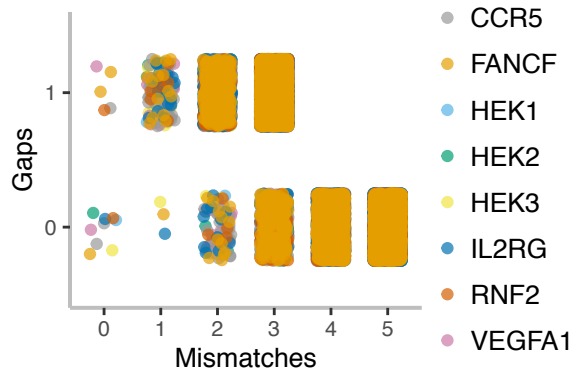
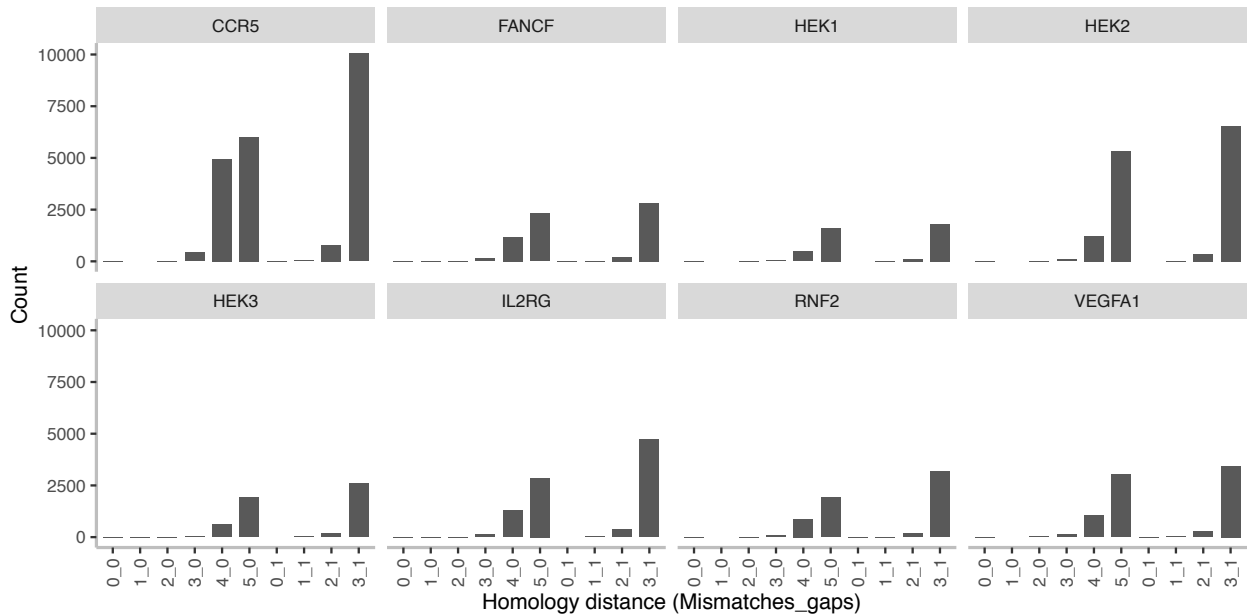


A**B**

Supplementary Fig. S1: A) Sites with up to 5 MM with 0 gaps or with up to 3 MM with 1 gap for eight gRNAs were interrogated with hybrid capture enrichment followed by sequencing. **B)** Number of bioinformatically predicted sites at different mismatch_gap homology distances for eight gRNAs used in this study.