

Supplementary material

Supplemental Figure 1. Primary root growth of maize seedlings is inhibited by auxin. Five days after germination (DAG) maize seedlings exhibiting shortened primary root growth when treated with 10 μ M indole-3-acetic acid (IAA) dissolved in 95% ethanol versus seedlings mock-treated with an equivalent volume of 95% ethanol for two days. Scale bar = 1 cm.

Supplemental Figure 2. UpSet plots of differentially expressed genes within maize root regions in response to auxin treatment at 30 min (t30) and 120 min (t120) when compared to mock. treatment (A) UpSet plot of genes with increased levels of transcript. (B) UpSet plot of genes with decreased levels of transcript. Only the top 20 most populated intersections are visualized. Abbreviations used: C = cortex, S = stele, EZ = elongation zone, MZ = meristem zone.

Supplemental Figure 3. UpSet plot comparing differentially expressed genes across maize root regions in “mock” treated samples. Only the top 50 most populated intersections are visualized. Abbreviations used: C = cortex, S = stele, EZ = elongation zone, MZ = meristem zone, up = up-regulated genes, down = down-regulated genes. Concordant gene expression differences are indicated in bluish green while discordant gene expression differences are in vermillion.

Supplemental Figure 4. Gene ontology (GO) terms enriched in differentially expressed genes between root regions profiled. Comparisons are indicated such that control condition is first and the control is second. For example, “S/C up” means that transcripts up in the stele (S) relative to the cortex (C) are enriched for the indicated GO terms. Abbreviations used: FDR = false discovery rate, C = cortex, S = stele, EZ = elongation zone, MZ = meristem zone, up = up-regulated genes in both tissues, down = down-regulated genes in both tissues. FDR values are colored according to the heatmap shown, going from blue to red.

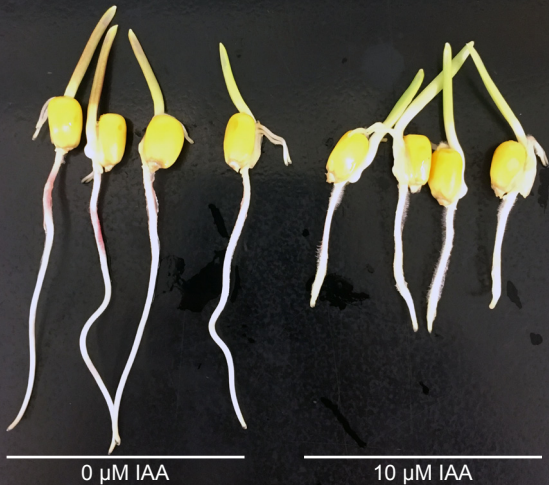
Supplemental Table 1. Differential expression analysis data from QuantSeq 3' mRNA-Seq. Workbook contains TMM-normalized expression values for all samples analysed with each additional sheet containing statistical analysis values for each pairwise comparison generated by PoissonSeq.

Supplemental Table 2. Gene Ontology (GO) enrichment analysis data of comparisons within tissue mock +IAA treated samples as well as between tissue samples.

Supplemental Table 3. Full gene regulatory network data. Independent Component Analysis (ICA) clustering assignments, SC-ION adapted GENIE3 output table, assigned tissue enrichment by cluster, and Cytoscape node table export data.

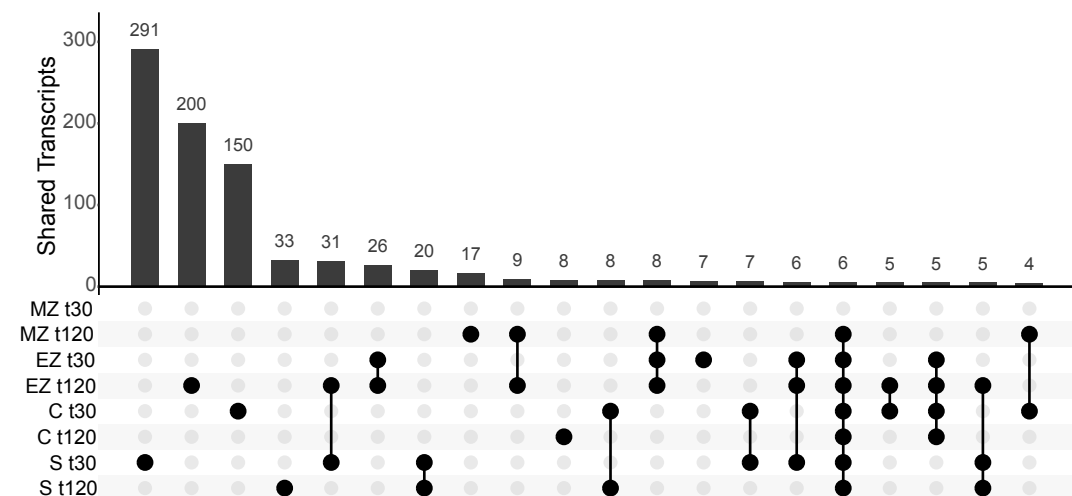
Supplemental Table 4. Auxin Response Factor (ARF) subnetwork data. SC-ION adapted GENIE3 output table and Cytoscape node table export data.

