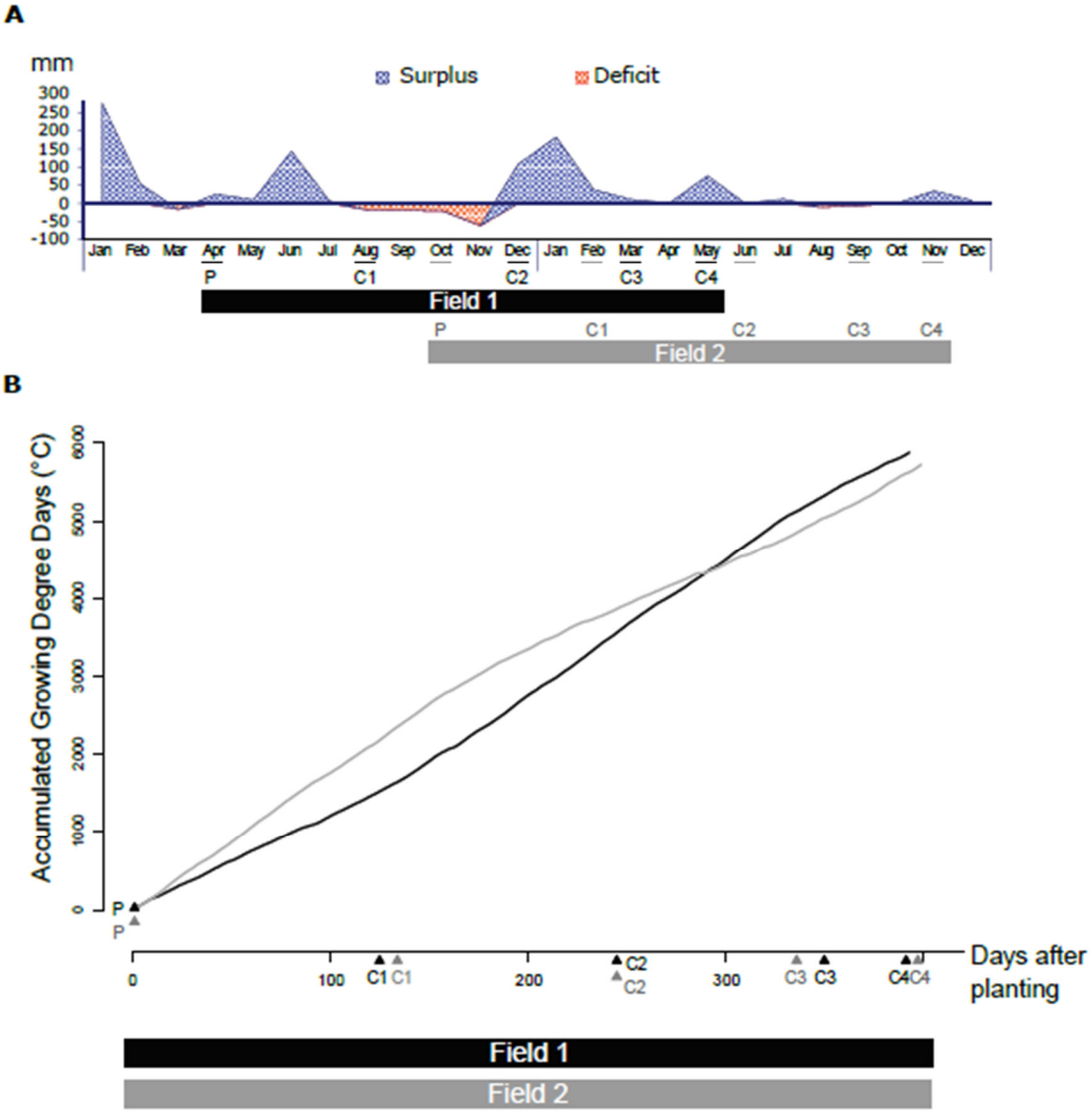


Figure S1. Soil water balance and Accumulated Growing Degree Days (AGDD) in field 1 (black bar) and field 2 (grey bar). C1, C2, C3 and C4 represent sampling points at 4, 8, 11 and 13 months after planting (P). (**A**) The Thornthwaite water balance in the soil is shown with surplus in blue and deficit in red. Inputs to the model are monthly temperature and precipitation. Data from UFSCar/CCA https://www.cca.ufscar.br/pt-br/servicos/dados-climatologicos/dados-climatologicos.xls (accessed on August 12, 2021). (**B**) AGDD values with triangles representing planting and sampling point, Black triangles in field 1 and grey triangles in field 2.

