

Supplementary Table 1: Oligonucleotide primers used for RT-qPCR analysis of *AtBrd* and *OsBrd* genes.

S. No.	Primer Name	Gene	Primer Sequence (5'-3')
1	AtBrd1a-ForP	^{BD5} <i>AtBrd1a</i> (AT3G01770)	GGCATTGCTTGAGATGGAGAAGTCGGTTG
2	AtBrd1a-RevP		CAAATACAGCCAACCCATCAGACTCAGAGCC
3	AtBrd1b-ForP	^{BD5} <i>AtBrd1b</i> (AT5G14270)	GCCAGGCATTGATGGAGATGGAGCAGTCAG
4	AtBrd1b-RevP		ACCCAACATCAGGCCCATCCTCCTCCTC
5	AtBrd3a-ForP	^{BD2} <i>AtBrd3a</i> (AT1G76380)	TAAACAATTAAC TCCAGTTGGACTGAAAGCTGAATATGGGT
6	AtBrd3a-RevP		CAACCCACCCGGGACCAAATTCGGTTCCA
7	AtBrd3b-ForP	^{BD2} <i>AtBrd3b</i> (AT1G20670)	GAGTTAAACAGTTGATTCCAGTTGGGCTGAACATGGAG
8	AtBrd3b-RevP		GGGCAATACAGTCTCGATTCTCCTCGATGC
9	AtBrdPG1a-ForP	^{BD1} <i>AtBrdPG1a</i> (AT1G17790)	AGTTACTGAATCAGGAAAAGC
10	AtBrdPG1a-RevP		GTCACTGTCAGTATCACTAGAG
11	AtBrdPG1b-ForP	^{BD1} <i>AtBrdPG1b</i> (AT1G73150)	GTCATGTGGCATCTACTGTTC
12	AtBrdPG1b-RevP		AGCTATCACTGTCAGAGCCACTA
13	AtBrdPG1b.1-ForP		AAGTTACTGAATTAGGTCATG
14	AtBrdPG1b.1-RevP		AGCTATCACTGTCAGAGCCACTA
15	AtBrdPG1b.2-ForP		TGTTTTTGACACTTGAAAAG
16	AtBrdPG1b.2-RevP		AGCTATCACTGTCAGAGCCACTA
17	AtBrd2a-ForP	^{BD3} <i>AtBrd2a</i> (AT2G42150)	GACTCGAACGTCAGGAAACAATTG
18	AtBrd2a-RevP		AACTCTGAAGATCCTCTGTG
19	AtBrd2b-ForP	^{BD3} <i>AtBrd2b</i> (AT3G57980)	GTAACCTGGTCTCGCCAGGATC
20	AtBrd2b-RevP		TTCAACTGCAATGACGAGATGG
21	AtBrd2c-ForP	^{BD4} <i>AtBrd2c</i> (AT2G44430)	AGGGTGGTGCCGGCGAGATC
22	AtBrd2c-RevP		AATCCTTAGTGTCTTGCTC
