

Supplementary figures and tables

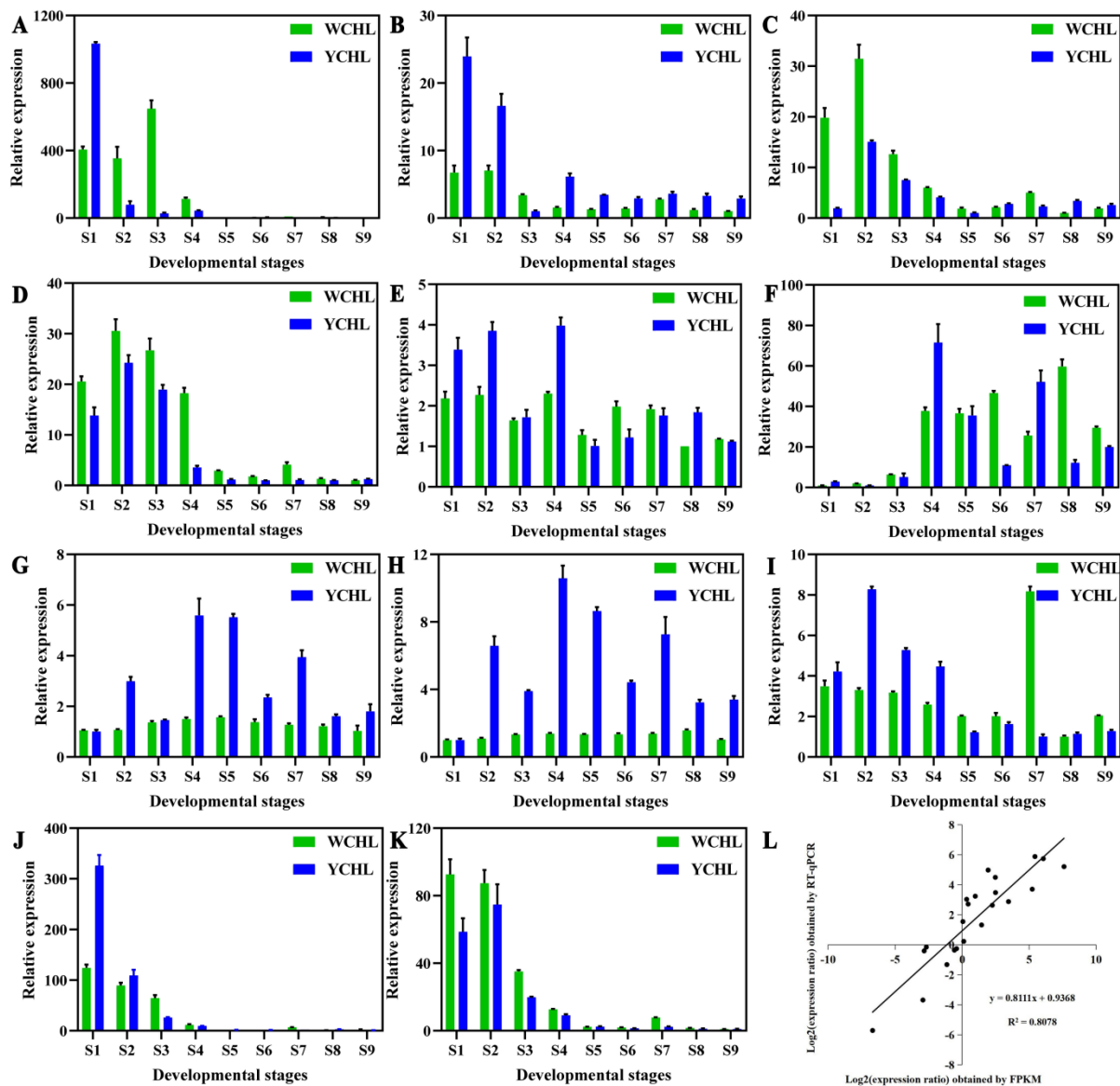


Figure S1. The RT-qPCR analyses of eleven candidate genes (A-K) in sugar and acid metabolic pathway and the coefficient analyses between FPKM values and RT-qPCR of those genes (L). A, *CMS1*; B, *CS6*; C, *FRK5*; D, *FRK9*; E, *MDAR1*; F, *PEPC4*; G, *PHS2*; H, *PHS3*; I, *PM11*; J, *SuSy5*; K, *SuSy11*.

Table S1 RNA-Seq data and corresponding quality control information

Samples	Raw reads	Clean reads	Clean_bases (G)	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
WCHL_17d_1	45918120	44088506	6.61	0.02	98.14	94.31	49.64
WCHL_17d_2	48264390	46108368	6.92	0.03	97.95	93.94	50.04
WCHL_17d_3	40405646	38763342	5.81	0.03	97.95	93.93	49.75
WCHL_25d_1	42257762	40626122	6.09	0.02	98.22	94.51	50.66
WCHL_25d_2	48071026	46752758	7.01	0.02	98.85	96.09	50.57
WCHL_25d_3	43826692	40976414	6.15	0.02	98.22	94.67	49.99
WCHL_29d_1	45988084	42674020	6.4	0.02	98.14	94.46	50.01
WCHL_29d_2	47180636	45564148	6.83	0.02	98.86	96.14	50.4
WCHL_29d_3	46150874	41831586	6.27	0.02	98.19	94.58	50.26
YCHL_35d_1	41089912	39661570	5.95	0.02	98.12	94.28	49.27
YCHL_35d_2	45494498	44206436	6.63	0.03	97.98	93.88	49.94
YCHL_35d_3	45244634	43577446	6.54	0.02	98.08	94.15	51.38
YCHL_65d_1	45518136	41775096	6.27	0.02	98.33	94.9	51.09
YCHL_65d_2	47612182	45114430	6.77	0.02	98.32	94.9	50.43
YCHL_65d_3	50410912	48703300	7.31	0.02	98.62	95.45	49.99
YCHL_75d_1	45291970	44124280	6.62	0.02	98.84	96.02	50.7
YCHL_75d_2	45216534	43936170	6.59	0.02	98.81	96	50.28
YCHL_75d_3	44770172	42611336	6.39	0.03	98.06	94.06	50.47

Table S2 Specific primers used in RT-qPCR assay.

Gene name	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>CMS1</i>	GTATGAACTTGATGGGCTT	TGGTATTGTGCTTGGAAAA
<i>CS6</i>	CAGTGGAACATGTGCAAGGC	CTGCTTCCCTGAGTGCTTGA
<i>FRK5</i>	TGCTGGCGATGCATTTGTTG	CCGGGAATTGCACCTCTCTT
<i>FRK9</i>	GAGGACGAGCCGAGATTGAG	GCTGGGATTGCTCCCTTCTT
<i>MDAR1</i>	TGGTCTTGAGCTCAGTGCAG	ATCAGCGGTGAAGAGTCGTG
<i>PEPC4</i>	CGTGCTCGAGTAGACGAACT	AGCACGTTCACGGGTATTGT
<i>PHS2</i>	TGAATCCCCCGAGTCCAGAT	GGAAAATCCCTCTGGGGCAA
<i>PHS3</i>	GCGGAGTGTTTGGCACATTT	ACCACGGCCAAATCCTTCAT
<i>PMI1</i>	GCTGGCCTAACACCTAAGCA	TGTGCATCCATCACTGCCAT
<i>SuSy5</i>	GTGAACCTTGTCGTGGTTGC	ATCTGGGCAGAGATCCACCT
<i>SuSy11</i>	GGAGCTGGACTTTGAGCCAT	TGTTGAGGAACTCGACACCG

Table S3 The transcript abundance of genes related to ascorbate pathways in ‘WCHL’ and ‘YCHL’ pitayas pulps.

