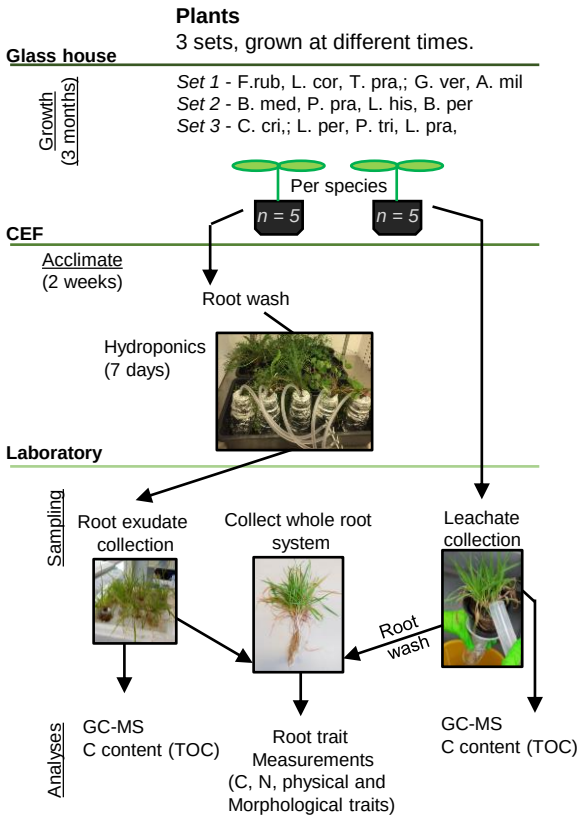
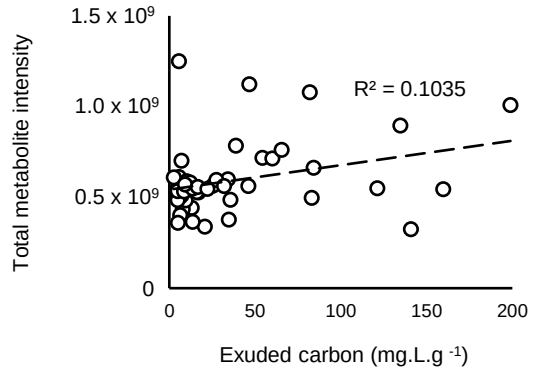
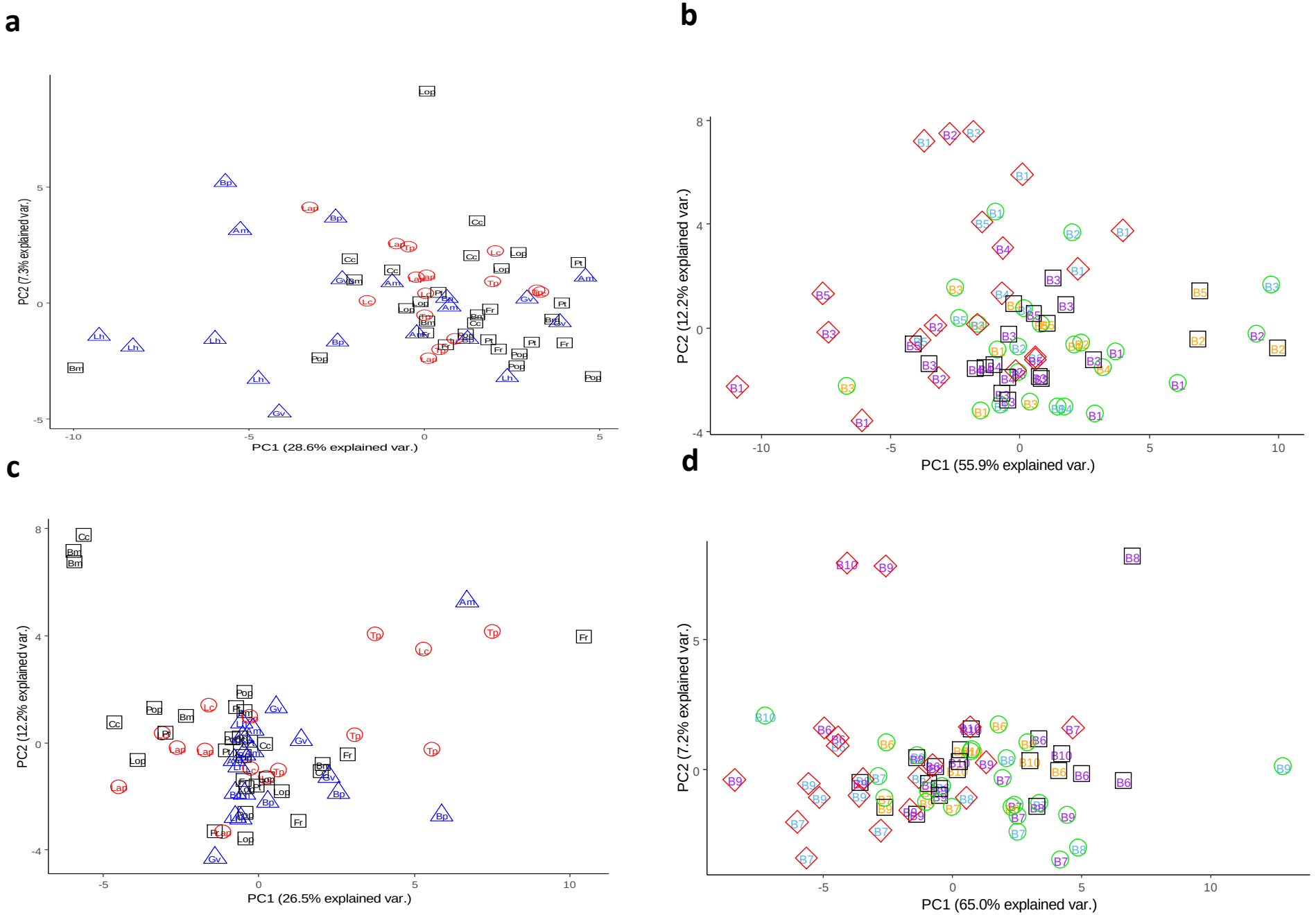


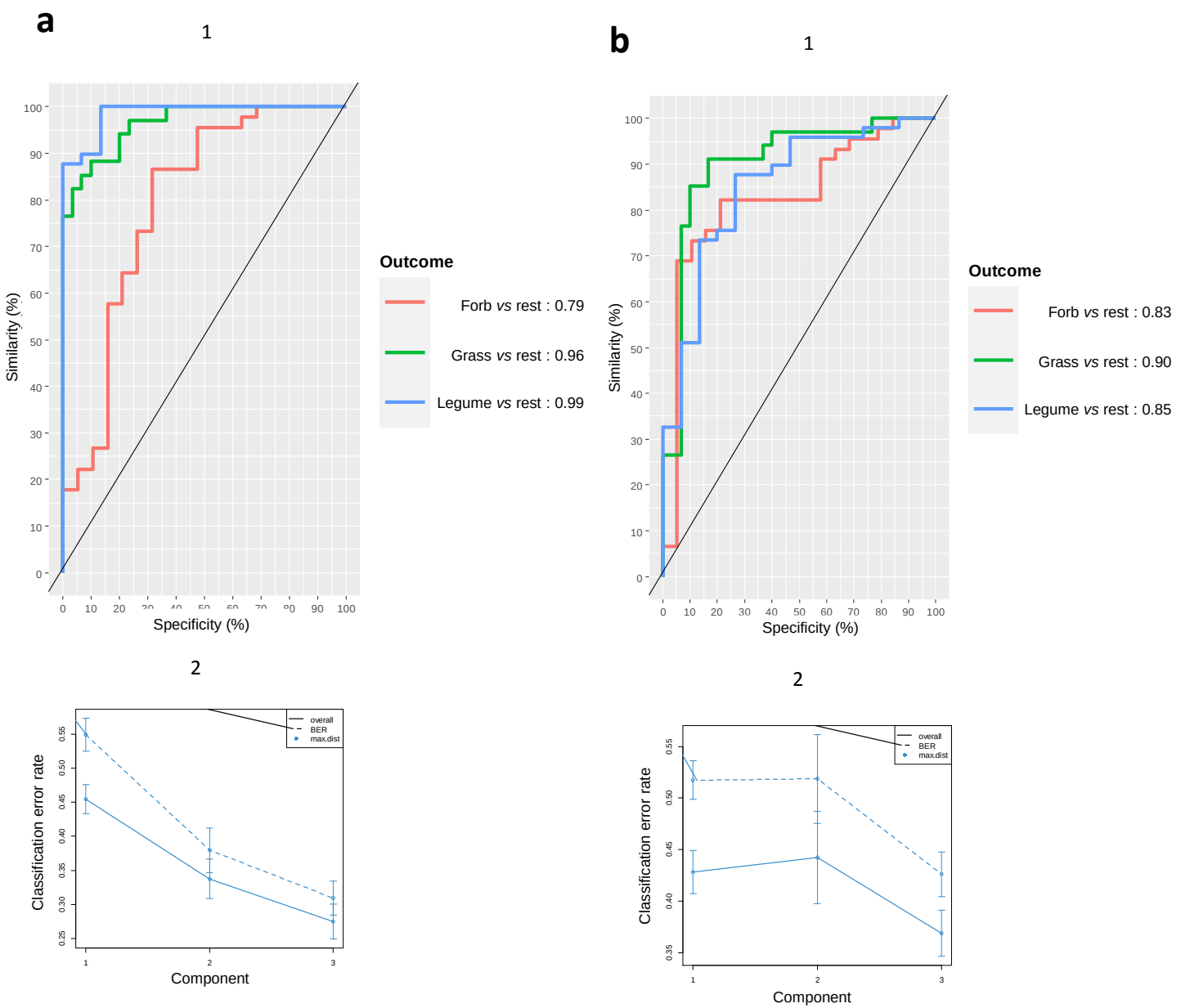
Supplemental Figure 1 Schematic of methodological design of root exudate and leachate sampling. Samples of each species were designated for either hybrid rot exudate collection or leachate collection. Plants were grown for 3 months in