

Table. S1. Correlations between variables determined using Pearson's coefficient. Asterisks indicate significant correlation at P<0.05 (*) or P< 0.01 (**). r= root, l= leaf, dw=dry weight, TP=total phenols, GS=glutamine synthetase, GOGAT=glutamate synthase, FRU=fructose, GLU=glucose, PROT=proteins.

[illegible]

Table S2. Loadings values of the plant variables on the axes identified by principal components (PC) analysis for the different types of treatment and control. r= root, l= leaf, dw=dry weight, TP=total phenols, GS=glutamine synthetase, GOGAT=glutamate synthase, FRU=fructose, GLU=glucose, PROT=proteins.

Variable	PC		
	1	2	3
GS_r	0.959	0.247	-0.107
GLU_r	-0.958	-0.233	0.137
GOGAT_r	0.954	0.248	-0.127
SPAD	0.954	0.249	-0.127
TP	0.952	0.241	-0.139
DW_r	0.868	-0.085	0.345
GLU_l	0.822	-0.485	0.046
RUBISCO	0.669	0.447	0.533
GOGAT_l	0.106	0.938	0.071
PROT	0.303	0.843	0.094
FRU_l	0.443	0.812	0.012
DW_l	0.093	-0.733	0.408
GS_l	0.297	-0.283	-0.872
FRU_r	-0.010	-0.452	0.825

