Supplementary Figure 1: Schematic representation of alternative splicing events in *Brd*-genes of *A. thaliana* (A) and *O. sativa* (B), belonging to different ortholog groups (OGs), paralog groups (PGs), and singleton category (STs). Block duplicated genes (BD), constitutive transcript (.1), alternative transcripts (.2 to .6), UTRs (white boxes), exons (dark grey boxes) and introns (dashed lines) are indicated in the figure. Scale on the top indicates the length of transcripts (kilobase, kb).



Supplementary Figure 2: Motif heterogeneity among BRD-proteins of *A. thaliana* (A) and *O. sativa* (B), belonging to thirteen ortholog groups (OG1-13), three paralog groups (PG1-3), and singleton category (STs). Motifs M1-M15 are shown in different color codes. Scale on the top indicates the protein length (number of amino acids). Duplicate BRD-pairs are indicated with the designations 'BD' (block duplication) and 'TD' (tandem duplication) in the names.



Supplementary Figure 3: Diversity of *cis*-elements (as per analysis at PlantCARE database) in the upstream regions of *A. thaliana Brd*-genes belonging to thirteen ortholog groups (OG1-13), two paralog groups (PG1-2), and singleton category (STs). Different types of elements are indicated by different symbols/colours, *cis*-elements belonging to six major functional categories are indicated below, and block-duplicated genes are indicated by the designation 'BD' in the gene name. Scale on the top indicates the length in kilobase.



Supplementary Figure 4: Diversity of *cis*-elements in the upstream regions of *O. sativa Brd*-genes belonging to thirteen ortholog groups (OG1-13), one paralog group (PG3), and singleton category (STs), as per analysis at PlantCARE database. Different types of elements are indicated by different symbols/colours, *cis*-elements specific to six functional categories are listed below, and genes affected by block or tandem duplications are indicated by the designation 'BD' or 'TD' in the gene names. Scale on the top indicates the length in kilobase.



Supplementary Figure 5: Multiple sequence alignment of the bromodomain-region of 28 AtBRD and 22 OsBRD-homologs. Scale on the top indicates the sites in the MSA file. The duplicate-pairs are indicated with designations 'BD' (block duplication) and 'TD' (tandem duplication) in names, while numerals (I-VI) indicates the six major clusters as per phylogenetic analysis (Figure 9A).

