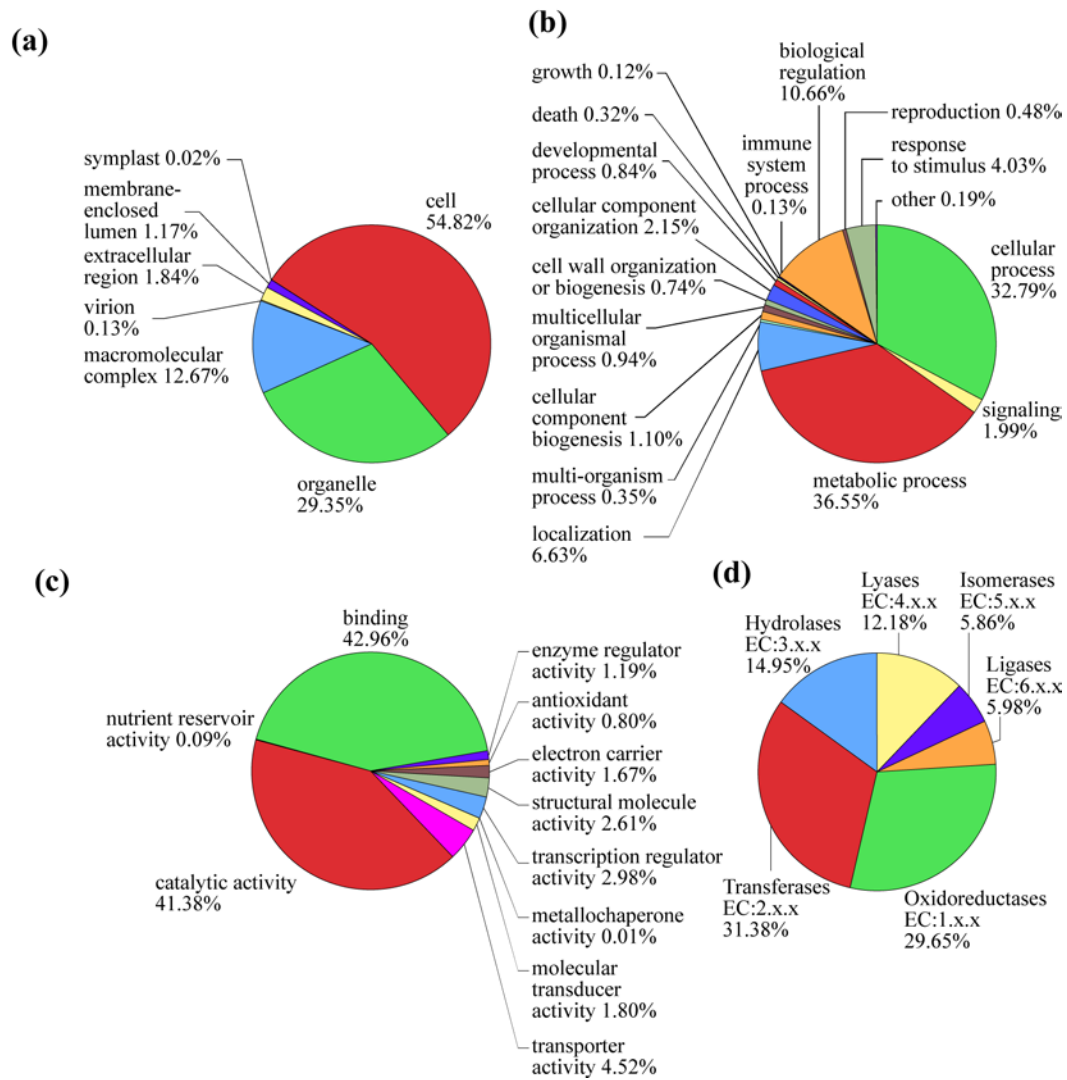
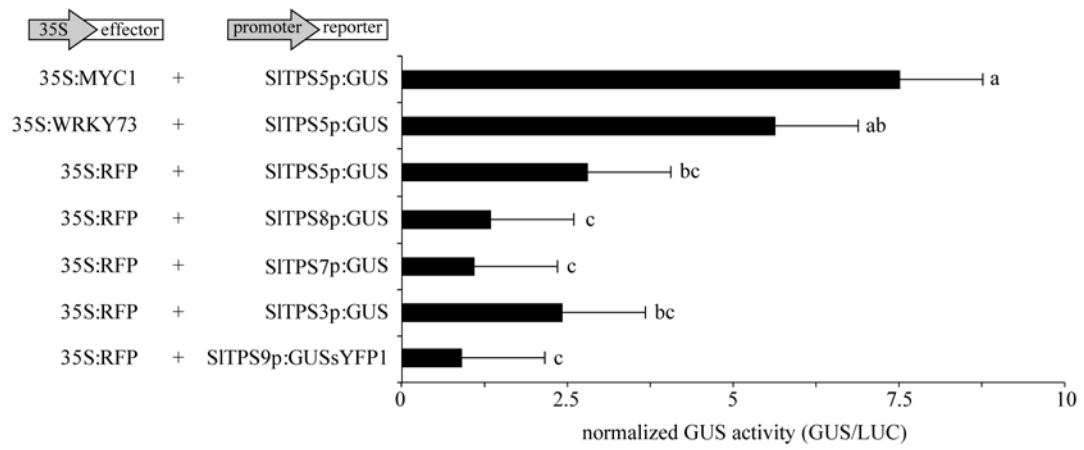


