












Summary

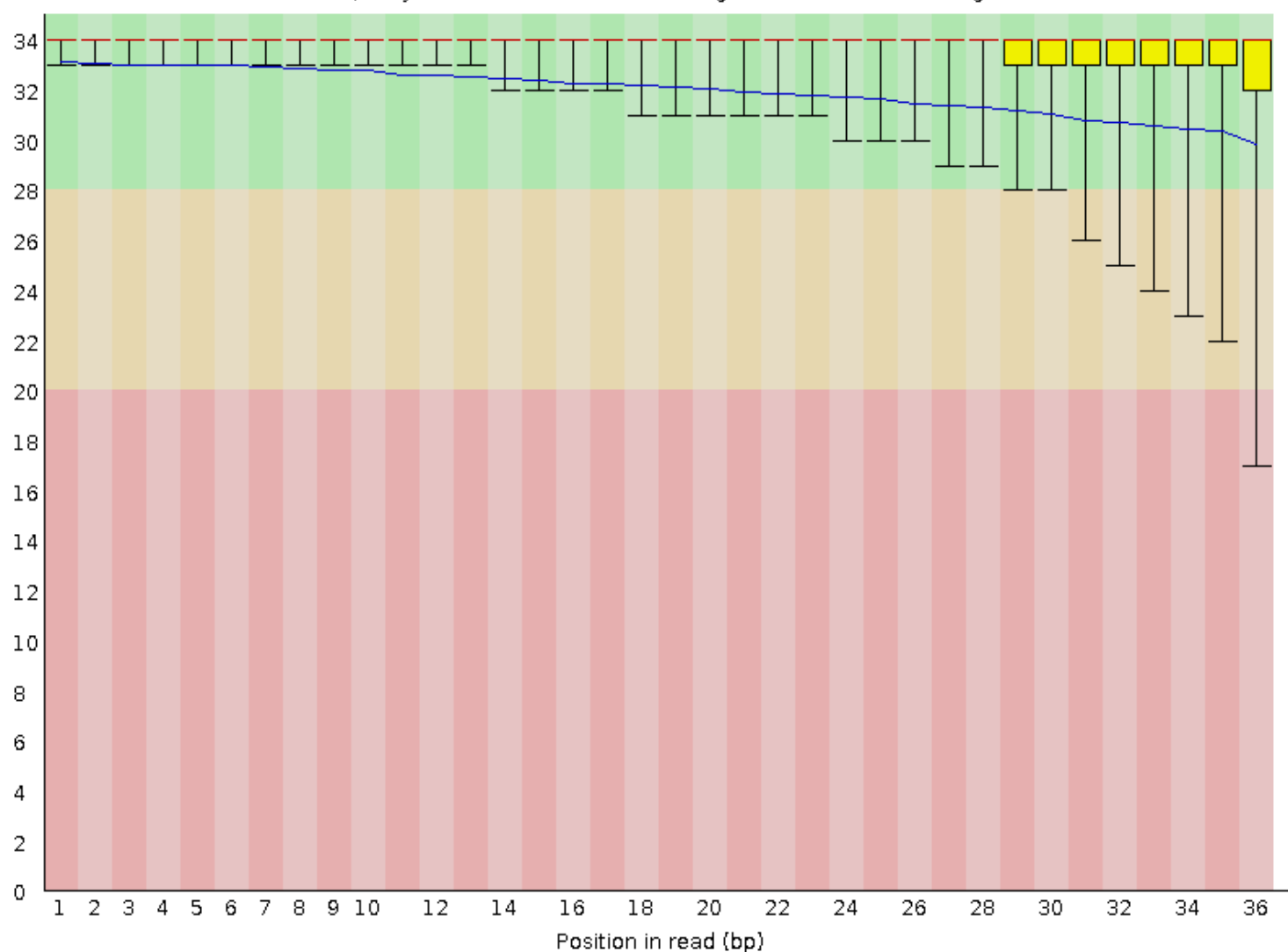
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Basic Statistics