Gene names	Gene ID	‘WCHL’ pitaya			‘YCHL’ pitaya		
		17 d	25 d	29 d	35 d	65 d	75 d
L-ascorbate oxidase							
AO1	HU01G01245.1	0	0	0	0	0	0
AO2	HU01G01270.1	0	0	0	5.44	0	0
AO3	HU01G01464.1	8.69	0	0	6.17	0.77	2.43
AO4	HU01G01815.1	0	0	0	0	0	0
AO5	HU02G01327.1	3.25	11.34	32.22	7.84	2.36	4.77
AO6	HU02G02455.1	0	0	0	0	0	0
AO7	HU02G03061.1	0	0	0	0	0	0
AO8	HU03G01567.1	0	0	0	0	0	0
AO9	HU03G01573.1	0	0	0	0	0	0
AO10	HU05G01813.1	0	0	0	0	0	0
AO11	HU05G01868.1	0.2	0	0	0	0	0
AO12	HU06G00762.1	21.26	1.59	4.01	70.48	7.37	8.26
AO13	HU06G00824.1	0	0	0	0	0	0
AO14	HU06G00825.1	3.45	1.48	4.27	1.67	1.6	6.9
AO15	HU07G01170.1	1.92	0.42	0.61	1.62	1.54	0.35
AO16	HU08G00550.1	3.53	5.73	4.62	3.04	7.24	7.32
AO17	HU08G01290.1	0.08	0	0	0	0	0
AO18	HU08G01291.1	0.95	0	0	0	0.07	0
AO19	HU08G01953.1	0.96	0.17	0.04	0.46	0.2	0.18
AO20	HU09G01170.1	0	0	0	0	0	0
AO21	HU09G01171.1	0	0	0	0	0	0
AO22	HU10G01971.1	0	0	0	0	0	0
L-ascorbate peroxidase							
APX1	HU01G00039.1	74.57	46.68	47.18	82.93	94.49	90.73

<i>APX2</i>	<i>HU01G01291.1</i>	272.97	461.8	401.56	582.28	485.69	468.56
<i>APX3</i>	<i>HU03G00392.1</i>	12.78	15.52	17.58	8.22	5.85	4.39
<i>APX4</i>	<i>HU06G00143.1</i>	0.13	0	0	0	0	0
<i>APX5</i>	<i>HU06G00147.1</i>	0	0	0	0	0	0
<i>APX6</i>	<i>HU06G00148.1</i>	0	0	0	0	0	0
<i>APX7</i>	<i>HU06G01014.1</i>	0.13	0.56	0.25	1.42	0.92	0
<i>APX8</i>	<i>HU07G00395.1</i>	1.61	1.53	1.41	1.28	2.6	2.14
<i>APX9</i>	<i>HU07G00844.1</i>	44.61	12.07	26.05	71.03	56.49	52.29
<i>APX10</i>	<i>HU09G00808.1</i>	31.33	89.6	30.18	9.96	63.5	90.36
<i>APX11</i>	<i>HU11G00172.1</i>	7.61	13.25	20.95	4.32	8.33	10.14
<i>APX12</i>	<i>HU11G01184.1</i>	10.57	16.62	22.54	14.95	23.02	26.83
dehydroascorbate reductase							
<i>DHAR</i>	<i>HU06G01275.1</i>	102.27	65.84	32.58	16.54	9.7	13
L-galactose dehydrogenase							
<i>GDH</i>	<i>HU03G00469.1</i>	24.04	12.52	13.43	13.47	10.16	8.41
GDP-L-galactose phosphorylase							
<i>GGP1</i>	<i>HU01G01690.1</i>	41.04	20.95	48.5	35.26	36.66	63.54
<i>GGP2</i>	<i>HU05G01762.1</i>	28.5	21.94	32.63	87.65	32.66	33.4
<i>GGP3</i>	<i>HU08G00238.1</i>	69.97	42.44	40	36.62	17.32	17.65
L-galactono-1,4-lactone dehydrogenase							
<i>GLDH</i>	<i>HU10G01073.1</i>	11.24	12.57	19.61	10.46	18.74	16.38
GDP-mannose 3,5-epimerase							
<i>GME1</i>	<i>HU03G01059.1</i>	25.03	15.77	23.54	10.66	19.54	20
<i>GME2</i>	<i>HU08G01094.1</i>	71.84	44.86	37.8	54.27	43.83	36.27
Mannose-1-phosphate guanylyltransferase							
<i>GMP1</i>	<i>HU05G01570.1</i>	11.46	10.73	11.32	7.84	4.77	8.47
<i>GMP2</i>	<i>HU05G01571.1</i>	8.69	5.98	5.95	2.59	5.88	9.27
<i>GMP3</i>	<i>HU05G01623.1</i>	10.73	7.09	3.47	11.19	9.49	8.02
<i>GMP4</i>	<i>HU06G00539.1</i>	56.89	26.42	26.47	70.57	63.34	55.22
L-galactose-1-phosphate phosphatase							

<i>GPP1</i>	<i>HU01G00275.1</i>	13.31	19.77	11.13	8.38	5.54	7.14
<i>GPP2</i>	<i>HU01G02287.1</i>	13.25	8.34	8.19	8.7	5.94	8.13
<i>GPP3</i>	<i>HU02G02148.1</i>	19.08	9.6	8.81	13.62	11.31	13.3
<i>GPP4</i>	<i>HU10G01800.1</i>	0.08	0	0.28	0	0	0
<i>GPP5</i>	<i>HU10G01801.1</i>	0.11	0	0.17	0.4	0.16	0
<i>GPP6</i>	<i>HU10G01803.1</i>	2.41	1.91	2.1	2.97	1.56	2.94
<i>GPP7</i>	<i>HU10G02033.1</i>	103.78	42.02	57.55	132.68	129.92	106.29
Monodehydroascorbate reductase							
<i>MDAR1</i>	<i>HU02G02424.1</i>	10.25	9.6	9.42	39.76	47.38	38.15
<i>MDAR2</i>	<i>HU05G00113.1</i>	38.84	79.42	74.26	25.12	49.93	40.96
<i>MDAR3</i>	<i>HU09G00954.1</i>	200.19	239.18	126.62	263.93	194.2	237.34
Mannose-6-phosphate isomerase							
<i>PMI1</i>	<i>HU05G01684.1</i>	14.47	21.35	31.8	9.15	6.5	7.23
<i>PMI2</i>	<i>HU05G01685.1</i>	0.06	8.58	1.19	0	0.5	1.18
<i>PMI3</i>	<i>HU06G00668.1</i>	13.9	33.02	27.09	4.03	11.9	7.27
Phosphomannomutase							
<i>PMM1</i>	<i>HU07G00464.1</i>	13.77	3.11	5.42	25.14	9.71	11
<i>PMM2</i>	<i>HU09G00757.1</i>	29.33	47.97	35.85	14.85	32.63	38.5

