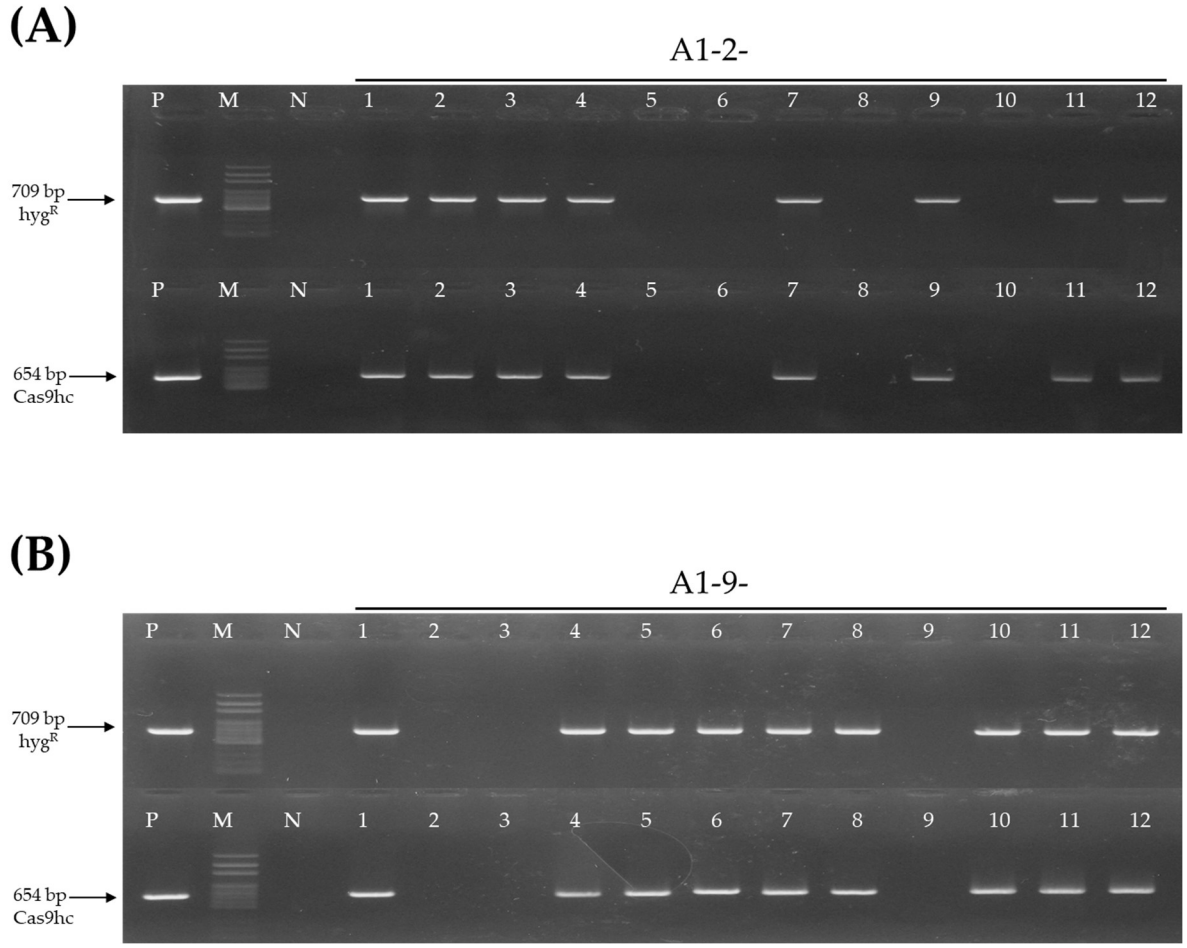


**Figure S1.** Selection of $E_1$ *AGL19*-edited lines using polymerase chain reaction (PCR) analysis. (**A**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A1-2-edited lines. (**B**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A1-9-edited lines. The 709 bp and 654 bp expected PCR products are indicated with an arrow, respectively. P, positive control; M, 100 bp DNA ladder; N, negative control; Numbering lane, gene-edited lines.

