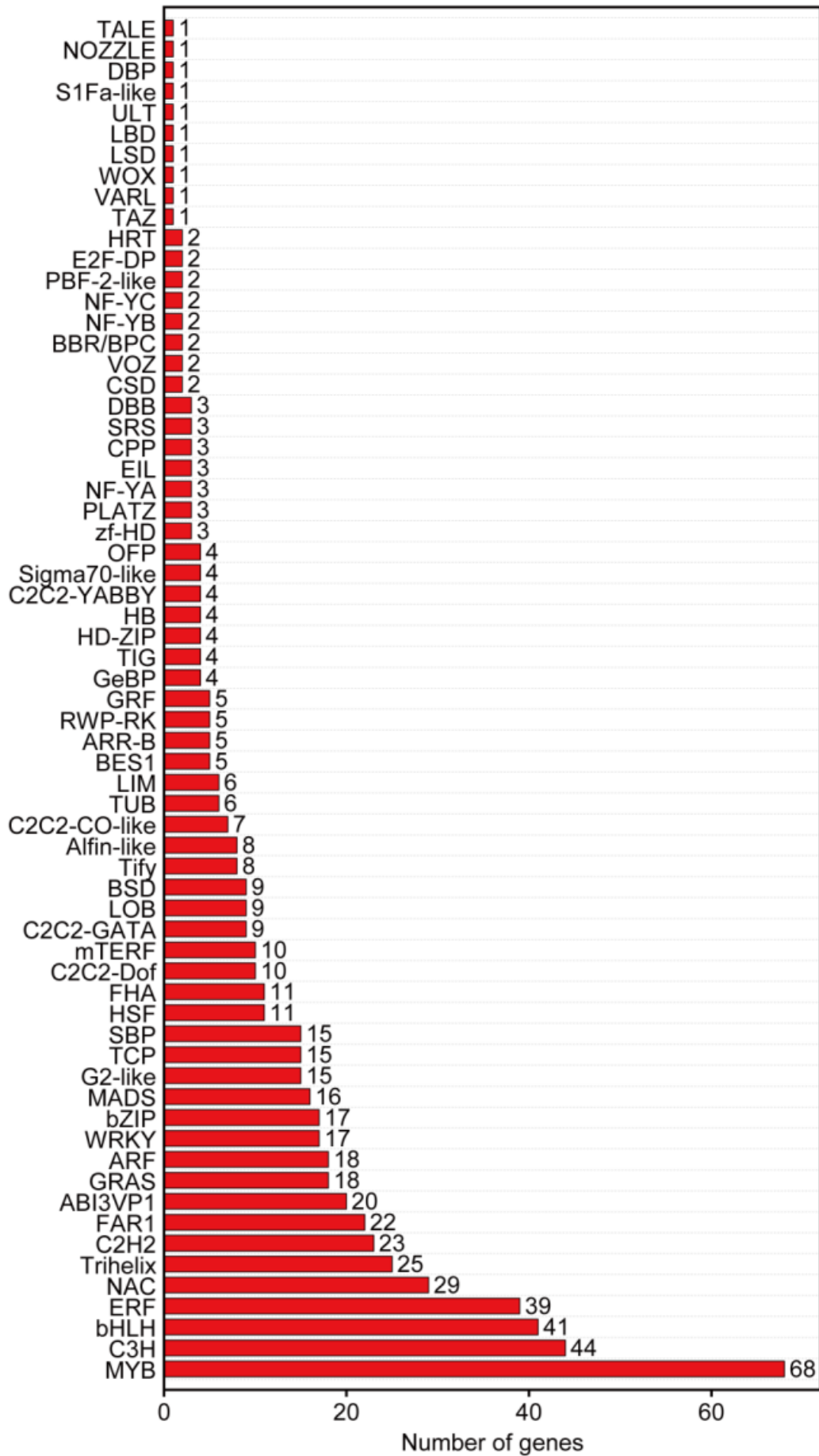
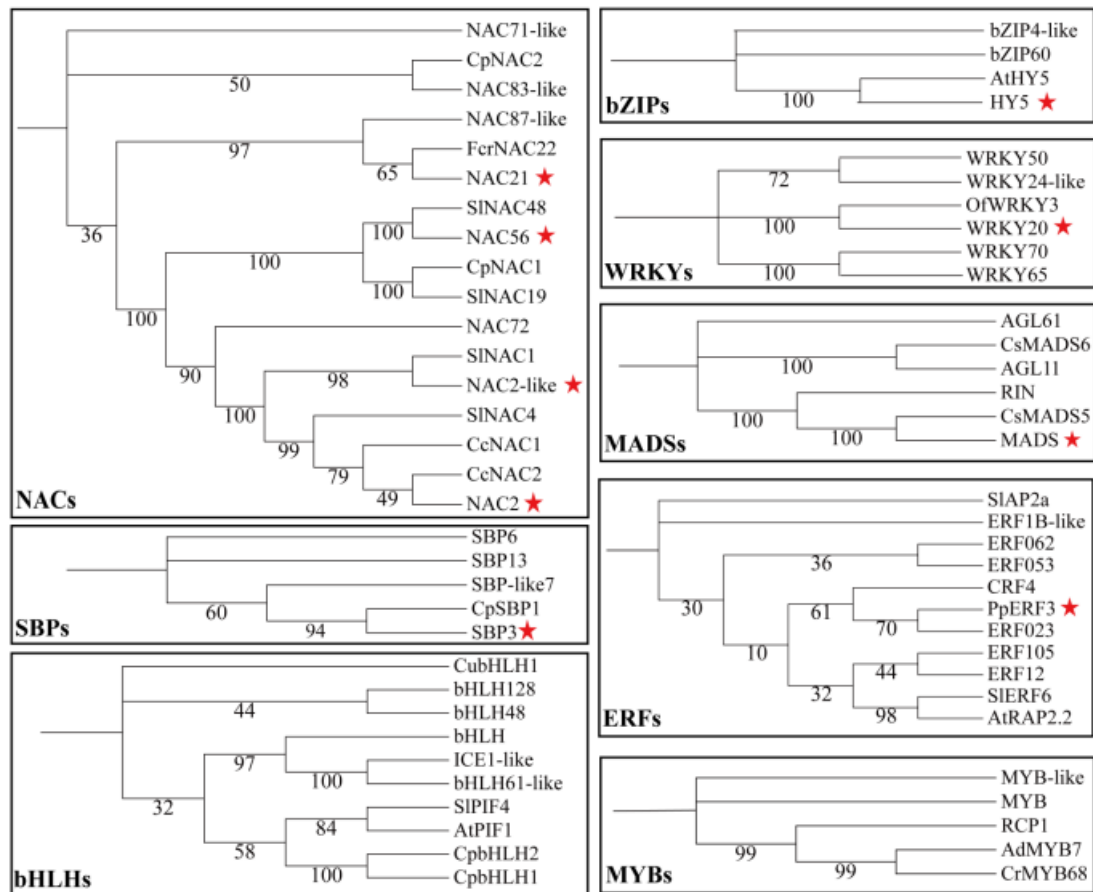


