













FastQC Report

Summary

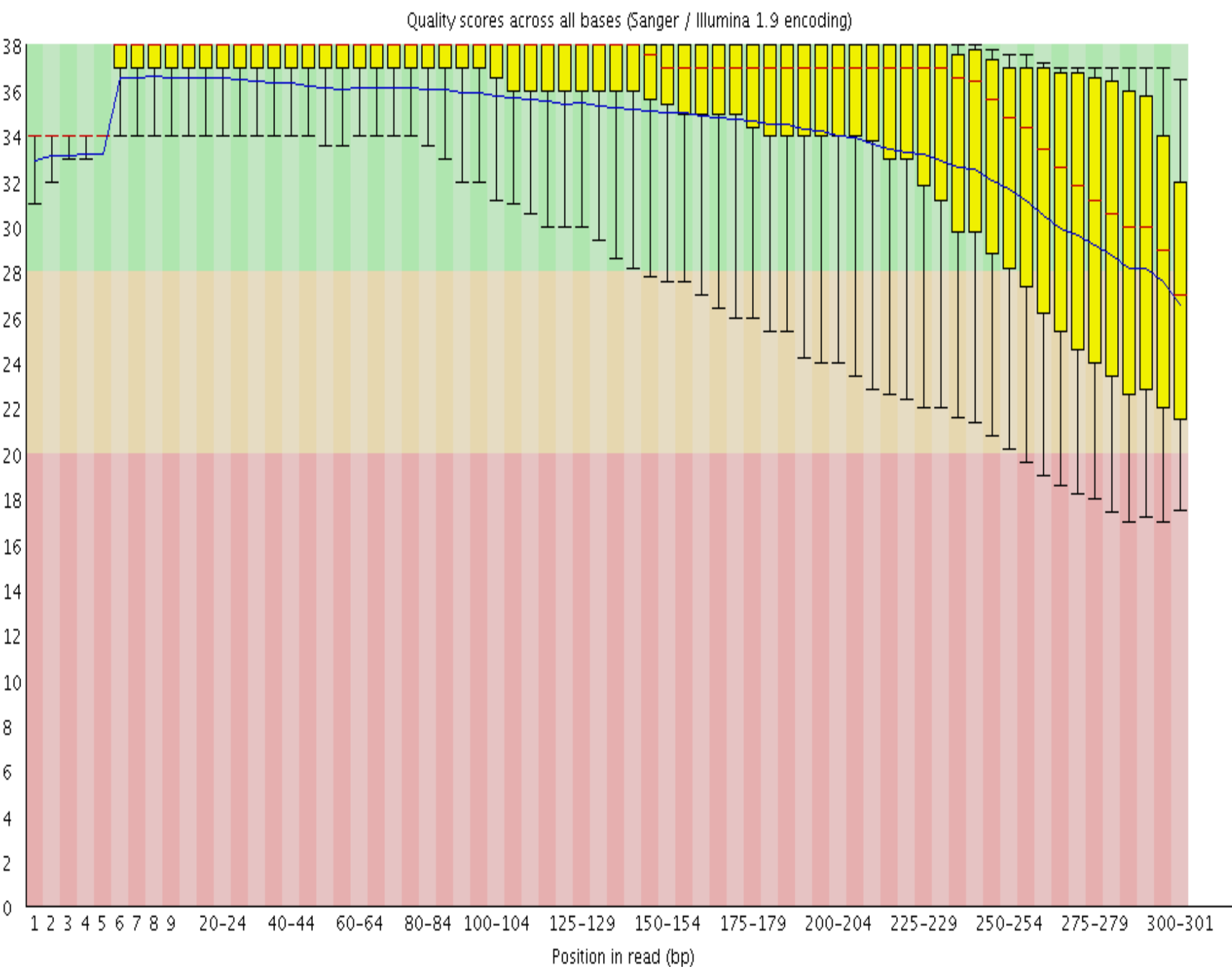
Fri 26 Apr 2019
output_R2_paired.fq.gz

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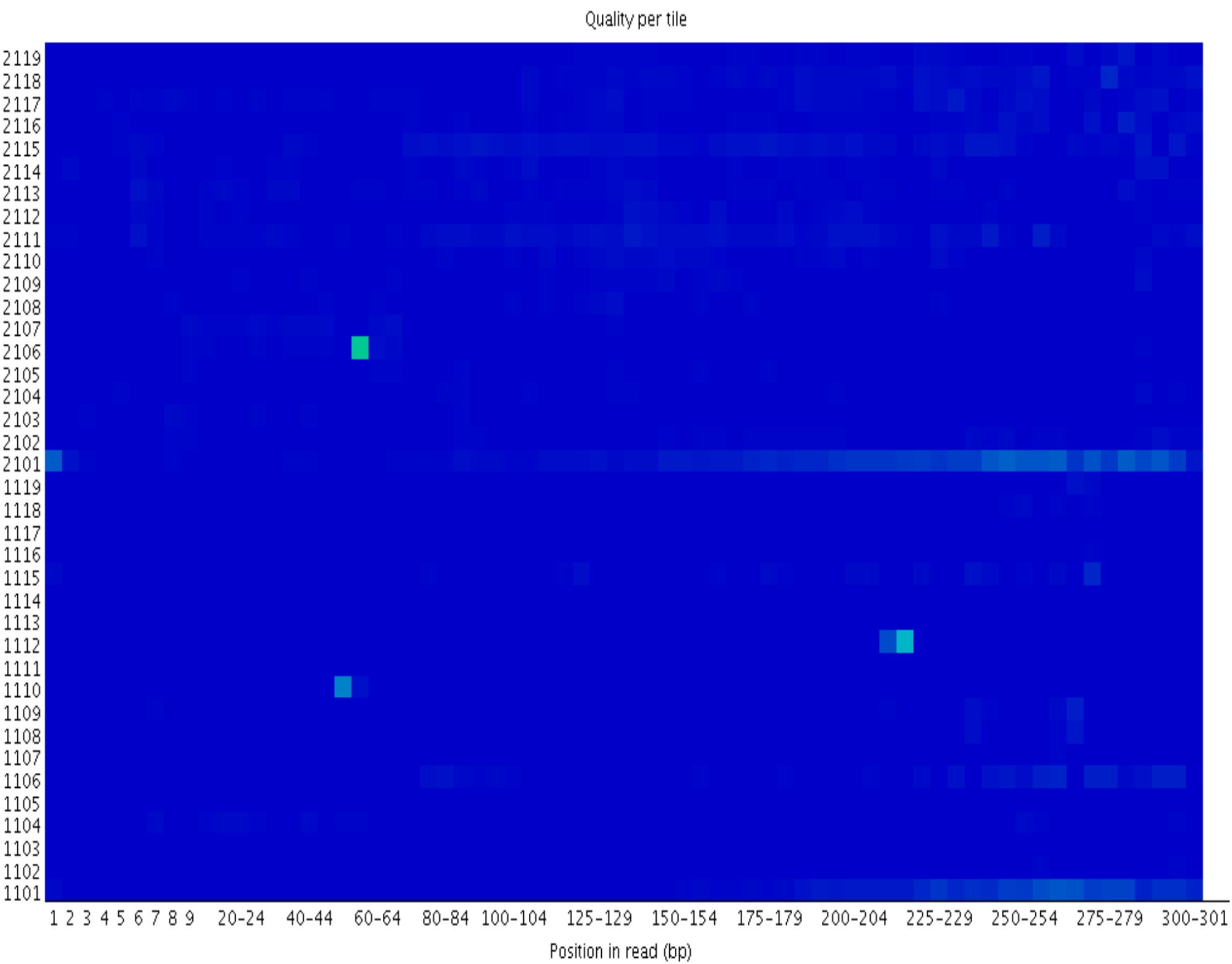
Basic Statistics

Measure	Value
Filename	output_R2_paired.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2503029
Sequences flagged as poor quality	0
Sequence length	36–301
%GC	36

