

Figure S1. Physiological indexes of peach fruit at picking time. The firmness of high-sugar, middle-sugar and low-sugar peach fruit at picking time (0 d) (A), the external color of peach fruit at 0 d (B) and TSS of peach fruit was measured by a detector during picking (C).

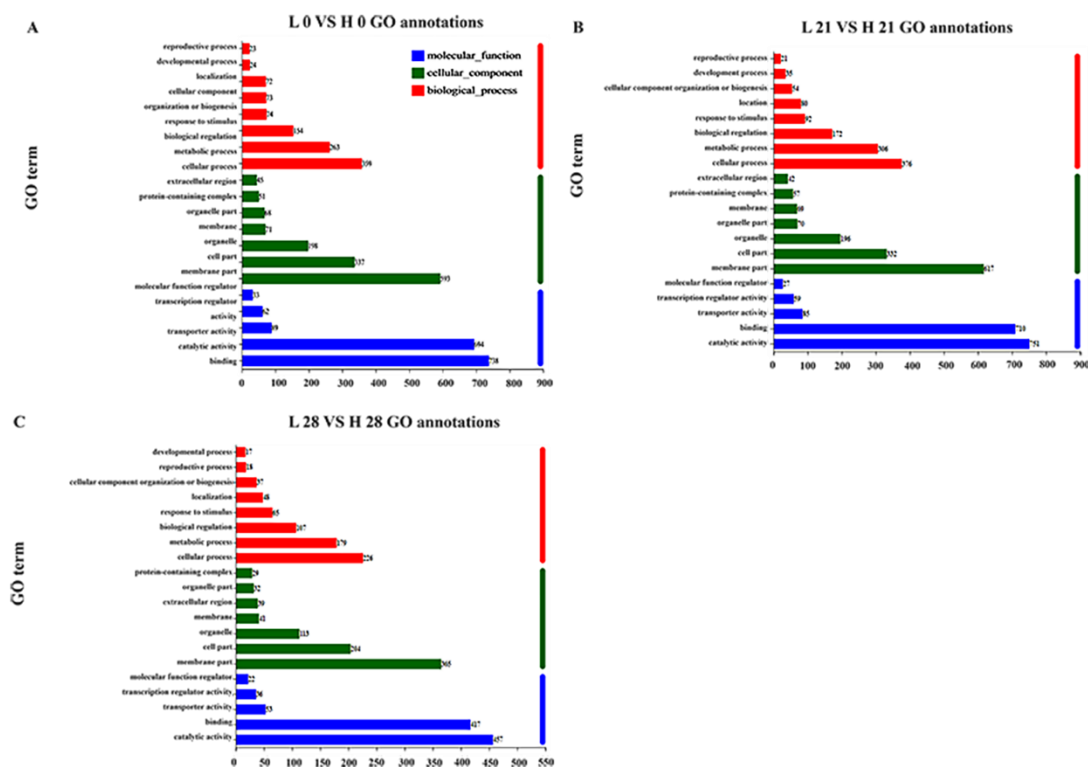


Figure S2. GO function of the DEGs in the three comparison groups of peach fruit. GO function classification of the DEGs in L 0 VS H 0 (A), GO function classification of the DEGs in L 21 VS H 21 (B), GO function classification of the DEGs in L 28 VS H 28 (C).

