

Figure S8 Sanger sequencing analysis of BE-PLUS-mediated iSTOP in the GFP-iSTOP reporter system.

Analysing the mutation of the GFP-iSTOP reporter system by Sanger sequencing. The PCR products were subjected to Sanger sequencing. The primers used for PCR amplification are listed (Supplementary information, Table 7S). The sequencing profiles of the PCR products are aligned to the wild-type genomic sequences of the target vector (top), including the protospacer (Cs are shown in red; others are indicated in black) and PAM (blue). Red arrows indicate the substituted nucleotides, which are represented as overlapped peaks in the sequence chromatogram. Different base editors are labelled on the left. The data shows a representative experiment from three independent experiments.