

Figure S1. Area of plants at 15 days (day of harvest) and day 21 (6 days post harvest) for the single and combined stresses. Each bar represents measurements from at least 4 plants. Error bars are represented by standard deviation and significance was determined by Student's two-tailed, t-test, $p < 0.05$. Control Day 15 and 21 contains 9 biologically independent plants for categories (A, B, G, H, J, M, O, P, Q, R, S, T, U, V, W), 8 (D, F, N), 7 (C, I, K), 5 (L). Heat day 15 and 21: 18 (Control), 9 (27, 30, 33, 36). Cold days 15 and 21: 15 (Control), 8 (3, 12), 9 (6), 7 (9). Mannitol: 17 (Control), 9 (50, 100, 200, 250, 300, 350, 400), 6 (150). Salt: 18 (Control), 8 (20, 60), 9 (40, 80, 100, 120, 140, 160, 180, 200). Light: 23 (Control), 7 (115), 5 (225), 9 (335,535), 8 (435). Nitrogen deficiency: 16 (Control), 8 (90, 80, 50, 40, 10), 9 (70, 20), 6 (30), 7 (0). Dark: 22 (Control), 4 (1), 8 (2,3), 6 (4, 6), 5 (5,7). Cross stress: 81 (Control), 9 (HS, HM, HN, SM, CN, SD, MD, ND, HD, CD, CL, HL, LS, SN), 18 (ML), 7 (CS, CM).

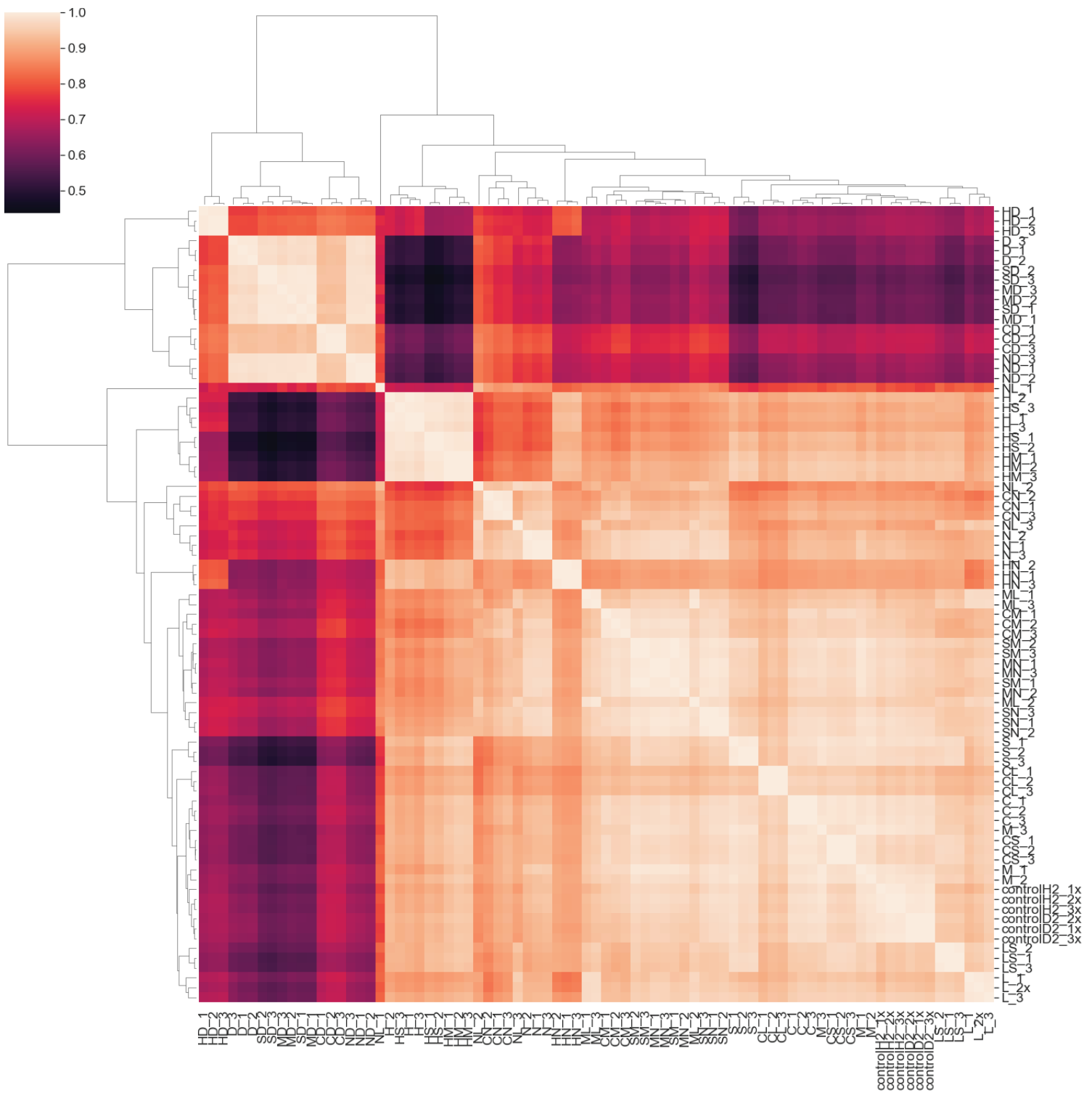


Figure S2. Hierarchical clustering of the *Marchantia* stress experiments. Transcript per million (TPM) gene expression values were scaled with standard scaler and clustered with `seaborn.clustermap()` function.

