

Supplementary Materials

Supplementary Figures



Figure S1. Transversal sections of L1 leaves from not-infected and infected plants. Images were obtained on fresh transverse thin sections of the main vein of L1 leaflet. A,B: Wild-type (WT), C,D: *SUT1*-AS, E,F: *SUT2*-AS transversal main vein sections of not-infected (NI) and infected (IF) plants respectively. Vascular tissues exhibit a typical organization with xylem vessels surrounded by abaxial and adaxial phloem. adp, adaxial phloem, abp, abaxial phloem, xy, xylem, pc, parenchyma cells. Bar, 100 µm.

MDPI



Figure S2. Amounts of sugars and starch in the leaves in response to the phytoplasma infection. Heat map and ANOVA for starch and soluble sugar contents at three leaf levels (L1, L4 and L6), sampled at 18 days after grafting. Left panel: the mean values for each compound and each genotype in not-infected (NI) and infected (I) plants. Data are expressed in nmol mg⁻¹ of fresh weight. Right panel: *p* values obtained by two-way ANOVA for each leaf level (*, *P* < 0.05; ***, *P* < 0.001; ns, not significant), with Inf: infection effect, G: genotype effect and G x Inf: genotype per infection interaction effect.



Figure S3. Transcript profiles of genes in not-infected *AS* plants compared to wild-type (WT) plants in L1 and L4 leaves. In A: *FRK* genes, in B, *GLO00/GOX2* gene (marker of the photorespiration), in C, *ICL* and *MLS* genes (markers of the glyoxylate cycle), and in D: *GLYR1* and *GLYR1* genes. Histograms show for each gene mean response +/- *SE* (*n*=4). Y-axis: Relative transcript accumulation, reported to the mean value of WT plants set to 1, Y-axis is drawn with a log₂ scale. RU: relative units for content. *P*-values: *, P < 0.05; **, P < 0.01; ***, P < 0.001. ns, not significant.



Figure S4. Enrichment of the exudates in phloem sap. The ratio of sucrose relative to soluble sugars (sucrose, fructose and glucose) is 0.97 in non-infected plants (NI) and to 0.95 in infected plants (I), showing that sucrose is the main sugar found in the exudate. High values for sucrose demonstrated that the exudates are enriched in phloem sap exudates [1]. The presence of hexoses could indicate minor contamination by apoplasmic fluids or invertase activity in the exudates during the period of exudation.



Figure S5. Workflow of metabolite data treatments. Workflow consists in data pairwise comparisons to verify homeostasis between samples, log₂ transformation, LOWESS normalization and statistical analysis. This procedure reveals the variations of exudation rates and corrects for dilution effects. RU: relative units

Supplementary Tables

Table S1. Symptoms after infection by '*Ca* Phytoplasma solani' in WT, *SUT1*-AS and *SUT2*-AS plants Number of plants for each class of symptoms. The classes of symptoms, from 0 to 4, correspond to no symptoms (class 0) to small crook-shaped and chlorotic leaves (class 4) (see details in the main text). Data were obtained on 4 plants. The first visible symptoms appeared at 17 DAG and the symptoms were recorded at 3 dates after grafting (DAG: days after grafting) from 18 to 27 DAG. Above panel: number of plants for each class of symptoms. Bottom panel: Kruskal Wallis tests followed by Dunn test performed on the symptoms level (classes from 0 to 4) for each date.

	WT	SUT1-AS	SUT2-AS	WT	SUT1-AS	SUT2-AS	WT	SUT1-AS	SUT2-AS
Class		18 DAG			24 DAG			27 DAG	
0	0	3	0	0	0	0	0	0	0
1	0	1	0	0	0	0	0	0	0
2	1	0	0	0	2	0	0	1	0
3	1	0	4	1	2	2	0	2	1
3.5	0	0	0	0	0	0	1	1	0
4	2	0	0	3	0	2	3	0	3

Kruskal Wallis tast a value	18 DAG	24 DAG	27 DAG
Kruskal Wallis test <i>p</i> -value	0.0207 *	0.0505	0.0455 *
Post hoc Dunn test adjusted with			
the Holm method	18 DAG	24 DAG	27 DAG
WT vs <i>SUT1</i> -AS	0.0304 *	0.0592	0.069
WT vs <i>SUT2</i> -AS	0.7188	0.5963	0.7915
SUT1-AS vs SUT2-AS	0.054	0.1433	0.0891

Table S2. Exudation rate of metabolites identified in the phloem-enriched exudates of non-infected and infected plants.



