Figure S4

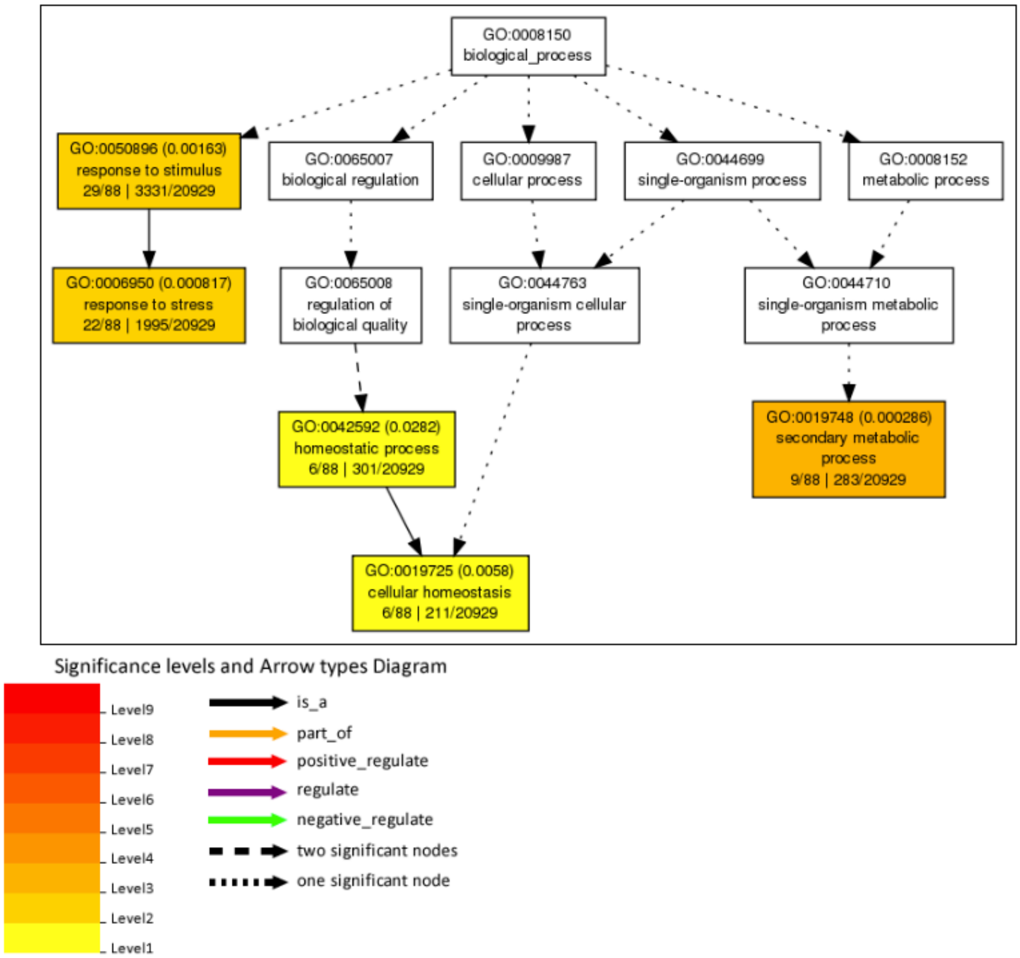


Figure S4. Results of Singular Enrichment Analysis (SEA) for the 88 out of 115 up-regulated transcripts between 1103P and SO4 grown in absence of Mg (-Mg) for 4 days with GO terms; the analysis was performed using agriGO v2.0 [126] using the locus ID (Gramene Release 5.0) as reference, Fisher as statistical test method, Yekutieli (FDR under dependency) as Multi-test adjustment method, 0.05 as significant level, 5 as minimum number of mapping entries and Plant GO slim as Gene Ontology type.