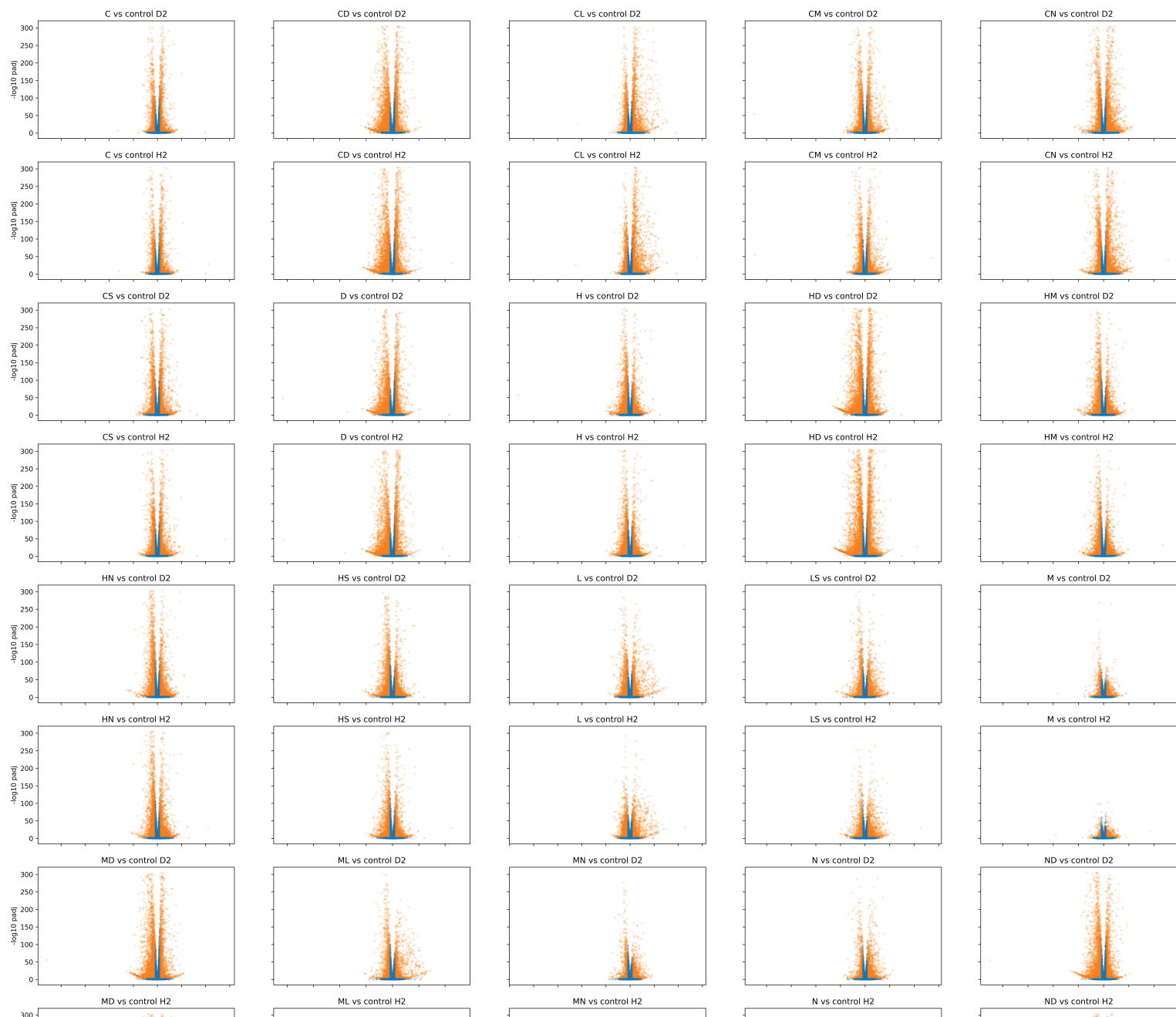


Figure S3. Volcano plots of stress experiments. The x-axis represents \log_2fc change, the y-axis indicates the $-\log_{10}$ of adjusted p-value. Each point represents a gene that has an absolute \log_2fc change > 1 and is significantly (adjusted $p\text{-value} < 0.05$, orange color) or not significantly ($p\text{-value} > 0.05$, blue point) differentially expressed.

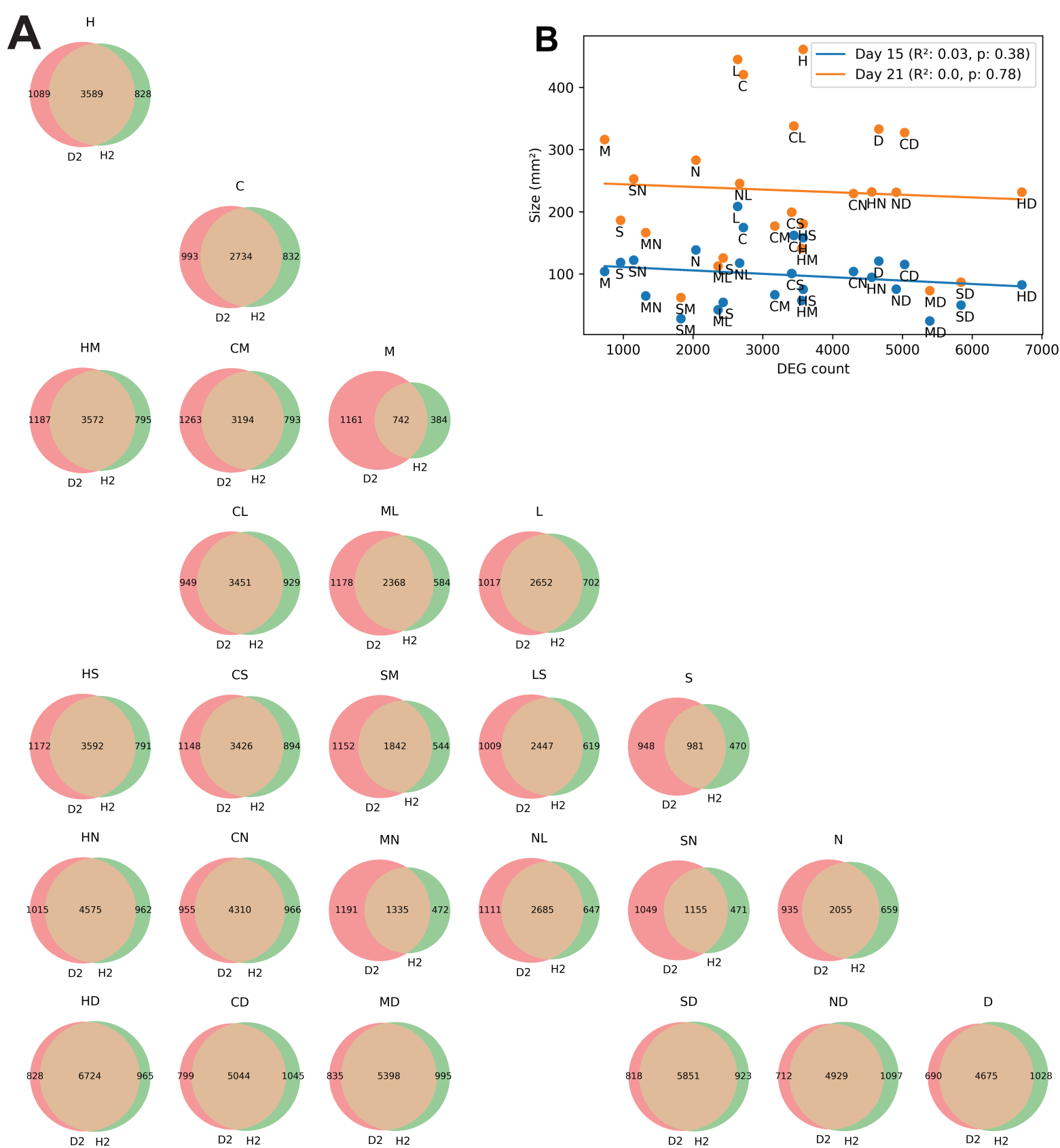


Figure S4. Comparison of found differentially expressed genes for the single and combined stressed. A) For each stress combination, we estimated significant DEGs (adjusted p -value <0.05) by using control D2 (red circle) and control H2 (green circle). The orange areas indicate the overlap between the found DEGs of the two controls. The overlapping DEGs were used for further study. The following abbreviations are used for the description of stresses: cold (C), dark (D), heat (H), light (L), mannitol (M), nitrogen deficiency (N) and salt (S). Combination of stresses is indicated by two letters, where e.g., HD indicates heat+darkness treatment. B) The number of DEGs (x-axis) versus the size (y-axis) of *Marchantia* plants on day 15 (blue) and day 21 (orange). The R^2 and p -values are shown in the legend.