Table S4 Correlation analyses between the ascorbic acid contents and expression patterns of candidate genes in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	ascorbic acid
<i>AO5</i>	<i>HU02G01327.1</i>	0.4
<i>AO12</i>	<i>HU06G00762.1</i>	-0.311
<i>APX1</i>	<i>HU01G00039.1</i>	-0.751**
<i>APX2</i>	<i>HU01G01291.1</i>	-0.294
<i>APX9</i>	<i>HU07G00844.1</i>	-0.676**
<i>APX10</i>	<i>HU09G00808.1</i>	-0.021
<i>DHAR</i>	<i>HU06G01275.1</i>	0.391
<i>GDH</i>	<i>HU03G00469.1</i>	0.266
<i>GGP1</i>	<i>HU01G01690.1</i>	-0.006
<i>GGP2</i>	<i>HU05G01762.1</i>	-0.036
<i>GGP3</i>	<i>HU08G00238.1</i>	0.404
<i>GLDH</i>	<i>HU10G01073.1</i>	0.153
<i>GME1</i>	<i>HU03G01059.1</i>	0.429
<i>GME2</i>	<i>HU08G01094.1</i>	-0.084
<i>GMP1</i>	<i>HU05G01570.1</i>	0.132
<i>GMP2</i>	<i>HU05G01571.1</i>	0.128
<i>GMP3</i>	<i>HU05G01623.1</i>	-0.497*
<i>GMP4</i>	<i>HU06G00539.1</i>	-0.603**
<i>GPP7</i>	<i>HU10G02033.1</i>	-0.366
<i>MDAR1</i>	<i>HU02G02424.1</i>	-0.531*
<i>MDAR2</i>	<i>HU05G00113.1</i>	0.669**
<i>MDAR3</i>	<i>HU09G00954.1</i>	-0.368
<i>PMI1</i>	<i>HU05G01684.1</i>	0.687**
<i>PMI2</i>	<i>HU05G01685.1</i>	0.358
<i>PMI3</i>	<i>HU06G00668.1</i>	0.761**
<i>PMM1</i>	<i>HU07G00464.1</i>	-0.577*
<i>PMM2</i>	<i>HU09G00757.1</i>	0.388

Note: The data was analyzed using SPSS 25 with Pearson's correlation. The significant positive correlation coefficients are indicated in red values while negative correlation coefficients are indicated in blue values.

* indicates correlation significant at the 0.05 level ($p < 0.05$, two-tailed) while ** indicates correlation significant at the 0.01 level ($p < 0.01$, two-tailed).

Table S5 The transcript abundance of genes related to starch synthesis and degradation pathways in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	‘WCHL’ pitaya			‘YCHL’ pitaya		
		17 d	25 d	29 d	35 d	65 d	75 d
Alpha-glucosidase							
AGL1	HU02G01725.1	1.02	0.67	0.33	2.96	3.66	4.94
AGL2	HU02G01726.1	1.13	1.04	0.73	5.49	6.44	6.1
AGL3	HU02G01727.1	8.19	5	6.53	7.22	5.14	7.53
AGL4	HU02G01728.1	1.19	0.65	0.48	0	0	0
AGL5	HU02G01729.1	0.91	0.2	0.78	0.54	1.74	3.44
AGL6	HU02G01730.1	6.93	4.74	7.04	2.39	1.26	1.81
AGL7	HU03G01386.1	23.77	26.53	26.47	16.25	21.31	16.17
AGL8	HU05G00176.1	53.86	68.41	44.28	18.17	55.74	53.64
AGL9	HU09G01939.1	4.59	12.68	5.42	0.81	1.53	1.24
Glucose-1-phosphate adenylyltransferase							
AGPS1	HU01G00286.1	14.46	24.98	22.71	25.52	79.08	66.24
AGPS2	HU03G00147.1	52.25	10.01	14.58	123.15	28.2	18.17
AGPS3	HU03G02063.1	63.03	14.95	12.89	50.09	68.08	76.34
AGPS4	HU06G01322.1	0.45	0.06	0	0	0.19	0.21
AGPS5	HU07G00703.1	26.56	1.87	0.77	7.01	5.8	3.57
Alpha-amylase							
AMY1	HU01G00458.1	0.55	0.8	3.03	2.52	3.16	1.68
AMY2	HU01G01364.1	4.48	6.89	13.06	1.95	3.58	4.03
AMY3	HU01G02422.1	0.76	0.7	1.68	0.35	0.92	0.53
AMY4	HU01G02675.1	1.19	2	3.19	1.23	2.69	3.39
AMY5	HU02G00188.1	1.99	2.4	4.39	1.33	2.44	4.13
AMY6	HU02G00293.1	38.78	210.71	76.22	20.37	220.68	194.78
AMY7	HU02G01323.1	23.59	97.01	74.82	10.59	53.44	64.52
AMY8	HU02G02922.1	1.6	1.74	2.69	1.27	1.04	2.24

AMY9	HU02G03420.1	0.62	1.16	1.63	1.11	2.11	2.88
AMY10	HU03G01593.1	0.72	0.88	2.42	0.27	0.98	1.3
AMY11	HU04G00245.1	0.35	0.86	1.83	1.27	1.38	1.09
AMY12	HU05G00001.1	0	0.06	0	0	0	0
AMY13	HU05G00002.1	0	0	0	0	0	0
AMY14	HU05G01323.1	3.9	4.3	5.25	8.14	1.16	1.45
AMY15	HU05G01802.1	0.34	0.99	2.79	0.29	1.18	1.21
AMY16	HU06G00016.1	0.21	0	0	0	0	0
AMY17	HU06G00973.1	0	0	0	0	0	0
AMY18	HU06G01277.1	1.76	3.12	3.43	0.9	2.48	2.54
AMY19	HU07G00472.1	1.25	1.65	3.12	1.98	1.45	0.68
AMY20	HU07G00886.1	0.68	1.05	4.06	0.54	1.53	1.63
AMY21	HU07G00912.1	0	0.09	0.15	0.06	0.04	0.04
AMY22	HU07G00913.1	0.14	0.56	0.42	0.2	0.57	1.16
AMY23	HU07G01462.1	0	0	0	0	0	0
AMY24	HU07G01511.1	55.71	0.24	0.09	12.41	0	0
AMY25	HU08G00353.1	0.12	0	0	0	0	0
AMY26	HU08G00466.1	2.22	3.97	10.3	2.68	14.69	12.55
AMY27	HU08G00990.1	0.56	0.68	2.55	2.68	3.84	4.42
AMY28	HU08G01940.1	0.49	1.01	2.44	1.35	0.5	1.39
AMY29	HU09G01705.1	0.51	0.42	1.27	0.2	0.32	0.22
AMY30	HU10G00319.1	0.68	0.07	0.07	0.2	0.07	0
AMY31	HU10G01279.1	0.13	0.18	0.22	1.17	2.01	2.14
AMY32	HU11G00819.1	0.43	1.78	3.17	0.81	1.01	1.3
AMY33	HU11G01508.1	0.17	1.22	0.23	0	0	0.34
AMY34	HU11G01790.1	1.8	2.36	7.11	1.62	2.26	2.37

