














FastQC Report

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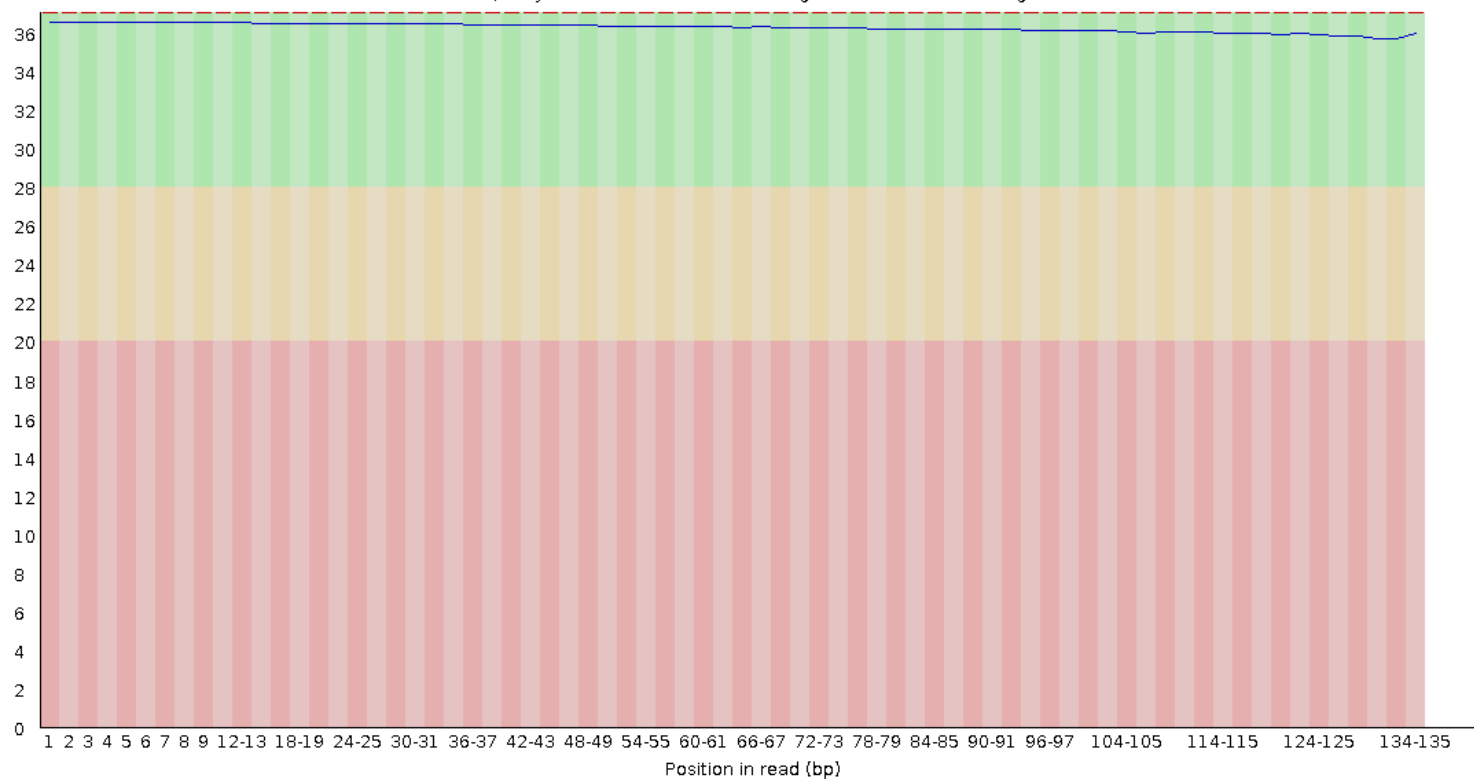
Basic Statistics

Measure	Value
Filename	WTC2_1_trPE.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	19434301
Total Bases	2.6 Gbp
Sequences flagged as poor quality	0
Sequence length	75–135
%GC	37



