

Figure S2 Differentially expressed genes (DEGs) GO enrichment analysis of AS1 and OE3.

(a) Downregulated DEGs GO of AS1. (b) Upregulated DEGs GO of OE3. Adjusted P-value (padj) for each ontology term are displayed with a color reflecting its level of significance.

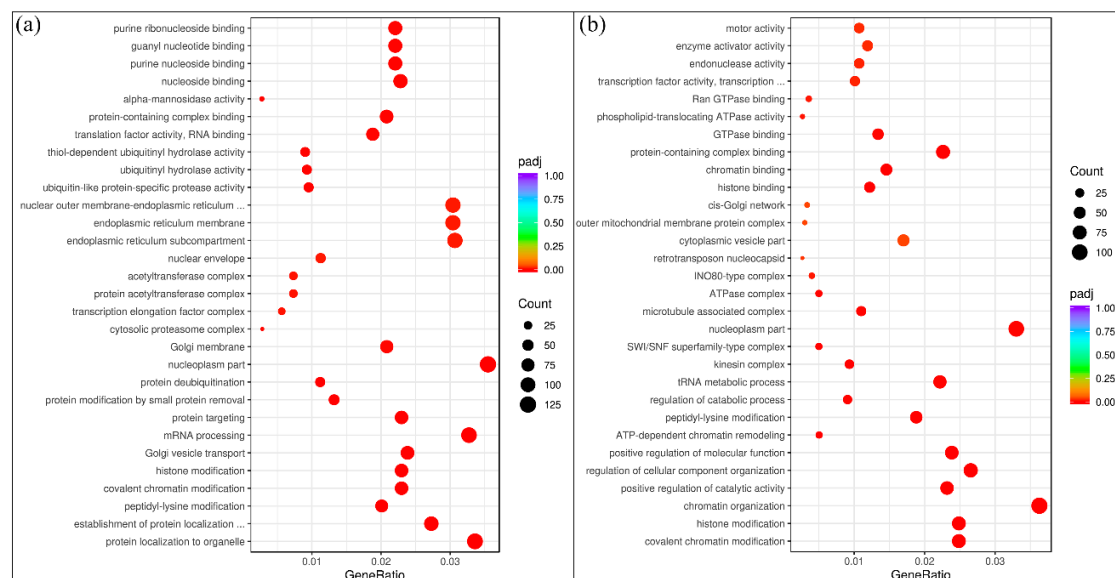


Figure S3 Significant GO terms on genes with downregulated H3K36me3 in AS1 (a) and upregulated H3K36me3 in OE3 (b). Adjusted P-value (padj) for each ontology term are displayed with a color reflecting its level of significance.

