FastQC Report

Wed 6 Jun 2018
ERR032068_2_REP1.fq

Summary

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- Per base sequence content
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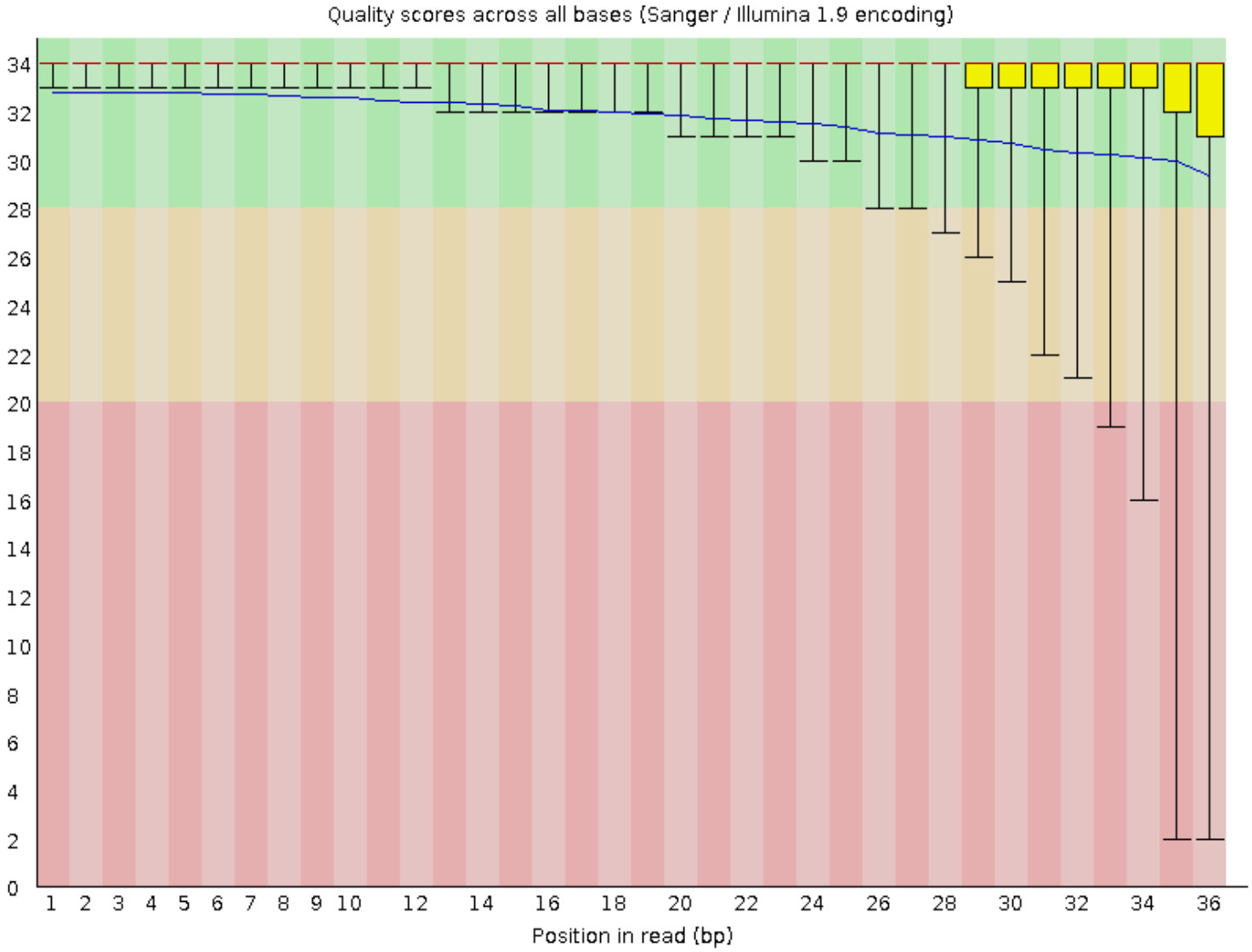
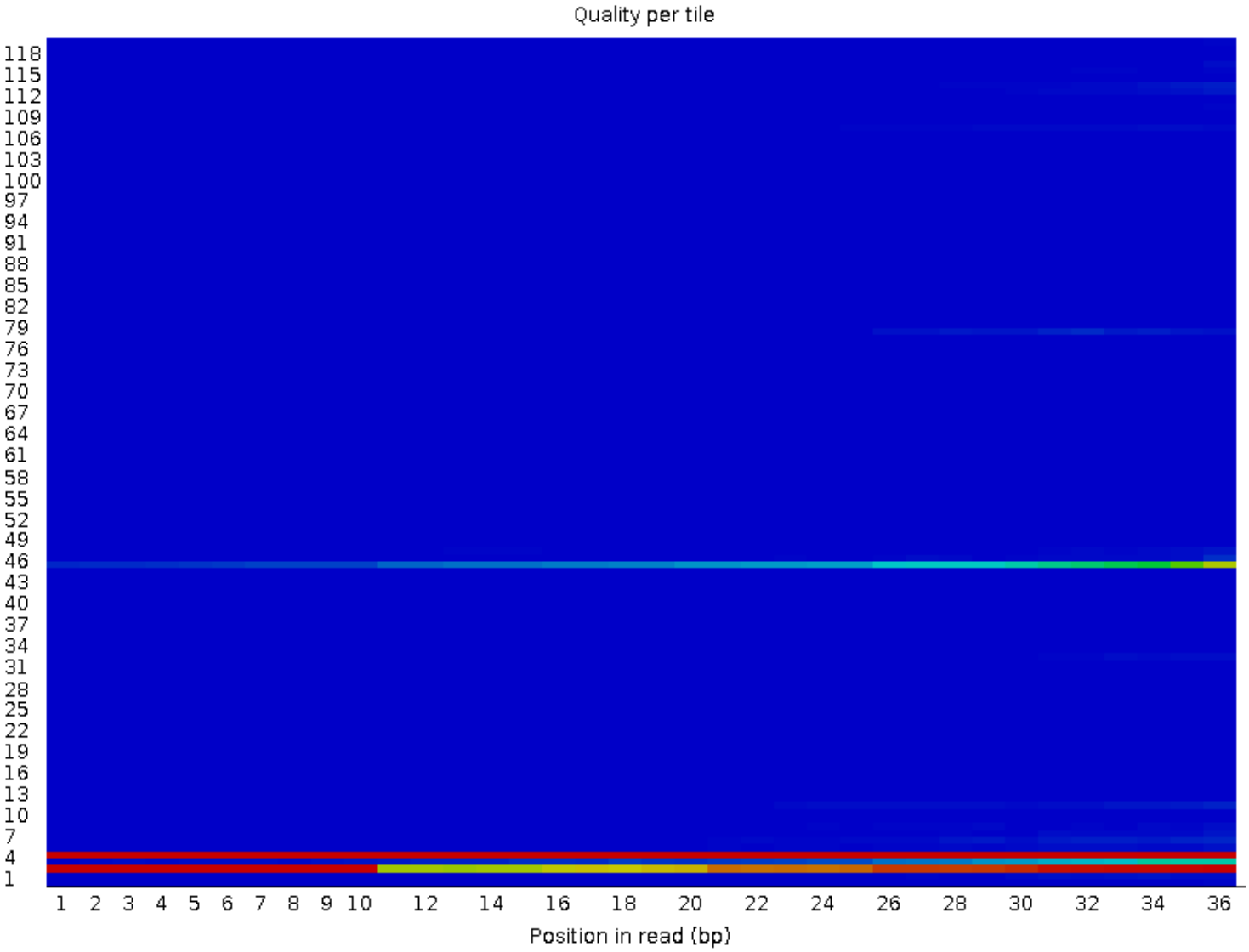
