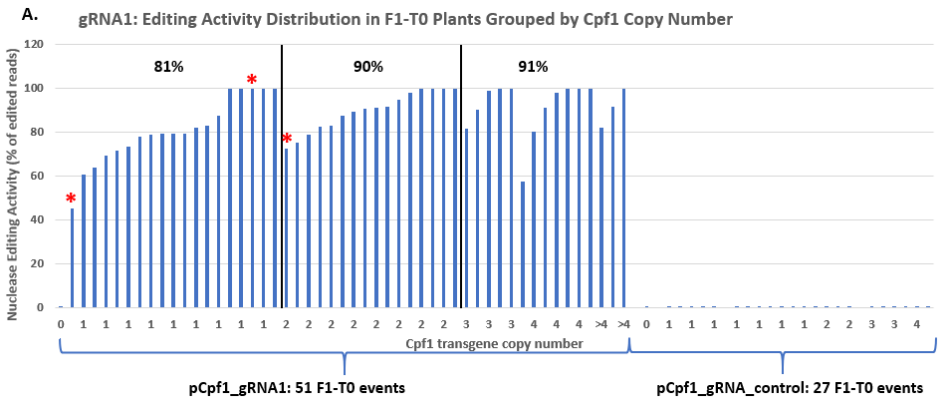
Supplementary Table 1: Total number of BC1-F1 seeds analyzed by genotyping in the first genome editing experiment using gRNA1 grouped by reciprocal backcrosses

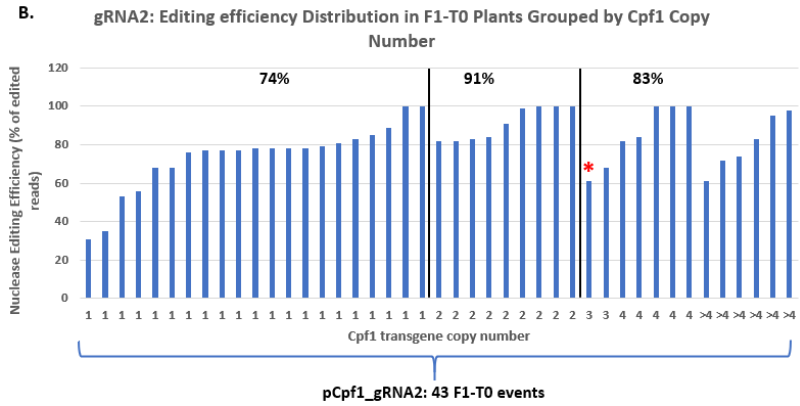
Construct	Back-Cross Type	Events # *	Total Seeds Genotyped
Editing: pCpf1_gRNA1	F1-T0(female) by Parent B(male)	26	2625 (62.5%)
Editing: pCpf1_gRNA1	Parent B(female) by F1-T0 (male)	21	1575 (37.5%)
Control: pCpf1_gRNA_control	F1-T0(female) by Parent B(male)	8	1015 (45%)
Control: pCpf1_gRNA_control	Parent B(female) by F1-T0 (male)	10	1250 (55%)

* BC1 seeds from both reciprocal backcrosses were genotyped for some F1-T0 events; some F1-T0 events were represented by only one type of the backcross

Supplementary Table 2: Genotyped BC1-F1 seeds grouped by reciprocal backcrosses

BC1-F1	F1-T0 (female) by Parent B (male)	Parent B (female) by F1-T0 (male)	Total Seeds Genotyped
Event1	308	0	308
Event2	270	41	311
Event3	329	132	461





Supplementary Figure 1: The guided nuclease editing activity in the F1-T0 plants. A. gRNA1 (pCpf1_gRNA1) or control (pCpf1_gRNA_control) plasmids. **B.** gRNA2 (pCpf1_gRNA2). The graphs show the distribution of editing activity grouped by T-DNA copy number. The numbers above the bar plot represent the average editing activity in events with T-DNA copy numbers from of 1, 2, or ≥3. Red stars indicate F1-T0 plants were guided CO was shown.

>Os.Act1:1:1 Promoter

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