Table 1 Suppl. Distribution of physical and chemical properties of amino acids in the *P. trichocarpa AP2/ERF* gene family.

Subfamily	Quantity	Numbering	Length	Mr [Da]	pI
AP2	32	PtAP2-001-PtAP2-032	120-721	13666.1-79224.7	5.27-8.77
DREB	69	PtERF-Ia-033-PtERF-IVb-101	155-473	17247.3-53117.8	4.51-10.12
ERF	102	PtERF-Va-102-PtERF-Xb-196	111-457	11988.4-49410.6	4.35-10.72
RAV	5	PtRAV-204-PtRAV-208	342-431	38710.7-48515.2	8.9-10.52
Soloist	1	Pt-soloist-210	232	26046.1	10.42
Average			296.22	32843.24	6.91

Table 2 Suppl. Distribution of physical and chemical properties of amino acids in the *P. deltoides AP2/ERF* gene family.

Subfamily	Quantity	Numbering	Length	Mr [Da]	pI
AP2	29	PdAP2-001-PdAP2-029	256-719	28656.3-78515.3	4.87-9.22
DREB	69	PdERF-Ia-030-PdERF-IVb-098	152-474	16679.5-52760.7	4.11-9.53
ERF	125	PdERF-Va-099-PdERF-Xb-215	67-456	7652.6-49349.6	4.2-11.53
RAV	5	PdRAV-224-PdRAV-228	348-382	39252.3-42740.4	8.09-9.51
Soloist	3	Pd-soloist-229-Pd-soloist-231	204-232	25976.0-23133.1	6.51-10.5
Average			278.77	30913.72	6.98718

Table 3 Suppl. Distribution of physical and chemical properties of amino acids in the *S. sinopurpurea AP2/ERF* gene family.

Subfamily	Quantity	Numbering	Length	Mr [Da]	pI
AP2	29	SpAP2-001-SpAP2-024	212-724	23341.8-79116.5	5.86-10.82
DREB	68	SpERF-Ia-025-SpERF-IVb-092	117-470	13349.1-51628.4	4.5-11.26
ERF	125	SpERF-Va-093-SpERF-Xb-179	121-458	13633.1-48997.3	4.4-10.67
RAV	4	SpRAV-188-SpRAV-191	353-385	39557.3-44835	6.9-9.79
Soloist	1	Sp-soloist-192	232	26133.2	10.42
Average			290.91	32203.77	6.95

Table 4 Suppl. Distribution of physical and chemical properties of amino acids in the *A. thaliana AP2/ERF* gene family.

