

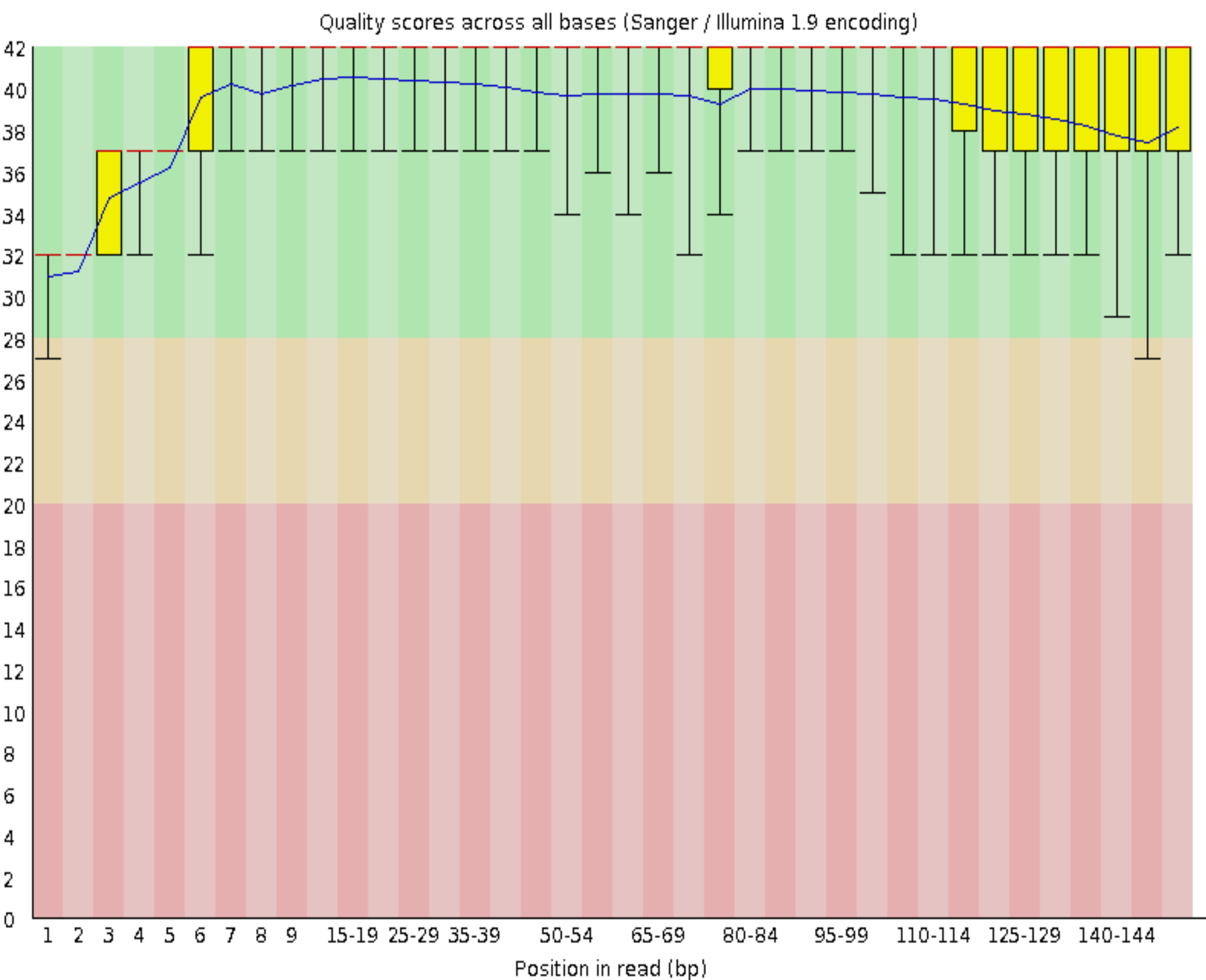
Summary

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Basic Statistics

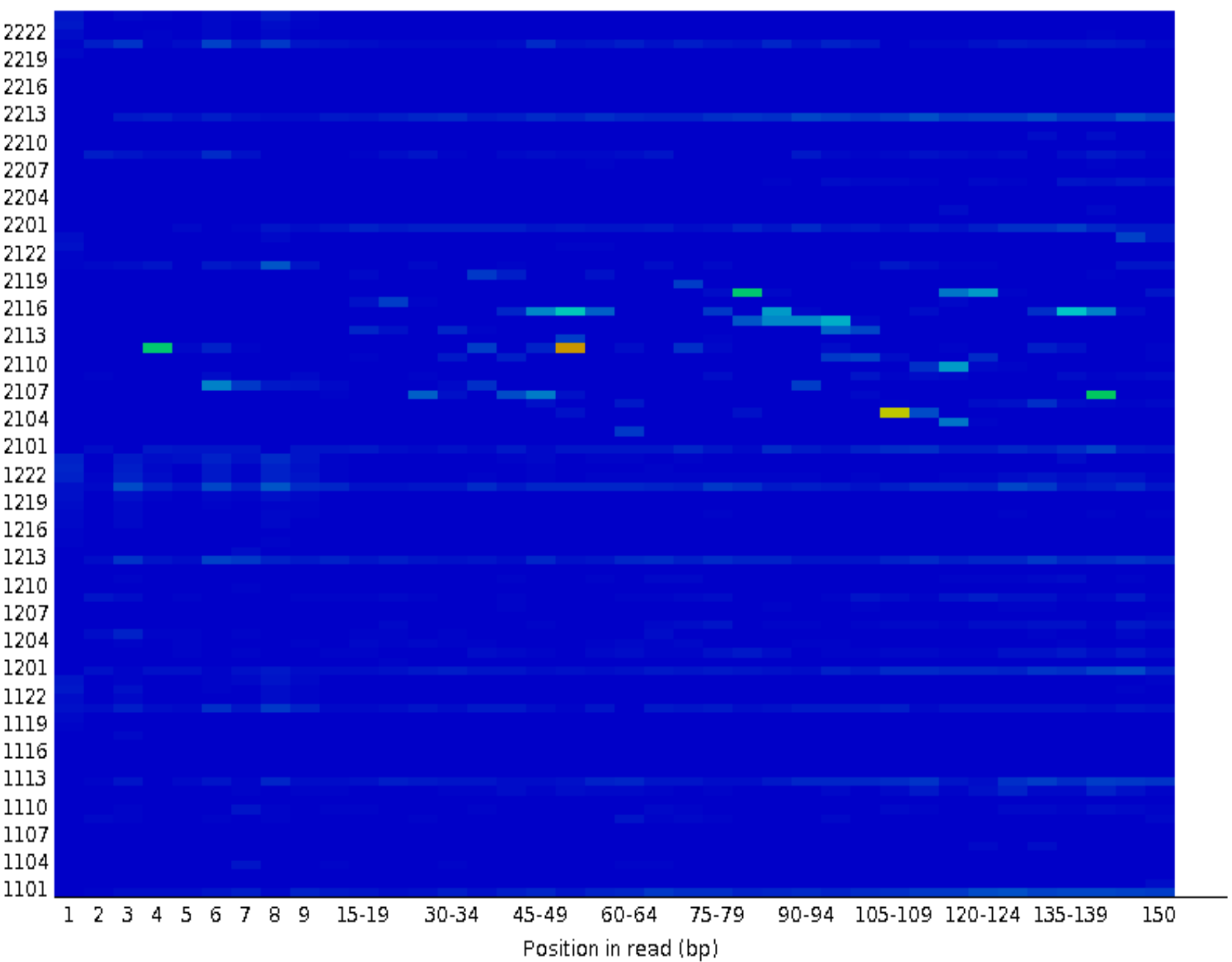
Measure	Value
Filename	IR23_L0_reverse_paired.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	20665282
Sequences flagged as poor quality	0
Sequence length	50-150
%GC	44

