

AtBRI1 1 ---MKTFSFFLSVTTLFFFSFF-SLSFQASPSQSLYREIHQLISFK--DVLDPKN-LLP
 AtBRL1 1 ---MKQRWLLVLIICFFTTSLV--MGIHGKHLINDDFNETALLLAFKQNSVKS DPNNVVG
 AtBRL2 1 MTTSPIRVIRIRTRIQISFIFLLTHLSQSSSSDQSSLKTDLSLSLSFK-TMIQDDPNNILS
 AtBRL3 1 ---MKQQWQF-LIILCLLVFLT--VDSRGRRLSDDVNDTALITAFKQTSIKSDPTNFLG
 OsBRI1 1 ---MDSLWAAIAALFVAAA VVR-GAAAAD-----DAQLLEEFR--QAVPNOA-ALK
 OsBRL1 1 ---MAASPPFMAAAFLT LVV--VLFRAPAPAI VGEAAAALLAFRRASVADDPDGALA
 OsBRL2 1 -----MDIL-IPLILSSIYVSSS-AAAETDAAALLRFK-AFVHKDPRGVLS
 OsBRL3 1 ---MAAVRVVAPAPSVLLLVAAAVLLHLARAIAGAADA EAAALLAFKDA SVAADDPGGALA
 ZmBRI1a 1 ---MESPGLVLVA VVALFVVVVA-ATASGD-----DAQLLEQFK--EAVPSQAPDLR
 ZmBRI1b 1 ---MESPG--LFAVVALFVVVVA-AAAAD-----DAQLLEQFK--EAVPSQATDLR
 ZmBRL1 1 ---MAASTTSAAWFFVAVVLL---VLLHATAAAIAGAE EAAALLAFRRASVADDPRGALS
 ZmBRL2 1 -----MDMLNLLLLVSSIYTSLAFT PVAATDADALLRFK-ASIQKDPGGVLS
 ZmBRL3 1 ---MGAARTAAPVFM LLLH-----LSPRAVAAGTGDEAAAALLAFKRASVAADQAGRLA

AtBRI1 54 DWSSNKN-----PCTFDGVTCRD---DKVTSIDLSSKPLNVGFSAVSSSLLSLTGLES
 AtBRL1 56 NWKYESG---RGSCSWRGVSCSD--DGRIVGLDLRNSGLTGTLN--LVNLTALPNLQNL
 AtBRL2 60 NWSPRKS-----PCQFSGVTCL---GGRVTEINLSG-SGLSG-IVSFNAFTSLDSLSVL
 AtBRL3 55 NWRYGSG---RDPCTWRGVSCSS--DGRVIGDLRNGGLTGTLN--LNNLTALS NLRSL
 OsBRI1 46 GWSGGDG-----ACRFPGAGCRN---GRLTSLSLAGVPLNAEFRAVAATLLQLGSVEVL
 OsBRL1 55 SWVLGAGGANSTAPCSWDGVSCAPPPDGRVAAVDLSGMSLAGELR--LDALLALPALQRL
 OsBRL2 45 SWVDPG-----PCRWRGVTCN--GDGRVTELDLAA-GGLAG-RAELAALSGLDTLCRL
 OsBRL3 58 GWAN-STTPG--SPCAWAGVSCAA---GRVRALDLSGMSLSGRLR--LDALLALSALRRL
 ZmBRI1a 48 GWSASDG-----ACRFPGAGCRG---GRLTSLSLAAVPLNADFRAVAATLLQLSSLET
 ZmBRI1b 44 GWSASDG-----ACRFPGAGCRG---GRLTSLSLAAVPLNADFRAVAATLLQLASLET
 ZmBRL1 55 GWAQAN--ATASAPCSWAGVSCAPQPDGRVVAVNLSGMALVGE LR--LDALLALPALQRL
 ZmBRL2 47 SWQPSGSD----GPCNWHGVACDS-GDGRVTRLDLAG-SGLVAGRASLAALS AVDTLQHL
 ZmBRL3 53 SWAEPNSTSGSASPCEWAGVSCVG---GHVRALDLSGMSLVGRLH--LDALLALPALRSV

AtBRI1 105 FLSNSHIN-----GSV
 AtBRL1 108 YLOGNYFS-----SGGDS
 AtBRL2 109 KLSNFFV-----LNS
 AtBRL3 107 YLOGNFS-----SGDSS
 OsBRI1 97 SLRGANVS-----GAL
 OsBRL1 113 NLRGNAFYGNLSHAAPSP---PCALVEVDISSNALNGTLP PPSFLAPCGVLRSVNLSRNL
 OsBRL2 94 NLSNGE-----LHV
 OsBRL3 110 DLRGNAFHGDL SRHGS PRAAPCALVEVDISSNTFN GTLPRAFLASC GGLQTLNLSRNL
 ZmBRI1a 99 SLRGTNVS-----GAL
 ZmBRI1b 95 SLRGANVS-----GTL
 ZmBRL1 111 DLRGNAFYGNLSHAAESAS--PCALVEADLSSNAFN GTLPAAFLAPCAALQSLNLSRNL
 ZmBRL2 101 NLSNGAA-----LRA
 ZmBRL3 108 LLGNAFHGDLTHRAPP R---CALVDVDLSSNALNGTLPRAFLASCSSLRLLNLSGNTF

AtBRI1 116 SGFK---CSASLTSLDLSRNS-LSGPVTTLTSLG-SCSGLKFLNVSSNTLD FFP--GKVSG
 AtBRL1 121 SGSD-----CYLQVLDLSSNS--ISDYSMV DYVFSKCSNLVSVNISNN--KLVGKLG FAP
 AtBRL2 120 TS--LLLLPLTLTHLELSSSG---LIGTLPENFFSKYSNLISITLSYN--NFTGKLPNDL
 AtBRL3 120 SSSG-----CSLEVL DLSNS--LTDSSIVDYVFSTCLNLVSVNF SHN--KLAGK LKSSP
 OsBRI1 108 SAAGGARCGSKLQALDLSGNAALRGSVADVAALASACGGLKTLNLSGDAVGA AKVGGGGG
 OsBRL1 170 AGGG-FPFAPSLRSLDLSRNR--LADAGLLNYSFAGCHGVGYLNLSAN--LFAGRLPE--
 OsBRL2 104 DAGDLVKLPRALLQLDLS DGG---LAGRLPDGFLACYPNLT DVSLARN--NLTGELPGML
 OsBRL3 170 TGGG-YFPFSLRRLDMSRNQ--LSDAGLLNYSLTGCHGIQYLNLSAN--QFTGSLPG--
 ZmBRI1a 110 AAP--RCGAKLQSLDLSGNAGLRGT VADVEALAASCTGLSALNLSGG SVGGPRSAGAVA
 ZmBRI1b 106 AAVP--RCGAKLQSLDLSANAGLRGSVDVEALVAACAGLSALNLSGGSIGGPRSAGVVA
 ZmBRL1 169 VGGG-FPFPSLWSLDLSRNH--LADAGLLNYSFAGCHGLRYLNLSAN--QFVGR LPE--
 ZmBRL2 112 DVTDLLSLPRALQTLDFAYGG---LGGSLPVDLLTLHPNLT TVSLARN--NLTGVLPE SL
 ZmBRL3 164 TGGGGFPFASLRITL DVS RNE--LSDAGLLNYSLSACHGIRHLNLSAN--QLTGELPPR-