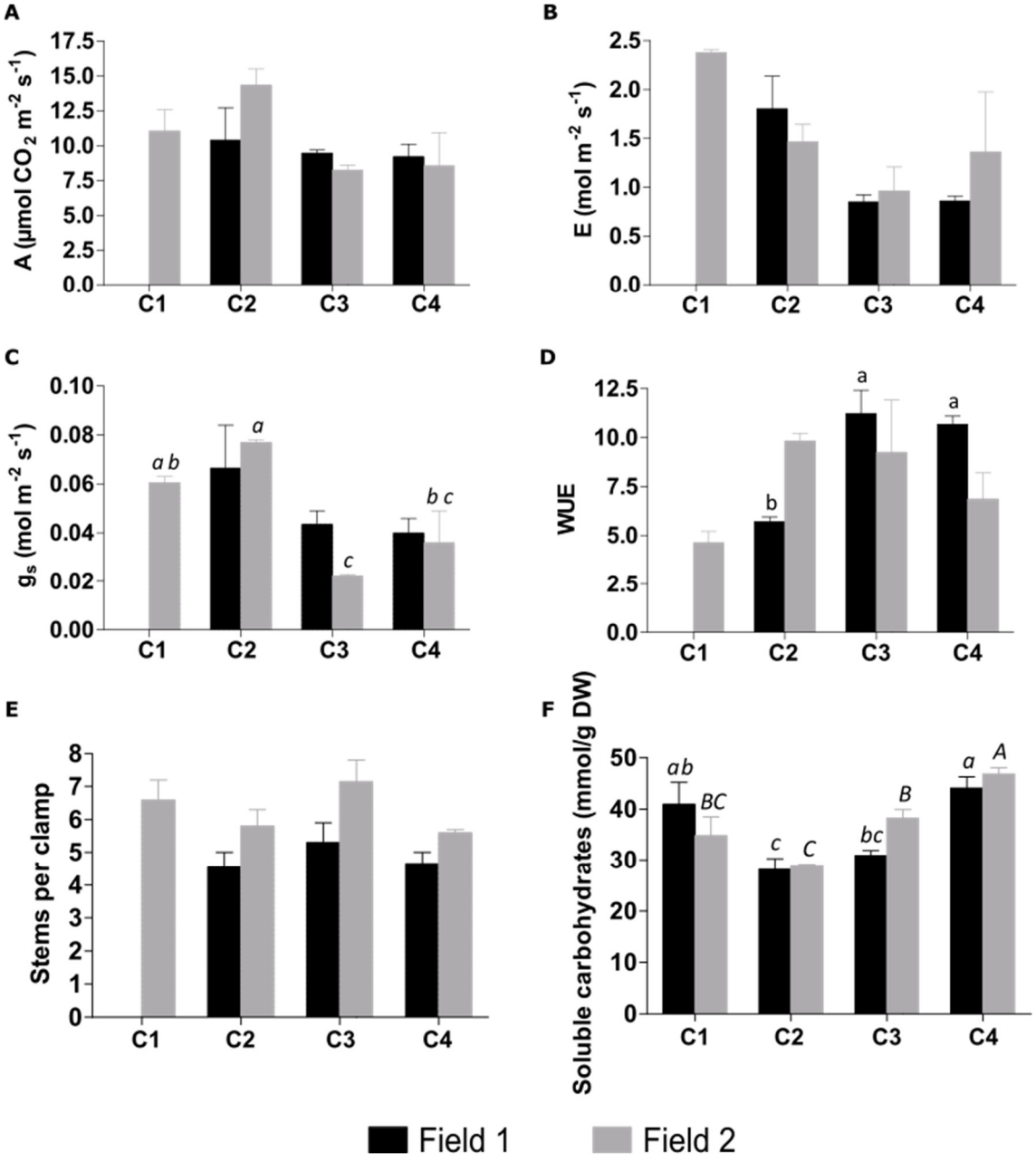


Figure S2. Instantaneous Photosynthetic rate (**A**), transpiration rate (**B**), stomatal conductance (**C**), water use efficiency (**D**), number of stems per clamp (**E**) and soluble carbohydrates in leaf (**F**) in field 1 and field 2 at 4 (C1), 8 (C2), 11 (C3) and 13 (C4)-month-old plants. Data was analyzed as split-plot scheme in balanced Completely Randomized Design (split2.crd). ANOVA and the multiple comparison test LSD were calculated. When the interaction between the two factors (field1 and field 2) was not significant, data was analyzed as Completely Randomized Design under one single factor. The analysis was done using ExpDes R Package. Regular letters and * are from split2.crd results. Bars with statistically different means are indicated by different letters (i.e. 'a' and 'b'). Bars with means that that are not statistically significant different are indicated with the same letter (i.e. 'a' and 'a') . Error bars show the standard error of the mean.

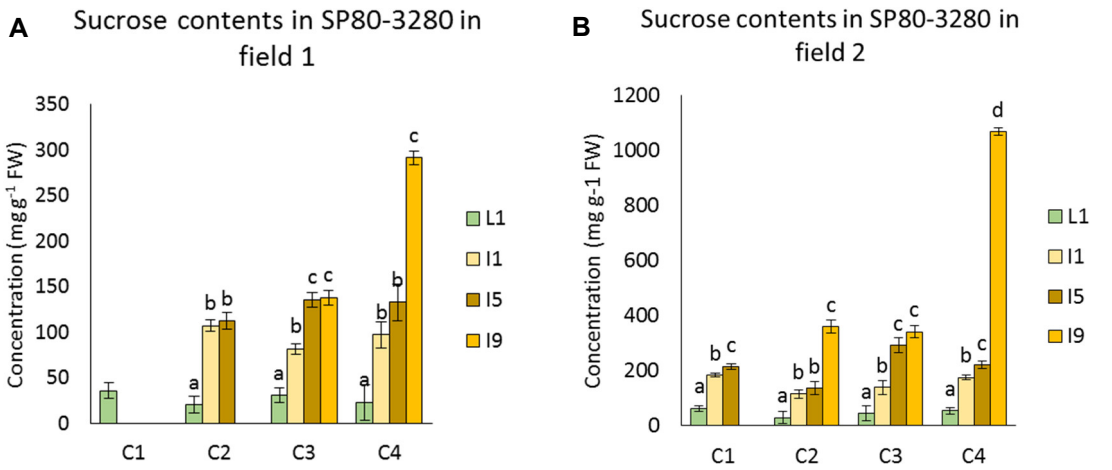


Figure S3. Sucrose contents in (**A**) field 1 and in (**B**) field 2. L1, I1, I5, and I9 refer to leaf +1 and immature, intermediate, and mature internodes. C1, C2, C3, and C4 refer to sampling points at 4, 8, 11, and 13 months after planting. The same letters (i.e. 'a' and 'a') indicate that the sucrose contents are not significantly different between the different developmental tissue within each sampling point based on ANOVA and Fisher's LSD (p-value < 0.05). Different letters (i.e. 'a' and 'b') indicate that sucrose contents are significantly different between the different developmental tissue within each sampling point based on ANOVA and Fisher's LSD (p-value < 0.05).

