

The glycolytic enzyme, phosphoglycerate mutase, has critical roles in stomatal movement, vegetative growth, and pollen production in *Arabidopsis thaliana*

Zhixin Zhao and Sarah M. Assmann

Supplemental Data

Table S1 Primer information.

Name	Primer sequence
iPGM1-1 LP	ATGTTCTATCAATCTCCGGGG
iPGM1-1 RP	TTGATGCTTTTTGGATTCATTG
iPGM1-2 LP	TCGCATTAATAATTATCACTCTTGTG
iPGM1-2 RP	AGAACCATCCAAAACATCACG
iPGM2-1 LP	GAGGTAGGCAATGCTTGTGAG
iPGM2-1 RP	TTACCTGGTCAAACCTGCCAC
iPGM2-2 LP	ATTGTCTGCAAACCAGGACAC
iPGM2-2 RP	GGTCCAATTGTTGATGGTGAC
LBb1	GCGTGGACCGCTTGCTGCAACT
RB1	ATTAAACTCCAGAAACCCGCGGCTGAG
RT iPGM1 LP (p1)	ATGGCTACCTCCTCCGCTTGG
RT iPGM1 RP (p2)	CTACTCCACTACTTCAATCAGGGT
RT iPGM1 RP (p3)	GTGGATACAGTTGTACTGATCAGG
RT iPGM1 RP (p4)	GAACTCCACCGTCACTGAGAAGTC
RT iPGM2 LP (p5)	ATGGGTAGCTCCGGCGACGTTAAC
RT iPGM2 RP (p6)	TCACTTCTCGACGACTTC
RT iPGM2 RP (p7)	CGAACGCCATTGTGTGCCAGAT

Table S2 Genes involved in photosynthesis in Arabidopsis

Proteins in bold were identified in Zhao et al., 2008. Plant Cell. 20: 3210-32226

Proteins in italics were identified in Zhao et al., 2010 J. Proteome Res. 9: 1637–1647

Gene list was downloaded from KEGG

(http://www.genome.jp/kegg-bin/show_pathway?org_name=ath&mapno=00195&mapscale=&show_description=hide)

Gene name and description were downloaded from TAIR (<http://www.arabidopsis.org/>).

Photosynthesis Name	Description
ATCG00120	ATPA the ATPase alpha subunit
AT4G04640	ATPC1 One of two genes encoding the gamma subunit of Arabidopsis chloroplast ATP synthase
AT1G15700	ATPC2 One of two genes that encode the gamma subunit of Arabidopsis chloroplast ATP synthase
AT4G09650	ATPD the chloroplast ATPase delta-subunit
ATCG00470	ATPE ATPase epsilon subunit
ATCG00130	ATPF ATPase F subunit
ATCG00140	ATPH ATPase III subunit
ATCG00150	ATPI a subunit of ATPase complex CF0
AT1G20340	DRT112 recombination and DNA-damage resistance protein (DRT112)
AT1G10960	FD1 ferredoxin 1 (FD1)
AT2G27510	FD3 ferredoxin 3 (FD3)
AT5G10000	FD4 ferredoxin 4 (FD4)
AT1G32550	FdC1 FdC1, a ferredoxin protein capable of alternative electron partitioning
AT4G14890	FdC2 2Fe-2S ferredoxin-like superfamily protein
AT1G60950	FED A a major leaf ferredoxin
AT5G66190	FNR1 a leaf-type ferredoxin:NADP(H) oxidoreductase
AT1G20020	FNR2 a leaf-type ferredoxin:NADP(H) oxidoreductase
AT1G44575	NPQ4 PSII-S (CP22)
ATMG00480	ORFB subunit 8 of the mitochondrial F(O) ATP synthase complex
ATCG00480	PB chloroplast-encoded gene for beta subunit of ATP synthase
ATCG00540	PETA cytochrome f apoprotein
ATCG00720	PETB the cytochrome b(6) subunit of the cytochrome b6f complex
AT4G03280	PETC the Rieske FeS center of cytochrome b6f complex
ATCG00730	PETD A chloroplast gene encoding subunit IV of the cytochrome b6/f complex
AT1G76100	PETE1 One of two Arabidopsis plastocyanin genes
ATCG00600	PETG Cytochrome b6-f complex, subunit V
AT3G55330	PPL1 PsbP-like protein 1 (PPL1)
AT3G01440	PQL1 a subunit of the NAD(P)H complex located in the chloroplast thylakoid lumen
AT1G14150	PQL2 a subunit of the NAD(P)H dehydrogenase complex located in the chloroplast thylakoid lumen
ATCG00350	PSAA psaA protein comprising the reaction center for photosystem I along with psaB protein
ATCG00340	PSAB the D1 subunit of photosystem I and II reaction centers

