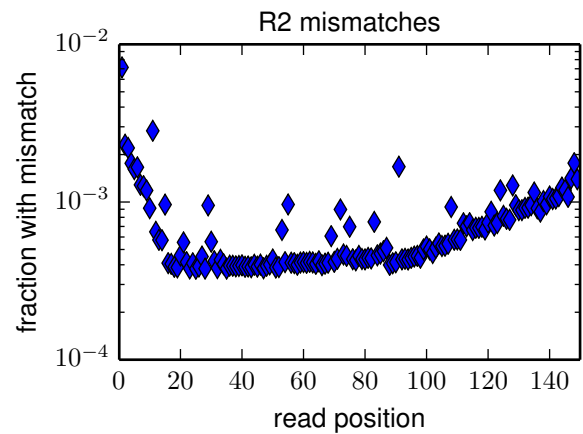
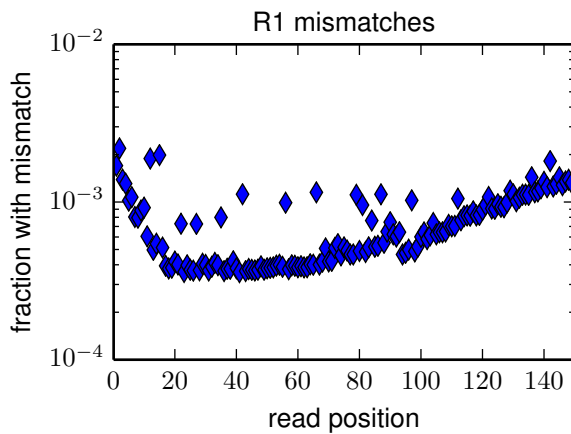
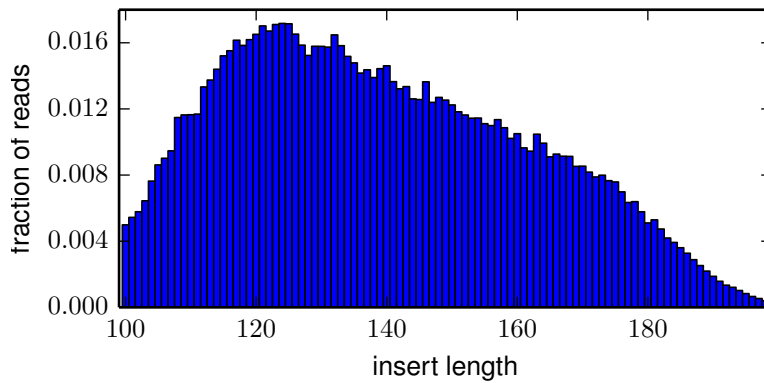
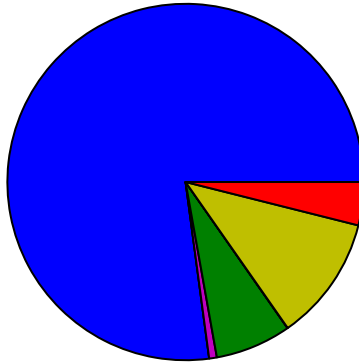


PR8_replicate_3, virus

number of read pairs

- aligned (1.3×10^7)
- outside gene (0)
- unaligned (1.2×10^5)
- unpaired (1.1×10^6)
- excess N (4.4×10^3)
- low Q (1.9×10^6)
- filtered (6.5×10^5)



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.