	Conten	t : mean	+/- SE										Student	t's t-test	(<i>p</i> -value	(î				Fold ch	ange (lo	og2)				
	Mean +/-5	SE for each	group (in r	elative un	its, RU)								<i>p</i> -value co	olor scale:		0.001	0.005	0.01	0.05	Fold cha (negativ	nge color s e values i	scale: in blue, po	n Sitive vali	AIN 0 Les in red)	000	IAX
	Metabol	ite conten	t (express	sed in rela	atve units,	-							INFEC	TION EFFEC genotype	Tper	Genotype in NI pl	e effect ants	Genotype in I pla	e effect ants	INFEC	TION EFFE genotype	CT per	Genotype in NI pl	effect (ŝenotype in I pla	effect nts
	March	ې د	SM SCOM		thug t	ت پير	tinsat	1.5K	thist	لا مىرد	Unsal	1.5K	TW 2V I TW IN	I 2A-LTU29J 2A-LTU29J 2 IN	I SA-STU251 2	2A-LTU29J IN TW 2V IN	2A-STU25J IN TW 2V IN	I 2A- 17U29. I TW 2V	I 2A- STU29	IN TW 2V I TW	I 2A-LTU25J 2 2A-LTU25J 2 IN	I SA-STUS51 SA-STUS512 IN	2A-LTU29J IN TW 2V IN	2A-STU25J IN TW 2V IN	I ZA- LTUZ9. I TW 2V	I 2A- STUS9. I TW 2V
	INIEan	25 25 25	INIEAN	S 11 1	NIEan	SE SE	Intean a	¥ 50	Mean	SE S 2 2 2 5 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Iviean	SE SE		N 1	A 000	1 000 0		1	7	10010	1	x 4			7	7
AlphaAlan Asparagine	2.4944 3.4445	0.2633	3.1618	0.3078	3.4557	0.2624	2.9587	0.2921	3.2636	0.3708	3.4723	0.3554	0.1493 0.4986	0.2790	0.6952	0.9804	0.6900	0.6741	0.5258	-0.2826	-0.4970	0.2087	0.0113	0.1809	0.2031 0	.3104
Aspartate	2.7180	0.2568	3.3349	0.1437	3.3874	0.1263	3.3208	0.1013	3.4958	0.1720	3.1504	0.1362	0.0492	0.6883	0.1414	0.0375	0.0271	0.9393	0.3723	0.6169	-0.0666	-0.3454	0.6694	0.7778 4	0.0140 -0	0.1845
BetaAlanir	3.5052	0.1591	3.0668	0.1853	3.0860	0.2849	3.0325	0.1302	2.7140	0.2104	2.7987	0.1611	0.1006	0.8496	0.7511	0.1973	0.0111	0.8816	0.2932	-0.4384	-0.0535	0.0846	-0.4192	0.7912	0.0343 -0	0.2682
Glutamate	4.3962	0.2008	3.4276	0.1633	3.2689	0.1785	3.6527	0.1587	4.6466 3.7474	0.2269	4.0383	0.1806	0.9901	0.1308	0.3840	0.5580	0.3167	0.3396	0.8043	-0.0033	0.3838	-0.2583	-0.4/03	0.3166	0 1202	0.0615
Glutamine	3.8238	0.2908	4.2272	0.2220	4.1693	0.2025	3.5868	0.1174	4.6777	0.2294	3.9097	0.3290	0.2835	0.0288	0.0856	0.3932	0.0398	7950.0	0.4370	0.4034	-0.5825	-0.7680	0.3455	0.8539	0.6405 -0	0.3175
Glycine	3.1610	0.1548	3.2545	0.3295	3.3040	0.2401	3.2339	0.2178	3.7032	0.1553	3.1388	0.3185	0.8017	0.8383	0.1423	0.6106	0.0318	0.9583	0.8072	0.0935	-0.0701	-0.5644	0.1430	0.5422 4	0.0206 -0	0.1156
Isoleucine	1.9107	0.0981	2.4601	0.1734	2.1763	0.0661	2.5626	0.1967	2.4778	0.2521	2.5375	0.2332	0.0143	0.1975	0.8681	0.1355	0.0480	0.7059	0.7966	0.5494	0.3864	0.0597	0.2656	0.5672 C	.1026 0	.0774
Leucine	2.0972	0.1036	2.3241	0.1741	2.6149	0.2935	2.3096	0.5168	2.6578	0.1424	2.2311	0.0830	0.2594	0.6587	0.0546	0.0672	0.0078	0.9735	0.6466	0.2270	-0.3052	-0.4268	0.5177	0.5607	0.0145 -0	0.0931
Lysine	1.8198	0.1160	1.7912	0.1050	1.8217	0.3536	1.4568	pu	2.0222	0.1411	1.6529	0.0395	0.9053	pu	0.2028	0.9951	0.2870	pu	0.3428	-0.0286	-0.3650	-0.3693	0.0019	0.2024	0.3345 -0	0.1383