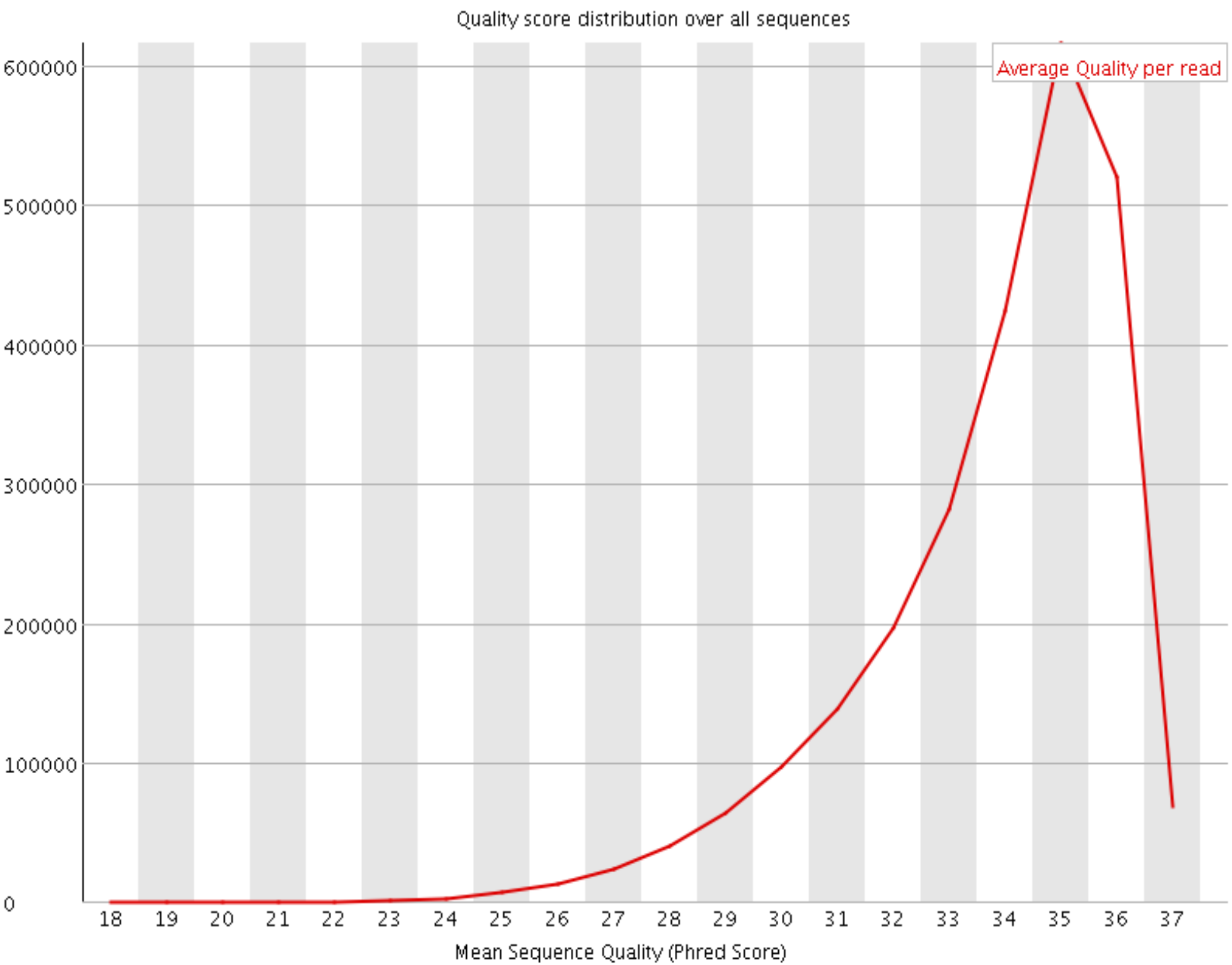
✔ Per base sequence quality



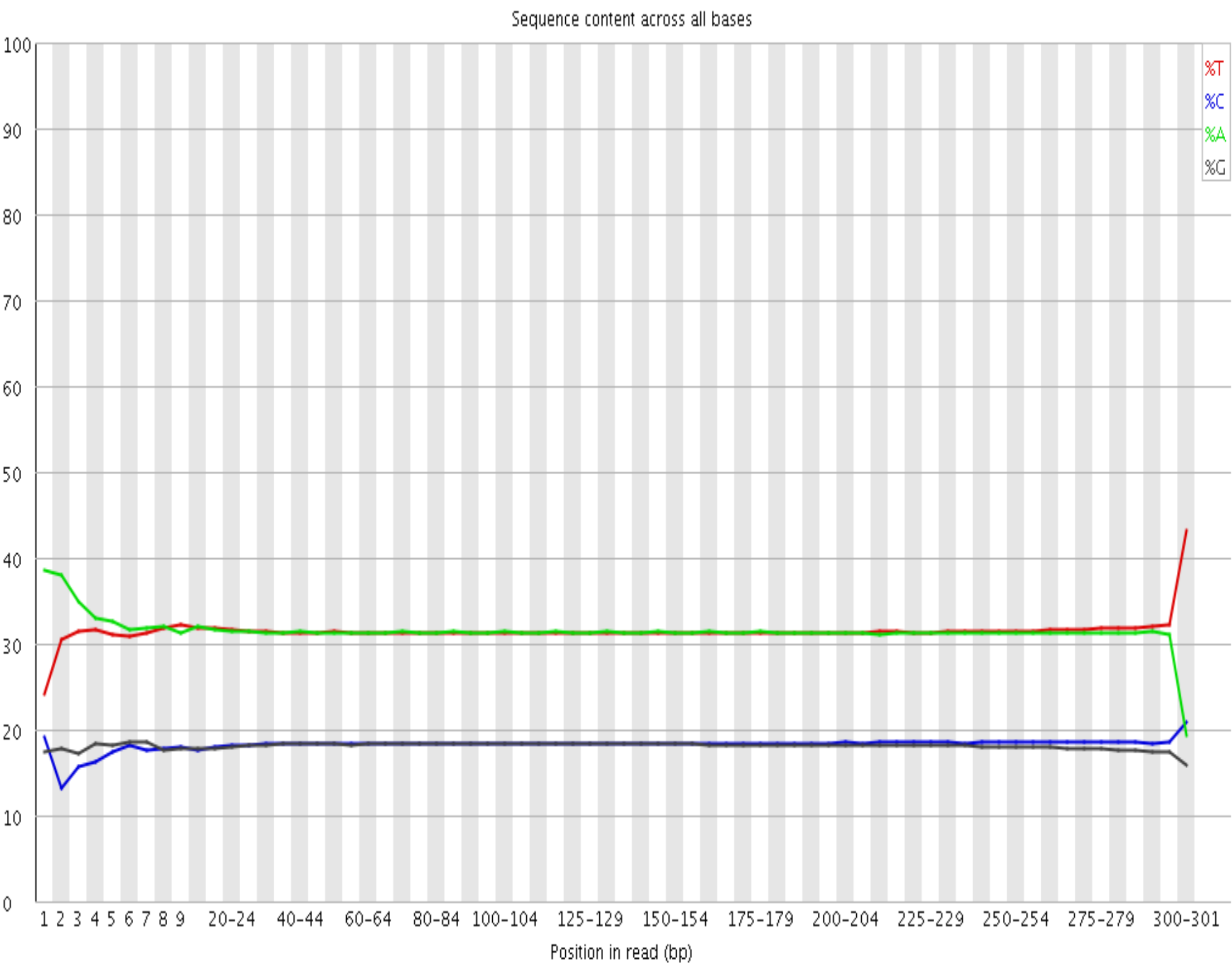
✔ Per tile sequence quality



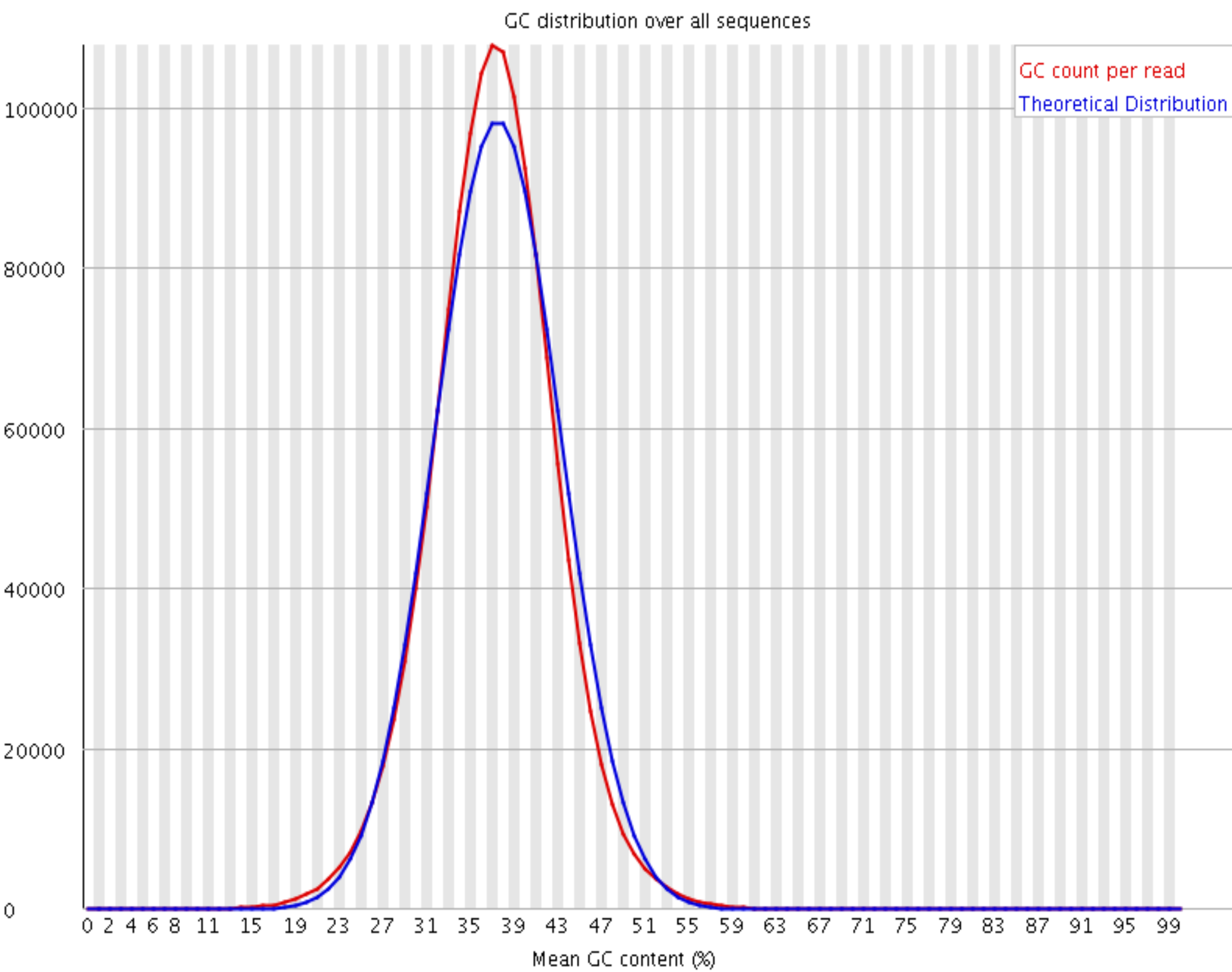
