

# SupplementaryMaterials: Functional Characterization of Soybean *Glyma04g39610* as a Brassinosteroid Receptor Gene and Evolutionary Analysis of Soybean Brassinosteroid Receptors

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**Table S1.** Sequence finger prints of the LLR domains in GmBRI1b. The cysteine residues in position 1 to 24 are shown in blue.

LRR	beg	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	end	No. res
1	47	L	T	S	I	D	L	S	S	V	P	L	S	T	N	L	T	V	I	A	S	F	L	L	S	70	24
2	71	L	D	H	L	Q	S	L	S	LK	S	T	N	L	S	G	P	A	A	M	P	P	L	S	H	95	25
3	99	S	S	S	L	T	S	L	D	L	S	Q	N	S	L	S	A	S	L	N	D	M	S	FL	AS	124	26
4	125	C	S	N	L	Q	S	L	N	L	S	S	N	L	L	Q	F	G		P	P	P	H	W	K	146	22
5	148	L	H	H	L	R	F	A	D	F	S	Y	N	K	I	S	G	P	G	V	V	S	WL	LN	P	173	26
6	174	V	I	E	L	L	S	L	K	G	N	K	V	T	G	E	T	D					F	S	G	193	20
7	194	S	I	S	L	Q	Y	L	D	L	S	S	N	N	F	S	V	T	L	P	T		F	G	E	216	23
8	217	C	S	S	L	E	Y	L	D	L	S	A	N	K	Y	L	G	D	I	A	R	T	L	S	P	240	24
9	241	C	K	S	L	V	Y	L	N	V	S	S	N	Q	F	S	G	P	V	P			S	L	P	262	22
10	263	S	G	S	L	Q	F	V	Y	L	A	A	N	H	F	H	G	Q	I	P	L	S	L	AD	L	287	25
11	288	C	S	T	L	L	Q	L	D	L	S	S	N	N	L	T	G	A	L	P	G	A	F	G	A	311	24
12	312	C	T	S	L	Q	S	L	D	I	S	S	N	L	F	A	G	A	L	P	M	SV	L	T	Q	336	25
13	337	M	T	S	L	K	E	L	A	V	A	F	N	G	F	L	G	A	L	P	E	S	L	S	K	360	24
14	361	L	S	A	L	E	L	L	D	L	S	S	N	N	F	S	G	S	I	P	A	S	L	C		383	23
15	392		N	N	L	K	E	L	Y	L	Q	N	N	R	F	T	G	F	I	P	P	T	L	S	N	414	22
16	415	C	S	N	L	V	A	L	D	L	S	F	N	F	L	T	G	T	I	P	P	S	L	G	S	438	24
17	439	L	S	N	L	K	D	F	I	I	W	L	N	Q	L	H	G	E	I	P	Q	E	L	M	Y	462	24
18	463	L	K	S	L	E	N	L	I	L	D	F	N	D	L	T	G	N	I	P	S	G	L	V	N	486	24
19	487	C	T	K	L	N	W	I	S	L	S	N	N	R	L	S	G	E	I	P	P	W	I	G	K	510	24
20	511	L	S	N	L	A	I	L	K	L	S	N	N	S	F	S	G	R	I	P	P	E	L	G	D	534	24
21	535	C	T	S	L	I	W	L	D	L	N	T	N	M	L	T	G	P	I	P	P	E	LF	K	Q	559	25
22	629		S	M	I	F	L	D	I	S	H	N	M	L	S	G	S	I	P	K	E	I	G	A		650	22
23	651	M	Y	Y	L	Y	I	L	N	L	G	H	N	N	V	S	G	S	I	P	Q	E	L	G	K	674	24
24	675	M	K	N	L	N	I	L	D	L	S	N	N	R	L	E	G	Q	I	P	Q	S	L	T	G	698	24
25	699	L	S	L	L	T	E	I	D	L	S	N	N	L	L	T	G	T	I	P	E	S		G	Q	721	23

**Table S2.** List of the quality criteria parameters in automatic modeling with modeller v9.10 at ModWeb (<http://modbase.compbio.ucsf.edu/ModWeb20-html/modweb.html>) [56].

Gene Name	Target Region	Protein Length	Template PDB Code	Template Region	Sequence Identity	E-Value	GA341	MPQS	z-DOPE	TSVMod Method	TSVMod RMSD	TSVMod NO35
GmBRI1a	21–761	762	3RGZ	30–770	60.00%	0	1.00	1.73604	−0.97	MSRED	2.024	0.84
GmBRI1b	3–744	745	3RGZ	30–770	60.00%	0	1.0	1.75347	−0.93	MSALL	1.006	0.913
GmBRL1a	68–824	825	3RGX	34–770	41.0%	0	1.00	1.39568	−0.38	MSRED	8.004	0.612
GmBRL1b	65–808	809	3RGX	50–770	44.00%	0	1.0	1.41525	−0.45	MSRED	2.051	0.8
GmBRL2a	34–724	725	3RGX	31–770	43.0%	0	1.0	1.4216	−0.49	MSRED	4.557	0.707
GmBRL2b	35–725	726	3RGX	31–770	43.00%	0	1.0	1.41229	−0.43	MSRED	5.131	0.645

**Table S3.** List of primers used in this study.

Primer Name	Sequence (5'-3')	Usage
GmBRI1b.F	ATGAAAGCTCTGTACTACAGAAGCT	Full <i>GmBRI1b</i> cloning
GmBRI1b.R	ATGCTTGCTCAATTCAGGGGC	Full <i>GmBRI1b</i> cloning
GmBRI1b.F1	GATGGCAATGTTCAAGGAGATTCAGGCG	sequencing
GmBRI1b.F2	CGAGTGTTCTTCGCTTGAGT	sequencing
GmBRI1b.R1	AATCCCTGTCCCCTTGTCGCTAA	sequencing
GmBRI1b.R2	CACATCCCCAAACCCGCCAGAGCCA	sequencing
GmEF1α.F	CTGGAGGTTTTGAGGCTGGTAT	qRT-PCR
GmEF1α.R	CCAAGGGTGAAAGCAAGAAGA	qRT-PCR
qGmBRI1b.F	TTGAAATGGTGGAGATGAGCA	qRT-PCR
qGmBRI1b.R	AGGGGAGCTGAATCCGTCA	qRT-PCR
qCPD.F	TTGCTCAACTCAAGGAAGAG	qRT-PCR
qCPD.R	TGATGTTAGCCACTCGTAGC	qRT-PCR
qDWF4.F	CATAAAGCTCTTCAGTCACGA	qRT-PCR
qDWF4.R	CGTCTGTTCTTTGTTTCCTAA	qRT-PCR
qBR6ox1.F	TCCCGTATCGGAGTCTTTGGT	qRT-PCR
qBR6ox1.R	TGGCCAATCTTTGGCGAA	qRT-PCR
qBR6ox2.F	CAATAGTCTCAATGGACGCAGAGT	qRT-PCR
qBR6ox2.R	AACCGCAGCTATGTTGCATG	qRT-PCR
qAtEF1a.F	GTCGATTCTGGAAAGTCGAC	qRT-PCR
qAtEF1a.R	AATGTCAATGGTGATACCACGC	qRT-PCR
GmBRI1bGFP.f	ATCGTCGACGATGAAAGCTCTGTACTACAGAAGCT	Subcellular localization
<i>GmBRI1b</i> .GFP.r	AAGCCCGGGCATGCTTGCTCAATTCAGGGGC	Subcellular localization
OX-GmBRI1b.F	ATCGTCGACATGAAAGCTCTGTACTACAGAAGCT	overexpression
OX-GmBRI1b.R	AAGCCCGGGATGCTTGCTCAATTCAGGGGC	Overexpression
GmBRI1b.RACE1	AATCCCTGTCCCCTTGTCGCTAA	5'RACE
GmBRI1b.RACE2	CACATCCCCAAACCCGCCAGAGCCA	5'RACE
GmBRI1b.RACE3	GATGGCAATGTTCAAGGAGATTCAGGCG	3'RACE
GmBRI1b.RACE4	CGAGTGTTCTTCGCTTGAGT	3'RACE
GmBRI1a.qF	TCCTCCTCATTAACCTCCCT	qRT-PCR
GmBRI1a.qR	TTGAGAAGCCAAGAAACGAC	qRT-PCR
GmBRI1b.qF	AACCTCCAATCCCTCAACCTC	qRT-PCR
GmBRI1b.qR	TTTGTGTCCTTTGAGAGAGA	qRT-PCR
GmBRL1a.qF	GTATGATCTACCTTGACCTTTCC	qRT-PCR
GmBRL1a.qR	AAGAAAGACCCTCCAATGCC	qRT-PCR
GmBRL1b.qF	AACAAACTAACGGGTCAACTCAG	qRT-PCR
GmBRL1b.qR	GAAGTAGATTCTTGACGAACC	qRT-PCR
GmBRL2a.qF	AATGACAACAGCCAAACCAC	qRT-PCR
GmBRI2a.qR	AAACCACCACACCCAATGAG	qRT-PCR
GmBRL2b.qF	CAAGAATGATAACAGCCAACCC	qRT-PCR
GmBRI2b.qR	AGCAACAGAGATGAGAATTCCC	qRT-PCR