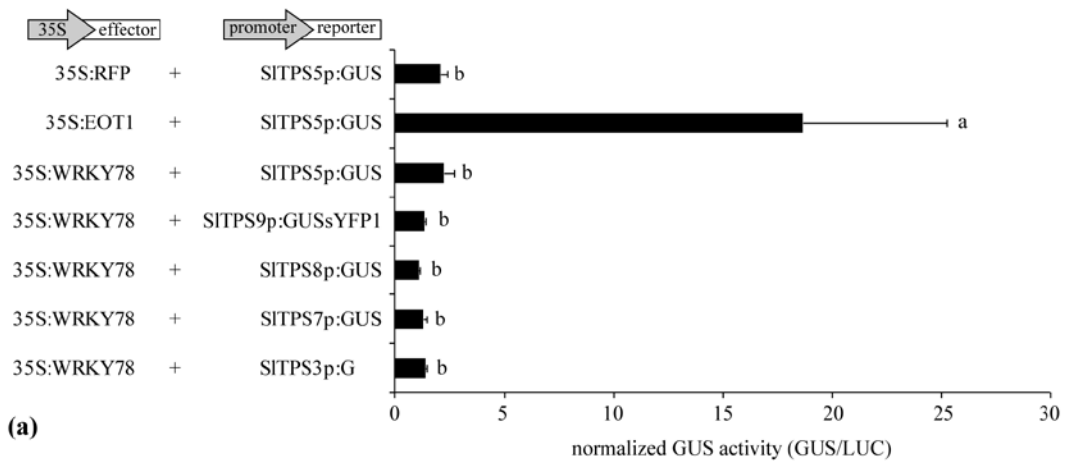
**Figure S1**



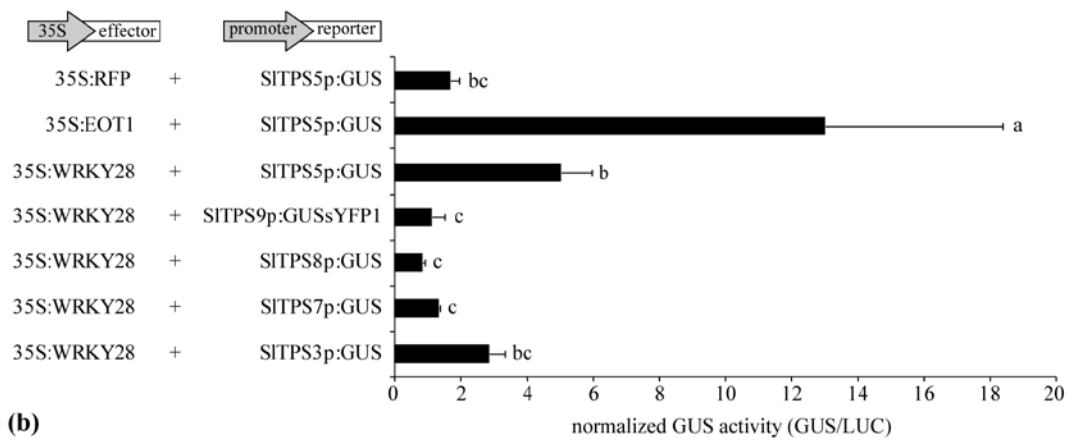
**Figure S2**



**Figure S3**



(a)



(b)

## Figure S4

### *SIMYCI*

ctcacctaacaacaaaatctctcattttctgtttttgtaaaattctcaatttaattga**ATG**ACGGACTATAGATTATGGAGTAA  
TACCAATACTACTAATACATGTGATGATACTATGATGATGGATTCTTTTTTATCTTCCGATC  
CATCCTCTTTTTGGCCTGCTTCCACTCCCAATCGTCCGACTCCGGTGAACGGAGTCGGAGA  
AACGATGCCGTTTTTCAATCAAGAATCACTACAGCAAAGGCTTCAGGCTTTAATTGACGGT  
GCTCGTGAATCATGGGCATATGCTATTTTCTGGCAATCGTCAGTTGTTGATTTTGCAGCC  
AAACTGTATTGGGTTGGGGAGATGGGTATTATAAAGGAGAAGAAGATAAGAATAAACGG  
AGAGGGTCGTCTAGTTCAGCAGCTAATTTTGTGCTGAGCAAGAGCATAGAAAGAAGGTG  
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GATGCAGTGGATGAGGAAGTGACGGATACTGAATGGTTTTTTCTGATTTCAATGACCCAAT  
CGTTTGTAAACGGTAACGGGCTTCCGGGCTTGGCGATGTACAGTTCAAGCCCAATTTGGGT  
TACTGGAACAGAGAAATTAGCTGCTTCTCAATGTGAACGGGCCAGGCAAGCCCAAGGTTT  
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GCCCCATCCTTCGGCCCTTGGCTTACGGATTCCATCTTCCTCGGTTGTGGAACCTAAGGAT  
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CAGCTGCCAGGCTAATGGCAGCCCTCAAGGACTTGGACCTAGACGTGCACCACGCTAGTG  
TTTCCGTGGTGAATGATTTGATGATCCAACAAGCCACAGTCAAAATGGGGAGCCGGCTTT  
ATGCTCAAGAACAGCTTAGGATAGCATTGACATCAAAAATTGCTGAATCGCGAT**G**Aaattatgt  
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ttc

### *SIWRKY78*

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GACAGTGACGTGGCGTTAATGTTGCCGATTTCGAGAAGAGGATCAGTCGTTGTACGGTGAT  
CTCGGTGAATTACCGGAATGTTCAAGTTGTTTTCCGGCGGTACAGTGTGAAACTCCCTGCT  
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tctgacccttttttaa

*SIWRKY28*

acttcataacgagtgccctcaaatcatattttcttcgccaaggacatccattgctattaccatcaagctacatactcttttttctctctccaaaacatt  
ctcatctatcatatctattttttattgcacaaaactatagtgtaatgtaatttaagaantcgaataatattttctccaat**ATGTCTGATAATCC**  
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AAAATCCTTCAAATTATAATAACCAACCAATAACTCCAAATATTCAAATCAACAATTTGT  
TCCTTCTTCTTATATGACTCTCACTGAGTGTTACATGGCTCTATGGACTACAACACACTAT  
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GGTCCAAAAACAAGAGCCATCT**TA**Gttcactacaaggtttctgtagcaatcgactattctatccatcaagaattttgtacaag  
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*SIWRKY73*

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tcagcgttattaatcaggtgtatttttaatgatttgagaatgtagtaccaaaatgtagatatttttagtatttagtaattgacgactctgt

**Table S1.** KEGG pathways found in the *S. lycopersicum* stem trichome transcriptome. The classification of the EC numbers in KEGG pathways was performed via Blast2GO ([www.blast2go.com](http://www.blast2go.com))

