

LEGENDS FOR SUPPORTING INFORMATION

Supplementary Figure 1. Double girdling promotes flowering in Citrus buds regardless of the presence of fruit, the node position and the date of treatment. A-B) Effect on the number of vegetative shoots and flowers, respectively, and C) in different dates and year. ON (with fruit, ungirdled), ON apical girdled (A-G), or apical and basal girdled (AB-G), and OFF (without fruit) shoots. D) Pictures showing the phenotype. All the shoots had the same number of nodes. Different letters or * indicate significant differences ($P < 0.05$; Data analyzed using ANOVA followed by Tukey's HSD test). Data are means and standard errors of 25 biological replicates.

Supplementary Figure 2. Double girdling promotes *CiFT3* upregulation and flowering in Citrus regardless of cold temperatures and the presence of fruit. A-B) Relative expression of *CiFT3* and *CcMADS19* genes in the leaf, respectively. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots. R.U. indicate relative units. Different letters indicate significant differences ($P < 0.05$; Data analyzed using ANOVA followed by Tukey's HSD test). Data are means and standard errors of 3 biological replicates.

Supplementary Figure 3. Principal Component Analysis (PCA) of RNA-seq data during floral induction reveals distinct transcriptional responses between leaves and buds in flowering versus non-flowering Citrus phenotypes. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots, SF (with small fruit, ungirdled).

Supplementary Figure 4. Functional analysis categories of RNA-seq data in the leaves during floral induction reveals the main transcriptional responses in flowering vs non-flowering Citrus phenotypes. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots, SF (with small fruit, ungirdled).

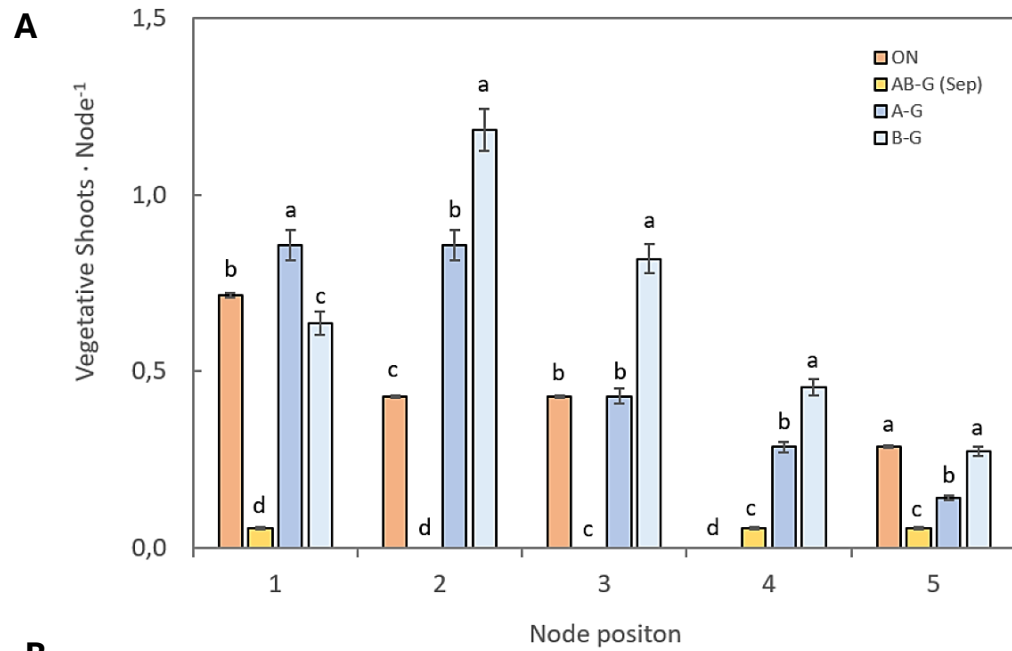
Supplementary Figure 5. Differentially Expressed Genes (DEGs) of the functional categories *polysaccharides hydrolysis* and *photosynthesis* of RNA-seq data in the leaves during floral induction in flowering vs non-flowering Citrus phenotypes.

Supplementary Figure 6. Differentially Expressed Genes (DEGs) of the functional category *Alpha-amino acid metabolic process* of RNA-seq data in the leaves during floral induction in flowering vs non-flowering Citrus phenotypes, and glutamine, tryptophan and methionine relative concentrations in leaves. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots. Different letters indicate significant differences ($P < 0.05$; Data analyzed using ANOVA followed by Tukey's HSD test). Data are means and standard errors of 3 biological replicates.

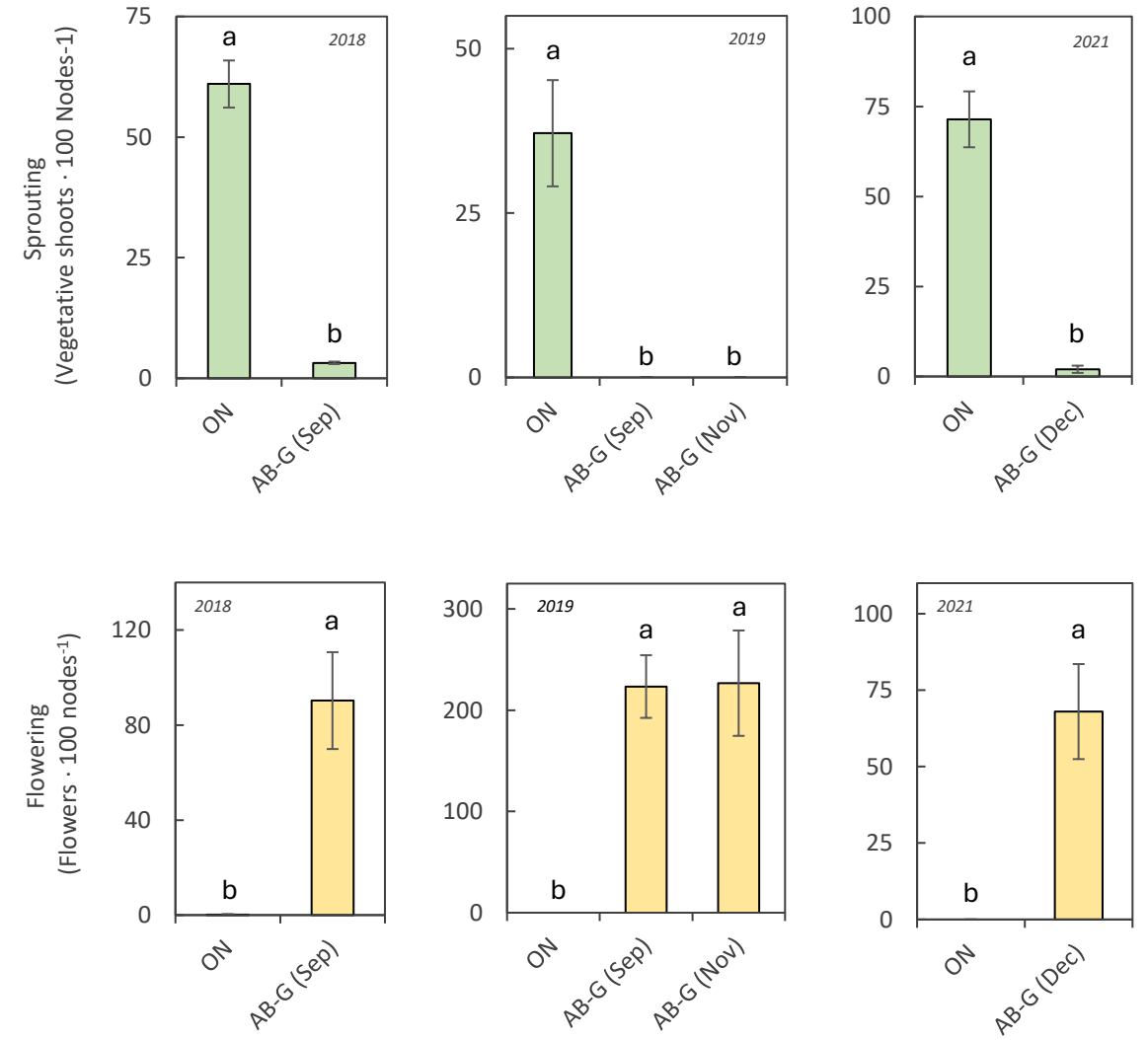
Supplementary Figure 7. Maltose (75mM) increases *CiFT3* expression in Citrus leaf protoplasts, incubated during 15 hours. Data analyzed using t-test. Data were obtained from 3 biological replicates with 3 technical replicates each.