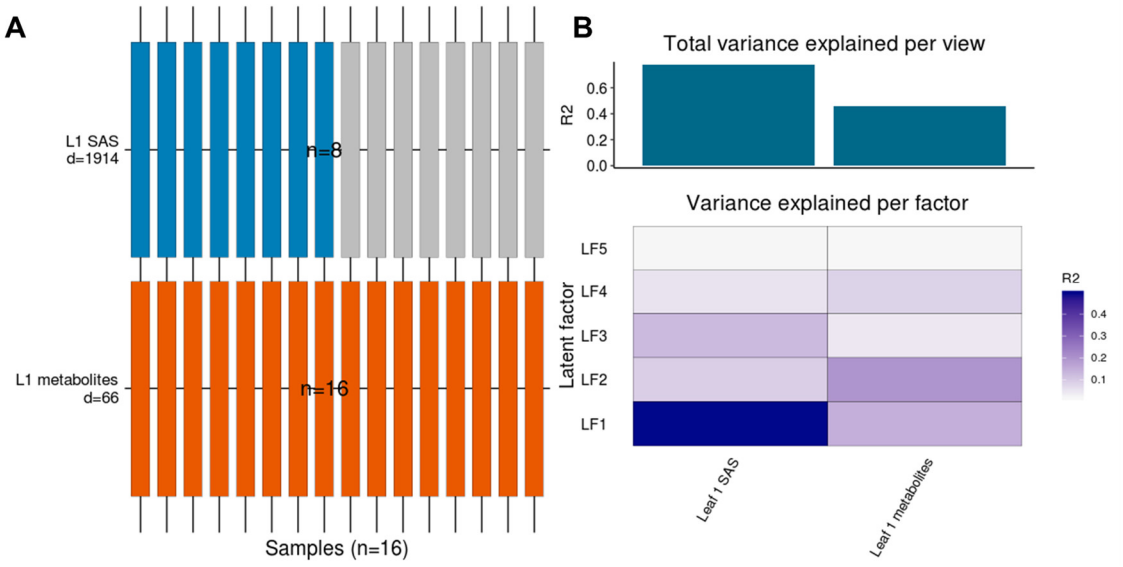


Figure S4. (**A**) Study overview and data types for leaf +1 (L1) collected from experimental field 1. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (**B**) Proportion of total variance explained (R^2) by individual data modalities (view) and the cumulative proportion of total variance explained per factor.

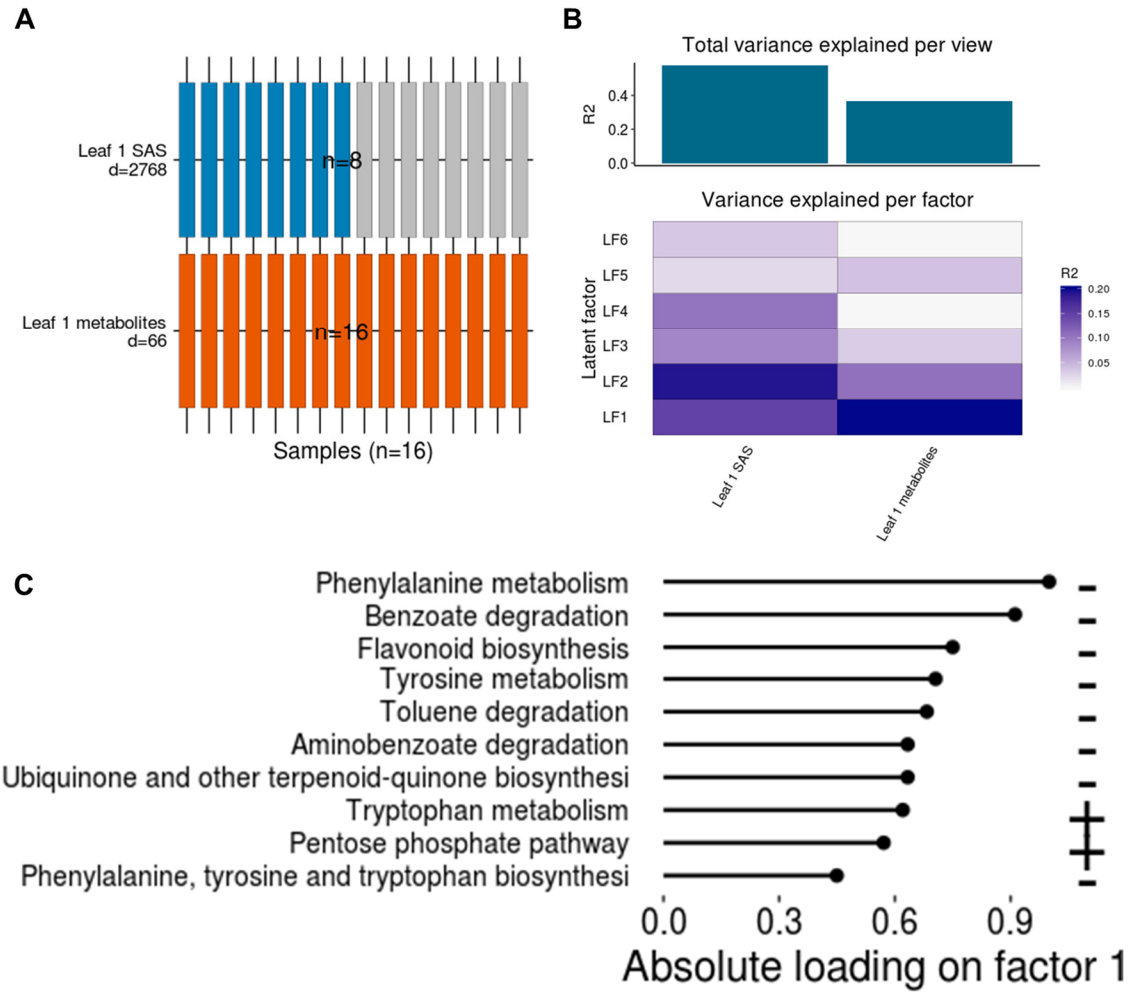


Figure S5. (**A**) Study overview and data types for leaf +1 (L1) collected from experimental field 2. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (**B**) Proportion of total variance explained (R^2) by individual data modalities (views) and the cumulative proportion of total variance explained per factor. (**C**) Absolute loadings of the top features of Latent Factors 1.

