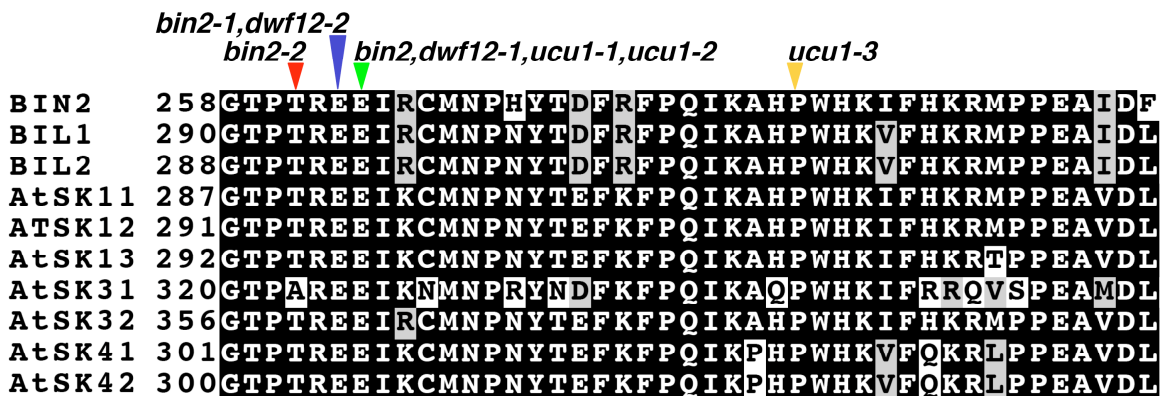**Supplemental Figure S1.** *BIN2* and its two homologs exhibit similar expression profiles. A, Comparison between *BIN2* and *BIL1*. B, Comparison between *BIN2* and *BIL2*. The two figures were generated using the Arabidopsis e-FP browser at http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi [Winter et al., 2007. PLoS One 2(8): e718]. The color scale at the right bottom corner indicates the relative expression levels of *BIN2, BIL1*, and *BIL2*: red means higher *BIN2* expression level, blue shows higher *BIL* expression, while yellow indicates similar expression levels between *BIN2* and *BIL1/BIL2*.

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                   bin2-1,dwf12-2
                     bin2-2        bin2,dwf12-1,ucu1-1,ucu1-2        ucu1-3

BIN2    258 GTPTREEIRCMNPHYTDFRFPQIKAHPWHKIFHKRMPPEAIDF
BIL1    290 GTPTREEIRCMNPNYTDFRFPQIKAHPWHKVFHKRMPPEAIDL
BIL2    288 GTPTREEIRCMNPNYTDFRFPQIKAHPWHKVFHKRMPPEAIDL
AtSK11  287 GTPTREEIKCMNPNYTEFKFPQIKAHPWHKIFHKRMPPEAVDL
ATSK12  291 GTPTREEIKCMNPNYTEFKFPQIKAHPWHKIFHKRMPPEAVDL
AtSK13  292 GTPTREEIKCMNPNYTEFKFPQIKAHPWHKIFHKRTPPEAVDL
AtSK31  320 GTPAREEIKNMNPRYNDFKFPQIKAQPWHKIFRRQVSPEAMDL
AtSK32  356 GTPTREEIRCMNPNYTEFKFPQIKAHPWHKIFHKRMPPEAVDL
AtSK41  301 GTPTREEIKCMNPNYTEFKFPQIKPHPWHKVFQKRLPPEAVDL
AtSK42  300 GTPTREEIKCMNPNYTEFKFPQIKPHPWHKVFQKRLPPEAVDL
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Supplemental Figure S2. Conservation of amino acids critical for BR-mediated inhibition of GSK3-like kinase activity. Sequence data for this analysis can be found in the GenBank database under the following accession numbers: BIN2, At4g18710, NP_193606; BIL1, At2g30980, NP_180655; BIL2, At1g06390, NP_973771, AtSK11, At5g26751, NP_568486; AtSK12, At3g05840, NP_187235; AtSK13, At5g14640, NP_196968; AtSK31, At3g61160, NP_191675; AtSK32, At4g00720, NP_191981; AtSK41, At1g09840, NP_001031013; AtSK42, At1g57870, NP_176096. The sequences were aligned using the Mcoffee program at http://tcoffee.vital-it.ch/cgi-bin/Tcoffee/tcoffee_cgi/index.cgi and shaded by the BoxShade Server at http://www.ch.embnet.org/software/BOX_form.html. Amino acids that are identical or similar in 60% of the analyzed sequences are shaded by black or grey background whereas amino acids that are not similar with the majority sequences are indicated by black letters with white background. Color arrows indicate amino acids mutated in 8 known gain-of-function *bin1/ucu1/dwf12* mutants.