Beta-amylase

BAM1	HU03G02052.1	2.13	0.56	0.2	3.58	0	0
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<i>BAM2</i>	<i>HU03G02053.1</i>	3.09	0.4	0	9.6	0	0
<i>BAM3</i>	<i>HU04G00443.1</i>	9.08	2.36	2.17	17.96	2.96	1.88
<i>BAM4</i>	<i>HU04G00659.1</i>	11.07	15.76	25.91	5.14	12.22	10.96
<i>BAM5</i>	<i>HU05G00342.1</i>	1.43	2.91	3.68	0.82	3.08	2.93
<i>BAM6</i>	<i>HU07G00441.1</i>	5.67	2.67	4.73	2.36	1.52	3.56
<i>BAM7</i>	<i>HU08G00306.1</i>	7.01	11.06	6.13	6.53	9.31	7
<i>BAM8</i>	<i>HU09G00508.1</i>	0.19	0	0	0	0	0
<i>BAM9</i>	<i>HU09G01694.1</i>	0	0	0	0	0	0
<i>BAM10</i>	<i>HU10G00777.1</i>	118.01	716.89	355.9	119.42	277.19	187.61
<i>BAM11</i>	<i>HU10G00778.1</i>	31.2	67.58	55.74	26.13	75.23	51.72
<i>BAM12</i>	<i>HU10G00833.1</i>	146.49	629.91	247.03	182.11	260.99	200.17
<i>BAM13</i>	<i>HU11G01792.1</i>	9.46	10.69	7.48	1.32	10.6	10.89
<i>BAM14</i>	<i>HU11G01794.1</i>	8.99	10.12	8.06	9.02	10.4	10.84

4-alpha-glucanotransferase

<i>DPE1</i>	<i>HU09G01260.1</i>	11.66	28.02	12.14	10.49	22.64	21.32
<i>DPE2</i>	<i>HU09G01976.1</i>	4.62	1.46	1.78	0.72	1.68	1.39
<i>DPE3</i>	<i>HU09G01977.1</i>	2.35	1.14	0.82	1.18	1.71	1.46
<i>DPE4</i>	<i>HU10G01164.1</i>	29.09	24.17	15.91	28.99	37.07	37.2

Glucan, water dikinase

<i>GWD1</i>	<i>HU01G01312.1</i>	39.35	47.53	61.78	0	0	0
<i>GWD2</i>	<i>HU02G00177.1</i>	28.76	51.71	24.07	16.49	69.88	60.45
<i>GWD3</i>	<i>HU0G00205.1</i>	2.72	8.4	12.69	7.38	6.07	4.92
<i>GWD4</i>	<i>HU10G00183.1</i>	17	47.68	32.45	1.53	7.98	14.5

Phosphoglucomutase

<i>PGM1</i>	<i>HU02G01892.1</i>	15.49	18.08	15.74	19.89	37.96	30.94
<i>PGM2</i>	<i>HU09G00757.1</i>	29.33	47.97	35.85	14.85	32.63	38.5
<i>PGM3</i>	<i>HU10G00720.1</i>	13.27	13.25	15.56	10.88	15.77	15.3
<i>PGM4</i>	<i>HU10G00736.1</i>	30.72	18.75	18.22	10.86	27.99	25.43

Glucan phosphorylase

<i>PHS1</i>	<i>HU02G00384.1</i>	21.33	3.81	7.97	5.41	6.11	8.15
<i>PHS2</i>	<i>HU06G01230.1</i>	60.24	140.56	80.34	29.64	338.64	210.85
<i>PHS3</i>	<i>HU06G01231.1</i>	73.35	209.78	109.27	42.98	374.6	273.23
<i>PHS4</i>	<i>HU07G02193.1</i>	42.73	82.33	50.14	19.11	150.08	115.6
Phosphoglucan, water dikinase							
<i>PWD1</i>	<i>HU09G02021.1</i>	16.79	44.53	34.75	10.33	24.01	32.25
<i>PWD2</i>	<i>HU09G02105.1</i>	1.81	5.13	4.37	3.35	9.24	9.78
Starch synthase							
<i>StSy1</i>	<i>HU02G03120.1</i>	18.3	15.84	15.87	16.13	14.04	15.85
<i>StSy2</i>	<i>HU05G01186.1</i>	24.34	35.77	28.49	8.42	14.06	13.16
<i>StSy3</i>	<i>HU05G01187.1</i>	38.95	57.58	46.68	20.36	31.67	20.99
<i>StSy4</i>	<i>HU05G02284.1</i>	13.98	12.78	11.62	6.24	10.92	12.19
<i>StSy5</i>	<i>HU06G02646.1</i>	10.56	18.33	10.32	6.94	12.34	12.98
<i>StSy6</i>	<i>HU07G01224.1</i>	17.25	20.69	18.86	15.4	24.95	24.71
<i>StSy7</i>	<i>HU09G00010.1</i>	3.16	0.73	0	1.73	0	0
<i>StSy8</i>	<i>HU10G00589.1</i>	45.6	51.86	15.35	46.61	101.75	90.26
<i>StSy9</i>	<i>HU10G01954.1</i>	2.15	1.83	1.33	2	2.88	3.83
<i>StSy10</i>	<i>HU10G01957.1</i>	4.69	4.86	4.47	2.67	4.9	5.32

Table S6 Correlation analyses between the starch contents or total soluble sugar and expression patterns of candidate genes in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	Starch
<i>AGL7</i>	<i>HU03G01386.1</i>	-0.406
<i>AGL8</i>	<i>HU05G00176.1</i>	-0.655**
<i>AGPS1</i>	<i>HU01G00286.1</i>	-0.379
<i>AGPS2</i>	<i>HU03G00147.1</i>	0.890**
<i>AGPS3</i>	<i>HU03G02063.1</i>	0.213
<i>AGPS5</i>	<i>HU07G00703.1</i>	0.522*
<i>AMY6</i>	<i>HU02G00293.1</i>	-0.689**
<i>AMY7</i>	<i>HU02G01323.1</i>	-0.832**
<i>BAM10</i>	<i>HU10G00777.1</i>	-0.520*
<i>BAM12</i>	<i>HU10G00833.1</i>	-0.426
<i>DPE1</i>	<i>HU09G01260.1</i>	-0.578*
<i>DPE2</i>	<i>HU09G01976.1</i>	0.101
<i>DPE3</i>	<i>HU09G01977.1</i>	0.18
<i>DPE4</i>	<i>HU10G01164.1</i>	0.072
<i>GWD1</i>	<i>HU01G01312.1</i>	-0.29
<i>GWD2</i>	<i>HU02G00177.1</i>	-0.589*
<i>GWD3</i>	<i>HU0G00205.1</i>	-0.162
<i>GWD4</i>	<i>HU10G00183.1</i>	-0.550*
<i>PGM1</i>	<i>HU02G01892.1</i>	-0.291
<i>PGM2</i>	<i>HU09G00757.1</i>	-0.835**
<i>PGM3</i>	<i>HU10G00720.1</i>	-0.246
<i>PGM4</i>	<i>HU10G00736.1</i>	-0.221
<i>PHS1</i>	<i>HU02G00384.1</i>	0.278
<i>PHS2</i>	<i>HU06G01230.1</i>	-0.587*
<i>PHS3</i>	<i>HU06G01231.1</i>	-0.636**
<i>PHS4</i>	<i>HU07G02193.1</i>	-0.651**
<i>PWD1</i>	<i>HU09G02021.1</i>	-0.793**
<i>PWD2</i>	<i>HU09G02105.1</i>	-0.439
<i>StSy2</i>	<i>HU05G01186.1</i>	-0.436
<i>StSy3</i>	<i>HU05G01187.1</i>	-0.401
<i>StSy6</i>	<i>HU07G01224.1</i>	-0.517*
<i>StSy8</i>	<i>HU10G00589.1</i>	-0.205

