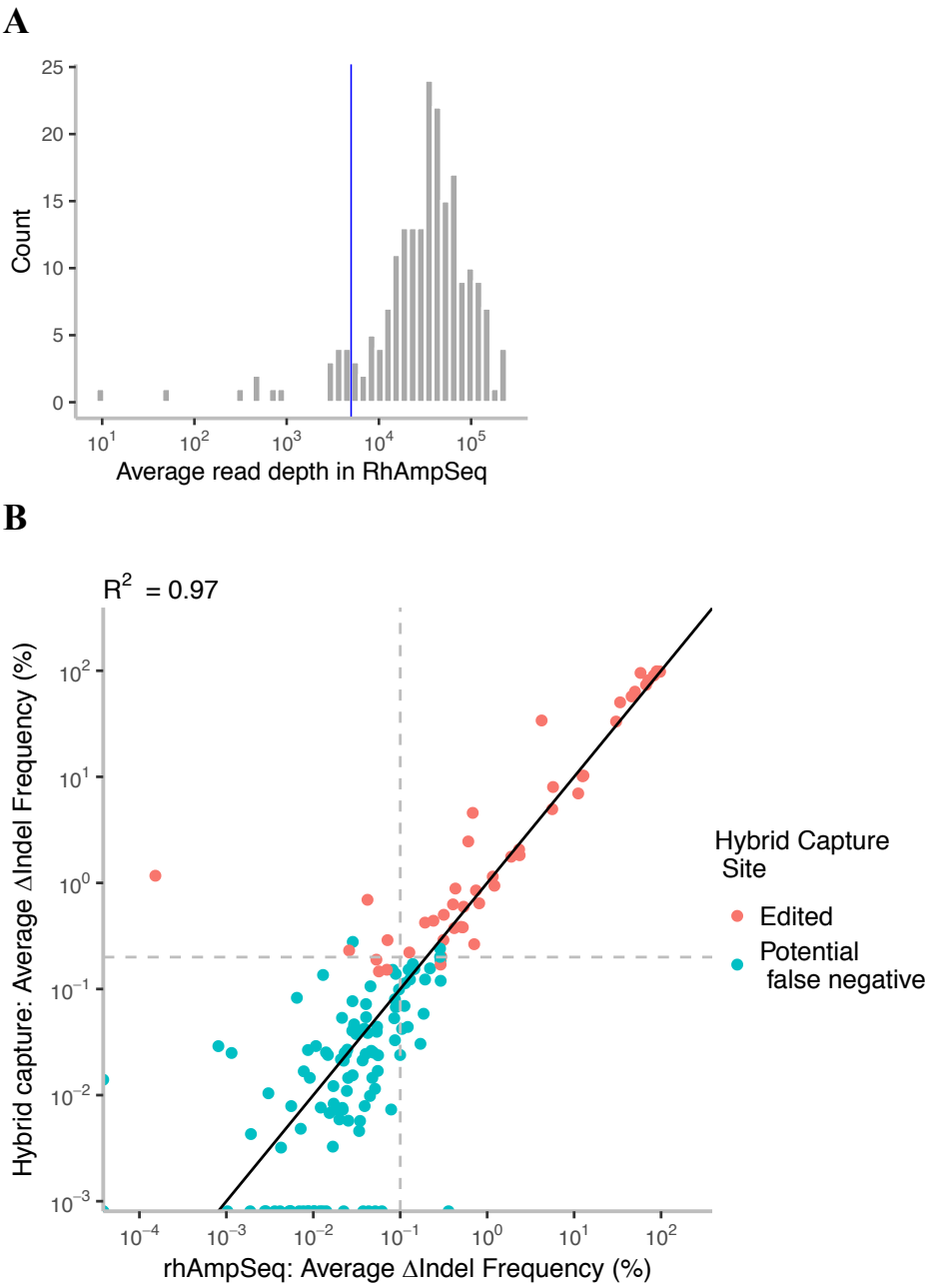

Supplementary Fig. S10: A) Average read depth obtained in rhAmpSeq amplicon sequencing on 207 sites in three replicates of treated and untreated samples (9 on-target sites, 40 sequence-confirmed off-target sites, and 152 potential false negatives of sequence confirmation step). Blue line denotes 5000 reads. **B)** Correlation between average difference in indel frequency measured by rhAmpSeq and hybrid capture for 201 sites with greater than 500 average read depth. Red points denote sites that were sequence-confirmed as edited by hybrid capture; blue points denote sites that were nominated by all three genome-wide assays but found to be unedited by hybrid capture. Dashed grey lines denote 0.2% indel frequency difference. Black line denotes $y = x$. The outlier (edited site, near the y-axis) is a potential false positive of the hybrid capture assay described in Supplementary Fig. S7.