a glass house, before transfer to controlled environment facility (CEF) to acclimate for 2 weeks. Hybrid plants were then root washed and left to recover in hydroponics solution for a week before exudate collection. Separate plants were taken for leachate collection, prior to root washing. Afterwards, clean roots were measured for various root traits and exudates and leachate were sent for metabolomics analysis with GC-MS or C quanitification with TOC. Species; B. med, *Briza media*; C. cri, *Cynosurus cristatus*; L. per, *Lolium perenne*; F.rub, *Festuca rubra*; P. pra, *Poa pratensis*; P. tri, *Poa trivialis*; L. cor, *Lotus corniculatus*; L. pra, *Lathyrus pratensis*; T. pra, *Trifolium pratense*; G. ver, *Galium verum*; L. his, *Leontodon hispidus*; A. mil, *Achillea millefolium*; B. per, *Bellis perennis.*



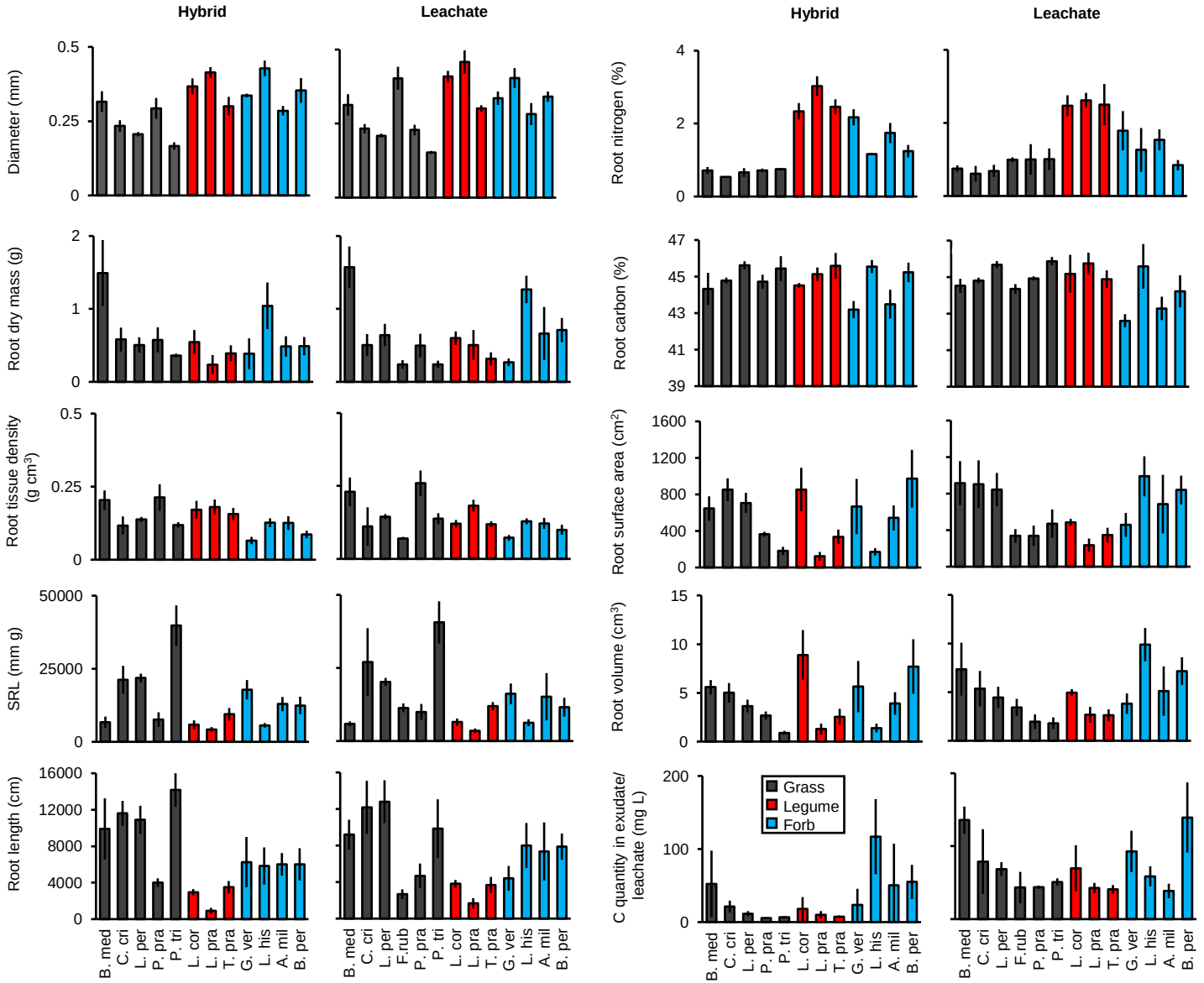
Supplemental Figure 2 Relationship between total metabolite area of exudates and exuded carbon. The significant positive relationship (linear regression $F_{1, 55}$=6.4, R^2=0.1035, p=0.0146) shows that the total metabolite intensity (calculated as total area under the peaks from GC-MS) are explained by the quantity of exuded carbon.