KEGG pathway	EC number	Enzyme Name	Nr of contigs
<b>Photosynthesis</b>	ec: 1.18.1.2	ferredoxin---NADP+ reductase	3
<b>Carbon fixation</b>	ec: 2.7.1.19	phosphoribulokinase	1
	ec: 4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	1
	ec: 4.1.1.39	ribulose-bisphosphate carboxylase	7
	ec: 4.1.1.31	phosphoenolpyruvate carboxylase	7
	ec: 5.3.1.6	ribose-5-phosphate isomerase	2
	ec: 5.3.1.1	triose-phosphate isomerase	3
	ec: 5.1.3.1	ribulose-phosphate 3-epimerase	3
	ec: 2.2.1.1	transketolase	2
	ec: 3.1.3.11	fructose-bisphosphatase	5
	ec: 2.7.2.3	phosphoglycerate kinase	2
	ec: 1.1.1.82	malate dehydrogenase (NADP+)	2
	ec: 4.1.2.13	fructose-bisphosphate aldolase	4
	ec: 1.1.1.39	malate dehydrogenase (decarboxylating)	2
	ec: 1.1.1.37	malate dehydrogenase	7
	ec: 2.6.1.1	aspartate transaminase	1
	ec: 1.2.1.13	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating)	2
	ec: 2.7.1.40	pyruvate kinase	4
	ec: 6.3.4.3	formate---tetrahydrofolate ligase	1
	ec: 4.1.1.31	phosphoenolpyruvate carboxylase	7
	ec: 1.5.1.20	methylenetetrahydrofolate reductase [NAD(P)H]	1
	ec: 6.4.1.2	acetyl-CoA carboxylase	7
	ec: 3.5.4.9	methenyltetrahydrofolate cyclohydrolase	2
	ec: 2.3.3.8	ATP citrate synthase	6
	ec: 6.2.1.5	succinate---CoA ligase (ADP-forming)	7
	ec: 6.2.1.1	acetate---CoA ligase	2
	ec: 1.1.1.42	isocitrate dehydrogenase (NADP+)	4
	ec: 1.1.1.37	malate dehydrogenase	7
	ec: 1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	1
	ec: 1.5.1.5	methylenetetrahydrofolate dehydrogenase (NADP+)	2
	ec: 4.2.1.3	aconitate hydratase	2
	ec: 4.2.1.2	fumarate hydratase	3
<b>Fructose and mannose metabolism</b>	ec: 2.7.1.11	6-phosphofructokinase	10
	ec: 5.3.1.8	mannose-6-phosphate isomerase	3
	ec: 5.3.1.5	xylose isomerase	1
	ec: 5.3.1.1	triose-phosphate isomerase	3
	ec: 2.7.1.4	fructokinase	3
	ec: 2.7.1.1	hexokinase	1
	ec: 3.2.1.78	mannan endo-1,4-beta-mannosidase	1
	ec: 3.1.3.46	fructose-2,6-bisphosphate 2-phosphatase	1

ec: 3.1.3.11	fructose-bisphosphatase	5
ec: 2.7.7.22	mannose-1-phosphate guanylyltransferase (GDP)	1
ec: 4.1.2.13	fructose-bisphosphate aldolase	4
ec: 3.6.1.21	ADP-sugar diphosphatase	1
ec: 2.7.1.105	6-phosphofructo-2-kinase	1
ec: 1.1.1.21	aldehyde reductase	1
	diphosphate---fructose-6-phosphate 1-	
ec: 2.7.1.90	phosphotransferase	6
ec: 5.4.2.8	phosphomannomutase	1
ec: 2.7.1.52	fucokinase	1

### Galactose metabolism

ec: 2.7.1.11	6-phosphofructokinase	10
ec: 2.7.1.6	galactokinase	2
ec: 2.7.1.2	glucokinase	1
ec: 2.7.1.1	hexokinase	1
ec: 5.1.3.2	UDP-glucose 4-epimerase	4
ec: 3.2.1.26	beta-fructofuranosidase	3
ec: 3.2.1.23	beta-galactosidase	20
ec: 3.2.1.22	alpha-galactosidase	4
ec: 3.2.1.20	alpha-glucosidase	6
ec: 2.7.7.9	UTP---glucose-1-phosphate uridylyltransferase	1
	UDP-glucose---hexose-1-phosphate	
ec: 2.7.7.12	uridylyltransferase	1
ec: 2.4.1.67	galactinol---raffinose galactosyltransferase	2
ec: 1.1.1.21	aldehyde reductase	1
ec: 5.4.2.2	phosphoglucomutase	3

### Pentose phosphate pathway

ec: 2.7.1.15	ribokinase	7
ec: 2.7.1.12	gluconokinase	1
ec: 2.7.1.11	6-phosphofructokinase	10
ec: 2.7.6.1	ribose-phosphate diphosphokinase	1
ec: 5.3.1.9	glucose-6-phosphate isomerase	3
ec: 5.3.1.6	ribose-5-phosphate isomerase	2
ec: 5.1.3.1	ribulose-phosphate 3-epimerase	3
ec: 3.1.1.31	6-phosphogluconolactonase	3
ec: 2.2.1.2	transaldolase	1
ec: 2.2.1.1	transketolase	2
ec: 3.1.3.11	fructose-bisphosphatase	5
ec: 4.1.2.13	fructose-bisphosphate aldolase	4
ec: 1.1.1.49	glucose-6-phosphate dehydrogenase	6
	phosphogluconate dehydrogenase	
ec: 1.1.1.44	(decarboxylating)	7
ec: 5.4.2.2	phosphoglucomutase	3

### Starch and sucrose metabolism

ec: 4.1.1.35	UDP-glucuronate decarboxylase	8
ec: 2.4.1.1	phosphorylase	3
ec: 5.3.1.9	glucose-6-phosphate isomerase	3
ec: 2.7.1.4	fructokinase	3
ec: 2.7.1.2	glucokinase	1

ec: 2.7.1.1	hexokinase	1
ec: 3.2.1.4	cellulase	10
ec: 3.2.1.2	beta-amylase	4
ec: 3.2.1.1	alpha-amylase	5
ec: 3.2.1.67	galacturan 1,4-alpha-galacturonidase	1
ec: 3.1.1.11	pectinesterase	28
ec: 3.2.1.39	glucan endo-1,3-beta-D-glucosidase	12
ec: 3.2.1.28	alpha,alpha-trehalase	2
ec: 3.2.1.26	beta-fructofuranosidase	3
ec: 3.2.1.21	beta-glucosidase	7
ec: 3.2.1.20	alpha-glucosidase	6
ec: 3.2.1.15	polygalacturonase	12
ec: 2.7.7.9	UTP---glucose-1-phosphate uridylyltransferase	1
ec: 3.1.3.24	sucrose-phosphate phosphatase	3
ec: 3.1.3.12	trehalose-phosphatase	7
ec: 2.7.7.27	glucose-1-phosphate adenyltransferase	3
ec: 2.4.1.34	1,3-beta-glucan synthase	8
ec: 3.6.1.21	ADP-sugar diphosphatase	1
ec: 2.4.1.25	4-alpha-glucanotransferase	3
ec: 2.4.1.21	starch synthase	11
ec: 2.4.1.18	1,4-alpha-glucan branching enzyme	2
ec: 2.4.1.15	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	6
ec: 2.4.1.14	sucrose-phosphate synthase	2
ec: 2.4.1.13	sucrose synthase	1
ec: 2.4.1.12	cellulose synthase (UDP-forming)	16
ec: 1.1.1.22	UDP-glucose 6-dehydrogenase	3
ec: 5.4.2.6	beta-phosphoglucomutase	1
ec: 5.4.2.2	phosphoglucomutase	3
<b>Glycolysis / Gluconeogenesis</b>		
ec: 2.7.1.11	6-phosphofructokinase	10
ec: 4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	1
ec: 5.3.1.9	glucose-6-phosphate isomerase	3
ec: 5.3.1.1	triose-phosphate isomerase	3
ec: 2.7.1.2	glucokinase	1
ec: 2.7.1.1	hexokinase	1
ec: 4.2.1.11	phosphopyruvate hydratase	5
ec: 5.1.3.3	aldose 1-epimerase	2
ec: 1.1.1.1	alcohol dehydrogenase	4
ec: 3.1.3.11	fructose-bisphosphatase	5
ec: 6.2.1.1	acetate---CoA ligase	2
ec: 2.7.2.3	phosphoglycerate kinase	2
ec: 4.1.1.1	pyruvate decarboxylase	1
ec: 1.2.1.9	glyceraldehyde-3-phosphate dehydrogenase (NADP+)	1
ec: 1.2.1.3	aldehyde dehydrogenase (NAD+)	4
ec: 4.1.2.13	fructose-bisphosphate aldolase	4
ec: 1.1.1.27	L-lactate dehydrogenase	1

ec: 1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	4
ec: 1.8.1.4	dihydrolipoyl dehydrogenase	2
ec: 1.2.1.12	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	7
ec: 5.4.2.2	phosphoglucomutase	3
ec: 5.4.2.1	phosphoglycerate mutase	2
ec: 2.7.1.40	pyruvate kinase	4

