

Table S5. Comparison of editing efficiency for *BnaRFL11*-promoters with other published gene-editing studies.

Promoter of sgRNA	Target sequence	Target genes ^b	GC % content (Without PAM)	Positive lines of T ₀	Editing lines	Editing efficiency ^c
U6-26	CAAGACTCAGAGGGATACG AGG	<i>BnaRFL11</i>	57%	108	70	64.81%
	GAGGTCGTCCGAGATGGCCG AGG	<i>BnaA9-RGA</i>	70%	29	28	96.60%
	CAAGGTGAGGTCGTCAGAGA TGG	<i>BnaC9-RGA</i>	55%	29	25	86.20%
	CAAGGTTAGGTCTTCGGAGA TGG	<i>BnaA6-RGA</i>	50%	29	28	96.60%
	CAGGTCGTCGGAGATGGCTG AGG	<i>BnaC7-RGA</i>	65%	29	27	93.10%
	GCACAAGACGACGGCATTGC TGG	<i>BnaA2-DA2</i>	60%	17	7	41.20%
	GAACACCTTAGGATTTGTGC TGG	<i>BnaC5-RGA</i>	50%	17	6	35.30%
U6-29	GTATCCCTCTGAGTCTTGG AGG	<i>BnaRFL11</i>	50%	108	50	46.29%
	ACCCGTCGGAGCTCTACTCG TGG	<i>BnaA9-RGA</i>	65%	29	8	27.6%
	ACCCGTCGGAGCTTTACTCG TGG	<i>BnaC9-RGA</i>	60%	29	9	31.00%
	ACCCCGCTGAGCTTTACTCG TGG	<i>BnaA6-RGA</i>	60%	29	10	34.50%
	ACCCTGCTGAGCTCTACTCT TGG	<i>BnaC7-RGA</i>	55%	29	12	41.40%
	GGGAGCTAAGTACGTAGACT TGG	<i>BnaA2-DA2</i>	50%	17	8	47.12%
	GAACACCTTAGGATTTGTGC TGG	<i>BnaC5-RGA</i>	45%	17	14	82.40%

^aThe PAM is in red.. ^bThe target genes *BnaRFL11* (Current study), *BnaA9*, *BnaC9*, *BnaA6*, *BnaC7*, *BnaA2*, *BnaC5* (Yang et al 2018). ^c for each target, the %age of modified plantations compared to the number of tested plants.