Dhenvlalar	1./2/9	0.1389	2.2549	9861.0	2.1504	0112.0	2.5834	0.3250	1.8954	0.3283	2.2349	0.4269	0.3386	0.4377	0.0971	0.4121	0.4814	0 7966	0.2094	-0.4970	0.4329	0.3394	-0 2265 -0 2265	J 2174 J	- 2825.	0.0200
Proline	3.3681	0.3381	3.8425	0.1439	4.3158	0.2347	3.6358	0.2444	3.4243	0.2441	3.3615 (0.1923	0.1989	0.0748	0.8476	0.0480	0.8951	0.4781	0.0631	0.4744	-0.6801	-0.0627	0.9477	0.0562	0.2067 -0	0.4809
Serine	4.2591	0.1173	3.7541	0.3039	3.4836	0.0480	3.8812	0.2971	4.2768	0.3507	3.7694	0.2224	0.1471	0.2159	0.2452	0.0001	0.9627	0.7724	0.9683	-0.5050	0.3975	-0.5074	-0.7755	0.0177 0	.1271 0	.0153
Threonine	2.9023	0.1199	2.2516	0.3531	2.0467	0.1970	2.5227	0.0979	2.7445	0.0799	2.4620	0.0979	0.0509	0.2131	0.0482	0.0028	0.2947	0.5982	0.4940	-0.6508	0.4760	-0.2825	-0.8557	0.1579	.2712 0	.2104
Tyrosine Valine	2.7189 2.4457	0.2705 0.0659	2.0965 2.1240	0.3709	2.4976 2.7747	0.1406 0.0675	1.8523 2.0710	0.2475 0.1325	2.5863	0.1570 0.1505	2.1252 2.6389	0.1725 0.3227	0.0949 0.1605	0.0479 0.0018	0.8737 0.8722	0.5355	0.0612 0.3859	0.3361 0.8808	0.8953 0.3901	-0.6224 -0.3217	-0.6454 -0.7037	0.0523 0.0526	-0.2213 0.3290	0.6461 4	0.2442 0 0.0530 0	.0287 .5149
				1		1						1					1									
Citrate	4.6061	0.1810	4.2207	0.1313	4.4410	0.0802	4.2571	0.1787	4.3822	0.0495	3.9650	0.1785	0.1028	0.2998	0.0256	0.4205	0.2557	0.8840	0.2649	-0.3855	-0.1839	-0.4172	-0.1651	0.2239 0	0365 -0	0.2557
Glvoxvlate	6.0923	0.4705	6.8162	0.1722	6.4579	0.1135	7.5741	0.1244	6.1955	0.0940	0.009U	0.0817	0.1118	0000.0	0.0000	0.3310	0.7685	0.0032	0.0031	0.7239	1.1162	1.3047	0.3656	0.1032	0 6/2/.	.6840
Malate	5.1053	0.1670	5.0686	0.1307	5.0802	0.1243	5.0810	0.1308	5.0139	0.1290	4.7415	0.1988	0.8634	0.9966	0.2863	0.9059	0.6724	0.9474	0.1909	-0.0367	0.0008	-0.2723	-0.0251	0.0914	.0124 -0	0.3270
Quinate	3.8423	0.3190	3.7049	0.0988	3.6011	0.2635	3.7858	0.0015	3.0139	0.1613	3.8154	0.2638	0.7087	0.6249	0.0461	0.6602	0.0504	0.6694	0.6320	-0.1374	0.1847	0.8015	-0.2412	0.8284	0 6080.	.1105
Succinate	4.6399	0.1564	4.6024	0.2361	5.0001	0.1420	4.7114	0.2618	4.8840	0.2172	4.3326	0.2692	0.8970	0.3690	0.2522	0.1138	0.3796	0.8258	0.5898	-0.0374	-0.2887	-0.5514	0.3602	0.2441 0	.1090	0.2699
Galactinol	1.8303	0.4307	pu	pu	1.5996	0.4171	1.7907	pu	1.4440	pu	2.0537	pu	pu	pu	pu	0.7373	pu	pu	pu	pu	0.1911	0.6097	-0.2307	0.3863	pu	pu
Myolnosit	5.8695	0.2080	5.5371	0.1521	5.6174	0.1565	5.4069	0.1622	5.4787	0.1404	5.3519	0.1763	0.2121	0.3710	0.5840	0.3519	0.1454	0.5675	0.4379	-0.3323	-0.2104	-0.1268	-0.2521	0.3908	0.1302 -0	0.1853
Sucrose Xvlose	9.0952 5.8213	0.3059	8.9412 6.2151	0.0228	8.9867 5.9935	0.0205	8.8248 5.3013	0.0293	9.0444 6.1048	0.0576	8.8/25	0.014/	0.2389	0.0075	0.2376	0.6110	0.2580	0.0331	0.0241	-0.1541 0.3937	-0.1619 -0.6922	-0.4006	0.1722	0.02835	1164 -(0.0686