AtBRI1 169 GLKLSNLEVLDSLANSISGANVVGWVLSGCGELKHLAISGNKISGDVDVSRVCVNLEFLD
 AtBRL1 172 -SSLQSLTTVDLSYNNILSD-KIPESFISDFPASLKYLDLTHNNLSG-----
 AtBRL2 173 FLSSKKLQTLDSLNNITGPI SGLTIP LSSCVSMTYLD FSGNSISG-----
 AtBRL3 171 SASNKRIITTVDSLNNRFSDEIPETFADFPNSLKHLDLSGNNVTG-----
 OsBRI1 168 P-GFAGLDSLDSLNNKITDDSDLRWVVDAGVAVRWLDLALNRIS-----
 OsBRL1 223 LAACSAVTTLDVSWNHMSG-GLPPGLVATAPANLTYLNIAGNNFTG-----
 OsBRL2 159 IAS--NIRSFVDSGNNMSGDISGVSIPAT----LAVLDLSGNRFTG-----
 OsBRL3 223 LAPCTEVSVLDLSWNLMSG-VLPPRFVAMAPANLTYLSIAGNNFSM-----
 ZmBRI1a 168 SSGFGRLDALDLSNKNISGDGLRWMVVGAGVAVRRLDLSGNKIS-----
 ZmBRI1b 164 S-GFARLDALDLSGNKNISGDGLRWMVVGAGVAVRQLDLSGNKIS-----
 ZmBRL1 222 LAPCSVSVLDVSWNHMSG-ALPAGLMSTAPSNLTSLSIAGNNFTG-----
 ZmBRL2 167 LAEAASTIQWFVDSGNNLSGDISRMSFADT----LTLLDLSENRFGG-----
 ZmBRL3 219 FAQCSQVSVLDLSGNLMSG-ALPGRLLATAPASLTRLSTIAGNNFSG-----

AtBRI1 229 VSSNNFSTGIPFLGDCSALQHLDISGNKLSG-DFS-RAISTCTELKLLNLISSN-QFVGPI
 AtBRL1 216 -----DFS DLSFGICGNLTF FLSLQNNLSG-DKFPITLPNCKFLET LNI SRN-NLAGKI
 AtBRL2 219 -----YISDSLINCTNLKSLNLSYNNFDG--QIPKSFGE LKLLQSLDLSHN-RLTGWI
 AtBRL3 216 -----DFSRLSFGLCENLTVFSLSONSISG-DRFPVSLSNCKLLET LNL SRN-SLIGKI
 OsBRI1 212 -----GVPEFTNCSGLQYLDLSGNLIVG-EVPGGALS DCRGLKVLNLSFN-HLAGVF
 OsBRL1 268 -----DVS GYDFGGCANLTVLDWSYNGLSS-TRLPGLINCR RLETLEM SGNKLLSGAL
 OsBRL2 199 -----AIPPSLSGCAGLTTLNLSYNGLAG--AIPEGIGAIAGLEVLDVSWN-HLTGAI
 OsBRL3 268 -----DISDYEFGGCANLTL DWSYNRLRS-TGLPRSLVD CRRLEALDMSGNKLLSGPI
 ZmBRI1a 213 -----RLPELTNCSGLE YLDLSGNLIAG-EVAGGILADCRGLRTRLNLSGN-HLVGPF
 ZmBRI1b 208 -----SLPEFTNCSGLE YLDLSGNLIAG-EVAGRTLADCRGLRTRLNLSGN-HLVGPF
 ZmBRL1 267 -----DVSAYEFGGCANLTVLDWSYNGLSS-SKLP PSLANCRLEVL DMSGNKVLLGGPI
 ZmBRL2 209 -----AIPPALSRCSGLRTRLNLSYNGLTG--PILESVAGIAGLEVFDVSSN-HLSGPI
 ZmBRL3 264 -----DISRYQFGGCANLSVLDLSYNRLSATIGLPPSLANCHHLREL DMSGNKILSGRV

AtBRI1 286 PP----LPLKSLQYLSLAENKFTGEIPDFLSGACD TLTGLDLSGNH FYGAVPPFFGSCSL
 AtBRL1 268 PNGEYWG SFQNLKQLSLAHNRLS GEIPPEL SLLCKTLVILDLSGNTFSGELPSQFTACVW
 AtBRL2 269 P-----PEIG-DTCRSLQNLRLSYNNFTGVIPESLSSCSW
 AtBRL3 268 PGDDYWG NFQNLRQLSLAHNLYS GEIPPEL SLLCRTLEVLDLSGNSITGQLPQSFTSCGS
 OsBRI1 262 P-----PDIAGLTS
 OsBRL1 321 P--TFLVGFSSLRRLALAGNEFTGAI PVELGQLCGRIVELDLSNRLV GALPASFAKCKS
 OsBRL2 249 P-----PGLGRNACASLRVLRVSSNNISGSIPELSLSSCHA
 OsBRL3 321 P--TFLVELQALRRLSLAGNRFTEISDKLSILCKTLVELDLSNQLIGSLPASFGQCRF
 ZmBRI1a 263 P-----PDVAALTA
 ZmBRI1b 258 P-----PDVAALTS
 ZmBRL1 320 P--AFLTGFSSLRRLALAGNEFSGP IPELSQLCGRIVELDLSGNRLV GGLPASFAKCRS
 ZmBRL2 259 P-----DSIG-NSCASLTILKVSSNNITGPIPASLSACHA
 ZmBRL3 318 P--EFLGGFRALRRLGLAGNRFTEEIPEL SLLCGTLVQLDLSNQLV GGLPASFSGCRS

AtBRI1 342 LESTALSSNNFSGELPMDTLLKMRGLKVLDLSFNEFSG--ELPESLITNLSASLITLDLSS
 AtBRL1 328 LQNLNLGNLYLSGDFLNTVVSKITGITYLYVAYNNISG--SVPI SLTNCS-NLRVLDLSS
 AtBRL2 303 LQSLDSLNNNISGFPNTILRSFGSLQILLNLSNLSG--DFPTSISACK-SLRIADFS
 AtBRL3 328 LQSLNLGNKLSGDFLSTVVSKLSRITNLYLPFNNSG--SVPI SLTNCS-NLRVLDLSS
 OsBRI1 271 LNALNLSNNNFSGELPGEAFALQQLTALSLSFNHFNG--SIPDTVASLP-ELQQLDLSS
 OsBRL1 379 LEVLDLGGNQLAGDFVASVSTIASLRELRLSFNNITGVNPLPVLAAGCP-LLEVIDLGS
 OsBRL2 284 LRLLDVANNVSGGIPAAVLGNLTAVESLLSNNFISG--SLPDTIAHCK-NLRVADLSS
 OsBRL3 379 LQVLDLGNQLSGDFVETVITNISSLRVLRLPFNNTIGANPLPALASRCP-LLEVIDLGS
 ZmBRI1a 272 LTA NLSNNNFSSLPADAYNELRQLKVL SLSFNHFNG--TIPDSLAAALP-ELDVLDLSS
 ZmBRI1b 267 LAGNLSNNNFSSLPADAFTELQQLKVVALSFNHFNG--SIPDSLAAALP-ELDVLDLSS
 ZmBRL1 378 LEVLDLGGNQLSGSFVDDVSTISSLRVLRLSFNNTIGQNPALAAAGCP-LLEVVDLGS
 ZmBRL2 293 LRMFDAA DNKLSGAI PAAVLGNLT SLESLLSNNFISG--SLPSTITSCT-SLRIADLSS
 ZmBRL3 376 LEVLDLGSNQLSGDFVITVISKISSLRVLRLPFNNTIGTNPLPTLAAGCP-LLEVIDLGS

AtBRI1 400 NNFSGPILPNLCQNPKNL--LQELYLQNNNGFTGKIPPTLSNCSSELVSLHLSFNLYLSGTIPS
 AtBRL1 385 NGFTGNVPSGFCSLQSSPVLEKILTIANNYLSGTVPMEELGKCKSLKTIIDLSFNELTGPPIPK
 AtBRL2 360 NFFSGVIPPDLCPGAAS--LEELRLPDNLVTGEIPPAISQCSELRTIDLSLNYLNGTIPP
 AtBRL3 385 NEFTGEVPSGFCSLQSSSVLEKLLIANNYLSGTVPVELGKCKSLKTIIDLSFNALTGLIPK
 OsBRI1 328 NTFSGTIPSSLCQDPNSK--LHLLYLQNNYLTGGIPDAVSNCTSLVSLDLSLNYINGSI
 OsBRL1 438 NELDGEIMPDLCSLPS--LRKLLLPNNYNGTVPVPSLGDANLESIDLSFNLLVKGKIP
 OsBRL2 341 NKISGALPAELCSPGAA--LEELRLPDNLVAGTIPPGLSNCSRRLRVIDFSINYLGRPIPP
 OsBRL3 438 NEFDGEIMPDLCSLPS--LRKLLLPNNYINGTVPSSLSNCSNLESIDLSFNLLVKGKIP
 ZmBRI1a 329 NTFSGTIPSSICQGNSS--LRMLYLQNNYLSGAIPEISNCTKLESIDLSLNNINGTIPA
 ZmBRI1b 324 NTFSGTIPSSICQGNSS--LRMLYLQNNYLSGAIPEISNCTRLESIDLSLNNINGTIPA
 ZmBRL1 437 NELVGEIMEDLCSLPS--LRKFLFPNNYNGTVPKSLGNCANLESIDLSFNLLVKGKIP
 ZmBRL2 350 NKISGVLPAELCSAGAA--LEELRMPDNMVTGIIPPGLSNCSRRLRVIDFSINYLKGPPIPP
 ZmBRL3 435 NMLEGEIMPELCSLPS--LRKLLLPNNYINGTVPVPSLGNCSNLESIDLSFNLMVGPITP

