












Summary

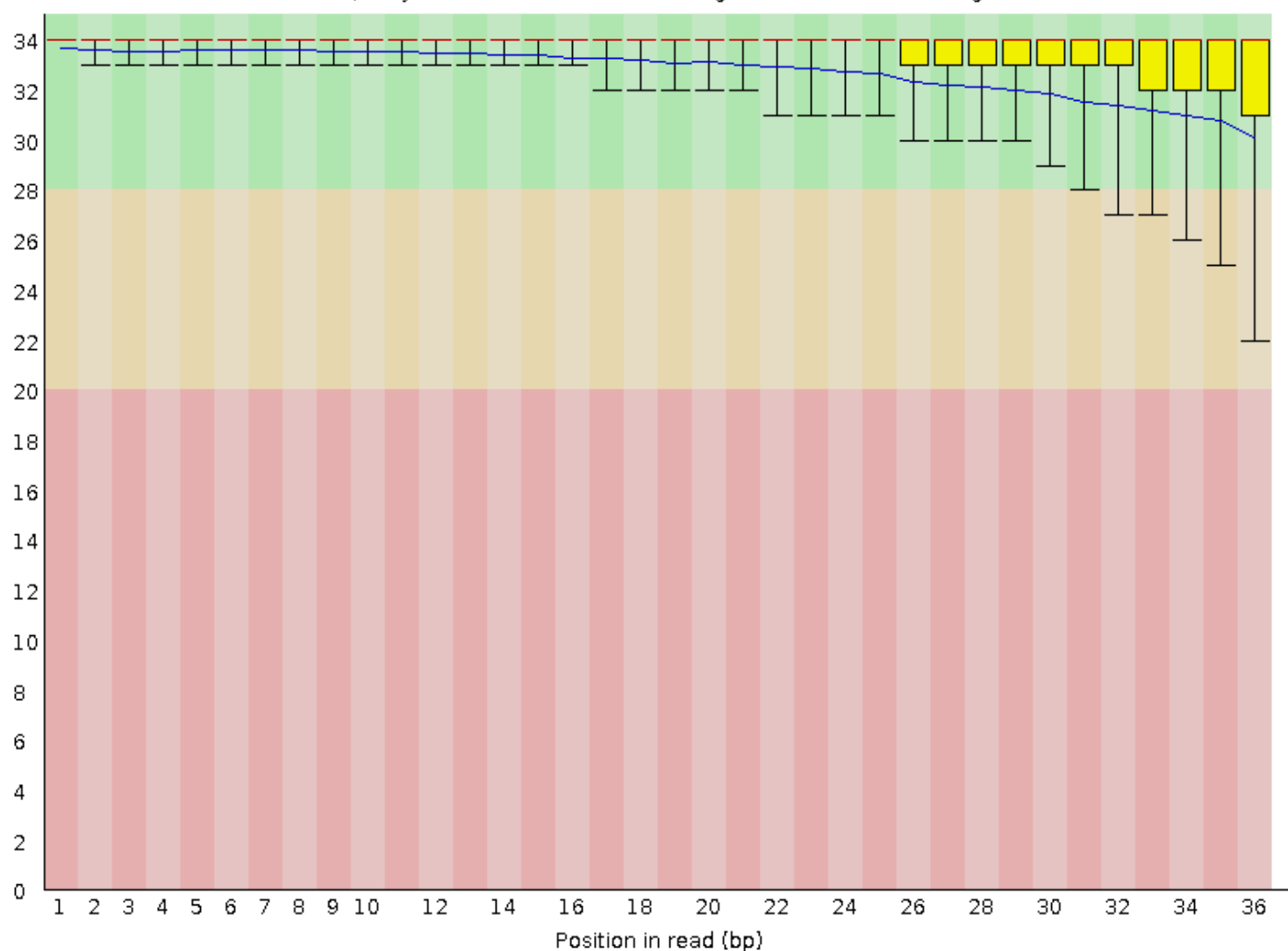
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Basic Statistics