#ID	length	Mr [Da]	pI	#ID	length	Mr [Da]	pI
AT1G16060.1(AP2)	345	39171.0	5.70	AT1G03800.1(ERF-VIIIa-B-1)	245	26392.3	4.84
AT1G51190.1(AP2)	568	62232.7	6.83	AT1G04370.1(ERF-IXc-B-3)	133	14742.9	7.75
AT1G72570.1(AP2)	415	47132.7	7.08	pAT1G06160.1(ERF-IXc-B-3)	244	27089.5	4.83
AT1G79700.2(AP2)	313	35410.6	7.60	AT1G12890.1(ERF-VIIIb-B-1)	219	25010.3	5.54
AT2G28550.3(AP2)	464	51156.7	6.79	AT1G12980.1(ERF-VIIIb-B-1)	328	36318.7	9.08
AT2G39250.1(AP2)	325	36440.0	9.25	AT1G15360.1(ERF-Va-B-6)	199	21696.1	7.45
AT2G41710.3(AP2)	458	50447.1	7.73	AT1G22985.1(ERF-VI-B-5)	159	17535.6	10.33
AT3G20840.1(AP2)	574	62875.1	6.36	AT1G24590.1(ERF-VIIIb-B-1)	306	33828.5	6.85
AT3G54320.1(AP2)	438	49301.9	4.91	AT1G25470.1(ERF-VI-L-B-6)	287	31991.3	4.56
AT3G54990.1(AP2)	346	38671.1	9.70	AT1G28160.1(ERF-VIIIb-B-1)	245	27702.9	4.95
AT4G36920.1(AP2)	432	47833.2	7.30	AT1G28360.1(ERF-VIIIa-B-1)	189	20946.4	9.91
AT4G37750.1(AP2)	555	61724.7	7.87	AT1G28370.1(ERF-VIIIa-B-1)	166	18611.9	9.91
AT5G10510.3(AP2)	604	67693.0	6.89	AT1G43160.1(ERF-Xa-B-4)	192	21962.5	7.50
AT5G17430.1(AP2)	584	64545.0	6.43	AT1G49120.1(ERF-VI-L-B-6)	329	37477.6	4.68
AT5G57390.1(AP2)	558	60305.7	7.92	AT1G50640.1(ERF-VIIIa-B-1)	225	25215.8	9.37
AT5G60120.2(AP2)	507	55889.1	7.46	AT1G53170.1(ERF-VIIIa-B-1)	185	20024.6	9.78
AT5G65510.1(AP2)	498	55447.6	6.51	AT1G53910.1(ERF-VIIa-B-2)	358	39800.6	4.95
AT5G67180.1(AP2)	352	39593.7	8.99	AT1G68550.1(ERF-VI-L-B-6)	324	35568.1	4.34
AT1G13260.1(RAV)	344	38596.9	9.89	AT1G71130.1(ERF-VI-B-5)	161	17951.1	10.21
AT1G25560.1(RAV)	361	40557.4	9.72	AT1G72360.2(ERF-VIIa-B-2)	262	29093.7	4.60
AT1G50680.1(RAV)	337	38473.2	7.08	AT1G80580.1(ERF-VIIIb-B-1)	256	28826.7	10.41
AT1G51120.1(RAV)	352	40307.3	7.27	AT2G20350.1(ERF-Xb-L-B-6)	158	17460.6	9.26
AT1G68840.1(RAV)	352	39492.5	9.87	AT2G31230.1(ERF-IXc-B-3)	243	27055.4	4.82
AT3G25730.1(RAV)	333	37755.6	9.72	AT2G33710.2(ERF-Xc-B-4)	231	25756.3	6.88
AT5G67190.1(ERF-IIa-A-5)	184	21048.0	6.31	AT2G44840.1(ERF-IXa-B-3)	226	25352.8	6.79
At1g63040(ERF-IIIb-A-4)	248	26016.9	4.49	AT2G46310.1(ERF-VI-B-5)	294	33155.5	4.85
AT1G01250.1(ERF-IIIa-A-4)	192	21050.7	5.85	AT2G47520.1(ERF-VIIa-B-2)	171	19346.4	6.81
AT1G12610.1(ERF-IIIc-A-1)	209	23616.3	5.01	AT3G14230.1(ERF-VIIa-B-2)	379	42525.6	4.65
AT1G12630.1(ERF-IIIb-A-4)	192	20770.0	4.84	AT3G15210.1(ERF-VIIIa-B-1)	222	23740.6	9.16