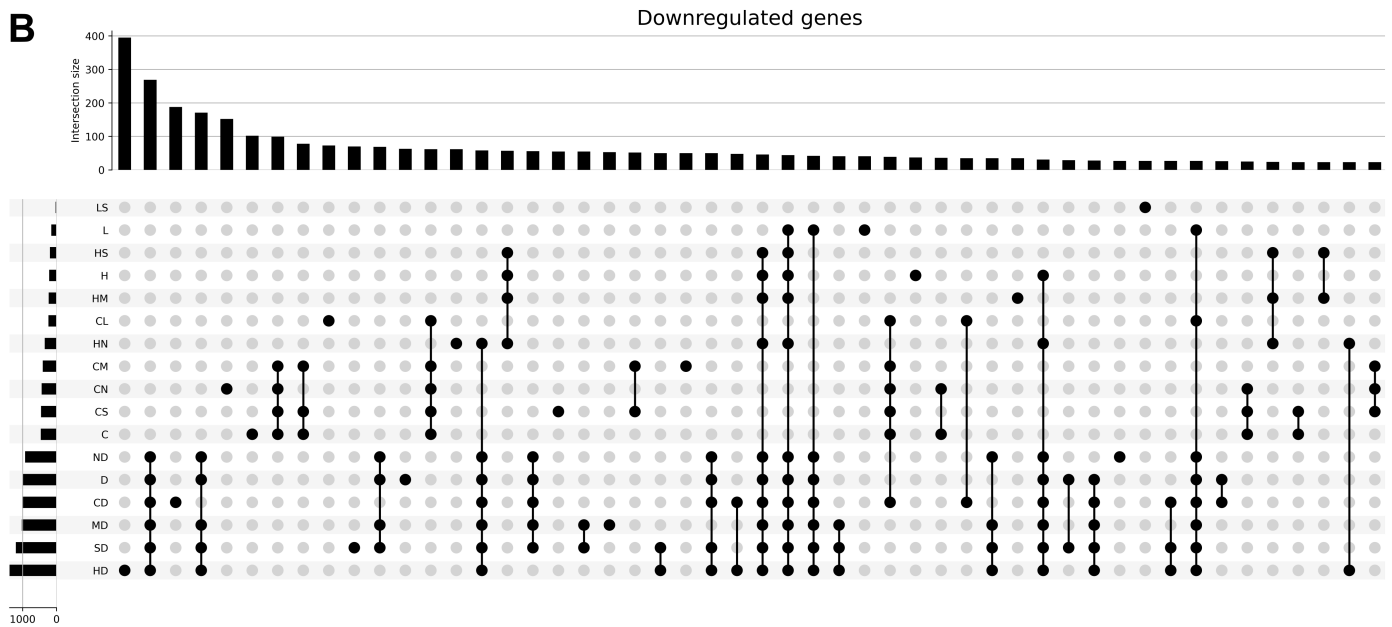
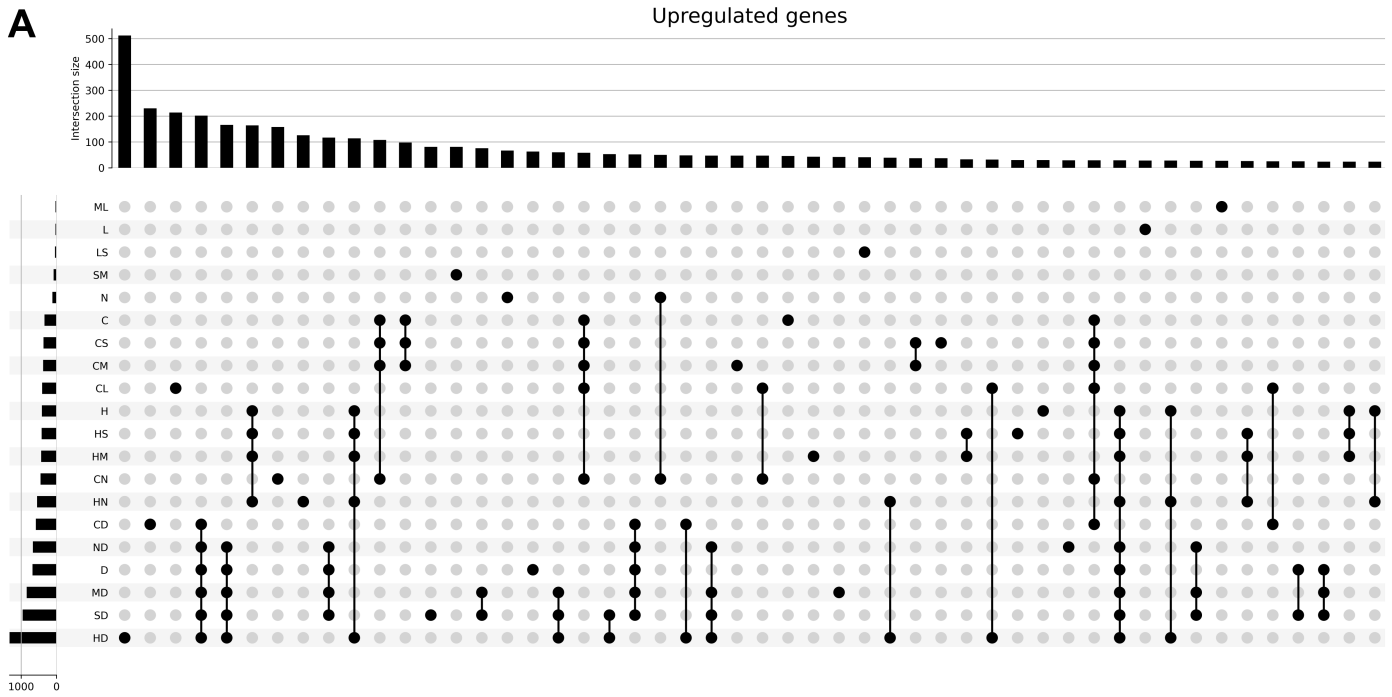


Figure S5. Upset plot showing the top 50 intersections of differentially expressed genes.
 A) Upregulated genes B) Downregulated genes. Rows represent the various stress conditions and columns represent the genes that are found in the particular group of sets indicated by the dots and connecting lines. The UpSet plot package is available from <https://upsetplot.readthedocs.io/en/stable/>.

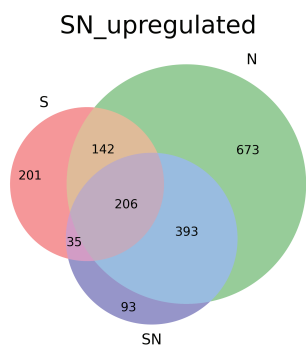
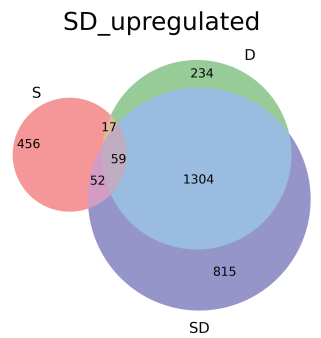
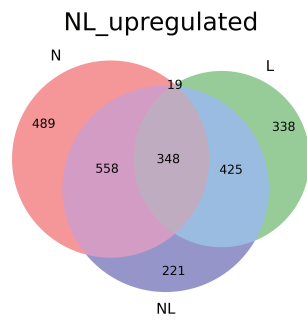
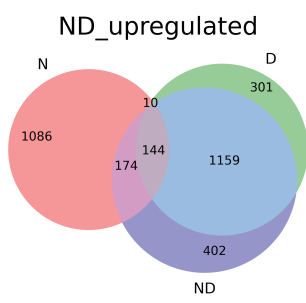
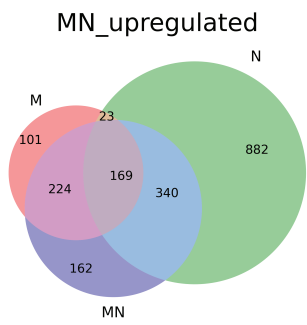
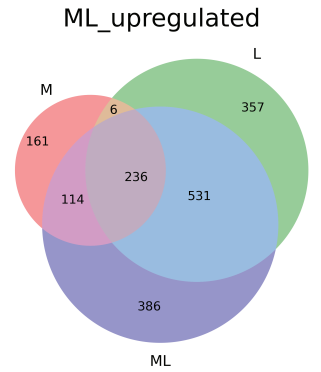
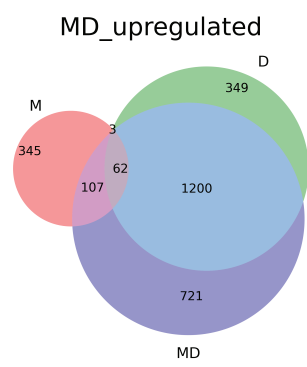
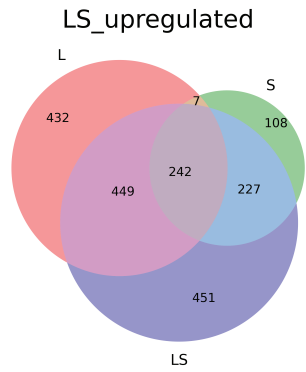
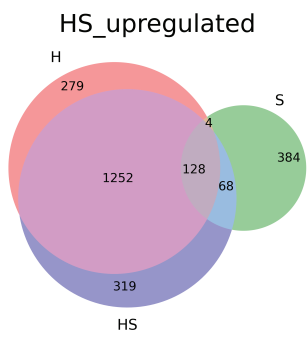
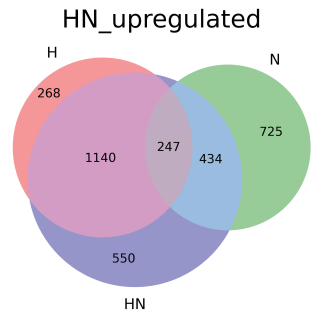
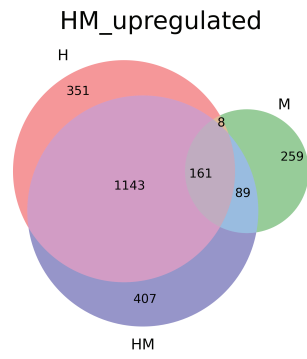
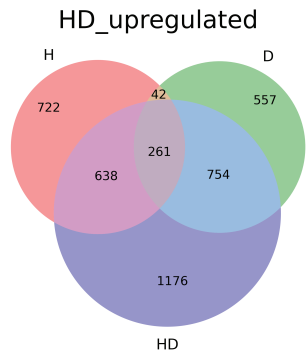
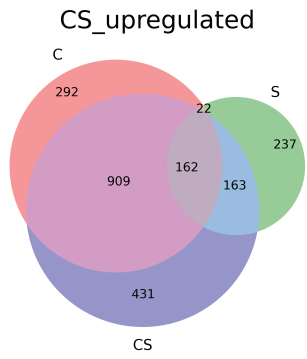
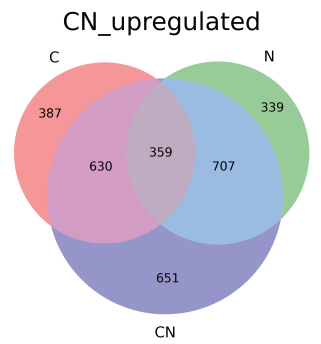
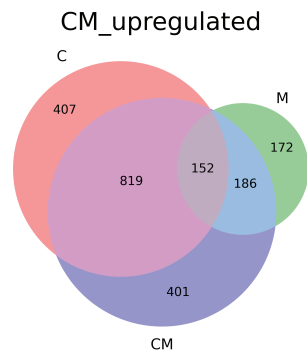
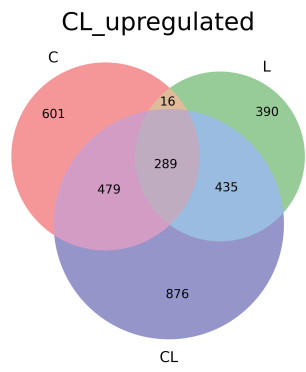
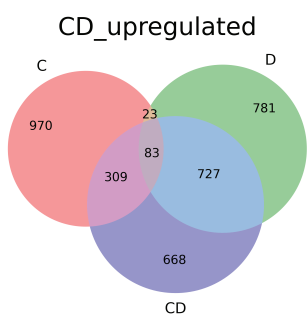


