

***New Phytologist* Supporting Information**

Article title: **Drought resistance is mediated by divergent strategies in closely related Brassicaceae**

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Supporting Information

Fig. S1 Effects of severe water deficit on photosynthetic efficiency and survival.

Fig. S2 Growth rates dynamics.

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Table S1 Overview of phenotypic characteristics (separate file).

Table S2 Differential regulated genes and GO enrichment (separate file).

Table S3 Orthologue relationships and complete expression matrix (separate file).

Table S4 Dynamic of transcriptional changes of drought-induced genes (separate file).

Table S5 Significant GO terms of dynamic transcriptional changes (separate file).

Table S6 Not shared GO terms and KEGG pathways at T11 (separate file).

Table S7 Significant GO terms and KEGG pathways of modules (separate file).

Table S8 Gene abundance of histone modification genes (separate file).

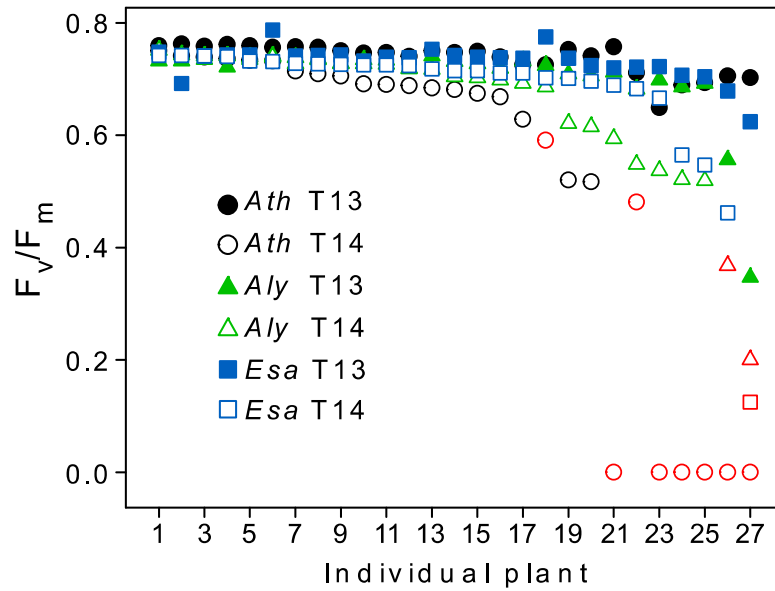
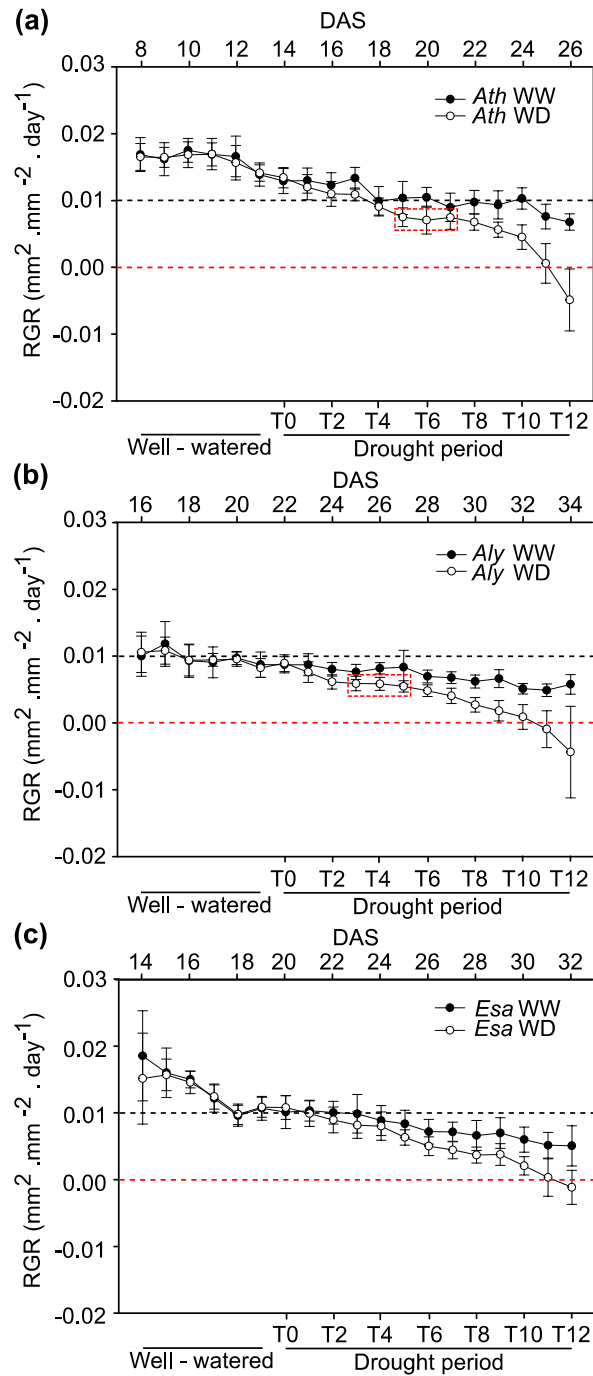


Fig. S1 Effects of severe water deficit on photosynthetic efficiency and survival. F_v/F_m ratio of individual plants at T13 and T14 (just before re-watering); red labeled individuals did not recover 3 days after re-watering. *Ath*, *Arabidopsis thaliana*. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*.



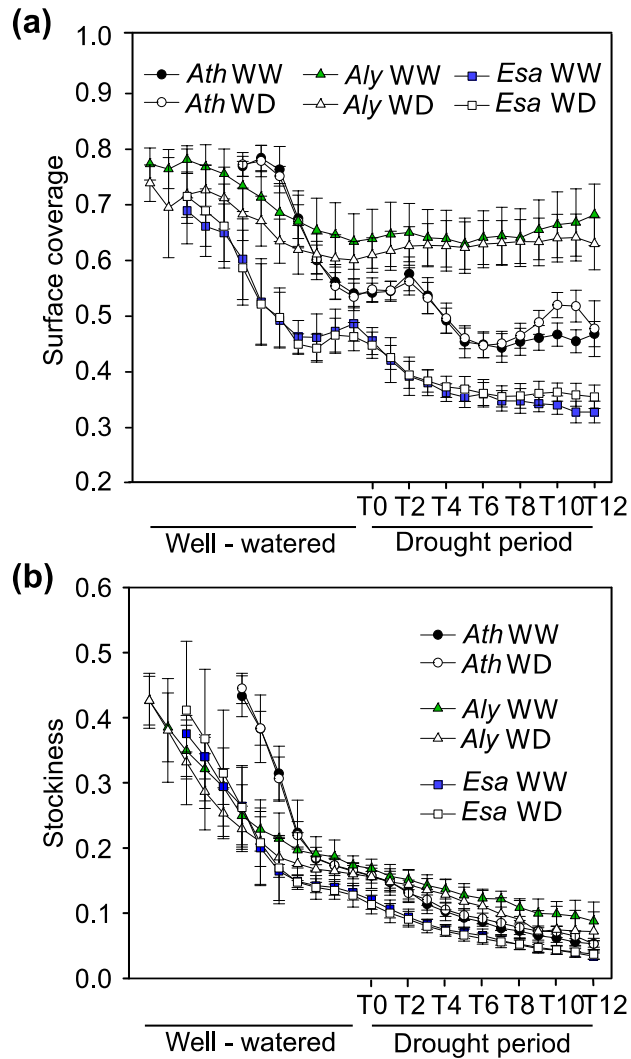


Fig. S3 Rosette morphology parameters. (a) Rosette surface coverage over time. Measure indicates occupancy of the rosette in the convex hull area. (b) Stockiness over time. Measure denotes rosette roundness. $n > 25$ plants per time point and treatment; data are represented as mean \pm SD. WW, well-watered. WD, water deficit. *Ath*, *Arabidopsis thaliana*. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*.

