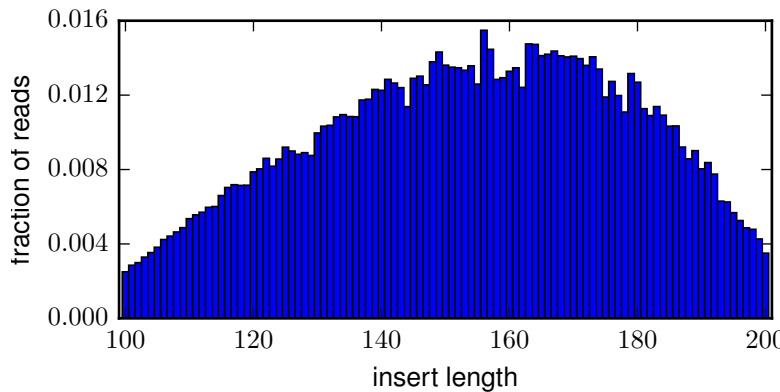
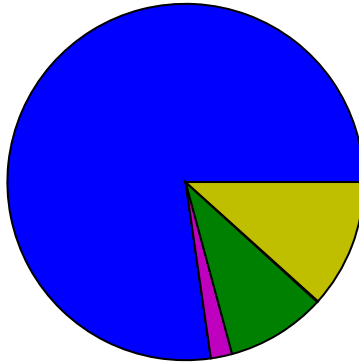


## replicate-1, mutvir\_MS

### number of read pairs

- aligned ( $5.9 \times 10^6$ )
- outside gene (0)
- unaligned ( $1.5 \times 10^5$ )
- unpaired ( $6.9 \times 10^5$ )
- excess N ( $6.1 \times 10^3$ )
- low Q ( $8.9 \times 10^5$ )
- 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.