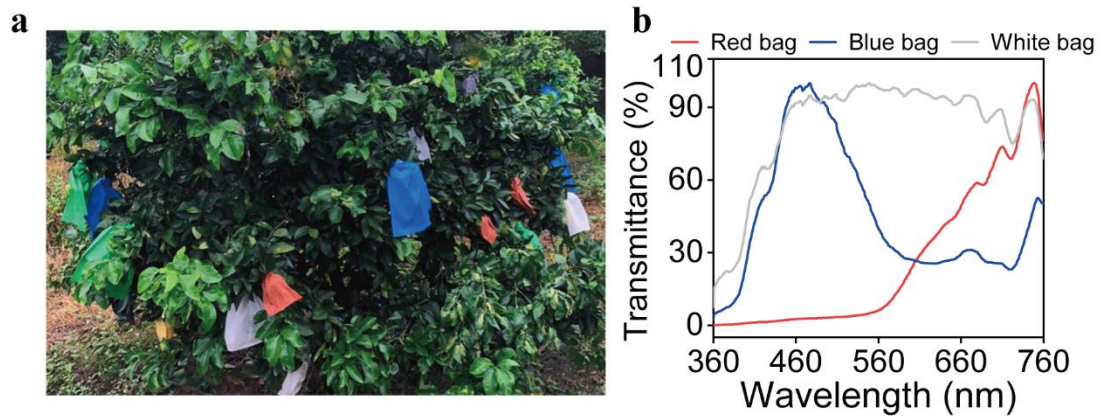
Supplementary Figure 1. Box-plot representation of distribution of gene expression level for RNA-seq during grapefruit ripening. RPKM, Reads Per Kilobase transcriptome per Million mapped reads; CK: control group; WL: white light treatment; RL: red light treatment; BL: blue light treatment; DAB184 and 220 represent 184 and 220 days after blossom, respectively. The grey, white, red and blue Box-plots represent the samples treated with control, white light, red light and blue light, respectively.