### Citrate cycle (TCA cycle)

ec: 4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	1
ec: 2.3.3.8	ATP citrate synthase	6
ec: 2.3.3.1	citrate (Si)-synthase	1
ec: 6.2.1.5	succinate---CoA ligase (ADP-forming)	7
ec: 2.3.1.61	dihydrolipoyllysine-residue succinyltransferase	1
ec: 1.3.5.1	succinate dehydrogenase (ubiquinone)	1
ec: 1.1.1.42	isocitrate dehydrogenase (NADP+)	4
ec: 1.1.1.41	isocitrate dehydrogenase (NAD+)	3
ec: 1.1.1.37	malate dehydrogenase	7
ec: 1.2.4.2	oxoglutarate dehydrogenase (succinyl-transferring)	4
ec: 1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	4
ec: 1.8.1.4	dihydrolipoyl dehydrogenase	2
ec: 4.2.1.3	aconitate hydratase	2
ec: 4.2.1.2	fumarate hydratase	3

### Pyruvate metabolism

ec: 4.1.1.49	phosphoenolpyruvate carboxykinase (ATP)	1
ec: 4.1.1.31	phosphoenolpyruvate carboxylase	7
ec: 6.4.1.2	acetyl-CoA carboxylase	7
ec: 3.1.2.6	hydroxyacylglutathione hydrolase	2
ec: 2.3.3.9	malate synthase	1
ec: 6.2.1.1	acetate---CoA ligase	2
ec: 1.1.1.82	malate dehydrogenase (NADP+)	2
ec: 4.4.1.5	lactoylglutathione lyase	3
ec: 1.2.1.3	aldehyde dehydrogenase (NAD+)	4
ec: 1.1.1.39	malate dehydrogenase (decarboxylating)	2
ec: 1.1.1.37	malate dehydrogenase	7
ec: 1.1.1.27	L-lactate dehydrogenase	1
ec: 1.1.1.21	aldehyde reductase	1
ec: 1.2.4.1	pyruvate dehydrogenase (acetyl-transferring)	4
ec: 2.3.3.13	2-isopropylmalate synthase	4
ec: 1.8.1.4	dihydrolipoyl dehydrogenase	2
ec: 2.7.1.40	pyruvate kinase	4

### Oxidative phosphorylation

ec: 1.10.2.2	ubiquinol---cytochrome-c reductase	5
ec: 3.6.3.6	H+-exporting ATPase	8
ec: 1.3.5.1	succinate dehydrogenase (ubiquinone)	1
ec: 1.6.5.3	NADH:ubiquinone reductase (H+-translocating)	13
ec: 3.6.1.1	inorganic diphosphatase ec: 3.6.1.10	9
ec: 1.9.3.1	endopolyphosphatase	9
ec: 1.9.3.1	cytochrome-c oxidase	7



<b>Pantothenate and CoA biosynthesis</b>	ec: 4.1.1.36	phosphopantothenoylcysteine decarboxylase	2
	ec: 2.2.1.6	acetolactate synthase	3
	ec: 1.1.1.86	ketol-acid reductoisomerase	2
	ec: 2.7.8.7	holo-[acyl-carrier-protein] synthase	1
	ec: 2.6.1.42	branched-chain-amino-acid transaminase	3
	ec: 2.7.1.33	pantothenate kinase	1
	ec: 4.2.1.9	dihydroxy-acid dehydratase	1
<b>Folate biosynthesis</b>	ec: 2.7.6.3	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	1
	ec: 3.5.4.16	GTP cyclohydrolase I	1
	ec: 4.1.2.25	dihydroneopterin aldolase	1
	ec: 1.5.1.3	dihydrofolate reductase	1
	ec: 2.5.1.15	dihydropteroate synthase	1
<b>One carbon pool by folate</b>	ec: 6.3.4.3	formate---tetrahydrofolate ligase	1
	ec: 2.1.2.10	aminomethyltransferase	1
	ec: 1.5.1.20	methylenetetrahydrofolate reductase [NAD(P)H]	1
	ec: 2.1.1.45	thymidylate synthase	1
	ec: 2.1.2.3	phosphoribosylaminoimidazolecarboxamide formyltransferase	2
	ec: 2.1.2.2	phosphoribosylglycinamide formyltransferase	1
	ec: 2.1.2.1	glycine hydroxymethyltransferase	6
	ec: 3.5.4.9	methenyltetrahydrofolate cyclohydrolase	2
	ec: 6.3.3.2	5-formyltetrahydrofolate cyclo-ligase	1
	ec: 1.5.1.5	methylenetetrahydrofolate dehydrogenase (NADP+)	2
	ec: 1.5.1.3	dihydrofolate reductase	1
<b>Fatty acid biosynthesis</b>	ec: 1.3.1.9	enoyl-[acyl-carrier-protein] reductase (NADH)	2
	ec: 6.4.1.2	acetyl-CoA carboxylase	7
	ec: 1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	7
	ec: 2.3.1.41	beta-ketoacyl-acyl-carrier-protein synthase I	6
	ec: 2.3.1.39	[acyl-carrier-protein] S-malonyltransferase	1
	ec: 1.14.19.2	acyl-[acyl-carrier-protein] desaturase	4
<b>Biosynthesis of unsaturated fatty acids</b>	ec: 4.2.1.17	enoyl-CoA hydratase	2
	ec: 1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase	7
	ec: 1.14.19.2	acyl-[acyl-carrier-protein] desaturase	4
	ec: 1.3.3.6	acyl-CoA oxidase	4
<b>alpha-Linolenic acid metabolism</b>	ec: 5.3.99.6	allene-oxide cyclase	1
	ec: 4.2.1.92	hydroperoxide dehydratase	2
	ec: 2.1.1.141	jasmonate O-methyltransferase	1
	ec: 4.2.1.17	enoyl-CoA hydratase	2
	ec: 1.13.11.12	linoleate 13S-lipoxygenase	9
	ec: 1.3.3.6	acyl-CoA oxidase	4
	ec: 3.1.1.4	phospholipase A2	4
	ec: 1.3.1.42	12-oxophytodienoate reductase	2

