

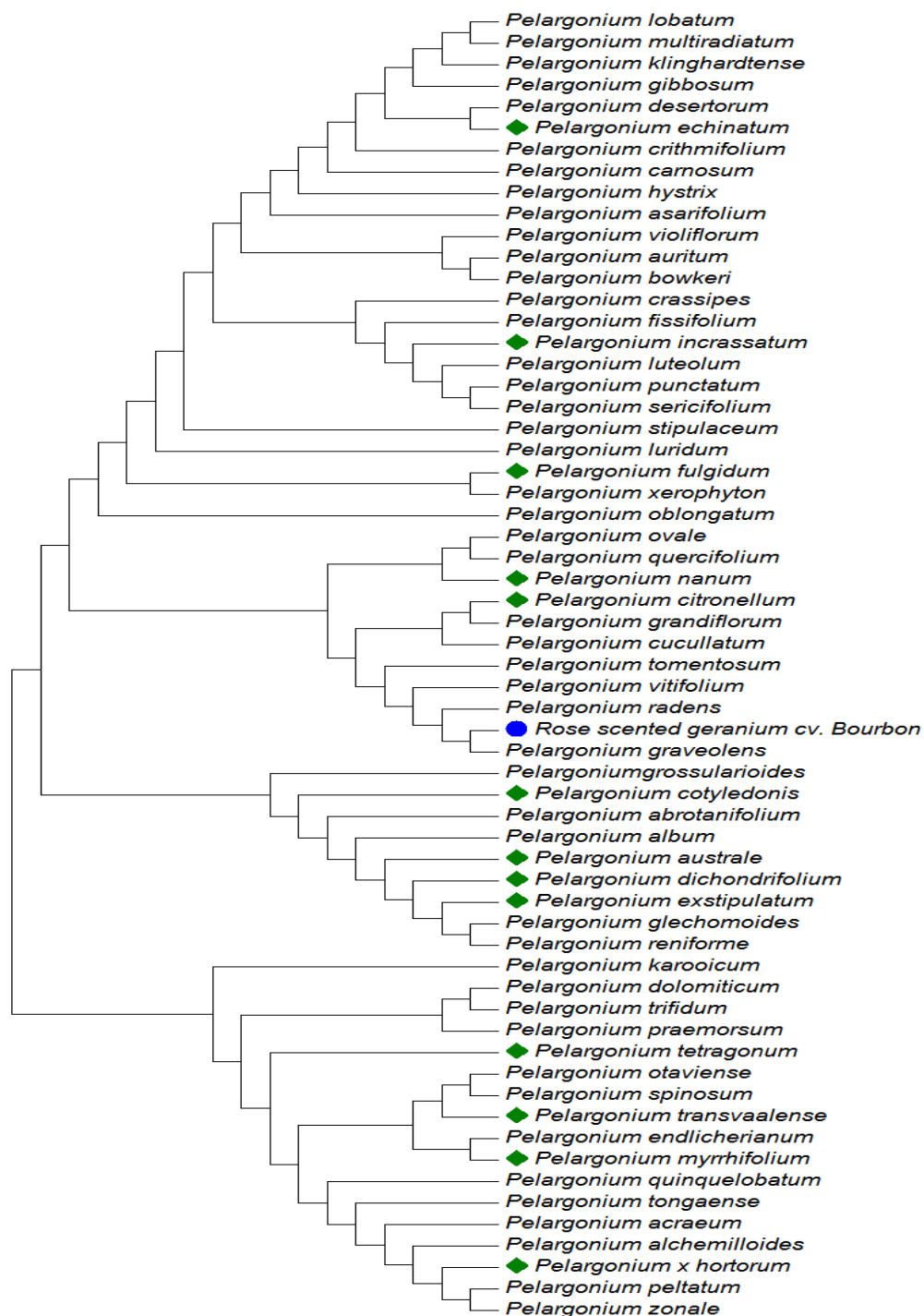
