Supplementary Figures



Supplementary Figure 1. AtMYB12 antibody detects both *Arabidopsis* and tomato MYB12 protein. (a) AtMYB12 antibody detects both SIMYB12 and AtMYB12 in tomato fruit. Both WT and *AtMYB12* tomato fruit were harvested three days after breaker. Nuclei from both fruit were isolated and nuclear protein extracts were assessed by western blot. Coomassie brilliant blue staining (CBB) showed equal loading of proteins from WT and *AtMYB12* tomato extracts. (b) AtMYB12 antibody detects both SIMYB12 and AtMYB12, but not AtMYB75 recombinant proteins. *AtMYB12, SIMYB12* and *AtMYB75* cDNAs were cloned into the pDEST17 plasmid (6 x His tag at N terminal). Recombinant proteins were produced in *E.coli* and total protein extracts were used for the western blots.



Supplementary Figure 2. Quantitative determination (nM g fresh wt⁻¹) of metabolite concentrations in fruit (10 dpb) of *AtMYB12* and *WT* tomato lines. The heat map compares the levels in *AtMYB12* tomato with those in WT fruit. Absolute values were scaled by log2. Asterisks indicate values that were determined by the Student's t test to be significantly different (p<0.05) (n=4, Student's t test).



Supplementary Figure 3. *AtMYB12* and *Del/Ros1* tomatoes showed different patterns of amino acid accumulation. Fruit were harvested and analysed 7 days after breaker. Data show levels in different lines compared to those in WT tomatoes. Error bars indicate SEM (n=4). * (p<0.05) and ** (p<0.01) (Student's *t* test) indicate significant differences compared to WT fruit.



Supplementary Figure 4. Acetyl-CoA contents of different fruit. Fruit were harvest at 7 days after breaker. Both peel and flesh were analyzed for different lines. Data show the relative values compared to WT fruit for the same tissue. Error bars show SEM (n=4). No significant differences (p<0.05, Student's *t* test) were observed for any of the genotypes compared to WT fruit.



Supplementary Figure 5. Genistin content in primary *LjIFS* **transformants of MicroTom tomato**. Extracts of ten different T0 *IFS* tomato lines were analysed by LC-MS. For every plant, ripe fruit were pooled and analysed. Genistin, the major isoflavone detected, was used as a standard as a standard to evaluate isoflavone contents in different lines. Line 8 had the highest content of genistin and was selected for later experiments.

а



Supplementary Figure 6. The *are* **mutation affects F3H activity.** (a) The *are* mutant (3-073) has a G to A change in the coding sequence of the *SlF3H* (Solyc02g083860) gene. This causes a change in the predicted amino acid sequence of F3H from S to N. (b) Phenotype of *AtMYB12* and *AtMYB12 are*^{-/-} tomatoes. The *AtMYB12* tomato was crossed with the *are* mutant. F2 plants were genotyped and plants with *AtMYB12* and *Are* (^{+/+} or ^{+/-}) or *AtMYB12 are*^{-/-} were selected. Pictures were taken at 10 days after breaker. (c) The content of major flavonols in *AtMYB12* and *AtMYB12 are*^{-/-} tomatoes. Fruit were harvested 10 days after breaker. Error bars indicate STDEV (n=3).



Supplementary Figure 7. Schematic representation of the crossing strategy for tomatoes with high isoflavone content. The $are^{-/-}$ mutant was first crossed with *AtMYB12* to make *AtMYB12 /are*^{-/-} which was then crossed with the best *IFS* line. In the F₂ generation, segregation of different genes was analysed by genotyping.

Supplementary Tables

Supplementary Table 1. The ratio of ¹⁴CO₂ evolution from C1 and C6 of glucose by fruits of wild type and *AtMYB12* tomatoes. Ratios were calculated from the cumulative release of CO₂ after 1, 2, 3, 4, 5 and 6 h incubation presented in **Fig 4a**. Each value represents the mean \pm SEM of four independent samples; and asterisks indicate values that were significantly different at (p≤0.05, Student's *t* test) from WT

	1 hr.		2hr. 3 hr			4 hr.		5 hr.		6 hr.								
Wild																		
Туре	0.60	±	0.06	0.42	±	0.06	0.38	±	0.04	0.39	±	0.04	0.41	±	0.04	0.45	±	0.06
MYB12	0.53	±	0.06	0.49	±	0.05	0.51	±	0.06	0.60	±	0.10	0.68	±	0.11	0.83*	±	0.13

Supplementary Table 2. Metabolism of $[U^{-14}C]$ Glucose in pericarp disks from *AtMYB12* and WT fruit at 10dpb. After 4 h of incubation, disks were extracted and fractioned. Values are means ±SEM of determinations on four independent samples. Asterisks indicate values that were determined by the t-test to be significantly different (P < 0.05, Student's *t* test) from the wild type. FW, fresh weight

Parmeter	Wild Type	MYB12
	$Bq(gFW)^{-1}$	
Total uptake	562.96 ± 34.09	576.86 ± 32.55
Insoluble		
Starch	4.74 ± 0.56	3.94 ± 0.36
Cell wall	0.60 ± 0.07	0.64 ± 0.13
Protein	0.19 ± 0.03	0.16 ± 0.03
Soluble		
Organic acids	118.90 ± 18.89	127.48 ± 17.57
Phosphates esters	105.98 ± 12.32	121.39 ± 6.44
Amino acids	94.37 ± 15.72	129.81 ± 13.67
Sucrose	238.18 ± 27.77	193.44 ± 26.49
	Bq (nmol) ⁻¹	
Specific activity of hexose phosphates	0.21 ± 0.01	0.26^{*} \pm 0.04
Metabolic flux	nmol $(gFW)^{-1}h^{-1}$	
Starch	55.35 ± 6.34	51.04 ± 9.11
Cell wall	6.95 ± 0.73	8.00 ± 1.52
Sucrose	2781.28 ± 318.90	2258.84 ± 371.90
Carbohydrate oxidation	2491.10 ± 112.85	$2999.54^{*} \pm 135.00$

Supplementary Table 3. Levels of major phenylpropanoids in WT, *AtMYB12*, *Del/Ros1* and Indigo (*AtMYB12* x *Del/Ros1*) tomatoes. Values are means \pm SEM of determinations on three independent samples. * (p<0.05) and ** (p<0.01) (Student's *t* test) indicate significant difference compared to WT fruit.

Compounds (mg g ⁻¹ DW)	WT	AtMYB12	Del/Ros1	Indigo
Chlorogenic Acid	0.150 ± 0.002	1.035**±0.163	0.363 ± 0.154	2.118**±0.406
Kaempferol-3-Rutinoside	0.073 ± 0.002	$4.050^{**} \pm 0.469$	0.276 ± 0.076	6.664*± 2.110
Rutin	0.894 ± 0.015	27.140**±2.070	5.183 ± 1.644	16.585**±0.981
Quercetin-(Coumaroyl)- Rutinoside	NA	NA	2.97**± 0.62	30.21**± 2.06
Myricetin-(Coumaroyl)- Rutinoside	NA	$0.68^{**} \pm 0.03$	$1.19^{**} \pm 0.19$	25.43**± 3.41
Methylmyricetin- (Coumaroyl)-Rutinoside	NA	NA	$0.72^{**} \pm 0.12$	16.43*± 4.55
Delphinidin-(Coumaroyl)- Rutinoside-Glucoside	NA	NA	$1.294^{**} \pm 0.187$	1.154**± 0.011
Petunidin-(Coumaroyl)- Rutinoside-Glucoside	NA	NA	$1.477^{**} \pm 0.163$	2.857**± 0.218
Petunidin-(Feruloyl)- Rutinoside-Glucoside	NA	NA	0.420 ± 0.211	0.922**± 0.102
Malvidin-(Coumaroyl)- Rutinoside-Glucoside	NA	NA	NA	0.598**± 0.011

Supplementary Table 4. Contents of major phenylpropanoids in WT, *StSy*, *AtMYB12* and *AtMYB12 StSy* tomatoes. Values are means \pm SEM of determinations on three independent samples. * (p<0.05) and ** (p<0.01) (Student's *t* test) indicate significant differences compared to WT fruit.