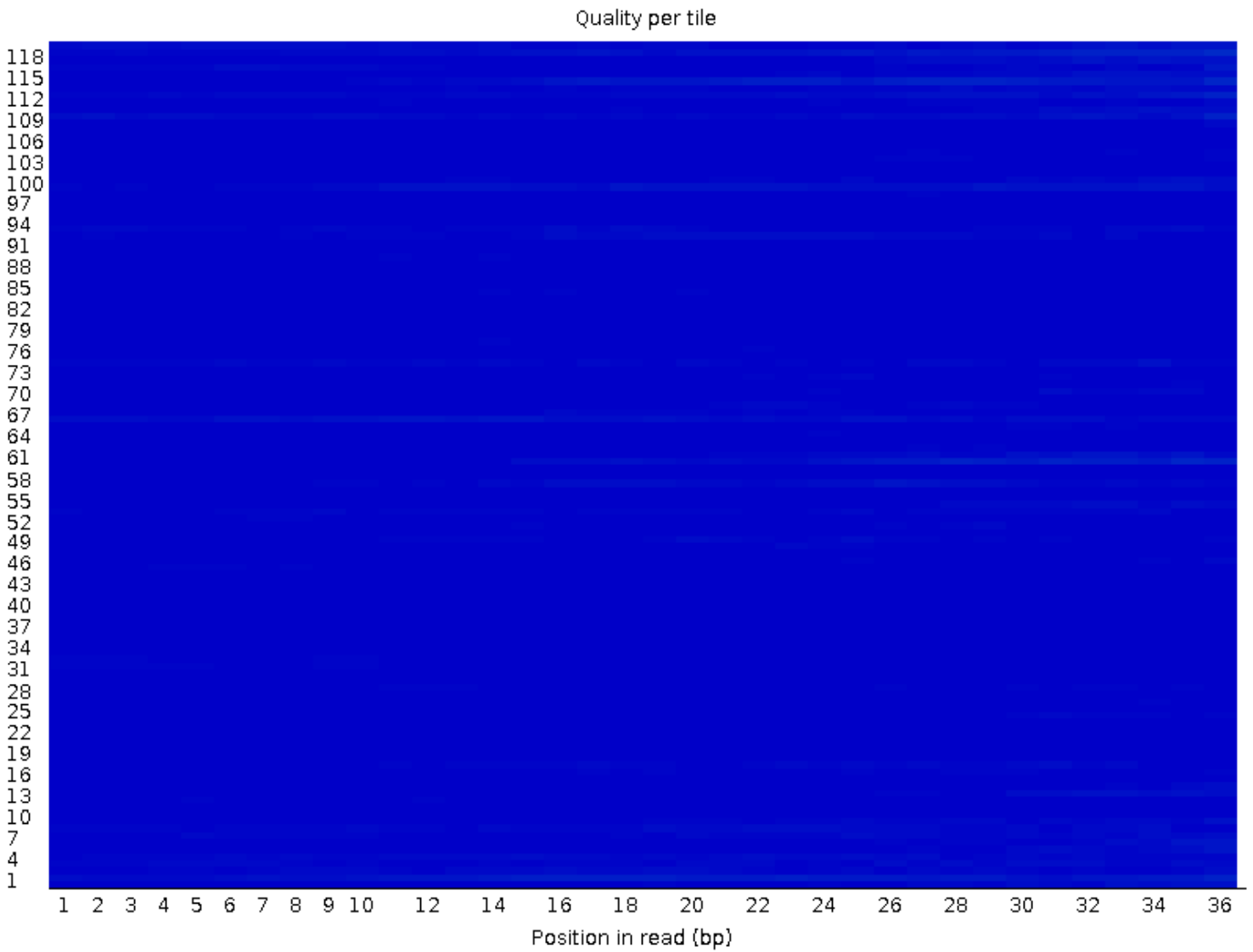
Measure	Value
Filename	ERR032066_2_REP1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	38