ATCG01060 PSAC the PsaC subunit of photosystem I
AT4G02770 PSAD-1 a protein predicted by sequence similarity with spinach PsaD to be photosystem I reaction center subunit II (PsaD1)
AT1G03130 PSAD-2 a protein predicted by sequence similarity with spinach PsaD to be photosystem I reaction center subunit II (PsaD2)
AT4G28750 PSAE-1 mutant has Decreased effective quantum yield of photosystem II
AT2G20260 PSAE-2 subunit E of photosystem I
AT1G31330 PSAF subunit F of photosystem I
AT1G55670 PSAG subunit G of photosystem I
AT3G16140 PSAH-1 subunit H of photosystem I reaction center subunit VI
AT1G52230 PSAH2 photosystem I subunit H2 (PSAH2)
ATCG00510 PSAI subunit I of photosystem I
ATCG00630 PSAJ subunit J of photosystem I
AT1G30380 PSAK subunit K of photosystem I reaction center
AT4G12800 PSAL subunit L of photosystem I reaction center
AT5G64040 PSAN the only subunit of photosystem I located entirely in the thylakoid lumen
AT1G08380 PSAO subunit O of photosystem I
AT1G03600 PSB27 PSB27
ATCG00020 PSBA chlorophyll binding protein D1, a part of the photosystem II reaction center core
ATCG00680 PSBB for CP47, subunit of the photosystem II reaction center
ATCG00280 PSBC chloroplast gene encoding a CP43 subunit of the photosystem II reaction center
ATCG00270 PSBD PSII D2 protein
ATCG00580 PSBE PSII cytochrome b559
ATCG00570 PSBF PSII cytochrome b559
ATCG00710 PSBH a 8 kD phosphoprotein that is a component of the photosystem II oxygen evolving core
ATCG00080 PSBI PSII I protein
ATCG00550 PSBJ PSII component
ATCG00070 PSBK PSII K protein
ATCG00560 PSBL PSII L protein
ATCG00220 PSBM PSII low MW protein
AT5G66570 PSBO1 a protein which is an extrinsic subunit of photosystem II
AT3G50820 PSBO2 a protein which is an extrinsic subunit of photosystem II
AT1G06680 PSBP-1 a 23 kD extrinsic protein that is part of photosystem II
AT2G30790 PSBP-2 a 23 kD extrinsic protein that is part of photosystem II
AT4G05180 PSBQ-2 the PsbQ subunit of the oxygen evolving complex of photosystem II
AT4G21280 PSBQA the PsbQ subunit of the oxygen evolving complex of photosystem II
AT1G79040 PSBR for the 10 kDa PsbR subunit of photosystem II (PSII)
ATCG00690 PSBT photosystem II 5 kD protein subunit PSII-T
AT2G30570 PSBW a protein similar to photosystem II reaction center subunit W
AT1G67740 PSBY PsbY precursor (psbY) mRNA
AT4G05390 RFNR1 a root-type ferredoxin:NADP(H) oxidoreductase
AT1G30510 RFNR2 a root-type ferredoxin:NADP(H) oxidoreductase

ATCG00210	YCF6	hypothetical protein
ATCG00300	YCF9	PsbZ, which is a subunit of photosystem II
AT2G07707		Plant mitochondrial ATPase, F0 complex, subunit 8 protein
AT4G28660		Similar to PsbW subunit of photosystem II
AT4G32260		ATPase, F0 complex, subunit B/B', bacterial/chloroplast
AT5G45040		Cytochrome c

Table S3 Genes involved in oxidative phosphorylation in Arabidopsis

Proteins in bold were identified in Zhao et al., 2008. Plant Cell. 20: 3210-32226

Proteins in italics were identified in Zhao et al., 2010 J. Proteome Res. 9: 1637–1647

Gene list was downloaded from KEGG

(http://www.genome.jp/kegg-bin/show_pathway?org_name=ath&mapno=00190&mapscale=&show_description=hide)

Gene name and description were downloaded from TAIR (<http://www.arabidopsis.org/>).