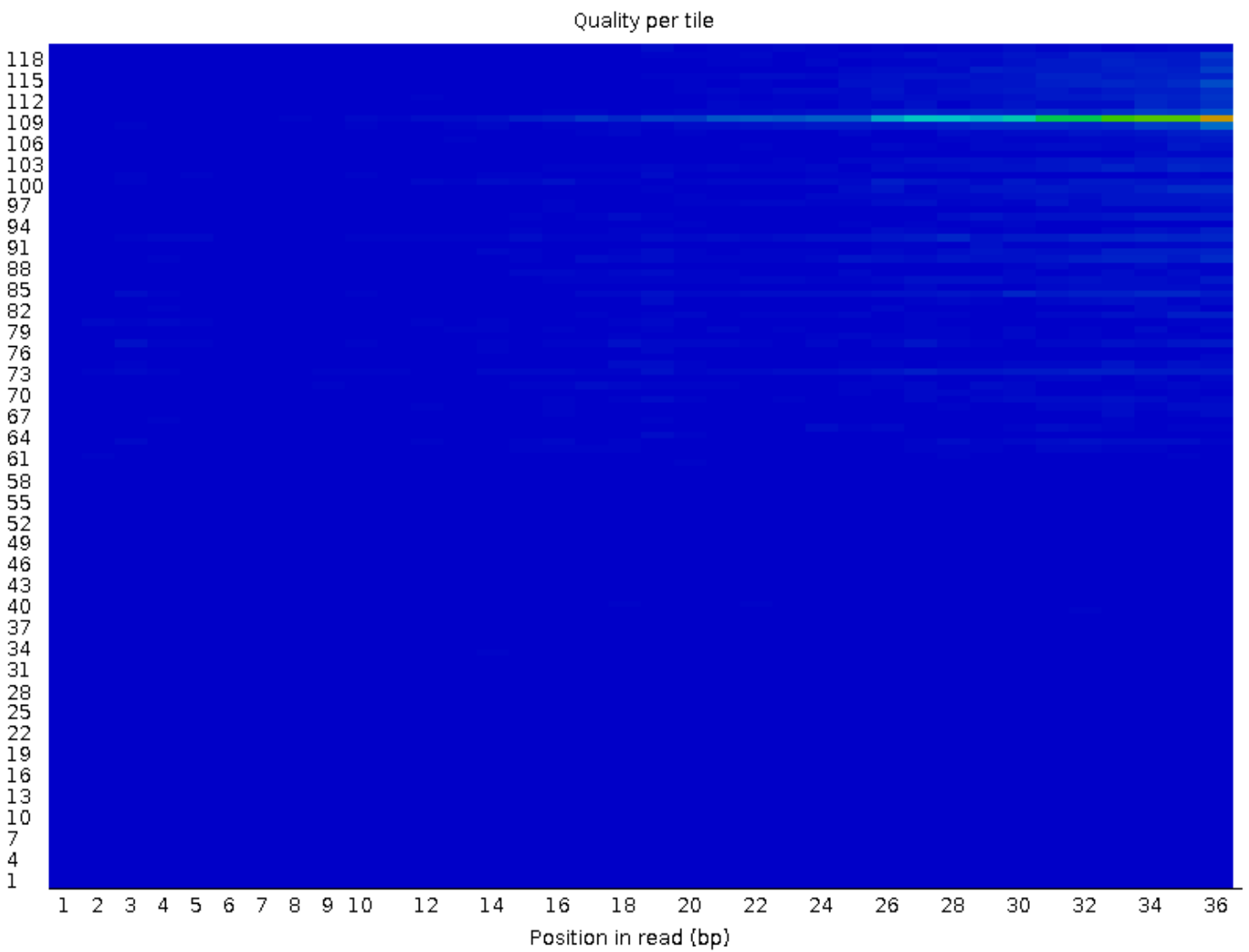
Measure	Value
Filename	ERR032066_1_REP2.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	38

