



Supplementary Fig. S9: A) Homology space covered by 2818 off-target sites sequenced with at least 500 read depth in second round of hybrid capture in HEK293T/Cas9 cells followed by targeted deep sequencing. **B)** Read depth from hybrid capture sequencing averaged across three replicates of treated and untreated samples for 2818 sites (Red line denotes median of 1581 reads). **C)** Indel frequency difference between treated and control samples for 2818 sites grouped by edit distance with respect to the gRNA sequence. Numbers in red indicate the number of nominated sites that have a certain edit distance.