Table S3. Content of metabolites in the phloem-enriched exudates of non-infected and infected plants (log₂ transformed and normalized values).

vice cinegrO

siegus

Table S4. List and characteristics of candidate genes.

* Gene pattern of expression, unless specifically indicated, with: l: leaf, yl: young leaf, sl: senescent leaf, s: stem, r: roots, s: seeds, yf: young fruit, mf: mature fruits, f: fruit, fl: flowers. TCMV: tomato chlorotic mottle virus infection. *P.s.: Pseudomonas syringae* pv. tomato DC3000, *F.s.: Fusarium lycopersici. R. s.: Ralstonia solanacearum. Ca.* P. s.: *'Candidatus* Phytoplasma solani', *RKN:* root-knot nematode. CC: companion cells. SE: sieve elements.

Gene name	Arabidopsis ortholog	Function	Expression*	References
		Defence rela	ited genes	
PR1a/P4	At4g33720 (putative <i>PR1</i>)	Pathogenesis related protein	l; SA dependent defence gene, upregulation by <i>Ca.</i> P. s. infection	[2]–[4]
PR2a	At4g16260 (β–1,3-glucanase)	Pathogenesis related protein (β-1,3-glucanase)	l; SA dependent defence gene, upregulation by <i>Ca.</i> P. s. infection	[2], [3]
CAS2	At2g31960 (GLS03)	Putative callose synthase	l, No response to <i>Ca</i> . P. s. infection	De Marco, personal communication
CAS7	At1g06490 (CAS7)	Putative callose synthase	l; Upregulation by <i>Ca.</i> P. s. infection	[5]
		Vascular	marker	
PP2	At4g19840 (PP2-A1)	Phloem protein 2 (lectin)	l, phloem; Downregulation by <i>Ca.</i> P. s. infection	[5]
		Sugar met	abolism	
FRK1	At5g51830 (FRK1)	Cytosolic fructokinase	l, st, r, f, vascular tissues	[6]–[8]
FRK2	At1g06030 (FRK2/6)	Cytosolic fructokinase	s, r, f, vascular tissues Increased protein amount in response to <i>R.s.</i>	[7], [9], [10]
FRK3	At1g66430 (FRK3/6)	Plastidial fructokinase	r, l, st, s. vascular tissues. Increased protein amount in response to TCMV infection	[7], [11]–[13]
SUSY1	At5g20830 (SUS1)	Sucrose synthase	st, vascular tissues (xylem)	[14]
SUSY3	At3g43190 (SUS4)	Sucrose synthase	r	[14]
		Sugar tra	nsport	
SUT1	At1g22710 (SUC2)	Sucrose transporter	l, st, source organs mRNA in CC, protein in SE	[15]–[17]
SUT2	At2g02860 (SUC3)	Sucrose transporter	l, st, sink organs mRNA in CC, Protein in SE. Upregulation by <i>RKN</i>	[17], [18]
SWEET2a	At3g14770 (SWEET2)	Sugar facilitator	l, st, r, fl, Upregulation by <i>RKN</i>	[19], [20]
SWEET5b	At5g62850 (SWEET5)	Sugar facilitator	l, fl, Upregulation in leaves and roots by <i>RKN</i>	[19], [20]
SWEET10c	At5g50790 (SWEET10)	Sugar facilitator	l, fl, Upregulation by sugars, salt and temperature	[19]
SWEE11a	At3g48740 (SWEET11)	Sugar facilitator	l, fl, Upregulation by sugars, salt and temperature	[19]

