













# FastQC Report

## Summary

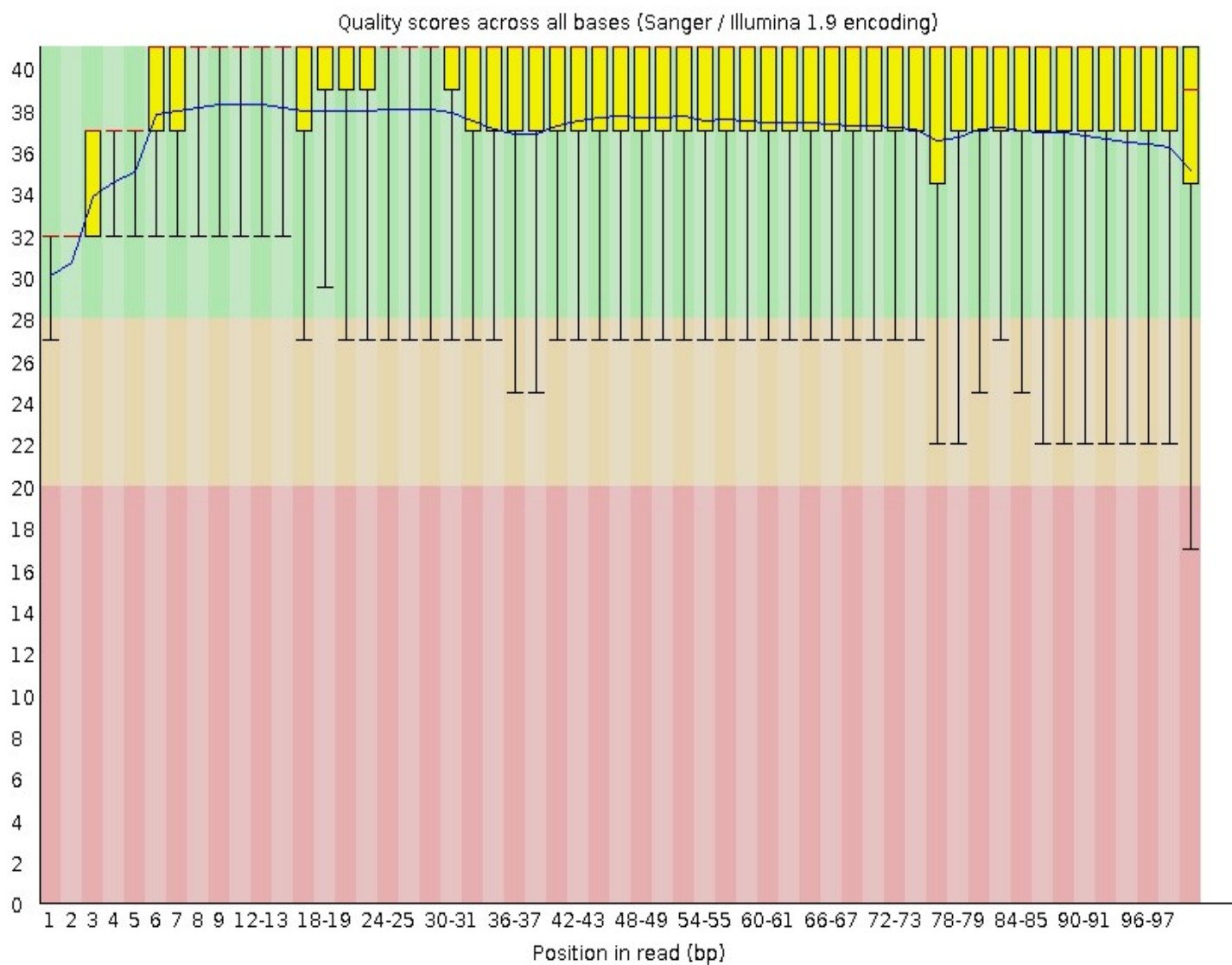
Mon 11 Sep 2023  
10\_2G\_both\_S8\_L008\_R2\_001.fastq.gz