Per base sequence quality

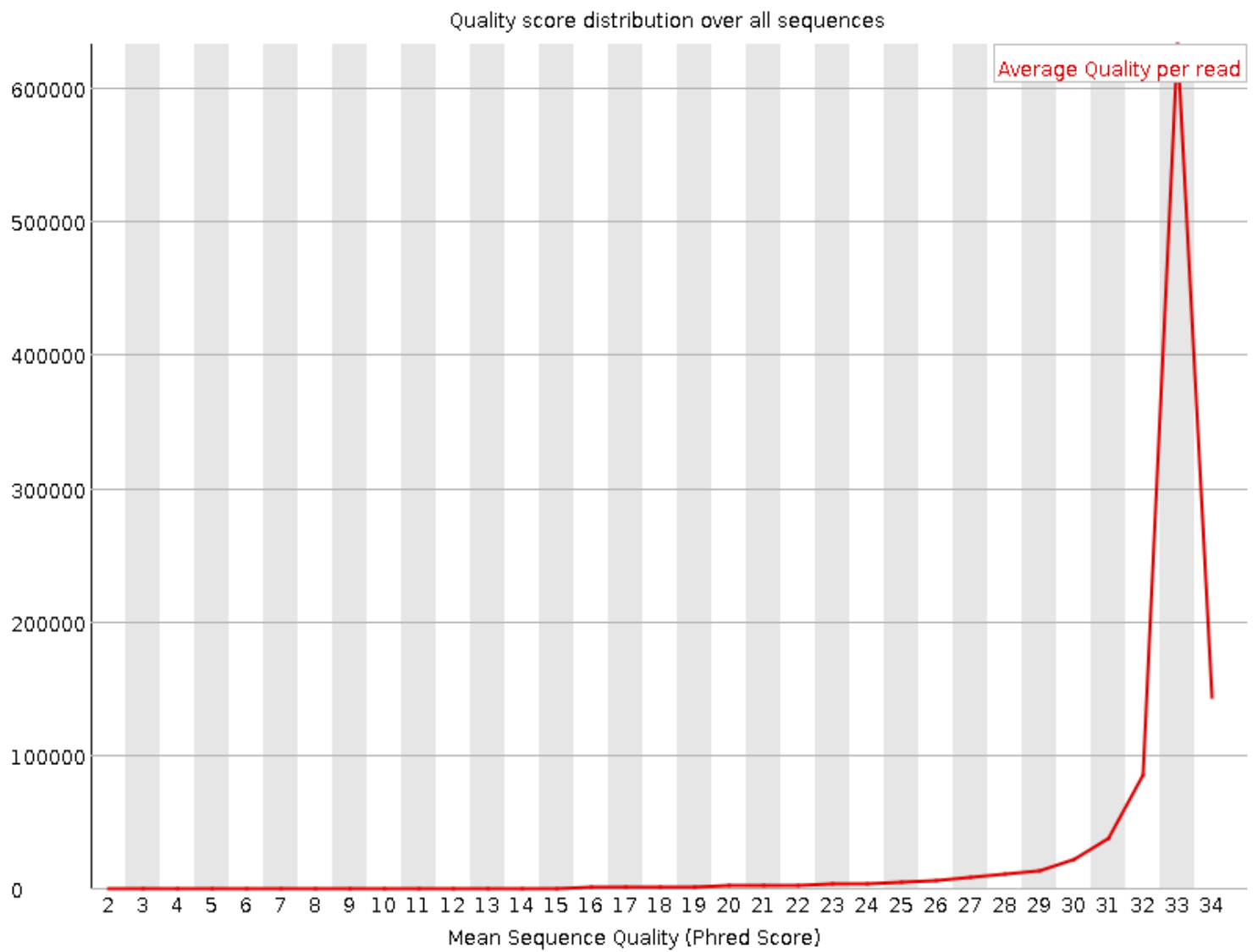
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



