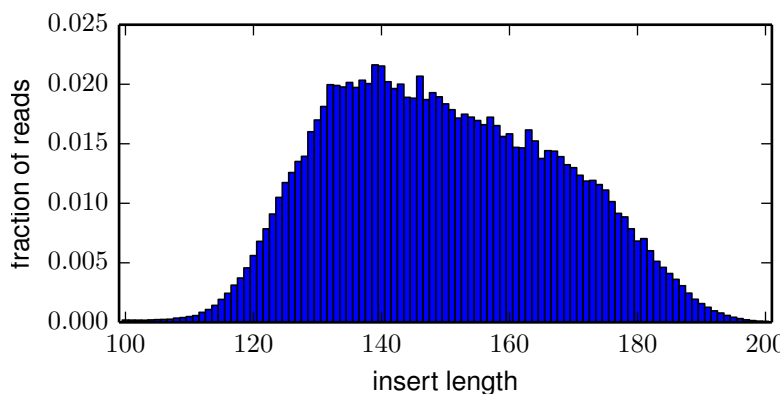
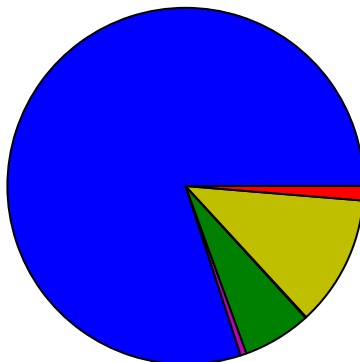
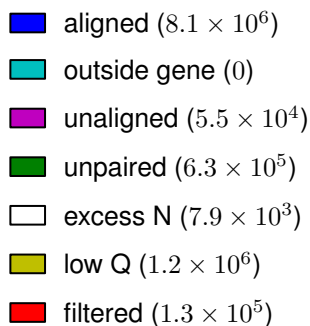


## PR8\_replicate\_1, DNA

### number of read pairs



### 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.

