FastQC Report

Wed 6 Jun 2018
ERR032068_1_REP2.fq

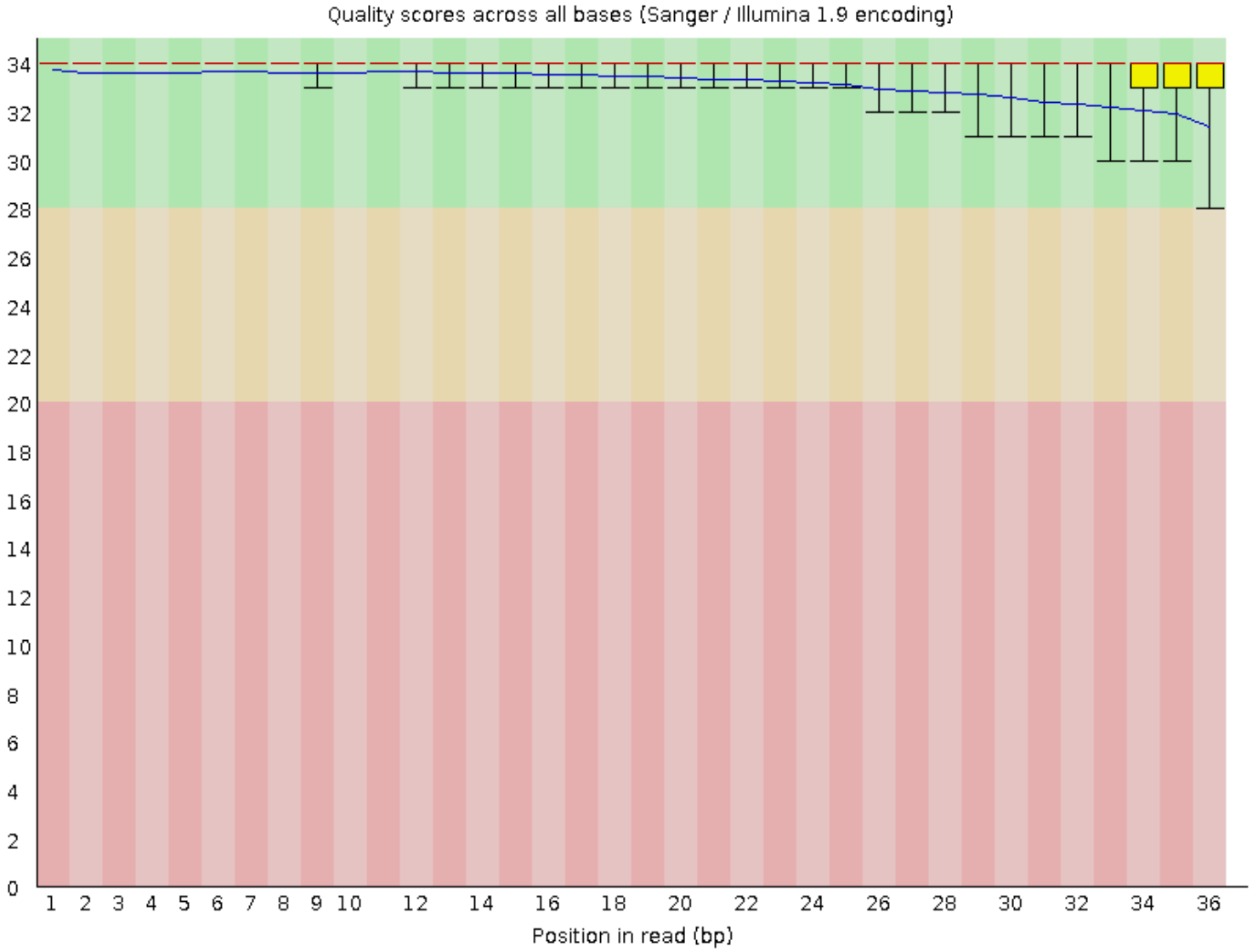
Summary

- Basic Statistics
- 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
- Adapter Content