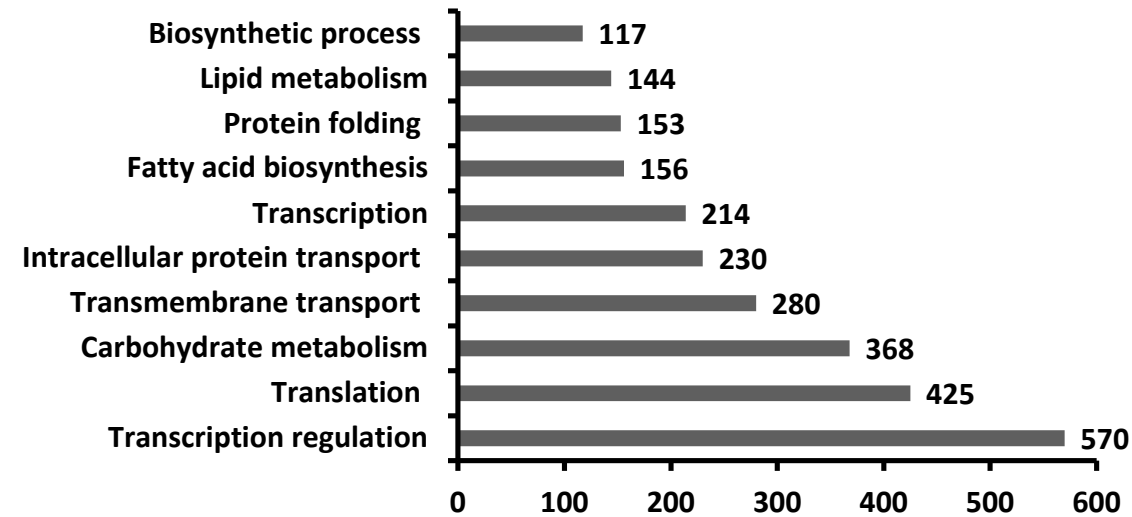


