Supplementary Material and methods

**Plant material and growth conditions.** The wild type used in all experiments was Columbia (Col0) and plants were grown on either soil or Petri dishes containing 0.5X Linsmaier and Skoog salts medium in long days. The **MAKR** genes are defined as: 

- **MAKR1**: At5g26230;
- **MAKR2**: At1g64080;
- **MAKR3**: At2g37380;
- **MAKR4**: At2g39370;
- **MAKR5**: At5g52870;
- **MAKR6**: At5g52900.

We used **bak1-3** (Chinchilla et al. 2007) and the null **bri1** allele GABI_134E10.

**Constructs, generation of transgenic lines, and phenotype analysis.** All the **BKI1** constructs (deletions and mutants included) are tagged with mCITRINE at their C-terminus. mCITRINE-tagged lines are resistant to glufosinate (Basta), 6xHA-tagged lines to kanamycin and mCHERRY-tagged lines to hygromycin. Rosette radius phenotypes were quantified on 5 week-old plants. **UBQ10prom** was PCR amplified from pNIGEL(Geldner et al. 2009) (gift from N. Geldner), **35Sprom** from pBJ36 (Gift from J. Long), **BRI1prom** (1.7 kb), **BAK1prom** (1.7 kb) and **BKI1prom** (2 kb) from Col0 genomic DNA and cloned into **pDONR-P4P1R** using gateway recombination (Invitrogen) (see supplementary table 1 for primers). **BKI1**, **BKI1 deletion**, **BRI1**, **BAK1** and **MAKR1** were PCR amplified from Col0 genomic DNA and recombined into **pDONR221** (Invitrogen). 

**mCITRINE** (a pH-resistant YFP variant), **mCHERRY** (gift from R. Tsien) and **6xHA** (pBK36, Gift from J. Long) were cloned into **pDONR-P2RP3** (Invitrogen). Final destination vectors were obtained by using three fragments recombination system using the **pB7m34GW**, **pH7m34GW** and **pK734GW** destination vectors(Karimi et al. 2007). The vectors created are listed in supplementary table 2. **BRI1** and **BAK1** constructs were transformed into heterozygous **bri1** (GABI_134E10) and homozygous **bak1-3** respectively and their transgenic expression fully rescued the **bri1** and **bak1** growth defect. For all constructs, more than 20 independent T1 lines were isolated and between
3 to 6 representative mono-insertion lines were selected in T2. Confocal microscopy, phenotypic analysis and protein extraction were performed on segregating T2 and homozygous T3 lines.

Supplementary References:


