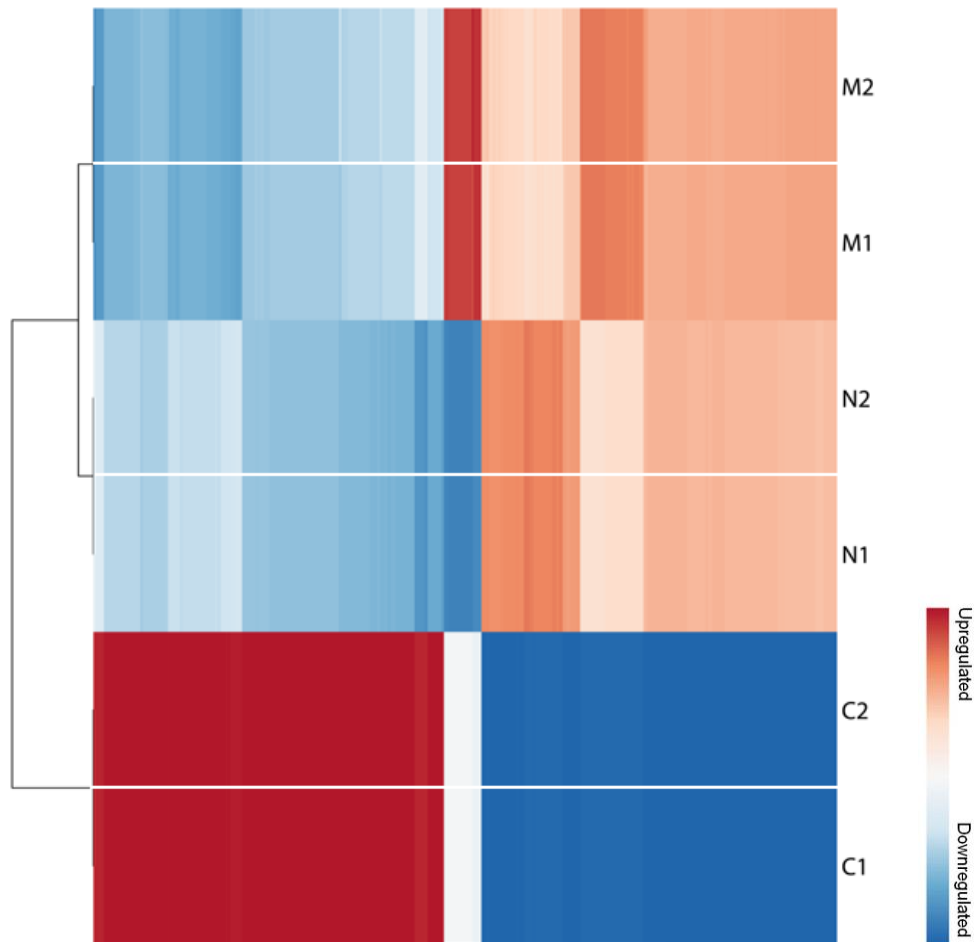S2 Fig. Heatmap showing hierarchical clustering based on expression values of the transcripts in control, mycorrhized, and nodulated root samples. Expression data from two biological replicates (1 and 2) of mycorrhized (M), nodulated (N), and control (C) roots were used. Hierarchical clustering results were visualized using TreeView by Clustvis web tool.