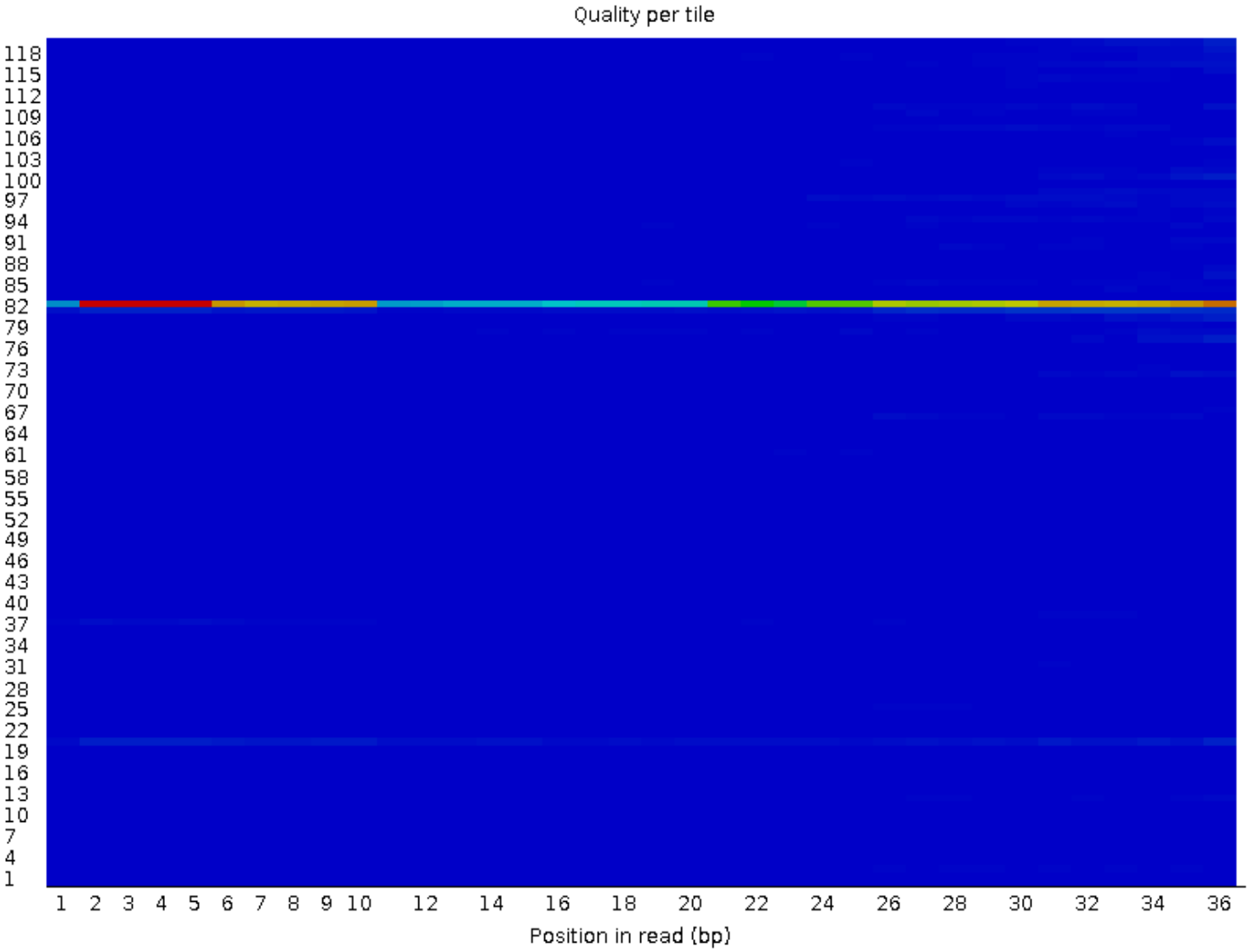
Basic Statistics

Measure	Value
Filename	ERR032068_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	38