AT1G19210.1(ERF-IIb-A-5)	185	20726.5	4.50	AT3G16770.1(ERF-VIIa-B-2)	248	27757.8	4.94
AT1G21910.1(ERF-IIb-A-5)	230	25475.9	7.76	AT3G20310.1(ERF-VIIIa-B-1)	244	26508.5	9.05
AT1G22190.1(ERF-Ib-A-6)	261	29137.1	6.37	AT3G23220.1(ERF-IXc-B-3)	139	15708.0	5.04
AT1G22810.1(ERF-IIc-A-5)	144	15816.4	6.51	AT3G23230.1(ERF-IXc-B-3)	139	16096.3	7.52
AT1G33760.1(ERF-IIIa-A-5)	184	21086.2	4.91	AT3G23240.1(ERF-IXc-B-3)	218	24694.9	4.77
AT1G36060.1(ERF-Ib-A-6)	314	34307.4	5.61	AT3G25890.1(ERF-VI-L-B-6)	332	36731.8	4.80
AT1G44830.1(ERF-IIb-A-5)	211	23039.1	5.24	AT3G61630.1(ERF-VI-B-5)	315	35573.0	4.69
AT1G46768.1(ERF-IIa-A-5)	153	17240.4	9.82	AT4G11140.1(ERF-VI-B-5)	287	31545.1	4.64
AT1G63030.1(ERF-IIIc-A-1)	181	20649.2	5.38	AT4G17490.1(ERF-IXb-B-3)	282	32108.0	4.93
AT1G64380.1(ERF-Ib-A-6)	335	36563.9	8.07	AT4G17500.1(ERF-IXa-B-3)	268	29189.5	8.78
AT1G71450.1(ERF-IIIa-A-4)	183	20315.4	5.32	AT4G18450.1(ERF-IXc-B-3)	303	34494.2	4.80
AT1G71520.1(ERF-IIc-A-5)	143	15695.2	4.98	AT4G23750.1(ERF-VI-B-5)	343	37872.2	6.68
AT1G74930.1(ERF-IIb-A-5)	195	21898.2	4.5	AT4G27950.1(ERF-VI-B-5)	335	38447.2	4.36
AT1G75490.1(ERF-IVb-A-2)	206	22579.8	6.51	AT4G28140.1(ERF-Ia-A-6)	292	33403.0	5.43
AT1G77200.1(ERF-IIIe-A-4)	244	26729.0	4.75	AT4G31060.1(ERF-IIb-A-5)	187	20810.4	6.79
AT1G77640.1(ERF-IIb-A-5)	244	26981.1	4.83	AT4G32800.1(ERF)	221	24857.3	4.62
AT1G78080.1(ERF-Ib-A-6)	334	36609.5	7.07	AT4G34410.1(ERF-Xb-B-3)	268	29446.5	6.29
AT2G20880.1(ERF-Ia-A-6)	336	38397.4	6.41	AT5G07310.1(ERF-Xa-B-4)	263	29405.6	7.09
AT2G22200.1(ERF-Ib-A-6)	261	29792.2	7.06	AT5G07580.1(ERF-IXb-B-3)	207	23146.1	4.59
AT2G23340.1(ERF-IIa-A-5)	176	19119.3	9.63	AT5G11190.1(ERF-Va-B-6)	189	21409.1	6.14
AT2G25820.1(ERF-IIIe-A-4)	225	24864.4	4.77	AT5G13330.1(ERF-Xa-B-4)	212	24287.6	9.11
AT2G35700.1(ERF-IIId-A-4)	194	21617.0	6.69	AT5G13910.1(ERF-VIIIb-B-1)	211	23680.7	4.80
AT2G36450.1(ERF-IIIb-A-4)	184	19790.0	4.55	AT5G18560.1(ERF-VIIIb-B-1)	348	38455.0	6.51
AT2G38340.1(ERF-IVa-A-2)	244	27370.1	8.58	AT5G19790.1(ERF-Vb-B-6)	253	28374.5	7.69
AT2G40220.1(ERF-IVb-A-3)	328	35670.8	6.68	AT5G25190.1(ERF-Va-B-6)	181	20606.0	7.60
AT2G40340.1(ERF-IVa-A-2)	341	37829.3	4.41	AT5G25390.2(ERF-Va-B-6)	189	21254.1	10.18
AT2G40350.1(ERF-IVa-A-2)	157	17791.4	10.6	AT5G43410.1(ERF-IXc-B-3)	131	14342.6	7.76
AT2G44940.1(ERF-IIId-A-4)	295	31984.7	4.62	AT5G44210.1(ERF-VIIIa-B-1)	200	22267.0	10.63