Oxidative Phos	Name	Description
AT1G17260	AHA10	belongs to H ⁺ -APTase gene family
ATMG01190	ATP1	ATPase subunit 1
AT2G33040	ATP3	gamma subunit of Mt ATP synthase (ATP3)
AT5G13450	ATP5	delta subunit of Mt ATP synthase (ATP5)
ATMG00410	ATP6-1	ATPase subunit 6
ATMG01170	ATP6-2	ATPase subunit 6
ATMG01080	ATP9	subunit 9 of mitochondrial F ₀ -ATPase
ATCG00120	ATPA	the ATPase alpha subunit
AT4G04640	ATPC1	One of two genes (with ATPC2) encoding the gamma subunit of Arabidopsis chloroplast ATP synthase
AT1G15700	ATPC2	One of two genes that encode the gamma subunit of Arabidopsis chloroplast ATP synthase
AT4G09650	ATPD	the chloroplast ATPase delta-subunit
ATCG00470	ATPE	ATPase epsilon subunit
ATCG00130	ATPF	ATPase F subunit
ATCG00140	ATPH	ATPase III subunit
ATCG00150	ATPI	a subunit of ATPase complex CF ₀
AT3G52300	ATPQ	ATP synthase D chain, mitochondrial (ATPQ)
AT4G34720	AVA-P1	vacuolar H ⁺ -pumping ATPase 16 kDa proteolipid (ava-p1)
AT1G19910	AVA-P2	vacuolar H ⁺ -pumping ATPase 16 kDa proteolipid (ava-p2)
AT1G15690	AVP1	a H ⁺ -translocating (pyrophosphate-energized) inorganic pyrophosphatase (H ⁺)-PPase
AT5G08530	CI51	51 kDa subunit of complex I (CI51)
ATMG00220	COB	Mitochondrial apocytochrome b (cob) gene a subunit of the ubiquinol-cytochrome c oxidoreductase
<i>ATMG01360</i>	COX1	cytochrome c oxidase subunit 1
AT2G44520	COX10	cytochrome c oxidase 10 (COX10)
AT5G56090	COX15	a homolog of COX15
AT3G15352	COX17	protein similar to yeast COX17
ATMG00160	COX2	cytochrome c oxidase subunit 2
ATMG00730	COX3	cytochrome c oxidase subunit 3
AT1G22450	COX6B	subunit 6b of cytochrome c oxidase
AT1G12840	DET3	subunit C of the vacuolar H ⁺ -ATPase (V-ATPase)
AT5G37510	EMB1467	a subunit of the 400 kDa subcomplex of the mitochondrial NADH dehydrogenase (complex I)
AT5G67590	FRO1	Mutant leaves have a reduced capacity for cold acclimation