Supplementary Figure 8. Functional analysis categories of RNA-seq data in the leaves during floral induction reveals the main transcriptional responses in flowering vs non-flowering Citrus phenotypes. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots, SF (with small fruit, ungirdled).

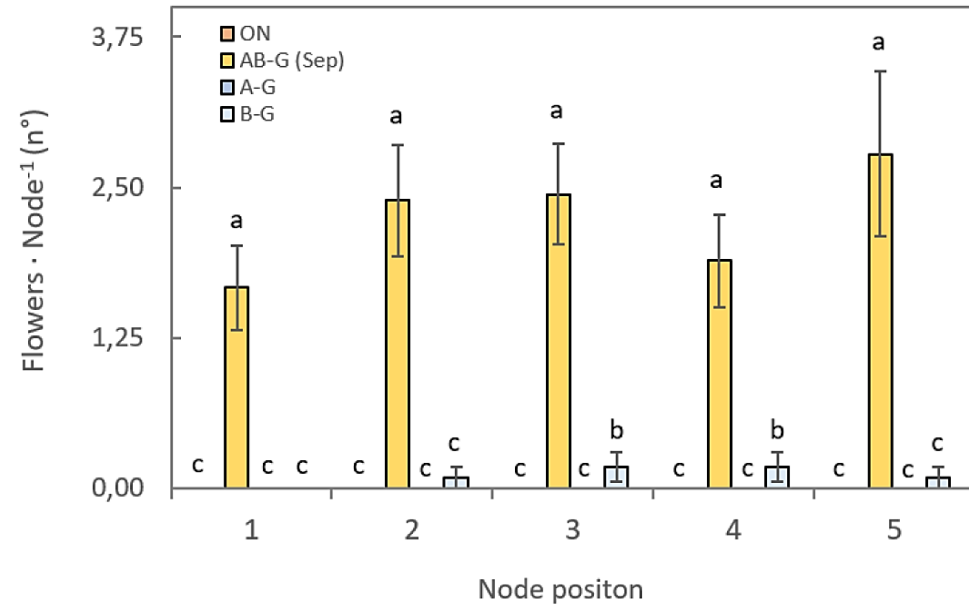
Supplementary Figure 9. Double girdling reduces GA1 content in Citrus buds. ON (with fruit, ungirdled), ON apical-basal girdled (AB-G) and OFF (without fruit) shoots. (* $P < 0.05$; ** $P < 0.01$; Data analyzed using ANOVA followed by Tukey's HSD test). Data are means and standard errors of 3 biological replicates. .



C



B



Supplementary Figure 1

D



ON



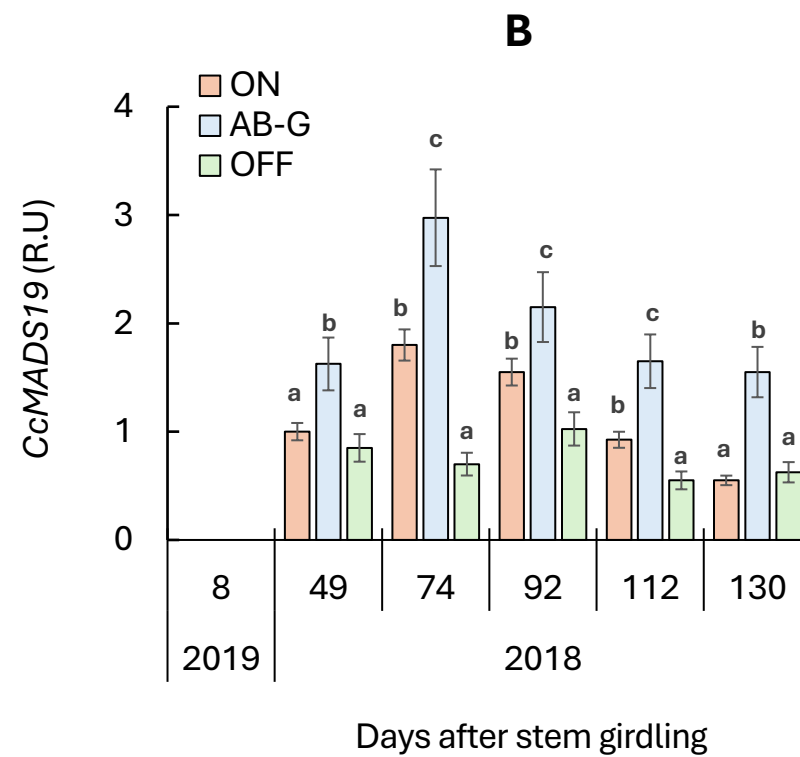
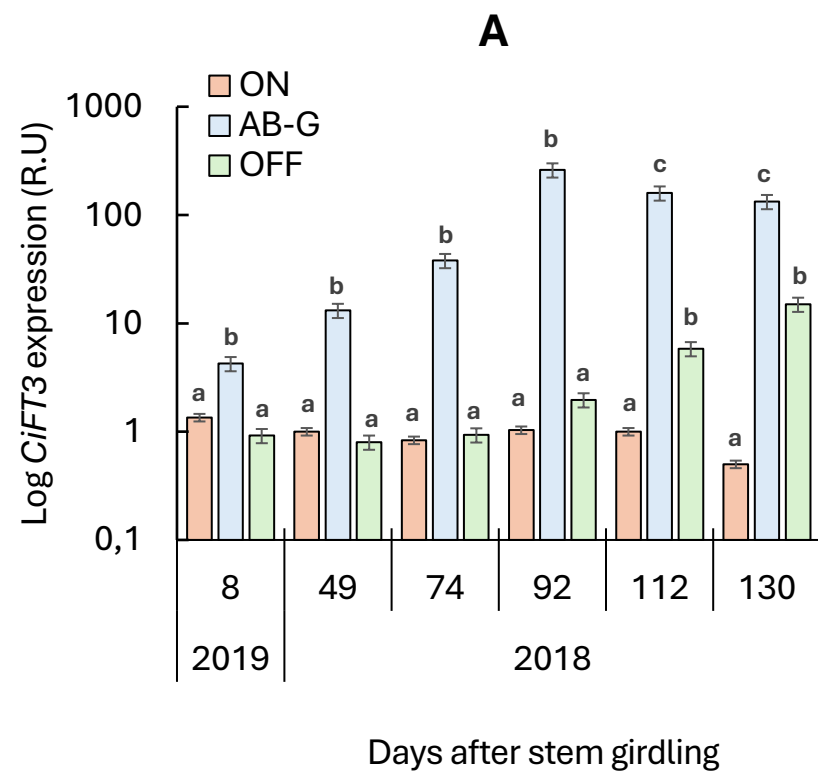
ON Apical Girdling (A-G)