Figure S6. Venn diagrams of upregulated genes in single and combined stresses. The abbreviates are cold (C), dark (D), heat (H), light (L), mannitol (M), nitrogen deficiency (N) and salt (S). Combination of stresses is indicated by two letters and purple circles. The first and second stress in a pair is colored red and green (e.g., cold is red in CD), while the combined stress is colored purple. The sizes of the circles and intersections and the numbers within indicate the number of significant DEGs.

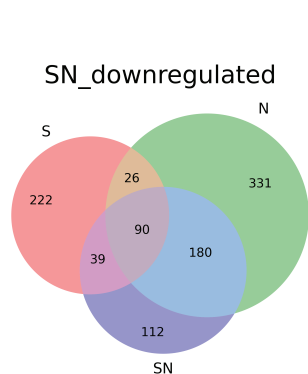
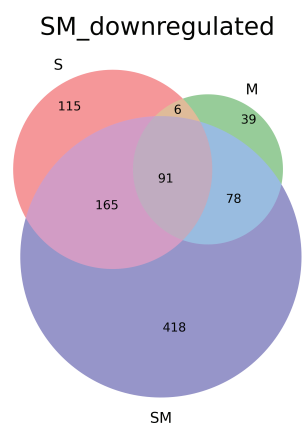
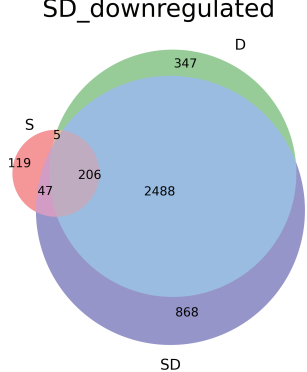
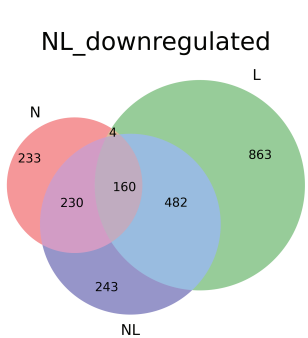
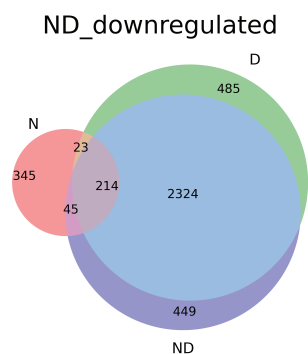
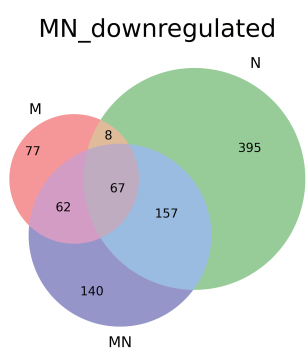
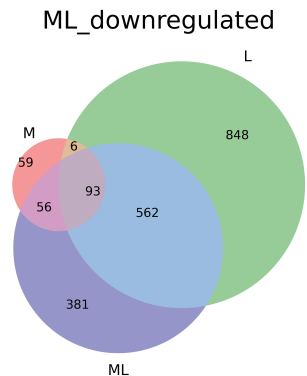
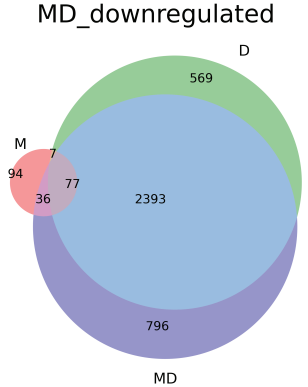
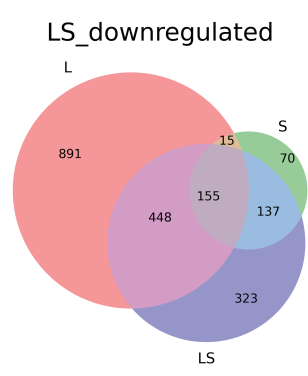
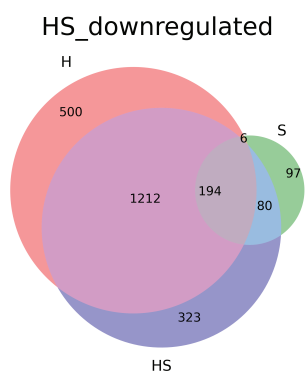
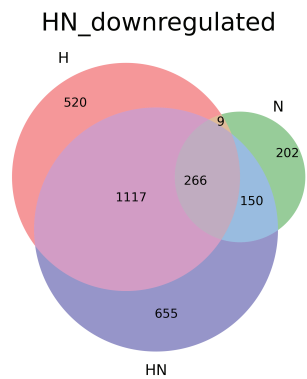
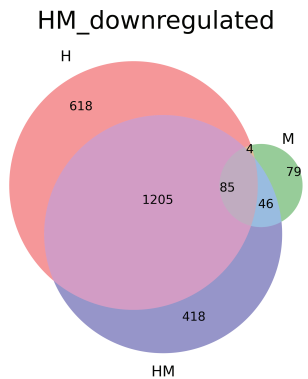
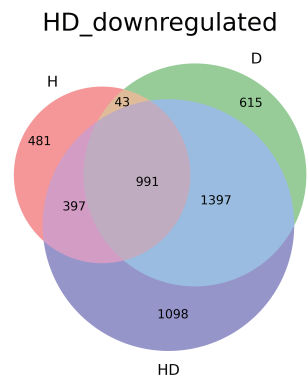
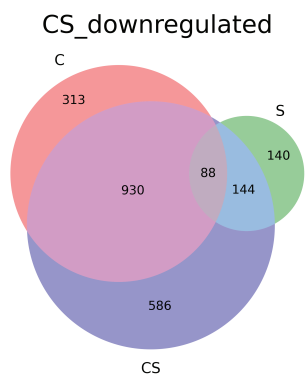
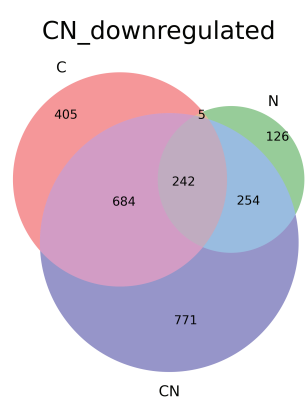
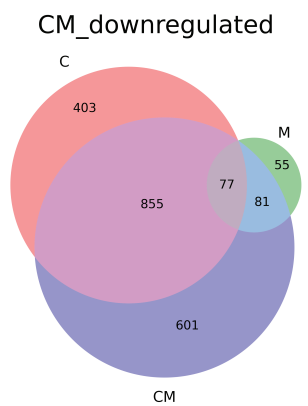
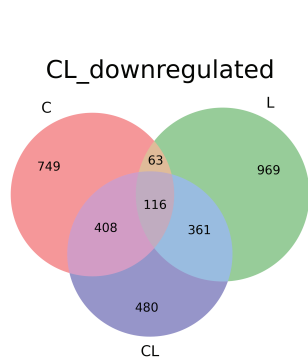
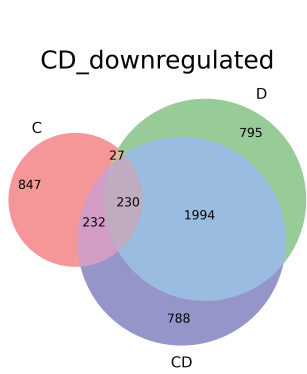
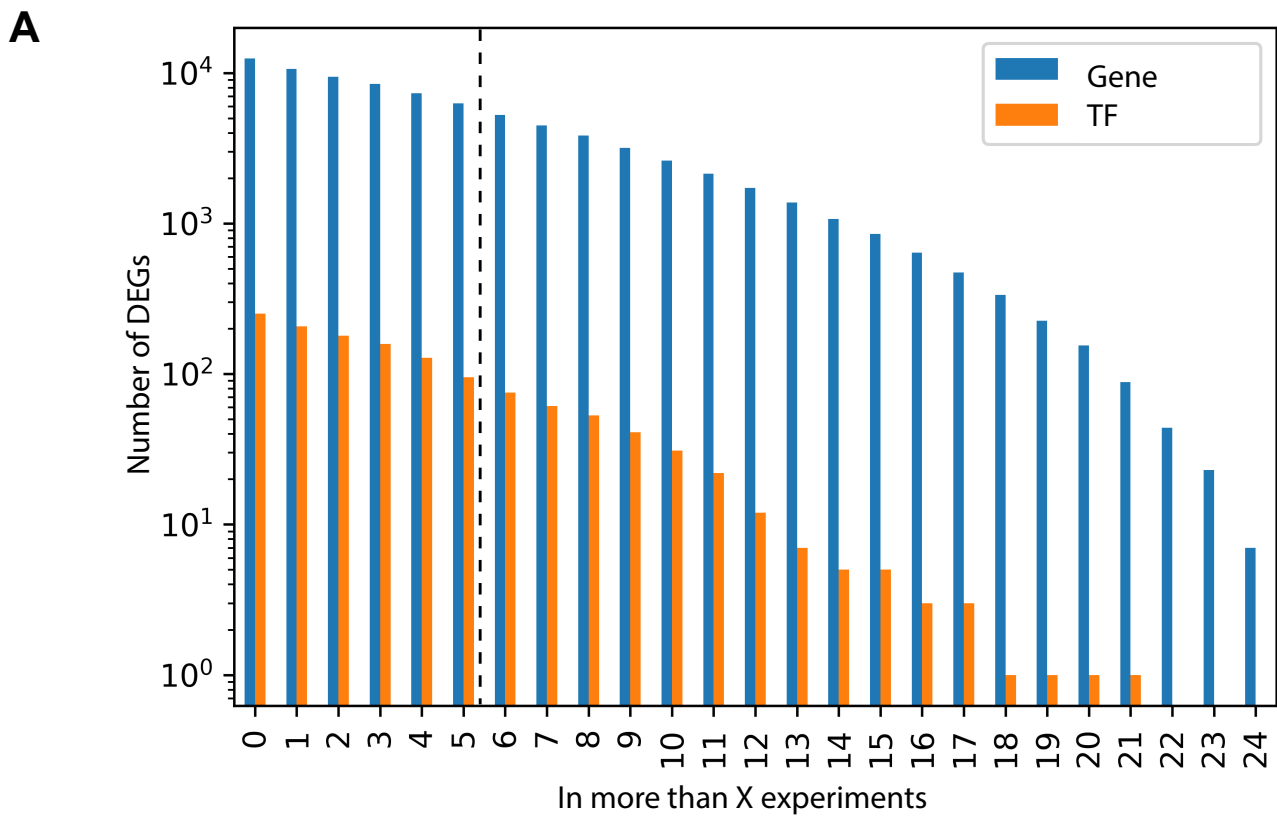