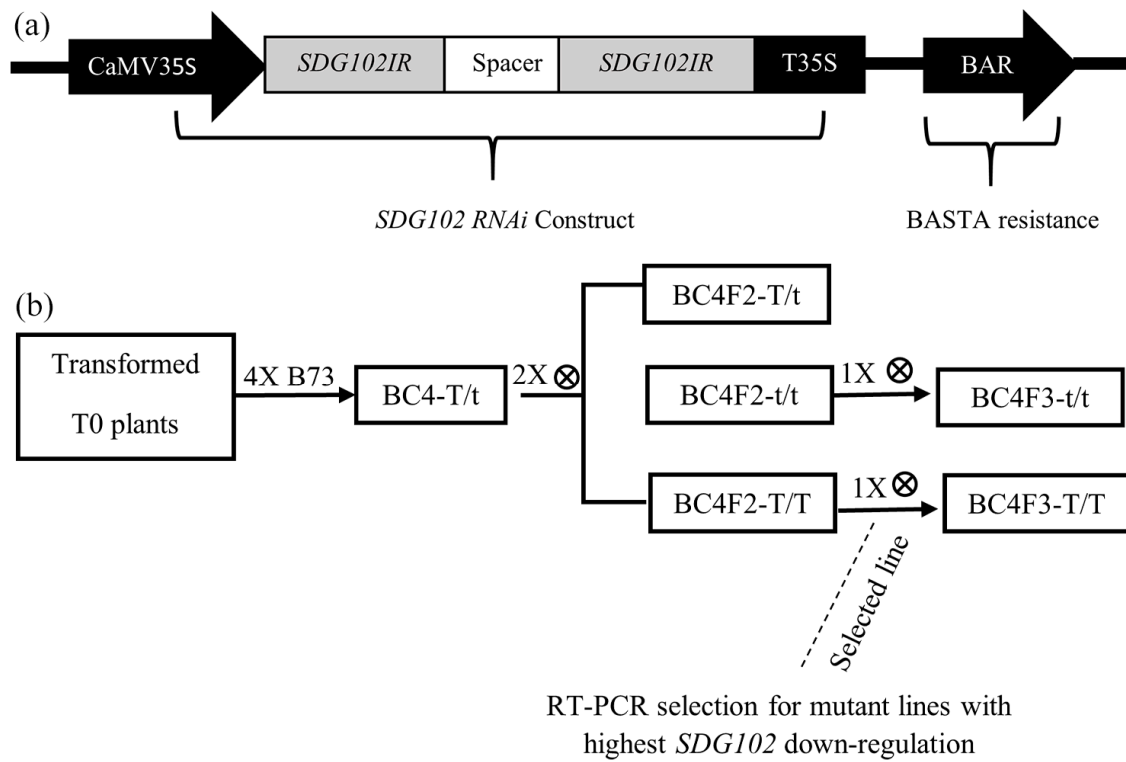


Figure S4 Schematic diagram of vector construction of *SDG102-RNAi* (a) and crossing scheme for *SDG102* down-regulation lines (b).

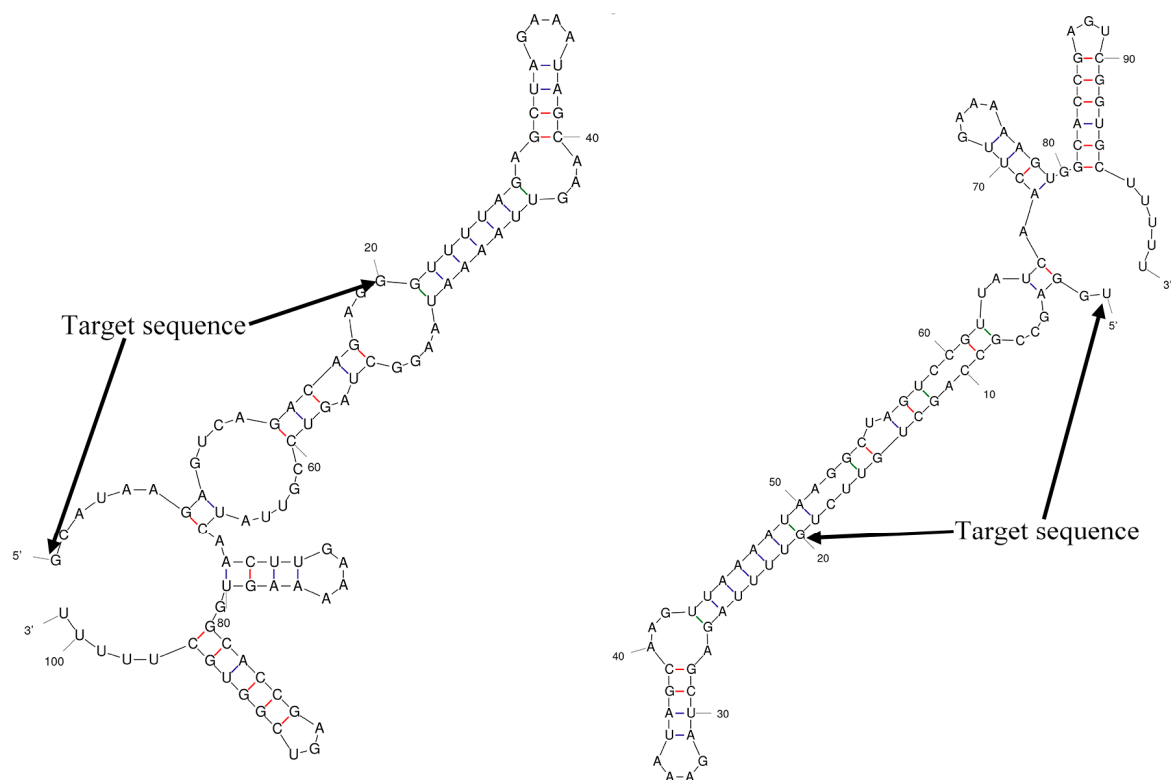


Figure S5 The secondary structures of target-sgRNAs targeting the third exon (left) and the seventh exon (right)