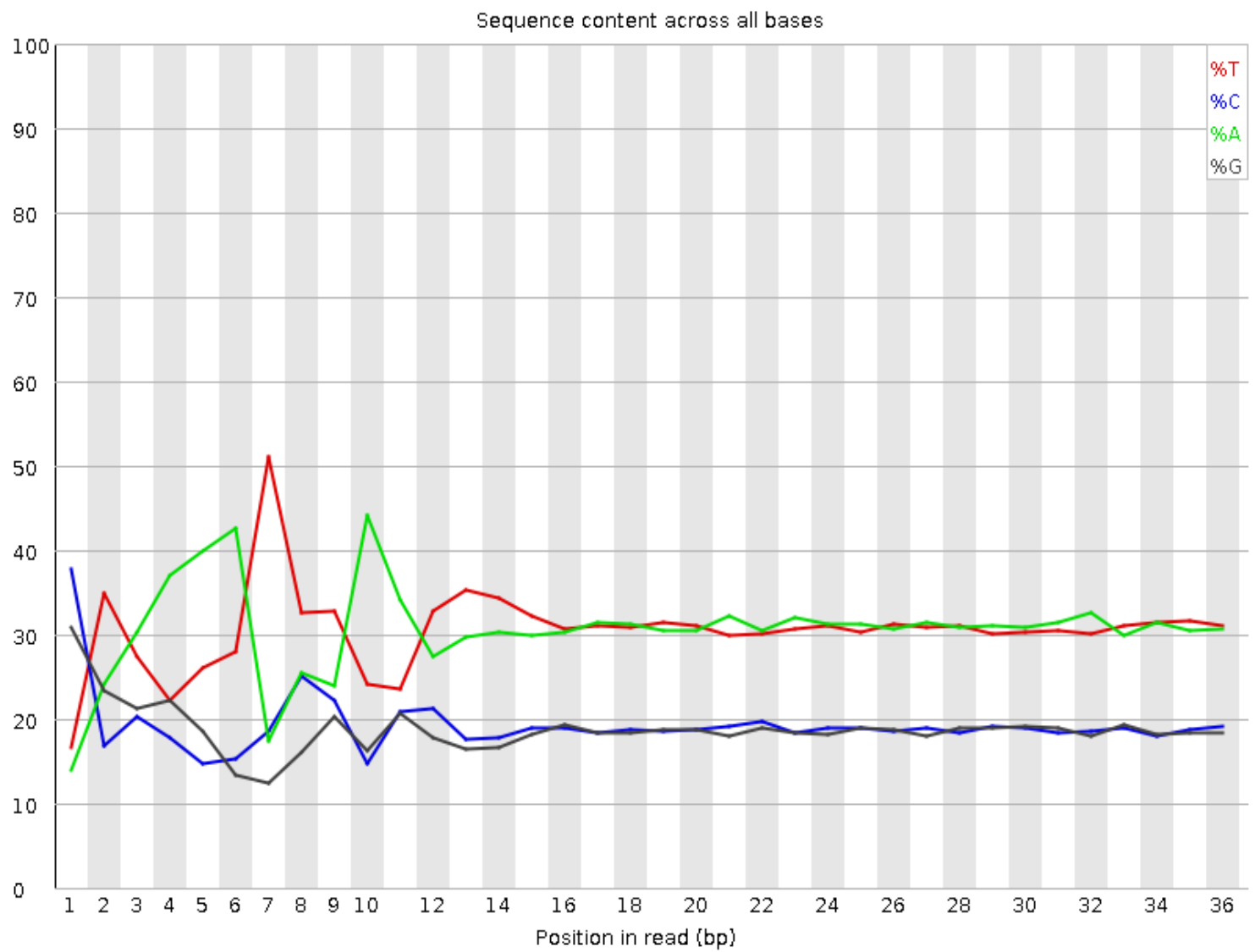
! Per tile sequence quality



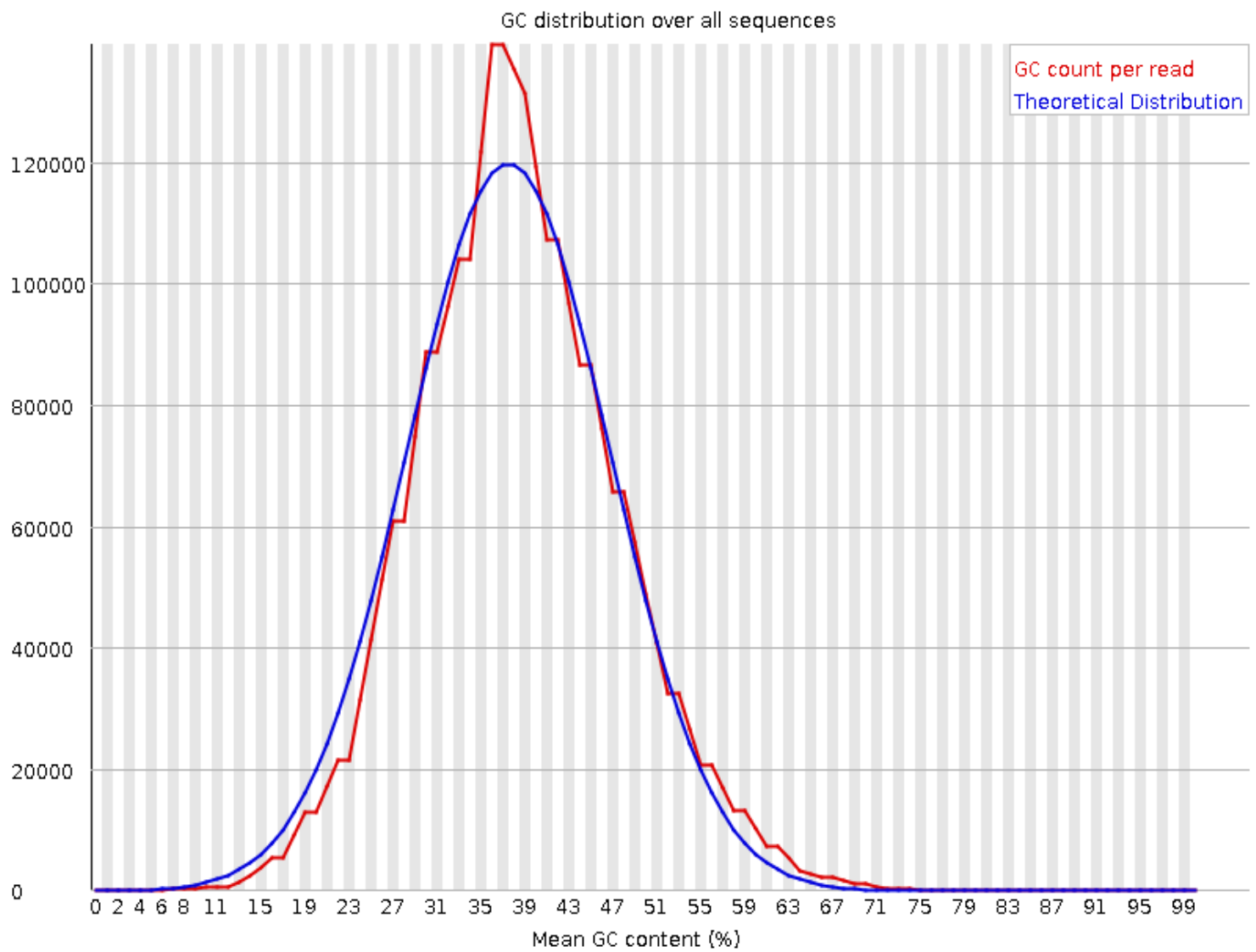
✓ **Per sequence quality scores**



✖ Per base sequence content

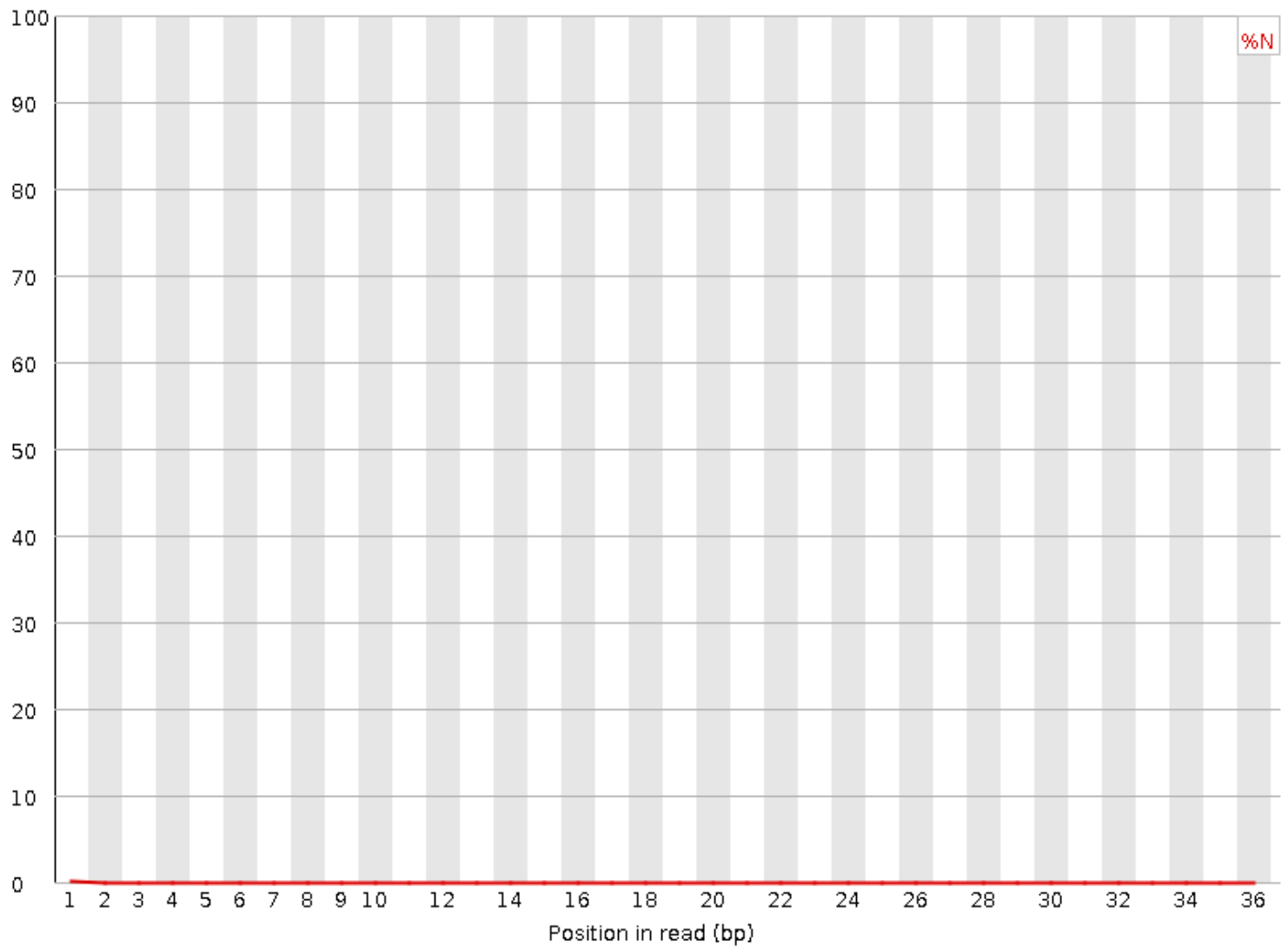


Per sequence GC content

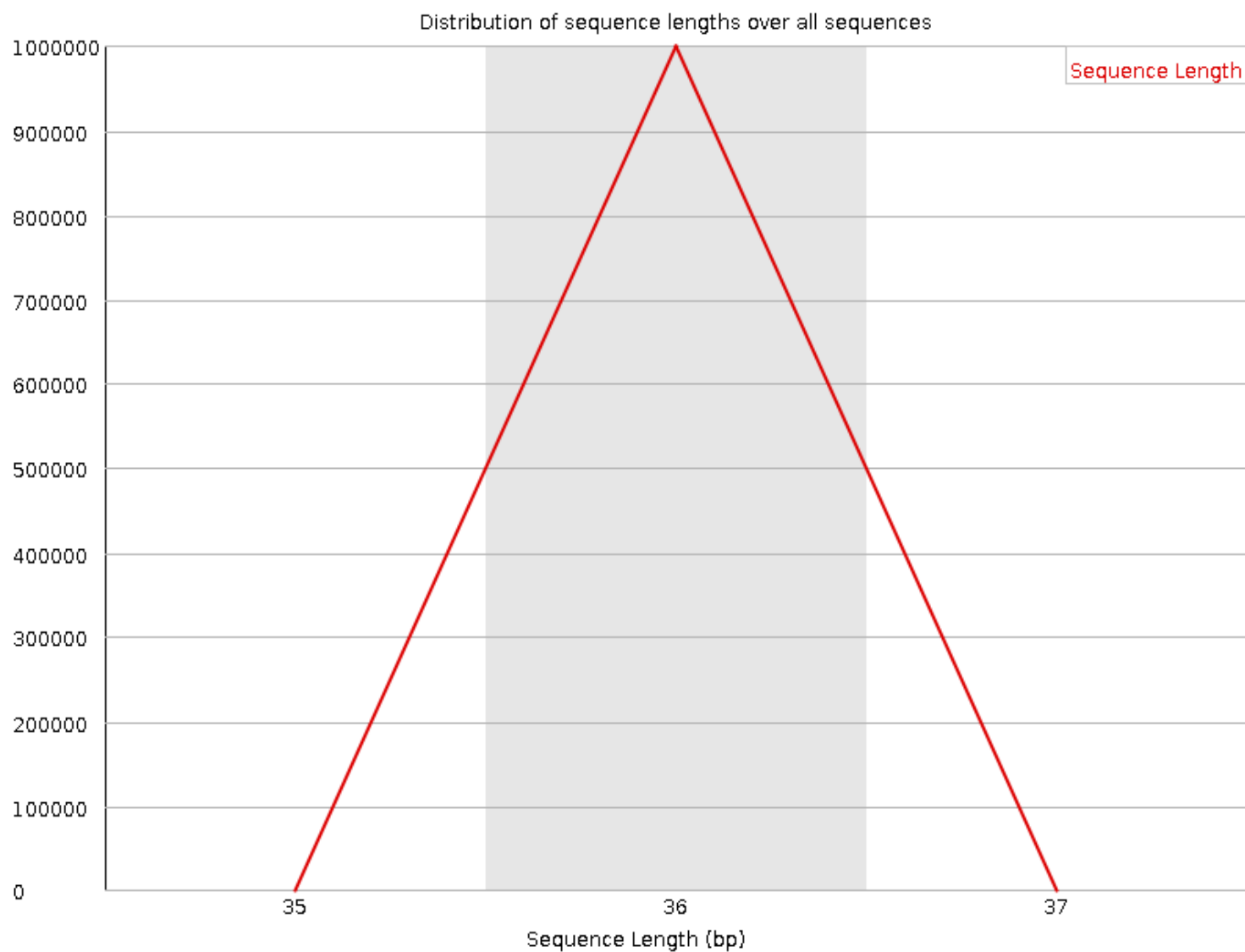


✅ Per base N content

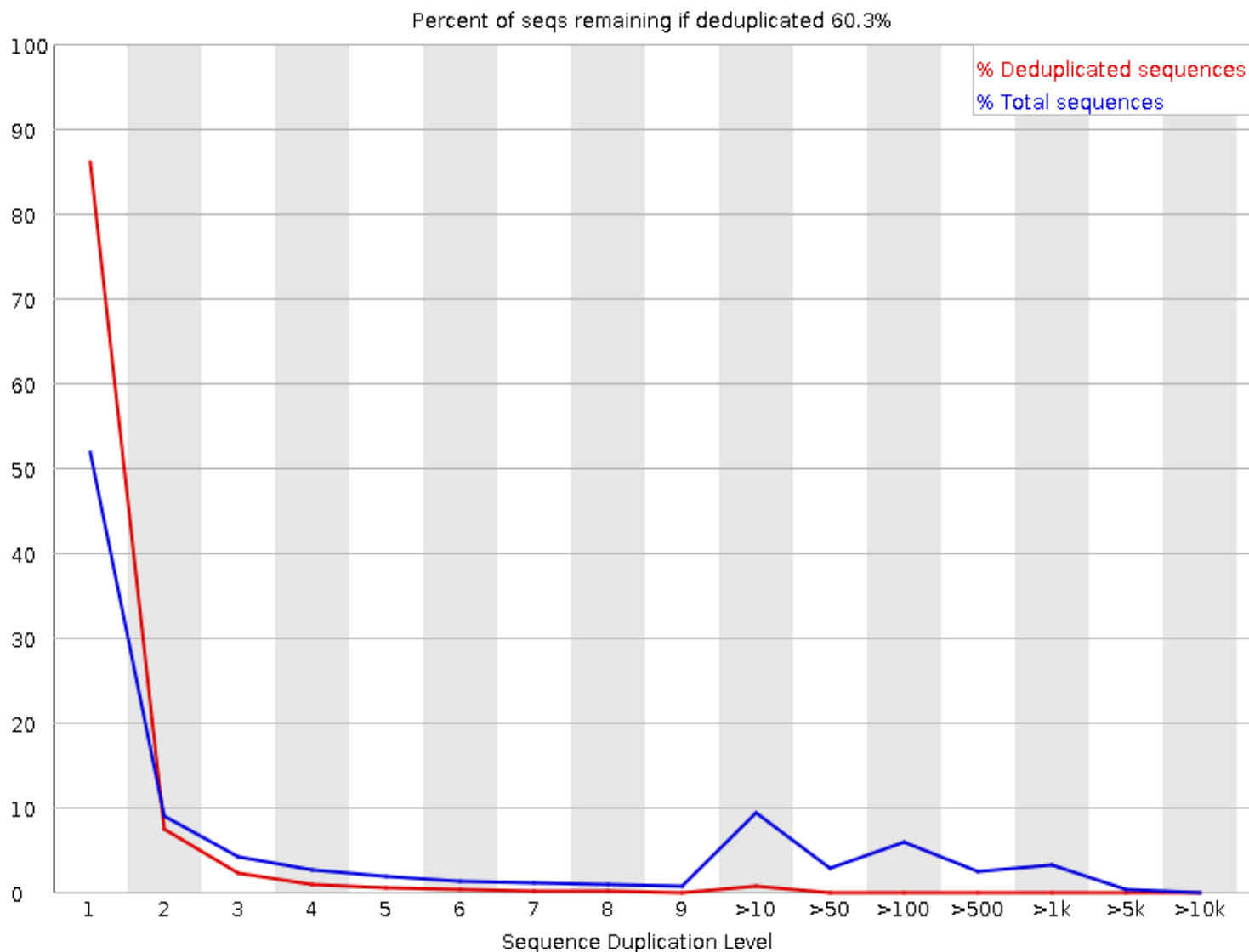
N content across all bases



Sequence Length Distribution