Figure S7. Venn diagrams of downregulated genes in single and combined stresses. The abbreviates are cold (C), dark (D), heat (H), light (L), mannitol (M), nitrogen deficiency (N) and salt (S). Combination of stresses is indicated by two letters and purple circles. The first and second stress in a pair is colored red and green (e.g., cold is red in CD), while the combined stress is colored purple. The sizes of the circles and intersections and the numbers within indicate the number of significant DEGs.

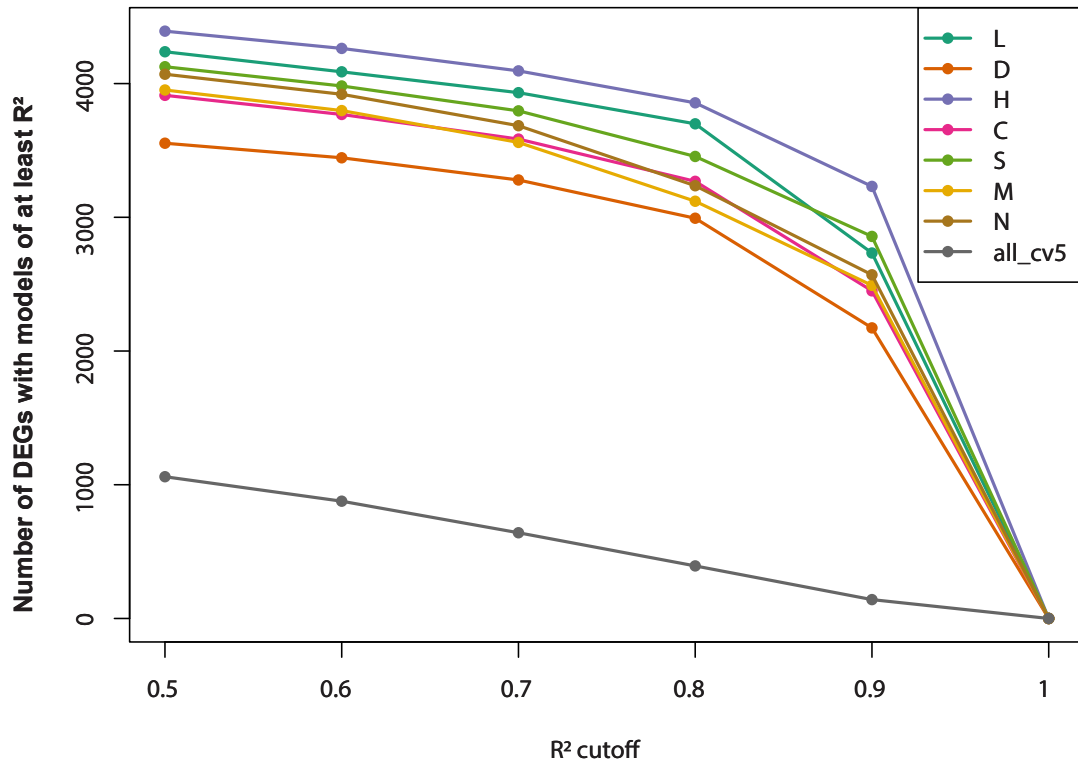


B

Stress-type	Cold	Dark	Heat	Light	Mannitol	Nitrogen	Salt
Experiment availability	C CS CM CN CD CL	D SD MD ND HD CD	H HS HM HN HD	L ML NL CL LS	M HM CM SM ML MN MD	N HN CN NL MN ND SN	S HS CS SM SD LS SN
Total (with replicates)	18	18	15	15	21	21	21

Figure S8. Considerations for reconstruction of the stress-specific gene regulatory networks.
 A) Number of differential genes in more than a certain number of experiments. B) List of experiments in each stress specific-network.