✔ **Per sequence quality scores**



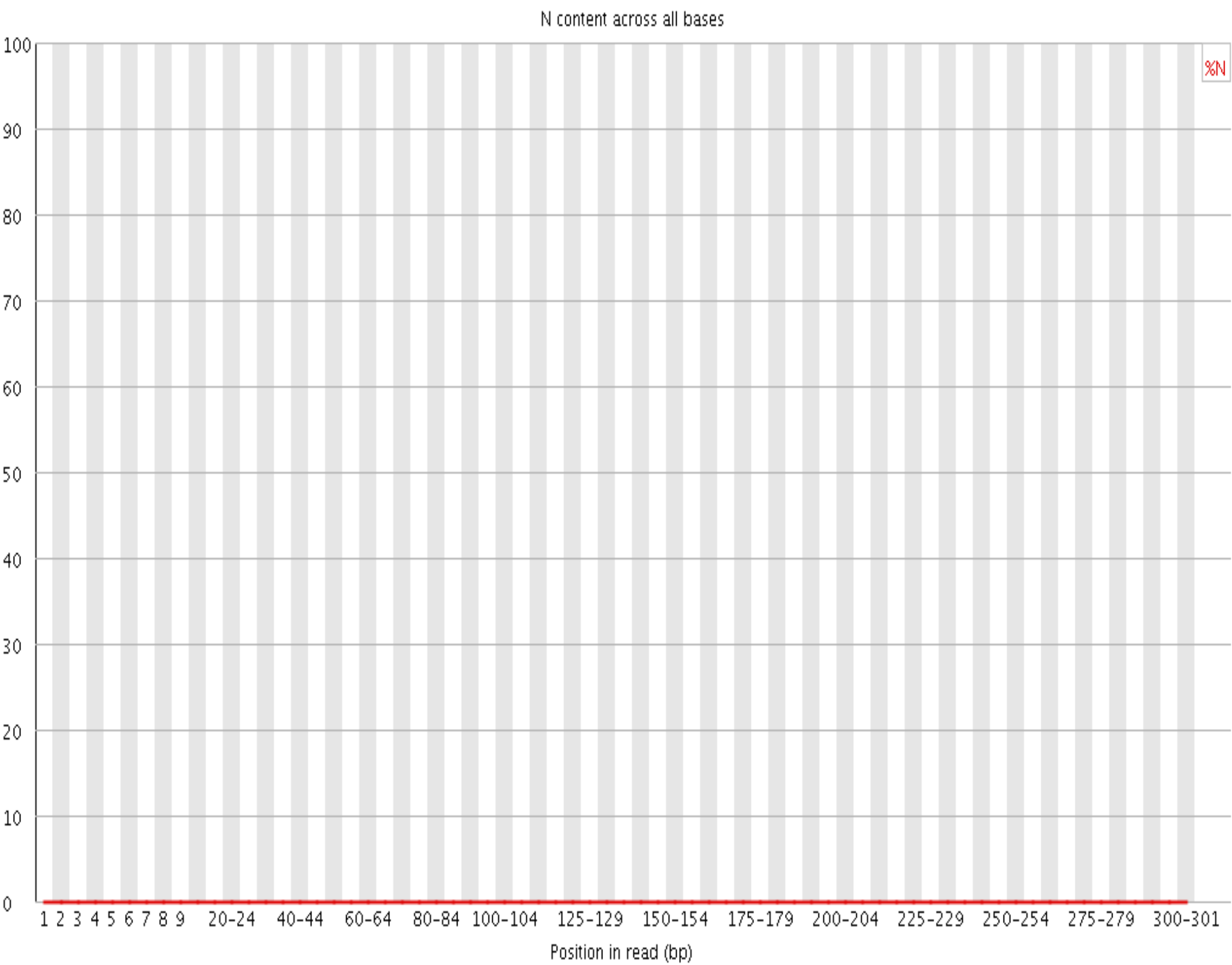
❌ Per base sequence content



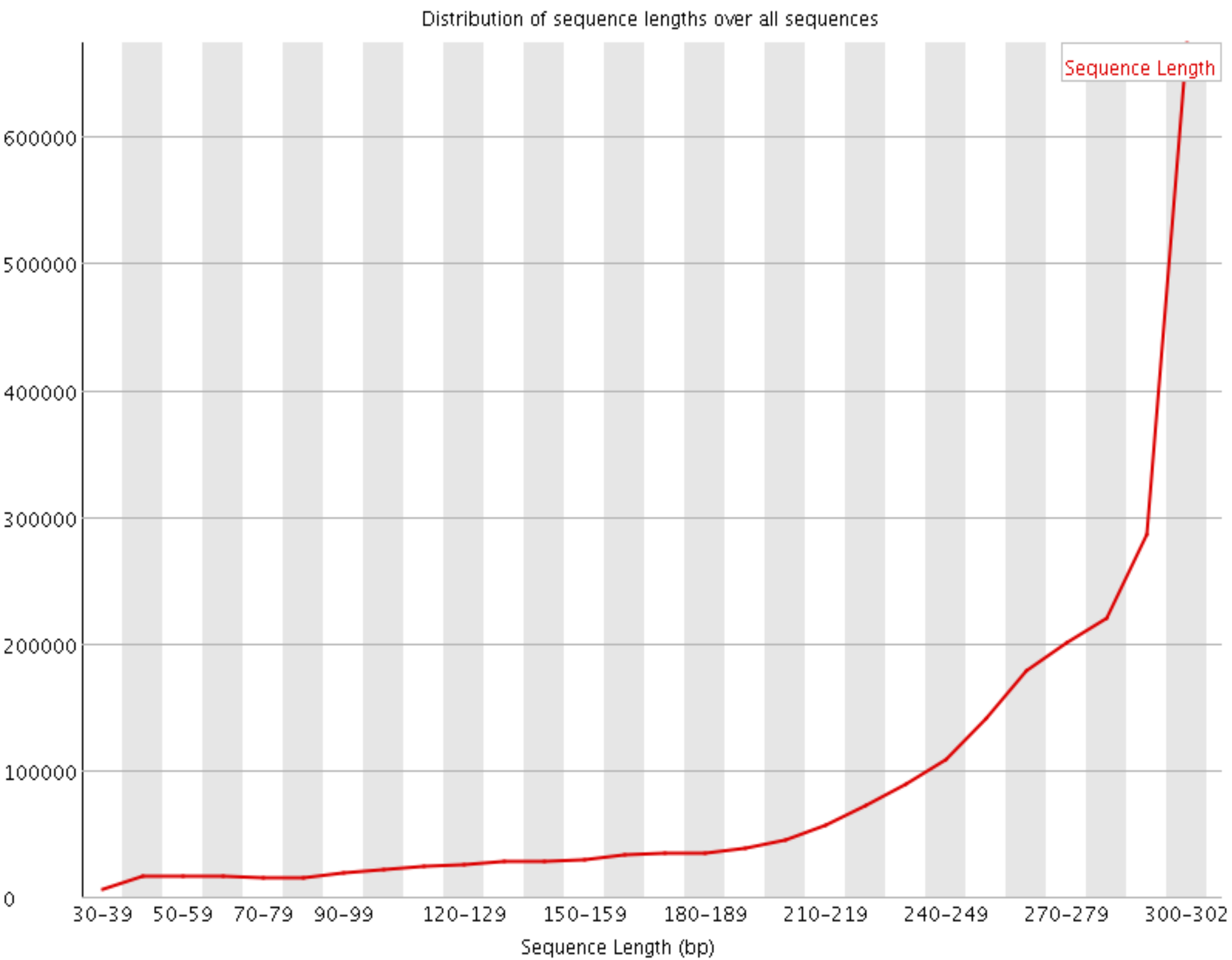
