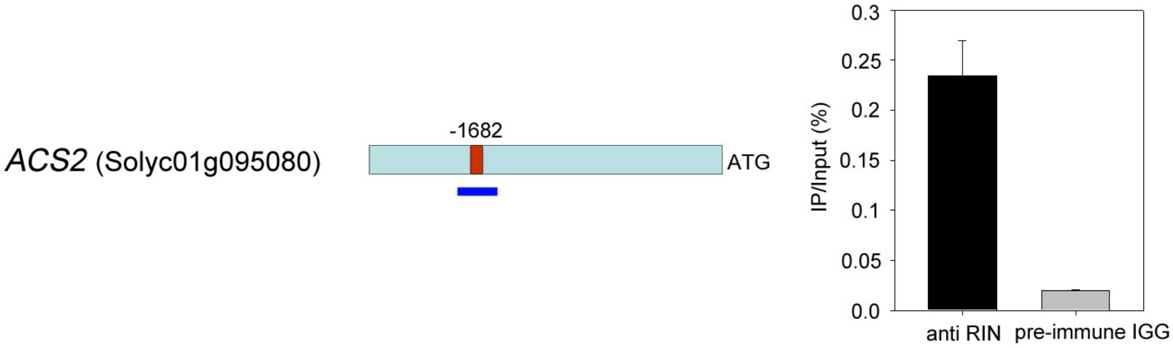
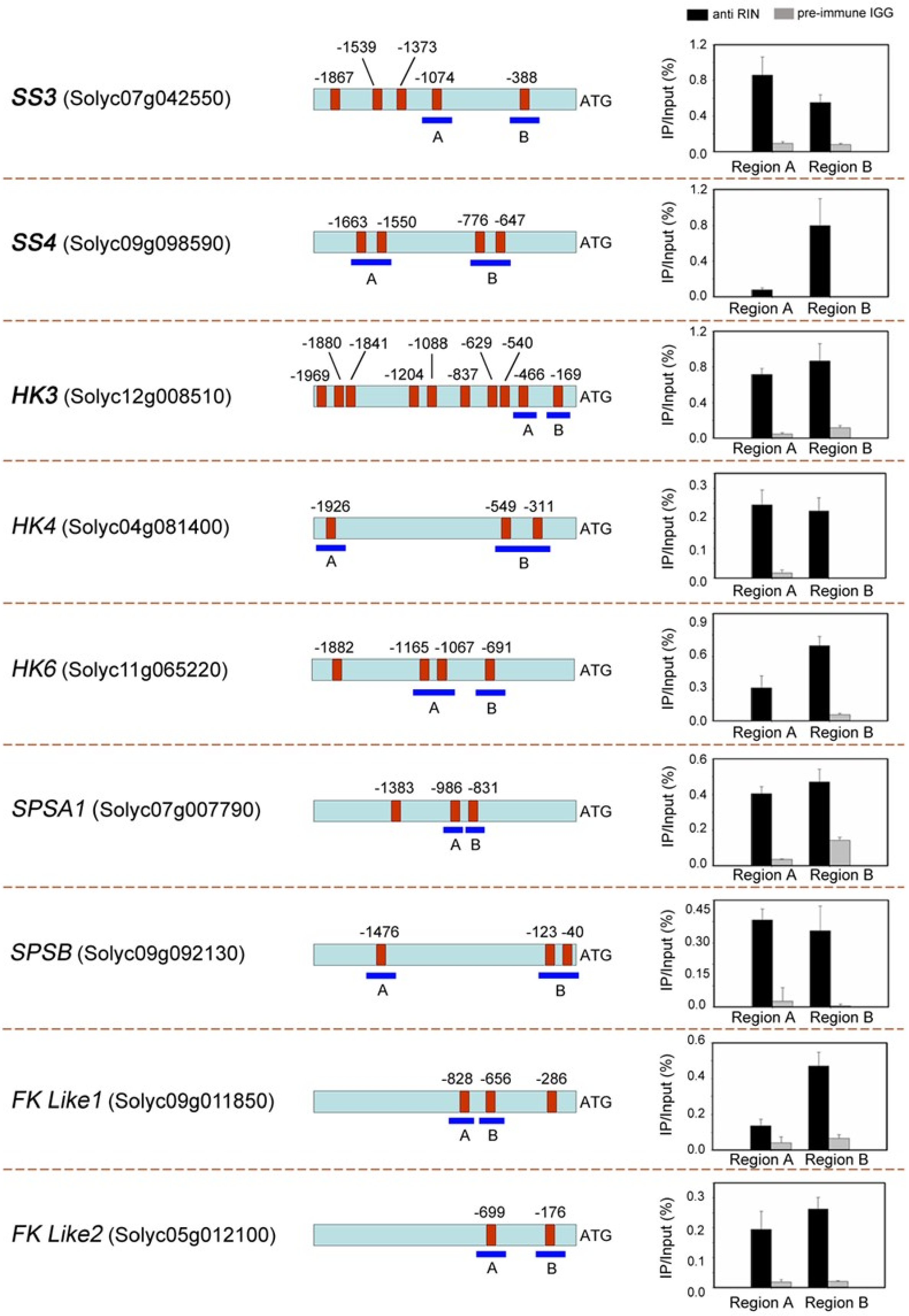
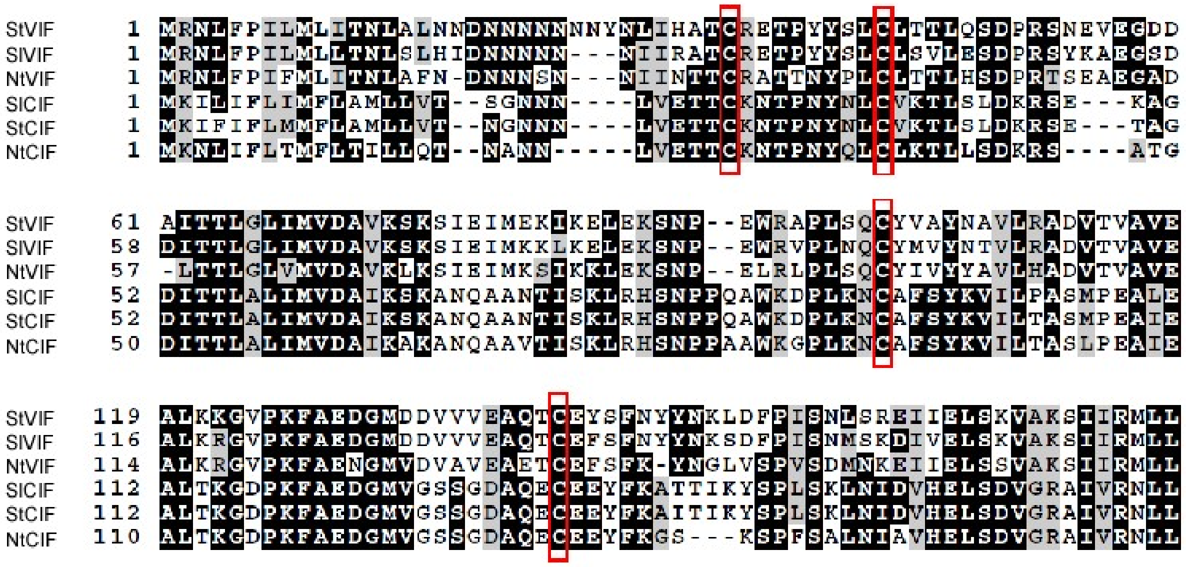


Supplemental Figure S1. The binding ability of RIN to the promoter of *ACS2* as revealed by chromatin immunoprecipitation. The promoter region of *ACS2* is indicated. Red box represents CArG box element and number above the box indicates the position of this motif relative to the translational start site. The blue fragment represents the region used for ChIP-qPCR. The value is percentage of DNA fragment that was co-immunoprecipitated with specific anti-RIN antibody or non-specific antibody (preimmune rabbit IgG) relative to the input DNA. Error bars represent the SD of three independent experiments.



Supplemental Figure S2. Chromatin immunoprecipitation reveals the direct binding of RIN to the promoters of genes involved in sucrose metabolism. The promoter regions of the target genes are indicated. Red boxes represent CArG box elements and numbers above the box indicate the position of these motifs relative to the translational start site. The blue fragments with upper-case letters represent the regions used for ChIP-qPCR. Values are the percentage of DNA fragments that were co-immunoprecipitated with specific anti-RIN antibodies or non-specific antibodies (preimmune rabbit IgG) relative to the input DNA. Error bars represent the SD of three independent experiments. SS, sucrose synthase; HK, hexokinase; SPS, sucrose phosphate synthase; FK, fructokinase.



Supplemental Figure S3. Alignment of amino acid sequences of invertase inhibitors from various plants. The sequences of invertase inhibitors are taken from tomato (SlCIF), tobacco (NtVIF and NtCIF) and potato (StVIF and StCIF). Four conserved Cys residues are boxed.