A

Number of models at various R² cutoffs

B

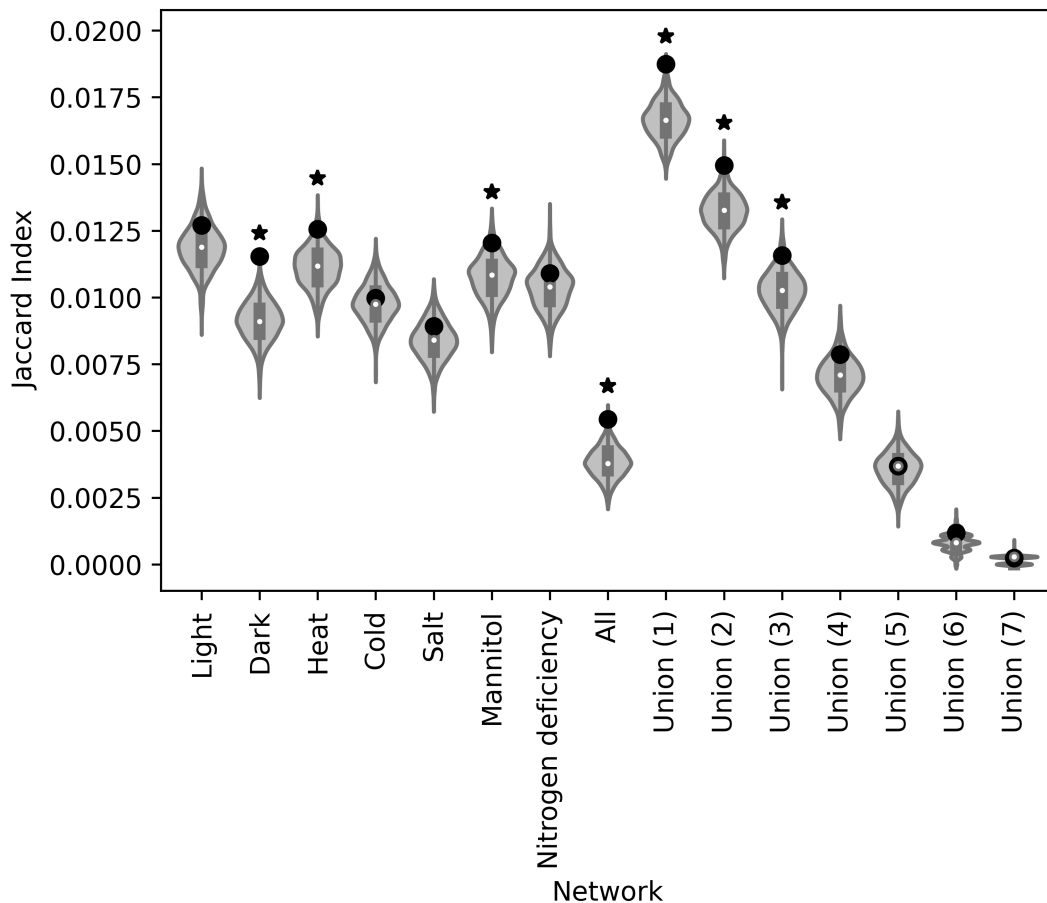


Figure S9. Metrics used to construct the unified GRN. A) Distribution of model counts across various R². B) Similarity of various gene regulatory networks against a shuffled AGRIS gene regulatory network. Union networks were generated by selecting for interactions found in at least X networks as indicated in the brackets. For example, 'Union (2)' will indicate that the interactions were found in at least 2 of the stress-specific networks. Point indicates observed similarity while asterisk indicates significance, hypergeometric test, p < 0.05. Maximum value of Jaccard index was observed in 'Union (1)' at 0.019.

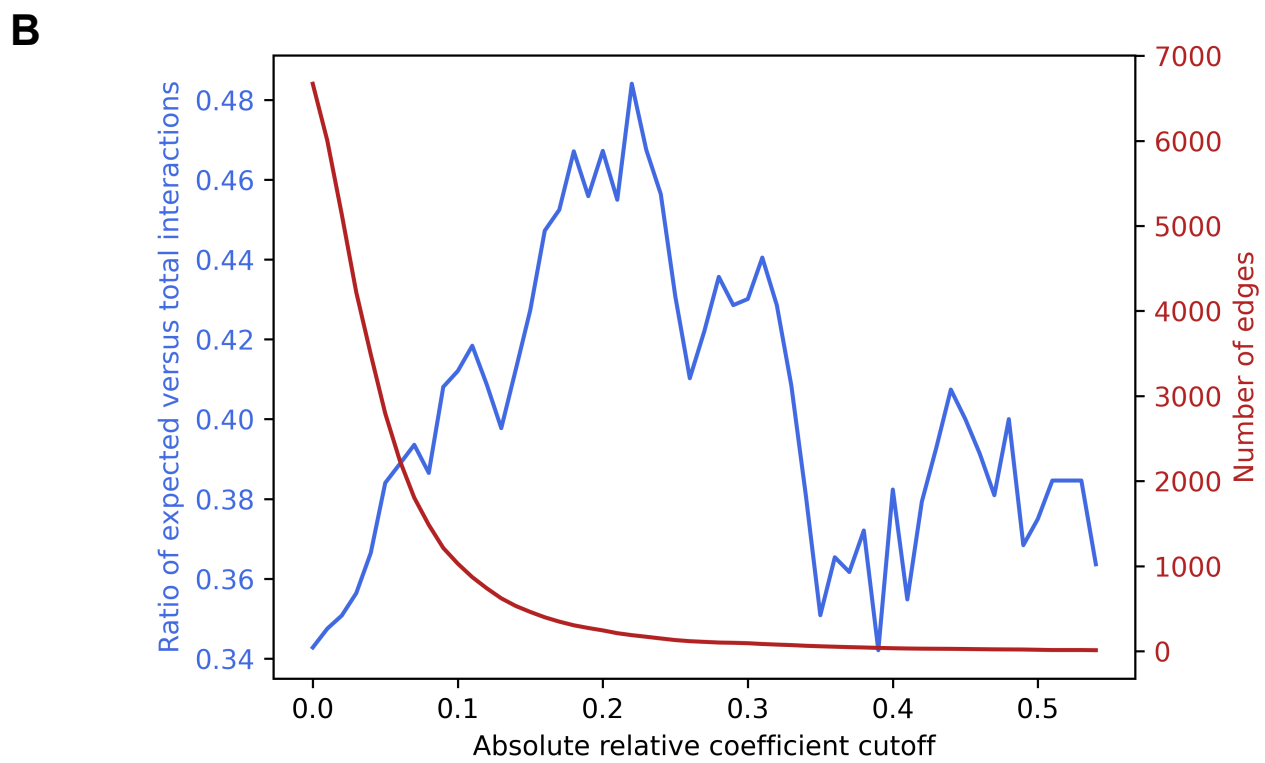
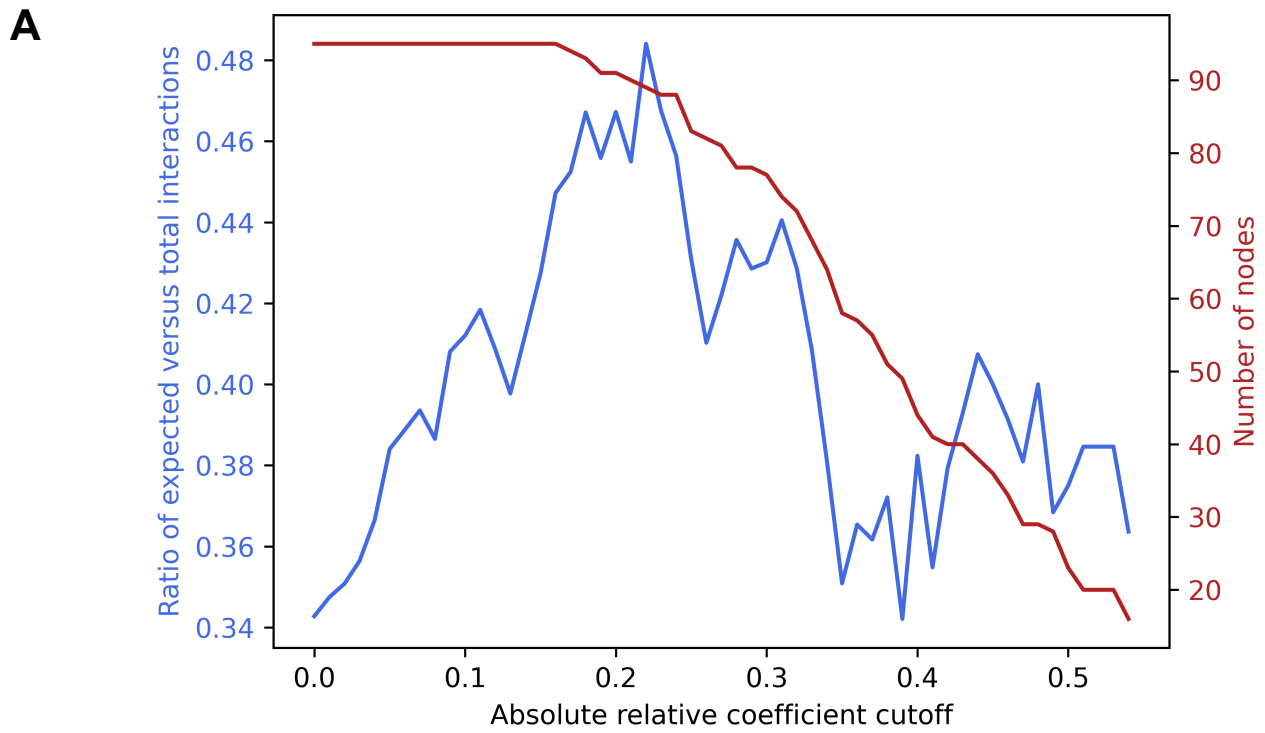