✔ Per sequence GC content



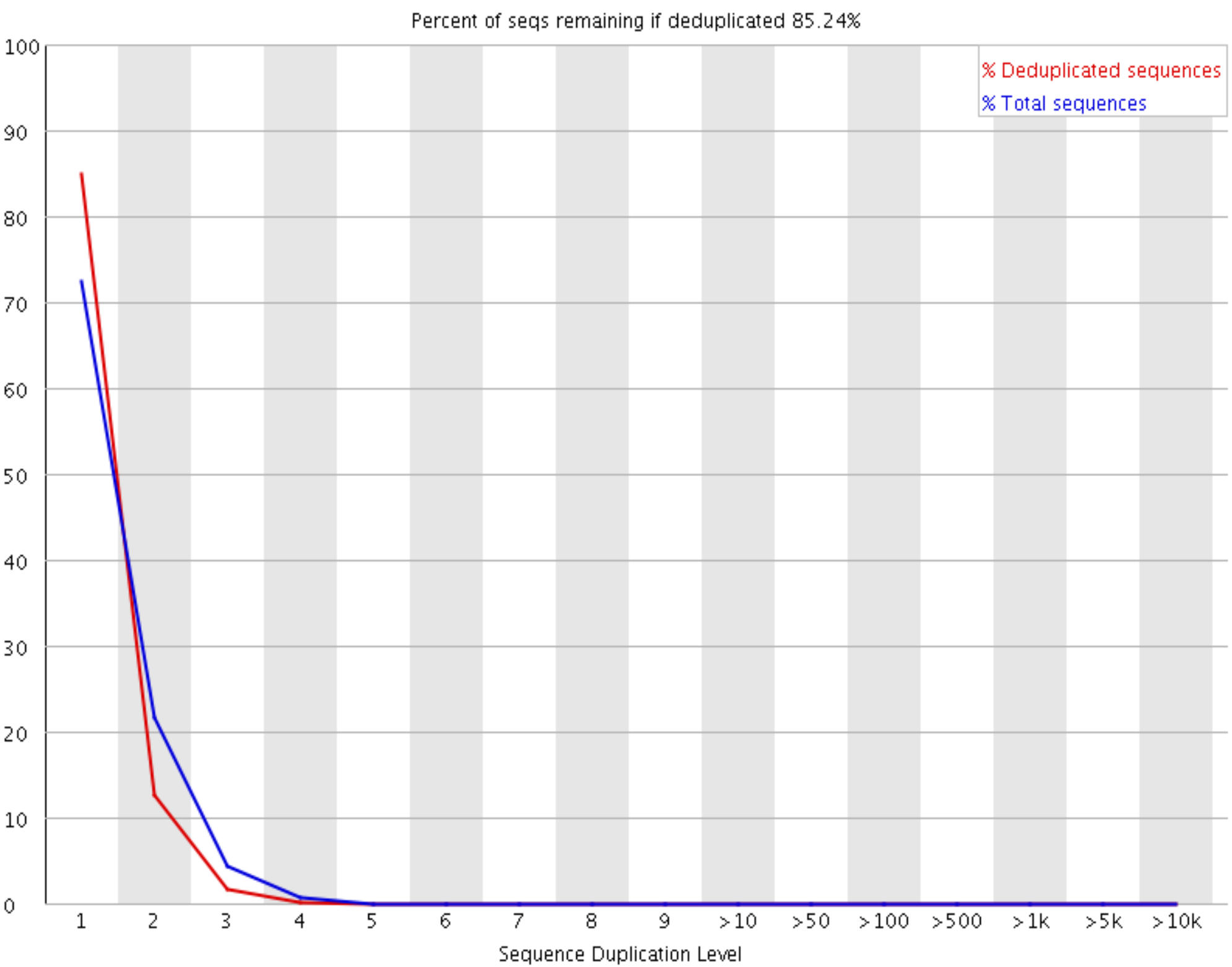
Per base N content



! Sequence Length Distribution

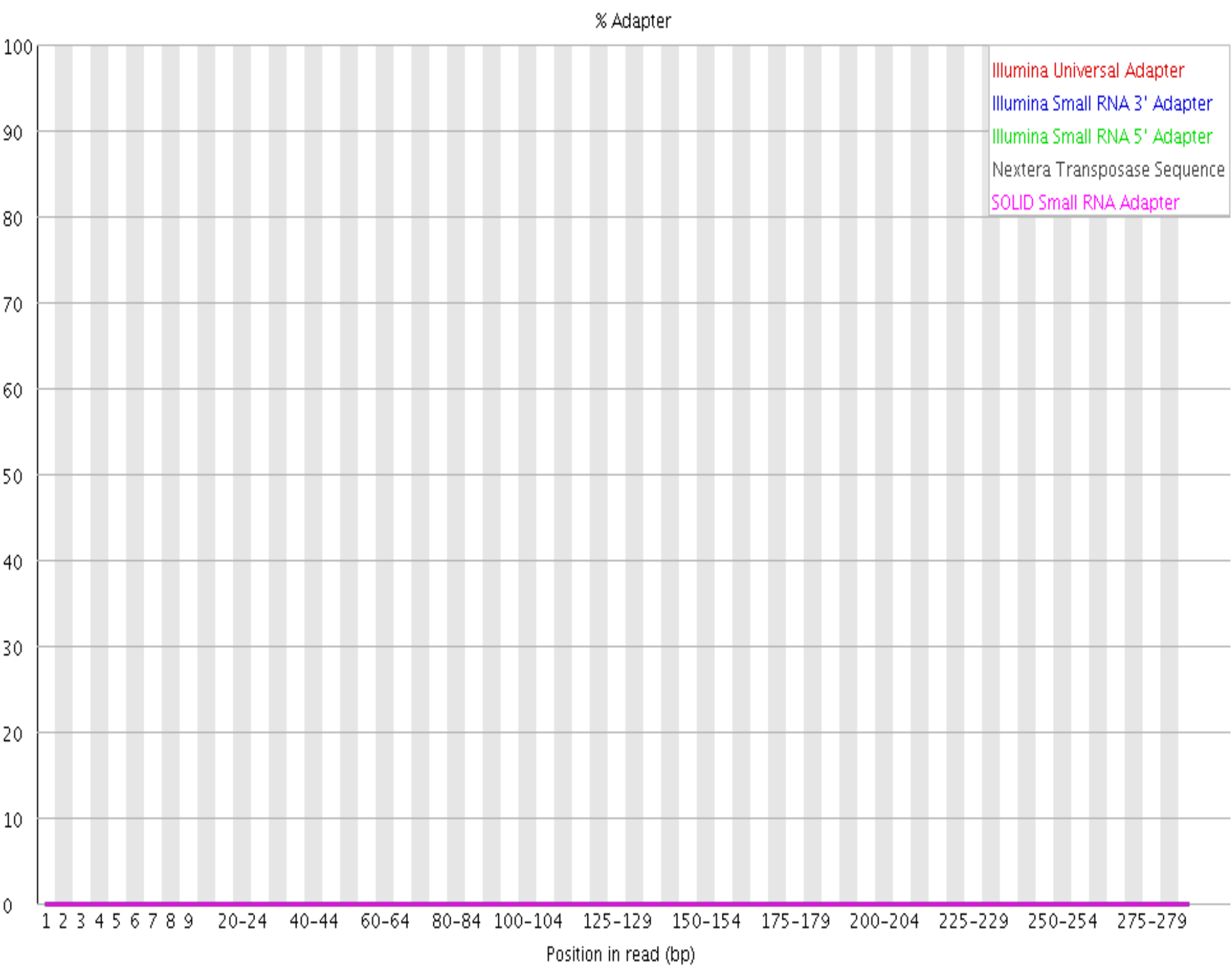


