chr20	DNMT3B	AGAGC$_{5}$C$_{6}$C$_{7}$C$_{8}$C$_{9}$C$_{10}$C$_{11}$TC$_{13}$AAAGAGAGGG
chr2	EMX1	TGC$_{3}$C$_{4}$C$_{5}$C$_{6}$TC$_{8}$C$_{9}$C$_{10}$TC$_{12}$C$_{13}$C$_{14}$TGGC$_{18}$C$_{19}$C$_{20}$AGG
chr2	FAP	GAC$_{3}$AATGC$_{8}$AC$_{10}$ATC$_{13}$AC$_{15}$C$_{16}$AATAAGG
chr8	IDO1	AGGTC$_{5}$ATGGAGATGTC$_{16}$C$_{17}$GTAAGG
chr11	MYOD1	C$_{1}$C$_{2}$AGC$_{5}$AGC$_{8}$TGGTC$_{13}$AC$_{15}$AAAGC$_{20}$TGG
chr4	PPEF2	GTTC$_{4}$ATAC$_{8}$TC$_{10}$AC$_{12}$TGTC$_{16}$GTTGTGG
chr12	IGF1	GAGC$_{4}$GTC$_{7}$TC$_{9}$C$_{10}$GGTC$_{14}$C$_{15}$AGC$_{18}$C$_{19}$GTGG

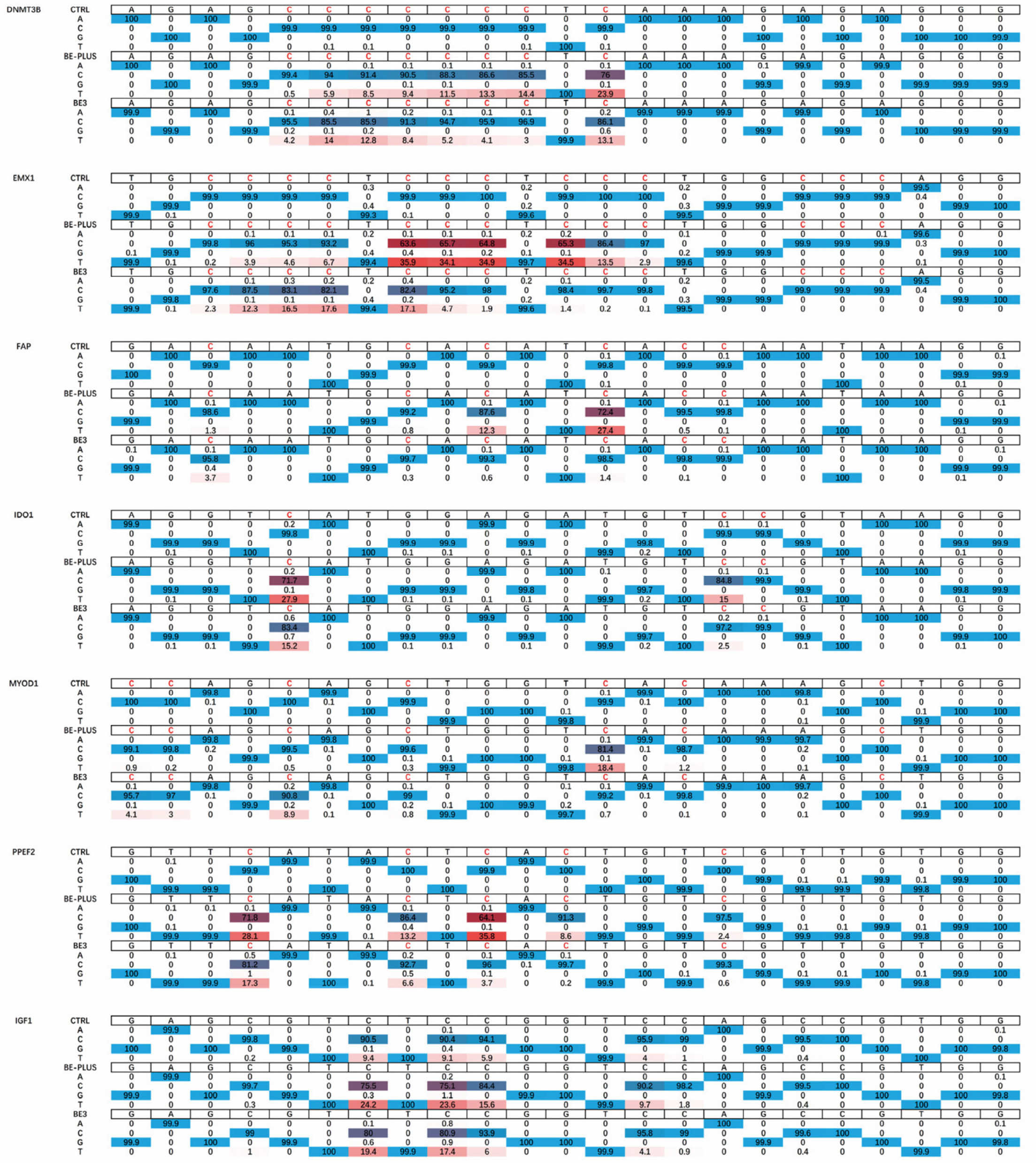

Figure S4 Detection of BE-PLUS activity in endogenous genes by deep sequencing. Deep sequencing assay of C-to-T conversions in all 7 endogenous loci. The target sequences of the 7 genomic loci targeted by BE-PLUS and BE3 are shown (top). PAM sequence are indicated in blue, and Cs are indicated in red. The positions of Cs in the protospacer are indicated by numbers. The chromosome distribution and gene names of each editing site is shown (left). The base editing of 7 genomic sites for BE-PLUS and BE3 were analysed by high-throughput sequencing.