












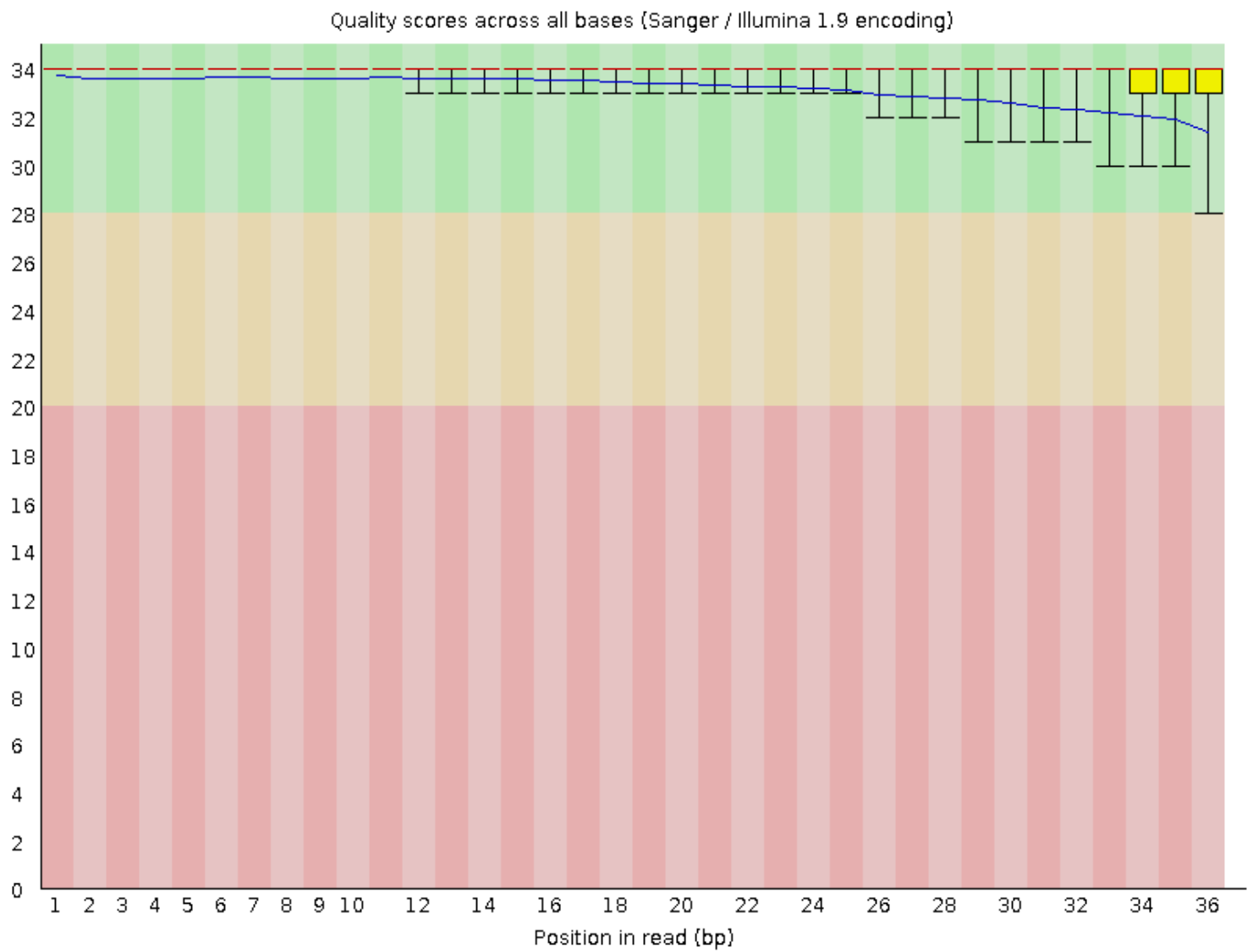
Summary

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