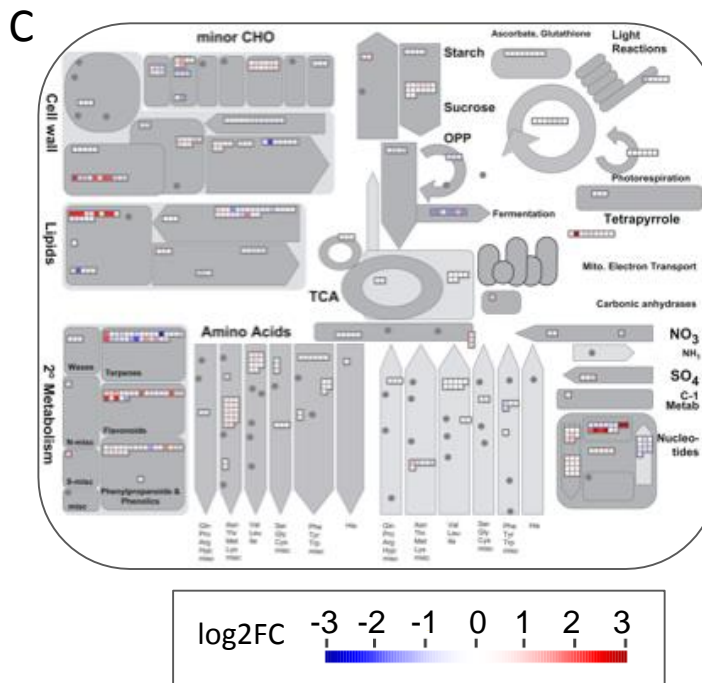
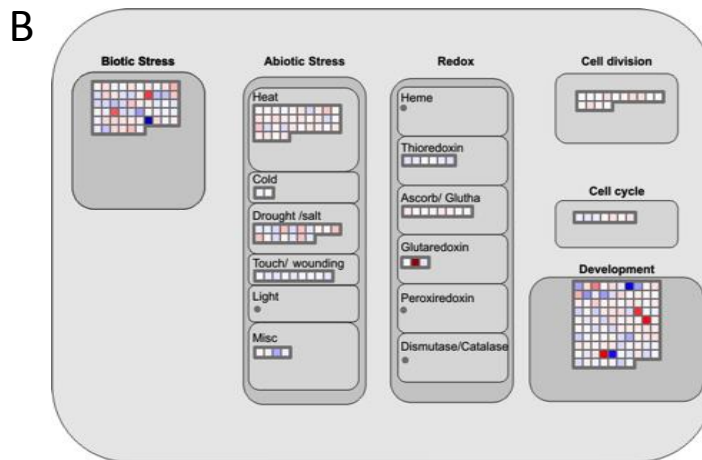
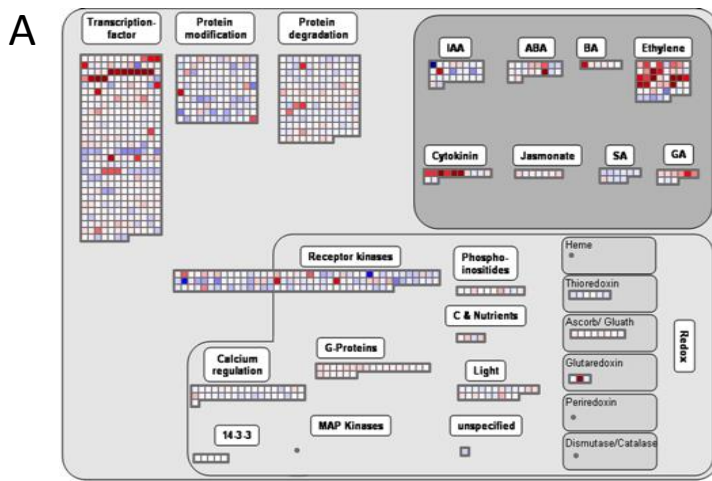




**Figure S7: GO categorization of genes induced by cytokinin in the shoot** Using the VirtualPlant (<http://virtualplant.bio.nyu.edu>) tool for gene ontology (GO) term enrichment, analysis was performed on genes induced by cytokinin the shoot tissues of rice. All terms have p-value cutoff of < 0.01 and the p-value of the GO group is depicted by the color scale below.



**Figure S8: GO categorization of genes repressed by cytokinin in the shoot** Using the VirtualPlant (<http://virtualplant.bio.nyu.edu>) tool for gene ontology (GO) term enrichment, analysis was performed on genes repressed by cytokinin in the shoot tissues of rice. All terms have p-value cutoff of < 0.01 and the p-value of the GO group is depicted by the color scale below.



**Figure SS9.** MapMan overviews of (A) metabolism, (B) cellular response and (C) regulation of cytokinin regulated genes in shoots in rice.