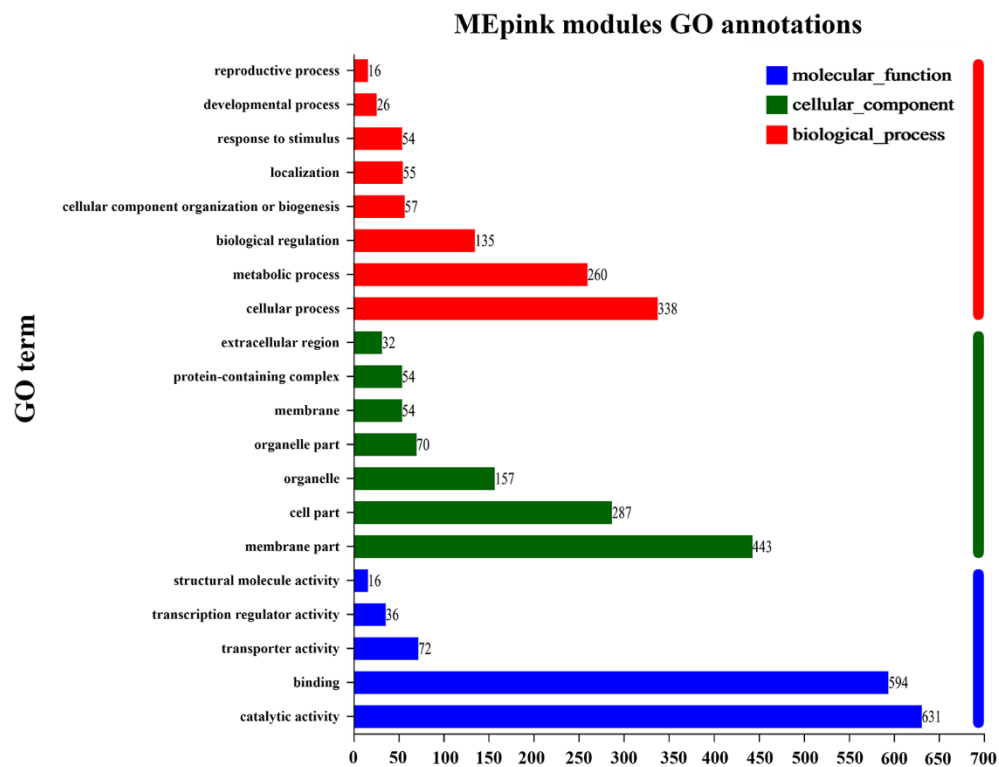


Figure S3. GO function classification of 1468 DEGs in MEpink module.

Supplementary Table S1.

Primers used for quantification of mRNA levels by qRT-PCR

Gene name	Accession no.	Sequence	Product (bp)
<i>PpSS</i> -FP	Prupe.5G241700	GGGCTGACCAATCTGTCTACT	102
<i>PpSS</i> -RP	Prupe.5G241700	CGTTTTCCGCCTTATTGTAGAG	
<i>PpMGAM</i> -FP	Prupe.4G103600	GGAGCTGCGAGGTAGGTGGTAAGCA	149
<i>PpMGAM</i> -RP	Prupe.4G103600	ATGTGAGGCGTGATAGGACTTTTTT	
<i>PpINV</i> -FP	Prupe.3G009500	TCAAGAAGGGATGGTCTGGACT	192
<i>PpINV</i> -RP	Prupe.3G009500	CATCTGCCTGTGCTGCTGTGAC	
<i>PpH XK</i> -FP	Prupe.3G057800	GTTTGACTACATTGCAGCAGAACT	208
<i>PpH XK</i> -RP	Prupe.3G057800	ACTCAATTCAGCCACAACATCTTG	
<i>PpFRK</i> -FP	Prupe.3G160500	GAAGAGTCAAGGGTATGAAGGTA	230
<i>PpFRK</i> -RP	Prupe.3G160500	TTTGAGCATGACATTCAGCACAG	
<i>PpMYB1</i> -FP	Prupe.6G229000	CGACAACGCCATCAAGAACCAC	102
<i>PpMYB1</i> -RP	Prupe.6G229000	TAGCCTCCGCTTCCACCTACAC	
<i>PpMYB3</i> -FP	Prupe.5G182000	TGGGAAATCTAACCTTGGGACA	149
<i>PpMYB3</i> -RP	Prupe.5G182000	GAGAGTTAGAGTCGACGTGTCCA	
<i>PpWRKY4</i> -FP	Prupe.8G265900	ACATTCAAGTCCCCAATTAGATC	104
<i>PpWRKY4</i> -RP	Prupe.8G265900	CAAGAGGAACCCAAGAGTGCTA	
<i>PpbHLH2</i> -FP	Prupe.6G159200	AATTACCACAACGTAATCCTGC	151
<i>PpbHLH2</i> -RP	Prupe.6G159200	GACTCTGACATCTTCCCTTCCT	
<i>PpbZIP1</i> -FP	Prupe.7G160600	GGGTCTTCTAGTGGGGTTTCT	116
<i>PpbZIP1</i> -RP	Prupe.7G160600	CCCGATTGGATAGCATTCTTTT	
<i>PpbZIP2</i> -FP	Prupe.8G091600	GATGATTTGATGGCTCAGATGG	234
<i>PpbZIP2</i> -RP	Prupe.8G091600	AGTGGGCTCATTGAAGCTGCTCGAA	
<i>PpbZIP3</i> -FP	Prupe.1G374400	AATTCCTCTGGTTCCACTCAGCTTC	216
<i>PpbZIP3</i> -RP	Prupe.1G374400	GGTCGTGATGTTTATGCTGGTC	
<i>PpMYB-related1</i> -FP	Prupe.2G176200	ATGGGCCTTCCGGGTCTCAATTCTA	180
<i>PpMYB-related1</i> -RP	Prupe.2G176200	CTCCCTGGACTTGGTAATCGTA	
<i>PpTEF2</i> -FP	Prupe.4G138900	GGTGTGACGATGAAGAGTGATG	129