Per base sequence quality

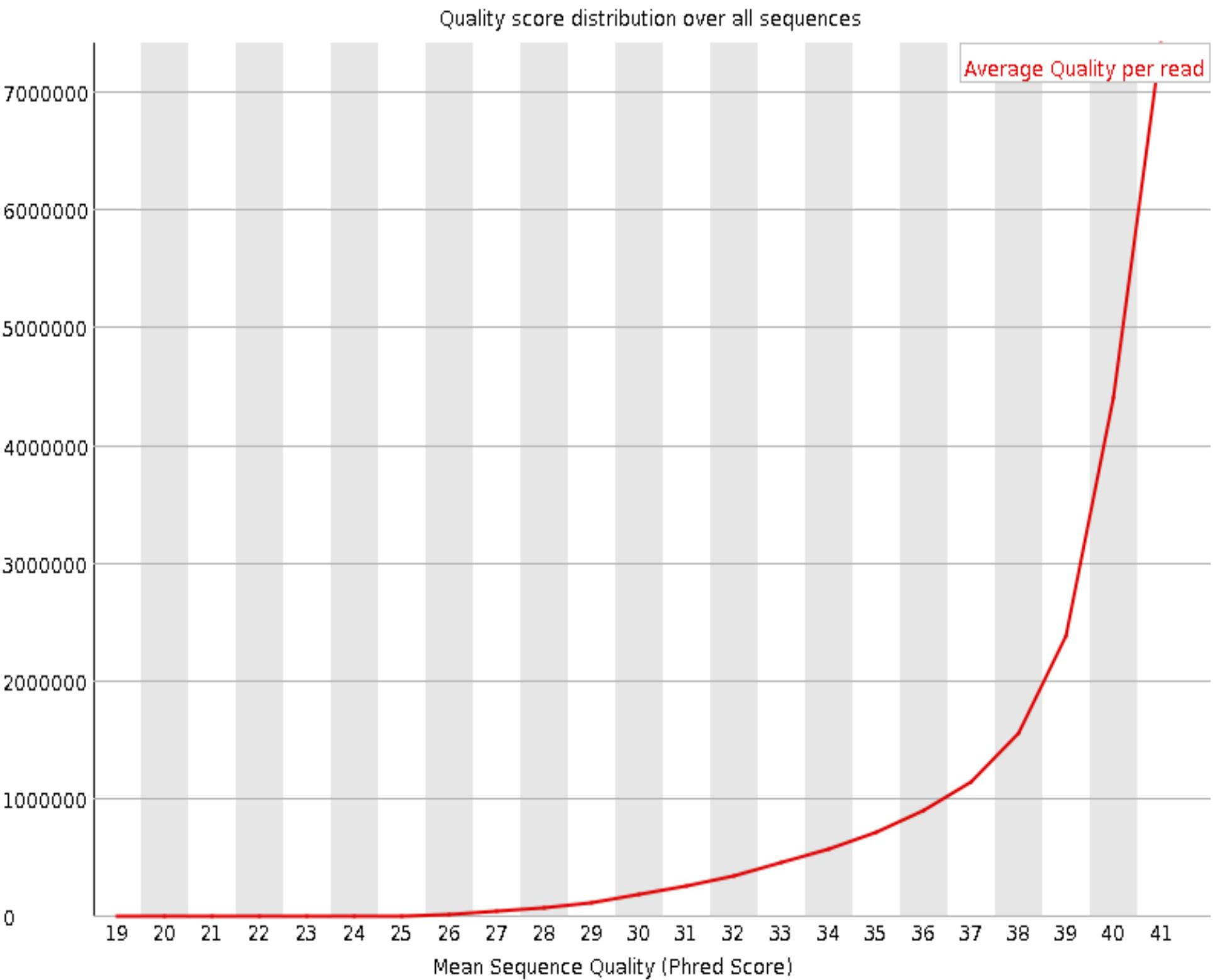


! Per tile sequence quality

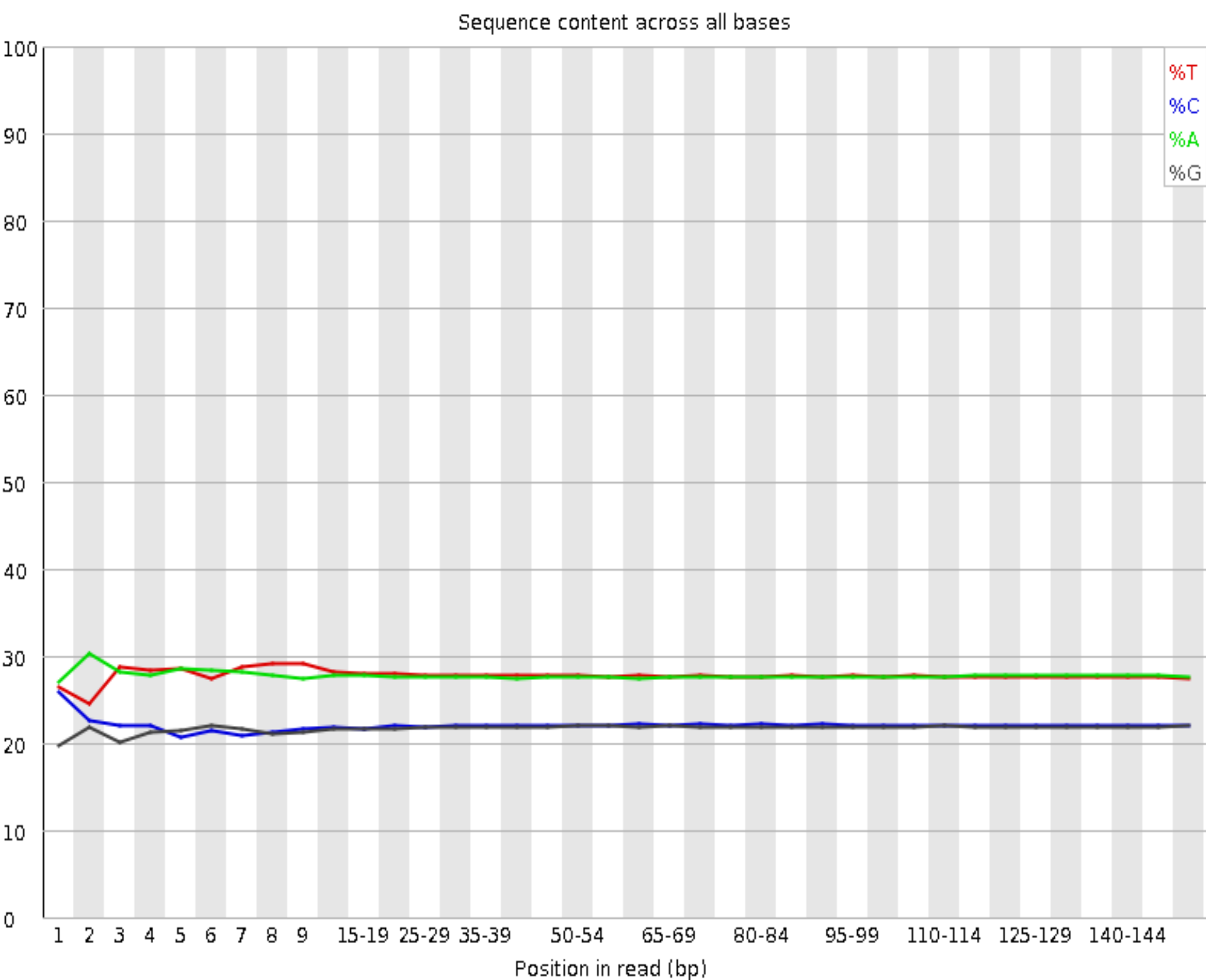
Quality per tile



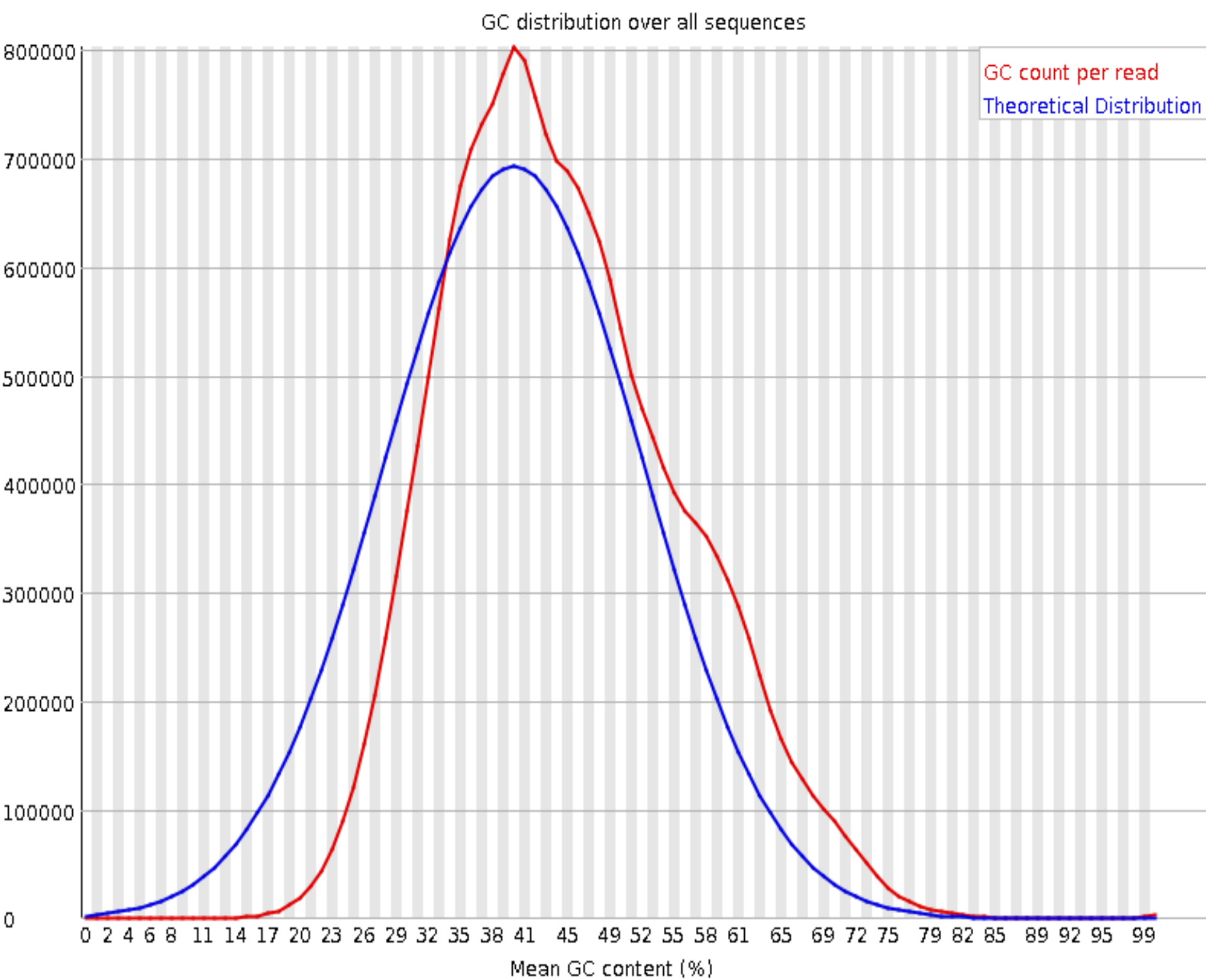
✔ Per sequence quality scores



