Figure S1. Phenotypic variation of soybean mutations. The variations of plant architecture (**a**) and seed (**b**) in soybean M3 mutants
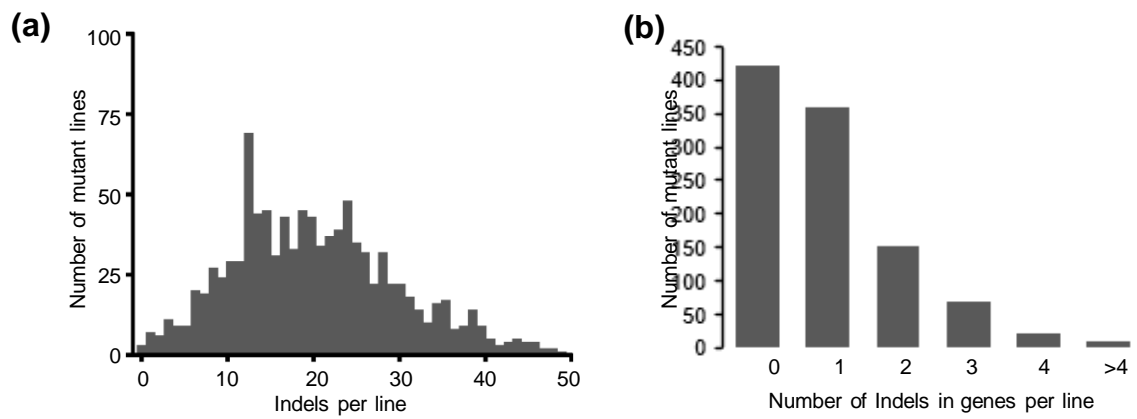
Figure S2. Distribution of small Indels in soybean mutant population.

(a) Distribution of small Indels per mutant line in mutant population.

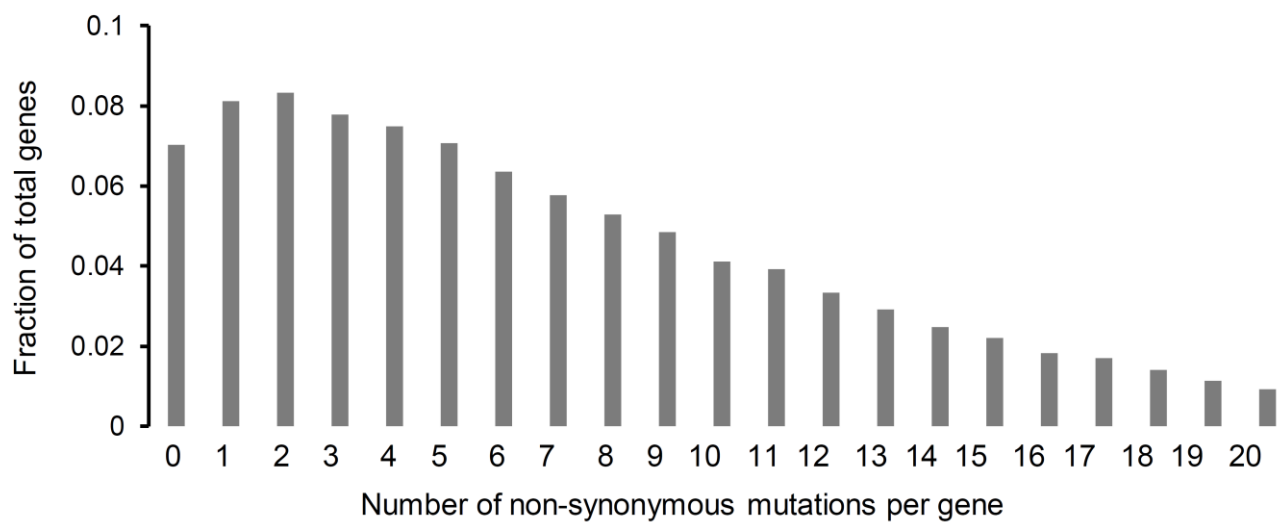**(b)** Frequency of mutant lines carrying different number of small Indels in gene region.