Basic Statistics

Measure	Value
Filename	ERR032068_2_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

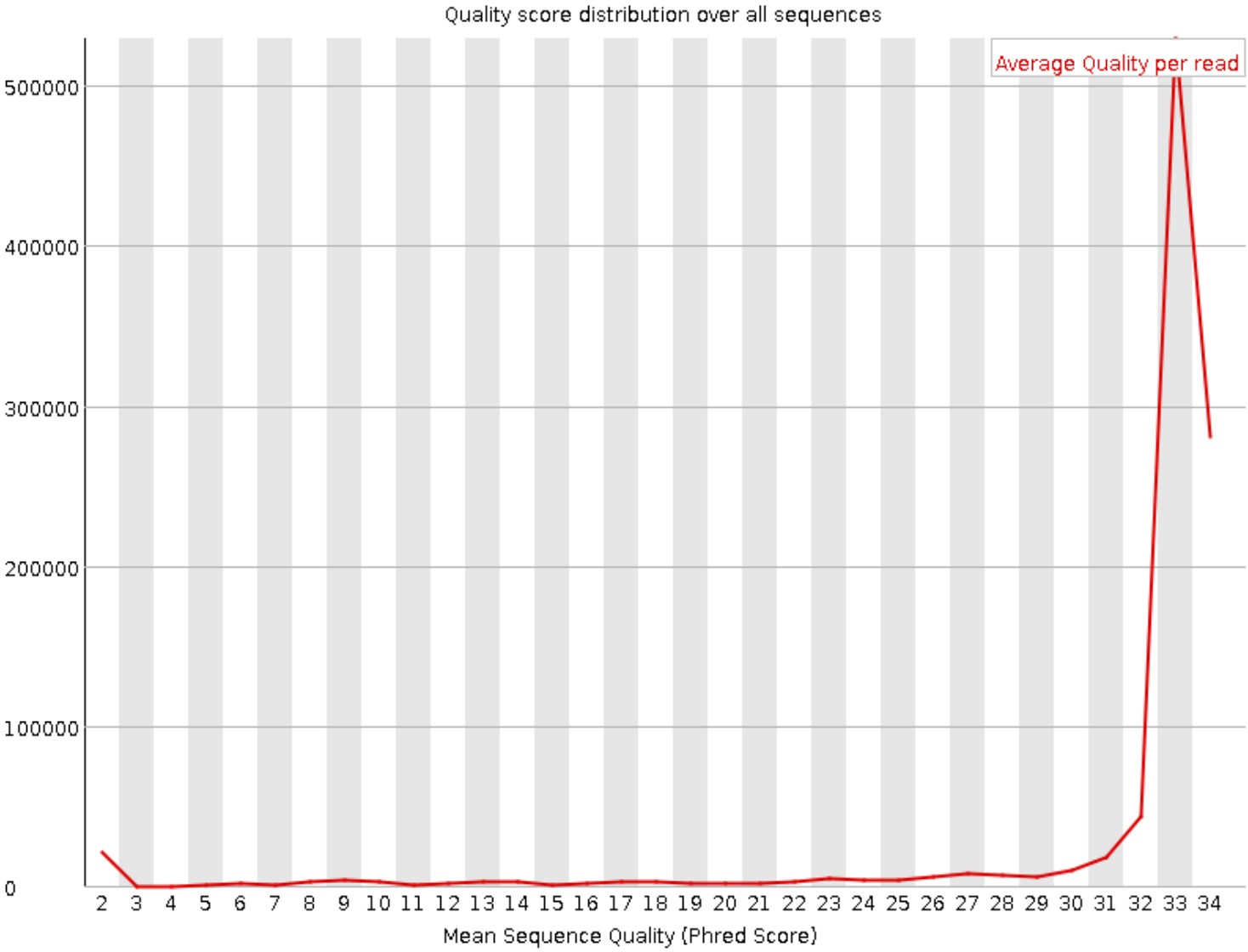
Per base sequence quality



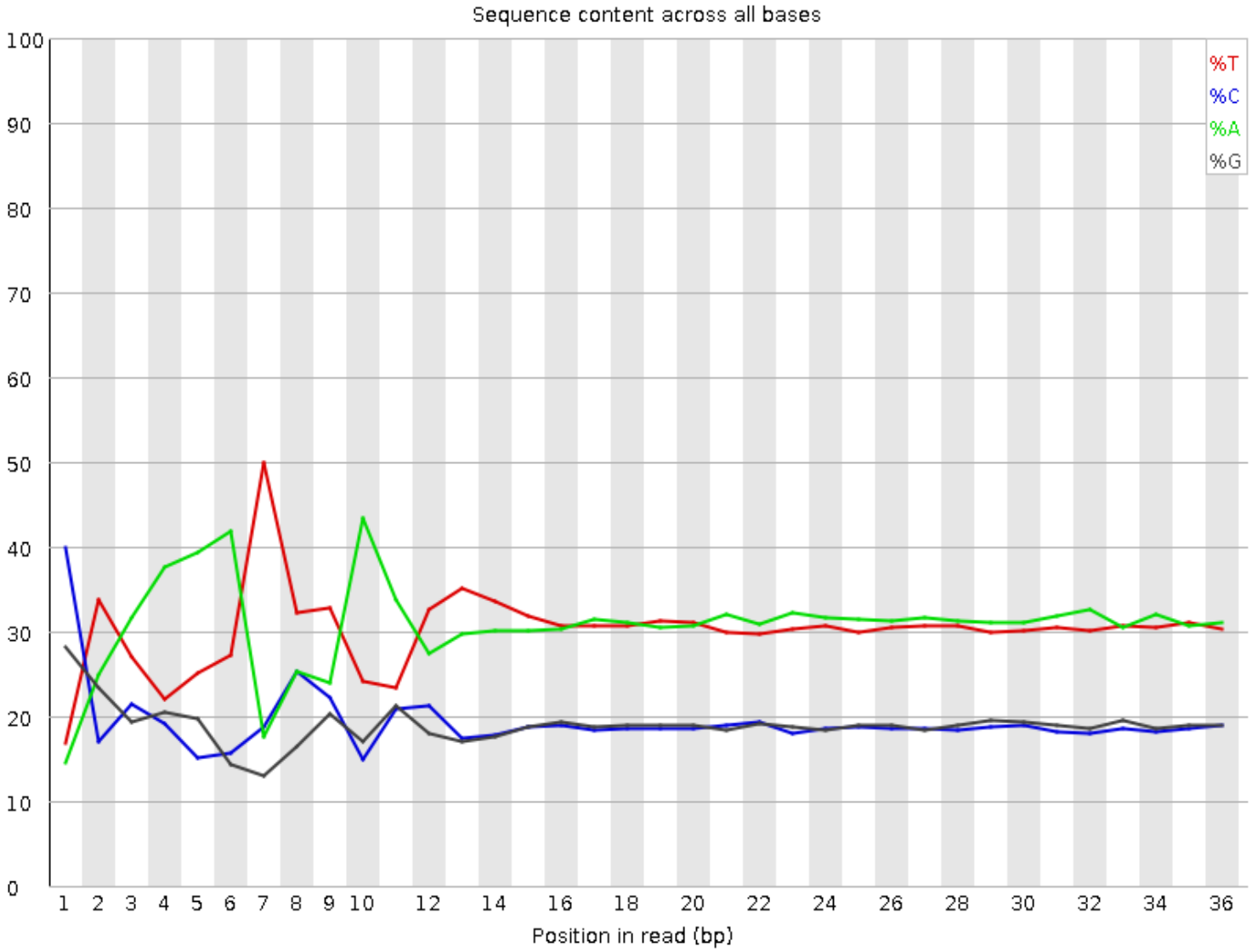
Per tile sequence quality