Supplemental Table S1. *Genes involved in sucrose metabolism*

Family	Name	ITAG gene locus	Genbank accession numbers	CArG box	Motif number
Invertase	*LIN5*	Solyc09g010080	NM_001247864	-269: CATAAAAATG -482: CTATTTATTG -1931: CAAAAAAATG -1982: CATATTTATG	4
	LIN6	Solyc10g083290	AF506005	—	0
	LIN7	Solyc09g010090	NM_001247772	-1266: CTAATATTTG -1603: CATTTATTTG	2
	LIN8	Solyc10g083300	XM_004249387	-250: CATATTAATG -690: CAAAATTTTG -1286: CAAAATTTTG -1388: CAAATTTAAG -1765: CAAAATAATG	5
	LIN9	Solyc08g079080	NM_001247140	-153: CTTAAAAAAG -379: CAAAATTAAG -412: CAATAATTAG	7

				-464: CTATTTAAAG	
				-736: CAATATTTAG	
				-822: CAATTTTATG	
				-1427: CTAAATTAAG	
	VI	Solyc03g083910	D11350	-1094: CTATAAATAG	2
				-1824: CTAAAAATAG	
	*NI1**	Solyc01g058010	XR_182330	-610: CAATTTTAAG	4
				-686: CATATTTATG	
				-993: CCATTAATGG	
				-1095: CATTTTATTG	
	*NI2**	Solyc01g100810	XM_004230281	-33: CATATATTTG	4
				-1015: CATATATTTG	
				-1417: CTAAATTAAG	
				-1959: CCTTTTTTGG	
	*NI3**	Solyc06g065210	XM_004241789	—	0
	*NI4**	Solyc11g020610	XM_004250368	-714: CTTTTATAAG	4
				-1386: CATTTTTTTG	
				-1848: CAAATTTAAG	
				-1987: CTTTTATTTG	

	*NI5**	Solyc11g067050	XM_004250984	-1168: CATAAAAAAG	1
Invertase inhibitor	*VIF**	Solyc12g099190	KC007445	-1511: CTATTAAAAG	4
				-1575: CTAATATATG	
				-1590: CATTATTTTG	
				-1780: CTATATTAAG	
	CIF1	Solyc12g099200	NM_001247862	-1320: CATAATAAAG	2
				-1641: CAATAATATG	
	*CIF2**	Solyc12g099210	XM_004252882	—	0
Sucrose synthase	*SS1*	Solyc12g009300	NM_001247726	-1759: CTATAAAAAG	1
	SS3	Solyc07g042550	NM_001247875	-388: CATTTATTTG	5
				-1074: CATTTTTTTG	
				-1373: CTAAAAAAAG	
				-1539: CTATAAAAAG	
				-1867: CATAAAAAAG	
	SS4	Solyc09g098590	HM180943	-647: CAATAAATTG	4
				-778: CTATATATTG	
				-1550: CAAATTTTAG	
				-1663: CTAAATTTTG	
	*SS5**	Solyc07g042520	XM_004243632	-449: CATTATAATG	4

				-516: CTATATATAG -772: CTTAAAATAG -1201: CCTAAATAGG	
	*SS6**	Solyc03g098290	XM_004235340	-724: CAAATTTATG -841: CTAATATTTG	2
	*SS7**	Solyc02g081300	XM_004232624	—	0
Sucrose phosphate synthase	*SPSA1**	Solyc07g007790	NM_001247910	-831: CCAAATTAGG -986: CATTTTTTTG -1383: CAAATTTTAG	3
	SPSA2	Solyc08g042000	JQ086765	-210: CAAAAATTTG -222: CATTTTTTTG -391: CATTTTAAAG -455: CTATTAATTG -969: CAAAATAATG -1251: CAAATTAAAG -1472: CATTATAAAG -1732: CCAATTTAGG -1934: CTAATATATG	9
	SPSB	Solyc09g092130	JQ086766	-40: CATTTTTTTG	3

				-123: CATTTTTTTG -1476: CAAATAATTG	
	*SPSC**	Solyc11g045110	XM_004250713	-324: CATATATTAG -378: CATATATTAG -843: CTTTTATTAG -1084: CTTTAAATAG -1333: CTTATATATG -1538: CAATATATAG -1717: CTTTATAAAG -1959: CTTTTTAAAG	8
Fructokinase	*FK1*	Solyc03g006860	NM_001246964	-539: CAATAAATAG	1
	FK2	Solyc06g073190	NM_001246959	-115: CTATATAAAG -337: CTTTTTTTTG -1020: CTATATTTAG -1274: CATTTTTTAG -1393: CTTATAATTG -1536: CAATAAAAAG	6
	FK3	Solyc02g091490	NM_001247467	-612: CTTTAATAAG -1642: CTTATTTTAG	2

	FK4	Solyc10g017620	AY099454	—	0
	*FK-Like1**	Solyc09g011850	XM_004246314	-286: CATTAATTTG	3
				-656: CAAATTATAG	
				-828: CATAAAATTG	
	*FK-Like2**	Solyc05g012100	XM_004238987	-176: CCATTATTGG	2
				-699: CAAAAAAAAG	
Hexokinase	*HK1*	Solyc03g121070	NM_001247028	-239: CAAAATTATG	7
				-327: CTTTTTTTTG	
				-551: CAATAAAATG	
				-624: CATATATAAG	
				-1141: CAAATATTTG	
				-1638: CAAATAAATG	
				-1656: CATTAATAAG	
	HK2	Solyc06g066440	NM_001247477	-692: CTTAAATAAG	3
				-729: CTATAAATAG	
				-749: CTTTTATTTG	
	HK3	Solyc12g008510	NM_001247781		10
				-169: CTTAAAAAAG	
				-446: CTAAAATAAG	
				-540: CAATTTTAAG	

				-629: CTTATTATAG -837: CTATATATAG -1088: CTTAAAAAAG -1204: CTAAAAAAAG -1841: CTTTTTTTTG -1880: CTAATTAATG -1969: CATATAAAAG	
	HK4	Solyc04g081400	NM_001247788	-311: CTAAATTTAG -549: CAAAATTTTG -1926: CTAATATAAG	3
	*HK5**	Solyc02g091830	XM_004251306	-1078: CAATTATATG -1276: CAATTATATG -1305: CAAATATATG	3
	*HK6**	Solyc11g065220	XM_004231915	-691: CAATTTAATG -1067: CTATTAAAAG -1165: CTTTATAATG -1882: CATATTAATG	4

Unreported genes were asterisked.

Supplemental Table S2. *Primers used in qRT-PCR analysis of sucrose metabolism genes*

Primer	Sequence
qFK1-F	GTTGCAGCCAACGAGACATG
qFK1-R	AAGGCTTTCCAGCATTTCCTT
qFK2-F	CGACGATGAGTTCGGTCACA
qFK2-R	GGCGCCCTTGTCAAAATTAA
qFK3-F	AGATGCGCTGTCAAAGCAACT
qFK3-R	CACTTGGCAATGCTCTTCCTT
qFK Like1-F	ACAGCTTCGCTTTGCTATTGC
qFK Like1-R	TTCTGTGTGGCGCTTTCAGT
qFK Like2-F	TTGCAAATGTTGATGCCGATA
qFK Like2-R	GGCCATCCATACGTGAAGCT
qHK1-F	TCTTGCTGCCTCTCATTCAATG
qHK1-R	TTCCCTCTAGCAAGATATGGCTTT
qHK2-F	TTCCTGGGAATGCCAACATATT
qHK2-R	GGGAGAATTAGCAGTTTGCTGAGT
qHK3-F	CTTGCTAAAGGGAACCCACTTCT
qHK3-R	GCATGACACAGTGCACAAGGA
qHK4-F	ACAGAGCTACTAGGCTCGGAAA
qHK4-R	GCAGCTAATAATGCAGCTCCAA
qHK5-F	GGGAGATGCTTGGCAATGAA
qHK5-R	AAGCGGCAATGTAGATGGAACT
qHK6-F	TACCCGATGTGCCAGTGAAA
qHK6-R	CCACTCCCATCTCGACCAAT
qSS1-F	CAAGTACCGTAAGATGGCTGAA
qSS1-R	TGAAACACTAAACAGAAGCCTCTAC
qSS3-F	TTTAGAAATTGTTTGCCCCACAT
qSS3-R	CTACAGAAGGGAAAAATGGCAAAT
qSS4-F	AGTTCCGTGAGTTGGTAAAATCTGT

qSS4-R	TGGTATGCTCCACGTTATTTATTCC
qSS5-F	TTATCACAGAGGCGCTCACAAT
qSS5-R	TTGCGTGTTATGGTTGACAATG
qSS6-F	GGGCAAAAGCAGGCTAAACA
qSS6-R	CAACTGGCAAGGGCTCTTCA
qSS7-F	TGGCCATTGATGAATAGTTGAAA
qSS7-R	GAGGAAGGAATTGCATTCAGAAA
qSPSA1-F	GCAAGTTACGTGCAAGGATCAA
qSPSA1-R	CCCAGGAGGAATTACAGCCATA
qSPSA2-F	GGAAGTTGCAGCAAGGAAGATATT
qSPSA2-R	TTTAACCTCCTCAGCGGAAATC
qSPSB-F	CCTGTGGCACGAGTGTAGGA
qSPSB-R	TTCCATTGCGGGTGTCTCAT
qSPSC-F	CCAGGAGCCGAAGTAAGGAA
qSPSC-R	TCAACCTTGATGCAGCATGTG
qLIN5-F	CTGAATGCTTGGAGCATGGAT
qLIN5-R	GAGGATTTTTGTGAACATCATCTACTG
qLIN6-F	AGCACATTTATTCGCCTTCAACAA
qLIN6-R	CTTTGTGACGTGGCATAATAAGAT
qLIN7-F	GAACGGAGCCAATCACAATTG
qLIN7-R	TCCCCCTTTTACCATAGTTCCTT
qLIN8-F	AGTCATTGAATGCATGGAGCAT
qLIN8-R	GAGCAATCAAATACGTCACCACAA
qLIN9-F	ACTGGGTCAACCAACGAATC
qLIN9-R	TGCCCTCATACTTGATCCAT
qVI-F	TCCTTCCCTTTGCAAGACTTGT
qVI-R	TCTCCCTCTTCCCTTTCTTGATG
qNI1-F	GCCTCTTGATGGAAGGAATGGT
qNI1-R	CCAGAATCAACAGGTGCAACAC