Per base sequence quality

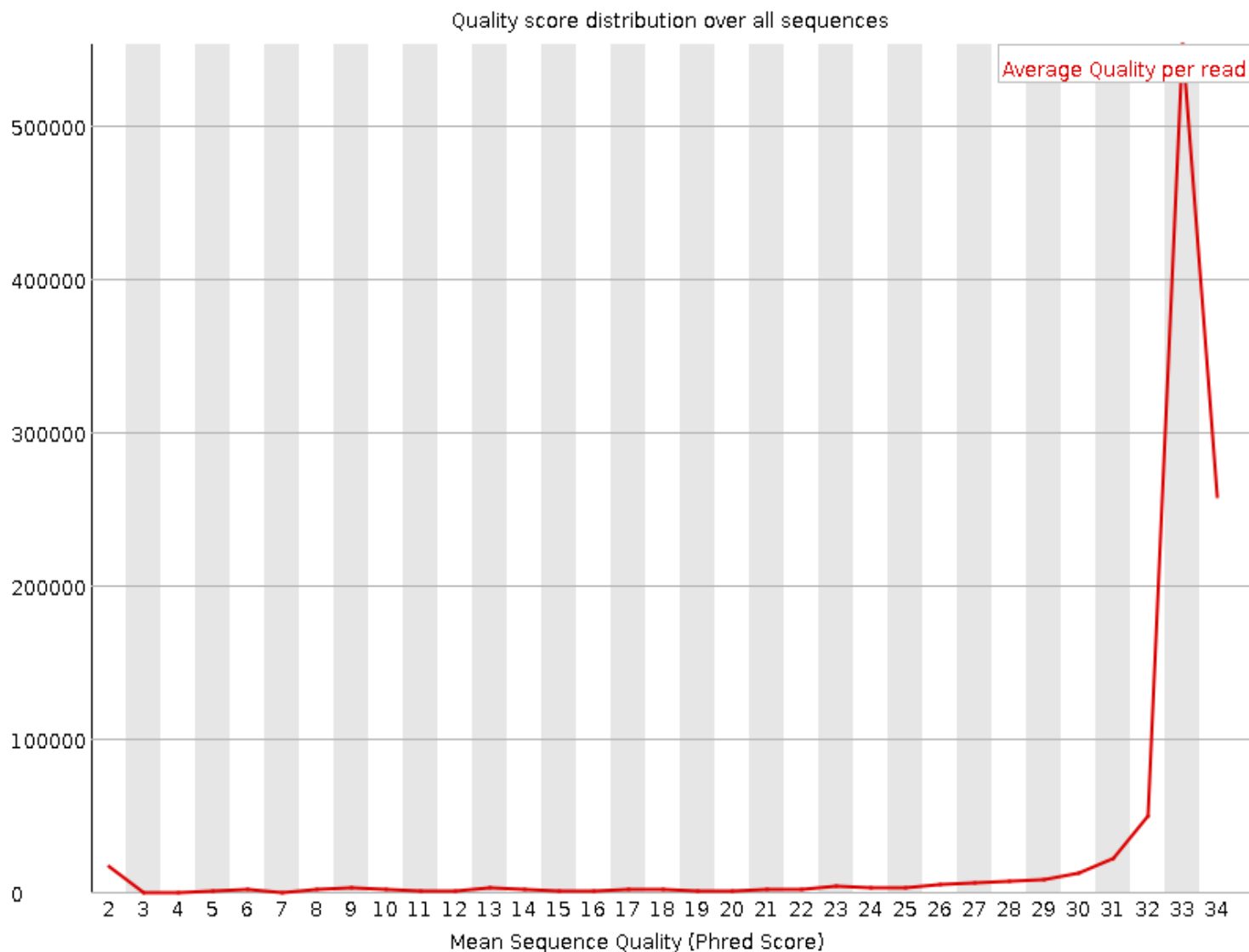
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



