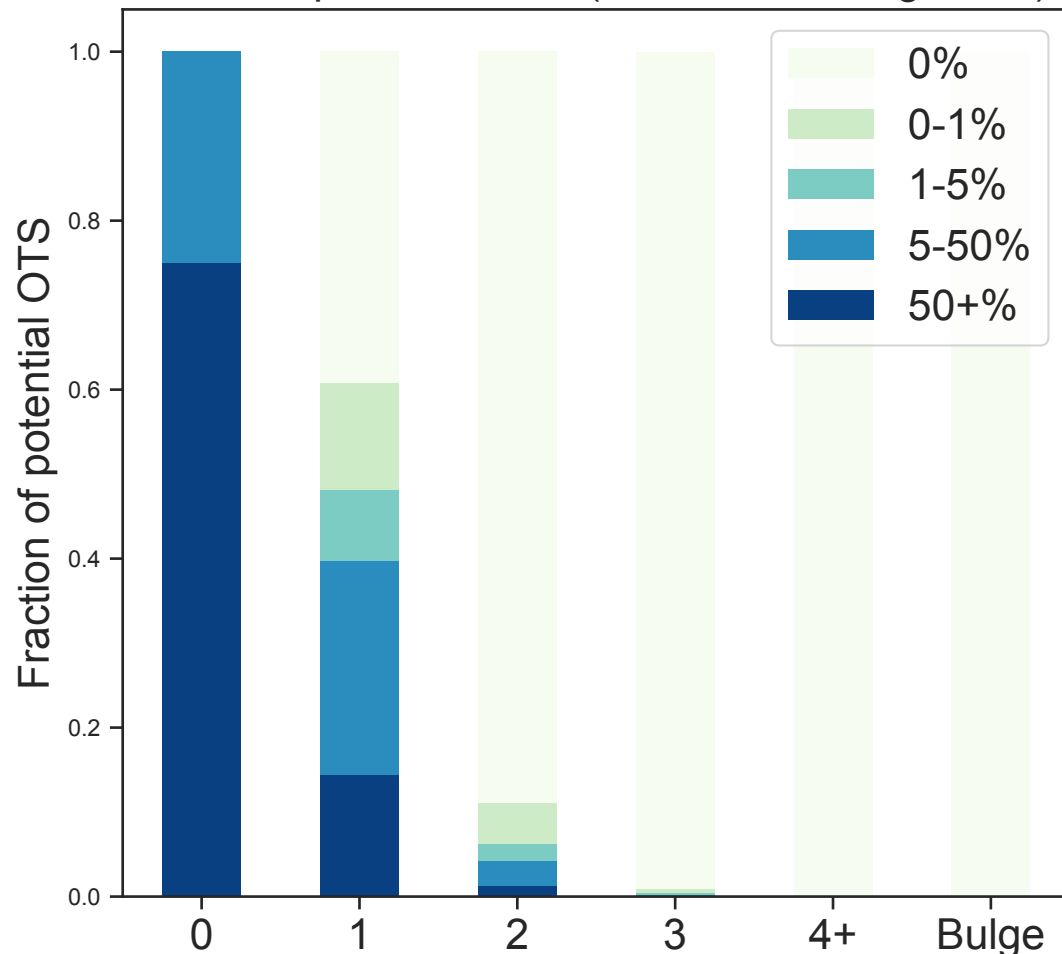
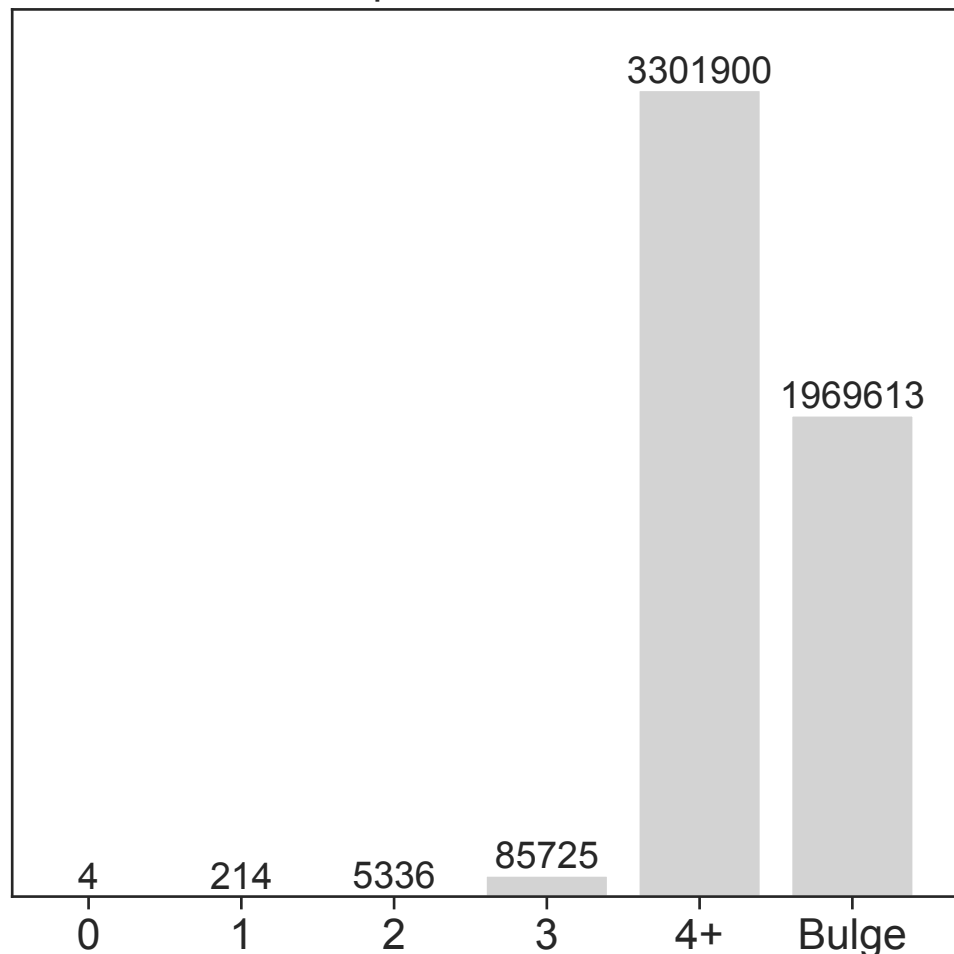


GUIDE-seq of off-target sites (OTS) for 114 sgRNAs (Yaish & Orenstein, 2024)

potential OTS

Reads at potential OTS (% relative to target site)



Mismatches in SDR to target site