**Supplemental Table 1 online.** Expression Data Showing Genes Clustering with *AtSAMT1*.

Arithmetic means of the three independent replicates contained in the AtGenExpress developmental series (Affymetrix ATH1 gene chip; 79 different conditions) were median centered for five consecutive times (rows and columns) and hierarchically clustered using the software Cluster 3.0. The resulting gene tree was visualized using the software Java Treeview (<a href="http://jtreeview.sourceforge.net">http://jtreeview.sourceforge.net</a>) and manually inspected for genes clustering with AtSAMT1. The gene/array tree showing an  $r^2$  value of > 0.85 was extracted and the corresponding AGI identifiers and annotations are listed in the table. All corresponding proteins were analyzed for their predicted subcellular localization using TargetP.

AGI	TargetP-prediction	Annotation
		protoporphyrinogen oxidase, putativel similar to protoporphyrinogen IX oxidase, mitochondrial (PPO II)
At5g14220	other	from Nicotiana tabacum (SPIO24164), Glycine max, AB025102, Spinacia oleracea (GI:14349153); contains
		Pfam amine oxidase, flavin-containing domain (PF015
At3g62000	mitochondria	O-methyltransferase family 3 proteinl several O-methyltransferases - different species; contains Pfam 01596
		O-methyltransferase domain
At5g39790	mitochondria	5'-AMP-activated protein kinase beta-1 subunit-related contains similarity to Swiss-Prot:P80387 5'-AMP-
		activated protein kinase, beta-1 subunit (AMPK beta-1 chain) (AMPKb) (40 kDa subunit) (Sus scrofa)
At5g64816	chloroplasts	expressed proteinl
At2g48120	chloroplasts	pale cress protein (PAC)
At3g18110	chloroplasts	pentatricopeptide (PPR) repeat-containing proteinl contains Pfam profile: PF01535 PPR repeat
At5g19620	chloroplasts	outer membrane OMP85 family protein
		cell division protein FtsZ, chloroplast, putative (FTSZ)l identical to SPlQ42545 Cell division protein ftsZ
At5g55280	chloroplasts	homolog, chloroplast precursor {Arabidopsis thaliana}; similar to FtsZ1 (Tagetes erecta) GI:8896066;
		contains Pfam profiles PF00091: Tubulin/FtsZ f

At4g23940	chloroplasts	FtsH protease, putative contains similarity to zinc dependent protease GI:7650138 from [Arabidopsis
		thaliana]
At3g46740	chloroplasts	chloroplast import-associated channel protein homolog chloroplast import-associated channel IAP75 - Pisum
		sativum,PIR2:S55344
At4g33680	chloroplasts	aminotransferase class I and II family proteinl low similarity to Aromatic Aminotransferase from
A14g33080		Pyrococcus horikoshii GPl14278621; contains Pfam profile PF00155 aminotransferase, classes I and II
Λ+1α1 <i>Λ</i> Λ1Ω	chloroplasts	DNA-binding protein p24, putative similar to DNA-binding protein p24 GI:9651810 from [Solanum
At1g14410		tuberosum]; supported by cDNA: gi_13877786_gb_AF370156.1_AF370156
At2g39290	chloroplasts	phosphatidylglycerolphosphate synthase (PGS1)l identical to phosphatidylglycerolphosphate synthase
A(2g3)2)0		GI:13365519 from (Arabidopsis thaliana)
At5g19210	other	eIF-4AII - like protein EUKARYOTIC INITIATION FACTOR 4A-II (EIF-4A-II), Homo sapiens,
At5g19210		SWISSPROT:IF42_HUMAN
At4g30720	chloroplasts	expressed protein hypothetical protein - Synechocystis sp. (strain PCC 6803), PIR2:S76076
At1g74850	chloroplasts	hypothetical protein predicted by genscan+
At3g49470	other	alpha NAC-like protein Nascent polypeptide associated complex protein alpha subunit - Drosophila
Allgarato		melanogaster, EMBL:AF017783; supported by cDNA: gi_13899100_gb_AF370545.1_AF370545
At4g32900	mitochondria	expressed proteinl
Λ+5α23310	chloroplasts	superoxide dismutase (Fe) / iron superoxide dismutase 3 (FSD3)l identical to iron superoxide dismutase 3
At5g23310		(Arabidopsis thaliana) gil3273757lgblAAC24834
At4g34290	chloroplasts	SWIB complex BAF60b domain-containing protein
At2g44640	chloroplasts	expressed proteinl

At3g04260	chloroplasts	SAP domain-containing protein
At3g54090	chloroplasts	Putative fructokinase; b3 pfkB-type carbohydrate kinase family proteinl contains Pfam profile: PF00294
		carbohydrate kinase
At1g69200	chloroplasts	putative fructokinase; b3 pfkB-type carbohydrate kinase family proteinl contains Pfam profile: PF00294
		pfkB family carbohydrate kinase
At1g06950	chloroplasts	The Chloroplast Envelope Anion Channel-forming Tic110 Family
At3g48500	chloroplasts	expressed proteinl
At2g34640	chloroplasts	expressed proteinl
At3g16260	chloroplasts	metallo-beta-lactamase family protein
At3g13180	chloroplasts	NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein
At1g10522	chloroplasts	expressed proteinl
At2g04530	chloroplasts	RNase Z
At1g30610	chloroplasts	pentatricopeptide (PPR) repeat-containing proteinl contains Pfam profile PF01535: PPR repeat
At1g63680	chloroplasts	Mur ligase family protein
At4g17540	other	expressed proteinl
		N2,N2-dimethylguanosine tRNA methyltransferase family proteinl low similarity to SPlQ9P804 N(2),N(2)-
At3g56330	chloroplasts	dimethylguanosine tRNA methyltransferase (EC 2.1.1.32) (tRNA(guanine-26,N(2)-N(2)) methyltransferase)
		{Schizosaccharomyces pombe}; contains Pfam profile P
At4g24175	mitochondria	expressed proteinl
At1g17850	chloroplasts	expressed proteinl
At2g14660	other	expressed proteinl contains Pfam PF04543: Family of unknown function (DUF589); similar to cThy28kD