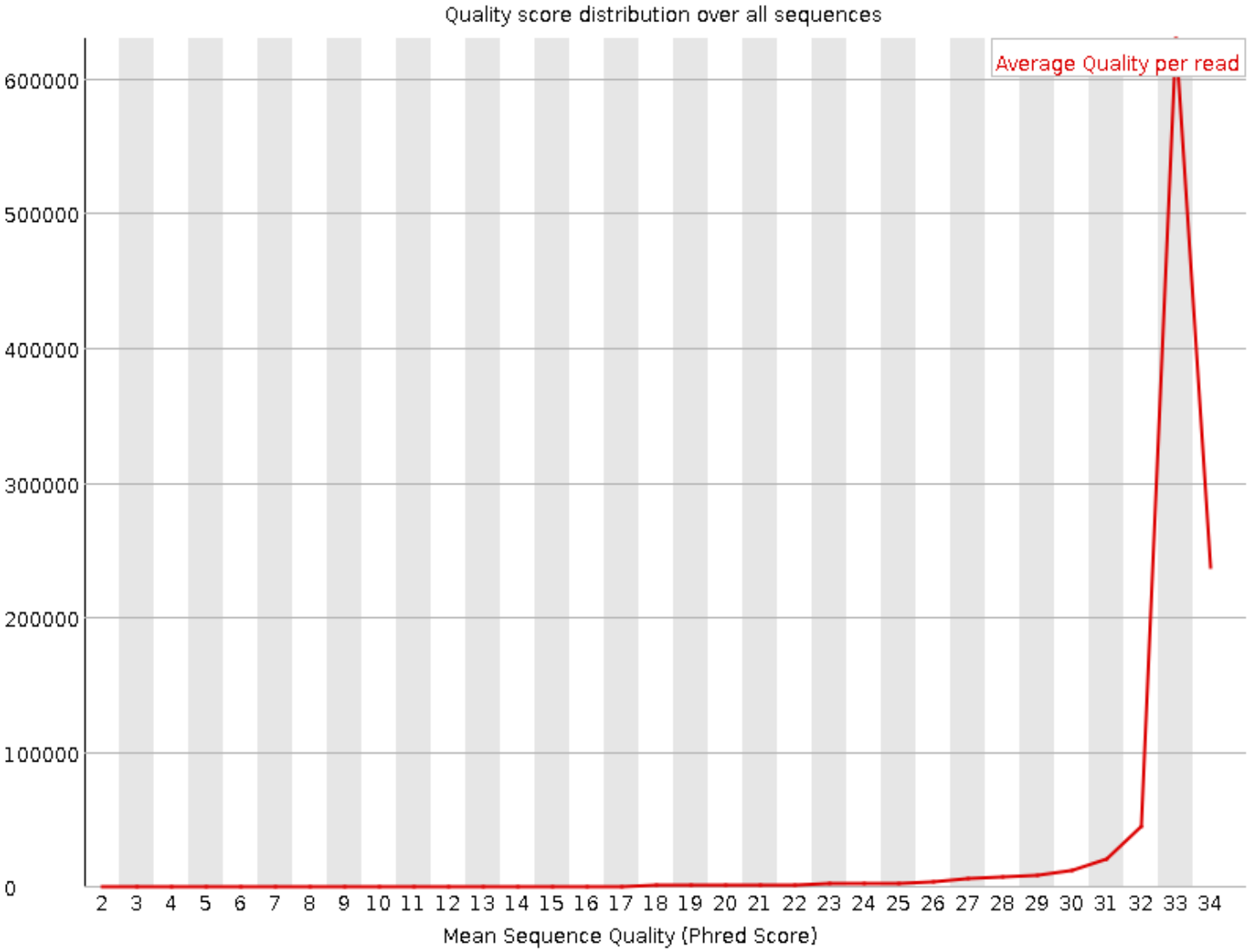
Per base sequence quality