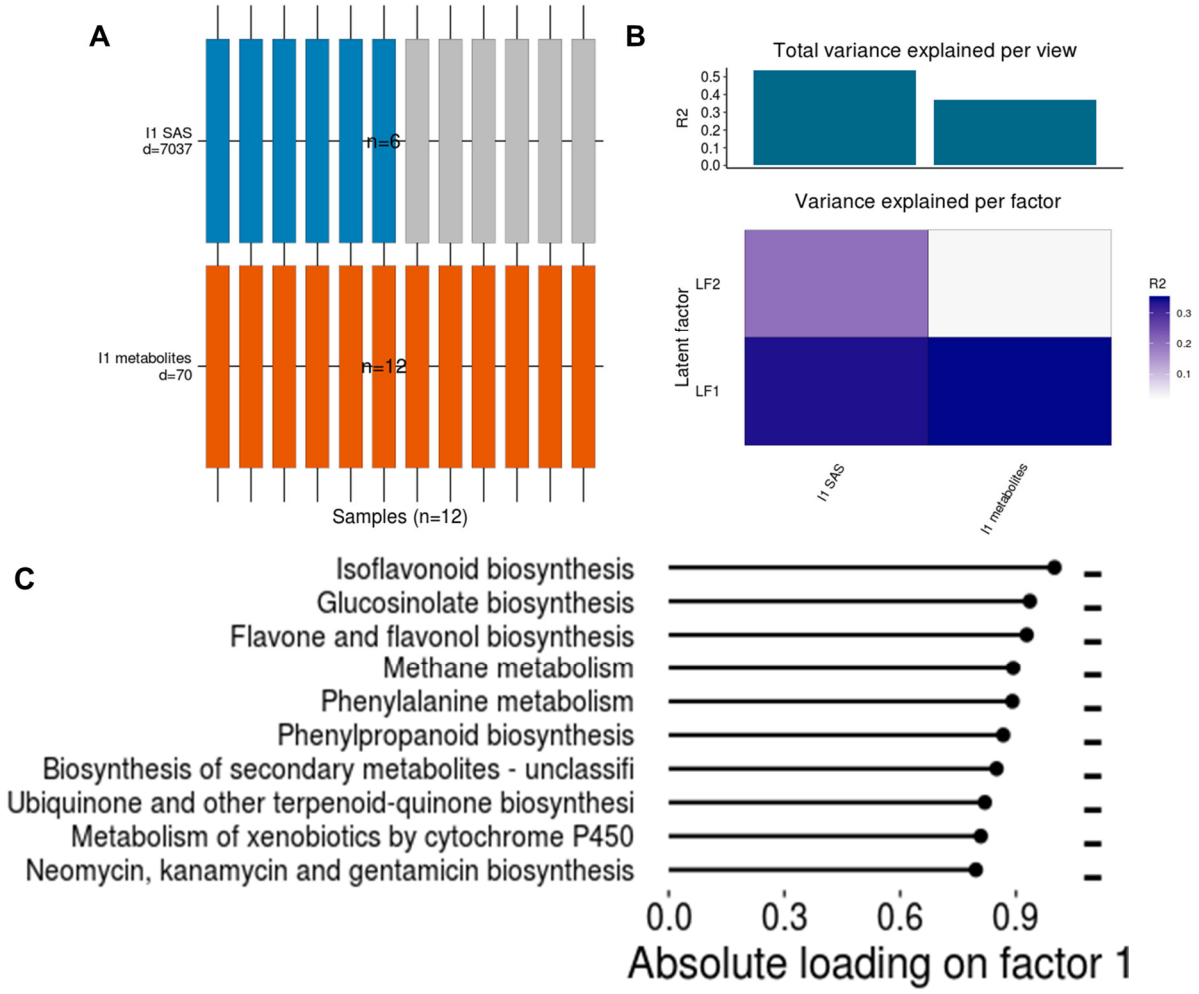
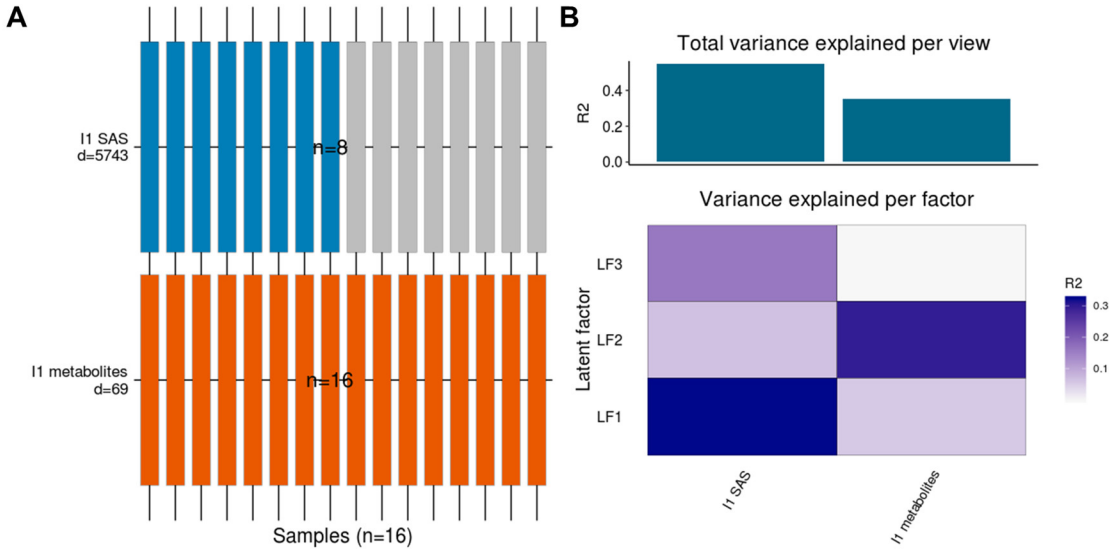


Figure S6. (**A**) Study overview and data types for immature internode (I1) collected from experimental field 1. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (**B**) Proportion of total variance explained (R^2) by individual data modalities (views) and the cumulative proportion of total variance explained per factor. (**C**) Absolute loadings of the top features of Latent Factor 1.



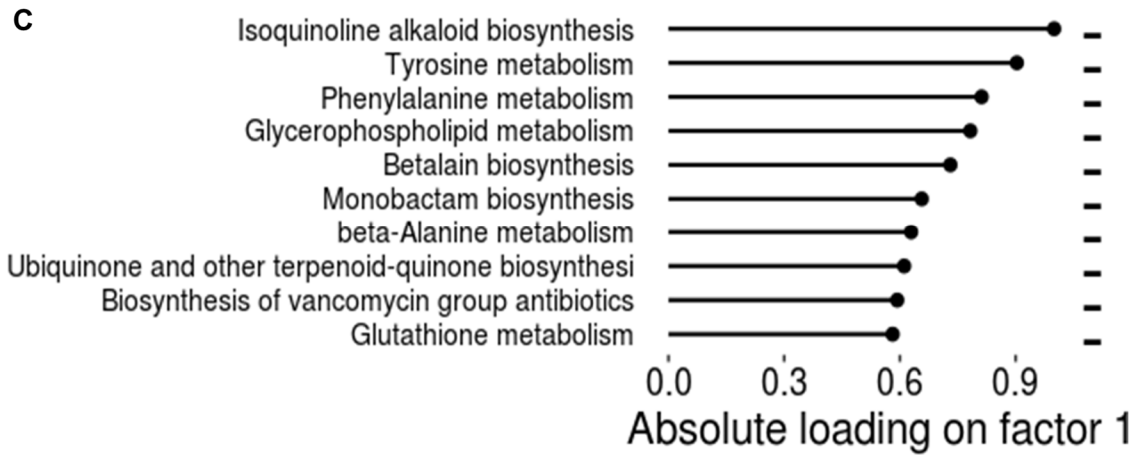


Figure S7. (**A**) Study overview and data types for immature internode (I1) collected from experimental field 2. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (**B**) Proportion of total variance explained (R^2) by individual data modalities (views) and the cumulative proportion of total variance explained factor (**C**). Absolute loadings of the top features of Latent Factors 1.

