

Table S1 primers for this study.

Primer name	Primer sequence(5'-3')
SC16908_c1_g2-F	GTCCGTGATATTCGTGGCTGGTC
SC16908_c1_g2-R	TGTGAGAACGGTTGACGCTTGG
SC16627_c2_g5-F	TGCTCCTCGTCGTACACCTATCTAC
SC16627_c2_g5-R	TACTGCGTTGACCTTCCAAGTTGTG
SC2555_c0_g1-F	GCTGTATGCGGACAAGGATCTGG
SC2555_c0_g1-R	GGTGAGTCAACGGTTAGCCATATCG
SC16598_c2_g1-F	TCGCCTGAACGCATTGAGAACG
SC16598_c2_g1-R	GACTCCGATGACAGCAACGAGATAC
SC16876_c1_g2-F	TCATTGGAAAGGTCGTCAAGGTTGG
SC16876_c1_g2-R	AGTAGTTCTCTTGGTCGGCATTGC
SC16337_c0_g3-F	CGACAAGGTCATCAACGACAAGTTC
SC16337_c0_g3-R	TCTTATGGGTGGCGGTGTAGGAG
SC16350_c0_g1-F	TGACCACCATCCACTCCTACACC
SC16350_c0_g1-R	AATGACCTTGCCGACAGCCTTG
SC14418_c0_g3-F	CGAATGCGGGTCTCTGTTCATG
SC14418_c0_g3-R	GACGAAACACGCTGGTCTGGAG
SC16410_c0_g3-F	CGCTCTCTCCTCTCCTTTCCTCTC
SC16410_c0_g3-R	GCCAACCTCAGCCTTCATCTCAG
SC16898_c5_g17-F	CTTGAGCGTGACGAGACTCTTAGC
SC16898_c5_g17-R	TTGCGGTTGTAGGAAGTGAAGATGG

Table S2 Candidate genes involved in antioxidation in SC.

Description	Gene ID	KEGG pathway	Expressd level
CAT1 catalase	SC16638_0_1	Glyoxylate and dicarboxylate	UP
	SC16638_0_2	metabolism	UP
	SC16638_0_3		UP
S-2-hydroxy-acid oxidase-like protein	SC4646_0_1	Glyoxylate and dicarboxylate	UP
		metabolism	
catalase-domain-containing protein	SC16908_1_2	Glyoxylate and dicarboxylate	UP
	SC16908_1_1	metabolism	UP
isocitrate lyase and phosphorylmutase	SC16145_0_1	Glyoxylate and dicarboxylate	UP
	SC16312_3_7	metabolism	UP
CAT2 catalase	SC16627_2_5	Glyoxylate and dicarboxylate	UP
	SC16627_2_3	metabolism	UP
malate dehydrogenase	SC16905_3_2	Pyruvate metabolism	UP
	SC16905_3_1		UP
	SC15936_0_2	Glycolysis / Gluconeogenesis	UP
malate synthase	SC13547_0_1	Glyoxylate and dicarboxylate	UP
		metabolism	
ATP-utilizing	SC16713_6_1	Glycolysis / Gluconeogenesis	UP
phosphoenolpyruvate	SC16713_4_4		UP
carboxykinase	SC16713_4_1		UP

	SC16713_4_6	Pyruvate metabolism	UP
L-lactate dehydrogenase	SC2555_0_1	Pyruvate metabolism	UP
acyl-CoA oxidase	SC16549_2_1	Fatty acid degradation	UP
	SC16598_2_1		UP
	SC16641_0_4		UP
	SC15352_1_1		UP
alcohol dehydrogenase	SC16055_0_2	Glycolysis / Gluconeogenesis	UP
	SC16055_0_1		UP
	SC16341_0_6		UP
	SC16876_1_2		UP
fructose-BISphosphate	SC15595_0_2	Pentose phosphate pathway	UP
ALDOLASE, class II	SC15595_0_1	Pentose phosphate pathway	UP
	SC15595_0_2	Fructose and mannose metabolism	UP
fructose-1,6-bisphosphatase	SC16924_2_1	Fructose and mannose metabolism	UP
glyceraldehyde-3-phosphate dehydrogenase	SC16337_0_3	Glycolysis / Gluconeogenesis	UP
	SC16350_0_1		UP
alpha-amylase	SC14418_0_3	Starch and sucrose metabolism	UP
	SC14418_0_1		

Table S3 Differential metabolite KEGG enrichment results in SC.

KEGG pathway	Total	Hits	Raw p	-LOG(p)
Nitrogen metabolism	8	3	0.20697	1.5752
beta-Alanine metabolism	7	2	0.42941	0.84535
Valine, leucine and isoleucine degradation	16	4	0.41035	0.89074
Arginine and proline metabolism	37	8	0.48088	0.73214
Tyrosine metabolism	19	4	0.55568	0.58755
Lysine biosynthesis	19	4	0.55568	0.58755
Propanoate metabolism	14	3	0.56118	0.57771
Nicotinate and nicotinamide metabolism	9	2	0.5712	0.56001
Pyrimidine metabolism	35	7	0.58235	0.54068
Alanine, aspartate and glutamate	20	4	0.59983	0.51112

metabolism				
Pantothenate and CoA biosynthesis	16	3	0.65809	0.41841
Tryptophan metabolism	27	5	0.6654	0.40736
Phenylalanine, tyrosine and tryptophan biosynthesis	22	4	0.67981	0.38593
Vitamin B6 metabolism	11	2	0.68579	0.37718
Purine metabolism	60	11	0.69879	0.3584
Pentose and glucuronate interconversions	12	2	0.73304	0.31055
Valine, leucine and isoleucine biosynthesis	24	4	0.74804	0.2903
Citrate cycle (TCA cycle)	20	3	0.80358	0.21868
Glycine, serine and threonine metabolism	26	4	0.80466	0.21733
Glyoxylate and dicarboxylate metabolism	14	2	0.80964	0.21117
Lysine degradation	16	2	0.8661	0.14376
Glutathione metabolism	23	3	0.8753	0.13318
Cyanoamino acid metabolism	10	1	0.89681	0.10891
Pentose phosphate pathway	18	2	0.90687	0.097757
Thiamine metabolism	11	1	0.91791	0.085654
Riboflavin metabolism	11	1	0.91791	0.085654
Inositol phosphate metabolism	19	2	0.92262	0.080542
Cysteine and methionine metabolism	33	4	0.9273	0.075482
Sulfur metabolism	13	1	0.9481	0.053296
Aminoacyl-tRNA	67	9	0.95052	0.050746

biosynthesis				
Amino sugar and nucleotide sugar metabolism	24	2	0.97026	0.030188
Fructose and mannose metabolism	17	1	0.97933	0.020888
Butanoate metabolism	17	1	0.97933	0.020888
Steroid biosynthesis	23	1	0.99485	0.005161
Glycolysis or Gluconeogenesis	24	1	0.99592	0.0040869
Glycerophospholipid metabolism	26	1	0.99744	0.0025613
Fatty acid metabolism	28	1	0.9984	0.0016035
Biosynthesis of unsaturated fatty acids	42	2	0.99928	0.00072046
Fatty acid biosynthesis	37	1	0.99981	0.00019215

Note: Total, total number of metabolites in the target metabolic pathway; Hits, number of differential metabolites in the target metabolic pathway, Raw p, p-value of the hypergeometric distribution test; -log(p): negative value for the natural logarithm of the p-value.