Table S7 The transcript abundance of genes related to major sugar biosynthesis pathways in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	‘WCHL’ pitaya			‘YCHL’ pitaya		
		17 d	25 d	29 d	35 d	65 d	75 d
Fructokinase							
<i>FRK1</i>	<i>HU02G00407.1</i>	10.97	10.51	13.56	10.63	11	19.75
<i>FRK2</i>	<i>HU02G00410.1</i>	0.49	0.18	1.19	0.27	0.32	0.83
<i>FRK3</i>	<i>HU02G00412.1</i>	0.39	0.28	0.34	1.88	0.87	1.23
<i>FRK4</i>	<i>HU02G01173.1</i>	14.8	27.63	35.05	5.41	18.75	24.92
<i>FRK5</i>	<i>HU02G01891.1</i>	113.54	19.18	23.79	22.62	9.19	16.56
<i>FRK6</i>	<i>HU02G03173.1</i>	5.05	3.12	2.53	0.83	0.58	1.12
<i>FRK7</i>	<i>HU02G03267.1</i>	3.03	0.55	0	20.62	4.53	10.88
<i>FRK8</i>	<i>HU05G01760.1</i>	9.48	2.1	4.12	12.37	9.04	8.98
<i>FRK9</i>	<i>HU06G02152.1</i>	271.62	33.4	24.63	235.29	73.1	42.2
<i>FRK10</i>	<i>HU06G02213.1</i>	171.04	124.8	122.54	240.79	321.37	323.58
<i>FRK11</i>	<i>HU07G01671.1</i>	0	0	0	0	0	0.09
Hexokinase							
<i>HXK1</i>	<i>HU01G00828.1</i>	28.98	6.16	2.64	6.68	1.35	1.38
<i>HXK2</i>	<i>HU02G01230.1</i>	6.26	1.87	5.67	14.24	14.24	18.24
<i>HXK3</i>	<i>HU02G01231.1</i>	4.01	5.6	14.36	0.85	3.52	7
<i>HXK4</i>	<i>HU03G01733.1</i>	6.03	8.83	13.04	8.36	5.02	5.95
<i>HXK5</i>	<i>HU03G02729.1</i>	28.13	36.44	21.24	31.02	44.5	32.77
<i>HXK6</i>	<i>HU05G00008.1</i>	12.06	10.64	14.91	3.79	4.77	4.29
<i>HXK7</i>	<i>HU06G00308.1</i>	0.07	0	0	0.57	2.1	1.26
<i>HXK8</i>	<i>HU08G00363.1</i>	2.86	6.13	17.46	2.82	9.21	17.44
<i>HXK9</i>	<i>HU08G01226.1</i>	6.67	31.06	46.67	13.27	15.69	29.31
<i>HXK10</i>	<i>HU0G00093.1</i>	0	0.15	0.14	0.5	1.47	1.15
<i>HXK11</i>	<i>HU0G00094.1</i>	1	0	1.85	0	1.16	3.34
<i>HXK12</i>	<i>HU11G00500.1</i>	42.44	35.63	19.52	45.91	34.39	25.44

Invertase

<i>Ivr1</i>	<i>HU01G00073.1</i>	0	0	0	0	0	0
<i>Ivr2</i>	<i>HU01G00074.1</i>	0	0	0	0	0.12	0
<i>Ivr3</i>	<i>HU02G01252.1</i>	29.19	20.81	23.08	20.24	12.11	12.04
<i>Ivr4</i>	<i>HU03G00349.1</i>	80.56	21.89	14.64	27.68	7.28	5.84
<i>Ivr5</i>	<i>HU03G00845.1</i>	3.36	3.09	4.04	2.37	4.19	4.04
<i>Ivr6</i>	<i>HU03G01461.1</i>	29.78	11.53	32.53	20.73	42.48	39.5
<i>Ivr7</i>	<i>HU03G02454.1</i>	1.05	0	0.11	0	0.14	0
<i>Ivr8</i>	<i>HU03G02455.1</i>	0.68	0.15	0	2.59	0	0.11
<i>Ivr9</i>	<i>HU03G02456.1</i>	0.05	0	0	0	0.25	0.72
<i>Ivr10</i>	<i>HU03G02457.1</i>	1.71	1.78	1.69	41.92	19.49	27.16
<i>Ivr11</i>	<i>HU04G00751.1</i>	0.07	0	0	0	0	0
<i>Ivr12</i>	<i>HU04G00755.1</i>	0	0	0	0	0	0
<i>Ivr13</i>	<i>HU05G00322.1</i>	0	0	0	0	0	0
<i>Ivr14</i>	<i>HU07G00113.1</i>	0.06	0	0	0	0	0
<i>Ivr15</i>	<i>HU07G00148.1</i>	0.79	0	0	0	0	0
<i>Ivr16</i>	<i>HU07G00250.1</i>	18.28	17.17	18.8	16.75	12.69	11.33
<i>Ivr17</i>	<i>HU07G00349.1</i>	7.97	0.95	0.77	0.42	0	0
<i>Ivr18</i>	<i>HU07G02013.1</i>	0.04	0.67	0.3	0.64	0.74	0.77
<i>Ivr19</i>	<i>HU07G02022.1</i>	0.28	0.72	1.14	1.57	2.13	1.42
<i>Ivr20</i>	<i>HU08G00679.1</i>	18.92	32.39	27.19	18.86	16.86	19.31
<i>Ivr21</i>	<i>HU08G01394.1</i>	2.38	0.88	2.27	0.17	0.81	0.92
<i>Ivr22</i>	<i>HU08G01398.1</i>	0	0	0	0	0	0
<i>Ivr23</i>	<i>HU11G00399.1</i>	2.36	0	0.41	13.61	2.96	2.02
<i>Ivr24</i>	<i>HU11G01556.1</i>	12.94	7.29	4.22	5.79	4.44	3.78
<i>Ivr25</i>	<i>HU11G01647.1</i>	0.14	0.9	0.07	0	0.05	0
<i>Ivr26</i>	<i>HU11G01656.1</i>	0	0	0	0	0	0
<i>Ivr27</i>	<i>HU11G01657.1</i>	0.87	0	0	1.43	0	0

Glucose-6-phosphate isomerase

<i>PGI1</i>	<i>HU01G02580.1</i>	2.13	1.45	0.28	1.39	2.2	1.01
<i>PGI2</i>	<i>HU01G02694.1</i>	5.57	8.04	10.2	18.69	5.49	11.6
<i>PGI3</i>	<i>HU04G01930.1</i>	0.57	1.1	2.93	1.05	0.2	0.31
<i>PGI4</i>	<i>HU05G00170.1</i>	52.99	50.53	37.64	37.41	42.92	31.51
<i>PGI5</i>	<i>HU05G00393.1</i>	3.29	1.42	0.6	2.09	2.13	2.71
<i>PGI6</i>	<i>HU07G00352.1</i>	10.42	7.38	7.44	5.27	8.79	9.15
<i>PGI7</i>	<i>HU07G00362.1</i>	2.54	6.62	3.88	2.13	4.54	3
<i>PGI8</i>	<i>HU07G01113.1</i>	14.88	17.14	17.81	15.86	19.27	16.26

