Smita *et al.* Gene regulatory networks associated with lateral root and nodule development in soybean
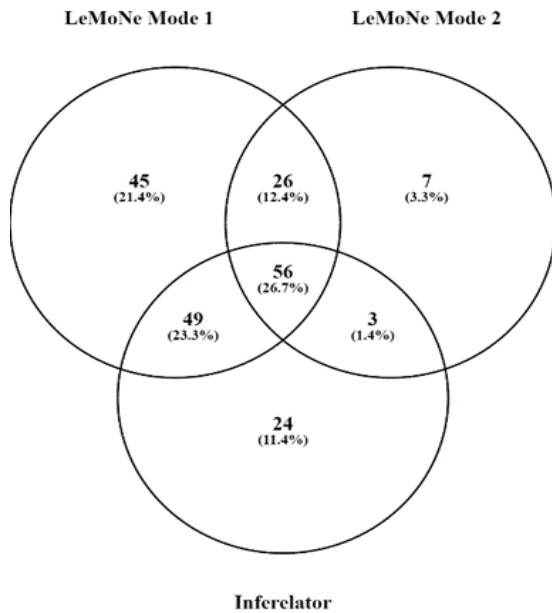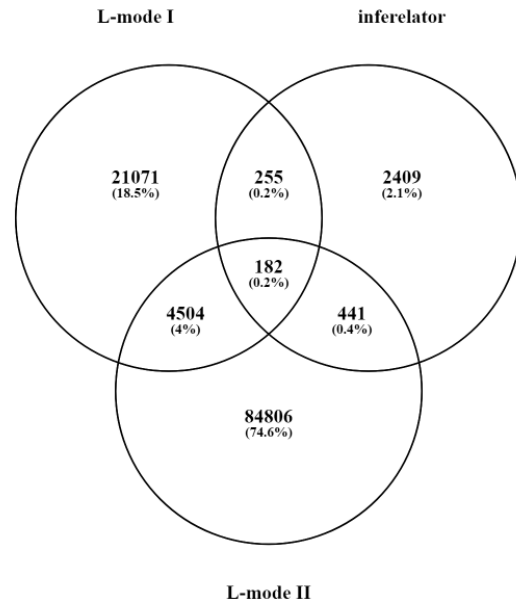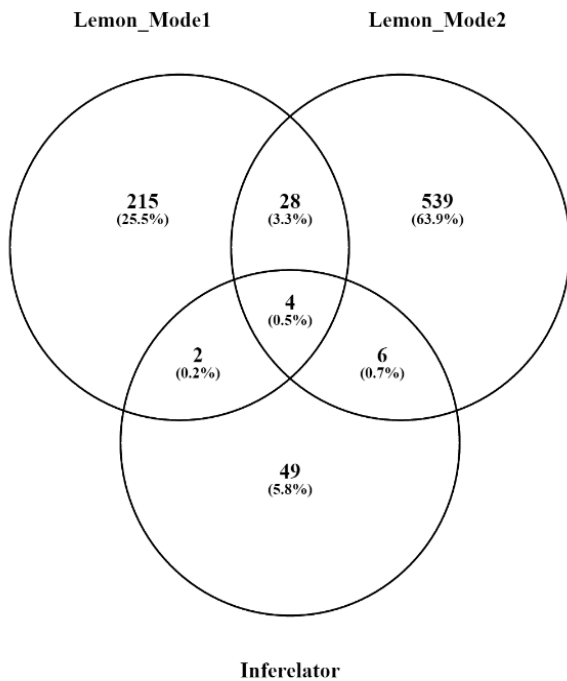
Supplementary Figures