AT2G18960	HA1	a plasma membrane proton ATPase
AT5G62670	HA11	H(+)-ATPase 11 (HA11)
AT5G57350	HA3	member of Plasma membrane H ⁺ -ATPase family
AT3G47950	HA4	mutant has Slight reduction in root and shoot growth
AT2G24520	HA5	H(+)-ATPase 5 (HA5)
AT2G07560	HA6	H(+)-ATPase 6 (HA6)
AT3G60330	HA7	H(+)-ATPase 7 (HA7)
AT3G42640	HA8	H(+)-ATPase 8 (HA8)
AT1G80660	HA9	H(+)-ATPase 9 (HA9)
AT1G04630	MEE4	maternal effect embryo arrest 4 (MEE4)
AT2G44620	MTACP-1	a member of the mitochondrial acyl carrier protein (ACP) family
AT1G65290	mtACP2	a member of the mitochondrial acyl carrier protein (ACP) family
ATMG00990	NAD3	NADH dehydrogenase subunit 3
ATMG00580	NAD4	NADH dehydrogenase subunit 4
ATMG00650	NAD4L	NADH dehydrogenase subunit 4L
ATMG00665	NAD5B	Mitochondrial NADH dehydrogenase subunit 5
ATMG00270	NAD6	NADH dehydrogenase subunit 6
ATMG00510	NAD7	NADH dehydrogenase subunit 7
ATMG00070	NAD9	NADH dehydrogenase subunit 9
AT2G29990	NDA2	alternative NAD(P)H dehydrogenase 2 (NDA2)
AT4G28220	NDB1	NAD(P)H dehydrogenase B1 (NDB1)
AT4G21490	NDB3	NAD(P)H dehydrogenase B3 (NDB3)
ATCG01100	NDHA	NADH dehydrogenase ND1
ATCG01250	NDHB	NADH dehydrogenase ND2
ATCG00440	NDHC	NADH dehydrogenase D3 subunit of the chloroplast NAD(P)H dehydrogenase complex
ATCG01050	NDHD	Represents a plastid-encoded subunit of a NAD(P)H dehydrogenase complex
ATCG01070	NDHE	NADH dehydrogenase ND4L
ATCG01010	NDHF	Chloroplast encoded NADH dehydrogenase unit
ATCG01080	NDHG	NADH dehydrogenase ND6
ATCG01110	NDHH	the 49KDa plastid NAD(P)H dehydrogenase subunit H protein
ATCG01090	NDHI	subunit of the chloroplast NAD(P)H dehydrogenase complex
ATCG00420	NDHJ	NADH dehydrogenase subunit J
ATMG01330	ORF107F	hypothetical protein
ATMG01260	ORF205	hypothetical protein
ATMG00480	ORFB	subunit 8 of the mitochondrial F(O) ATP synthase complex
ATCG00480	PB	chloroplast-encoded gene for beta subunit of ATP synthase
AT1G01050	PPa1	a soluble protein with inorganic pyrophosphatase activity that is highly specific for Mg-inorganic pyrophosphate
AT2G18230	PPa2	a protein that might have inorganic pyrophosphatase activity
AT2G46860	PPa3	a protein that might have inorganic pyrophosphatase activity
AT3G53620	PPa4	a soluble protein with inorganic pyrophosphatase activity that is highly specific for Mg-inorganic pyrophosphate

AT4G01480	PPa5	a protein that might have inorganic pyrophosphatase activity
AT5G09650	PPa6	a protein with inorganic pyrophosphatase activity
ATCG00430	PSBG	its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase
AT5G66760	SDH1-1	One of two genes in Arabidopsis that encode a flavoprotein subunit of the mitochondrial succinate dehydrogenase complex
AT2G18450	SDH1-2	Nuclear encoded mitochondrial flavoprotein subunit of succinate dehydrogenase complex
AT3G27380	SDH2-1	One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT5G40650	SDH2-2	One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT5G65165	SDH2-3	One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT4G11150	TUF	a vacuolar H ⁺ -ATPase subunit E isoform 1 which is required for Golgi organization and vacuole function in embryogenesis
AT4G23710	VAG2	vacuolar ATP synthase subunit G2 (VAG2)
AT4G25950	VATG3	V-ATPase G-subunit like protein
AT1G78900	VHA-A	catalytic subunit A of the vacuolar ATP synthase
AT2G28520	VHA-A1	Vacuolar proton ATPase subunit VHA-a isoform 1
AT2G21410	VHA-A2	Vacuolar proton ATPase subunit VHA-a isoform 2
AT4G39080	VHA-A3	Vacuolar proton ATPase subunit VHA-a isoform 3
AT4G38920	VHA-C3	vacuolar-type H ⁽⁺⁾ -ATPase C3 (VHA-C3)
AT3G08560	VHA-E2	vacuolar H ⁺ -ATPase subunit E isoform 2 (VHA-E2)
AT1G64200	VHA-E3	vacuolar H ⁺ -ATPase subunit E isoform 3 (VHA-E3)
AT1G16780	VHP2	a type II H ⁺ -Ppases
AT3G01390	VMA10	Subunit G of the vacuolar membrane ATPase complex
AT5G08690		the mitochondrial ATP synthase beta-subunit
AT4G38510		ATPase, V1 complex, subunit B protein
AT4G30190		belongs to the P-type ATPase superfamily of cation-transporting ATPases, nutrients by proton symport
AT1G20260		ATPase, V1 complex, subunit B protein
AT5G47030		the mitochondrial ATP synthase subunit delta
AT5G40810		Cytochrome C1 family
AT5G13440		Ubiquinol-cytochrome C reductase iron-sulfur subunit
AT5G13430		Ubiquinol-cytochrome C reductase iron-sulfur subunit
AT5G11770		NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial
AT5G08680		the mitochondrial ATP synthase beta-subunit
AT5G08670		the mitochondrial ATP synthase beta-subunit
AT4G29480		Mitochondrial ATP synthase subunit G protein
AT4G05020		NAD(P)H dehydrogenase B2 (NDB2)
AT4G02580		NADH-ubiquinone oxidoreductase 24 kDa subunit, putative
AT3G42050		vacuolar ATP synthase subunit H family protein
AT3G27240		Cytochrome C1 family
AT3G03100		NADH:ubiquinone oxidoreductase, 17
AT2G20360		NAD(P)-binding Rossmann-fold superfamily protein
AT1G76030		the vacuolar ATP synthase subunit B1
AT1G02410		cytochrome c oxidase assembly protein CtaG / Cox11 family