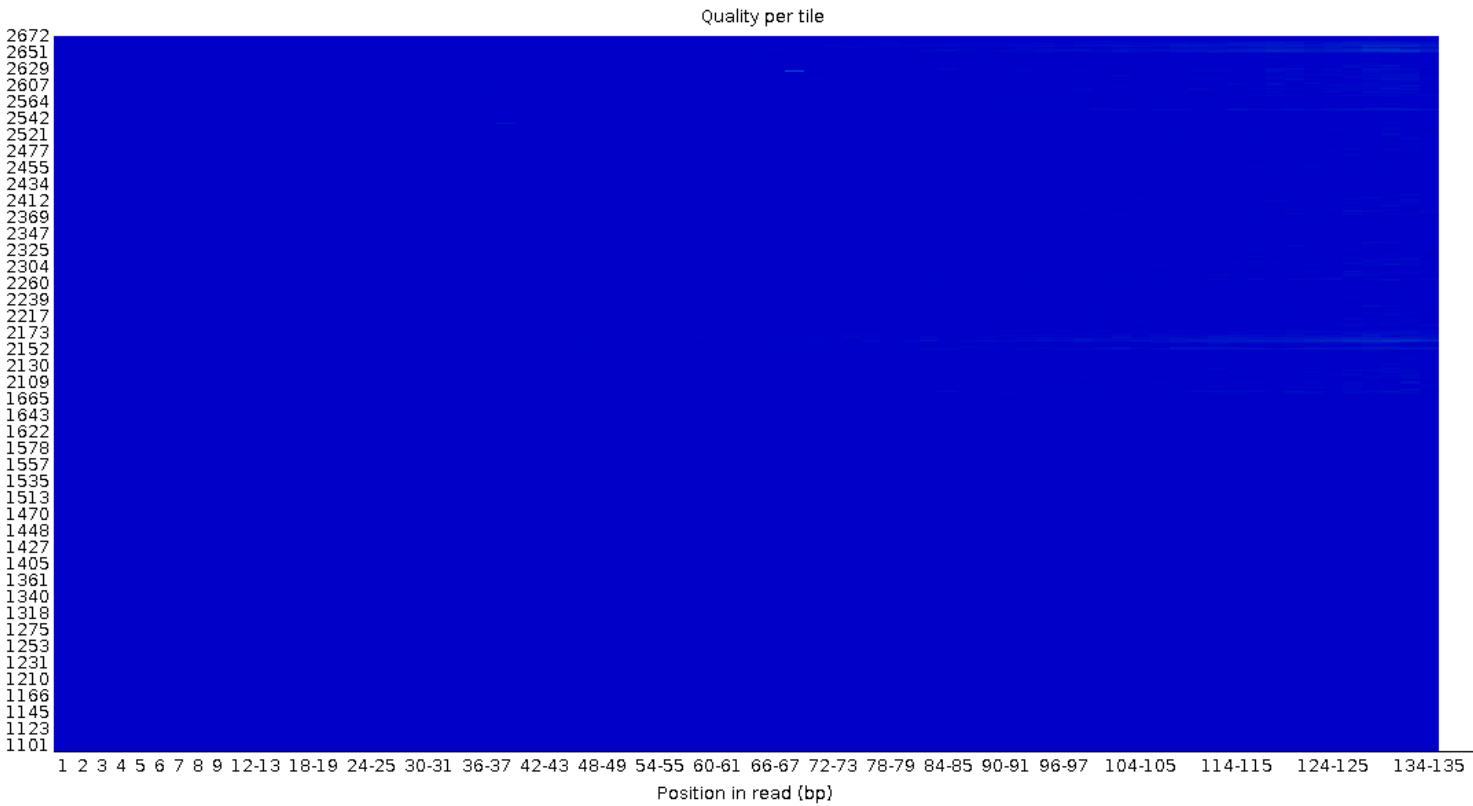
Per base sequence quality

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