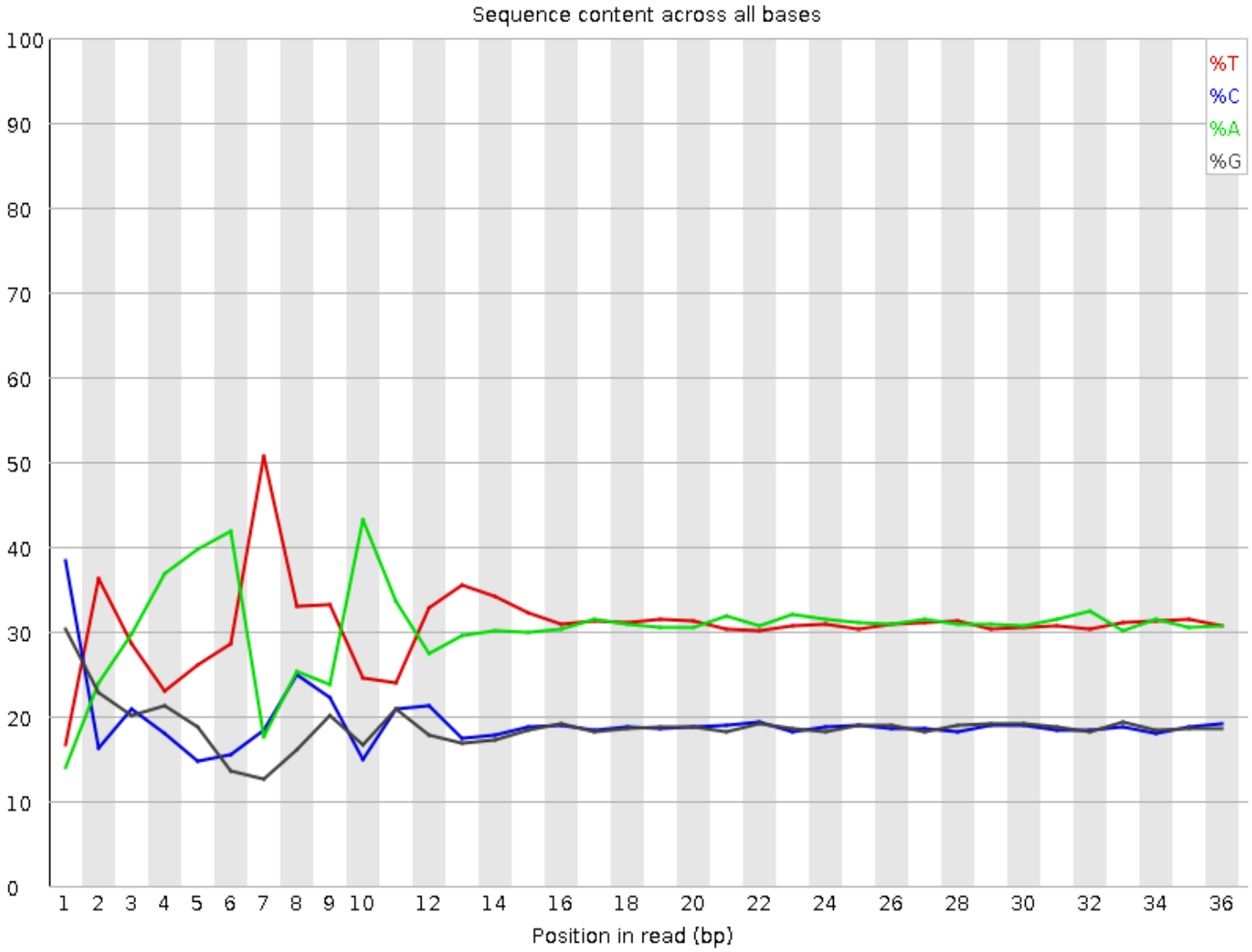
Per tile sequence quality



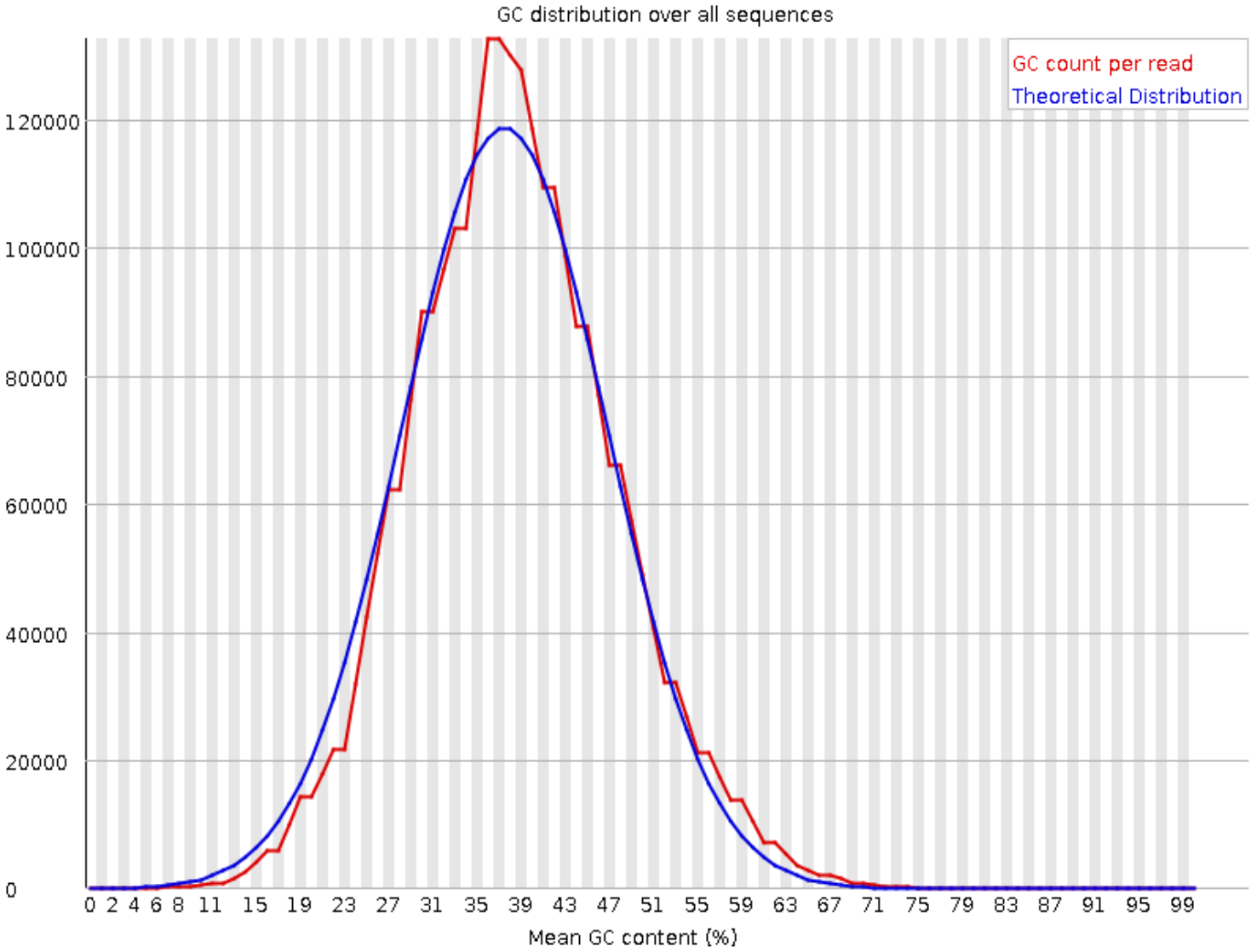