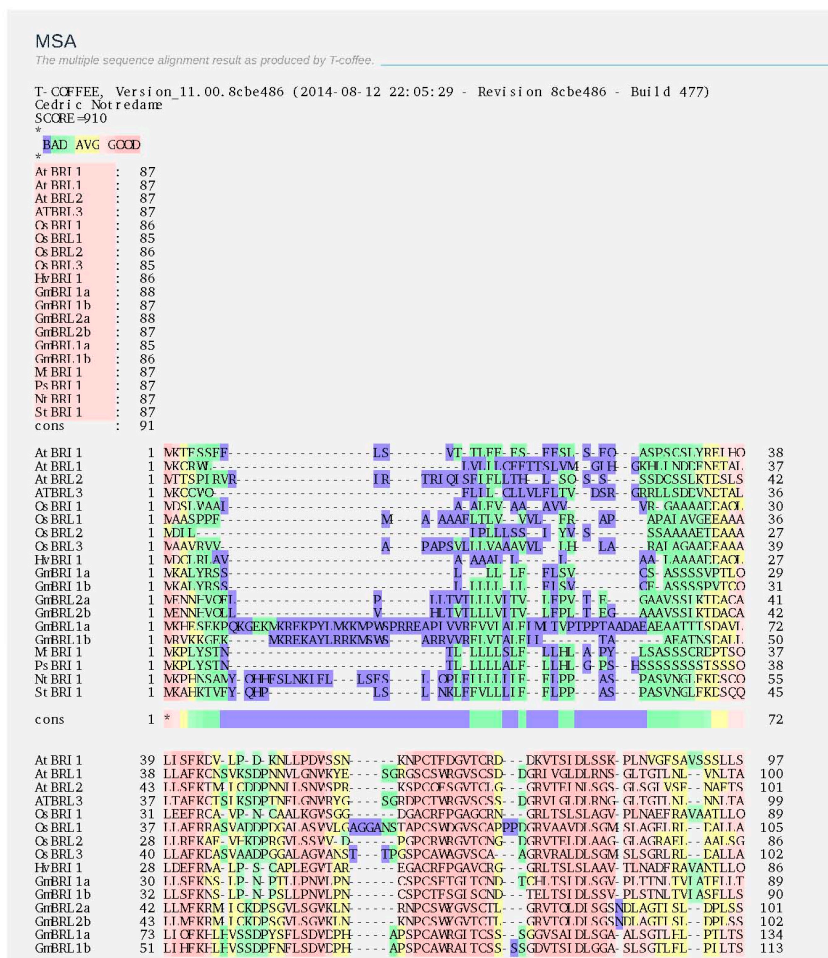


Figure S1. Cont.

M BRI 1	38	LLNFRCS-LP-N-PSLLHNLVLPN-----NNPCSFTGTCNO--TTITSDLTSL-PLNINLTTITTYLLT	96
Ps BRI 1	39	LLYFRCS-LP-N-PSLLHDLVLPY-----KNPCSFTGTCNO--TTVTSLDLTSL-PLNINLTVAVATYLLT	97
Nt BRI 1	56	LI.SFRSS-LP-NCTCTI.ONVLS-----TDPCSFTGVSCRN--SRVSSI.DTNT-FI.SVDFTI.VSSVYI.G	115
St BRI 1	46	LLSFKAA-LP-PTPILLQNVLP-----TDPCSFTGVSCRN--SRVSSIDLNT-FLSVDFLSVTSYLLP	105
cons	73	* * : : * * : * : * : : : *	144
At BRI 1	98	ITGIFSLFINSNH-INGSV-----SGFKCSASITSLDIRNS-LSGP-VTTLTSL-GSCSGIKFLNVSSNT	159
At BRI 1	101	LPNLONLYLOGNY-FSSGGDS-----SGSDCYLCVLDLSSNS-LSDYSMVD-YVF-SKCSNLVSVNI-SNNK	162
At BRI 2	102	LDSTSVIKISFNF-FVINS--T-SLI.I.PI.TI.THIFISSG-IIGT-IPF-NFF-SKYNSI.I.SITISYNN	163
At BRI 3	100	LSNI.RSIVIOGNN-FSSGDS-----SSSGCSI.FVLDLSSNS-ITDSIVD-YVF-STCI.NI.VSVNFSHNK	161
Os BRI 1	90	LGSVEVLSLRGAN-VSGAL--SAAGGARCGSKLCALDLSGNAALRGS-VALVAALASACGGLKTLNLSGDA	156
Os BRI 1	106	LPALORLNLRGNA-FYGNLSH-A--APSPPCALVEVDLSSNA-LNGT-LPP-SFL-APCGVLSRVNLSRNG	168
Os BRI 2	87	ITDTICRINI.SGNGEIHVDA--G-DIVKIPRAI.I.OIDSDGG-IAGR-IPD-GFI-ACYPNI.TT.VSIARNN	149
Os BRI 3	103	LSALRRLLDRGNA-FHGDLSR-IGSPRRAAPCALVEVDLSSNT-FNGT-LPR-AFL-ASCGGLOTLNLSRNS	168
Hv BRI 1	87	LSAVERLSLRGAN-VSGAL--A--AACCGKLEELDLSGNAALRGS-VALVAALASCGALRTLNLSGDA	150
Gn BRI 1a	90	ITDN.OSTISIKSTN-LSGPAAMPPI.SHSKCASTITSLDIRSONA-LSGS-INTASFI-SSCSNI.OSTISIKSTN	157
Gn BRI 1b	91	LDHLOSLSLKSTN-LSGPAAMPPI.SHSKCSSTLSDLSONS-LSAS-LNDSFL-ASCSNLKSLNLSNL	157
Gn BRI 2a	102	LDL.SVLKMSLNS-FSVNS--T-SLLNLPYSLTOLDLDFGG-VTGP-VPE-NLF-SKCPNLVVNLVSYNN	163
Gn BRI 2b	103	ITDM.SVLIKISINS-FSVNS--T-SLVNIPYSITOIDLDFGG-VTGP-VPE-NLF-SKCPNLVVNLVSYNN	164
Gn BRI 1a	135	ISSI.OI.IIRGNS-FSSFNLT-----VSPICITITITSHNN-FSGK-FPF-ANF-APCIRISYINISNNI	195
Gn BRI 1b	114	LDPSLONILRGNS-FSSFNLT-----VSPICITITITSHNN-FSGK-FPF-ADF-APCNRISYINISNNI	174
M BRI 1	97	IPHI.OITIKSTN-ITSSPP--IPITHTKCTTTITSLDIRNT-LSGS-FSTLSFI-STCISIKSINISNNI	162
Ps BRI 1	91	LDHLOSLSLKSTN-ITSSPP--ISLHTKCTTTITSLDIRNT-LSGS-FSTLSFI-STCISIKSINISNNI	162
Nt BRI 1	116	LSNLESLVLKNAN-LSGSL--TSAAKSCCGVLSNIDLAENT-LSGP-VSEISSF-GACSNLKSLSNLSKNL	180
St BRI 1	106	LSNLESLVLKNAN-LSGSL--TSAAKSCCGVLSNIDLAENT-LSGP-ISEISSF-GVCSNLKSLSNLSKNL	170
cons	145	* : * : : * : : : : * : : : : *	216
At BRI 1	160	LDFPGKVS--GGLKLSLEVLDSLANSISGANVVGWLSGCGGELKHLAISGNKISGDVDV--SRC---	221
At BRI 1	163	LVGKIGFA--PSSLQSLTTVDLSYNI LS-----LSS-----	188
At BRI 2	164	FTGKLPN--DLP-----LSS-----	176
At BRI 3	162	LAKLKSS--PSASNKRI.TTVDLSNNRFS-----LSS-----	188
Os BRI 1	157	VGAAGVCG--GGGFGAGIDSLDIRNNKIDTDSIRVWVD-----ACV-----	197
Os BRI 1	169	IAAGGF--PFAPSLRSLDLRNLADAGLLNYSFA-GCHGVGYLNSANL.FAGRLPEL--AACSAVT	230
Os BRI 2	150	LTGELDG--ML-----A-----	160
Os BRI 3	169	ITGGGY--PPPPSIRRIDMRNCISDAGIINYSIT-GCHKI.QYLNLSANQFTGSLPGL--APCTEVS	230
Hv BRI 1	151	VGAAGPAGGGGGGGAFAI.TAIDSSNKIACDADI.RVWVG-----AGI-----	193
Gn BRI 1a	158	LEFDSSH--WK-LHLLVAEFSYNKISGPGILPVLIN--PEI.EHLALKGNKVTGETDF--SGS--	212
Gn BRI 1b	158	LCFGPPP--HMKLHLRFADFYNKISGPGVSVLLN--PVEILLSLKGNKVTGETDF--SGS--	214
Gn BRI 2a	164	ITGPIPE--NFF-----CNS--	176
Gn BRI 2b	165	LTGPIPE--NFF-----CNS--	177
Gn BRI 1a	196	ITAGP--GPWPELAQLDLRNRVSDVLLVSA-L-GSSTLVFLNFSNKLACGLSETLVSKSLNLS	257
Gn BRI 1b	175	ITAGI.VPG--PGWPPEIACDIDRNRVSDVLLVSA-L-GSSTLVFLNFSNKLACGLSETLVSKSLNLS	240
M BRI 1	163	LCFDSPK--WGLASSLSLSDENKISGPNFHHMLN--HELELLSLRGNKISGVTGETDF--SGY--	219
Ps BRI 1	163	LDSDSPK--WGLASSLSLSDENKISGPGFFVLLN--HELELLSLRGNKISGVTGETDF--SGY--	219
Nt BRI 1	181	MDPPSGEI--KASTFSIOIDISFNINISGONIPFVLSNRVFEI.FYFVSKGNKISAGNIPF--LTF--	241
St BRI 1	171	LDPPGKEI--LKGAIFSLQVLDLSYNNISGFNLFPWSSVGFGELEFFSLKGNKLAGSIPF--LDF--	232
cons	217	: : : : * : : : : *	288
At BRI 1	222	-----VNI.FFIDVSSNNFSTGI--PFI-GTCSAIOHIDISGNKISGDFSRAT	265
At BRI 1	189	-----DKIPESFISDFP-ASLKYL.DLTHNLSGDFS--DLSP-GICGNLTFFSLSONLSGLKFPITL	247
At BRI 2	177	-----KRI.OITIDSYNNITGPI.SGLTIP-SSCVSMYIDFSGNSISGY-LSIST	224
At BRI 3	189	-----DEIPETFIADFP-NSIKHIDISGNNVTGDFS--RISF-GICGNLTFFSLSONLSGLRFPVSL	247
Os BRI 1	198	-----GAVRWLDLALNRI.SG-V--PEF-TNCSGLCYLLDLSGNLIVGE	235
Os BRI 1	231	TLDSWNHMGGLPPGLVATAPANI.TYNTAGNNFTGDVS--GYDF-GGCANI.TVTDWYNGISSTRI.PPGI	299
Os BRI 2	161	-----SNIRSFIDVSGNNISGDIS--GV-SIPATTAVIDISGNRFTGA-IPPSI	204
Os BRI 3	231	VLDDL.SWNL.MGVLPPRFVAMAPANLTYLSIAGNNFSMDIS--DYEF-GGCANLTLLDWYNNLRSLTGLPRSL	299
Hv BRI 1	194	-----GSVRWLDLAVNKISGGL--SDF-TNCSGLCYLLDLSGNLIVAGD	232
Gn BRI 1a	213	-----NSICFIDISNNFVSIT--PTR-GFCSSTFYITDISANKYFGD-IARTI	256
Gn BRI 1b	215	-----ISLOYLDLSSNNFVSIT--PTR-GECSSTFYITDISANKYFGD-IARTI	258
Gn BRI 2a	177	-----EKLQVLDLSYNNLSGPIF--GLKMECISLLQVLDLSDIS-IPLSL	221
Gn BRI 2b	178	-----EKLQVLDLSYNNLSGPIF--GLKMECISLLQVLDLSDIS-IPLSL	222
Gn BRI 1a	258	TTIDISYNI.FSGKVPPII.I-NEAVCMIDFSFNNESEFD--FGF-GSCFNIVRISFHNALSSNFFPRGI	321
Gn BRI 1b	241	YLDLSYNVLSGKVPSSRLI-NEAVRVLDFSFNNESEFD--FGF-GSCFNIVRISFHNALSSNFFPRGI	304
M BRI 1	220	-----NNIRHIDISNNFVSIT--PSF-GFCSSTFYITDISANKYFGD-IARTI	263
Ps BRI 1	220	-----TTIRYIDISNNFVSIT--PSF-GFCSSTFYITDISANKYFGD-IARTI	263
Nt BRI 1	242	-----TNLSYLDLSANNFSTGF--PSF-KDCSNLEHLLDLSNKFYGD-IGASL	285
St BRI 1	233	-----KNLSHLLDLSANNFSTVF--PSF-KDCSNLQHLDLSNKFYGD-IGSSL	276
cons	289	: : : : * : : : : *	360
At BRI 1	266	STCTFIRKIDINISNOF-VGPI.PPI--PIKSI.OYI.SIAFNKFTGEPIDFIS-GACTIT.TGIDISGNHFGA	331
At BRI 1	248	PNCKFI.FITNISNNI-AGKIPNGEYVGSFCNISKI.SIAHNRI.SGPI.PPEIS-I.IKCTIVIIDISGNIFSGF	317
At BRI 2	225	INCTNLKSLNLSYNNF-DGOIPRS--FGELKLLCSLDLSHNRLTGWIPPEIG-DICRSLONLRLSYNNFTGV	292
At BRI 3	248	SNCKLLETNLNRSL-I.GKIPGLYVGNFCNLRQLSLAHNLSYGEIPPEIS-LLCRTLVLVLDLSGNISLIGO	317
Os BRI 1	236	-----VPCGAI-SDCRGIVKINISFNHAGV	260
Os BRI 1	300	INCRRLLETLEMBGNKLSGALPTF--LVGFSSLRRLLAGNEFTGAI.PVELG-OLCGRI.VELDLSNRLVGA	368
Os BRI 2	205	SGCAGLTITLNL.SYNGI-AGAI.PEG-I.GAIGLEVLVDSWNHITGAI.PPGLGRNACASLRVLVSSNNISGS	273