Figure S3. Frequency of genes carrying different number of non-synonymous mutations, including stop gained, mis-splicing, start lost, and missense mutations.
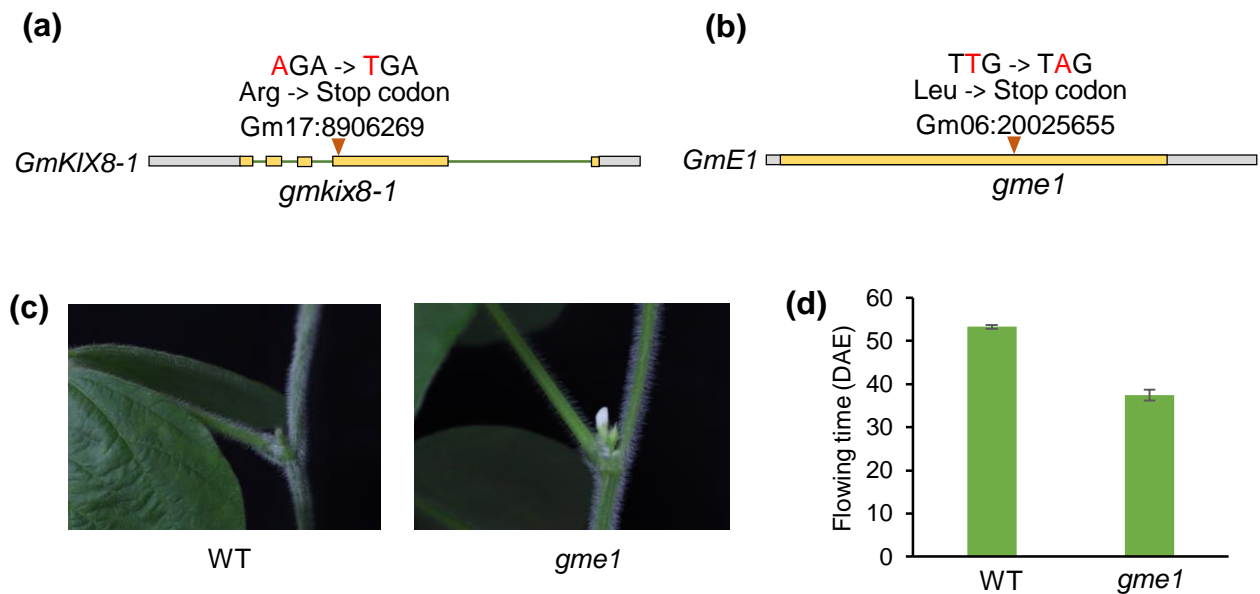
Figure S4. Knockout of *GmKIX8-1* and *GmE1* genes in mutant population.

(a) Genomic location and amino acid change of homozygous EMS-induced mutation in *gmkix8-1* mutant (NJAU1840).

(b) Genomic location and amino acid change of homozygous EMS-induced mutation in *gme1* mutant (NJAU0143).

(c) Phenotype of wild type (WT) and *gme1* mutant. WT did not bloom when *gme1* mutant was flowering in long-day condition (16 h/8 h, light/dark).

