












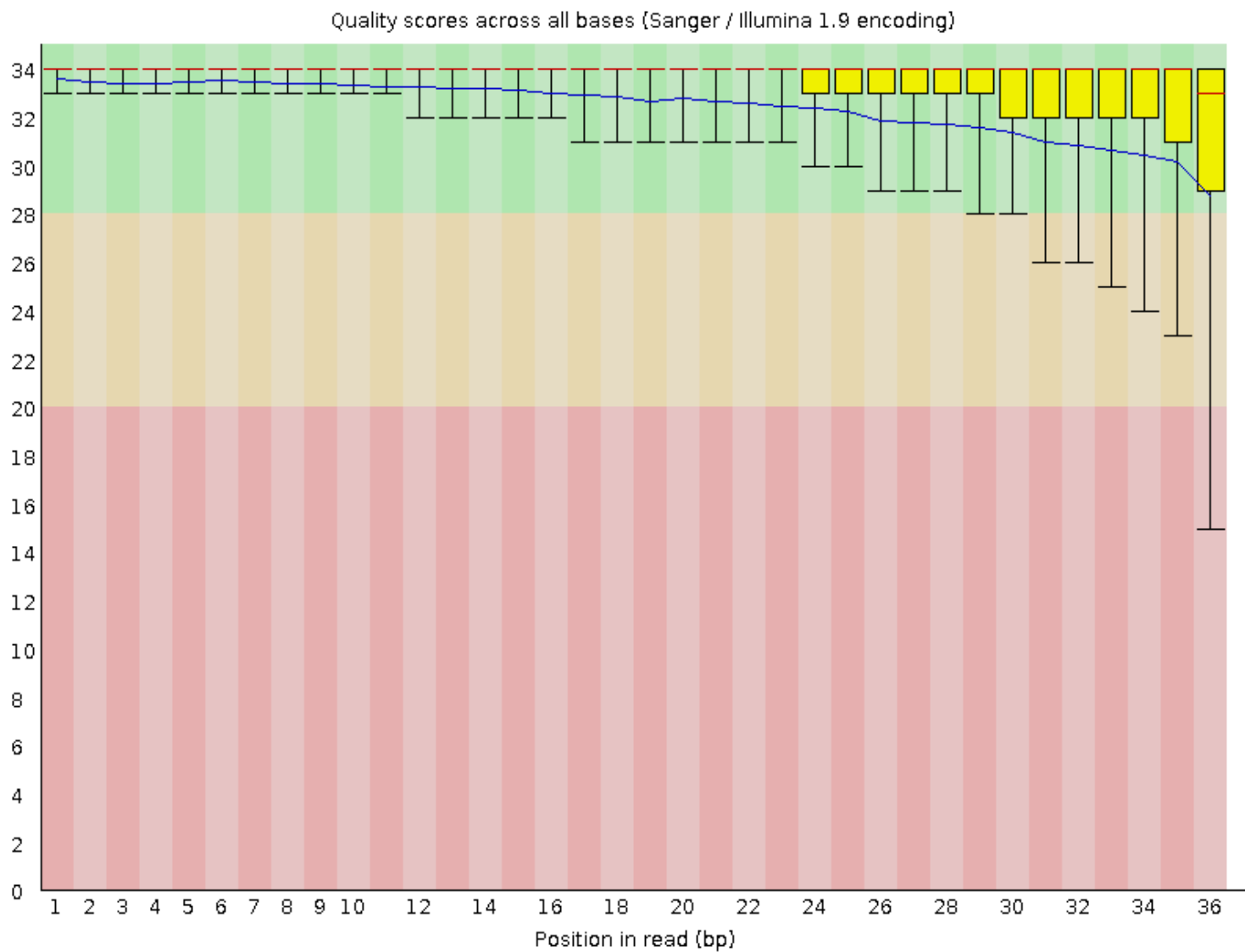
Summary

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