Sucrose-phosphate synthase

<i>SPS1</i>	<i>HU03G00894.1</i>	20.77	27.66	15.06	20.59	21.48	24.69
<i>SPS2</i>	<i>HU05G00771.1</i>	58.92	42.4	51.66	50.28	78.01	77.51
<i>SPS3</i>	<i>HU09G02070.1</i>	0.06	0.02	0.02	0	0	0
<i>SPS4</i>	<i>HU11G00237.1</i>	20.08	25.17	16.84	2.78	10.12	9.76

Sucrose synthase

<i>SuSy1</i>	<i>HU02G00890.1</i>	50	296.75	109.37	117.09	258.88	236.68
<i>SuSy2</i>	<i>HU02G01574.1</i>	4.58	17.4	0.35	3.48	0.14	0.48
<i>SuSy3</i>	<i>HU02G02087.1</i>	9.65	11.78	12.71	7.95	11.97	16.78
<i>SuSy4</i>	<i>HU03G00958.1</i>	1.71	3.24	4.83	0.88	2.57	3.25
<i>SuSy5</i>	<i>HU03G02498.1</i>	146.58	4.67	3.9	130.53	2.26	1.96
<i>SuSy6</i>	<i>HU03G02967.1</i>	28.37	53.1	33.85	8.47	9.62	9.13
<i>SuSy7</i>	<i>HU05G00839.1</i>	13.21	19.9	18.85	7.55	13.29	12.64
<i>SuSy8</i>	<i>HU07G01441.1</i>	10.82	55.53	57.16	3.61	6.03	6.63
<i>SuSy9</i>	<i>HU07G01442.1</i>	6.11	24.03	33.17	2.77	3.4	4.45
<i>SuSy10</i>	<i>HU08G01008.1</i>	0.42	0.42	0.51	0.29	0	0
<i>SuSy11</i>	<i>HU11G00421.1</i>	353.84	33.53	62.84	83.81	26.09	21.84

Table S8 Correlation analyses between the main sugar contents and expression patterns of candidate gene in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	Glucose	Fructose	Sucrose	Sorbitol	Galactose	Inositol
<i>FRK5</i>	<i>HU02G01891.1</i>	-0.564*	-0.616**	-0.356	-0.394	-0.444	-0.296
<i>FRK9</i>	<i>HU06G02152.1</i>	-0.821**	-0.875**	-0.565*	-0.642**	-0.777**	-0.349
<i>FRK10</i>	<i>HU06G02213.1</i>	-0.321	0.199	0.546*	-0.457	-0.368	0.692**
<i>HXK1</i>	<i>HU01G00828.1</i>	-0.625**	-0.709**	-0.475*	-0.473*	-0.531*	-0.337
<i>HXK5</i>	<i>HU03G02729.1</i>	-0.263	0.11	0.186	-0.491*	-0.387	0.646**
<i>HXK9</i>	<i>HU08G01226.1</i>	0.796**	0.593**	0.254	0.766**	0.817**	-0.106
<i>HXK12</i>	<i>HU11G00500.1</i>	-0.741**	-0.783**	-0.610**	-0.698**	-0.751**	-0.217
<i>Ivr4</i>	<i>HU03G00349.1</i>	-0.600**	-0.731**	-0.514*	-0.428	-0.510*	-0.406
<i>Ivr6</i>	<i>HU03G01461.1</i>	-0.025	0.225	0.442	0.004	-0.01	0.325
<i>Ivr10</i>	<i>HU03G02457.1</i>	-0.321	-0.168	0.053	-0.327	-0.361	0.117
<i>Ivr20</i>	<i>HU08G00679.1</i>	0.587*	0.201	-0.22	0.561*	0.600**	-0.378
<i>PGI4</i>	<i>HU05G00170.1</i>	-0.278	-0.389	-0.455	-0.277	-0.286	-0.148
<i>SPS1</i>	<i>HU03G00894.1</i>	-0.126	-0.04	-0.06	-0.311	-0.151	0.156
<i>SPS2</i>	<i>HU05G00771.1</i>	-0.166	0.385	0.718**	-0.322	-0.183	0.765**
<i>SPS4</i>	<i>HU11G00237.1</i>	0.282	0.066	-0.215	0.258	0.328	-0.2
<i>SuSy1</i>	<i>HU02G00890.1</i>	0.284	0.454	0.295	0.021	0.186	0.434
<i>SuSy5</i>	<i>HU03G02498.1</i>	-0.761**	-0.908**	-0.642**	-0.569*	-0.699**	-0.495*
<i>SuSy11</i>	<i>HU11G00421.1</i>	-0.607**	-0.666**	-0.396	-0.426	-0.496*	-0.316

Table S9 The transcript abundance of genes related to TCA cycle pathways in ‘WCHL’ and ‘YCHL’ pitayas.

Gene names	Gene ID	‘WCHL’ pitaya			‘YCHL’ pitaya		
		17 d	25 d	29 d	35 d	65 d	75 d
Aconitate hydratase							
<i>ACO1</i>	<i>HU01G01718.1</i>	35.63	84.96	54.41	47.16	70.54	63.8
<i>ACO2</i>	<i>HU01G01740.1</i>	25.97	57.35	28.71	11.55	25.87	18.51
<i>ACO3</i>	<i>HU08G00194.1</i>	21.99	30.09	20.84	26.33	27.45	32.12
2-isopropylmalate synthase							
<i>CMS1</i>	<i>HU01G02605.1</i>	173.29	0.89	0.89	4.33	0	0
<i>CMS2</i>	<i>HU06G01828.1</i>	22.46	32.57	28.19	7.79	16.09	14.98
<i>CMS3</i>	<i>HU08G00711.1</i>	67.82	32.98	22.81	31.18	15.46	10.87
Citrate synthase							
<i>CS1</i>	<i>HU01G00929.1</i>	153.83	130.68	65.25	80.49	120.89	90.4
<i>CS2</i>	<i>HU02G00183.1</i>	53.36	6.07	7.12	8.69	12.68	7.84
<i>CS3</i>	<i>HU02G03260.1</i>	22.37	24.66	21.63	17.04	14.58	13.29
<i>CS4</i>	<i>HU03G01582.1</i>	62.81	46.63	39.22	37.82	42.27	39.99
<i>CS5</i>	<i>HU04G00898.1</i>	0.31	1.11	0.92	0	9.98	10.05
<i>CS6</i>	<i>HU06G02202.1</i>	88.34	29.9	32.27	48.52	36.3	24.6
<i>CS7</i>	<i>HU07G00576.1</i>	0	0	0	0	0	0
<i>CS8</i>	<i>HU07G00635.1</i>	0.86	0.63	0.27	0.23	0.16	0.15
<i>CS9</i>	<i>HU07G01303.1</i>	11.49	15.74	14.41	33.19	12.33	20.86
<i>CS10</i>	<i>HU08G00662.1</i>	59.65	48.16	29.09	46.04	53.3	42.8
<i>CS11</i>	<i>HU08G01468.1</i>	7.52	0.55	0.17	11.63	2.03	1.9
<i>CS12</i>	<i>HU10G00190.1</i>	97.88	10.18	3.46	30.99	12.43	6.87
<i>CS13</i>	<i>HU11G01933.1</i>	0.43	0	0	1.08	0	0
<i>CS14</i>	<i>HU11G01978.1</i>	0	0	0	0.34	0	0
Dihydrolipoyllysine-residue succinyltransferase							
<i>DLST1</i>	<i>HU01G01093.1</i>	0.34	0.2	0.59	0	0	0
<i>DLST2</i>	<i>HU08G00217.1</i>	0.76	0.49	1.79	1.37	1.25	0.82

