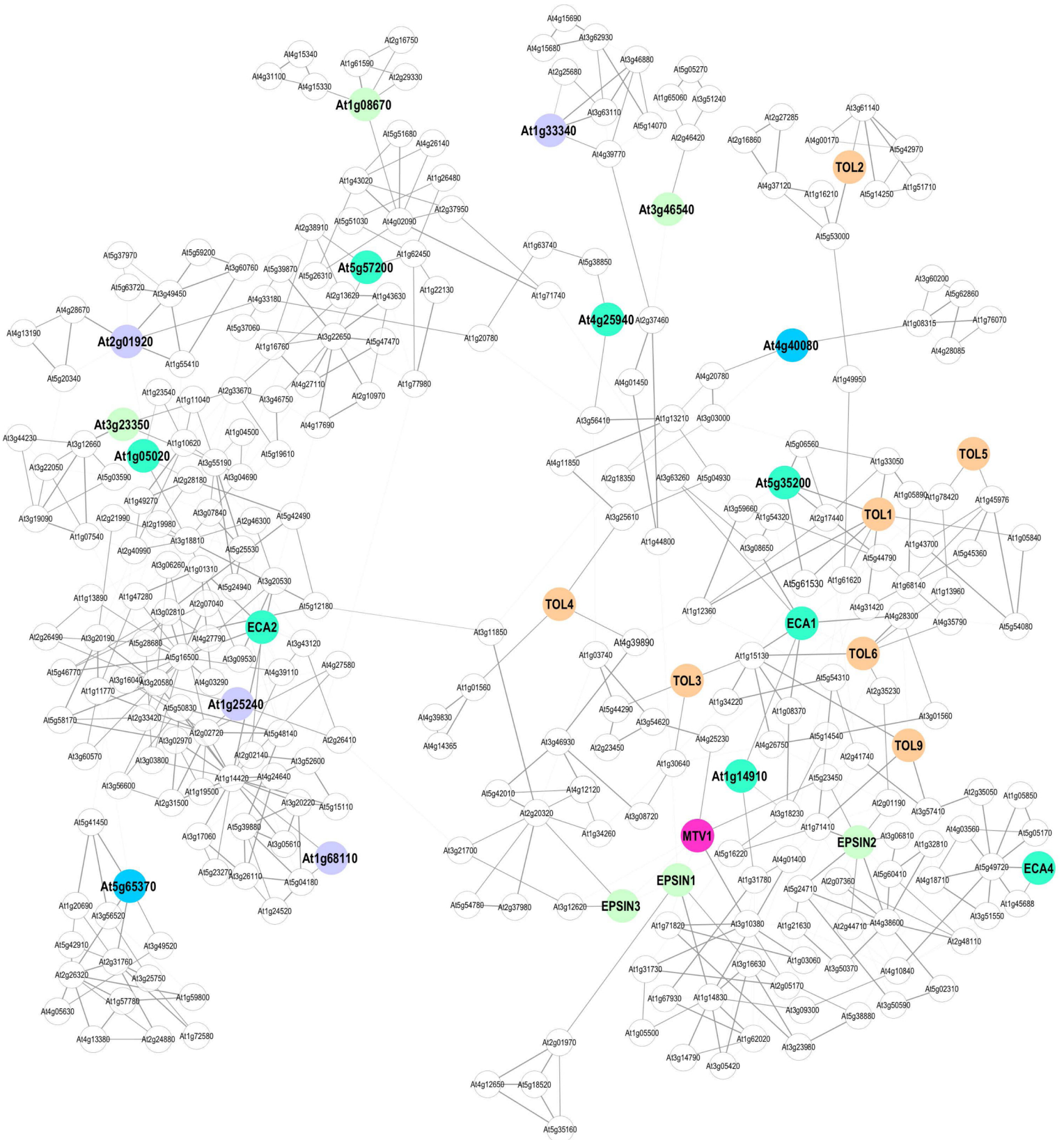


Supplemental Figure 1

Phylogenetic analysis of only the first 200 amino acids

Maximum likelihood tree of 35 Arabidopsis ENTH/ANTH/VHS domain containing genes, using an alignment of only the first 200 amino acids of each protein with essentially the same tree topology as the full length tree of Figure 1. See methods section for details of analysis. Common name in bold, preceding the AGI. Groups colored like in Figure 1.



Supplemental Figure 2.
Transcriptional network analysis as in Figure 2 with all gene identifiers displayed.