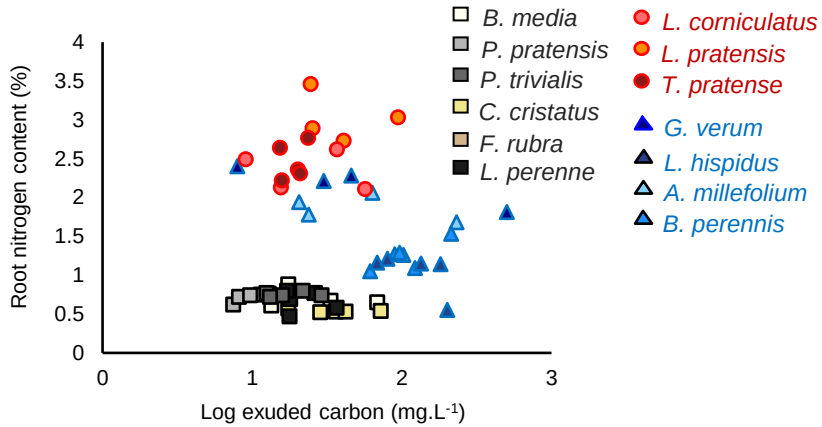
Supplemental Figure 3 PCA scores plots of root exudate profiles across different species. Comparison of the raw root metabolome profiles between grasses (dark grey squares), legumes (red circles) and forbs (blue triangles) from hydroponic exudates (a) and leachate (c). After a dry-weight correction was applied, these samples were checked for random effect of growth set (b and d) where no clear pattern is discernible.



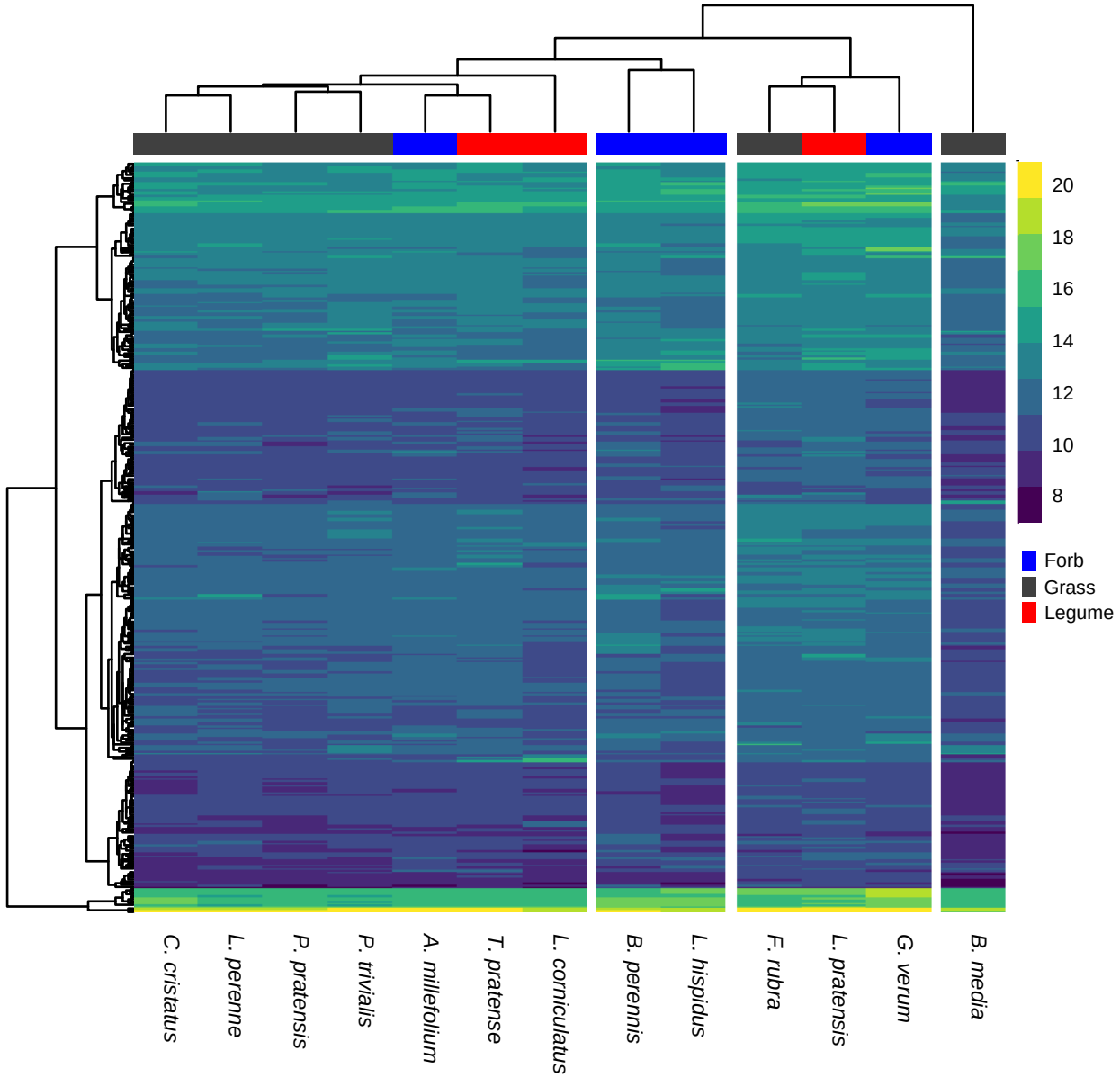
Supplemental Figure 4 sPLS-DA model performance and validation. For hydroponics (a) and leachate (b). Area under curve plots are shown for the 3rd components, which