Figure S1 A phylogenetic tree generated on the basis of a plastid marker *trnL-F* in 57 *Pelargonium* species, and rose-scented geranium cv. Bourbon. The molecular phylogenetic analysis was done by Maximum Likelihood method method based on the Tamura-Nei model [1], by using MEGA7 [2]. The nucleotide sequence information of *trnL-F* in 57 *Pelargonium* species was extracted from NCBI, and that of rose-scented geranium cv. Bourbon (marked with blue bullet) was taken from the transcriptome assembly data. The 13 *Pelargonium* species, for which raw sequencing reads are available in SRA database, are marked with green bullets in the phylogenetic analysis to show its possible genetic distance from rose-scented geranium cv. Bourbon

Reference:

1. Tamura K and Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* 1993; 10:512-526.
2. Kumar S, Stecher G, and Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 2016; 33:1870-1874.

Biological process



Molecular function

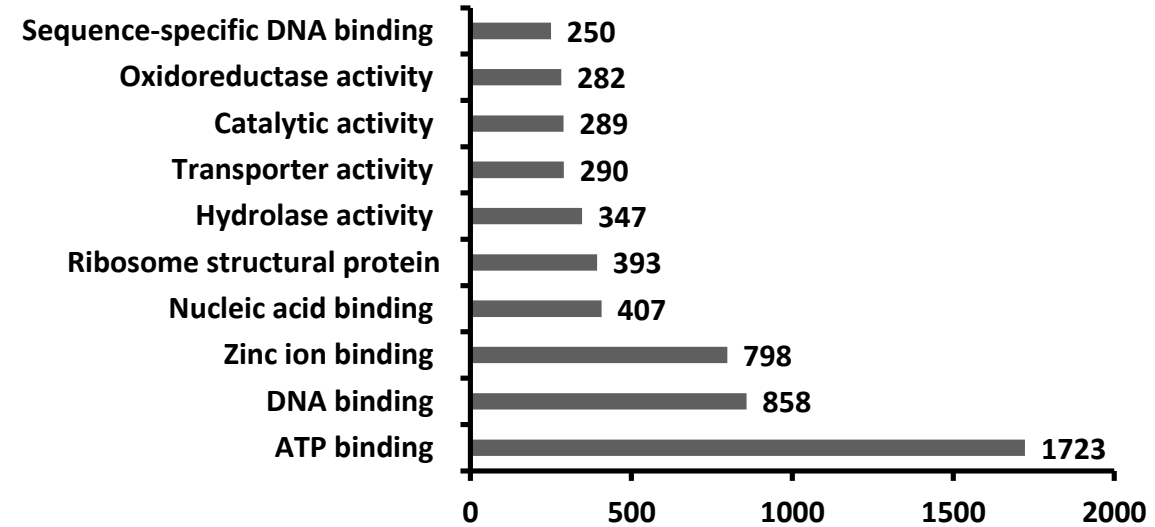
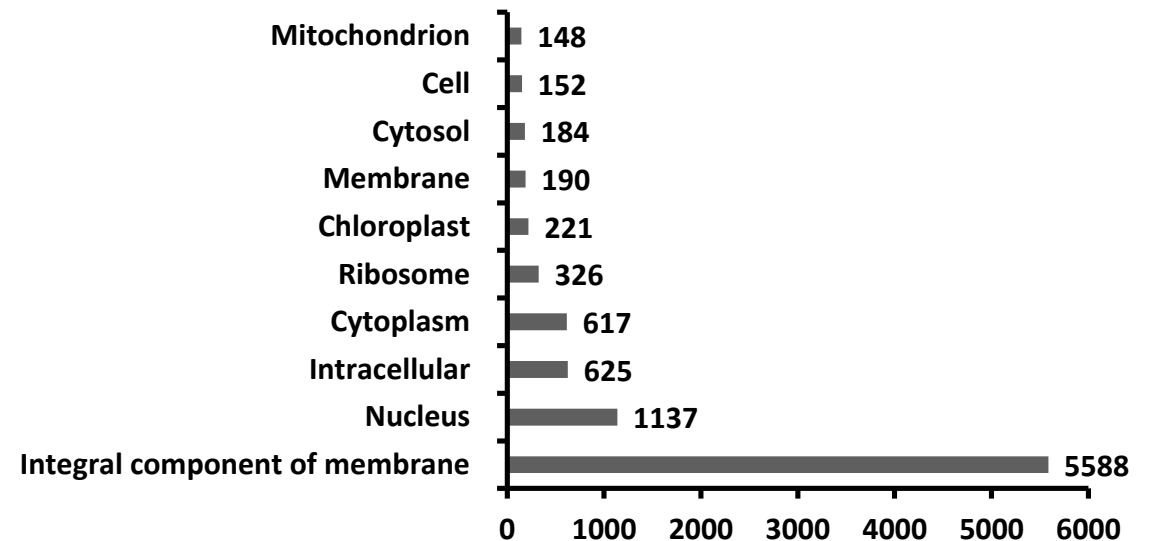


Figure S2 Categorization of rose-scented geranium transcriptome contigs based on gene ontology (biological processes, cellular components and molecular functions). Top 10 hits of each categories presented here.

