FastQC Report

Wed 6 Jun 2018
ERR032066_1_REP1.fq

Summary

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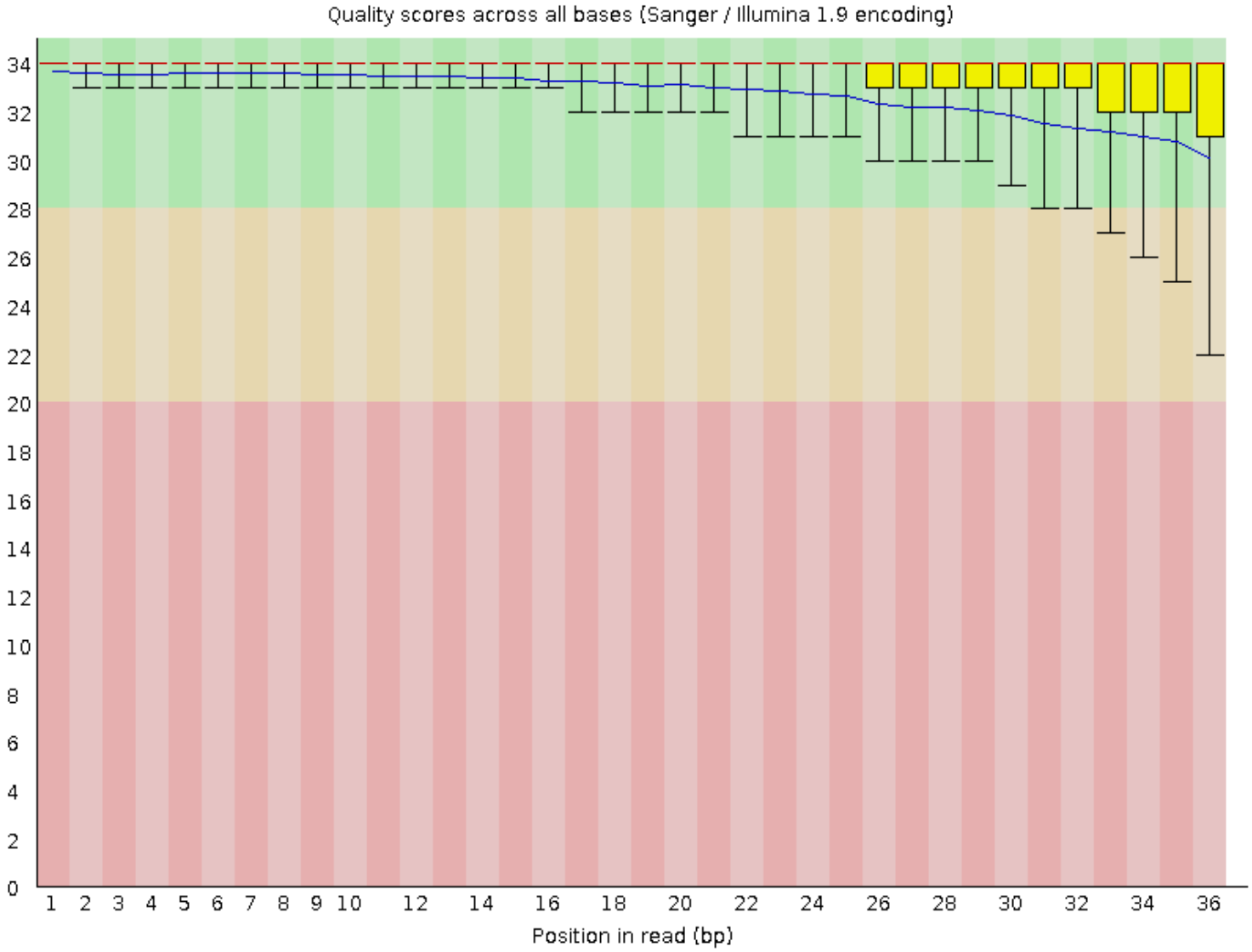
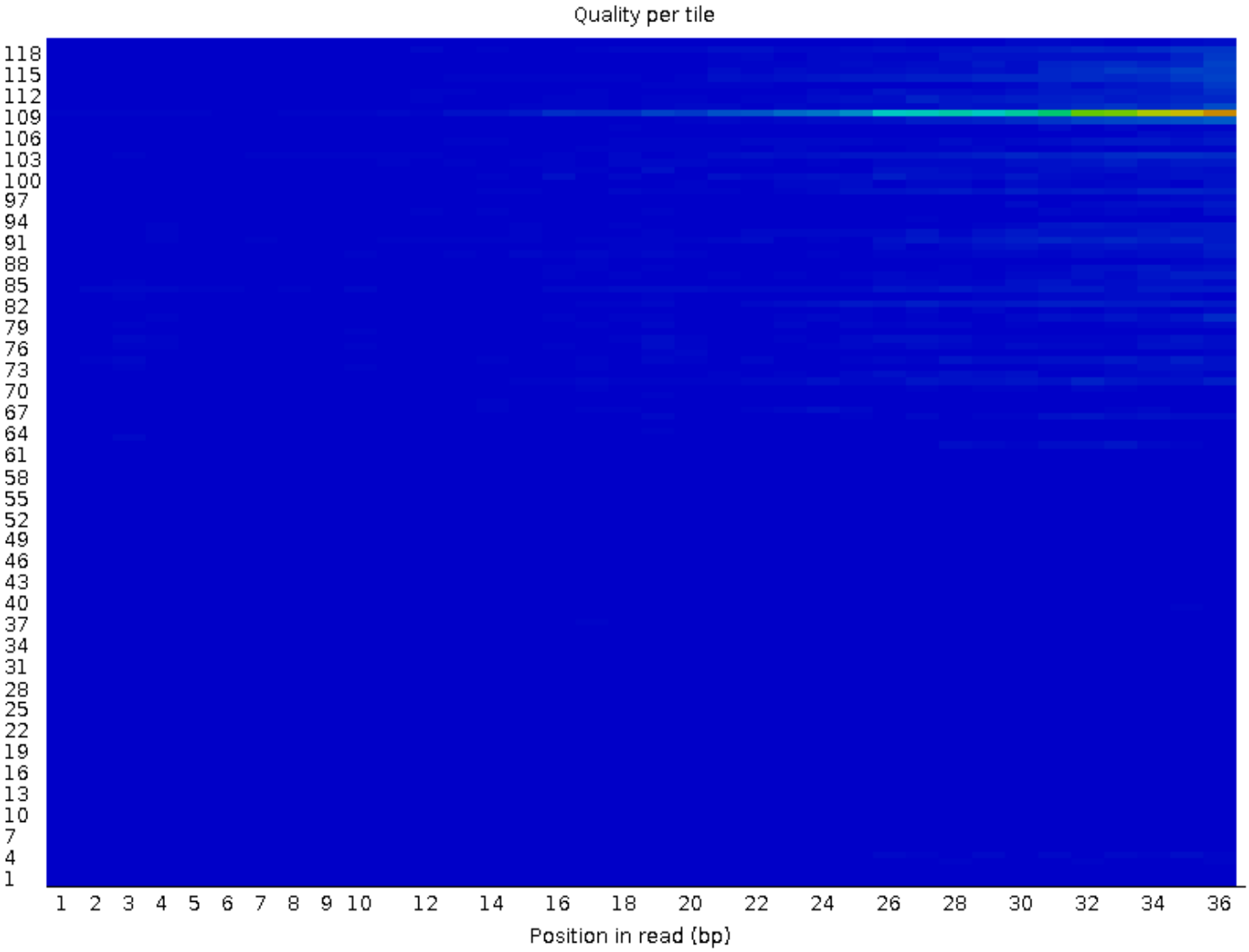
Basic Statistics

Measure	Value
Filename	ERR032066_1_REP1.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

