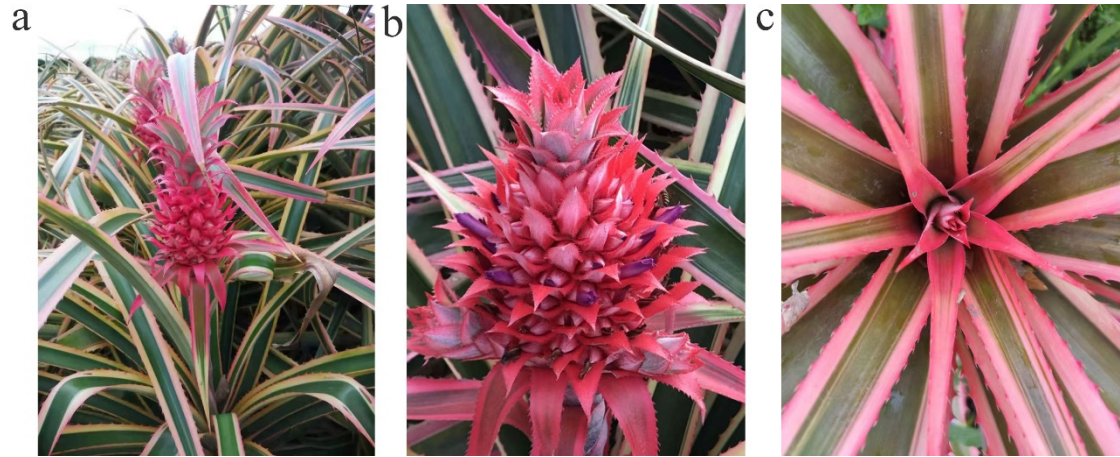


Supplementary Material

Supplementary Figures



Supplementary Figure S1. The red Phenotype of different tissues in *Ananas comosus* var. *bracteatus*

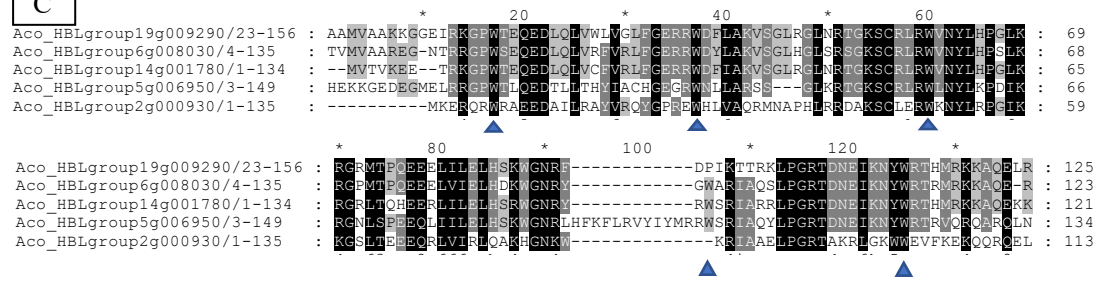
A	Helix 1		Helix 2		Helix 3	
	*	20	*	40	*	
Aco_HBLgroup6g007080/76-348	: CARGH	RPAAE	AKL	EL	SSQY	: FQNNL
Aco_HBLgroup14g001960/35-500	: LVKGS	THEE	NKLI	HL	KKHG	: QSK
Aco_HBLgroup19g007590/21-278	: LRGGP	NTVEE	ELI	LV	NYIT	: AHG
Aco_HBLgroup13g006020/14-225	: --NKG	ANTKEE	DER	LI	AHRE	: HGC
Aco_HBLgroup19g006990/12-344	: LKKG	RTAEE	EEI	LV	KYIT	: THG
Aco_HBLgroup8g005940/34-310	: VKG	PTADE	EEV	LS	YV	: RREG
Aco_HBLgroup11g000160/14-358	: LNKGS	NTPEE	DMR	LI	AY	: HKY
Aco_HBLgroup13g006350/12-241	: VKRGP	NTAEE	EKK	LI	GL	: LFL
Aco_HBLgroup22g003930/16-284	: --KGP	NTPEE	DI	TV	SY	: QEHG
Aco_HBLgroup17g0010760/12-258	: QNKGS	SVSEE	EKI	LEY	KL	: HGC
Aco_HBLgroup1g007530/122-428	: VVKG	NTAEE	ERL	LV	QL	: DQHG
Aco_HBLgroup15g004150/12-235	: VKRGP	NSPEE	EAI	RS	YV	: EMT
Aco_HBLgroup16g006310/12-316	: VKKGP	NSPEE	EAK	LI	YEE	: HGT
Aco_HBLgroup5g000200/70-513	: LVKGP	NSKOE	EII	IQ	MY	: KKY
Aco_HBLgroup13g0010320/16-313	: --KGP	NTPEE	EKL	VE	YQ	: KNC
Aco_HBLgroup11g004390/23-325	: LKKG	PTAAB	EEL	TE	YV	: RREG
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Aco_HBLgroup22g007150/28-338	: LRKGL	NSPEE	DDK	LS	MY	: LSHG
Aco_HBLgroup17g0010760/16-310	: CPBGH	NRPEE	EKK	LI	QY	: QKHG
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Aco_HBLgroup15g005990/12-269	: LRKGL	NSPEE	EKK	LI	YEE	: HGT
Aco_HBLgroup24g005180/13-195	: --NKG	ANTKEE	DER	LI	AY	: QAHG
Aco_HBLgroup12g001980/14-256	: --KGP	NTPEE	ELM	LV	SY	: QEHG
Aco_HBLgroup13g003940/13-276	: YRKGL	NSPEE	QDR	LD	Y	: LSHG
Aco_HBLgroup11g006600/155-450	: VVKG	NTLEE	ERL	LV	QL	: DQHG
Aco_HBLgroup18g003400/16-290	: --KGP	NTPEE	EKK	LI	QY	: QKHG
Aco_HBLgroup13g009340/12-345	: VKRGL	NSPEE	EKK	LI	YEE	: HGT
Aco_HBLgroup16g004820/84-364	: CVRGH	NRPAE	ESK	REL	V	: SQFG
Aco_HBLgroup23g002090/12-329	: VKKGP	NTAEE	EAK	LI	YEE	: HGT
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Aco_HBLgroup10g001000/14-264	: --NKG	ANTKEE	DER	LI	AY	: QAHG
Aco_HBLgroup1g005280/16-303	: --KGP	NTPEE	EII	LV	SY	: QEHG
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B