PpTEF2-RP Prupe.4G138900 TGAAGGAGAGGGAAGGTGAAAG

*Primers are indicated in the 5'→3' direction

Supplementary Table S2.

The quality and statistical summary of the transcriptome study data mapped to the peach genome

Sample	Raw reads	Clean reads	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
H0_01	44994492	44551998	0.03	97.91	93.93	46.42
H0_02	43697494	43336662	0.03	97.97	94.11	46.56
H0_03	43606334	43094710	0.03	97.86	93.86	46.57
L0_01	43922994	43412198	0.02	98.09	94.40	46.60
L0_02	43471474	42975876	0.03	97.90	93.97	46.58
L0_03	43865902	43292868	0.03	97.82	93.77	46.71
H21_01	44226152	43677818	0.03	97.91	93.99	46.56
H21_02	43896830	43266204	0.03	97.95	94.10	46.61
H21_03	42163572	41538068	0.02	98.03	94.29	46.60
L21_01	43189442	42741282	0.03	97.93	94.04	46.49
L21_02	43842088	43316462	0.03	97.96	94.08	46.59
L21_03	43836170	43382696	0.03	97.88	93.94	46.57
H28_01	43316782	42780332	0.03	97.81	93.77	46.48
H28_02	44317212	43613994	0.03	97.94	94.09	46.72
H28_03	44473576	43788868	0.03	97.87	93.92	46.67
L28_01	43592032	42932950	0.03	97.85	93.88	46.56
L28_02	43501166	42973864	0.03	97.83	93.83	46.65
L28_03	43745074	43164166	0.03	97.81	93.76	46.51

Supplementary Table S3.

Pearson's correlation coefficients analysis among the transcriptome study samples