AtBRI1 459 SLEGSLSKLRDLKLVLMLEGEIQELMY-VKTLETLILDFNDLTGEIPSGLSNCTNINLWI
 AtBRL1 445 EIWMLPNLSDLVMWANNLTGTIPEGVCVKGGNLETILILNLLTGSIPESISRCTNMIWI
 AtBRL2 418 ETGNLQKLEQFTAWYNNIAGEIPPEIGK-LQNLKDLILNLLTGEIPPEFFNCSNIEWV
 AtBRL3 445 EIWTLPKLSDLVMWANNLTGGIPESICVDGGNLETILILNLLTGSIPESISKCTNMLWI
 OsBRI1 387 SLEGLGNLQDLILWQNELEGEIPASLSR-IQGLEHLILDYNGLTGSIPPELAKCTKLNWI
 OsBRL1 496 EITIRLPKIVDLVMWANGLSGEIPDVLCSNGTTLETLVISYNNFTGSIPRSITKCVNLIWV
 OsBRL2 399 ETGRRLALEKLVWVFNGLDGRIPADLQ-CRNLRTLILNLLTGGIPVELFNCTGLEWV
 OsBRL3 496 EITLFLKLVDLVWANNLSGEIPDKFCFNSTALETLVISYNSFTGNIPESITRCVNLIWL
 ZmBRI1a 388 SLEKLRDLILWQNLLEGEIPASLEN-LVRLEHLILDYNGLTGGIPRELSKCKELNWI
 ZmBRI1b 383 SLEKLGELRDLILWQNFLEGEIPASLEN-LDKLEHLILDYNGLTGSIPPELSKCKELNWI
 ZmBRL1 495 EIMVLPKLVDLVMWANGLSGEIPDMLCSNGTTLETLVISYNNFTGGIPASIFRCVNLIWV
 ZmBRL2 408 ETGQLRGLKLVWVFNGLGRIPAELGQ-CRGLRTLILNLLTGGIPVELFNCTGLEWV
 ZmBRL3 493 EIVLLPKLVDLVMWANSLSGEIPDTLCSNSTALKTLVISYNNITGVIPVSI TRCVNLIWL

AtBRI1 518 SLSNRLTGEIPKWIGRLENLAILKLSNNSFSGNIPAEIGDCRSLIWLDLNTNLNFGTIP
 AtBRL1 505 SLSNRLTGKIPSGIGNLSKLAILQLGNNLSLGNVPRQLGNCKSLIWLDLNSNLTGDLIP
 AtBRL2 477 SFTSNRLTGEVPKDFGILSRLAVLQLGNNNFTGEIPPELGKCTTLVWLDLNTNLHLTGEIP
 AtBRL3 505 SLSNRLTGEIPVGIGKLEKLAAILQLGNNSLTGNIPSELGNCKNLIWLDLNSNLTGNLIP
 OsBRI1 446 SLASNRLSGPIPSWLGKLSYLAAILKLSNNSFSGPIPELGDQCOSLVWLDLNSNQLNGSIP
 OsBRL1 556 SLSGNRLTGSVPGGFGKLOKLAAILQLKNNLSGHVPAELGSCNLIWLDLNSNSFTGTIP
 OsBRL2 458 SLTASNRTGTIRPEFGRLSRLAVLQLANNSLAGEIPRELGNCSLWLDLNSNRLTGEIP
 OsBRL3 556 SLAGNRLTGSIPSGFGNLQNLAILQLKNSLSGKVPALGSCSNLIWLDLNSNELTGTIP
 ZmBRI1a 447 SLASNQLSGPIPAWLGQLSNLAAILKLSNNSFSGPIPAELGNCOSLVWLDLNSNQLKGSIP
 ZmBRI1b 442 SLASNQLSGPIPAWLGQLSNLAAILKLSNNSFSGPIPAELGNCOSLVWLDLNSNQLNGSIP
 ZmBRL1 555 SLSGNRLTGSVPRGFSKLOKLAAILQLKNNLSGVPALGSCNLIWLDLNSNSFTGTIP
 ZmBRL2 467 SLTASNRTGTIRPEFGRLSRLAVLQLANNSLGGVIPKELGKCSLWLDLNSNRLTGEIP
 ZmBRL3 553 SLAGNSMTGSVPAGFGNLQKLAAILQLHRNSLSGVPALGRCNLIWLDLNSNNSFSGAI

AtBRI1 578 AAMFKQSG-KTAAANFTAGKRYVYIKNDGMKKECHGAGNLLFEQGRSEQLNRLSTRNPCN
 AtBRL1 565 GELASQAG-LVMPGSVSGKQFAFVRNE--GGTDCRGAGGLVEFEGIRAERLERLPMVHSCP
 AtBRL2 537 PRLGRQPGSKALSGLLSGNTMAFVRNV--GNSCKGVGGLVEFEGIRPERLLQIPSLKSCD
 AtBRL3 565 GELASQAG-LVMPGSVSGKQFAFVRNE--GGTDCRGAGGLVEFEGIRAERLEHFPMVHSCP
 OsBRI1 506 KELAKQSG-KMNVGLIVGRPYVYLRNDELSSECRGKGSLEFTSIRPDDL SRMPSKKL CN
 OsBRL1 616 PQLAQAG-LVPGGIVSGKQFAFLRNE--AGNICPGAGVLEFFFGIRPERLAEFPAVHLCP
 OsBRL2 518 RRLGRQLGSTPLSGILSGNTLAFVRNV--GNSCKGVGGLLEFAGIRPERLLQVPTLKSCD
 OsBRL3 616 PQLAAQAG-LITGAVVSGKQFAFLRNE--AGNICPGAGVLEFFLDIRPDRLANFPAVHLCS
 ZmBRI1a 507 AELAKQSG-KMNVGLVLRPYVYLRNDELSSECHGKGSLEFTSIRPEELSRMPSKKL CN
 ZmBRI1b 502 AELAKQSG-KMNVGLVLRPYVYLRNDELSSECHGKGSLEFTSIRPEELSRMPSKELCN
 ZmBRL1 615 PELASQAG-LVPGGIVSGKQFAFLRNE--AGNICPGAGVLEFFFGIRPERLAAFPVHLCP
 ZmBRL2 527 RRLGRQLGSTPLSGILSGNTLAFVRNV--GNSCKSVGGLLEFAGIRPERLLQVPTLKSCD
 ZmBRL3 613 PQLAAQAG-LITGMVSGKQFAFLRNE--AGNICPGAGVLEFFDIRPERLAQFPVHSCA

