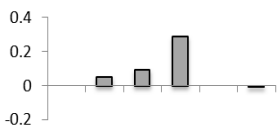
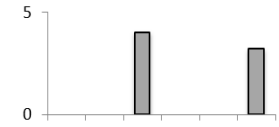
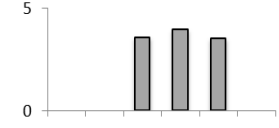
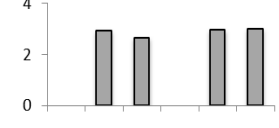
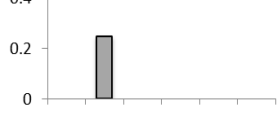
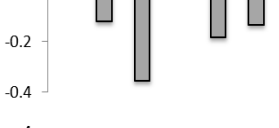
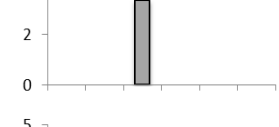
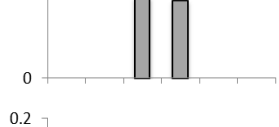
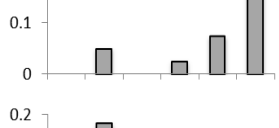
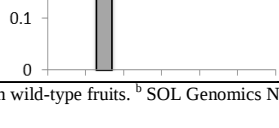


Supplementary Table S1. List of unique proteins identified from wild-type fruits by MS/MS analysis

Functional Categories	Spot ID ^a	SOL ID ^b	Protein Name	Stage kinetics ^c						Score	NP ^d	% coverage	Thr. Mw/ pI	Exp. Mw/ pI
				C	24h	48h	72h	96h	120h					
Metabolism	*SRP 219	Solyc02g062500.2.1	2-oxoglutarate-dependent dioxygenase				3.5			138	3	9	36.73/5.17	47.26/5.01
	SRP 556	Solyc01g109300.2.1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase		0.3	0.6	0.4	0.1	0.1	265	28	24	52.14/5.38	68.5197/5.62
	SRP 290	Solyc06g053200.2.1	6-phosphogluconolactonase			3.5				284	18	30	28.70/5.22	41.95/5.15
	*SRP 215	Solyc01g108560.2.1	Acetyl esterase		-0.02				0.02	59	2	8	33.700/5.55	50.95/4.97
	*SRP 313	Solyc03g083910.2.1	Acid beta-fructofuranosidase		0.25					584	10	16	71.602/5.54	55.56/5.28
	SRP 507	Solyc09g092380.2.1	Adenosylhomocysteinase		0.3	0.4	0.4	0.3	-0.1	940	51	26	53.63/5.57	47.12/5.76
	*SRP 324	Solyc03g113800.2.1	Betaine aldehyde dehydrogenase		0.1		-0.1		0.1	216	13	6	53.63/5.57	62.67/5.16
	SRP 169	Solyc09g09020.2.1	Enolase		-0.25	-0.15		-0.1	-0.15	432	15	17	48.05/5.68	21.22/5.08
	SRP 220	Solyc09g064940.2.1	Phenazine biosynthesis protein PhzF family		0.1	-0.4		-0.1	-0.1	424	41	34	32.56/5.04	46.59/5.04
	*SRP 382	Solyc01g111120.2.1	Triosephosphate isomerase		2.8					137	3	11	35.043/6.45	35.17/5.36
Protein folding, modification, degradation	*SRP 505	Solyc08g080790.1.1	Carboxyl-terminal proteinase					0.5		33	1	1	46.89/6.52	59.38/4.38

Redox homeostasis	SRP 212	Solyc04g015340.2.1	Serine carboxypeptidase K10B2.2		92	6	6	52.596/5.71	41.30/4.98
	*SRP 499	Solyc07g056490.2.1	Glutathione transferase		33	1	3	25.594/5.42	33.64/6.95
	*SRP 1206	Solyc01g007740.2.1	Peroxiredoxin		56	2	7	29.412/6.18	30.85/4.64
Signalling	*SRP 305	Solyc01g100320.2.1	Thioredoxin/protein disulfide isomerase		81	4	13	39.886/5.43	51.51/5.33
	*SRP 464	Solyc05g053620.2.1	F-box protein PP2-B1		41	2	14	19.097/5.63	22.55/5.70
	*SRP 0105	Solyc01g099770.2.1	Translationally-controlled tumor protein homolog		56	2	11	19.015/4.55	32.36/4.69
Stress Response	*SRP 878	Solyc03g093360.2.1	Universal stress protein family protein		89	2	12	19.84/6.31	28.07/6.88
	SRP 1002	Solyc03g093360.2.1	Wound/stress protein		79	2	6	19.905/6.29	12.06/6.93
Transcriptional regulator & Chromatin remodelling	*SRP 742	Solyc02g070500.1.1	Susceptibility homeodomain transcription factor (Fragment)		57	1	11	17.00/6.20	23.43/6.41
Transport	SRP 402	Solyc01g111760.2.1	V-type ATP synthase beta chain		101	10	21	53.40/5.03	48.71/5.46

^a Spot number as given on the 2-D gel images. SRP, storage responsive protein in wild-type fruits. ^b SOL Genomics Network ID. ^c Normalized protein expression value for different timepoints. ^d NP represents the number of peptides