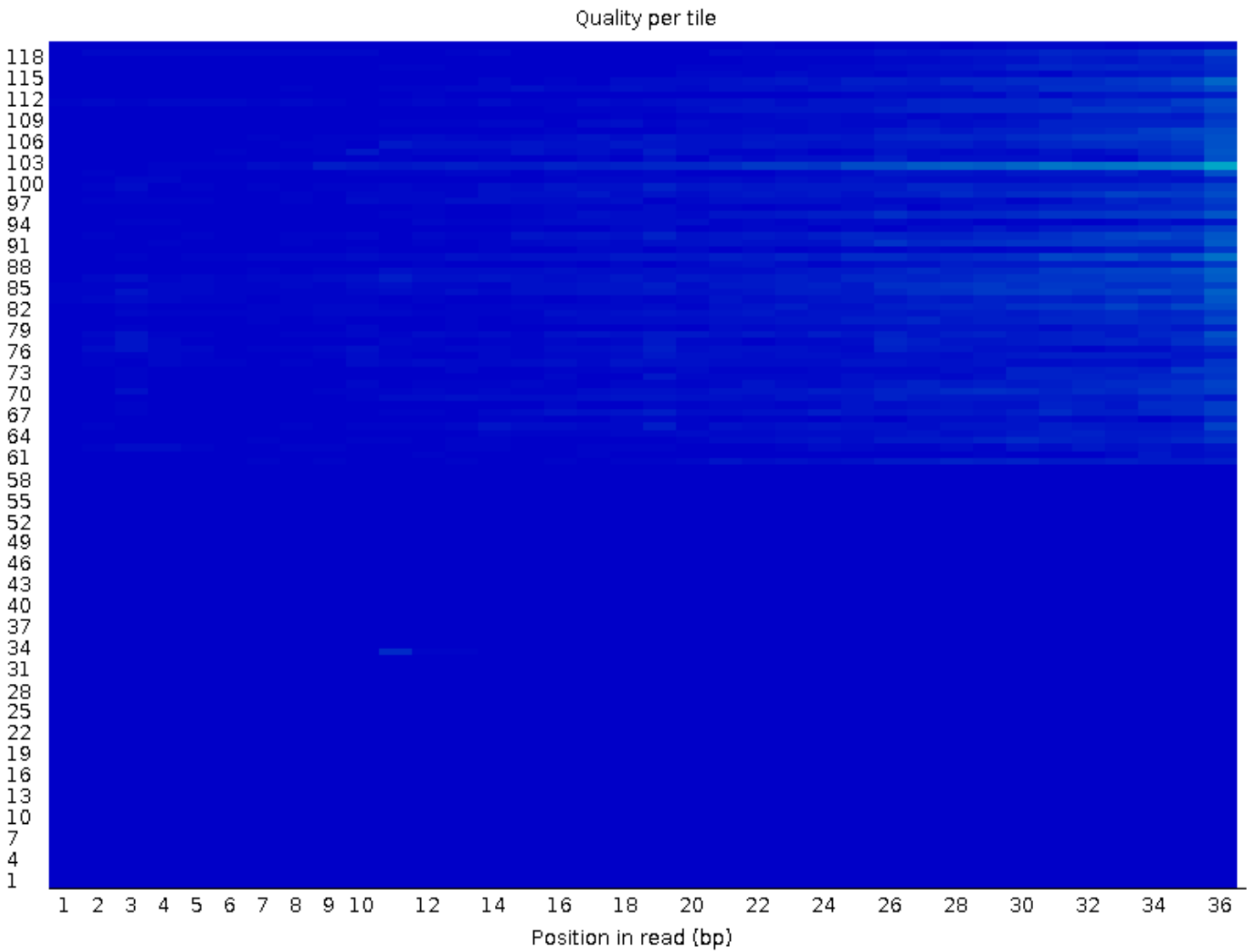
Basic Statistics

Measure	Value
Filename	ERR032071_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

