

Quality Filtering:

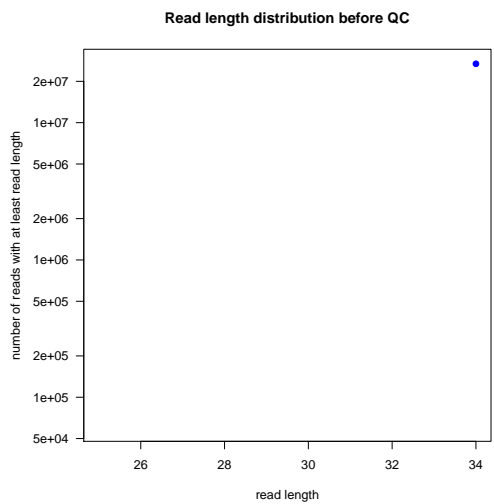


Figure 1: Read length reverse cumulative distribution before filtering

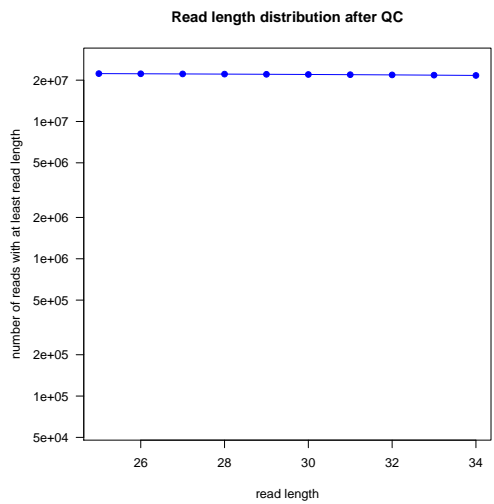


Figure 2: Read length reverse cumulative distribution after filtering

Adaptor Finding:

0.1

Chosen adaptor: GATCGGAAGAGCTCGTATGCCGTCCTCTGCTTG

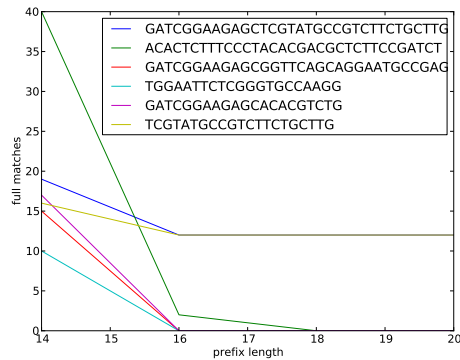


Figure 3: Plot for Adaptor Finding: Length of Adaptor versus Full Matches

Adaptor Removal and Quality Filtering:

0.2

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# 5'/3' adaptors      : / GATCGGAAGAGCTCGTATGCCGTCTTCTGCTTG
# 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 19:36:52 2014: READING SEQUENCES
# Thu Dec 4 19:41:03 2014: done reading sequences (n=20515658)
# Thu Dec 4 19:41:03 2014: REMOVING ADAPTORS
# Thu Dec 4 20:01:36 2014: done removing adaptors (n=20513540)
# Thu Dec 4 20:01:36 2014: FILTERING AND OUTPUT
# Thu Dec 4 20:06:34 2014: done FILTERING AND OUTPUT
# SUMMARY:
# Number of sequences:
#
#           input sequences : 22325260 (100.0%)
#           unique sequences : 20515658 ( 91.9%)
#
# 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 : 1072 ( 0.0%)
#   inexact prefix matches to 3'-adaptor : 25748 ( 0.1%)
#     exact prefix matches to 3'-adaptor : 6600653 ( 29.6%)
#
#           total matches to 5'-adaptor : 0 ( 0.0%)
#           total matches to 3'-adaptor : 6627473 ( 29.7%)
#
#           unique sequences (w/o adaptors) : 20513540 ( 91.9%)
#
# Sequence filtering:
#           5'-adaptor alignment too short : 0 ( 0.0%)

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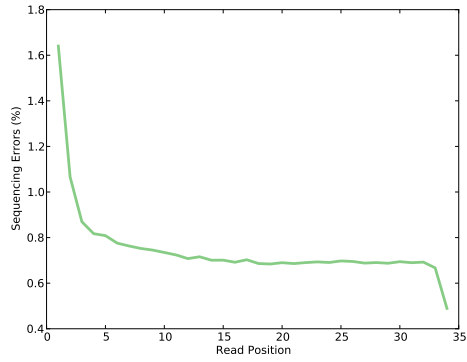



Figure 4: Fraction of all reads that had an error at read position

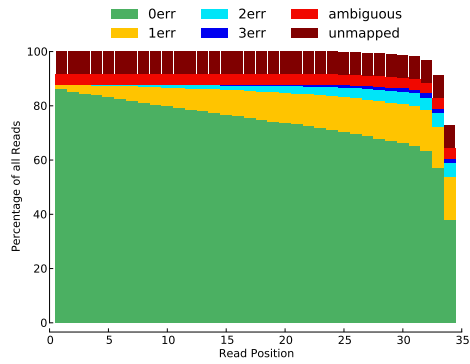


Figure 5: Fraction of all reads that have a certain mapping error up to read position

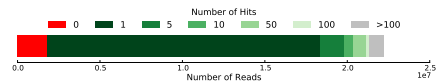


Figure 6: Number of reads that have a certain number of hits

Fragment Size Estimation:

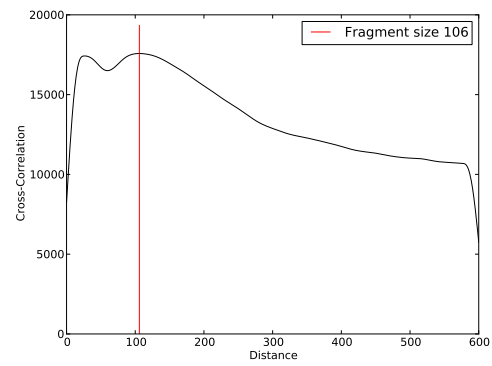


Figure 7: Fragment size correlation plot