De Marco et al. Int. J. Mol. Sci. 2021, 22, SUPPLEMENTARY MATERIALS

10 o	f 16
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SWEE12a	At5g23660 (SWEET12) At3g48740 (SWEET11)	Sugar facilitator	l, fl, Upregulation by sugars, salt and temperature	[19]
	(Glyoxylate cycle and	l photorespiration	
ICL	At3g21720 (ICL)	Isocitrate lyase	yl, sl. Protein in yl. and sl., less in mat. leaves	[21], [22]
MLS	At5g03860 (MLS)	Malate synthase	yl, sl. Protein in yl. and sl., lower activity in the roots by <i>R.s.</i> infection	[21]–[23]
GLO40/GOX1/ SlGlo1/ TomGlo.1	At3g14420 (GOX1) At3g14415 (GOX2)	Glycolate oxidase	<i>l,</i> Decreased activity in response to <i>F. l.</i> . No response to <i>P.s.</i>	[4], [24], [25]
GLO00/GOX2 /SIGlo2	At3g14420 (GOX1) At3g14415 (GOX2)	Glycolate oxidase	yf, l, Decreased activity in response to <i>F.s.</i> Upregulation by <i>P.s</i> . Involved in the photorespiration	[4], [24], [25]
GLO50/GOX3/ SlGlo3	At4g18360 (GOX3)	Glycolate oxidase	L, Decreased activity in response to <i>F. l.</i>	[24]
GLYR1	At3g25530 (GLYR1)	Glyoxylate reductase	L, Increased activity by F. l. infection	[24]
GLYR2	At1g17650 (GLYR2)	Glyoxylate reductase	L, Increased activity by F. l. infection	[24]

Table S5. Two-way ANOVA of the expression of candidate genes in not-infected and infected plants.

The ANOVA was determined on gene expression data obtained at 3 leaf levels for the 3 genotypes (WT, *SUT1*-AS, *SUT2*-AS). G: Genotype; L: leaf position; GxL= Genotype per leaf position interaction. *p*-value (2-way ANOVA): *, P < 0.05, **; P < 0.01; ***, P < 0.001. *n*=72.

Gene	G	L	GxL	G	L	GxL
		Not-infected			Infected	
SUS1	0.0132 *	4.07e-05 ***	0.4750	0.2085	3.83e-05 ***	0.6739
SUS3	0.2073	0.0053 **	0.7242	0.0057 **	0.0006 ***	0.0888
FRK1	0.1837	0.0004 ***	0.6185	0.0004 ***	8.59e-05 ***	0.6609
FRK2	0.0017 **	0.0085 **	0.2882	0.3586	0.0001 ***	0.5379
FRK3	0.0226 *	0.0031 **	0.3118	0.1911	0.0033 **	0.5541
CAS2	0.0055 **	2.16e-07 ***	0.0239 *	0.0124 *	2.63e-06 ***	0.3743
CAS7	0.0747	2.32e-10 ***	0.9559	0.5643	4.46e-06 ***	0.6072
PR1a	0.0584	0.0854	0.5372	0.0122 *	0.2525	0.3696
PR2a	0.4755	0.0265 *	0.4345	0.1518	0.2261	0.5719
SWEET2a	0.0089 **	0.0008 ***	0.5491	0.0268*	0.0016**	0.5703
SWEET5b	0.1581	6.03e-06 ***	0.7338	0.3010	9.37e-06 ***	0.0906
SWEET10c	0.2010	0.0007 ***	0.5131	0.4201	5.20e-05 ***	0.8110
SWEET11a	0.4628	0.0033 **	0.4946	0.0417 *	3.57e-05 ***	0.7356
SWEET12a	0.3217	0.0004 ***	0.5877	0.0497 *	0.0001***	0.8447
PP2	0.5485	3.74e-07 ***	0.5769	0.472	2.79e-06 ***	0.6045
ICL	0.0640	0.0370 *	0.6605	0.0145 *	0.3298	0.5561
MLS	0.0568	0.4368	0.9470	0.0002 ***	0.9635	0.9771
GLO00/GOX2	0.0035 **	0.3770	0.6526	0.0142 *	0.0025 **	0.4767
GLO40/GOX1	0.5239	0.0206 *	0.9951	0.3176	0.0009 ***	0.7862
GLO50/GOX3	0.2170	0.2787	0.9831	0.5420	0.1109	0.5444
GLYR1	0.4658	0.0318 *	0.4585	0.6818	0.0355 *	0.6063
GLYR2	0.0012 **	0.0025 **	0.0951	0.0356 *	0.6020	0.0756

Table S6. Correlations in gene expression.