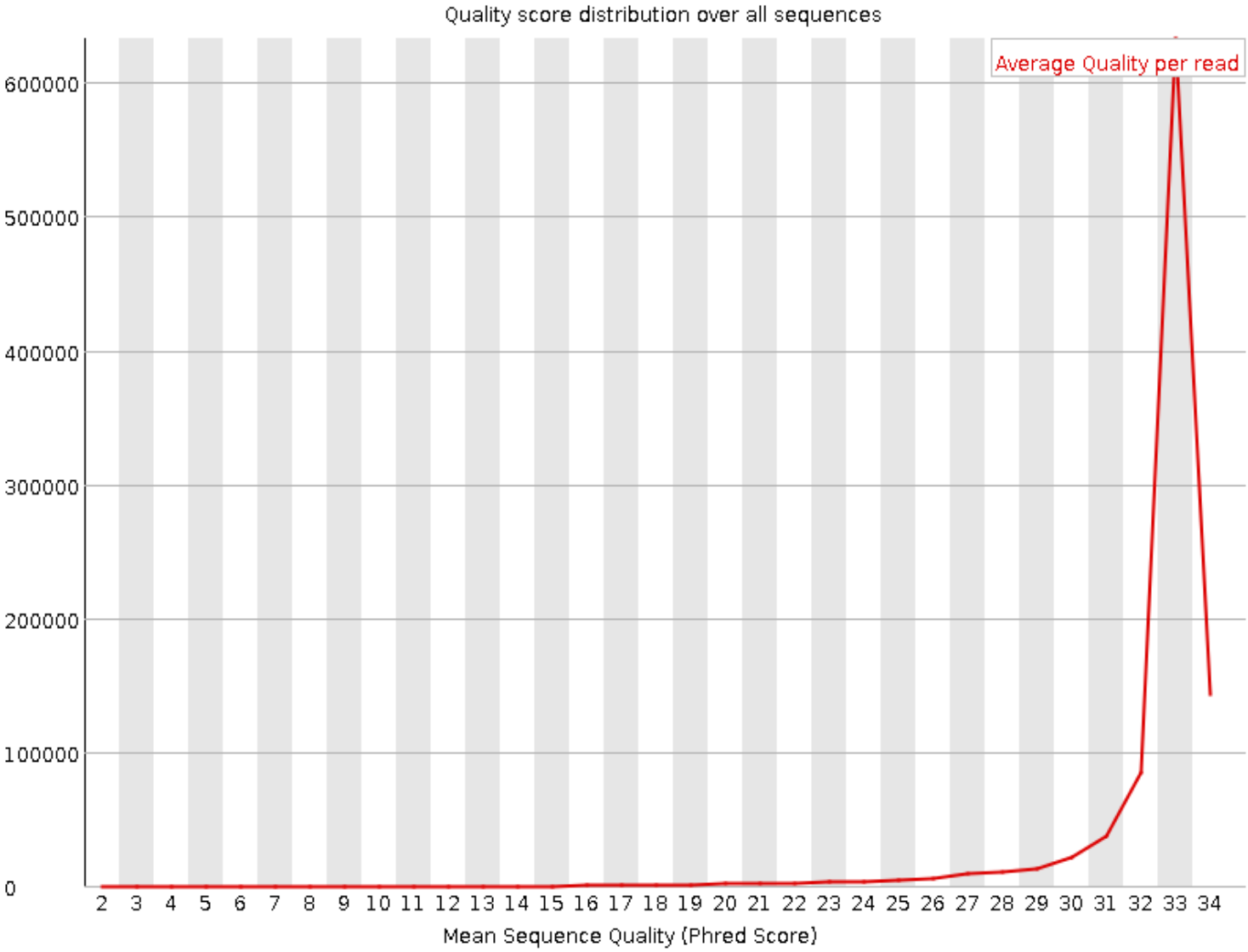
Per base sequence quality



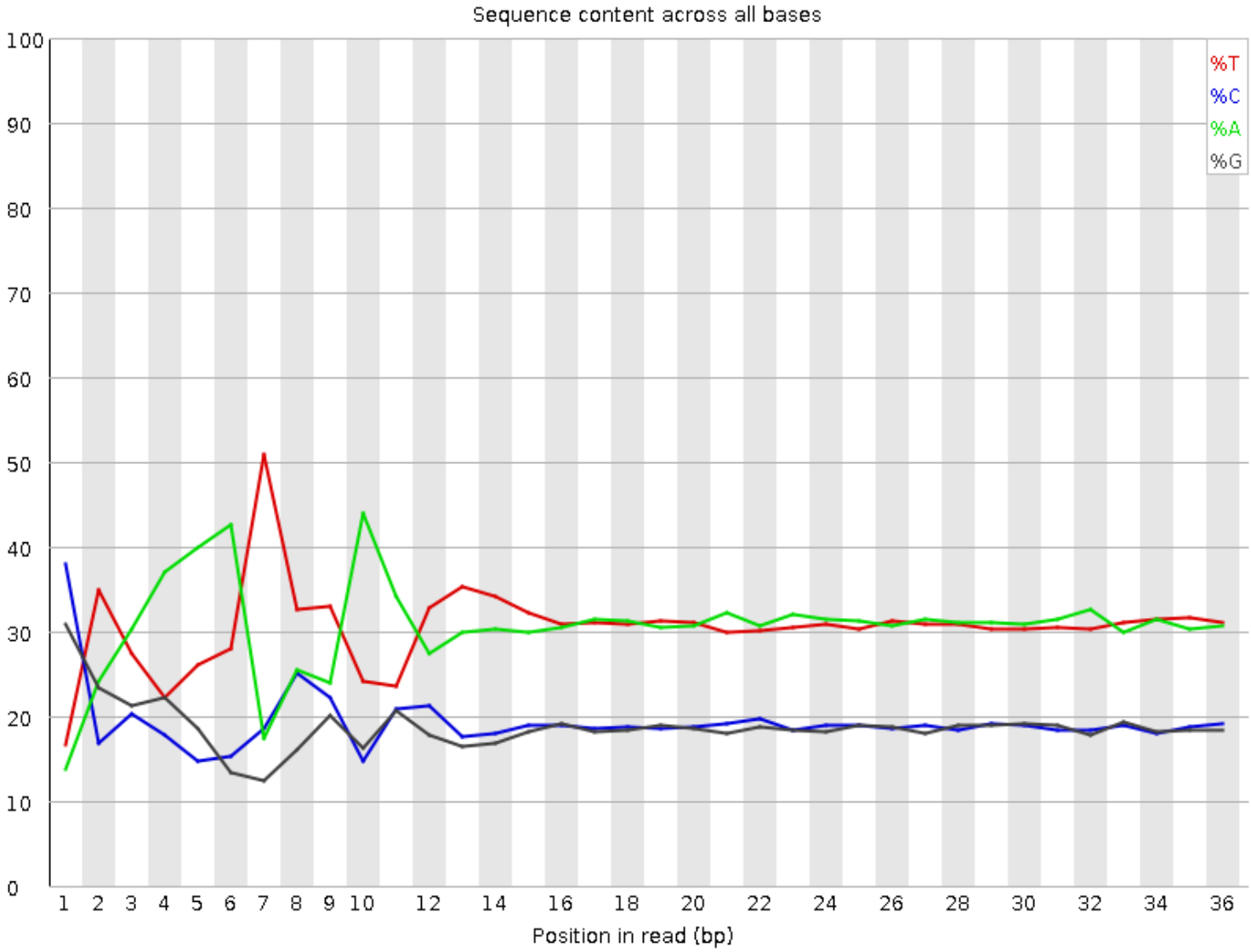
Per tile sequence quality



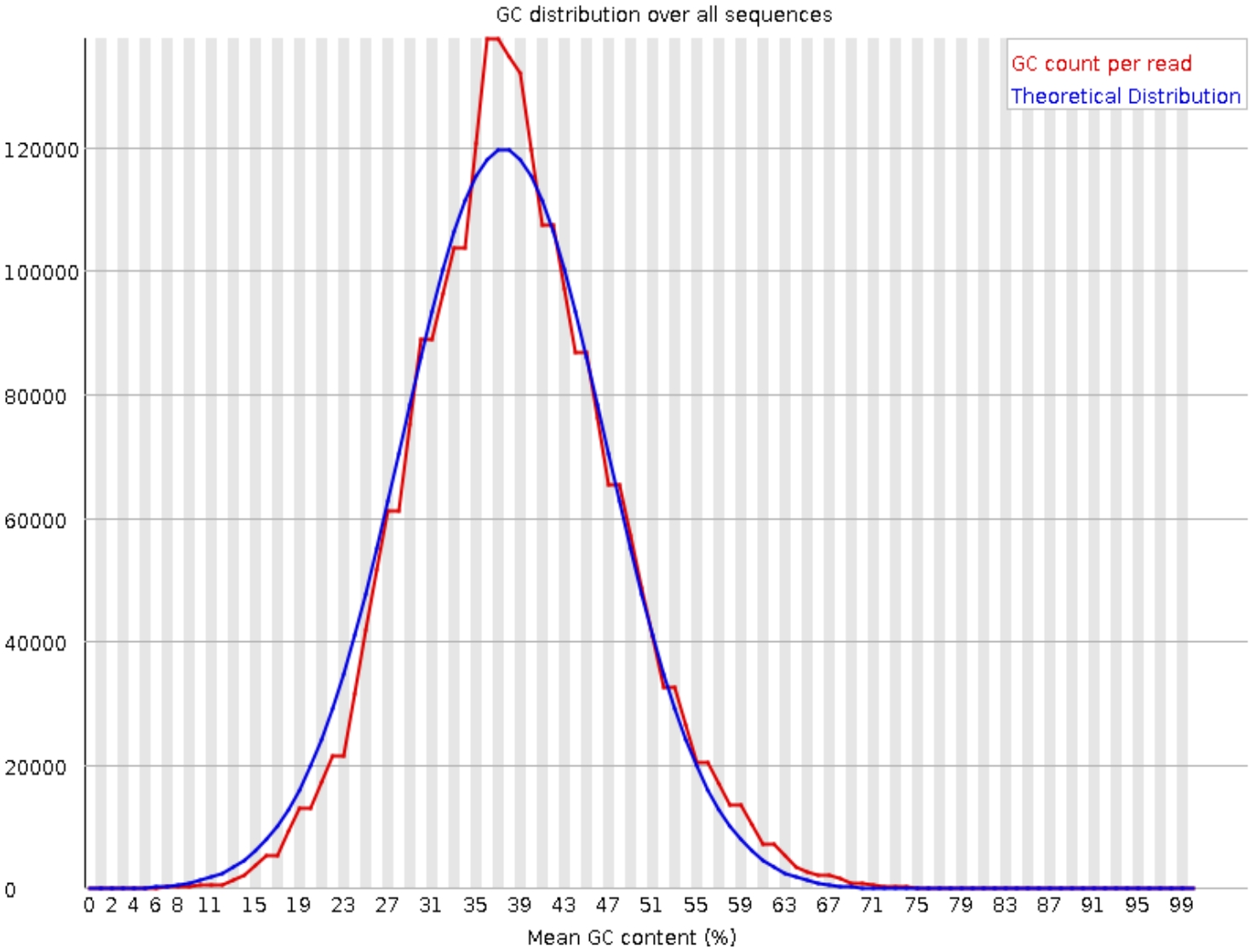
Per sequence quality scores



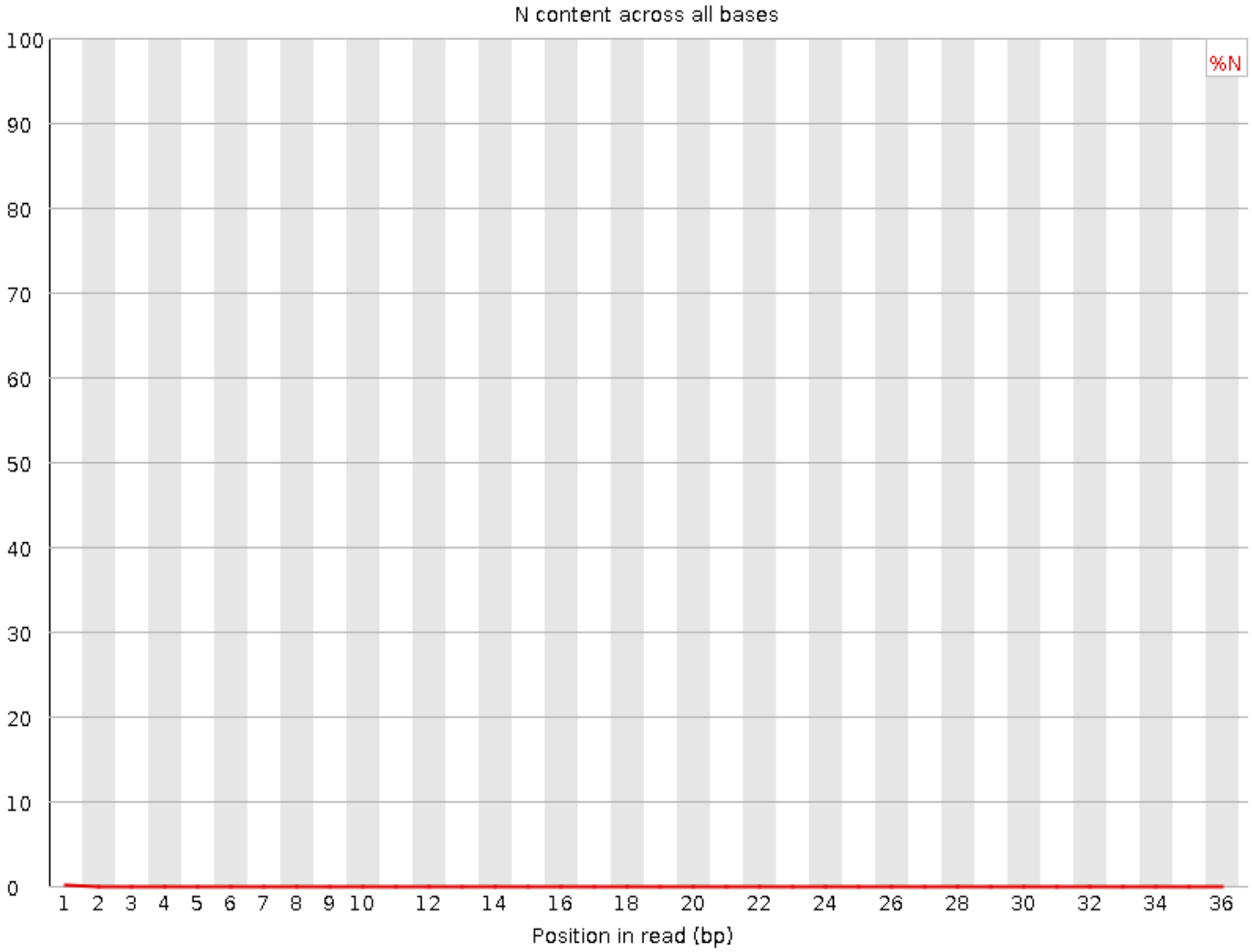
Per base sequence content