Figure S1. Cont.

Os BRL3	300	VDCRRLEALDMSGNKL	SGPI PTF	LVEL QALRRLSLAGNRTGEI	SDKLS	ILCKTLVELDLSSNNLI	GS	368																
Hv BRL1	233				VAAL	SGGRSLRALNLSSNNHL	AGA	257																
GnBRL1a	257	SPCKNI.VYI.NFSSNOF	SGPVPSI	PSGSI CFVYI ASNHFGQI	PI PI A	DL CSTI I.CI.DI SSNNI	SGA	322																
GnBRL1b	259	SPCKSI.VYI.NVSSNOF	SGPVPSI	PSGSI CFVYI AANHFHGOI	PI SI A	DL CSTI I.CI.DI SSNNI	TGA	324																
GnBRL2a	222	SNCTSLKLI LNANMM	SGDI PKA	FGCLNKL DTL SHNOLNGW	PSEFG	NACASLLEKL SFNNI	SGS	289																
GnBRL2b	223	SNCTSI.KNI.NI.ANNM	SGDI PKA	FGCLNKL CTTI.DI SHNOI I	GW PSEFG	NACASTI I.FI.KI SFNNI	SGS	290																
GnBRL1a	232	GNONNI.FVI.DI SHNEI	MMFI PSE	ITLI.NI.KSI.KSI.FI AHNFSGEI	PSEI.G	SI CKTI VFI.DI SFNNI	SGS	390																
GnBRL1b	305	SNONNLVL.DL SHNEF	AMEI PSE	LLVSLKSLKSLFLAHNFSGEI	PSELG	GL CETLVELDLSENKLS	SGS	373																
M BRL1	264	SPCKNLHL.NVSGNCF	TGPVPEL	PSGSLKFVFLAANHFSGEI	PKI PARLA	ELCSTLVELDLSSNNLTGD		329																
Ps BRL1	264	SPCKNI.I.H.NI.SGNCF	TGPVPSI	PSGSI CFYI YI AFNFHAGKI	PARI A	DL CSTI VFI.DI SSNNI	TGP	329																
Nt BRL1	286	SSCGKLSFLNLNNQF	VGL VPKL	PSESLQFVFLYLRGNDFQGVY	PQOLA	DLCKTVVELDL SFNNFSG	L	351																
St BRL1	277	SSCGKLSFLNLNNQF	VGL VPKL	CSESLQVFLYLRGNDFQGVY	PQOLA	DLCKTVVELDL SYNNFSGM		342																
cons	361							432																
At BRL1	332	VPPFFGSCSLLESAL	SSNNFSGEL	PMDTLLKMRGLKVL	DL SFNEFSGELPE	- SLTNLS	ASLLTDLSSNN	401																
At BRL1	318	LPSSOTACVWQNI	NI.GNNYI	SGDFI TVVUSKI	TGI VYI	VYAYNNI	SGSVPI	- SI TNCS	NI RVFI.DI SSNG	386														
At BRL2	293	LPESLSGSCVLSL	DLSSNNI	SGPFPNTI	LRSGFSGLI	LLLSNNLI	SGDFPT	- SI SACK	SLRI ADFSSNR	361														
AtBRL3	318	LPQSFSTCGSLOSL	LNQNLK	SGDFLS	TVSVKSL	RI TNLY	LPFNFI	SGSVPI	- SLTNCS	NI LRVLVDI SSNG	386													
Os BRL1	261	FDPDI ACI.TSI.NAI	NI SSNNFSGEI	PGCAF AKI	COI TAI	SI SI SFNHFNGSI	PD	- TVASI P	FI COI.DI SSNT	329														
Os BRL1	369	LPASFAKCKSI	FVI.DI GNNQI	ACGFVASVSTI	ASI RF	RI SFNNI	TGVNDI	PVLAAGCP	- I.FVI.DI GSNE	432														
Os BRL2	274	LPESLSCHARLL	LDVANNQSGEI	PAAVLGNL	TAVESLL	SSNNI	SGSLPD	- TI AHCK	NI RVAIDLSSNK	349														
Os BRL3	369	LPASFGCGRFI	QVI.DI GNNQI	SGDFVETVI	TNI SSI	RVI RI PFNNI	TGANDI	PAI	ASRCP	- I.FVI.DI GSNE	439													
Hv BRL1	258	FDPNI ACI.TSI.TAI	NI SSNNFSGE	VPADAFGT	COI OSI	SI SI SFNHFSGSI	PD	- SVAAI P	DI FVI.DI SSNN	326														
GnBRL1a	323	LPEAFGACTSL	SDSI	SSNLFAGAL	PMVLTOMKSL	KELAVAFNAFL	GPLPE	- SLTKLS	TLES	LDLSSNL	391													
GnBRL1b	325	LPGAFGACTSL	SDSI	SSNLFAGAL	PMVLTOMKSL	KELAVAFNAFL	GPLPE	- SLTKLS	AL	ELLDLSSNN	393													
GnBRL2a	291	LPSPFSSSCV	QO.I.DI SSNNM	GGCOPDAI	FONI	SGSI OFI	RI GNNAI	TGQFSS	- SI SSCK	KI KI VDFSSNK	358													
GnBRL2b	291	LPSPGSSCTV	QLLDI	SSNNM	GGCOPDAI	FONI	SGSI OFI	RI GNNAI	TGQFSS	- SI SSCK	KI KI VDFSSNK	359												
GnBRL1a	391	LPLSFTCCSSLOSL	ARNARY	SGNFI	VS	VNKL RSLKY	NAAFNNI	TGPVPS	- SLVSSK	EL RVLDI SSNNR	459													
GnBRL1b	374	LPLSFTCCSSLOSL	ARNARY	SGNFI	VS	VNKL RSLKY	NAAFNNI	TGPVPS	- SLVSSK	NI KI RVFI.DI SSNR	443													
M BRL1	330	LPREFGACTSI	TSFDI	SSNIFAGCI	OVFI	VFMSI	KFI	SVAFNDFVGPVPI	- SI SKI T	GL I.FI.DI SSNN	398													
Ps BRL1	330	LPREFGACTSVTSF	SDSI	SSNIFAGCM	PEVLI	TEMNSL	KEL	TVAFNEFAGLPE	- SL SKLT	GL	ESLDLSSNN	398												
Nt BRL1	352	VPENI GACCSI	RFI.DI SSNNFSGEI	PVDITI	I.KI	SNL	IKTMI	SFNNFI	GGI	PF	- SFSNI I	KI FTDI SSNN	420											
St BRL1	343	VPESLGCSSLELD	VDI	SSNNFSGEL	PVDITL	KL	SNMKTML	SFNKFGVGL	PD	- SFSNLL	KL	ETLDVSSNN	411											
cons	433												504											
At BRL1	402	FSGPI I.PNI.CCNP	---	KNTI	CEI	YI.ONNGFTGKI	PPTI	SNCSEI	VSI	FI	SFNVI	SGTI	PSGI	SKI	RDI	469								
At BRL1	387	FTGVNVPFSG	CLCS	---	SPVLEKI	LI	ANNYLS	SGTVPMEL	GKCKSL	KTI	DL	SFNELT	TGPI	PKFI	WML	PNLS	SDL	455						
At BRL2	362	FSGVI	PPDI	CPGA	---	ASI	FEI	RI	PDNI	VTGFI	PPAI	SOCSEI	RTI	DI	SI	NYI	NGTI	PPI	GNI	CKI	FCF	428		