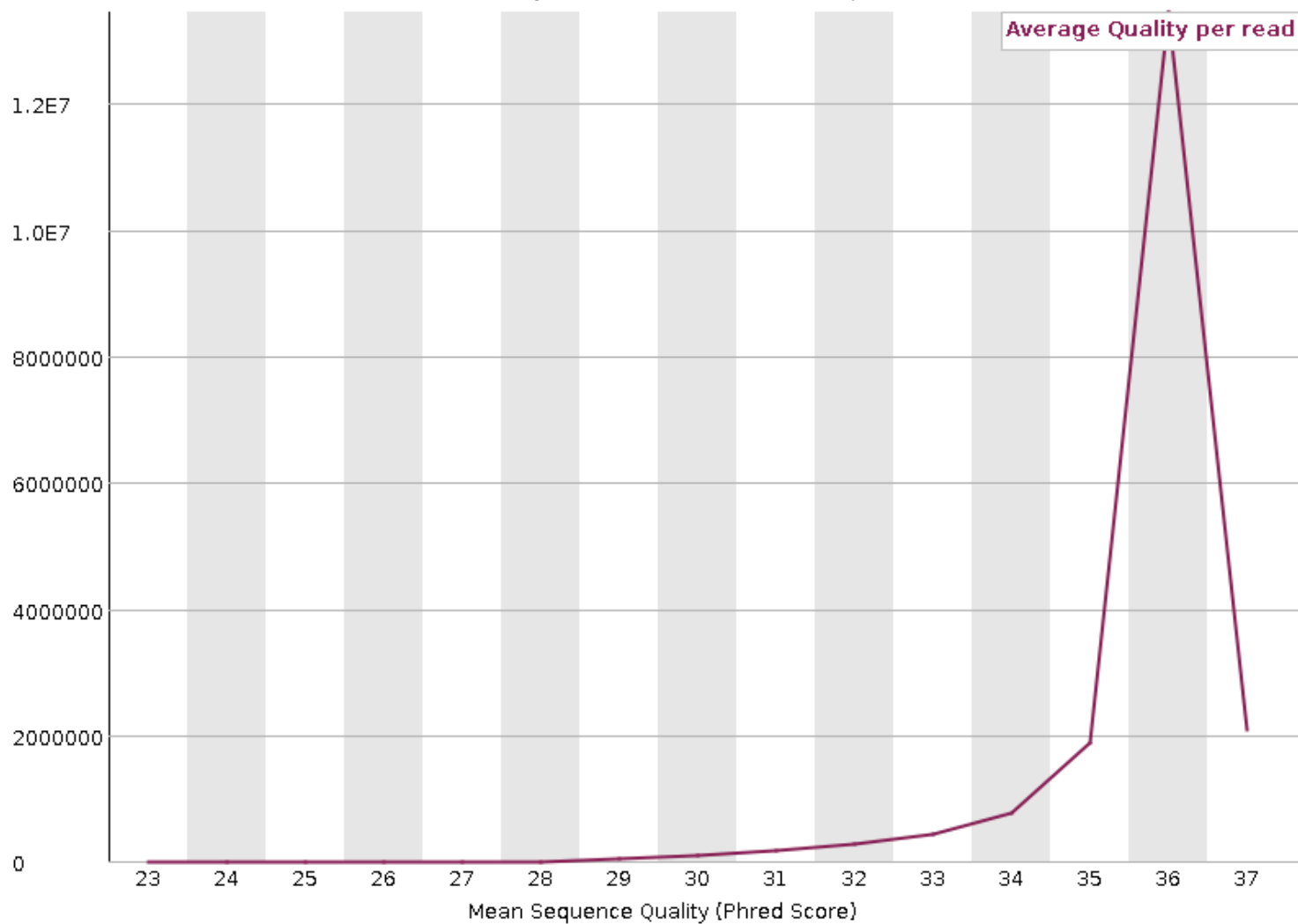


Per tile sequence quality

