

BRI1 sgRNA2 site

Mutation detected from 28 out of 71 sequenced clones

Plant ID	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTCC--TGAGGGATCTC	WT
1	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTC--TGAGGGATCTC	D1
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAG-----GGATCTC	D8 (×2)
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTCCCTGAGGGATCTC	+1 (×10)
2	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTC--TGAGGGATCTC	D1
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAG-----GAGGGATCTC	D5
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTCCTTGAGGGATCTC	+1
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTCCCTGAGGGATCTC	+1 (×8)
3	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTC--TGAGGGATCTC	D1
	GGATCAGAGTCTCTAAGGTCTTGACATACATGAGCTCCTTGAGGGATCTC	+1 (×3)

Supplementary information, Figure S4 Targeted indel mutations induced by engineered sgRNA:Cas9 at the *BRI1* gene sgRNA2 site in *Arabidopsis*.

Alleles shown were amplified from genomic DNA isolated from 3 independent T1 transgenic plants separately and sequenced after cloned into vectors. The wild type sequence is shown at the top with the PAM sequence highlighted in magenta and the target sequence in cyan. Red dashes, deleted bases; red bases, insertions or mutations. The net change in length is to the right of each sequence (+, insertion; D, deletion). The number of clones representing each mutant allele is shown in brackets.