AtBRL3	387	FTGTVPSFG	CFI.CS	---	SVI	FKI	I.I	ANNYI	SGTVPMFI	GKCKSI	KTI	DI	SFNAI	FTI	I	PKFI	WML	PKI	SDI	457				
Os BRL1	330	FSGTI	PPDI	CPGA	---	NSKL	H.LYI	ONNYLTGGI	PDVANSCTLS	VLSLDL	SLNY	NGSI	PASL	GDLGN	LOD							397		
Os BRL1	404	LDGEI	MPDI	CSSL	---	PSLR	KLLP	PNNYL	NGTVPPSL	GDCANLEI	DL	SFNLL	VGKI	PETI	I	RLPKI	VDL					506		
Os BRL2	343	ISGAI	PAFI	CPSG	---	AAI	FEI	RI	PDNI	VAGTI	PPGI	SNCSEI	RVI	DFSI	NYI	RPGI	PPFI	GRI	RAI	FEI		409		
Os BRL3	404	FDGEI	MPDI	CSSL	---	PSLR	KLLP	PNNYI	NGTVPPSL	SNCVNLEI	DL	SFNLL	VGSI	PPFI	L	FLLK	VDL					506		
Hv BRL1	327	FSGSI	PPDI	CCDP	---	NSRL	RVLY	LYI	ONNYLS	SGSI	PEAVNSCTDL	VLSLDL	SLNY	NGSI	PESL	GEL	SRL	LOD				394		
GnBRL1a	392	FSGSI	PTTI	CGGAD	NNNI	I	KFI	YI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI				462		
GnBRL1b	394	FSGSI	PASTI	CGGAD	AGLI	NNNI	I	KFI	YI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI			462		
GnBRL2a	359	YIGSI	PRDI	CPGA	---	VS	LEELR	MPDNI	I	TGEI	PAEL	SKCSQ	KTL	DF	SLNYL	NGTI	PDGI	GELEN	LEO			425		
GnBRL2b	360	FYSGI	PRDI	CPGA	---	ASI	FEI	RPDNI	I	TGKI	PAFI	SKCSQ	KTI	DF	SI	NYI	NGTI	PDGI	GEI	FN	FCI	426		
GnBRL1a	404	FSGNVPSI	CPG	---	I	GE	NI	I	AGNYI	SGTVPSQ	GE	CRNI	KTI	DF	SFNFI	NGSI	PQWVWAI	PN	DI			524		
GnBRL1b	444	FSGNVPSI	CPG	---	E	LEKI	I	L	AGNYI	SGTVPSQ	GE	CRNI	KTI	DF	SFNFI	NGSI	PQWVWAI	PN	DI			508		
M BRL1	399	FTGTI	PRW	CEEF	---	GNN	KEI	YI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI				467		
Ps BRL1	399	FTGTI	PRW	CEEF	---	GNN	KEI	YI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI				467		
Nt BRL1	421	ITGFI	PSGI	CKDP	---	N	S	L	KVLYI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI			488		
St BRL1	412	ITGVI	PSGI	CKDP	---	N	N	L	KVLYI	ONNRTGFI	PPTI	SNCSEI	VAI	DI	SFNFI	TGPI	PSGI	SKI	RDI			479		
cons	505																					576		
At BRL1	470	KLWNLMEGEI	POELMY	-	VKTLET	LI	LD	FNDLT	TGEI	PSGL	SNCNTNL	NW	SL	SSNNRL	TGEI	PKW	GRLEN	LA	I			540		
At BRL1	456	VMANNI	TGFI	PEGVCG	KGGNI	FTI	I	NNNI	I	TGSI	PSTI	SRTCTM	NI	W	SSNNI	TGKI	PSGI	GNI	SKI	AI		527		
At BRL2	429	I	AWNNI	AGEI	PEGI	GR	-	CLNKL	LDI	LNNNLT	TGEI	PEEFNCSNI	EW	SFNTS	NRIT	GTEVPKDF	GI	LSRLAV				499		
AtBRL3	456	VMANNI	TGFI	PSTI	CEVDG	GNLET	I	LNNNLT	TGSL	PSTI	SRTCTM	NI	W	SSNNI	TGKI	PSGI	GNI	SKI	AI			527		
Os BRL1	398	I	WNNFI	TGFI	PASTI	SR	-	ICG	FHI	I	TDYNGI	TGSI	PPFI	AKCTKI	NW	SI	ASNNI	SGPI	PSW	GKI	SYI	468		
Os BRL1	507	VMANGI	SGFI	PSTI	CSNGT	LI	FTI	I	VY	SFNNTGSI	PSSTI	TRCVNI	I	W	SI	ASNNI	TGSGV	PGFG	GKI	AKI	478			
Os BRL2	410	VMWF	NGDI	RADI	GO	CRNL	RTI	I	NNNI	I	GGDI	PVFNCT	GLEW	SLT	SNOI	TGPI	REFP	GR	LSRLAV			580		
Os BRL3	507	I	WANNI	SGFI	PKPFC	FNSTAI	FTI	I	VY	SFNNTGSI	PSSTI	TRCVNI	I	W	SI	ASNNI	TGSGI	PSFG	GNI	AKI	478			
Hv BRL1	395	I	WNNI	I	EGFI	PASTI	SS	-	I	PGI	FHI	I	TDYNGI	TGSI	PPFI	AKCTKI	NW	SI	ASNNI	SGPI	PSW	GKI	SYI	465
GnBRL1a	463	I	W	NOL	HGEI	POELMY	-	LKSELEN	I	LD	FNDLT	TGNI	PSGL	VNCTKL	NW	SL	SSNNRL	TGEI	PRW	GR	LSNL	533		
GnBRL1b	466	I	W	NOL	HGEI	POELMY	-	LKSELEN	I	LD	FNDLT	TGNI	PSGL	VNCTKL	NW	SL	SSNNRL	TGEI	PPW	GR	LSNL	536		
GnBRL2a	426	I	AWNNI	EGSI	PPKI	GO	---	CRNI	KTI	I	NNNI	TGGI	PI	I	F	FNCSNI	FW	SI	TSNFI	SWFI	PRKFI	FTI	496	
GnBRL2b	427	I	AW	NLEGI	EPFI	PKPI	GO	---	CRNI	KTI	I	NNNI	TGGI	PI	I	ELF	FNCSNI	FW	SI	TSNFI	SWFI	PRKFI	FTI	497
GnBRL1a	525	I	W	ANNI	TGFI	PEGI	CEVG	GNLET	I	LNNNLI	I	SGSI	PKSI	ANCTM	NW	W	SSANNI	TGFI	TAGI	GN	NALAI	596		
GnBRL1b	509	I	W	ANNI	NGFI	PEGI	CEVG	GNLET	I	LNNNLI	I	SGSI	PKSI	ANCTM	NW	W	SSANNI	TGFI	TAGI	GN	NALAI	580		
M BRL1	468	I	W	NOL	HGEI	POELMY	-	LKSELEN	I	LD	FNDLT	TGNI	PSGL	VNCTKL	NW	SL	SSNNRL	TGEI	PAW	GR	LSNL	538		
Ps BRL1	468	I	W	NOL	HGEI	POELMY	-	LKSELEN	I	LD	FNDLT	TGNI	PSGL	VNCTKL	NW	SL	SSNNRL	TGEI	PAW	GR	LSNL	538		
Nt BRL1	489	I	W	NOL	SGFI	POELMY	-	LKSELEN	I	LD	FNDLT	TGSI	PASTI	SNCNTNI	NW	W	SSANNI	I	SGFI	PASTI	GKI	PNAI	559	
St BRL1	480	I	W	NOL	SGFI	POELMY	-	LKSELEN	I	LD	FNDLT	TGSI	PASTI	SNCNTNI	NW	W	SSANNI	I	SGFI	PASTI	GKI	PNAI	550	
cons	577																					642		

