Supporting Information

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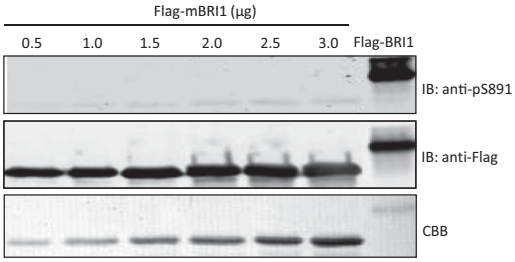

Fig. S1. The anti-pS891 antibodies do not cross-react with the kinase inactive Flag–mBRI1(K911E) and are therefore phospho specific. The indicated amount of Flag–mBRI1 protein was electrophoresed and transferred to a PVDF membrane before probing with the indicated antibodies or staining with Coomassie Brilliant Blue.

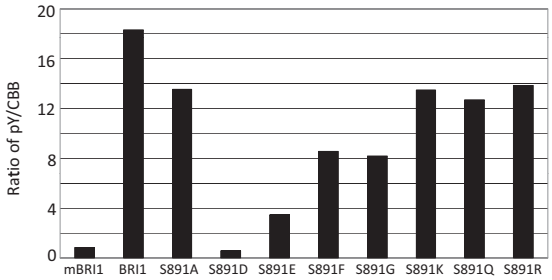

Fig. S2. Tyrosine autophosphorylation of recombinant Flag-BRI1 proteins with various substitutions at the 891 position, normalized for the amount of BRI1 protein. The immunoblots shown in Fig. 2 were analyzed by densitometry and the ratio of phosphotyrosine content (from the anti-pY immunoblots) and protein (CBB stain) is plotted.

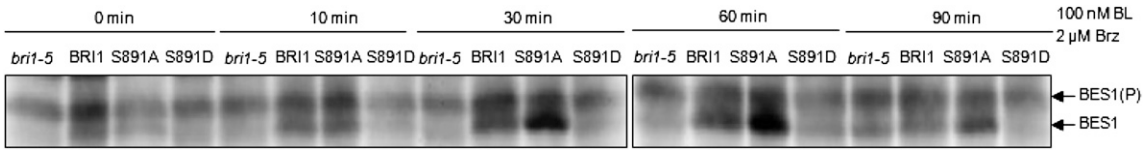

Fig. S3. Representative immunoblots showing BES1 phosphorylation status in the *bri1-5* mutant and transgenics (in the *bri1-5* background) expressing wild-type BRI1–Flag or the S891A- or S891D-directed mutants in response to BL treatment. P-BES1, phospho-BES1. Seedlings were grown in shaking liquid culture in continuous light. On day 6, the cultures were treated with 2 μM Brz and on day 11, 100 nM BL was added and samples were collected at 0, 10 min, 30 min, 1 h, and 1.5 h after BL addition. Microsomal membranes were isolated and BRI1–Flag was immunopurified before SDS/PAGE and immunoblotting. The immunoblot signals from unphosphorylated BES1 were quantified by densitometry using the LI-COR Odyssey infrared imaging system.

Table S1. Sixteen arginine-aspartate (RD)-type LRR-RLKs with a phosphorylatable residue at the position corresponding to serine-891 in the subdomain I ATP-binding domain of BRI1

Gene locus	G-rich loop sequence
AT1G72180	**G**S**G**SA**G**KVY
AT5G6571O	**G**S**G**G**S**G**L**VY
AT5G25930	**G**S**G**G**S**G**K**VY
AT4G20140	**G**S**G**G**S**G**K**VY
AT5G44700	**G**S**G**G**S**G**K**VY
AT1G35710	**G**T**G**GY**S**K**VY
AT4G08850	**G**T**G**GH**G**K**VY
AT5G07180	**G**Y**G**AS**S**T**VY
AT5G62230	**G**Y**G**AS**S**T**VY
AT5G62710	**G**S**G**GF**G**T**VY
AT1G55610	**G**S**G**GF**G**E**VY
AT3G13380	**G**S**G**GF**G**D**VY
AT4G39400 (BRI1)	**G**S**G**GF**G**D**VY
AT1G66150	**G**S**G**GF**G**V**VY
AT1G79620	**G**Y**G**GY**G**K**VY**
AT2G37050	**G**S**G**GF**G**I**VY**

The glycine residues in the GXGXXG motif are in bold and the phosphorylatable residue is underlined. The sequences are arranged in order, on the basis of alignment of the kinase domain sequence. LRR–RLKs, leucine-rich receptor–receptor-like kinases.