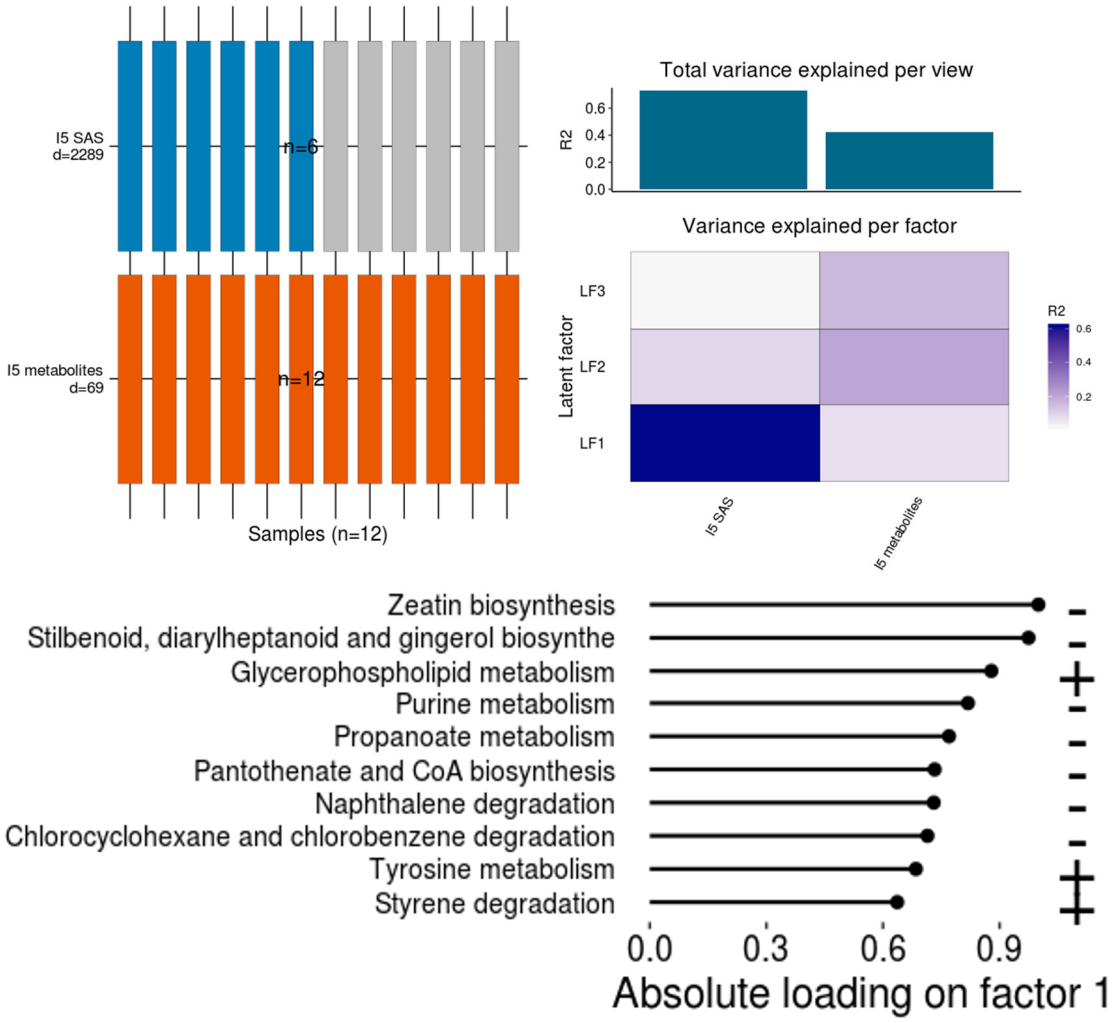


Figure S8. (A) Study overview and data types for the intermediate internodes (I5) collected from experimental field 1. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (B) Proportion of total variance explained (R^2) by

individual data modalities (views) and the cumulative proportion of total variance explained. (C) Absolute loadings of the top features of Latent Factors 1. No correlations or shared variance between the metabolomics and transcriptomics data modalities could be identified by MOFA in samples from the I5 collected from experimental field 2.