Compounds (mg g ⁻¹ DW)	WT	StSy	AtMYB12	AtMYB12 StSy	AtMYB12 StSy are-/-
Chlorogenic Acid	0.117 ± 0.008	0.192 ± 0.024	$0.912^{**} \pm 0.022$	0.180 ± 0.106	0.200 ± 0.135
Kaempferol-3-Rutinoside	0.351 ± 0.020	$0.118^{*} \pm 0.014$	20.934**±0.450	$0.779^{*} \pm 0.089$	1.393 ± 0.267
Rutin	1.649 ± 0.153	0.118**±0.009	12.770**±0.382	0.129**± 0.016	1.011 ± 0.213
Resveratrol	0.018 ± 0.007	0.519**±0.044	0.011 ± 0.004	0.447 ± 0.106	0.297 ± 0.130
Piceid	0.011 ± 0.011	0.688**±0.056	NA	2.824**± 0.074	2.597*± 0.418
Resveratrol-Glucoside Isoform	0.047 ± 0.003	0.608**±0.051	0.038 ± 0.038	1.513**± 0.081	1.717*± 0.244
Resveratrol-di-Glucosides	0.053 ± 0.053	$0.379^* \pm 0.070$	NA	$0.487^{**} \pm 0.069$	$1.004^{**} \pm 0.124$
Methyl-Resveratrol-Glucosides	0.005 ± 0.005	0.036**±0.003	NA	0.992**± 0.070	0.306 ± 0.088

+ this could be an under estimate due to difficulties of extracting resveratrol and resveratrol derivatives completely by the protocol used.

Supplementary Table 5. Content of major phenylpropanoids in WT, *IFS*, *AtMYB12 IFS* and *AtMYB12 IFS are^{-/-}* tomatoes. Values are means \pm SEM of determinations on three independent samples. * (p<0.05) and ** (p<0.01) (Student's *t* test) indicate significant differences compared to WT fruit.

Compounds (mg g^{-1} DW)	WT	IFS	AtMYB12 IFS	AtMYB12 IFS are-/-	IFS are-/-
Chlorogenic Acid	0.102 ± 0.006	$0.280^{*} \pm 0.029$	$0.589^{**} \pm 0.040$	$0.495^{**} \pm 0.025$	$0.150^{*} \pm 0.017$
Kaempferol-3-Rutinoside	0.298 ± 0.027	$0.105^{\star}\pm0.008$	41.693**±2.774	$3.88^{**} \pm 0.283$	$0.094^{\star} \pm 0.010$
Rutin	1.458 ± 0.093	0.799**± 0.096	22.197**±1.258	$3.032^{**} \pm 0.200$	0.148**±0.017
Genistein	0.105 ± 0.007	$0.278^{*} \pm 0.032$	$0.220^{**} \pm 0.013$	$0.738^{**} \pm 0.053$	$0.160^{\star} \pm 0.018$
Genistin	0.011 ± 0.001	NA	10.854**±0.706	76.221**±4.078	0.170**±0.012
Genistein-di-Glucosides	NA	0.013 ± 0.007	NA	1.729* ± 0.127	NA

†These data were derived from the best lines segregating in the F2 population.