Per sequence quality scores



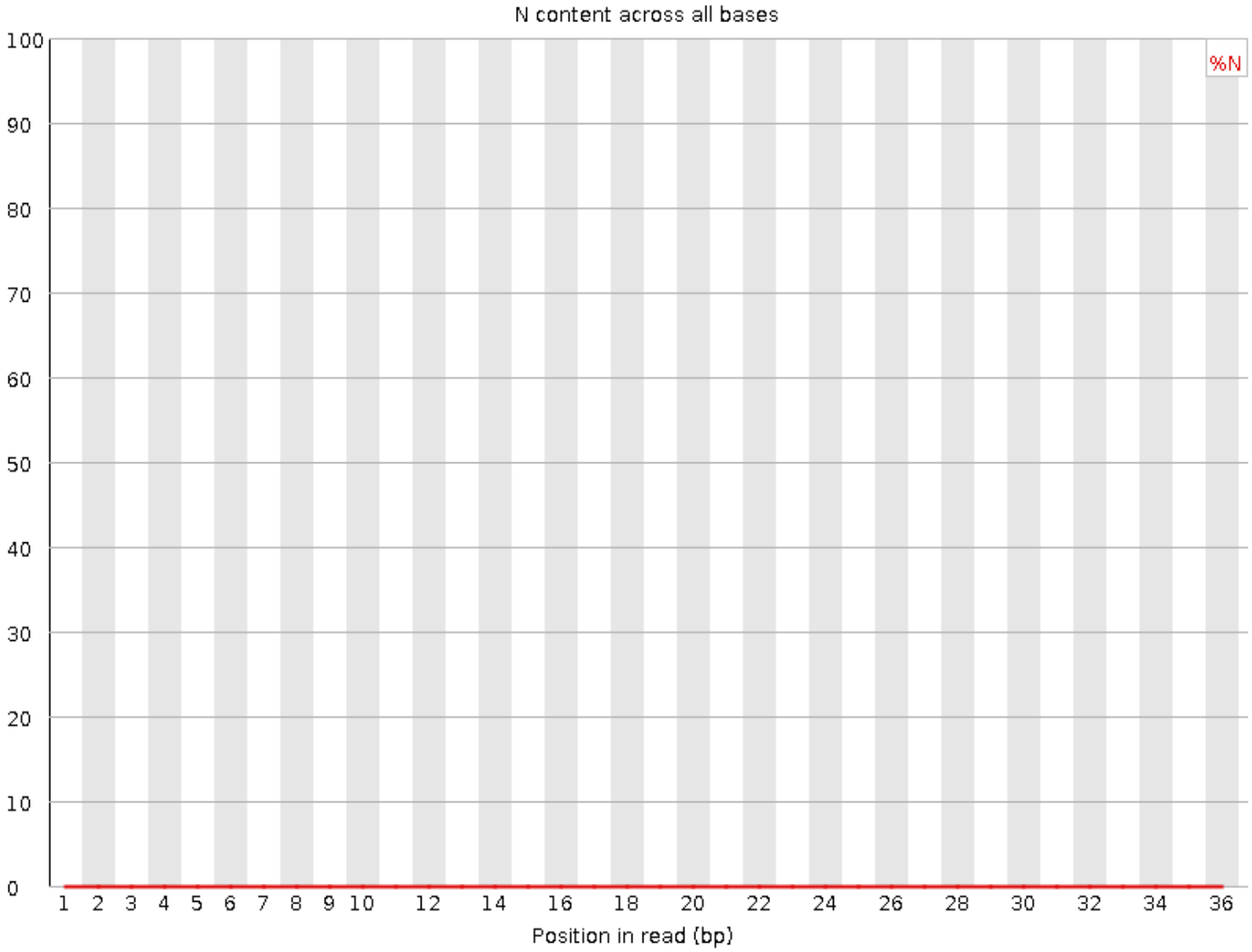
Per base sequence