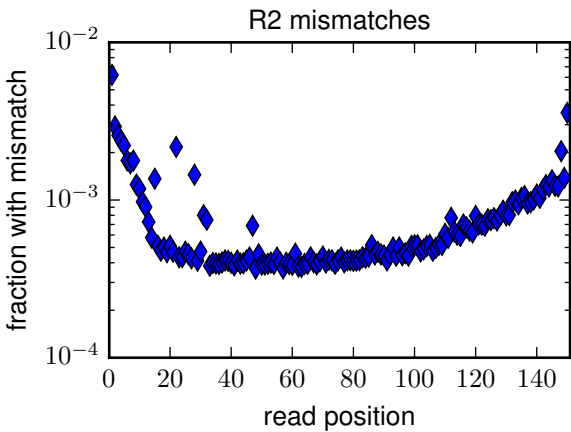
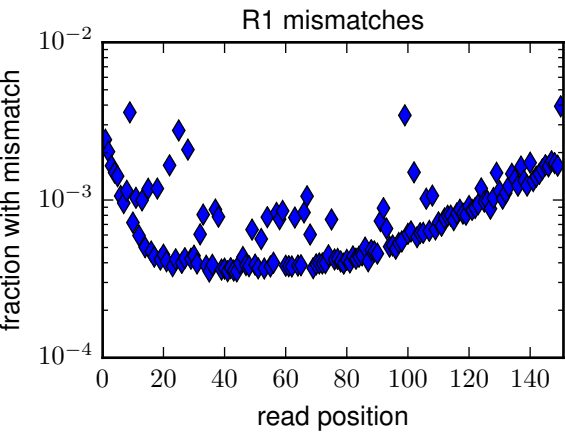
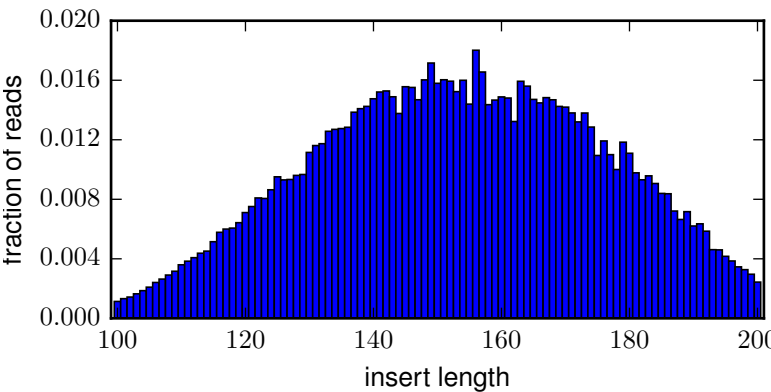
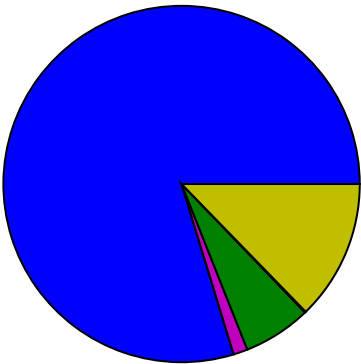


replicate-2, vir

number of read pairs

- aligned (1.2×10^7)
- outside gene (0)
- unaligned (2.0×10^5)
- unpaired (9.6×10^5)
- excess N (1.5×10^4)
- low Q (2.0×10^6)
- 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.