cover most of the variation (panel 1). The balanced error rates are shown for 3 components in the optimised model (panel 2).



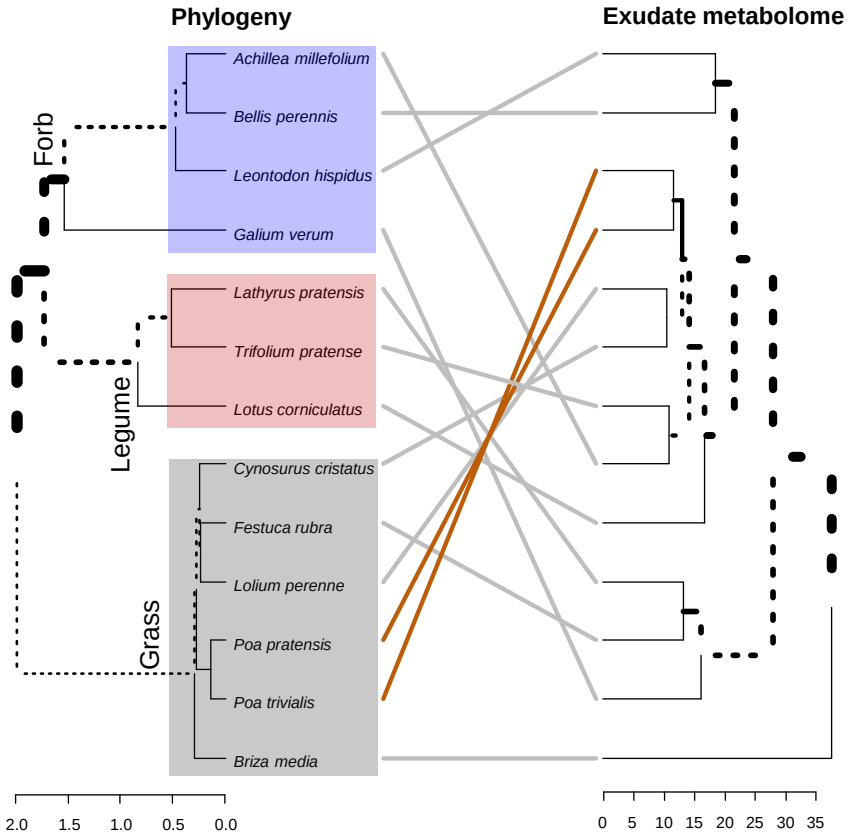
Supplemental Figure 5 Raw root trait data for the species of grass, forb and legume used in this work. Species are coloured by functional group and are annotated as follows; B. med, Briza media; C. cri, Cynosurus cristatus; L. per, Lolium perenne; F.rub, Festuca rubra; P. pra, Poa pratensis; P. tri, Poa trivialis; L. cor, Lotus corniculatus; L. pra, Lathyrus pratensis; T. pra, Trifolium pratense; G. ver, Galium verum; L. his, Leontodon hispidus; A. mil, Achillea millefolium; B. per, Bellis perennis.