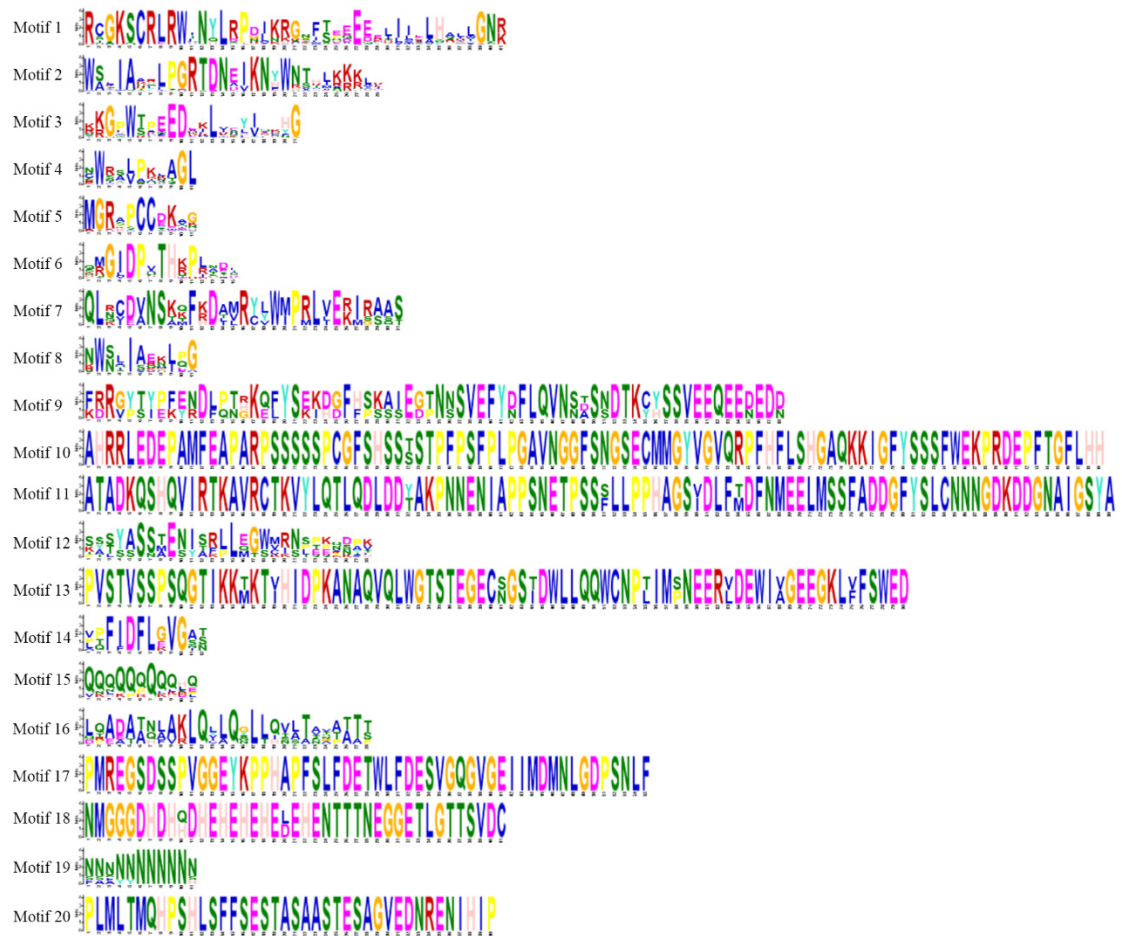
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Aco_HBLgroup17g007460/16-317 : G-KFSLQEEQTIILHALLGNRWAAIATHLPKRTDNEIKNYQNTHSKKRLA
Aco_HBLgroup1g005020/19-131 : D-PMSPEDAEIIVLHAILGNKWAIAVQ-----FIMILR

