

### ROC5 sgRNA1 site

Mutation detected from 136 out of 165 sequenced clones

Plant ID	Sequence	WT
	GACGAGGGACACTGAGGCGGAGAACGACAGCCG-GTCGGGAAGCGAC	WT
1	GACGAGGGACACTGAGGCGGAGAACGACAGCCGAGTCGGGAAGCGAC	+1 (×27)
2	GACGAGGGACACTGAGGCGGAGAACGACAGCC--GTCGGGAAGCGAC	D1 (×7)
	GACGAGGGACACTGAGGCGGAGAACGACA-----GTCGGGAAGCGAC	D4 (×2)
	GACGAGGGACACTGAGGCGGAGAACGAC-----GTCGGGAAGCGAC	D5
	GACGAGGGACACTGAGGCGGAGAACGACAGCCGAGTCGGGAAGCGAC	+1 (×6)
	GACGAGGGACACTGAGGCGGAGAACGACAGCCGTGTCGGGAAGCGAC	+1 (×3)
3	GACGAGGGACACTGAGGCGGAGAACGACAGCCGTGTCGGGAAGCGAC	+1 (×29)
4	GACGAGGGACACTGAGGCGGAGAACGACAGCCGAGTCGGGAAGCGAC	+1 (×22)
	GACGAGGGACACTGAGGCGGAGAACGACAGCCGTGTCGGGAAGCGAC	+1 (×6)
5	GACGAGGGACACTGAGGCGGAGAACGACAGCCGAGTCGGGAAGCGAC	+1 (×17)
	GACGAGGGACACTGAGGCGGAGAACGACAGCCGTGTCGGGAAGCGAC	+1 (×16)

**Supplementary information, Figure S8** Targeted indel mutations induced by engineered sgRNA:Cas9 at the *ROC5* gene sgRNA1 site in rice.

Alleles shown were amplified from genomic DNA isolated from 5 independent T0 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.