

Table S1 Sequence alignment results of 25 Ba-clade DREBs using IKP BLAST.

	Gene	Length (aa)	Moss Species	E-value	Identity
1	TR125756_c0_g1_i1	216	<i>Funaria</i>	1.59737e-144	200/202(100%)
2	TR60912_c0_g1_i1	279	<i>Funaria</i>	2.57357e-121	176/187(95%)
3	TR76229_c0_g1_i1	284	<i>Funaria</i>	3.74832e-132	211/227(93%)
4	TR97947_c2_g1_i1	381	<i>Funaria</i>	0.0	319/360(89%)
5	TR55251_c0_g3_i1	193	<i>Funaria</i>	1.86953e-87	138/156(89%)
6	TR65794_c0_g1_i1	207	<i>Racomitrium_varium</i>	1.92769e-105	164/185(89%)
7	TR51295_c0_g1_i1	315	<i>Funaria</i>	1.16271e-85	125/143(88%)
8	TR88428_c1_g1_i3	219	<i>Racomitrium_varium</i>	5.59893e-71	101/117(87%)
9	TR122227_c0_g1_i1	163	<i>Funaria</i>	1.72466e-72	106/123(87%)
10	TR44863_c0_g1_i1	197	<i>Funaria</i>	2.08436e-67	107/126(85%)
11	TR29644_c0_g1_i1	273	<i>Funaria</i>	2.86133e-126	180/220(82%)
12	TR50045_c0_g1_i1	496	<i>Funaria</i>	0.0	277/352(79%)
13	TR65949_c0_g1_i1	326	<i>Funaria</i>	1.2845e-180	251/325(78%)
14	TR101997_c0_g1_i1	333	<i>Racomitrium_varium</i>	2.19047e-62	97/126(77%)
15	TR126346_c7_g1_i1	649	<i>Golenkinia_longispicula</i>	1.85319e-35	57/78(74%)
16	TR121202_c1_g1_i1	235	<i>Neckera_douglasii</i>	1.56115e-64	118/181(66%)
17	TR31778_c0_g1_i1	269	<i>Scouleria_aquatica</i>	8.1443e-67	104/159(66%)
18	TR83728_c1_g1_i2	380	<i>Encalypta_streptocarpa</i>	1.88475e-144	232/376(62%)
19	TR88531_c0_g1_i1	232	<i>Buxbaumia_aphylla</i>	2.66208e-32	89/144(61%)
20	TR111064_c1_g1_i1	266	<i>Neckera_douglasii</i>	9.94306e-27	60/103(59%)
21	TR61348_c0_g1_i1	312	<i>Aulacomnium_heterostichum</i>	6.56064e-37	71/126(57%)
22	TR73547_c0_g1_i1	345	<i>Pseudotaxiphyllum_elegans</i>	8.72126e-64	115/205(57%)
23	TR111064_c2_g1_i3	416	<i>Neckera_douglasii</i>	5.1885e-22	50/93(54%)
24	TR110075_c0_g3_i1	218	<i>Racomitrium_varium</i>	2.30651e-23	55/104(53%)
25	TR78180_c0_g1_i2	260	<i>Aulacomnium_heterostichum</i>	8.42958e-27	66/140(48%)

Table S2 Primer information of 12 BaAP2/ERF genes for RT-qPCR analysis.

Gene	Subfamily	Primer sequence (5'→3')	Length (bp)
TR129622 c4_g8_i3	AP2	GGTCCTGGAAGTGTCAATCAAC CCAAAGGTGCCAAGGTAGA	230
TR119737 c13_g1_i1	DREB (A-2)	TCTGGACCGGATTGATTTGGA AACGCTGTCTGATGCTTTGCA	151
TR27842 c0_g1_i1	DREB (A-5)	CTTCCCAGACTCCATCCCTTCG TTGTCGTCATTTGCGGTTTCC	285
TR1991 c0_g3_i1	DREB (A-5)	CCGACCACGAGGCTTCAAATC CAATACTGGGCGACAATGGCTTA	285
TR42033 c0_g1_i1	DREB (A-6)	GTCGAGGTCTGGGTACGTGAGT CGTGGTGGTGACGGAAGTGA	238
TR125756 c0_g1_i1	DREB unclassified	CATTATAGAACACGGGAAGAAAGC ACGGCACCTTATTCAAATCAAA	272
TR29644 c0_g1_i1	DREB unclassified	CAACATCGTCGCAGAGTCCA CAGGTTCTTCTTGACACACAGA	245
TR113906 c0_g1_i1	ERF(B1)	AACGGCACCACCACCCAT TCGTGAGGCTGAGCAAGGA	132
TR54730 c0_g1_i1	ERF(B3)	GGCTGGGCACTTACGACA	126

		CGAGGTTGGCTGAGTAGACG	
TR138719 c0_g1_i1	ERF(B6)	AGAGGCGCAGTCGCAGTCA GCAAGATGCCCAGGTTGGAT	122
TR86276 c0_g2_i1	Soloist	ACACTCCTTTCGTTCTTTACT TGGATGATGCCAATCTTAT	187
TR86276 c0_g3_i1	Soloist	ACTTGGGCACCGTTGATT GCTTCTCTTCTTACTCAAGATGGA	180

Table S3 Primer information of 12 *BaAP2/ERF* genes for gene cloning.