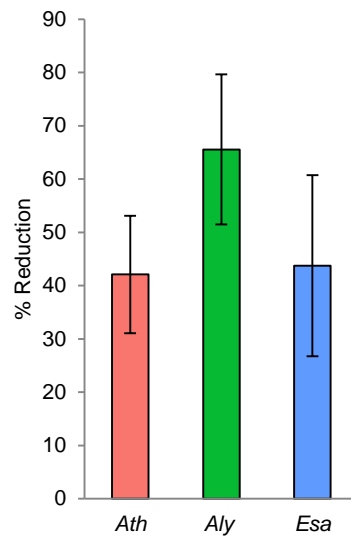


Fig. S4 Reduction in area of detached leaves at T11. The decrease in leaves area is expressed as percent. ($n = 10$ plants per species and treatment; data are represented as mean \pm SD). *Ath*, *Arabidopsis thaliana*. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*.

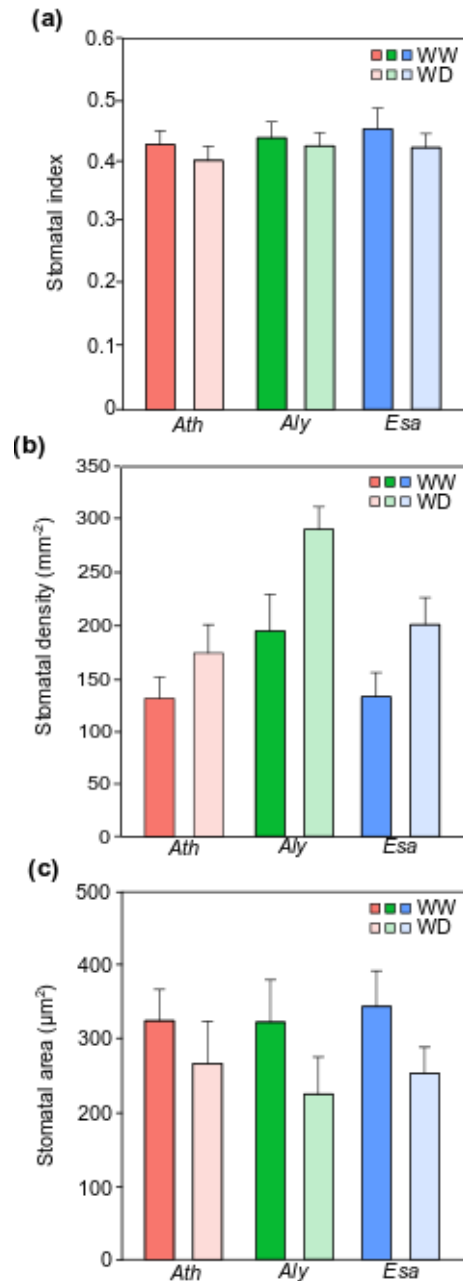


Fig. S5 Measurements of stomatal parameters. (a) Stomatal index, (b) stomatal density and (c) stomatal area of leaf six at WW (well-watered) and WD (water deficit) conditions ($n = 5 - 8$ plants per species and treatment). Data are represented as mean \pm SD. *Ath*, *Arabidopsis thaliana*. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*. Numeric data provided in Table S1.

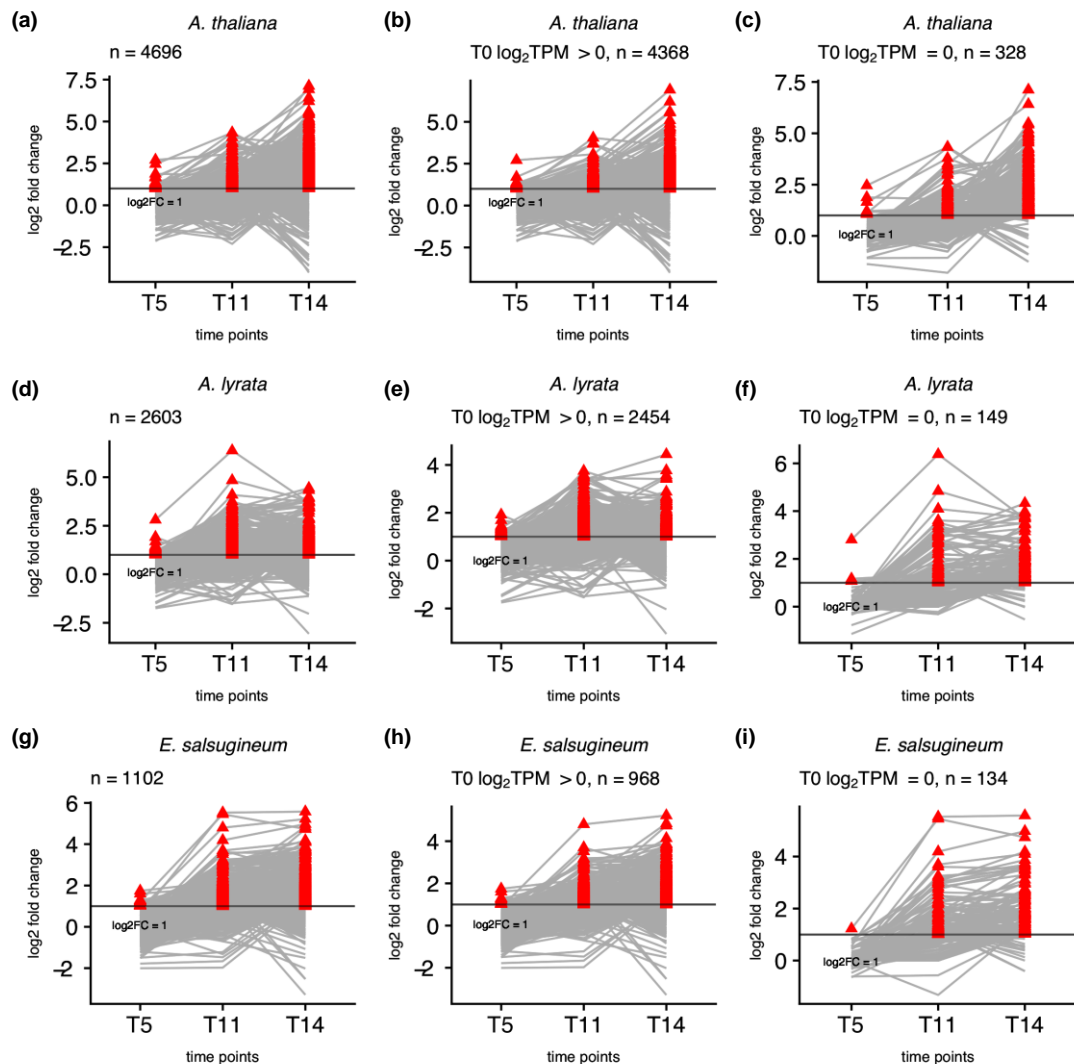


Fig. S6 Dynamic of transcriptional changes. Upregulated genes (T5-T14) were classified into not expressed at T0 (log₂TPM = 0; basal -) and expressed at T0 (log₂TPM > 0; basal +). *Ath* upregulated (a), *Ath* basal + (b), *Ath* basal - (c), *Aly* upregulated (d), *Aly* basal + (e), *Aly* basal - (f), *Esa* upregulated (g), *Aly* basal + (h), *Aly* basal - (i).

