

Table S1. Statistics of RNA-seq data of ‘CM’ and ‘CX’ peach fruit sample.

Sample name	UMI reads	UMI mapped (%)	Multiple mapped reads (%)	Uniquely mapped reads (%)	Read-1 (%)	Read-2 (%)	Reads mapped to positive strand (%)	Reads mapped to negative strand (%)	Non-splice reads (%)	Splice reads (%)
CM_CK01	3656584	34591929	849748	33742181	17120213	16621968	16877994	16864187	21765222	11976959
1	2	(94.6%)	(2.32%)	(92.28%)	(46.82%)	(45.46%)	(46.16%)	(46.12%)	(59.52%)	(32.75%)
CM_CK01	4072244	38426860	862241	37564619	19083882	18480737	18782288	18782331	24751075	12813544
1	6	(94.36%)	(2.12%)	(92.25%)	(46.86%)	(45.38%)	(46.12%)	(46.12%)	(60.78%)	(31.47%)
CM_CK01	3785692	35890976	837280	35053696	17766671	17287025	17533249	17520447	22883183	12170513
1	8	(94.81%)	(2.21%)	(92.6%)	(46.93%)	(45.66%)	(46.31%)	(46.28%)	(60.45%)	(32.15%)
CM_L1_1	3620234	34378875	699243	33679632	17136039	16543593	16857112	16822520	22297921	11381711
0		(94.96%)	(1.93%)	(93.03%)	(47.33%)	(45.7%)	(46.56%)	(46.47%)	(61.59%)	(31.44%)
CM_L1_2	3672248	34773001	701272	34071729	17309791	16761938	17035042	17036687	22430051	11641678
8		(94.69%)	(1.91%)	(92.78%)	(47.14%)	(45.64%)	(46.39%)	(46.39%)	(61.08%)	(31.7%)
CM_L1_3	5678149	54163134	1311648	52851486	26739740	26111746	26448626	26402860	34617037	18234449
2		(95.39%)	(2.31%)	(93.08%)	(47.09%)	(45.99%)	(46.58%)	(46.5%)	(60.97%)	(32.11%)
CM_L2_1	3741501	35654308	900668	34753640	17559694	17193946	17399071	17354569	22887590	11866050
0		(95.29%)	(2.41%)	(92.89%)	(46.93%)	(45.95%)	(46.5%)	(46.38%)	(61.17%)	(31.71%)
CM_L2_2	7295371	68368930	1813292	66555638	33916771	32638867	33317684	33237954	43756501	22799137
4		(93.72%)	(2.49%)	(91.23%)	(46.49%)	(44.74%)	(45.67%)	(45.56%)	(59.98%)	(31.25%)
CM_L2_3	3789351	35704728	866640	34838088	17781893	17056195	17435311	17402777	23347139	11490949
8		(94.22%)	(2.29%)	(91.94%)	(46.93%)	(45.01%)	(46.01%)	(45.93%)	(61.61%)	(30.32%)
CX_CK01	3636128	34456648	482812	33973836	17272135	16701701	16981278	16992558	22161790	11812046
4		(94.76%)	(1.33%)	(93.43%)	(47.5%)	(45.93%)	(46.7%)	(46.73%)	(60.95%)	(32.49%)

CX_CK01	3894731 36898576 0 (94.74%)	513110 (1.32%)	36385466 (93.42%)	18453421 (47.38%)	17932045 (46.04%)	18190681 (46.71%)	18194785 (46.72%)	24019915 (61.67%)	12365551 (31.75%)
CX_CK01	4136194 39150676 8 (94.65%)	552248 (1.34%)	38598428 (93.32%)	19615537 (47.42%)	18982891 (45.89%)	19274951 (46.6%)	19323477 (46.72%)	24969883 (60.37%)	13628545 (32.95%)
CX_L1_1	3609403 34141551 4 (94.59%)	1644363 (4.56%)	32497188 (90.03%)	16500416 (45.72%)	15996772 (44.32%)	16299730 (45.16%)	16197458 (44.88%)	22141254 (61.34%)	10355934 (28.69%)
CX_L1_2	3882781 36824603 6 (94.84%)	1748488 (4.5%)	35076115 (90.34%)	17852510 (45.98%)	17223605 (44.36%)	17618671 (45.38%)	17457444 (44.96%)	23891319 (61.53%)	11184796 (28.81%)
CX_L1_3	3939061 37421618 (95%) 4 (4.4%)	1731290 (4.4%)	35690328 (90.61%)	18172928 (46.14%)	17517400 (44.47%)	17943150 (45.55%)	17747178 (45.05%)	24282094 (61.64%)	11408234 (28.96%)
CX_L2_1	3675599 34915871 4 (94.99%)	1160303 (3.16%)	33755568 (91.84%)	17046100 (46.38%)	16709468 (45.46%)	16884475 (45.94%)	16871093 (45.9%)	22309410 (60.7%)	11446158 (31.14%)
CX_L2_2	4144059 39448579 8 (95.19%)	1369794 (3.31%)	38078785 (91.89%)	19279116 (46.52%)	18799669 (45.37%)	19052864 (45.98%)	19025921 (45.91%)	25095994 (60.56%)	12982791 (31.33%)
CX_L2_3	3625715 34508976 2 (95.18%)	1189683 (3.28%)	33319293 (91.9%)	16832311 (46.42%)	16486982 (45.47%)	16661409 (45.95%)	16657884 (45.94%)	21889346 (60.37%)	11429947 (31.52%)

Abbreviations used are as follows: CK0, immediately after harvest; L1, at the start of ethylene; L2, at the peak of ethylene release.

Table S2. Quality of reads obtained by RNA-seq analysis of ‘CM’ and ‘CX’ peach fruit sample.

