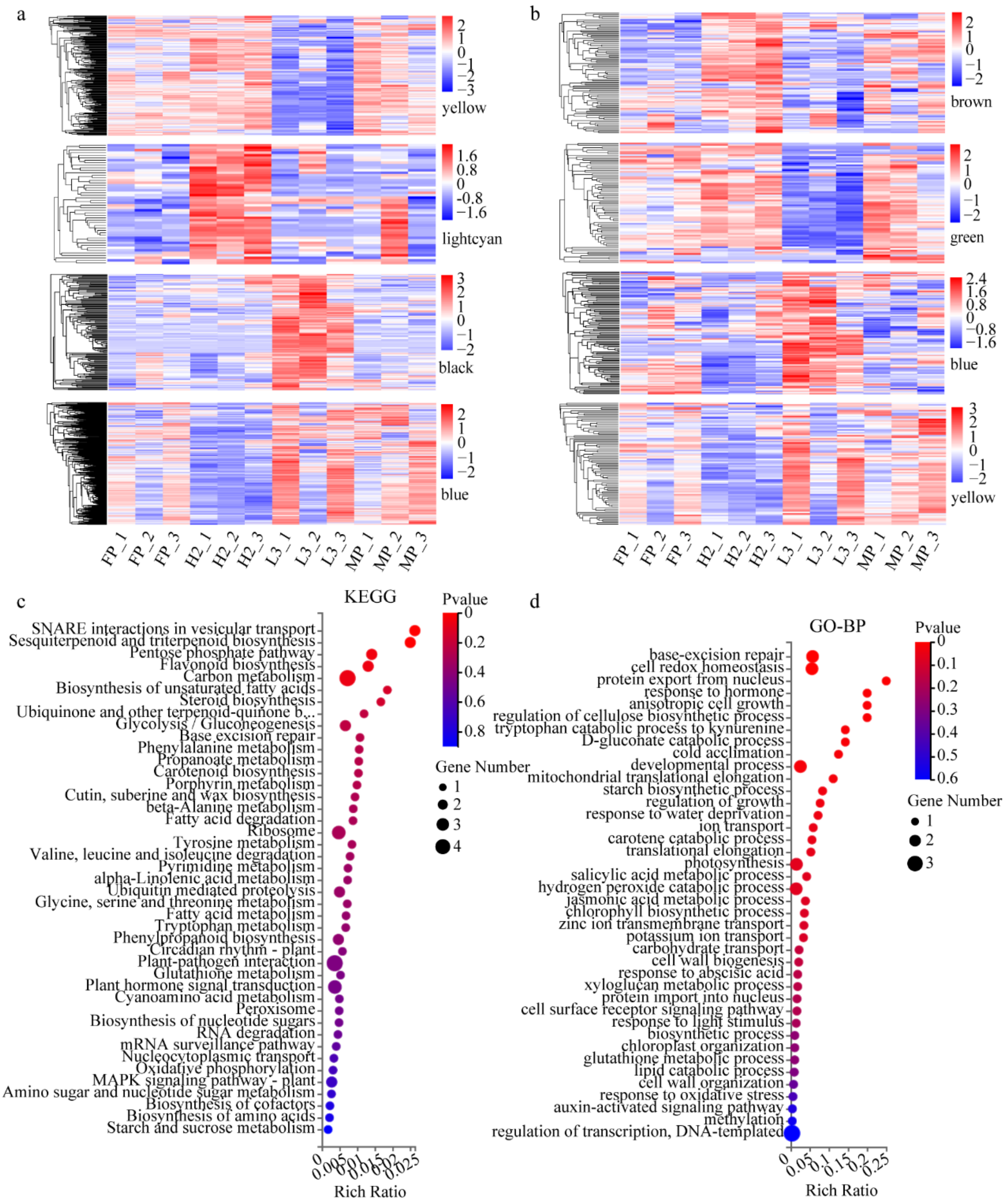

Supplementary Fig. 5 Gene heatmap of 8 key modules regulating growth in WGCNA.

(a) 4 modules significantly correlated with growth in parental SMRs. (b) 4 modules significantly correlated with growth in parental DMRs. (c) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis and (d) Gene Ontology (GO) in the biological processes (BP) function annotations of genes in co-expression network.