

*BR1* sgRNA3 site

Mutation detected from 22 out of 34 sequenced clones

Plant ID	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-C-CTGAGGAATCC	WT
1	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG---CTGAGGAATCC	D1 (×3)
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CCCTGAGGAATCC	+1
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CACTGAGGAATCC	+1
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CTCTGAGGAATCC	+1
2	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG---CTGAGGAATCC	D1
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CACTGAGGAATCC	+1 (×6)
3	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACA-----TGAGGAATCC	D5 (×2)
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CTCTGAGGAATCC	+1
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CACTGAGGAATCC	+1
4	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG---CTGAGGAATCC	D1
	CAAATCGATTTCCGTAAGCATAGTAAGAGCTGACATAG-CACTGAGGAATCC	+1 (×4)

**Supplementary information, Figure S5** Targeted indel mutations induced by engineered sgRNA:Cas9 at the *BR1* gene sgRNA3 site in *Arabidopsis*.

Alleles shown were amplified from genomic DNA isolated from 4 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.