FastQC Report

Wed 6 Jun 2018
ERR032071_1_REP2.fq

Summary

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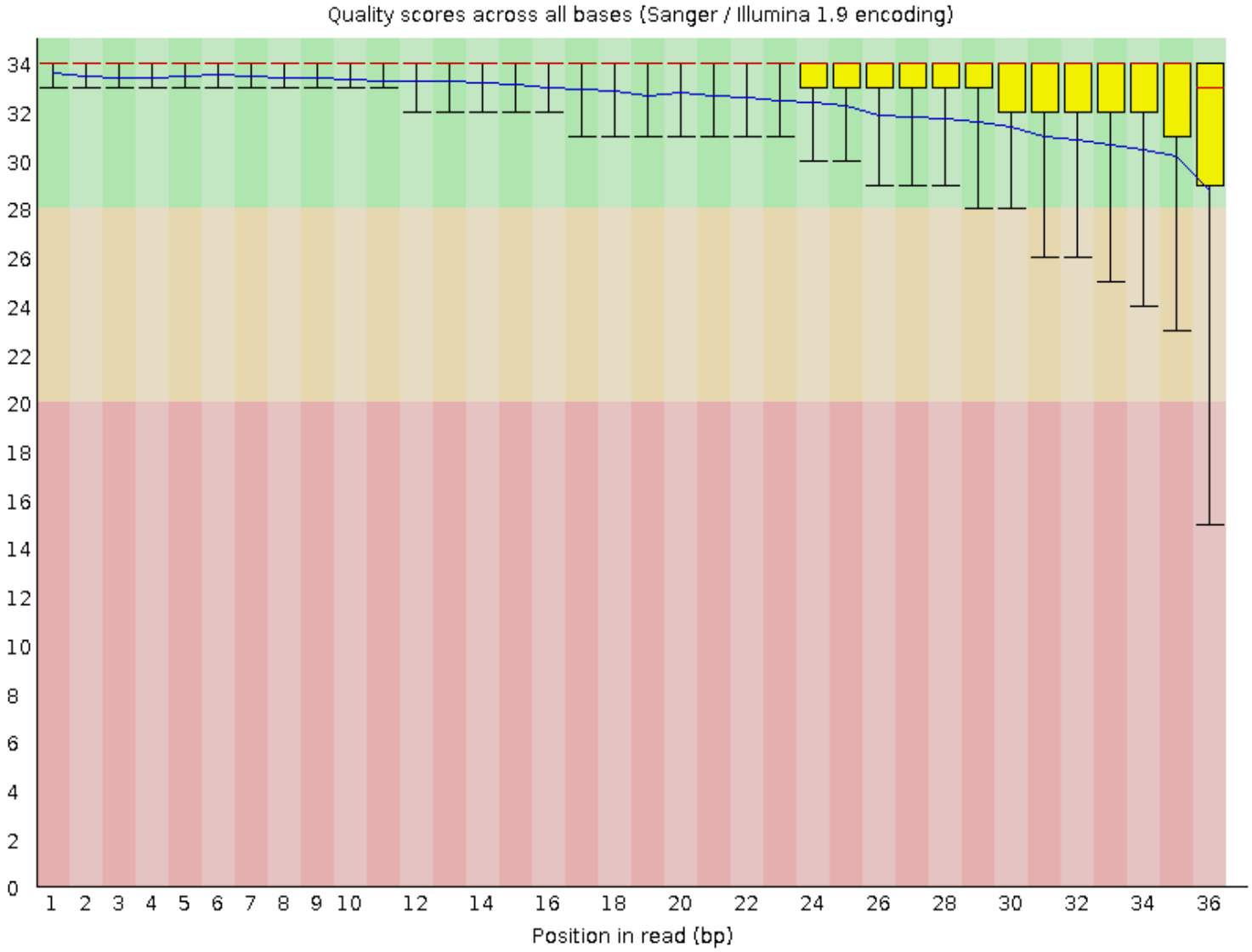
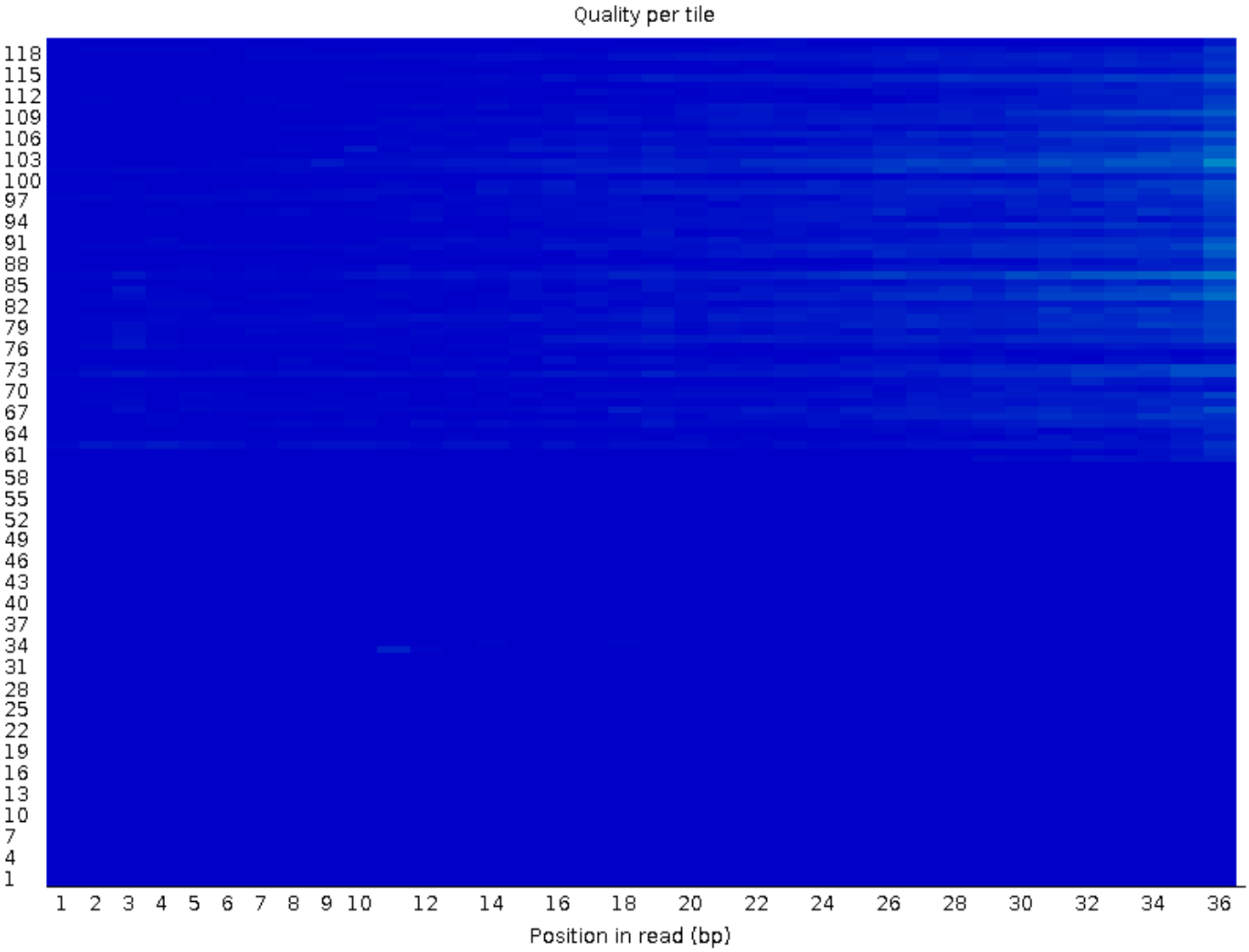
Basic Statistics

Measure	Value
Filename	ERR032071_1_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	39