<b>Glycerolipid metabolism</b>	ec: 3.2.1.22	alpha-galactosidase	4
	ec: 2.3.1.15	glycerol-3-phosphate O-acyltransferase	1
	ec: 2.4.1.46	monogalactosyldiacylglycerol synthase	2
	ec: 1.2.1.3	aldehyde dehydrogenase (NAD+)	4
	ec: 2.7.1.107	diacylglycerol kinase	8
	ec: 1.1.1.21	aldehyde reductase	1
	ec: 2.4.1.241	digalactosyldiacylglycerol synthase	1
	ec: 3.1.1.3	triacylglycerol lipase	23
<b>Glycerophospholipid metabolism</b>	ec: 2.7.1.29	glycerone kinase	1
	ec: 3.1.4.46	glycerophosphodiester phosphodiesterase	2
	ec: 4.1.1.65	phosphatidylserine decarboxylase	2
	ec: 3.1.4.4	phospholipase D	9
	ec: 3.1.4.3	phospholipase C	1
		CDP-diacylglycerol---inositol 3-	
	ec: 2.7.8.11	phosphatidyltransferase	1
	ec: 1.1.1.8	glycerol-3-phosphate dehydrogenase (NAD+)	1
	ec: 2.7.7.41	phosphatidate cytidyltransferase	3
	ec: 2.3.1.43	phosphatidylcholine---sterol O-acyltransferase	6
	ec: 2.3.1.15	glycerol-3-phosphate O-acyltransferase	1
	ec: 2.7.1.107	diacylglycerol kinase	8
		CDP-diacylglycerol---glycerol-3-phosphate 3-	
	ec: 2.7.8.5	phosphatidyltransferase	1
	ec: 3.1.1.4	phospholipase A2	4
<b>Sphingolipid metabolism</b>	ec: 3.2.1.45	glucosylceramidase	2
	ec: 3.2.1.23	beta-galactosidase	20
	ec: 3.2.1.22	alpha-galactosidase	4
	ec: 1.1.1.102	3-dehydrosphinganine reductase	1
	ec: 2.3.1.50	serine C-palmitoyltransferase	2
	ec: 3.5.1.23	ceramidase	1
	ec: 2.7.1.138	ceramide kinase	1
	<b>Carotenoid biosynthesis</b>	ec: 1.10.99.3	violaxanthin de-epoxidase
ec: 1.14.13.90		zeaxanthin epoxidase	1
ec: 2.5.1.32		phytoene synthase	2
<b>Porphyrin and chlorophyll metabolism</b>	ec: 4.1.1.37	uroporphyrinogen decarboxylase	1
	ec: 4.99.1.3	sirohydrochlorin cobaltochelata	1
	ec: 4.99.1.1	ferrochelata	1
	ec: 5.4.3.8	glutamate-1-semialdehyde 2,1-aminomutase	2
	ec: 1.3.7.4	phytychromobilin:ferredoxin oxidoreductase	1
	ec: 1.14.99.3	heme oxygenase	2
		magnesium protoporphyrin IX methyltransferase	
	ec: 2.1.1.110	sterigmatocystin 8-O-	
	ec: 2.1.1.11	methyltransferase	1
	ec: 1.14.13.81	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	1

ec: 2.5.1.61	hydroxymethylbilane synthase	1
ec: 6.1.1.17	glutamate---tRNA ligase	1
ec: 1.2.1.70	glutamyl-tRNA reductase	1
ec: 1.3.3.5	bilirubin oxidase	1
ec: 1.3.3.4	protoporphyrinogen oxidase	2
ec: 1.3.3.3	coproporphyrinogen oxidase	1
ec: 1.3.1.33	protochlorophyllide reductase	5
ec: 6.6.1.1	magnesium chelatase	4

**Nitrogen  
metabolism**

ec: 2.1.2.10	aminomethyltransferase	1
ec: 4.2.1.104	cyanase	1
ec: 3.5.1.1	asparaginase	1
ec: 6.3.5.4	asparagine synthase (glutamine-hydrolysing)	2
ec: 1.13.12.16	nitronate monooxygenase	1
ec: 1.4.1.2	glutamate dehydrogenase	1
ec: 1.7.1.1	nitrate reductase (NADH)	2
ec: 4.4.1.8	cystathionine beta-lyase	1
ec: 1.7.7.1	ferredoxin---nitrite reductase	1
ec: 6.3.1.2	glutamate---ammonia ligase	4
ec: 4.2.1.1	carbonate dehydratase	5

**Alanine, glutamate  
and aspartate  
metabolism**

ec: 4.1.1.15	glutamate decarboxylase	4
ec: 4.2.1.17	enoyl-CoA hydratase	2
ec: 1.4.3.21	primary-amine oxidase	4
ec: 1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	4
ec: 2.5.1.16	spermidine synthase	2
ec: 1.2.1.19	aminobutyraldehyde dehydrogenase	1
ec: 1.3.99.3	acyl-CoA dehydrogenase	6
ec: 2.6.1.19	4-aminobutyrate transaminase	6
ec: 6.3.4.4	adenylosuccinate synthase	4
ec: 4.1.1.15	glutamate decarboxylase	4
ec: 1.4.3.2	L-amino-acid oxidase	1
ec: 1.4.3.16	L-aspartate oxidase	1
ec: 2.4.2.14	amidophosphoribosyltransferase	1
ec: 3.5.1.1	asparaginase	1
ec: 6.3.5.4	asparagine synthase (glutamine-hydrolysing)	2
ec: 1.4.1.2	glutamate dehydrogenase	1
ec: 4.3.2.2	adenylosuccinate lyase	1
ec: 2.1.3.2	aspartate carbamoyltransferase	1
ec: 2.6.1.1	aspartate transaminase	1
ec: 6.3.1.2	glutamate---ammonia ligase	4
ec: 2.6.1.19	4-aminobutyrate transaminase	6
ec: 2.6.1.16	glutamine---fructose-6-phosphate transaminase (isomerizing)	1