Supplemental Figure 1

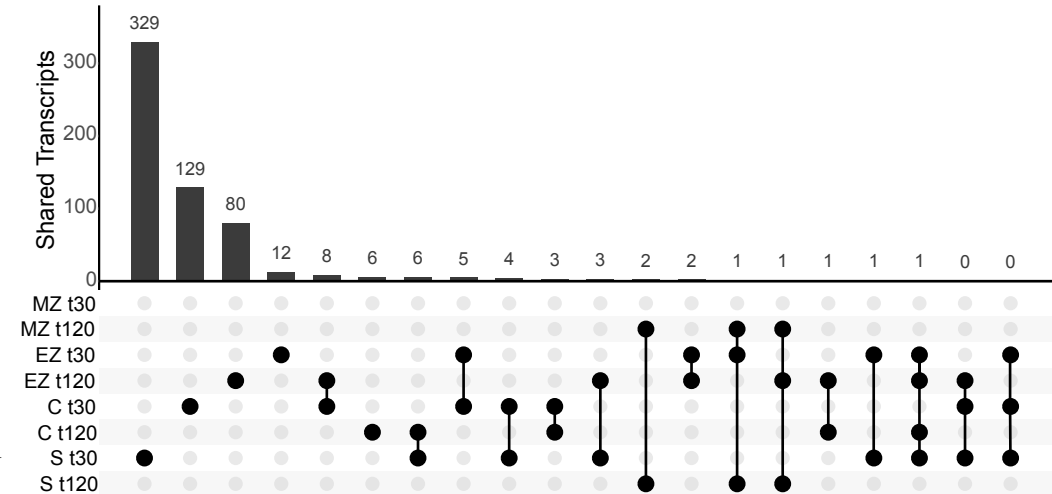


Supplemental Figure 2

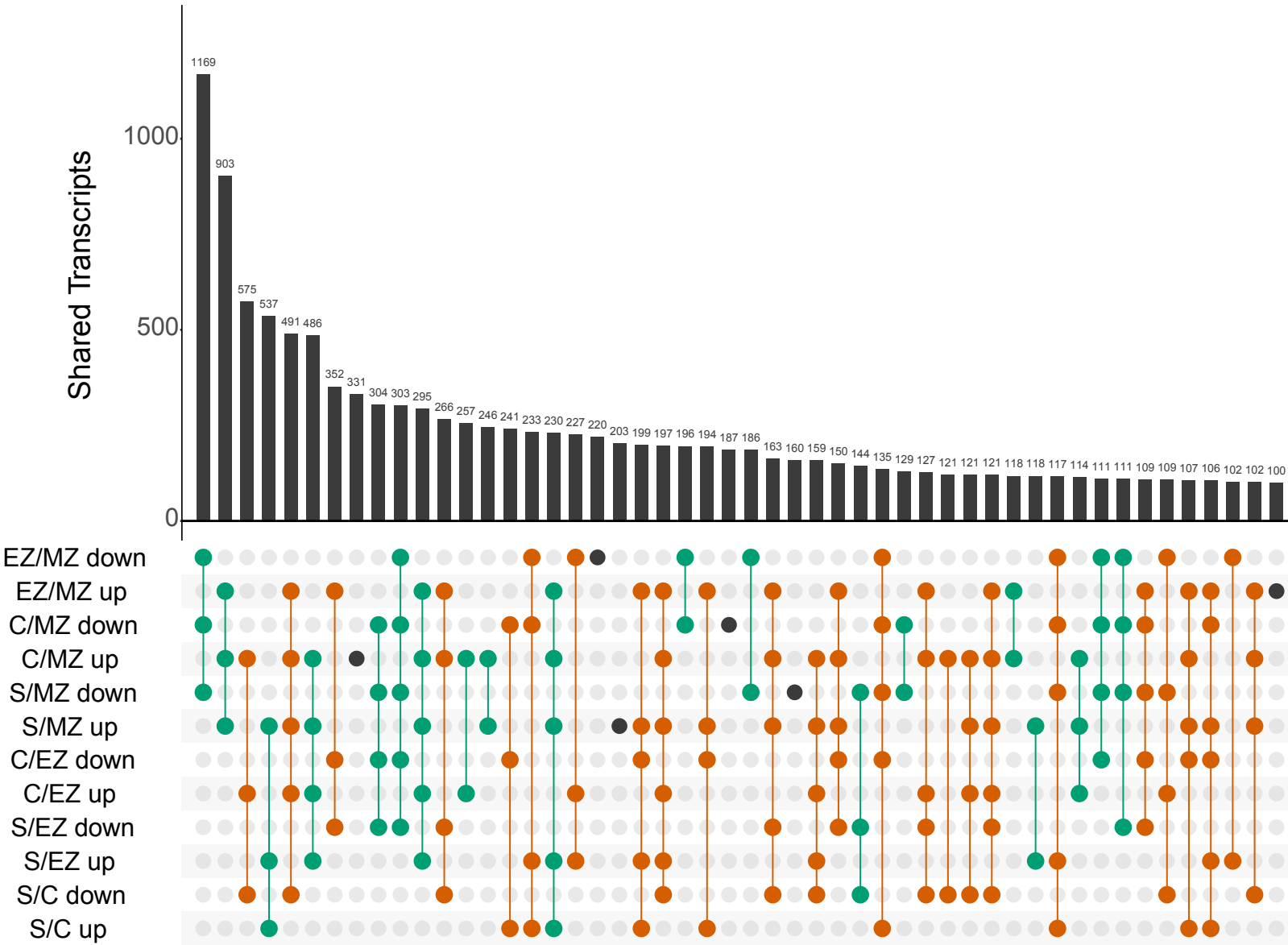
A



B



Supplemental Figure 3



Supplemental Figure 4