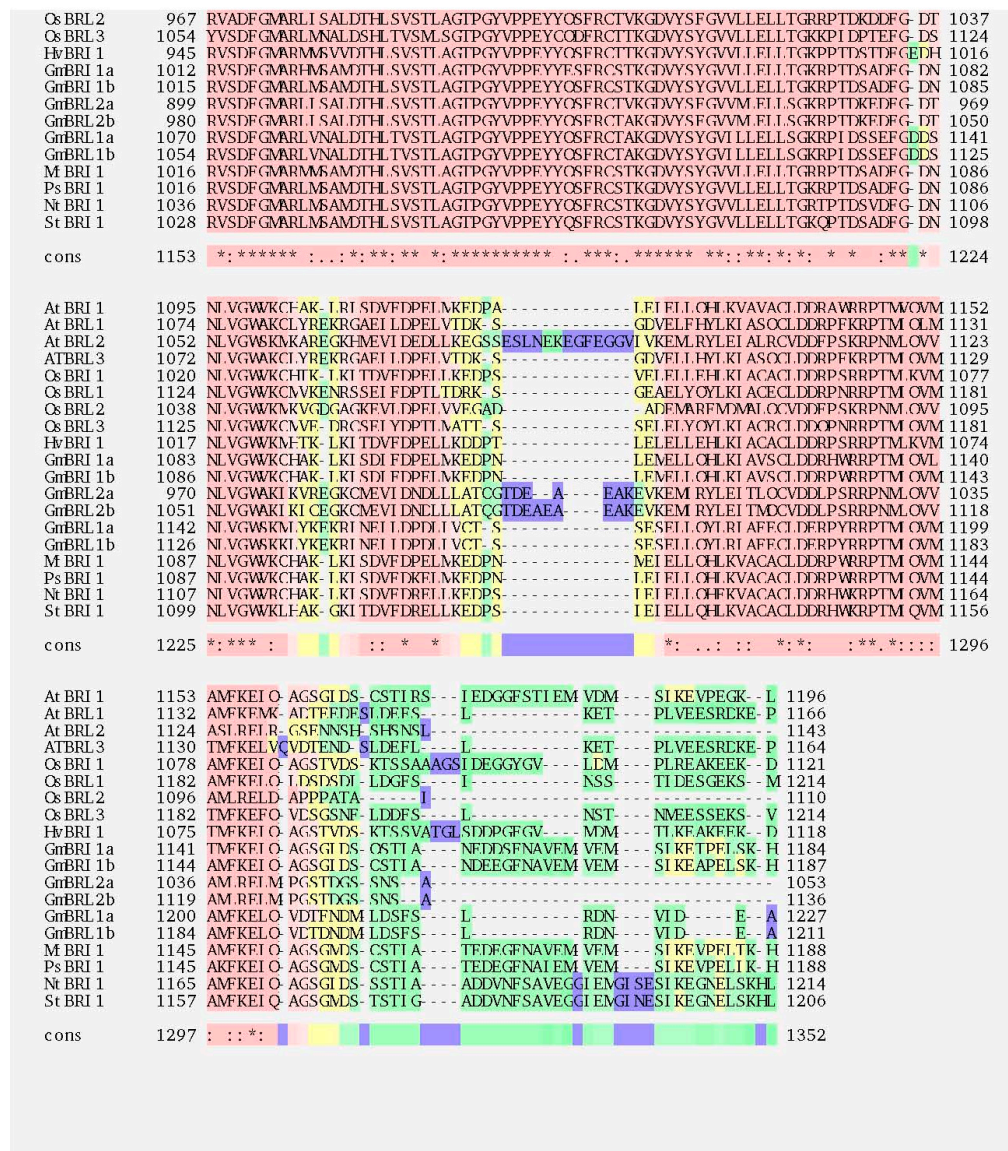
**Figure S1. Cont.**

[illegible]