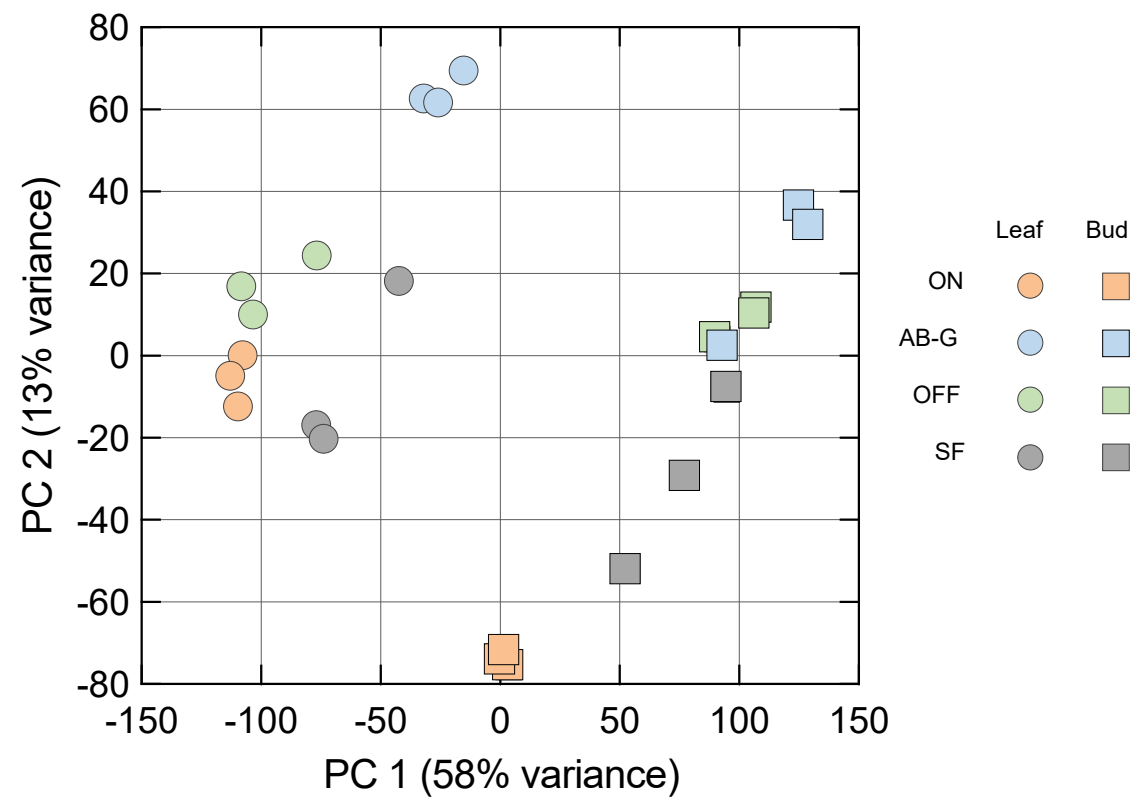


ON Double Girdling
(apical and basal, AB-G)