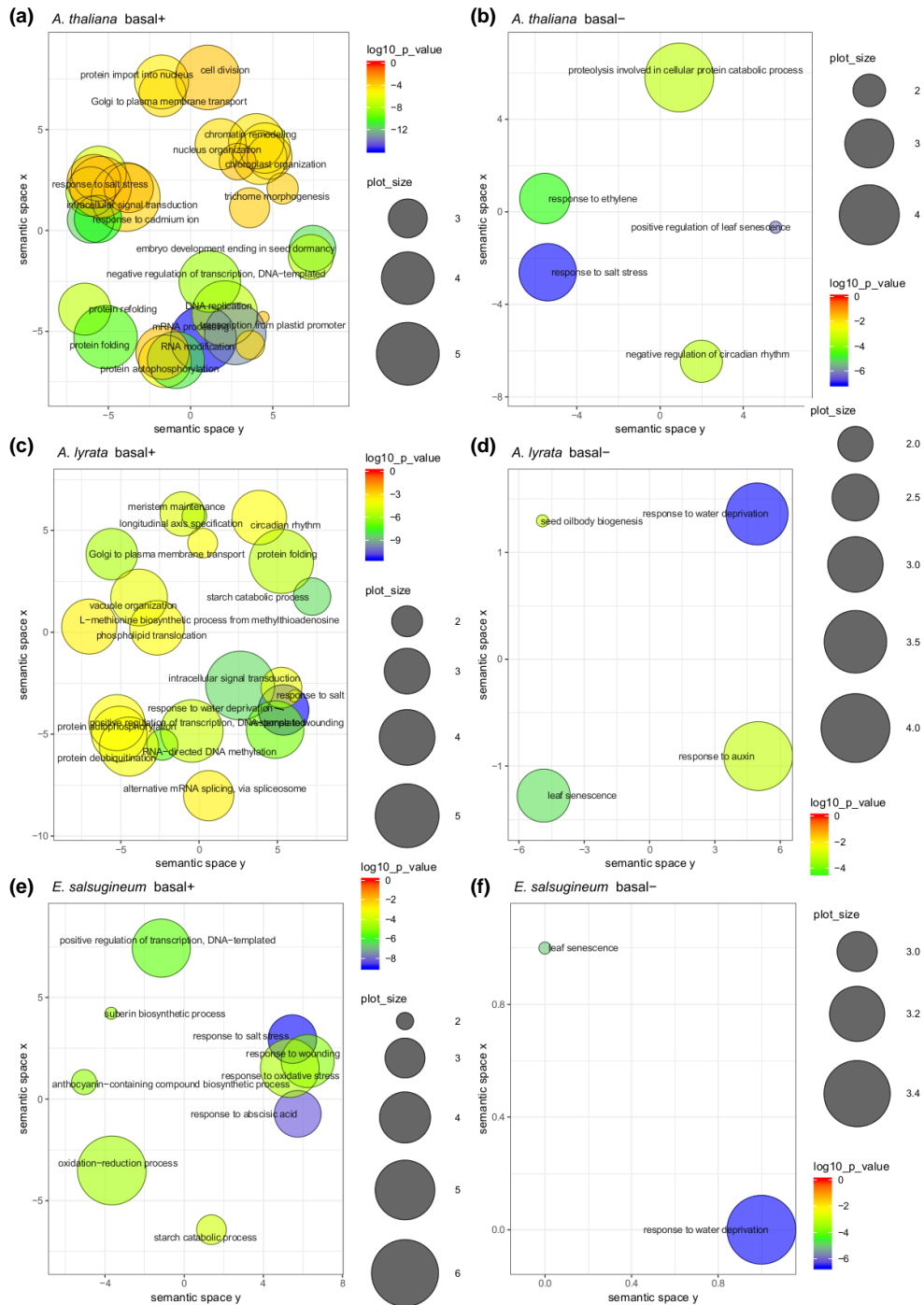


Fig. S7 Dynamic of transcriptional changes and their GO-based functional classification. Gene ontology classifications visualized as scatter plot. Summarized GO terms related to biological processes at baseline. Circle color indicates the $\log_{10} p$ -value and circle size indicates the frequency of the GO term in the underlying EBI GOA databases. The scatter plots represent *Ath* basal + (a), *Ath* basal - (b), *Aly* basal + (c), *Aly* basal - (d), *Esa* basal + (e), *Esa* basal - (f).

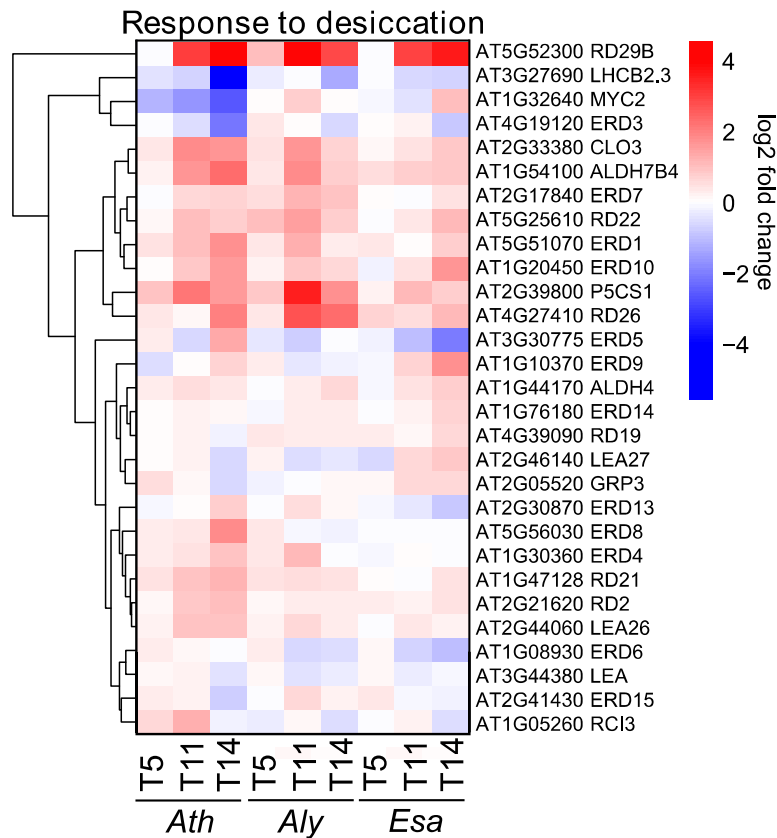


Fig. S8 Drought stress response gene expression. Heatmap visualization of expression levels for “response to desiccation” (RD) and “early-response to desiccation” (ERD) gene families, and genes annotated with GO term “response to desiccation” (GO:0009269). Color scale represents log₂ fold change (WD/WW). Gene names are based on *Arabidopsis thaliana* (*Ath*) locus identifiers and annotation (TAIR10). WW, well-watered. WD, water deficit. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*.

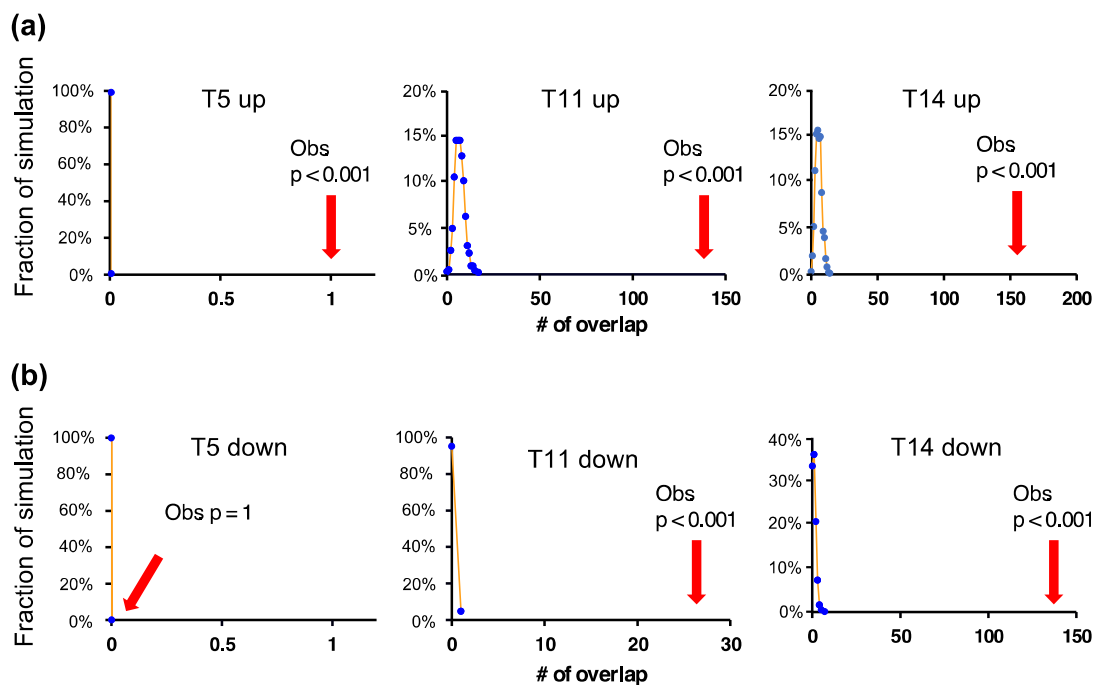


Fig. S9 Significant overlap of differentially regulated genes. Random permutation simulation showing the significance of observed overlap between *Arabidopsis thaliana* (*Ath*), *Arabidopsis lyrata* (*Aly*) and *Eutrema salsugineum* (*Esa*) (a) up- and (b) down-regulated genes at T5, T11 and T14.

