

Supplementary information to:

## The genome-wide mutational consequences of DNA hypomethylation

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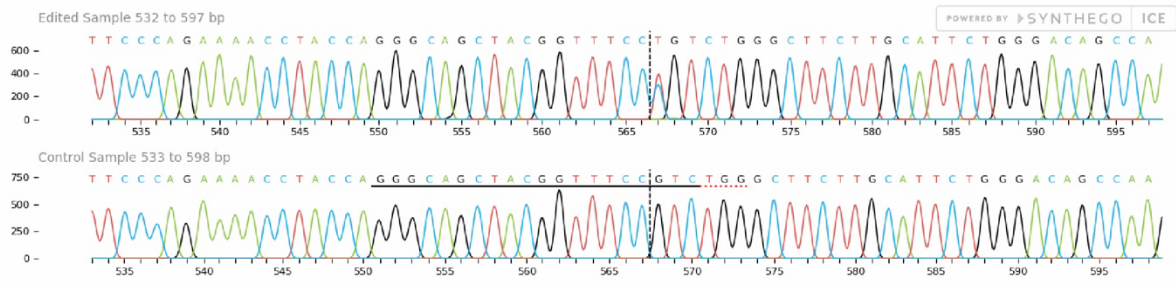
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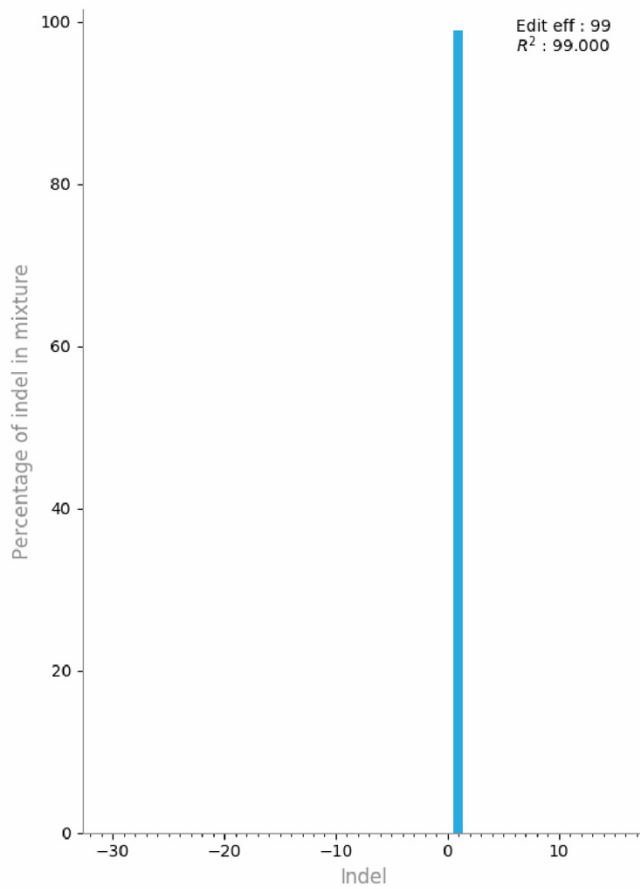
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**a**



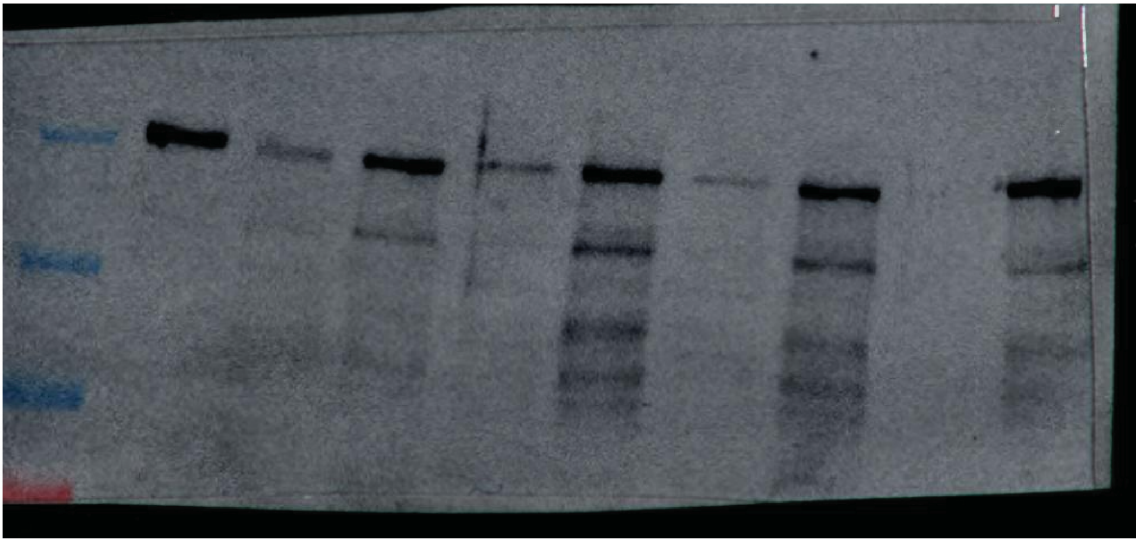
**b**



Supplementary Figure 1: Validation of TP53 knockout

(a) Sanger sequencing result of PCR amplified region in TP53 from RPE-1 cells targeted by CRISPR/CAS9 (top panel) and control cells (bottom panel). Line indicates the sgRNA sequence that was used for targeting. (b) CRISPR edits were inferred from the Sanger trace with the ICE CRISPR Analysis Tool from Synthego<sup>69</sup>.

a



b



Supplementary Figure 2: Full length original western blots for which cropped versions are shown in Figure 1c. (a) Uncropped image for DNMT1. (b) Uncropped image for Tubulin. For both panels: lane 1 is protein ladder, lane 2 are untreated cells at start of the experiment, lanes 3-8 are *DNMT1kd* knockdown cells treated with or without doxycycline for 1 week (lanes 3+4), 2 weeks (lanes 5+6), 3 weeks (lanes 7+8), and 4 weeks (lanes 9+10).