Sample name	Raw data (Gb)	Clean data (Gb)	Error rate (%)	Q20 (%)	Q30 (%)
CM_CK01	7.02G	5.94G	0.03	98.05	94.07
CM_CK01	7.91G	6.64G	0.03	97.88	93.72
CM_CK01	7.12G	6.13G	0.03	97.90	93.73

CM_L1_1	7.08G	5.89G	0.03	97.91	93.73
CM_L1_2	7.03G	5.98G	0.03	98.03	93.95
CM_L1_3	10.29G	9.23G	0.03	97.97	93.92
CM_L2_1	6.45G	6.07G	0.03	97.46	92.77
CM_L2_2	13.99G	11.76G	0.03	97.29	92.50
CM_L2_3	7.58G	6.16G	0.03	97.95	93.77
CX_CK01	7.03G	5.88G	0.03	97.93	93.74
CX_CK01	7.54G	6.28G	0.03	97.96	93.88
CX_CK01	7.82G	6.72G	0.03	97.95	93.86
CX_L1_1	7.02G	5.89G	0.03	97.96	93.87
CX_L1_2	7.39G	6.31G	0.03	97.82	93.51
CX_L1_3	7.43G	6.42G	0.03	97.91	93.74
CX_L2_1	6.9G	5.97G	0.02	98.10	94.26
CX_L2_2	8.1G	6.78G	0.03	97.97	93.91
CX_L2_3	6.79G	5.92G	0.03	98.04	94.04

Table S3. Correlation matrix of RNA-seq samples.

Sample	CM_CK	CM_CK	CM_CK	CM_L1	CM_L1	CM_L1	CM_L2	CM_L2	CM_L2	CX_CK	CX_CK	CX_CK	CX_L1	CX_L1	CX_L1	CX_L2	CX_L2	CX_L2	
	01	02	03	_1	_2	_3	_1	_2	_3	01	02	03	_1	_2	_3	_1	_2	_3	
CM_CK 01		1	0.994	0.994	0.819	0.825	0.861	0.863	0.864	0.861	0.94	0.941	0.945	0.815	0.817	0.811	0.754	0.755	0.757
CM_CK	0.994		1	0.994	0.819	0.825	0.861	0.862	0.863	0.862	0.939	0.941	0.944	0.815	0.817	0.811	0.755	0.756	0.757

02

CM_CK
03

0.994	0.994	1	0.819	0.824	0.86	0.862	0.863	0.861	0.941	0.943	0.945	0.815	0.817	0.811	0.754	0.755	0.756
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CM_L1
_1

0.819	0.819	0.819	1	0.99	0.961	0.897	0.904	0.906	0.85	0.856	0.863	0.869	0.872	0.879	0.904	0.905	0.901
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CM_L1
_2

0.825	0.825	0.824	0.99	1	0.968	0.904	0.909	0.908	0.862	0.865	0.87	0.876	0.879	0.878	0.908	0.908	0.907
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CM_L1
_3

0.861	0.861	0.86	0.961	0.968	1	0.97	0.971	0.969	0.889	0.891	0.893	0.923	0.924	0.918	0.912	0.912	0.914
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CM_L2
_1

0.863	0.862	0.862	0.897	0.904	0.97	1	0.994	0.991	0.877	0.879	0.88	0.929	0.93	0.925	0.879	0.879	0.881
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CM_L2
_2

0.864	0.863	0.863	0.904	0.909	0.971	0.994	1	0.995	0.876	0.878	0.882	0.93	0.931	0.929	0.884	0.884	0.885
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CM_L2
_3

0.861	0.862	0.861	0.906	0.908	0.969	0.991	0.995	1	0.872	0.875	0.879	0.927	0.929	0.929	0.882	0.883	0.882
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CX_CK
01

0.94	0.939	0.941	0.85	0.862	0.889	0.877	0.876	0.872	1	0.994	0.99	0.806	0.807	0.795	0.786	0.787	0.79
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CX_CK
02

0.941	0.941	0.943	0.856	0.865	0.891	0.879	0.878	0.875	0.994	1	0.991	0.808	0.808	0.798	0.789	0.79	0.791
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CX_CK
03

0.945	0.944	0.945	0.863	0.87	0.893	0.88	0.882	0.879	0.99	0.991	1	0.809	0.81	0.805	0.794	0.795	0.796
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CX_L1
_1

0.815	0.815	0.815	0.869	0.876	0.923	0.929	0.93	0.927	0.806	0.808	0.809	1	0.993	0.986	0.9	0.9	0.902
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CX_L1
_2

0.817	0.817	0.817	0.872	0.879	0.924	0.93	0.931	0.929	0.807	0.808	0.81	0.993	1	0.988	0.901	0.902	0.903
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CX_L1_3	0.811	0.811	0.811	0.879	0.878	0.918	0.925	0.929	0.929	0.795	0.798	0.805	0.986	0.988	1	0.901	0.902	0.9
CX_L2_1	0.754	0.755	0.754	0.904	0.908	0.912	0.879	0.884	0.882	0.786	0.789	0.794	0.9	0.901	0.901	1	0.994	0.993
CX_L2_2	0.755	0.756	0.755	0.905	0.908	0.912	0.879	0.884	0.883	0.787	0.79	0.795	0.9	0.902	0.902	0.994	1	0.993
CX_L2_3	0.757	0.757	0.756	0.901	0.907	0.914	0.881	0.885	0.882	0.79	0.791	0.796	0.902	0.903	0.9	0.993	0.993	1

Table S4. List of names and IDs of genes involved in ethylene and ABA biosynthesis and signaling, lipid metabolism. The abbreviations used are listed in the legend to Fig. 3.