**Glycine, serine and  
threonine  
metabolism**

ec: 2.1.2.10	aminomethyltransferase	1
ec: 4.2.1.20	tryptophan synthase	5

	ec: 1.4.3.21	primary-amine oxidase	4
	ec: 4.3.1.19	threonine ammonia-lyase	2
	ec: 1.1.1.3	homoserine dehydrogenase	3
	ec: 1.1.1.1	alcohol dehydrogenase	4
	ec: 2.1.2.1	glycine hydroxymethyltransferase	6
	ec: 1.4.4.2	glycine dehydrogenase (decarboxylating)	1
	ec: 2.7.2.4	aspartate kinase	2
	ec: 1.1.1.95	phosphoglycerate dehydrogenase	2
	ec: 4.2.3.1	threonine synthase	2
	ec: 1.1.1.29	glycerate dehydrogenase	1
	ec: 1.8.1.4	dihydrolipoyl dehydrogenase	2
<b>Lysine biosynthesis</b>	ec: 4.2.1.52	dihydrodipicolinate synthase	3
	ec: 1.1.1.3	homoserine dehydrogenase	3
	ec: 2.7.2.4	aspartate kinase	2
	ec: 1.3.1.26	dihydrodipicolinate reductase	2
<b>Valine, leucine and isoleucine degradation</b>			
	ec: 1.4.3.2	L-amino-acid oxidase	1
	ec: 4.2.1.18	methylglutaconyl-CoA hydratase	1
	ec: 4.2.1.17	enoyl-CoA hydratase	2
	ec: 1.3.99.10	isovaleryl-CoA dehydrogenase	1
	ec: 4.1.3.4	hydroxymethylglutaryl-CoA lyase	2
	ec: 1.2.3.1	aldehyde oxidase	5
		dihydrolipoyllysine-residue (2-methylpropanoyl)transferase	1
	ec: 2.3.1.168		1
	ec: 1.2.1.3	aldehyde dehydrogenase (NAD+)	4
	ec: 1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	1
	ec: 1.1.1.31	3-hydroxyisobutyrate dehydrogenase	2
	ec: 2.3.3.10	hydroxymethylglutaryl-CoA synthase	6
	ec: 1.8.1.4	dihydrolipoyl dehydrogenase	2
	ec: 2.6.1.42	branched-chain-amino-acid transaminase	3
		methylmalonate-semialdehyde dehydrogenase (acylating)	1
	ec: 1.2.1.27		1
	ec: 1.3.99.3	acyl-CoA dehydrogenase	6
<b>Methionine and cysteine metabolism</b>			
	ec: 4.1.1.50	adenosylmethionine decarboxylase	3
	ec: 1.4.3.2	L-amino-acid oxidase	1
	ec: 1.1.1.3	homoserine dehydrogenase	3
	ec: 4.4.1.14	1-aminocyclopropane-1-carboxylate synthase	13
	ec: 2.1.1.37	DNA (cytosine-5-)-methyltransferase	4
		5-methyltetrahydropteroyltriglutamate---	
	ec: 2.1.1.14	homocysteine S-methyltransferase	1
	ec: 2.5.1.6	methionine adenosyltransferase	5
	ec: 2.1.1.10	homocysteine S-methyltransferase	1
	ec: 2.7.2.4	aspartate kinase	2
	ec: 2.3.1.30	serine O-acetyltransferase	4
	ec: 3.3.1.1	adenosylhomocysteinase	6
	ec: 4.4.1.8	cystathionine beta-lyase	1
	ec: 2.5.1.47	cysteine synthase	8

ec: 2.7.1.100	S-methyl-5-thioribose kinase	1
ec: 1.1.1.27	L-lactate dehydrogenase	1
ec: 2.5.1.16	spermidine synthase	2
ec: 2.6.1.1	aspartate transaminase	1
ec: 1.14.17.4	aminocyclopropanecarboxylate oxidase	4

### Arginine and proline metabolism

ec: 4.1.1.50	adenosylmethionine decarboxylase	3
ec: 1.5.99.8	proline dehydrogenase	3
ec: 3.5.3.1	arginase	2
ec: 4.1.1.19	arginine decarboxylase	2
ec: 4.1.1.17	ornithine decarboxylase	1
ec: 3.5.1.5	urease ec: 3.5.1.50 pentanamidase	1
ec: 3.5.1.4	amidase	4
ec: 1.4.1.2	glutamate dehydrogenase	1
ec: 3.5.1.53	N-carbamoylputrescine amidase	2
ec: 2.7.2.11	glutamate 5-kinase	3
ec: 1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	4
ec: 2.3.1.1	amino-acid N-acetyltransferase	1
ec: 2.5.1.16	spermidine synthase	2
ec: 1.2.1.41	glutamate-5-semialdehyde dehydrogenase	2
ec: 3.5.3.12	agmatine deiminase	1
ec: 2.6.1.1	aspartate transaminase	1
ec: 1.2.1.38	N-acetyl-gamma-glutamyl-phosphate reductase	1
ec: 1.2.1.19	aminobutyraldehyde dehydrogenase	1
ec: 6.3.1.2	glutamate---ammonia ligase	4

### Ascorbate and aldarate metabolism

ec: 5.1.3.18	GDP-mannose 3,5-epimerase	2
ec: 1.11.1.11	L-ascorbate peroxidase	6
ec: 1.8.5.1	glutathione dehydrogenase (ascorbate)	2
ec: 1.13.99.1	inositol oxygenase	4
ec: 1.3.2.3	L-galactonolactone dehydrogenase	1
ec: 1.6.5.4	monodehydroascorbate reductase (NADH)	3
ec: 1.10.3.3	L-ascorbate oxidase	6
ec: 1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	4
ec: 1.1.1.22	UDP-glucose 6-dehydrogenase	3

### Tryptophan metabolism

ec: 4.1.1.28	aromatic-L-amino-acid decarboxylase	4
ec: 1.4.3.2	L-amino-acid oxidase	1
ec: 4.2.1.17	enoyl-CoA hydratase	2
ec: 1.11.1.6	catalase	3
ec: 3.5.1.4	amidase	4
ec: 1.2.3.1	aldehyde oxidase	5
ec: 1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	4
ec: 1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	1
ec: 1.2.4.2	oxoglutarate dehydrogenase (succinyl-transferring)	4
ec: 1.14.14.1	unspecific monooxygenase	1

### Histidine metabolism

ec: 4.1.1.28	aromatic-L-amino-acid decarboxylase	4
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ec: 4.1.1.22	histidine decarboxylase	3
ec: 4.2.1.19	imidazoleglycerol-phosphate dehydratase	1
ec: 1.2.1.3	aldehyde dehydrogenase (NAD <sup>+</sup> )	4
ec: 1.1.1.23	histidinol dehydrogenase	1
ec: 2.6.1.9	histidinol-phosphate transaminase	1

**Phenylalanine,  
tyrosine and  
tryptophan  
biosynthesis**

ec: 4.2.1.91	arogenate dehydratase	1
ec: 5.4.99.5	chorismate mutase	2
ec: 4.2.1.51	prephenate dehydratase	5
ec: 1.4.3.2	L-amino-acid oxidase	1
ec: 4.2.1.20	tryptophan synthase	5
ec: 4.2.1.10	3-dehydroquinate dehydratase	3
ec: 4.1.3.27	anthranilate synthase	4
ec: 2.4.2.18	anthranilate phosphoribosyltransferase	1
ec: 4.2.3.5	chorismate synthase	3
ec: 4.2.3.4	3-dehydroquinate synthase	1
ec: 2.5.1.54	3-deoxy-7-phosphoheptulonate synthase	3
ec: 1.1.1.25	shikimate dehydrogenase	4
ec: 2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase	3
ec: 2.6.1.9	histidinol-phosphate transaminase	1