Supplenmentary Table S1. Primers Used for Genotyping, Sequencing, and RT-PCR Analyses.

Name	Sequence (from 5' to 3')	Comment
gBIN2For/Rev	For: CGTGTCTGCGTAATTAACCAGCAATTTCAA Rev: GCAAAGAGGAGACTGTGTTTTTCACCAAA	to amplify and sequence the entire BIN2 gene from putative ucu1-3 suppressors
BIN2SG1	GGTTTTGTGCTGATATTAAA	sequence BIN2
BIN2SG2	ACCGCTACAAGTCGAATGA	sequence BIN2
BIN2SG3	CTGTGATCTTGTCATTTAC	sequence BIN2 and genotype bin2-1 and bin2-3
BIN2SG4	TGAAGAAACCTCAAGACC	sequence BIN2 and genotype bin2-1 and bin2-3. (Xho I can't cut SG3/SG4 fragment in bin2-1)
ucu1-3dCAPS	For: CAGGTTTCCACAGATAAAGGCAGAT Rev: ATCTGCCTTTATCTGTGGAAACCTGAAATC	Hinf I cuts the mutant PCR product
LB4	CGTGTGCCAGGTGCCCACGGAATAGT	with BIN2SG3 to amplifying T-DNA from bin2-3 T-DNA insertional mutant
BIL1EK	For: GTACTCCAACTCGCAAAGAAATCCGGTG Rev: CACCGGATTTCTTTGCGAGTTGGAGTAC	Used for site-directed mutagenesis to change E295(GAA) to K(AAA) in BIL1
BIL1Seq	3: AGGTAACCTTATACATGGTAG 4: CTTACATGATTGAATTCTCTG	Used for genotyping bil1 T-DNA insertional mutation
JL270	TTTCTCCATATTGACCATCATACTCATTG	with BIL1Seq4 to genotype bil1 mutation with BIL2Seq1 to genotype bil2 mutation
BIL1RT	For: TCCACAAGCGGATGCCTCCG Rev: CAGCTTGAAATGGAAAGCCA	RT-PCR analysis of BIL1 expression
BIL2EK	For: GTACTCCAACTCGTAAAGAAATTCGATG Rev: CATCGAATTTCTTTACGAGTTGGAGTAC	Site-directed mutagenesis to change E293(GAA) to K(AAA) in BIL2
BIL2Seq	1: TCGTGCTCCAGAACTGATC 2: GCAAGGTCTATTGCTTCTG	To genotype the bil2 T-DNA insertional mutation
BIL2RT	For: TTCATAAACGGATGCCTCCA Rev: ACTGTTTTGTAATCCTGTGC	RT-PCR analysis of BIL2 gene expression in the bil2 mutant
SAUR-AC1RT	For: GAGGAGTTTCTTGGGTGCTAAG Rev: CATTGTATCTGAGATGTGACTG	RT-PCR analysis of the SAUR-AC1 gene expression
DWF4RT	For: CACGAGCAACGATATTGAAGTTC Rev: CCTAAGCTCTTCAACGGCTTTAG	RT-PCR analysis of the DWF4 gene expression
β–TubulinRT	For: ATTCCAGGTTTGTCACTCGTTG Rev: TATGAAGAAGTGAAGACGGG	used to analyze β-Tubulin expression as a control for RT-PCR experiments
bri1-5dCAPS	For: GTGTACTTTCGATGGCGTTACCT Rev: GGTTAAAGAAGCAGAGCA	genotype bri1-5 mutation, Pst I cuts the DNA fragment with bri1-5 mutation