Cellular component



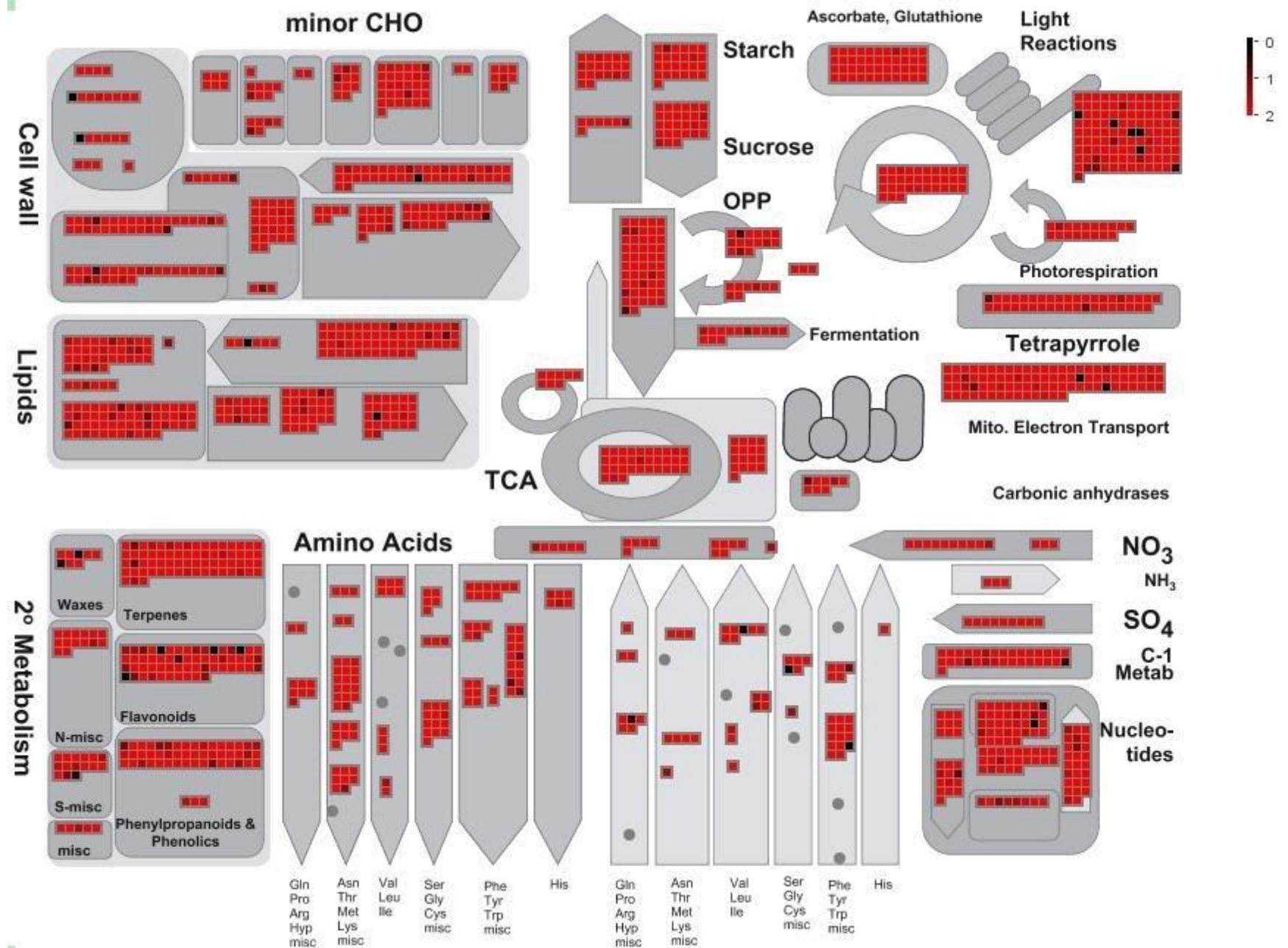


Figure S3 MapMan visualized genes associated with primary metabolic biosynthesis pathways.