	H0_01	H0_02	H0_03	L0_01	L0_02	L0_03	H21_03	H21_01	H21_02	L21_02	L21_01	L21_03	H28_02	H28_01	H28_03	L28_01	L28_02	L28_03
H0_01	1.00	1.00	1.00	0.96	0.97	0.94	0.53	0.50	0.51	0.53	0.53	0.53	0.51	0.50	0.52	0.40	0.41	0.41
H0_02	1.00	1.00	1.00	0.96	0.97	0.96	0.51	0.48	0.49	0.52	0.51	0.51	0.49	0.48	0.50	0.39	0.40	0.39
H0_03	1.00	1.00	1.00	0.97	0.97	0.96	0.52	0.50	0.51	0.54	0.53	0.52	0.51	0.50	0.52	0.40	0.41	0.40
L0_01	0.96	0.96	0.97	1.00	0.98	0.99	0.51	0.49	0.50	0.54	0.52	0.51	0.49	0.48	0.50	0.39	0.39	0.39
L0_02	0.97	0.97	0.97	0.98	1.00	0.99	0.48	0.46	0.47	0.49	0.48	0.48	0.45	0.44	0.46	0.36	0.37	0.36
L0_03	0.94	0.96	0.96	0.99	0.99	1.00	0.46	0.44	0.45	0.48	0.47	0.46	0.43	0.42	0.44	0.34	0.35	0.34
H21_03	0.53	0.51	0.52	0.51	0.48	0.46	1.00	0.99	0.99	0.90	0.93	0.94	0.91	0.92	0.91	0.94	0.94	0.94
H21_01	0.50	0.48	0.50	0.49	0.46	0.44	0.99	1.00	0.99	0.89	0.91	0.92	0.89	0.89	0.89	0.95	0.94	0.94
H21_02	0.51	0.49	0.51	0.50	0.47	0.45	0.99	0.99	1.00	0.93	0.93	0.93	0.91	0.90	0.90	0.94	0.94	0.94
L21_02	0.53	0.52	0.54	0.54	0.49	0.48	0.90	0.89	0.93	1.00	0.98	0.97	0.93	0.92	0.92	0.86	0.87	0.88
L21_01	0.53	0.51	0.53	0.52	0.48	0.47	0.93	0.91	0.93	0.98	1.00	0.99	0.94	0.95	0.94	0.88	0.90	0.91
L21_03	0.53	0.51	0.52	0.51	0.48	0.46	0.94	0.92	0.93	0.97	0.99	1.00	0.94	0.95	0.95	0.89	0.91	0.92
H28_02	0.51	0.49	0.51	0.49	0.45	0.43	0.91	0.89	0.91	0.93	0.94	0.94	1.00	0.99	0.99	0.93	0.94	0.94
H28_01	0.50	0.48	0.50	0.48	0.44	0.42	0.92	0.89	0.90	0.92	0.95	0.95	0.99	1.00	0.99	0.93	0.94	0.94
H28_03	0.52	0.50	0.52	0.50	0.46	0.44	0.91	0.89	0.90	0.92	0.94	0.95	0.99	0.99	1.00	0.92	0.93	0.93
L28_01	0.40	0.39	0.40	0.39	0.36	0.34	0.94	0.95	0.94	0.86	0.88	0.89	0.93	0.93	0.92	1.00	1.00	0.99
L28_02	0.41	0.40	0.41	0.39	0.37	0.35	0.94	0.94	0.94	0.87	0.90	0.91	0.94	0.94	0.93	1.00	1.00	1.00
L28_03	0.41	0.39	0.40	0.39	0.36	0.34	0.94	0.94	0.94	0.88	0.91	0.92	0.94	0.94	0.93	0.99	1.00	1.00

Supplementary Table S4.

The information of regulatory network of related gene

<i>Gene name</i>	Accession no.	Gene symbol	Gene description
<i>PpSS</i>	Prupe.5G241700	LOC18777229	sucrose synthase 6
<i>PpMGAM</i>	Prupe.4G103600	LOC18781275	alpha-glucosidase
<i>PpINV</i>	Prupe.3G009500	LOC18788064	insoluble isoenzyme CWINV1
<i>PpH XK</i>	Prupe.3G057800	LOC18781930	hexokinase-1
<i>PpFRK</i>	Prupe.3G160500	LOC18783524	fructokinase-6
<i>PpERF1</i>	Prupe.2G272500	LOC18785268	ethylene-responsive transcription factor ERF106
<i>PpERF2</i>	Prupe.2G289500	LOC18787317	dehydration-responsive element-binding protein 1A
<i>PpERF3</i>	Prupe.1G130300	LOC18789727	ethylene-responsive transcription factor RAP2-3
<i>PpERF4</i>	Prupe.4G176200	LOC18778290	ethylene-responsive transcription factor 4