content



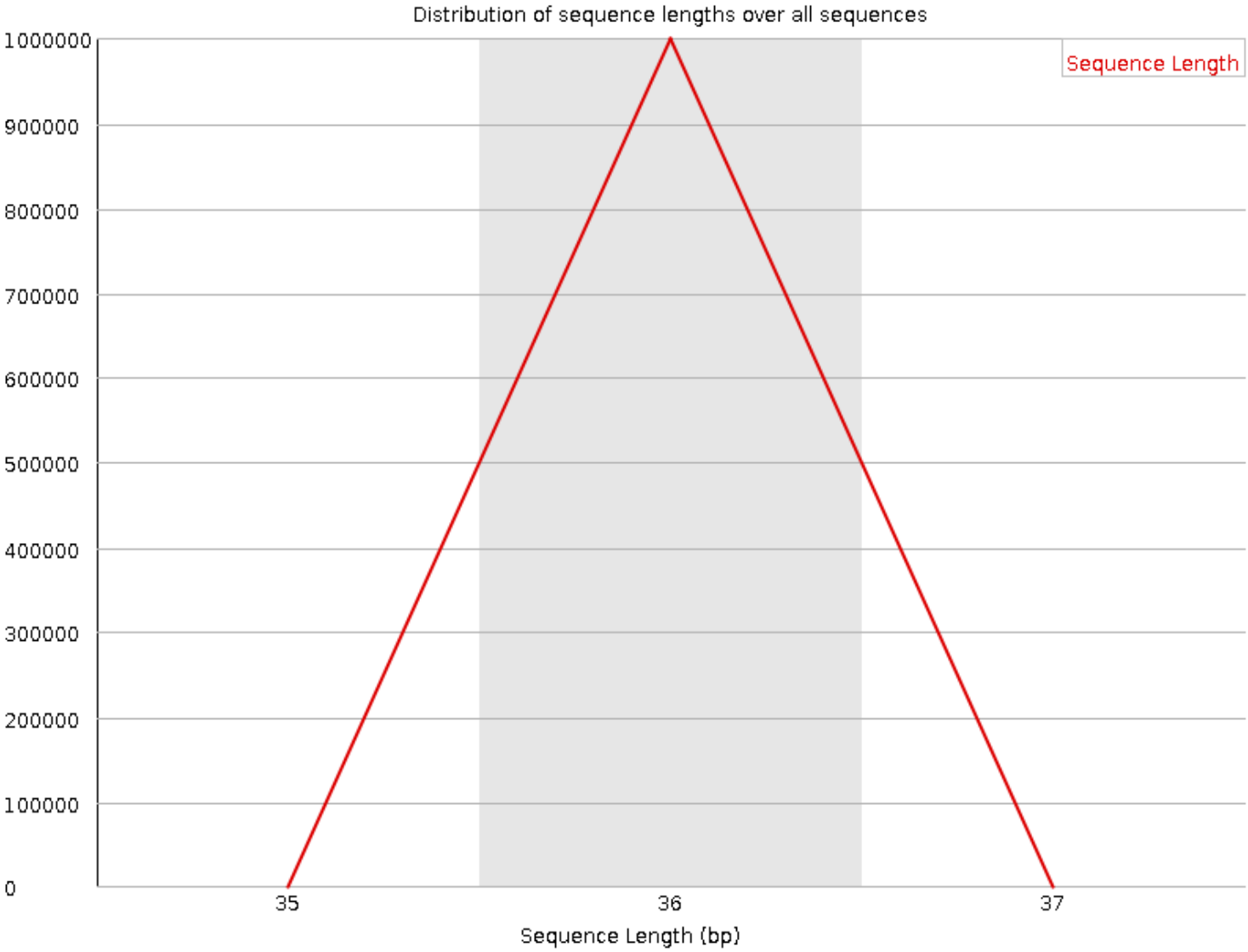
Per sequence GC content