23	AtBrd2d-ForP	^{BD4} <i>AtBrd2d</i> (AT3G60110)	AGAGGAAAGGACAGAAATAC
24	AtBrd2d-RevP		AATCCTTAGTGTCTTGCTC
25	AtBrdPG2a-ForP	^{BD6} <i>AtBrdPG2a</i> (AT5G10550)	CTCCACCAAGAAACATGCCTCCGG
26	AtBrdPG2a-RevP		TAGAGCCACCACTAGCAGCGGCAGCTG
27	AtBrdPG2b-ForP	^{BD6} <i>AtBrdPG2b</i> (AT5G65630)	CTCCACCTAGGAACATGGCTTC
28	AtBrdPG2b-RevP		CACTACTAGCAGCAGCTGCAA
29	AtAct-ForP	<i>AtActin</i> (AT3G18780)	CACAGCACTTGCACCAAGCAGCAT
30	AtAct-RevP		TGGAGATCCACATCTGCTGGAATG
31	OsBrd4a-ForP	^{BD1} <i>OsBrd4a</i> (LOC_Os01g11580)	ATGATAATGAGAGGTATGTAGGCTCATCATCACC
32	OsBrd4a-RevP		CACTAGACGAAGAGCCTGAATCGC
33	OsBrdST1-ForP	^{BD1} <i>OsBrdST1</i> (LOC_Os01g46040)	CGGGATGATGGAGGTGGACCTGGA
34	OsBrdST1-RevP		TCATGGCTCCTGCTTCACCTTAACC
35	OsBrdPG3a-ForP	^{TD1} <i>OsBrdPG3a</i> (LOC_Os04g53130)	CCGCTACGATGGTGGACAACGGTGATGTGACG
36	OsBrdPG3a-RevP		GGGCGGACCCAGGGCCAGGACA
37	OsBrdPG3b-ForP	^{TD1-BD2} <i>OsBrdPG3b</i> (LOC_Os04g53170)	ACAATGGCAATAGAGAGCAAGGATCCTGA
38	OsBrdPG3b-RevP		CCTCAGTATCCTTCTCAATCTCCACTGATTGGT
39	OsBrdPG3c-ForP	^{BD2} <i>OsBrdPG3c</i> (LOC_Os08g09340)	GATATTGGCGATGAGATGCCGACGGCA
40	OsBrdPG3c-RevP		GAGCTCCTCGAGTCAGAATCACTGGATG
41	OsBrd5a-ForP	^{BD3} <i>OsBrd5a</i> (LOC_Os06g24870)	AGAGCTTATGAAACGGGTGAAGAAGGGCTTCA
42	OsBrd5a-RevP		TCATCGCCTGTGTTATCATTGCCACCATTCTCCTG
43	OsBrd5b-ForP	^{BD3} <i>OsBrd5b</i> (LOC_Os08g01794)	GAGGATGAAGGCTCCAGACCATACTTTGACG
44	OsBrd5b-RevP		TGGCTTGTTTCTGTTGGCTCCTTATGTTGG
45	OsBrd2-ForP	^{BD4} <i>OsBrd2</i>	GAAATACGATCTCTCGATCGGGTCGTTGCAATCA