<i>PpERF5</i>	Prupe.5G090100	LOC18776409	dehydration-responsive element-binding protein 1E
<i>PpERF6</i>	Prupe.6G039700	LOC18772665	pathogenesis-related genes transcriptional activator PTI6
<i>PpERF7</i>	Prupe.6G064700	LOC18772983	chromatin modification-related protein eaf-1
<i>PpERF8</i>	Prupe.7G194400	LOC18771728	ethylene-responsive transcription factor ERF017
<i>PpHB-other1</i>	Prupe.1G271400	LOC18792206	homeobox-leucine zipper protein ATHB-13
<i>PpHB-other2</i>	Prupe.2G156900	LOC18787087	homeobox-leucine zipper protein ANTHOCYANINLESS 2
<i>PpHB-other3</i>	Prupe.2G241700	LOC18784831	BEL1-like homeodomain protein 9
<i>PpHB-other4</i>	Prupe.6G102300	LOC18773641	homeobox-leucine zipper protein REVOLUTA
<i>PpHB-other5</i>	Prupe.6G263900	LOC18772447	BEL1-like homeodomain protein 9
<i>PpHB-other6</i>	Prupe.7G079300	LOC18771696	homeobox-leucine zipper protein HOX11
<i>PpHB-other7</i>	Prupe.7G149700	LOC18769821	homeobox-leucine zipper protein ATHB-40
<i>PpMYB1</i>	Prupe.6G229000	LOC18775054	transcription factor MYB44
<i>PpMYB2</i>	Prupe.1G323400		Myblike DNA-binding domain containing protein
<i>PpMYB3</i>	Prupe.5G182000	LOC18777189	transcription factor MYB1R1
<i>PpMYB4</i>	Prupe.4G035100	LOC18781079	transcription repressor MYB6
<i>PpMYB5</i>	Prupe.6G267600	LOC18772814	transcription factor MYB1
<i>PpMYB6</i>	Prupe.6G303300	LOC18772237	transcription factor MYB86
<i>PpMYB7</i>	Prupe.6G085000	LOC18773813	transcription factor MYB59
<i>PpNAC1</i>	Prupe.1G383200	LOC18791355	NAC domain-containing protein 79
<i>PpNAC2</i>	Prupe.2G202000	LOC18787361	NAC domain-containing protein 67
<i>PpNAC3</i>	Prupe.2G202600	LOC109947178	NAC domain-containing protein 100-like
<i>PpNAC4</i>	Prupe.3G014400	LOC18782146	NAC domain-containing protein 86
<i>PpNAC5</i>	Prupe.4G143600	LOC18780262	NAC domain-containing protein 21/22
<i>PpNAC6</i>	Prupe.7G217000	LOC18771576	protein BEARSKIN2
<i>PpWRKY1</i>	Prupe.1G071400	LOC18789894	probable WRKY transcription factor 11
<i>PpWRKY2</i>	Prupe.1G114800	LOC18789015	probable WRKY transcription factor 48
<i>PpWRKY3</i>	Prupe.3G214800	LOC18782434	probable WRKY transcription factor 31
<i>PpWRKY4</i>	Prupe.8G265900	LOC18766660	WRKY transcription factor 69
<i>PpWRKY5</i>	Prupe.6G286000	LOC18772845	probable WRKY transcription factor 33
<i>PpbHLH1</i>	Prupe.1G304900	LOC18793925	transcription factor bHLH30
<i>PpbHLH2</i>	Prupe.6G159200	LOC18775069	transcription factor HEC2
<i>PpbHLH3</i>	Prupe.3G312800	LOC18782429	transcription factor ICE1
<i>PpbHLH4</i>	Prupe.7G071500	LOC18770320	transcription factor bHLH130