Figure S5

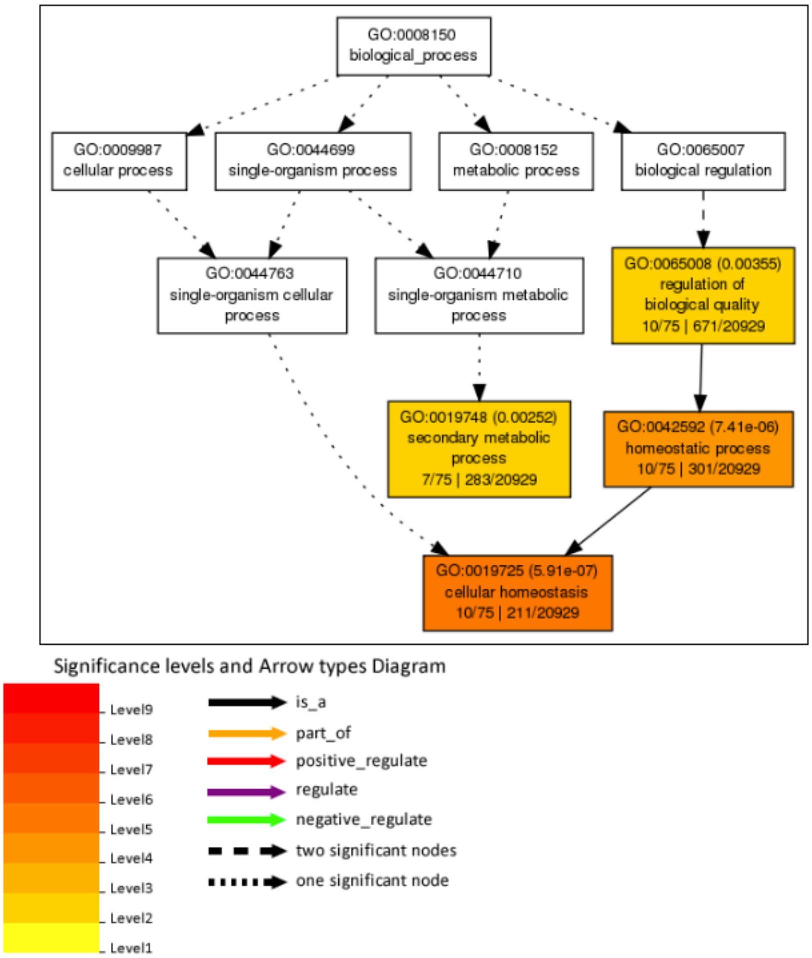


Figure S5. Results of Singular Enrichment Analysis (SEA) for the 75 out of 104 down-regulated transcripts between 1103P and SO4 grown in absence of Mg (-Mg) for 4 days with GO terms; the analysis was performed using agriGO v2.0 [126] using the locus ID (Gramene Release 5.0) as reference, Fisher as statistical test method, Yekutieli (FDR under dependency) as Multi-test adjustment method, 0.05 as significant level, 5 as minimum number of mapping entries and Plant GO slim as Gene Ontology type.

Figure S6

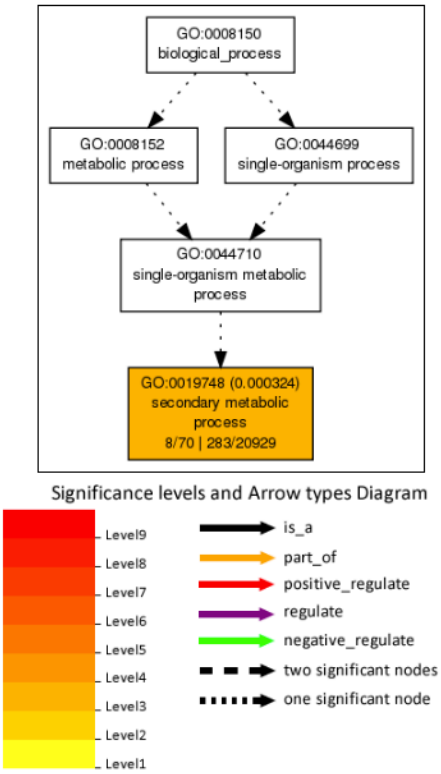


Figure S6. Results of Singular Enrichment Analysis (SEA) for the 70 out of 128 up-regulated transcripts between 1103P and SO4 grown in absence of Mg (-Mg) for 14 days with GO terms; the analysis was performed using agriGO v2.0 [126] using the locus ID (Gramene Release 5.0) as reference, Fisher as statistical test method, Yekutieli (FDR under dependency) as Multi-test adjustment method, 0.05 as significant level, 5 as minimum number of mapping entries and Plant GO slim as Gene Ontology type.