qNI2-F	TTCTTTTCTGGGTCTTCCATTCA
qNI2-R	TCCATTGCCCAAAATACGAGAT
qNI3-F	GACTGGACGGCCACAAATTG
qNI3-R	CCAATGTATCTGCCGAGCTTT
qNI4-F	CATTAAGACGGGACGACCACAA
qNI4-R	ACCAATATATCTTCCAACTGTACCA
qNI5-F	AATGGGAAGTCGATGCACACT
qNI5-R	CCATTTTCCTGCTTCATGTTCTG
qVIF-F	CATGGTGGATGCGGTGAA
qVIF-R	GCCACTCAGGGTTCGATTTC
qCIF1-F	GTTGGTAGAGCCATTGTAAGAAATTT
qCIF1-R	TGATCATAATGTGACGAATCGAAT
qCIF2-F	CTGGAGATGCACAAGAATGTGA
qCIF2-R	TATTAAGAGAGGCTTATTGATTCAC
qRIN-F	GGATACGATAATGTACAACCCGAAA
qRIN-R	CAAAGCATCCATCCAGGTACAA
qNOR-F	AGAGAACGATGCATGGAGGTTTGT
qNOR-R	ACTGGCTCAGGAAATTGGCAATGG
qLePG-F	TGGACAAGTATGGTGGCCAAGTTC
qLePG-R	TCCAGAAGGTTAAGGCCGTTGG
qEXP1-F	CTGCCCACCAAATTACGCGTTG
qEXP1-R	TGGGATCCTGCGATAAGTTACAGG
qACS2-F	AATGTCAAGAGCCAGGGTGGTTCC
qACS2-R	TCCTCGCGAGCGCAATATCAAC
qACO1-F	ACGGGAAGTACAAGAGTGTGCTG
qACO1-R	ACATTCGTGTCCCGTCTGTTTGTG
qPSY1-F	ATGAGGCAGAGAAAGGCGTGAC
qPSY1-R	CAAGACCAAAGATGCCCATACAGG
qPDS-F	TTTGTGTTTGCCGCTCCAGTG

qPDS-R	ACAGGTACTCCGACTAACTTCTCC
qACTIN-F	TGTCCCTATTTACGAGGGTTATGC
qACTIN-R	AGTTAAATCACGACCAGCAAGAT

Supplemental Table S3. *Ripening marker genes used for qRT-PCR analysis in this study*

Gene	**ITAG gene ID**[a]	**Description**
RIN	Solyc05g012020	Ripening inhibitor
NOR	Solyc10g006880	Non-ripening
LePG	Solyc10g080210	Polygalacturonase A
EXP1	Solyc06g051800	Expansin 1
ACS2	Solyc01g095080	1-aminocyclopropane-1-carboxylate synthase 2
ACO1	Solyc07g049530	1-aminocyclopropane-1-carboxylate oxidase
PSY1	Solyc03g031860	Phytoene synthase 1
PDS	Solyc03g123760	Phytoene desaturase

[a] ITAG, the International Tomato Annotation Group release version 2.3.

Supplemental Table S4. *Gene-specific primers used in ChIP-qPCR assay*

Primer	**Sequence**
VI-F1	CGTTTTTGGACAAATCTTCATTATC
VI-R1	GAATTGGAGATGATATGACAATACT
VI-F2	ATGGTAACCTTTGGAGTGATTTCTC
VI-R2	AGAGAAGTAAAATGGAAGATAAGAC
CIF1-F1	TAGATTCGCCTCAAAGAAATACACA
CIF1-R1	TTGAGTGGTGCAATATAAGTCTAGT
CIF1-F2	GTTCCAAGGAATCAACCCAAAAAG
CIF1-R2	CATTATCCTTGTGAAAGTGGAATGC
SPSA1-F1	ATGGTAAGCTCACATTCCTTCTGAA
SPSA1-R1	GATTGGTGAAGCGCCTAAATTAATC
SPSA1-F2	AAGTATTGATGACTAGCGGCGAT
SPSA1-R2	ATGTGTTAGAATGAGAATCGTCGAA
SPSB-F1	CTACCTTAGCATATGTGTCACCCTT
SPSB-R1	GAAGAGGAAAACCATGTGAAAGGAA
SPSB-F2	ATCTCTCATTCACATATCTCACCAT
SPSB-R2	TTTGCTATTTCTAACTTACCCACCT
FK like1-F1	GCCCGATGTTTTATTTCGATTCATT
FK like1-R1	TAAATCGATGACAACCTTTCCATTC
FK like1-F2	CCTTGATTTCCTCCAACTGCTT
FK like1-R2	GGGACATCTTGATTGTAATTTTACC
FK like2-F1	GAAACTTTATCACTGATAGAGCACA
FK like2-R1	AAATCGTGTTATGGTAACTTCAAGC
FK like2-F2	CCAATTTCTCTTTACTACTTCACAG
FK like2-R2	ATCTTTACAACCCTGAAGACCCAAT
HK4-F1	CATATTTGCATAATGTGTTCCATAGC
HK4-R1	TCGTCCTACCTGCGCAATTTTC
HK4-F2	CCTTCCTTTTATTTCGTGTGTTTTG

HK4-R2	CTGTTCGTTACTTTCATAGTGCTGA
SS4-F1	CTCATCCCACCCATTGTCATCCCC
SS4-R1	CAACCATTTGTCACCGTACCCTCA
SS4-F2	CGTTTTGGAATCCGTTGAATGGTA
SS4-R2	GTATAGTTCACTATTCTTGGATGAC
SS6-F1	AGGATAACGTGAAGAGGGTCA
SS6-R1	CAGTTGGAAGGAAGGGGGGA
VIF-F1	GCCACGTTTTCATGTTGTAATGTC
VIF-R1	GGACAACATCGCAAGTTGGATC
VIF-F2	GAGTTGTAAGGAGCATCAAATCGTA
VIF-R2	ATGAATCACCATTAATAGGTGCAAG
LIN7-F1	AAGGGTGTATCCAACTTTAGCGA
LIN7-R1	GCTCCAAGCATTCAGAGTCTCAA
LIN7-F2	TTTGTTAGCTTTCCTTTTTGTTTTG
LIN7-R2	CATCTTTATTCATTTGCGATTGTTT
LIN8-F1	ATAGTGAATGACAAAGACGGGTG
LIN8-R1	TATCTTCCTTTCTCCCCACTCTT
LIN8-F2	GATCACTTCAACTTTGATGAGAACC
LIN8-R2	TTGGGAGGTTACATTACGCTGAA
NI2-F1	CTCAAATGACAAATATACTGGAGAAG
NI2-R1	TGGAGATTTTATACCTTACAGCTAAC
NI2-F2	GTGAGCAATTTAGAGCGAAAATAACT
NI2-R2	GAAAGCAAAAAGCCTATCGCAAAC
NI4-F1	GAGGAATAATATGAGTGGAAATAAG
NI4-R1	AACCTTAATATCCTACTTGACATGA
NI4-F2	GGTCTATCTCTGGACTCTACTC
NI4-R2	GAACAAGAGCGAAACAAAAGATAGT
SS3-F1	GTTCATGTACCTTTCGTTTTCAGAG
SS3-R1	CATTGTTTTCTATCCGTGACGGT

SS3-F2	GGTCGTTTACGTATCCTATTCTGC
SS3-R2	TCAACTCGTCCGATCAAACTAAC
HK3-F1	TGCGGCCTAATTTGATTTAATACGA
HK3-R1	TCGTTTCAATTTATCTTACTCCGTC
HK3-F2	TGGGACCTACTCTTTGTTATCATC
HK3-R2	TTGATGTGTGGGAGTGACAGAGA
HK6-F1	TCAAGAACACATAATACGAAAAATC
HK6-R1	AGACTCTTGTTATTTTCTTTTCACT
HK6-F2	TCAAACTTAAATGGCAATTACCGTA
HK6-R2	GTTATTTGTGAAAGCGAAGGTCTGA
ACS2-F1	TCACAAACGAGCTATTCTAAAAA
ACS2-R1	CCTTACATCATTTATTATTACAA

Supplemental Table S5. *Primers used for probes of EMSA*

Primer	**Sequence**
VI-F	TTCTCACTCTATAAATAGGGTTGTTT
VI-R	AAACAACCCTATTTATAGAGTGAGAA
VIF-F	AGTAATAACTATTAAAAGTGTAAAATAC
VIF-R	GTATTTTACACTTTTAATAGTTATTACT
CIF1-F	GAGAAAGCATAATAAAGTGATGCAT
CIF1-R	ATGCATCACTTTATTATGCCTTTCTC
LIN7-F	ATGTAGAACTAATATTTGGTAATATT
LIN7-R	GTTAAAAACAAATAAATGTGCATTAT
LIN8-F	ATGAGAACCATATTAATGTATTGAGG
LIN8-R	CCTCAATACATTAATATGGTTCTCAT
NI2-F	TTTGTAAACAAATTTATGTTCAAATA
NI2-R	TATTTGAACATAAATTTGTTTACAAA
NI4-F	ACTCTACTCTCTTTTATAAGTTTTCTAT
NI4-R	ATAGAAAACTTATAAAAGAGAGTAGAGT

Supplemental Table S6. *Identification of the differentially expressed proteins in the SlVIF silenced tomato fruit (vif) using iTRAQ-based quantitative proteomic analysis*