! Sequence Duplication Levels



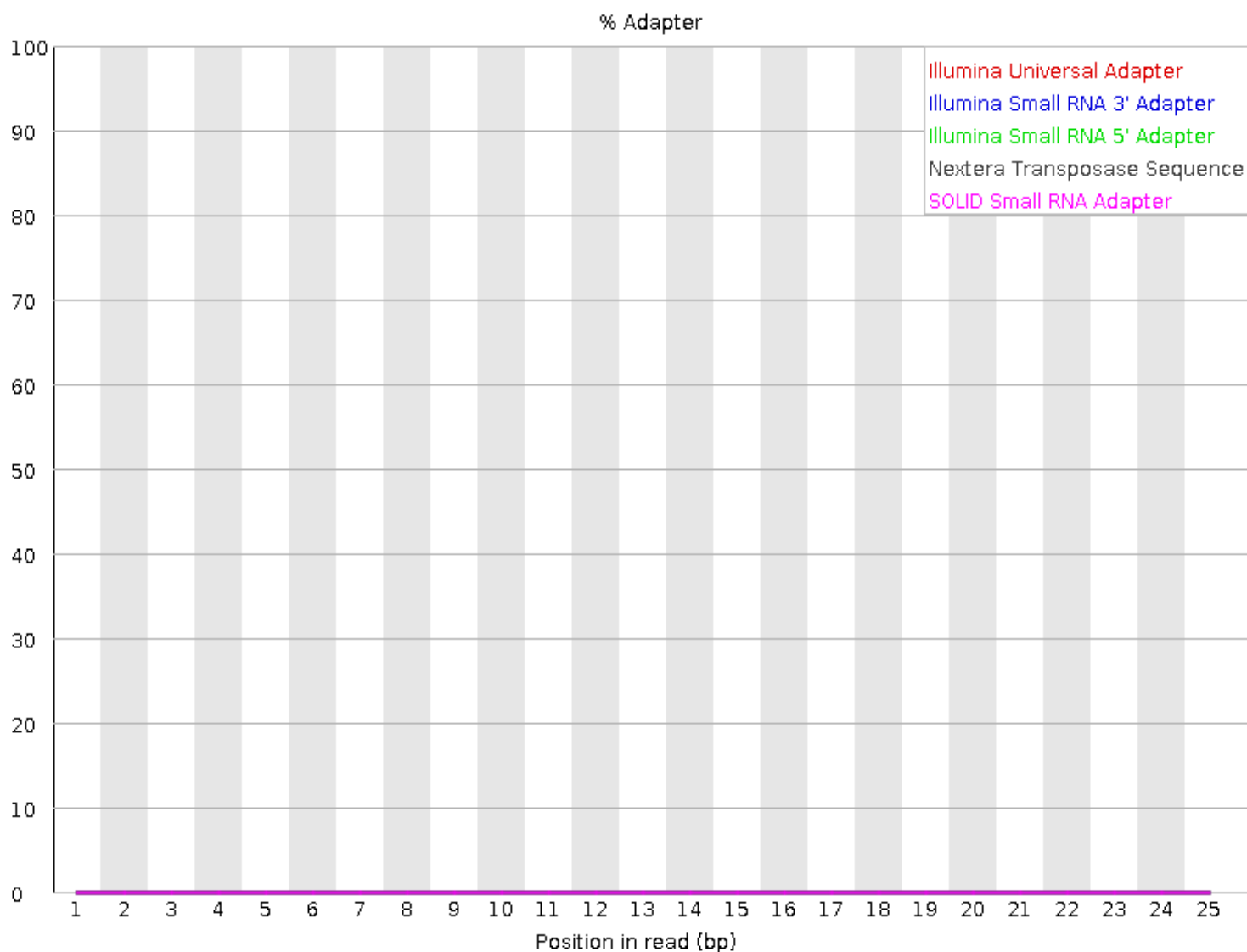
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	5557	0.5557000000000001	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3677	0.3677	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	3291	0.3291	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	2602	0.2602	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2466	0.24659999999999999	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1873	0.18730000000000002	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1811	0.18109999999999998	No Hit
GTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1693	0.1693	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1685	0.1685	No Hit

Sequence	Count	Percentage	Possible Source
GTAAAGATAGGTGTAGAGGCCTTTACTTTTAGTCT	1379	0.1379	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1294	0.12940000000000002	No Hit
CTTGAGGACATATCGAAGATTTTGTCTTCTACCTC	1292	0.1292	No Hit
CTAACTCAAATCACGAATAATATTATTAGTCGAAC	1267	0.12669999999999998	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	1263	0.1263	No Hit
CTTAGGATAACAGGGATATAGAATCTTGGAGGACA	1262	0.1262	No Hit
AAATACTAAAGTAAGAAACACCACTAAGTTAAAAA	1237	0.1237	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1226	0.12260000000000001	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1183	0.1183	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1076	0.10759999999999999	No Hit
TTTGAATACTTATTTATTACATTATGAACTTCCTTA	1072	0.1072	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1068	0.10679999999999999	No Hit



Adapter Content



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