The *Pearson* correlation was determined on the full gene expression dataset obtained at the three leaf levels (L1, L4 and L6) of the infected and non-infected plants of the 3 genotypes (WT, *SUT1*-AS and *SUT2*-AS). *n*=72.

Correlations	Pearson correlation	Pairwise two- sided <i>n</i> -values	Adjusted
Glycolysis and peroxison	ne metabolism	staca p varaes	p vulues
FRK1 - ICL	-0.406	0.000	0.019
FRK1 - GLYR2	-0.384	0.001	0.037
FRK3 - GLO40/GOX1	0.394	0.009	0.028
FRK3 - GLO50/GOX3	0.416	0.005	0.014
FRK3 - GLYR1	0.401	0.030	0.022
SUS1 - GLO40/GOX1	0.438	< 0.0001	0.006
SUS3 - GLO40/GOX1	0.450	< 0.0001	0.004
SUS3 - GLO50/GOX3	0.470	< 0.0001	0.002
SUS3 - GLYR1	0.473	< 0.0001	0.001
Glycolysis			
SUS1 - FRK1	0.446	< 0.0001	0.004
SUS1 - FRK2	0.649	< 0.0001	< 0.0001
SUS1 - FRK3	0.687	< 0.0001	< 0.0001
SUS1 - SUS3	0.518	< 0.0001	0.000
SUS3 - FRK2	0.486	< 0.0001	0.001
SUS3 - FRK3	0.599	< 0.0001	< 0.0001
FRK1 - FRK2	0.527	0.000	0.000
FRK2 - FRK3	0.724	0.000	0.000
Peroxisomal meta	bolism		
GLO00/GOX2 - ICL	0.644	< 0.0001	< 0.0001
GLO00/GOX2 - MLS	0.835	< 0.0001	< 0.0001
ICL- MLS	0.734	< 0.0001	< 0.0001
GLO50/GOX3- GLO40/GOX1	0.626	< 0.0001	< 0.0001
GLO50/GOX3- GLYR1	0.653	< 0.0001	< 0.0001
GLO40/GOX1- GLYR1	0.884	< 0.0001	< 0.0001
Others			
CAS7 - PP2	0.906	<0.0001	< 0.0001
CAS7- FRK3	0.734	< 0.0001	< 0.0001
PP2 - FRK3	0.742	<.0001	<.0001

Table S7. List of Primers.

When more than one sequence was identified, primers amplify each variant. E (%): Efficiency of the primers.