AT1G15120	Ubiquinol-cytochrome C reductase hinge protein
AT1G16700	Alpha-helical ferredoxin
AT1G32710	Cytochrome c oxidase, subunit Vib family protein
AT1G49140	Complex I subunit NDUFS6
AT1G51650	ATP synthase epsilon chain, mitochondrial
AT1G53030	a copper chaperone, can functional complements the yeast COX17 null mutant
AT1G75630	vacuolar H ⁺ -pumping ATPase 16 kD proteolipid (ava-p) mRNA,
AT1G79010	Alpha-helical ferredoxin
AT1G80230	Rubredoxin-like superfamily protein
AT2G01090	Ubiquinol-cytochrome C reductase hinge protein
AT2G02050	NADH-ubiquinone oxidoreductase B18 subunit, putative
AT2G07671	ATP synthase subunit C family protein
AT2G07687	Cytochrome c oxidase, subunit III
AT2G07698	ATPase, F1 complex, alpha subunit protein
AT2G07707	Plant mitochondrial ATPase, F0 complex, subunit 8 protein
AT2G07727	Di-haem cytochrome, transmembrane
AT2G07741	ATPase, F0 complex, subunit A protein
AT2G07751	NADH:ubiquinone/plastoquinone oxidoreductase, chain 3 protein
AT2G07785	NADH dehydrogenase family protein
AT2G16510	ATPase, F0/V0 complex, subunit C protein
AT2G19680	Mitochondrial ATP synthase subunit G protein
AT2G25610	ATPase, F0/V0 complex, subunit C protein
AT2G33220	GRIM-19 protein
AT2G47690	NADH-ubiquinone oxidoreductase-related
AT3G03070	NADH-ubiquinone oxidoreductase-related
AT3G06310	Cox19-like CHCH family protein
AT3G08610	unknown protein
AT3G12260	LYR family of Fe/S cluster biogenesis protein
AT3G15640	Rubredoxin-like superfamily protein
AT3G18410	Complex I subunit NDUFS6
AT3G28710	ATPase, V0/A0 complex, subunit C/D
AT3G28715	ATPase, V0/A0 complex, subunit C/D
AT3G52730	ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein
AT3G58730	vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD)
AT3G62790	NADH-ubiquinone oxidoreductase-related
AT4G02620	vacuolar ATPase subunit F family protein
AT4G26210	Mitochondrial ATP synthase subunit G protein
AT4G26710	ATPase, V0 complex, subunit E
AT4G28060	Cytochrome c oxidase, subunit Vib family protein
AT4G32260	ATPase, F0 complex, subunit B/B', bacterial/chloroplast

AT4G32470	Cytochrome bd ubiquinol oxidase, 14kDa subunit
AT4G32530	ATPase, F0/V0 complex, subunit C protein
AT4G34700	LYR family of Fe/S cluster biogenesis protein
AT4G37830	cytochrome c oxidase-related
AT5G18800	Cox19-like CHCH family protein
AT5G25450	Cytochrome bd ubiquinol oxidase, 14kDa subunit
AT5G47890	NADH-ubiquinone oxidoreductase B8 subunit, putative
AT5G52840	NADH-ubiquinone oxidoreductase-related
AT5G55290	ATPase, V0 complex, subunit E
AT5G57815	Cytochrome c oxidase, subunit Vib family protein

Table S4 Genes involved in the TCA cycle in Arabidopsis

Proteins in bold were identified in Zhao et al., 2008. Plant Cell. 20: 3210-32226

Proteins in italics were identified in Zhao et al., 2010 J. Proteome Res. 9: 1637–1647

Gene list was downloaded from KEGG

(http://www.genome.jp/kegg-bin/show_pathway?org_name=ath&mapno=00020&mapscale=1.0&show_description=show)

Gene name and description were downloaded from TAIR (<http://www.arabidopsis.org/>).