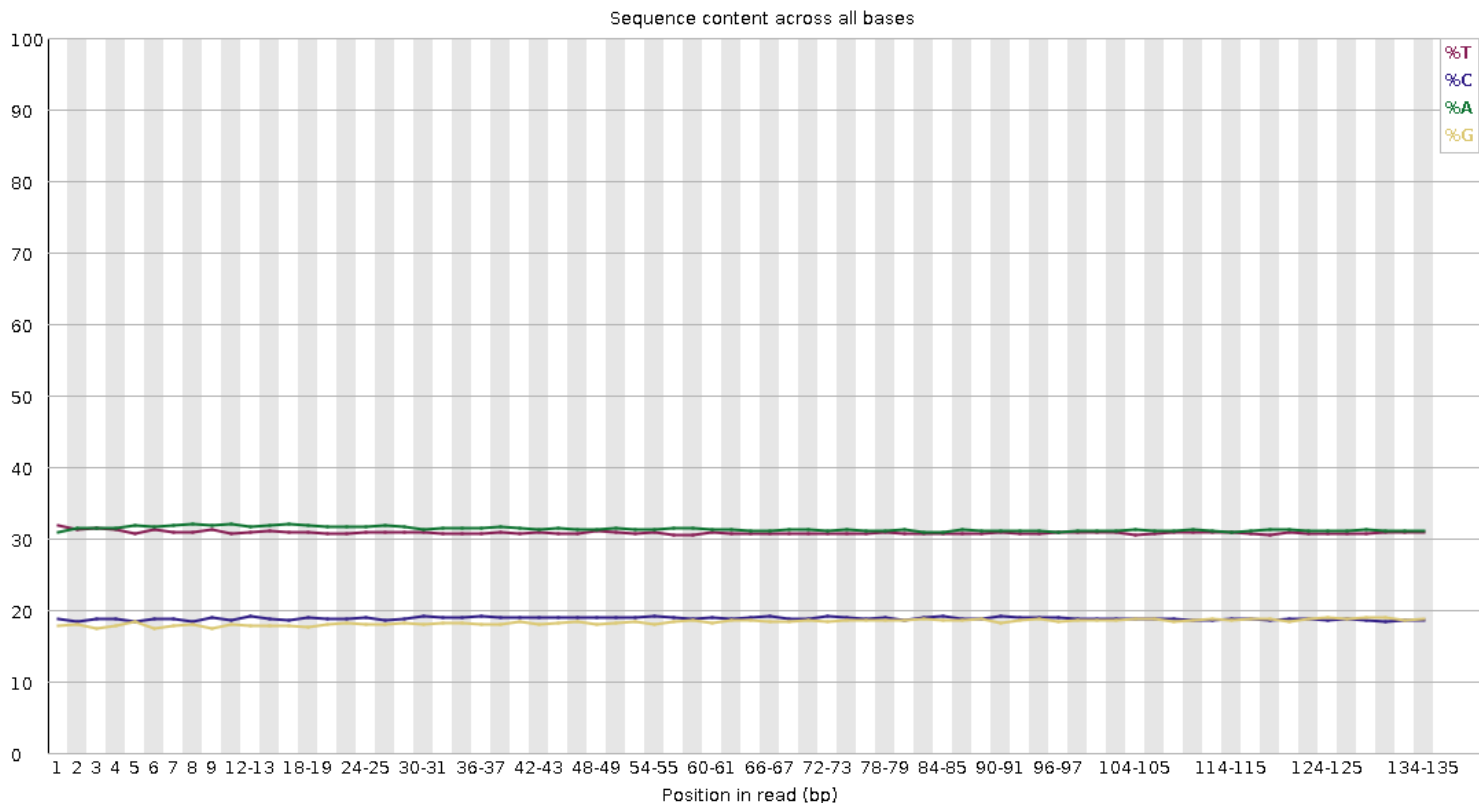


✓ Per sequence quality scores

Quality score distribution