	Sample	CM_CK0	CM_L1	CM_L2	CX_CK0	CX_L1	CX_L2
Ethylene	Prupe.1G034300 ETR	17.61055658	112.3402637	127.4228872	33.15224792	74.31544703	182.9672569
	Prupe.7G254900 CTR1	8.943620495	6.399910964	11.68846564	9.436605371	3.561679619	4.793696263
	Prupe.7G117700 CTR1	9.778313373	12.18927085	20.15137746	13.97316972	19.06586873	24.86293016
	Prupe.6G235600 EIN2	60.53339978	38.34609981	66.1455199	41.31351843	57.89960713	29.47634763
	Prupe.7G244300 EBF1	8.125526651	18.91585491	42.49044703	10.10430316	40.09389863	48.15697243
	Prupe.1G480700 EBF	52.13443035	45.96194992	101.7419015	83.5253074	74.95320044	102.1319139
	Prupe.1G107000 SAM1	1425.012297	2818.913931	1670.150785	1576.065365	1622.878833	2781.648657
	Prupe.2G176900 ACS1	92.73336001	262.5432466	577.9011357	150.2282406	410.5892546	1891.585457
	Prupe.5G083500 ACS2	3.574899782	11.66545147	18.24605937	5.404841197	8.92815028	6.665613501
	Prupe.3G209900 ACO1	3580.110469	22323.05886	18935.71298	10279.38723	14159.01408	30567.95912
	Prupe.4G013800 ACO2	26.25556246	5.701482667	19.58441932	3.780487888	66.69378716	145.9510381
ABA	Prupe.7G133100 ZEP	461.2284828	597.0990826	684.3769574	184.5947431	1833.625172	449.3352452
	Prupe.6G154100 ZEP	10.82033	1.731277315	3.962552864	14.40037322	1.128231982	0.267731707
	Prupe.4G082000 NCED3	23.56190926	304.4085517	1047.663118	129.3110318	357.5750975	216.3042515
	Prupe.4G150100 NCED2	2787.317951	1106.302223	3624.508861	2592.495543	1512.191043	576.8497661
	Sample	CM_CK0	CM_L1	CM_L2	CX_CK0	CX_L1	CX_L2

ABA	Prupe.2G029900 ABA2	18.82872757	12.224371	5.355887192	23.98803774	6.830283201	9.756307875
	Prupe.6G150900 AAO3	11.09910745	2.1859919 21	4.238392581	8.498545903	4.350667868	2.167447964
	Prupe.7G051800 BG	0	0.0570408	0.259734807	0	4.099213903	23.16698763
	Prupe.7G267900 UGT	1332.726701	2020.729769	1876.255514	679.9141341	2883.073982	1243.011285
	Prupe.5G013100 CYP707A	0.018127565	1.56414632	0.523328437	0.733758353	1.7776714	22.48157823
	Prupe.1G413500 PYL/PYR	139.3504487	81.5618451	35.31965007	132.6589839	214.6025973	54.64570541
	Prupe.6G284000 PYL/PYR	157.1548208	391.057638	87.26424581	139.4162555	30.99051298	146.1010791
	Prupe.7G204800 PYL/PYR	243.2953517	168.3214592	746.8861846	207.0675733	471.4591622	183.6790531
	Prupe.2G239700 PP2C	261.8836167	289.6044474	730.8857143	176.0815911	824.2263197	387.8008546
	Prupe.5G054500 SnRK2	101.9096429	171.9580103	370.7242878	104.2480168	280.6235295	195.8611338
Lipid	Prupe.8G041800 CK	18.07394893	79.40128877	35.66904066	86.68853143	25.55906634	50.20138487
	Prupe.5G233000 PMT	11.88996516	0.739594224	2.811955774	5.52606567	1.943416838	1.622881735
	Prupe.7G262100 AAPT	37.48398794	46.10544441	72.40727782	37.31996456	164.7124058	46.12735442
	Prupe.3G228600 DGK	12.39024855	24.08739152	11.81574551	20.9116645	10.76975727	36.12334715
	Prupe.1G317400 PAP	45.14666773	3.297032827	4.139631203	12.48145049	83.34268427	101.3817589

	Sample	CM_CK0	CM_L1	CM_L2	CX_CK0	CX_L1	CX_L2
Lipid	Prupe.1G319700 PSS	15.22872014	6.048495202	7.605324528	3.895729952	22.35935953	9.567023379
	Prupe.4G011700 CDS	14.69829409	12.754630 92	17.17576219	14.54615167	23.26011015	17.01828055
	Prupe.6G325200 LACS	9.545025834	9.652592863	10.82955535	24.79695194	7.078295383	6.14308022
	Prupe.2G098700 PLC	7.826068397	59.48045181	68.66648564	8.510372969	133.160452	211.7426126
	Prupe.6G058400 PLC	36.20930494	47.88609371	61.37298373	37.58377317	84.02754356	77.67902364
	Prupe.2G250000 PLC	21.52050613	19.95460922	49.54659556	30.11070003	57.31326162	21.67794216
	Prupe.2G250100 PLC	49.31598494	47.34748958	46.92820319	40.73668606	85.69910138	53.06359773
	Prupe.6G056900 PLC	9.986569066	11.46299729	17.66751367	12.61591304	21.95484682	16.04491942
	Prupe.3G084800 PLDα	373.6323758	77.11037615	130.8848406	283.6904719	113.2969335	62.85047423
	Prupe.1G130000 PLDζ	12.30271773	12.36913803	17.28731255	11.14653405	20.572862	12.63907718
	Prupe.4G259400 FAD	3.574358455	16.86240422	2.183374316	4.047676762	3.59935588	6.178756365
	Prupe.6G056100 FAD	0.173637343	321.2727487	98.8387297	7.334752792	166.3958413	435.5096503
	Prupe.6G278800 FAD	25.14539753	11.45328865	6.425438548	38.35079963	4.325625108	11.7591029
FA	Prupe.4G082200 PDH	47.64556456	46.91621221	15.37260596	64.97160716	17.43319359	42.7389643
	Prupe.1G512000 ACCase	42.4466727	58.67288955	24.93310197	18.55755129	45.23580936	26.22652871

	Sample	CM_CK0	CM_L1	CM_L2	CX_CK0	CX_L1	CX_L2
FA	Prupe.4G015900 MCD	14.38861553	6.058510466	4.949429415	6.592078875	3.357416946	2.459237762
	Prupe.5G154900 KAR	25.71565527	26.612104 39	15.6890292	40.89238502	9.378781081	24.82750312
	Prupe.6G365200 SAD	84.41168235	41.69365618	30.17323222	85.4466629	15.61391601	44.32453025
	Prupe.7G221100 ENR	1607.390966	429.2204113	651.0712911	922.2554044	770.4389618	375.295089
	Prupe.6G015200 ENR	19.19026802	10.83028997	6.763071489	25.41237247	3.333196107	4.332844036

Table S5. List of genes in the co-expression network of Fig. S9A and B.