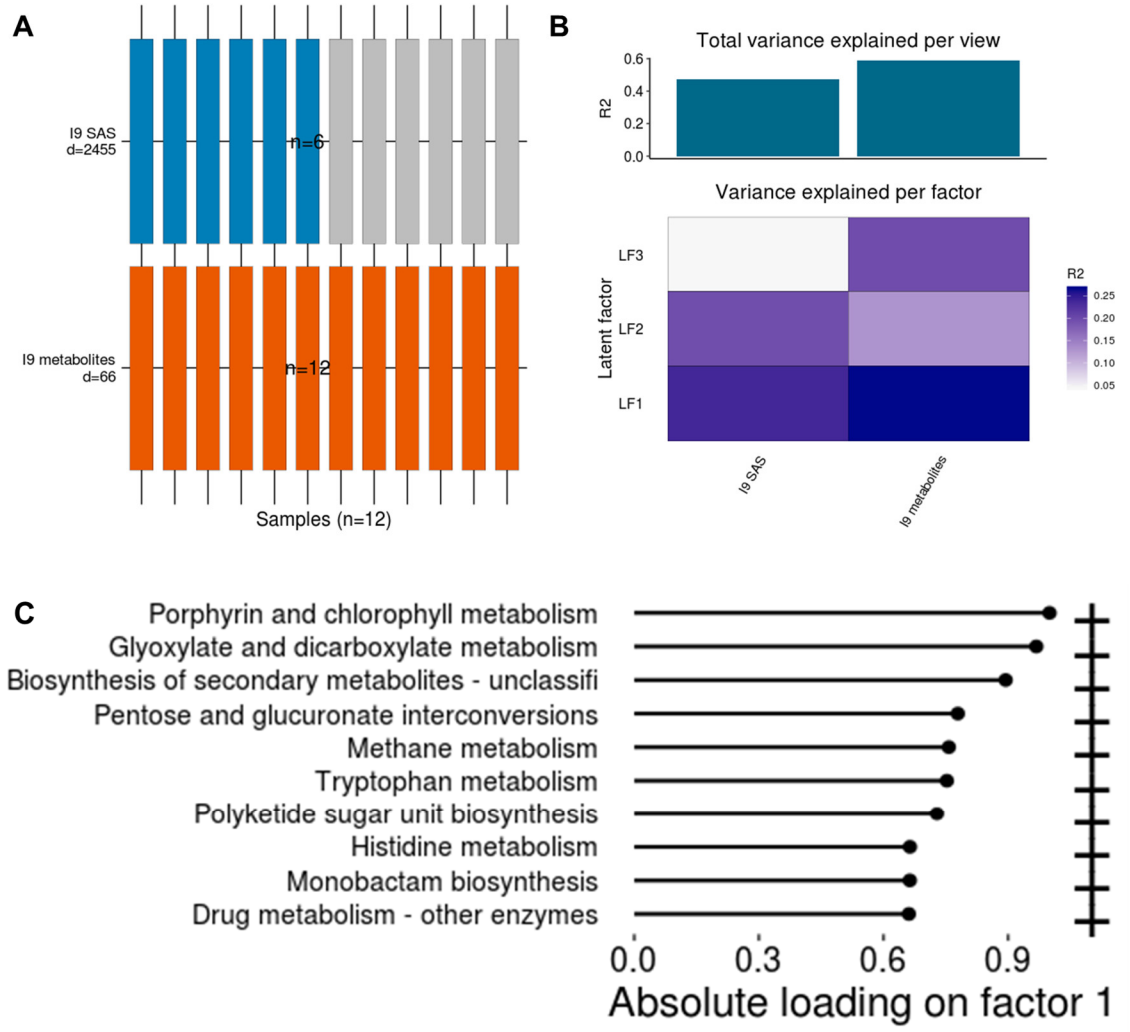


Figure S9. (**A**) Study overview and data types for mature internodes (I9) collected from experimental field 2. No correlations or shared variance between the metabolomics and transcriptomics data modalities could be identified by MOFA in I9 tissue collected from experimental field 1. Data modalities are shown in different rows (d = number of features) and samples (n) in columns, with missing samples shown using grey bars. (**B**) Proportion of total variance explained (R^2) by individual data modalities (views) and the cumulative proportion of total variance explained. (**C**) Absolute loadings of the top features of Latent Factors 1.

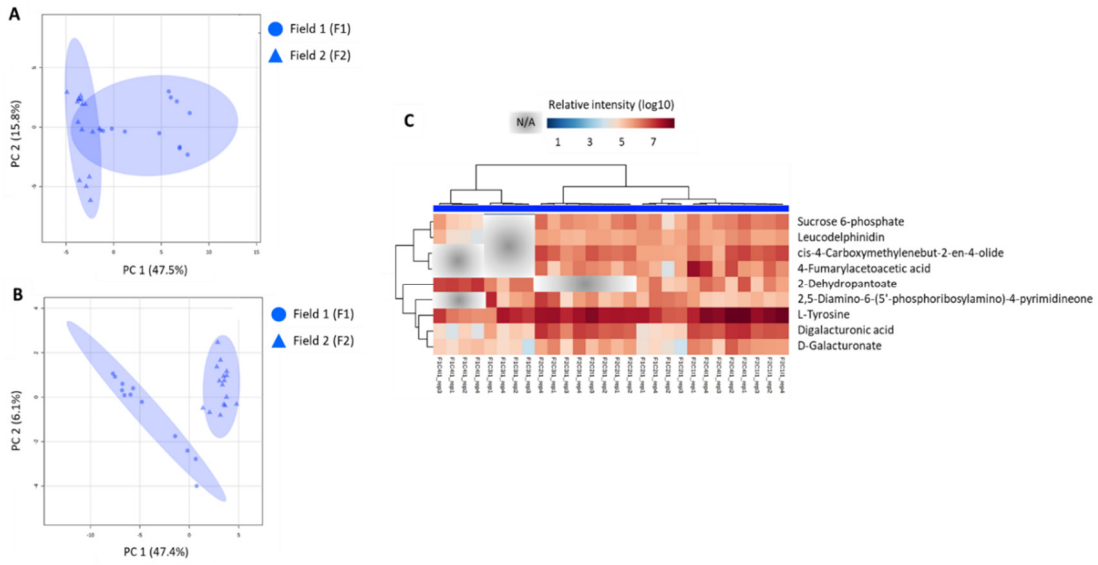


Figure S10. Discriminant models for the immature internode (I1) between fields. Discriminant models between field comparisons generated from the normalized and log10 transformed metabolomics data from the I1 tissues, combining sampling points (C1, C2, C3 and C4) and experimental fields (F1 and F2). (**A**) PCA and (**B**) PLS-DA models for I1 (component 1 Q2 = 0.70928, R2 = 0.75463 and component 2, Q2 = 0.8062, R2 = 0.91727); (**C**) Heatmap representation of the 9 main metabolites responsible for the separations (VIP scores ≥ 1.0 from PLS-DA analysis) and NA refers to non-detected metabolites.

