FastQC Report

Wed 6 Jun 2018
ERR032066_2_REP2.fq

Summary

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- Per base sequence content
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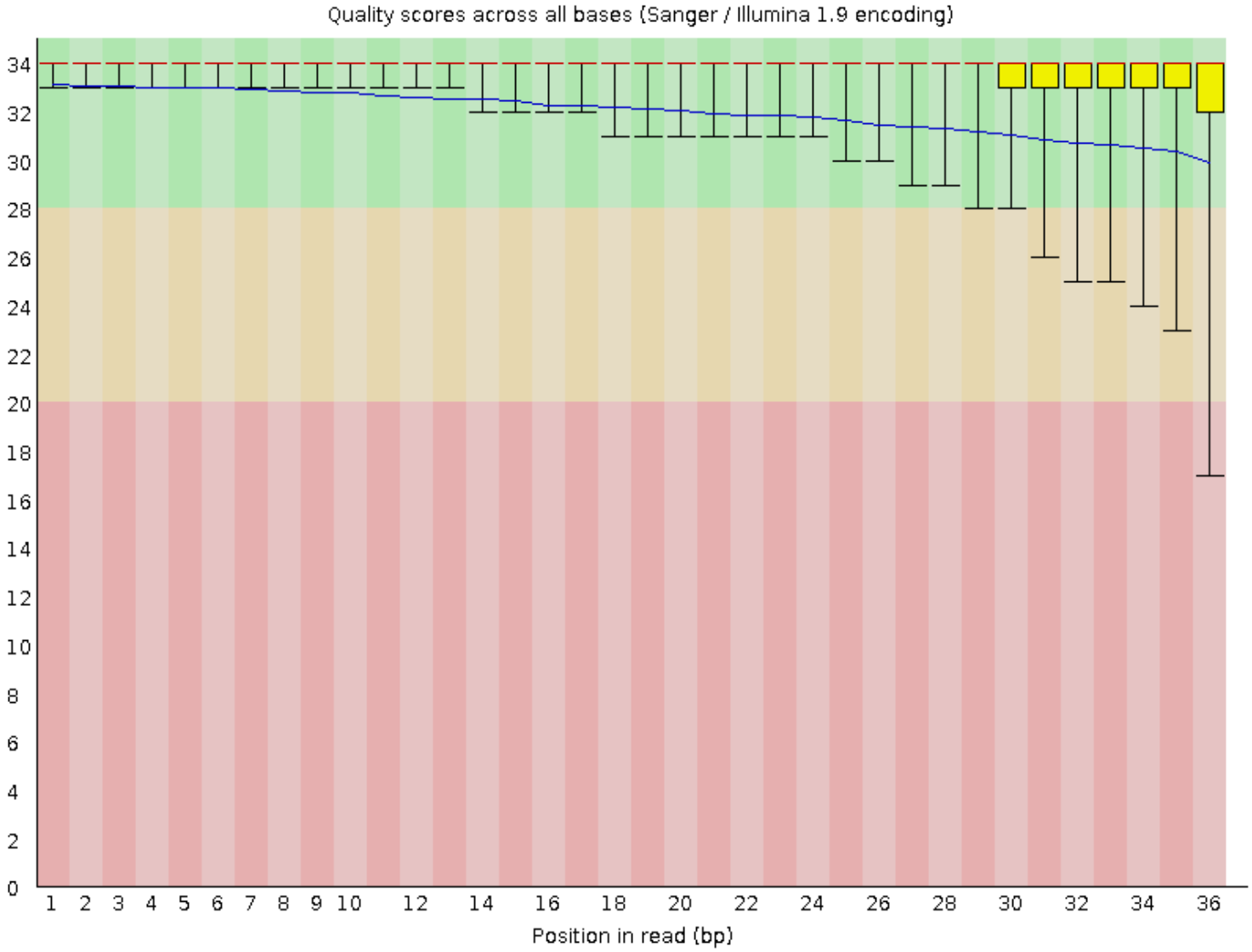
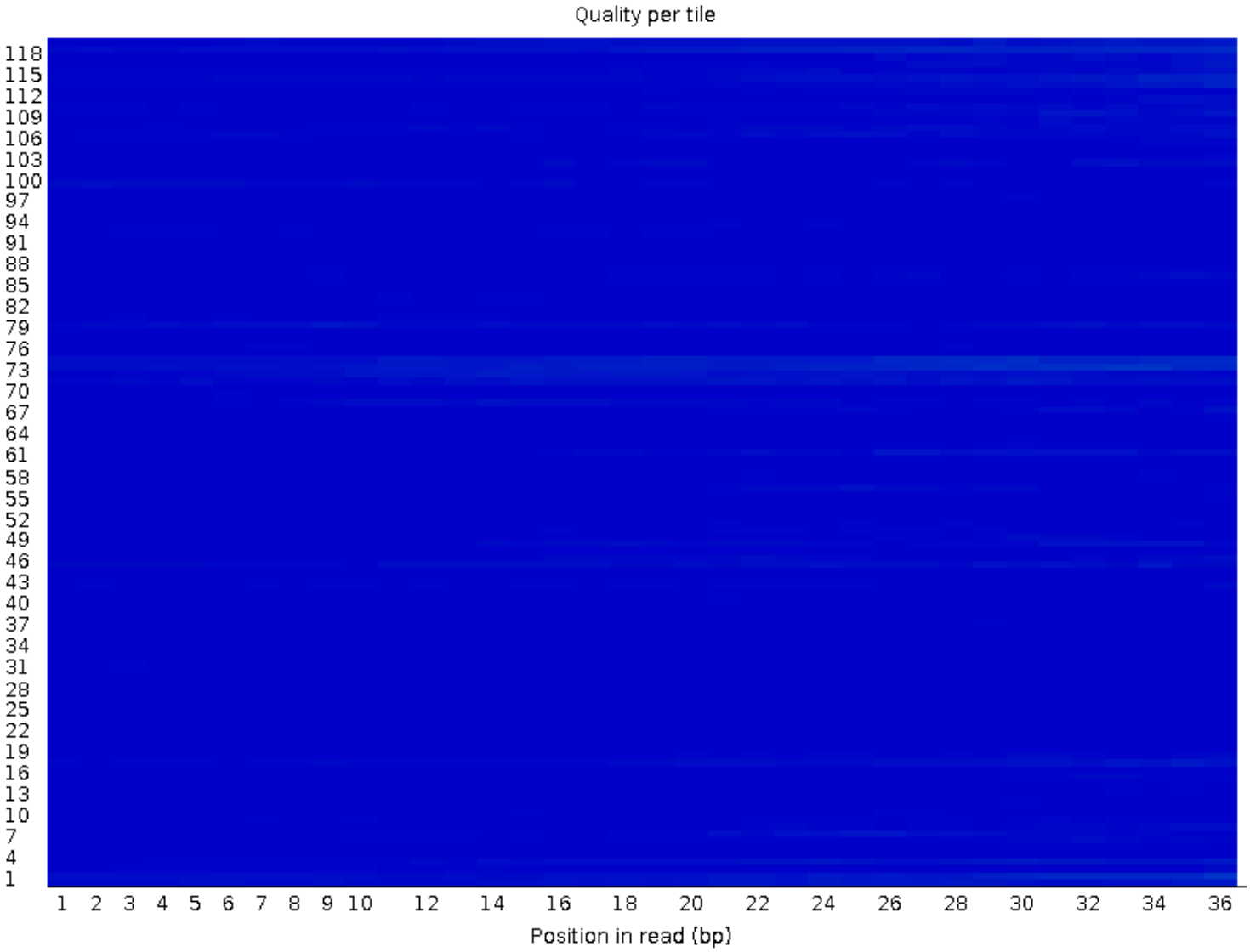
Basic Statistics

Measure	Value