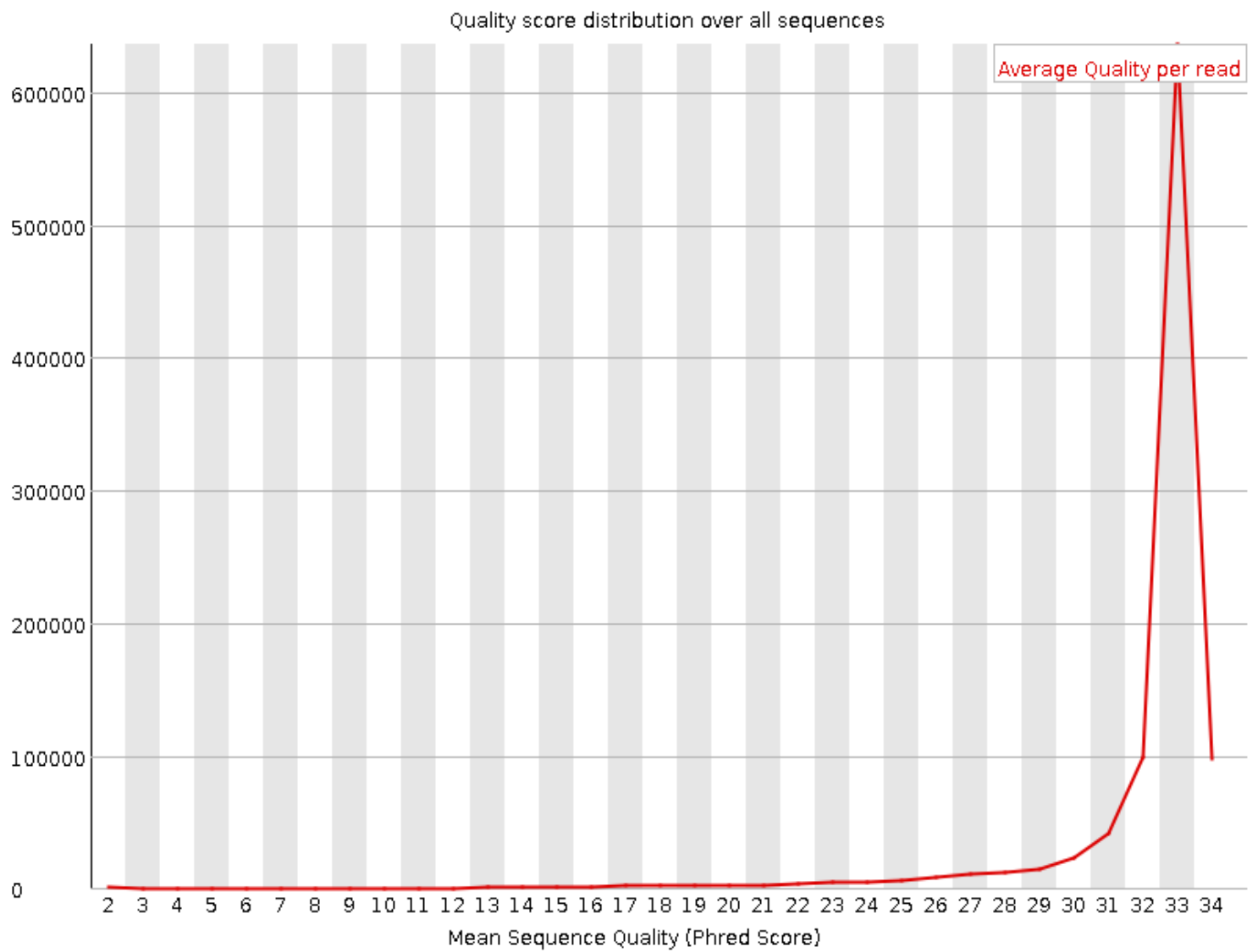
Per base sequence quality



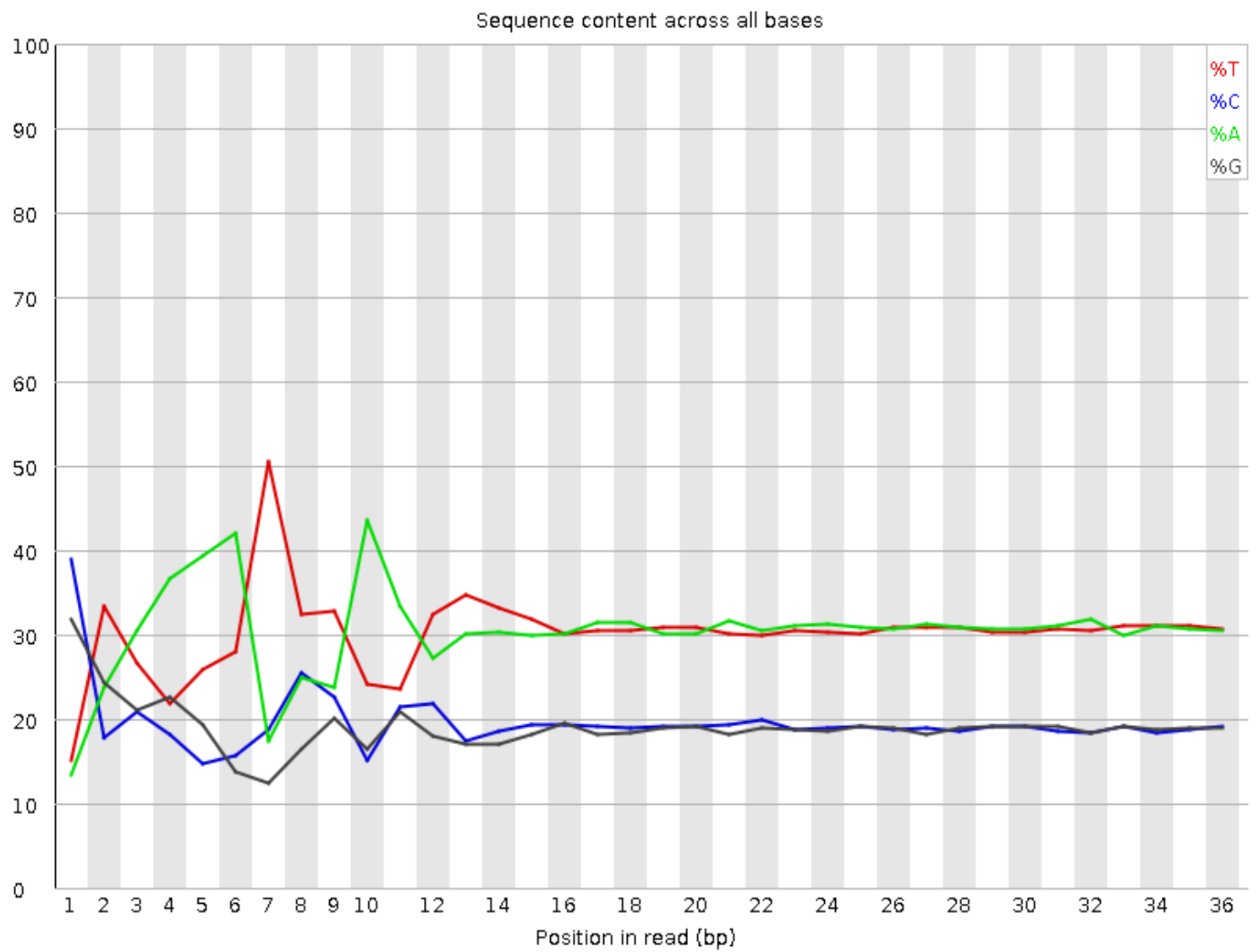
✔ Per tile sequence quality



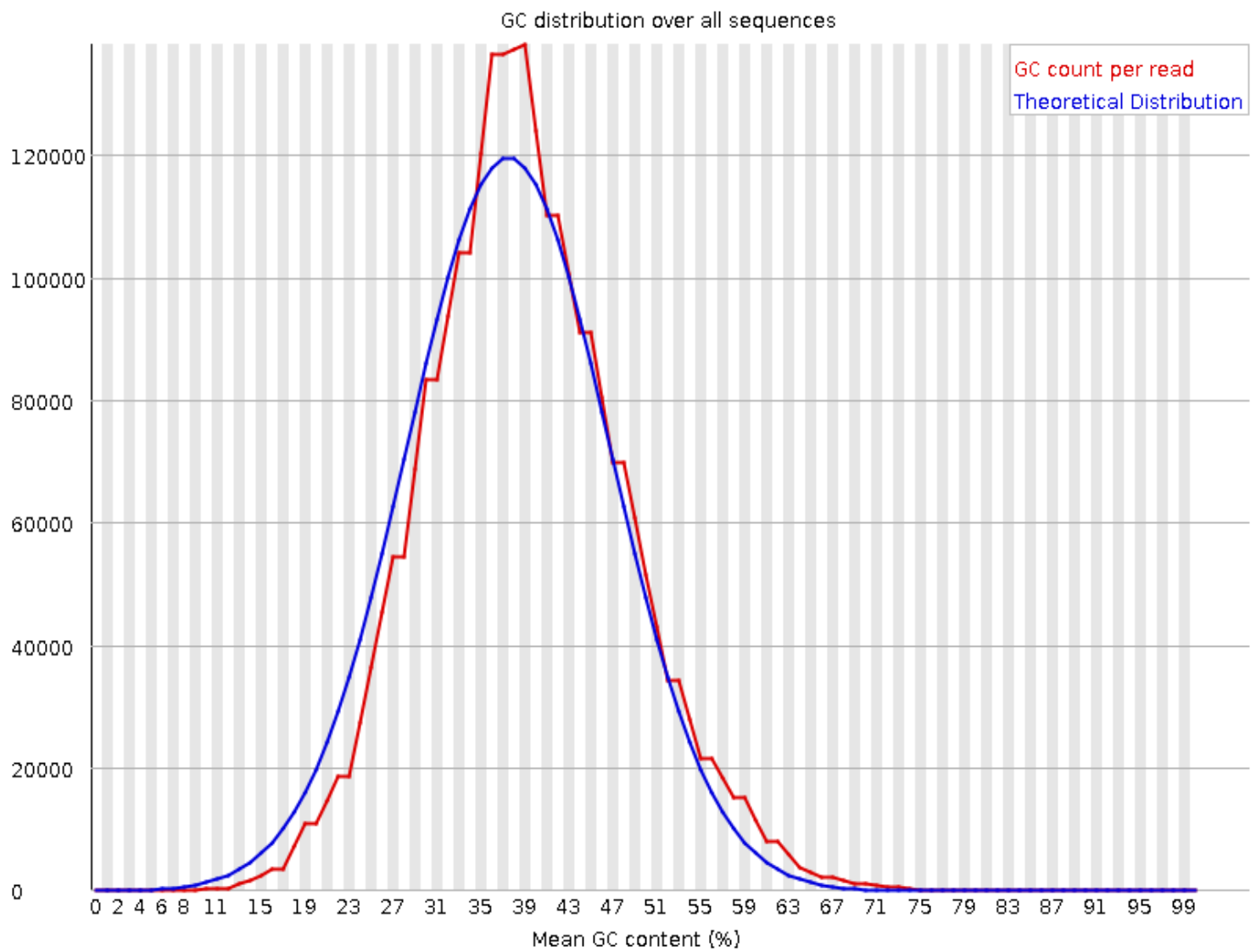
Per sequence quality scores



✖ Per base sequence content

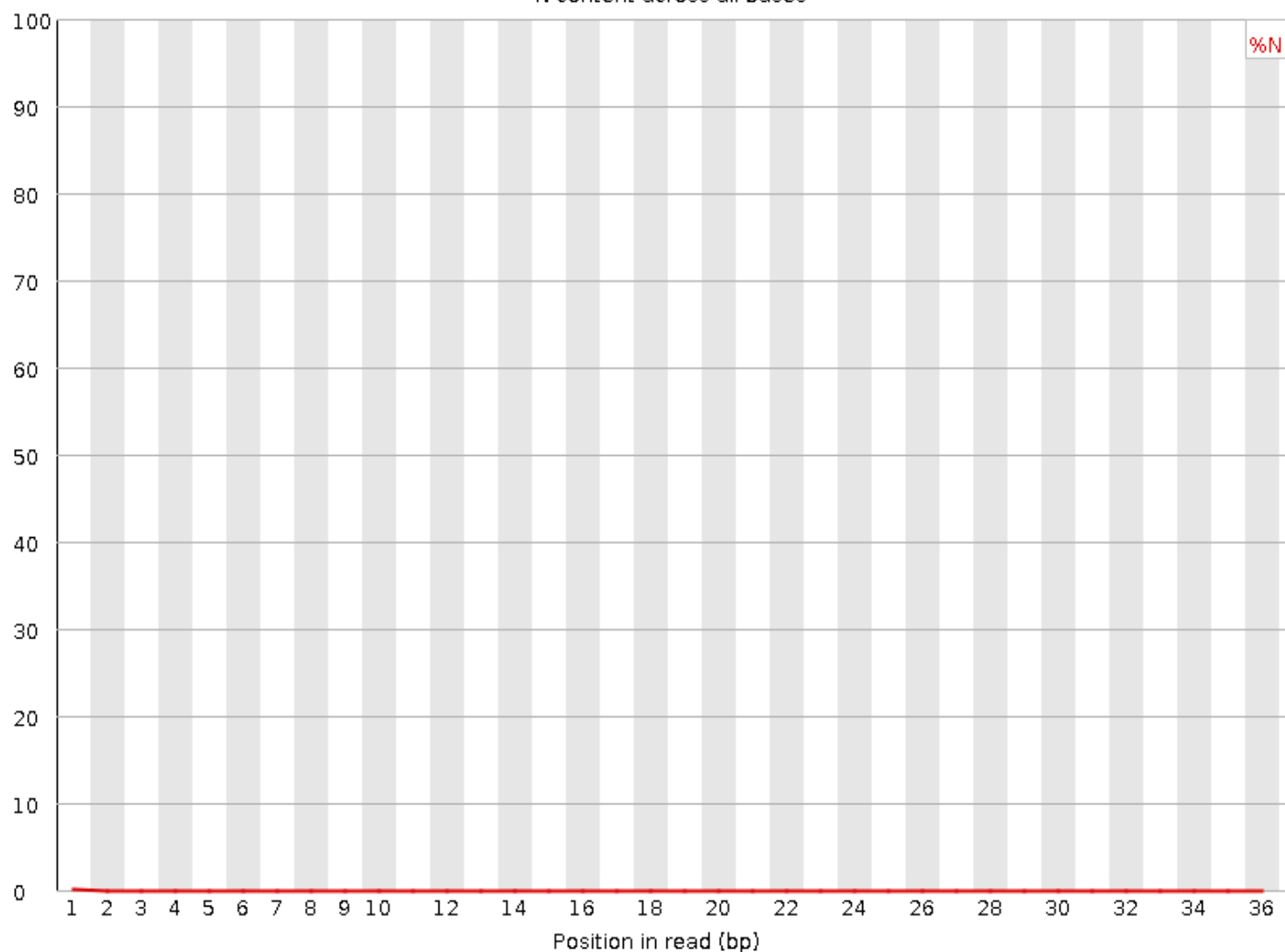


Per sequence GC content

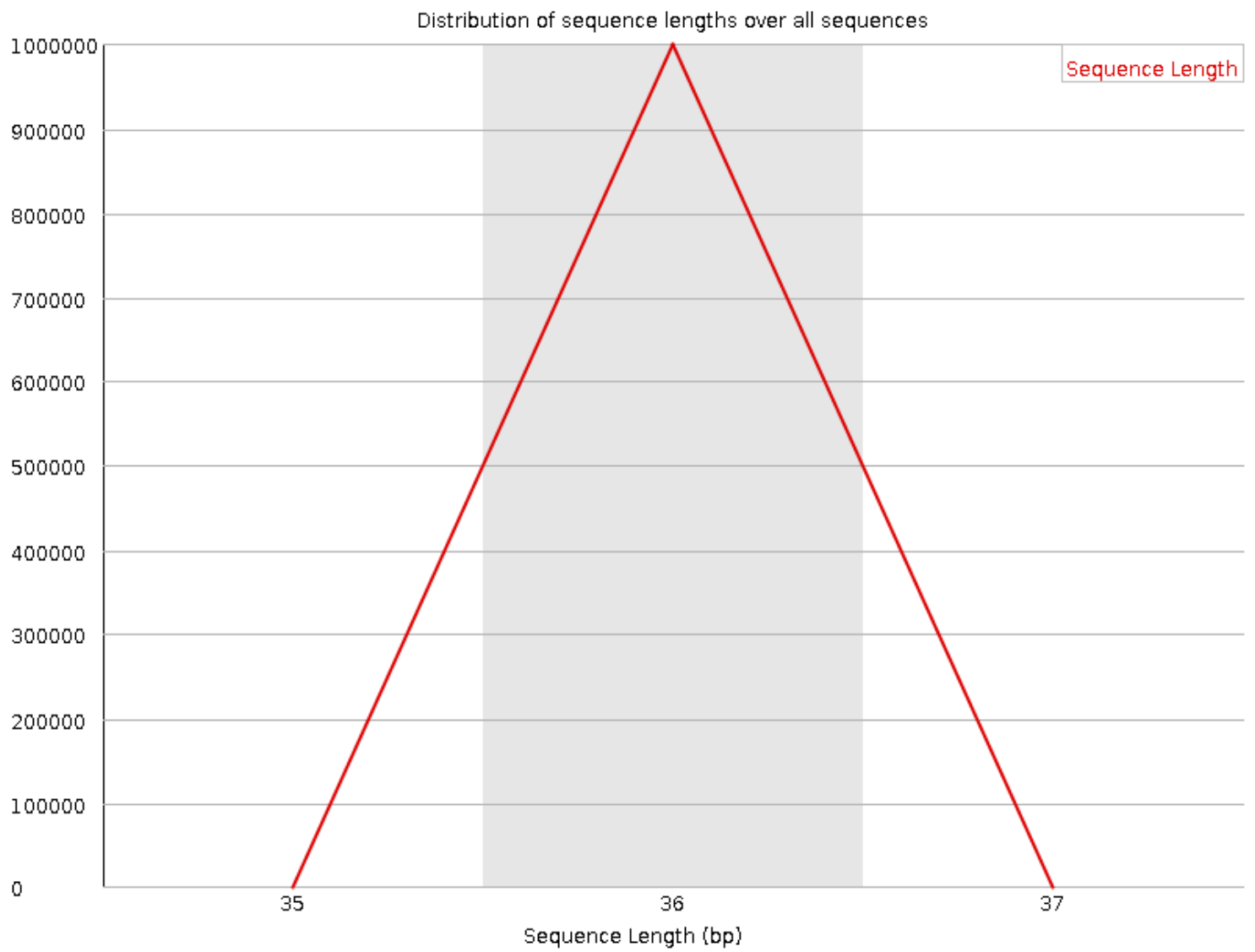