Supplementary Figure 2. Enrichment analysis of TFs in carotenoid co-expression modules.



Supplementary Figure 3. Phylogenetic analysis of candidate NACs, SBPs, bHLHs, bZIPs, WRKYs, MADSs, ERFs and MYBs transcription factor. Accession number for transcription factors in phylogenetic tree were listed in **Supplementary Table 6**.



c

	CK	WL	RL	BL
Light intensity ($\mu\text{mol m}^{-2} \text{s}^{-1}$)	250.21 \pm 5.35	183.72 \pm 3.44	145.39 \pm 3.11	123.78 \pm 2.16
Temperature ($^{\circ}\text{C}$)	19.61 \pm 0.58	20.37 \pm 0.74	20.63 \pm 0.56	20.6 \pm 0.41
Relative humidity (%)	55.67 \pm 2.11	53.57 \pm 1.94	55.63 \pm 1.87	54.97 \pm 1.69
CO ₂ concentration (%)	0.20 \pm 0.03	0.23 \pm 0.04	0.22 \pm 0.03	0.23 \pm 0.04
O ₂ concentration (%)	20.10 \pm 1.01	20.21 \pm 0.86	20.20 \pm 0.74	20.21 \pm 0.62

Supplementary Figure 4. Grapefruit-bagging treatment in the field. **a** Grapefruit bagged with light-transmitting bags in the field. **b** Light-transmitting property of bags used for bagging. **c** The micro-climate condition of different light-transmitting bags. Data are expressed as means \pm standard deviation of triplicate samples ($n = 3$). CK: control group; WL: white-light treatment; RL: red-light treatment; BL: blue-light treatment. All parameters were measured at 10:00 AM in October 20, 2020 (a sunny day).

Supplementary Table 1. Retention time and maximum absorption peaks of carotenoids standards.

NO.	Carotenoids	Rt (min)	λ_{\max} (nm) observed			λ_{\max} (nm) literature ^a		
			Peak I	Peak II	Peak III	Peak I	Peak II	Peak III
1	9-cis-violaxanthin	18.15	412	436	462.7	411	434	463
2	phytofluene	32.41	329	347.1	364	331	347	364
3	ζ -carotene	39.53	380	398.5	422.7	380	400	426
4	β -carotene	46.62	426	451.8	478.5	426	451	473
5	lycopene	49.00	446.9	474.8	/	446	473	503

^aCharacterization of Pinalate, a novel *Citrus sinensis* mutant with a fruit-specific alteration that results in yellow pigmentation and decreased ABA content.

Supplementary Table 2. Total RNA quality of RNA-seq samples during grapefruit ripening.