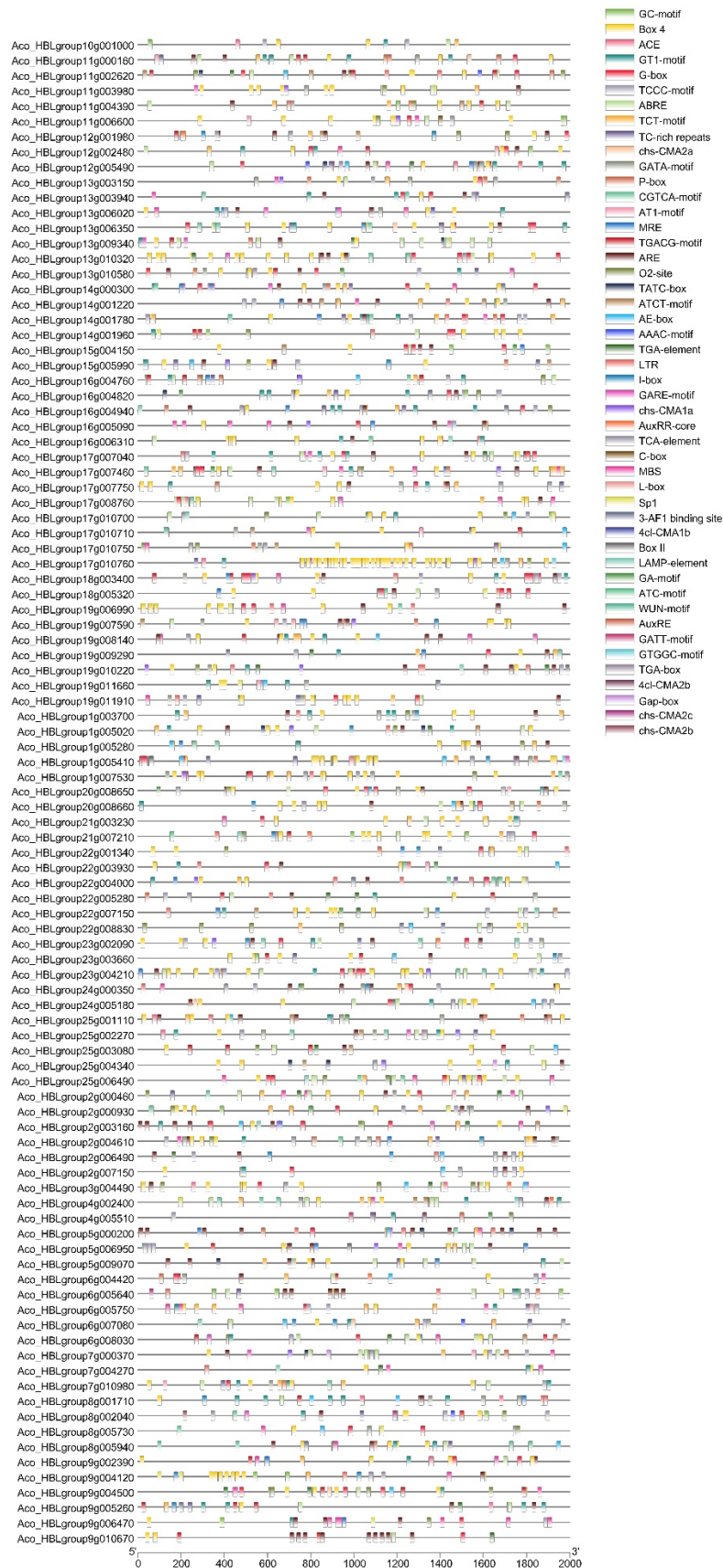
C



Supplementary Figure S2 Multiple sequence alignment of the AbR2R3-MYB conserved domain in *Ananas comosus* var. *bracteatus*. The shading of the alignment represents different degrees of conservation among sequences; the dark shading indicates identical residues, the light shading indicates conservative changes. The positions of the three α -helices that form each R2 (A) and R3 (B) repeat are marked as Helix 1 to Helix 3. (C), few insertions and deletions in 5 AbR2R3-MYBs, the blue triangles indicate the highly conserved tryptophan residues (W) in the MYB domain.



Supplementary Figure S3 A total of 20 conserved motifs were screened and visualized with different colors by using the MEME server.



Supplementary Figure S4 Identified pivotal *cis*-elements in the promoters of AbR2R3-MYB genes in *A. comosus* var. *bracteatus*. The black line represents the upstream of the AbR2R3-MYB genes. Different colored boxes represent different *cis*-elements.

Table S1. List of AbR2R3-MYB protein family genes and their physiochemical properties.

Genome ID	CDS/bp	ORF/aa	MW/kD	pI	GRAVY	Subcellular localizations
Aco_HBLgroup15g004150	708	235	26077.02	10.44	-0.536	Nucleus
Aco_HBLgroup8g001710	2115	704	76880.84	8.05	-0.266	Nucleus