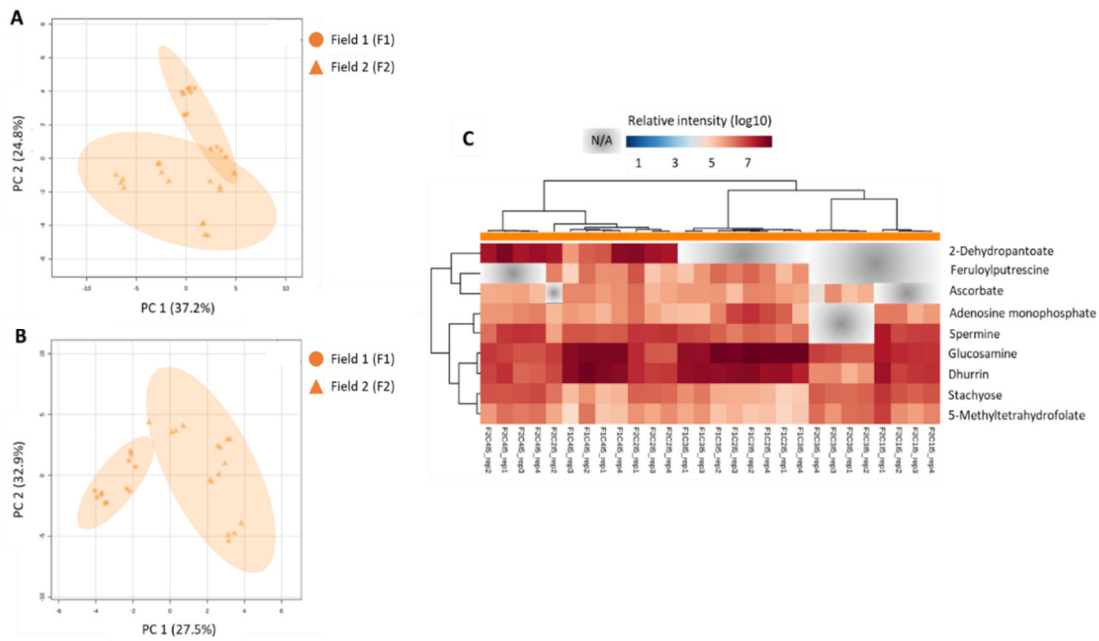


Figure S11. Discriminant models for the intermediate internode (I5) between fields. Discriminant models for between field comparisons generated from the normalized and log10 transformed metabolomics data from the I5 tissues, combining sampling points (C1, C2, C3 and C4) and experimental fields (F1 and F2). (**A**) PCA and (**B**) PLS-DA models for I5 (component 1 Q2= 0.7642, R2 = 0.82433 and component 2 Q2 = 0.78814, R2= 0.861); (**C**) Heatmap representation of the 9 main metabolites responsible for the separations (VIP scores ≥ 1.0 from PLS-DA analysis) and NA refers to non-detected metabolites.

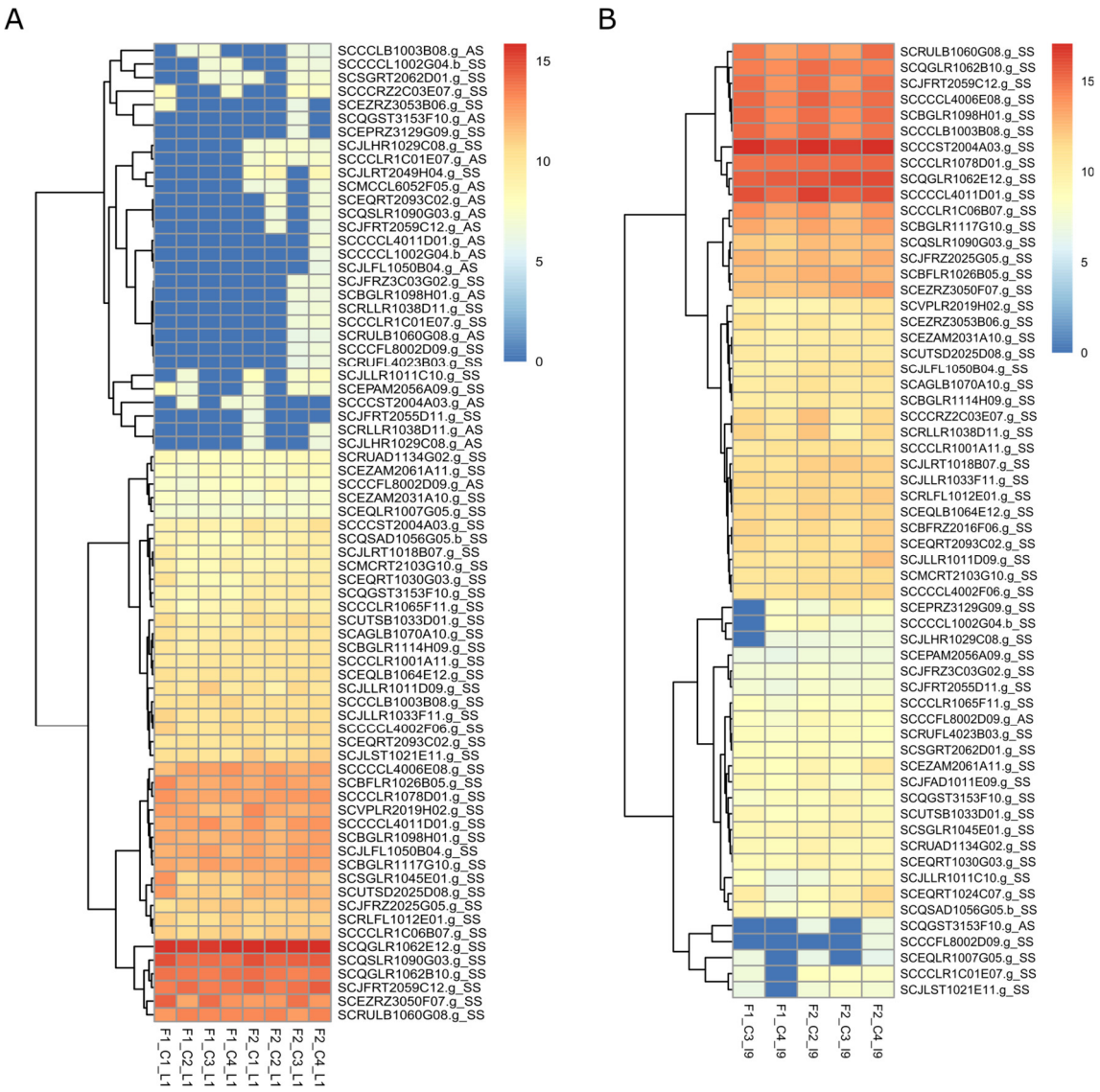


Figure S12. Natural antisense transcript expression of genes from the Phenylalanine, tyrosine and tryptophan biosynthesis pathways differs between field 1 and field 2 in leaves. Heatmap of gene expression level from genes in the (**A**) leaf +1 (L1) and in the (**B**) mature internode (I9) tissues in field 1 (F1) and field 2 (F2), and sampling points (C1, C2, C3 and C4).