ID Symbol Full Name ChIP_qPCR Primer Sequence (5:3) Solyc02g093830 G6PD Glucosc-6-phosphale 1- dehydrogenase GTCGTGTCTTATGATTCTGG Solyc05g012110 PGLS 6-phosphogluconate dehydrogenase ATCCAGTACAAATGAAAGTT Solyc05g010260 6PGD2 6-phosphogluconate dehydrogenase ATCCAGTACAAATGAAAATGAAAACA Solyc05g000260 6PGD2 6-phosphogluconate dehydrogenase TCGTGACTTTGGTGTCTTCTTTATA Solyc05g008370 Rpi Ribose-5-phosphate isomerase GATGAAAAATCAAGAAAACAGAAGGAA ATGCAAAATCAAGAAACCAAAGGAA Solyc05g007260 Rpe Ribulosc-phosphate 3-epimerase TGGAGCATAATAAGCAAAATAAGCAAAAG Solyc00g006800 TALDO1 Transketolase 1 ATGGACCAAAAATAAGCAAAAGAAAACCA Solyc02g042505 SUS1 Sucrose synthase GGAAAATCAGCAAAAAGCAAAAGGAAAACCATAAGGAAAACCA Solyc02g011010 GADPH Glyceraldehyde-3-phosphate dehydrogenase ACGATAGTGAAAGGCCAAACA Solyc02g04g009030 GADPH Glyceraldehyde-3-phosphate dehydrogenase CCCAACAATAAGCAAAACACAA AACAGAGGTAGGTCCCTTTAT Solyc04g072800 PFK1 Diphosphate-fructose-6- phosphotmaferase CAAAACAATAAGGAAATCCCCAACAGA				
Solyc02g093830 G6PD Clucose-6-phosphoplate 1- dehydrogenase GTCACTGCCTCTTATGATTCTGG Solyc05g012110 PGLS 6-phosphogluconolactonase GTGGTATCCCACAAGGTAAAGTT AATACAACATGAATGGAAGATGG Solyc04g005160 6PGD1 6-phosphogluconate dehydrogenase ATCCAACATGAAATGGAAGAATGGA Solyc05g010260 6PGD2 6-phosphogluconate dehydrogenase ATGGTATTTTGGTAGCATCCACTC Solyc05g008370 Rpi Ribose-5-phosphate isomerase ATGGCAAAGAAACAAGAAACAAGAAAAGAAAACA Solyc05g008370 Rpe Ribulose-phosphate isomerase GGCATTCAATATATAAGAAACAAGAGAAAA Solyc05g007260 Rpe Ribulose-phosphate - argimerase GGCATTCAATAATTAAAAGAAAATAAGAAAAAA Solyc00g006800 TALDO1 Transaldolase TTAAAGGCTTGTGAAATTGAAAATA Solyc02g042550 SUS1 Sucrose synthase TAAAAGAGCTTAGCAGGCAAAAT Solyc03g111010 GADPH Glyceraldehyde-3-phosphate dehydrogenase like CGCATTGAAATGAAAATACAGA Solyc04g072800 PGKI Diphosphate-fnctose-6- phosphoplycreate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplycerate dependent phosphoplenetacaCACAGGTTGTGCCCAGAAAGAGACATGG GGTAACTCGTCCAGAAAA	ID	Symbol	Full Name	ChIP-qPCR Primer Sequence (5'-3')
Solyc05g012110 PGLS 6-phosphogluconalectonase GTCTTCTGGATGACCACAAGGTAAAGGT Solyc05g012100 PGLS 6-phosphogluconate ATTACAACATGAAATGGAAAACG Solyc05g010260 6PGD2 6-phosphogluconate ATTCCATAAGGAATGGAAACGA Solyc05g010260 6PGD2 6-phosphogluconate ATCCATTCATGAATGAAAAACA Solyc05g008370 Rpi Ribose-5-phosphate isomerase TTCCCAAGGTTCCAATCTGATAA Solyc05g007260 Rpe Ribulose-phosphate 3-epimerase GGGAGCATAATTAAAAACTAAGGAAAATCAAAGGAAAT Solyc00g006800 TKT Transketolase 1 AGGAGCCAAAATAAGCAAAAGGAAAATCAA Solyc00g006800 TALDO1 Transaldolase TTAAAGGGTTGTGTGCCACCACTT Solyc03g111010 GADPH Diphosphate-fructose-6- CAAAACAATAAGGACAATTGCAAACCAA Solyc03g111010 GADPH Gilyceraldehyde-3-phosphate CCCGCTCTGAAAATACCAA Solyc04g072800 PGM depardrogenase ACCAAAAGGACAATGGTAGAGGTCCTTTT Solyc04g072800 PGM depardrogenase ICCATTCGTAAAATCCCAACGA Solyc04g072800 PGM depardrogenase ICCATTCTGTGAAAATCCCAACA Solyc04g074480 <td>Solvc02g093830</td> <td>G6PD</td> <td>Glucose-6-phosphate 1-</td> <td>GTCAGTGGCTCTTATGATTCTGG</td>	Solvc02g093830	G6PD	Glucose-6-phosphate 1-	GTCAGTGGCTCTTATGATTCTGG
Solyc05g012110PGLS6-phosphogluconate dehydrogenaseGTGGTATCCCACAAGTAAATGAAATGG AATCAAACATGAAATGGAAATGG ATCACAATGGAAATGGAAATGG TCCCTTACAATGGAAATGGAAAACASolyc05g0102606PGD26-phosphogluconate dehydrogenaseTCCCTTACAATGAAATGGAAAACASolyc05g008370RpiRibose-5-phosphate isomeraseTCGGACATAATTAAATCAAACGAGGAASolyc05g007260RpeRibulose-phosphate 3-epimeraseTGGAGCATAATTAAATCAAACCCACTCSolyc05g007260RpeRibulose-phosphate 3-epimeraseTGGAGCATAATTAAATCAAACCCATSolyc00g006800TKTTransketolase 1ATGCTACATGAGAAATGAAAATGASolyc00g006800TALDO1TransaldolaseTTAAAGGGCTGAAATTAGAAAATCASolyc07g042550SUS1Sucrose synthaseGAAACCAAAATAAGGACCATTTCCSolyc03g111010GADPHIGiyccraldehyde-3-phosphateCAAAACAAATAAGGAAAATCAGAGSolyc04g009030GADPHLGiyccraldehyde-3-phosphateACGATAGTGAAATTGGAATTTGGATGTGTGGTGSolyc04g072800PGMENOEnolaseCATTTCGTAAGGTGTGTGTGTGTGGTGSolyc04g072800PGMENOEnolaseCACTATGTGTAAGTGAAATCCCATASolyc04g072800PGMEnolaseCACATATTTTGTAAGGGAGGGTGGTGCCTTGSolyc04g072800PGMEnolaseCACATATTTTGTAAGGAGGTCGTGGCSolyc04g072800PGMEnolaseCACATATTTGTACGCCGTGTCCCAAASolyc04g072800PGMEnolaseCACATATTTTGTAAGGAGGTGGGGTTGTAAGGAGGGTSolyc04g072800PGMEnolaseCACATATTTTGTAAGGAGGTGGGGGTTGACAGGAAAAGGGGGGGG		0012	dehydrogenase	GTCTTCTGGATGATCCTTCTGTG
Solyc04g005160 6PGD1 6-phosphogluconate dehydrogenase ATACAAACATGGAATGGAAGAATGG Solyc04g005160 6PGD2 6-phosphogluconate dehydrogenase ATGCAGACAATGGAAAACA Solyc05g008370 Rpi Ribose-5-phosphate isomerase dehydrogenase ATGCAGAAAACAGAGGGAA Solyc05g008370 Rpi Ribose-5-phosphate isomerase ATGCAAAAATCAAAACAGAGGAA Solyc05g007260 Rpe Ribulose-phosphate 3-epimerase GCGATCAATAATAAAACGAGGGAA Solyc00g006800 TKT Transaketolase 1 AGGAGCCAAAATAAGCAAAATAGGAAAAT Solyc00g006800 TALDO1 Transaketolase 1 AAACCAAAAAGGTAATTAGAAAATCAA Solyc00g006800 TALDO1 Transaketolase 1 AAACCAAAAAGGTAATTAGAAATCCA Solyc00g006800 TALDO1 Transaketolase 1 AAACCAAAAAGGTAATTAGAAATCCA Solyc00g006800 TALDO1 Transaketolase TTAAAGGGTTGTTGACCACACTTAT Solyc00g006800 GLID Transaketolase TAAACAAAGGGTAATTAAATAGGACACAT Solyc01g001200 PFK1 Diphosphate-fructose-6 CAAAACCAATAAGGCTAACGGGACACTTTCCATC Solyc03g111010 GADPH Glyceraldehyde-3-phosphate GCGTAACTTGGAAGTGTTGTGGTGT Solyc04g072800 PGM Glyceraldeh	Solvc05g012110	PGLS	6-phosphogluconolactonase	GTGGTATCCCACAAGGTAAAGTT
Solyc04g0051606PGD16-phosphogluconate dehydrogenaseATCCAGTACAATGAAAAGAAACASolyc05g0102606PGD26-phosphogluconate dehydrogenaseTCGTGACTTTGGTTCTTTGTTTGTTATGSolyc05g008370RpiRibose-5-phosphate isomeraseATTCCACAAGTACAAATCAGAAACAGAGGAASolyc05g007260RpeRibulose-phosphate 3-epimeraseATTCCACAAATTAAACCAGGGAAAASolyc05g007260RpeRibulose-phosphate 3-epimeraseGATGAAAAATCAAGAAACCAAGGGAAAASolyc00g006800TKTTransketolase 1AGGAGCCAAAATAAACTAGGGAAAATSolyc07g042550SUS1Sucrose synthaseTAAAAGGTTGTTGTACCTCACTTTATSolyc03g111010GADPHDiphosphate-1-phosphateCAAAACATAAGGAGTTACCAACGGSolyc03g111010GADPHLGlyceraldehyde-3-phosphateCGATACTGGAAGATGTGGAGGTGTTGGTGSolyc03g114500ENOEnolaseTCATTTTGGTACCTCCACTASolyc02g083590DHQSDehydroquinate synthaseGATGGAACACTCGGCCAAAATAAGGAGTTAGSolyc02g083590DHQSDehydroquinate synthaseGATGGAGACGTTAGCCGCCAAAATAAGGAGGTTGGSolyc02g083590DHQSDehydroquinate synthaseGATGGGACACCTCGTCCAAAGAGAGGTGGSolyc02g083590DHQSDehydroquinate synthaseGATGGGACAAATGAAAGAAAGAAAGAAASolyc02g083590DHQSDehydroquinate 1-CCCCTCTTGGAGAAGGTGGGGSolyc02g083590DHQSDehydroquinate synthaseGATGGGACCACTGGTCCAAASolyc02g083590DHQSDehydroquinate synthaseGATGGGACAAATAGAAAGAAAAGAASolyc04g071800Skikimate la enolaseCCTCTATGTGGGCCAAAAGGAGGTSolyc01g06		1 GES	o phosphograeonolaetonase	AATACAACATGAATTTTGCTATGCT