Per base N content

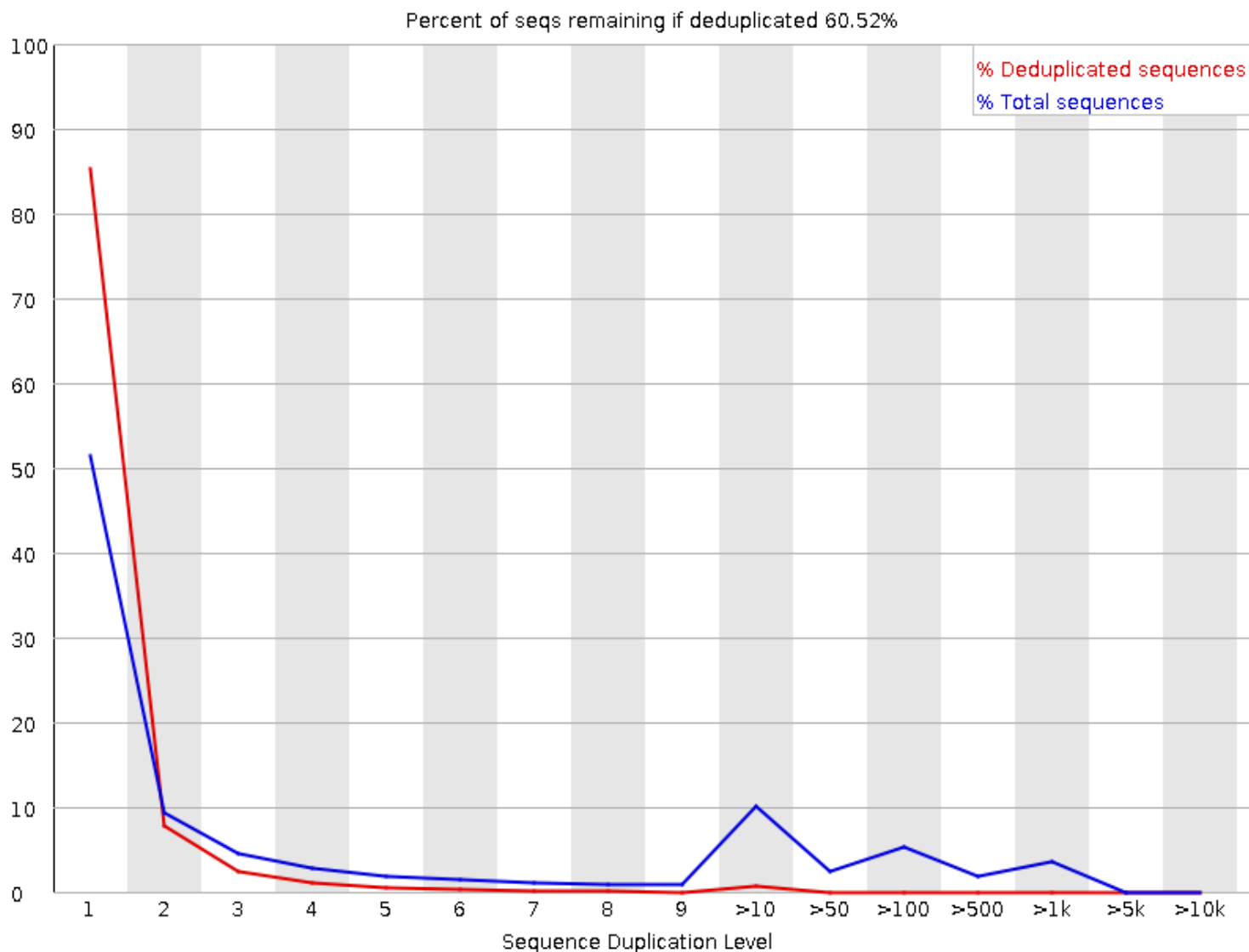
N content across all bases



Sequence Length Distribution



! Sequence Duplication Levels

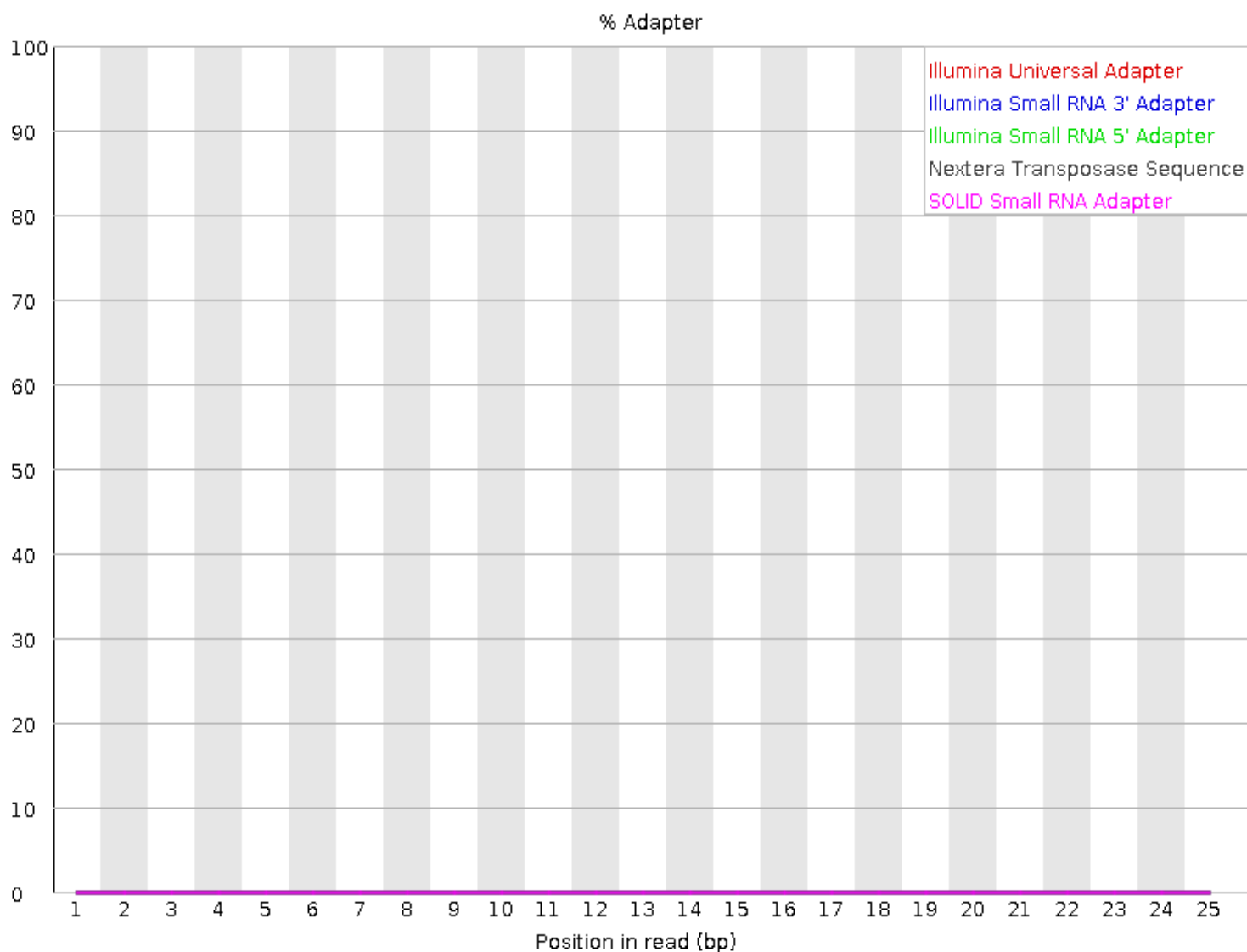


! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3275	0.3275	No Hit
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3269	0.3269	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	