BD1	10 I	20 I	30 I	40 I	50 I	60 ₁	70 I	90 80 I	90 I	100 I	11 	0 12 I	20 13 I	0 140 I	150 I
AtBRDPG1a			FKNC	NSLLTK LMKHI	KSAW VE	NVPVDAKG	LGLHDYHNIV	KEPMDLGTVK	rKLGK	SLYKSPL D	FAEDVRLTF	NNAILYNPIG	HDVYRFA	ELLLNMFEDK	W
AtBRDPG1b			LKSC	NNLLTK LMKH	KSGW IF	NTPVDVVT	LGLHDYHNII	KEPMDLGTVK	TRLSK	SLYKSPL E	FAEDVRLTF	NNAMLYNPVG	HDVYHMA	EILLNLFEEK	W
BD6 A+PPDPG2b			MMTTC	GOILVK LMKHI	KWSW VE	LNPVDVVG	LGLHDYHRIV	DKPMDLGTVK I	MNLEK	GLYRSPID	FASDVRLTF	DNAMSYNPKG	ODVYLMA	EKLLSQFDVW	E
BD1 BD1 BD1			MLINIC	SQITAK TWEE	KWAW VE	NIPVDVVG	LGLHDINGVV	KKPMDLGIVK I	GNLDK	GFIVSPID	CAIDVRLIE	DNAMIINPKG	DVIFMA	DKLLDHFDGM	E
OsBRD4a			A FRES		KHSW VE	NTPVDASA	LGLHDYFATT	KHPMDLGTVK :		COVENDE E	FAGDVRLTE	UNAMRINPKG	ODVHEMA	FOLLCIFFAO	W
AtBRD4			V FKNC	SALLER LMKH	KHGW VE	NAPUDVKC	LGLLDYYTT	EHPMDLGTTK	SALMK	NIVKSPRE	FAEDVRLTE	HNAMTYNDEC	ODVHIMA	VTLLOTFEER	W
AtBRD1c			T. MKOC	DTLLEK LWSHI	PHSW VE	OAPVDVVK	LNTPDYLTTT	KHPMDI.GTVK	INT.AS	GVYSSPH E	FAADVRLTE	TNAMTYNPPG	HDVHTMG	DTLSKLEEAR	W
OsBRD1			FKOC	DAILKK LMTO	KCSN IF	DSPVDAVK	LNIPDYFOII	KKPMDLGTIR	KLDS	GSYTSPS E	FAADVRLTF	SNAMTYNPRO	HVVHDYA	IOLNKMFESR	W
TD1-BD2 OsBRDPG3c			MRKRC	TOILTR LRKO	KISV WE	NSPVDVER	LKLHDYHAII	RNPMDLGTVK I	ENLAF	GRYPSHE A	FATDVRLTF	SNALRYNPAL	HHVHRYA	SNLLATFE	
^{TD1} OsBRDPG3a			M RKRC	DOILAK LRKDI	KRSI WE	NAPVEVDR	LGLQDYHAVI	KCPMDLGTVR	ANLAA	GRYPSHD D	FAADIRLTF	SNALRYNPAG	HEVHTFA	GDLLASFEKM	¥
BD2 OsBRDPG3b			MRKRC	EQILAK LRKDI	KRSI WE	NAPVEVDR	LGLHDYHAVI	KCPMDLGTVR	ANLAA	GRYPSHD D	FAADVRLTF	SNALRYNPAG	HEVHTFA	GDLLASFEKM	¥
AtBRD1d			V MKEC	ETLLNR LWSH	KSGW PE	RTPVDPVM	LNIPDYFNVI	KHPMDLGTIR S	SRLCK	GEYSSPL D	FAADVRLTE	SNSIAYNPPG	NQFHTMA	QGISKYFESG	W
AtBRD12			W SSQC	LALLRF LMEH	RGGW LE	KEPVDPVK	MEIPDYFNVI	QKPMDLGTVK S	SKLLK	NVYSNAD E	FAADVRLTF	ANAMHYNPLW	NEVHTIA	KEINEIFEVR	W 1
OsBRD12			SRQC	GSILKK LMDH	KSGW IF	NTPVDPVV	YGIPDYFDVI	RNPMDLGTVK H	RKLTS	KQYSNPY E	FAADVRLTF	SNAMKYNPPG	NDVHGIA	DQLNKIFDSE	W
^{BD5} AtBRD1a			MKQC	ESLLKR LMSQ	QHCW LF	NTPVDVVK	LNIPDYFTII	KHPMDLGTVK S	SKLTS	GTYSSPS E	FSADVRLTF	RNAMTYNPSE	NNVYRFA	DTLSKFFEVR	W
^{BD5} AtBRD1b			L MKQC	EALLKR LMSH	QYGW VE	NTPVDVVK	LNILDYFNVI	EHPMDLGTVK 1	KLTS	GTYSCPS E	FAADVRLTF	SNAMTYNPPG	NDVYVMA	DTLRKFFEVR	W
^{BD1} OsBRDST1			A LLRC	GKLLDK LLEHI	EDGW VE	AEPVDARA	LRLVDYYLRI	SDPMDLGTVR H	RRLER	RRYADPW A	FAADVRLTF	NNAMSYNSAG	DPVYESA	AELSEIFEAG	W
AtBRD9			L MRQF	ATMFRQ IAQHI	KWAW PE	LEPVDVKG	LGLHDYYKVI	EKPMDLGTIK H	KKMES	SEYSNVR E	IYADVRLVF	KNAMRYNEEK	EDVYVMA	ESLLEKFEEK	W
AtBRDST1			L MRQF	GTIFRQ ITQH	KCAW PE	MHPVNVEG	LGLHDYFEVI	DKPMDFSTIK 1	NQMEA	KDGTGYKHVM Q	IYADMRLVF	ENAMNYNEET	SDVYSMA	KKLLEKFEEK	W
OsBRD9			L MRQF	GTIVRQ ITSH	EWAE PE	LKPVDVVG	LQLDDYYKII	TKPMDFSTIQ H	KKMEG	KDDNKYNNVR E	IYSDVRLIF	ANAMKYNDEF	R HDVHIMA	KSLLEKFEEK	W
AtBRD5		N	KQE LEDS	LIVIKK IMKM	EAAD PE	NVPVNPEA	LGIPDYFDII	KTPMDFGTIC N	NNFEK	GNKYMNSE D	VYKDVNYIW	NNCSKYNKKG	DYIVDLM	KRVKKNFMKY	W
BD3 OsBRD5a				IKK VMKM	DAAE PE	NTPVDPVA	LGIPDYFDII	DTPMDFGTIC (QNLER	GDKYMNSE D	VYKDVQFIW	DNCTKYNSKG	DYIIELM	KRVKKGFMKN	W
OsBRD5b				IKK VMKM	DAAE PE	NTPVDPVA	LGIPDYFDII	DTPMDFGTIC (2NLER	GDKYMNSE D	VYKDVQFIW	DNCTKYNSKG	DYIIELM	KRVKKGFMKN	W
OsBRD10			- QL TNLM	RSLLKN MNEH	PDAW PE	KEPVDSRD	VPDYYDII	KDPIDLKTMS H	KRVES	EYYVTLE M	FVADMKRMF	SNAKTYNSPE	TIYYKCA	SRLESFFSNK	v]11