Accession number[a]	**Name**	**Fold-change (*vif*:WT) at 38 dpa[b]**	**±SD**	**Fold-change (*vif*:WT) at 41 dpa[c]**	**±SD**	**Confident peptides[d]**	**%Seq cov[e]**
Amino acid metabolic process							
Solyc01g112280.2.1	Succinyl-diaminopimelate desuccinylase	1.40	0.11	0.12	0.00	17.00	46.32
Solyc02g091560.2.1	Serine hydroxymethyltransferase (SHMT)	3.09	0.11	0.53	0.06	43.25	59.94
Solyc03g098240.2.1	Glutamate decarboxylase (GAD1)	1.69	0.11	0.50	0.01	29.25	39.89
Solyc04g054310.2.1	Alanine-glyoxylate aminotransferase,class-III (AGT)	0.37	0.04	0.61	0.04	13.25	33.88
Solyc06g019170.2.1	Gamma-glutamyl phosphate reductase (GPR)	1.28	0.06	0.50	0.02	27.00	35.08
Solyc07g032740.2.1	Aspartate aminotransferase (AST)	1.00	0.05	0.46	0.02	25.25	59.73
Solyc07g053720.2.1	Tyrosine aminotransferase-like protein (TAT)	2.18	0.86	2.46	1.19	2.50	9.48
Solyc08g014130.2.1	2-isopropylmalate synthase 1 (leuA)	0.37	0.04	0.33	0.01	38.50	55.01
Solyc08g065220.2.1	Glycine dehydrogenase P protein (GLDC)	2.19	0.13	1.06	0.16	25.25	28.98

Solyc09g007910.2.1	Phenylalanine ammonia-lyase (PAL)	0.35	0.11	2.30	1.04	6.75	19.45
Solyc09g008670.2.1	Threonine ammonia-lyase	2.04	1.09	1.34	0.23	3.25	8.40
Solyc11g011920.1.1	Glutamate decarboxylase (GAD2)	1.22	0.08	2.42	0.03	23.25	39.86
Solyc11g012970.1.1	Aminoacylase-1 (ACY1)	1.24	0.15	0.17	0.05	10.00	41.72
Solyc12g005860.1.1	3-isopropylmalate dehydratase large subunit (leuC)	0.49	0.02	0.70	0.04	70.25	56.78
Solyc12g088220.1.1	Branched-chain amino acid aminotransferase II (BCAT2)	0.39	0.12	0.66	0.09	4.25	18.23
Solyc12g096190.1.1	Tryptophan synthase, beta chain-like	2.12	0.24	1.04	0.08	16.00	32.72
Carbohydrate metabolic process							
Solyc01g008710.2.1	Mannan endo-1 4-beta-mannosidase (MAN4)	0.08	0.03	0.24	0.02	6.50	17.36
Solyc01g060020.2.1	Beta-glucanase	0.37	0.01	1.80	0.36	5.50	19.79
Solyc01g074030.2.1	Beta-glucosidase 01	0.47	0.11	1.22	0.09	4.75	11.02
Solyc01g099630.2.1	Xyloglucan endotransglucosylase/hydrolase 5 (XTH1)	0.78	0.04	3.29	0.21	9.50	31.93
Solyc01g104950.2.1	Alpha-L-arabinofuranosidase/β-D-xylosidase	0.50	0.01	1.02	0.03	15.50	21.78

Solyc01g107830.2.1	UDP-glucosyltransferase family 1 protein (UGT1)	0.87	0.18	0.40	0.01	7.25	23.55
Solyc01g110360.2.1	Fructose-bisphosphate aldolase, class-I	2.10	0.02	0.66	0.02	8.00	51.01
Solyc02g062340.2.1	Fructose-bisphosphate aldolase, class-I	1.83	0.07	0.46	0.13	8.75	50.76
Solyc02g070020.1.1	UDP-glucosyltransferase (UGT)	0.14	0.04	0.41	0.01	7.00	18.21
Solyc02g087770.2.1	Aldose-1-epimerase-like protein	0.72	0.10	2.18	0.08	12.25	24.93
Solyc03g019790.2.1	Alpha-galactosidase	2.14	0.25	1.27	0.15	21.00	44.31
Solyc03g065340.2.1	Glycogen/starch/alpha-glucan phosphorylase	2.10	0.19	1.50	0.10	53.75	52.61
Solyc03g083910.2.1	Acid beta-fructofuranosidase/ vacuolar invertase (VI)	0.19	0.03	1.15	0.06	66.25	51.00
Solyc03g098290.2.1	Sucrose synthase (SuSy6)	0.33	0.03	0.67	0.12	3.75	4.29
Solyc03g113030.2.1	Aldose 1-epimerase-like protein	0.46	0.03	0.56	0.03	10.50	30.84
Solyc03g123830.2.1	Phosphoglycerate dehydrogenase (PHGDH)	4.46	0.50	2.95	0.20	22.25	39.95
Solyc04g016470.2.1	Beta-1, 3-glucanase	0.45	0.05	0.89	0.04	4.25	19.64
Solyc05g007070.2.1	Alpha amylase 2 (IC)	2.47	0.68	0.94	0.06	6.75	10.90
Solyc05g050800.2.1	Phosphoglycerate mutase family protein (PGAM)	0.43	0.05	1.63	0.21	12.00	44.61

Solyc07g007790.2.1	Sucrose phosphate synthase (SPSA1)	1.21	0.14	0.49	0.04	37.75	32.57
Solyc07g009380.2.1	Xyloglucan endotransglucosylase/hydrolase 2 (XET2)	0.90	0.04	4.46	1.40	3.50	14.55
Solyc07g052480.2.1	Isocitrate lyase	0.44	0.09	3.45	1.44	2.75	6.30
Solyc07g056140.2.1	Glucose-1-phosphate adenylyltransferase	2.25	0.28	1.13	0.09	12.25	29.27
Solyc07g065900.2.1	Fructose-bisphosphate aldolase, class-I (FBA)	1.43	0.15	0.47	0.32	5.50	34.80
Solyc08g083320.2.1	Granule-bound starch synthase (GBSS)	7.28	1.74	0.99	0.46	6.25	14.53
Solyc09g009020.2.1	Enolase (ENO)	2.18	0.25	1.16	0.16	102.50	76.41
Solyc09g031970.2.1	Glycogen/starch/alpha-glucan phosphorylase	2.62	0.18	0.94	0.07	16.25	33.81
Solyc09g092330.1.1	NAD dependent epimerase/dehydratase family protein expressed	1.49	0.21	2.03	0.04	1.00	2.21
Solyc09g092500.1.1	UDP-glucosyltransferase family 1 protein (UGT1)	0.43	0.06	1.02	0.08	11.00	30.27
Solyc09g098040.2.1	Phosphoglucan water dikinase	3.86	1.34	0.85	0.19	15.50	18.86
Solyc10g007600.2.1	L-lactate dehydrogenase (LDHA)	0.12	0.02	1.60	0.21	16.75	43.94

Solyc10g085220.1.1	Mitochondrial carrier protein expressed	1.04	0.12	2.42	0.60	4.00	6.52
Solyc10g085230.1.1	UDP-glucosyltransferase (UGT)	0.31	0.05	0.88	0.02	8.00	20.53
Solyc10g085880.1.1	UDP-glucosyltransferase family 1 protein (UGT1)	0.08	0.02	0.55	0.01	39.50	50.73
Solyc12g009300.1.1	Sucrose synthase (SuSy1)	1.88	0.10	2.33	0.19	62.25	55.25
Solyc12g094640.1.1	Glyceraldehyde-3-phosphate dehydrogenase B (GAPB)	0.68	0.10	0.46	0.05	3.50	37.17
Solyc12g098600.1.1	UDP-glucosyltransferase family 1 protein (UGT1)	2.38	0.53	0.96	0.23	8.25	21.54
Solyc12g099200.1.1	Cell-wall Invertase inhibitor	2.66	0.61	1.28	0.07	9.25	56.29
Cell wall biogenesis/degradation							
Solyc03g111690.2.1	Pectate lyase	0.04	0.01	0.62	0.05	13.75	32.01
Solyc03g116230.2.1	Agglutinin isolectin I (Fragment)	2.18	0.63	1.19	0.02	5.25	10.51
Solyc03g123630.2.1	Pectinesterase (PMEU1)	1.07	0.07	2.58	0.28	47.00	42.54
Solyc04g049070.2.1	Alpha glucosidase II	0.94	0.04	0.40	0.07	14.50	17.97
Solyc05g050130.2.1	Acidic chitinase	0.44	0.10	2.10	0.34	4.75	17.55
Solyc07g005100.2.1	Chitinase II (Cht2)	4.88	0.53	1.02	0.21	16.25	28.59
Solyc07g064180.2.1	Pectinesterase (PME2.1)	4.07	1.75	0.58	0.03	8.00	36.95