TCA	Name	Description
AT1G60810	ACLA-2	One of the three genes encoding subunit A of the trimeric enzyme ATP Citrate lyase
AT1G09430	ACLA-3	subunit A of the heteromeric enzyme ATP citrate lyase (ACL)
AT3G06650	ACLB-1	One of the two genes encoding subunit B of the trimeric enzyme ATP Citrate lyase
AT5G49460	ACLB-2	One of the two genes encoding subunit B of the cytosolic enzyme ATP Citrate Lyase (ACL)
AT4G35830	ACO1	an aconitase that can catalyze the conversion of citrate to isocitrate through a cis-aconitate intermediate
AT4G26970	ACO2	an aconitase that can catalyze the conversion of citrate to isocitrate through a cis-aconitate intermediate
AT2G05710	ACO3	an aconitase that can catalyze the conversion of citrate to isocitrate through a cis-aconitate intermediate
AT2G44350	ATCS	a mitochondrion targeted citrate synthase
AT1G65930	ciCDH	a NADP+-isocitrate dehydrogenase that is believed to function in the cytosol
AT3G58740	CSY1	a peroxisomal citrate synthase that is expressed in siliques and developing seeds
AT3G58750	CSY2	a peroxisomal citrate synthase that is expressed throughout seedling and shoot development
AT2G42790	CSY3	a peroxisomal citrate synthase that is expressed throughout seedling and shoot development
AT3G60100	CSY5	citrate synthase 5 (CSY5)
AT1G59900	E1 ALPHA	the e1 alpha subunit of the pyruvate dehydrogenase complex (PDC)
AT1G34430	EMB3003	embryo defective 3003 (EMB3003)
AT2G47510	FUM1	a mitochondrial-localized protein
AT5G50950	FUM2	a fumarase enzyme
AT1G24180	IAR4	Arabidopsis thaliana pyruvate dehydrogenase E1a-like subunit
AT1G54340	ICDH	NADP-specific isocitrate dehydrogenase (ICDH)
AT4G35260	IDH1	a regulatory subunit of the mitochondrially-localized NAD+- dependent isocitrate dehydrogenase
AT2G17130	IDH2	a regulatory subunit of the mitochondrially-localized NAD+- dependent isocitrate dehydrogenase
AT4G35650	IDH-III	a regulatory subunit of the mitochondrially-localized NAD+- dependent isocitrate dehydrogenase
AT1G32480	IDH-IV	Predicted to encode a protein related isocitrate dehydrogenases
AT5G03290	IDH-V	a catalytic subunit of the mitochondrially-localized NAD+- dependent isocitrate dehydrogenase
AT3G09810	IDH-VI	a catalytic subunit of the mitochondrially-localized NAD+- dependent isocitrate dehydrogenase
AT3G16950	LPD1	a plastid lipoamide dehydrogenase
AT5G50850	MAB1	MACCI-BOU (MAB1)
AT3G47520	MDH	a protein with NAD-dependent malate dehydrogenase activity, located in chloroplasts
AT1G53240	mMDH1	Lactate/malate dehydrogenase family protein
AT3G15020	mMDH2	Lactate/malate dehydrogenase family protein
AT1G48030	mtLPD1	a mitochondrial lipoamide dehydrogenase whose expression is induced by light