AT3G11020.1(ERF-IVa-A-2)	330	37116.8	4.77	AT5G47220.1(ERF-IXa-B-3)	243	26796.7	5.48
AT3G16280.1(ERF-IIIe-A-4)	236	26204.4	4.49	AT5G47230.1(ERF-IXb-B-3)	300	33809.6	4.79
AT3G50260.1(ERF-IIa-A-5)	153	17007.4	10.3	AT5G50080.1(ERF-Xa-B-4)	220	24256.7	9.45
AT3G57600.1(ERF-IVb-A-2)	277	31571.8	5.11	AT5G51190.1(ERF-IXb-B-3)	221	24576.6	9.73
AT3G60490.1(ERF-IIId-A-4)	256	28215.8	5.16	AT5G53290.1(ERF-VI-B-5)	354	40099.8	4.29
AT4G06746.1(ERF-IIa-A-5)	150	17198.9	10.55	AT5G61590.1(ERF-IXb-B-3)	201	22727.0	5.17
AT4G13620.1(ERF-Ib-A-6)	388	44254.4	9.98	AT5G61600.1(ERF-IXb-B-3)	241	26824.8	6.69
AT4G16750.1(ERF-IIId-A-4)	179	19908.9	6.69	AT5G61890.1(ERF-Xa-B-4)	248	27725.8	6.16
AT4G25470.1(ERF-IIIc-A-1)	216	24264.0	4.75	AT5G64750.1(ERF-Xa-B-4)	391	42813.4	8.42
AT4G25480.1(ERF-IIIc-A-1)	216	24235.9	4.87	AT5G67000.1(ERF-Xb-L-B-6)	184	20614.1	9.5
AT4G25490.1(ERF-IIIc-A-1)	213	23829.4	4.74	AT5G67010.1(ERF-Xb-L-B-6)	162	17604.4	7.03
AT4G36900.1(ERF-IIa-A-5)	196	21361.6	8.24				
AT4G39780.1(ERF-Ib-A-6)	272	30951.0	4.60				
AT5G05410.1(ERF-IVa-A-2)	335	37702.3	4.93				
AT5G11590.1(ERF-IIIe-A-4)	236	26043.6	5.16				
AT5G18450.1(ERF-IVb-A-2)	307	34233.8	6.77				
AT5G21960.1(ERF-IIb-A-5)	216	24400.3	4.38				
AT5G25810.1(ERF-IIIe-A-4)	218	23941.3	5.11				
AT5G51990.1(ERF-IIIc-A-1)	224	24955.6	5.44				
AT5G52020.1(ERF-IIIb-A-4)	232	25105.9	4.58				
AT5G65130.1(ERF-Ib-A-6)	277	31210.1	7.04				
		length	Mr [Da]	pI			
Average		270.79	30187.11	6.72			