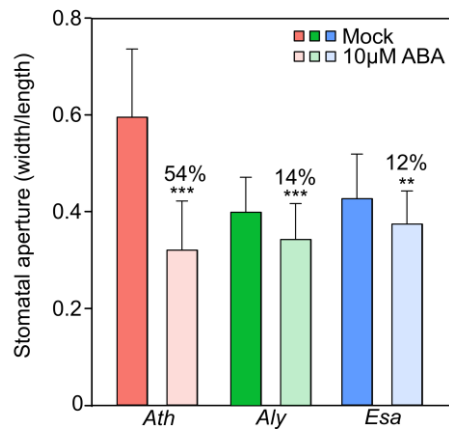
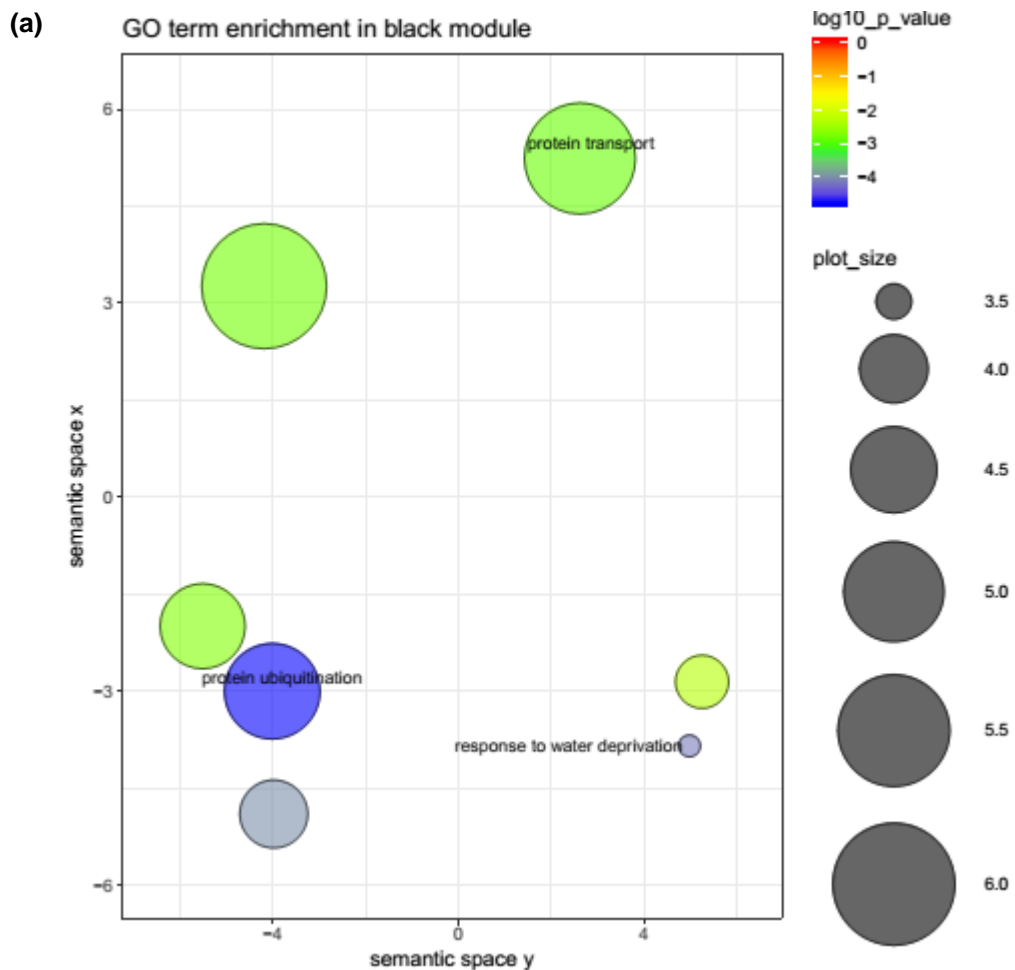
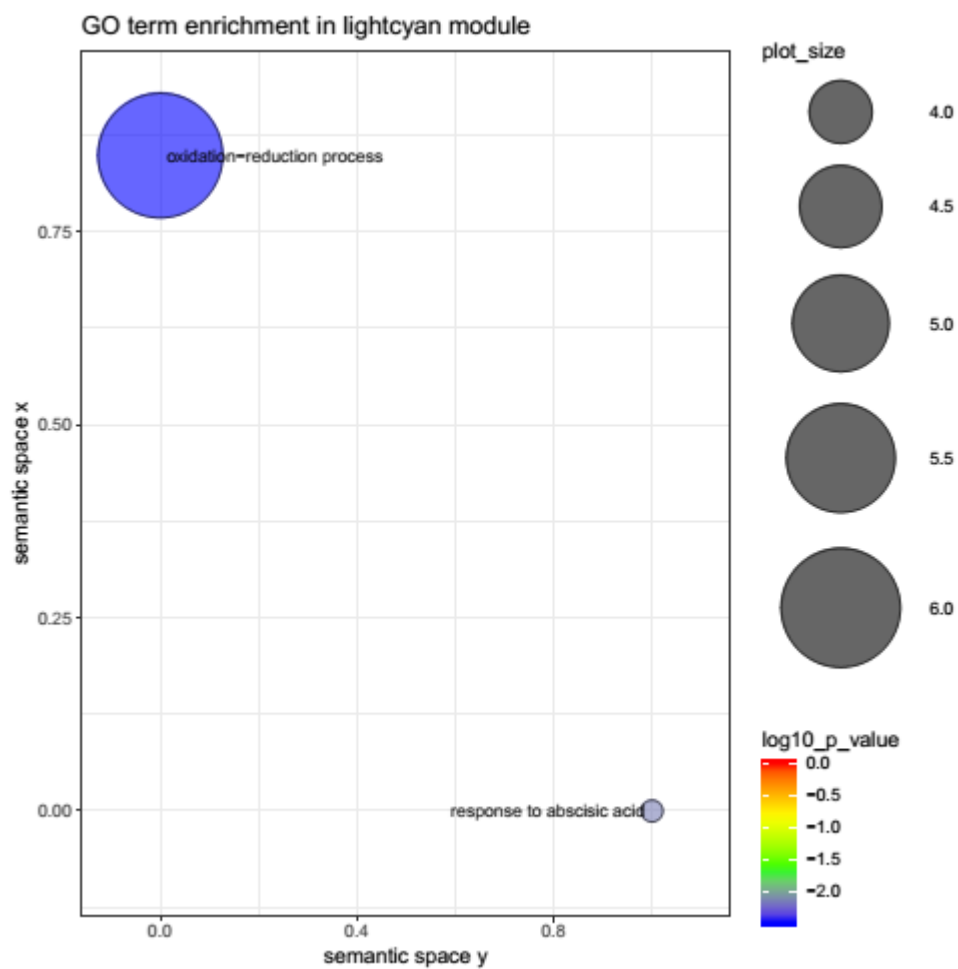


Fig. S11 Stomatal aperture in response to 10 µM ABA. “%” indicates relative decrease of ABA treated plants relative to mock. Data are represented as mean \pm SD (** $P < 0.01$; *** $P < 0.001$, Student’s t-test). $n > 40$ stomata per treatment. *Ath*, *Arabidopsis thaliana*. *Aly*, *Arabidopsis lyrata*. *Esa*, *Eutrema salsugineum*.