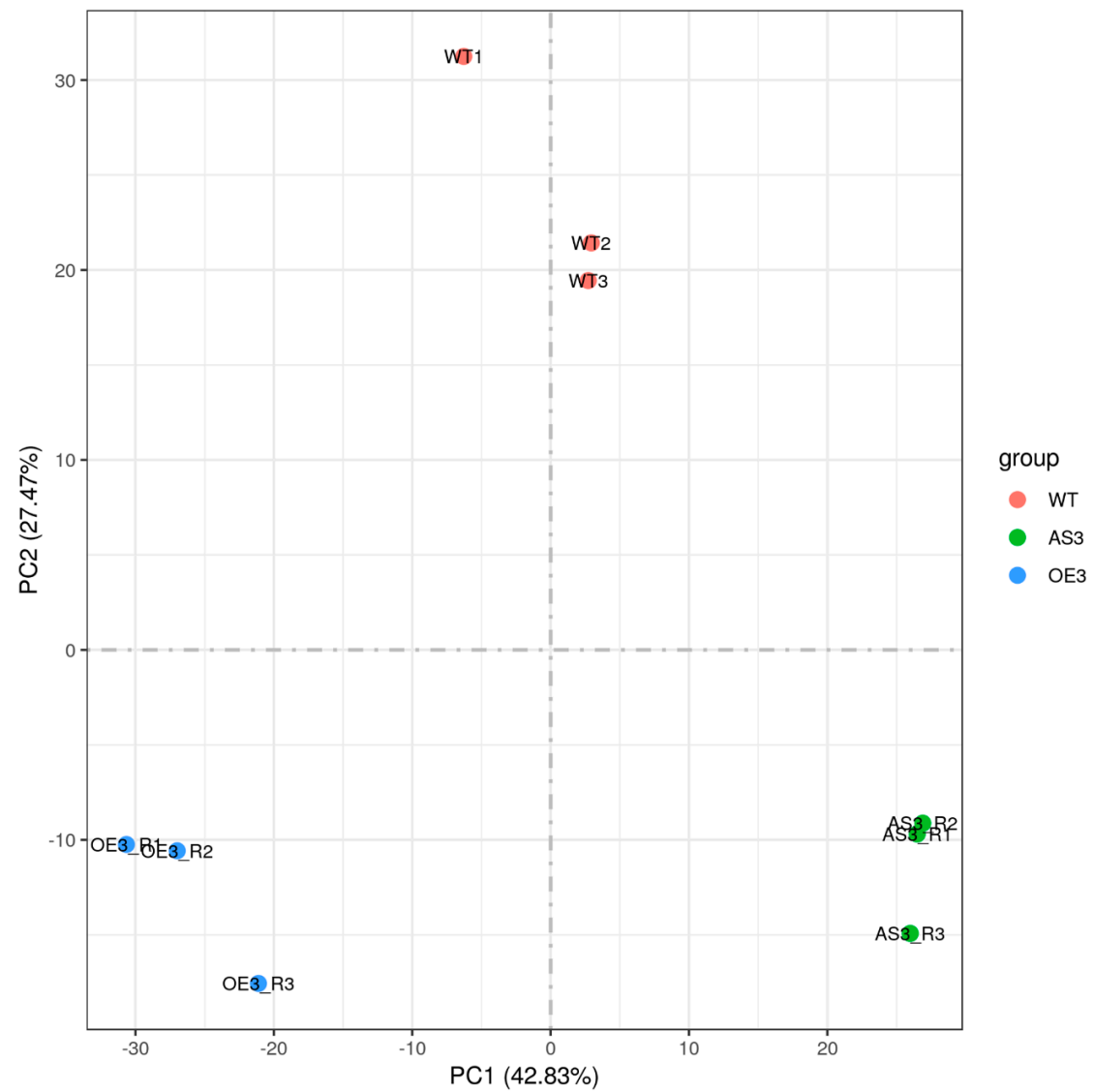


Figure S6 PCA of RNA-Seq data quality. PCA = principal component analysis