Aco_HBLgroup15g005990	810	269	30218.3	5.07	-0.729	Nucleus
Aco_HBLgroup13g010580	771	256	29315	6.95	-0.748	Nucleus
Aco_HBLgroup1g005020	396	131	15032.47	9.6	-0.411	Nucleus
Aco_HBLgroup2g003160	1596	531	58719.61	4.79	-0.75	Nucleus
Aco_HBLgroup16g004760	1230	409	44995.59	8.69	-0.438	Nucleus
Aco_HBLgroup16g004820	1095	364	41056.51	6.31	-0.795	Nucleus
Aco_HBLgroup18g003400	867	288	31579.35	5.59	-0.577	Nucleus
Aco_HBLgroup16g006310	951	316	35491.63	5.39	-0.693	Nucleus
Aco_HBLgroup19g006990	1035	344	38962.26	5.29	-0.924	Nucleus
Aco_HBLgroup24g000350	846	281	31607.94	5.49	-0.656	Nucleus
Aco_HBLgroup14g001780	792	263	30568.3	8.43	-0.996	Nucleus
Aco_HBLgroup2g006490	477	158	18291.49	10.44	-0.508	Nucleus
Aco_HBLgroup23g004210	978	325	35838.72	4.89	-0.718	Nucleus
Aco_HBLgroup8g002040	987	328	36656.88	6.89	-0.63	Nucleus
Aco_HBLgroup23g002090	990	329	36305.6	6.21	-0.603	Nucleus
Aco_HBLgroup19g010220	774	257	27959.12	5.54	-0.652	Nucleus
Aco_HBLgroup11g006600	1353	450	51160.6	6.56	-0.743	Nucleus
Aco_HBLgroup22g004000	1428	475	52547.4	5.16	-0.633	Nucleus
Aco_HBLgroup8g005940	933	310	34432.3	6.95	-0.823	Nucleus
Aco_HBLgroup25g006490	867	288	32426.22	5.84	-0.85	Nucleus
Aco_HBLgroup6g005750	1095	364	40837.44	5.79	-0.678	Nucleus