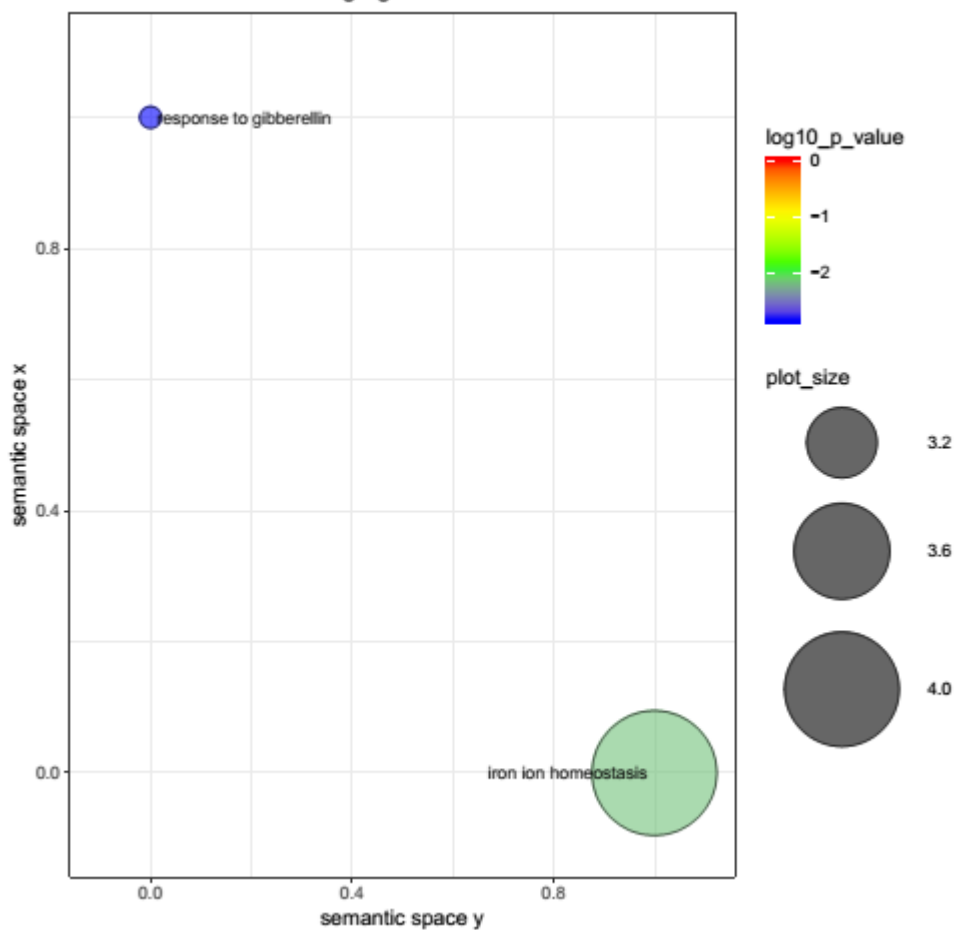
Fig. S12 GO-based functional classification of treatment associated modules. Gene ontology classifications of significant modules visualized as scatter plot. Summarized GO terms related to biological processes at baseline. Circle color indicates the log10 p-value and circle size indicates the frequency of the GO term in the underlying EBI GOA databases. The scatter plots represent black (a), lightcyan (b), lightgreen (c), magenta (d), orange (e), pink (f), purple (g) and skyblue (h) module.



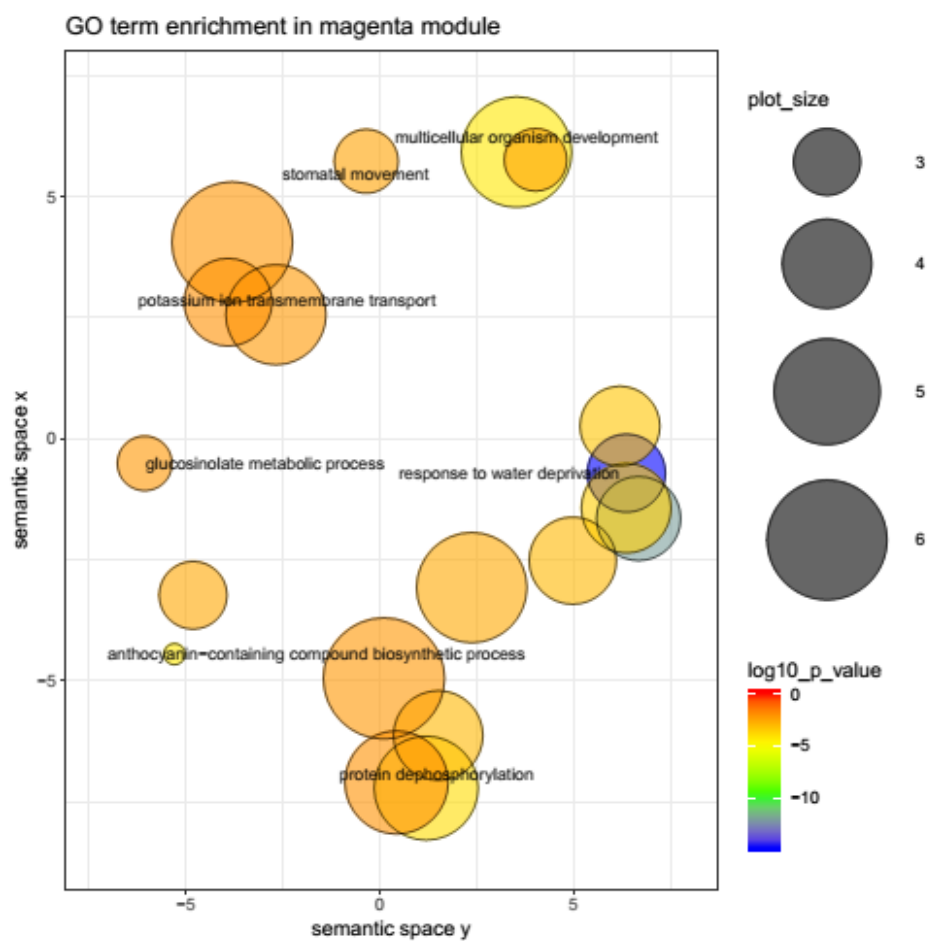
(b)



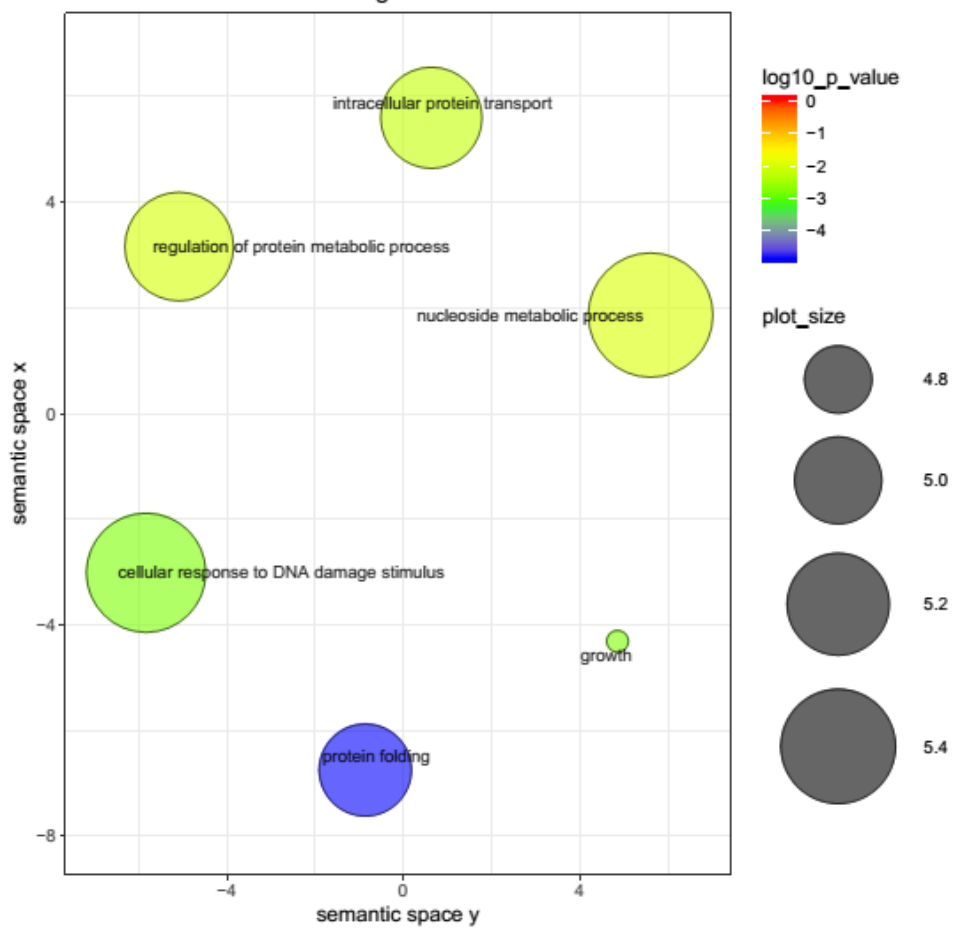
(c) GO term enrichment in lightgreen module



