**Supplementary Table S4.** Hub genes and CRGs in the depicted co-expression networks of WGCNA modules

| Module & Gene ID | Description | $K_{ME}$ | Hubs (connections) |
|---|---|---|---|
| **Chocolate1** | | | |
| AT5G58900 | Homeodomain-like transcriptional regulator | 1.00 | Y (61) |
| AT1G06410 | Trehalose-phosphatase/synthase 7 (TPS7) | 1.00 | Y (99) |
| AT5G07920 | Diacylglycerol kinase1(DGK1) | 1.00 | Y (43) |
| CRGs | AT1G12450; AT1G14330; AT1G16370; AT1G22360; AT1G27910; AT1G44350; AT1G51090; AT1G72470; AT1G72510; AT1G75310; AT1G76160; AT2G17840; AT2G19780; AT2G22770; AT2G31010; AT2G34770; AT2G38310; AT2G39130; AT2G40130; AT2G40140; AT4G19530; AT5G03150; AT5G24030; AT5G25350; AT5G38710; AT5G40380; AT5G44050; AT5G52120; AT5G56160; AT5G58680; AT5G58900; AT5G64750; AT5G65470; AT5G65630 | >0.98 | |
| **Darkorange2** | | | |
| AT2G21050 | LIKE AUXIN RESISTANT 2 (LAX2) | 1.00 | Y (5) |
| AT1G02270 | Calcium-binding endonuclease/exonuclease/phosphatase family | 1.00 | Y (108) |
| AT5G51130 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | 1.00 | Y (89) |
| CRGs | AT1G61120; AT2G03090; AT2G15020; AT2G15760; AT2G28550; AT2G30930; AT2G44670; AT3G25870; AT4G15233; AT4G27260; AT4G29930; AT4G37530; AT5G12340; AT5G58670; AT5G63370 | >0.96 | |
| **Cornflowerblue** | | | |
| AT1G66090 | Disease resistance protein (TIR-NBS class) | 1.00 | Y (63) |
| AT5G09400 | $K^+$ uptake permease 7 (KUP7) | 1.00 | Y (64) |
| AT1G19300 | Nucleotide-diphospho-sugar transferases superfamily protein (PARVUS) | 1.00 | Y (73) |
| CRGs | AT1G12540; AT1G72920; AT2G17040; AT2G28120; AT2G32510; AT2G46370; AT4G03390; AT4G32350; AT5G09400; AT5G10410; AT5G59580; AT5G62360; AT5G63450; AT5G67420 | >0.98 | |

Note: WGCNA (Weighted Correlation Network Analysis) was performed to determine co-expression modules. The top-ranking 10% of genes with highest $K_{ME}$ in the module (Supplementary Data S7) were used to depict a subnetwork, and hub genes (indicated by "Y") were determined as those with at least 4 depicted connections in the network (Figure 7c-e). $K_{ME}$ represents eigengene connectivity measured for each gene by correlating its gene expression profile with the module eigengene (ME) which is defined as the first principal component of gene expression values and represents the gene expression profiles in the module. CRGs, cAMP-responsive genes. The underline of Gene ID indicates that the hub genes belong to the CRGs.