Figure S11. Ratio of expected interactions across absolute coefficient cutoffs. A) Number of nodes retained. B) Number of edges retained

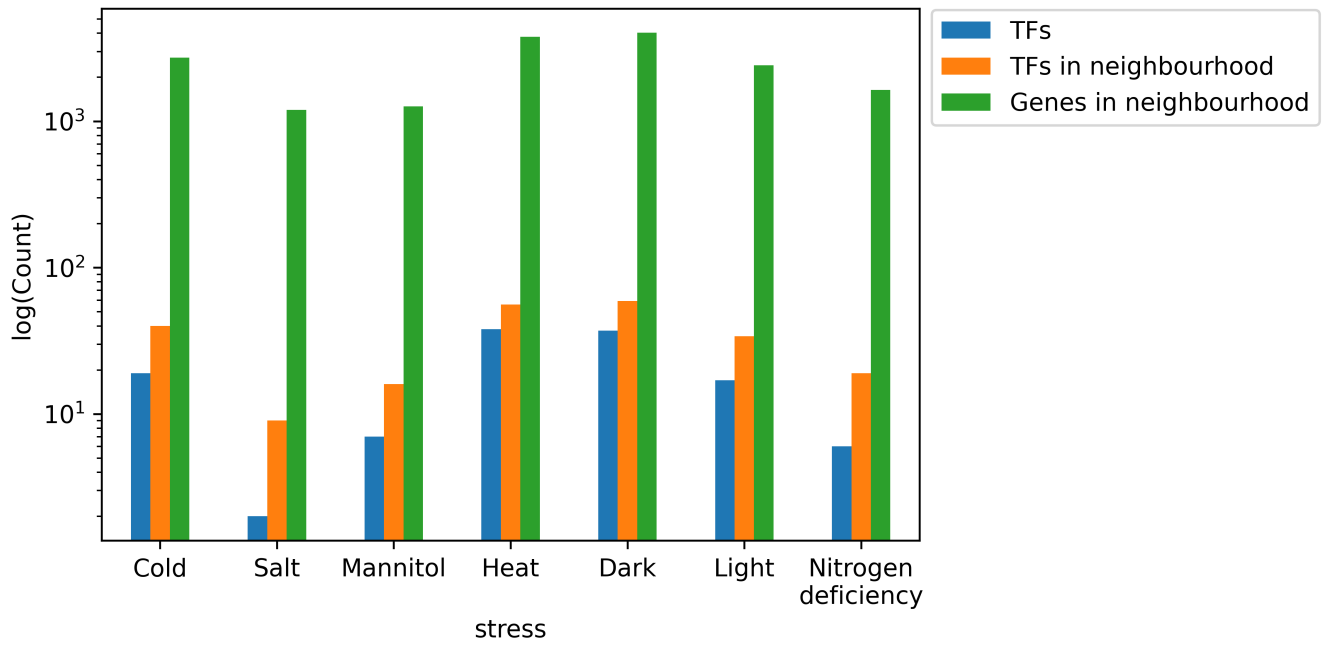


Figure S12. Magnitude of response in GRN for each stress. Blue, orange and green bars reflect the number of stress-specific TFs, number of TFs in the first neighborhood of the former and genes associated to the first neighborhood respectively.

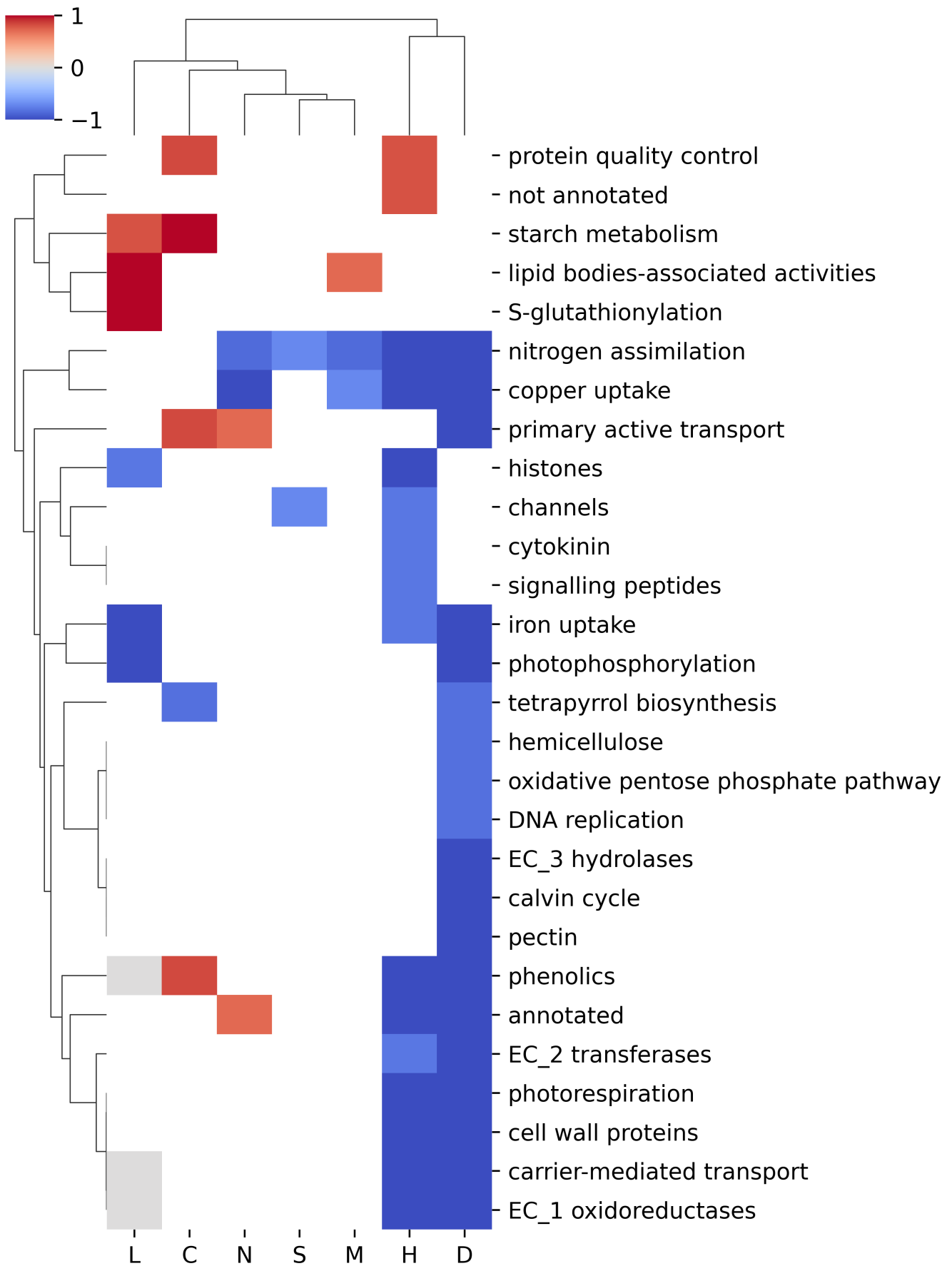


Figure S13. Robustly responding second level mapman bins across the 7 abiotic stresses. Red, blue and gray cells correspond to specifically up-, down-regulated and no change respectively. Cells that do not contain enrichment for stress are in white.