Solyc07g065090.1.1	Polygalacturonase inhibitor protein	4.92	0.72	1.29	0.11	9.25	24.77
Solyc09g010860.2.1	Expansin (EXPA4)	0.18	0.09	0.86	0.22	2.00	11.41
Solyc09g014480.1.1	Polygalacturonase inhibitor protein	0.50	0.04	1.37	0.30	1.00	6.72
Solyc10g055800.1.1	Chitinase	0.58	0.16	2.61	0.63	6.50	28.57
Solyc10g055810.1.1	Endochitinase (CHI9)	0.08	0.02	2.12	0.31	4.50	29.89
Solyc10g080210.1.1	Polygalacturonase A (LePG)	0.03	0.00	0.07	0.01	49.75	49.45
Solyc11g005150.1.1	Leucine-rich repeat Extensin-like family protein (LRX)	0.62	0.08	0.47	0.05	7.25	11.27
Solyc11g008720.1.1	Beta-glucosidase G4	0.27	0.11	0.53	0.11	5.00	13.19
Solyc12g099660.1.1	Glucosidase 2 subunit beta	1.02	0.07	0.48	0.05	9.00	17.56
Cellular metabolic process							
Solyc01g090230.2.1	GRAM domain containing protein	2.95	2.16	1.27	0.07	1.00	4.11
Solyc01g097880.2.1	Cytidine deaminase-like	0.23	0.03	0.48	0.05	9.75	49.46
Solyc01g099590.2.1	Glutathione-S-transferase (GST)	2.73	0.67	0.44	0.01	2.75	19.20
Solyc01g101060.2.1	S-adenosylmethionine synthase (SAM1)	3.29	0.52	2.82	0.04	40.00	73.15
Solyc01g108560.2.1	Acetyl esterase	0.25	0.17	0.45	0.03	2.00	22.51
Solyc02g036350.2.1	1-aminocyclopropane-1-carboxylate oxidase	0.20	0.03	3.54	0.51	10.75	49.69

Solyc02g071150.2.1	DNA-binding TFAR19-related protein	0.70	0.26	0.41	0.08	8.00	58.40
Solyc02g091100.2.1	Oxalyl-CoA decarboxylase	2.11	0.10	1.01	0.08	26.25	44.12
Solyc03g025320.2.1	Hydroxycinnamoyl transferase (AAT2)	0.93	0.09	2.01	0.14	10.50	25.45
Solyc03g095900.2.1	1-aminocyclopropane-1-carboxylate oxidase-like protein (E8)	0.26	0.06	1.12	0.19	2.50	14.08
Solyc03g097700.2.1	O-methyltransferase (OMT)	0.47	0.04	0.78	0.08	13.25	42.50
Solyc03g117430.2.1	Cobalamin synthesis protein P (CobP)	0.81	0.09	0.47	0.08	11.25	31.92
Solyc03g117870.2.1	4-coumarate CoA ligase (4CL)	0.47	0.26	0.82	0.17	3.25	9.95
Solyc03g123760.2.1	Phytoene desaturase (PDS)	0.73	0.05	0.40	0.01	8.50	17.79
Solyc04g071140.2.1	Pyridoxal phosphate-dependent decarboxylase	0.42	0.21	0.87	0.15	1.00	2.90
Solyc05g052240.2.1	Chalcone isomerase (CHI)	0.38	0.10	0.63	0.12	5.00	35.36
Solyc05g052480.2.1	Multiple inositol polyphosphate phosphatase	1.10	0.45	0.19	0.04	2.75	6.57
Solyc05g053550.2.1	Chalcone synthase (CHS2)	0.25	0.18	0.67	0.09	6.50	14.78
Solyc07g006180.2.1	Tetratricopeptide repeat protein 4 homolog	0.52	0.04	0.44	0.03	10.75	52.87

Solyc07g049530.2.1	1-aminocyclopropane-1-carboxylate oxidase (ACO1)	0.15	0.04	1.08	0.28	32.25	72.54
Solyc07g056420.2.1	Glutathione S-transferase-like protein	1.25	0.21	0.29	0.04	11.00	41.02
Solyc07g056510.2.1	Glutathione S-transferase	0.45	0.19	0.24	0.07	2.50	25.12
Solyc07g061790.2.1	SOUL Heme-binding protein 2 (HEBP2)	2.85	0.24	0.84	0.06	21.75	53.82
Solyc07g062530.2.1	Phosphoenolpyruvate carboxylase 2 (PPC2)	2.89	0.35	1.26	0.16	122.00	71.14
Solyc08g005770.2.1	Alcohol acetyltransferase	0.04	0.01	0.49	0.02	22.50	43.49
Solyc08g006770.2.1	Anthocyanidin synthase (Fragment)	0.26	0.06	1.48	0.07	6.75	19.16
Solyc08g006890.2.1	Tubulin alpha-3 chain (TUB)	1.86	0.36	2.09	0.61	23.75	57.65
Solyc08g066240.2.1	Pyridoxal phosphate-dependent decarboxylase	0.06	0.02	0.39	0.03	16.25	36.20
Solyc08g075210.1.1	Acyltransferase-like protein	2.22	0.27	1.05	0.12	16.25	41.57
Solyc08g076970.2.1	Acetylornithine deacetylase or succinyl-diaminopimelate desuccinylase	2.71	0.19	1.25	0.10	30.00	59.85
Solyc08g077300.2.1	Adenylate kinase (ADK)	0.59	0.10	0.42	0.17	6.00	30.67
Solyc08g079110.2.1	Pentapeptide repeat	1.48	0.20	2.67	0.39	3.75	27.37
Solyc08g079430.2.1	Primary amine oxidase	4.96	2.33	1.92	0.49	0.75	1.87
Solyc08g080510.2.1	Replication factor C subunit 4	2.54	2.20	1.33	0.57	1.25	8.08

Solyc09g008280.1.1	S-adenosylmethionine synthase (SAM3)	1.32	0.10	2.96	0.43	9.75	57.69
Solyc09g010930.2.1	NAD-dependent epimerase/dehydratase	0.80	0.06	0.44	0.03	16.50	66.47
Solyc09g011580.2.1	Glutathione S-transferase-like protein	0.16	0.03	1.06	0.22	9.50	36.52
Solyc09g064940.2.1	Phenazine biosynthesis protein PhzF family	0.43	0.03	0.85	0.04	10.00	38.45
Solyc09g089580.2.1	1-aminocyclopropane-1-carboxylate oxidase-like protein (ACO3)	0.05	0.01	0.25	0.02	47.50	56.47
Solyc10g076510.1.1	Pyruvate decarboxylase (PDC)	5.92	2.17	0.32	0.06	23.50	35.45
Solyc10g081650.1.1	Carotenoid isomerase, chloroplastic (CRTISO)	0.30	0.04	0.42	0.02	11.00	18.98
Solyc10g084400.1.1	Glutathione S-transferase/chloride channel	2.58	0.95	0.31	0.00	15.25	66.60
Solyc10g085040.1.1	Soul heme-binding family protein (SOUL/HBP)	0.32	0.10	0.37	0.00	6.75	36.93
Solyc10g085830.1.1	O-methyltransferase 1 (OMT1)	0.31	0.03	0.50	0.06	15.25	47.85
Solyc11g013110.1.1	Anthocyanidin synthase (ANS)	0.18	0.03	1.76	0.20	15.00	42.83
Solyc11g066290.1.1	Icc family phosphohydrolase	0.47	0.03	0.65	0.04	10.00	26.28
Solyc12g011310.1.1	Glutathione S-transferase	0.45	0.22	0.16	0.00	11.25	42.46

Solyc12g044600.2.1	NADP-dependent malic enzyme, chloroplastic (ME1)	2.11	0.04	0.81	0.02	30.00	51.13
Defense response							
Solyc00g060810.2.1	Major latex-like protein	0.71	0.09	0.35	0.02	4.25	28.42
Solyc00g174340.1.1	Pathogenesis-related protein 1b (PR-1b)	0.03	0.01	28.38	2.41	16.50	55.97
Solyc01g105410.2.1	Phosphate-induced protein 1 conserved region	0.72	0.03	2.61	0.53	3.50	15.03
Solyc02g065470.1.1	Pathogenesis-related protein	1.07	0.16	2.18	0.08	9.00	44.45
Solyc03g020060.2.1	Proteinase inhibitor II (PI-II)	11.20	2.35	1.42	0.20	6.25	29.37
Solyc05g053620.2.1	F-box protein PP2-B1	0.62	0.07	2.01	0.41	3.50	26.97
Solyc06g054320.1.1	Plant disease resistance response protein	3.18	1.14	1.95	0.32	3.00	19.83
Solyc07g006380.2.1	Defensin-like protein	3.68	1.99	0.53	0.06	1.00	7.62
Solyc07g007750.2.1	Defensin protein	3.04	0.45	1.34	0.40	5.75	35.20
Solyc08g080640.1.1	Osmotin-like protein (NP24)	0.25	0.01	0.83	0.12	5.50	29.56
Solyc09g084440.2.1	Proteinase inhibitor I (PI-I)	1.58	0.17	2.36	0.89	2.00	26.57
Solyc09g090330.2.1	Harpin binding protein 1 (HrBP1)	1.24	0.17	0.48	0.04	14.75	51.09
Solyc09g091000.2.1	Major allergen Mal d 1	0.32	0.08	5.47	3.49	2.00	19.35

Lipid metabolic process							
Solyc01g006540.2.1	Lipoxygenase (LoxC)	0.06	0.01	0.34	0.07	36.50	38.28
Solyc01g088090.2.1	Hydrolase alpha/beta fold family protein	0.38	0.30	0.47	0.18	2.50	8.74
Solyc01g088400.2.1	CER1, Fatty acid hydroxylase	0.27	0.08	1.14	0.02	5.25	10.99
Solyc01g098110.2.1	Hydrolase alpha/beta fold family protein	0.80	0.25	0.46	0.13	5.25	12.17
Solyc01g099160.2.1	Lipoxygenase (CEVI34)	0.53	0.02	0.50	0.02	31.50	45.30
Solyc01g099190.2.1	Lipoxygenase (LoxB)	0.27	0.10	0.33	0.03	119.75	66.93
Solyc01g111260.2.1	Phosphatidylinositol-specific phospholipase c	2.55	0.46	1.52	0.19	8.25	35.69
Solyc02g065240.2.1	Hydrolase alpha/beta fold family protein	0.45	0.08	0.15	0.02	10.75	52.00
Solyc02g069800.1.1	CXE carboxylesterase	0.36	0.03	0.56	0.07	13.75	54.11
Solyc02g081170.2.1	Plastid-lipid-associated protein, chloroplastic (ChrC)	1.88	0.12	0.40	0.01	20.25	64.42
Solyc03g005020.2.1	Lipase	0.07	0.02	0.61	0.13	6.25	15.99
Solyc03g025720.2.1	Long-chain-fatty-acid--CoA ligase	2.32	0.23	0.58	0.06	17.25	34.61
Solyc03g065250.2.1	CER1, Fatty acid hydroxylase	0.25	0.12	2.76	1.48	1.00	2.72
Solyc04g054990.2.1	Lipoxygenase, LH2	2.28	0.24	2.73	0.12	6.50	37.39