(d) Flowering time of WT and *gme1* mutant in long-day condition (16 h/8 h, light/dark). DAE: days after emergence.
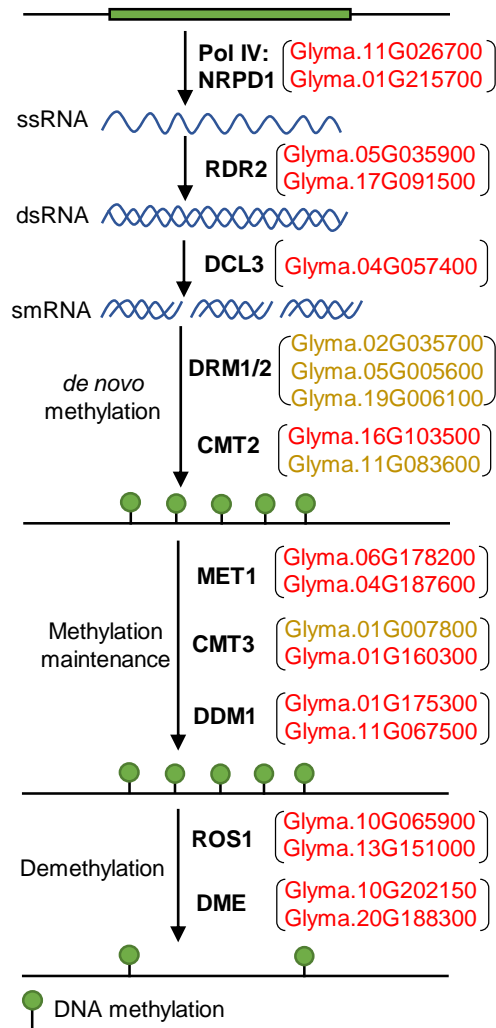
Figure S5. Mutations identified in genes involved in DNA methylation and demethylation. Genes in Red indicate genes carrying truncation mutations, including stop gained, mis-splicing, start lost. Genes in brown indicates genes carrying missense mutations.
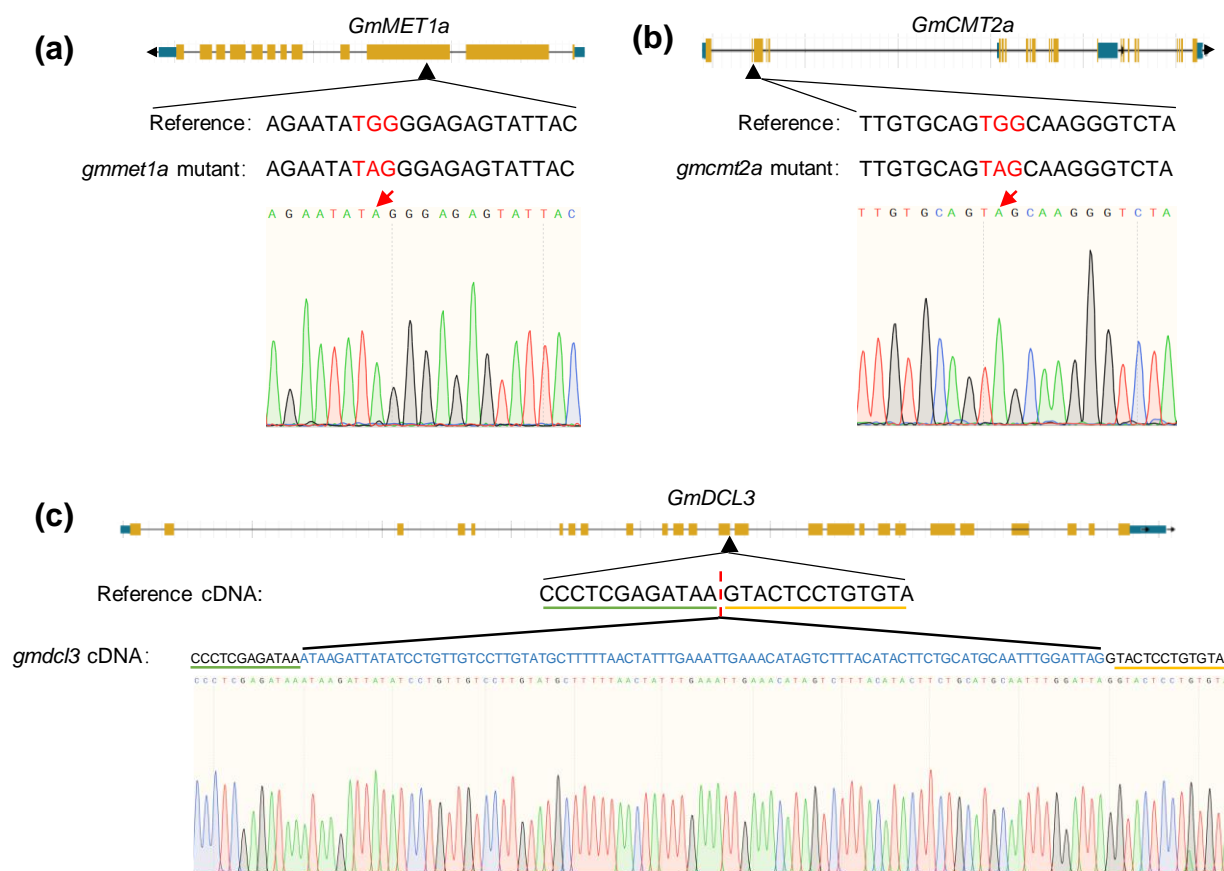
Figure S6. Validation of truncation mutations in DNA methylation related genes. **(a-c)** Sanger sequencing validation of truncation mutations in *GmMET1a* **(a)**, *GmCMT2a* **(b)** and *GmDCL3* **(c)**, respectively. Black triangles indicate positions of mutations on genes. Retained intron in mature mRNA in *gmdcl3* mutant is indicated in blue.