(A – Regulator TFs)
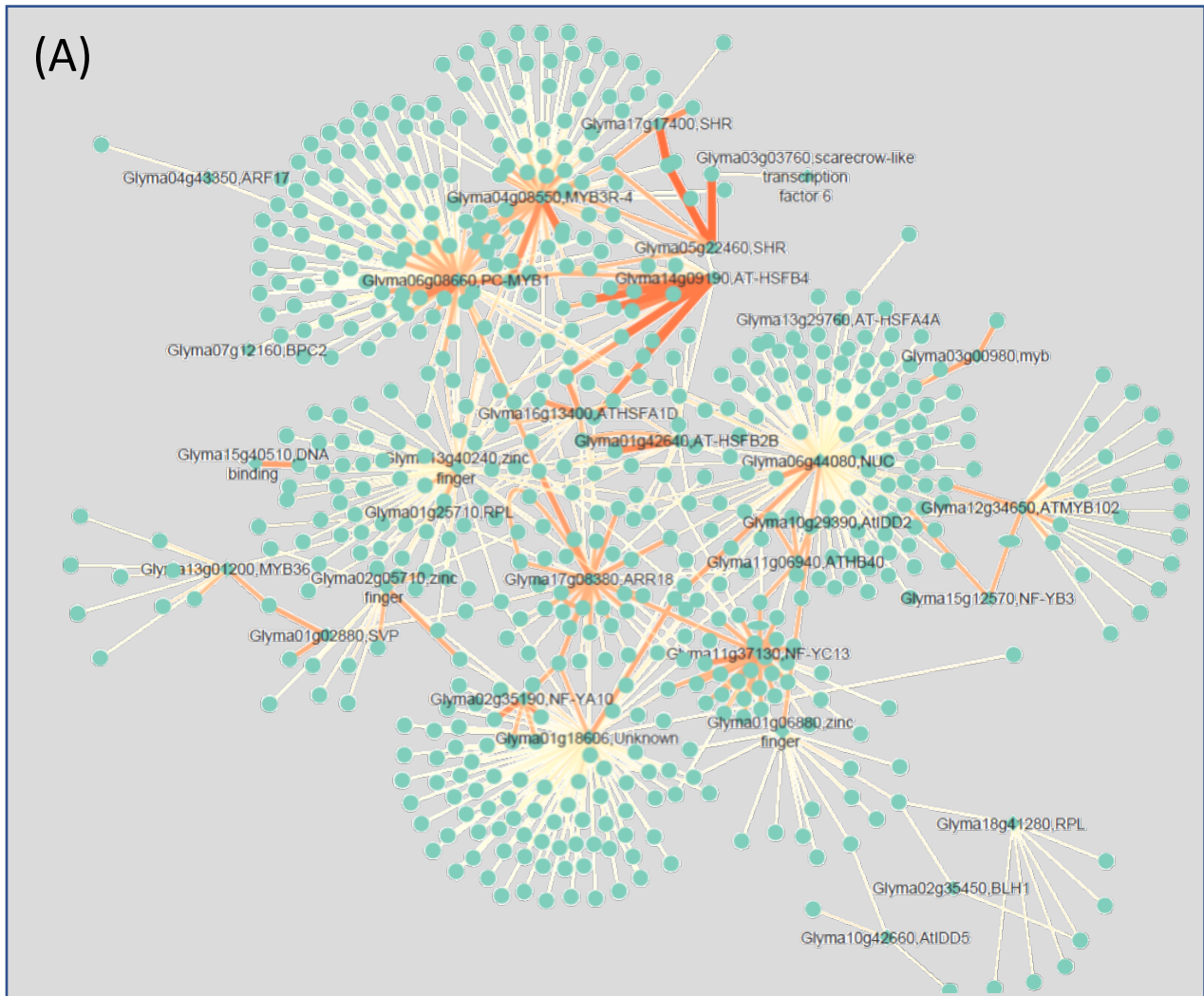

(B – TF-target pairs)

(C – STRING PPIs)

Supplementary Figure 1

Venn diagrams outlining overlaps and differences in the outputs among the three different network approaches: (A) Regulator TF prediction; (B) Identification of targets for predicted TFs; (C) Protein-Protein Interactions.
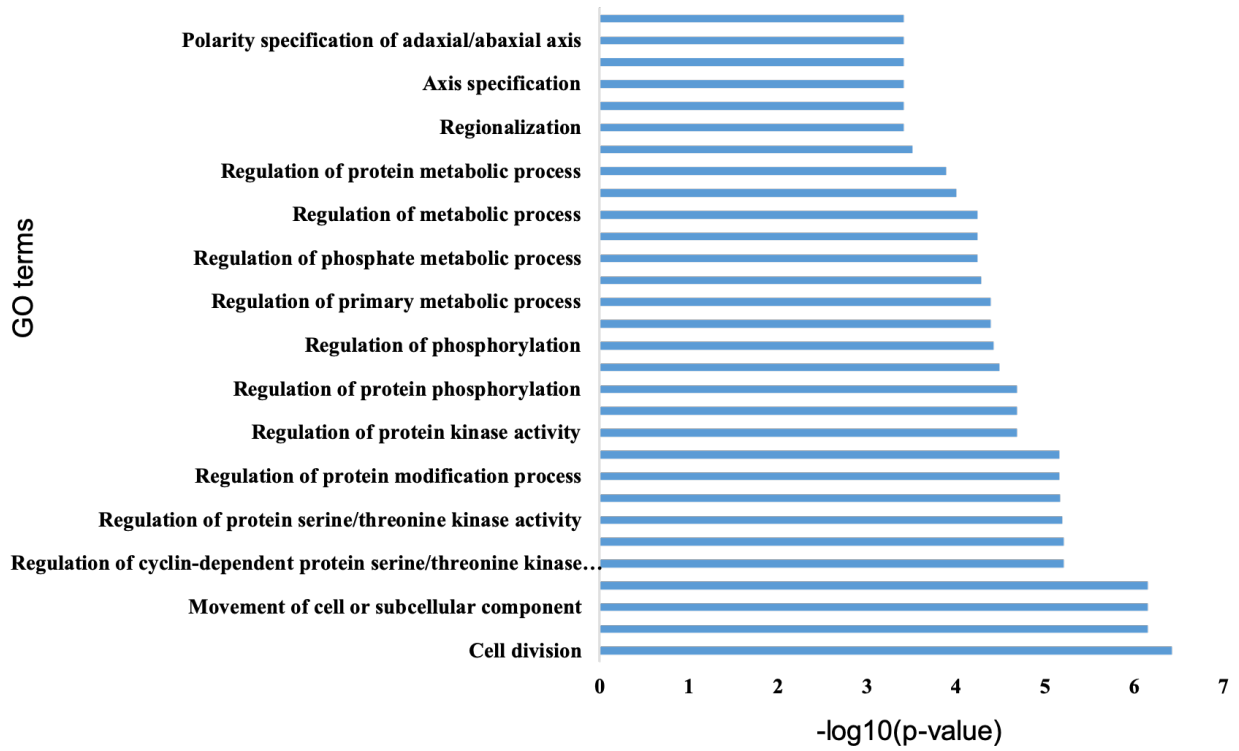
Supplementary Figure 2A