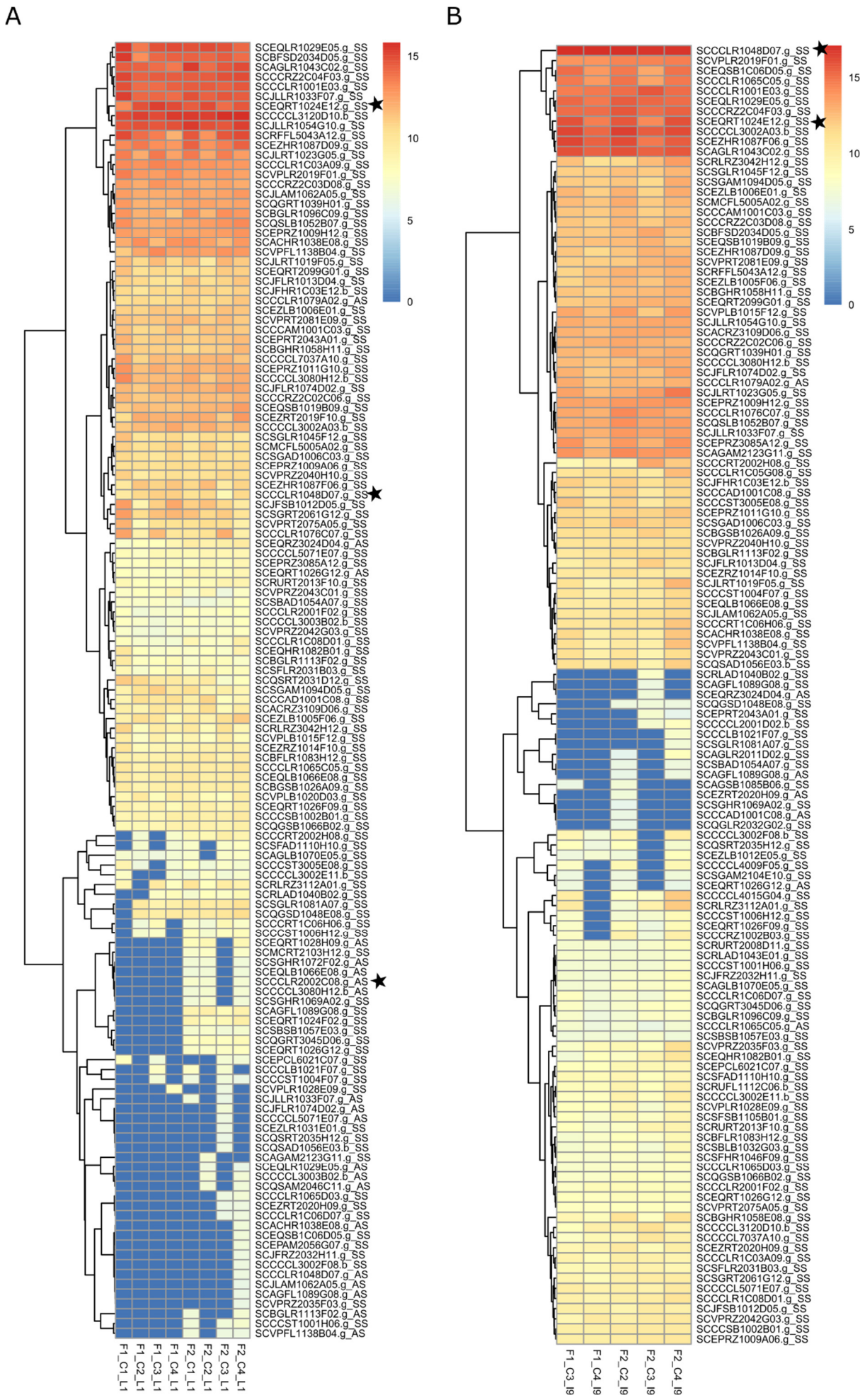

A
B
15
10
5
0
F1_C1_L1
F1_C2_L1
F1_C3_L1
F1_C4_L1
F2_C1_L1
F2_C2_L1
F2_C3_L1
F2_C4_L1
F1_C3_I9
F1_C4_I9
F2_C2_I9
F2_C3_I9
F2_C4_I9

Figure S13. Natural antisense transcript expression of genes from the Phenylpropanoid biosynthesis pathways differs between field 1 and field 2 in leaves. Heatmap of gene expression level from genes in the (**A**) leaf +1 (L1) and in the (**B**) mature internode (I9) tissues in field 1 (F1) and field 2 (F2), and sampling points (C1, C2, C3 and C4). The five-pointed stars indicate transcripts cited in the manuscript.

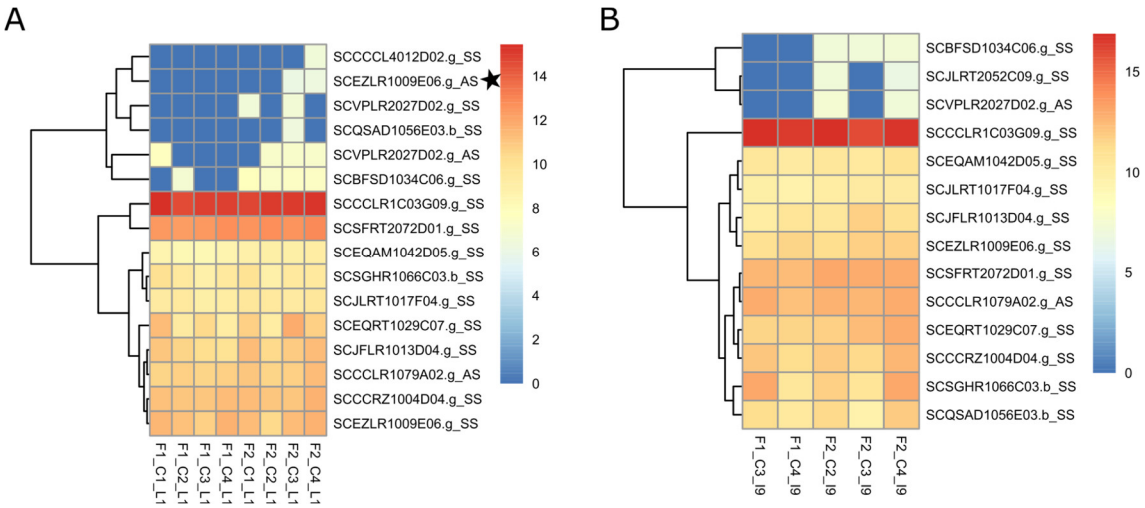


Figure S14. Gene expression of genes from the Flavonoid biosynthesis pathways in field 1 and field 2. Heatmap of gene expression level from genes in the (**A**) leaf +1 (L1) and in the (**B**) mature internode (I9) tissues in field 1 (F1) and field 2 (F2), and sampling points (C1, C2, C3 and C4). The five-pointed star indicates transcripts cited in the manuscript.