replicate-2, mutvir_MS
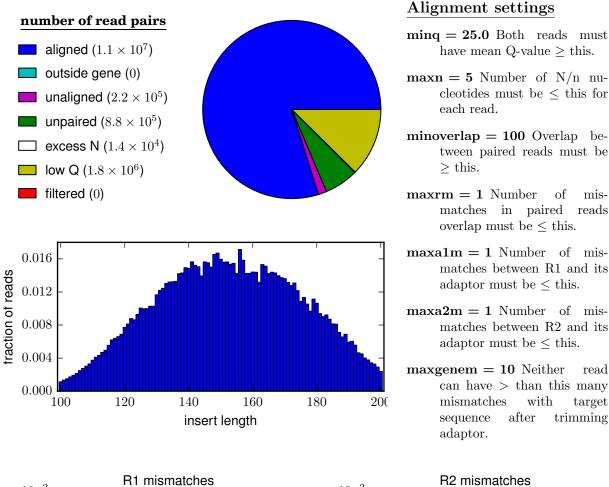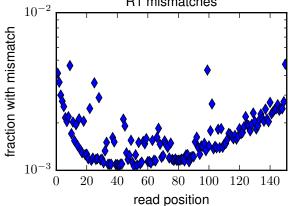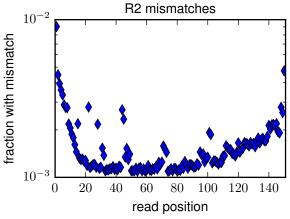
number of read pairs

- ■ aligned (1.1×10^7)
- ■ outside gene (0)
- ■ unaligned (2.2×10^5)
- ■ unpaired (8.8×10^5)
- □ excess N (1.4×10^4)
- ■ low Q (1.8×10^6)
- ■ 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.