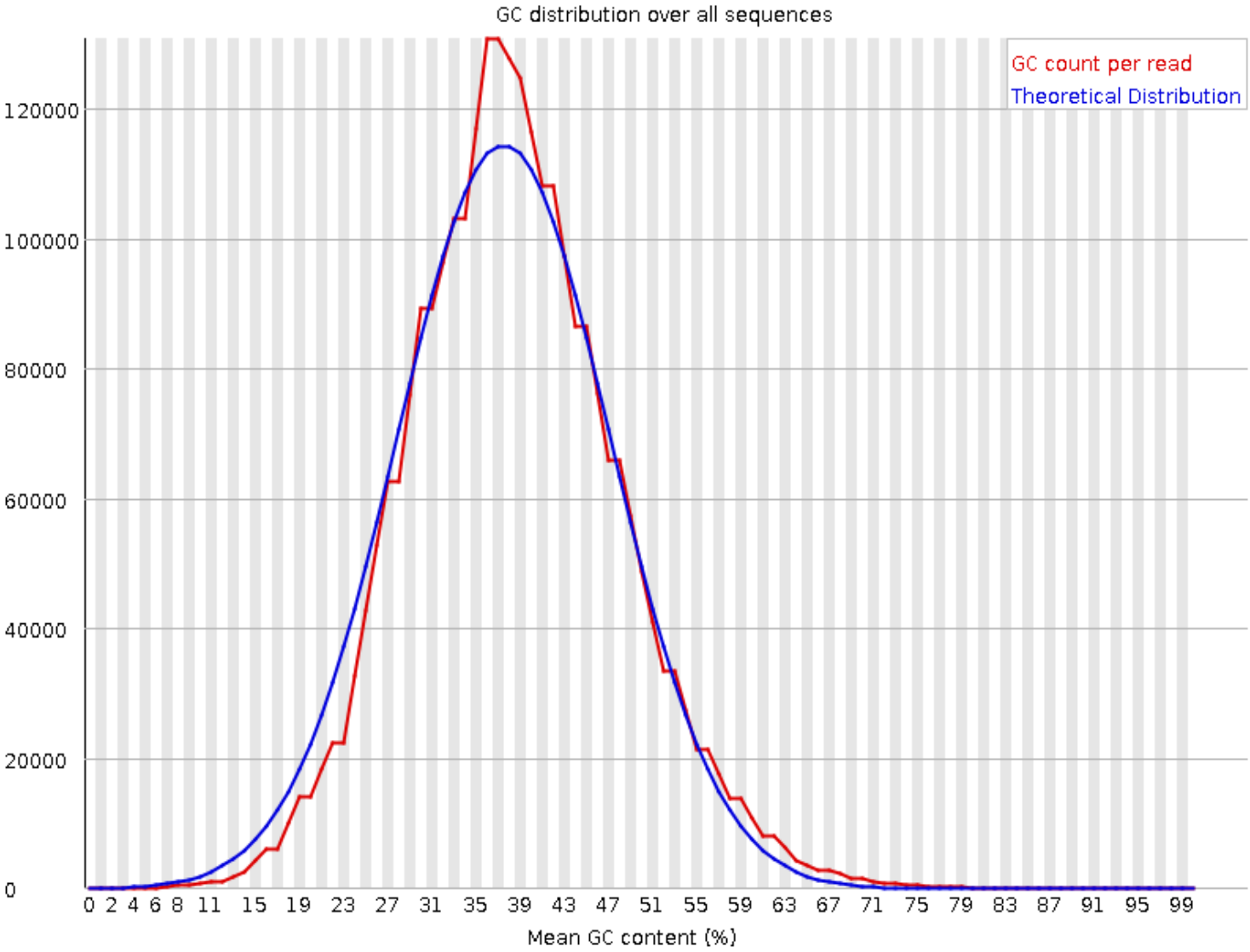
Per sequence quality scores



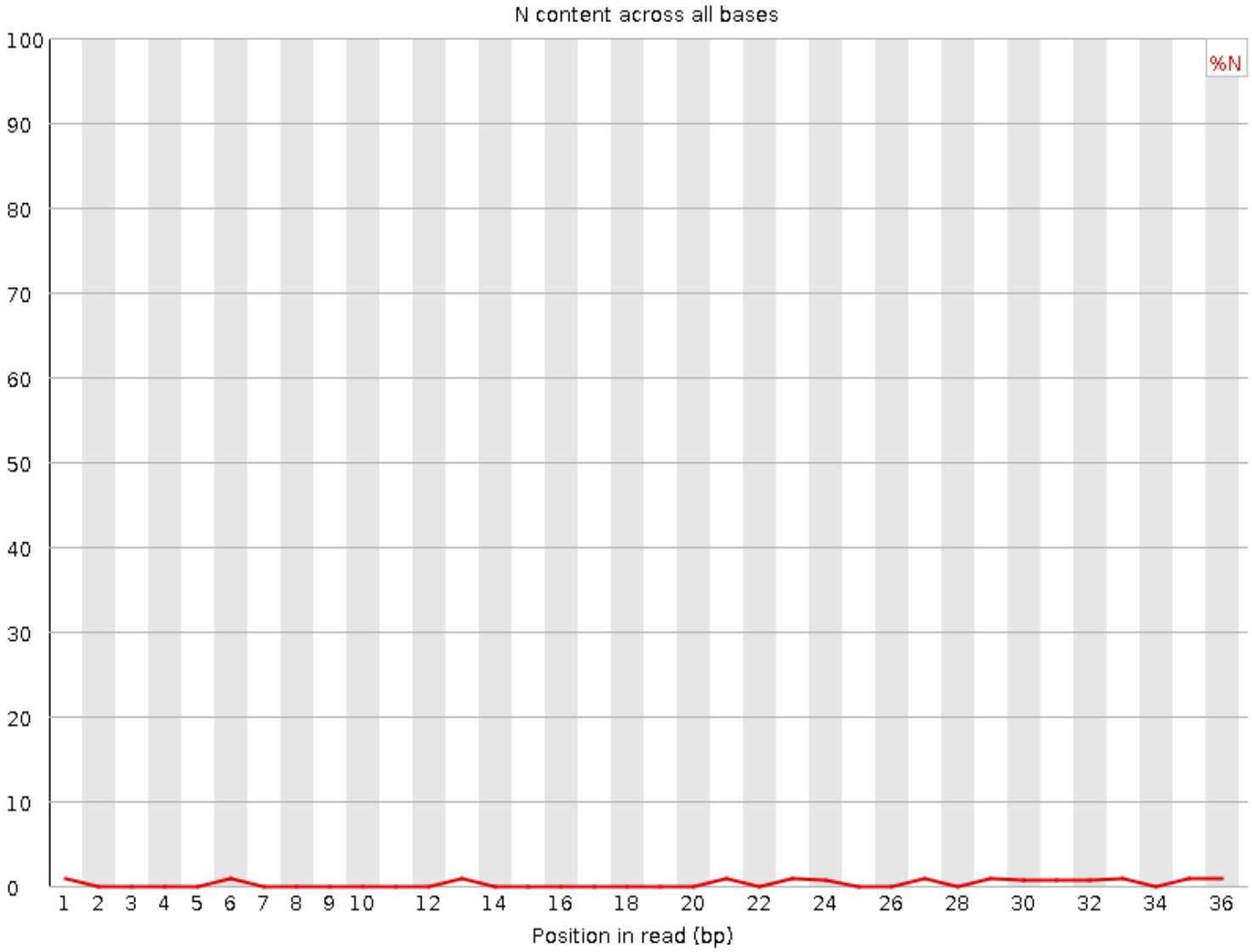
Per base sequence content



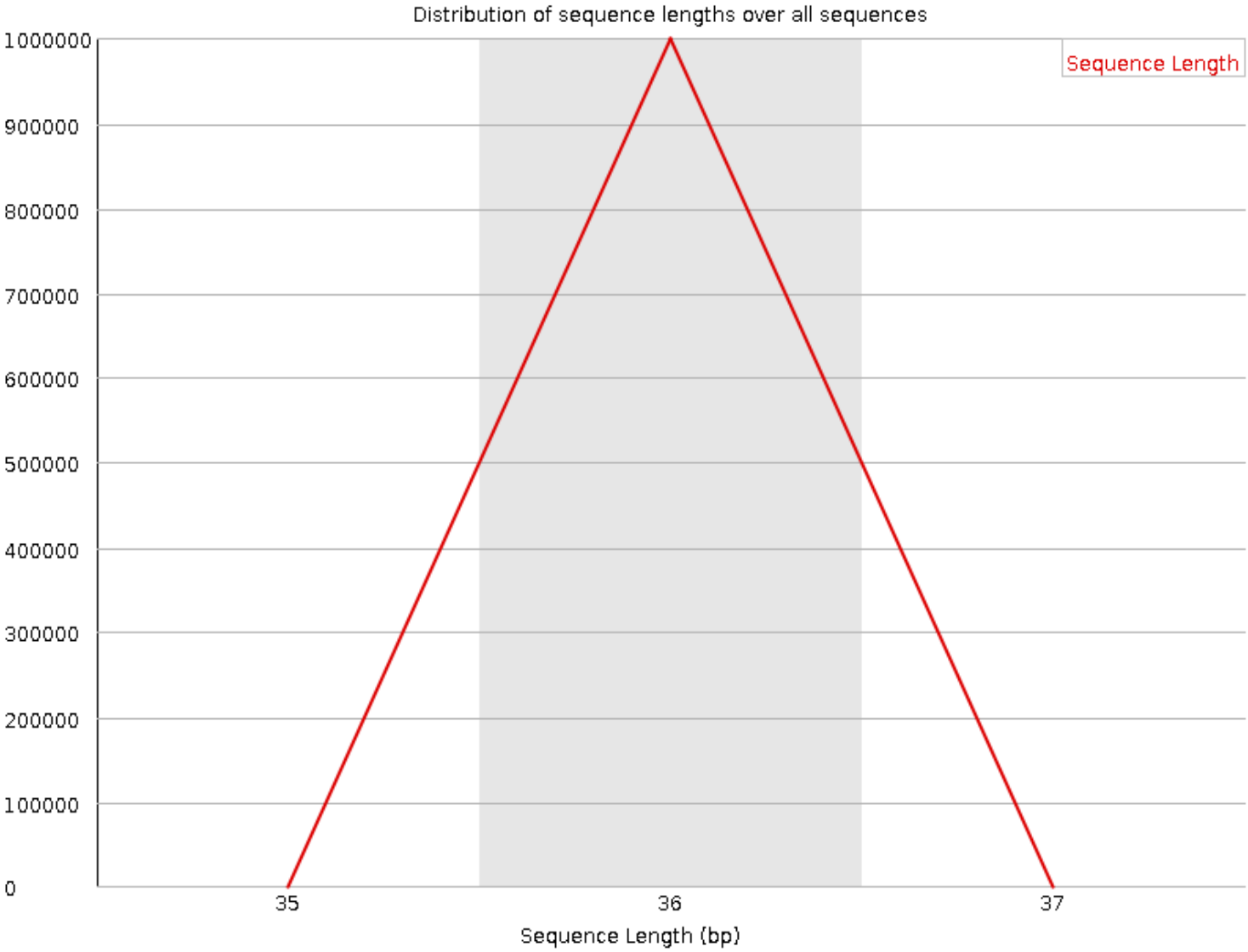
Per sequence GC content



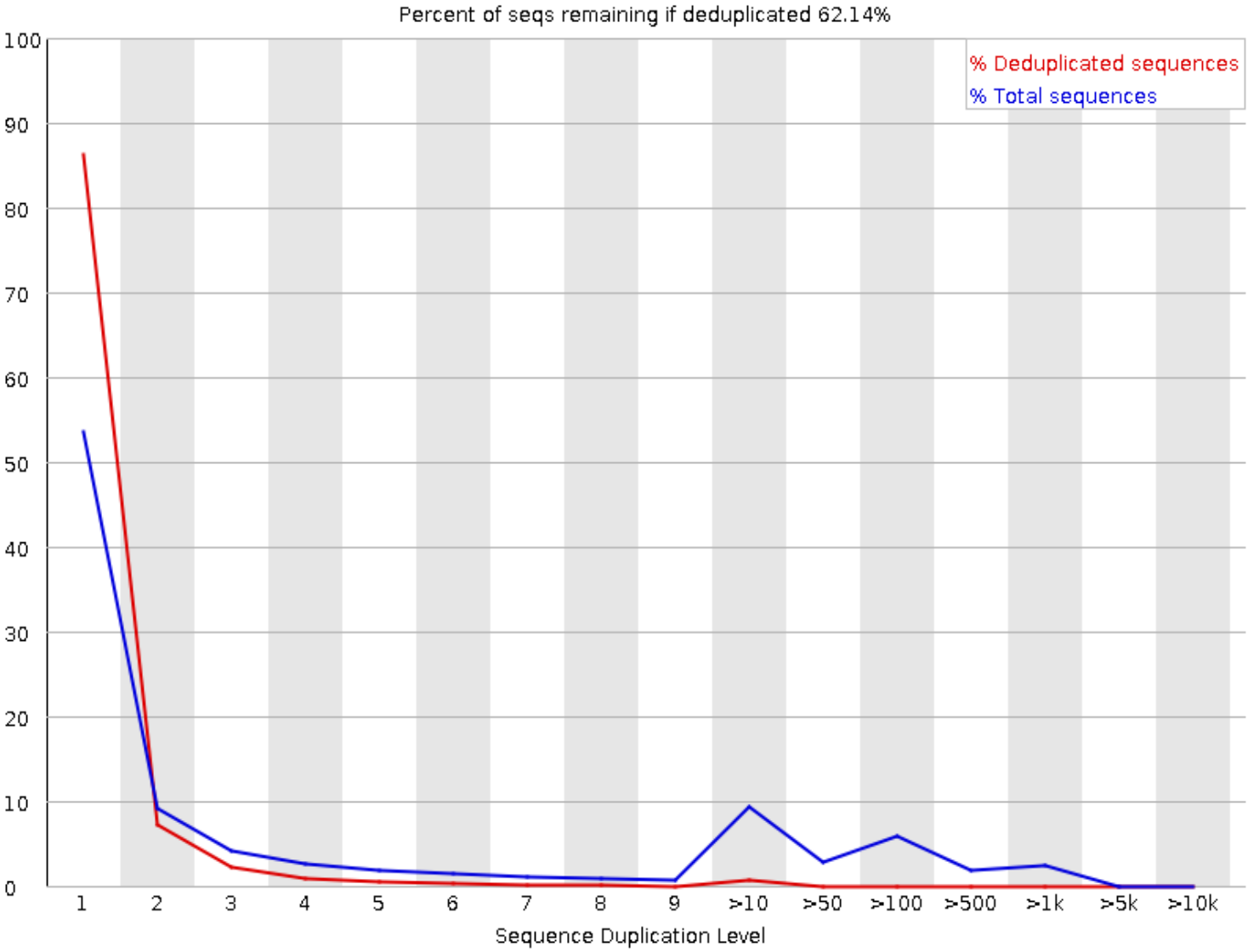