AtBRD10			- QL NALM	RALLKT MQDH	ADAW PF	KEPVDSRD	VPDYYDII	KDPIDLKVIA H	KRVES	EQYYVTLD M	FVADARRMF	NNCRTYNSPE	TIYYKCA	TRLETHFHSK	VQA 11
AtBRD3b			D KKLL	LFILDR LOKK	DTYG VY	SDPVDPEE	LPDYFEII	KNPMDFSTLR 1	KLDS	GAYSTLE Q	FERDVFLIC	TNAMEYNSAL	TVYYRQA	RAIQELAKKD	F
AtBRD3a			D KKLL	FFILDR VQKK	DTYG VY	SDPADPEE	LPDYYEII	KNPMDFTTLR H	KKLES	GAYTTLE Q	FEQDVFLIC	TNAMEYNSAL	TVYYRQA	RAMLELAKKD	F
AtBRD3c			D KKSL	ELILDK LQKKI	DIYG VY	AEPVDPEE	LPDYHDMI	EHPMDFSTVR H	KKLAN	GSYSTLE E	LESDVLLIC	SNAMQYNSSE	TVYYKQA	RTIQEMGKRK	F II
OsBRD3b			D KKLL	VFVLDR LQKK	DTYG VE	SDPVDPEE	LPDYHDII	KHPMDFSTIR H	KKLNK	GAYGNLE Q	FEDDVFLLT	SNAMCYNSPE	TIYYRQA	RAIQELAKKD	F 11
OsBRDST3				ILDT LEMRI	DTHE LF	AMP-DDIQ	VTDYAERV	NRPGDFATLR (5KNKD	GMYNTLE Q	FENDVYMVF	QKAMSINSED) TIPYREA	MSLLHQAKQV	F
OsBRD3a								MDFSTIR I	CKLLN	DSYTTLE Q	FENDVFLLT	SNAMSYNSDE	TVYYRQA	RSIEALAKKD	F
OsBRD13		V	RRM RMCL	RDICNR ILYNI	KRFN VE	HFPVSEEE	VPDYRSVV	HNPMDMATVL (20 VD S	GQYLTRA S	FMKDIDLIV	SNAKTYNGSE	YNGSRIVSRA	CELRDVVQGM	LSQMDPSLV
AtBRD13		I	RRL RMCL	RDVCNR ILYDI	KRFS AF	HFPVTDED	APNYRSII	QIPMDTATLL (QRVDT	GQYLTCT P	FLQDVDLIV	RNAKAYNGDD	YAGARIVSRA	YELRDVVHGM	LSQMDPALL
OsBRD7			L SNIL	EKIVDH LRTM	SCSF LF	RKPVTKKE	APDYFDII	ERPMDLGTIR I	KVRK	MEYKNRE D	FRHDVAQIA	LNAHTYNLNF	R HPHIPPLA	DELLELCDYL	LEESADVLDD AEYAI
AIBRD/a			T DNITT	ERIVDT LRLK	EE-VSR LE	LKPVSKKE	APDYLDIV	ENPMOLSTIR I	DKVRK	TEYRNRE Q	E.KHDVWQIK	YNAHLYNDGR	NPGIPPLA	DOTTEICDAT	
ALDKD/0			LANIL	ESIVDT LRVK	EVNVSI LE	LKPVTKKE	APNILEIV	KCPMDLSTIR I	JKVRR	MEIRDRQ Q	ERHDVWQIK	. FNAHLINDGR	KNLSIPPLA	DELLVKCDRL	LDEIRDELKE AEKGI
OsBRD8			L	AEILKT ISTQ:	SDCY ML	QRRLDVQR	-KRTRYKKMI	RRHIDFRILH S	SKIKS	GATSSTK E	LLRDILLFV	NNVLAFYPKA	A TLEHMAA	IELRNIAFRT	VQE
AtBRD8			L PKEL	MKIYNT IAQN	ECAL VE	RRRLDSQ-	-KRGRYKKLV	RRHMDLDTVQ S	SRING	CSISSAK E	LFRDFLLVA	NNAAIFYSKN	TREYKSA	VGLRDIVTKS	LRHY
BD3			EPL	VAFLES VRTS	KAGA VE	ERRLDSQD	-GE-RYSGTI	RRHVDLETVR S	SRLVGATAAA	AAAACYASAS E	FYRDMMLLC	ANALVFFPRG	SPEHAAA	LQLRALVSKQ	VSK
AtBRD2a		SAKDE	TVE SQPL	ISFVEI LLSH	PCGS HE	SRRLERQ-	-ETIEYGTII	REHVDFEIIR	KRVEG	GLYKSWRI N	FFRDLLLLV	NNARVFYHRG	SSEFKFA	EQLHQLVKKQ	MTT V
AtBRD2b			L	SDFIEI LQSHI	PIGS HE	SRRLETQE	TSDYYRII	ROHIDFEMIR S	SRVEE	GYYKTART K	FFRDLLLLI	NNVRVFYGE	P SPEFNAA	KÖLÄÖTIKKÖ	M
AtBRD2c			SQPL	ISLLDL IRSHI	PRGS LF	ERRLRSQE	AKDYKSMV	KQHLDIETIQ H	RKLKQ	GSYDSSSL I	FYRDLQLLF	TNAIVFFPLS	S SSESMAA	HELRAVVSQE	MRKE
AtBRD2d			SQPL	IDIIKL IRSHI	PRGS VE	ESRLRSQD	TKDYKRLI	RQHLDMKTIE H	KKMEK	GSYVSSSL S	FYRDLKLLF	TNAIVFFPTS	S SSESIAA	QELRTLVSNE	мкк
OsBRDST2							V	SRPLDFRTID	IRLAM	GAYYGSWE A	FLEDVQEVI	RNLHTAFGDF	R PDVLEMV	VALSQSFE	7
OsBRD11			QRK CKNV	INKLWR RIDK	EGH-QI IF	NISSWWRR	NENSSFKGLA	SSTLDLQKIE (2RVDG	FEYGGVN E	FIADMQQML	KSVVQHFSYF	R HEVRVEA	ETLHNLFFNI	MKIA
AtBRD11]	QKR CKIV	ISKLOR RIDK	EGQQIV - F	MLTNLWKR	IQNGYAAGGV	NNLLELREID	RVER	LEYAGVM E	LASDVQLML	RGAMQFYGFS	HEVRSEA	KKVHNLFFDL	LKM
OsBRD6	GSDHPHSPWE LHDTGNI	WVPWKHPHI	LGI KDKL	LSELDN LLEL	SHRNQD RY	GVLKLNSV	AEKSDFINRE	PVQFSIEVIR	IRLEN	NYYRTLE A	IRHDATVML	ANAQSYFSKS	TDMTKKI	RRLSDWIEQT	F SSL V
AtBRD6a	GETSLHSPWE FDNPE	- FPWEKSTIE	DER REKL	LSLFAG LVKS	ISKHQD SY	GIQKLNEA	AQKMDFCNRF	PVPLYPELIH	ERLEN	QYYRSIE S	FKHDVDAML	SNAELYFVRS	AHMLSKI	KRLRDKLTKT	LRKL
AtBRD6b	AETHLHSPWE LFDAD	- TKWEQPHIE	DEQRNRL	LSALTK LETS	DKRTQD SE	GLRKLNQT	VGNSSYSNRF	PVPLSLEVIR	SRLEN	NYYRSVE A	LRHDVSVML	SNAETFFGRN	KSVAAKI	SNLSNWFDRT	LPSS