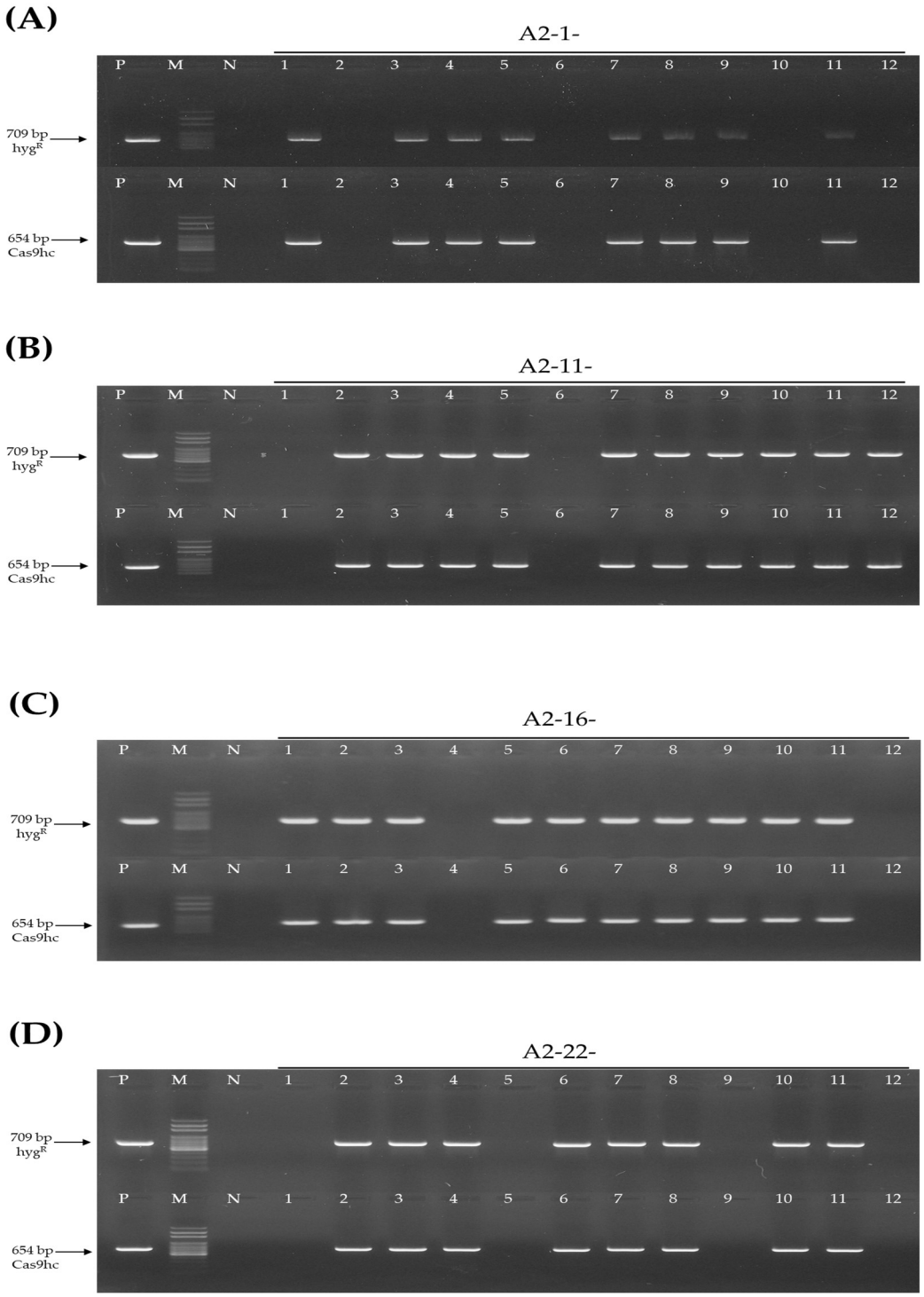


**Figure S2.** Selection of $E_1$ *AGL24*-edited lines using polymerase chain reaction (PCR) analysis. (**A**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A2-1-edited lines. (**B**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A2-11-edited lines. (**C**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A2-16-edited lines. (**D**) PCR analysis with $hyg^R$ and Cas9hc primer sets of $E_1$ A2-22-edited lines. The 709 bp and 654 bp expected PCR products are indicated with an arrow, respectively. P, positive control; M, 100 bp DNA ladder; N, negative control; Numbering lane, gene-edited lines.

**Table S1.** List of primer sets for polymerase chain reaction (PCR) analysis.

| Name | Primer | Sequence (5'→3') | Expected product size (bp) |
|---|---|---|---|
| **Hyg$^R$** | F[z] | CGT CTG CTG CTC CAT ACA AG | 709 |
| | R | TGT CGA GAA GTT TCT GAT CGA | |
| **Cas9hc** | F | CCG CCA GGA GGA CTT CTA CC | 654 |
| | R | ATG TTC TCG GGC TTG TGG CG | |
| **CT001_A03121400** | F | GGA GTT TCT TGG ATT GTC TTG G | 297 |
| | R | GTT GTC AAA ATC TCA GGA GAG G | |
| **CT001_A08282630** | F | GAA GAA ATT GAT AAG CTG AAG | 476 |
| | R | TTT CTT GGA TTG TCT TGG CT | |
| **CT001_A03122450** | F | AAA CCA CAC ATG CAA AGT CG | 1381 |
| | R | GCT GAT GAA CTT TCG GTT CT | |
| **CT001_A01013460** | F | ATG GCG AGA GAG AAG ATA AG | 318 |
| | R | CTC CGA GCC CAA GAA TAA ATT | |

[z]: F, forward primer; R, reverse primer.

**Table S2.** List of degenerate primers for variable argument-thermal asymmetric interlaced polymerase chain reaction (VA-TAIL PCR) analysis.

| Target domain | Name | Sequence (5'→3') | Variable argument[z] |
|---|---|---|---|
| **Zinc finger protein LSD1** | **BrAD1**[y] | GAM RTG NCT VAM WTT G[x] | 192 |
| | **BrAD2** | DTA ASA TGN HNT TGC T | 288 |

[z]: The number of primer combinations of AD primers.

[y]: BrAD primers are degenerate primers.

[x]: Mixed bases. M = A/C; R = A/G; V : A/C/G; W : A/T; D = A/G/T; S : G/C; H = A/C/T; N = any base.

**Table S3.** List of nested long T-DNA-specific primers for variable argument-thermal asymmetric interlaced polymerase chain reaction (VA-TAIL PCR) analysis.

| Primer | Sequence (5'→3') | GC% | TM(℃) |
|---|---|---|---|
| LSP1 | ATA GTG GAA ACC GAC GCC CCA GCA[z] | 58.3 | 66.6 |
| LSP2 | CCA GCA CTC GTC CGA GGG CAA AG | 65.2 | 66.8 |
| RSP1 | AAA GTA TAC CCC TAC GAC GTG CCC G | 56.0 | 63.8 |
| RSP2 | GCC CGA CTA CGC CTA ACA CCC AG | 65.2 | 66.2 |

[z]: Underlined nucleotide sequences indicate the overlapping sequence.