Filename	ERR032066_2_REP2.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	38

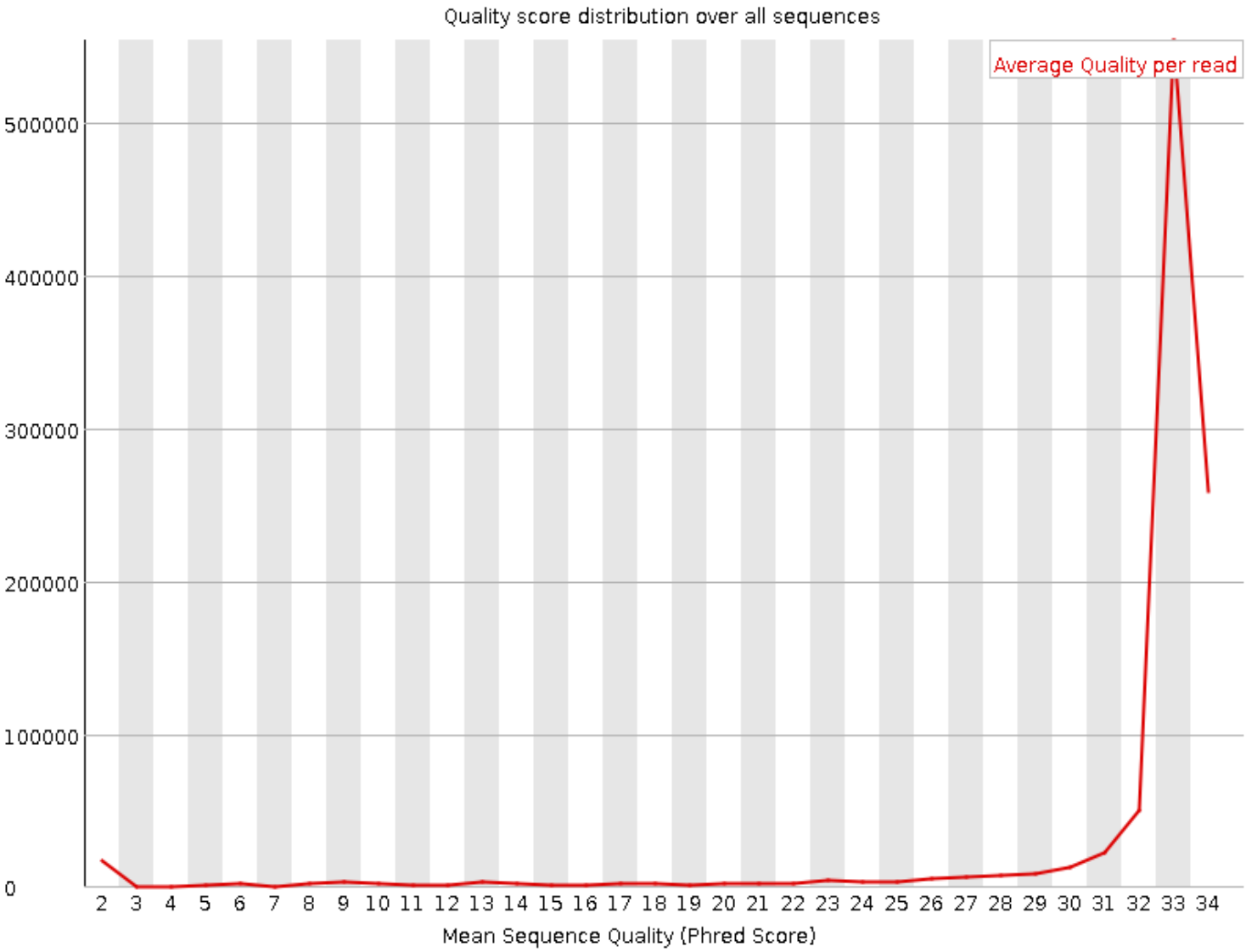
Per base sequence quality



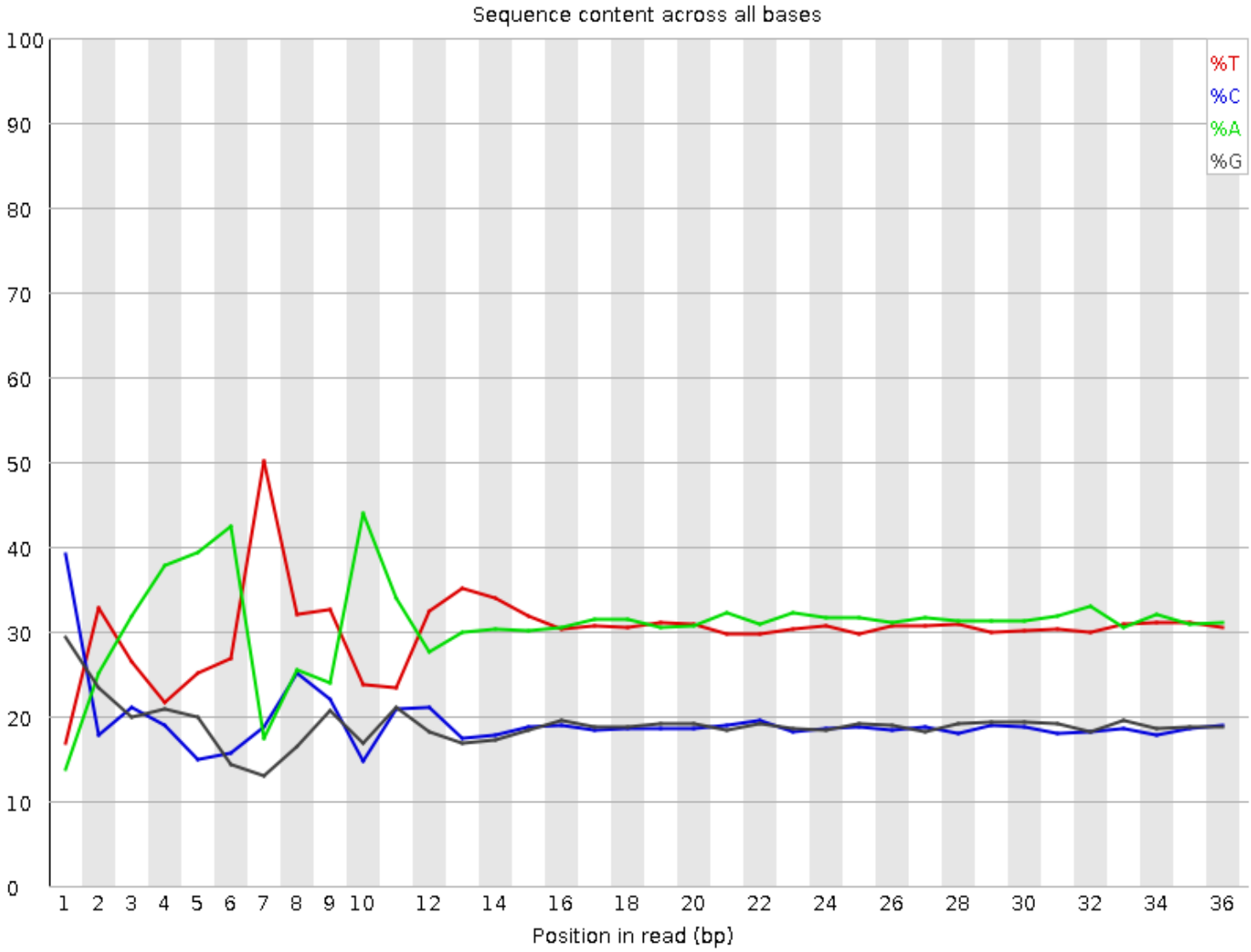
Per tile sequence quality



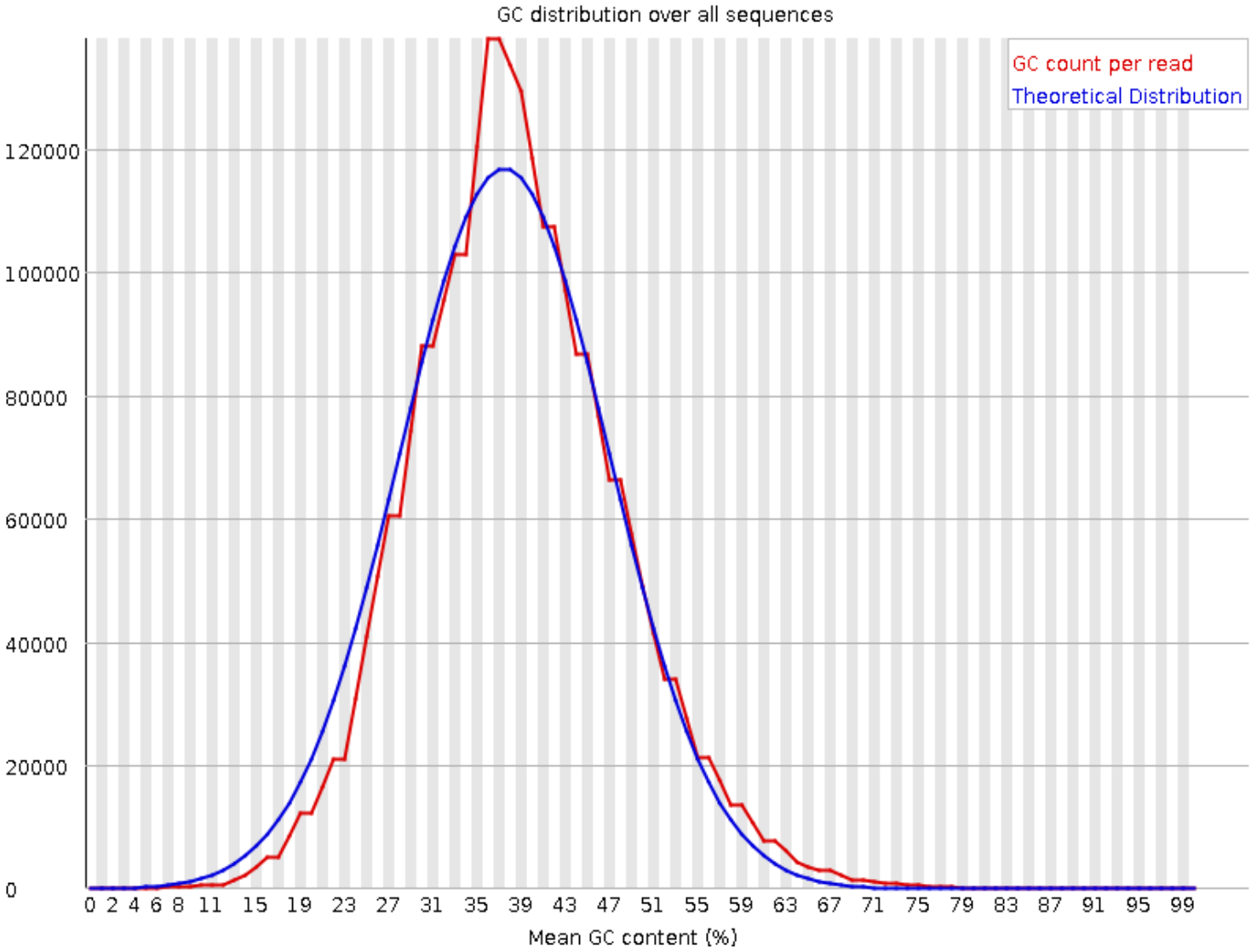
Per sequence quality scores



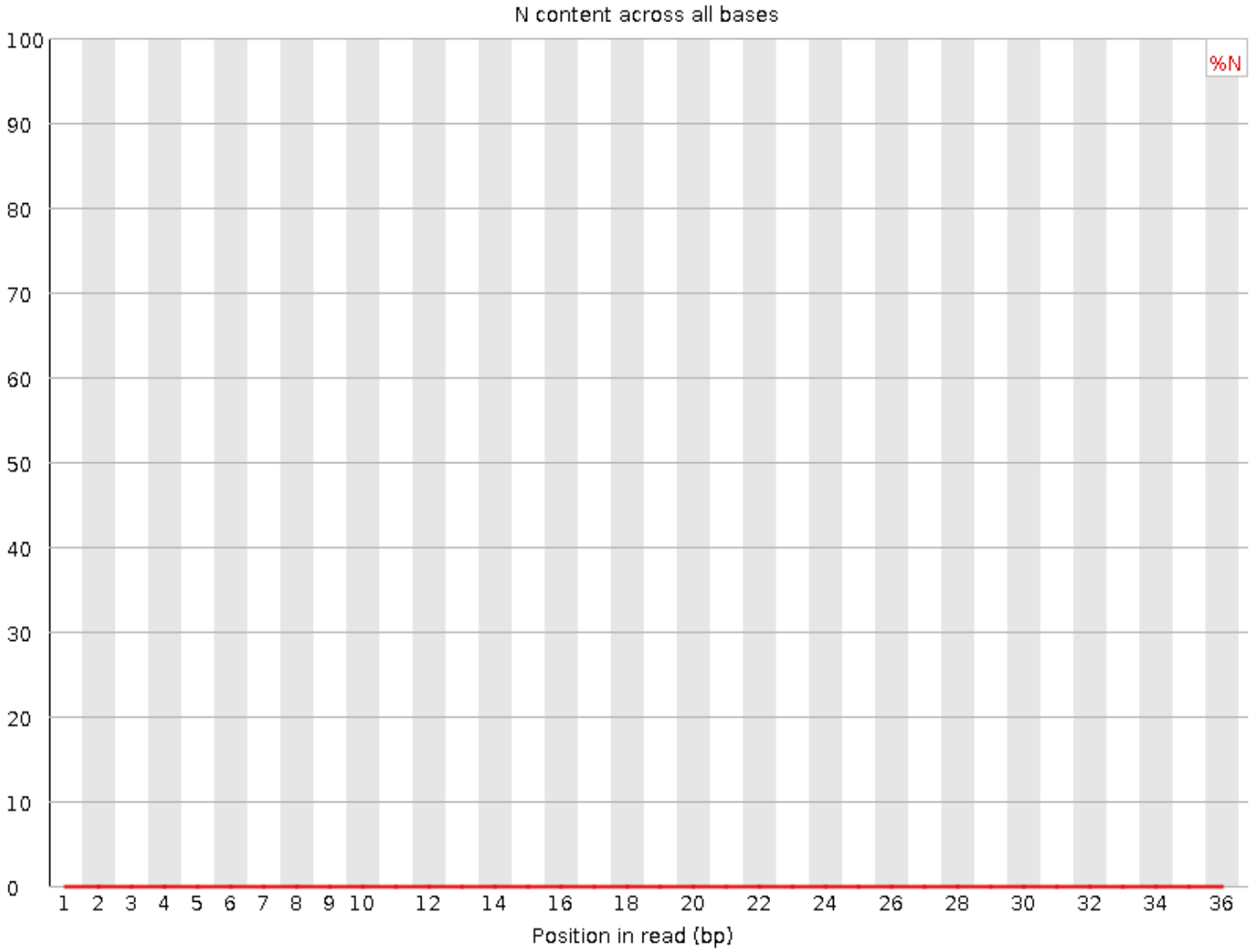
Per base sequence content



