replicate-1, vir

number of read pairs

- aligned (8.1×10^6)
- outside gene (0)
- unaligned (1.4×10^5)
- unpaired (8.5×10^5)
- excess N (8.4×10^3)
- low Q (1.2×10^6)
- filtered (0)
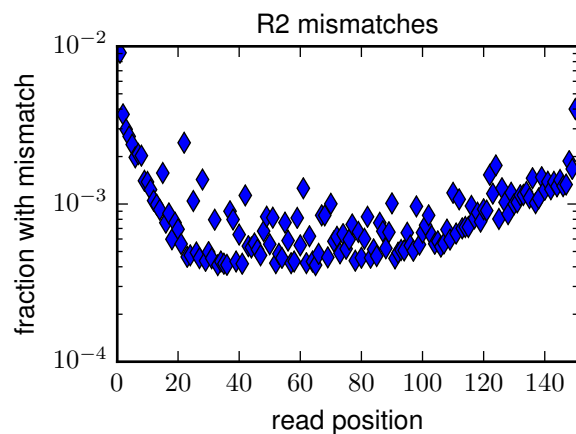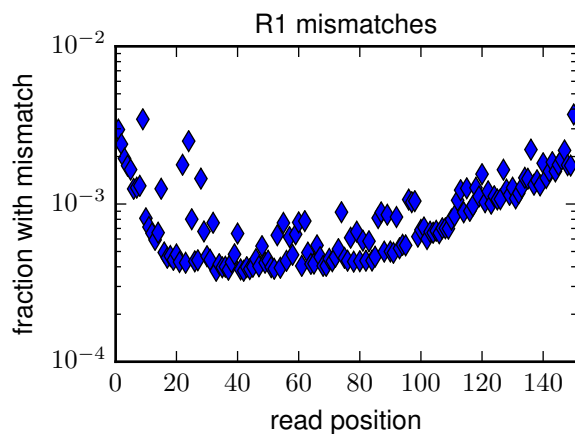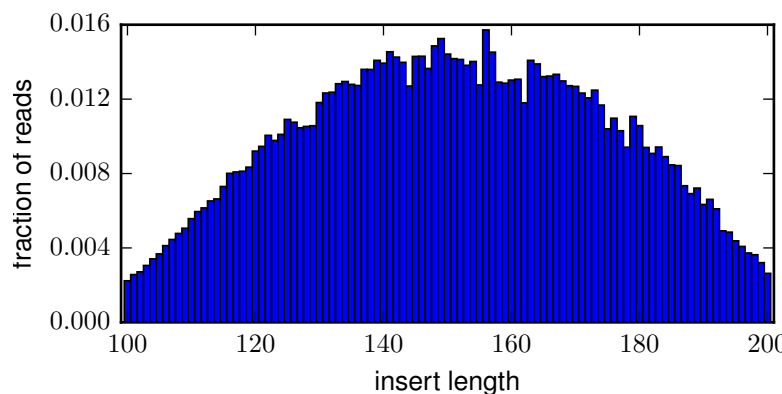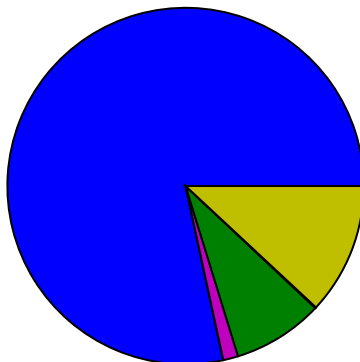
Alignment settings

minq = 25.0 Both reads must have mean Q-value $\geq$ this.

maxn = 5 Number of N/n nucleotides must be $\leq$ this for each read.

minoverlap = 100 Overlap between paired reads must be $\geq$ this.

maxrm = 1 Number of mismatches in paired reads overlap must be $\leq$ this.

maxa1m = 1 Number of mismatches between R1 and its adaptor must be $\leq$ this.

maxa2m = 1 Number of mismatches between R2 and its adaptor must be $\leq$ this.

maxgenem = 10 Neither read can have > than this many mismatches with target sequence after trimming adaptor.