Solyc05g051850.2.1	Inositol-3-phosphate synthase	2.91	0.19	1.34	0.11	3.00	8.34
Solyc07g061990.2.1	Solanesyl diphosphate synthase	0.66	0.06	0.47	0.03	5.25	22.05
Solyc08g014000.2.1	Lipoxygenase (LoxA)	1.41	0.02	0.38	0.03	77.50	60.14
Solyc09g091470.2.1	3-ketoacyl CoA thiolase 2	0.36	0.03	0.51	0.04	30.25	60.27
Solyc10g080900.1.1	3-oxoacyl-reductase	0.15	0.05	0.51	0.03	25.75	65.77
Solyc11g006250.1.1	GDSL esterase/lipase (G1DEX3)	0.80	0.23	2.79	0.41	9.50	31.77
Solyc12g017460.1.1	GDSL esterase/lipase At1g28590	0.76	0.08	2.38	0.34	4.00	14.09
Solyc12g056940.1.1	Acetyl-CoA carboxylase (ACC)	0.38	0.07	0.72	0.04	32.00	18.89
Oxidation-reduction process							
Solyc01g067740.2.1	Superoxide dismutase (SODCC.1)	1.04	0.10	0.43	0.07	12.75	61.84
Solyc01g073640.2.1	Uncharacterized oxidoreductase Mb1385 (yfe37)	0.90	0.06	2.34	0.03	19.25	47.30
Solyc01g103920.2.1	Ferredoxin I	0.90	0.04	0.48	0.08	2.50	48.21
Solyc02g030170.2.1	FAD linked oxidase domain protein	2.18	0.56	0.84	0.06	15.75	29.40
Solyc02g062500.2.1	2-oxoglutarate-dependent dioxygenase	0.38	0.03	0.57	0.02	35.50	66.74
Solyc02g079500.2.1	Peroxidase (TAP1)	1.30	0.12	2.37	1.10	16.00	27.61
Solyc02g086880.2.1	Formate dehydrogenase	2.68	0.28	1.02	0.13	43.50	66.93
Solyc02g087110.2.1	Alpha-dioxygenase	0.24	0.05	0.23	0.02	13.50	26.82

Solyc03g111720.2.1	Peptide methionine sulfoxide reductase msrA (E4)	0.06	0.02	0.57	0.03	17.75	52.04
Solyc03g111970.2.1	Cytochrome P450 (CYP450)	0.40	0.06	0.65	0.08	3.25	9.68
Solyc03g120720.2.1	Protein disulfide isomerase L-3b	0.97	0.07	0.23	0.05	8.75	18.03
Solyc03g121040.2.1	Taurine catabolism dioxygenase TauD/TfdA family	0.38	0.06	0.44	0.05	5.75	25.93
Solyc03g122350.2.1	Cytochrome P450 (CYP450)	0.32	0.08	0.67	0.06	6.00	25.42
Solyc04g049450.2.1	Protein disulfide isomerase L-2	0.63	0.03	0.29	0.02	11.50	24.87
Solyc04g071890.2.1	Peroxidase 4	0.46	0.04	3.40	0.25	20.25	36.57
Solyc04g080550.2.1	Phenylcoumaran benzylic ether reductase	0.46	0.01	0.32	0.04	5.75	29.55
Solyc05g005460.2.1	Nucleoredoxin 2	0.33	0.07	1.82	0.26	7.25	17.81
Solyc05g005480.2.1	Oxidoreductase zinc-binding dehydrogenase (EO)	1.43	0.03	0.47	0.05	26.00	63.27
Solyc05g005700.2.1	Aldehyde dehydrogenase 1	2.27	0.16	1.10	0.04	23.75	41.78
Solyc05g008450.2.1	Oxidoreductase FAD/NAD(P)-binding domain protein	0.86	0.14	0.46	0.02	16.50	44.04
Solyc05g054760.2.1	Dehydroascorbate reductase	2.45	0.22	1.06	0.07	21.75	79.29
Solyc06g005940.2.1	Protein disulfide isomerase	1.16	0.08	0.39	0.03	31.75	46.40
Solyc06g048410.2.1	Superoxide dismutase	2.00	0.39	0.64	0.07	6.00	25.30
Solyc06g059740.2.1	Alcohol dehydrogenase 2 (ADH2)	0.78	0.03	0.26	0.05	38.25	45.64

Solyc06g060290.2.1	Protein disulfide isomerase	0.94	0.07	0.25	0.01	24.00	44.06
Solyc07g005390.2.1	Aldehyde dehydrogenase	3.28	0.22	1.14	0.10	34.75	57.26
Solyc07g043570.2.1	Aldo/keto reductase family protein	1.90	0.27	0.48	0.05	8.00	26.62
Solyc07g047800.2.1	Short-chain dehydrogenase/reductase family protein	0.18	0.02	0.58	0.01	20.50	55.07
Solyc08g005630.2.1	Glucose-methanol-choline oxidoreductase	0.18	0.04	0.27	0.01	24.25	30.65
Solyc09g066150.1.1	Cytochrome P450 (CYP450)	0.19	0.02	0.62	0.03	16.25	34.46
Solyc10g080840.1.1	Cytochrome P450 (CYP450)	0.22	0.04	0.59	0.04	8.50	17.83
Solyc10g081440.1.1	NADH cytochrome b5 reductase	0.48	0.05	0.82	0.04	7.25	24.19
Solyc10g083650.1.1	Peroxiredoxin ahpC/TSA family (AhpC)	0.53	0.05	0.32	0.03	12.75	55.05
Solyc10g087010.1.1	cytochrome P450 (CYP450)	3.77	2.77	0.91	0.13	1.75	6.86
Solyc11g010960.1.1	Alcohol dehydrogenase	1.24	0.05	6.99	2.26	10.00	25.70
Solyc11g066390.1.1	Superoxide dismutase (SODCP.2)	1.06	0.07	0.44	0.06	12.25	57.15
Solyc11g069400.1.1	Protein disulfide isomerase L-2	1.12	0.09	0.27	0.06	11.25	23.02
Solyc11g069800.1.1	cytochrome P450 (CYP450)	0.49	0.03	0.63	0.06	20.25	42.89
Solyc11g069860.1.1	Glutaredoxin	0.83	0.07	0.35	0.09	2.00	26.05
Solyc12g010950.1.1	Alcohol dehydrogenase superfamily, zinc-containing	0.38	0.02	1.57	0.17	5.00	22.40

Solyc12g013690.1.1	Aromatic-ring hydroxylase-like	0.28	0.07	0.51	0.05	11.00	34.03
Solyc12g094620.1.1	Catalase (CAT1)	0.39	0.02	1.01	0.08	55.25	68.39
Photosynthesis							
Solyc01g007330.2.1	Ribulose bisphosphate carboxylase large chain (rbcL)	0.73	0.03	0.35	0.09	69.50	60.27
Solyc01g007500.2.1	Photosystem II CP47 chlorophyll apoprotein (PsbB)	1.49	0.25	2.99	0.63	18.75	26.67
Solyc01g105030.2.1	Chlorophyll a-b binding protein, chloroplastic (CAP10A)	1.28	0.03	4.17	0.18	6.00	24.80
Solyc01g106090.2.1	Photosystem II oxygen evolving complex protein (PsbP)	1.08	0.05	2.83	0.72	5.00	19.78
Solyc05g005490.2.1	Carbonic anhydrase (CA1)	0.24	0.04	0.54	0.03	25.00	65.67
Solyc06g060340.2.1	Chloroplast photosystem II-associated protein (PSBS)	1.05	0.01	0.38	0.02	10.00	23.91
Solyc06g063370.2.1	Chlorophyll a-b binding protein 1A, chloroplastic	1.54	0.14	4.27	0.80	12.00	44.23
Solyc08g013670.2.1	Photosystem I reaction centre subunit N	1.67	0.08	2.76	0.37	6.50	37.12
Solyc09g014520.2.1	Chlorophyll a-b binding protein 6A, chloroplastic	1.48	0.07	4.05	0.48	11.75	39.82