✔ Sequence Duplication Levels

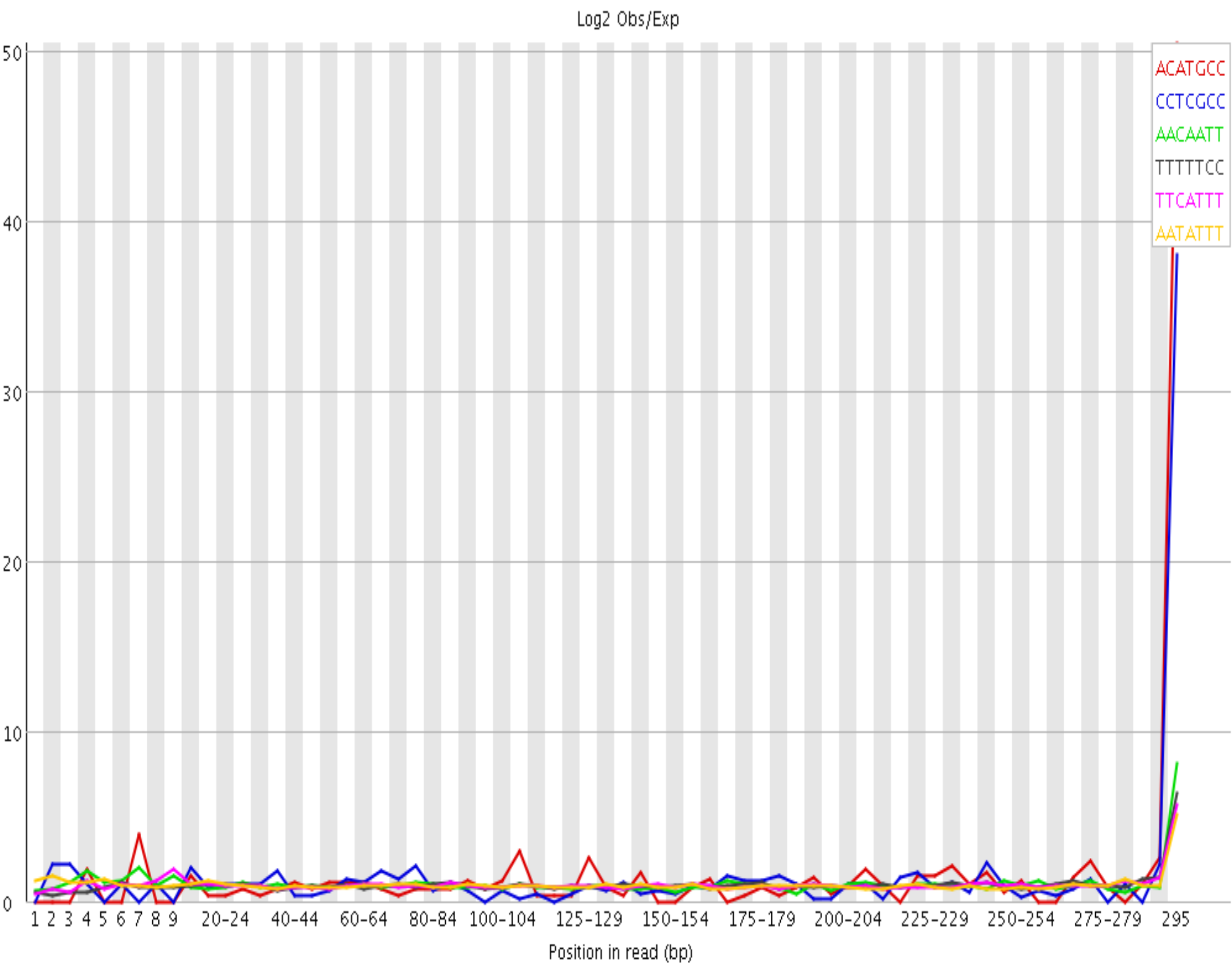


✔ **Overrepresented sequences**
No overrepresented sequences

✔ **Adapter Content**



 **Kmer Content**



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACATGCC	605	0.008125042	50.460766	295
CCTCGCC	1070	0.0016051822	38.042076	295
AACAATT	12450	0.0012260086	8.173698	295
TTTTCC	20430	4.9730315E-4	6.4753466	295
TTCATTT	21270	0.005497334	5.7411876	295
AATATTT	31275	4.918081E-4	5.206078	295
ATTATTT	27965	0.0036779947	5.094496	295