Aco_HBLgroup1g007530	1287	428	48196.82	6.96	-0.794	Nucleus
Aco_HBLgroup5g006950	924	307	35109.25	7.15	-0.685	Nucleus
Aco_HBLgroup22g008830	708	235	27607.65	8.62	-1.054	Nucleus
Aco_HBLgroup13g003150	951	316	34510.72	8.59	-0.632	Nucleus
Aco_HBLgroup25g003080	696	231	26168.24	5.8	-0.694	Nucleus
Aco_HBLgroup25g004340	1068	355	39374.68	5.56	-0.534	Nucleus
Aco_HBLgroup12g001980	768	255	28294.17	8.65	-0.478	Nucleus
Aco_HBLgroup19g007590	837	278	31380.09	6.08	-0.687	Nucleus
Aco_HBLgroup1g003700	1206	401	44796.21	6.7	-0.638	Nucleus
Aco_HBLgroup2g000460	1110	369	39808.37	5.97	-0.545	Nucleus
Aco_HBLgroup7g000370	1062	353	40028.92	5.78	-0.645	Nucleus
Aco_HBLgroup12g005490	813	270	30839.69	8.87	-0.973	Nucleus
Aco_HBLgroup18g005320	873	290	32747.74	5.13	-0.742	Nucleus
Aco_HBLgroup10g001000	792	263	29573.62	8.19	-0.654	Nucleus
Aco_HBLgroup3g004490	891	296	34114.54	8.06	-0.59	Nucleus
Aco_HBLgroup22g007150	1017	338	37214.59	5.43	-0.585	Nucleus
Aco_HBLgroup7g010980	1005	334	37000	7.56	-0.508	Nucleus
Aco_HBLgroup22g005280	678	225	26073.58	8.67	-0.819	Nucleus
Aco_HBLgroup14g001960	1578	525	58691.49	8.8	-0.67	Nucleus
Aco_HBLgroup19g008140	1257	418	45961.82	5.91	-0.707	Nucleus
Aco_HBLgroup7g004270	660	219	24721.98	6.14	-0.632	Nucleus
Aco_HBLgroup14g000300	774	257	29394.99	5.76	-0.656	Nucleus
Aco_HBLgroup6g005640	834	277	29452.73	7.22	-0.538	Nucleus
Aco_HBLgroup8g005730	747	248	27722.21	6.24	-0.66	Nucleus
Aco_HBLgroup21g003230	1329	442	46707.24	6.32	-0.422	Nucleus
Aco_HBLgroup5g000200	2925	974	108600.75	5.06	-0.621	Nucleus

Aco_HBLgroup20g008660	1038	345	37119.14	8.93	-0.322	Nucleus
Aco_HBLgroup24g005180	588	195	22783.38	5.53	-0.867	Nucleus
Aco_HBLgroup9g010670	897	298	32362.82	5.94	-0.532	Nucleus
Aco_HBLgroup9g002390	702	233	26854.63	6.92	-0.617	Nucleus
Aco_HBLgroup5g009070	1545	514	57568.58	5.89	-0.628	Nucleus
Aco_HBLgroup11g002620	612	203	23283.64	8.78	-0.716	Nucleus
Aco_HBLgroup17g007750	945	314	34547.39	6.33	-0.729	Nucleus
Aco_HBLgroup23g003660	828	275	31455.08	5.18	-0.76	Nucleus
Aco_HBLgroup17g007460	948	315	34534.59	6.68	-0.628	Nucleus
Aco_HBLgroup6g004420	819	272	30524.36	7.58	-0.624	Nucleus
Aco_HBLgroup9g005260	1077	358	39318.59	6.06	-0.265	Nucleus
Aco_HBLgroup22g001340	708	235	27599.54	6.77	-1.054	Nucleus
Aco_HBLgroup19g009290	834	277	31319.75	5.46	-0.878	Nucleus
Aco_HBLgroup1g005280	906	301	33498.56	6.09	-0.621	Nucleus
Aco_HBLgroup19g011910	879	292	32761.64	5.87	-0.695	Nucleus
Aco_HBLgroup21g007210	831	276	29571.3	8.49	-0.582	Nucleus
Aco_HBLgroup9g004120	807	268	29839.42	6.54	-0.705	Nucleus
Aco_HBLgroup14g001220	1623	540	59492.37	5.28	-0.528	Nucleus
Aco_HBLgroup2g007150	1086	361	39526.02	5.38	-0.673	Nucleus
Aco_HBLgroup22g003930	849	282	31049.75	5.31	-0.479	Nucleus
Aco_HBLgroup17g010700	777	258	29364.85	7.59	-0.873	Nucleus
Aco_HBLgroup13g003940	831	276	30461.8	5.99	-0.623	Nucleus
Aco_HBLgroup12g002480	933	310	35132.69	9.23	-0.864	Nucleus
Aco_HBLgroup4g002400	687	228	26483.37	7.1	-0.982	Nucleus
Aco_HBLgroup13g006350	726	241	26973.35	7.15	-0.777	Nucleus
Aco_HBLgroup17g010750	648	215	24750.07	8.64	-0.717	Nucleus