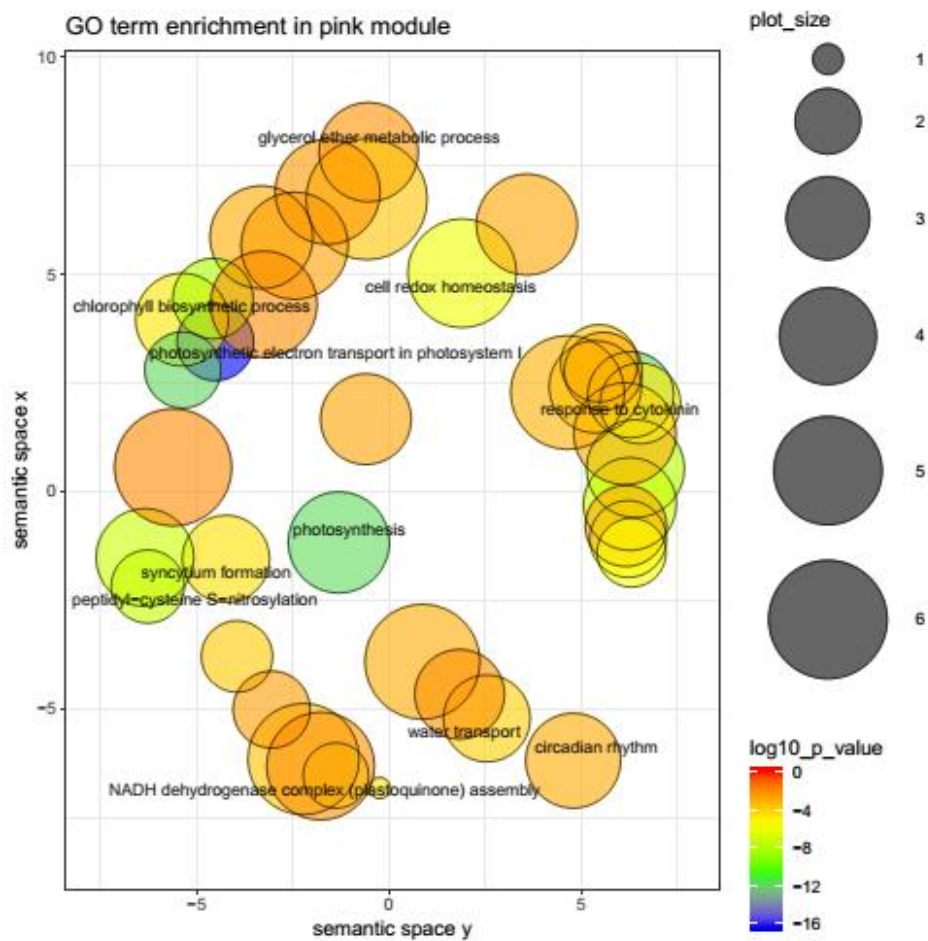
(d)



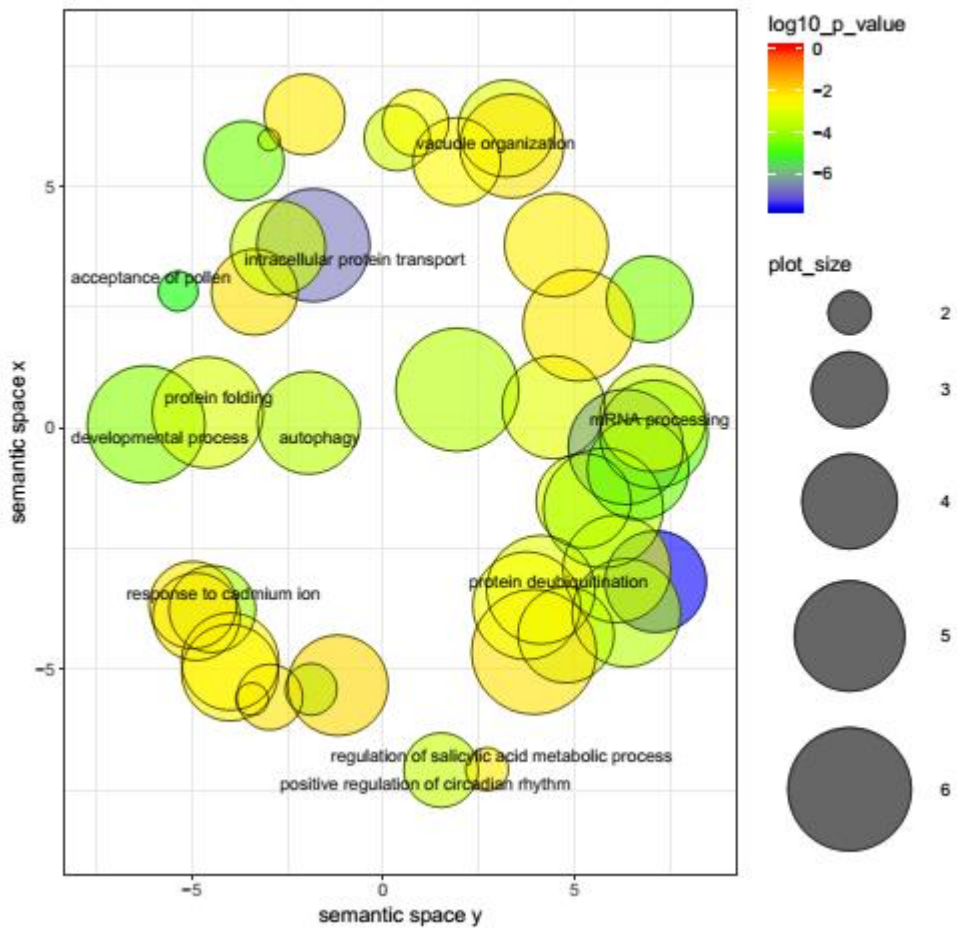
(e) GO term enrichment in orange module



(f)