<i>DLST3</i>	<i>HU10G01974.1</i>	74.68	106.46	84.94	78.33	95.45	78.05
Enolase							
<i>Eno1</i>	<i>HU02G01933.1</i>	0	0.19	0.15	4.56	8.97	7.68
<i>Eno2</i>	<i>HU04G01426.1</i>	73.53	10.45	13.18	27.58	21.15	17.49
<i>Eno3</i>	<i>HU07G02203.1</i>	22.9	16.26	17.92	27.08	21.53	22.65
<i>Eno4</i>	<i>HU09G00620.1</i>	285.93	309.69	100.97	144.21	276.51	271.38
<i>Eno5</i>	<i>HU09G00621.1</i>	623.52	201.32	132.05	315.07	181.19	174.38
Fumarate hydratase							
<i>FUM1</i>	<i>HU02G00881.1</i>	42.42	25.84	29.08	42.32	44.18	43.09
<i>FUM2</i>	<i>HU06G01498.1</i>	31.19	33.24	27.3	20.55	23.94	26.85
Malate dehydrogenase							
<i>MDH1</i>	<i>HU06G02301.1</i>	482.2	174.33	152.57	467.01	425.44	397.99
<i>MDH2</i>	<i>HU07G00587.1</i>	13.47	1.7	0.69	28.87	2.19	3.01
<i>MDH3</i>	<i>HU11G01942.1</i>	1.17	0	0	0.85	0.29	0.54
<i>MDH4</i>	<i>HU11G01943.1</i>	0.56	0	0	0.39	0.39	0.99
2-oxoglutarate dehydrogenase							
<i>OGDH1</i>	<i>HU01G01093.1</i>	0.34	0.2	0.59	0	0	0
<i>OGDH2</i>	<i>HU01G02567.1</i>	15.67	18.05	36.54	5.6	37.22	45.16
<i>OGDH3</i>	<i>HU04G02070.1</i>	58.94	92.45	77.58	38.57	45.66	37.77
<i>OGDH4</i>	<i>HU06G01674.1</i>	0.42	0.96	0.3	0.07	1.17	2.67
<i>OGDH5</i>	<i>HU08G00217.1</i>	0.76	0.49	1.79	1.37	1.25	0.82
<i>OGDH6</i>	<i>HU10G01974.1</i>	74.68	106.46	84.94	78.33	95.45	78.05
Pyruvate dehydrogenase							
<i>PDH1</i>	<i>HU02G00259.1</i>	0.82	0.06	0.5	2.62	4.11	3.29
<i>PDH2</i>	<i>HU02G02870.1</i>	24.87	32.76	34.45	28.84	35.09	33.3
<i>PDH3</i>	<i>HU07G00191.1</i>	109.24	35.16	25.44	39.63	19.4	21.42
<i>PDH4</i>	<i>HU10G00282.1</i>	99.89	58.41	43.15	48.42	52.11	43.38
Phosphoenolpyruvate carboxylase							
<i>PEPC1</i>	<i>HU01G00450.1</i>	0.88	0	0	0	0	0
<i>PEPC2</i>	<i>HU01G00894.1</i>	25.5	51.62	21.3	15.52	58.34	56.87

<i>PEPC3</i>	<i>HU01G00987.1</i>	5.88	170.05	43.39	4.45	620.03	513.18
<i>PEPC4</i>	<i>HU01G00988.1</i>	2.9	86.75	22.02	3.08	314.72	315.79
<i>PEPC5</i>	<i>HU01G00989.1</i>	0.57	2.35	3.06	0.1	0.88	0.72
<i>PEPC6</i>	<i>HU01G00990.1</i>	2.88	2.27	1.77	39.71	72.07	48.41
<i>PEPC7</i>	<i>HU01G00991.1</i>	13.77	7.7	21.5	104.68	24.4	14.17
<i>PEPC8</i>	<i>HU02G00490.1</i>	1.96	1.7	1.51	0.08	0.19	0.19
<i>PEPC9</i>	<i>HU02G02553.1</i>	1.49	0.7	0.81	0.57	0.37	0.37
<i>PEPC10</i>	<i>HU02G02555.1</i>	0.1	0	0.05	1.08	0.78	0.26
<i>PEPC11</i>	<i>HU02G02556.1</i>	4.74	3.1	3.57	1.17	1.58	2.08
<i>PEPC12</i>	<i>HU02G03351.1</i>	0.06	0.63	0.91	0.21	0.79	0
<i>PEPC13</i>	<i>HU03G01008.1</i>	102.25	181.3	125.63	120.33	35.27	21.17
<i>PEPC14</i>	<i>HU03G01874.1</i>	295.76	93.13	87.12	103.75	116.19	103.5
<i>PEPC15</i>	<i>HU04G00337.1</i>	0	0	0	0	0	0
<i>PEPC16</i>	<i>HU08G01056.1</i>	42.11	11.62	9.38	104.78	7.23	4.34
<i>PEPC17</i>	<i>HU08G02244.1</i>	5.42	1.96	3.23	2.36	3.35	2.95
<i>PEPC18</i>	<i>HU09G00446.1</i>	0	0	0	0	0	0
<i>PEPC19</i>	<i>HU09G00447.1</i>	0	0	0	0	0.36	0
<i>PEPC20</i>	<i>HU09G01073.1</i>	9.35	8.03	8.83	5.07	6.49	8.11
<i>PEPC21</i>	<i>HU10G01889.1</i>	0.05	0	0	0	0	0
<i>PEPC22</i>	<i>HU10G01890.1</i>	0.74	0.25	0.05	0.03	0	0
<i>PEPC23</i>	<i>HU10G02036.1</i>	0.04	0	0	0	0	0
<i>PEPC24</i>	<i>HU10G02037.1</i>	0.19	0.08	0	0	0	0

Phosphoenolpyruvate carboxykinase

<i>PEPCK</i>	<i>HU10G00784.1</i>	3.51	92.48	36.01	0.31	9.23	14.93
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Phosphoglycerate kinase

<i>PGK1</i>	<i>HU03G02104.1</i>	69.42	40.4	34.77	17.24	9.99	12.27
<i>PGK2</i>	<i>HU03G02313.1</i>	6.06	4.5	7.25	4.8	5.79	7.91
<i>PGK3</i>	<i>HU05G00547.1</i>	23.81	20.02	24.91	10.42	35.89	34.58

<i>PGK4</i>	<i>HU06G01772.1</i>	546.86	359.49	135.71	397.25	366.86	338.26
<i>PGK5</i>	<i>HU06G02389.1</i>	13.51	15.17	9.66	8.49	14.74	12.14
<i>PGK6</i>	<i>HU10G01770.1</i>	7.56	8.18	10.63	2.86	1.81	1.64