Table 5 Suppl. Genes and upstream and downstream primers used for RT-qPCR analysis.

Gene ID	Primer name	Primer sequence（5’-3’）
Actin	Actin-F	GTCCTCTTCCAGCCATCTC
	Actin-R	TTCGGTCAGCAATACCAGG
PeERF037	PeERF037-F	ACTGGATATCATGGGCTCTA
	PeERF037-R	TGGGGACATCGAAAATCAAT
PeERF002	PeERF002-F	TGGAAACTTGACACAGCAGGAGATT
	PeERF002-R	AACAGCATAAGAAGGCGGGTTTA
PeERF082	PeERF082-F	TGGAGCAAAGCTTTATCTGTCAC
	PeERF082-R	AGAAAATCAAGCTCAAGGGTCGT
PeDREB57	PeDREB57-F	TTCGTGAAATCCGTAAGTATCA
	PeDREB57-R	ACGCAGATCAGTCTTAAAAT

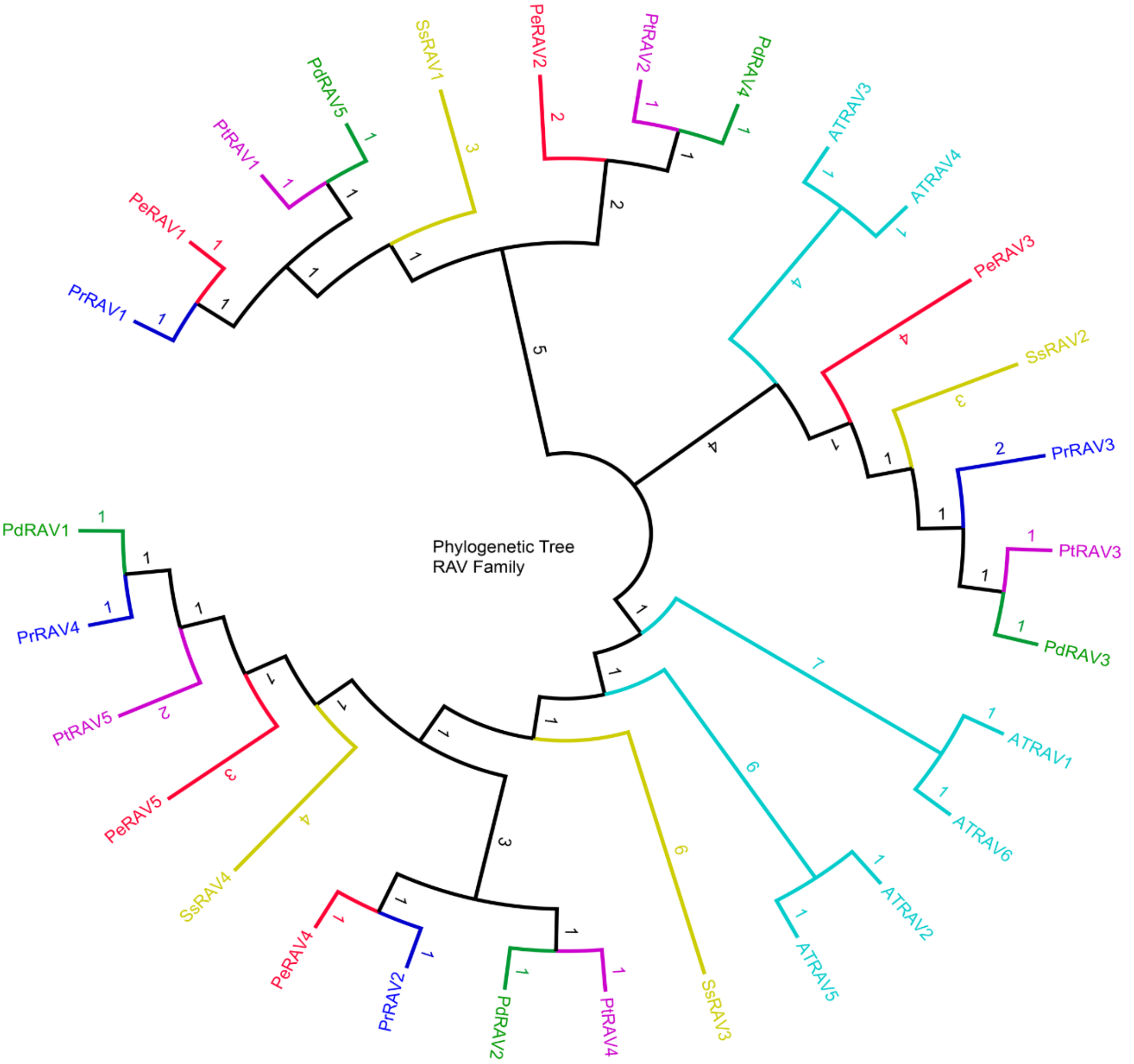

Fig. 1 Suppl. Phylogenetic analysis of the RAV subfamily of *Populus*.