Solyc09g015290.1.1	Photosystem I P700 chlorophyll a apoprotein A1	1.09	0.10	2.11	0.22	1.00	11.25
Solyc09g063130.2.1	Photosystem I reaction center subunit IV A	0.87	0.04	2.05	0.28	7.00	46.78
Solyc10g007690.2.1	Chlorophyll a-b binding protein 8, chloroplastic	1.44	0.04	2.62	0.36	4.75	25.18
Protein metabolic process							
Solyc01g028810.2.1	Chaperonin Cpn60	0.65	0.05	0.40	0.04	63.75	64.98
Solyc01g079610.2.1	Heat shock protein DnaJ	0.84	0.08	2.35	0.72	4.50	17.83
Solyc01g080410.2.1	Peptide methionine sulfoxide reductase msrB	0.96	0.04	0.43	0.04	0.75	28.33
Solyc01g088610.2.1	Chaperonin Cpn10	0.93	0.05	0.42	0.02	3.00	37.40
Solyc01g100380.2.1	Calreticulin 2 calcium-binding protein	0.93	0.07	0.38	0.05	13.25	36.63
Solyc01g103450.2.1	Chaperone DnaK	0.74	0.10	0.46	0.03	40.75	56.15
Solyc02g077670.2.1	Chaperone protein dnaJ 2	0.41	0.05	0.32	0.12	6.25	26.60
Solyc02g088610.2.1	ATP-dependent chaperone ClpB	0.54	0.05	0.31	0.04	65.50	56.61
Solyc03g082890.2.1	Pentapeptide repeat protein	1.01	0.08	2.13	0.25	5.50	29.51
Solyc03g098780.1.1	Kunitz-type protease inhibitor (KTI3)	2.55	0.65	1.86	0.33	1.00	5.43

Solyc03g118040.2.1	Calcium-binding protein Calnexin (CNX61.0)	0.79	0.04	2.18	0.25	27.50	45.96
Solyc04g079470.2.1	Serpin (Serine protease inhibitor)	0.97	0.11	2.37	0.19	0.50	5.83
Solyc05g010670.2.1	Chaperone protein htpG (HSP90)	0.54	0.09	0.39	0.01	42.25	52.00
Solyc05g056230.2.1	Calreticulin 2 calcium-binding protein	1.02	0.09	0.21	0.01	15.75	36.43
Solyc06g083190.2.1	Peptidyl-prolyl cis-trans isomerase	0.57	0.08	0.40	0.02	39.25	59.10
Solyc07g042250.2.1	Chaperonin Cpn10 (CPN21)	0.57	0.09	0.43	0.03	17.25	66.11
Solyc07g062060.2.1	Peptide methionine sulfoxide reductase msrB	0.75	0.11	0.38	0.04	5.75	39.36
Solyc09g057670.2.1	Peptidyl-prolyl cis-trans isomerase	0.57	0.03	0.09	0.02	6.25	48.15
Solyc10g081240.1.1	GrpE nucleotide exchange factor	0.69	0.25	0.24	0.05	15.00	41.05
Solyc11g020040.1.1	Chaperone DnaK (HSP70)	0.84	0.09	0.27	0.02	52.00	56.39
Solyc11g021060.1.1	Proteinase inhibitor (ARPI)	1.23	0.21	2.66	1.04	1.25	8.72
Solyc11g022590.1.1	Kunitz trypsin inhibitor 4 (Fragment)	4.63	0.93	4.65	0.78	7.25	41.22
Solyc11g069790.1.1	Chaperonin Cpn60	0.69	0.09	0.34	0.02	42.50	60.80
Solyc11g071830.1.1	Chaperone protein DnaJ	0.76	0.17	0.34	0.08	3.75	18.12
Solyc12g056850.1.1	Co-chaperone protein DnaJ	0.86	0.09	0.45	0.09	1.00	6.14
Proteolysis							

Solyc01g068390.2.1	Zinc finger family protein	0.69	0.44	3.28	3.30	1.50	3.10
Solyc01g087850.2.1	Subtilisin-like protease	0.32	0.04	0.64	0.08	10.75	16.03
Solyc01g108490.2.1	Serine carboxypeptidase 1	1.81	0.37	2.84	1.30	8.50	18.46
Solyc01g111400.2.1	Subtilisin-like protease	1.34	0.25	2.25	0.27	7.50	14.02
Solyc02g068380.2.1	N-carbamoyl-L-amino-acid amidohydrolase	0.71	0.12	0.41	0.08	4.25	12.02
Solyc03g119690.1.1	Aspartic proteinase nepenthesin-1	2.21	0.14	1.89	0.36	4.00	10.86
Solyc03g121270.2.1	IAA-amino acid hydrolase	1.19	0.09	0.32	0.05	13.75	35.11
Solyc04g007120.2.1	UV excision repair protein RAD23	0.40	0.13	0.73	0.11	5.00	20.48
Solyc04g015340.2.1	Serine carboxypeptidase K10B2.2	0.62	0.04	0.49	0.05	5.50	17.27
Solyc04g077650.2.1	Serine carboxypeptidase 1	0.34	0.05	0.49	0.08	7.25	17.05
Solyc04g077670.2.1	Serine carboxypeptidase 1	1.40	0.34	2.58	0.35	2.25	8.64
Solyc06g073060.2.1	Iaa-amino acid hydrolase 6	0.96	0.02	0.30	0.05	11.50	31.63
Solyc07g008900.2.1	Subtilisin-like serine protease	2.82	0.73	1.48	0.34	3.25	6.43
Solyc08g079870.1.1	Subtilisin-like protease (P69B)	0.11	0.03	4.44	0.91	18.00	30.54
Solyc08g082820.2.1	Heat shock protein 70 (BiP/grp78)	0.94	0.05	0.41	0.01	17.50	51.61
Regulation of gene expression							
Solyc01g100760.2.1	Susceptibility homeodomain transcription factor (Fragment)	0.10	0.02	0.87	0.11	8.25	47.56

Solyc01g111280.2.1	Cold shock protein-1	3.61	1.74	2.07	0.84	4.00	43.42
Solyc01g112060.2.1	NmrA family protein	1.47	0.15	2.09	0.04	5.50	17.75
Solyc02g068200.1.1	TCP family transcription factor	0.43	0.12	0.56	0.07	2.00	8.32
Solyc02g070500.1.1	Susceptibility homeodomain transcription factor (Fragment)	0.48	0.15	0.97	0.17	7.50	44.22
Solyc07g006560.2.1	Hypersensitive response assisting protein	3.10	1.17	5.36	0.77	6.75	50.00
Solyc07g006570.2.1	S8-RNase (Fragment)	2.13	0.65	6.35	0.52	7.75	29.83
Solyc07g049150.2.1	Ribonuclease III family protein	0.41	0.20	8.56	3.94	3.00	12.78
Solyc09g092380.2.1	Adenosylhomocysteinase (SAHH)	0.47	0.12	0.47	0.02	60.75	63.82
Solyc10g051390.1.1	RNA-binding glycine-rich protein-1b	0.81	0.06	4.79	3.03	6.75	62.29
Regulation of translation							
Solyc01g095900.2.1	Protein TIF31 homolog	0.48	0.13	0.81	0.04	5.25	6.47
Solyc02g081810.2.1	tRNA pseudouridine synthase B	1.13	0.27	2.46	1.03	6.50	13.53
Solyc03g117330.2.1	Prolyl-tRNA synthetase	1.01	0.37	2.40	1.72	1.25	21.97
Solyc07g006030.2.1	Protein TIF31 homolog	0.47	0.10	0.69	0.10	10.00	7.47
Solyc07g018360.2.1	Elongation factor Ts	0.71	0.09	0.46	0.19	25.50	28.77
Solyc11g069700.1.1	Protein biosynthesis elongation factor EF1A	0.14	0.03	2.46	0.31	3.00	60.07

Response to stimulus							
Solyc01g100370.2.1	Universal stress protein	0.88	0.13	0.21	0.02	10.75	47.89
Solyc01g102960.2.1	class IV heat shock protein Hsp20	0.65	0.11	0.04	0.01	15.75	57.41
Solyc02g084850.2.1	Dehydrin	21.93	10.65	0.52	0.30	2.00	22.31
Solyc03g007890.2.1	Heat shock protein Hsp90	0.61	0.22	0.29	0.03	61.00	63.81
Solyc03g082420.2.1	Heat shock protein Hsp20	1.47	1.18	0.09	0.00	23.75	54.47
Solyc03g113930.1.1	class IV heat shock protein Hsp20	0.89	0.38	0.04	0.01	6.75	44.81
Solyc03g116390.2.1	Late embryogenesis abundant protein (LEAP)	8.13	2.26	0.30	0.10	6.00	42.25
Solyc03g117630.1.1	Heat shock protein 70	0.84	0.59	0.17	0.01	17.00	55.66
Solyc03g123540.2.1	class II heat shock protein Hsp20	1.29	0.38	0.45	0.05	4.50	34.20
Solyc04g014480.2.1	class I heat shock protein 3 Hsp20	1.02	0.27	0.32	0.01	10.00	59.48
Solyc04g014600.2.1	Universal stress protein family protein	1.64	0.37	0.39	0.03	14.00	55.86
Solyc04g071620.2.1	ABA/WDS induced protein, ASR4 (Fragment)	3.10	0.54	1.77	0.37	21.50	65.41
Solyc05g014280.2.1	Heat shock protein Hsp20 (VIS1)	0.19	0.05	0.17	0.00	18.50	51.81
Solyc05g015390.2.1	Rubber elongation factor-like stress related protein 1	0.51	0.17	0.36	0.12	8.00	38.48