Solyc0sg00106 OFD/1 dehydrogenase TTCCCTTACAATGAAATGAAATGAAATGAAATGAAATGA	Solvc04g005160	6PGD1	6-phosphogluconate	ATCCAGTACAAATGGAAGAATGG
Solyc05g0102606PGD26-phosphogluconate dehydrogenaseTCGTGACTTTTGGTTCTTCTTTTAG ATGATATTTCTGCAAGGTCCACTCSolyc05g008370RpiRibose-5-phosphate isomeraseATGATAATTTCTGCAAGTCCAAGGAA ATTCACAAGTCCAATTCTGATAA GATGAAAATAAGGAAAACAGAGGAASolyc05g007260RpeRibulose-phosphate 3-epimerase GCATTCAATAATTAAAACTAGGGAAAA AGGAGCCAAAATAAGGAAAATAAGT AGGAGCCAAAATAAGGAAAATAAGT AGGAGCCAAAATAAGGAAAATAAGT AGGAGCCAAAATAAGGAAATAAGT AACCAAAAGAGATAAATGAAAATCCA TTTAAGGGTTGTTGGATGAAATTGAAAAT CAAAACAAAAAGAGATAAATAAGCAAAAAGAGAAAAAAA TAAAGGAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAA	50190042005100	01 001	dehydrogenase	TTCCCTTACAATGAAATGAAAACA
Solycogo 10000 OF DE2 dehydrogenase ATTCCACAAGTTCCAACATCCACTC Solyc05g008370 Rpi Ribose-5-phosphate isomerase ATTCCACAAGTTCCAATCTTGATAA Solyc05g007260 Rpe Ribulose-phosphate 3-epimerase TGGAGCATAATTAAAACTAAGGAAAATCAAGCAAAATCAAGCAAAATAAGT Solyc10g018300 TKT Transketolase 1 ATGTTTTTGGAGTAAATTAAAACTAAGGAAAAT Solyc00g006800 TALDO1 Transaldolase AAACCAAAAGGATAATTAAAACTAAGGAAAATCAA Solyc00g006800 TALDO1 Transaldolase TAAAAGGAGTAATTAGAAAATCAA Solyc00g006800 TALDO1 Transaldolase TAAAAGGAGTAATTAGAAAATCAA Solyc00g0042550 SUS1 Sucrose synthase GAAACCAAAAAAGGACATTACCACCTCACTTAT Solyc03g111010 GADPH Giyceraldehyde-3-phosphate ACGATAGTGAAATCGGAGTTGTTGGTG Solyc04g009030 GADPHL Giyceraldehyde-3-phosphate CGCTCAACTTGACGAGGAGTGTTGA Solyc04g072800 PGM Giyceraldehyde-3-phosphate GGTAACTCCGGATTGTGGAGTGTCG Solyc04g072800 PGM Enolase TGCTTTGAAGTGAGAGCGTTAA Solyc04g072800 PGM Enolase ACGATAATGGAGAGCGTTAAG Solyc0	Solvc05g010260	6PGD2	6-phosphogluconate	TCGTGACTTTTGGTTCTTTCTTTAG
Solyc05g008370RpiRibose-5-phosphate isomeraseATTCCACAAGTTCCAATCTTGATAA GATGAAAAATCCAAGAAAAGAAGGAASolyc05g007260RpeRibulose-phosphate 3-epimeraseTGGAGCATAATTAAAATCAAAGCAGGAAAASolyc10g018300TKTTransketolase 1AGGAGCCAAAATAAGCAAAATAAGT ATGTTTTGTGGAAATTGAAAATSolyc00g006800TALDO1TransaldolaseAAACCAAAAGGATAATTGAAAAT ATGTTTGTGGACCTCACTTATSolyc00g006800TALDO1TransaldolaseTAAAAGAGGTTAGCAGGCAAAATAAGCAAAAAASolyc01g002500SUS1Sucrose synthaseGAAATGAGAGGGCCAAAATAAGCAACAACA GGAATGGTAGAGGCCCTTTTASolyc01g009200GADPHDiphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAAACAATAAGGACCATTGCACCATC CCGCTCTGAAAATACGGGGTTGTTGTGGGGSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenase likeCGTAACTTGGATTGTGAGGGTGTGGTGGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeGGTAACTCTGGATTGTGCTCGAC GGTAACTCGGATTGTGCCTGASolyc04g072800PGMdepedent phosphoglycerate- depedent phosphoglycerate- depedent phosphoglycerate- depedent phosphoglycerate- gGAATGGAGCAGTAGGCAAAAACTTCCTCTCAACAASolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTGTGGAGAAATACCCTTT GGAATGGACTTGCTCGAGAAAGAAAAGAASolyc01g06750SHDShikimate dehydrogenaseACTGATCATCGGCTGAAAAGAAAAGAA AATCCAACTGTGAAAGAAACCAGGAAAAGAAAAGAASolyc01g051860SKShikimate hinaseCACATATTTTGCGAAAAGAAAAGAAAAGAA AATCCTACGCGGTGCAACAGCCAAAACCAGTTAAATACCAGGACATTGGGCT CAAAAACTTGGCAAAAAACACCAGTTAAATAACCACAGT AAAACCAGTTAAATAACACAGTAAAATCA CC	50192052010200	01 002	dehydrogenase	ATGATATTTCTGCTAGCATCCACTC
SolyCo2g03030Hp1H00505-phosphate 3-epimeraseGATGAAAAATCAAGAAACAGAAGAASolyc05g007260RpeRibulose-phosphate 3-epimeraseTGGAGCATAATTAAAACAAACCTASolyc10g018300TKTTransketolase 1AGGAGCCAAAATAAGCAAAATAAGTSolyc00g006800TALDO1TransaldolaseTTTAAGGATGAAATTGAAAATSolyc00g006800TALDO1TransaldolaseTTAAAGGATGTAGAAATAGAAATASolyc00g006800TALDO1TransaldolaseTAAAACAAAGAGGTAATTAGAAAATASolyc07g042550SUS1Sucrose synthaseTAAAAGAGGTCTAGCAGGCAAACASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotansferaseCAAAACAATAAGGACCATTCCCATCSolyc03g111010GADPHGlyceraldehyde-3-phosphateACGATAGTGAAAATACGGATTTTGTGGGGSolyc04g009030GADPHLGlyceraldehyde-3-phosphateCGTTACTTGGATGTGTGTGTGGTGSolyc04g072800PGMelendent phospholglycerate- mutaseGGTAACTCTGGATTGTGTCCTGASolyc04g074480DAHPS3-deoxy-7-phosphohepluonate synthaseCACATATTTGGAGAGAGTTAGTSolyc02g083590DHQSDehydroquinate dehydrataseACTGGTTGACAAAAGAGAAAGAAAGAT AATCCACTTGGTTGAAAAGAGACAAAGAAAGAASolyc01g067750SHDShikimate heinaseGATGGATGATGAGAGAAAAGAAAGAT AATCCACTTGTGTGAAAAGAGCC GTATCTGGTCCAACTTGTGGACAAGTAAAGAAAGAASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAAACGTTAAATAACCCTTGTGGCTCAG CAAAAACTTGTCGCCCTCTTGAAATCASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAACACGTCAAATCA CAAAACGTTGTGTGCCCTCTGAAATCA </td <td>Solve05c008370</td> <td>Rni</td> <td>Ribose-5-phosphate isomerase</td> <td>ATTCCACAAGTTCCAATCTTGATAA</td>	Solve05c008370	Rni	Ribose-5-phosphate isomerase	ATTCCACAAGTTCCAATCTTGATAA
Solyc05g007260RpeRibulose-phosphate 3-epimeraseTGGAGCATAATTAAATCAAACCCTA GCATTCAATTAAAATTAAAACTAGGGAAAASolyc10g018300TKTTransketolase 1AGGAGCCAAAATAAGCAAAATAGG AAATTGAAAATTGAAAATSolyc00g006800TALDO1TransaldolaseAAACCAAAAGGCTAATTAGAAAATSolyc07g042550SUS1Sucrose synthaseGGAATGGTAGAGGCCCTTTTASolyc07g042550SUS1Sucrose synthaseCAAAACAATAAGGACTCACTTATSolyc02g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCCCGCTCTGAAATTAGGAGCACATTTCCATCSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATACGA ACGATAGTGAAAATACGTSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenaseCCAAAACCTTCCTCTCACACAA ACCAGAGTAGTGAAGTGTCG CGCTCAACTTGGATGTGCTCG CGCTCAACTTGGATGGTGTCG CGCTCAACTTGGTCTTCAACAASolyc04g072800PGMEnolaseTCATTTTCGTACGTGGAGGTGTCG CGCTCAACTTGGTCCTCAACAASolyc04g074480DAHPS3-deoxy-7-phosphohepluonate synthaseGATGGATCACTCGGGCCAAAAGAAAAGGT AATCCTACTTGGATCAGAAAAGGGTSolyc04g075800DHQSDehydroquinate synthaseGATGGATCACTCGTCACAGTAGGG GCACAGTTGGTCCCTTTGAAGGAGGASolyc02g083590DHQSDehydroquinate synthaseGATGGATCACCGCAAAAGAAAAGAT AATCCTACTTGGAGACACAGGCC GCACAGTTGGTATACCTTGGGGGTTACCCTGTGAAGSolyc01g067750SHDShikimate linaseCCCCCATCTTGAAGAAAAGAGA AATCCTGGCTCACAGTCAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCCAAACGTTAAGTGAAAATCGCCCCTCTTGAAAASolyc01g091190EPSPS2 <td< td=""><td>30190032008370</td><td>Крі</td><td>Ribbse-5-phosphate isomerase</td><td>GATGAAAAATCAAGAAACAGAGGAA</td></td<>	30190032008370	Крі	Ribbse-5-phosphate isomerase	GATGAAAAATCAAGAAACAGAGGAA