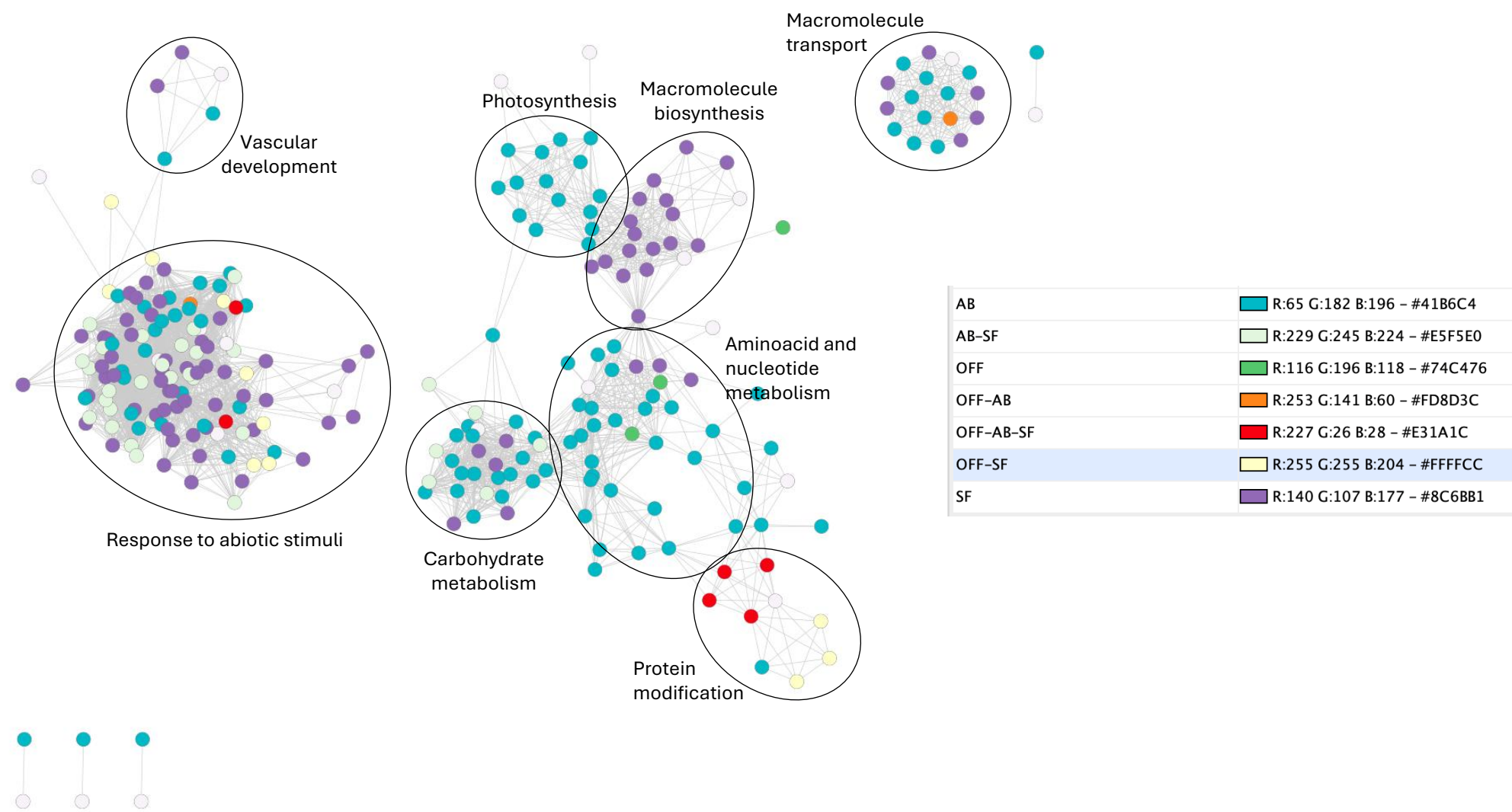
OFF





Supplementary Figure 3

Leaves



Supplementary Figure 4

Polysaccharides hydrolysis

Supplementary Figure 5

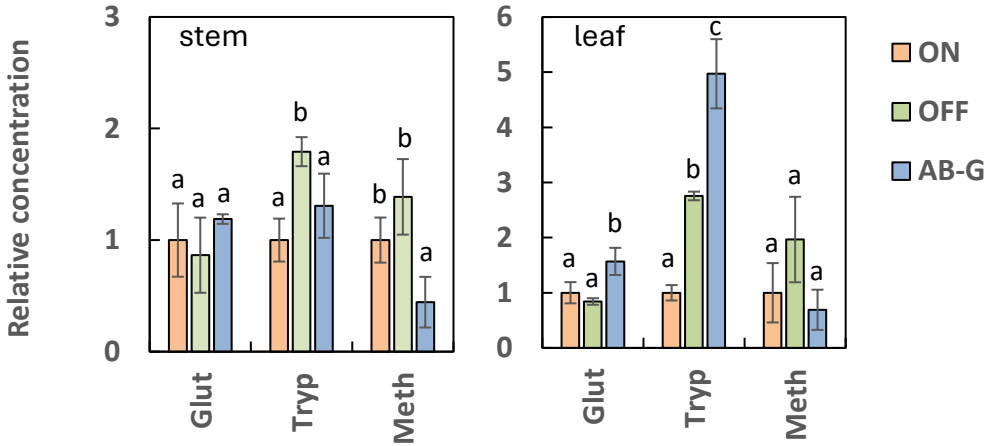
Photosynthesis

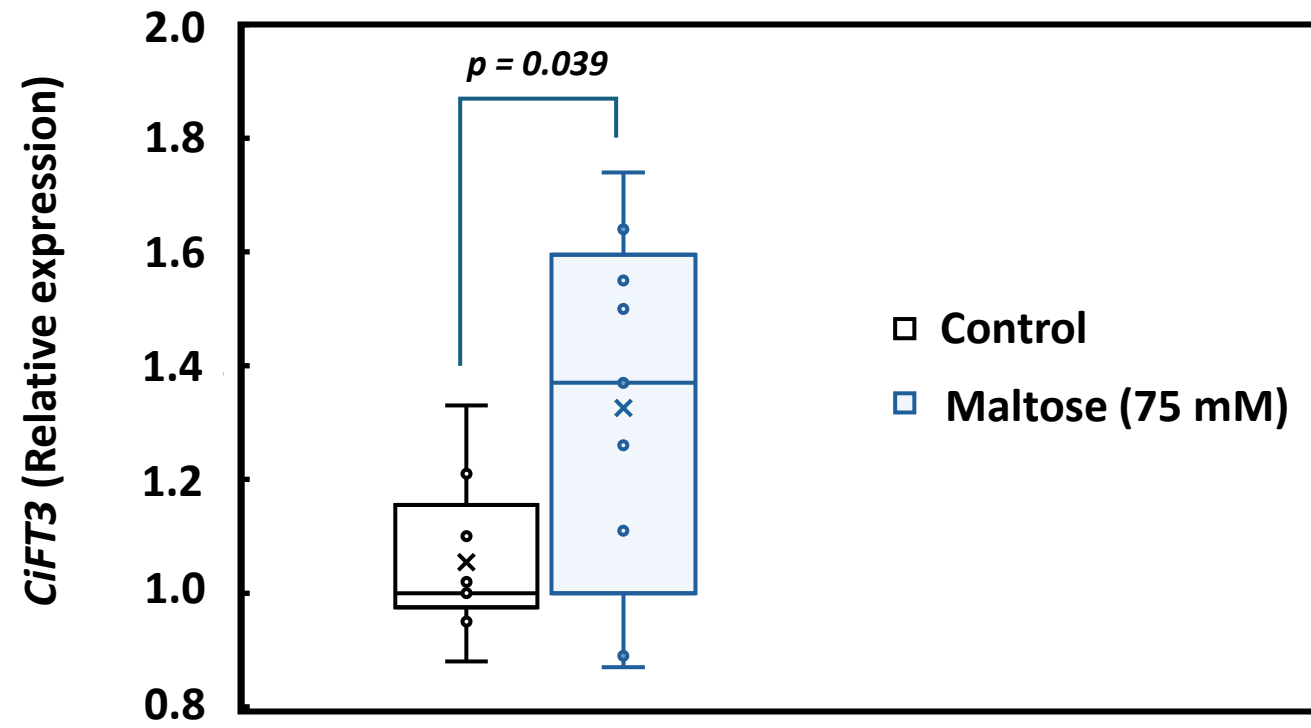
ID	Code	Fold Change	
GH9C2	Ciclev10019301m	-6.4	ENDOGLUCANASE 19-RELATED
XTH9	Ciclev10016129m	-5.6	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE PROTEIN 9
GH17	Ciclev10015086m	-5.3	O-GLYCOSYL HYDROLASES FAMILY 17 PROTEIN
PGF9	Ciclev10019597m	-4.7	POLYGALACTURONASE-LIKE PROTEIN
GH3	Ciclev10027856m	-4.5	PERIPLASMIC BETA-GLUCOSIDASE-RELATED
BGAL1	Ciclev10024886m	-4.3	BETA-GALACTOSIDASE 1
GH16	Ciclev10031440m	-4.1	O-GLYCOSYL HYDROLASES FAMILY 17 PROTEIN
CEL5	Ciclev10019883m	-3.9	ENDOGLUCANASE 3-RELATED
BGLC1	Ciclev10028018m	-3.5	BETA-D-GLUCAN EXOHYDROLASE-LIKE PROTEIN-RELATED
BGAL3	Ciclev10024881m	-3.1	BETA-GALACTOSIDASE 3
BGLU45	Ciclev10014887m	-3.0	BETA-GLUCOSIDASE 45-RELATED
XYL1	Ciclev10033422m	-2.9	ALPHA-D-XYLOSIDASE XYLOHYDROLASE / ALPHA-XYLOSIDASE
BGAL10	Ciclev10020391m	-2.7	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE 10-RELATED
BGAL8	Ciclev10027805m	-2.7	BETA-GALACTOSIDASE / LACTASE
BGLU4	Ciclev10015028m	-2.6	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE 4
PGF10	Ciclev10020035m	-2.5	PECTATE LYASE SUPERFAMILY PROTEIN (PECTATE_LYASE_3)
BGLU3	Ciclev10014990m	-2.4	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE 3
A/N-InvB	Ciclev10030393m	-2.3	BETA-FRUCTOFURANOSIDASE / SACCHARASE
BGLU12	Ciclev10031212m	-2.2	BETA-GLUCOSIDASE / GENTOBIASE
GDSL-like	Ciclev10025415m	-2.1	FASCIN
VI1	Ciclev10019134m	-2.0	ACID BETA-FRUCTOFURANOSIDASE 3, VACUOLAR-RELATED
GM38	Ciclev10024800m	-2.0	ALPHA-MANNOSIDASE
HCHIB	Ciclev10028959m	-1.9	BASIC ENDOCHITINASE B
BXL6	Ciclev10024911m	-1.8	BETA-D-XYLOSIDASE 6-RELATED
XTH6	Ciclev10026210m	-1.8	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE PROTEIN 6-RELATED
PR3	Ciclev10028831m	-1.7	BASIC ENDOCHITINASE B
DBE1	Ciclev10023436m	-1.6	ISOAMYLASE 2, CHLOROPLASTIC