AtBRI1 637 ITSRVYGGHTSPTFDNNGSMFLDMSYNMLSGYIPKEIGSMPYLFILNLGHNDISGSIPTD
AtBRL1 623 AT-RIYSGMTMYTFSANGSMIYFDISYNAVSGFIPPGYGNMGYLQVLNLGHNRITGTIPD
AtBRL2 595 FT-RMYSGPILSLFTRYQTIEYLDLSYNQLRGKIPDEIGEMIALQVLELSHNQLSGEIPF
AtBRL3 623 KT-RIYSGMTMYMFSSNGSMIYLDLSYNVSGSIPPLGYGAMGYLQVLNLGHNLLTGTIPD
OsBRI1 565 FT-RMYVGSSTEYTFNKNGSMIFLDLSYNQLDSAIPGELGDMFYLMIMNLGHNLLSGTIPS
OsBRL1 674 ST-RIYTGTVYTFNNGSMIFLDLSYNGLTGTIPGSLGNMMLYQVLNLGHNELNGTIPD
OsBRL2 576 FT-RLYGAAVSGWTRYQTLEYLDLSYNLDGEIPEELGDMVVLQVLDLARNNLTGEIPA
OsBRL3 674 ST-RIYTGTVYTFNNGSMIFLDLSYNGLTGTIPASFGNMTYLEVLNLGHNELTGAIPD
ZmBRI1a 566 FT-RVYMGSTEYTFNKNGSMIFLDLSFNQLDSEIPKELGNMYYLMIMNLGHNLLSGVIPP
ZmBRI1b 561 FT-RVYMGSTEYTFNKNGSMIFLDLSFNQLDSXIPKELGNMYYLMILNLGHNLLSGVIPP
ZmBRL1 673 ST-RIYTGTVYTFDKNGSMIFLDISYNRLTGAIPAGLGNMMLYEVNLGHNDLNGTIPY
ZmBRL2 585 FT-RLYGAAVSGWTRYQTLEYLDLSYNALSGGIPEEFGDMVVLQVLDLARNNLTGEIPA
ZmBRL3 671 ST-RIYTGTVYTFNQSGSMIFLDLSYNGLTGTIPASLGNMTYLDVNLGHNDLTGAIPD

AtBRI1 697 EVGDLRGLNILDLSNNKLDGRIPQAMSAITMLTEIDLNNNLSGPIPEMGQFETFPFAKF
AtBRL1 682 SFGGLKATGVLDLSHNQLQGYIPGSLGSLFSLSDLDVSNNNLTGPIPFGGQLTTFPVSRY
AtBRL2 654 TIGQLKNLGVFDASDNRLQGOIPESFSNLSFLVQIDLSNNELTGPQPORGQLSTLPATQY
AtBRL3 682 SFGGLKATGVLDLSHNDLQGFIPGSLGGLSFLSDLDVSNNNLTGPIPFGGQLTTFPLTRY
OsBRI1 624 RLAEAKKLAVLDLSYNQLEGPIPNFSFALS-LSEINLSNNQLNGTIPELGSLATFPKSOY
OsBRL1 733 AFQNLKSTGALDLSNNQLSGGIPPGGLGGLNFLADFDVSNNNLTGPIPSSGQLTTFPPSRY
OsBRL2 635 SLGRLHNLGVFDVSRNRLQGGIPDSFSNLSFLVQIDISDNNLSGEIPORGQLSTLPASOY
OsBRL3 733 AFTGLKATGALDLSHNHLTGVIIPGFCGLHFLADFDVSNNNLTGEIPTSGQLITFPASRY
ZmBRI1a 625 ELGAKKLAVLDLSHNQLQGPINFSFSTLS-LSEINLSNNQLNGSIPELGSLTFPFRISY
ZmBRI1b 620 ELGAKKLAVLDLSHNQLQGPINFSFSTLS-LSEINLSNNQLNGSIPELGSLTFPFRISY
ZmBRL1 732 EFSGLKLVGALDLSNNHLTGVIIPGGLGGLTFLADLDVSNNNLSGPIPSTGQLTTFPOSRY
ZmBRL2 644 SLGRLHNLGVFDVSHNALSGGIPDSFSNLSFLVQIDVSDNNLSGEIPORGQLSTLPASOY
ZmBRL3 730 AFTGLKATGVLDLSHNHLTGVIIPAGLGLNFLADFDVSNNNLTGEIPTSGQLSTFPASRF

AtBRI1 757 LNNPGLCGYPLPRCDPSNADGYAHQRSHGRRPASLAGSVAMGLLFSFVCFIFGLILVGRE
AtBRL1 742 ANNSGLCGYPLRPGCSAPRR--PITSRIHAKKQT-VATAVIAGIAFSFMCVVMLVMA---
AtBRL2 714 ANNPGLCGYPLPECKNGNQLPAG---TEEGKRAKHGTRAASWANSIVLGVLSAASVC-
AtBRL3 742 ANNSGLCGYPLPPCSSGSR---PTRSHAHPKKQS-IATGMSAGIVFSFMCIVMLIMA---
OsBRI1 683 ENNTGLCGYPLPPCDHSS-PRSSNDHQSH-RRQASMASSIAMGLLFSLFCII-VIIIAIG
OsBRL1 793 DNNPGLCGYPLPPCGHNPPWGGRRPRGSPDGKRKV-IGASILVGVALSVLILLILLVVT---
OsBRL2 695 AGNPGLCGMPLPCCGDRLPATMSGLAAAASDPPPRRAVATWANGVILAVLVSAGLAC-
OsBRL3 793 ENNSGLCGYPLNPCVHNSGAGGLPQT-SYGHNF-ARQSVFLAVTSLVILIFSLLIITHYK
ZmBRI1a 684 ENNSGLCGYPLPPCGHNAGSSSSGDHRSH-RTQASLAGSVAMGLLFSLFCIVGIVIIAIE
ZmBRI1b 679 ENNSGLCGYPLPPCGHNAGSSSSGDHRSH-RNQASLAGSVAMGLLFSLFCIVGIVIIIVVE
ZmBRL1 792 ANNSGLCGYPLPPCGHDPGQGSVPSASSDGRRKV-VGGSSILVGVIVLSMLTLLILLVTT--
ZmBRL2 704 TGNPGLCGMPLPCCG-TPRATASVLAPPDGSFRDR---SLWV--VILAVLVTGVVACG
ZmBRL3 790 ENNSGLCGYPLDPCTHNASTGGVQPONS NVRRKF-LEEFVLLAVSLTVLMVATLVVVTAYK

AtBRI1 817 MRKRKRKKE---AELEMYAEGHNSGDRTANNINWK-LTGVKEALSINLAAFEKPLRKLK
AtBRL1 796 -LYRVRKVQKKEQKREKYIESLPTSG-----SCSWK-LSSVPEPLSINVATFEKPLRKLK
AtBRL2 770 ILTVWAIAVRARRRDADAKMLHSLQAVN-SATTWKIEK-EKEPLSINVATFQRQLRKLK
AtBRL3 795 -LYRARKVQKKEQKREKYIESLPTSG-----SSSWK-LSSVHEPLSINVATFEKPLRKLK
OsBRI1 740 SKRRRLKNEEASTSRDIYIDSRSHSA---TMNSDWRQNLSGTNLLSINLAAFEKPLQNLK
OsBRL1 849 -LCKLRMNRKTEEVRTGYVESLPTSG-----TSSWK-LSGVREPLSINVATFEKPLRKLK
OsBRL2 754 AAIIWAVAAARRREVRSAMMLSSLDGTRTATTWKLKGAKEALSINVATFQRQLRKLK
OsBRL3 851 -LWKFHKNKTKEIQ-AGCSESLPGSS-----KSSWK-LSGIGEPLSINMAIFENPLRKLK
ZmBRI1a 743 CKRKRQINEEASTSRDIYIDSRSHSG---TMNSNWR--LSGTNALSINLAAFEKRLQKLT
ZmBRI1b 738 CKRKRQINEEASTSRDIYIDSRSHSG---TMNSNWR--LSGTNALSINLAAFEKRLQKLT
ZmBRL1 849 -LCKLRMNRKTEEMRTGYIQSLPTSG-----TTSWK-LSGVHEPLSINVATFEKPLKLT
ZmBRL2 758 MAVACFVVARARRKEAREARMLSSLDGTRTATTWKLKGAKEALSINVATFQRQLRRLK
ZmBRL3 849 -LRRPRGSKTEEIQTAGYSDSPASST-----STSWK-LSGSKEPLSINLAIIFENPLRKLK