Gene	Accession no. (NCBI)	Forward (F) and Reverse (R) primers (5'-3')	E (%)	Reference
Stolbur markers				
STOL-rRNA	AF248959	F: AGGGTAGCTAAAGCGTAAGC R: CATCAACCCTACCTTAGACG	92.4	[26]
STOL-gDNA	AM990981	F: ATTTGATGAAACACGCTGGATAA R: TCCCTGGAACAATAAAAGTYGCA	99.2	[27]
Tomato candidate genes				
Sugar transport				
SUT1	NM_001302901.2	F: TTCCATAGCTGCTGGTGTTC R: TACCAGAAATGGGTCCACAA	109.5	Forward: [16]
SUT2	NM_001247392.2 NM_001313887.1	F: CCTACAGCGTCCCTTTCTCT R: CGATACAACCATCTGAGGTACAA	109.8	Forward: [16]
SWEET2a	XM_004244249.3 XM_019215006.1 XM_010326104.2	F: TGTTTGCCTCCCACTGTTA R: TAGGAAGGTGGAGAGGGACA	95.3	This study
SWEET5b	NM_001320885.1	F: TGTACACCTCACCACTGACC R: CATGCCCAAACAATGCCATT	93.8	This study
SWEET10c	XM_004235291.3	F: GATGGCTATTGCTGGTCATTGG R: ACCCTGGCTTTCTTTGGTGC	103.2	[19]
SWEET11a	XM_004235278.3	F: CTACGCACCAAAGAAAGCCAG R: GTCTCACAATGCCTAAGGGAGC	102.4	[19]
SWEET12a	XM_004235286.3	F: TCTCACAATGCCTAAGGGTGC R: ACCAAACAAAGCCAGGGTCC	108.2	[19]
Sugar metabolism	1			
SUS1	XM_019211274.1	F: CTGCTGAGTGAATGAAGGTC R: GATACTAATGGAAATGAAACAC	103.6	[14]
SUS3	XM_019214635.2	F: GGTTTCTGTCTGATTGTTATCC R: ACAGAAGGGAAAAATGGCAAA	89	[14]
FRK1	NM_001246964.2 XM_010319082.1	F: CTCCGTTACATATCTGATCCTT R: GACAGCATTGAAGTCACCTT	105.4	[28]
FRK2	NM_001246959.2	F: TTGTTGGTGCCCTTCTAACCA R: ACGATGTTTCTATGCTCCTCCCT	110.9	[28]
FRK3	NM_001247467.2	F: GTGGTGCATTGACCGTGATG R: GGTCGGATGGTATTATGCAACTG	99.2	[11]
Stress markers	1			
CAS2	XM_026031249.1	F: CGTCAGTGGGCTTGAAGAAG R: GCACAAAAGACTGAGAGGCA	102.1	This study
CAS7	XM_010325327.2 XM_010325328.2	F: GGGACTTGGAATTTGGGATT R: CTCTGATACGAATGGGAACCA	101.9	[5]
PR1a	AJ011520.1	F: CTGTAGGCAACTGGGTTGGA R: TCAATCCGATCCCACTTATCATTT	95.7	This study
PR2a	NM_001247869.2	F: AGGGCTAAACGATGCAGGAT R: GCCAACCACTTTCCGATACA	93.8	This study
Vascular markers	1			
PP2	XM_004233183.4	F: TGAAGGTGGGAACTGGAAGA R: CTGGGCTTAACGCCAAATC	94.7	[5]

Glyoxylate cycle				
ICL	NM_001246949.2	F: CGACACGTTTGCCAAGGATT R: ACACCATTGCTCCTCTCCTC	101.7	This study
MLS	XM_010320762.1 XM_004236297.3 XM_004236298.3	F: GTGGCTGATCGGAGGGTG R: GGCCTCTCATTAAATTCTCCCA	94.3	This study
GLO00/GOX2	NM_001347977.1 NM_001347978.1	F: ATCAGGCGTGTTTATTGGGC R: CTTCAGTGAACGACAGCCAC	99.6	This study
GLO40/GOX1	NM_001307942.1 XM_004243141.3 XM_010325318.2	F: CTGTCGCTCACTGAAGGAGA R: GTACATGCTCACAACCTTGGG	98.0	This study
GLO50/GOX3	XM_010326599.2 XM_010326600.2 XM_010326601.2 XM_004244918.3 XM_019215374.1	F: CCTGTTTTCCTTGACGGTGG R: CTAACTCCTGCCTCCCCATC	99.2	This study
GLYR1	NM_001246903.2	F: AGCAGAAGGACATGAGGCTG R: AAGTCAAGGTCTCCCAAGCC	98.7	This study
GLYR2	NM_001246907.2	F: GTGCTCCAATGTATGCCGTT R: AACCCAGAGCTAGACGAAGG	97.6	This study
Tomato reference genes	•			
UBI3 Ubiquitin	NM_001346406.1	F: TCGTAAGGATGCCCTAATGCTGA R: CAATCGCCTCCAGCCTTGTTGTAA	100.2	[29]
UPL3 E3 ubiquitin-protein ligase	XM_004230989.3 XM_010317077.2	F: AGCGCTGATCCCTCATTGCAT R: GCTGTTTACAAATTCCTCCGAGG	98.5	[5]
PGK Phosphoglycerate kinase	NM_001329592.1 NM_001329591.1	F: TCTACAAGGCCCAAGGTTATG R: GCAGCAAACTTGTCCGCAATC	97.1	[30]
UrK UMP-CMPkinase 3	NM_001309811.1	F: TGGTAAGGCACCCAATGTGCTAA R: ATCATCGTCCCATTCTCGGAACCA	99.7	[29]

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