**Figure S1. Cont.**

GnBRL1b	793	RYENNSSLGCVPLP-ACGASKNHSV-----A-VG-DW-KKOCPPVAGVVI-GLLCFLVFALGLVLALYR	851
M BRL1	751	KFLNLSNGSGCVPLP-PCGKLTGANA-----ACHOKSH-RROASTAGSVAMGLFSLFCVFGLIITIAFE	811
Ps BRL1	751	KFLNLSNGSGCVPLP-PCGKLTSGGGA-----GSHRSH-RRCASTAGSVAMGLFSLFCVFGLIITIAFE	811
Nt BRL1	772	RFANTN-SL-CGYPLP-PCGSGVNSNS-----SCHOKSH-RROASTAGSVAMGLFSLFCVFGIIVATFE	831
St BRL1	763	RFANNT-SL-CGYPLP-PCGSGPKSDA-----NCHOKSH-RRQASLAGSVAMGLFSLFCVFGIIVATFE	823
cons	865	::. . . * * * * *	936
At BRL1	817	MKRRRRKKKEAF--LEM-YAEG-GNSGDR-TANNNTWKLT-G-VKEALSI-NLAAEFKPLRLKLTFAADLLQATNG	882
At BRL1	799	VRVK-ORFKCP--REK-YFESLPT-----SGGSSWKLS-S-VPEPLSI-NVATFEKPLRLKLTFAHILFATNG	858
At BRL2	778	VRRRRDAEDA--K-M-HSLPT-----VNSATTWKI-G-KFKPLSI-NVATFEORLRLKLTKEFSQIFATNG	837
ATBRL3	798	ARKV-CKKEKO--REK-YFESLPT-----SGGSSWKLS-S-VPEPLSI-NVATFEKPLRLKLTFAHLEATNG	857
Os BRL1	740	SKRRRLKNEEASTSDRI-YLISRSF-S-----ATMSDLWRNLS-GTNNLSI-NLAAEFKPLRLTLADILEATNG	806
Os BRL1	852	LRYN-OKTFEV--RTG-VYVESLPT-----SGT'SWKLS-S-G-VREPLSI-NVATFEKPLRLKLTFAHILFATNG	911
Os BRL2	762	ARARRVERSA--M-M-SSSLCDG-TTRTATWKL-G-KAEKALSI-NVATFEORLRLKLTFTQLILEATNG	823
Os BRL3	851	LWKFHNKTKE--I-OAGCSSELPG-----SSKSSWKLS-G-I-GEPLSI-NMAIFENPLRLKLTFSDLHATNG	912
Hv BRL1	739	SKRRLKNEEFASTSDRI-YLISRSF-S-----GTMSNWKLS-S-G-T-NAISI-NLAAEFKPLRLKLTGIVVFATNG	802
GnBRL1a	808	TKRRRRKKKEAA--LEA-YDGNLFS-----GPANVSWKLT-S-TREALSI-NLATEFKPLRLKLTFAADLLDATNG	870
GnBRL1b	811	TKRRRRKKKEAA--LEA-YDGSFS-----GPANVSWKLT-S-TREALSI-NLATEFKPLRLKLTFAADLLDATNG	873
GnBRL2a	732	-----TTNPSTDRRLRLKLTFSQILFATNG	755
GnBRL2b	777	MRARRKFAFEV--K-I-LNSLQ-A-----CHAAITWKI-G-KFKPLSI-NVATFEORLRLKLTKEFSQIFATNG	836
GnBRL1a	868	VRKT-ORKEEM--REF-YFESLPT-----SGGSSWKLS-S-FPEPLSI-NVATFEKPLRLKLTFAHLEATNG	927
GnBRL1a	852	VRKA-ORKEEM--REF-YFESLPT-----SGGSSWKLS-S-FPEPLSI-NVATFEKPLRLKLTFAHILFATNG	911
M BRL1	812	TKRRRRKKKFAA--LDG-YLDNSHSG-----NANNSGWKT-T-SAREALSI-NLATEFKPLRLKLTFAHILFATNG	874
Ps BRL1	812	TKRRRRKKKFAA--LDG-YLDNSHSG-----NANNSGWKT-T-SAREALSI-NLATEFKPLRLKLTFAADLLAATNG	874
Nt BRL1	832	TKRRRRKKKFAA--LEA-YMDGSFNS-----VTANSWKFT-S-SAREALSI-NLAAEFKPLRLKLTFAADLLAATNG	894
St BRL1	824	TKRRRRKKKFAA--LEA-YMDGFS-----ATANSWKFT-S-SAREALSI-NLAAEFKPLRLKLTFAADLLAATNG	886
cons	937	* * * * *	1008
At BRL1	883	FHNDISI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GGGRFFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	954
At BRL1	859	PSAETWSSGGGGEVYKAQLRDGSVAIKKLI-ITGODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	930
At BRL2	838	PSAASM-GHGGGGEVFKATLDGSAVAIKKLI-RLSCODREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	909
ATBRL3	858	PSADSM-GGCGGGEVYKATLDGSAVAIKKLI-OVTCODREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	929
Os BRL1	807	PHACOI-GSGGFGDVYKATLDGSAVAIKKLI-HVSGODREFMAEMFTIKIKHRLNVPLI-GYCKAGGERILL	878
Os BRL1	912	PSAEITLI-GSGGFGDVYKATLDGSAVAIKKLI-HFTGODREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	983
Os BRL2	824	FSTASIT-GSGGFGGEVFKATLDGSAVAIKKLI-HI-SYOGREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	895
Os BRL3	913	FCFATLI-GSGGFGGEVFKATLDGSAVAIKKLI-HI-SYOGREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	984
Hv BRL1	804	FHNDISLI-GSGGFGDVYKATLDGSAVAIKKLI-HVSGODREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	875
GnBRL1a	871	FHNDISI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	942
GnBRL1b	874	FHNDISI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	942
GnBRL2a	756	PSAASLI-GCGGGEVFKATLDGSAVAIKKLI-RLSCODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	827
GnBRL2b	837	PSAASLI-GCGGGEVFKATLDGSAVAIKKLI-RLSCODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	908
GnBRL1a	928	PSASFIT-GSGGFGGEVFKATLDGSAVAIKKLI-IHVTGODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	999
GnBRL1b	912	PSAESLI-GSGGFGGEVFKATLDGSAVAIKKLI-IHVTGODREFMAEMFTIKIKHRLNVPLI-GYCKIGERILL	983
M BRL1	875	FHNDISLI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	946
Ps BRL1	875	FHNDISI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	946
Nt BRL1	895	FHNDISI-GSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	966
St BRL1	887	FHNDISLVSGGFGDVYKATLDGSAVAIKKLI-IHVS-GODREFMAEMFTIKIKHRLNVPLI-GYCKVGGERILL	958
cons	1009	* * * * *	1080
At BRL1	955	VYEFMYKGSLEDVLHDCK-K-AGVGLNWSRRKAI-IA-GAARGALFLHNCSPHII-HRDMKSSNVLLDENLEA	1023
At BRL1	931	VYFMYKWSITFTVHDFK-SKK-GGIYLNAAARKAI-IA-GAARGALFLHNCSPHII-HRDMKSSNVLLIDENFA	1001
At BRL2	910	VYFMYKWSITFEVHDFK-TGKERRI-I-GWFFRCKI-AGAARGCFI-HNCSPHII-HRDMKSSNVLLIDENFA	980
ATBRL3	930	VYEFMYKGSLEVLHEDK-KK-GGFLDWSARKAI-IA-GAARGALFLHNCSPHII-HRDMKSSNVLLIDENFA	999
Os BRL1	879	VYDMYKWSITFDVHDK-K-I-GKKI-NWARRKAI-AGAARGAFI-HNCSPHII-HRDMKSSNVLLIDENFA	947
Os BRL1	984	VYFMYKWSITDVIHDK-K-ASVKI-DWSARKAI-IA-GAARGAFI-HNCSPHII-HRDMKSSNVLLIDENFA	1052
Os BRL2	896	VYEFMHSGLEDLTHDGK-GSAPASVW-ORCKVARGAARGCFI-HNCSPHII-HRDMKSSNVLLIDENFA	966
Os BRL3	985	VYEFMNGSLDVLHDGK-E-ANMLDNWARRKAI-IA-GAARGALFLHNCSPHII-HRDMKSSNVLLIDENFA	1053
Hv BRL1	876	MDYFMYKWSITFDVHDK-K-I-GVRI-NWARRKAI-IA-GAARGAFI-HNCSPHII-HRDMKSSNVLLIDENFA	944
GnBRL1a	943	VYEFMYKGSLEDVLHDCK-K-AGI-KLNAARRKAI-IA-GAARGALFLHNCSPHII-HRDM	

**Figure S1. Cont.**



**Figure S1.** Alignment of the full amino acid sequences of the BR receptors from *Arabidopsis thaliana* (At), *Oryza sativa* (Os), *Glycine max* (Gm), *Solanum tuberosum* (St), *Medicago truncatula* (Mt), *Nicotiana tabacum* (Nt), and *Pisum sativum* (Ps). T-COFFEE V11.0 was used to construct the alignments [81]. The amino acid sequences that are identical in all aligned BR receptors are indicated with an asterisk (\*), sequences that are conserved are indicated with a dot (.) and (:).

## MSA

The multiple sequence alignment result as produced by T-coffee.

T-COFFEE, Version\_11.00.8cbe486 (2014-08-12 22:05:29 - Revision 8cbe486 - Build 477)

Cedric Notredame

SCORE=920

\*

\* BAD AVG GOOD

At BRI 1 : 85  
 At BRI 1 : 84  
 At BRI 3 : 84  
 GnBRI 1a : 86  
 GnBRI 1b : 88  
 GnBRI 1a : 82  
 GnBRI 1b : 82  
 GnBRI 2a : 84  
 GnBRI 2b : 84  
 Ps BRI 1 : 85  
 Os BRI 1 : 83  
 Hv BRI 1 : 83  
 Nt BRI 1 : 85  
 Sl BRI 1 : 89  
 cons : 92

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At BRI 1 1 MKTFSSFF-----LS-----VTILFFSFSSLSF--QASPSCSLYREI 36
At BRI 1 1 MKCRVL-----LVLI-LCFFTSLVM--GI-FGKHLINDFNET 35
At BRI 3 1 MKCCVO-----FL-I-LCLIVIFITV--DS-RGRIISDFVNDT 34
GnBRI 1a 1 MKALYRSS-----L-----LLFFLS--VC--SASSSSVPT 27
GnBRI 1b 1 F-----ASSSSVPT 9
GnBRI 1a 1 MKHFSFKPQGEKMKRFKPYIMKKMPWSPRREAPIVVRFFV-IATFIMTVPTPTAA-DAEAFATTTSDA 70
GnBRI 1b 1 MRVKKGFK-----MKREKAYLRKMEWS-----ARRVVRFI-V-TAIFIT--TAAAFATNSDA 48
GnBRI 1a 1 MENNEVO-----FLPLLTVILLVI TVLFP-----VT-EG-AAVSSI KTDA 39
GnBRI 2a 1 MENNEVO-----LLVHLTVILLVI TVLFP-----LT-EGAAAVSSI KTDA 40
GnBRI 2b 1 MKPIYSTN-----TLIIIIATFIH-----LGPSSSSSSSSSTSS 36
Ps BRI 1 1 NDSLWAAL-----A-ALFVAAAVVV-----RGAAAADDA 28
Os BRI 1 1 NDCLRLAV-----A-AAALL--LA-----ALAAAADDA 25
Hv BRI 1 1 MKPHNSAMY-QHFSLNKI FL--LSFSLQP-----LFILLIIFFLP--PA--SPASVNGIFKDS 53
Sl BRI 1 1 VN-----GLYKDS 8

