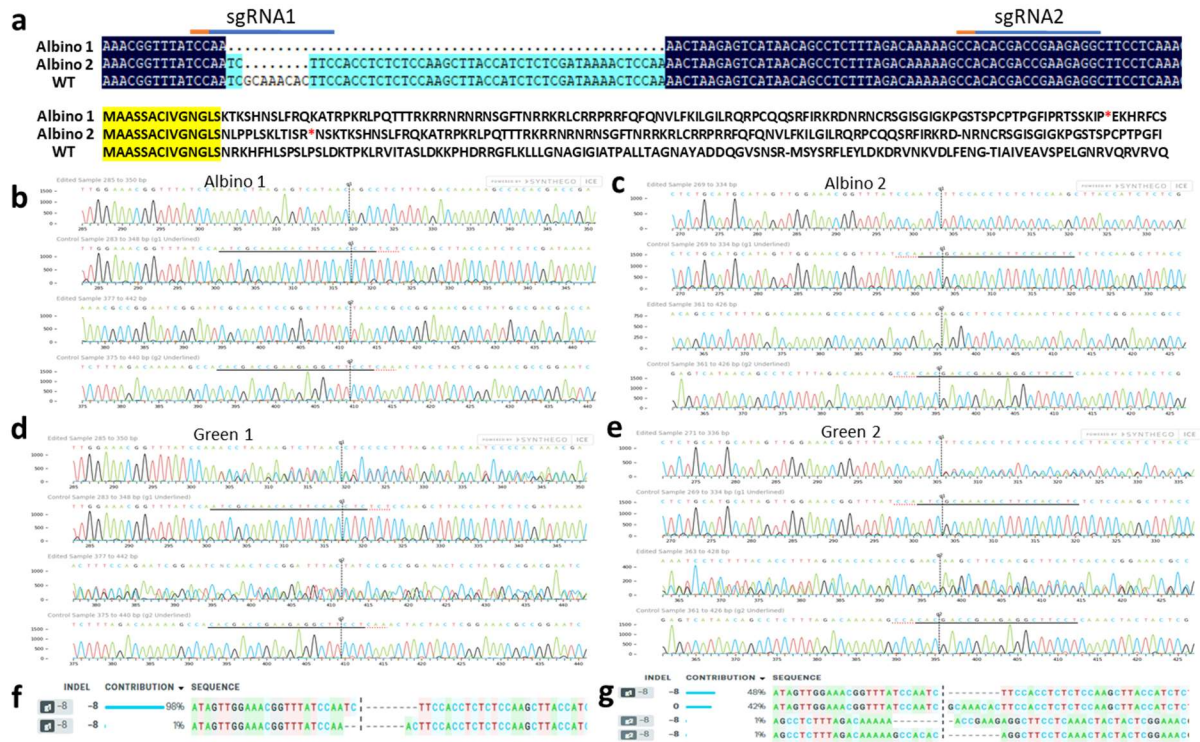


Supplemental Information



Supplemental Figure 1: Sequence analysis of *lsvr2* from two mutants created by CRISPR/Cas9. (a) Nucleic acid sequence alignment revealed 53bp deletion and 8bp deletion in albino cotyledons from the genetic line 26-VAR-1-F_R (albino 1) and 25-VAR-1-F_R (albino 2), respectively (top). Protein sequence alignment showed amino acid change and premature stop codons (asterisks) in both genetic lines (bottom). **(b and c)** Clean peaks in chromatogram alignment of albino phenotype indicated homozygous knockout mutation. **(d and e)** Mixed peaks starting at sgRNA1 in chromatogram alignment of variegated phenotype indicated heterozygous mutation. **(f)** 98% of sequencing contribution are 8bp deletion in the homozygous mutant albino 2. **(g)** 48% of 8bp deletion and 42% wild type sequence were detected in the heterozygous variegated mutant.