Sample	Concentration(ng/ μ L)	Volume(μ L)	Total content(μ g)	RIN/RQN	28S/18S	Results
CK184_1	645	30	19.35	9.1	1.3	A
CK184_2	470	30	14.1	8.9	1.2	A
CK184_3	305	30	9.15	9.2	1.3	A
CK220_1	420	30	12.6	8.6	1.1	A
CK220_2	520	30	15.6	8.6	1.2	A
CK220_3	347	30	10.41	8.4	1.2	A
WL184_1	233	30	6.99	8.4	1.2	A
WL184_2	219	30	6.57	8.4	1.1	A
WL184_3	440	30	13.2	8	1.2	A
WL220_1	350	30	10.5	8.5	1.3	A
WL220_2	505	30	15.15	8.8	1.3	A
WL220_3	365	30	10.95	8.7	1.4	A
RL184_1	620	30	18.6	8.9	1.2	A
RL184_2	735	30	22.05	9	1.3	A
RL184_3	500	30	15	9	1.5	A
RL220_1	219	30	6.57	7.8	1	A

RL220_2	310	30	9.3	8.4	1.1	A
RL220_3	156	30	4.68	8.4	1	A
BL184_1	545	30	16.35	8.7	1.2	A
BL184_2	640	30	19.2	8.2	1.2	A
BL184_3	600	30	18	9.2	1.1	A
BL220_1	320	30	9.6	8.3	1	A
BL220_2	290	30	8.7	8.6	1.1	A
BL220_3	480	30	14.4	8.5	1.1	A

Note: CK: control group; WL: white light treatment; RL: red light treatment; BL: blue light treatment; 184, 220 represent 184, 220 days after blossom, respectively. "A" refers to the samples which quality meet the requirements of library construction and sequencing.

Supplementary Table 3. Throughput and quality of RNA-Seq data in grapefruit fruit.

Sample	Total Raw	Total Clean	Total Clean	Clean Reads	Clean Reads	Clean Reads
	Reads (M)	Reads (M)	Bases (Gb)	Q20 (%)	Q30 (%)	Ratio (%)
CK184_1	48.93	43.94	6.59	96.88	90.8	89.79
CK184_2	48.93	45.43	6.81	97.01	91.14	92.83
CK184_3	48.93	45.27	6.79	96.82	90.62	92.52
CK220_1	48.93	45.12	6.77	96.95	90.98	92.21
CK220_2	48.93	44.3	6.65	96.96	91	90.54
CK220_3	48.93	44.88	6.73	96.97	91.02	91.71
WL184_1	48.93	45.28	6.79	96.76	90.44	92.54
WL184_2	48.93	45.29	6.79	96.88	90.78	92.56
WL184_3	48.93	44.97	6.75	96.89	90.81	91.9
WL220_1	48.93	45.46	6.82	96.82	90.63	92.9
WL220_2	48.93	44.92	6.74	96.87	90.76	91.79
WL220_3	48.96	42.58	6.39	96.72	90.21	86.98
RL184_1	50.68	45.07	6.76	97.03	91.13	88.93
RL184_2	50.68	44.29	6.64	96.98	90.98	87.38
RL184_3	50.68	44.97	6.75	96.6	89.91	88.74
RL220_1	50.68	44.09	6.61	96.66	90.08	87

RL220_2	50.14	43.09	6.46	96.72	90.21	85.95
RL220_3	50.64	43.99	6.6	96.45	89.46	86.87
BL184_1	50.68	44.8	6.72	96.88	90.67	88.39
BL184_2	47.19	44.65	6.7	96.65	90.04	94.62
BL184_3	47.19	44.45	6.67	96.59	89.86	94.21
BL220_1	47.19	44.92	6.74	96.62	89.97	95.19
BL220_2	47.19	44.93	6.74	96.48	89.59	95.21
BL220_3	47.19	44.67	6.7	96.62	89.95	94.68

Note: CK: control group; WL: white light treatment; RL: red light treatment; BL: blue light treatment; 184, 220 represent 184, 220 days after blossom, respectively. Q20: the rate of bases which quality is greater than 20; Q30: the rate of bases which quality is greater than 30.

Supplementary Table 4. Summary of reference genome and gene sequence mapping of grapefruit during ripening after RNA-seq.