over all sequences

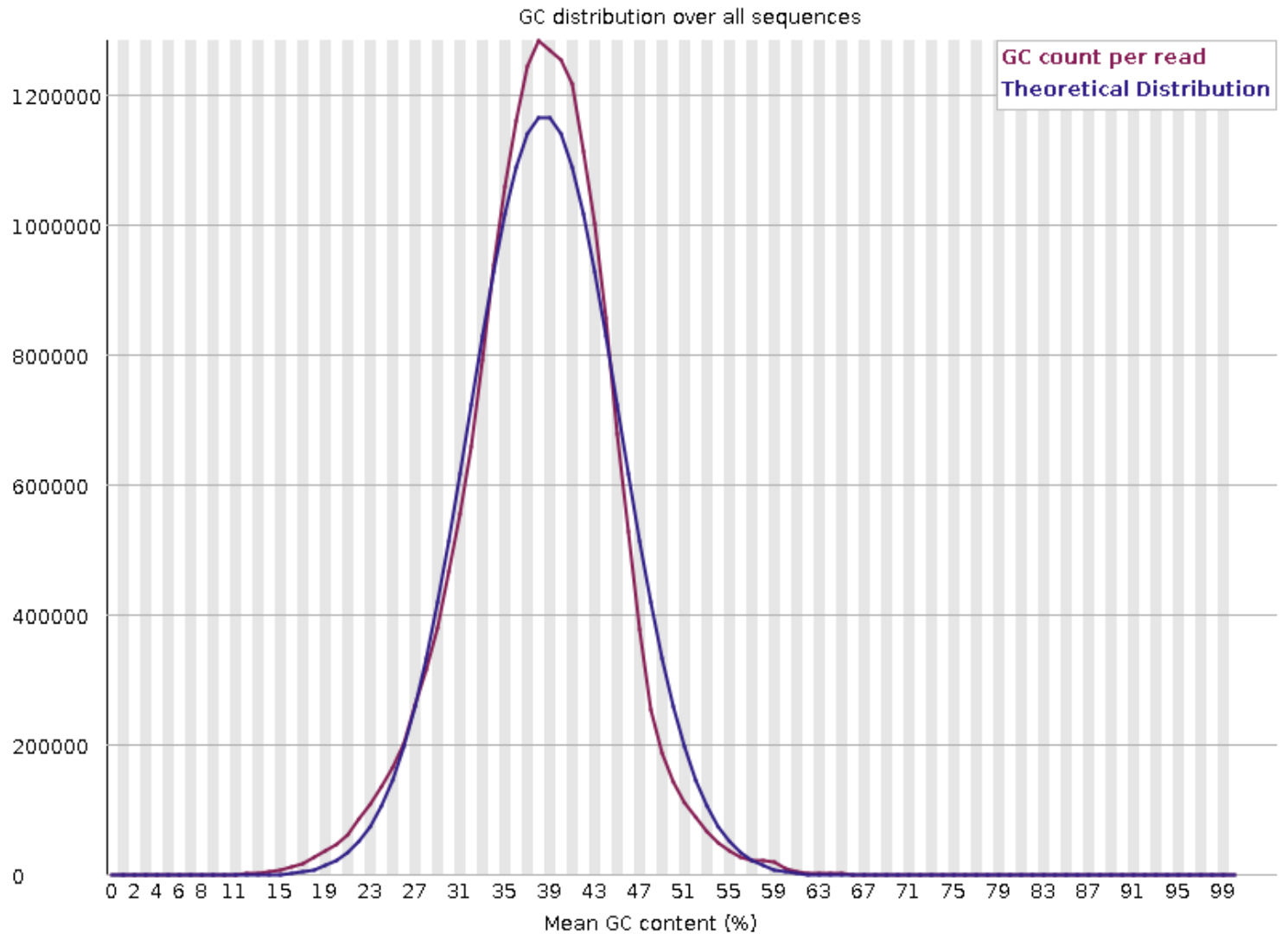


Per base sequence content