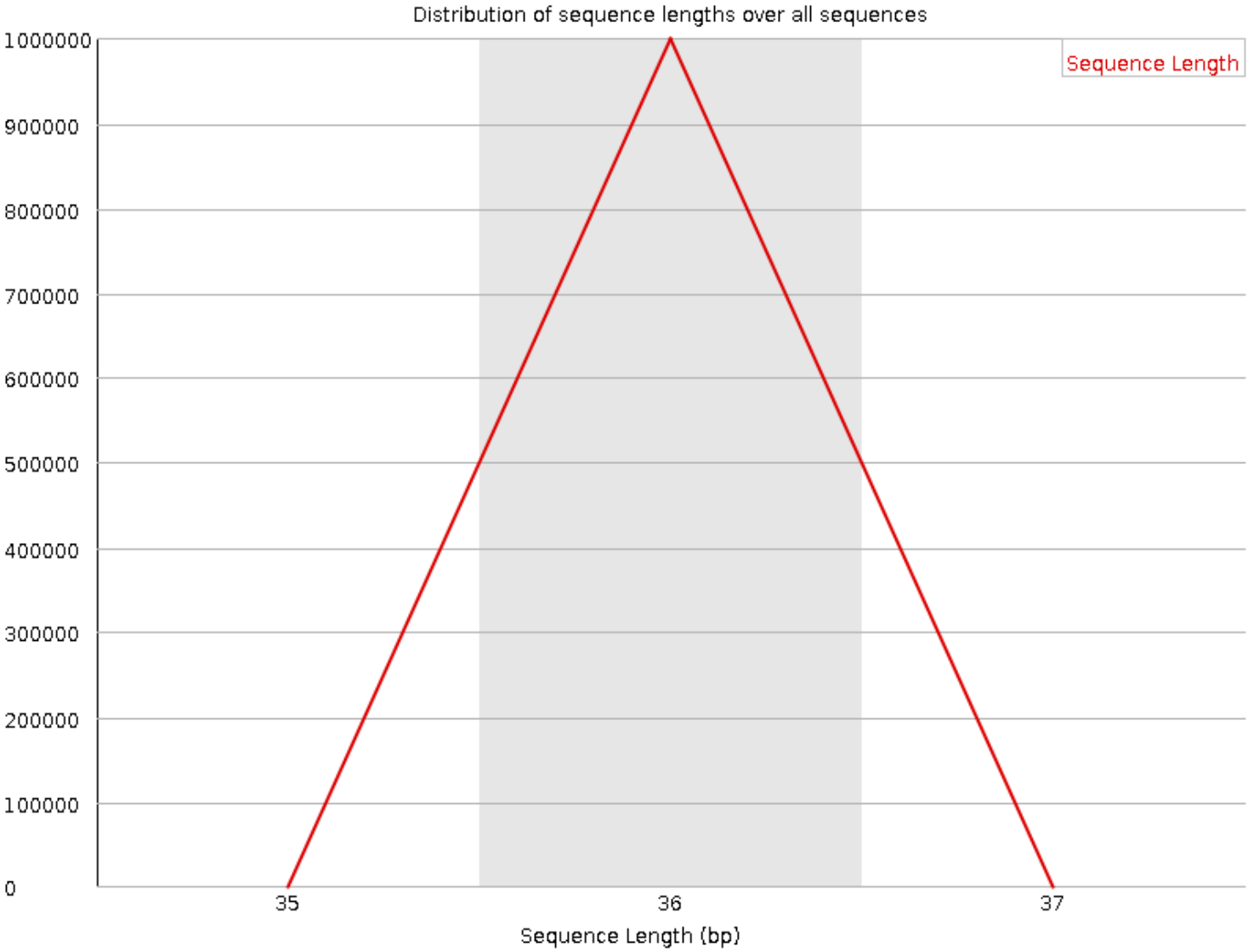
Per sequence GC content



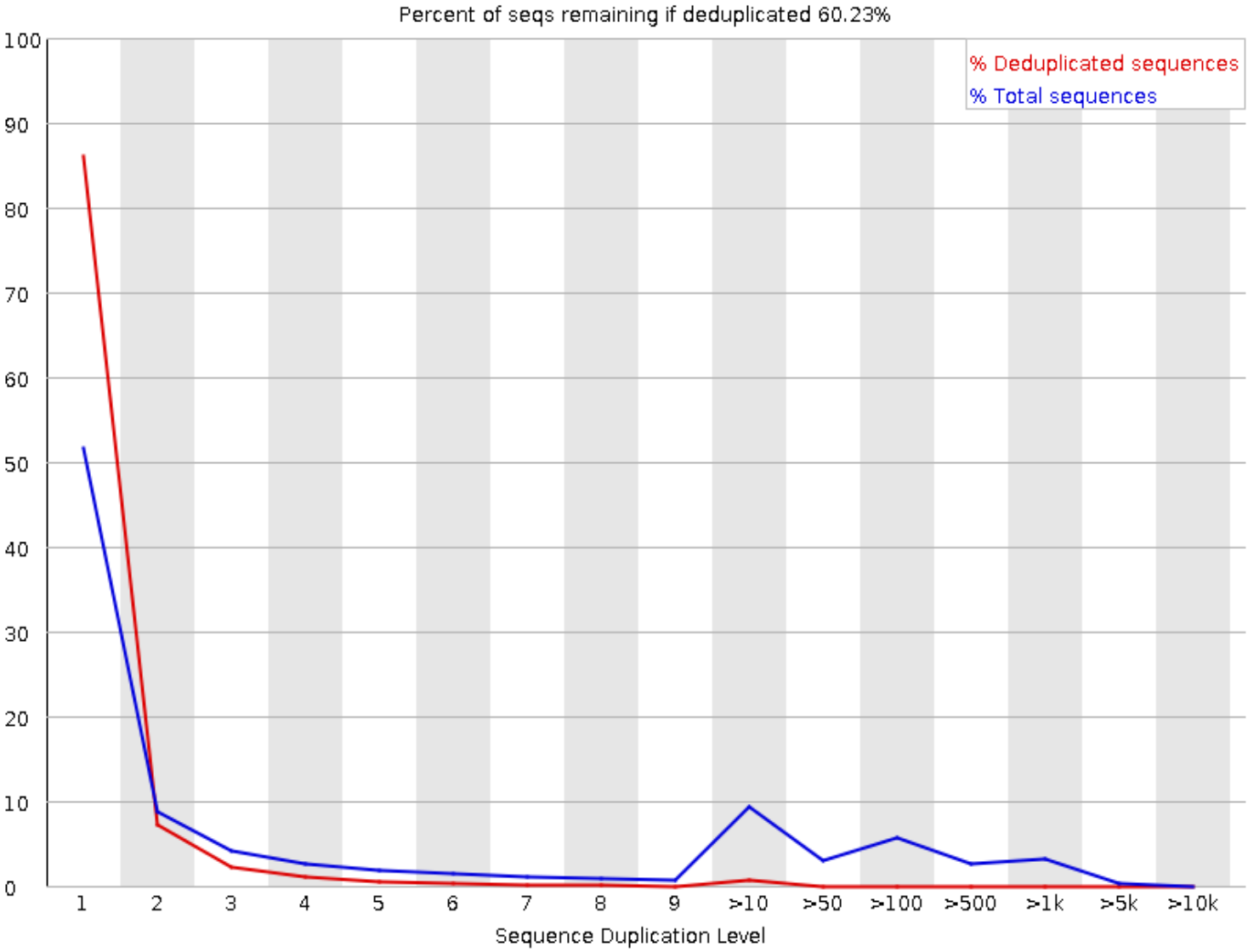
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

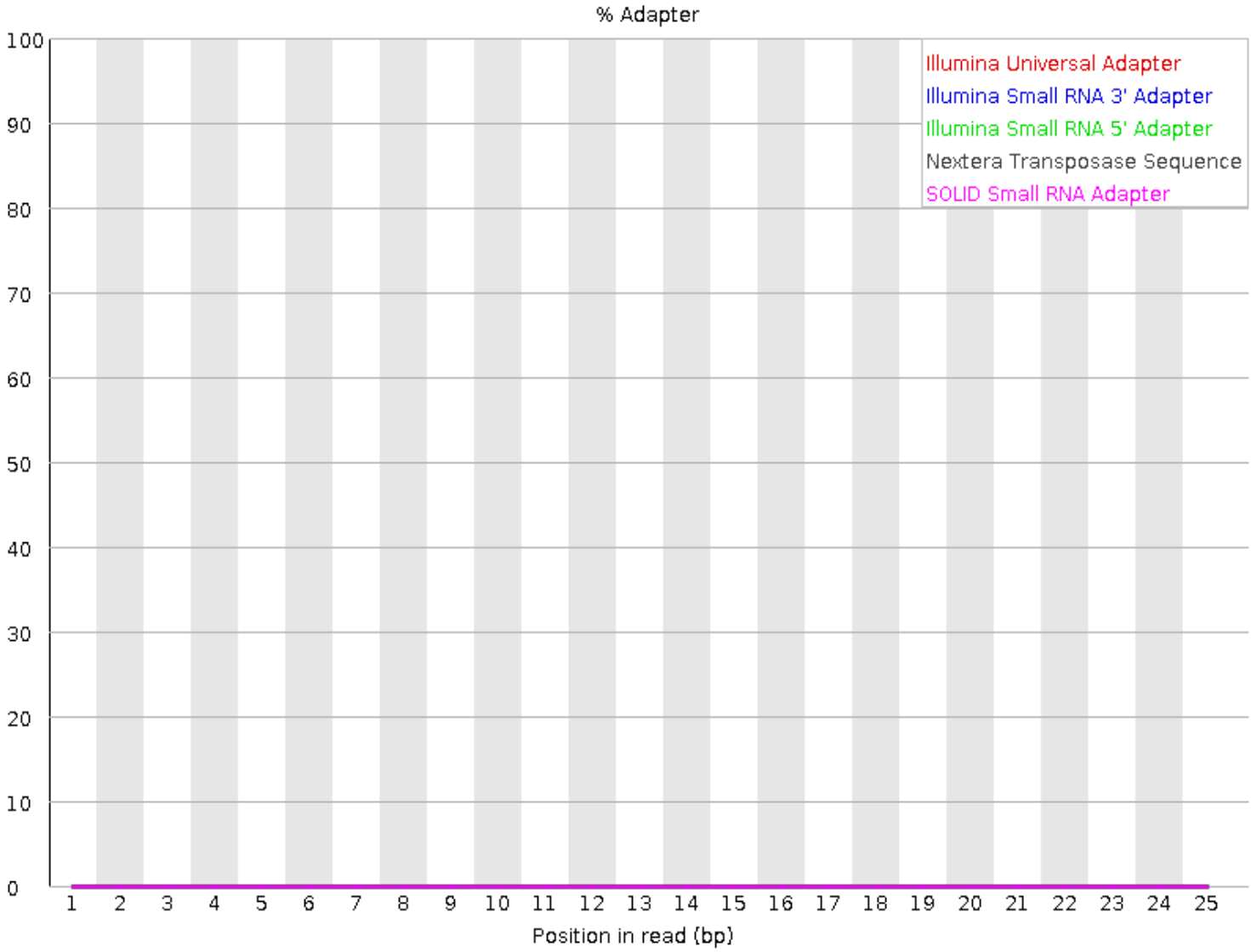


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	5427	0.5427000000000001	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3692	0.3692	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	3228	0.3228	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	2689	0.2689	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2466	0.24659999999999999	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1929	0.1929	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1849	0.1849	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1715	0.17149999999999999	No Hit
GTTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1640	0.164	No Hit

Sequence	Count	Percentage	Possible Source
GTTAAAGATAGGTGTAGAGGCCTTTACTTTTAGTCT	1322	0.1322	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1302	0.1302	No Hit
CTTGGAGGACATATCGAAGATTTTGTTTTCTACCTC	1287	0.12869999999999998	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1258	0.1258	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	1253	0.1253	No Hit
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1242	0.1242	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	1203	0.1203	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1164	0.1164	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1089	0.1089	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1047	0.1047	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1023	0.1023	No Hit
AAACAATTCTAGAATTAGTAGACAAGTAATTATGCT	1003	0.1003	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)