Solyc03g0/1200RpcRobinse-phosphate 5-ephinetaseGCATTCAATAATTAAAACTAGGGAAAASolyc10g018300TKTTransketolase 1AGGAGCCAAAATAAGCAAAATAAGTSolyc00g006800TALDO1TransaldolaseAAACCAAAAGAGTAATTAGAAAATSolyc01g0042550SUS1Sucrose synthaseGGAATGGTAGAAGGTCCACGCAAACAGGATGGTAGGAAGGTCACAGGCAAACAGGAATGGTAGGAGGCCCATTTCCATCCCCCGCTCTGAAAATACGGTTTATSolyc01g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAACAATAAGGACCTTTTCATCSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATACGGATGTGGTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeCGCTCAACTTGTGTAGCAACAASolyc04g072800PGMEnolaseTCATTTGTAAGTTGGAGTGTCCTGASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCCSolyc04g07480DAHPS3-deoxy-7-phosphoheptulonate synthaseGAATGGTATCAACAAAAGAGGTSolyc01g067750SHDShikimate dehydrogenaseACTGGATTGTGCCAGAAAGGGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGAACTCTGAAAGGGTSolyc01g067750SHDShikimate kinaseGGACGGTGTATCACAGAAGGGTSolyc01g067750SHDShikimate haseGGACGGTGTGATAACCGAGGGGSolyc01g067750SHDShikimate kinaseCACGTTTGGACCCAACTGTGTGGGSolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCCCCTCTTGAAATAAGGCCAAAATCASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCCAACAGT	Solve05c007260	Pne	Pibulosa phosphoto 3 opimorosa	TGGAGCATAATTAAATCAAACCCTA
Solyc10g018300TKTTransketolase 1AGGAGCCAAAATAAGCAAAATAAGT ATGTTTTGTGGATGAAATTGAAAATSolyc00g006800TALDO1TransaldolaseATACCAAAAGAGTAATTGAAAATSolyc00g006800TALDO1TransaldolaseTTAAAGGGTTGTTGTACCTCACTTATSolyc07g042550SUS1Sucrose synthaseTAAAAGAGGTTAGCAGGGCAAACA GGAATGGTAGGAGGCCCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6CAAAACAATAAGGACCCATTCCATC CCCGCTCTGAAAATACGGTTATSolyc03g111010GADPHGilyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCGAGGAGGTGTTGGGG CGCTCAACTGGAGTGTGTGGGGSolyc04g009030GADPHLGilyceraldehyde-3-phosphate dehydrogenase likeCGCTCCAACTGGGATTGTGGCG CGCTCAACTGGGATTGTGGCCG CGCTCAACTGGGATTGTGGCCCGGSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phospholplycerate- mutaseGGAAACTCCGGAGGAGGAGGTTGASolyc04g072800ENOEnolaseATTTCGTAGGTCGTGCC TGCTTTGAAGGAGAGAGCTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGATGGATCACTCGTCCAGGAGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCAGAGAAGGAT AATCCTACTAGAGAGATCAACGGGTTGATACCTTGGAAAAAGAAAG	S01yc05g007200	кре	Ribulose-phosphate 3-epimerase	GCATTCAATAATTAAAACTAGGGAAAA
Solyclog016500TATTransaldolase IATGTTTTGTGGATGAAATTGAAAATTSolyc00g006800TALDO1TransaldolaseAAACCAAAAGAGTAATTAGAAATACCA TTTAAGGGTTGTTGTACCTCACTTATSolyc07g042550SUS1Sucrose synthaseTAAAAGAGGTTAGCAGGGCAAACA GGAATGGTAGAGGGCCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCACAAATAAGGACCAATCAGGGGTGTTATSolyc03g111010GADPHGilyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA ACCATAGTGAAATCCTGGGGTTCGGSolyc04g009030GADPHLGilyceraldehyde-3-phosphate dehydrogenaseCGCTCAACTTGGCTGTAGGGGTTCG GGTAACTCTGGATGTGGTCCTGASolyc04g072800PGM2 3-bisphosphoglycerate- mutaseGGTAACTCTGGATGGAGGAGCTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTCCTAAAATACCCTTTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCAGAGGGGGSolyc01g067750SHDShikimate dehydrogenaseCACGTTTTGGTAACTCTGGAGGAGACGTTGGSolyc04g051860SKShikimate kinaseCCCCCTCTATGGGTTCCAAAAAGGGGSolyc01g067750SHDShikimate kinaseCCTCCTATGGGTTGCCAAAAGGGAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGGGCTTGCCAAAAAGCAAACAASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAACAAGTAAAGCCCTGTTGCAACAGSolyc01g091190EPSPS2Chorismate synthaseTAGAAATTGGCCCTGTTGCAACAG	Salva10a019200	TVT	Translateless 1	AGGAGCCAAAATAAGCAAAATAAGT
Solyc00g006800TALDO1TransaldolaseAAACCAAAAGAGTAATTAGAAATACCA TTTAAGGGTTGTTGTACCTCACTTATSolyc07g042550SUS1Sucrose synthaseTAAAAGAGCTAGCAGGCAAACA GGAATGGTAGAGGTCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAACAATAAGGACCATTTCCATC CCCGCTCTGAAAATACGGTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTGAGAGTGGGGTTGTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenaseCCGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGMGlyceraldehyde-3-phosphate depidrogenaseCGAAAACTTCCTCCTCTCAACAASolyc04g072800PGM2 3-bisphosphoglycerate- mutaseGGTAACTCTGGATTGTGTCCTGASolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTSolyc06g084460DHQDDehydroquinate dehydrataseGATGGGTCACTCGTCCAGAAAAGGAT AATCCTACTTAGAGACTCAAGSolyc01g067750SHDShikimate kinaseGCACGTTTGTGACCTTGTAAGTGG GTACTCTGGTACTCTGAAGTGAAAAGAASolyc04g051860SKShikimate kinaseCCTCCTATGGGACTTGTGAAG GTACGAGTGATATTAGAAGTCAAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCAAAACTTAGCCCTCTTGAAAATCASolyc04g091900EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCACCTATAAAAACTTGCCCCTCTTGAAATCASolyc04g09350CSChorismate synthaseTATAGAGCCTGTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATTGCCCCTCTTGAAATCA	Solyc10g018500	INI	Transketolase 1	ATGTTTTGTGGATGAAATTGAAAAT
Solycolg006800TALDOTTransiduolaeTTTAAGGGTTGTTGTACCTCACTTATSolyc07g042550SUS1Sucrose synthaseTAAAAGAGCTTAGCAGGCAAACA GGAATGGTAGAGGTCCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAACAATAAGGACCATTCCACTC CCCCCTCTGAAAATACGGTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTAGTGAAGTGTAAGGTGTTGGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeCGCTCAACTGGCAGGTTGTTGGTGSolyc04g072800PGMGlyceraldehyde-3-phosphate dependent phosphoglycerate- mutaseCAAAAACTTCTCTCCTCAACAASolyc04g072800PGMEnolaseCAATATTTTTCGTAGGTGTCC TGCTTTGGAGGAGAGCGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGTCCAGTAAAGSolyc02g083590DHQSDehydroquinate dehydrataseACTGATTTGGACAAGAAGTCAAG AATCCTACTTGGTCCAAGAAAGAAAAGAT AATCCTACTTGGTCCAACAAGGAGGTTGGATCAACGGTGGAACACTGTTTGGAAGAGGC GATGGATCACTCGTCCAAAAGAAAAGAASolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACCTGTCGAAA CTCATCTGGTCCAACTGTCTGAASolyc04g051860SKShikimate kinaseCCCCCTCTATGTGGTTTGCAAGA GGACGATGTTACCTTGGTGG GTATCTGGTCCAACAGTCAAAATCASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferase TATATAGAGCCTGTTGGAAAAATCASolyc04g049350CSChorismate synthaseTAGAAATTGCGCTCCTTGAAAATCA	Selve00~006800	TALDOI	Transaldalasa	AAACCAAAAGAGTAATTAGAAATACCA