Sample	Total	Reference genome		Reference gene sequence	
	Clean Reads	Total	Uniquely	Total	Uniquely
	(M)	Mapping (%)	Mapping (%)	Mapping (%)	Mapping (%)
CK184_1	43.94	86.03	82.82	75.21	71.41
CK184_2	45.43	87.19	83.86	78.7	74.46
CK184_3	45.27	86.73	83.46	77.16	73.25
CK220_1	45.12	87.58	83.74	77.37	72.91
CK220_2	44.3	87.15	83.35	76.64	72.23
CK220_3	44.88	87.25	83.38	76.18	71.51
WL184_1	45.28	86.73	83.49	76.15	72.36
WL184_2	45.29	87.29	83.99	77.11	73.13
WL184_3	44.97	87.08	83.8	76.35	72.47
WL220_1	45.46	85.75	82.1	76.05	71.8
WL220_2	44.92	87.21	83.5	75.71	71.54
WL220_3	42.58	87.43	83.6	76.63	72.41
RL184_1	45.07	86.6	83.35	76.46	72.61
RL184_2	44.29	86.04	82.87	75.08	71.27

RL184_3	44.97	86.55	83.38	76.23	72.48
RL220_1	44.09	86.03	82.34	75.33	71.09
RL220_2	43.09	86.2	82.51	75.24	71.06
RL220_3	43.99	86.54	82.89	75.83	71.58
BL184_1	44.8	86.48	83.32	75.64	71.79
BL184_2	44.65	87.11	83.92	77.7	73.76
BL184_3	44.45	86.27	83.09	75.73	71.97
BL220_1	44.92	87.73	84.07	77.46	73.28
BL220_2	44.93	86.46	82.81	76.27	72.21
BL220_3	44.67	87.02	83.42	76.08	71.95

Note: CK: control group; WL: white light treatment; RL: red light treatment; BL: blue light treatment; 184, 220 represent 184, 220 days after blossom, respectively.

Supplementary Table 5. Expression pattern of differentially expressed genes (DEGs) involved in carotenoid metabolism during grapefruit ripening (from 184 DAB to 220 DAB).

Gene ID	module	Gene name	Other ID	CK184	WL184	RL184	BL184	log ₂ (RL184/CK184)
102622692	blue	ZEP6	Cs1g04870	1.05	1.34	2.48	1.207	1.27
Gene ID	module	Gene name	Other ID	CK220	WL220	RL220	BL220	log ₂ (RL220/CK220)
102619293	-	ZEP7	orange1.1t04051	0.00	0.000	0.02	0.00	2.40
102621234	-	CCD4-1	Cs8g14150	2.057	2.75	7.92	2.873	1.83
102578064	-	NCED3	Cs5g14370	42.947	7.42	20.557	8.267	-1.17

Note: CK: control group; WL: white light treatment; RL: red light treatment; BL: blue light treatment; 184 and 220 represents 184, 220 days after blossom, respectively.

Supplementary Table 6. Gene ID for protein sequence in phylogenetic tree.

Gene name	Gene ID	Gene name	Gene ID
SINAC48	NM_001279348	CrMYB68	KY612511
FcrNAC22	XM_006440961	AdMYB7	AXP34749.1
CpNAC2	XP_021899904	RCP1	KR053165
SINAC4	KC453999	CubHLH1	BAU09296.1
SINAC1	AY498713	CpbHLH1	XP_021890297.1

CcNAC1	KC814686	CpbHLH2	XP_021907394.1
CcNAC2	KC814687	SIPIF4	Solyc07g043580
SINAC19	XM 004236996	AtPIF1	At2g20180
CpNAC1	evm.model.supercontig_1.48	PpERF3	Prupe.7G194400
CpSBP1	evm.model.supercontig_27.40	AtRAP2.2	At3g14230
CsMADS6	MG594037	SIAP2a	SGN-U314860
CsMADS5	MK431890	SIERF6	JN616265
RIN	NP_001234670.1	AtHY5	AT5G11260
OfWRKY3	KM504380		