Gene ID in Fig. S9A	Label in Fig. S9A	Gene ID in Fig. S9B	Label in Fig. S9B
Prupe.1G478400	bZIP	Prupe.1G455300	bZIP
Prupe.2G098700	PLC	Prupe.2G182800	bZIP
Prupe.2G176900	ACS1	Prupe.2G202500	NAC
Prupe.3G098100	WRKY	Prupe.2G202600	NAC
Prupe.3G209900	ACO1	Prupe.2G202700	NAC
Prupe.3G228600	DGK	Prupe.3G269500	bHLH
Prupe.4G013800	ACO2	Prupe.4G077100	bHLH
Prupe.4G055500	ERF	Prupe.4G082000	NCED2
Prupe.5G013100	CYP707A	Prupe.5G040400	NAC
Prupe.5G061800	ERF	Prupe.6G303500	bHLH
Prupe.5G117800	ERF	Prupe.7G094500	DGD
Prupe.6G056100	FAD	Prupe.7G114400	bZIP
Prupe.7G051800	DGK		
Prupe.8G126600	bZIP		
Prupe.5G054500	SnRK2		

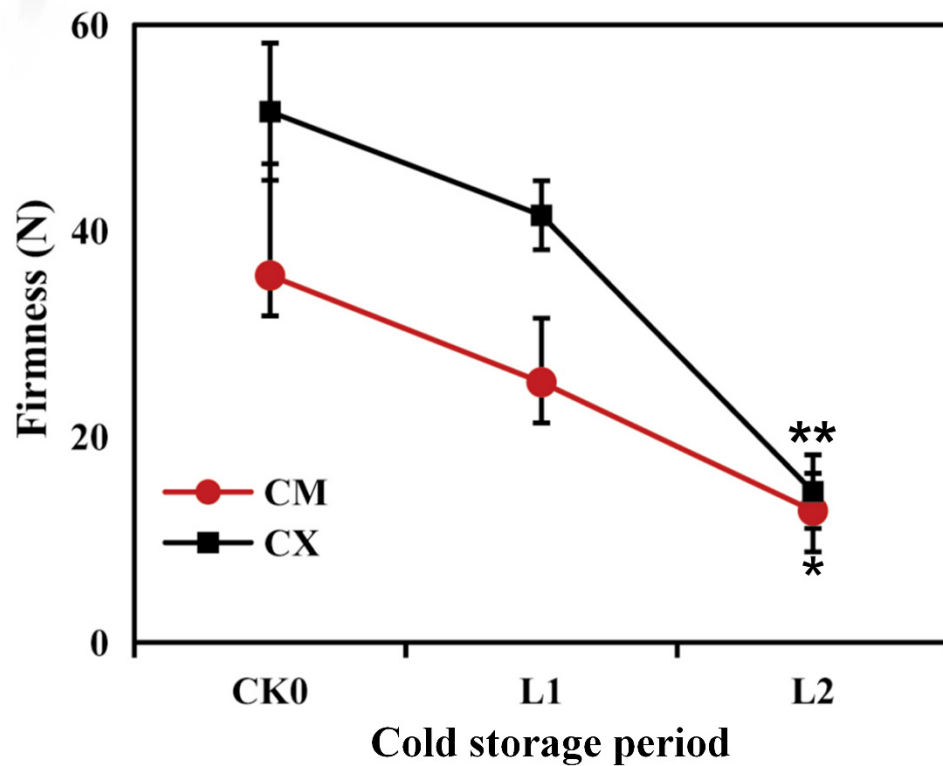


Fig. S1. Changes of firmness of CX and CM fruits during low temperature storage

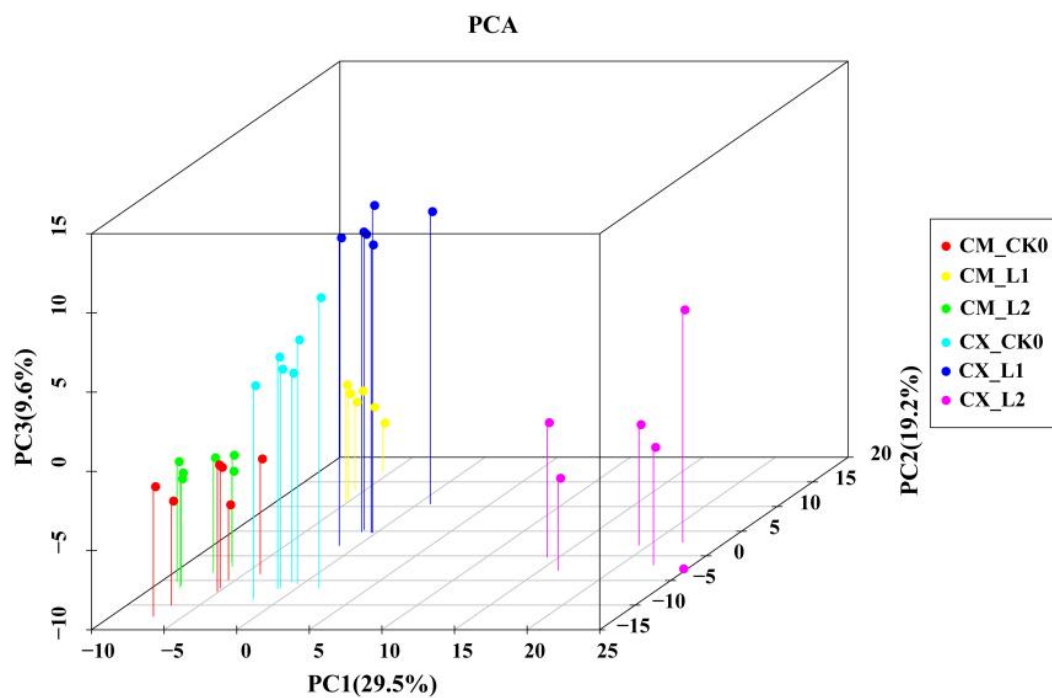


Fig. S2. Principal component analysis (PCA) of the lipidome data in 'CM' and 'CX' peaches stored at low temperature.