Solyc07g042550SUS1Sucrose synthaseTAAAAGAGCTTAGCAGGCAAACA GGAATGGTAGAGGTCCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAACAATAAGGACCATTTCCATC CCCGCTCTGAAAATACGGTTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenase likeACCGATAGTGAAAATACGGTTGTGGGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeCGCTCAACTTGTCAACGA CGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGMC12-3-bisphosphoglycerate- mutaseGGTAACTCTGGACTGTGTGCC CGCTCAACTTGTCTCAACAASolyc04g072800PGMEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACCTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTGCTAAAATACCCTTT GGATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATTCACTCGTCCAGTAAAG GTCAGGTTGATCACAGGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrataseACTGGATCAAGGACATTGTTGGGG GTACTCGGTCCAACTGTCGAAASolyc04g051860SKShikimate kinaseCACGTTGGTTGACAGGGTTGCAAAAGGAA AATCCTACAGCTGTCGAAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGGTGTGCAAAAAGAAAACA AACGAAAATTGCGCCGTGTCAAGGGG GTAACTGGCCGTGTCAAAATCASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTGTTGCGAGC AACGAAAATTGCGCTGTTGGCTCAGSolyc04g049350CSCbrisimate synthaseTAGAAATCTGCCCTCTTGAAATCA	S01yc00g006800	TALDOT	Transaldolase	TTTAAGGGTTGTTGTACCTCACTTAT
Solyc0/g042530S031Sucrose synthaseGGAATGGTAGAGGTCCCTTTTASolyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphate 1-phosphateCAAAACAATAAGGACCATTTCCATC CCCGCTCTGAAAATACGGTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTAGTGGAAGTGTTCGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenaseTCATTTTGTAAGTTGAAGTGTTCG CGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGMGlycerate- dependent phosphoglycerate- dependent phosphoglycerate synthaseGGAAAACTTCTCGGATTGTGTCCTGASolyc04g072800ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACGTTAGSolyc04g07480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGTGTTTATAAGGAGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGGTACCAGGTSolyc01g067750SHDShikimate dehydrogenase carboxyvinyltransferaseCACGTTGTGTAAAGGAGAGT CACGTTGTATACGCTGTCGTGCAGAASolyc01g051860SKShikimate kinaseCCCCCCCTTTGGAACTGGTGTCAAAAAGAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCCCCCCTCTTGAAATAAGTCAAAAATACA TATAAGAGCCTGTTGCAAAATSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCACATTGCCCCCCTCTTGAAATCA TATAAGAGCCTGTTGCAAAATCASolyc04g049350CSChrismate synthaseTAGAAATTTGCCCCCCTCTTGAAATCA	9-1-07-040550	CLIC 1	C	TAAAAGAGCTTAGCAGGCAAACA
Solyc12g095760PFK1Diphosphate-fructose-6- phosphate 1-phosphotransferaseCAAAACAATAAGGACCATTTCCATC CCCGCTCTGAAAATACGGTTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTAGTGGAGTTGTTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeCGCTCAACTTGTAGGTGTAGGTTCG CGCTCAACTTGTCTTAAAATGCTSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate- mutaseGGTAACTTCGCACTGTGTCCTCAACAASolyc03g114500ENOEnolaseTGCTTTGGAGGAGAGGTGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTCCTAAAATAACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGGACAAAAGAAAAGAASolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGAACATTGTTGGGG GTATCTGGTCCAACATGTTTGGASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGGGGTTGCCAAGTGAAC AACCGTTAGAACATTGCGCCCCCTCTGAAAATCA CCAAACAGTTAAAATAAGGAGCSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACGTTAAATAAGCCCTCTTGAAATCA CCAACAGTTAAAATAAGCCCTCTTGAAATCA CCAAACAGTTAAAATAAGCCCCTCTTGAAATCA	501yc0/g042550	SUSI	Sucrose synthase	GGAATGGTAGAGGTCCCTTTTTA
Solyc12g095760PFA1phosphate 1-phosphotransferaseCCCGCTCTGAAAATACGGTTTATSolyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTAGTGGAGTGTTGGTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeTCATTTTGTAAGTTGAAGTGTAGTGGTGGSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate- mutaseGGTAACTCTGGATTGTGTCCTGASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACGTTAGSolyc04g072800DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGTTTATATAAGGAGGTSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCCAGGSolyc02g083590DHQSDehydroquinate dehydrataseGATGGATCACTCTGAAAAAGAAAAGAA AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACCATGAGAAAAGAA AATCCTACTGGTCCAAACAGTGAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferase AACGAAAATTGGGTTGCAAAAAAGAAAAAACASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferase AACGAAAATTGGCGTTTGGCACAGSolyc04g049350CSChorismate synthaseCCAAACAGTTAAAAAAACCCCTTTGAAAAAAACCA	Solyc12g095760	PFK1	Diphosphate-fructose-6-	CAAAACAATAAGGACCATTTCCATC
Solyc03g111010GADPHGlyceraldehyde-3-phosphate dehydrogenaseACGATAGTGAAAATCCTCAACGA AACAGAGTAGTGGAGTTGTTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeTCATTTTGTAAGTGAAGTGTCG CGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate mutaseGGTAACTCTGGATTGTCCTCAACAASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGAGCGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACCTGTCGAA GGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCCAAAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTGTTGGAG GAACGATGTTGGTCCAACAGTCAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferase arboxyvinyltransferaseCCAAAATTGCCCCTCTTGAAATAACACAT TATAAGACCTTTTGGCAAAASolyc04g049350CSChorismate synthaseTAGAAATCGCCCTCTTGAAAT			phosphate 1-phosphotransferase	CCCGCTCTGAAAATACGGTTTAT
Solyc03g111010GADPHdehydrogenaseAACAGAGTAGTGGAGTTGTTGGTGSolyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeTCATTTTGTAAGTTGAAGTGTCG CGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate mutaseGGTAACTCTGGATTGTGTCCTGASolyc03g114500ENOEnolaseCAAAAACTTCCTCCTCTCAACAASolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAGATAGCCTCTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAAGAAAAGAT AATCCTACTTAGAGACACTTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACACTGTCAAGAAGTGG GTATCTGGTCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGATACCTTGTGGAA GTACGTGGTTGCCAAGTAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCAAAAATTGCCCTCTTGAAATAASolyc04g091490350CSChorismate synthaseTAGAAATCTGCCCTCTTGAAATA	Solyc03g111010	GADPH	Glyceraldehyde-3-phosphate	ACGATAGTGAAAATCCTCAACGA