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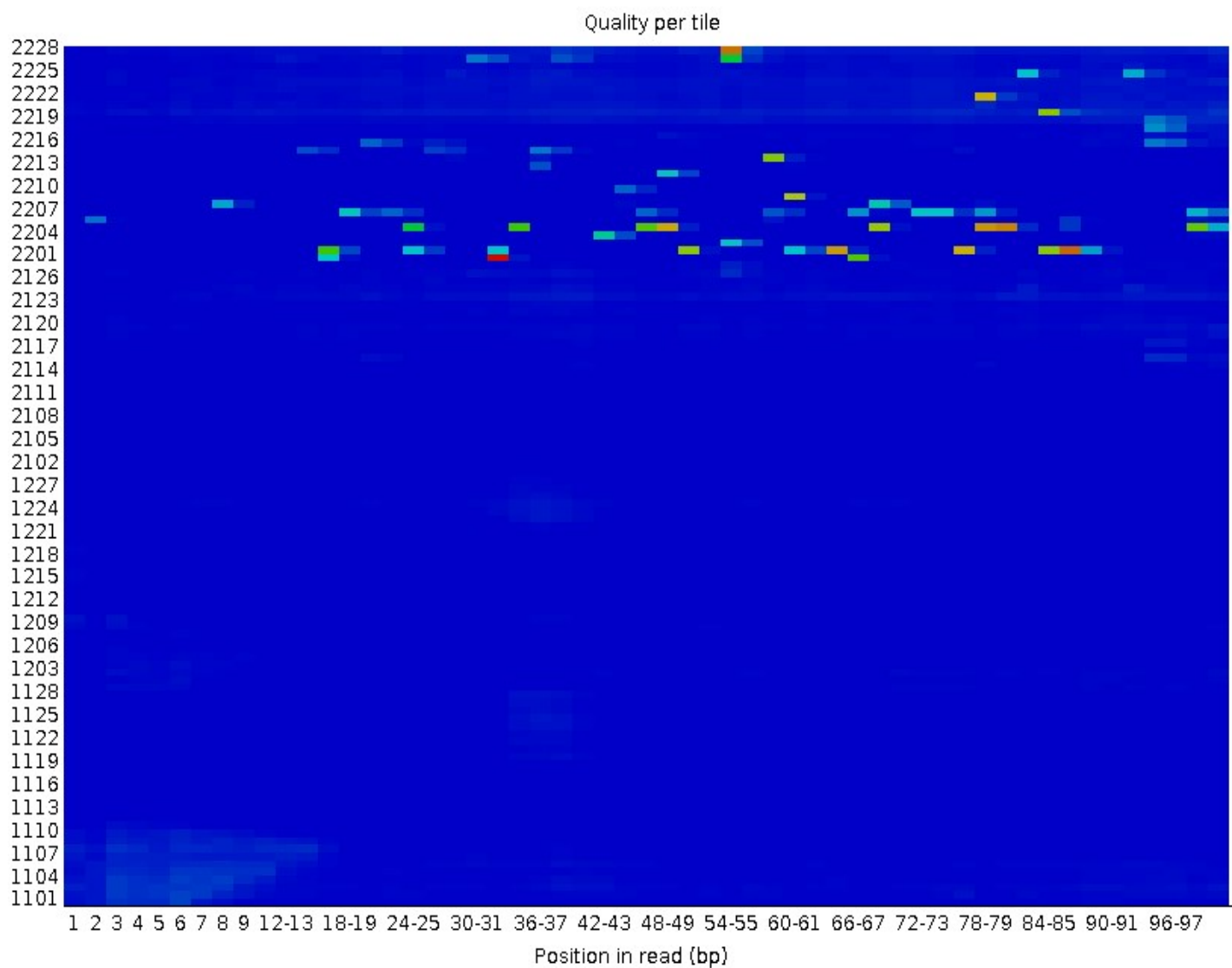
## Basic Statistics

Measure	Value
Filename	10_2G_both_S8_L008_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	81477069
Sequences flagged as poor quality	0
Sequence length	101
%GC	50