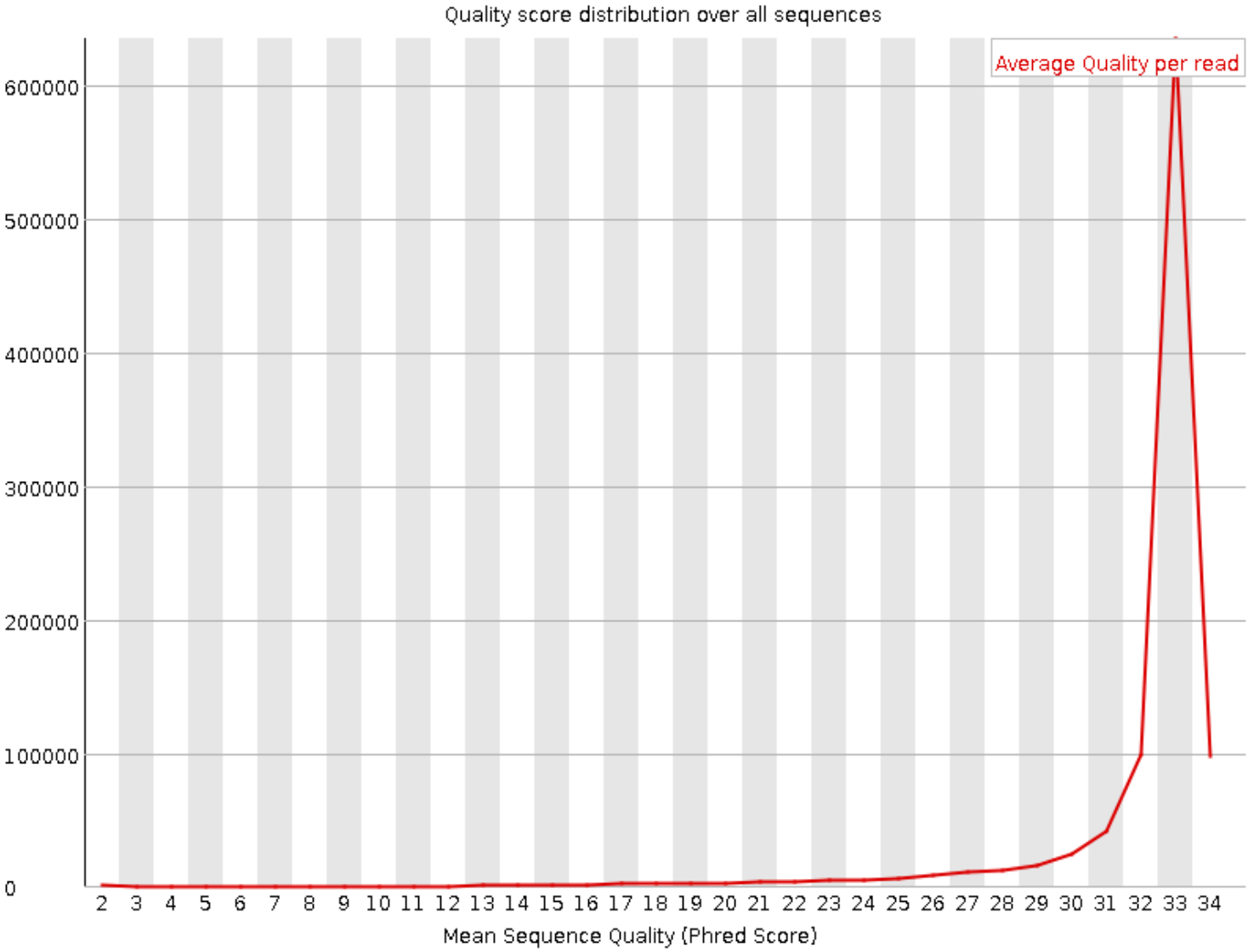
Per base sequence quality



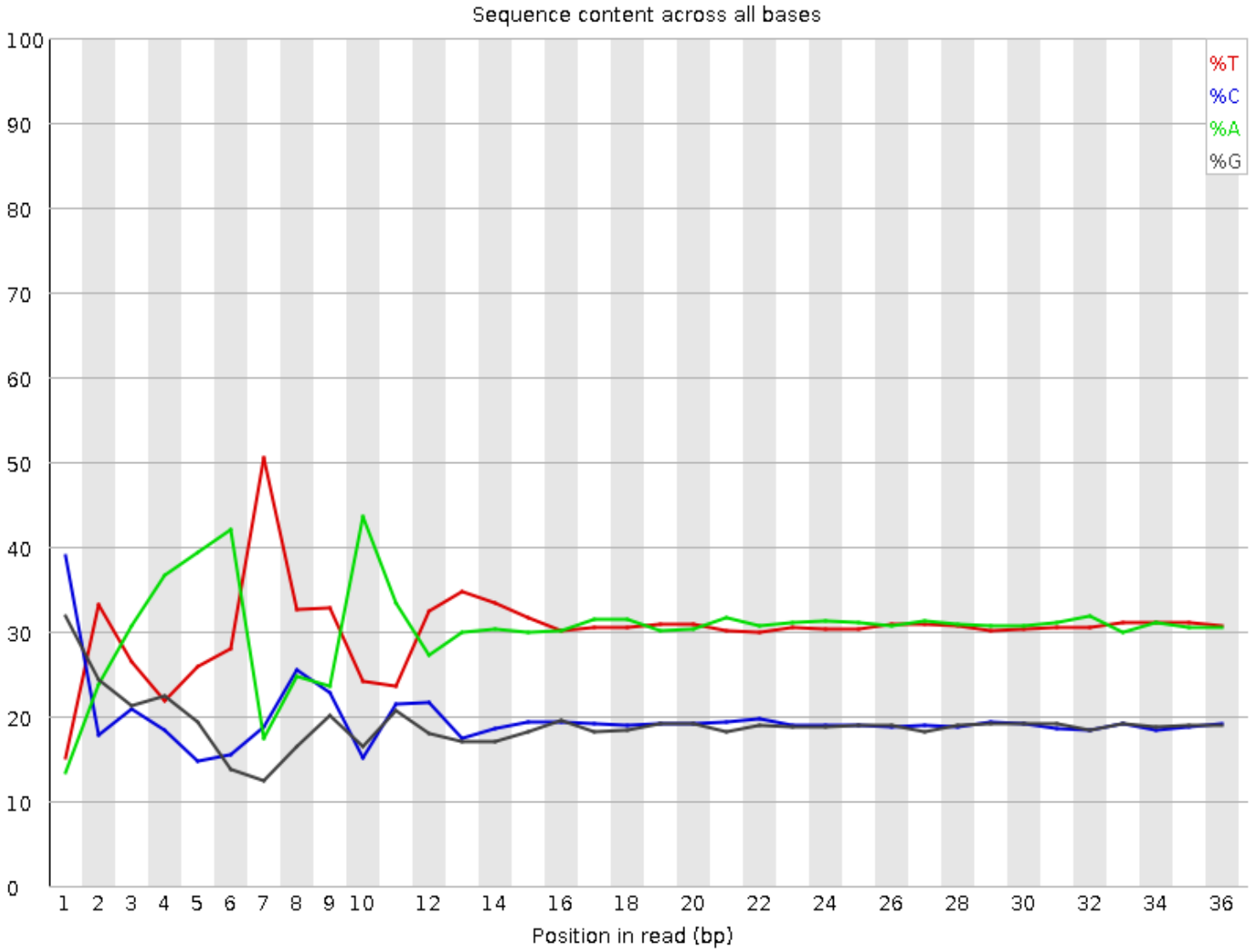
Per tile sequence quality



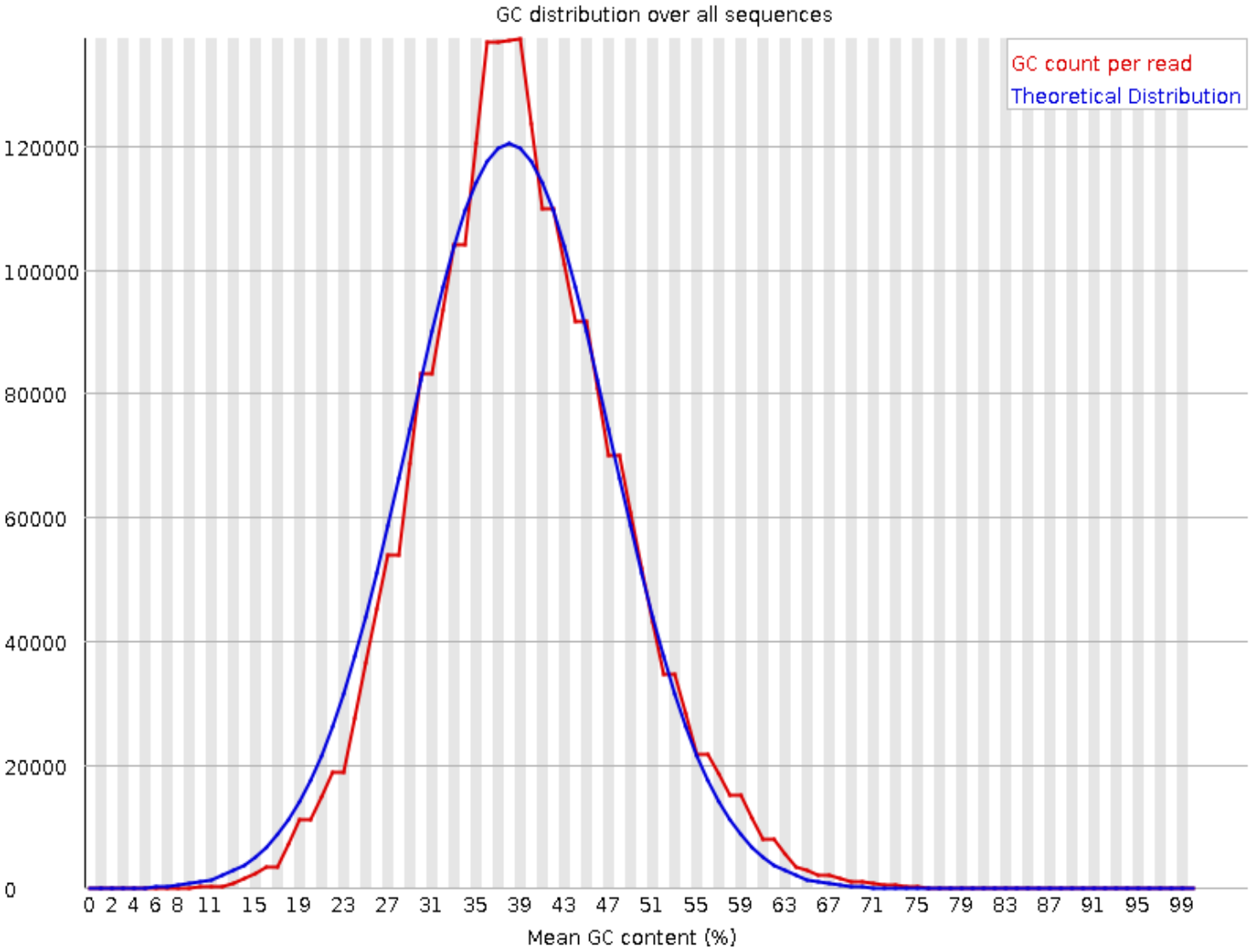
Per sequence quality scores



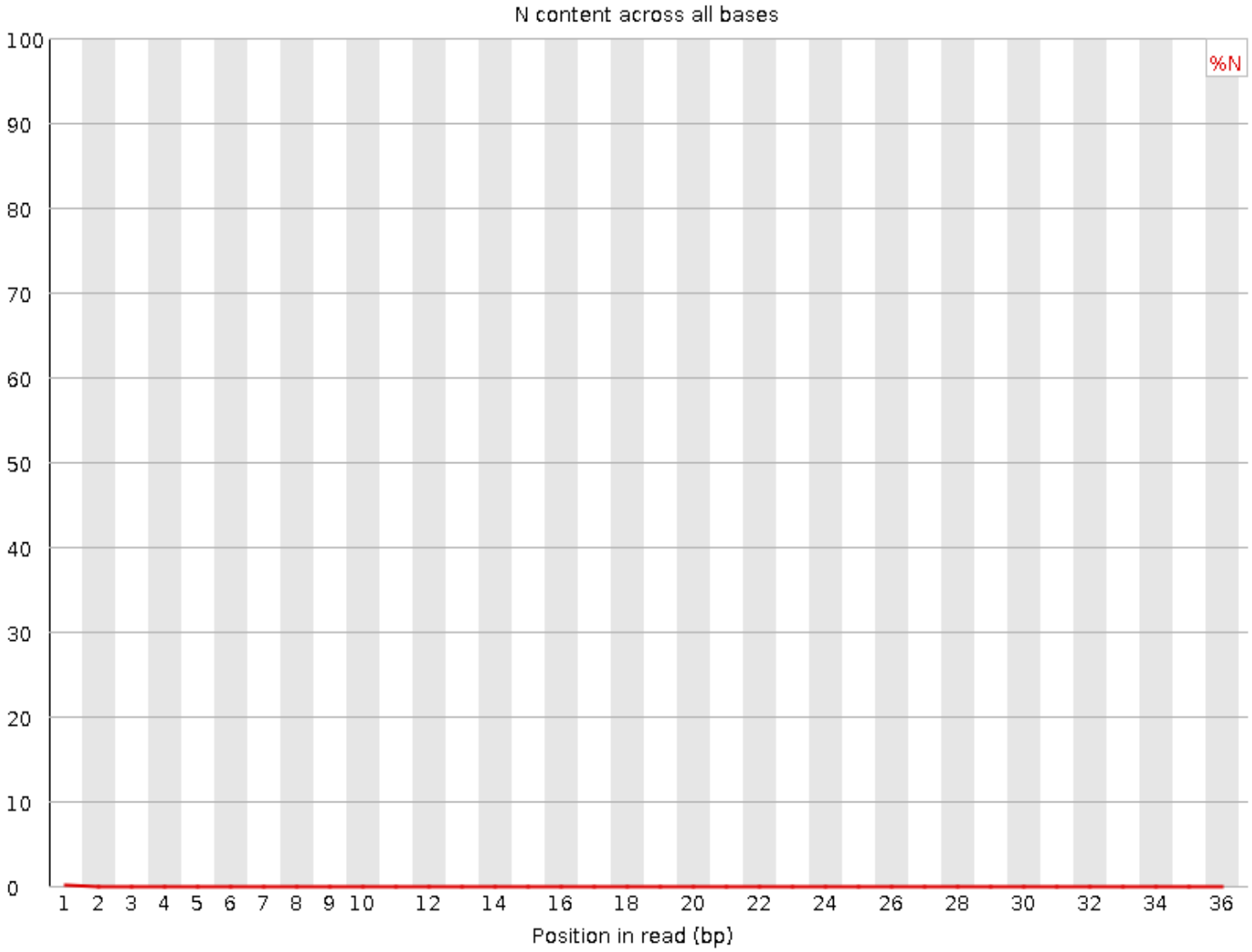