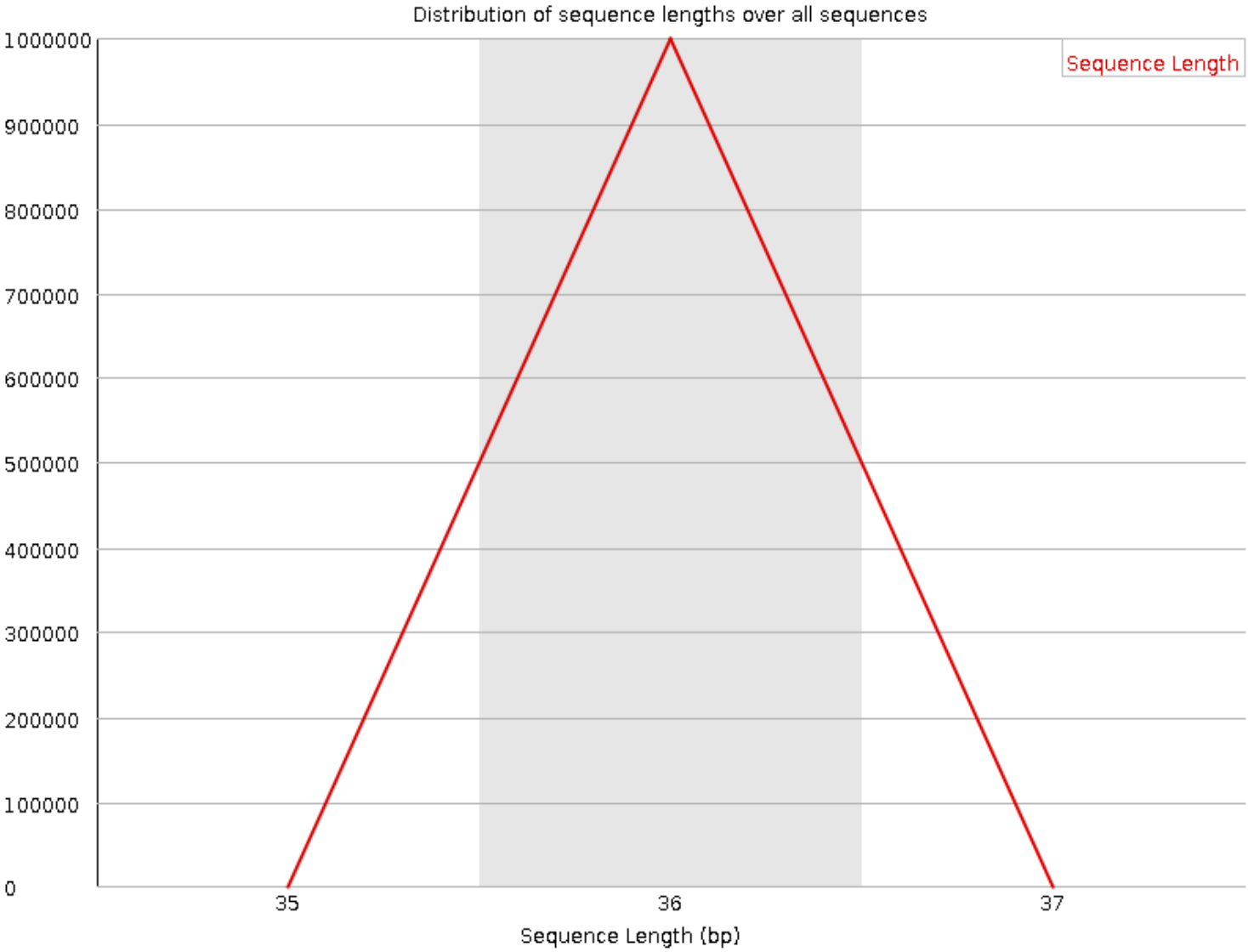
Per sequence GC content



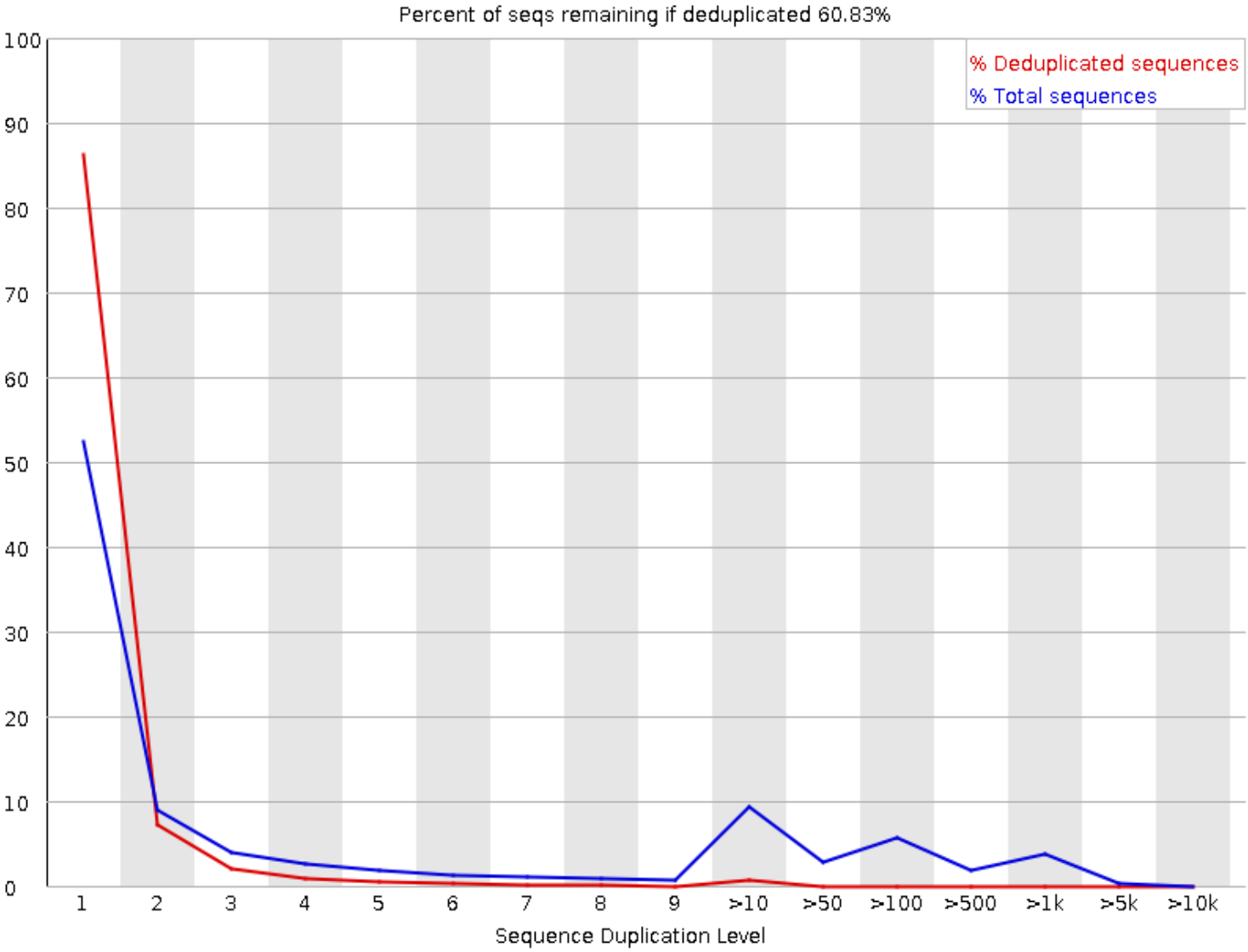
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

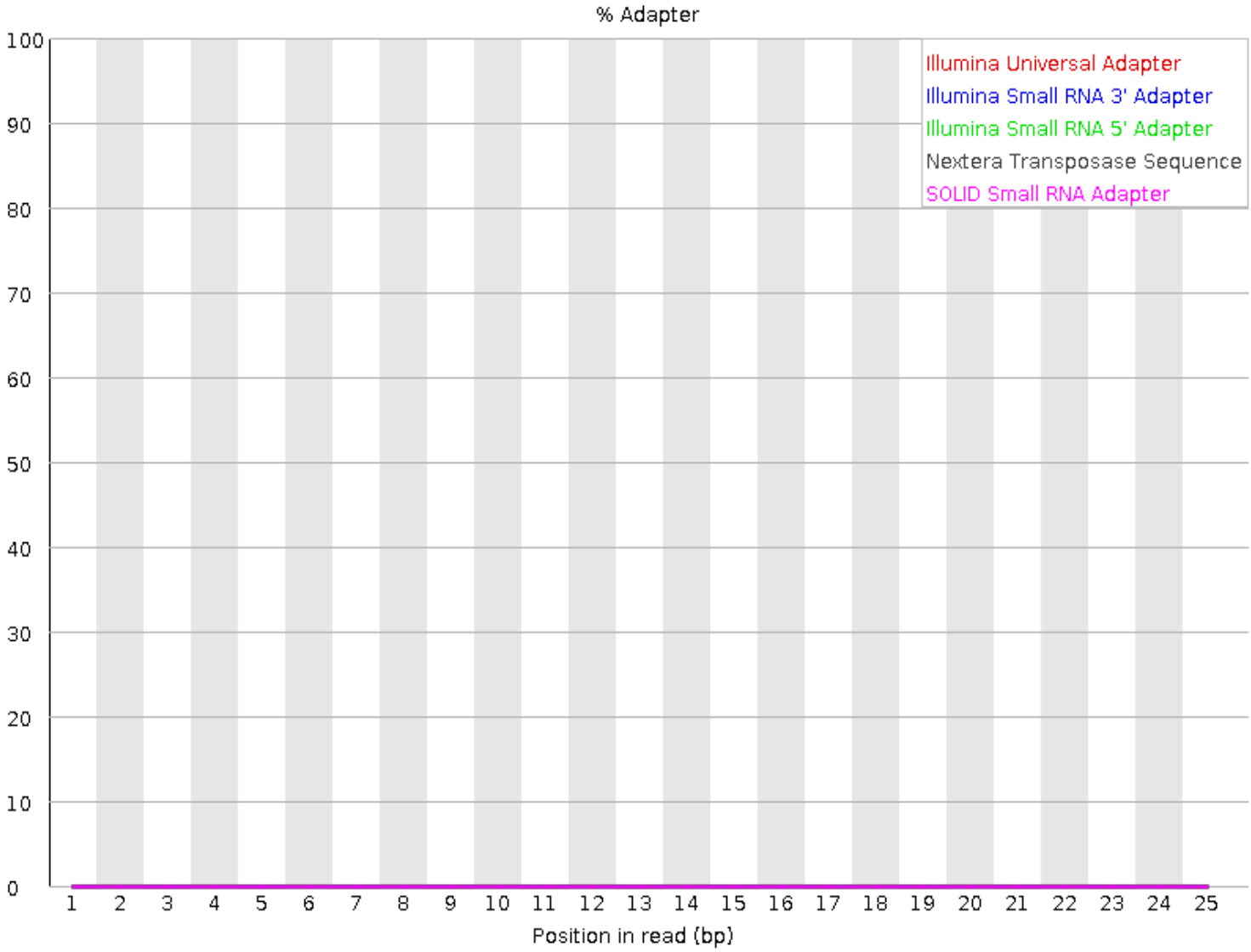


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	5646	0.5646	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3563	0.3563	