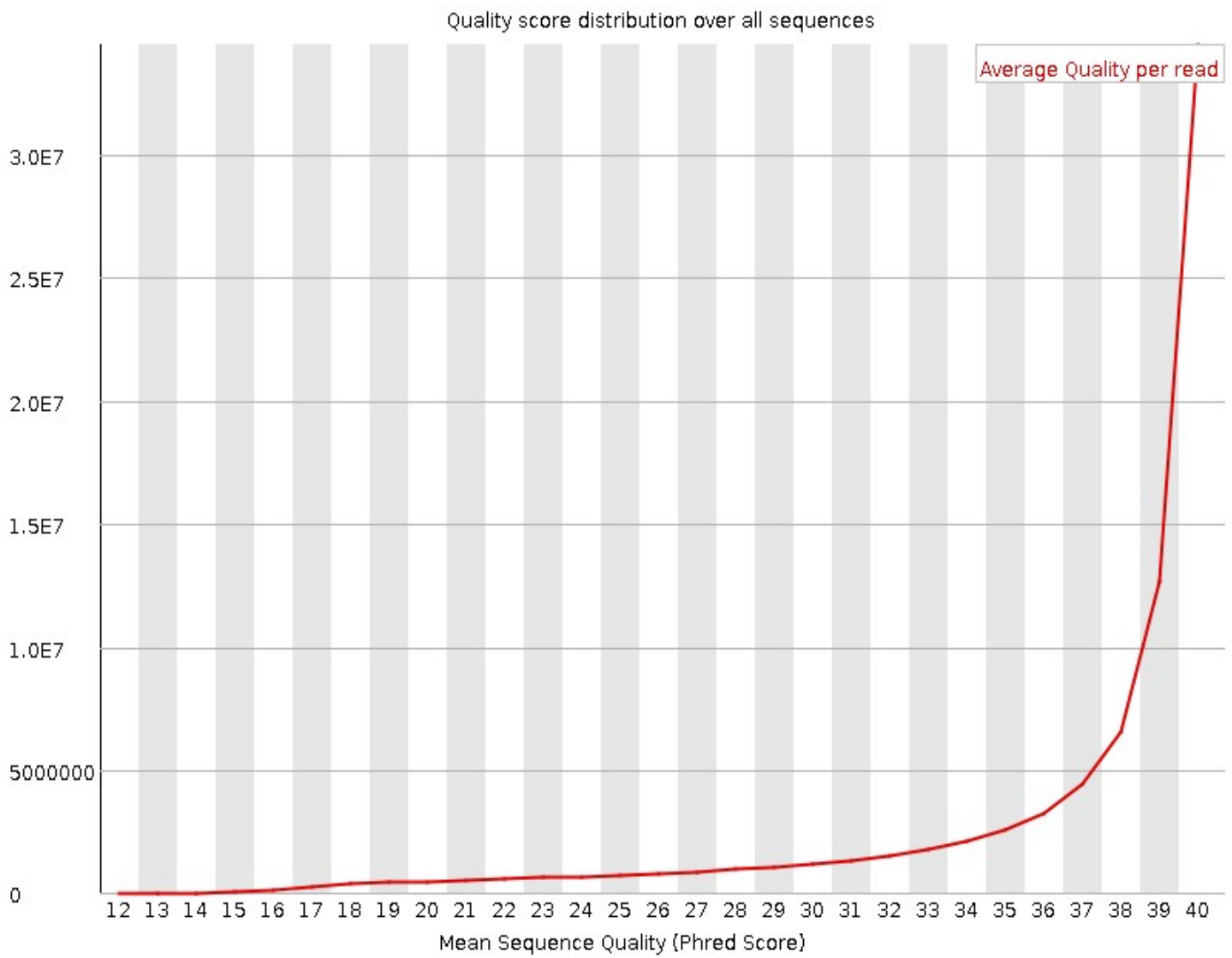
## Per base sequence quality



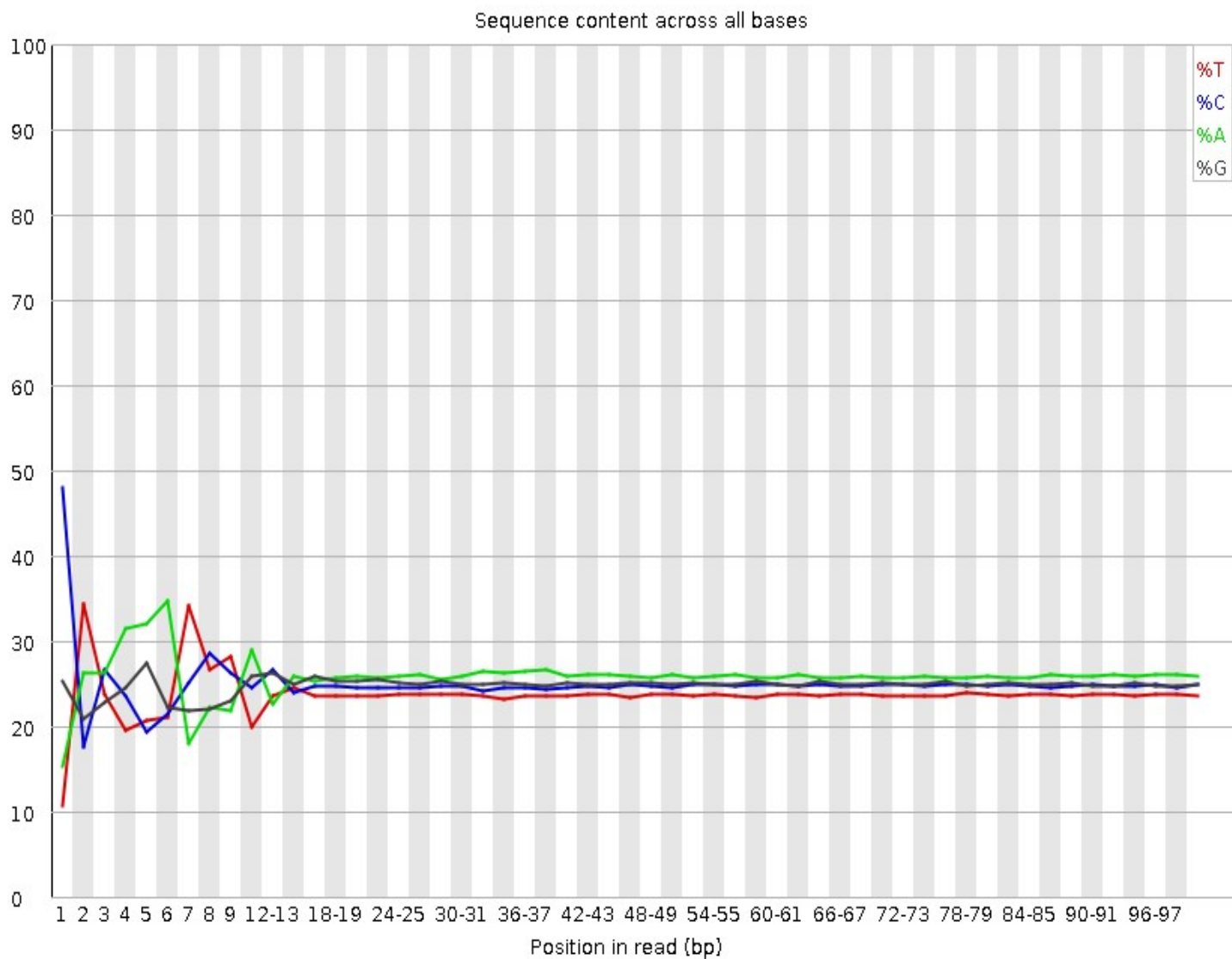
## ! Per tile sequence quality



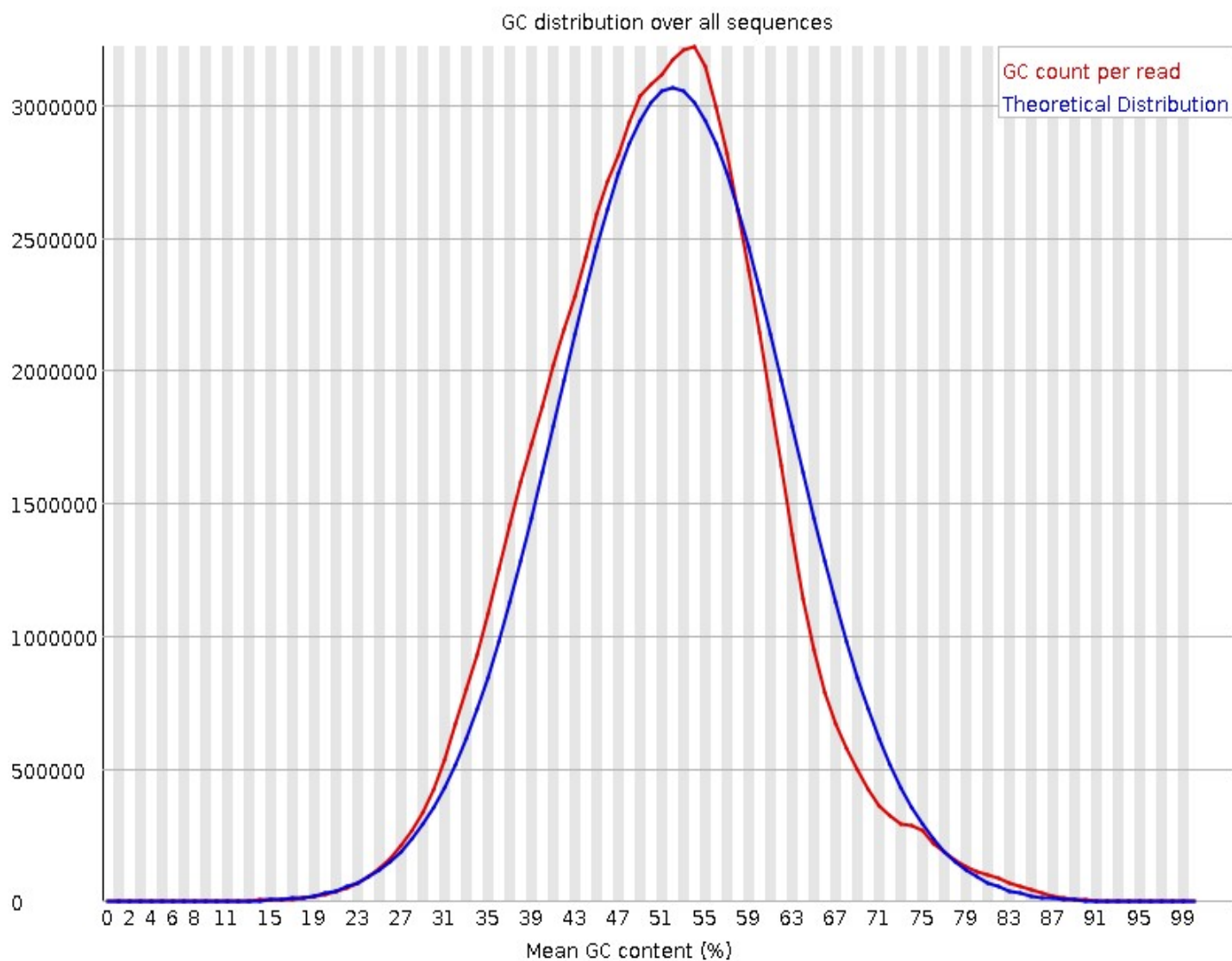
## Per sequence quality scores



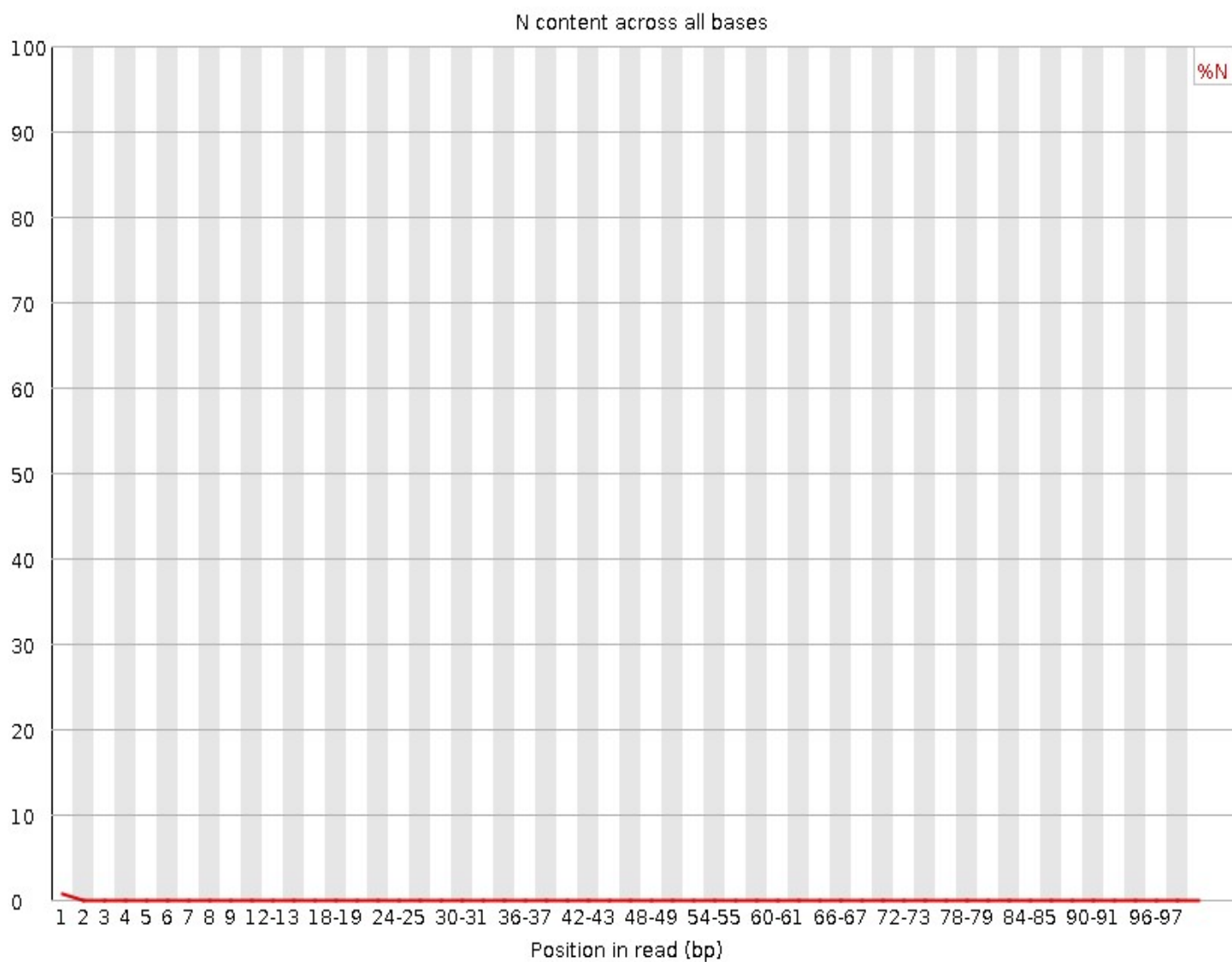