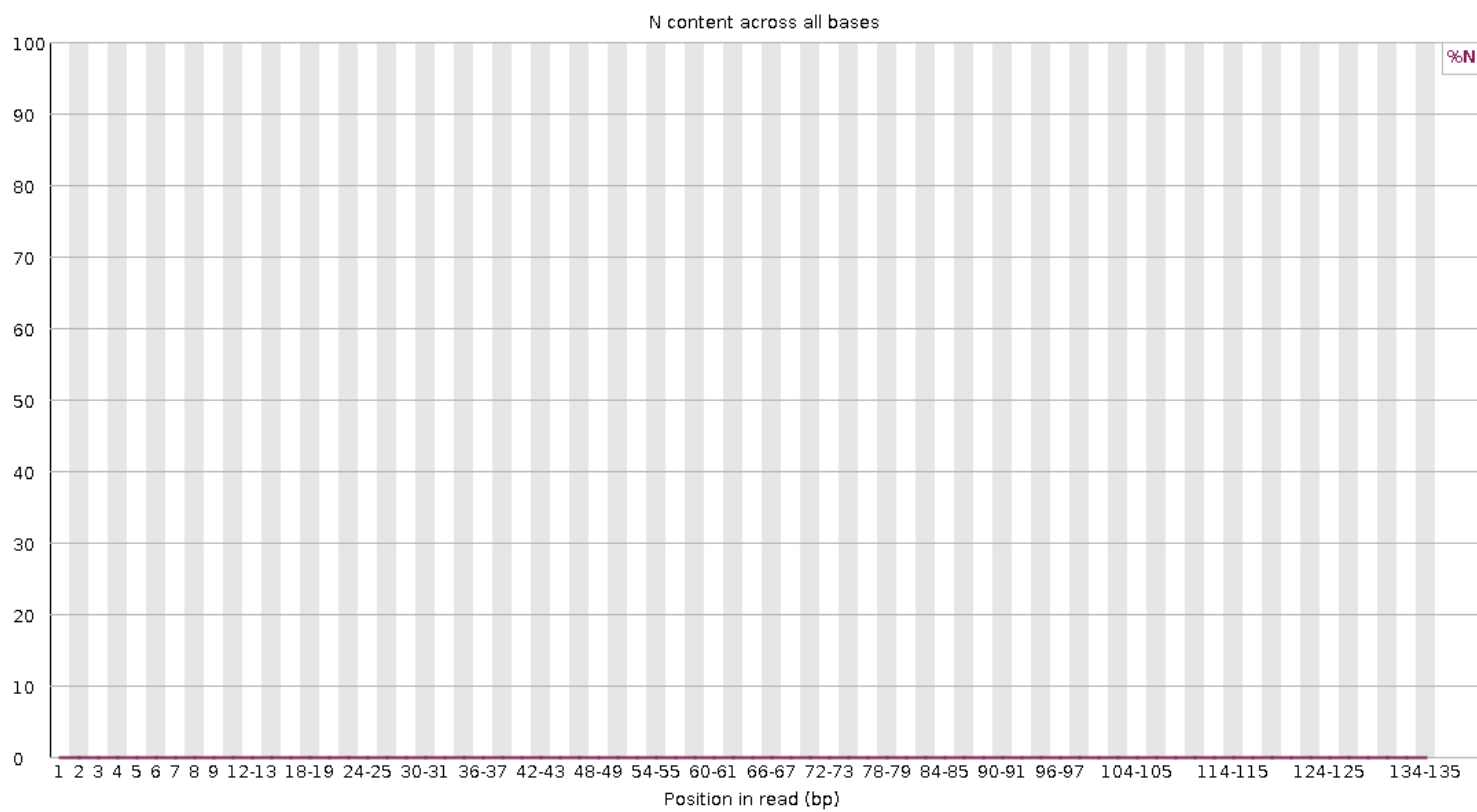


Per sequence GC content

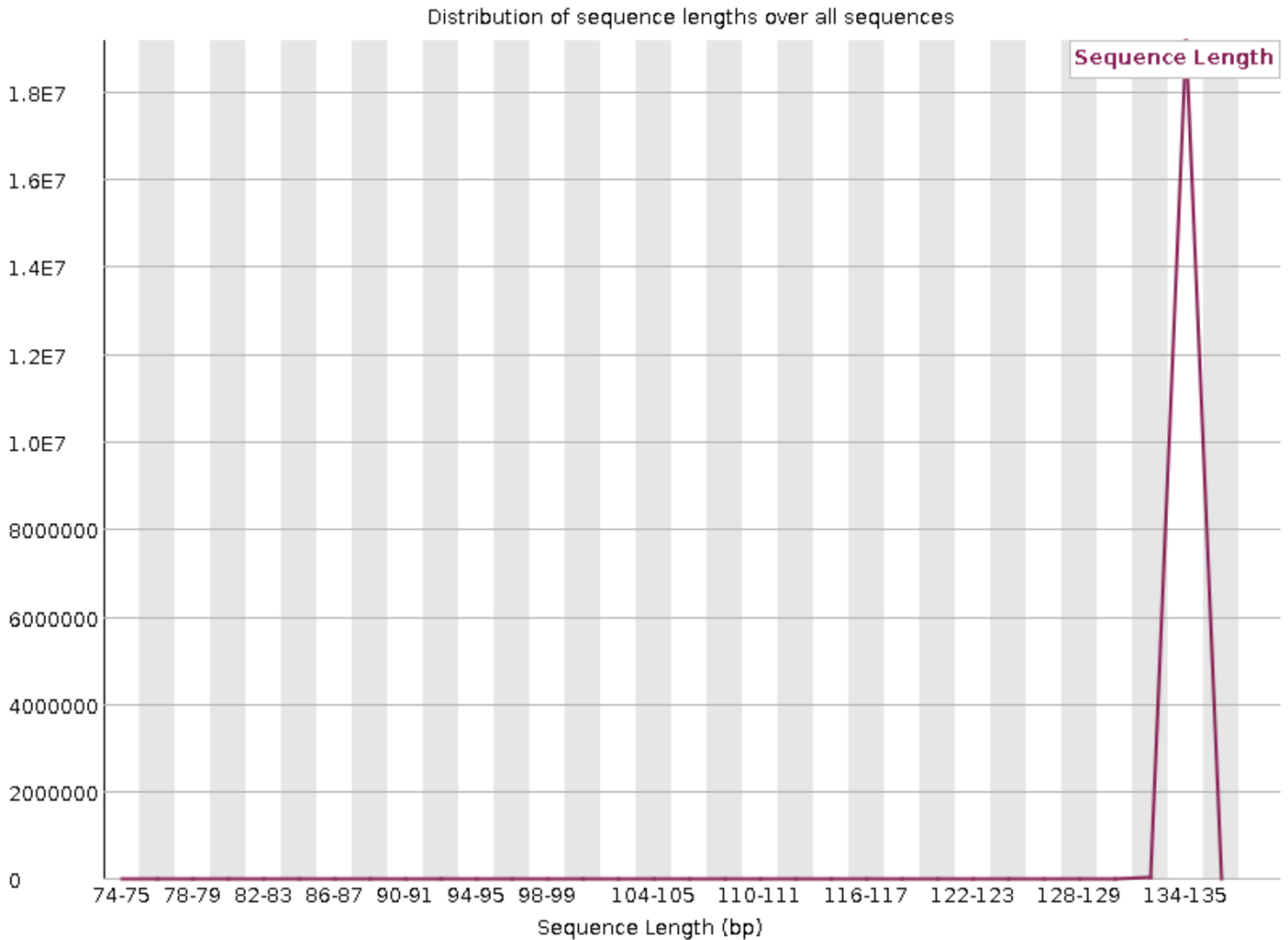