AtBRI1 873 FADLLQATNGFHNDSLIGSGGFGDVYKAILKDGSAVAIKKLIHVSGQGDREFMAEMETIG
 AtBRL1 849 FAHLLEATNGFSAETMVGSGGFGGEVYKAQLRDGSSVVAIKKLIRITGQGDREFMAEMETIG
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AtBRL2 1067 MEVIDEDLLKEGSSSESLNEKEGFEGGVIVKEMLRYLEIALRCVDDFPSKRPNMLQVVASL
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OsBRI1 1034 TDVFDPELLKEDPSVEL-----ELLEHLKIACACLDDRPSRRPTMLKVMAMF
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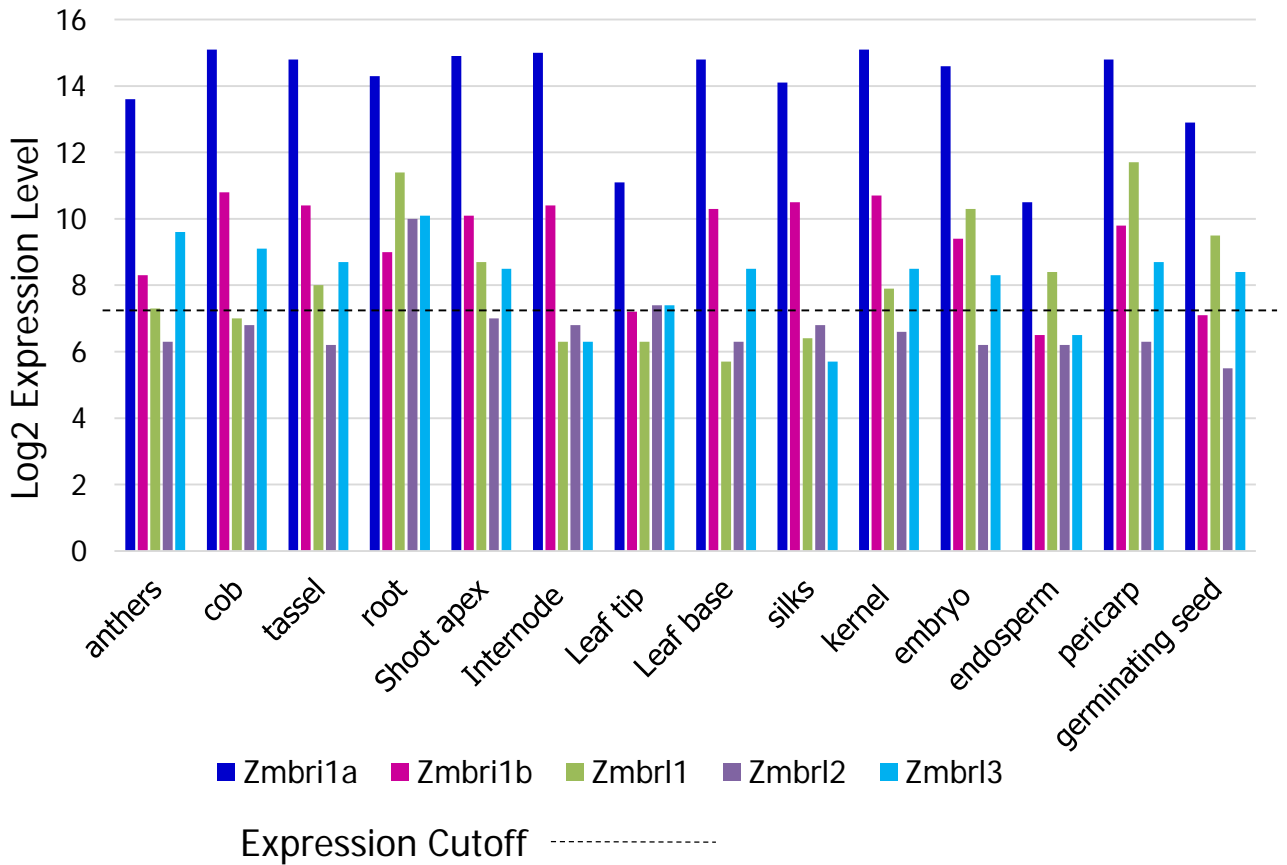
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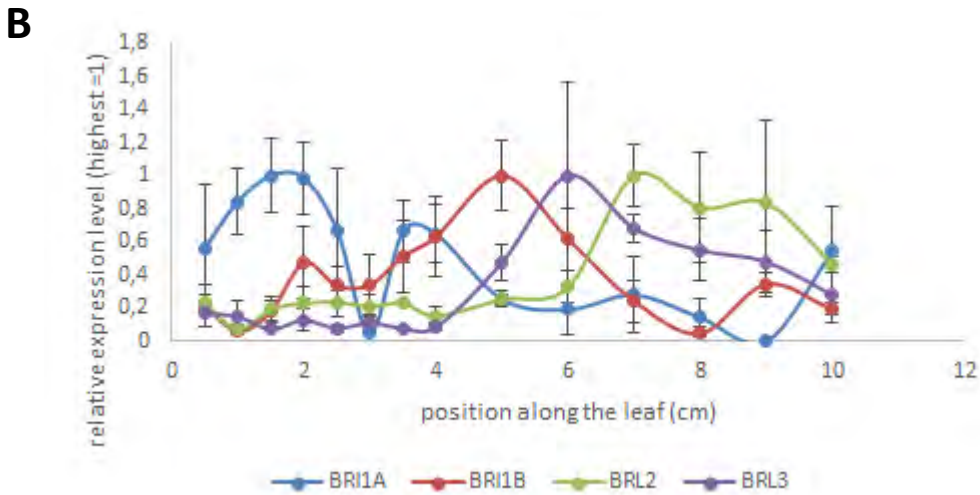
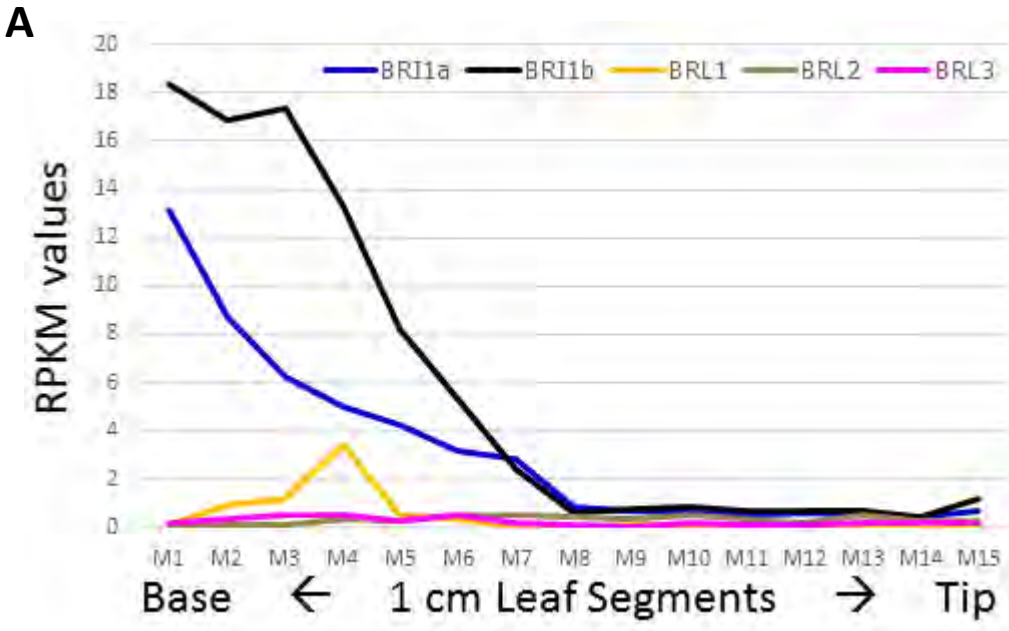
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ZmBRI1b 1077 KEMQASSTVDSKTSACT----DDACFADVEMTTLKEDKEEKD--
ZmBRL1 1186 KDIHLDP-DSDF-----LDGFSINSSTIDESAEKPT----
ZmBRL2 1100 RELDDAPPSHQQA-----PASACD-----
ZmBRL3 1185 SEFQIDS-GSFF-----LDGFSLD-----SDRGII-----

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Supplemental Figure S1. Amino acid sequence alignment of BRI1 homologs from Arabidopsis (At), rice (Os) and maize (Zm).