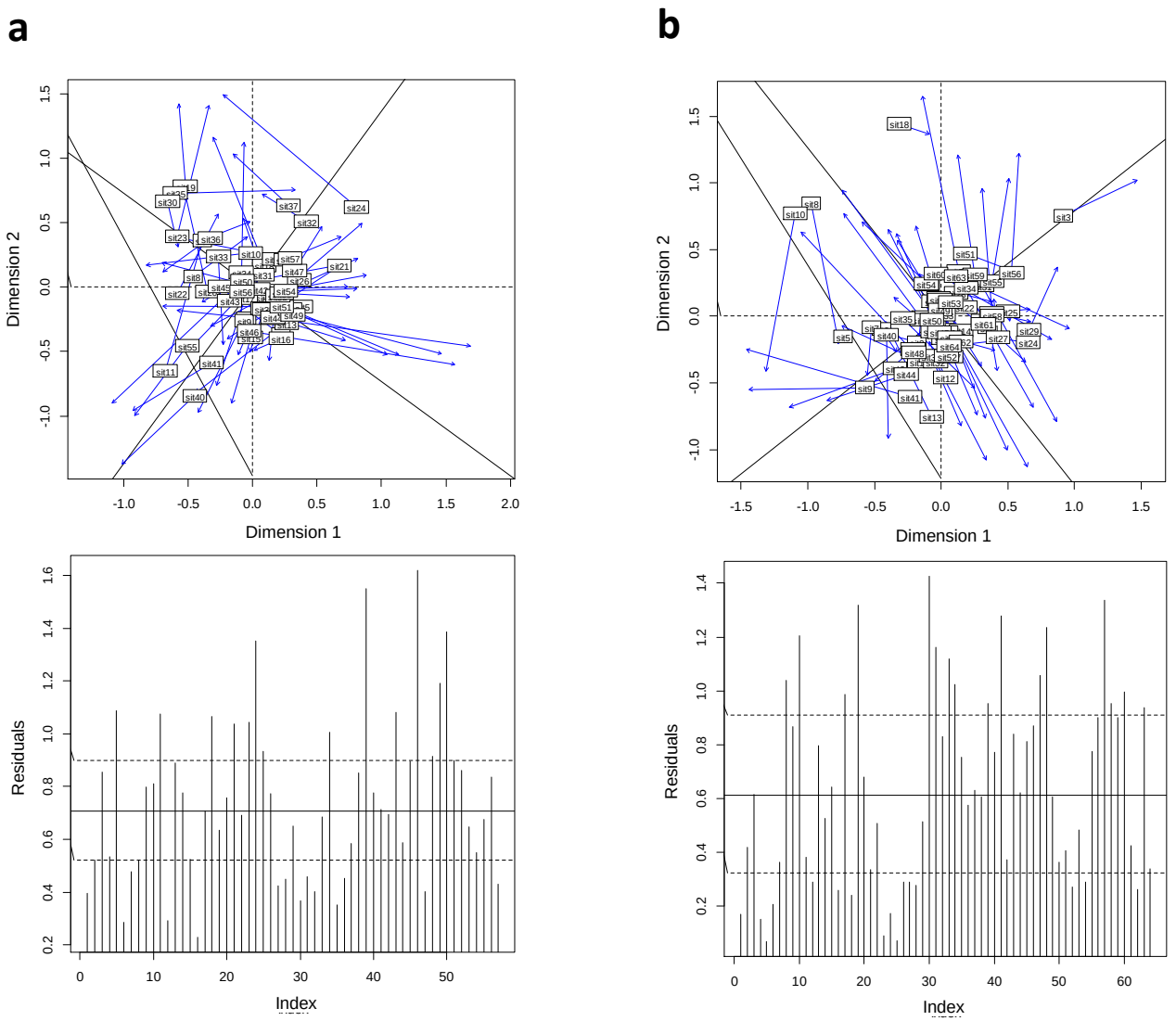
Supplemental Figure 6 Scatter plots of specific exudation rate against root nitrogen content across different species. Grasses (dark grey squares), legumes (red circles) and forbs (blue triangles). Exuded is mg per litre of exudate.