## ❌ Per base sequence content



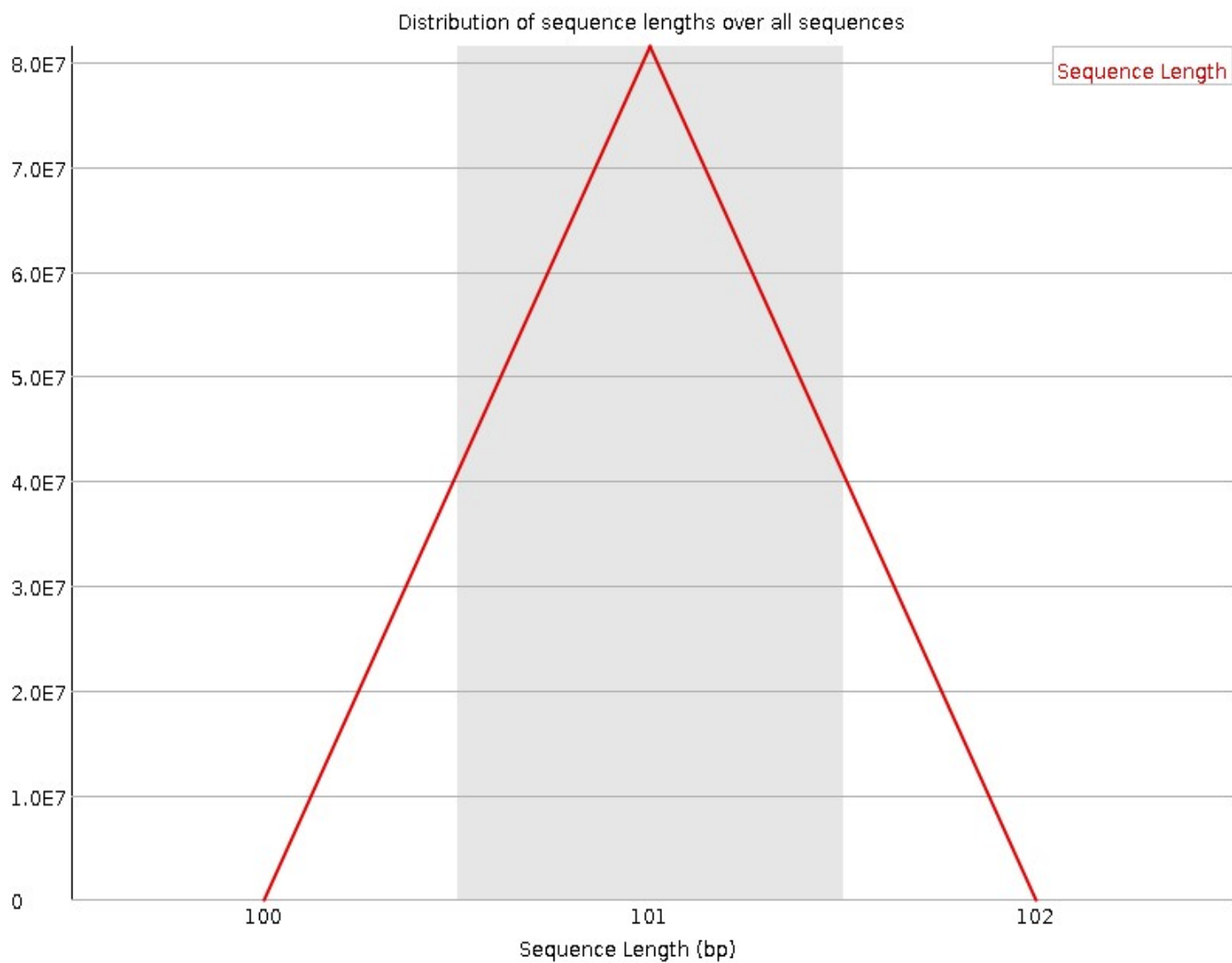
**Per sequence GC content**



## Per base N content

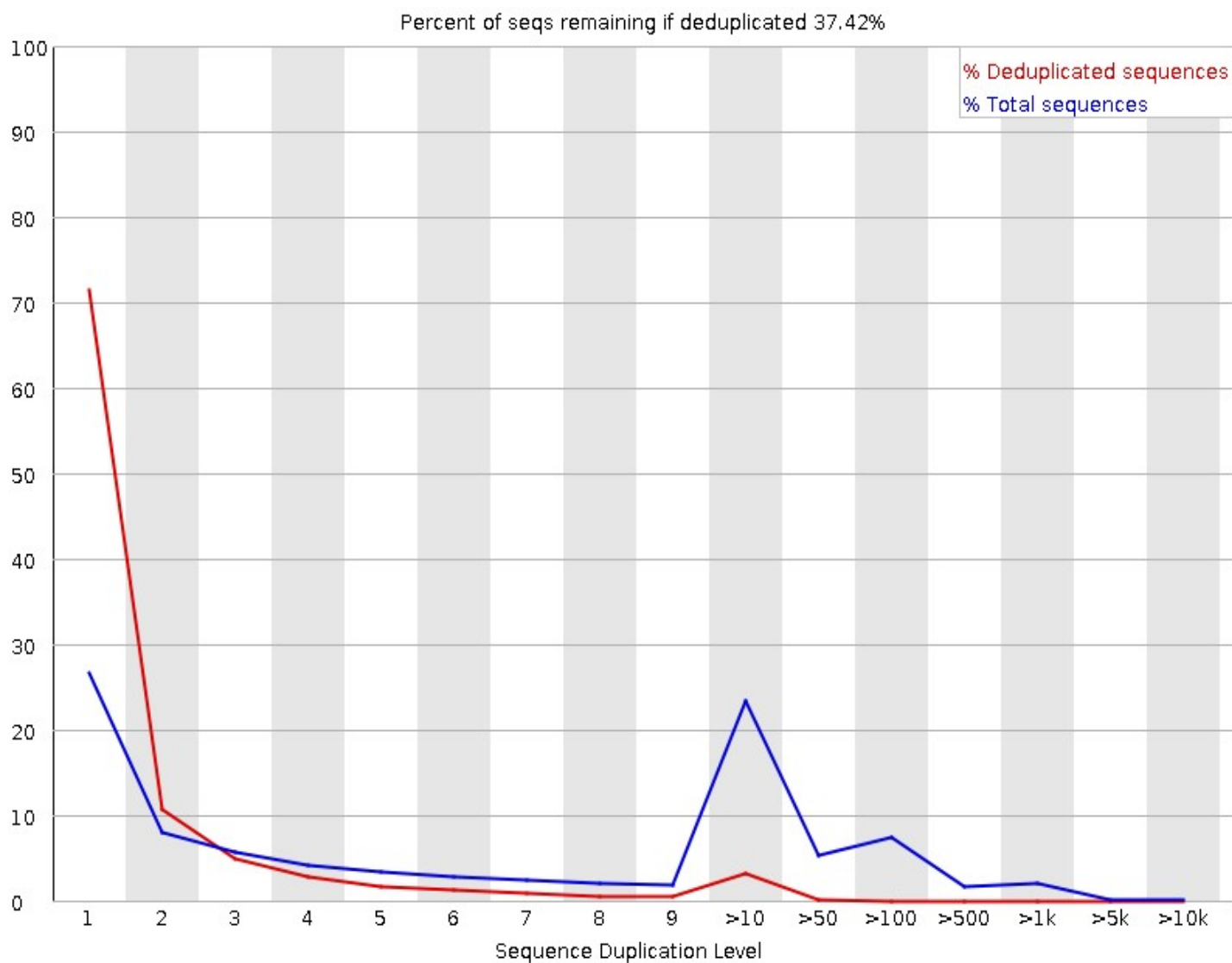


## Sequence Length Distribution



## ❌ Sequence