<i>PpbHLH5</i>	Prupe.8G242100	LOC18767836	basic helix-loop-helix protein A
<i>PpbZIP1</i>	Prupe.7G160600	LOC18769167	bZIP transcription factor 44
<i>PpbZIP2</i>	Prupe.8G091600	LOC18767767	bZIP transcription factor 11
<i>PpbZIP3</i>	Prupe.1G374400	LOC18788985	bZIP transcription factor 11
<i>PpbZIP4</i>	Prupe.6G343100	LOC18773097	light-inducible protein CPRF2
<i>PpARF1</i>	Prupe.2G190400	LOC18786825	auxin response factor 18
<i>PpARF2</i>	Prupe.6G097700	LOC18772269	auxin response factor 4
<i>PpARF3</i>	Prupe.8G252300	LOC18768867	auxin response factor 2
<i>PpHSF1</i>	Prupe.1G021200	LOC18790318	heat stress transcription factor A-6b
<i>PpHSF2</i>	Prupe.1G433500	LOC18788483	heat stress transcription factor B-4
<i>PpHSF3</i>	Prupe.4G046000	LOC18779732	heat stress transcription factor B-2a
<i>PpMYB_related1</i>	Prupe.2G176200	LOC18784574	protein REVEILLE 3
<i>PpMYB_related2</i>	Prupe.6G106200	LOC18772343	
<i>PpDof1</i>	Prupe.1G388600	LOC109946797	dof zinc finger protein DOF3.4
<i>PpDof2</i>	Prupe.5G173100	LOC18776482	dof zinc finger protein DOF5.6
<i>PpGRAS</i>	Prupe.5G091700	LOC18776291	scarecrow-like protein 28
<i>PpTCP</i>	Prupe.4G171100	LOC18780672	transcription factor TCP4
<i>PpLBD (AS2/LOB)</i>	Prupe.4G105700	LOC18781496	LOB domain-containing protein 4
<i>PpLBD (AS2/LOB)</i>	Prupe.3G290800	LOC18781820	LOB domain-containing protein 25
<i>PpSBP</i>	Prupe.4G050400	LOC18778248	squamosa promoter-binding-like protein 3
<i>PpSBP</i>	Prupe.1G290200	LOC18790408	squamosa promoter-binding-like protein 6
<i>PpSBP</i>	Prupe.7G074200	LOC18769457	squamosa promoter-binding-like protein 9
<i>PpDBB</i>	Prupe.3G155900	LOC18784147	B-box zinc finger protein 24
<i>PpMIKC</i>	Prupe.1G549600	LOC18789032	agamous-like MADS-box protein AGL11
<i>PpMIKC</i>	Prupe.3G170600	LOC18783633	agamous-like MADS-box protein AGL1
<i>PpB3</i>	Prupe.4G049500	LOC18779046	B3 domain-containing transcription factor LEC2
<i>PpAP2</i>	Prupe.1G084900	LOC18791311	AP2-like ethylene-responsive transcription factor AIL5
<i>PpNF-YA</i>	Prupe.3G043900	LOC18782250	nuclear transcription factor Y subunit A-3
<i>PpCPP</i>	Prupe.1G019100	LOC18789798	CRC domain-containing protein TSO1
<i>PpGRAS</i>	Prupe.7G236100	LOC18769184	DELLA protein DWARF8
<i>PpM_type2</i>	Prupe.7G164100	LOC18769016	floral homeotic protein DEFICIENS
<i>PpZF-HD</i>	Prupe.7G155700	LOC18769526	zinc-finger homeodomain protein 6
<i>PpAP23</i>	Prupe.6G203000	LOC18773090	AP2-like ethylene-responsive transcription factor AIL6