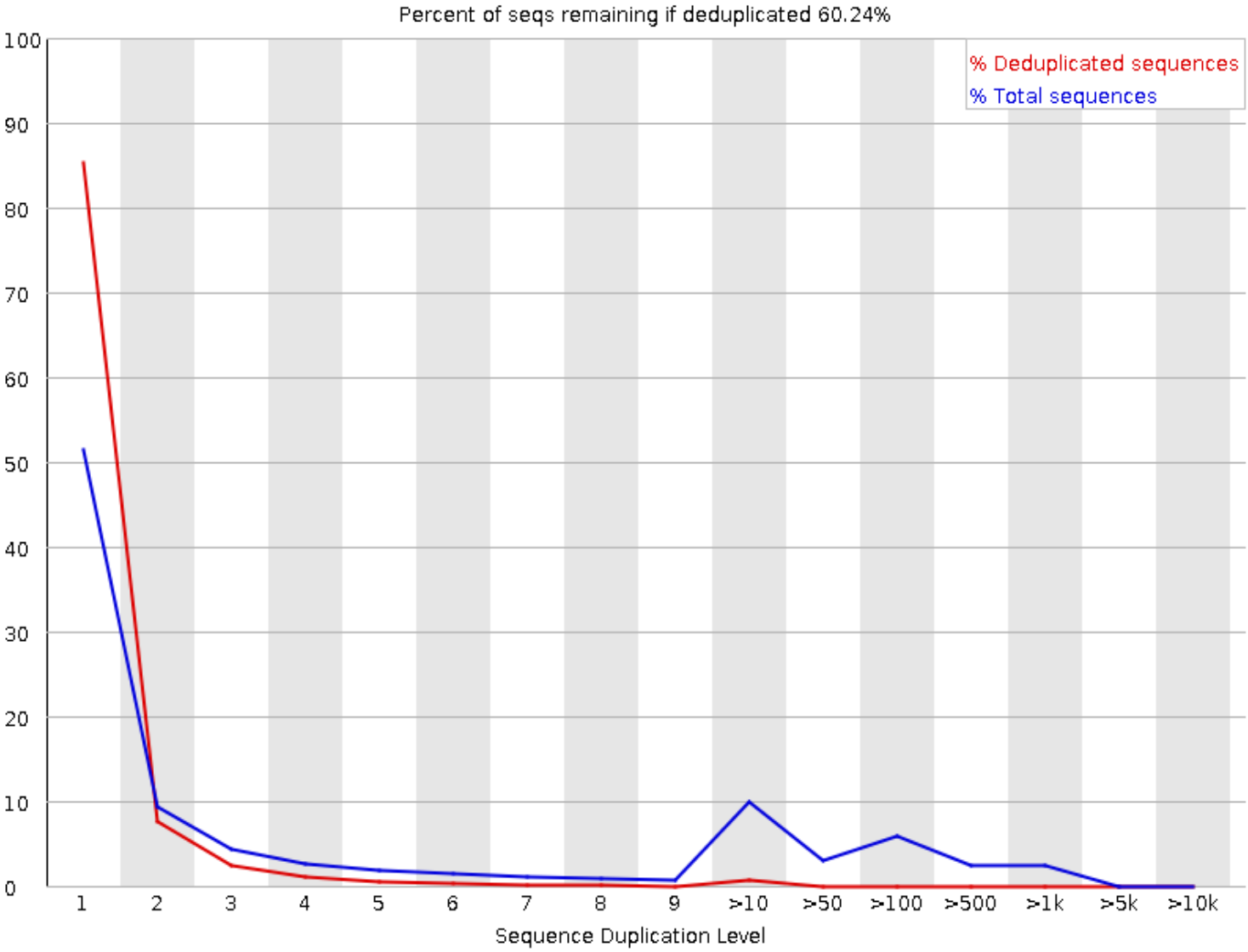
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

