



Supplemental Fig S2. Phenotypic observation and molecular detection of the target sites in progenies of F1 lines. (A) The silkworm mutant lines of *DHX8* (KWMTBOMO05973), named by Mutant-1. Compared to WT, the larvae of mutant-1 showed developmental delay and a little small size. The pie chart shows 46% of 12,149 alleles were edited. The top of sequence alignment plot shows the sgRNA and its target gene sequences, the sequences and frequency of edited alleles is shown below. (B) The silkworm mutant lines of *DNA primase large subunit* (KWMTBOMO01805), named by Mutant-2. Compared to WT, the larvae of mutant-2 showed different degrees of developmental delay and the size was obviously smaller. The relatively small individuals cannot cocooning, while the cocoon and pupa of relative large one are significantly smaller than WT. The pie chart shows 82% of 22,422 alleles were edited. The top of sequence alignment plot shows the sgRNA and its target gene sequences, the sequences and frequency of edited alleles is shown below.