A total of 843 STRING protein-protein interaction (PPI) predictions matched our co-regulatory expression prediction. The large network is shown here and smaller discrete networks are shown in Supplementary Figure 2B.
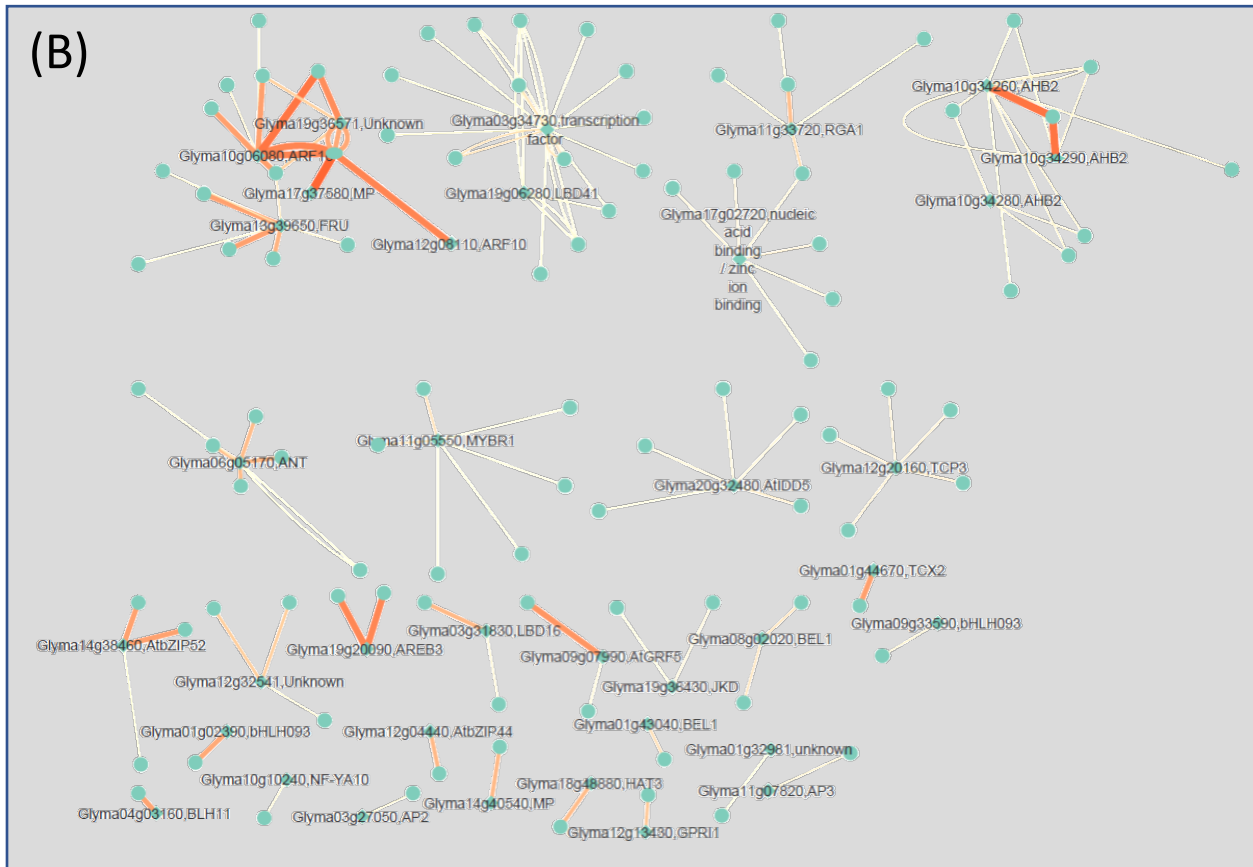
Supplementary Figure 2B

A total of 843 STRING protein-protein interaction (PPI) predictions matched our co-regulatory expression prediction. Smaller discreate networks are shown here and the large network is shown in Supplementary Figure 2A.

Supplementary Figure 3

Gene Ontology biological process enrichment of target genes in consensus 182 co-regulatory gene network predicted for root lateral organ development in soybean.