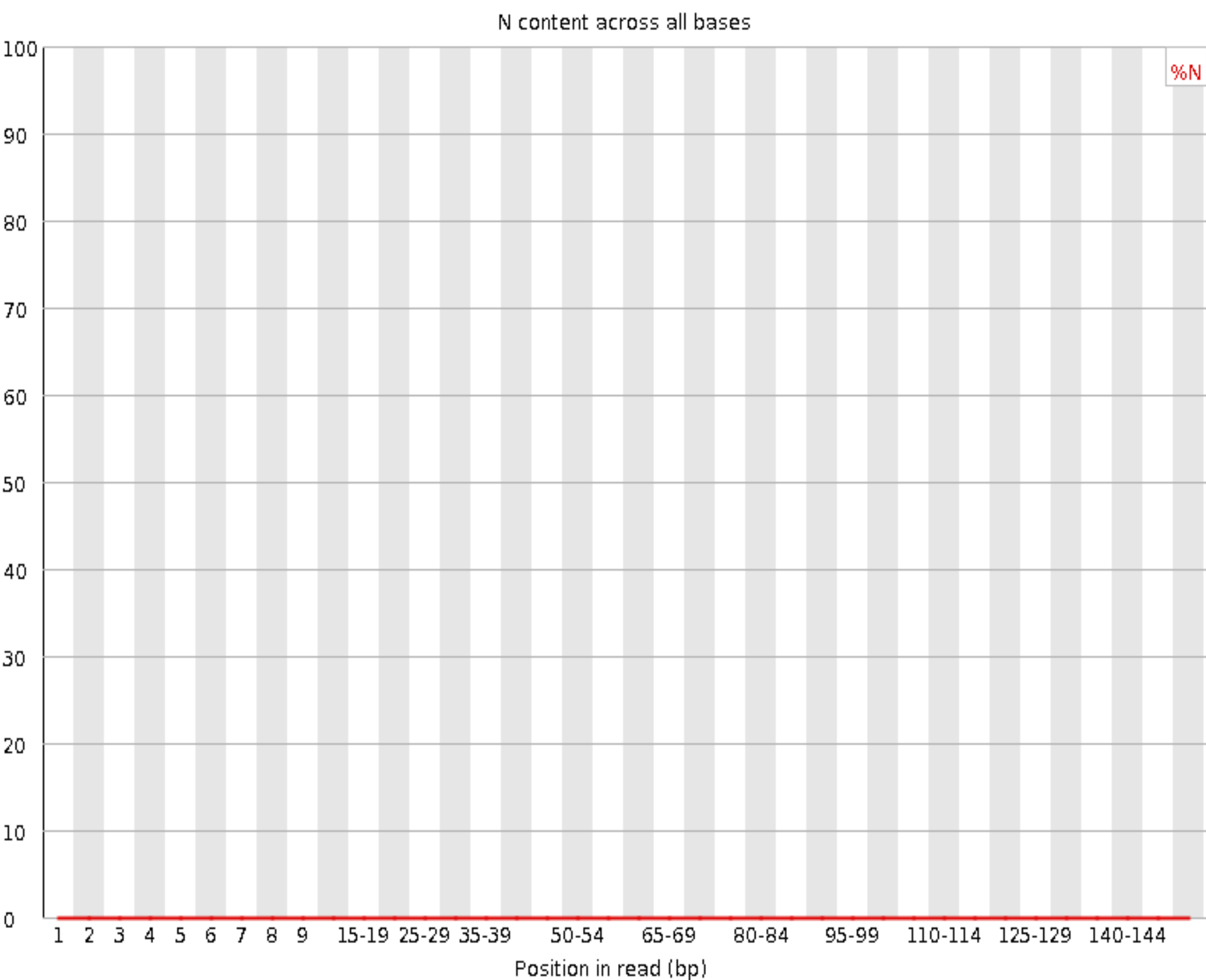
✅ Per base sequence content



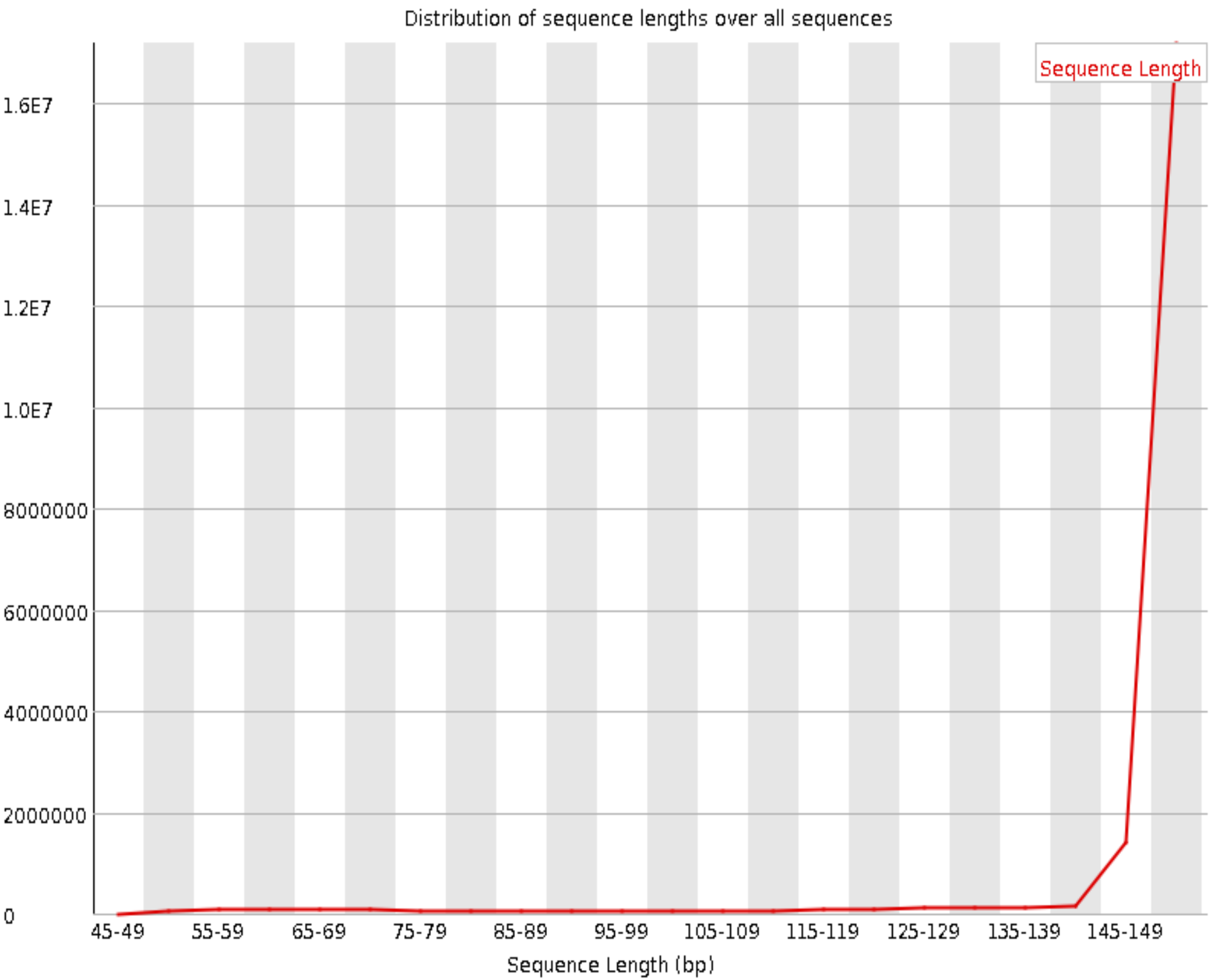
! Per sequence GC content



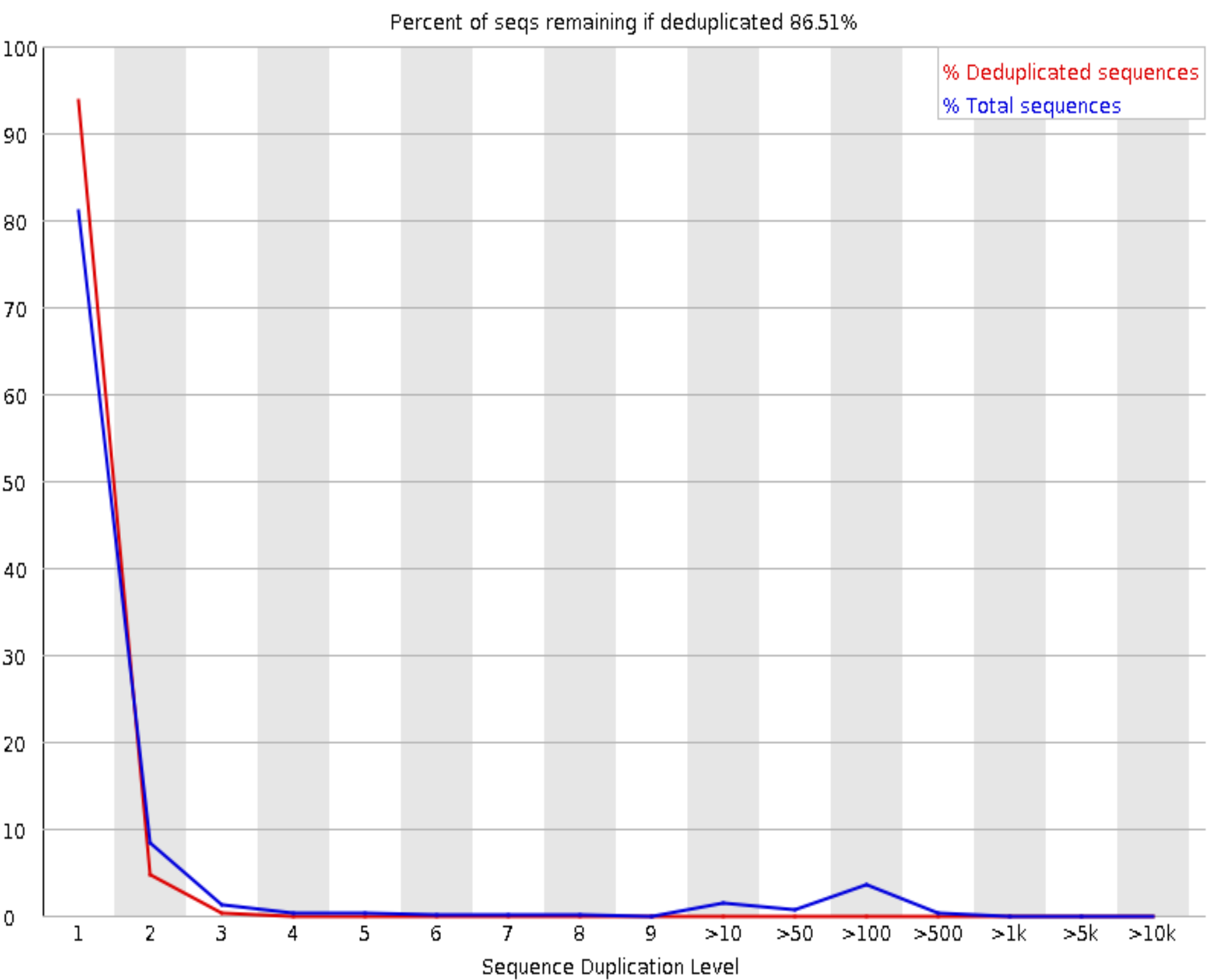
Per base N content



