

# Quality Filtering:

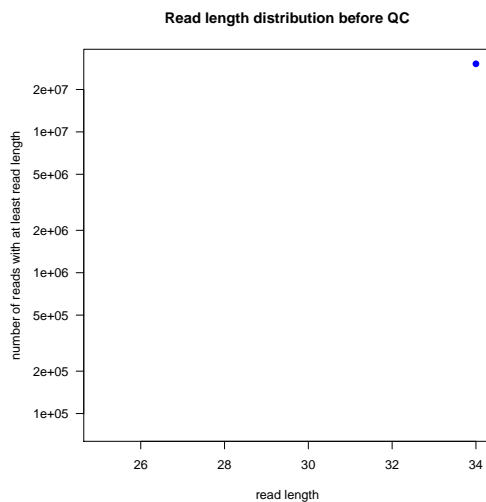


Figure 1: Read length reverse cumulative distribution before filtering

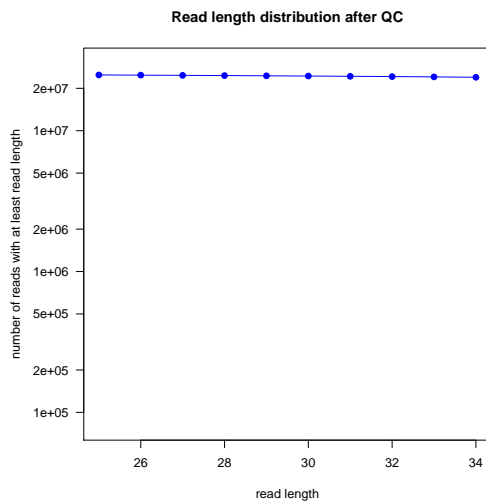


Figure 2: Read length reverse cumulative distribution after filtering

# Adaptor Finding:

## 0.1

Chosen adaptor: `ACACTCTTTCCCTACACGACGCTCTTCCGATCT`

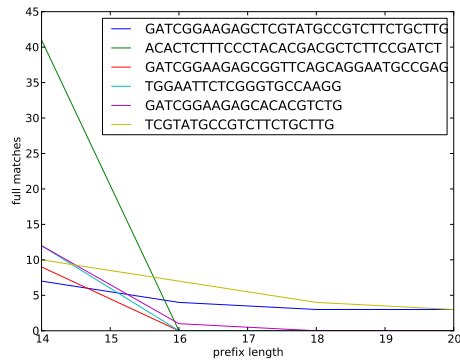


Figure 3: Plot for Adaptor Finding: Length of Adaptor versus Full Matches

## Adaptor Removal and Quality Filtering:

### 0.2

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# 5'/3' adaptors      : / ACACTCTTTCCTACACGACGCTCTCCGATCT
# 5'/3' min aln. len. : 0 / 0
# min len (1 mm)     : 7
# min len (2 mm)     : 10
# max mm (full)      : 2
# sequence filter     : on
# Thu Dec 4 19:42:51 2014: READING SEQUENCES
# Thu Dec 4 19:47:42 2014: done reading sequences (n=22982671)
# Thu Dec 4 19:47:42 2014: REMOVING ADAPTORS
# Thu Dec 4 20:10:12 2014: done removing adaptors (n=22980769)
# Thu Dec 4 20:10:12 2014: FILTERING AND OUTPUT
# Thu Dec 4 20:15:45 2014: done FILTERING AND OUTPUT
# SUMMARY:
# Number of sequences:
#
#           input sequences : 24887763 (100.0%)
#           unique sequences : 22982671 ( 92.3%)
#
# Adaptor removal:
#           full matches to 5'-adaptor : 0 ( 0.0%)
#   inexact suffix matches to 5'-adaptor : 0 ( 0.0%)
#     exact suffix matches to 5'-adaptor : 0 ( 0.0%)
#           full matches to 3'-adaptor : 0 ( 0.0%)
#   inexact prefix matches to 3'-adaptor : 80576 ( 0.3%)
#     exact prefix matches to 3'-adaptor : 8733777 ( 35.1%)
#
#           total matches to 5'-adaptor : 0 ( 0.0%)
#           total matches to 3'-adaptor : 8814353 ( 35.4%)
#
#           unique sequences (w/o adaptors) : 22980769 ( 92.3%)
#
# Sequence filtering:
#           5'-adaptor alignment too short : 0 ( 0.0%)

```



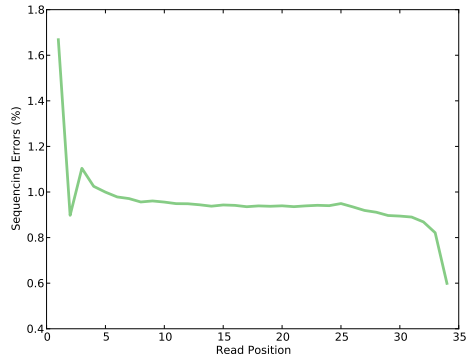


Figure 4: Fraction of all reads that had an error at read position

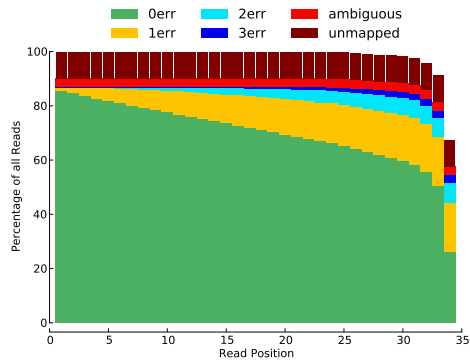


Figure 5: Fraction of all reads that have a certain mapping error up to read position

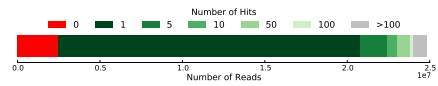


Figure 6: Number of reads that have a certain number of hits

## Fragment Size Estimation:

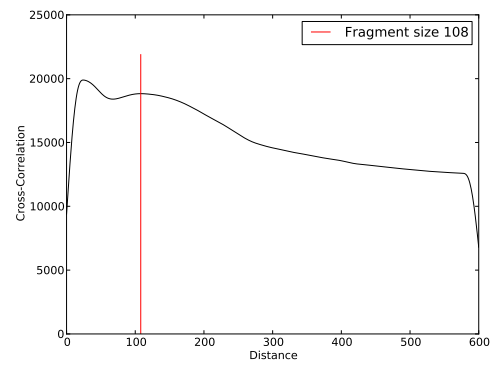


Figure 7: Fragment size correlation plot