Solyc05g056580.2.1	Dehydration-responsive family protein	1.27	0.12	2.37	0.32	7.50	12.79
Solyc06g009050.2.1	Universal stress protein	0.79	0.16	0.40	0.09	7.00	18.48
Solyc06g036290.2.1	Heat shock protein 90 (Fragment)	0.92	0.09	0.40	0.01	12.50	62.03
Solyc06g076520.1.1	class I heat shock protein Hsp20	2.07	0.25	0.35	0.02	26.75	77.92
Solyc06g076560.1.1	class I heat shock protein Hsp20 (HSP17.6)	1.79	0.97	0.19	0.02	6.75	77.92
Solyc06g076570.1.1	class I heat shock protein Hsp20	0.83	0.15	0.43	0.15	12.50	75.16
Solyc07g043560.2.1	Heat shock protein 4 (HSP70)	1.04	0.06	0.33	0.07	15.75	23.54
Solyc07g064160.2.1	Thiamine biosynthesis Thi4 protein	2.17	0.09	0.98	0.19	16.50	37.85
Solyc08g016670.2.1	Calcyclin-binding protein (CACYBP)	1.01	0.08	0.36	0.03	10.50	55.25
Solyc08g062340.2.1	Class II small heat shock protein Le-HSP17.6	1.14	0.23	0.45	0.02	11.00	59.20
Solyc08g062450.1.1	class II heat shock protein Hsp20	2.53	0.22	0.38	0.03	30.50	61.08
Solyc08g075870.2.1	Dehydration-responsive family protein-like	2.01	0.40	4.16	0.30	13.75	25.75
Solyc08g076480.2.1	Plastid lipid-associated protein 3, chloroplastic	2.76	0.60	0.58	0.01	17.00	53.71
Solyc08g078510.2.1	GRAM-containing/ABA-responsive protein (Fragment)	0.35	0.05	0.76	0.03	6.25	30.37

Solyc08g078700.2.1	Heat shock protein 22 (MTSHP)	1.42	0.32	0.36	0.02	17.50	54.05
Solyc09g015000.2.1	class I heat shock protein Hsp20	2.59	2.35	0.29	0.05	10.25	59.89
Solyc09g015020.1.1	class I heat shock protein 3 Hsp20	2.03	0.62	0.28	0.01	13.00	48.38
Solyc09g075950.1.1	Heat shock protein 1	0.98	0.30	0.36	0.00	20.75	41.49
Solyc11g020330.1.1	class IV heat shock protein Hsp20 (er-sHSP)	1.48	0.40	0.04	0.00	11.75	49.47
Solyc11g066100.1.1	Heat shock protein 70	1.02	0.14	0.35	0.05	95.25	75.65
Solyc12g013700.1.1	Aluminum-induced protein-like protein	0.20	0.03	0.94	0.03	8.25	35.04
Solyc12g042830.1.1	class I heat shock protein, HSP20-like chaperone	0.50	0.13	0.33	0.03	1.75	24.05
Signal transduction							
Solyc01g008850.2.1	CBL-interacting protein kinase 18	0.45	0.04	1.06	0.11	7.75	21.80
Solyc01g097770.2.1	Serine/threonine protein kinase	2.38	0.11	1.97	0.43	10.25	11.62
Solyc05g055860.2.1	Serine/threonine-protein kinase	4.42	1.08	1.31	0.29	0.50	2.47
Solyc07g007140.2.1	Serine/threonine-protein kinase B-raf	0.66	0.37	0.44	0.32	1.00	2.21
Solyc07g056150.2.1	Ras-related protein Rab-2-A	1.65	0.43	2.03	0.76	1.00	56.61
Solyc10g052880.1.1	LRR receptor-like serine/threonine-protein kinase, RLP	0.40	0.05	1.06	0.03	7.00	18.36

Solyc11g056680.1.1	LRR receptor-like serine/threonine-protein kinase, RLP	2.77	0.17	0.70	0.06	23.25	44.78
Transport							
Solyc01g111040.2.1	EF-Hand containing protein-like	0.74	0.03	0.40	0.01	21.50	48.87
Solyc02g032930.2.1	B-cell receptor-associated protein 31-like containing protein	0.46	0.15	0.70	0.08	10.75	36.15
Solyc03g082660.2.1	Major facilitator superfamily domain containing protein 5 (MFSD)	1.04	0.06	2.93	0.37	3.25	7.63
Solyc03g117300.2.1	Nodulin-like protein	1.07	0.10	2.04	0.40	1.50	3.55
Solyc03g120980.2.1	ATP-binding cassette transporter	0.42	0.06	1.05	0.16	10.25	9.05
Solyc04g014570.2.1	Transmembrane 9 superfamily protein member 1	1.34	0.09	2.09	0.62	2.25	11.91
Solyc05g054210.2.1	Proline-rich protein	2.34	0.31	1.04	0.11	2.50	11.97
Solyc06g076750.2.1	Peptide transporter	1.61	0.14	2.20	0.07	4.25	8.63
Solyc07g005210.2.1	Outer membrane lipoprotein blc (TIL)	1.39	0.48	0.41	0.02	4.25	31.08
Solyc07g052470.2.1	Syntaxin	0.36	0.09	0.64	0.05	6.75	23.28
Solyc08g074480.1.1	Plant lipid transfer protein and hydrophobic protein	0.39	0.10	0.81	0.06	1.00	8.59
Solyc08g081910.2.1	V-type proton ATPase subunit E	3.30	0.83	0.95	0.12	24.25	54.76

Solyc09g015650.2.1	Non-green plastid inner envelope membrane protein	20.99	7.88	1.44	0.28	5.50	18.08
Solyc10g075090.1.1	Non-specific lipid-transfer protein (LE16)	6.19	5.40	0.99	0.20	4.25	45.04
Solyc10g075110.1.1	Non-specific lipid-transfer protein (TSW12)	5.02	1.16	0.50	0.34	1.25	37.07
Solyc11g051160.1.1	Phosphatidylinositol transfer protein SFH5	0.33	0.05	0.63	0.04	19.75	39.22
Solyc12g010320.1.1	Lipocalin	0.37	0.06	0.59	0.05	14.50	43.92
Solyc12g055800.1.1	V-type ATP synthase alpha chain	2.35	0.48	1.45	0.08	97.50	76.48
Unknown							
Solyc02g086460.2.1	Unknown Protein	0.19	0.05	1.57	0.21	83.00	31.26
Solyc04g080540.2.1	ST225	0.68	0.14	0.28	0.02	6.00	46.63
Solyc04g081330.2.1	Chromosome 11 contig 1 DNA sequence. (Fragment)	0.89	0.04	0.34	0.02	3.00	16.55
Solyc06g063240.2.1	Os03g0169000 protein	1.52	0.36	4.11	0.26	13.75	35.90
Solyc06g066030.2.1	Os02g0200800 protein (Fragment)	1.12	0.14	2.29	1.26	0.50	3.47
Solyc09g008970.1.1	Unknown Protein	0.36	0.15	0.26	0.03	5.75	44.30

[a] Accession number from the International Tomato Annotation Group release version 2.4.

[b] The average fold change of protein expression levels in *vif* versus wild-type at 38 days post-anthesis (dpa) from three independent biological replicates. The meaningful cut-off was fixed at 2 fold corresponding to the iTRAQ ratio of >2.0 for up-regulation and <0.5 for down-regulation.

[c] The average fold change of protein expression levels in *vif* versus wild-type at 41 dpa from three independent biological replicates. The meaningful cut-off was fixed at 2 fold corresponding to the iTRAQ ratio of >2.0 for up-regulation and <0.5 for down-regulation.

[d] The average number of unique peptides identified (95% confidence) from three independent biological replicates.

[e] The average sequence coverage of amino acid for the identified proteins from three independent biological replicates.

Supplemental Table S7. *Primers for qRT-PCR analysis of selected genes identified in iTRAQ*

Accession Number	Primer	Sequence
Solyc03g123760	qPDS-F	TTGACAGAAAACTGAAGAACACATA
	qPDS-R	TGCAAAAACCAATTCCAACATAGAC
Solyc10g081650	qCRTISO-F	TCGTGTTGCAGCTGACTTAGGG
	qCRTISO-R	AGAAGAGCACTGTCCAGCACATC
Solyc07g049530	qACO1-F	ACGGGAAGTACAAGAGTGTGCTG
	qACO1-R	ACATTCGTGTCCCGTCTGTTTGTG
Solyc03g111720	qE4-F	TGCCCGTATTCCAATCTCCT
	qE4-R	CTGCTTACAACCTCTGCCCC
Solyc09g089580	qE8-F	GATGTTCCTCCTACACCCGGTTCT
	qE8-R	TTCACTGTGGTTGCGCGATATTTT
Solyc01g101060	qSAM1-F	AGGCAGGCTGCAAAGAGTATCG
	qSAM1-R	GGCACACCGATGGCATAAGATACC
Solyc09g008280	qSAM3-F	ACTTGCTCGCCGCTGTATTGTG
	qSAM3-R	ACGGAAAGTGGTTCAGCCACAC
Solyc01g006540	qLOXC-F	CTTTCCAAATAGGCCAACAACTGC
	qLOXC-R	CCATTCCTCAGCTGTTGGATCCTC
Solyc09g007910	qPAL-F	TGTTGGACCTAATGGCGAGAAGC
	qPAL-R	GTAACACCAGCCACATGAAACGC
Solyc03g083910	qVI-F	TCCTTCCCTTTGCAAGACTTGT
	qVI-R	TCTCCCTCTTCCCTTTCTTGATG
Solyc10g080210	qLePG-F	TGGACAAGTATGGTGGCCAAGTTC
	qLePG-R	TCCAGAAGGTTAAGGCCGTTGG
Solyc01g008710	qMAN4-F	TTTGGCAAGTATTGGGCCAAGG
	qMAN4-R	CTAGAAGTTGATGGGCTCTCTTGC
Solyc07g064180	qPME2.1-F	TTCCACTCTGCCACTCTTGCTG
	qPME2.1-R	AGCTTGGTGTTTAGCTGGTCCTG

Solyc01g104950	qXYLOSIDASE-F	GATATCACAATCCAGGTGGAAGGC
	qXYLOSIDASE-R	ACAGTTGGACCTTTGTAGAACCTG
Solyc09g010860	qEXPA4-F	TTATACCGGCGGACCATGGCAAAC
	qEXPA4-R	AGCTCCACCCATAGTTCCAGATGC