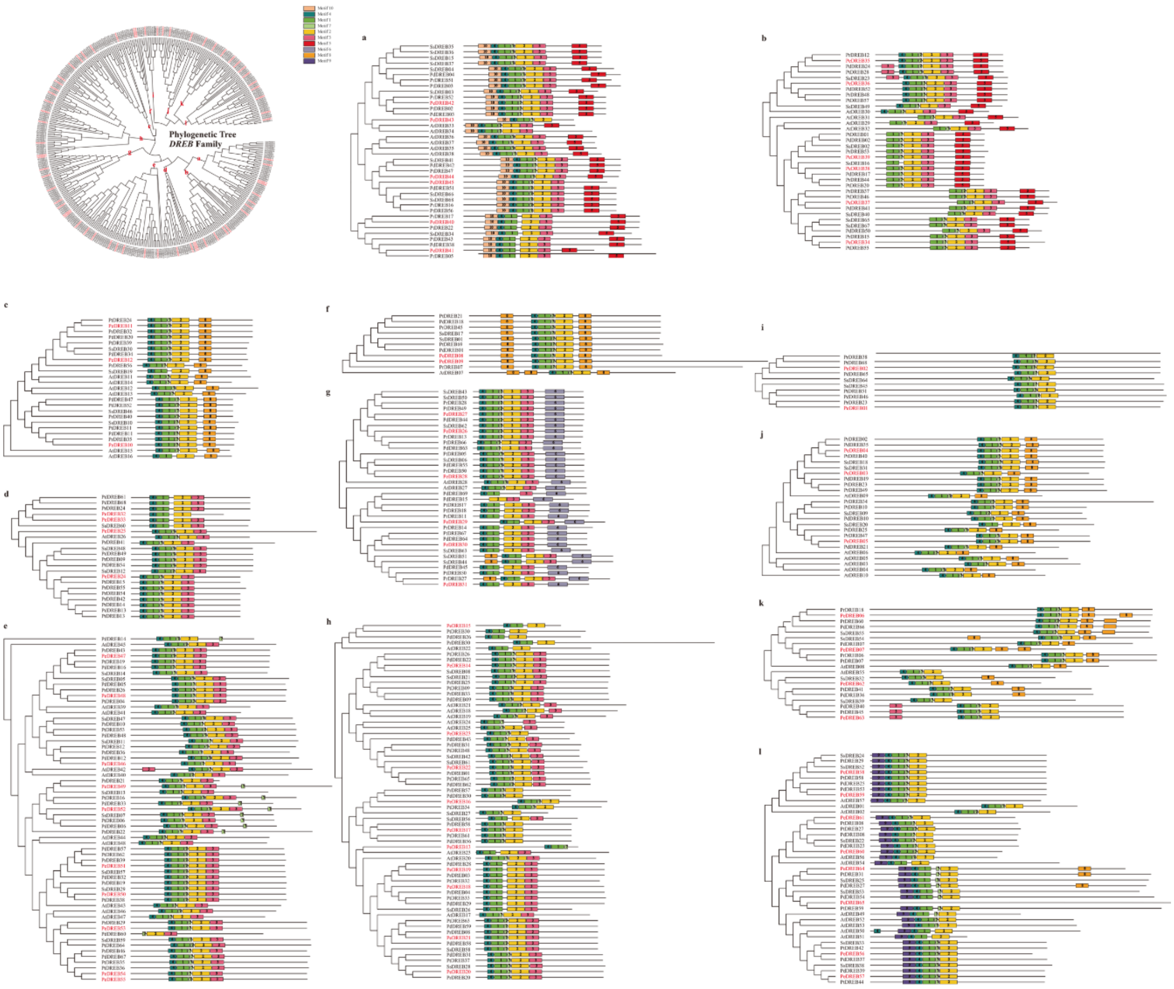

Fig. 2 Suppl. Phylogenetic relationship and conserved motifs of six different plant DREB proteins. Left image: NJ phylogenetic tree constructed using MEGA 7, right image: Distribution of conserved motifs in DREB protein. (Different colored squares represent different motifs and their positions in each DREB protein sequence). a-l: 12 groups of DREB subfamily members.

