

At BRL3	547	KNNI I WLDLNSNNITCNI L GELASQAG. LVMPGSVSCKQFAFVRN EGGT . DCRGAGGLVEF	604
At BRL1	547	KSN I WLDLNSNNITCD I LPGE L ASQAG. LVMPGSVSCKQFAFVRN EGGT . DCRGAGGLVEF	604
Os BRL1	598	NN I WLDLNSNSFTCT I PPQLAGOAG. LVPGGIVSCKQFAFLRN E AGN. ICPGAGVLFEF	655
Os BRL3	598	SNI I WLDLNSNE I TCT I PPQLAAQAG. LITGAIVSCKQFAFLRN E AGN. ICPGAGVLFEF	655
Sl BRI1	571	QSL I WLDLNTNF I NGS I PPPLFK O SG. NIAVALLT E KRYVYIKNDGSK. ECHGAGNLLEF	628
Spi BRI1	571	QSL I WLDLNTNF I NGS I PPPLFK O SG. NIAVALLT E KRYVYIKNDGSK. ECHGAGNLLEF	628
Spv BRI1	571	QSL I WLDLNTNF I NGS I PPPLFK O SG. NIAVALLT E KRYVYIKNDGSK. ECHGAGNLLEF	628
St BRI1	570	QSL I WLDLNTNF I NGS I PPPLFK O SG. NIAVALLT E KRYVYIKNDGSK. ECHGAGNLLEF	627
Nb BRI1	579	QSL I WLDLNTNLL I NGS I PGPLFK O SG. NIAVALLT E KRYVYIKNDGSK. ECHGAGNLLEF	636
Ps BRI1	558	PSL I WLDLNTNF I TCG I PPPLFK O SG. KVVNFISCKTYVYIKNDGSK. ECHGAGSLLEF	615
At BRI1	560	RS I WLDLNTNLF I NG I PAAMFK O SG. KIAANFI A QKRYVYIKNDGMK E CHGAGNLLEF	618
Os BRI1	488	QS I VWLDLNSNQ I NGS I P E LA O SG. KMNVGLIVERPYVYL R ND E LS S CCR G K S LL E F	546
Hv BRI1	485	KSL I VWLDLNSNQ I NGS I P E LA O SG. KMTVGLI C RPYVYL R ND E LS S CCR G K S LL E F	543
At BRL2	519	TT I VWLDLNTNHL I TC E IP P RL G RO P SK A LS G LL C NT M AF V R N VG N S..CKGVGG L VEF	576
Os BRL2	500	SS I M W LDLNSNRL I TC E IP P RL G RO P ST P LS G IL C NT L AF V R N VG N S..CKGVGG L LEF	557

At BRL3	605	EG I RAERLEHFPMVHS O PKT. RI I SC M IMYM F SSNGSM I Y L DD I SYNAVSG S I PLGYGAMG	663
At BRL1	605	EG I RAERLERLPMVHS O PAT. RI I SC M IMYM F TSANGSM I Y F DISYNAVSG F I PPGYGNMG	663
Os BRL1	656	FG I RPERLA E FPAV H LC P ST. RI I Y T CT V Y T FT N NGSM I F L DD I SYNG I T G T I PG S LC N M	714
Os BRL3	656	LD I RP D R L ANFP A V H LC S ST. RI I Y T CT V Y T FT N NGSM I F L DD I SYNS I T G T I P A S F GN M T	714
Sl BRI1	629	GG I RQE Q LD R ISTR R HP C NFT. RV V RC I TOPT F NH G SM I F L DD I SYNK L E G SI P K E LG A MY	687
Spi BRI1	629	GG I RQE Q LD R ISTR R HP C NFT. RV V RC I TOPT F NH G SM I F L DD I SYNK L E G SI P K E LG A MY	687
Spv BRI1	629	GG I RQE Q LD R ISTR R HP C NFT. RV V RC I TOPT F NH G SM I F L DD I SYNK L E G SI P K E LG A MY	687
St BRI1	628	GG I RQE Q LD R ISTR R HP C NFT. RV V RC I TOPT F NH G SM I F L DD I SYNK L E G SI P K E LG T MY	686
Nb BRI1	637	GG I RQE Q LD R ISTR R HP C NFT. RV V RC I TOPT F NH G SM I F L DD I SYNK L E G SI P K E LG S MY	695
Ps BRI1	616	AG I N Q E Q LR R ISTR R NP C NFT. RV V GG K L Q PT F TL N GS I F L D V SH N ML S GT I P K E I G E MT	674
At BRI1	619	Q I G R SE Q LN R LR L STR R NP C NFT. SRV V Y G HT S PTFD N NG S MM F LD M SY N ML S GY I P K E I G S MP	678
Os BRI1	547	TS I RP D DL S R M PS K K I C NY VG S TE Y TF N NG S MI F LD L SY N Q L DS A I P G E I G D MF	605
Hv BRI1	544	SS I RS E DL S R M PS K K I C NY VG S TE Y TF N NG S MI F LD L SY N Q L DS E I P K E I G N MF	602
At BRL2	577	SC I R E RL L Q I P S LK S CD F T. RM Y SG P IL S LF T RY Q T I E Y LD L SY N Q L R K I P D E I G E MI	635
Os BRL2	558	AG I R E RL L Q V PT L K S CD F T. RLY S AA V SG W TRY Q T L E Y LD L SY N Q L D E I P E EL G DM V	616

Supplementary Figure 4: Sequence alignment of the BL binding region of BRI1 and related proteins

The sequence alignment encompasses the BL binding region of At BRI1 (amino acids 580-673). Sequences present in the alignment are (numbers in parenthesis indicate Genbank accession numbers): At BRL3 (Q9LJF3); At BRL1 (Q9ZWC8); Os BRL1 (NP_001062792); Os BRL3 (BAD01717) Sl BRI1 (Q8GUQ5); Spi BRI1 (ABO27626); Spv BRI1; (Q8L899); St BRI1 (ABO27627); Nb BRI1 (ABO27628); Ps BRI1 (BAC99050); At BRI1 (O22476); Os BRI1 (NP_001044077) Hv BRI1 (BAD06331); At BRL2 (Q9ZPS9); Os BRL2 (AAK52544). At, *Arabidopsis thaliana*; Os, *Oryza sativa*; Sl, *Solanum Lycopersicum*; Spi, *Solanum pimpinellifolium*; Spv, *Solanum peruvianum*; St, *Solanum tuberosum*; Nb, *Nicotiana benthamiana*; Ps, *Pisum sativum*; Hv, *Hordeum vulgare*. Amino acids highlighted in black are identical in all sequences and those highlighted in grey are conserved. The NGSM motif conserved in BL responsive proteins is indicated by asterisks.