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	3404	0.3404	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	2566	0.2566	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2294	0.2294	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	2204	0.22039999999999998	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1713	0.17129999999999998	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1497	0.1497	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	1451	0.1451	No Hit

Sequence	Count	Percentage	Possible Source
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1427	0.14270000000000002	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1421	0.1421	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1415	0.14150000000000001	No Hit
GTTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1355	0.1355	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1334	0.1334	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1272	0.12719999999999998	No Hit
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1235	0.1235	No Hit
TAAAGATACAGTTTGTTATTTCAAGGACGAAAAGAC	1226	0.12260000000000001	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1225	0.1225	No Hit
GTTAAAGATAGGTGTAGAGGCCTTTACTTTTAGTCT	1212	0.1212	No Hit
CCCATTCAAACAATTCTAGAATTAGTAGACAAGTAA	1144	0.1144	No Hit
CTTGGAGGACATATCGAAGATTTTGTTTTCTACCTC	1126	0.1126	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAAATCTTC	1075	0.1075	No Hit
AAACAATTCTAGAATTAGTAGACAAGTAATTATGCT	1075	0.1075	No Hit
CTAAAGTAAGAAACACCACTAAGTTAAAAACTCTCT	1033	0.1033	No Hit
CAAAATCTTCGATATGTCCTCCAAGATTCTATATCC	1012	0.10120000000000001	No Hit
CTCTACACCTATCTTTAACTACAATTCAACATCGAG	1011	0.1011	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)