46	OsBrd2-RevP	(LOC_Os08g39980)	CGCCGGCCTCCTCCGGTGATCC
47	OsBrd13-ForP	^{BD4} <i>OsBrd13</i>	CGCCTGTTGCTCAGCTGGTATCTG
48	OsBrd13-RevP	(LOC_Os09g33980)	TGGTGGATTGTCAGTTTCTTTCAGAACACC
49	Ose1F1 α -ForP	<i>Ose1F1α</i>	GCTGCAACAAGATGGATGCCACCA
50	Ose1F1 α -RevP	(LOC_Os03g08010)	GAAGGGAATCTTGTCAGGGTTGTAGC

Note: The locus numbers of the *AtBrd*-genes are as per The Arabidopsis Information Resource (TAIR, <https://www.arabidopsis.org/>) and of *OsBrd*-genes, as per Rice Genome Annotation Project (RGAP, <http://rice.uga.edu/>).

Supplementary Table 2: List of conserved motifs identified among twenty-eight *Arabidopsis thaliana* bromodomain (BRD) containing proteins at per analysis using MEME suite software.

Motif	Motif Sequence	E-Value	Sites	Width	Functional Annotation
M1	EJPDYNNIIKHPMDLGTIKKKLEKG	3.10E-213	24	25	BRD
M2	YSSPLEFAADVRLTFNNAMTY	1.10E-166	24	21	BRD
M3	MKQCETLLRKLMMKHKGWVFNTPVDDVGL	1.90E-134	12	29	BRD
M4	NPEGNDVYVMAEKLLKLFEERWKTIEKKY	3.80E-87	12	29	BRD
M5	QIVKKSNPESLQGDDEIEJDIDALDDETLWELRRF VDEYLN	9.30E-83	12	41	ET
M6	QTWGTWEELLLACAVKRHGTGDWDSVASEVQ	2.80E-47	5	31	Myb-like DBD
M7	EPAKRDMTDEEKRLGEDLQSLPPDKLZ	2.10E-33	11	28	ET
M8	PWLEELRKLRLVAELRREVERYDLSINSLQLKVKK LEEERE	3.90E-32	7	40	-
M9	AAEAKRKRELEREAARQALLEMEKSVEINENSRL LEDLELL	2.20E-29	4	41	-
M10	DGVSKMVLSSGLSSSERRELKRRLKSELEZVRSL RKRIE	9.40E-28	8	40	BRD
M11	PEKRYRAAJLKNRFADIILKAREKPLNQN	5.70E-25	5	29	-
M12	PVGLNAEYGYARSLARYAANLGPVAVKIASQRI EKVLPSTGIKFGRGWVGE	4.30E-27	3	50	-
M13	KGDPEKLQRERELELQKKKEKARLQAEAKAAE EARRKA	1.60E-24	5	39	-
M14	ICVWNAADGSLVHCLTGHSESSYVLDVHPFNPRI AMSAGYDGKTIIWDIW	2.10E-21	2	50	WD
M15	WFLHDNFVTCSDGRANIWRPEIRGVGGPSGRGL GFYHLKVPPPLPP	4.10E-29	4	48	TFIID, subunit TAF1

Analysis of conserved motifs was carried out online using MEME software, available at MEME online Suite (version 5.4.1, <http://meme-suite.org/tools/meme>, Bailey et al., 2015).

Supplementary Table 3: List of conserved motifs identified among twenty-two *Oryza sativa* bromodomain (BRD) containing proteins, as per analysis using MEME suite software.

Motif	Motif Sequence	E-Value	Sites	Width	Functional Annotation
M1	YGSLEEFAADVRLTFSNAMTYNPKGHDVH	9.10E-187	22	29	BRD
M2	DVVALGJPDYFDIHKPMDLGTIRKKLE	2.00E-145	15	28	BRD
M3	LPPEKLDNVLQIVKKRNGSPELVGDEIELDIDEMD VETLWELDRFVANYK	6.80E-84	7	50	ET
M4	LKRCGEILKKLMKHKAAEPFNTPV	2.30E-27	9	24	BRD
M5	ATFENMYKPAHSWFEQEPKILEPPMPVPPPPEPEK PAPSTV	4.40E-23	5	41	-
M6	MKKPKAREPNKREMTLEEKNKLRVGLZ	1.10E-20	5	27	-
M7	YVDIGDEMPATYQSVIEKDTEAASSGSSSSSDS GSSKDSVSESGNAH	3.90E-15	3	49	-
M8	IVNGENADVIDASVANDSDMLVNGSTATMVDNG DVTMAIESKDPDKITTQ	5.10E-13	2	50	-
M9	MKRVKKGFMMKNWLAAGLYSDVQENGNDNTG DEDVKSGSKGSKQKRRRLG	4.00E-11	2	50	-
M10	MAEQLLEIFEAKWPEIEAKV	6.10E-07	6	20	BRD
M11	VQNAKPKVYSRVRLKFKSAKVLETHQGPSEAKA PVDGGGGKPAASAAPEA	5.70E-06	2	49	-
M12	HHHHHHQW	9.00E-06	3	8	-
M13	NQDRKADSVSEPLPSKQETVLENVESETALEPRSS QELEVKQATPERQRD	5.00E-04	2	50	-
M14	VAEKAIVSPDGQKDAQAAELSGSDKDKMARKVA SIKIKSVGLSSVEDK	4.90E-02	2	48	-
M15	MKRKRGRKMGKKGKLKASITADASPMSPSPST VDASSKSP	9.80E-01	2	41	-

Analysis of conserved motifs was carried out online using MEME software, available at MEME online Suite (version 5.4.1, <http://meme-suite.org/tools/meme>, Bailey et al., 2015).