Aco_HBLgroup19g011660	801	266	29417.98	10.22	-0.89	Nucleus
Aco_HBLgroup4g005510	552	183	21267.55	9.85	-0.62	Nucleus
Aco_HBLgroup13g010320	936	311	34610.55	9.27	-0.438	Nucleus
Aco_HBLgroup11g004390	1101	366	39443.85	5.79	-0.324	Nucleus
Aco_HBLgroup9g006470	1251	416	45743.15	6.36	-0.491	Chloroplast
Aco_HBLgroup1g005410	1089	362	39468.34	5.6	-0.688	Nucleus
Aco_HBLgroup17g007040	639	212	23571.74	7.57	-0.423	Nucleus
Aco_HBLgroup11g003980	999	332	37135.86	6.39	-0.567	Nucleus
Aco_HBLgroup17g010760	777	258	29341.87	7	-0.851	Nucleus
Aco_HBLgroup13g006020	675	224	25607.68	9.02	-0.603	Nucleus
Aco_HBLgroup25g001110	1026	341	37559.32	6.99	-0.83	Nucleus
Aco_HBLgroup17g008760	936	311	34591.95	5.83	-0.462	Nucleus
Aco_HBLgroup20g008650	1038	345	37745.54	5.99	-0.446	Nucleus
Aco_HBLgroup6g008030	720	239	27437.65	5.73	-0.843	Nucleus
Aco_HBLgroup6g007080	1047	348	38148.19	6.6	-0.708	Nucleus
Aco_HBLgroup16g005090	807	268	29853.49	6.96	-0.706	Nucleus
Aco_HBLgroup25g002270	840	279	31907.45	7.79	-1.008	Nucleus
Aco_HBLgroup9g004500	810	269	30410.06	6.51	-0.693	Nucleus
Aco_HBLgroup2g004610	834	277	31665.86	9.11	-0.402	Nucleus
Aco_HBLgroup11g000160	1077	358	39860.15	4.9	-0.825	Nucleus
Aco_HBLgroup13g009340	1038	345	38960.62	5.33	-0.634	Nucleus
Aco_HBLgroup16g004940	1236	411	45848.07	6.32	-0.631	Nucleus
Aco_HBLgroup2g000930	1056	351	40173.88	9.86	-0.865	Nucleus
Aco_HBLgroup17g010710	648	215	24674.98	8.25	-0.688	Nucleus

Table S2. Estimated Ka/Ks ratios of the duplicated R2R3-MYB genes in *Ananas comosus* var. *bracteatus*