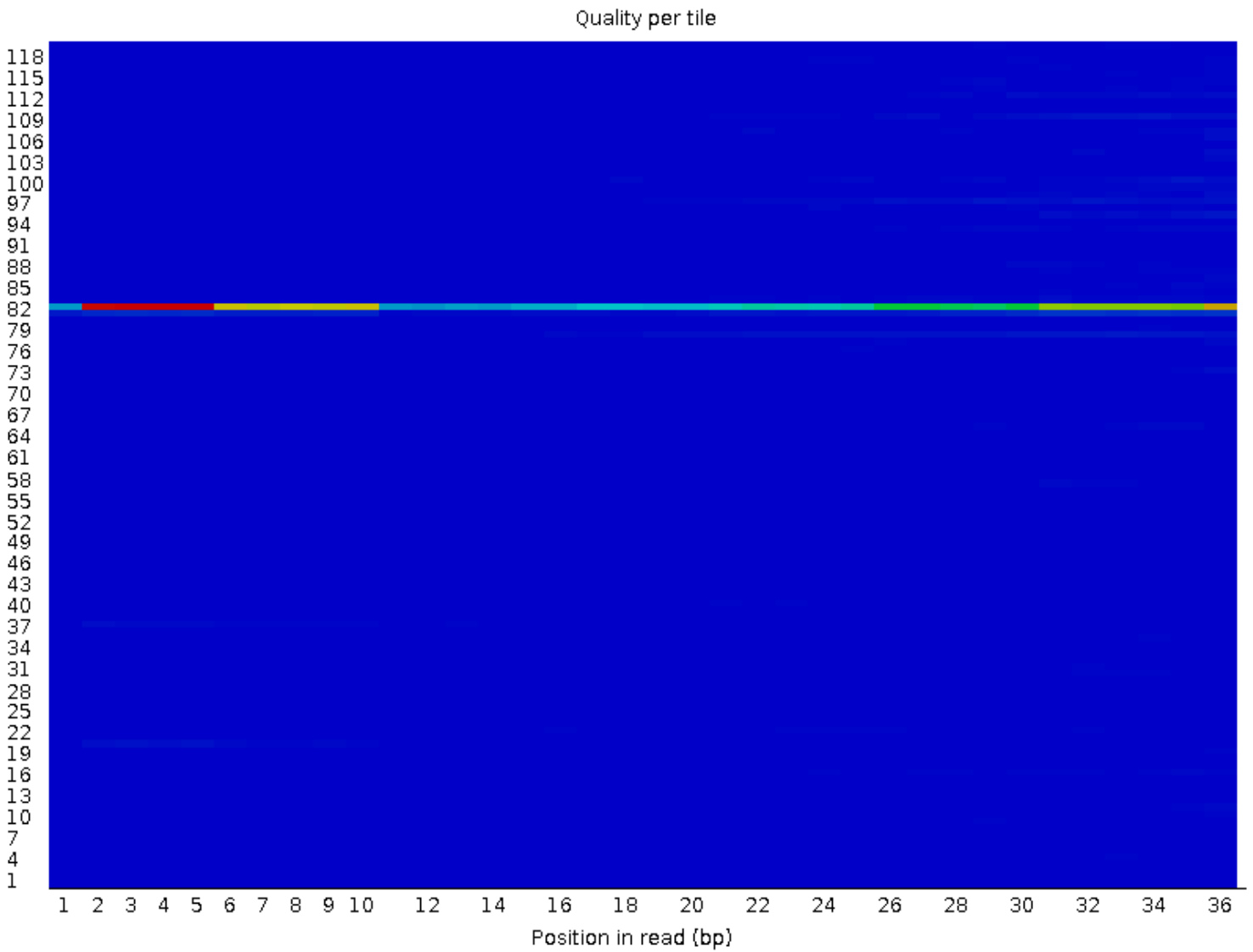
Basic Statistics

Measure	Value
Filename	ERR032068_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

