

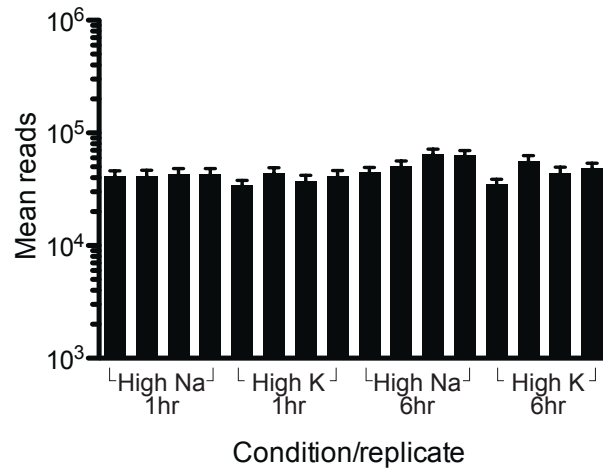
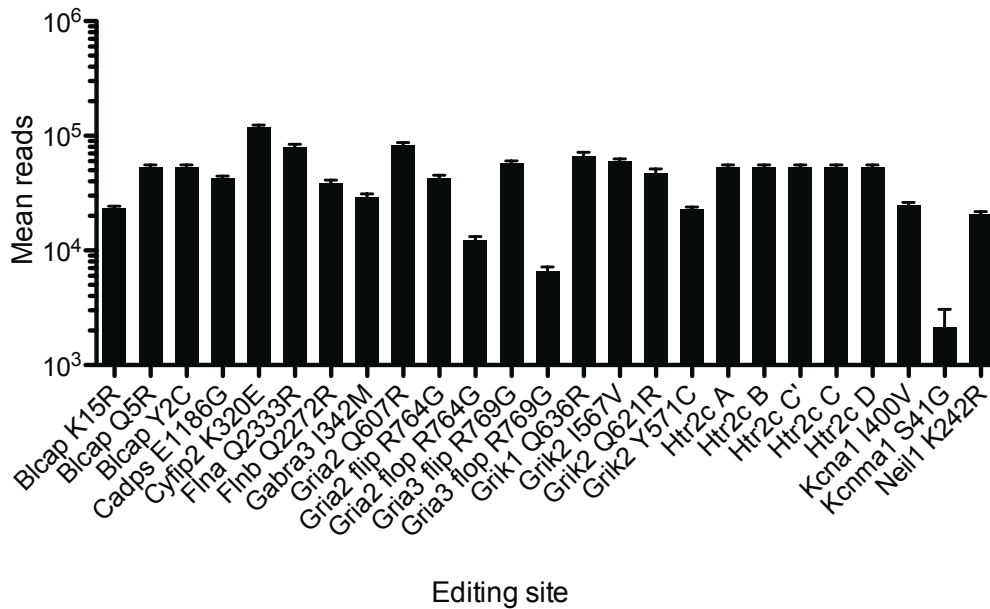
A**B**

Figure S1 Read uniformity across conditions and editing sites. Counts of the average number of sequencing reads per editing site and per condition in one multiplexed Illumina sequencing run. **a**, Mean number of sequencing reads per condition/replicate averaged across editing sites ($n=25$). In each condition in the sequencing run (High Na 1hr, High K 1hr, High Na 6hr, High K 6hr), reads counts are plotted for 4 separate biological replicates. **b**, Mean number of sequencing reads per editing site averaged across different conditions/replicates ($n=12$). In both panels, error bars indicate s.e.m.