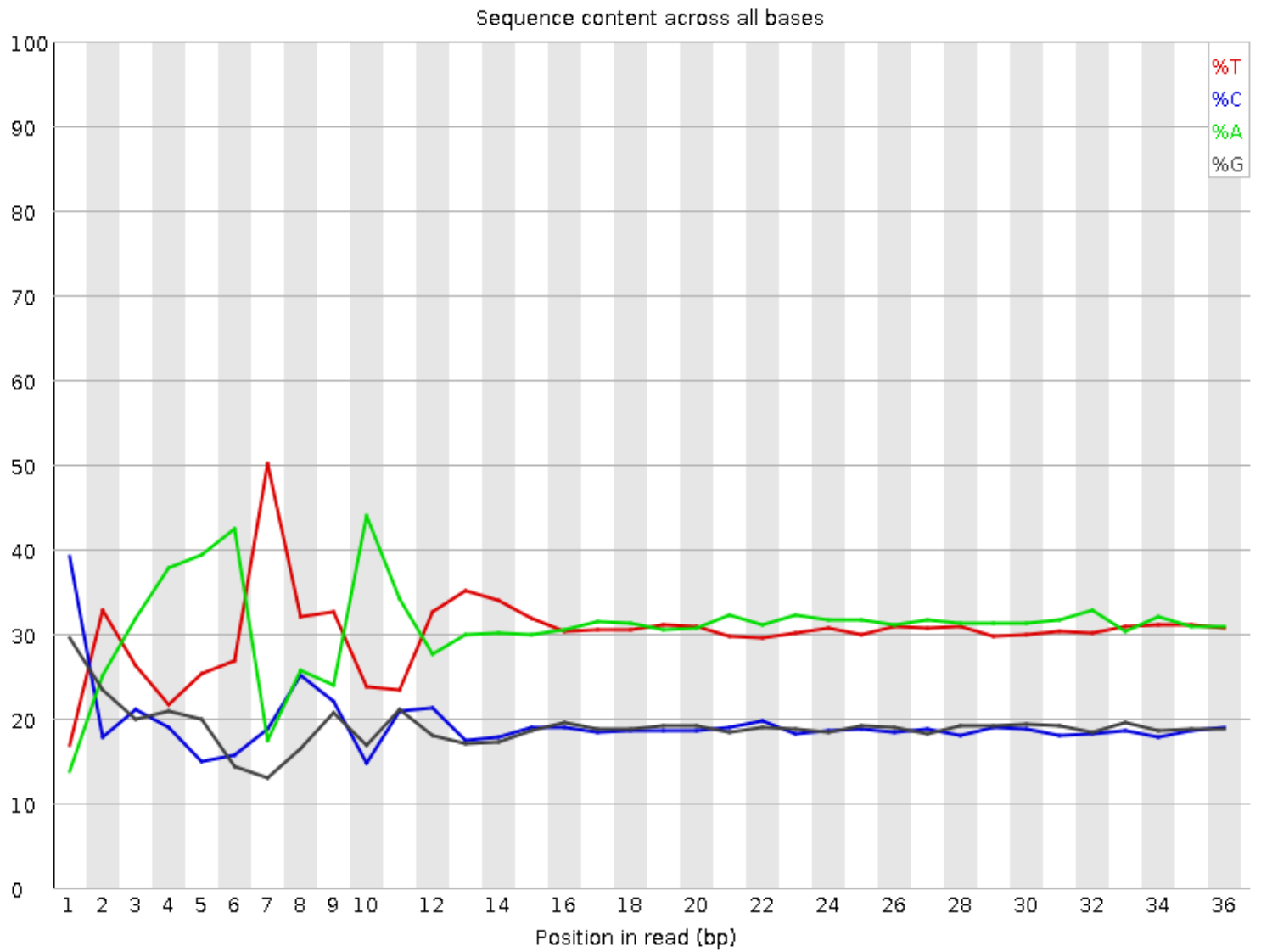
Per tile sequence quality



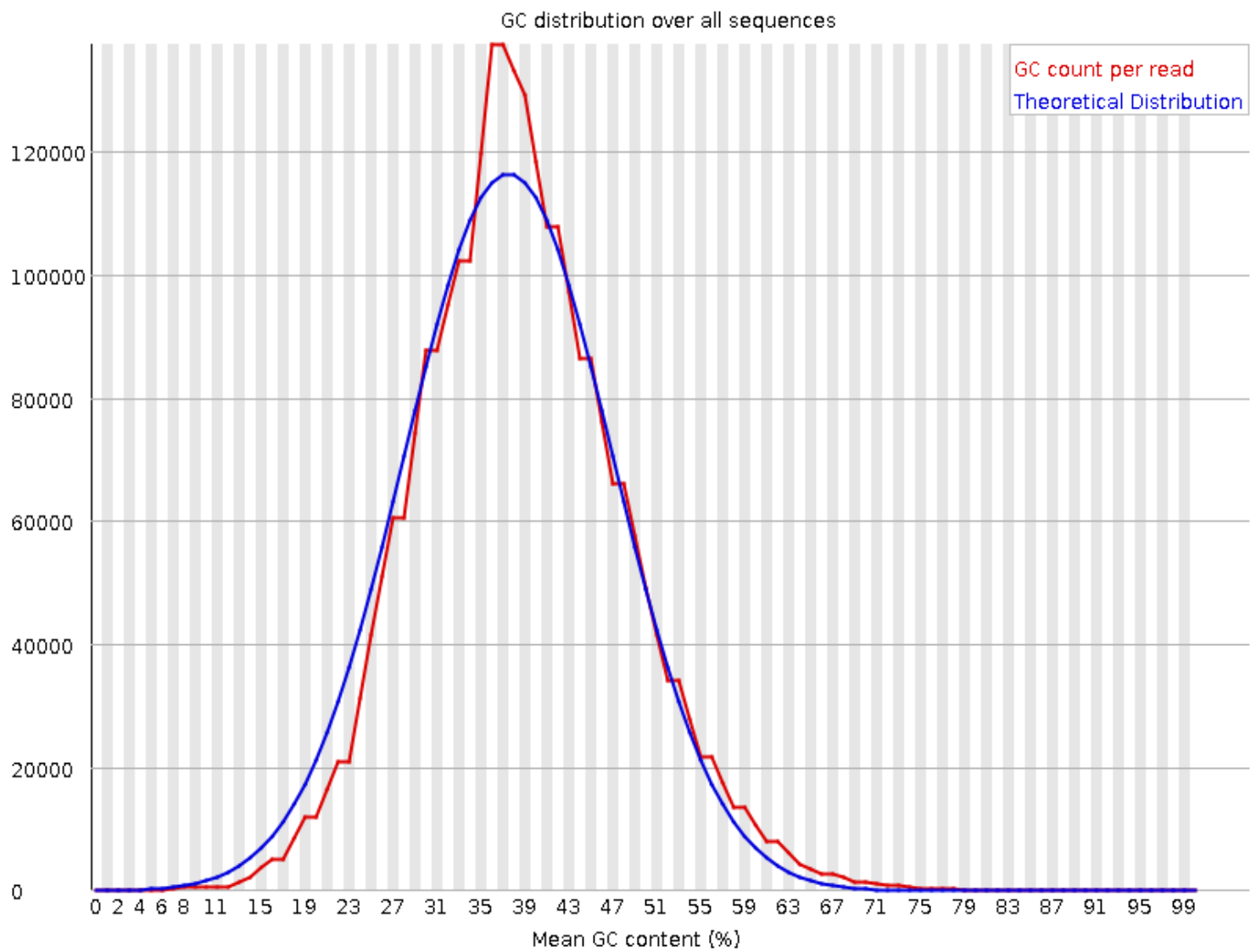
Per sequence quality scores



❌ Per base sequence content

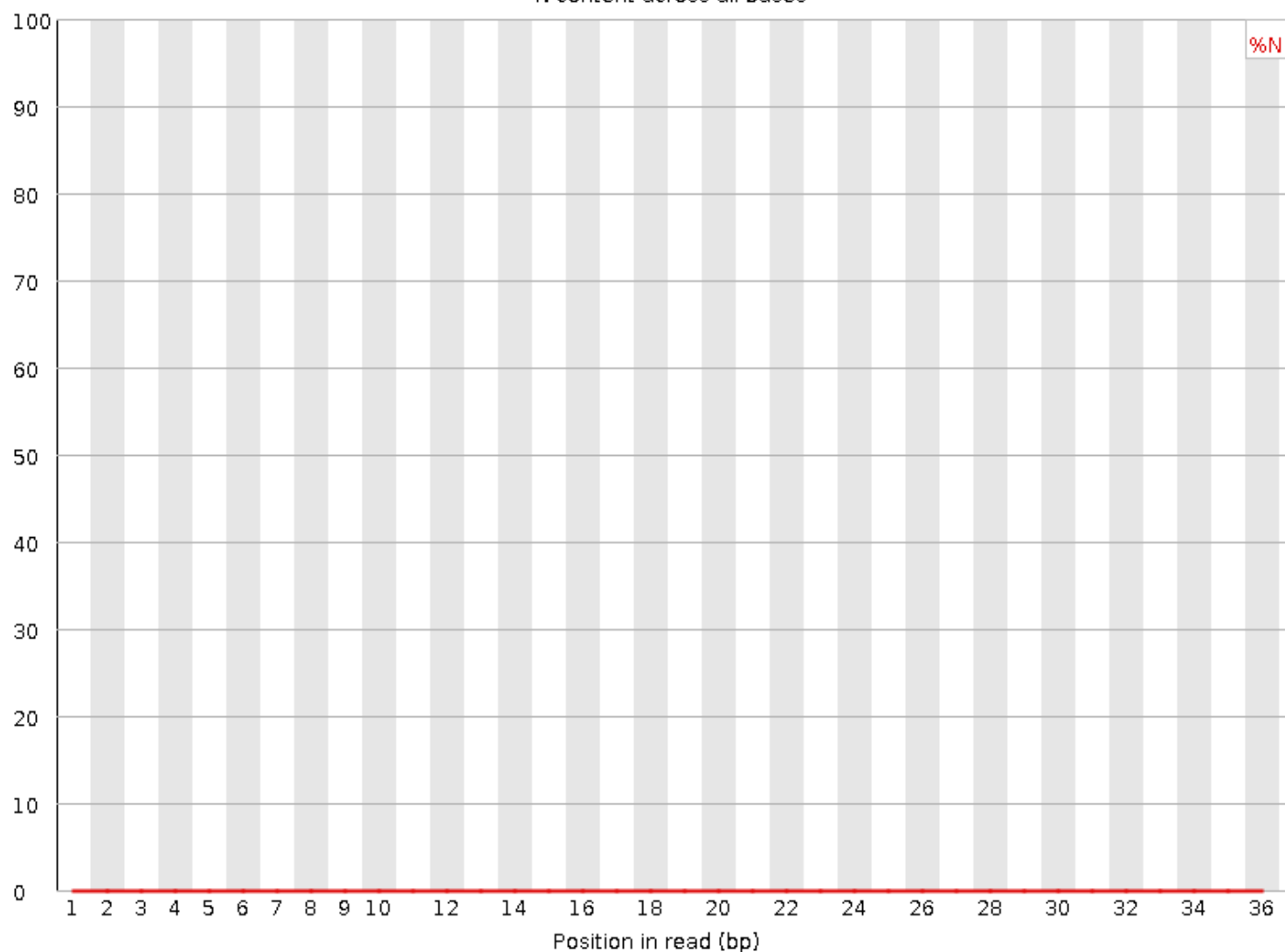


Per sequence GC content

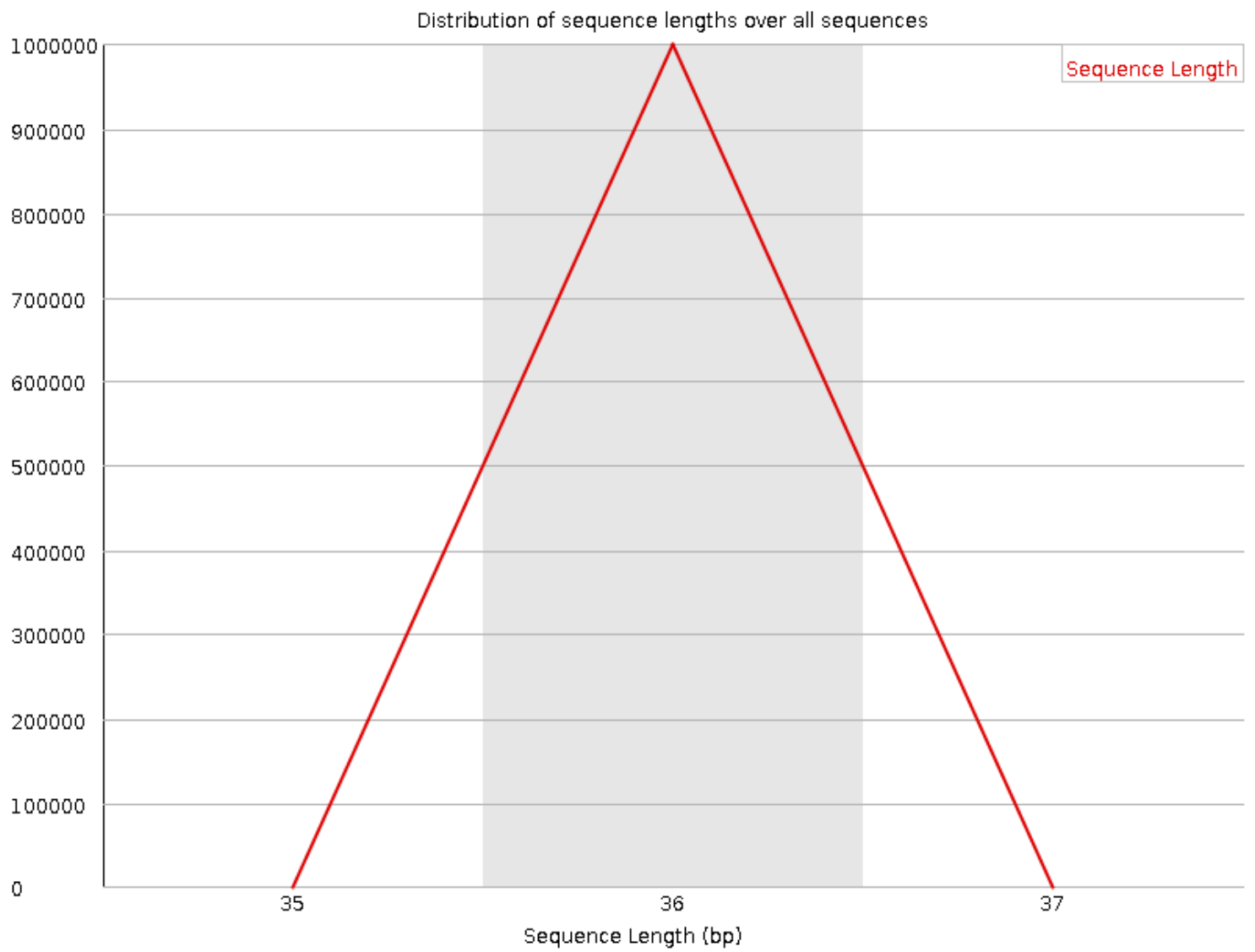


Per base N content

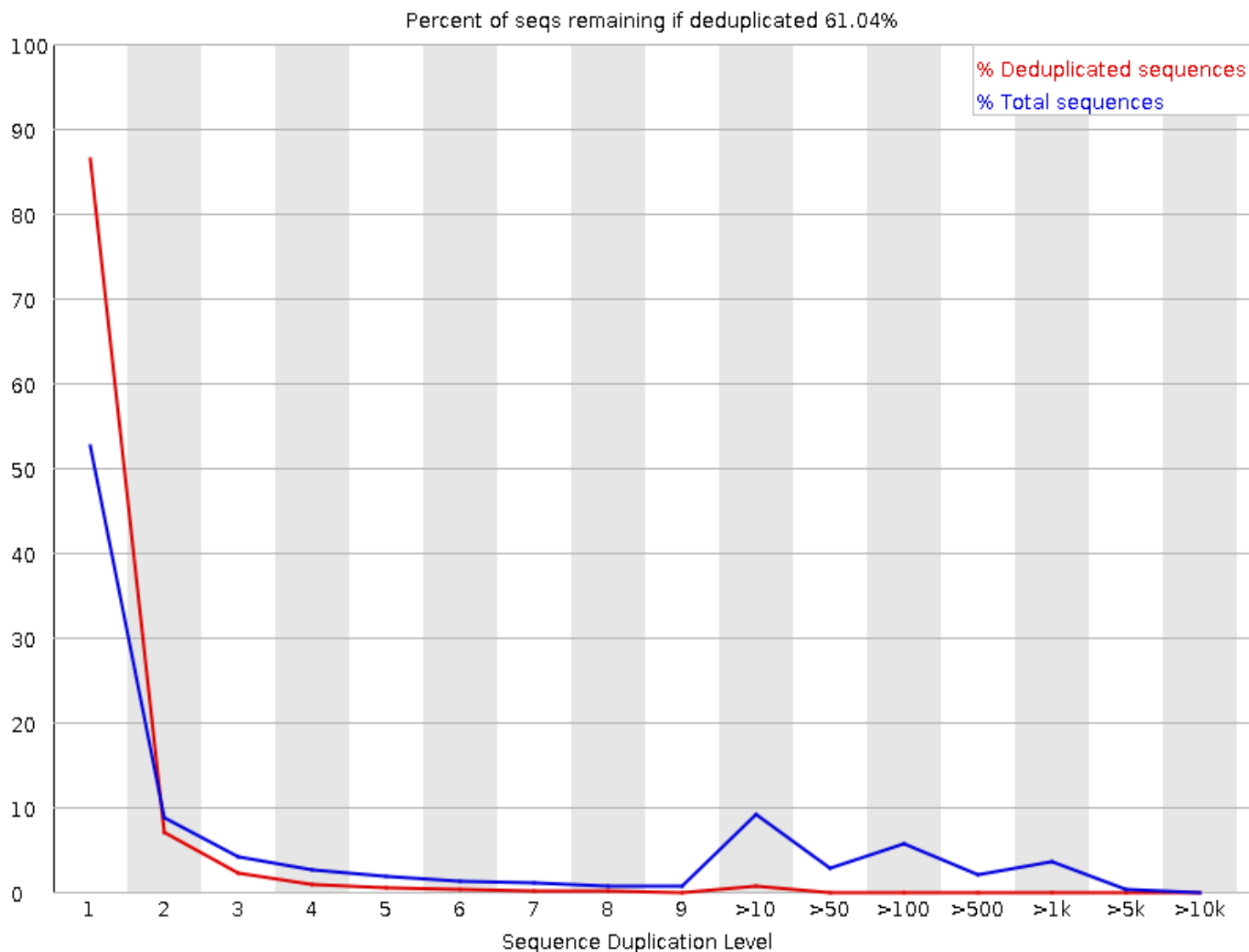
N content across all bases



Sequence Length Distribution



! Sequence Duplication Levels