AT3G17240 mtLPD2 lipoamide dehydrogenase precursor
AT4G37870 PCK1 a putative phosphoenolpyruvate carboxykinase (ATP-dependent)
AT5G65690 PCK2 a putative phosphoenolpyruvate carboxykinase (ATP-dependent)
AT1G01090 PDH-E1 AL pyruvate dehydrogenase E1 alpha subunit
AT1G30120 PDH-E1 BE a putative plastid pyruvate dehydrogenase E1 beta subunit
AT2G22780 PMDH1 an peroxisomal NAD-malate dehydrogenase
AT5G09660 PMDH2 a microbody NAD-dependent malate dehydrogenase
AT5G66760 SDH1-1 One of two genes in Arabidopsis that encode a flavoprotein subunit of the mitochondrial succinate dehydrogenase complex
AT2G18450 SDH1-2 Nuclear encoded mitochondrial flavoprotein subunit of succinate dehydrogenase complex
AT3G27380 SDH2-1 One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT5G40650 SDH2-2 One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT5G65165 SDH2-3 One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex
AT5G65750 2-oxoglutarate dehydrogenase, E1 component
AT5G43330 Lactate/malate dehydrogenase family protein
AT5G23250 Succinyl-CoA ligase, alpha subunit
AT5G08300 Succinyl-CoA ligase, alpha subunit
AT3G55410 2-oxoglutarate dehydrogenase, E1 component
AT3G13930 Dihydrolipoamide acetyltransferase, long form protein
AT1G04410 Lactate/malate dehydrogenase family protein
AT5G55070 Dihydrolipoamide succinyltransferase
AT4G26910 Dihydrolipoamide succinyltransferase
AT4G16155 dihydrolipoamide dehydrogenases
AT3G52200 dihydrolipoamide S-acetyltransferase (LTA3) mRNA, nuclear
AT2G20420 ATP citrate lyase (ACL) family protein
AT1G10670 One of the three genes encoding subunit A of the trimeric protein ATP Citrate Lyase
AT1G54220 Dihydrolipoamide acetyltransferase, long form protein
AT2G34590 Transketolase family protein
AT5G14590 Isocitrate/isopropylmalate dehydrogenase family protein
AT5G56720 Lactate/malate dehydrogenase family protein

Table S5 Genes involved in the Calvin cycle in Arabidopsis

Proteins in bold were identified in Zhao et al., 2008. Plant Cell. 20: 3210-32226

Proteins in italics were identified in Zhao et al., 2010 J. Proteome Res. 9: 1637–1647

Gene list was downloaded from KEGG

(http://www.genome.jp/kegg-bin/show_pathway?org_name=ath&mapno=00710&mapscale=&show_description=hide)

Gene name and description were downloaded from TAIR (<http://www.arabidopsis.org/>).

Calvin Cycle	Name	Description
	AT1G17290	AlaAT1 for alanine aminotransferase (ALAAT1), involved in alanine catabolism during plants recovery from hypoxia
	AT1G70580	AOAT2 a protein with glyoxylate aminotransferase activity
	AT5G19550	ASP2 Nitrogen metabolism
	AT5G11520	ASP3 the chloroplastic isozyme of aspartate aminotransferase
	AT1G62800	ASP4 aspartate aminotransferase (Asp4)
	AT4G31990	ASP5 a plastid-localized aspartate aminotransferase
	AT2G21330	FBA1 fructose-bisphosphate aldolase 1 (FBA1)
	AT4G38970	FBA2 Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds
	AT3G26650	GAPA one of the two subunits forming the photosynthetic glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
	AT1G12900	GAPA-2 glyceraldehyde 3-phosphate dehydrogenase A subunit 2 (GAPA-2)
	AT1G42970	GAPB chloroplast localized glyceraldehyde-3-phosphate dehydrogenase
	AT1G23310	GGT1 Identified by cloning the gene that corresponded to a purified protein having glyoxylate aminotransferase activity
	AT3G54050	HCEF1 HCEF1 (High Cyclic Electron Flow 1)
	AT3G47520	MDH a protein with NAD-dependent malate dehydrogenase activity, located in chloroplasts
	AT1G53240	mMDH1 Lactate/malate dehydrogenase family protein
	AT3G15020	mMDH2 Lactate/malate dehydrogenase family protein
	AT2G13560	NAD-ME1 an NAD-dependent malic enzyme (NAD-ME) that does not act on oxaloacetate
	AT4G00570	NAD-ME2 an NAD-dependent malic enzyme (NAD-ME) that does not act on oxaloacetate
	AT2G19900	NADP-ME1 The malic enzyme (EC 1)
	AT5G11670	NADP-ME2 The malic enzyme (EC 1)
	AT5G25880	NADP-ME3 The malic enzyme (EC 1)
	AT1G79750	NADP-ME4 The malic enzyme (EC 1)
	AT4G37870	PCK1 a putative phosphoenolpyruvate carboxykinase (ATP-dependent)
	AT5G65690	PCK2 a putative phosphoenolpyruvate carboxykinase (ATP-dependent)
	AT1G79550	PGK cytosolic phosphoglycerate kinase (PGK)
	AT3G12780	PGK1 nuclear phosphoglycerate kinase (PGK1)
	AT1G32440	PKp3 a chloroplast pyruvate kinase beta subunit
	AT3G22960	PKP-ALPHA a chloroplast pyruvate kinase alpha subunit
	AT5G52920	PKP-BETA1 a dominant chloroplast pyruvate kinase beta subunit
	AT2G22780	PMDH1 an peroxisomal NAD-malate dehydrogenase
	AT5G09660	PMDH2 a microbody NAD-dependent malate dehydrogenase