		(GI:995778) (Gallus gallus); similar to thymocyte protein mThy28 (GI:23978374) (Mus musculus)
At3g25680	chloroplasts	expressed proteinl
At5g39980	chloroplasts	pentatricopeptide (PPR) repeat-containing proteinl contains Pfam profile PF01535: PPR repeat
At1g11290	chloroplasts	pentatricopeptide (PPR) repeat-containing proteinl contains Pfam profile PF01535: PPR repeat
		DEAD box RNA helicase (RH26) strong similarity to RNA helicase RH26 (Arabidopsis thaliana)
At5g08610	chloroplasts	GI:3776025; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-
		terminal domain; identical to cDNA DEAD box RNA helicase, RH26 GI
At4g31210	chloroplasts	DNA topoisomerase like- protein Bacillus subtilis DNA Topoisomerase I; PID:G520753
A+1~66520	ablaranlasts	formyltransferase, putativel similar to methionyl-tRNA formyltransferase (strain N315- Staphylococcus
At1g66520	chloroplasts	aureus) SWISS-PROT:Q99UQ2
At3g21300	other	RNA methyltransferase family proteinl contains TIGRfam TIGR00479: RNA methyltransferase, TrmA
	omei	family
A+1 a70560	other	FtsH protease, putative contains similarity to chloroplast FtsH protease GI:5804782 from [Nicotiana
At1g79560	omei	tabacum]
A+2~24120	ahlaranlasts	DNA-directed RNA polymerase, chloroplast (RPOPT)I identical to SPIO24600 DNA-directed RNA
At2g24120	chloroplasts	polymerase, chloroplast precursor (EC 2.7.7.6) {Arabidopsis thaliana}
At4g09730	mitochondria	DEAD/DEAH box helicase, putativel RNA helicase -Mus musculus,PIR2:I84741
At2g22870	mitochondria	expressed proteinl
At3g10270	other	putative DNA gyrase subunit B similar to putative DNA gyrase subunit GB:O50627 [Bacillus halodurans]
At1g48570	chloroplasts	zinc finger (Ran-binding) family proteinl contains Pfam domain, PF00641: Zn-finger in Ran binding protein
		and others

		DEAD/DEAH box helicase, putative (RH22)l similar to RNA helicase GI:3776015 from (Arabidopsis
At1g59990	chloroplasts	thaliana); contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00270: DEAD/DEAH
		box helicase; matches EST OAO811-2
		heat shock protein, putativel strong similarity to heat shock protein (Arabidopsis thaliana) GI:1906830;
At2g04030	chloroplasts	contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain
		protein, PF00183: Hsp90 protein
At1g49630	chloroplasts	peptidase M16 family protein / insulinase family proteinl contains Pfam domain, PF05193: Peptidase M16
		inactive domain
At4g10470	chloroplasts	expressed proteinl
At5g17660	chloroplasts	expressed proteinl contains Pfam profile PF02390: Putative methyltransferase
		NAD-dependent glycerol-3-phosphate dehydrogenase family proteinl low similarity to SPlQ26756 Glycerol-
At2g40690	other	3-phosphate dehydrogenase (NAD+), glycosomal (EC 1.1.1.8) {Trypanosoma brucei rhodesiense}; contains
		Pfam profile PF01210: NAD-dependent glycerol-3-phosp
		phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2)l identical to
At3g09150	chloroplasts	SPlQ9SR43 Phytochromobilin:ferredoxin oxidoreductase, chloroplast precursor (EC 1.3.7.4)
		(Phytochromobilin synthase) (PFB synthase) (PPhiB synthase)
At4g39460	chloroplasts	AtSAMT1; plastidic S-adenosylmethionine transporter
Δτ3σ13470	chloroplasts	chaperonin 60 beta, putative very similar to GB:JT0901 from [Arabidopsis thaliana] (Gene 111 (2), 175-181
At3g13470		(1992))
At1g50575	chloroplasts	lysine decarboxylase family proteinl contains Pfam profile PF03641: lysine decarboxylase family
At2g43630	chloroplasts	expressed proteinl

At3g49560	other	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family proteinl contains
		Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17
At1g04110	secretory pathway	subtilisin-like serine protease, putative contains similarity to subtilisin-like protease GI:3687307 from
		[Lycopersicon esculentum]
At4g26520	other	fructose-bisphosphate aldolase, cytoplasmicl identical to SPIP22197 Fructose-bisphosphate aldolase,
		cytoplasmic isozyme (EC 4.1.2.13) {Arabidopsis thaliana}
At3g10840	mitochondria	hydrolase, alpha/beta fold family protein
At2g18940	chloroplasts	pentatricopeptide (PPR) repeat-containing proteinl contains Pfam profile: PF01535 PPR repeat
At1g78180	other	mitochondrial substrate carrier family proteinl contains Pfam profile: PF00153 mitochondrial carrier protein