**Tyrosine  
metabolism**

ec: 2.6.1.1	aspartate transaminase	1
ec: 2.7.1.71	shikimate kinase	2
ec: 1.3.1.13	prephenate dehydrogenase (NADP <sup>+</sup> )	1
ec: 4.1.1.68	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase	1
ec: 2.1.1.6	catechol O-methyltransferase	1
ec: 3.7.1.2	fumarylacetoacetase	3
ec: 4.1.1.28	aromatic-L-amino-acid decarboxylase	4
ec: 1.4.3.2	L-amino-acid oxidase	1
ec: 1.4.3.21	primary-amine oxidase	4
ec: 1.1.1.1	alcohol dehydrogenase	4
ec: 1.2.3.1	aldehyde oxidase	5
ec: 1.13.11.5	homogentisate 1,2-dioxygenase	1
ec: 1.10.3.1	catechol oxidase	8
ec: 5.2.1.2	maleylacetoacetate isomerase	1
ec: 2.6.1.9	histidinol-phosphate transaminase	1
ec: 2.6.1.1	aspartate transaminase	1

**Phenylalanine  
metabolism**

ec: 4.1.1.28	aromatic-L-amino-acid decarboxylase	4
ec: 1.4.3.2	L-amino-acid oxidase	1
ec: 1.4.3.21	primary-amine oxidase	4
ec: 2.1.1.104	caffeoyl-CoA O-methyltransferase	4
ec: 1.11.1.7	peroxidase	56
ec: 3.5.1.4	amidase	4
ec: 2.6.1.9	histidinol-phosphate transaminase	1
ec: 2.6.1.1	aspartate transaminase	1
ec: 1.14.13.11	trans-cinnamate 4-monooxygenase	1

<b>N-Glycan biosynthesis</b>	ec: 6.2.1.12	4-coumarate---CoA ligase	4
	ec: 2.4.2.38	glycoprotein 2-beta-D-xylosyltransferase	1
	ec: 3.2.1.52	beta-N-acetylhexosaminidase	2
	ec: 2.4.1.119	dolichyl-diphosphooligosaccharide---protein glycotransferase	1
		alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	2
ec: 2.4.1.101	mannosyl-oligosaccharide 1,2-alpha-mannosidase	1	
<b>Purine metabolism</b>	ec: 3.2.1.113	adenylosuccinate synthase	4
	ec: 6.3.4.4	ribose-phosphate diphosphokinase	1
	ec: 2.7.6.1	phosphoribosylaminoimidazole carboxylase	1
	ec: 4.1.1.21	factor-independent urate hydroxylase	1
	ec: 1.7.3.3	phosphoribosylaminoimidazolesuccinocarboxamide synthase	2
	ec: 6.3.2.6	guanylate kinase	2
	ec: 2.7.4.8	nucleoside-diphosphate kinase	2
	ec: 2.7.4.6	adenylate kinase	6
	ec: 2.7.4.3	amidophosphoribosyltransferase	1
	ec: 2.4.2.14	urease ec: 3.5.1.50 pentanamidase	1
	ec: 3.5.1.5	phosphoribosylformylglycinamide synthase	2
	ec: 6.3.5.3	GMP synthase (glutamine-hydrolysing)	1
	ec: 6.3.5.2	adenylate cyclase	4
	ec: 4.6.1.1	phosphoribosylaminoimidazolecarboxamide formyltransferase	2
	ec: 2.1.2.3	phosphoribosylglycinamide formyltransferase	1
	ec: 2.1.2.2	IMP cyclohydrolase	2
	ec: 3.5.4.10	polyribonucleotide nucleotidyltransferase	1
	ec: 2.7.7.8	DNA-directed DNA polymerase	7
	ec: 2.7.7.7	DNA-directed RNA polymerase	25
	ec: 2.7.7.6	sulfate adenylyltransferase	5
	ec: 2.7.7.4	AMP deaminase	1
	ec: 3.5.4.6	adenosine deaminase	2
	ec: 3.5.4.4	RNA-directed RNA polymerase	6
	ec: 2.7.7.48	hypoxanthine phosphoribosyltransferase	1
	ec: 2.4.2.8	adenine phosphoribosyltransferase	1
	ec: 2.4.2.7	ribonucleoside-diphosphate reductase	4
	ec: 1.17.4.1	phosphoribosylformylglycinamide cyclo-ligase	1
	ec: 6.3.3.1	5'-nucleotidase	3
	ec: 3.1.3.5	adenosinetriphosphatase	26
	ec: 3.6.1.3	adenylosuccinate lyase	1
	ec: 4.3.2.2	ADP-sugar diphosphatase	1
	ec: 3.6.1.21	phosphoribosylamine---glycine ligase	1
	ec: 6.3.4.13	nucleoside-triphosphatase	53
ec: 3.6.1.15	exopolyphosphatase	1	
ec: 3.6.1.11	IMP dehydrogenase	1	
ec: 1.1.1.205	phosphoglucomutase	3	
ec: 5.4.2.2	pyruvate kinase	4	
ec: 2.7.1.40	adenylyl-sulfate kinase	2	
ec: 2.7.1.25			