Duplication Levels



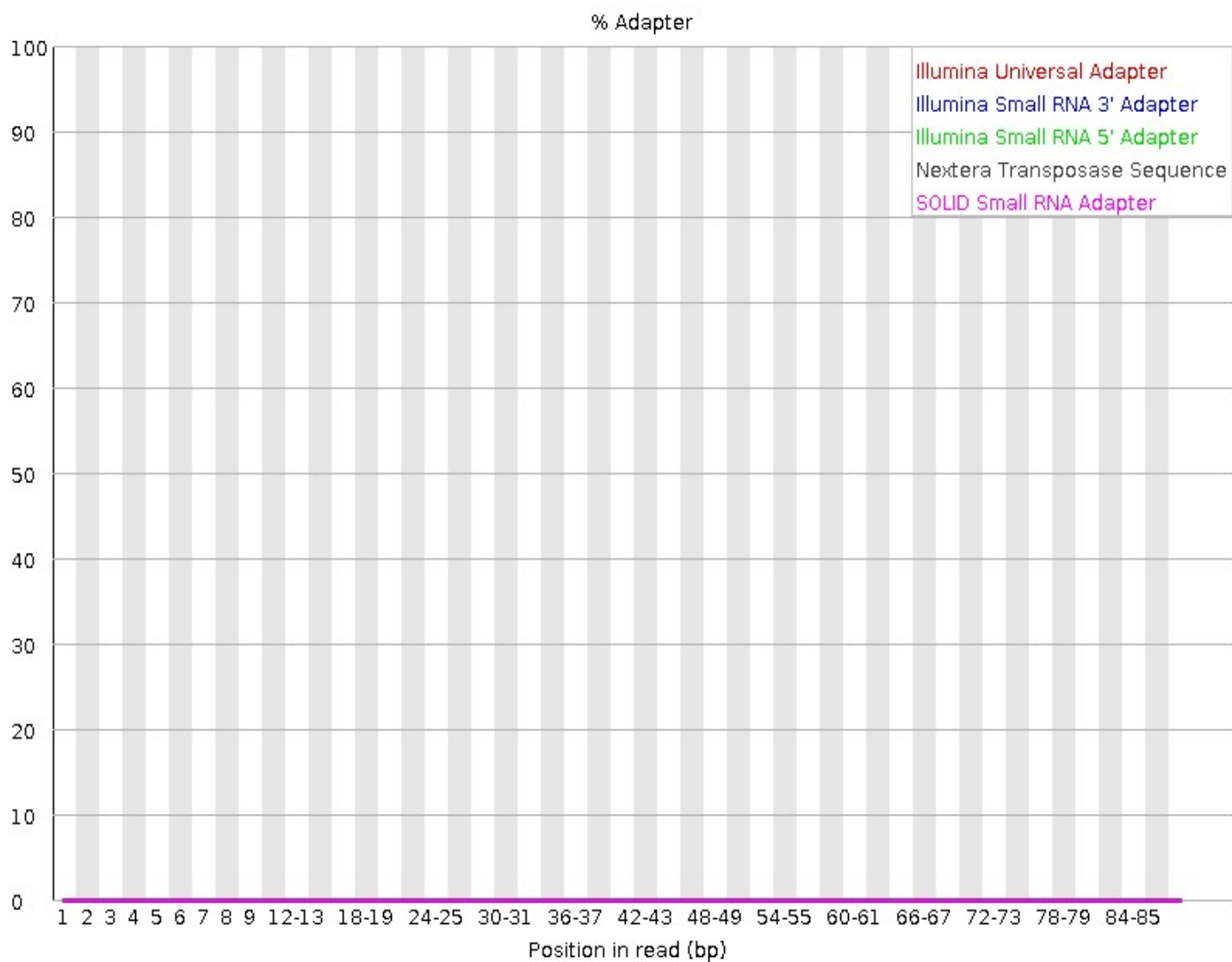


## Overrepresented sequences

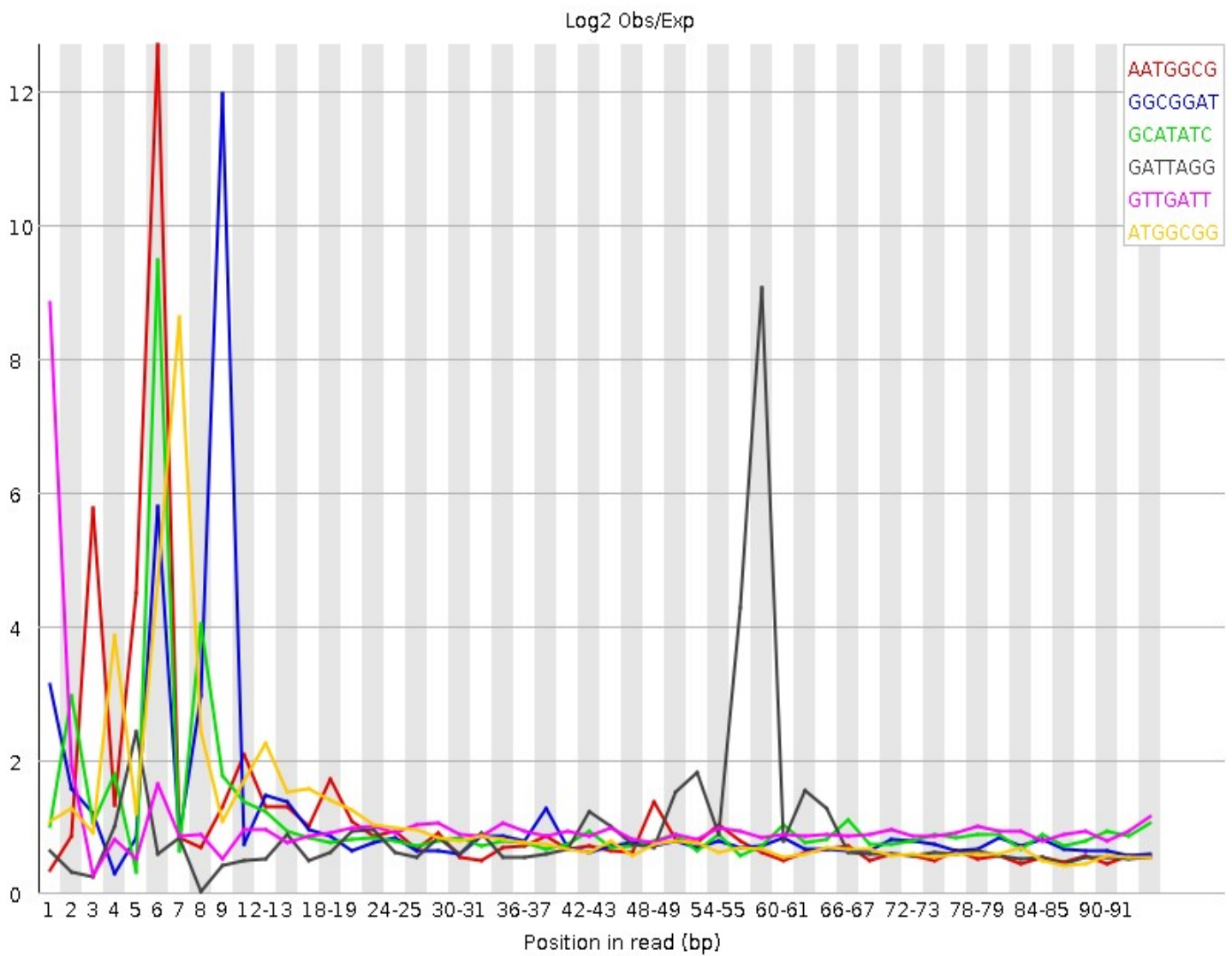
No overrepresented sequences



## Adapter Content



 **Kmer Content**



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AATGGCG	32235	0.0	12.686145	6
GGCGGAT	29480	0.0	11.954383	9
GCATATC	23745	0.0	9.481136	6
GATTAGG	22505	0.0	9.053755	58-59
GTTGATT	30555	0.0	8.834536	1
ATGGCGG	64650	0.0	8.617569	7
CGACGAT	15565	0.0	8.532735	1
TTCCGCG	24120	0.0	8.4967575	78-79
GTATAGG	13040	0.0	8.340884	6
CTTAAAT	38730	0.0	8.306778	1
CTCGACT	16940	0.0	8.009966	1
TGGCGGA	54585	0.0	7.9703503	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGCCGG	27885	0.0	7.715734	16-17
CGACCGT	8520	0.0	7.6928835	20-21
CGCCGGT	22905	0.0	7.682589	18-19
TTGATTA	28925	0.0	7.586198	2
CATATCA	31275	0.0	7.5780683	7
ATATCAC	31115	0.0	7.540713	8
CGAAGAT	30205	0.0	7.540018	1
CGAAAAG	36655	0.0	7.5082088	1

Produced by [FastQC](#) (version 0.11.5)