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

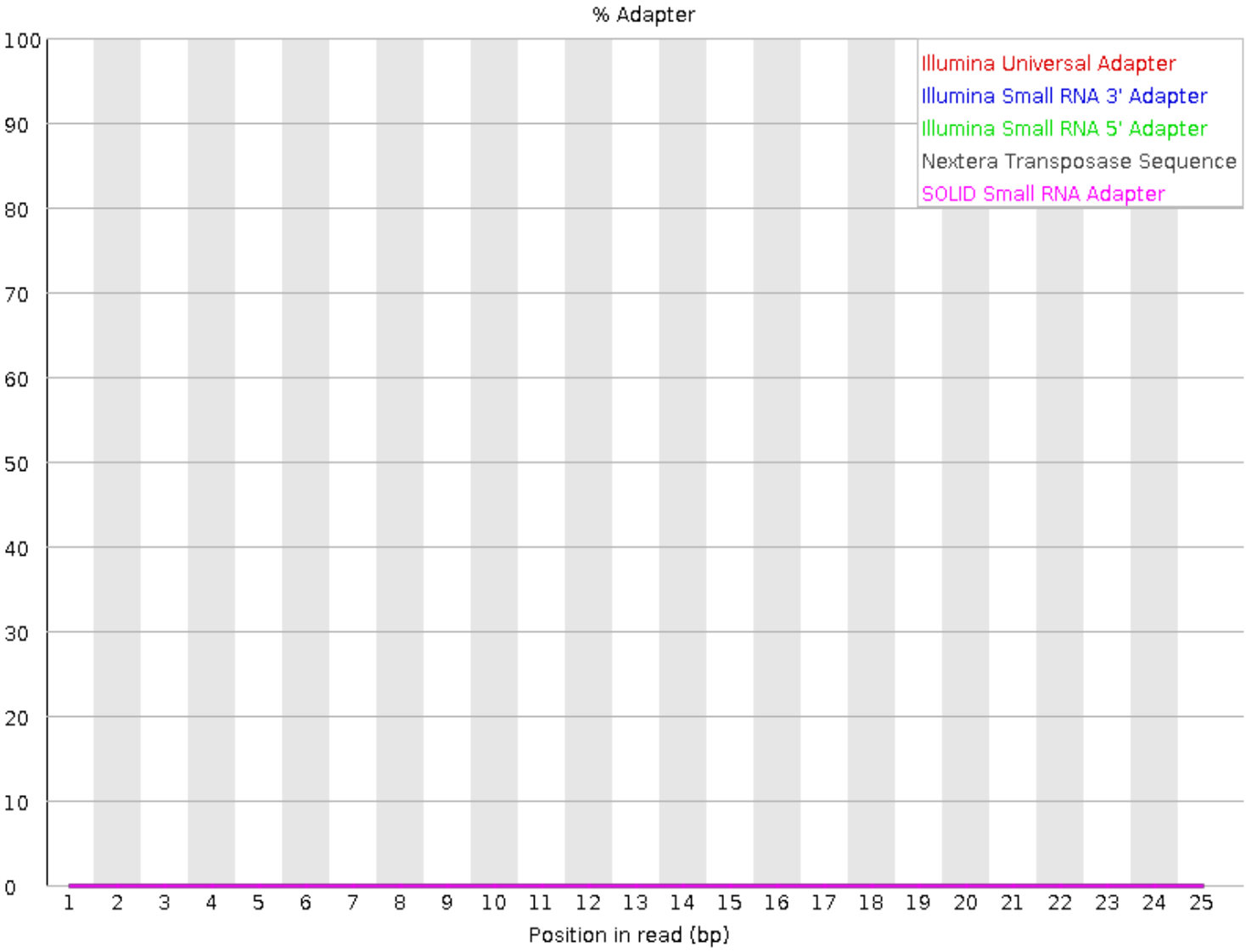


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3289	0.32889999999999997	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	2911	0.29109999999999997	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2613	0.2613	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	2118	0.21180000000000002	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	1973	0.1973	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1785	0.1785	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1426	0.1426	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1380	0.13799999999999998	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1350	0.135	No Hit

Sequence	Count	Percentage	Possible Source
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1347	0.13470000000000001	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1157	0.1157	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1117	0.1117	No Hit
CAGAAATTCAGGATAAAAACCAACCTGATTCACATC	1071	0.10709999999999999	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1068	0.10679999999999999	No Hit
CTTCCTTAGGGATAACAGGGATATAGAATCTTGGAG	1061	0.10610000000000001	No Hit
CGAAGATTTTGTTTTCTACCTCGATGTTGAATTGTA	1050	0.105	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)