

Figure S1. Sequencing results of the targeted region in transgenic hairy roots. (A) Target sequences were designed to the 5' end of the *GUS* gene. (B) Target sequences were designed to the 3' end of the *GUS* gene. Each hairy root is an independent event. Base substitutions are indicated with orange capital letters. The targeted sequences are shown on the top. The genotype of the mutation is indicated at the right of each sequence. -n, nucleotide deletion of the indicated number; +n, nucleotide of the inserted number; Percentages next to sequences indicate the number of amplicons with sequence over the number of total amplicons sequenced. There were 10 amplicons per event from the 5'-target and 3'-target events, respectively.

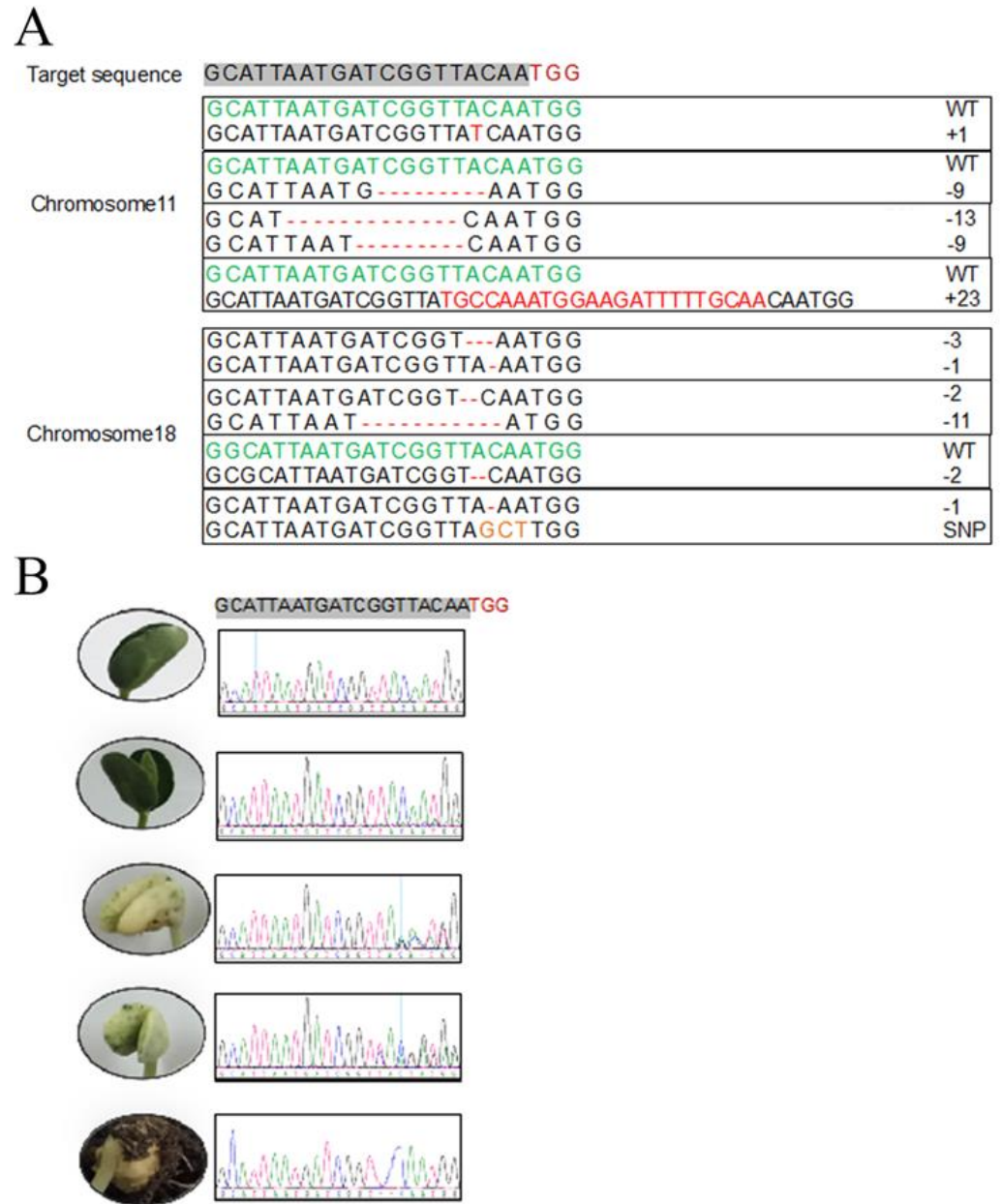


Figure S2. GmPDS sequencing results of the targeted region in transgenic hairy roots. (A) Sequencing of Cas9-induced GmPDS mutation in the T0 transgenic soybean plants. Wild-type sequences are in green, deletions and insertions are shown in red. Base substitutions are indicated with orange capital letters. The targeted sequences are shown on the top. -n, number of nucleotide deleted; +n, number of nucleotide inserted; Percentages next to the sequences is the ratio of amplicons with this sequence over the number of total amplicons sequenced. Ten amplicons per event were sequenced. (B) Sequencing analysis of GmPDS-CRISPR/Cas9 T1 soybean plants.

Non-mutation gRNA5-2, 03G168700

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Mutation gRNA5-2, 03G168700

CGAAATCTCTTCACCGCTCTCTGCCACACCGATGCTTACACTTGGGGCGGCAAGTACAGCGTCTTTTTTTTTTCTTGAATCAAAATCAAT
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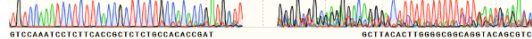
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ACAGGTTTAAAGAGAGTGGCGAGAGACGGTGTGGCTACGAATGTGAACCCGCC GTCCATGTCGCAAAAAAAAAAAGAACTTAAGTTTAA

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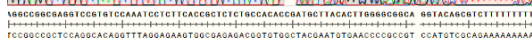
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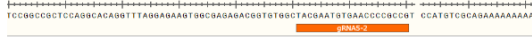


gRNA5-2

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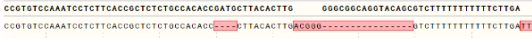


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