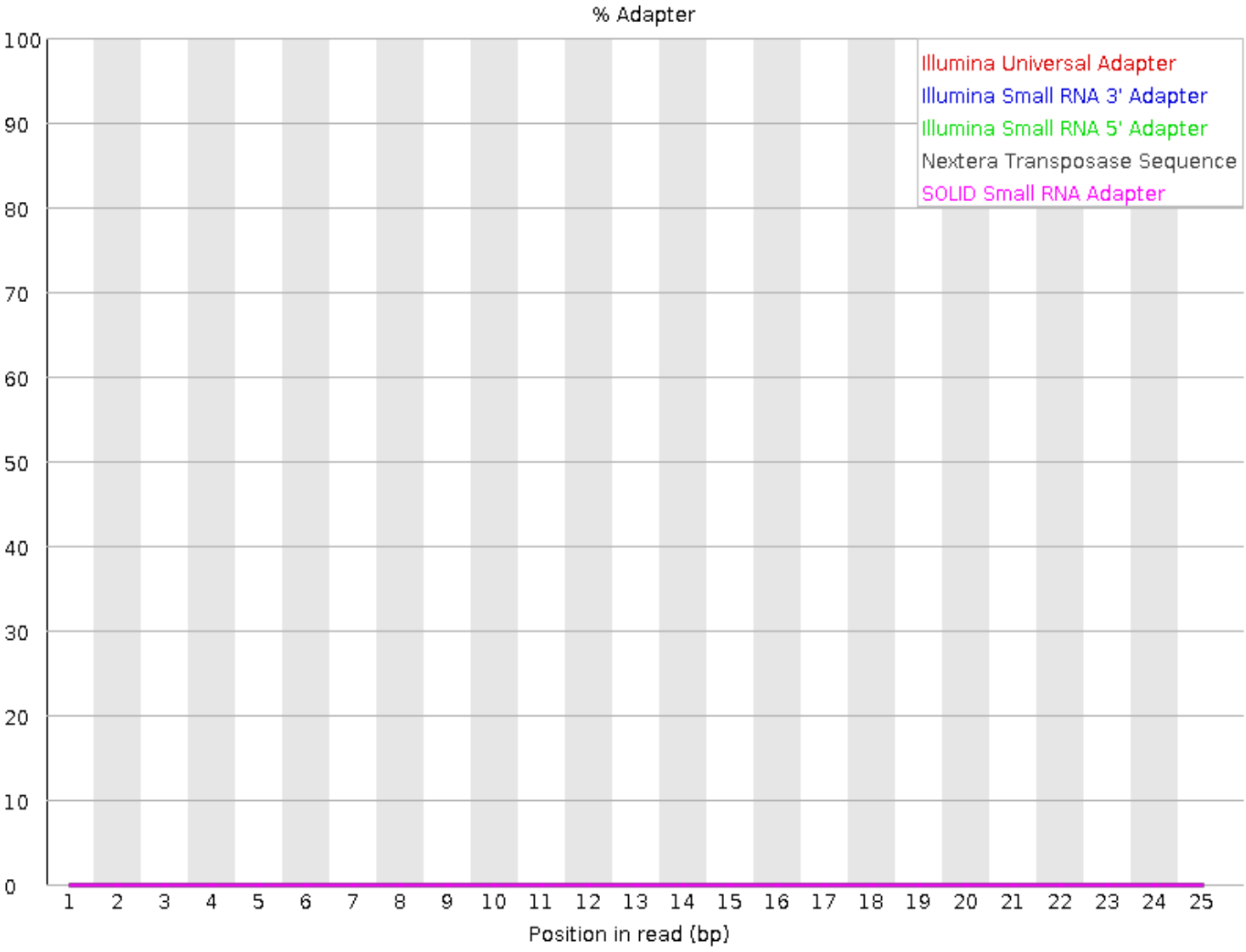


Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3306	0.3306	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3083	0.30829999999999996	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2543	0.2543	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	2068	0.20679999999999998	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2027	0.20270000000000002	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1918	0.1918	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1808	0.1808	No Hit
GTTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1347	0.13470000000000001	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1219	0.12190000000000001	No Hit

Sequence	Count	Percentage	Possible Source
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1181	0.1181	No Hit
CAGAAATTCAGGATAAAAACCAACCTGATTCACATC	1127	0.1127	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1122	0.1122	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1120	0.11199999999999999	No Hit
CTTACTTTAGTTATTTGTTGGGGTAACGGTATTTAT	1014	0.10139999999999999	No Hit
CTCACTGATAAGTTAAATAGCTGCAGTACTTTGACT	1012	0.10120000000000001	No Hit

Adapter Content



Produced by FastQC (version 0.11.7)