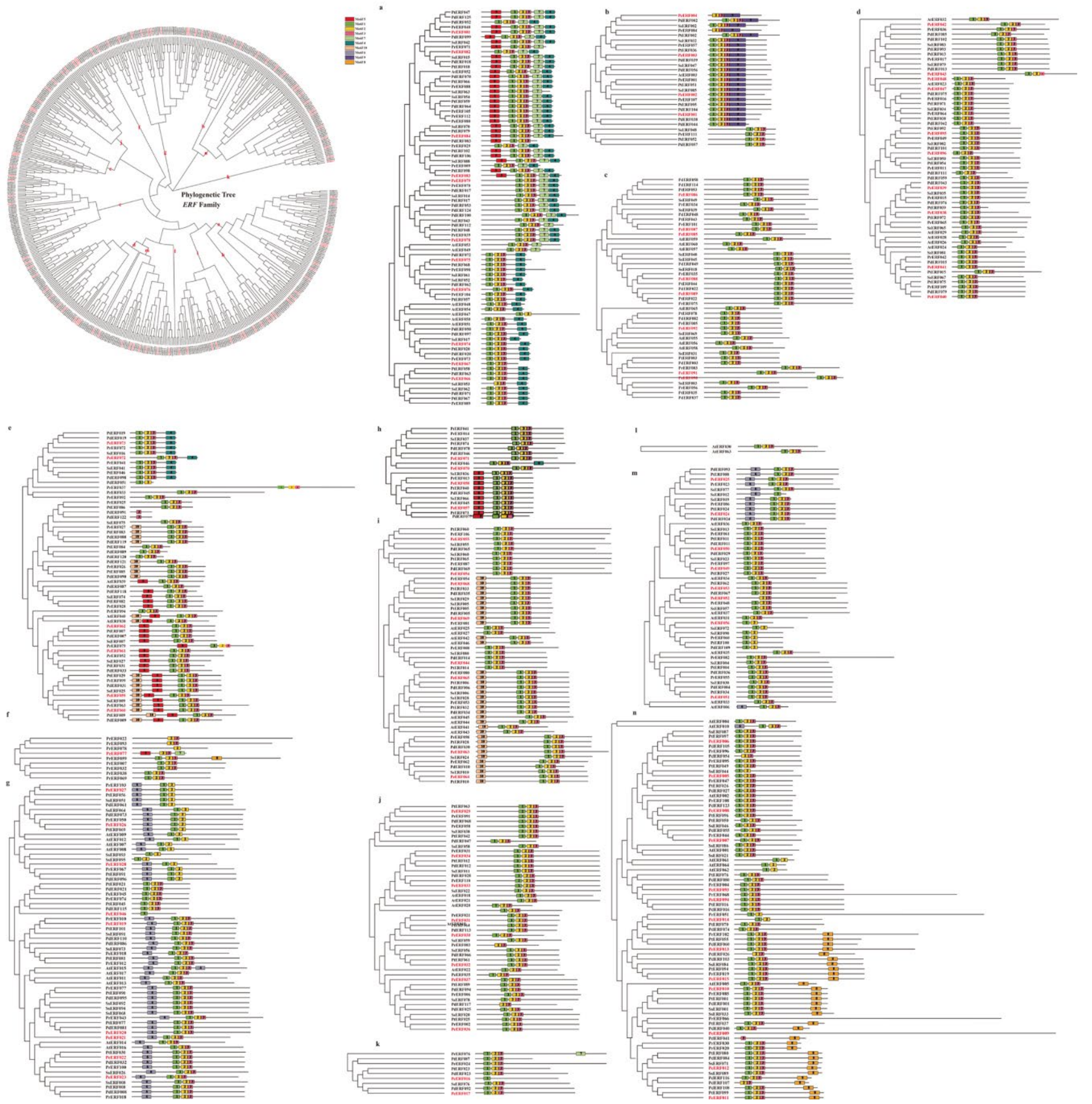

Fig. 3 Suppl. Phylogenetic relationship and motif composition of six different plant ERF proteins. Left image: NJ phylogeny tree constructed using MEGA 7, right image: Distribution of conserved motifs in ERF protein. (Different colored squares represent different motifs and their positions in each ERF protein sequence). a-n: 14 groups of ERF subfamily members.

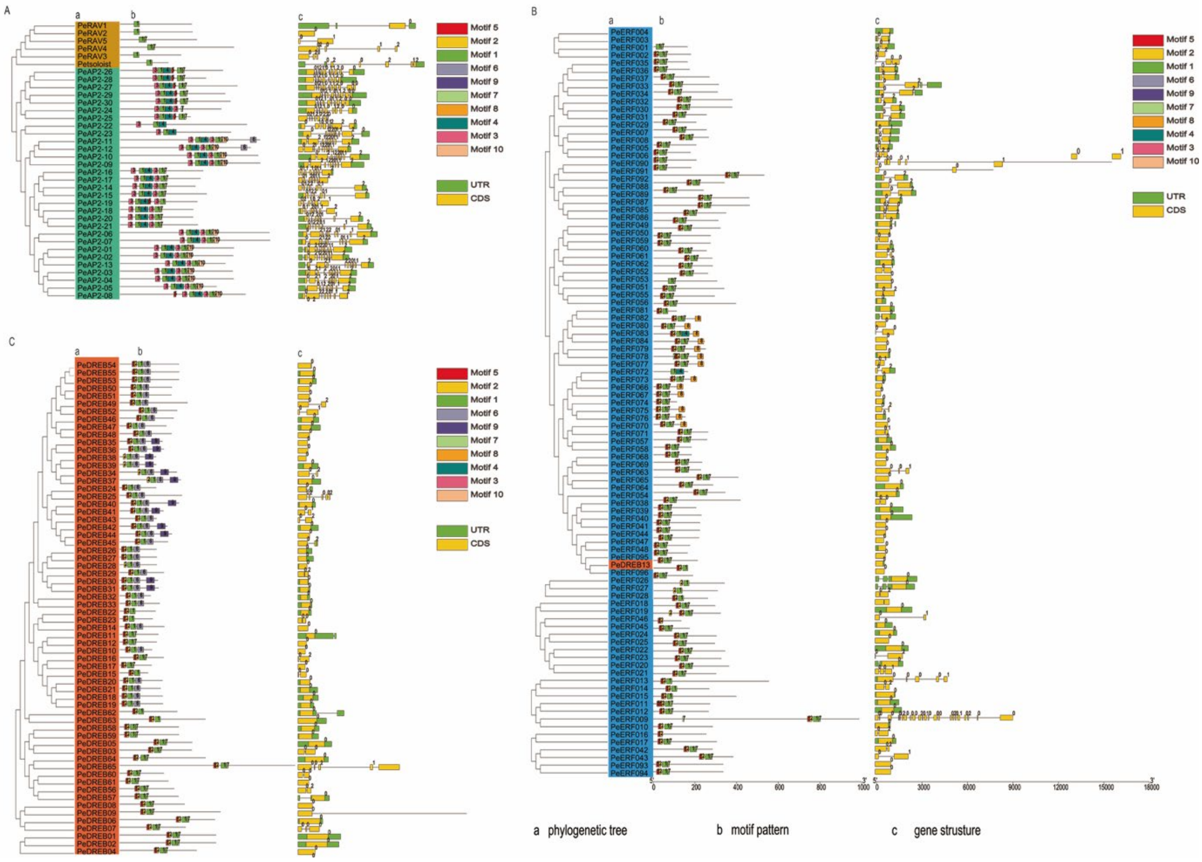

Fig. 4 Suppl. Phylogenetic relationships, gene structure and architecture of conserved protein motifs in *AP2/ERF* genes from *P. euphratica.* A shows AP2 and RAV subfamily, B shows ERF subfamily, and C shows DREB subfamily. a: Phylogenetic tree. b: Conservative motif. (The motifs, numbers 1-10, are displayed in different colored boxes. The sequence information for each motif is provided in Table 2 Suppl. The protein length can be estimated using the scale at the bottom) c: gene structure. (Yellow boxes indicate untranslated 5′- and 3′-regions; green boxes indicate exons; black lines indicate introns. The number indicates the phases of the corresponding introns).