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cons 1 . 72

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At BRI 1 37 HOLI SFKEV-LP-D-KNLLPDVSSN-KNPCTFDGVTCD--D-KVTSIDLSSKP-LNVGFSAVSSSLSLT 99
At BRI 1 36 ALLLAFKCNVKSDDPNVNLGNVYSGRGSCSVRGVSCSD--G-RI-VGLDLRNSG-LTGILNL--VNLALP 102
At BRI 3 35 AIITAFKCTSIKSDPTNFI.GNRYGSGRDPCTVRGVSCSD--G-RVI-GIDIRNGG-LTGILNL--NNITAI.S 101
GnBRI 1a 28 I.CI.I.SFRNS-I-P-N-PTI.I.PNW.PN--CSPCFTGTICND--TCHI.TSIDI.SGVP-I.TNI.TVIATFI.I.TID 91
GnBRI 1b 10 CCLLSFRNS-LP-N-PSLLPNWLPN--CSPCTFSGISCND--T-ELTSIDLSSVP-LSTNLTVIASFLLSLD 72
GnBRI 1a 71 VI.I.I.CFKH.FVSSDPYSFI.SDWCPH-APSPCAWRGITCASS--G-GVSAID.SGAA-I.SGIT.HI--PTI.TSI.S 136
GnBRI 1b 49 I.I.I.I.HFKH.FVSSDPYSFI.SDWCPH-APSPCAWRGITCASS--G-DVTSIDI.GGAS-I.SGIT.FI--PII.TSI.P 115
GnBRI 2a 40 QALLMFKRMICKDPGVLSGVKLN--RNPSCWVGVSCTIL--G-RVTOLDISGSNDLAGTISL--LPLSSLD 103
GnBRI 2b 41 QALLMFKRMICKDPGVLSGVKLN--RNPSCWVGVSCTIL--G-RVTOLDISGSNDLAGTISL--LPLSSLD 104
Ps BRI 1 37 SCTI.YFKCS-I-P-N-PSI.I.HDW.PY--KNPCSFGTICND--T-TVTSIDI.TSIP-I.NINI.TVVATYI.I.TID 99
Os BRI 1 29 QLEEFRCV-LP-N-CAALKGVSOG--DGACRFPAGACRN--G-RLTSLSLAGVP-LNAEFRAVAATLLCLG 91
Hv BRI 1 26 QLLDEFRCV-LP-S-CAPLEGVTAR--EGACRFPAGACRN--G-RLTSLSLAGVP-LNAEFRAVAATLLCLG 88
Nt BRI 1 54 OCTI.SFRSS-I-P-NTCTCI.QNVI.SS--TDPCSFGTGVSCKN--S-RVSSI.DI.TNTF-I.SVDFTI.VSSYI.I.GI.S 117
Sl BRI 1 9 QQLSFRKA-LP-PTPILLQNLSS--TGPCSFGTGVSCKN--S-RVSSI.DI.TNTF-I.SVDFSLVTSYLLPLS 72

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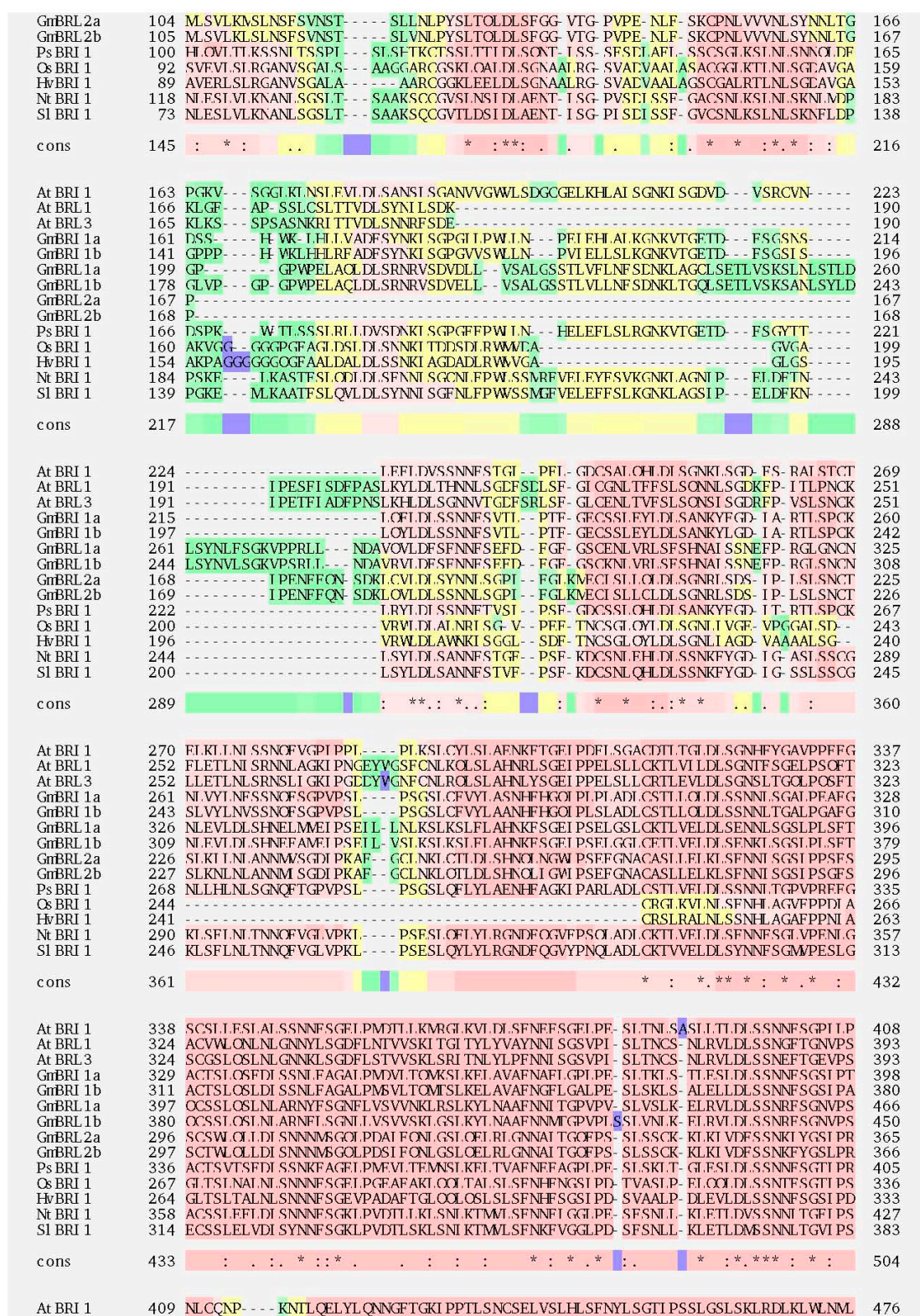
cons 73 \* \* : : \* \* . . \* : : : \* : \* \* 144