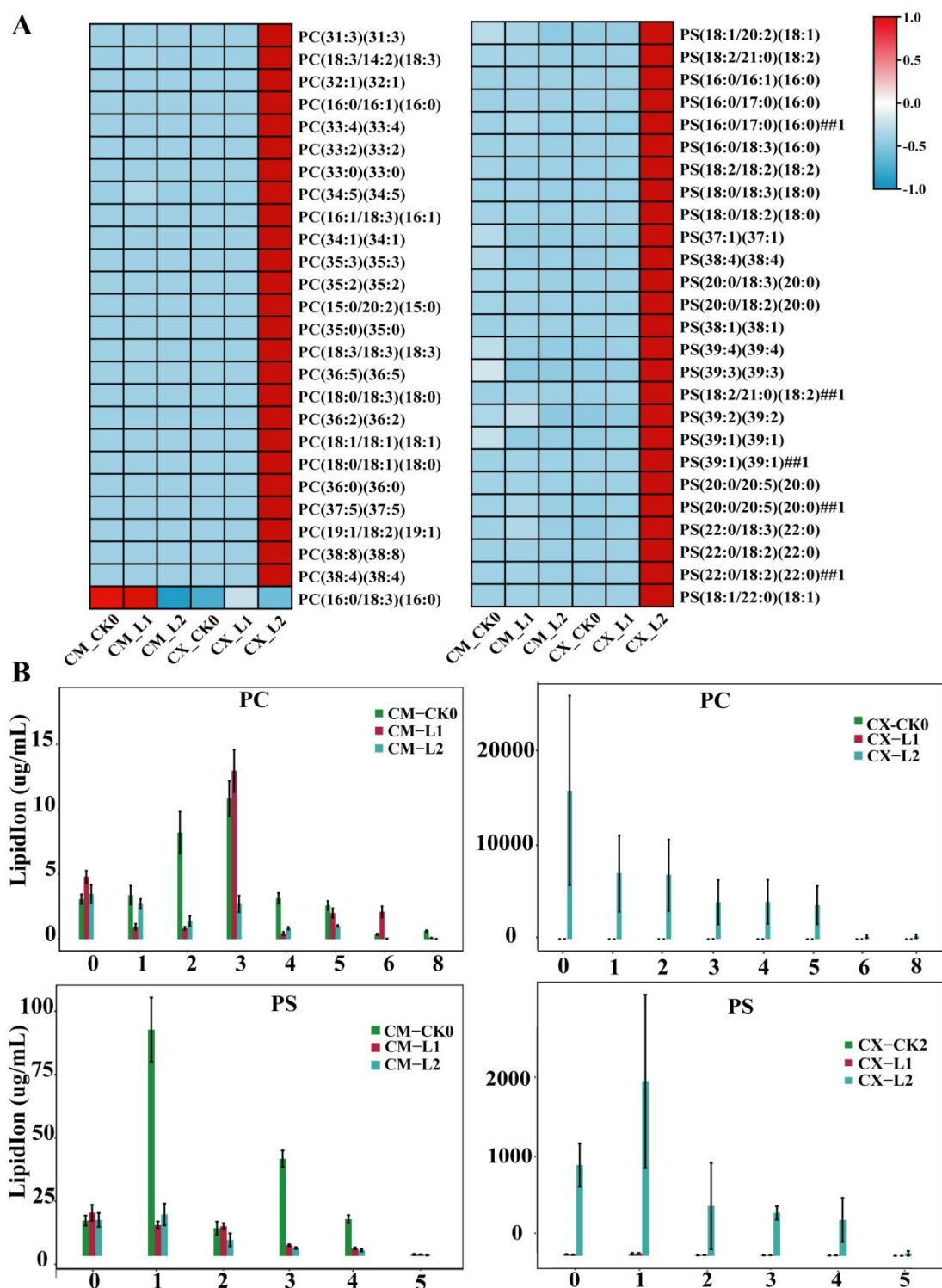


Fig. S3. Lipid type and saturation analysis of 'CM' and 'CX' peaches stored at low temperature. (A) Changes in mainly lipid types; (B) Changes in lipid saturation of PC and PS. Blue, white, and red colors indicate low, medium, and high contents, respectively. The error bars represent the standard error (SE) calculated according to six independent biological replicates.