AT1G53310	PPC1	one of four Arabidopsis phosphoenolpyruvate carboxylase proteins
AT2G42600	PPC2	one of four Arabidopsis phosphoenolpyruvate carboxylase proteins
AT3G14940	PPC3	a cytosolic phosphoenolpyruvate carboxylase (PEPC) that has activity when expressed in E
AT1G68750	PPC4	one of four Arabidopsis phosphoenolpyruvate (PEP) carboxylase proteins
AT4G15530	PPDK	a dual-targeted protein believed to act as a pyruvate, orthophosphate dikinase
AT1G32060	PRK	phosphoribulokinase (PRK)
ATCG00490	RBCL	large subunit of RUBISCO
AT1G67090	RBCS1A	ribulose biphosphate carboxylase small chain 1A (RBCS1A)
AT5G61410	RPE	Arabidopsis thaliana ribulose-5-phosphate-3-epimerase mRNA
AT2G01290	RPI2	Cytosolic ribose-5-phosphate isomerase
AT1G71100	RSW10	a ribose 5-phosphate isomerase involved in the formation of uridine used for the synthesis of UDP-sugars
AT3G55800	SBPASE	the chloroplast enzyme sedoheptulose-1,7-bisphosphatase (SBPase), involved in the carbon reduction of the Calvin cycle
AT2G21170	TIM	a plastidic triose phosphate isomerase
AT3G55440	TPI	triosephosphate isomerase
AT5G43330		Lactate/malate dehydrogenase family protein
AT5G38420		Ribulose biphosphate carboxylase (small chain) family protein
AT5G38410		Ribulose biphosphate carboxylase (small chain) family protein
AT3G60750		Transketolase
AT3G52930		Aldolase superfamily protein
AT2G36580		Pyruvate kinase family protein
AT2G01140		Aldolase superfamily protein
AT1G04410		Lactate/malate dehydrogenase family protein
AT5G38430		Ribulose biphosphate carboxylase (small chain) family protein
AT3G52990		Pyruvate kinase family protein
AT3G04790		Ribose 5-phosphate isomerase, type A protein
AT2G45290		Transketolase
AT2G36460		Aldolase superfamily protein
AT1G56190		Phosphoglycerate kinase family protein
AT1G43670		Inositol monophosphatase family protein
AT1G63290		Aldolase-type TIM barrel family protein
AT1G72330		for alanine aminotransferase ALAAT2
AT3G01850		Aldolase-type TIM barrel family protein
AT3G04050		Pyruvate kinase family protein
AT3G25960		Pyruvate kinase family protein
AT3G49160		Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress
AT3G55650		Pyruvate kinase family protein
AT3G55810		Pyruvate kinase family protein
AT4G26390		Pyruvate kinase family protein
AT4G26520		Aldolase superfamily protein
AT4G26530		Aldolase superfamily protein

AT5G03690	Aldolase superfamily protein
AT5G08570	Pyruvate kinase family protein
AT5G44520	NagB/RpiA/CoA transferase-like superfamily protein
AT5G56350	Pyruvate kinase family protein
AT5G56720	Lactate/malate dehydrogenase family protein
AT5G63680	Pyruvate kinase family protein
AT5G64380	Inositol monophosphatase family protein