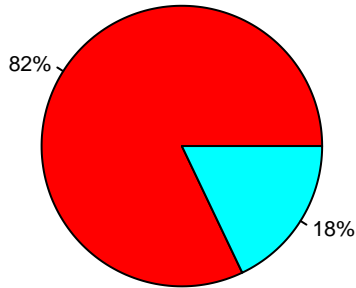
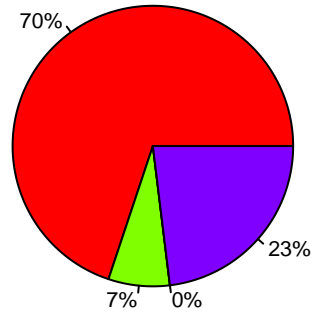
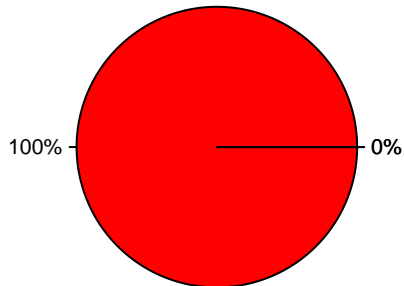


Percentage of reads that map at least 30bp

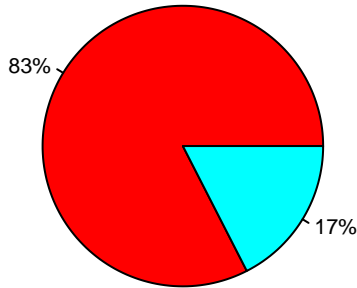
● Mapped 30bp ● Unmapped 30bp

Statistics of reads that mapped to 30bp

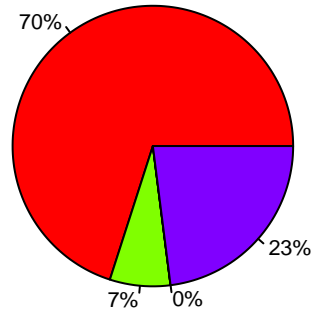
● Map 40bp, m = 0 ● Read size < 37bp
● Map 40bp, 1<=m<=3 ● Map 40bp, m > 3

Statistics of reads that did not map to 30bp

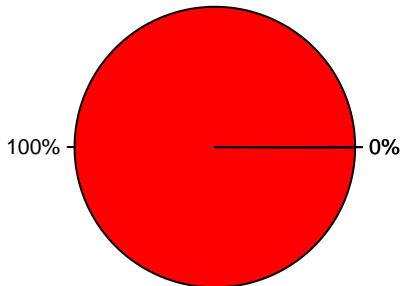
● Map 1 guide ● Map < 1 guide
● Map 1 guide multiple times

Percentage of reads that map at least 30bp

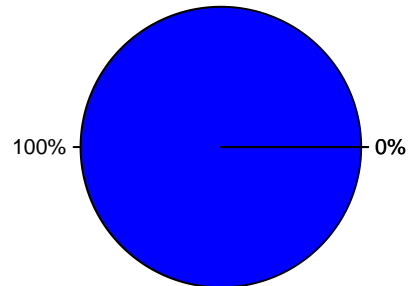
● Mapped 30bp ● Unmapped 30bp

Statistics of reads that mapped to 30bp

● Map 40bp, m = 0 ● Read size < 37bp
● Map 40bp, 1 <= m <= 3 ● Map 40bp, m > 3

Statistics of reads that did not map to 30bp

● Map 1 guide ● Map < 1 guide
● Map 1 guide multiple times

Statistics of reads that mapped a guide multiple times

● Repeated sgRNA ● Other
● Recombination

Alignment information