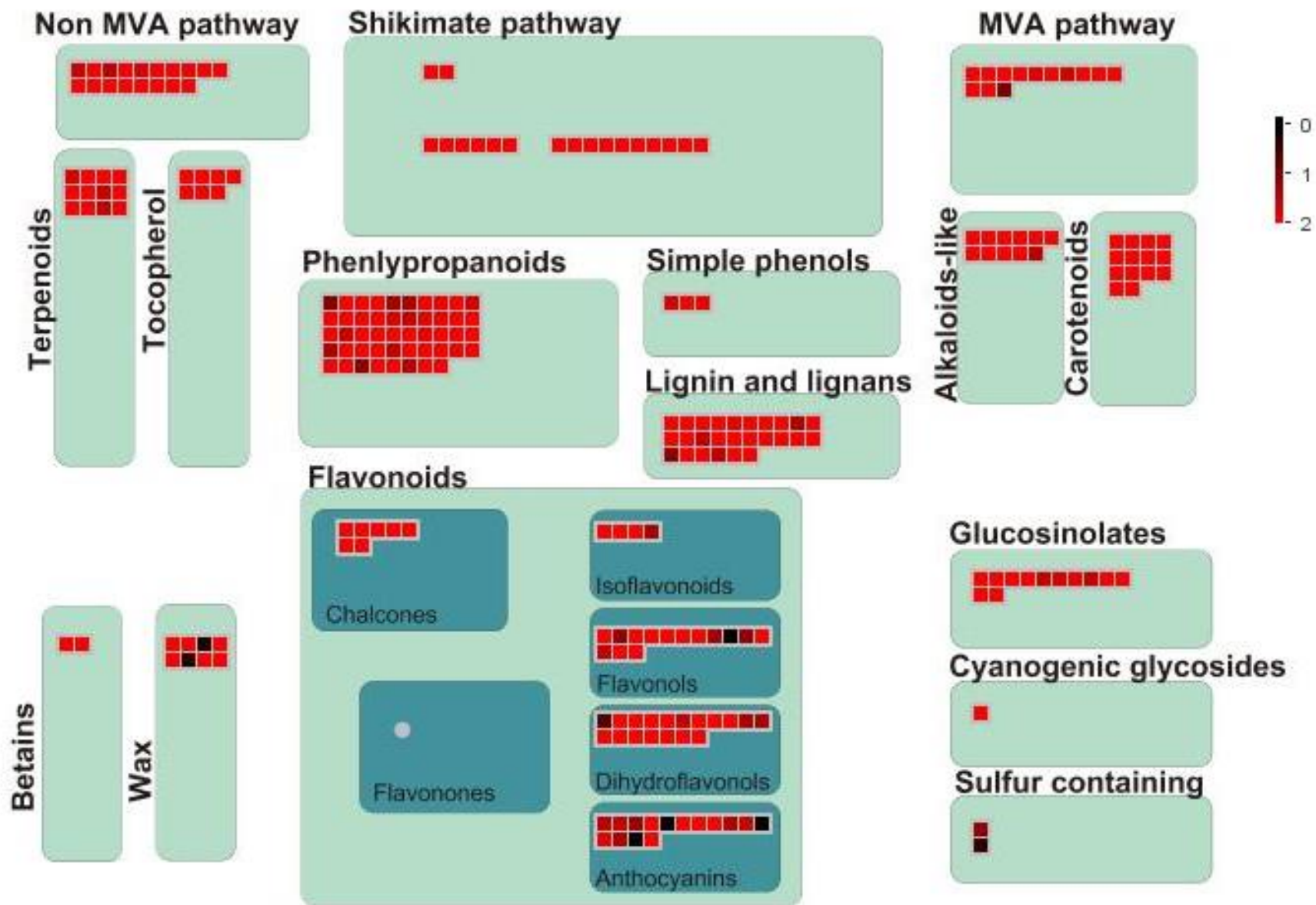