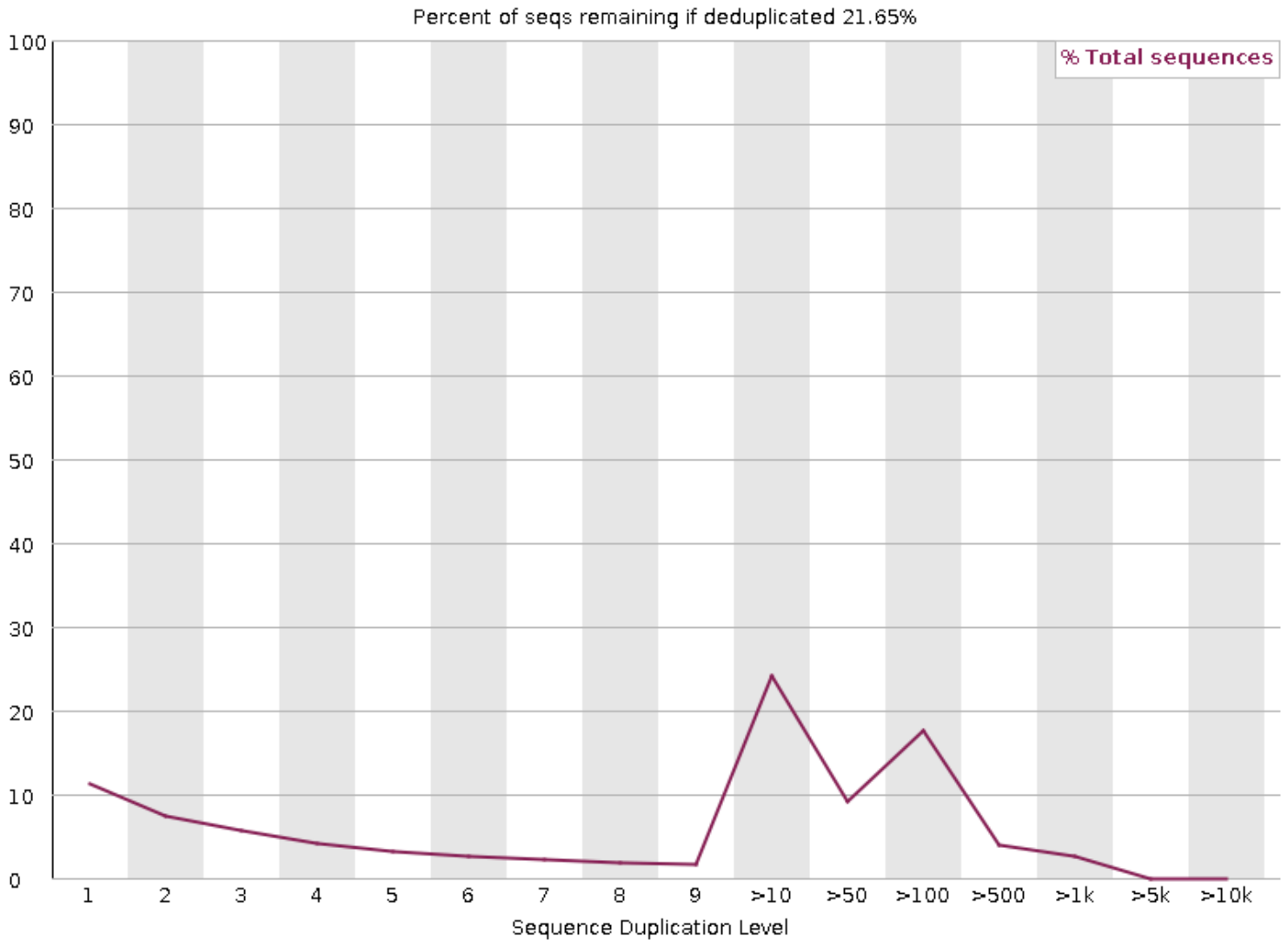
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

