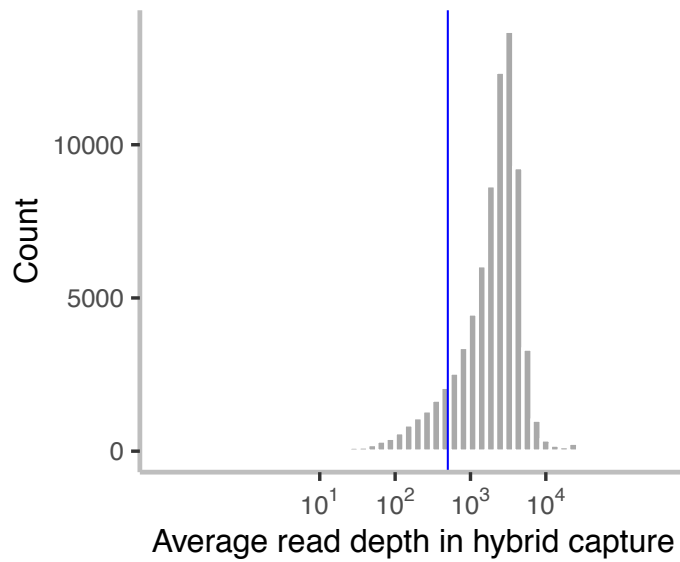
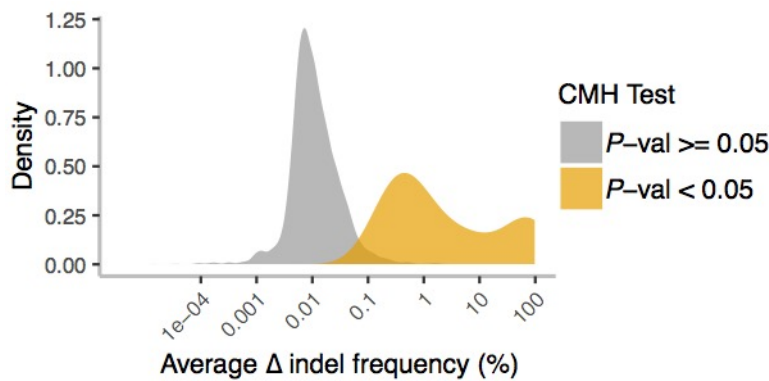


**A****B**

**Supplementary Fig. S5: A)** Distribution of read depth obtained from hybrid capture followed by sequencing at all sites across eight gRNAs in HEK293T/Cas9 cells, averaged across three treated and three untreated control samples for each site. Blue line denotes the 500 read threshold. Median coverage at sites across eight gRNAs was 2313.33 reads. **B)** Distribution of average indel frequency difference between treated and untreated control samples. Sequence-confirmed edited sites (i.e. sites with at least 500 average read depth across all samples, a statistically significant difference (CMH test  $P$ -value with BH correction  $< 0.05$ ) in indel frequency between treated and control samples, and indel frequency difference of at least 0.2% in at least one pair of treated and untreated samples) are shown in ochre.