Supplemental Figure S2. Transcript levels of maize *bri1* homologs in B73 maize tissues. Data were retrieved from the Maize Gene Expression Atlas (Sekhon et al., 2011) using the eFP tool (Winter et al., 2007) available through MaizeGDB (Monaco et al., 2013). The histogram contains data from the following subset of available samples that were chosen to survey expression patterns: (anthers, immature cob, immature tassel stage v13, primary root stage v1, shoot apex stage v4, internode 4 stage v9, tip expanding leaf stage v7, base expanding leaf v7, silks stage r1, whole kernel 2 DAP, embryo 16 DAP, endosperm 16 DAP, pericarp 16 DAP, and germinating seed 24 hr after radicle emergence). The dotted line represents the gene expression cutoff value below which the authors consider a gene as not expressed.



Supplemental Figure S3. A, Transcript levels of maize BRI1 homologs in developing B73 maize seedling leaf 3. Data were retrieved from publically accessible RNAseq transcriptomic analysis along the maturation gradient of a growing leaf (Wang et al., 2014). RNA was extracted from 1cm segments beginning at the base of the leaf (M1) and going to the tip (M15). The base is the meristematic zone of active cell division whereas tissues at the tip are fully differentiated and mature. B, Relative transcript levels in 1 cm increments along maize seedling leaf 4 as determined by quantitative reverse transcriptase polymerase chain reaction.

RNAi 1 TGGACCTCTCCGGAACAAGAT---CTCTCGG-----CTCCCAGAGCTCACCAACT
ZmBRI1a 1 TGGACCTCTCCGGAACAAGAT---CTCTCGG-----CTCCCAGAGCTCACCAACT
ZmBRI1b 1 TGGACCTCTCCGGAACAAGAT---CTCTAGC-----CTGCCGGAGTTTACCAACT
ZmBRL1 1 TGGACTGGTCCCTTCAACGGCCTGAGCAGCAGCAAG---CTGCCGCCGAGCTCTGCCAACT
ZmBRL2 1 TCGACCTGTCCGAGAACCCTT---CGGTGGCGCG---ATCCCGCCGGCCTGTCTACGCT
ZmBRL3 1 TTGATCTTTCGTACAACAGACTGAGCGCCACCATAGGGTTGCCACCGAGTCTTGCCAATT

RNAi 49 GCTCTGGGCTTGAGTACCTCGACCTCTCCGG---CAACCTCATCGCGGG---CGAGGTAGC
ZmBRI1a 49 GCTCTGGGCTTGAGTACCTCGACCTCTCCGG---CAACCTCATCGCGGG---CGAGGTAGC
ZmBRI1b 49 GCTCTGGGCTGGAGTACCTCGACCTCTCCGG---CAACCTCATCGCGGG---CGAGGTAGC
ZmBRL1 58 GCGGCCGCTTGAGGTGCTGGACATGTCCGGGAAACAAGGCTCTCGCGGCCCGCATCCCGG
ZmBRL2 55 GCTCGGGGCTCAGGACGCTCAACTTGTCTGTA---CAACGGCTCACCGGGCCGATACTGG
ZmBRL3 61 GCCACCACCTCAGGGAAGTAGACATGTCTGGGAAACAAGATTCTGTCTGGGCCGAGTACCGG

RNAi 104 CCGCGGGATTCTCGCTGACTGCCGTGGCCTGAGAACGCTCAACCTCTCAGGCAACCACCT
ZmBRI1a 104 CCGCGGGATTCTCGCTGACTGCCGTGGCCTGAGAACGCTCAACCTCTCAGGCAACCACCT
ZmBRI1b 104 CCGCAGGACTCTCGCTGACTGCCGTGGTCTGAGAACGCTCAACCTCTCAGGCAACCACCT
ZmBRL1 118 CGTTCC-----TGACTGGCTTCTCCTCGCTGAAGCGGCTGGCATTGGCCGGCAACGAGTT
ZmBRL2 112 AGTCCG-----TGGCTGGAATCGCCGGCCTTGAGGTGTTCCGACGTCTCGTCAACCACCT
ZmBRL3 121 AGTTCC-----TGGGGGCTTCCGAGCATTCCGGCGACTCGGACTTGCCGGGAACAACCTT

RNAi 164 GGTCCGCCCG---TTCCCGCCGGACGTCGCCGCCCTC---ACCGCTCTCACCGCGCTAAACCT
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ZmBRI1b 164 GGTCCGCCCG---TTCCCGCCGGACGTCGCCGCCCTC---ACCTCGCTCGCCGGACTCAACCT
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ZmBRI1b 221 CTCAAACAACAACCTTCTCCAGCGACTCCCCGCCGACGCTTTCACCGAGCTACAGCAGCT
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ZmBRL2 227 GTCAGCAACAACATCACGGGA---CCCATCCCCGGCGTCTCTGTCCGGCGTCCATG---CGCT
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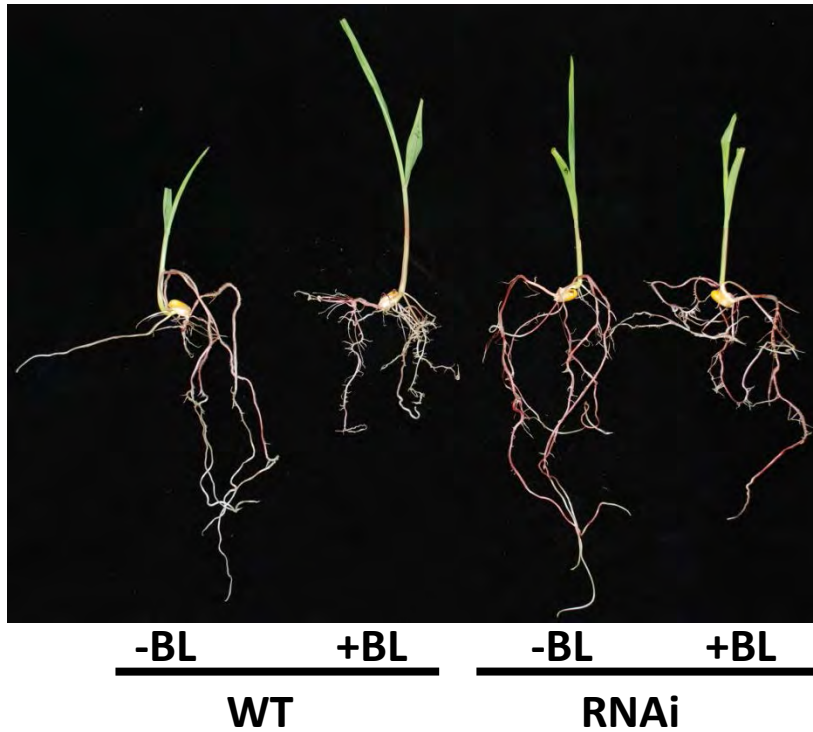
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ZmBRI1b 281 CAAGGTGCTCGCCTCTCCTTCAACCACTTCAACGGCAGTATTCCGGACTCCTT---GG
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ZmBRL3 293 TAGGTGCTCGATCTGGGTAGCAACCAGCTGTCAAGTACTTTGTGATCACTGTGATCAG