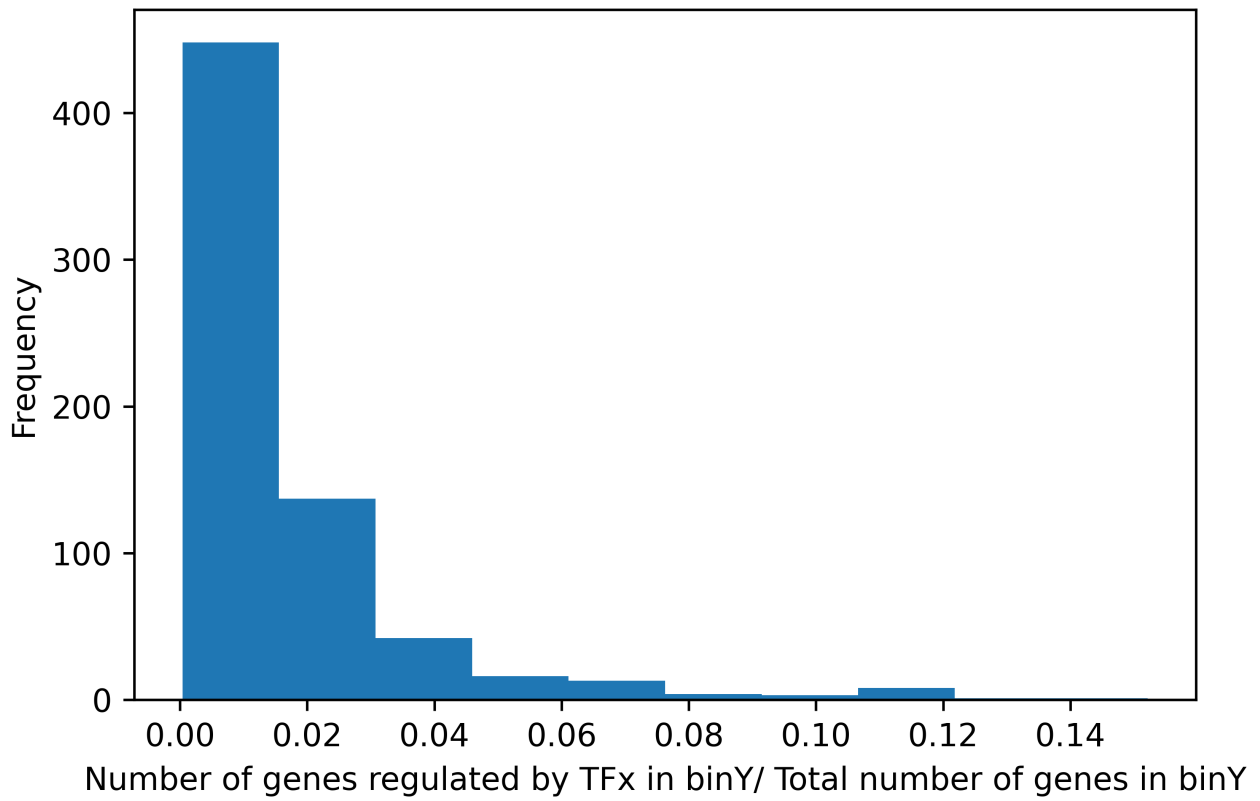
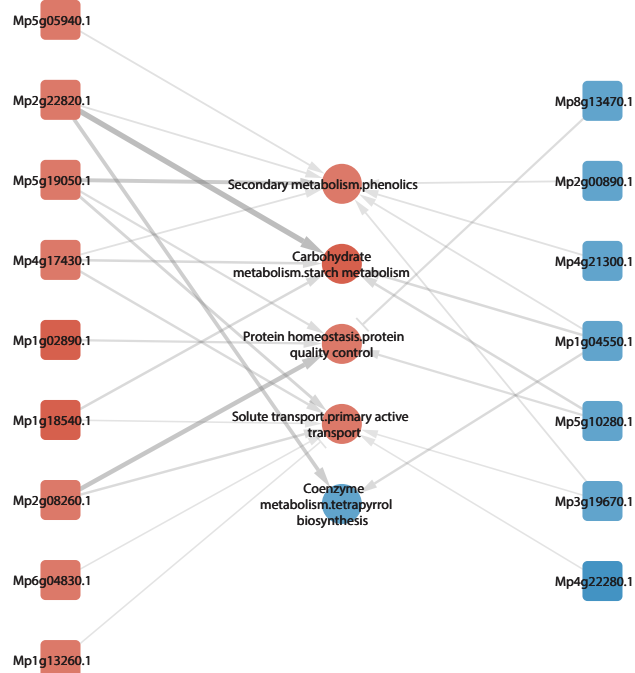
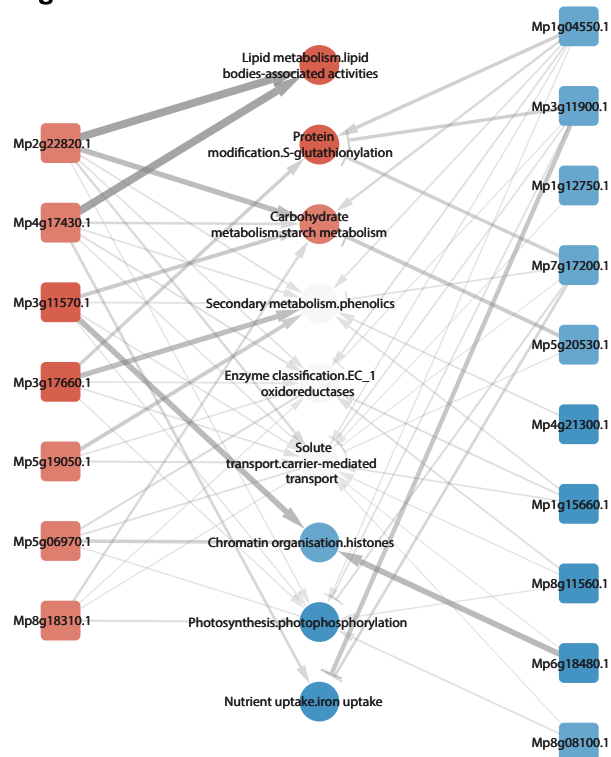


Figure S14. Frequency of ratio of robustly responding mapman bins regulated by robustly responding transcription factors.

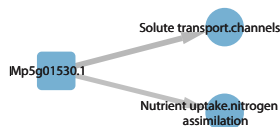
Cold



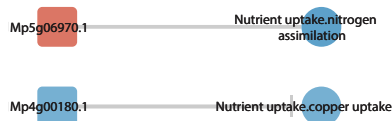
Light



Salt



Mannitol



Nitrogen deficiency

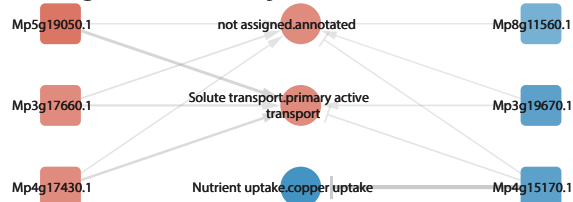


Figure S15. Representation of enriched second level mapman bins under the regulation of specifically expressed transcription factors in A) Cold, B) Light, C) Salt, D) Mannitol and E) Nitrogen deficiency stresses. Node colors red and blue reflect the degree where the nodes are specifically up or downregulated in the stress respectively. The edge width represents the ratio of genes under regulation as a fraction of the total number of genes found in that particular MapMan bin. Edges with arrow, blunt arrow and no arrow reflect the general trend of regulation of the TF, representing positive, negative and ambiguous regulation respectively.