Gene	Primer sequence (5'→3')	Product length(bp)	CDS length(bp)	ORF length(aa)
TR129622 c4_g8_i3	TTGAAGGGGGAGAGTGTTGTT TTTCCACCGAGCTCTCCATCA	818	594	198
TR119737 c13_g1_i1	CTGACATTGCTACAGAGTTCGT AAACCAGCTCCCGGGTCAAT	879	789	263
TR27842 c0_g1_i1	GATTCGGCAGTGAGCAATTGTA TGCATCTCCAACACCAATATG	732	618	206
TR1991 c0_g3_i1	ATGCTTGGGATTTGGGAGCTC GATCACGCTCCAAACAATTGTA	1131	1041	347
TR42033 c0_g1_i1	AGCACGTTTGAAGTTTGTGCG CACCAGAACTGTCAACCAAGAT	1561	1482	494
TR125756 c0_g1_i1	TTGTGTGTGCAATTGAGACCGT TGATTGCTTGAGTGAAGCTTCA	757	648	216
TR29644 c0_g1_i1	ATCGTGTATTTAGACACGGTGT CGGAATGGTTGCTAATGAAACT	924	819	273
TR113906 c0_g1_i1	TTACATGCGGTGGGAGTACTG ACCTAAGCATGATGTTTGCAAG	757	699	233
TR54730 c0_g1_i1	TCGAGTGGAGCTAATTCGATC CAGCATCGTCTGCAAGAACGA	1134	1011	337
TR138719 c0_g1_i1	GTCAGAAGTTCTGTATCTTGCA GTGTCAGCAATCATGTGAAGTA	802	621	207
TR86276 c0_g2_i1	ATCCTACCACGAGCTTCATATC CATAATTCAGTACCATCCACAG	844	759	253
TR86276 c0_g3_i1	ATCCTACCACGAGCTTCATATC GCAGGCTATCATGATAATTCCT	684	612	204

Table S4 Primer information of 12 *BaAP2/ERF* genes for fusing to pGBKT7 vector. The vector sequence was labeled in red.

Gene	Primer sequence (5'→3')
TR129622 c4_g8_i3	CATGGAGGCCGAATTCATGGAGGTGGTGTCTGAAATT GCAGGTCGACGGATCCCATATACGATTTTGGACAAC
TR119737 c13_g1_i1	CATGGAGGCCGAATTCATGCAGTTGGGAAACAACAG GCAGGTCGACGGATCCCAATGCTGGTCCCGACC
TR27842 c0_g1_i1	CATGGAGGCCGAATTCATGGTGGACAACGGCAGGAG GCAGGTCGACGGATCCTCAGGAGAAAGACCAGAGCTC
TR1991 c0_g3_i1	CATGGAGGCCGAATTCATGGTTGACAAGCAGAGGA GCAGGTCGACGGATCCCTTAAGCTCCGGGGAAGCT
TR42033 c0_g1_i1	CATGGAGGCCGAATTCATGGCAGCAGTGGCACAC GCAGGTCGACGGATCCCATACACACTGTCTCCAG
TR125756 c0_g1_i1	CATGGAGGCCGAATTCATGAATTTGACAATATCCAGC GCAGGTCGACGGATCCCTAGCTGGACGAGGGCAC
TR29644 c0_g1_i1	CATGGAGGCCGAATTCATGTCATCGGGGAAGTGC GCAGGTCGACGGATCCCAATAGAGATAGAAAACGTC
TR113906 c0_g1_i1	CATGGAGGCCGAATTCATGGGGTCTCGAGAAGGG GCAGGTCGACGGATCCTCAGAAATATACCTCACAAGA
TR54730 c0_g1_i1	CATGGAGGCCGAATTCATGACCATCATTCCGGGTG GCAGGTCGACGGATCCCTCAGAATGGCGGACTTCG
TR138719 c0_g1_i1	CATGGAGGCCGAATTCATGTGCAGGAAGATGAGAG GCAGGTCGACGGATCCCTACGCGGAGGCGGCCGT
TR86276 c0_g2_i1	CATGGAGGCCGAATTCATGGTTAGTATCAGAAAACGG GCAGGTCGACGGATCCCTTATGATGACCTCTTAAATGTT
TR86276 c0_g3_i1	CATGGAGGCCGAATTCATGGTTAGTATCAGAAAACGG GCAGGTCGACGGATCCCTTATGATGAGCATTTGAGAGC

Table S5 Primer information of *BaAP2/ERF* genes for infusing to pYES2 vector. The vector sequences were labeled in red.

Gene	Primer sequence (5'→3')
TR1991 c0_g3_i1	CAGTGTGCTGGAATTCATGGTTGACAAGCAGAGGA CATGCTCGAGCGGCCGCTTAAGCTCCGGGGAAGCT
TR29644 c0_g1_i1	CAGTGTGCTGGAATTCATGTCATCGGGGAAGTGC CATGCTCGAGCGGCCGCTCAATAGAGATAGAAAACGTC
TR54730 c0_g1_i1	CAGTGTGCTGGAATTCATGACCATCATTCCGGGTG CATGCTCGAGCGGCCGCTCAGAATGGCGGACTTCG
TR138719 c0_g1_i1	CAGTGTGCTGGAATTCATGTGCAGGAAGATGAGAG CATGCTCGAGCGGCCGCTACGCGGAGGCGGCCGT
TR86276 c0_g2_i1	CAGTGTGCTGGAATTCATGGTTAGTATCAGAAAACGG CATGCTCGAGCGGCCGCTTATGATGACCTCTTAAATGTT
TR86276 c0_g3_i1	CAGTGTGCTGGAATTCATGGTTAGTATCAGAAAACGG CATGCTCGAGCGGCCGCTTATGATGAGCATTTGAGAGC