Per base sequence content



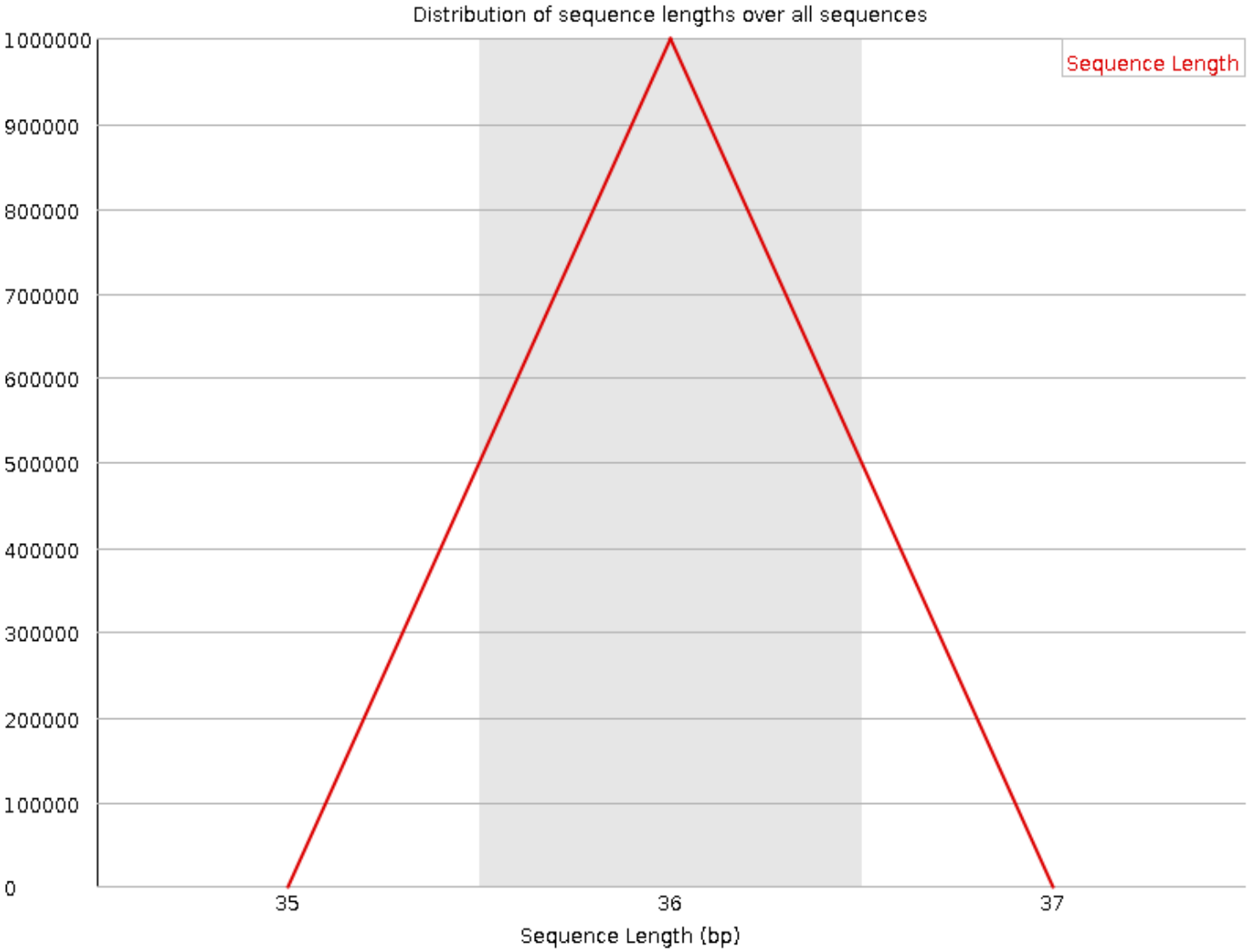
Per sequence GC content



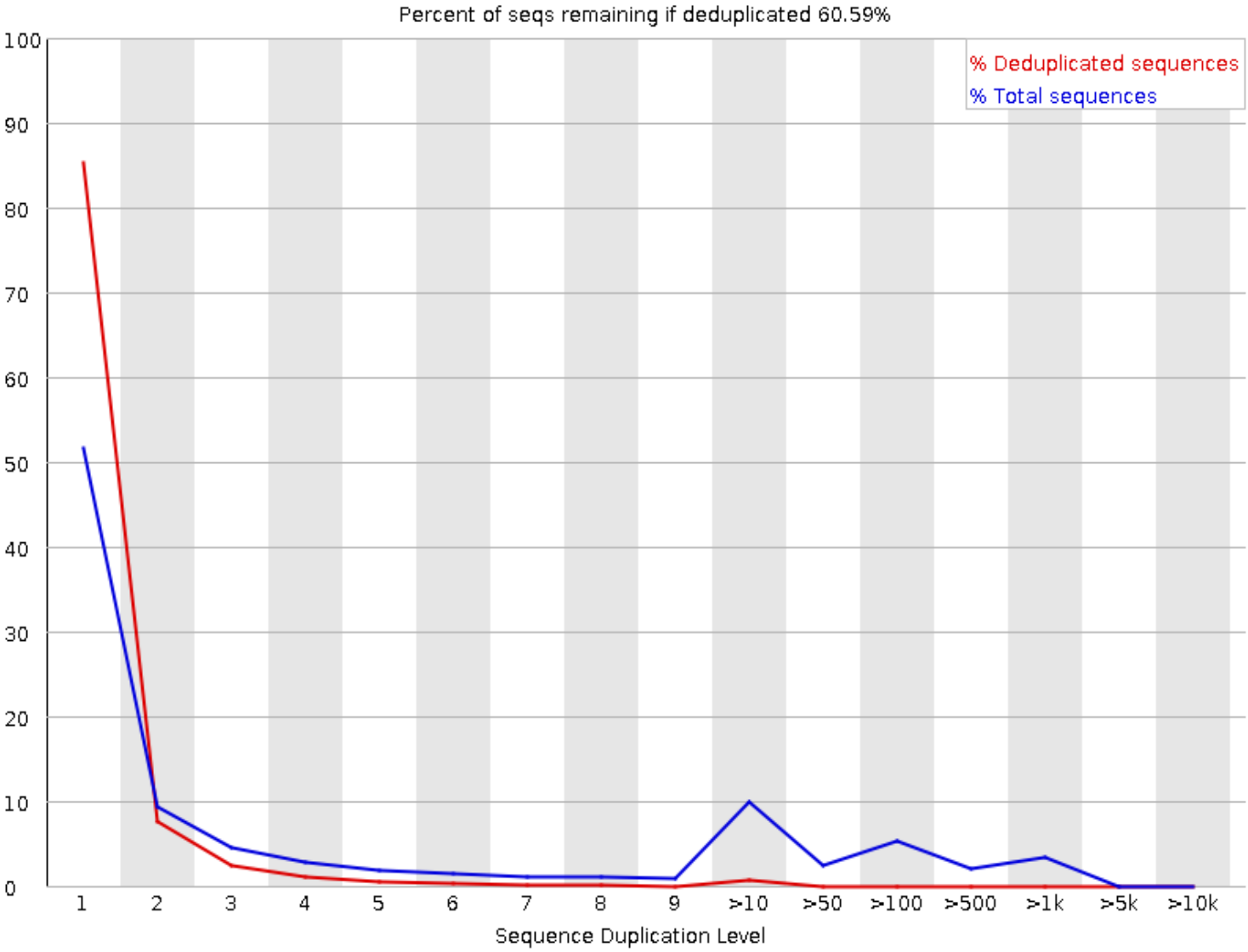
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

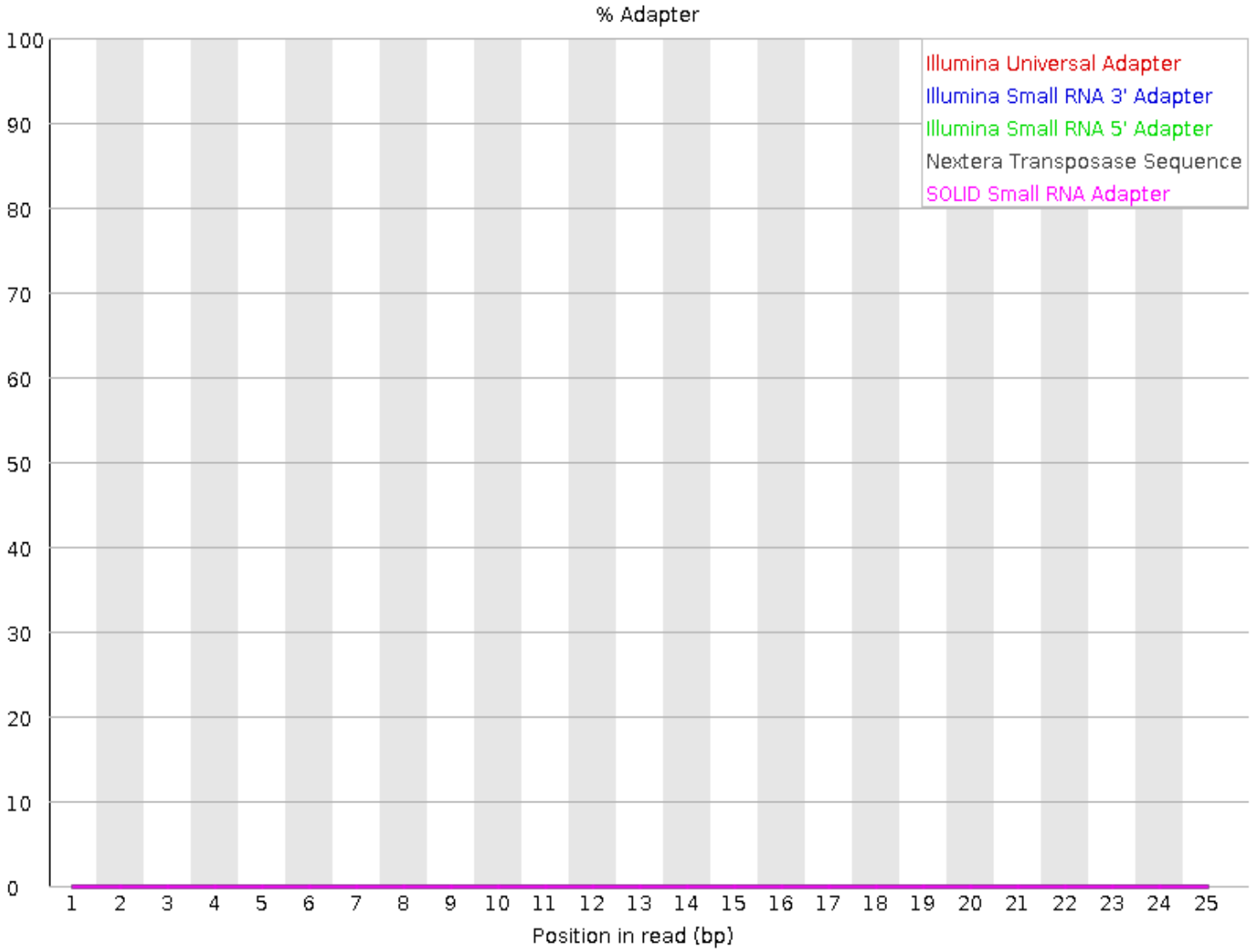


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3276	