Gene_1	Gene_2	Ka	Ks	Ka/Ks	Effective Length (bp)	AverageS-sites	AverageN-sites	Duplication Type
Aco_HBLgroup1g008320	Aco_HBLgroup14g001960	0.391894	1.022078	0.383429	1209	264.92	944.08	segmental
Aco_HBLgroup1g003700	Aco_HBLgroup19g008140	0.260106	1.962444	0.132542	1104	238.42	865.58	segmental
Aco_HBLgroup1g005280	Aco_HBLgroup19g011910	0.254155	1.583335	0.160519	834	185.33	648.67	segmental
Aco_HBLgroup1g005410	Aco_HBLgroup19g011660	0.415646	1.091040	0.380963	771	168.00	603.00	segmental
Aco_HBLgroup10g001000	Aco_HBLgroup12g001980	0.216943	1.764469	0.122951	702	166.75	535.25	segmental
Aco_HBLgroup10g001000	Aco_HBLgroup3g004490	0.229569	2.676690	0.085766	762	181.33	580.67	segmental
Aco_HBLgroup13g006350	Aco_HBLgroup7g004270	0.338766	0.698805	0.484778	621	141.33	479.67	segmental
Aco_HBLgroup13g003940	Aco_HBLgroup9g010670	0.491340	3.734796	0.131557	795	185.83	609.17	segmental
Aco_HBLgroup14g000300	Aco_HBLgroup19g007590	0.241417	1.837748	0.131366	747	172.92	574.08	segmental
Aco_HBLgroup15g004150	Aco_HBLgroup8g005730	0.414147	1.624802	0.254891	633	149.08	483.92	segmental
Aco_HBLgroup16g004820	Aco_HBLgroup16g004940	0.005894	0.004335	1.359532	1083	231.33	851.67	tandem
Aco_HBLgroup16g004760	Aco_HBLgroup17g007460	0.171706	1.243373	0.138097	906	209.33	696.67	segmental
Aco_HBLgroup16g005090	Aco_HBLgroup17g007750	0.201515	1.018050	0.197942	786	179.08	606.92	segmental
Aco_HBLgroup16g005090	Aco_HBLgroup22g003930	0.340588	1.993741	0.170829	762	173.25	588.75	segmental
Aco_HBLgroup16g005090	Aco_HBLgroup9g004120	0.001608	0.016714	0.096217	804	181.50	622.50	segmental
Aco_HBLgroup17g007040	Aco_HBLgroup18g005320	0.146895	0.646526	0.227206	609	139.25	469.75	segmental
Aco_HBLgroup17g008760	Aco_HBLgroup18g003400	0.198171	1.001056	0.197962	765	171.17	593.83	segmental
Aco_HBLgroup17g007750	Aco_HBLgroup22g003930	0.244771	2.235645	0.109486	753	172.42	580.58	segmental
Aco_HBLgroup17g010700	Aco_HBLgroup22g005280	0.462982	1.698785	0.272537	591	137.25	453.75	segmental
Aco_HBLgroup17g008760	Aco_HBLgroup4g005510	0.160713	1.206373	0.133220	534	118.08	415.92	segmental
Aco_HBLgroup17g007040	Aco_HBLgroup4g001840	0.340427	1.549228	0.219740	450	101.92	348.08	segmental
Aco_HBLgroup18g005320	Aco_HBLgroup4g009920	0.356364	2.427242	0.146818	639	141.33	497.67	segmental

Aco_HBLgroup18g003400	Aco_HBLgroup4g005510	0.232726	1.534717	0.151641	531	118.67	412.33	segmental
Aco_HBLgroup18g005320	Aco_HBLgroup4g001840	0.233265	2.022556	0.115332	453	102.58	350.42	segmental
Aco_HBLgroup19g007590	Aco_HBLgroup2g004610	0.276877	1.454797	0.190320	726	170.25	555.75	segmental
Aco_HBLgroup19g006990	Aco_HBLgroup23g004210	0.309376	1.443415	0.214336	861	177.58	683.42	segmental
Aco_HBLgroup19g007590	Aco_HBLgroup23g003660	0.200221	1.314296	0.152341	795	178.50	616.50	segmental
Aco_HBLgroup2g006490	Aco_HBLgroup2g007150	0.039619	0.153185	0.258634	381	83.00	298.00	tandem
Aco_HBLgroup22g001340	Aco_HBLgroup22g008830	0.010946	0.019891	0.550297	705	152.83	552.17	tandem
Aco_HBLgroup22g001340	Aco_HBLgroup4g002400	0.156896	0.988617	0.158703	639	138.67	500.33	segmental
Aco_HBLgroup22g008830	Aco_HBLgroup4g002400	0.146106	1.077750	0.135565	639	139.33	499.67	segmental
Aco_HBLgroup22g001340	Aco_HBLgroup4g009300	0.228640	1.272632	0.179659	543	115.50	427.50	segmental
Aco_HBLgroup25g003080	Aco_HBLgroup9g002390	0.262922	1.418641	0.185334	675	150.08	524.92	segmental
Aco_HBLgroup4g002400	Aco_HBLgroup4g009300	0.011228	0.024525	0.457802	573	124.33	448.67	tandem
Aco_HBLgroup5g000200	Aco_HBLgroup8g007840	0.313663	1.117426	0.280701	2469	548.67	1920.33	segmental
Aco_HBLgroup5g006950	Aco_HBLgroup8g002040	0.302289	2.064544	0.146419	825	186.92	638.08	segmental

Table S3. Functionally annotated *cis*-elements identified in the promoters of AbR2R3-MYB genes in *Ananas comosus* var. *bracteatus*