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At BRI 1 100 GLESLFLSNHNGSV-----SGFKCSASLTSLDLSSNS-LSG-PVTTLTSL-GSCSGLKFLNVSSNTLDF 162
At BRI 1 103 NLQNYLOGNYFSSGGD-----SSGSDCYLOVLDLSSNS-ISDYSMVD-YVF-SKCSNLVSVNI.SNNKLVG 165
At BRI 3 102 NLRSIYICGNFSSGDS-----SSSGCSIFVIFDI.SSNS-ITDSI.VD-YVF-STCI.NI.VSVNF.SNNKLVG 164
GnBRI 1a 92 NLRSIYIKSTNLSGPAAMPPI.SHSKCASTITSLDI.SNA-LSG-SINEMFI-SSCSNLSI.NI.SNNI.I.FF 160
GnBRI 1b 73 HLCSLSKSTNLSGPAAMPPLSHSCSSSLTSLDLSSNS-LSA-SINEMFI-ASCSNLSI.NI.SNNI.I.FF 140
GnBRI 1a 137 SIQNI.I.LRGNSFSFNL-----TVSPICIT.FITDI.SHN-FSG-KFPF-ANI-APCI.RI.SYI.NI.SNNI.I.FF 198
GnBRI 1b 116 SLQNI.I.LRGNSFSFNL-----TVSPICITQLDLSHNN-FSG-KFPF-ADF-APCNRLSYL.NI.SNNI.I.FF 177

```

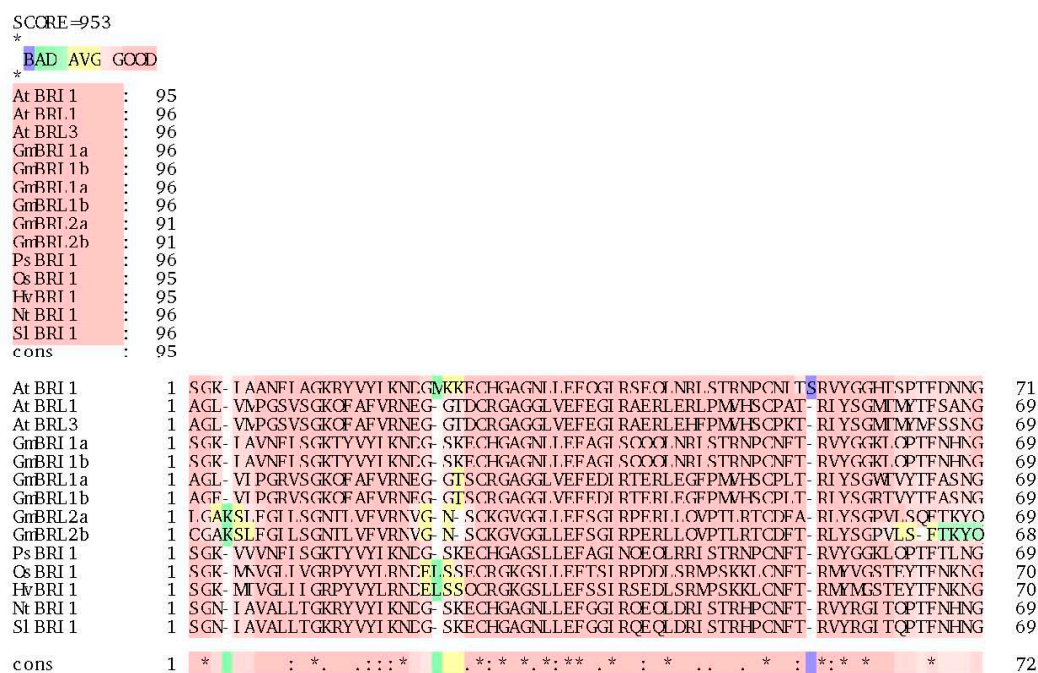
Figure S2. Cont.



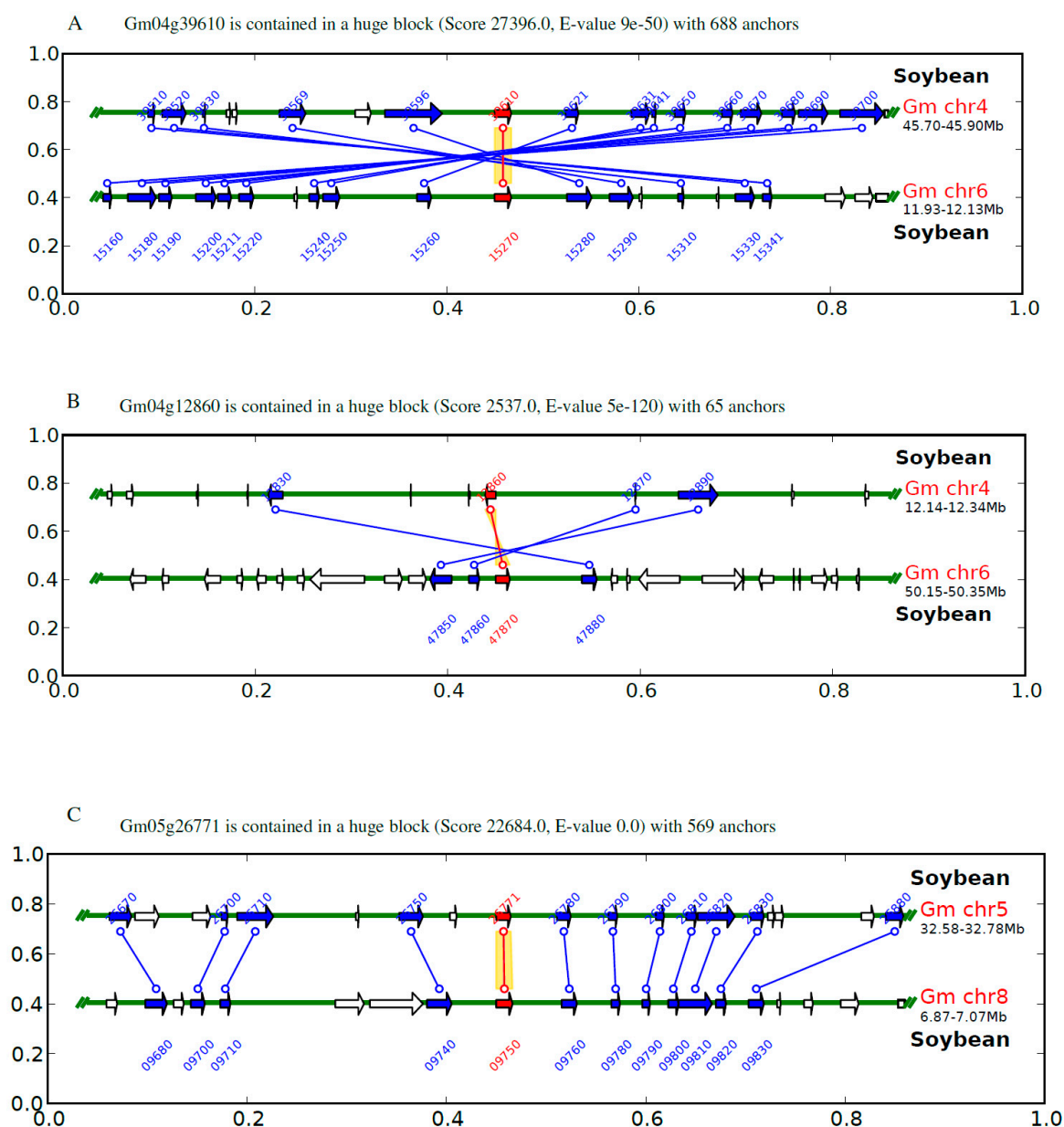
**Figure S2. Cont.**



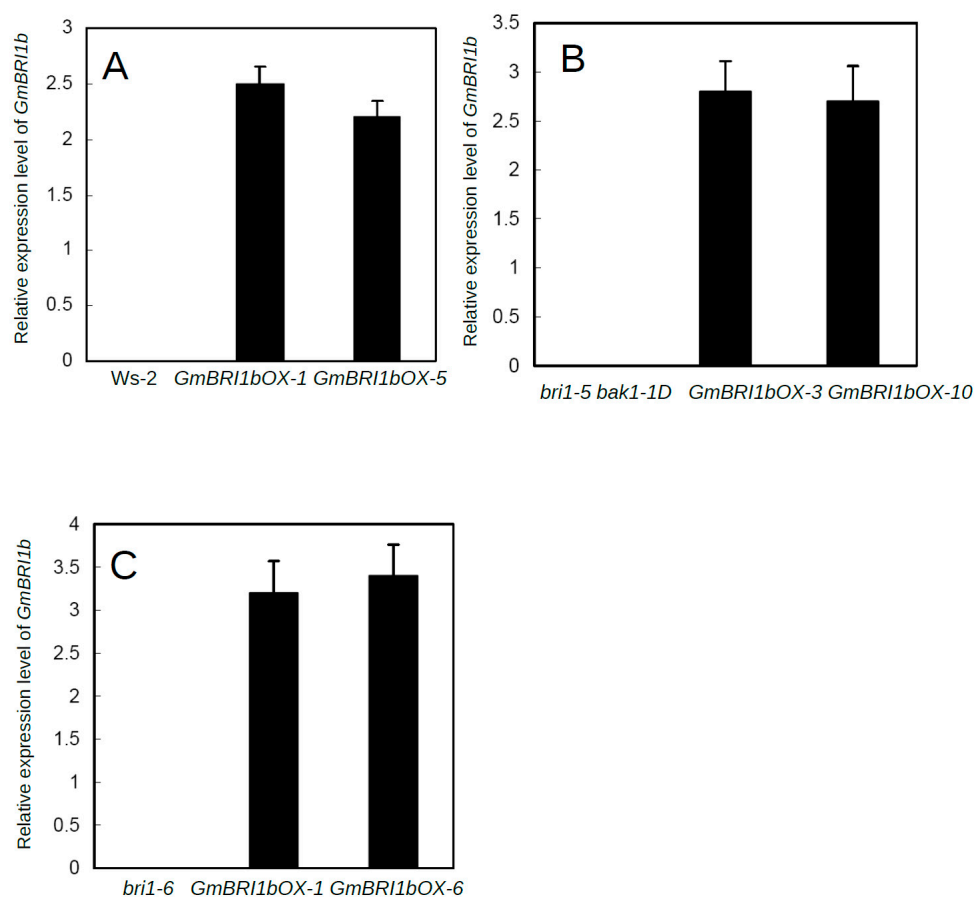
**Figure S2.** Alignment of the ectodomains of the BR receptors from *Arabidopsis thaliana* (At), *Oryza sativa* (Os), *Glycine max* (Gm), *Solanum lycopersicum* (Sl), *Nicotiana tabacum* (Nt), *Pisum sativum* (Ps), and *Hordeum vulgare* (Hv). T-COFFEE V11.0 was used to construct the alignments [81]. The amino acid sequences that are identical in all aligned BR receptors are indicated with an asterisk (\*), sequences that are conserved are indicated with a dot (.) and (:).



**Figure S3.** Alignment of the island domain sequences of the BR receptors from *Arabidopsis thaliana* (At), *Oryza sativa* (Os), *Glycine max* (Gm), *Solanum lycopersicum* (Sl), *Nicotiana tabacum* (Nt), *Pisum sativum* (Ps), and *Hordeum vulgare* (Hv). T-COFFEE V11.0 was used to construct the alignments [81]. The amino acid sequences that are identical in all aligned BR receptors are indicated with an asterisk (\*), sequences that are conserved are indicated with a dot (· and :).



**Figure S4.** Duplication analysis of the BR receptor genes in soybean. Three gene duplication events can be found in soybean, *Glyma04g39610* (*GmBRI1b*) to *Glyma06g15270* (*GmBRI1a*) (A); *Glyma04g12860* (*GmBRL1a*) to *Glyma06g47870* (*GmBRL1b*) (B); and *Glyma05g26771* (*GmBRL2a*) to *Glyma08g09750* (*GmBRL2b*) (C). The intra-species blocks for *GmBRI1a*, *GmBRL1a*, and *GmBRL2a* are shown in A, B, and C, respectively. Graphs display 100-kb regions. Blue arrows indicate the other anchor genes in the region, red indicates the query locus.



**Figure S5.** The relative expression levels of *GmBRI1b* in transgenic lines in Ws-2 (A), *bri1-5 bak1-1D* (B), and *bri1-6* (C) background, respectively. Quantitative real-time PCR was used to determine the relative transcription levels of *GmBRI1b* in transgenic lines. *AtEF-1a* was used to normalize the relative expression levels of *GmBRI1b*. Results are means  $\pm$  SD from three independent experiments.