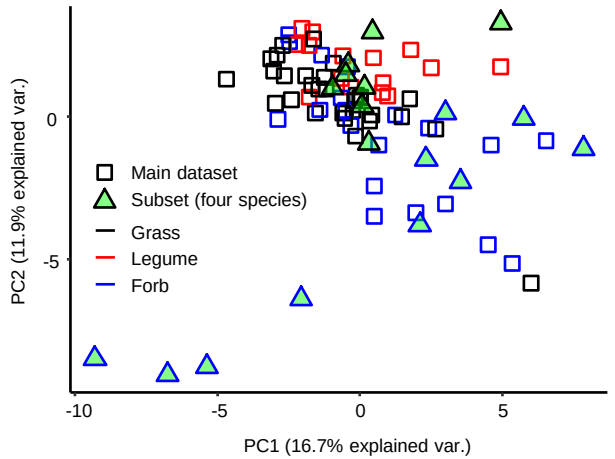
Supplemental Figure 7 Heatmap of all metabolites of all 14 species showing the phylogenetic signal of the entire dataset. Rows on Y-axis indicate individual $\log_{10}$ transformed metabolites, corrected for root dry weight. Columns are the average values of each species. Abundance of metabolites is represented by colour gradient, with yellow indicating high values and blue low values. The tree indicates how related the profile of each species is. Functional groups are indicated below the tree (grass, grey; legume, red; forb, blue); species are named beneath the heatmap.



Supplemental Figure 8 Tanglegram between dendograms generated for phylogenetic relationship (left) and exudate metabolome (right). Functional groups are coloured in boxes to the left and species are labelled. Similar sub-trees are connected by lines of the same colour, while branches leading to distinct sub-trees are marked by a dashed line.



Supplemental Figure 9 Procrustes matching of root-trait profiles and metabolome datasets. Ordination plots represent a visual indication of the degree of match between the two ordinations (top panels) in hydroponics (a) and leachate (b). Symbols show the position of the samples in the first ordination (root traits), and arrows point to their positions in the target ordination (metabolome). The rotation factor to match the two ordinations is indicated by the degree of offset between the black lines and the dotted lines Line plots (bottom panel) show the residuals for each sample. The horizontal lines are the 25% (dashed), 50% (solid), and 75% (dashed) quantiles.



Supplemental Figure 10 PCA scores plots of root exudate profiles across main dataset and subset. Comparison of the raw root metabolome profiles show that the subset and main dataset roughly match in terms of the metabolites identified. The subset are displayed in green highlighted triangles, the main dataset are shown in open squares. Line colour corresponds to functional group.

Supplemental Table 1 Spearman's rank correlation of root traits against specific exudation rate.

Root trait	Rho	*p*-value	R^2
RTD	-0.51	0.00005	0.2739
D	0.35	0.00771	0.1281
RN	0.09	0.49380	0.0016
RC	0.05	0.73090	0.0569
DW	0.03	0.84050	0.0014
SA	-0.03	0.80030	0.0031
Length	-0.02	0.87640	0.0105
Vol	0.02	0.85400	0.0014
SRL	0.01	0.94220	0.0078

DW, root dry biomass; RTD, root tissue density; SRL, specific root length; RC, root carbon; RN, root nitrogen; SA surface area; Vol, root volume.