BGLU7	Ciclev10028372m	-1.5	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE 7-RELATED
XTH4	Ciclev10028851m	-1.5	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE PROTEIN 4-RELATED
MAN2	Ciclev10015394m	-1.4	MANNAN ENDO-1,4-BETA-MANNOSIDASE 2-RELATED
LH17	Ciclev10014935m	-1.3	LYCOSYL HYDROLASES FAMILY 17 PROTEIN
B-CHI	Ciclev10028964m	-1.2	BASIC ENDOCHITINASE B
CTL1	Ciclev10021187m	-1.2	CHITINASE-LIKE PROTEIN 1
BGLU14	Ciclev10031178m	-1.2	BETA-GLUCOSIDASE / GENTOBIASE
BGLU11	Ciclev10028386m	-1.2	BETA-GLUCOSIDASE 1-RELATED
BGLU2	Ciclev10028241m	-1.1	GLUCOSIDASE-LIKE PROTEIN
BGLU15	Ciclev10031179m	-1.1	BETA-D-GLUCOPYRANOSYL ABSICISATE BETA-GLUCOSIDASE-RELATED
MAN7	Ciclev10025631m	-1.0	MANNAN ENDO-1,4-BETA-MANNOSIDASE 3-RELATED
BAM5	Ciclev10014929m	-1.0	BETA-AMYLASE 5-RELATED
PG13	Ciclev10020162m	-0.9	GLYCOSIDE HYDROLASE FAMILY 28 PROTEIN / POLYGALACTURONASE (PECTINASE) FAMILY PROTEIN
AGAL	Ciclev10030938m	-0.9	ALPHA-GALACTOSIDASE / MELIBIASE
BGLU8	Ciclev10019922m	-0.8	LUCAN ENDO-1,3-BETA-GLUCOSIDASE 8-RELATED
CTL	Ciclev10022123m	-0.6	CHITINASE / POLY-BETA-GLUCOSAMINIDASE
Pectin lyase	Ciclev10030577m	-0.6	PENTATRICOPEPTIDE REPEAT-CONTAINING PROTEIN
AGAL3	Ciclev10034010m	0.7	ALPHA-GALACTOSIDASE/ALPHA-N-ACETYL GALACTOSAMINIDASE
A/N-INV	Ciclev10030925m	0.7	ALKALINE AND NEUTRAL INVERTASE (GLYCO_HYDRO_100)
INV	Ciclev10028002m	0.8	ALKALINE AND NEUTRAL INVERTASE (GLYCO_HYDRO_100)
CTL	Ciclev10022063m	0.8	CHITINASE / POLY-BETA-GLUCOSAMINIDASE
TRE1	Ciclev10033306m	1.0	ALPHA,ALPHA-TREHALASE / TREHALASE
CTL	Ciclev10023611m	1.1	CHITINASE-RELATED
HEX02	Ciclev10024601m	1.3	BETA-N-ACETYLHEXOSAMINIDASE / N-ACETYL-BETA-GLUCOSAMINIDASE
MAN1	Ciclev10020376m	1.3	MANNAN ENDO-1,4-BETA-MANNOSIDASE 1
B_lectin	Ciclev10027866m	1.4	PROTEIN KINASE DOMAIN (PKINASE) // GLYCOSYL HYDROLASES FAMILY 18 (GLYCO_HYDRO_18)
CWINV5	Ciclev10025259m	1.8	BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME CWINV1-RELATED
BAM3	Ciclev10019566m	3.4	BETA-AMYLASE / SACCHAROGEN AMYLASE