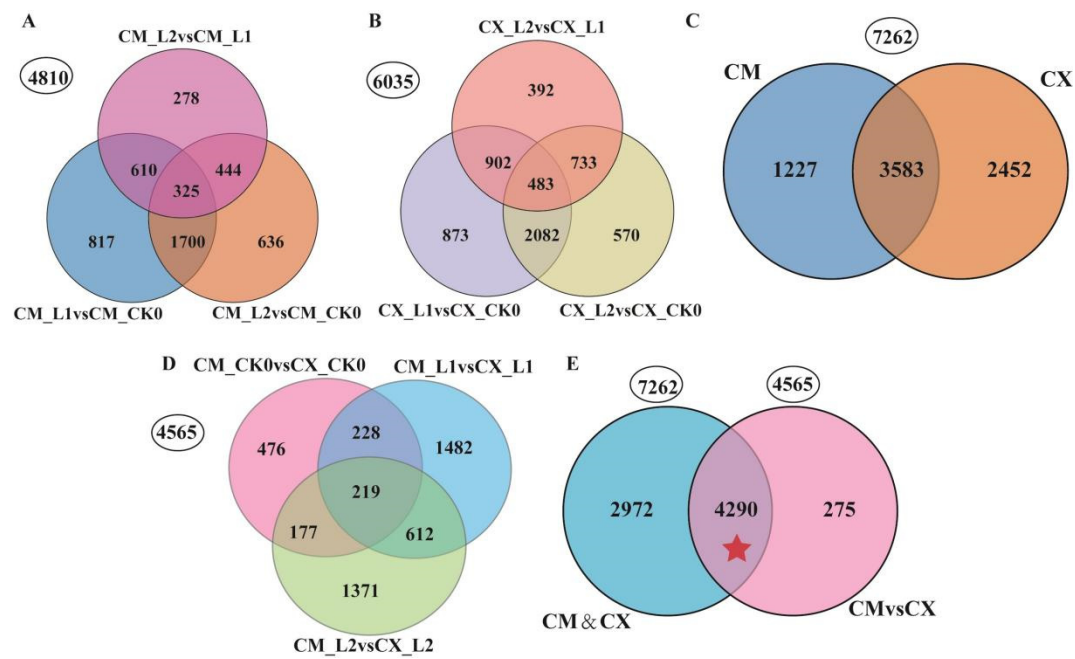


Fig. S4. Venn diagrams of DEGs among the different comparison groups. (A) CM responds to low temperature differential genes; (B) Spring snow responds to low temperature differential genes; (C) Spring beauty and spring beauty responds to low temperature differential genes Veen; (D) Different genes in each period of the two varieties.

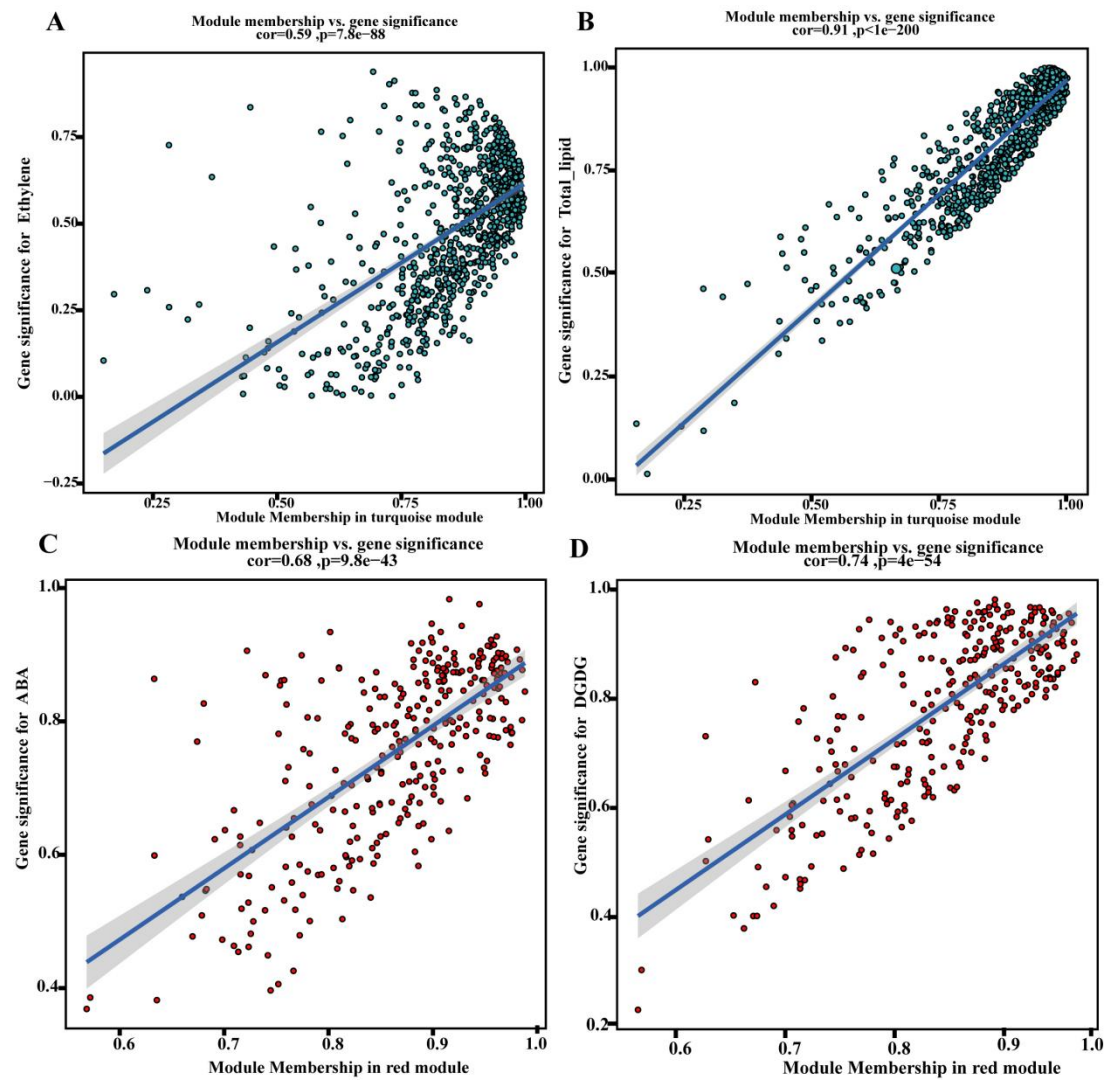


Fig. S5. The gene significance (GS) for ethylene (y-axis), total lipid(y-axis), ABA(y-axis) and DGDG (y-axis) vs. the module membership (x-axis) in modules turquoise and red. (A-B) Gene significance (GS) for ethylene and total lipid vs. module membership in module turquoise. (C-D) Gene significance (GS) for ABA and DGDG vs. module membership in module red. Module membership (KME) is the module eigengene-based network connectivity.