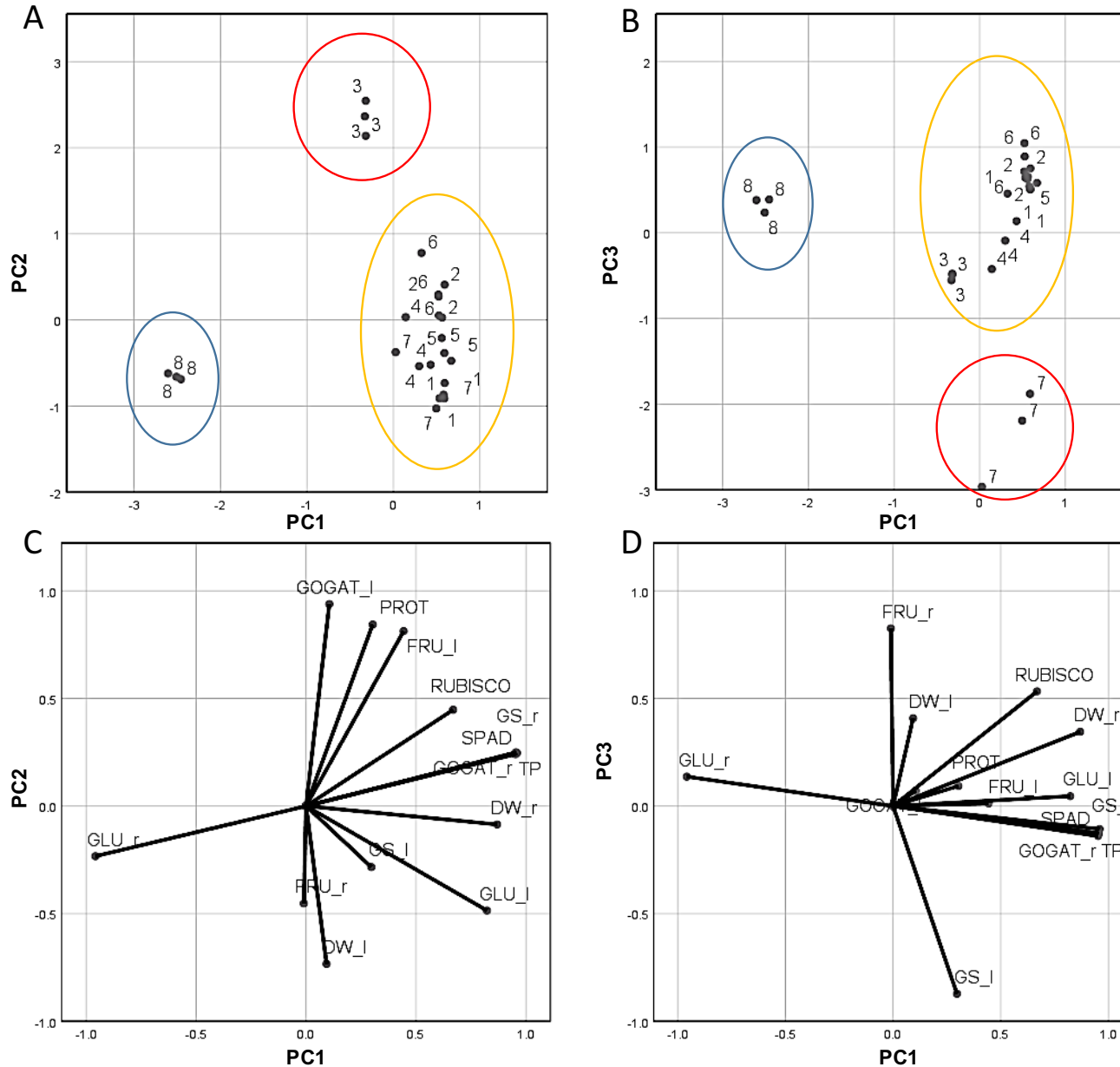


Figure S1. Position of the treated and untreated plants (1=LS1, 2=LS2, 3=LS3, 4=LS4, 5=LS5, 6=PH, 7=LH, and 8=control) in the reduced space of the first two principal components (PC1 and PC2) (A) and on PC1 and PC3 (B); variables projected in the plane determined by PC1 and PC2 (D) and PC1 and PC3 (C). r= root, l= leaf, dw=dry weight, TP=total phenols, GS=glutamine synthetase, GOGAT=glutamate synthase, FRU=fructose, GLU=glucose, PROT=proteins.

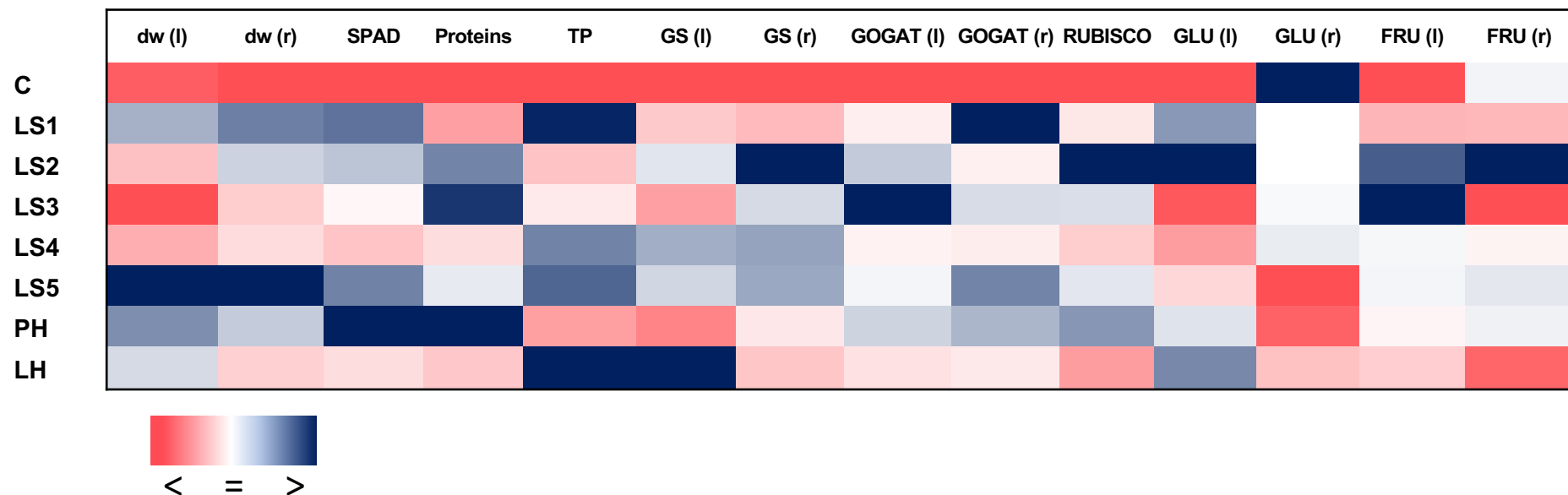


Figure S2. Heat map of plant-associated parameters influenced by individual humates. Different colors indicate different levels of induction/repression (more red more repression, more blue more induction). r= root, l= leaf, dw=dry weight, TP=total phenols, GS=glutamine synthetase, GOGAT=glutamate synthase, FRU=fructose, GLU=glucose, PROT=protein.