ID	Code	Fold Change	PSAK	Ciclev10002020m	1.11
DAC	Ciclev10009532m	-1.71	PSAK	Ciclev10017170m	1.12
CRK14	Ciclev10015210m	-1.65	NdhS	Ciclev10002129m	1.13
RK3	Ciclev10007570m	-1.33	Lhca6	Ciclev10009205m	1.16
AT1G12000	Ciclev10014760m	-1.10	AT1G13990	Ciclev10032568m	1.19
P5CR	Ciclev10005922m	0.60	PSAE-2	Ciclev10022750m	1.19
AT1G60670	Ciclev10002793m	0.61	AT1G60670	Ciclev10005510m	1.22
AT5G03420	Ciclev10012082m	0.64	AT2G30020	Ciclev10028615m	1.23
PSAK	Ciclev10001894m	0.65	AT2G39130	Ciclev10031289m	1.23
CSK	Ciclev10030964m	0.66	GSTZ2	Ciclev10022571m	1.23
PSBX	Ciclev10009915m	0.69	UNE16	Ciclev10016540m	1.24
AT4G25740	Ciclev10022793m	0.69	AT5G64180	Ciclev10029515m	1.24
AT4G14385	Ciclev10002108m	0.71	mtACP3	Ciclev10017019m	1.24
P5CR	Ciclev10005924m	0.74	AT1G59960	Ciclev10032377m	1.28
#iVALOR!	Ciclev10009198m	0.75	FAD6	Ciclev10028238m	1.29
PHYLLO	Ciclev10030492m	0.76	FD3	Ciclev10016927m	1.33
PYD1	Ciclev10021452m	0.77	AT1G03250	Ciclev10002687m	1.35
PnsB3	Ciclev10026544m	0.77	TFIIIA	Ciclev10002351m	1.40
AT5G07580	Ciclev10005892m	0.78	TFIIIA	Ciclev10012370m	1.40
AT3G02710	Ciclev10011842m	0.80	AT2G36360	Ciclev10031886m	1.41
PSB29	Ciclev10016098m	0.81	PSBX	Ciclev10009914m	1.44
CRK14	Ciclev10015214m	0.84	AT3G26700	Ciclev10016002m	1.46
NdhS	Ciclev10000422m	0.84	AT4G14385	Ciclev10006216m	1.49
RSH1	Ciclev10018801m	0.86	MIPS2	Ciclev10025544m	1.50
AT1G71500	Ciclev10002268m	0.87	TFIIIA	Ciclev10012378m	1.51
AT5G63620	Ciclev10025812m	0.89	GSTZ2	Ciclev10022248m	1.57
AT2G40935	Ciclev10012893m	0.89	MSD1	Ciclev10032629m	1.58
PPL1	Ciclev10032564m	0.90	APC2	Ciclev10015874m	1.59
#iVALOR!	Ciclev10026034m	0.90	OTP81	Ciclev10004760m	1.66
AGY1	Ciclev10018714m	0.91	NdhS	Ciclev10024562m	1.67
psbB	Ciclev10003146m	0.92	ADT2	Ciclev10028591m	1.68
AT4G10790	Ciclev10020858m	0.95	AT4G10790	Ciclev10020542m	1.70
AT1G03250	Ciclev10001734m	0.96	APC2	Ciclev10015680m	1.70
PSAH2	Ciclev10026722m	1.01	psbA	Ciclev10023978m	1.70
MENG	Ciclev10032789m	1.02	PnsL3	Ciclev10009429m	1.72
AT5G22920	Ciclev10029116m	1.02	PETC	Ciclev10016706m	1.74
TFIIIA	Ciclev10002532m	1.04	AT4G10790	Ciclev10020692m	1.81
AT1G03250	Ciclev10021861m	1.04	IBR5	Ciclev10016637m	1.83
PSBW	Ciclev10029551m	1.06	PGR5-LIKE A	Ciclev10021127m	1.85
UNE16	Ciclev10016525m	1.06	AT5G13760	Ciclev10031094m	2.03
AT1G71500	Ciclev10021386m	1.06	PSBW	Ciclev10024455m	2.06
AT4G31290	Ciclev10009769m	1.08	AT3G02710	Ciclev10011855m	2.11
MIRO2	Ciclev10020312m	1.08	MIPS2	Ciclev10002178m	2.18
PSAK	Ciclev10002001m	1.10			

Alpha-amino acid metabolic process			
	Code	Fold Change	Description
	Ciclev10004120m	-4.53	Glutamate synthase (NADH) / NADH-glutamate synthase
	Ciclev10004713m	-3.59	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE, MITOCHONDRIAL
	Ciclev10019406m	-3.46	Methylenetetrahydrofolate reductase (NAD(P)H) / N(5,10)-methylenetetrahydrofolate reductase
	Ciclev10003581m	-2.84	ATP phosphoribosyltransferase / Phosphoribosyl-ATP pyrophosphorylase
	Ciclev10032203m	-2.63	NAC DOMAIN-CONTAINING PROTEIN 6-RELATED
	Ciclev10005007m	-2.45	GLUTAMINE SYNTHETASE, CHLOROPLASTIC/MITOCHONDRIAL
	Ciclev10001438m	-1.86	PROTEIN WALLS ARE THIN 1
	Ciclev10019860m	-1.69	Argininosuccinate synthase / Citrulline–aspartate ligase
	Ciclev10020798m	-1.59	L-threonine aldolase / L-threonine acetaldehyde-lyase
	Ciclev10032371m	-1.54	6-PHOSPHOGLUCONATE DEHYDROGENASE
	Ciclev10028700m	-1.40	HOMOSERINE KINASE
	Ciclev10011434m	-1.15	Cystathionine gamma-synthase / O-succinylhomoserine synthetase
	Ciclev10007310m	-1.15	Glycine dehydrogenase (aminomethyl-transferring) / Glycine-cleavage complex P-protein
	Ciclev10005931m	-1.12	Acireductone dioxygenase (Ni(2+)-requiring) / E-2
	Ciclev10015017m	-1.12	Glutamate decarboxylase / L-glutamate 1-carboxy-lyase
	Ciclev10015433m	-1.06	Aminomethyltransferase / Tetrahydrofolate aminomethyltransferase
	Ciclev10018988m	-0.99	Methylcrotonoyl-CoA carboxylase / Methylcrotonyl-CoA carboxylase
	Ciclev10015131m	-0.92	Arogenate dehydratase / Carboxycyclohexadienyl dehydratase
	Ciclev10020608m	-0.88	Gamma-glutamyl hydrolase / Pteroyl-poly-alpha-glutamate hydrolase
	Ciclev10018921m	-0.84	5-methyltetrahydropteroyltriglutamate–homocysteine S-methyltransferase / Tetrahydropteroylglutamate-homocysteine transmethylase
	Ciclev10025372m	-0.82	SERINE HYDROXYMETHYL TRANSFERASE
	Ciclev10005510m	-0.80	4-hydroxy-tetrahydrodipicolinate reductase / Dihydrodipicolinate reductase
	Ciclev10004137m	-0.80	Glutamate synthase (ferredoxin) / Ferredoxin-dependent glutamate synthase
	Ciclev10030821m	-0.80	HISTIDINE AMMONIA-LYASE
	Ciclev10011175m	-0.80	HISTIDINE AMMONIA-LYASE
	Ciclev10028779m	-0.79	Inositol-phosphate phosphatase / Myo-inositol-1-phosphatase
	Ciclev10031010m	-0.76	Thymidylate synthase (FAD) / Flavin dependent thymidylate synthase
	Ciclev10015356m	-0.76	Nicotianamine aminotransferase / Nicotianamine transaminase
	Ciclev10017047m	-0.76	GLYCINE CLEAVAGE SYSTEM H PROTEIN
	Ciclev10020605m	-0.74	HOMOCYSTEINE S-METHYLTRANSFERASE 2
	Ciclev10028055m	-0.74	Phosphoglycerate dehydrogenase / Phosphoglyceric acid dehydrogenase
	Ciclev10008557m	-0.69	GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT
	Ciclev10004902m	-0.68	SERINE HYDROXYMETHYL TRANSFERASE
	Ciclev10005146m	-0.64	S-ADENOSYLMETHIONINE SYNTHASE 4
	Ciclev10025659m	-0.62	Phosphoserine transaminase / PSAT
	Ciclev10032092m	-0.62	HOMOCYSTEINE S-METHYLTRANSFERASE 3
	Ciclev10001793m	0.58	Cysteine synthase / OAS sulfhydrylase
	Ciclev10000875m	0.60	SERINE HYDROXYMETHYL TRANSFERASE 2, MITOCHONDRIAL
	Ciclev10008463m	0.65	PEROXISOMAL SARCOSINE OXIDASE
	Ciclev10007313m	0.65	Saccharopine dehydrogenase (NADP(+), L-lysine-forming) / Lysine-ketoglutarate reductase
	Ciclev10020218m	0.71	2-isopropylmalate synthase / Isopropylmalate synthetase
	Ciclev10028078m	0.76	Asparagine synthase (glutamine-hydrolyzing) / Glutamine-dependent asparagine synthetase
	Ciclev10028359m	0.78	PREPHENATE DEHYDRATASE P PROTEIN
	Ciclev10019831m	0.85	Glutamate decarboxylase / L-glutamate 1-carboxy-lyase
	Ciclev10025514m	0.87	ALANINE–GLYOXYLATE AMINOTRANSFERASE 2, MITOCHONDRIAL
	Ciclev10028518m	1.03	S-methyl-5-thioribose kinase / MTR kinase
	Ciclev10011176m	1.04	Glutamate-5-semialdehyde dehydrogenase / Glutamyl-gamma-semialdehyde dehydrogenase
	Ciclev10019562m	1.17	L-glutamate gamma-semialdehyde dehydrogenase / Pyrroline-5-carboxylate dehydrogenase
	Ciclev10029027m	1.27	Arylformamidase / Kynurenine formamidase
	Ciclev10011584m	1.29	PROLINE OXIDASE
	Ciclev10021870m	1.33	L-serine ammonia-lyase / Serine deaminase
	Ciclev10032942m	1.61	INE CLEAVAGE SYSTEM H PROTEIN 3, MITOCHONDRIAL
	Ciclev10025846m	1.68	AROGENATE DEHYDROGENASE 2, CHLOROPLASTIC
	Ciclev10021719m	1.83	Gamma-glutamyl hydrolase
	Ciclev10025148m	2.49	Phosphoglycerate dehydrogenase / Phosphoglyceric acid dehydrogenase

