

Fig. S3.

a

WT_BAX	CCCGGCACTGGTTCTCCTCTCCTGCAGGATGATTGCCGCCGTGGACACAGACTCCCCCGAGAGGTCTTTCCGAGTGGCAGCTGACATGTTTCTG
Octa/MCL-1/BAX KO BAX	CCCGGCACTGGTTCTCCTCTCCTGCAGGATGATTGCC-CCGTGGACACAGACTCCCCCGAGAGGTCTTTCCGAGTGGCAGCTGACATGTTTCTG

b

WT BAK	GCATGCCTCCTGCTCCTACAGCACCATGGGCAGGTGGACGGCAGCTGCCATC-ATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCA
Octa/MCL-1/BAK KO BAK	GCATGCCTCCTGCTCCTACAGCACCATGGGCAGGTGGACGGCAGCTGCCATC A ATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCCAGACCA

Fig. S3 Mutations in the targeted *BAX* and *BAK* loci of Octa/*MCL-1/BAX* KO and Octa/*MCL-1/BAK* KO cells.

(a) Genomic sequence of *BAX* around the CRISPR target site in Octa/*MCL-1/BAX* KO cell aligned with the wild-type sequence. (b) Genomic sequence of *BAK* around the CRISPR target site in Octa/*MCL-1/BAK* KO cells aligned with the wild-type sequence. CRISPR target sites are underlined.