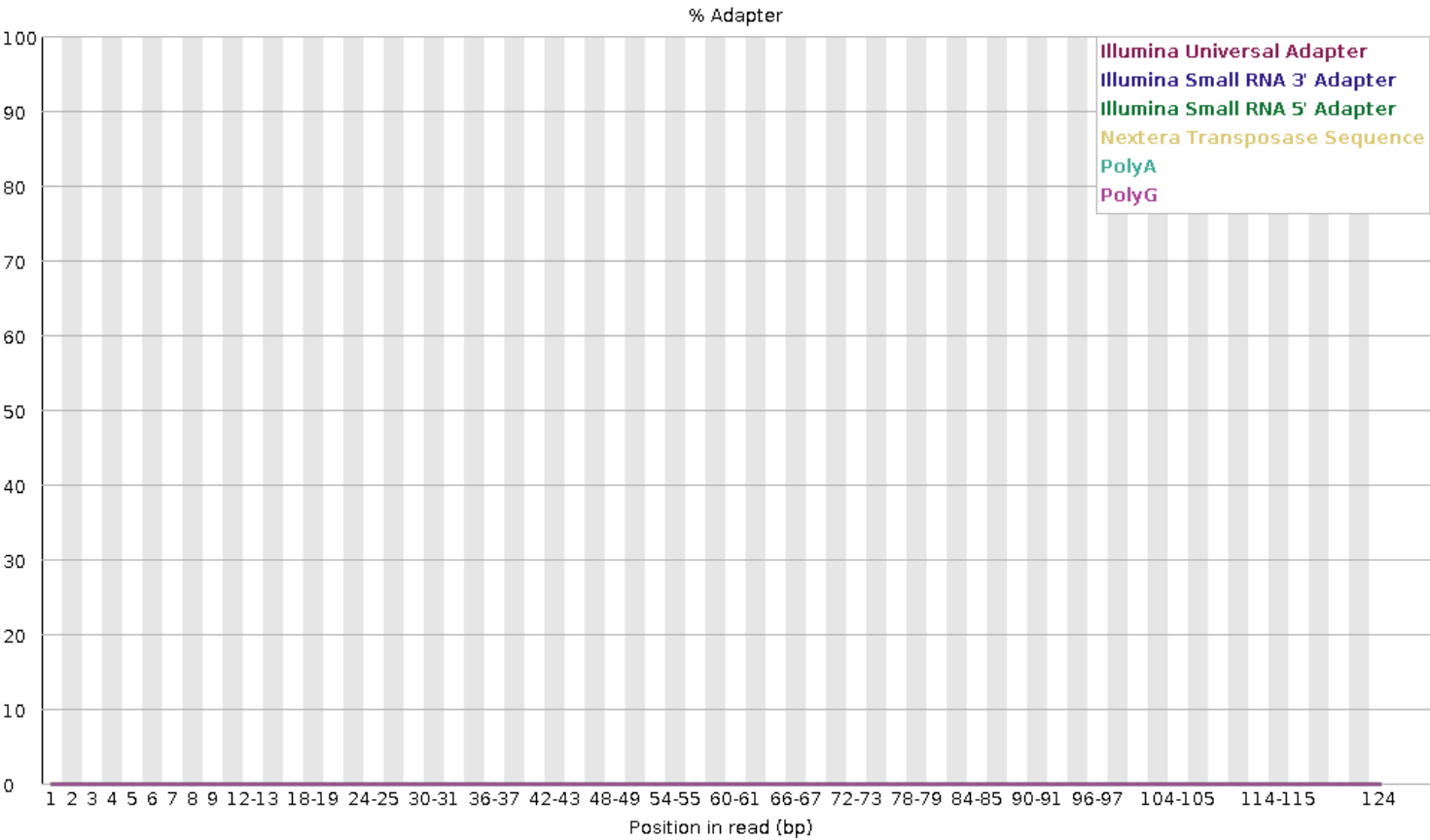


Overrepresented sequences

No overrepresented sequences



Adapter Content



Produced by [FastQC](#) (version 0.12.0)