Supplementary Figure 6



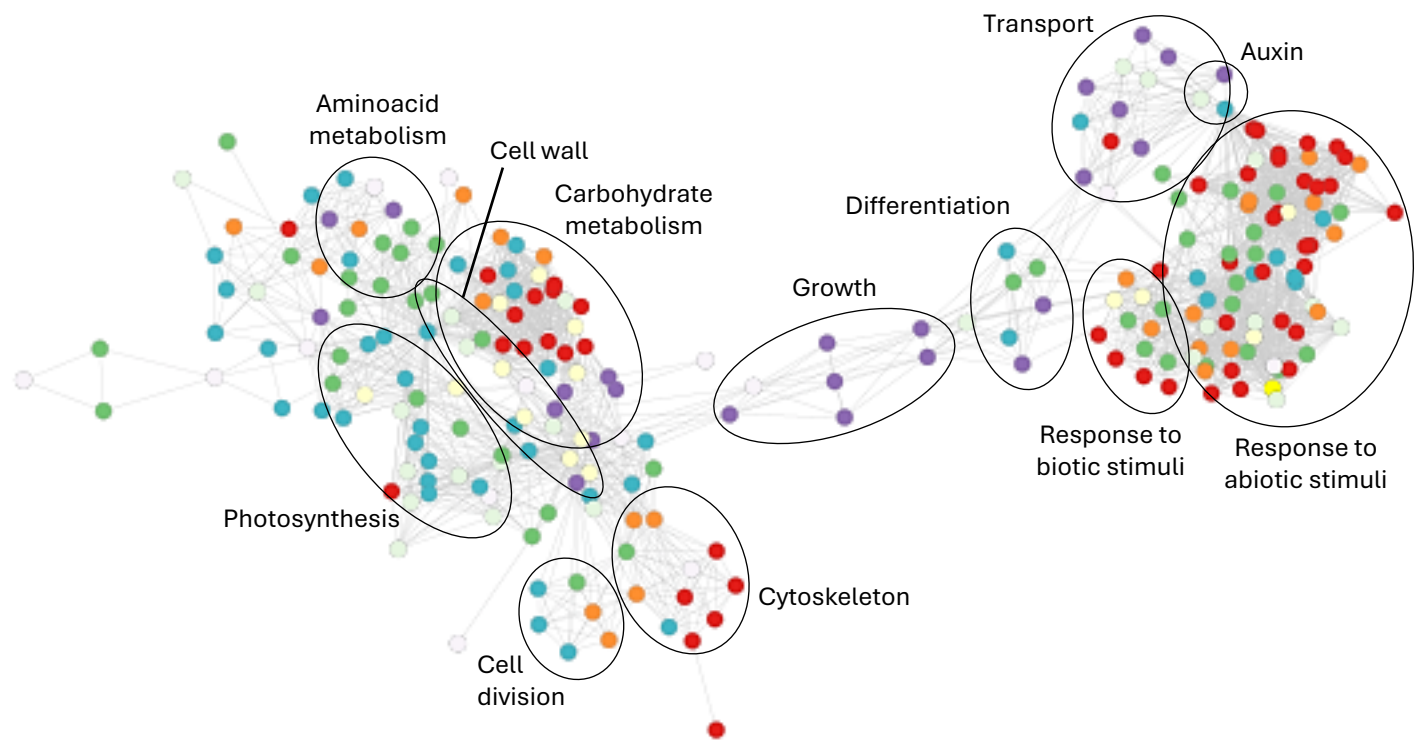


Supplementary Figure 7

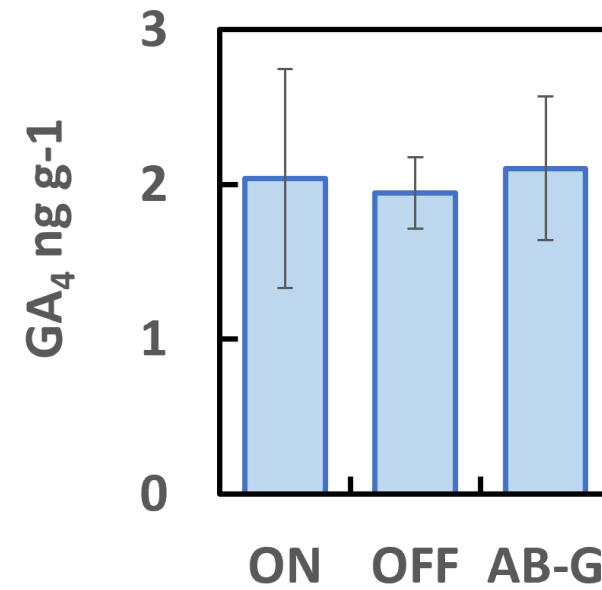
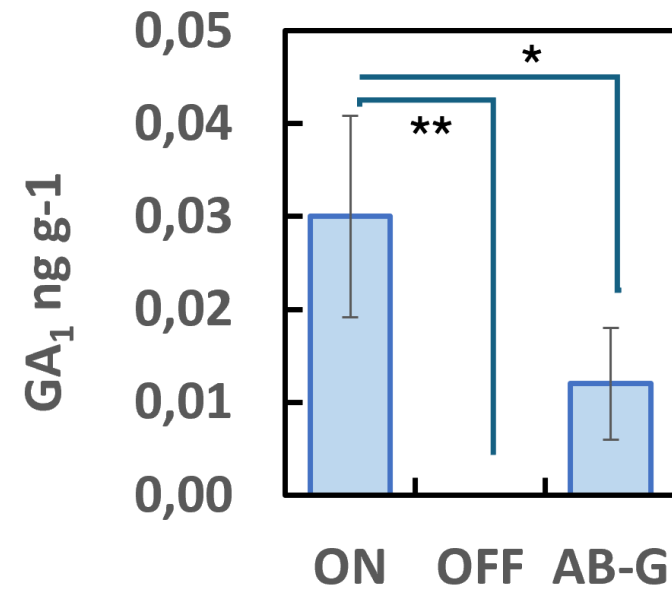
Buds



AB	R:65 G:182 B:196 – #41B6C4
AB-SF	R:229 G:245 B:224 – #E5F5E0
OFF	R:116 G:196 B:118 – #74C476
OFF-AB	R:253 G:141 B:60 – #FD8D3C
OFF-AB-SF	R:227 G:26 B:28 – #E31A1C
OFF-SF	R:255 G:255 B:204 – #FFFFCC
SF	R:140 G:107 B:177 – #8C6BB1



Supplementary Figure 8



* p<0.05
** p<0.01

Supplementary Figure 9

Supplementary Table 1. Primer sequences used in this study

Gene	Phytozome ID	Description	Forward primer (5'-3')	Reverse primer (5'-3')	Reference
<i>PIN1</i>	Ciclev10007787m	Auxin efflux carrier	CTCTCTTTGCAGTCCCCTTG	CCCTTTTGCTCAACTTGCTC	Liu et al., 2015
<i>α-AMY</i>	Ciclev10001266m	Alpha-amylase	ACCGAACTGCAGAGAGGAAA	ATGTTCCACCCTCGAAAATG	Mesejo et al., 2019
<i>CWIN</i>	Ciclev10025259m	Cell wall invertase	ACCATTTCCAGCCTCCCAAG	GTTGCCCCATACTGCTCCTT	Unpublished data
<i>CIN</i>	Ciclev10003220m	Cytosolic invertase	TGAAGCACGATGGGAGGAAC	GACTGGCCAAGAACCTCCAT	Unpublished data
<i>VIN</i>	Ciclev10019134m	Vacuolar invertase	CAATGGCCAGTGGAGGAAGT	ACATCAAGCGGCATCACTGA	Unpublished data
<i>SUS1</i>	orange1.1g003661m	Sucrose Synthase	CAAATCCTCATTATTACCCGTCTC	ACTTGCGGACAACTCCCTTC	Hussain et al., 2020
<i>CYCB2</i>	Ciclev10025564m	Cyclin B type. Cell cycle regulator	GAAAGCAGCAACAGGGAAGC	TCCAAAAGAAATTGCGCCGG	Mesejo et al., 2022
<i>CDKB2</i>	Ciclev10002132m	Cyclin dependent kinase	GAGGTCTCCATCTTGCGCAT	CGTCCTGCCTTCCTTGTCT	Mesejo et al., 2022
<i>LFY</i>	Ciclev10033942m	LEAFY, flowering integrator	TCTTGATCCAGGTCCAGAACATC	TAGTCACCTTGGTTGGGCATT	Muñoz-Fam et al., 2011
<i>AP1</i>	Ciclev10032490m	AGAMOUS Like MADS box protein	CAAAACCAGGTCCCAACAC	ACGAACATACGGGTCAAGG	Muñoz-Fam et al., 2011
<i>TFL</i>	Ciclev10013475m	TERMINAL FLOWER	TCCGTCCACAGTTGTTTCAA	TCACTAGGGCCAGGAACATC	Muñoz-Fam et al., 2011
<i>CEN</i>	Ciclev10029782m	Phosphatidylethan olamine protein	CAGCTTCAAGGGATCGGTT	GAGCAGCAGTCTCCCTTTGT	Zhang et al., 2021