Figure S7

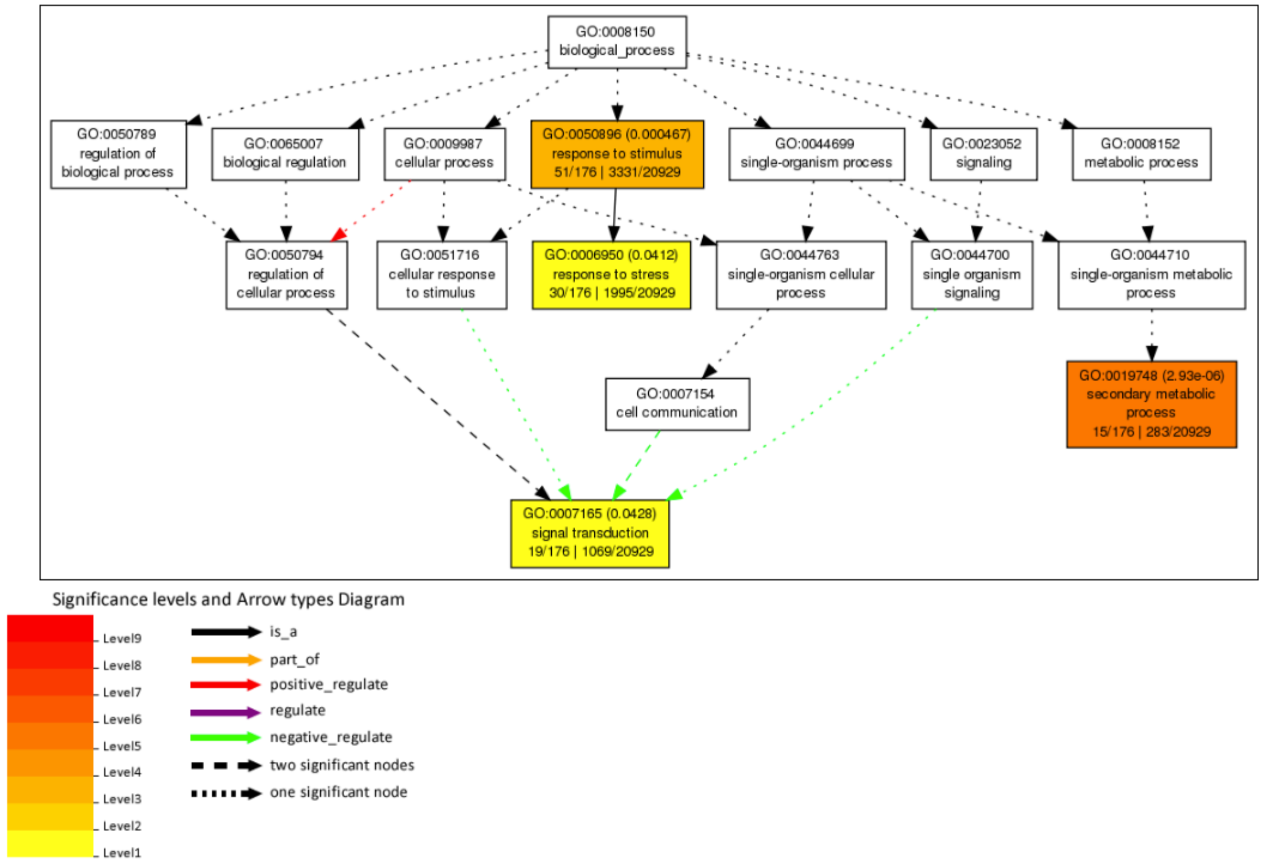
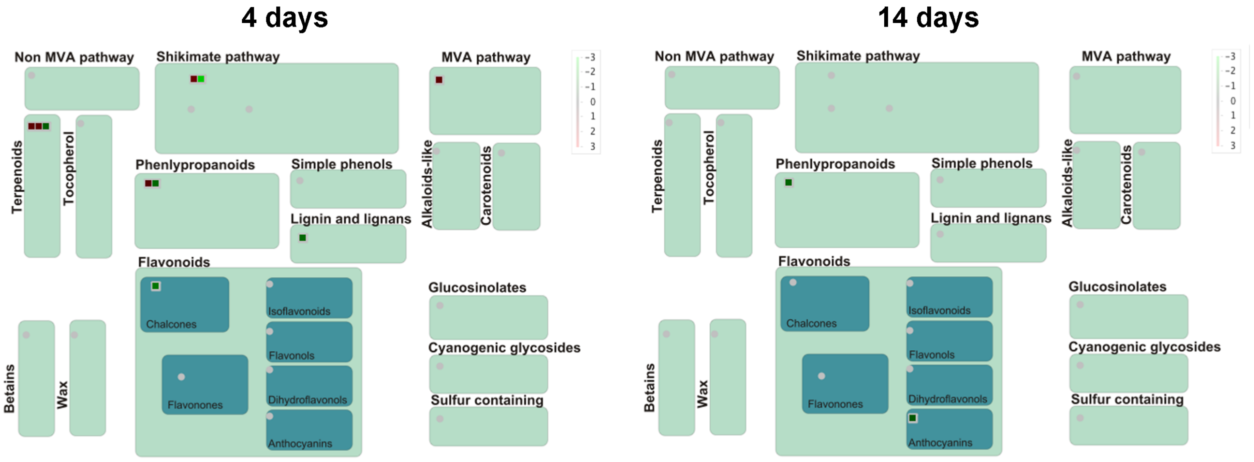


Figure S7. Results of Singular Enrichment Analysis (SEA) for the 176 out of 233 down-regulated transcripts between 1103P and SO4 grown in absence of Mg (-Mg) for 14 days with GO terms; the analysis was performed using agriGO v2.0 [126] using the locus ID (Gramene Release 5.0) as reference, Fisher as statistical test method, Yekutieli (FDR under dependency) as Multi-test adjustment method, 0.05 as significant level, 5 as minimum number of mapping entries and Plant GO slim as Gene Ontology type.

Figure S8


4 days

14 days

Figure S8. MapMan overview display of differentially expressed transcripts between 1103P and SO4 concerning the secondary metabolism. The Log_2(ratio) is shown by the color scale (green indicates a decrease and red an increase in transcript abundance between 1103P and SO4). The analysis was carried out using MapMan software [123].