Solyc04g009030GADPHLGlyceraldehyde-3-phosphate dehydrogenase likeTCATTTTGTAAGTTGAAGTGTTCG CGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate mutaseGGTAACTCTGGATTGTGTCCTGASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCTAAAATACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAAGAAAAGAT AATCCTACTTAGAGACACTTGTTTTGTSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACCTTGTGAAGTGG GTATCCTGTCCAACTGTCTGAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTGGCTCAG Solyc04g091190Solyc04g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAATCA TTATTAGAGCCTGTTTGGCTCAG			dehydrogenase	AACAGAGTAGTGGAGTTGTTGGTG
Solyc04g009030GADPHLdehydrogenase likeCGCTCAACTTGTCTTTAAATGCTSolyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate- mutaseGGTAACTCTGGATTGTGTCCTGASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGAGACGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGACCAGGASolyc06g084460DHQDDehydroquinate dehydrataseACTTGGTACTAGAAAAGAAAAAGAA AATCCTAGTTTGGAACATGTTTTGTSolyc01g067750SHDShikimate dehydrogenase GAACGTTGGTACCAACTGTCTGAAGGACGATGTGTATAACCTGGTGGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseCCTCCTATGTGGTATACCTTGTGG CTTATCAGCTGTCACAGTCAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAATCA TTATTAGAGCCTGTTGGCCCAAGTSolyc04g09350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solyc04g009030	GADPHL	Glyceraldehyde-3-phosphate	TCATTTTGTAAGTTGAAGTGTTCG
Solyc04g072800PGM2 3-bisphosphoglycerate- dependent phosphoglycerate- mutaseGGTAACTCTGGATTGTGTCCTGASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGAGCGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGACATGGGTSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAGAAAAGAA AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenase carboxyvinyltransferaseGGACGATGTGTATACCTGTCGAG GACGATAAATAAGTCAAAAATCA CCACGTTAGGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTGGCCCAACTSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT			dehydrogenase like	CGCTCAACTTGTCTTTAAATGCT
Solyc04g072800PGMdependent phosphoglycerate mutaseCAAAAACTTCCTCCTCTCAACAASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGAGCGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAAATACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTAGG CTCTATCAGCCTGTCACAGTCAASolyc01g091190EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT		PGM	2 3-bisphosphoglycerate-	GGTAACTCTGGATTGTGTCCTGA
mutaseCAAAAACTTCCTCCTCTCAACAASolyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGAGCAGTSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTGGCTCAGSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCTCTTGAAAT	Solyc04g072800		dependent phosphoglycerate	
Solyc03g114500ENOEnolaseATTTTCGTACGCTCGTGTCC TGCTTTGGAGGAGACGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTGAAGAGGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTGCCGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT			mutase	CAAAAACTTCCTCCTCTCAACAA
Solycolg111500EntrieTGCTTTGGAGGAGACGTTAGSolyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGACATGGTTGATCAAGAAGTCCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAAACASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAAACASolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvc03g114500	ENO	Enolase	ATTTTCGTACGCTCGTGTCC
Solyc04g074480DAHPS3-deoxy-7-phosphoheptulonate synthaseCACATATTTTTCCTAAAATACCCTTT GGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTGCGAGC AACGAAAATTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT			Liionuse	TGCTTTGGAGGAGACGTTAG
Solycolg07100DAIN 5synthaseGGAATGGGGTTTTATAAGGAGGTSolyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGGGTTGCT AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvc04g074480	DAHPS	3-deoxy-7-phosphoheptulonate	CACATATTTTTCCTAAAATACCCTTT
Solyc02g083590DHQSDehydroquinate synthaseGATGGATCACTCGTCCAGTAAAG GTCAGGTTGATCAAGAAGTCAGSolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTAGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT		Dinns	synthase	GGAATGGGGTTTTATAAGGAGGT
Solyc02g000000DHQDDenydroquinate dynamic syntaseGTCAGGTTGATCAAGAAGATCAAGASolyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAACAGTTAAATAAGTCAAAAATCASolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvc020083590	DHOS	Dehydroquinate synthase	GATGGATCACTCGTCCAGTAAAG
Solyc06g084460DHQDDehydroquinate dehydrataseACTTGATTTGGCAAAAAGAAAAGAT AATCCTACTTAGAGACATTGTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	50190026003590	DHQS	Denyaroquinate synthuse	GTCAGGTTGATCAAGAAGTCCAG
Solycoog 004400DHQDDenydroqunate denydroqunatesAATCCTACTTAGAGACATTGTTTTTGTSolyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvc06g084460	ЛНОЛ	Dehydroquinate dehydratase	ACTTGATTTGGCAAAAAGAAAAGAT
Solyc01g067750SHDShikimate dehydrogenaseCACGTTTGGTACTCTTGAAGTGG GTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	50190002004400	DIIQD	Denyuloquinate denyulatase	AATCCTACTTAGAGACATTGTTTTTGT
Solyc01g007750SHDSHRMAR delydrogenaseGTATCTGGTCCCAACTGTCTGAASolyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solve01c067750	SHD	Shikimate dehydrogenase	CACGTTTGGTACTCTTGAAGTGG
Solyc04g051860SKShikimate kinaseGGACGATGTGTATACCTTGTTGG CTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	S01yc01g007750	SIID	Sinkinate denydrogenase	GTATCTGGTCCCAACTGTCTGAA
Solyc04g051800SKSinkmate kinaseCTCTATCAGCCTGTCACAGTCAASolyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvo04c051860	SK	Shikimata kinasa	GGACGATGTGTATACCTTGTTGG
Solyc05g050980EPSPS13-phosphoshikimate 1- carboxyvinyltransferaseCCTCCTATGTGGTTTGCGAGC AACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	S01yC04g051800	SK	Shikimate kinase	CTCTATCAGCCTGTCACAGTCAA
Solyc03g030980EPSP31carboxyvinyltransferaseAACGAAAATTTGCGGTTGCTSolyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Salva05~050090		3-phosphoshikimate 1-	CCTCCTATGTGGTTTGCGAGC
Solyc01g091190EPSPS23-phosphoshikimate 1- carboxyvinyltransferaseCCAAACAGTTAAATAAGTCAAAAATCA TTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	20190028020980	LFSFSI	carboxyvinyltransferase	AACGAAAATTTGCGGTTGCT
Solycolg091190EFSP32carboxyvinyltransferaseTTATTAGAGCCTGTTTGGCTCAGSolyc04g049350CSChorismate synthaseTAGAAATCTGCCCCTCTTGAAAT	Solvo01~001100	EDCDCO	3-phosphoshikimate 1-	CCAAACAGTTAAATAAGTCAAAAATCA
Solyc04g049350 CS Chorismate synthase TAGAAATCTGCCCCTCTTGAAAT	S01yc01g091190	EFSF52	carboxyvinyltransferase	TTATTAGAGCCTGTTTGGCTCAG
	Solyc04g049350	CS	Chorismate synthase	TAGAAATCTGCCCCTCTTGAAAT