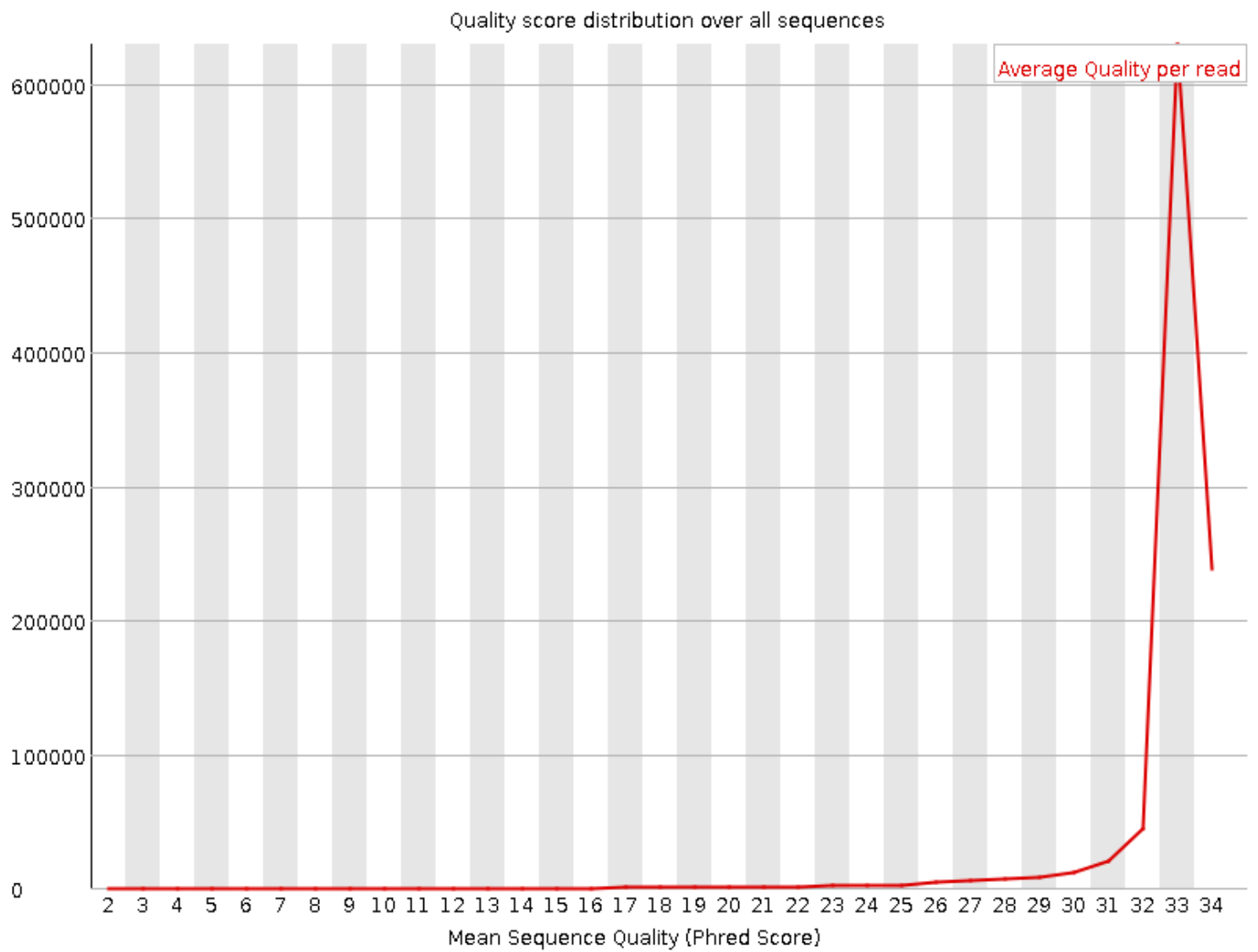
Per base sequence quality



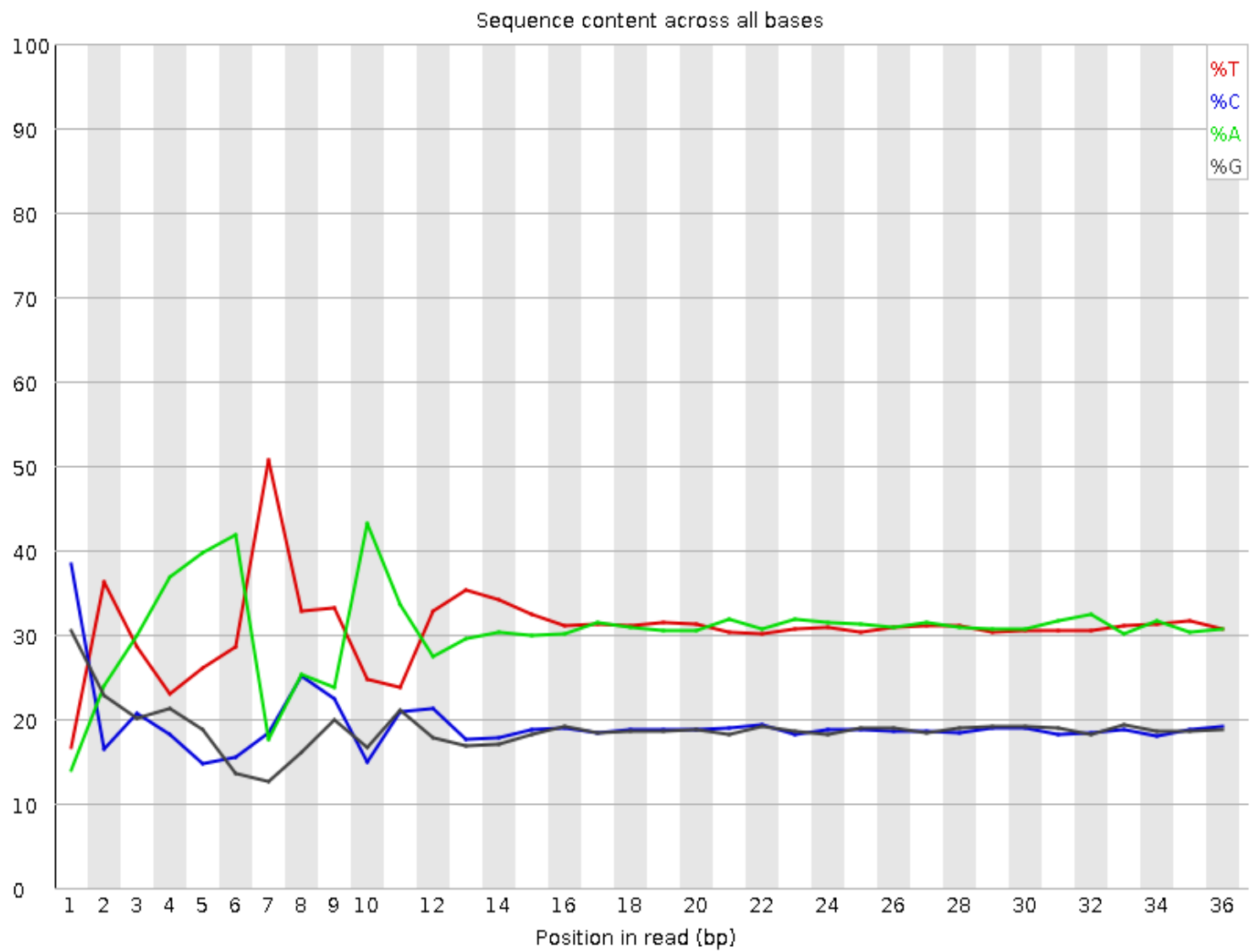
✖ Per tile sequence quality



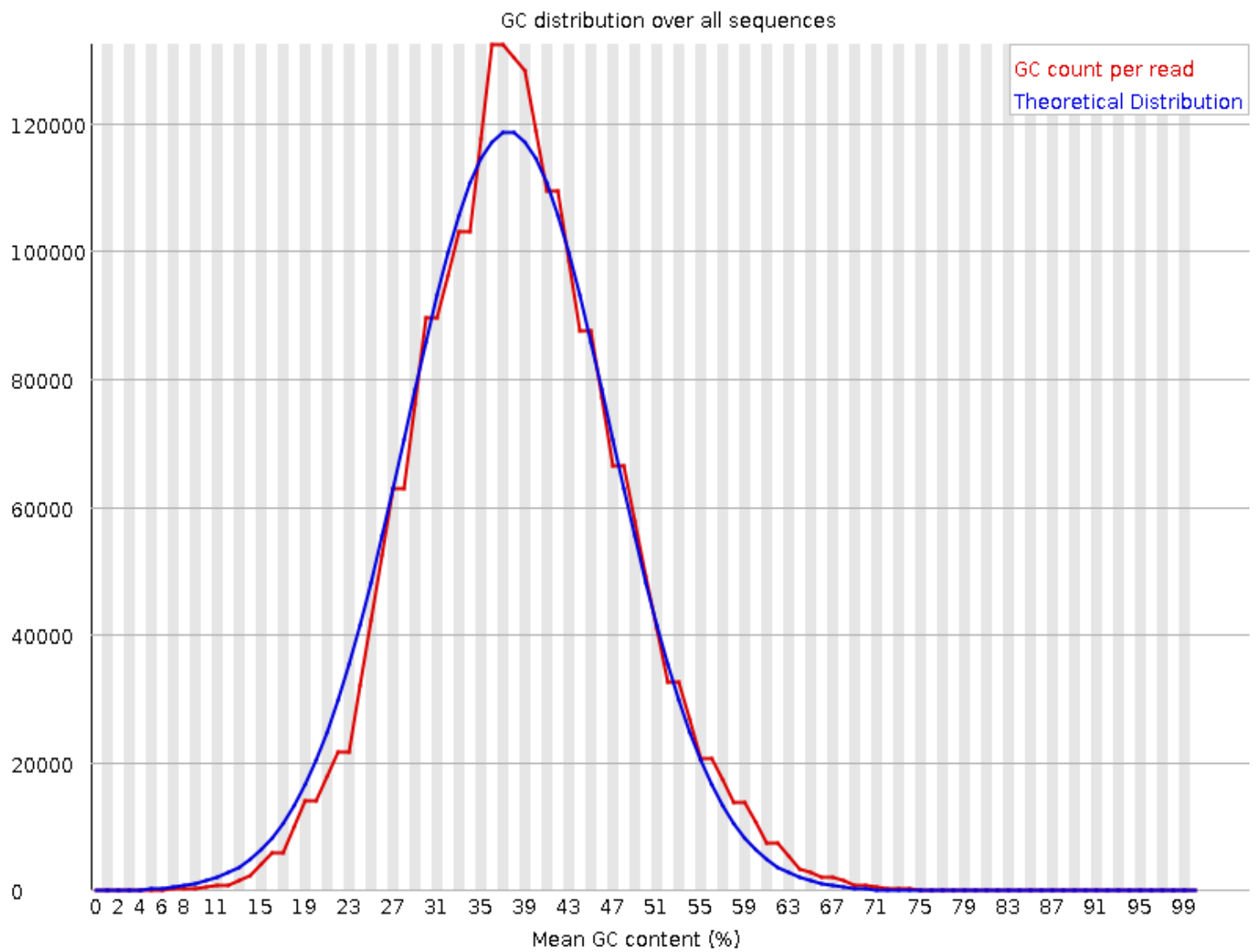
Per sequence quality scores



✖ Per base sequence content