Categories	<i>Cis</i> -Elements	Functions of <i>Cis</i> -Elements
Light-response elements	Box 4, ATCT-motif, ATC-motif	part of a conserved DNA module involved in light responsiveness
	ACE	cis-acting element involved in light responsiveness
	GT1-motif, AAAC-motif, Sp1, 3-AF1 binding site, 4cl-CMA1b, 4cl-CMA2b	light responsive element
	G-Box, C-box	cis-acting regulatory element involved in light responsiveness
	TCCC-motif, TCT-motif, chs-CMA2a, GATA-motif, AT1-motif, I-box, chs-CMA1a, L-box, Box II, LAMP-element, GA-motif, GATT-motif, GTGGC-motif, chs-CMA2c, chs-CMA2b, Gap-box	part of a light responsive element
	MRE	MYB binding site involved in light responsiveness
Stress-response elements	AE-box	part of a module for light response
	GC-motif	enhancer-like element involved in anoxic specific inducibility
	TC-rich repeats	cis-acting element involved in defense and stress responsiveness

Hormone- response elements	ARE	cis-acting regulatory element essential for the anaerobic induction
	LTR	cis-acting element involved in low-temperature responsiveness
	MBS	MYB binding site involved in drought-inducibility
	WUN-motif	wound-responsive element
	ABRE	cis-acting element involved in the abscisic acid responsiveness
	P-box, GARE-motif	gibberellin-responsive element
	TATC-box	cis-acting element involved in gibberellin-responsiveness
	CGTCA-motif, TGACG-motif	cis-acting regulatory element involved in the MeJA- responsiveness
	O ₂ -site	cis-acting regulatory element involved in zein metabolism regulation
	TGA-element	auxin-responsive element
	AuxRR-core	cis-acting regulatory element involved in auxin responsiveness
	AuxRE, TGA-box	part of an auxin-responsive element

TCA-element	cis-acting element involved in salicylic acid responsiveness
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Table S4. List of primers used for qRT-PCR.

Gene Name	Primer Sequences (5'-3')	
<i>Unigene.16454</i>	Forward: TCTCACGCCCTCTTTCTTCCA	Reverse: GCTCTAACTCGCCACGCCTTT
<i>Unigene.16459</i>	Forward: GGATTTGAAGCATCATGGCACA	Reverse: AGCACAACCCACCTCATTTTCG
<i>SDP</i>	Forward: TGGGCGGCGTATTTACTGTGG	Reverse: CCAAACCTATCCTTCGCCATC
<i>IDH</i>	Forward: GAGTCTATTCGGGCCTTTGCT	Reverse: CCCAGACATACCCTCCCTCAC
<i>Aco_HBLgroup8g001710</i>	Forward: CTAAGCAACGCCCCGCAGTATG	Reverse: TGGCAGGAAGAATGACGCTATCG
<i>Aco_HBLgroup3g004490</i>	Forward: CTCTCCCCAAAGCCGCAGG	Reverse: CGACCAGCAATCAAGGACCAT
<i>Aco_HBLgroup10g001000</i>	Forward: CCTCTCAATAATAAGCCTCCCG	Reverse: CCAAGGTGGTAGCACAAGC
<i>Aco_HBLgroup8g005940</i>	Forward: CCCTACTCCTGCTCCCGCTGAAG	Reverse: GCTGGTGCTGCTGTAGGAAGATG
<i>Aco_HBLgroup22g005280</i>	Forward: TCACAAGAAGCACCAAGAACTCCTC	Reverse: ACTCCAACCTTGCCGCGAACTTAG
<i>Aco_HBLgroup13g006020</i>	Forward: CCTCCTCGGCAACAAATGGTCTC	Reverse: CCTCCTTATGTGCGTGTTCCAGTAG
<i>Aco_HBLgroup12g001980</i>	Forward: GGACGAAGGAGGAGGACCAGAG	Reverse: GAAGAAGACCTGCGGCTTTGGG
<i>Aco_HBLgroup17g010710</i>	Forward: TTTGATAGCGGGAAGGATACC	Reverse: CTTGAGATGGGCTTGACACG
<i>Aco_HBLgroup17g010750</i>	Forward: GAACCCACCCTTGCTCTCA	Reverse: CGGTATCCTCCCCGCTATC
<i>Aco_HBLgroup11g002620</i>	Forward: ACCACTGGAACACGCACATCA	Reverse: CAAAAGAAGCGGCGAAATC