! Sequence Length Distribution

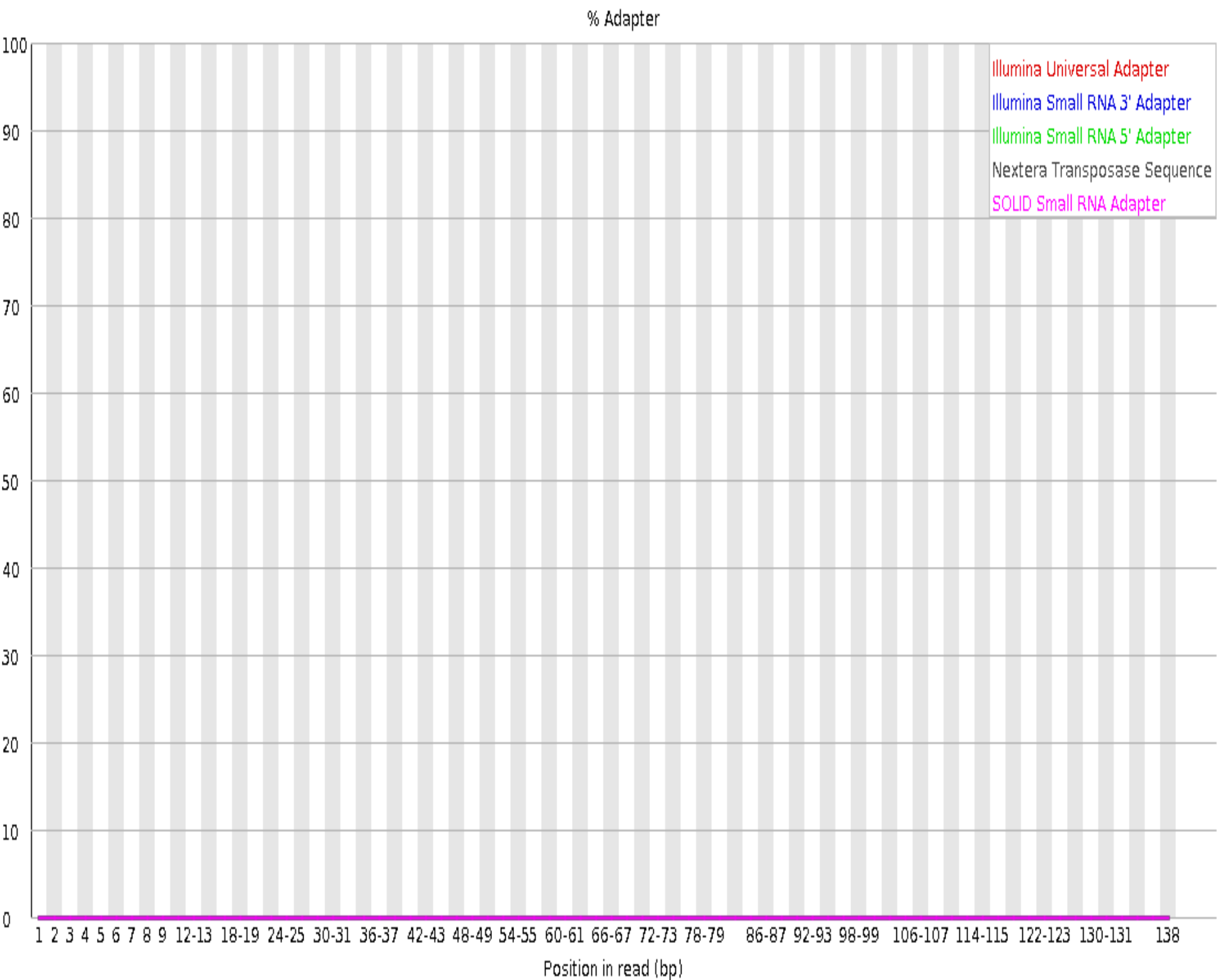


✔ Sequence Duplication Levels

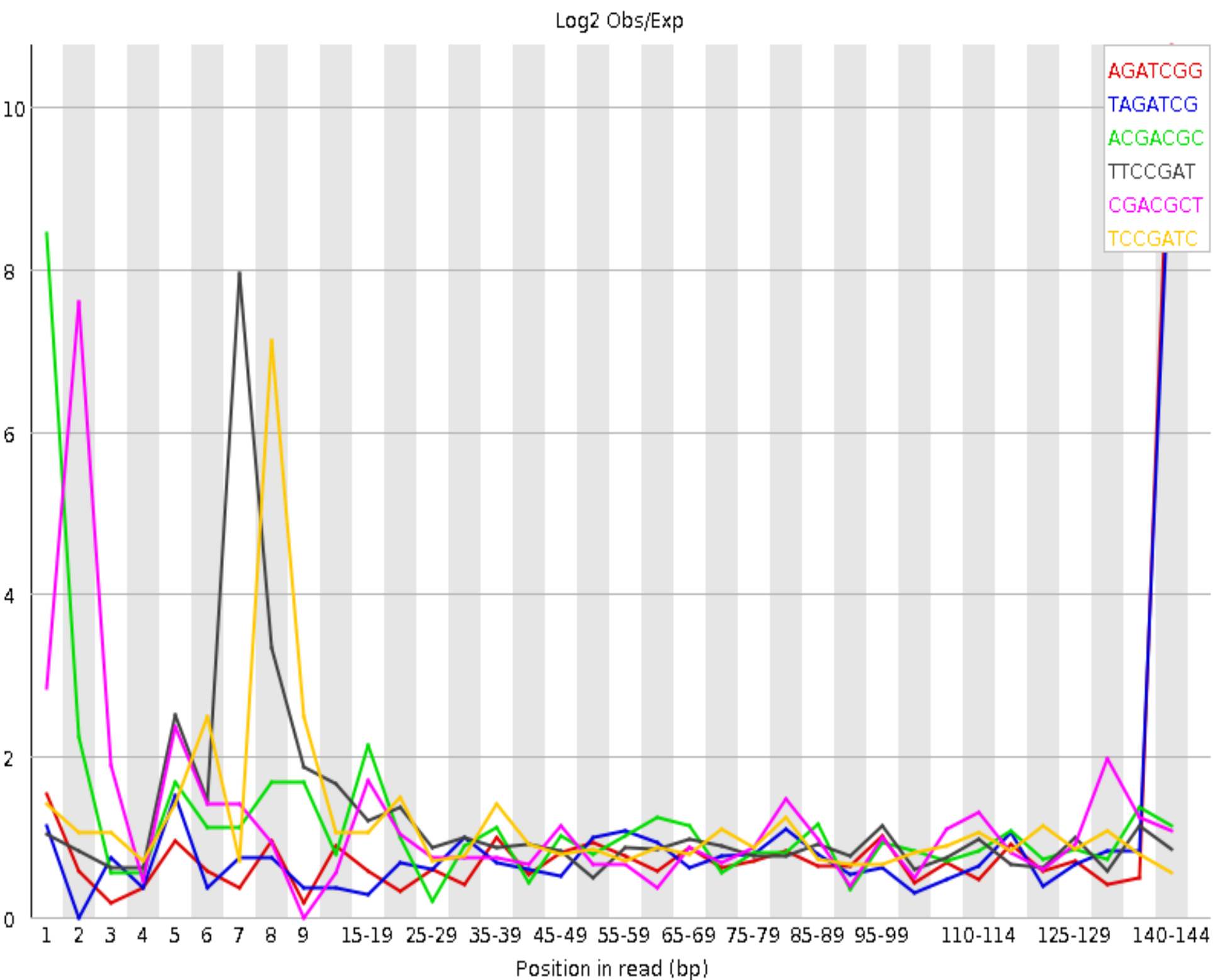


 **Overrepresented sequences**
No overrepresented sequences

 **Adapter Content**



✖ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGATCGG	3590	0.0	10.7646675	140–144
TAGATCG	1820	0.0	9.966792	140–144
ACGACGC	1235	1.4225516E-6	8.45682	1
TTCCGAT	3325	0.0	7.9508214	7
CGACGCT	1465	1.9724066E-6	7.604402	2
TCCGATC	1950	5.592301E-8	7.135094	8
GAGATCG	3660	0.0	6.5507565	140–144
AAGATCG	3105	0.0	6.3500533	140–144
TACACTC	11105	0.0	6.207252	1
CTTCCGA	4835	0.0	5.755507	6
CGCTCTT	5210	0.0	5.746633	2
TCCGATT	3215	1.5734258E-8	5.6259604	8
CCGATCT	2475	2.4308973E-5	5.34091	9
ACGCTCT	5530	0.0	5.288188	1

CAGATCG	3310	0.0	5.003689	140–144
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Produced by [FastQC](#) (version 0.11.5)