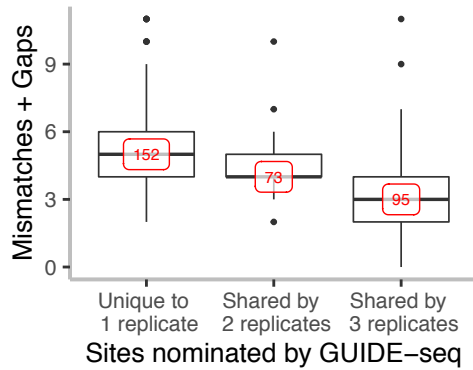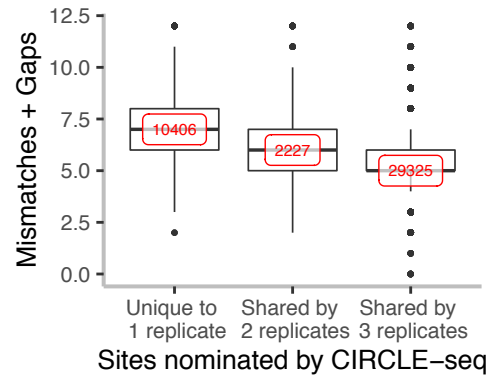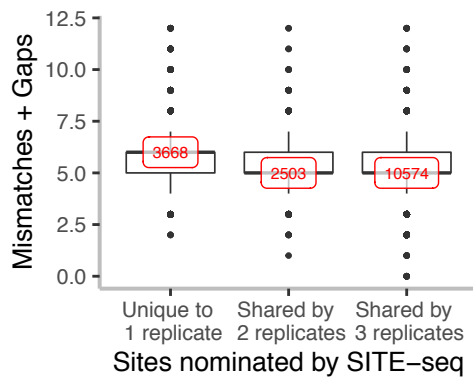**A**

B

C

Supplementary Fig. S3: Edit distances (mismatches + gaps) of site nominated by single or multiple replicates of homology-independent nomination methods across eight gRNAs are shown for **A)** GUIDE-seq **B)** CIRCLE-seq and **C)** SITE-seq. The x-axis represents overlap within the replicates of the genome-wide assays. The y-axis shows the edit distances. The distribution of edit distances for sites nominated by all three replicates (3rd box in each plot) were significantly different from the distributions of edit distances for sites nominated by one or two replicates (1st and 2nd box in each plot) for all three methods (Wilcoxon *P*-value < 0.05).