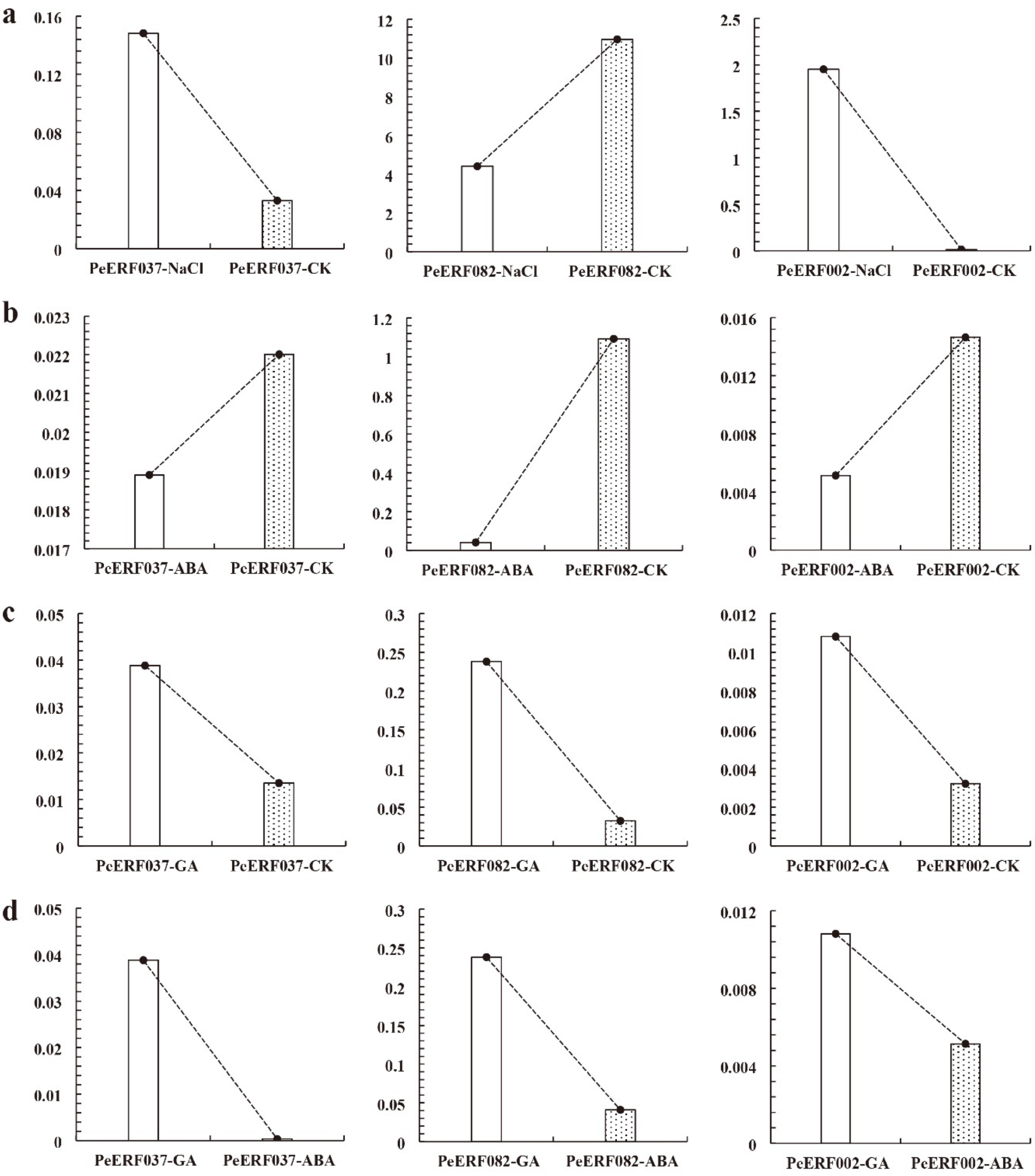

Fig. 5 Suppl. RT-qPCR analysis of *PeERF037, PeERF082* and *PeERF002*. a, b, c and d represent ABA versus ABA_CK, GA$_3$ versus GA$_3$_CK, NaCl versus NaCl_ CK and GA$_3$ versus ABA, respectively.