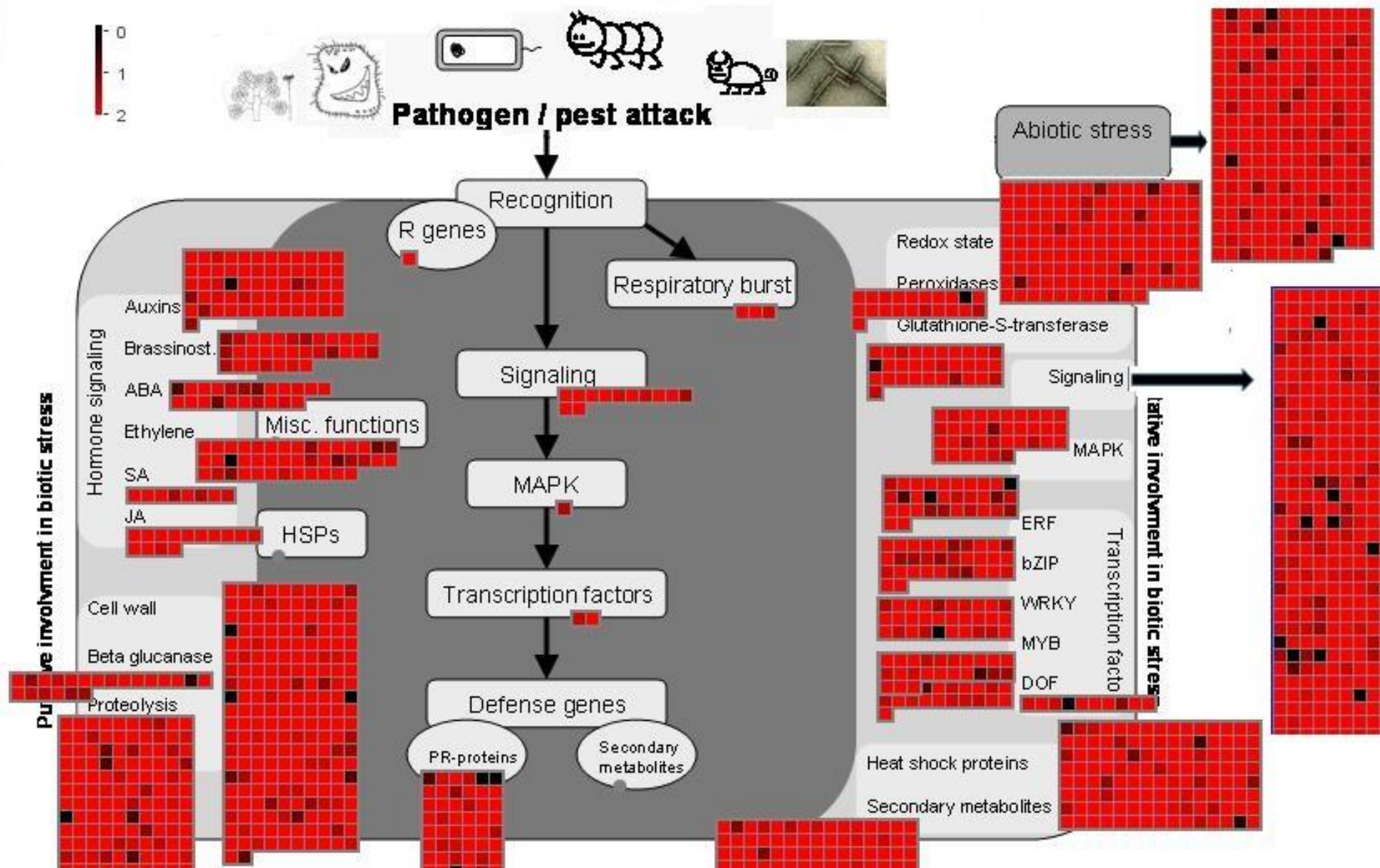