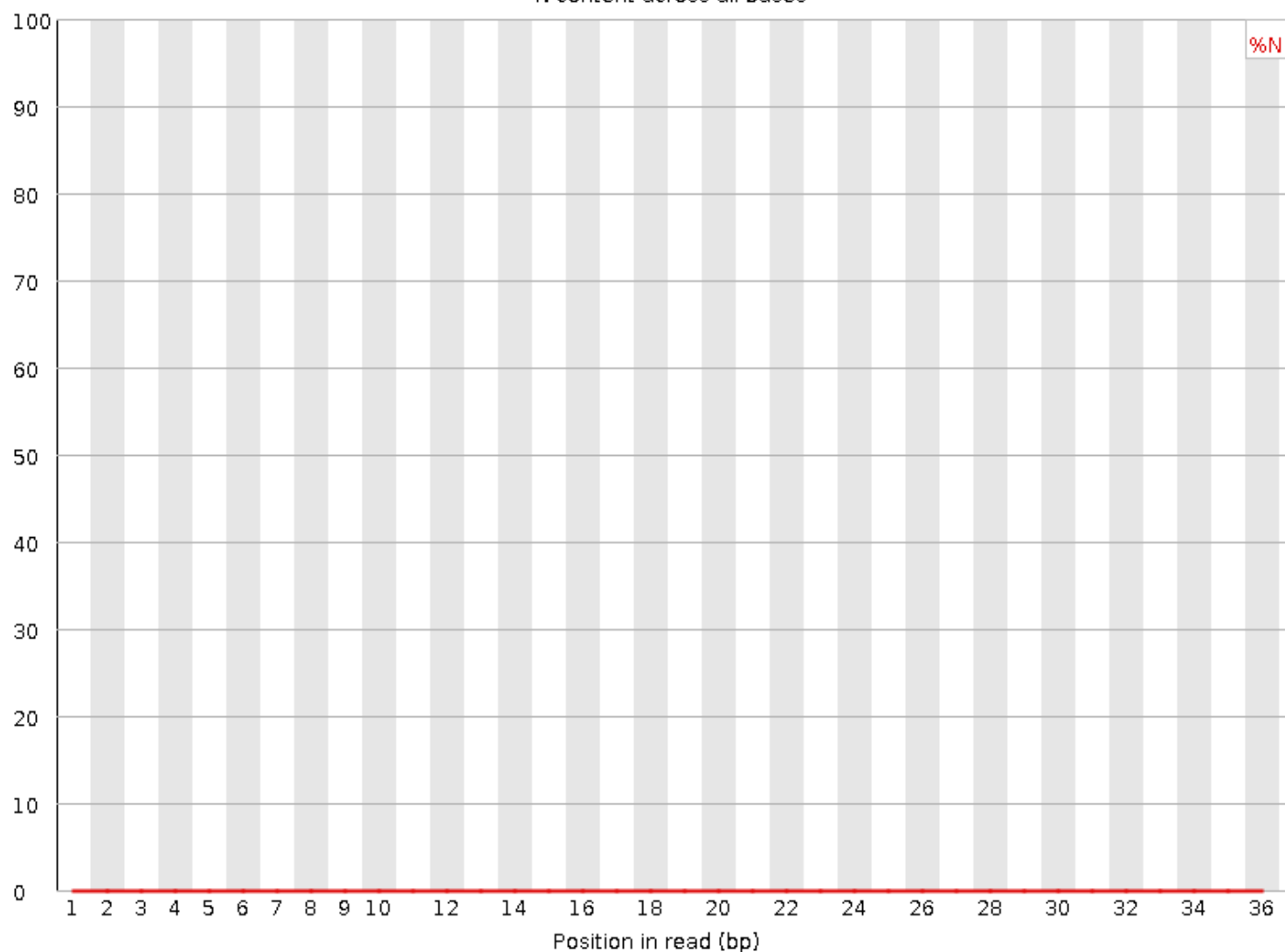


Per sequence GC content

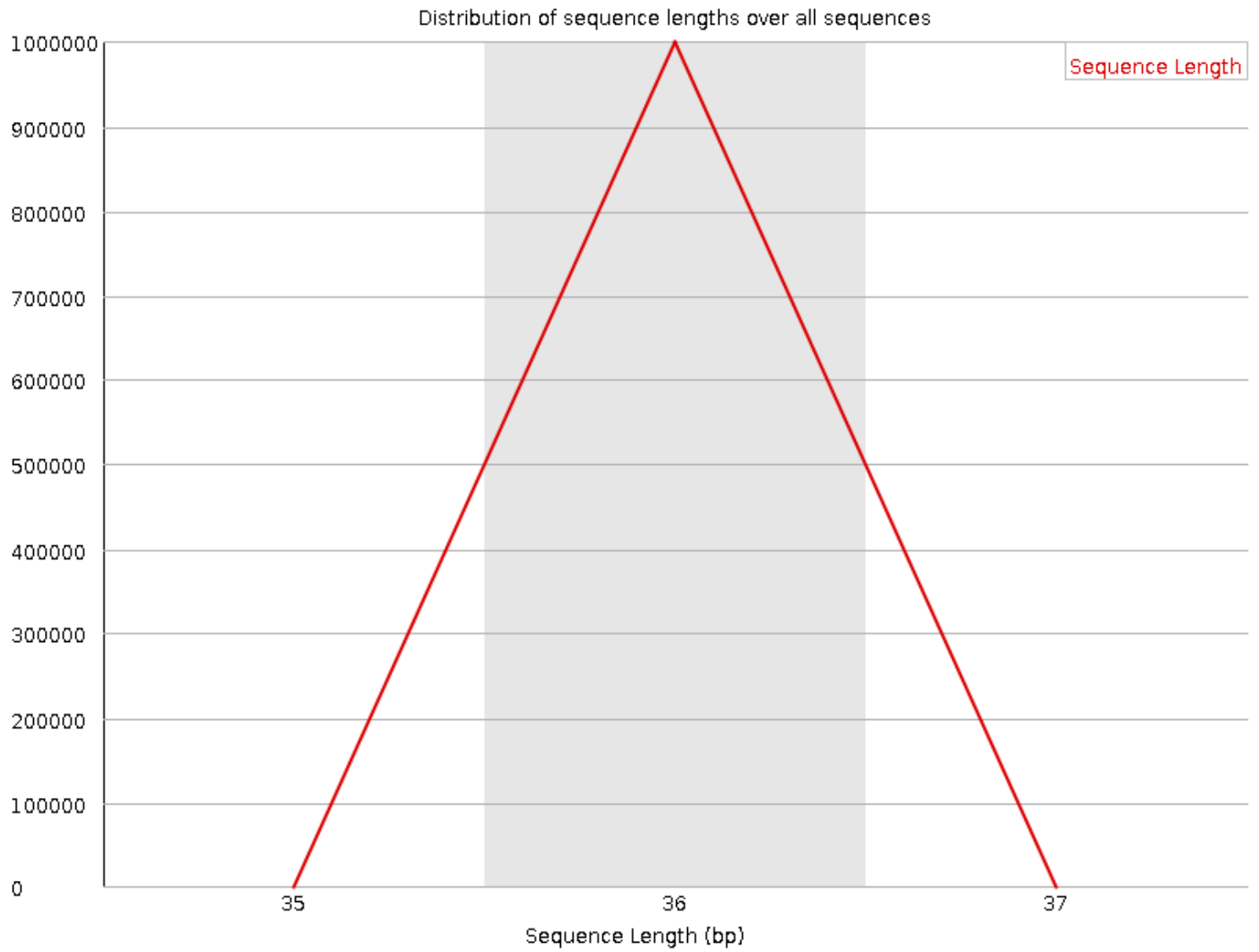


Per base N content

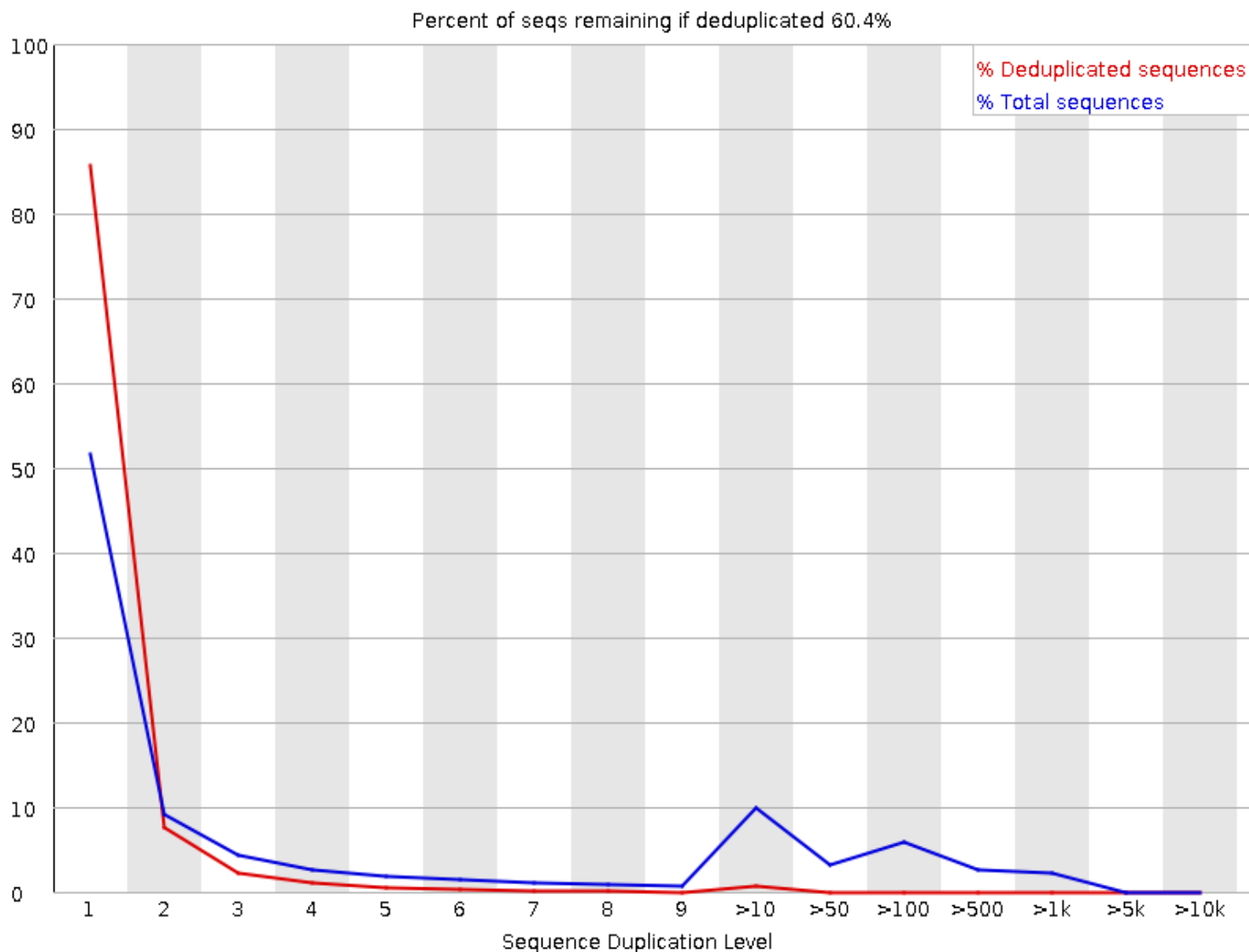
N content across all bases



Sequence Length Distribution



! Sequence Duplication Levels



! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3331	0.3331	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3149	0.3149	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2549	0.2549	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	2123	0.2123	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2017	0.20170000000000002	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1974	0.19740000000000002	No Hit
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1776	0.1776	No Hit
GTAAATAGCTGCAGTACTTTGACTGTACGAAGGTA	1380	0.13799999999999998	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1247	0.1247	No Hit

Sequence	Count	Percentage	Possible Source
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1168	0.1168	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1140	0.11399999999999999	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1098	0.10980000000000001	No Hit
CAGAAATTCAGGATAAAAACCAACCTGATTCACATC	1021	0.1021	No Hit
CTTACTTTAGTTATTTGTTGGGGTAACGGTATTTAT	1013	0.1013	No Hit

Adapter Content

