Aichi68C_replicate_2, DNA

number of read pairs

- aligned (1.3×10^7)
- outside gene (0)
- unaligned (1.3×10^5)
- unpaired (9.8×10^5)
- excess N (1.6×10^4)
- low Q (1.9×10^6)
- filtered (2.1×10^5)
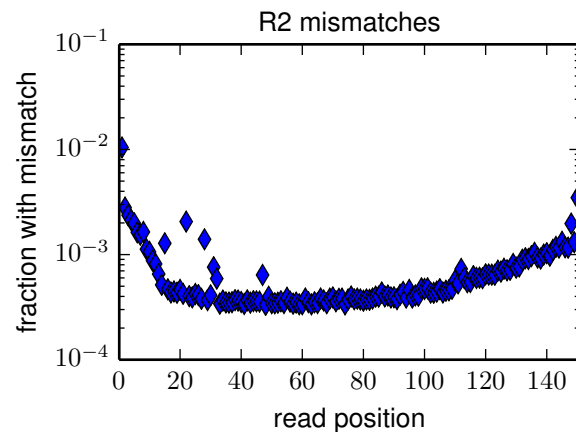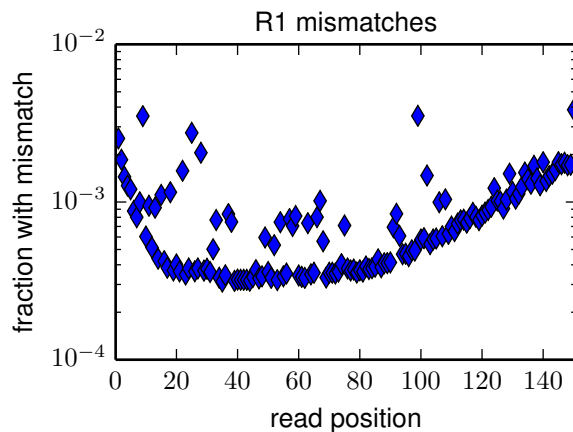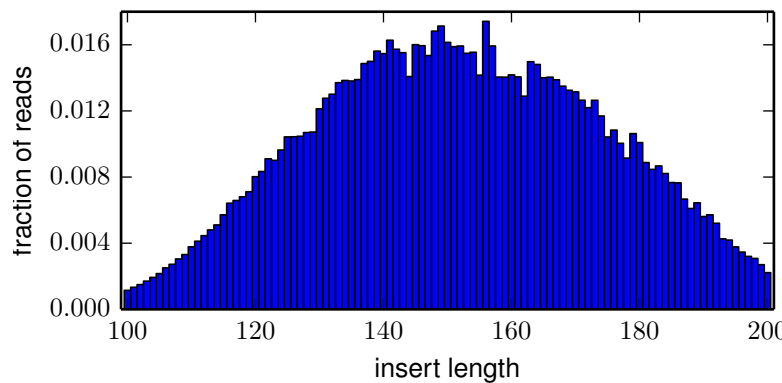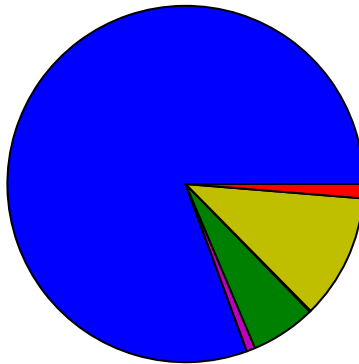
Alignment settings

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.