(g) GO term enrichment in purple module



(h) GO term enrichment in skyblue module

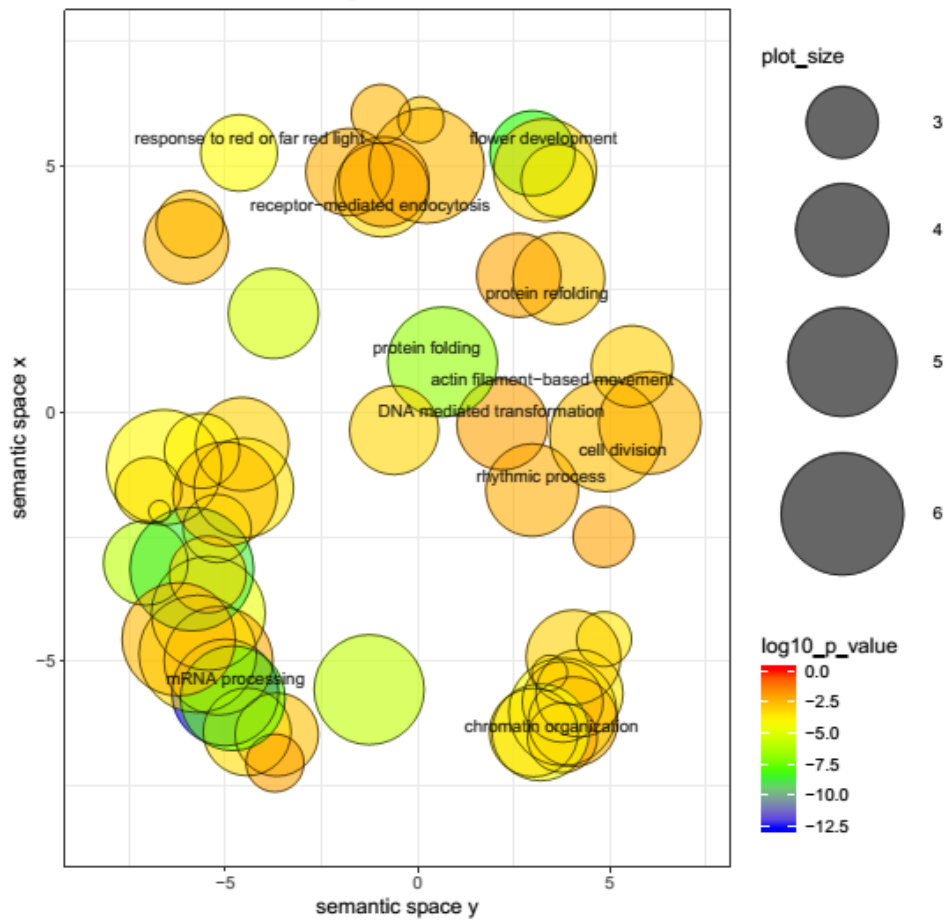
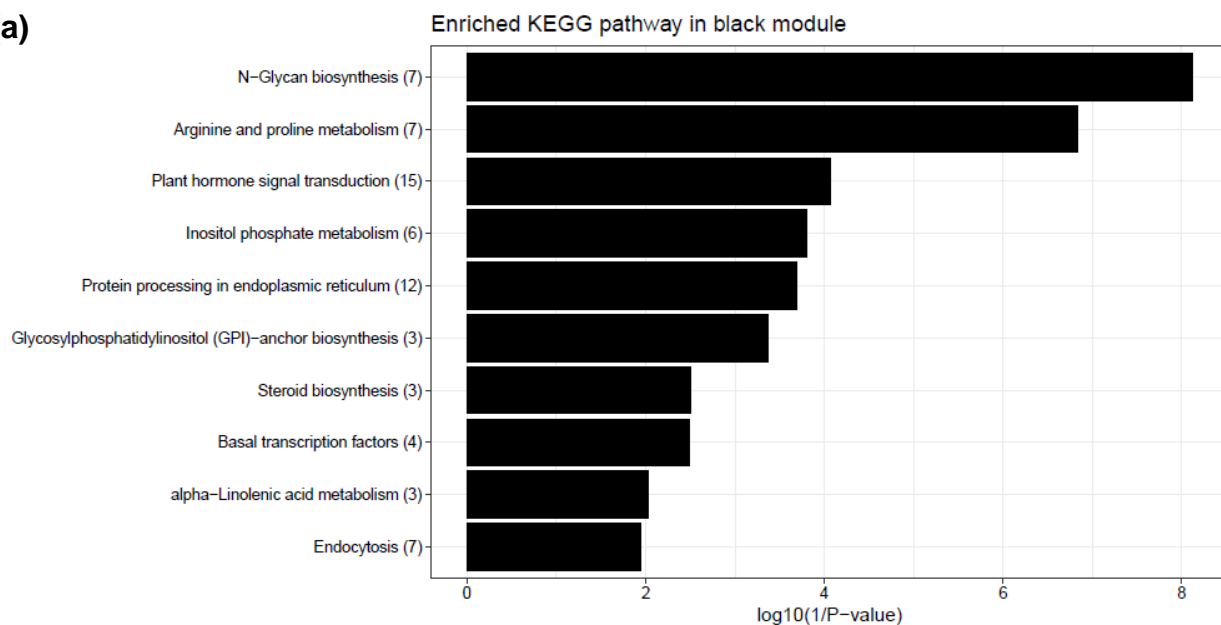
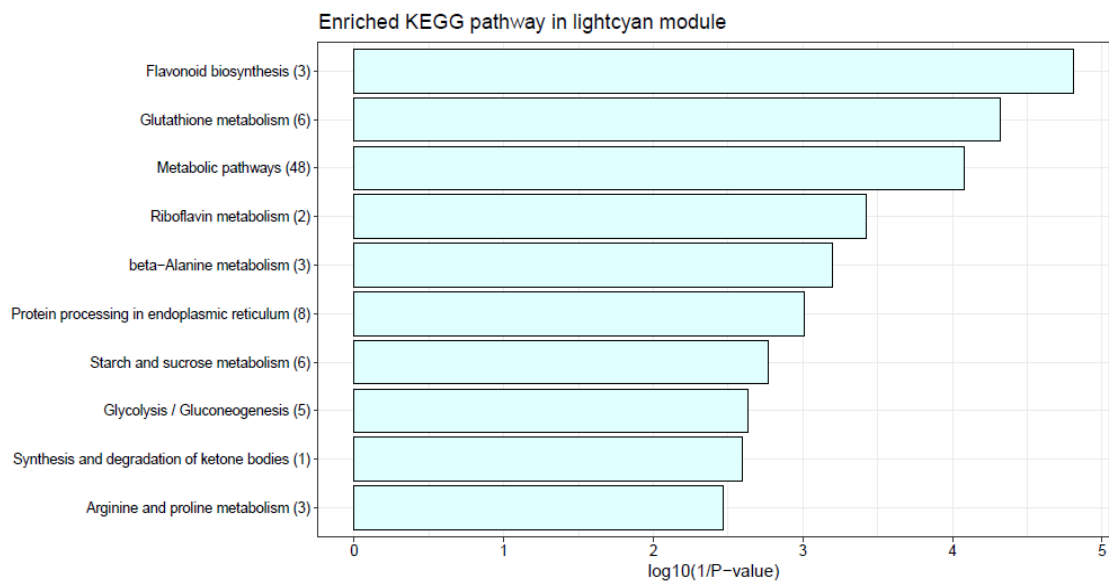


Fig. S13 KEGG-based functional classification of treatment associated modules. The x-axis indicates the log10 p-value and the y-axis indicates the number of genes on each enriched pathway. The top-10 ranking KEGG pathways of black (a), lightcyan (b), lightgreen (c), magenta (d), orange (e), pink (f), purple (g) and skyblue (h) modules are shown as bar plots.

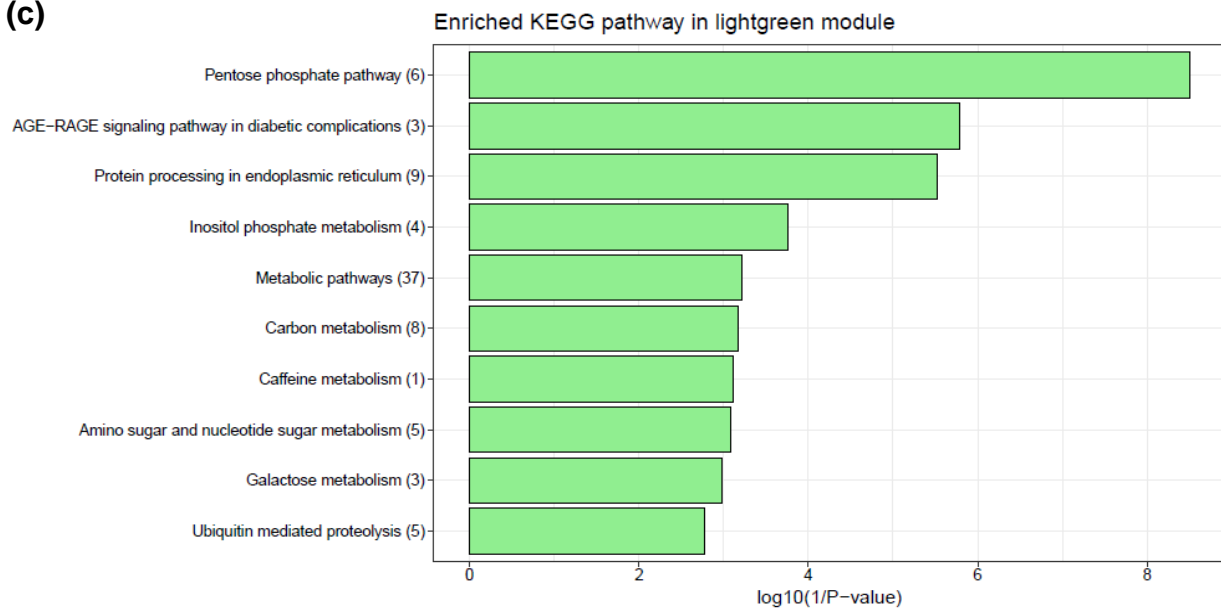
(a)