Figure S4 MapMan visualized genes associated with secondary metabolic biosynthesis pathways.



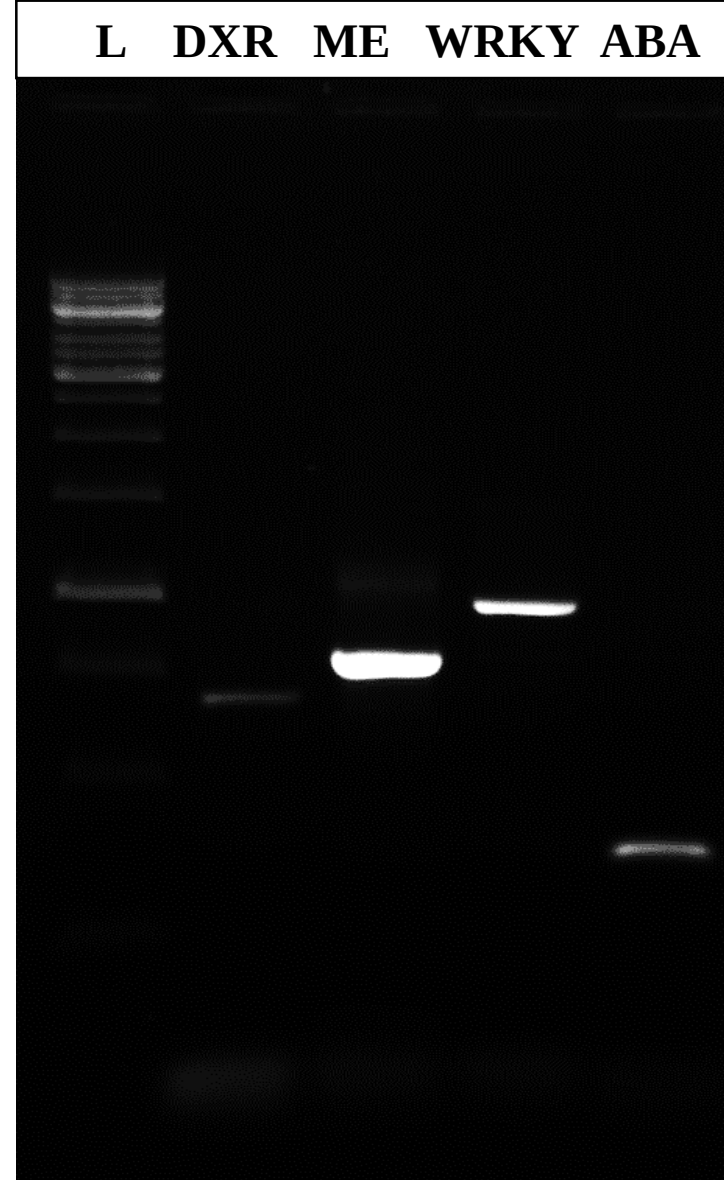


Figure S6 PCR amplifications of selected putative genes for assembly validation. Ladder; DXR- 1-Deoxy- D -xylulose 5-phosphate reductoisomerase; ME- GDP-mannose-3',5'-epimerase; WRKY- WRKY transcription factor and ABA- Absciscic acid biosynthesis (Zeaxanthin epoxidase).

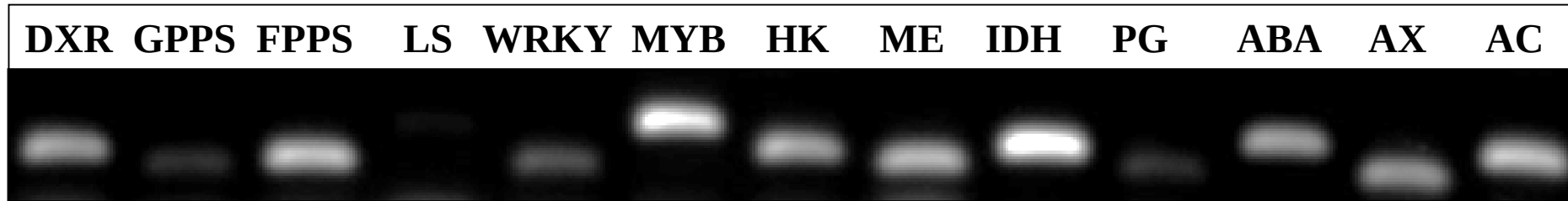


Figure S7 Semi-quantitative PCR analysis of selected putative genes. DXR- 1-Deoxy- D -xylulose 5-phosphate reductoisomerase; GPPS- Geranyl diphosphate synthase; FPPS- Farnesyl pyrophosphate synthase; LS- Linalool synthase; WRKY- WRKY transcription factor; MYB- MYB transcription factor; HK- Hexokinase; ME- GDP-mannose-3',5'-epimerase; IDH- L-Idonate 5-dehydrogenase; PG- Polygalacturonase; ABA- Absciscic acid biosynthesis (Zeaxanthin epoxidase); AX- Auxin biosynthesis (Cytochrome P₄₅₀) and AC- Actin