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ZmBRI1b 337 CAGCGCTGCCGGAGCTCGACGTGCTGGACCTCAGCTCCAACACCTTCTCCGGCACCATCC
ZmBRL1 350 CACC-ATCTCTCGCTCCCGGTGCTGCGGCTGTGCTTCAACAACATCACCGGGCAGAAACC
ZmBRL2 344 CAAC-CTGACATCGCTGGAGAGCCTGCTGTAAGCAACAACCTTTCATCTCGGGCTCCCTCC
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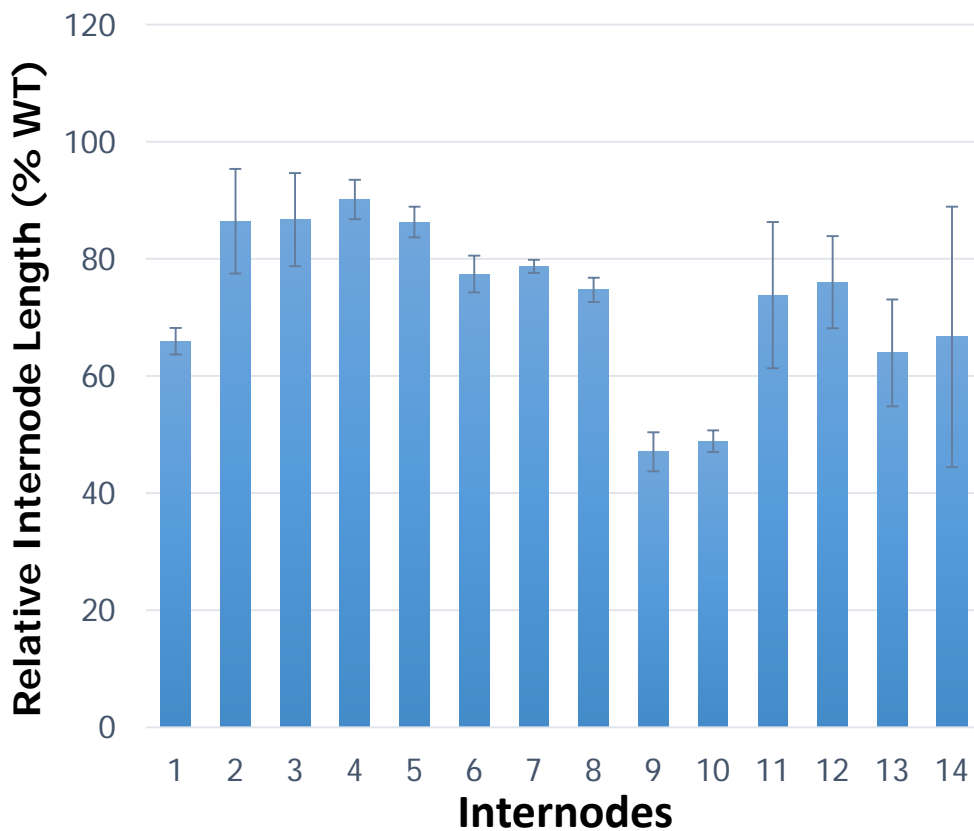
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ZmBRI1a 397 C-----TTCGTCCATCTGCCAAGG---CCCCAACTCCAGC-----CT
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ZmBRL1 409 CG-----CTGCCGGCGCTGGCGGCGGGTTGCCATTGCTCGAGG---TGGTCTGACCT
ZmBRL2 403 CGAGCACGATCACCTCCTGACCCAGCCTCAGGATCGCCGACCTCAGCAGCAACAAGATCT
ZmBRL3 412 CT-----CTGCCACGCTAGCAGCTGGCTGCCCTTTGCTTGAAG---TCATTGATCT

RNAi	431	CCG-----CATGCT-----GTACCTC-----
ZmBRI1a	431	CCG-----CATGCT-----GTACCTC-----
ZmBRI1b	431	CCG-----CATGCT-----GTACCTC-----
ZmBRL1	458	CGGGTCCAAAGCTTGTCGGTGAGATCATGGAAGATCTCTGCTCATCACTGCCGTTCGCT
ZmBRL2	463	CCGG-----CGTGCTG-----CCGGCGACCTCTGCTCGGCTGGCGCCGCGCT
ZmBRL3	461	CGGGTCTAAACATGCTGGAAGGAGAGATCATGCCGAGCTGTGTTTCATCTTTGCCATCACT
RNAi	447	-----CAGAACAACCTACCTCTCCGGCGCCATCCCGGAGTCAAATCTCCAA
ZmBRI1a	447	-----CAGAACAACCTACCTCTCCGGCGCCATCCCGGAGTCAAATCTCCAA
ZmBRI1b	447	-----CAGAACAACCTACCTCTCCGGCGCCATCCCTTGAAGTCAAATCTCCAA
ZmBRL1	518	GCGGAAGCTGTTCCCTCCCAACAATACCTCAATGGCACAGTGCCGAAGTCCGTGGGTAA
ZmBRL2	506	TGAGGAGCTCCGGATGCCGGACAACATGGTCAACCGGCATCATCCCACCGGGTCTTTCCAA
ZmBRL3	521	CAGAAAGCTGCTCCTACCCAACAACCTACATCAATGGAACCGTGCCGCCCTCACCTGGCAA
RNAi	491	CTGCACCA
ZmBRI1a	491	CTGCACCA
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ZmBRL2	566	CTGCTCGC
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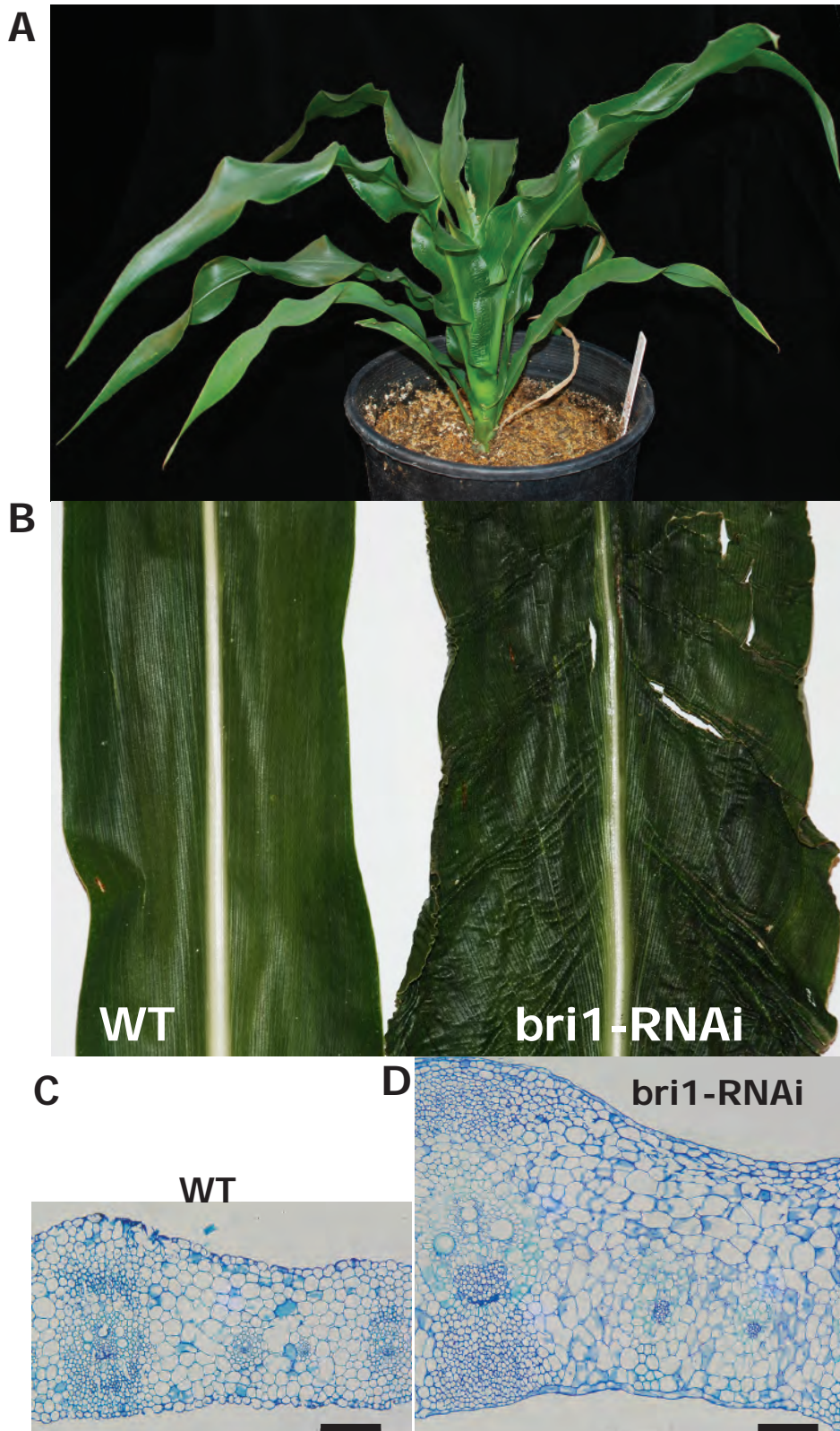
Supplemental Figure S4. Nucleotide sequence of the *zmbri1a* cDNA used for RNAi construct aligned with BRI1 homologs. Nucleotide base 1 of the RNAi fragment corresponds to base 721 of *Zmbri1a*, 745 of *Zmbri1b*, 1180 of *zmbri1*, 751 of *zmbri2*, and 919 of *zmbri3*.



