



Supplementary Fig. S6: Average indel frequency (%) differences between treated and control samples for 51 edited sites grouped by nomination in genome-wide assays. The first box contains sites nominated by all three replicates of all three genome-wide assays (n = 45). The second box contains the one site not nominated by any genome-wide assay. The third box has sites that were nominated by fewer than 3 replicates of one or more genome-wide assays (n= 5). Red line denotes 0.5% indel frequency difference.