

Table S1 Detection of mutations on off-target sites in T0 edited plants.

Name of off-target site	Off target position	Sequence of the off-target site	Region	No. of plants sequenced	No. of plants with off-target
Ms10 ³⁵ -off1	SL2.50ch05: 37905349	AGACGAAACCACTTACATTAGGG	Intergenic	5	0
Ms10 ³⁵ -off2	SL2.50ch08: 8941450	AGACCCTATGACCTACATTAAGG	Intergenic	5	0
GSTAA-off1	SL2.50ch09: 55914395	TCATTTAAGAGGGTGATTTAGG	Intergenic	5	0
GSTAA-off2	SL2.50ch08: 20856153	TCATTGAAGAAGAGATTTCAG	Intergenic	5	0
F3H-off1	SL2.50ch08: 25722311	GGGCTAGAGACAATACTAGATGG	Intergenic	5	0
F3H-off2	SL2.50ch12: 42487968	GGGCTAGAGACAATACTAGACGG	Intergenic	5	0

Using CRISPR-GE offTarget(<http://skl.scau.edu.cn/offtarget/>) to predict off-target sites. A mismatching bases are marked in red.