Supplementary Table S9: Impact of hybrid capture parameters on number of sites sequence-confirmed as edited. Read depth threshold was varied from 100 to 500 reads. Benjamini-Hochberg adjusted CMH *P*-value threshold was varied from 0.05 to 0.15. An additional site was observed when the Benjamini-Hochberg adjusted CMH *P*-value threshold was raised to 0.15 at 500 read depth threshold. This site had an average frequency difference of 0.201% between treated and control samples.

Read depth threshold	**Number of sites sequenced above threshold**	**Multiple hypothesis correction**	**BH adjusted CMH *P*-value threshold**	**Number of sites edited**
500	66165	Benjamini-Hochberg	0.05	51
400	67771	Benjamini-Hochberg	0.05	51
300	69454	Benjamini-Hochberg	0.05	51
200	71230	Benjamini-Hochberg	0.05	51
100	73174	Benjamini-Hochberg	0.05	51
500	66165	Benjamini-Hochberg	0.1	51
500	66165	Benjamini-Hochberg	0.15	52