<i>CiFT3</i>	Ciclev10012905m	Flowering Locus T	AGACTGTTTATGCACCGGGG	AGTTGAAGTAGACAGCGGCC	Mesejo et al., 2022
<i>CcMADS19</i>	Ciclev10033420m	FLC ortholog	GGCAACTTGAAGGTCCAAAC	GCCCAATGAGCATAGGAATG	Agustí et al., 2020
<i>LYC</i>	Ciclev10025866m	Housekeeper	GAACCAGGAGCTTAGGTCTG	GCTAGGTCTACAACAAGGCC	Alquezar et al., 2009
<i>ACT</i>	Ciclev10025866m	Housekeeper	TTAACCCCAAGGCCAACAGA	TCCCTCATAGATTGGTACAGTATGAGA	Mesejo et al., 2022

Supplementary Table 2. Experiment I. Apical girdling (A-G), basal girdling (B-G) and double girdling (AB-G) were applied to ON shoots of Citrus trees. Ungirdled ON shoots and OFF shoots were used as control. The treatment was made in September, sampling in September-January and flowering was evaluated in the next spring.

Treatments	Number of shoots	
	Phenotype evaluation	Hormones and RT-PCR
ON	30	50
OFF	30	50
ON+ apical girdling (A-G)	30	50
ON+ basal girdling (B-G)	30	50
ON+ double girdling (AB-G)	30	50
Total	150	250

Supplementary Table 3. Experiment II. Double girdling (AB-G) was applied to ON shoots of Citrus trees at different dates (September, December, January). Ungirdled ON shoots and OFF shoots were used as control. Sampling was made in September-January and flowering was evaluated in the next spring.

Treatments	Number of shoots	
	Phenotype evaluation	Hormones and RT-PCR
ON	20	40
OFF	20	40
ON+ double girdling (Sept)	20	40
ON+ double girdling (Dec)	20	40
ON+ double girdling (Jan)	20	40
Total	100	250

Supplementary Table 4. Experiment III. Experimental design for the RNA-seq experiment. Three Citrus flowering phenotypes, Double girdling (AB-G), OFF (without fruit), and ON shoots with a small fruit (SF) were compared to ON (with a mature fruit) shoots unable to flower. AB-G was applied in September.

Treatments	Number of shoots	
	Phenotype evaluation	RNA for RNA-seq
ON	20	12
OFF	20	12
ON+ double girdling (Sept)	20	12
ON+ small summer fruit (SF)	20	12
Total	100	68