Supplementary Figure 6: (A) Homology model of a normal bromodomain (BRD) region containing all typical structural features of the BRD-fold (four α helices: αZ , αA , αB , αB and three loops: ZA, AB, BC). (B) Homology model of BRD-region of a human protein (K2026_Human, UniProt ID: Q5HYC2) with a long deletion at N-terminal region (similar to deletion in OsBRD3a and OsBRDST2), leading to loss of αZ and ZA-loop elements.



Supplementary Figure 7: CDD-NCBI based conserved domain analysis of OsBRDST2 (LOC_Os02g09920, BRD-homolog with BRD-PHD-WHIM1-ZnF domain combination (A) and its tandem duplicate gene locus (LOC_Os02g09910) encoding protein containng only PHD domain (B).

(A)							
Query seq.	1	125 2	50 375 	500	625	750	875 979
putative histon	Zn binding site e H3 binding site			z putative charged b	zinc cluster 1 📐 👗 inding surface 🏊		
Specific hits		PHD1_Li					
Superfamilies	Bromo	PHD_SF HHIM1 s			ZZÇ		
(B)							
Query seq.	50	100	150 	280	259		
Specific hits			PHD				
Superfamilies			PHD_SF superfamily				

Supplementary Figure 8: Heatmap-based analysis of RNA-Seq data of constitutive and alternative transcripts of *OsBrd*-genes in different tissues (A) and stress conditions (B). The *OsBrd*-transcript designations (constitutive transcript: .1; alternative transcripts: .2 to .5) are mentioned on the left side of the heat maps, tissues and stress conditions are listed on the top, and a gradient color scale indicating expression level from blue (low) to red (high) is shown on the bottom of the figure.