Pyruvate kinase

<i>PK1</i>	<i>HU01G02685.1</i>	0.68	0.67	2.01	1.1	0.38	0.44
<i>PK2</i>	<i>HU01G02786.1</i>	0.31	0.21	0.66	0	0.07	0.13
<i>PK3</i>	<i>HU02G01707.1</i>	37.2	22.1	24.03	13.33	11.08	12.62
<i>PK4</i>	<i>HU02G02411.1</i>	65.91	51.51	28.16	57.65	61.36	57.94
<i>PK5</i>	<i>HU03G00827.1</i>	53.4	7.82	3.55	40.42	46.3	38.4
<i>PK6</i>	<i>HU03G02352.1</i>	164.91	107.49	70.4	105.15	101.53	93.18
<i>PK7</i>	<i>HU04G00494.1</i>	37.08	3.89	2.86	10.51	4.44	2.76
<i>PK8</i>	<i>HU05G00291.1</i>	40.26	6.56	11.17	23.65	13.01	16.2
<i>PK9</i>	<i>HU09G00466.1</i>	84.95	57.56	39.68	38.22	40.14	39.74
<i>PK10</i>	<i>HU09G00634.1</i>	49.96	60.01	66.39	49.06	35.65	41.81
<i>PK11</i>	<i>HU09G01922.1</i>	29.1	9.26	5.64	18.85	17.56	14.8

Succinyl-CoA synthetase

<i>SCS1</i>	<i>HU02G02193.1</i>	51.55	36.82	36.58	70.71	71.57	60.29
<i>SCS2</i>	<i>HU03G02309.1</i>	61.28	32.26	40.91	60.23	47.14	44.04
<i>SCS3</i>	<i>HU10G01334.1</i>	55.71	48.42	40.46	52.02	62.17	46.27

Succinate dehydrogenase

<i>SDH1</i>	<i>HU01G02379.1</i>	6.11	8.27	13.87	6.76	5.93	5.11
<i>SDH2</i>	<i>HU05G02019.1</i>	78.08	60.99	54.24	64.92	80.64	65.92
<i>SDH3</i>	<i>HU06G00028.1</i>	0.93	3.96	1.22	0.18	2.25	2.71

Table S10 Correlation analyses between the main organic acid contents and expression patterns of candidate genes in ‘WCHL’ and ‘YCHL’ pitayas.

<i>Gene names</i>	<i>Gene ID</i>	Malic acid	Citric acid	Citromalic acid	Oxalic acid	Fumaric acid	Succinic acid
<i>ACO1</i>	<i>HU01G01718.1</i>	0.672**	0.35	-0.433	-0.560*	-0.023	0.222
<i>ACO2</i>	<i>HU01G01740.1</i>	0.827**	-0.302	0.201	-0.364	.572*	-0.001
<i>ACO3</i>	<i>HU08G00194.1</i>	0.082	0.331	-0.319	-0.442	-0.272	0.198
<i>CMS1</i>	<i>HU01G02605.1</i>	-	-	0.948**	-	-	-
<i>CMS2</i>	<i>HU06G01828.1</i>	-	-	0.327	-	-	-
<i>CMS3</i>	<i>HU08G00711.1</i>	-	-	0.924**	-	-	-
<i>CS1</i>	<i>HU01G00929.1</i>	-0.02	-0.094	-	-0.139	0.477*	0.295
<i>CS2</i>	<i>HU02G00183.1</i>	-0.480*	-0.368	-	0.302	0.476*	-0.007
<i>CS4</i>	<i>HU03G01582.1</i>	-0.118	-0.376	-	0.156	0.702**	0.174
<i>CS6</i>	<i>HU06G02202.1</i>	-0.459	-0.431	-	0.28	0.495*	0.077
<i>CS10</i>	<i>HU08G00662.1</i>	-0.307	0.14	-	-0.114	0.238	0.517*
<i>CS12</i>	<i>HU10G00190.1</i>	-0.507*	-0.449	-	0.316	0.480*	0.048
<i>DLST1</i>	<i>HU01G01093.1</i>	0.312	-0.626**	-	0.146	0.631**	-0.286
<i>DLST2</i>	<i>HU08G00217.1</i>	-0.085	0.043	-	0.25	-0.267	-0.278
<i>DLST3</i>	<i>HU10G01974.1</i>	0.611**	0.143	-	-0.252	0.025	0.029
<i>Eno4</i>	<i>HU09G00620.1</i>	0.039	0.245	0.363	-0.33	0.206	0.454
<i>Eno5</i>	<i>HU09G00621.1</i>	-0.471*	-0.424	0.838**	0.316	0.458	0.071
<i>FUM1</i>	<i>HU02G00881.1</i>	-0.745**	0.504*	-	-0.032	-0.297	0.524*
<i>FUM2</i>	<i>HU06G01498.1</i>	0.252	-0.367	-	-0.015	0.273	-0.378
<i>MDH1</i>	<i>HU06G02301.1</i>	-0.762**	0.35	-	0.053	-0.195	0.487*
<i>OGDH2</i>	<i>HU01G02567.1</i>	-0.001	0.522*	-	-0.131	-0.329	-0.007
<i>OGDH3</i>	<i>HU04G02070.1</i>	0.844**	-0.577*	-	-0.112	0.689**	-0.266
<i>OGDH6</i>	<i>HU06G01674.1</i>	-0.112	0.451	-	-0.212	-0.418	0.024
<i>PDH3</i>	<i>HU07G00191.1</i>	-0.343	-0.547*	0.892**	0.314	0.577*	-0.037

<i>PDH4</i>	<i>HU10G00282.1</i>	-0.25	-0.447	0.938**	0.192	0.654**	0.108
<i>PEPC3</i>	<i>HU01G00987.1</i>	-0.102	0.804**	-0.431	-0.468	-0.499*	0.375
<i>PEPC4</i>	<i>HU01G00988.1</i>	-0.143	0.768**	-0.425	-0.415	-0.532*	0.31
<i>PEPC7</i>	<i>HU01G00991.1</i>	-0.193	-0.011	-0.195	-0.109	-0.184	0.136
<i>PEPC13</i>	<i>HU03G01008.1</i>	0.529*	-0.661**	0.234	0.147	0.45	-0.28
<i>PEPC14</i>	<i>HU03G01874.1</i>	-0.482*	-0.363	0.899**	0.241	0.489*	0.055
<i>PEPC16</i>	<i>HU08G01056.1</i>	-0.338	-0.21	0.067	0.198	-0.008	0.152
<i>PEPCK</i>	<i>HU10G00784.1</i>	0.803**	-0.288	-0.044	-0.131	0.346	-0.226
<i>PGK4</i>	<i>HU06G01772.1</i>	-0.374	-0.004	0.529*	0.037	0.202	0.351
<i>PK6</i>	<i>HU03G02352.1</i>	-0.331	-0.258	0.815**	0.171	0.518*	0.305
<i>PK9</i>	<i>HU09G00466.1</i>	-0.092	-0.549*	0.937**	0.126	0.706**	-0.014
<i>SCS1</i>	<i>HU02G02193.1</i>	-0.608**	0.607**	-	-0.255	-0.517*	0.546*
<i>SCS2</i>	<i>HU03G02309.1</i>	-0.741**	-0.049	-	0.367	-0.096	0.072
<i>SCS3</i>	<i>HU10G01334.1</i>	-0.24	0.423	-	-0.378	0.104	0.746**
<i>SDH1</i>	<i>HU01G02379.1</i>	0.314	-0.324	-	0.418	-0.037	-0.640**
<i>SDH2</i>	<i>HU05G02019.1</i>	-0.357	0.325	-	-0.337	0.07	0.539*
<i>SDH3</i>	<i>HU06G00028.1</i>	0.536*	0.243	-	-0.272	0.056	0.095