2589	0.2589	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2506	0.2506	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	2374	0.23739999999999997	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2304	0.2304	No Hit
CTTGGAGGACATATCGAAGATTTTGTCTTCTACCTC	1944	0.1944	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1782	0.1782	No Hit
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1604	0.1604	No Hit

Sequence	Count	Percentage	Possible Source
CGAAGATTTTGTCTTCTACCTCGATGTTGAATTGTA	1588	0.1588	No Hit
GGAGGACATATCGAAGATTTTGTCTTCTACCTCGAT	1542	0.1542	No Hit
TTTGAATACTTATTTATTACATTATGAACTTCCTTA	1376	0.1376	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1370	0.13699999999999998	No Hit
CTAAAGTAAGAAACACCACTAAGTTAAAACTCTCT	1323	0.1323	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAATCTTC	1185	0.11850000000000001	No Hit
CGAAAAGACCCTAGAGAGTTTTTAACCTAGTGGTGT	1140	0.11399999999999999	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1125	0.11249999999999999	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1068	0.10679999999999999	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1063	0.10629999999999999	No Hit
ATTTCAAGGACGAAAAGACCCTAGAGAGTTTTTAAC	1039	0.10389999999999999	No Hit
CAAGGACGAAAAGACCCTAGAGAGTTTTTAACCTAG	1037	0.1037	No Hit
GACATATCGAAGATTTTGTCTTCTACCTCGATGTTG	1002	0.10020000000000001	No Hit

Adapter Content



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