

Supplementary Information Legends

Fig. S1. Process to generate the family nodes and edges from two different single-species coexpression networks. **A)** Genes that are orthologous to each other are grouped. **B)** Gene family nodes are created to represent a group of orthologous genes. Edges are inherited by the new nodes, resulting in pairs of nodes linked by more than one edge. **C)** The previous single-species coexpression edges are replaced by a “gene family” coexpression edge only if all genes within both families are coexpressed ($PCC > 0.7$). In the case some genes are not coexpressed, the gene family nodes are not linked.

Suppl. Table 1. Full set of results from OC analysis in rice, tomato and *A. thaliana*, listing the OCs to which each gene belongs to, if any.

Suppl. Table 2. GO enrichment analysis results of the rice genes in the CCD7/8 OC.

Suppl. Table 3. GO enrichment analysis results of the tomato genes in the CCD7/8 OC.

Suppl. Table 4. Uniprot annotations of the tomato genes in the CCD8 OC.

Suppl. Table 5. Rice and tomato genes in the OC-DEG targeting day 10 from the start phosphate starvation experiment. The Pfam domains, logFC and P-value of each gene is also listed.

Suppl. Table 6. Uniprot annotations of the tomato and rice genes identified in “cluster II” of the untargeted comparative time-series gene expression analysis.