<b>Pyrimidine metabolism</b>	ec: 2.7.1.20	adenosine kinase	2
	ec: 6.3.4.2	CTP synthase	1
	ec: 4.1.1.23	orotidine-5'-phosphate decarboxylase	1
	ec: 2.7.4.6	nucleoside-diphosphate kinase	2
	ec: 2.4.2.10	orotate phosphoribosyltransferase	1
	ec: 2.1.1.45	thymidylate synthase	1
	ec: 2.7.7.8	polyribonucleotide nucleotidyltransferase	1
	ec: 2.7.7.7	DNA-directed DNA polymerase	7
	ec: 2.7.7.6	DNA-directed RNA polymerase	25
	ec: 2.4.2.9	uracil phosphoribosyltransferase	1
	ec: 1.17.4.1	ribonucleoside-diphosphate reductase	4
	ec: 3.1.3.5	5'-nucleotidase	3
	ec: 3.6.1.23	dUTP diphosphatase	2
	ec: 2.1.3.2	aspartate carbamoyltransferase	1
	ec: 2.7.1.48	uridine kinase	3
	ec: 2.7.1.21	thymidine kinase	2
	<b>Nicotinate and nicotinamide metabolism</b>	ec: 1.4.3.16	L-aspartate oxidase
ec: 2.4.2.19		nicotinate-nucleotide diphosphorylase (carboxylating)	1
ec: 2.4.2.11		nicotinate phosphoribosyltransferase	1
ec: 6.3.5.1		NAD <sup>+</sup> synthase (glutamine-hydrolysing)	1
ec: 1.2.3.1		aldehyde oxidase	5
ec: 3.1.3.5		5'-nucleotidase	3
ec: 3.6.1.22		NAD <sup>+</sup> diphosphatase	1
ec: 2.7.1.23		NAD <sup>+</sup> kinase	1
<b>Inositol phosphate metabolism</b>	ec: 3.1.4.3	phospholipase C	1
	ec: 3.1.4.11	phosphoinositide phospholipase C	8
	ec: 2.7.8.11	CDP-diacylglycerol---inositol 3-phosphatidyltransferase	1
	ec: 5.3.1.1	triose-phosphate isomerase	3
	ec: 1.13.99.1	inositol oxygenase	4
	ec: 3.1.3.57	inositol-1,4-bisphosphate 1-phosphatase	1
	ec: 3.1.3.25	inositol-phosphate phosphatase	1
	ec: 2.7.1.159	inositol-1,3,4-trisphosphate 5/6-kinase	1
	ec: 2.7.1.150	1-phosphatidylinositol-3-phosphate 5-kinase	2
	ec: 2.7.1.137	phosphatidylinositol 3-kinase	2
	ec: 2.7.1.134	inositol-tetrakisphosphate 1-kinase	1
	ec: 2.7.1.127	inositol-trisphosphate 3-kinase	2
	ec: 5.5.1.4	inositol-3-phosphate synthase	3
	ec: 2.7.1.68	1-phosphatidylinositol-4-phosphate 5-kinase	3
	ec: 2.7.1.67	1-phosphatidylinositol 4-kinase	3
	ec: 4.1.1.28	aromatic-L-amino-acid decarboxylase	4
	<b>Riboflavin metabolism</b>	ec: 1.1.1.193	5-amino-6-(5-phosphoribosylamino)uracil reductase
ec: 3.5.4.26		diaminohydroxyphosphoribosylaminopyrimidine deaminase	1



ec: 3.5.4.25	GTP cyclohydrolase II	6
ec: 2.5.1.9	riboflavin synthase	3
ec: 3.1.3.2	acid phosphatase	10
ec: 4.1.99.12	3,4-dihydroxy-2-butanone-4-phosphate synthase	6
ec: 2.7.1.26	riboflavin kinase	1

### Glutathione metabolism

ec: 4.1.1.17	ornithine decarboxylase	1
ec: 2.3.2.2	gamma-glutamyltransferase	1
ec: 6.3.2.2	glutamate---cysteine ligase	1
ec: 1.11.1.9	glutathione peroxidase	4
ec: 1.11.1.15	peroxiredoxin	1
ec: 1.11.1.12	phospholipid-hydroperoxide glutathione peroxidase	1
ec: 1.11.1.11	L-ascorbate peroxidase	6
ec: 1.8.5.1	glutathione dehydrogenase (ascorbate)	2
ec: 1.17.4.1	ribonucleoside-diphosphate reductase	4
ec: 1.1.1.49	glucose-6-phosphate dehydrogenase	6
ec: 1.1.1.44	phosphogluconate dehydrogenase (decarboxylating)	7
ec: 1.1.1.42	isocitrate dehydrogenase (NADP+)	4
ec: 2.5.1.18	glutathione transferase	6
ec: 2.5.1.16	spermidine synthase	2
ec: 1.8.1.7	glutathione-disulfide reductase	1

### Glyoxylate and dicarboxylate metabolism

ec: 4.1.1.39	ribulose-bisphosphate carboxylase	7
ec: 4.1.3.1	isocitrate lyase	1
ec: 3.1.3.18	phosphoglycolate phosphatase	2
ec: 2.3.3.9	malate synthase	1
ec: 2.3.3.1	citrate (Si)-synthase	1
ec: 1.2.1.2	formate dehydrogenase	1
ec: 1.1.1.60	2-hydroxy-3-oxopropionate reductase	1
ec: 1.1.1.37	malate dehydrogenase	7
ec: 1.1.1.29	glycerate dehydrogenase	1
ec: 1.1.1.26	glyoxylate reductase	1
ec: 4.2.1.3	aconitate hydratase	2
ec: 1.1.3.15	(S)-2-hydroxy-acid oxidase	2

### Aminoacyl-tRNA biosynthesis

ec: 6.1.1.9	valine---tRNA ligase	2
ec: 6.1.1.6	lysine---tRNA ligase	2
ec: 6.1.1.5	isoleucine---tRNA ligase	1
ec: 6.1.1.4	leucine---tRNA ligase	2
ec: 6.1.1.1	tyrosine---tRNA ligase ec: 6.1.1.10 methionine---tRNA ligase	2
ec: 6.1.1.22	asparagine---tRNA ligase	1
ec: 6.1.1.21	histidine---tRNA ligase	1
ec: 6.1.1.20	phenylalanine---tRNA ligase	2
ec: 6.1.1.19	arginine---tRNA ligase	1
ec: 6.1.1.17	glutamate---tRNA ligase	1
ec: 6.1.1.15	proline---tRNA ligase	3

**Table S2.** Selected regulatory motifs in the sequence of *SITPS5*, 3 and 7 promoters analyzed by PLACE [61]. The A of the start codon ATG was designated as +1. The promoter sequences have been described elsewhere [43].

Promoter	Cis- element	Name	Position (Strand)	Putative function
SITPS5	TGAC(C/T)	W-box	-1166 (-) -688 (+) -633 (-) -465 (-) -267 (-)	WRKY recognition site
	CACATG	E-box (G-box-like)	-343 (+) -208 (-)	MYC recognition site
	AACGTG	T/G-box	-1199 (-)	MYC recognition site
	TACGTG	T/G-box-like	-955 (-)	
SITPS3	CACATG	E-box (G-box-like)	-1315 (+)	MYC recognition site
	AACGTG	T/G-box	-147 (+)	MYC recognition site
	TGAC(C/T)	W-box	-803 (+) -1682 (-) -1151 (-) -973 (-)	WRKY recognition site
SITPS7	AACGTG	T/G-box	-260 (+)	MYC recognition site
	TGAC(C/T)	W-box	-1055 (-)	WRKY recognition site

**Table S3.** List of primers used.

Primer name	Sequence 5' -> 3'
SIMYC1_QF2	TGCTGAATCGCGATGAAATTATGTC
SIMYC1_QR2	GCCTCAACTCGAGATCTCTAGTA
SIWRKY78_QF	GGATCAGTCGTTGTACGGTG
SIWRKY78_QR	CTTCCTGACTTTTTGGTTCCACG
SIWRKY28_QF	CAACAACATCAAGGTTCAGAATATAC
SIWRKY28_QR	TAGTCAATGCTACAAGAACTTGTAC
SIWRKY73_QF	GAAGGTTACTGAGCCATTTCCAG
SIWRKY73_QR	AACCTGATTAATAACGCTGATACCAG
SIACT_QF	TCAGCACATTCCAGCAGATGT
SIACT_QR	AACAGACAGGACACTCGCACT