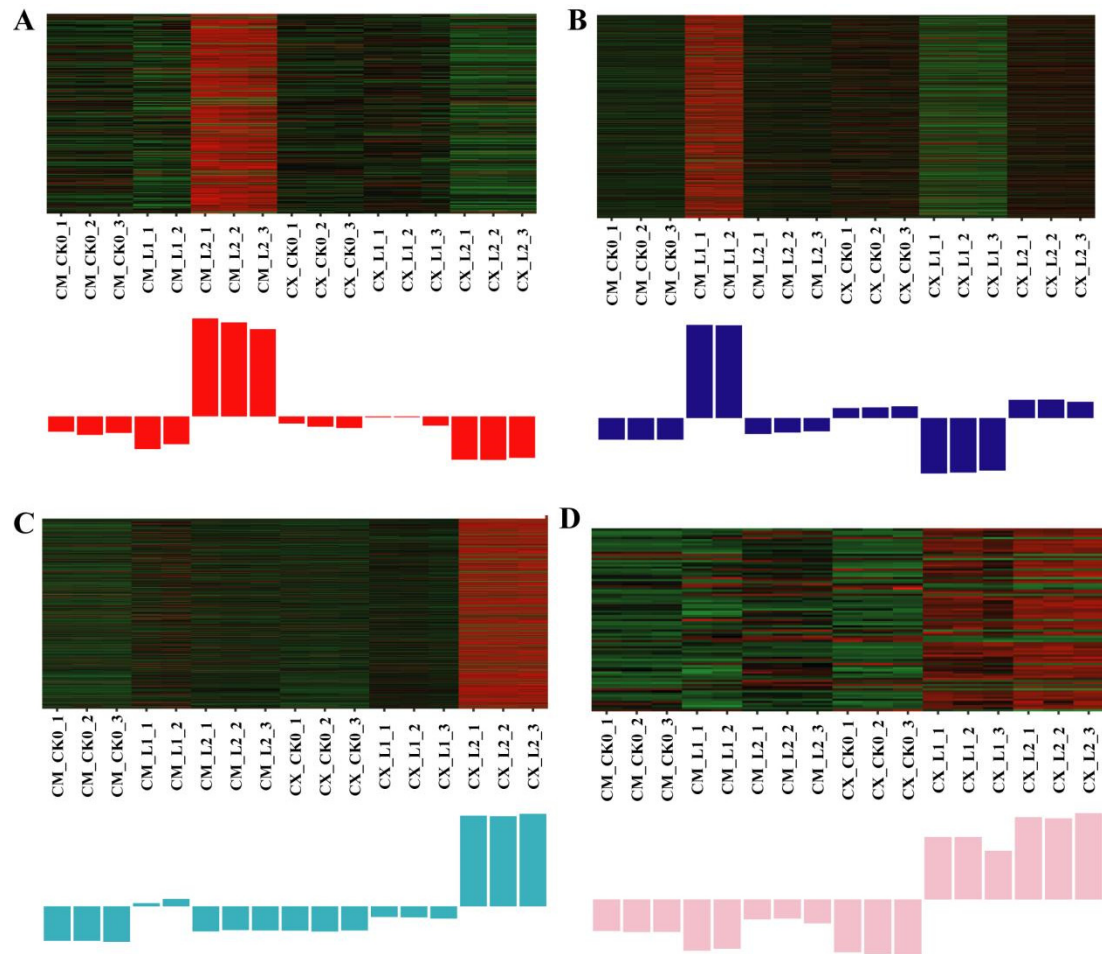


Fig. S6. Expression heatmaps and profiles of DEGs and eigengenes in modules red, blue, turquoise and pink in response to cold storage in 'CM' and 'CX'. Red indicates upregulated genes, and green indicates downregulated genes. The bar graph of eigengene expression shows the eigengene value variance calculated from the singular value composition for each module.

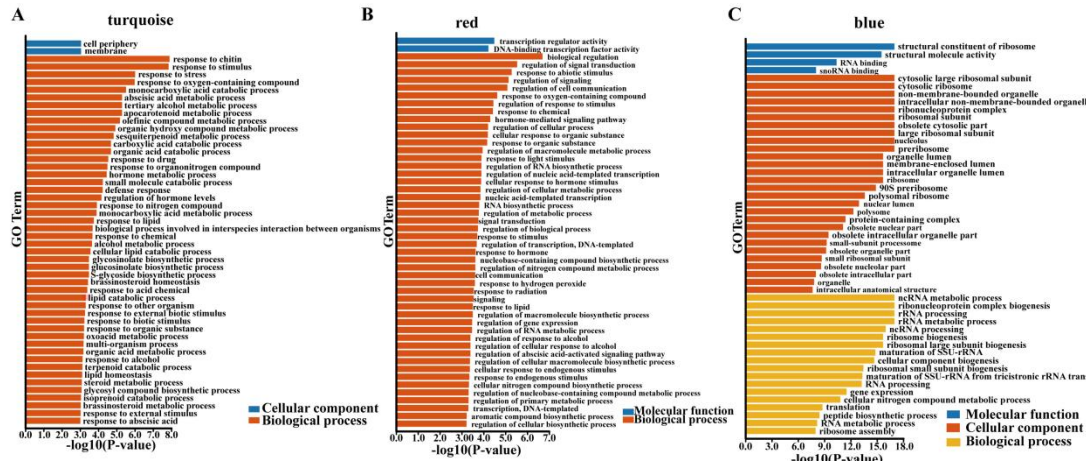


Fig. S7. GO enrichment analysis of DEGs in turquoise (A), red (B) and blue (C).