Supplementary Table 6. Oligonucleotides used in ChIP-qPCR experiments

			TAGACGAGTCATTTGATCCACCA
Salwa02a099460	CM1	Chariamata mutaga 1	GGTAGTAGGAGGATATCGCATCA
S01yc02g088400	CMI	Chorisinate mutase 1	TGGGTTTTGGAGTTAGGTGAGT
ID	Symbol	Full Name	ChIP-qPCR Primer Sequence (5'-3')
<u> </u>			TACTTCACCAACCAAAGAGGAAA
Solyc04g054710	PAT	Prephenate aminotransferase	GTGAGTGAAACAGAAGAGGGTTG
		Prephenate dehydrogenase	GAAATCGAAGCCGATTTACACAA
Solyc07g007590	ADT	family protein	AGAGGACTTTTTCCACGAAGCAC
		V 1	ТССТАТААТТААТСТТССААСААССА
Solyc09g007920	PAL5A	Phenylalanine ammonia-lyase	
			ТСССАТСАТТААТСТТТСААСАА
Solyc09g007910	PAL5B	Phenylalanine ammonia-lyase	CCCCCA ACTA ATAGATCCTA CCTA A A
Solyc09g007900	PAL5C	Phenylalanine ammonia-lyase	
Solyc09g007890	PAL5D	Phenylalanine ammonia-lyase	
Solyc10g086180	PAL	Phenylalanine ammonia-lyase	CGGICCATATAATICCITATGICCA
			AGGTGAGTTGATAAGGGGTCCAT
Solvc03g117870	4CL	4-coumarate CoA ligase	TTGTATCCCCCAAAAAGGAAAAA
, 0		6	CCTGTGGTAGGTGAAAGGGAGTT
Solvc06ø035960	4CL-Like	4-coumarate-CoA ligase-like	ATTGAGGAAATATGCCCTCTCCA
			GCGGCAATATAAATGCAATGAAG
$S_0 v_0 0_0 0_0 1510$	CHS-1	Chalcone synthase -1	TCTTAAATTTAGAAAGGAAAACCAAAA
50190096091510			TCCAAAAGAAAAAGAATGGTAGC
Solve05c052550	CHS 2	Chalcone synthese 2	ACGAAAAATAAGAGTTGGGGAAA
301yc03g033330	CH5-2	Charcone synthase -2	CATAACAAACTGGTAGGCGGTAG
Solvo05c010220	СШ	Chalcona flavonona isomarasa	TCTCGAAATACGAAATAATTGAGG
301yc03g010320	CIII	Charcone-mavonone isomerase	GTACGGTTAATGGCTCACAGTTC
S = 1 0.5 = 0.5 22.40	CUU	Chalcone-flavonone isomerase	CTTTCCAAATACTCGTGTCAAGC
S01yc05g052240	CHIL	like	AGCTACCACACAATCTACCTTCC
G 1 00 0000 (0	5311		CATAATTTTCAAACCAAGTATGGTGGT
Solyc02g083860	F3H	Flavanone 3-nydroxylase	CGTGCCAACTAACAACATTTCAC
			AATTAAAGGCAAAAAGTAGGTTTGAA
Solyc11g013110	FLS	Flavonol synthase	TTATAGGAAAGTGACGCGGTGT
~		Dihydroflayonol-4-reductase	AACTCCTGCAATTAGTCTTTCACA
Solyc02g089770	DFRLI	like	CATCCGAGCATATAAGAAACCAA
		Dihydroflayonol-4-reductase	AGTACAACGCGGCGTATCACTAT
Solyc01g068080	DFRL2	like	TTCTATGGCTTCGAGTTAGAAAAA
Solyc08g080040	ANS	Anthocyanidin synthase	
		LIDD flavonoid 2 O	
Solyc10g083440	3GT	ducosyltransferase	
Solvc03g117600	HCT	shikimate/quinate	
50190052117000	ner	hydroxycinnamovltransferase	TGAGTTTCTTATATAGTATTGGGAAGG
		,	ACCAGCCACGTGATTGAGAAAT
Solyc10g078240	СЗН	<i>p</i> -coumarate 3' -hydrolase	TTGCGTTTGGAGTTTTGGTAGGT

ID	Symbol	RT-qPCR Primer Sequence (5'-3')
Salwa02a002920	CADD	GTCAGTGGCTCTTATGATTCTGG
S01yc02g095850	GOPD	GTCTTCTGGATGATCCTTCTGTG
G 1 05 000250	ъ ·	TCTTCCTCTGTTTCCCCTGTTA
Solyc05g008370	Крі	CTGTTGACCCTGTACCTAAACCA
~		GTCTAGGAGAAGACGGTCCAACT
Solyc10g018300	TKT	TAAGCTCCTGCTGTCTCATTACC
		GTTAGGTGTAACACAGTGCACCA
Solyc07g042550	SUS1	AGCTGTGAACTGAGCTGAGAAGT
		GCACTCTGCAGTCACATCCTAAT
Solyc12g095760	PFK1	ТСАСССТАССТТСААСТСТАТС
		GACAAGCTAACATCCCAAGAGGT
Solyc04g072800	PGM	
		GGATGTAGCAGCATCTGAGTTCT
Solyc03g114500	ENO	GCTCTGAGCACTAACTACATGA
Solyc04g074480	DAHPS	
Solyc02g083590	DHQS	
Solyc01g067750	SHD	
· · ·		GTATCIGGICCCAACIGICIGAA
Solvc04g051860	SK	GGACGATGTGTATACCTTGTTGG
	~	CTCTATCAGCCTGTCACAGTCAA
Solvc049049350	CS CAGGGCGGTATATCAAATGG	CAGGGCGGTATATCAAATGG
	0.5	GCGATGAGTTCTGTTTCGTG
Solvc02g088460	CM1	CAGTATCCAAAGGTTCTGCACTC
50190025000100	emi	TGCCTTCCTTCACTAATCTTGG
Solvc07c007590	ADT	GTCACAAGTCAGTCACCACCAT
501yc07g007590	ADI	AGCCTACCTGACTGAGCATATTG
Solve00g282510	DAI	AATTGCTTCGAGTCGTGGATAG
301yc00g282310	TAL	ACAAGGACTTGTCTCAGCTTCTG
Salwa00a001510	CUS 1	CCTTTATTTGAACTCGTCTCAGC
S01yc09g091510	CHS-1	CAGGAACATCCTTGAGTAAGTGG
9-1-05-052550	CHE 2	CGGGCTACTAGGCAAGTTTTAAG
Solycu5g053550	CHS-2	CCTGTGGTACTAAGCCCTTCTTT
G 1 05 010220	CIU	TTGTCAACTCGGTCTAATGTGTC
Solyc05g010320	CHI	TAAAGTGGGACCTTATTGCACAC
~		ATGGATGAGCCGATTACATTTG
Solyc02g083860	F3H	TGGCCTCTTCAGTTTGTATCTTC
		CTCAACGCCACTAAATCTCCCTA
Solyc11g066580	F3'5'H	TTGCCCATATGTTGACACTAAGC
		TATAGCTGGGACAGACACATCCT
Solyc03g115220	F3'H	CTACTTTGTCGATCTCCTGTTGG
		GACTTGCCGACAGAAGCAAT
Solyc02g085020	DFR	
Solyc08g080040	ANS	
Solyc11g013110	FLS	
		ICACCAATGIGGACAATTATAGCA

Supplementary Table 7. Oligonucleotides used in RT-qPCR experiments