Supplemental Figure S5. BR root growth assay. RNAi lines have decreased BR sensitivity compared to WT siblings. 100nM BL treated WT seedlings' primary root length was ~40% decreased compared to untreated WTs, while primary root length of BL treated RNAi plants is 20% decreased compared to untreated RNAi seedlings.



Supplemental Figure S6. Internode length of mild *bri1*-RNAi plants. Bars show proportional internode length of the mild *bri1*-RNAi plants as a percentage of the corresponding internode in non-transgenic siblings. There is a fairly uniform decrease over all internodes in RNAi lines, except a more pronounced shortening of internodes 9 and 10 just past the ear node.



Supplemental Figure S7. Leaf traits of *bri1*-RNAi plants. A, *bri1*-RNAi dwarves show characteristic wavy margins producing the appearance of a corkscrew twist. B, Compared to WT (left), strong *bri1*-RNAi leaves have a wrinkled surface and are dark green in color. C and D, Histological sections through the auricle regions of WT (C) and *bri1*-RNAi (D) leaves. RNAi leaves do not show normal auricle anatomy, with thickened tissue, enlarged vascular bundles and enlarged cortical parenchyma (size bar 100 μ m).

Table S1. Fluorescence intensity of nuclei in the auricle bands of WT vs. *zmbri1*-RNAi leaves.

Expt	CTCF (+/- SE)		T-test
	WT	bri1-RNAi	
1	8666.9 (369.0)	6949.1 (246.6)	9.70195E-05
2	10131.7 (327.5)	8332.2 (302.6)	4.85517E-05
3	1529.7 (90.0)	805.9 (46.2)	1.13561E-09

Table S2. Primers and sequences used

Primers used for constructing transgenic lines		
<u>Construct</u>	<u>Primer</u>	<u>Sequence (5'-3')</u>
<i>bri1</i> -RNAi-sense fragment	XmaIBRI-F	ATTCCCGGGTGGACCTCTCCGGGAACAAGAT
<i>bri1</i> -RNAi-sense fragment	SpeIBRI-R	CGGACTAGTTGGTGCAGTTGGAGATTGAC
<i>bri1</i> -RNAi-anti sense fragment	AVRIIBR-F	ATGCCTAGGTGGACCTCTCCGGGAACAAGAT
<i>bri1</i> -RNAi- anti sense fragment	ASCIBR-R	TAAGGCGCGCCTGGTGCAGTTGGAGATTGAC
BES1-YFP - promoter&genomic coding sequence-	BES1_3GW p1	GGGGACAAGTTTGTACAAAAAAGCAGGCTGCATTG ATGCTATCGGAGAT
BES1-YFP - promoter&genomic coding sequence-	BES1_3GW p4	GGGGACAAGTTTGTATAGAAAAGTTGGGTGCTTGG CGCCGACGCCGA
BES1YFP-native terminator	BES1_3GW p3	GGGGACAAGTTTGTATAATAAAGTTGAGTGAAGCG ATTGGCAGCAA
BES1-YFP-native terminator	BES1_3GW p2	GGGGACCACTTTGTACAAGAAAGCTGGGTACGTTT GTTCCATCTCCTCTC
Primers used for genotyping transgenic lines		
<i>bri1</i> -RNAi	Waxy-gk1	CCAGTTCAAATTCTTTTAGGCTCACC
	Mu278-F	GAACAACCTACCTCTCCGGCG
BES1-YFP	Bes1yfp-F2	TGGATCAGCTTCCAGGCCACCA
	Bes1yfp-R	GAAGAAGTCGTGCTGCTTCATGTG
Primers used for Quantitative PCR		
Gene / Accession #	Primer	Sequence (5'-3')
BRI1a / XM_008658585	qbri1-F	TCGTCACACTTTAGTAAGAGCTG
	qbri1-R	CGTTGGTCAAAGCAAGGTA
BRI1b / KP099562	qbri1-5F	AGCTCCGGGACCTCATTCTT
	qbri1-5R	AGAGTTCCGACGGGATGATG
BRL1 / XM_008654300	qbri1L-F	GATAGACGAATCGGCAGAGAAA
	qbri1L-R	GCTAGCTGCTGTTGTATCGTAC
BRL2 / XM_008660956	qbri1L2-F	CCTCTGCCTGTGACTGATG
	qbri1L2-R	ATTAGTACAGAATTACGGACCAGG
BRL3 / XR_565429	qbri1L3-F	AATGTTTCAGTGAGTTTCAGATTGAC
	qbri1L3-R	CTGCAGGGATCAATAACATTTACAC
CPD / NM_001147124	qcpd-F	GATAGAGTAAGGTGGATGTCGTG
	qcpd-R	GTCCAGGTTACAGAGCAAGAG
BRD1 / NM_001138467	qbrd1-F	GAAATAACCCATGCGATGCTG
	qbrd1-R	ACATTACTATCGGCATGGACAC
DWF4 / XM_008669815	qdwf4-F:	TTTGACCGAGAGCACAAGAG
	qdwf4-R:	CAATCTACATAAAACACGAGACCAC

BAS1 / XM_008647147	qbas1-F	TAACTTTCTGTCCTAGCCTGCG
	qbas1-R	CACATACCACACAAACGCCA
BAS2 / NM_001159622	qbas2-F	GACCGGAGCAGAGTTTTGGA
	qbas2-R	CAATCAATCCCATCTATACTGCCA
BAS3 / XM_008674900	qbas3-F	ACTAGAAGGAGCACCACCGT
	qbas3-R	GGCACTGGTCAAGCCTTCT
RS1 / NM_001111861	qcpd-F	CACTTCCATGGACACGACTG
	qcpd-R	CCACAACAATGTCCTTGCAC
Ubiquitin / XM_008681532	q378-F	AACATCCTAACCCAGCTCAAG
	q378-R	CTGTTGGATCCCATGACGG
Primers&sequences used for cloning and sequencing of BRI1b		
Primer	Sequence (5'-3')	
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Chr5-R1	CTAGTCCTTCTCCTCCTTGTCTTCTTTTCAGGGTCG	
Chr5-R2	CTAGTCCTTCTCCTCCTTGTCTTCTTTTCAGGGTCC	
Chr5-R3	CTAGTCCTTCTCCTCCTTGTCTTCTTTTCAGGGTCA	
Chr5-R4	CTAGTCCTTCTCCTCCTTGTCTTCTTTTCAGGGTCT	
Chr5W-F7	CTCGAGACGCTCAGCCTG	
Chr5W-F8	TGCAGCTGAGCAGCCTC	
Chr5-N1	TTTCTTCTGCTCCTCTCTCTAGGT	
Chr5-UR	GTGGATTTGGCACCGAAGAAAAAAT	
Sequence-#1	TGAACTCGTGAAGGAAGATCCAGCCCTGGAGCTCGAG CTACTGGAGCACCTAAAA	
Sequence-#2	AGAGGCTCAGCCTGCGCGGGCGCCAACGTCAGCGGCACGC TGGCCGCGGTGCCGAGGTGCGGGGCAAGCTGCAGTCGC TCGACCTGTCAGCGAATGCCGGCCTGCGGGGCTCCGT	