0.3276	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3276	0.3276	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	2669	0.26689999999999997	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2559	0.2559	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	2299	0.2299	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2266	0.22659999999999997	No Hit
CTTGGAGGACATATCGAAGATTTTGTTTTCTACCTC	2051	0.20509999999999998	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1755	0.17550000000000002	No Hit
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1571	0.1571	No Hit

Sequence	Count	Percentage	Possible Source
CGAAGATTTTGTTTTCTACCTCGATGTTGAATTGTA	1558	0.1558	No Hit
GGAGGACATATCGAAGATTTTGTTTTCTACCTCGAT	1524	0.1524	No Hit
TTTGAATACTTATTTATTACATTATGAACTTCCTTA	1384	0.1384	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1305	0.1305	No Hit
CTAAAGTAAGAAACACCACTAAGTTAAAAACTCTCT	1290	0.129	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAAATCTTC	1205	0.1205	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1153	0.1153	No Hit
CGAAAAGACCCTAGAGAGTTTTTAACTTAGTGGTGT	1112	0.1112	No Hit
CAAGGACGAAAAGACCCTAGAGAGTTTTTAACTTAG	1070	0.107	No Hit
ATTTCAAGGACGAAAAGACCCTAGAGAGTTTTTAAC	1054	0.10540000000000001	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1050	0.105	No Hit
GACATATCGAAGATTTTGTTTTCTACCTCGATGTTG	1041	0.1041	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)