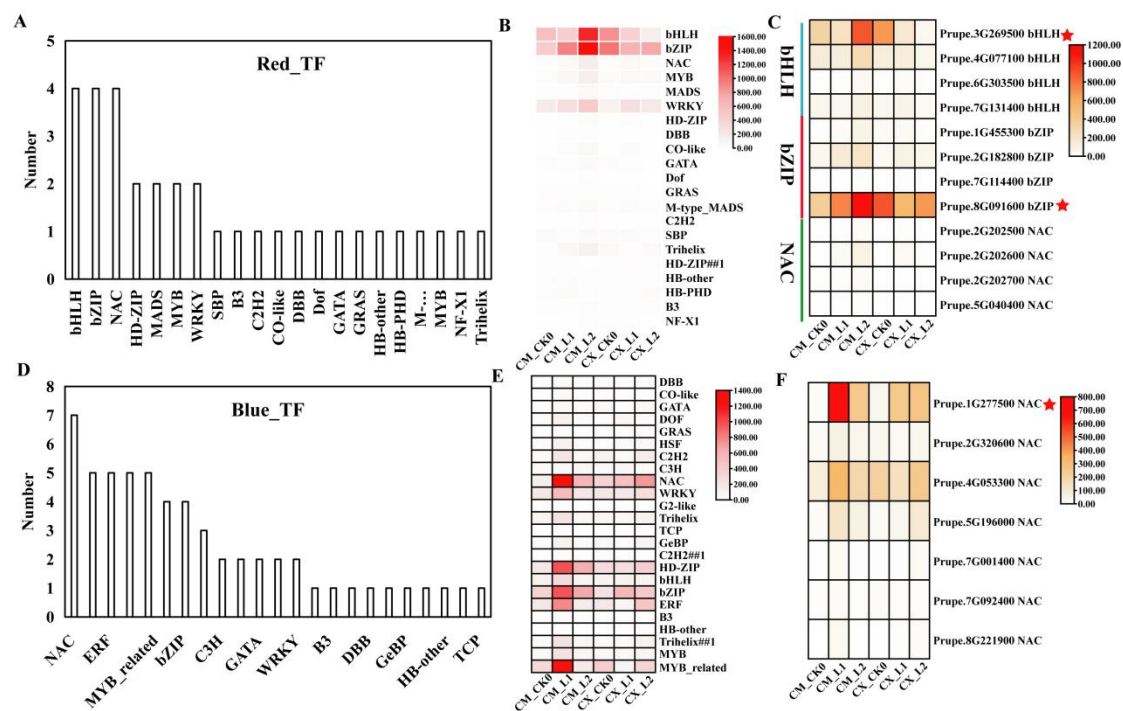


Fig. S8. Transcription factors and correlation between diffierentially TFs family and ABA, ethylene and lipid in red and blue modules.

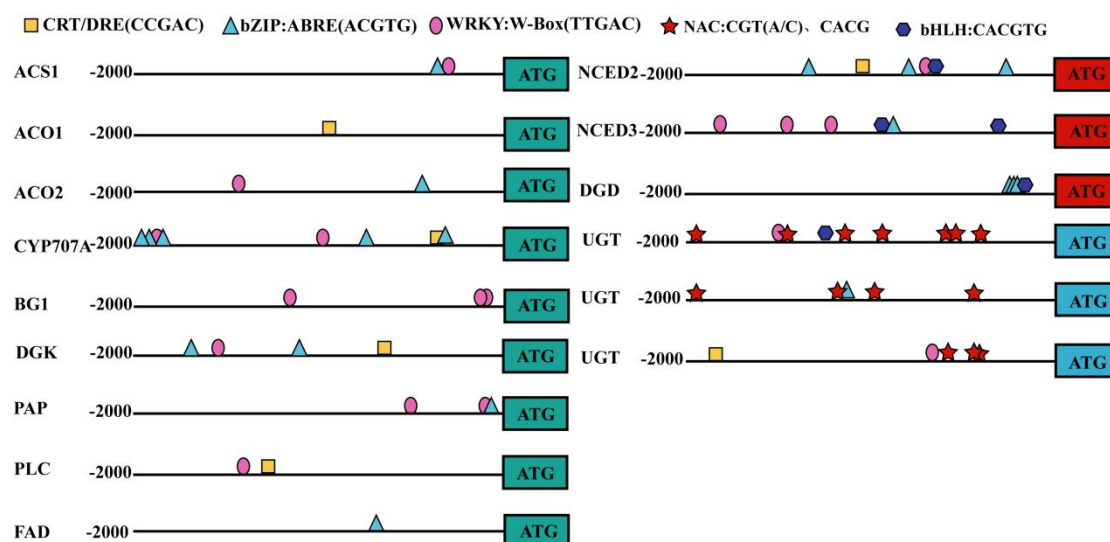


Fig. S9. Prediction of the cis-acting elements in the 2000-bp *ACS1*, *ACO1*, *ACO2*, *CYP707A*, *BG1*, *DGK*, *PAP*, *PLC*, *FAD*, *NCED2*, *NCED3*, *DGD* and *UGT* promoter region was performed by searching the PLACE databases.

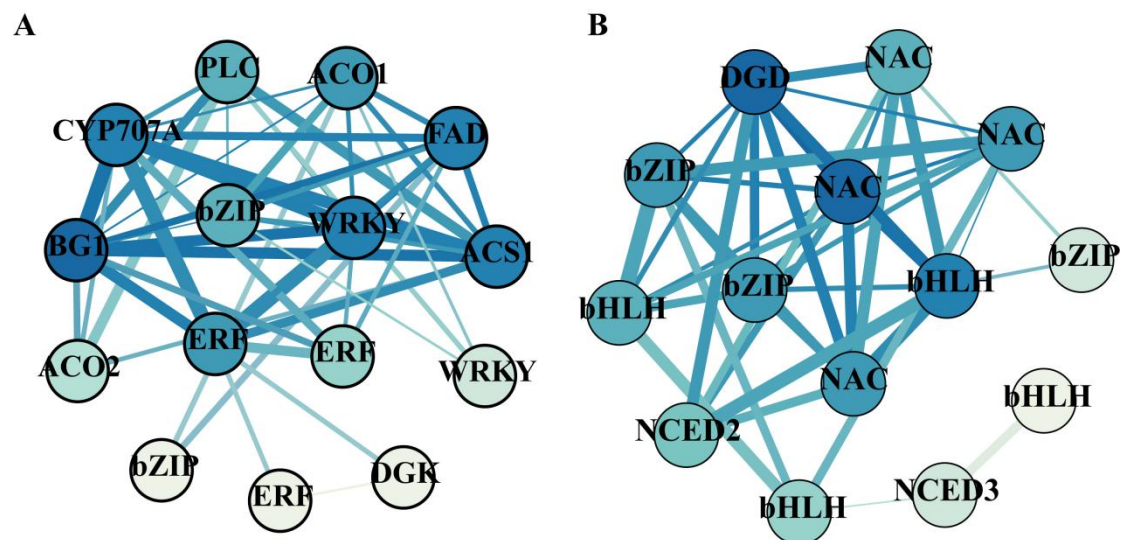


Fig. S10. Transcription factor and structural gene co-expression regulatory network. (A) Turquoise module differential TF and structural gene co-expression regulatory network; (B) Red module differential TF and structural gene co-expression regulatory network.