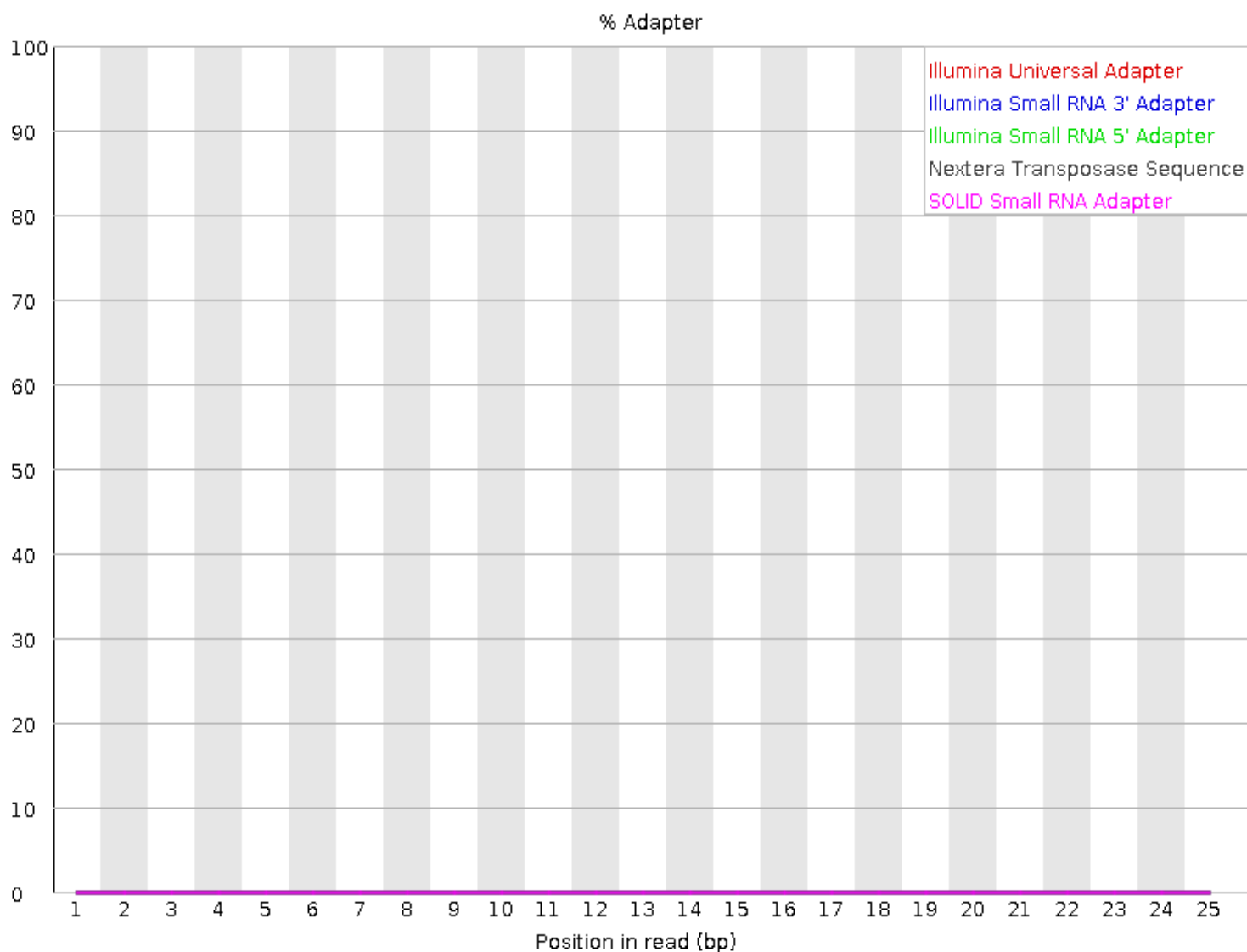
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	5738	0.5738	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	3438	0.3438	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3385	0.3385	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	2560	0.256	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2355	0.2355	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	2207	0.2207	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1797	0.1797	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1524	0.1524	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1483	0.1483	No Hit

Sequence	Count	Percentage	Possible Source
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	1434	0.1434	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1397	0.1397	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1390	0.13899999999999998	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1336	0.1336	No Hit
GTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1271	0.1271	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1250	0.125	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1244	0.12440000000000001	No Hit
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1211	0.1211	No Hit
GTAAAGATAGGTGTAGAGGCCTTTACTTTTAGTCT	1161	0.1161	No Hit
CTTGGAGGACATATCGAAGATTTTGTCTTCTACCTC	1158	0.1158	No Hit
TAAAGATACAGTTTGTTATTTCAAGGACGAAAAGAC	1143	0.11429999999999998	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAATCTTC	1102	0.11019999999999999	No Hit
CCCATTCAAACAATTCTAGAATTAGTAGACAAGTAA	1057	0.1057	No Hit
AAACAATTCTAGAATTAGTAGACAAGTAATTATGCT	1057	0.1057	No Hit
CAAAATCTTCGATATGTCCTCCAAGATTCTATATCC	1033	0.1033	No Hit



Adapter Content



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