

Table 3. List of genes shown in Fig. 3 in the main text

abbreviation	AraCyc	DART	gene name	MIPS code	Expression level
ATP-PRT	ATP PHOSPHORIBOSYL TRANSFERASE	ATP phosphoribosyltransferase		AT1g58080	1 2 3 4 5 6
AS	ANTHRANILATE SYNTHASE SUBUNIT B	unknown protein		AT1g25170	1 2 3 4 5 6
	anthranilate synthase	anthranilate synthase beta subunit		AT1g25220	1 2 3 4 5 6
	anthranilate synthase	anthranilate synthase component I precursor (sp P32068)		AT5g05730	1 2 3 4 5 6
TS	tryptophan synthase	tryptophan synthase beta chain		AT5g38530	1 2 3 4 5 6
TyrAT	TYROSINE AMINOTRANSFERASE	putative tyrosine aminotransferase		AT2g24850	1 2 3 4 5 6
GHMT	GLYCINE HYDROXYMETHYLTRANSFERASE	glycine hydroxymethyltransferase like protein		AT4g37930	1 2 3 4 5 6
AlaAT	ALANINE AMINOTRANSFERASE	putative alanine aminotransferase		AT1g23310	1 2 3 4 5 6
AAT	ASPARTATE AMINOTRANSFERASE	aspartate aminotransferase (AAT1)		AT2g30970	1 2 3 4 5 6
AsnS		glutamine-dependent asparagine synthetase		AT3g47340	1 2 3 4 5 6
MetS	5-METHYLtetrahydropteroyltriglutamate--HOMOCYSTEINE S-METHYLTRANSFERASE	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase		AT5g17920	1 2 3 4 5 6
NRT		nitrate transporter		AT3g21670	1 2 3 4 5 6
NR	nitrate reductase	nitrate reductase 1 (NR1)	Nra1	AT1g77760	1 2 3 4 5 6
			Nra2	AT1g37130	1 2 3 4 5 6
GS		glutamate-ammonia lyase (EC 6.3.1.2) precursor; chloroplast (clone AmbdaAtgs1) (pI 518600)		AT5g35630	1 2 3 4 5 6
	GLUTAMINE SYNTHETASE	glutamine synthetase, putative		AT1g66200	1 2 3 4 5 6
GO GAT		ferredoxin-dependent glutamate synthase	Fd-GOGAT	AT5g04140	1 2 3 4 5 6
GDH		glutamate dehydrogenase 2	GDH2	AT5g07440	1 2 3 4 5 6
		glutamate dehydrogenase (EC 1.4.1.-) 1 (pI 571217)		AT5g18170	1 2 3 4 5 6
ATPS	ATP sulfurylase		APS1	AT3g22890	1 2 3 4 5 6
APSK		adenosine-5-phosphosulfate-kinase	akn2	AT4g39940	1 2 3 4 5 6
APR	APS reductase	5'-adenylylphosphosulfate reductase, putative	APR2	AT1g62180	1 2 3 4 5 6
	APS reductase	PRH26 protein	APR3	AT4g21990	1 2 3 4 5 6
SAT	serine acetyltransferase	serine acetyltransferase (Sat-1)	SAT-m	AT3g13110	1 2 3 4 5 6
CS	CYSTEINE SYNTHASE	cysteine synthase AtcysC1	Bsas3i1	AT3g61440	1 2 3 4 5 6
γECS	GAMMA-GLUTAMYL CYSTEINE SYNTHETASE	gamma-glutamylcysteine synthetase		AT4g23100	1 2 3 4 5 6
fructosidase	BETA-FRUCTOSIDASE	beta-fructosidase		AT1g62660	1 2 3 4 5 6
HXK	HEXOKINASE	hexokinase, putative		AT1g50460	1 2 3 4 5 6
G6PDH	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE	glucose-6-phosphate 1-dehydrogenase, putative		AT3g27300	1 2 3 4 5 6
PP+PFK		pyrophosphate-dependent phosphofructo-1-kinase-like protein		AT4g29220	1 2 3 4 5 6
abbase	FRUCTOSE-BISPHOSPHATE ALDOLASE	putative fructose-bisphosphate aldolase		AT4g38970	1 2 3 4 5 6
	FRUCTOSE-BISPHOSPHATE ALDOLASE	fructose-bisphosphate aldolase - like protein		AT4g26530	1 2 3 4 5 6
	FRUCTOSE-BISPHOSPHATE ALDOLASE	putative fructose-bisphosphate aldolase, plastidic form		AT2g01140	1 2 3 4 5 6
	FRUCTOSE-BISPHOSPHATE ALDOLASE	putative fructose bisphosphate aldolase		AT2g21330	1 2 3 4 5 6
G3PDH	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C	glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)	GAPC	AT3g04120	1 2 3 4 5 6
	glyceraldehyde-3-phosphate dehydrogenase		GAPB, GAPA	AT1g42970	1 2 3 4 5 6
	glyceraldehyde-3-phosphate dehydrogenase	glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA)	GAPB, GAPA	AT3g26650	1 2 3 4 5 6
	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	glyceraldehyde-3-phosphate dehydrogenase, putative		AT1g13440	1 2 3 4 5 6
PGK	PHOSPHOGLYCERATE KINASE	phosphoglycerate kinase, putative		AT3g12780	1 2 3 4 5 6
	PHOSPHOGLYCERATE KINASE	phosphoglycerate kinase, putative	PGK	AT1g79550	1 2 3 4 5 6
aconitase	ACONITASE HYDRATASE	cytoplasmatic aconitate hydratase (aconitate hydratase) (aconitase) (EC 4.2.1.3)		AT4g35830	1 2 3 4 5 6
2-O-G DH	2-OXOGLUTARATE DEHYDROGENASE	2-oxoglutarate dehydrogenase, E1 component		AT5g65750	1 2 3 4 5 6
MaDH		mitochondrial NAD-dependent malate dehydrogenase		AT1g53240	1 2 3 4 5 6
NADP-MaDH		NADP-dependent malate dehydrogenase		AT5g58330	1 2 3 4 5 6
ATP CL		ATP citrate lyase, putative		AT3g06650	1 2 3 4 5 6

Annotations given in AraCyc

Pathways of TAIR (The *Arabidopsis* Information Resource; www.arabidopsis.org), DART (the Database for *Arabidopsis* Research and Tools; http://biochem.agr.nagoya-u.ac.jp/atgenome/index.html), and MIPS (Munich Information Center for Protein Sequences) codes are shown. Statistically significant changes in gene expression (SAM, the false discovery rate <10%) are shown in the boxes (1, H-le-S/C; 2, H-le-N/C; 3, H-le-SN/C; 4, H-ro-S/C; 5, H-ro-N/C; 6, H-ro-SN/C) as red (induced) or green (repressed).