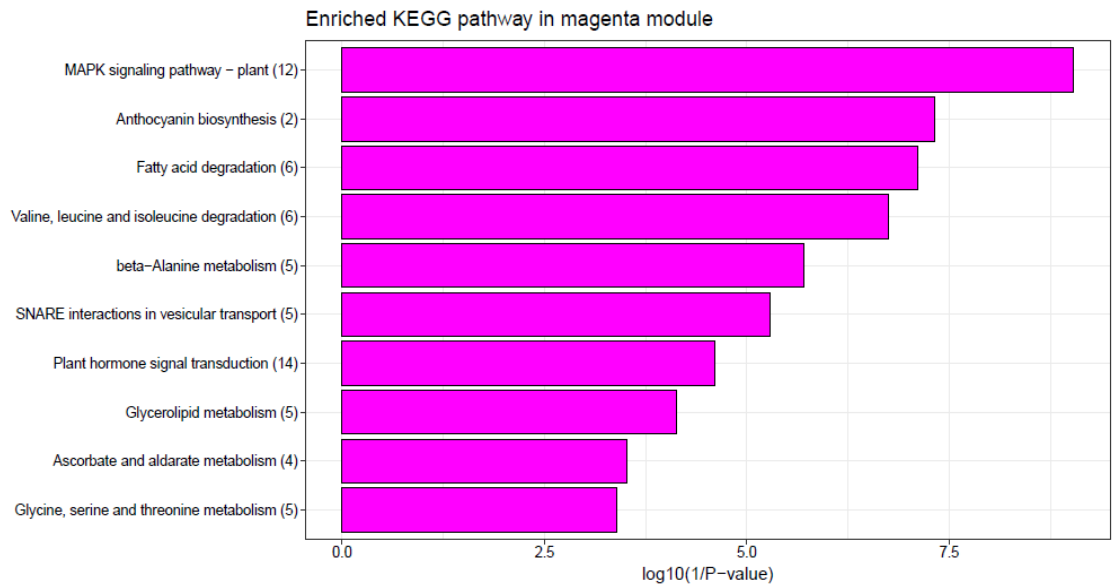
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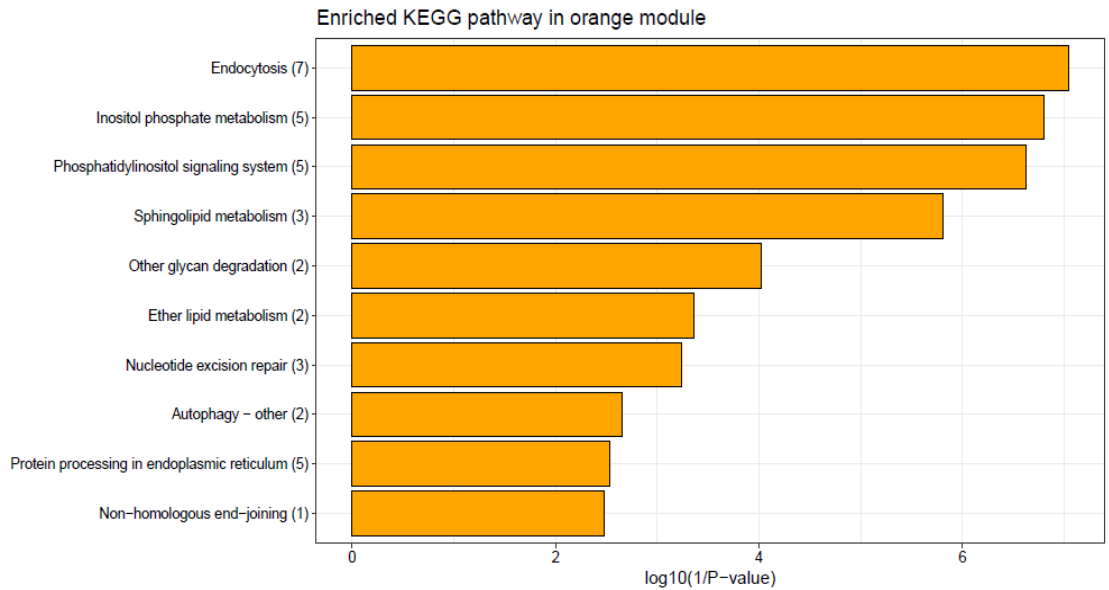
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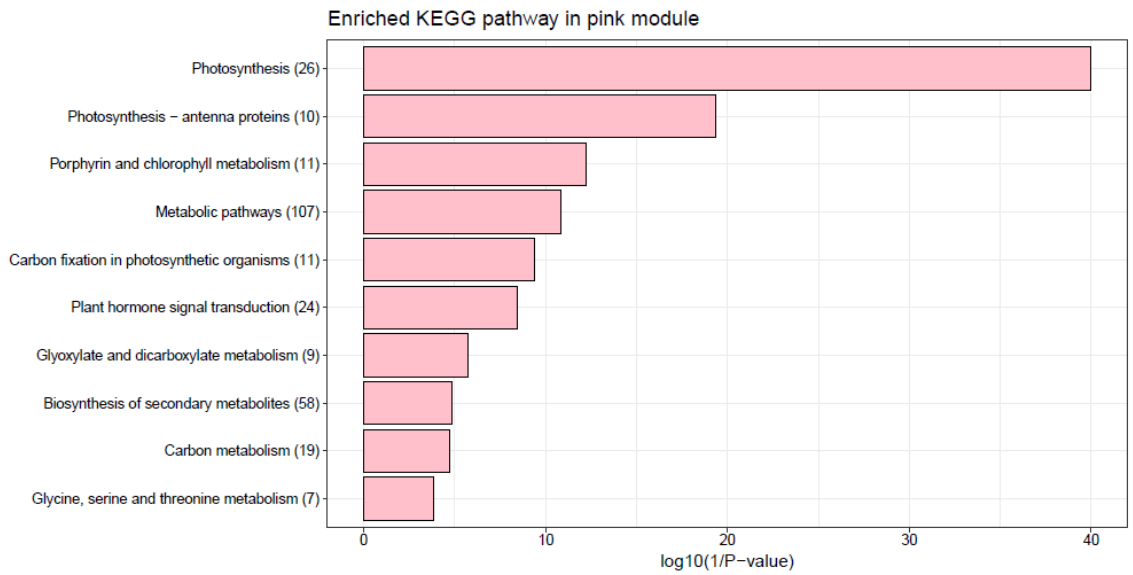
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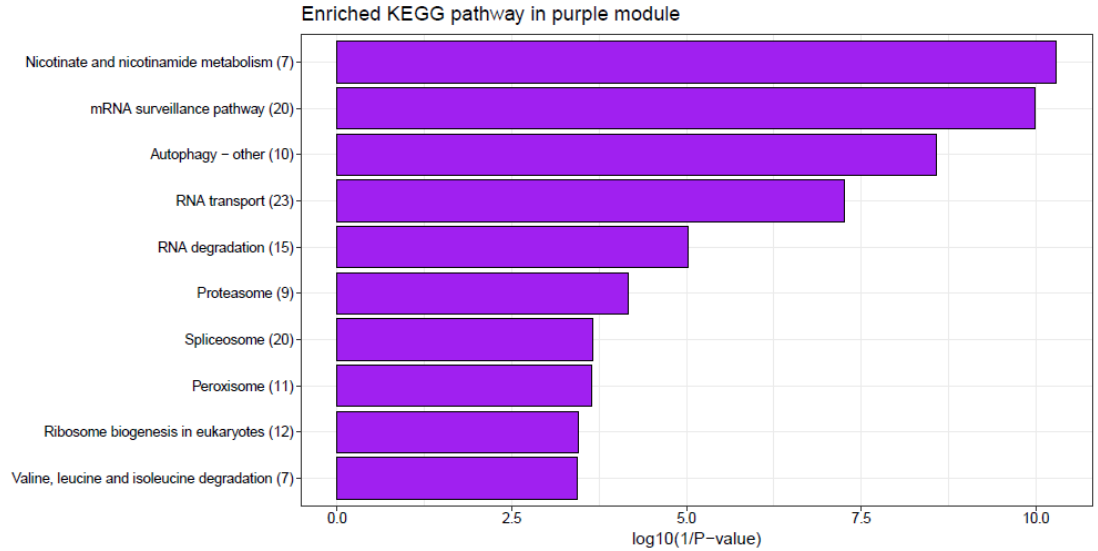
(e)



(f)



(g)



(h)

