FastQC Report

Mon 11 Sep 2023
31_4F_fox_S22_L008_R2_001.fastq.gz

Summary

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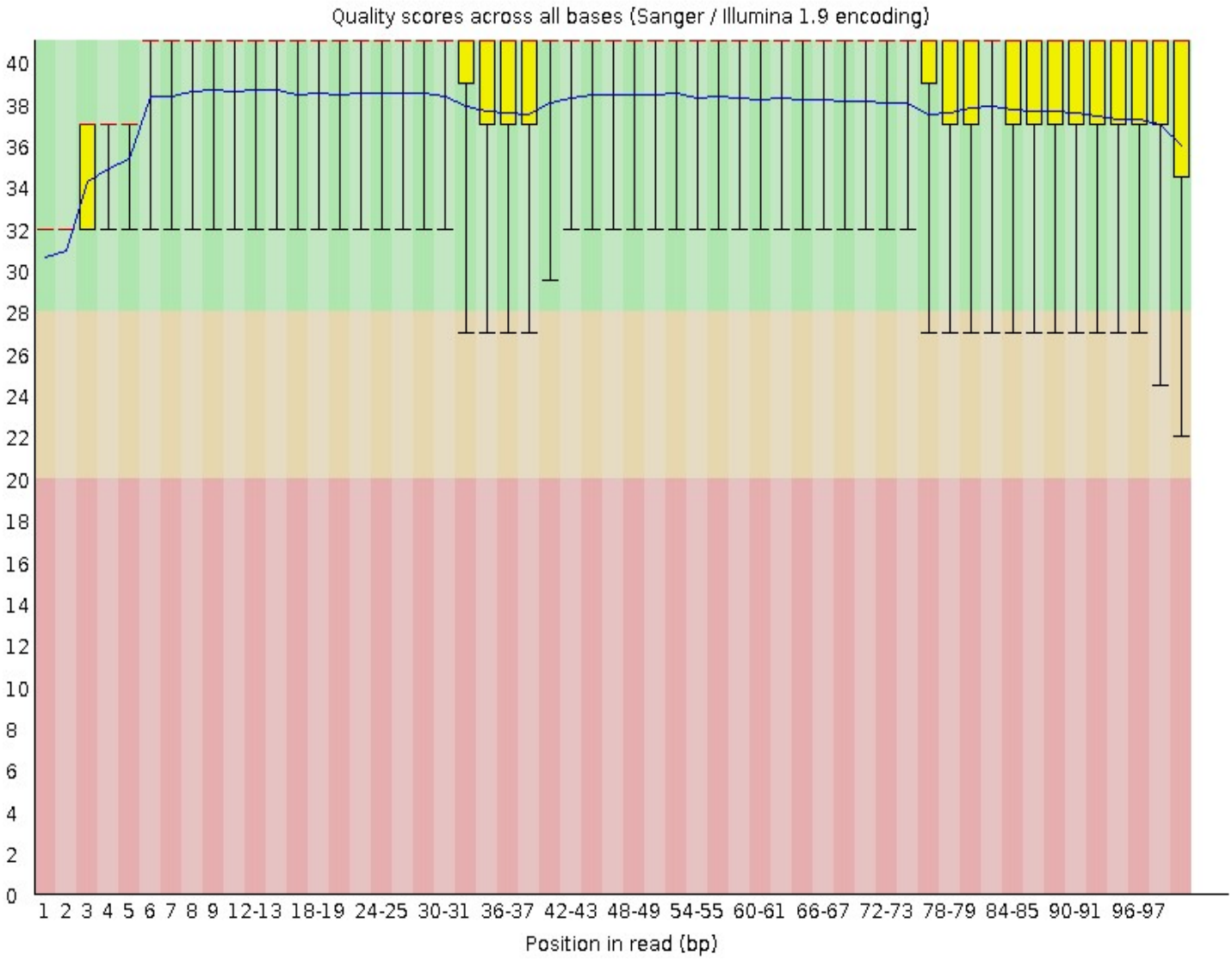
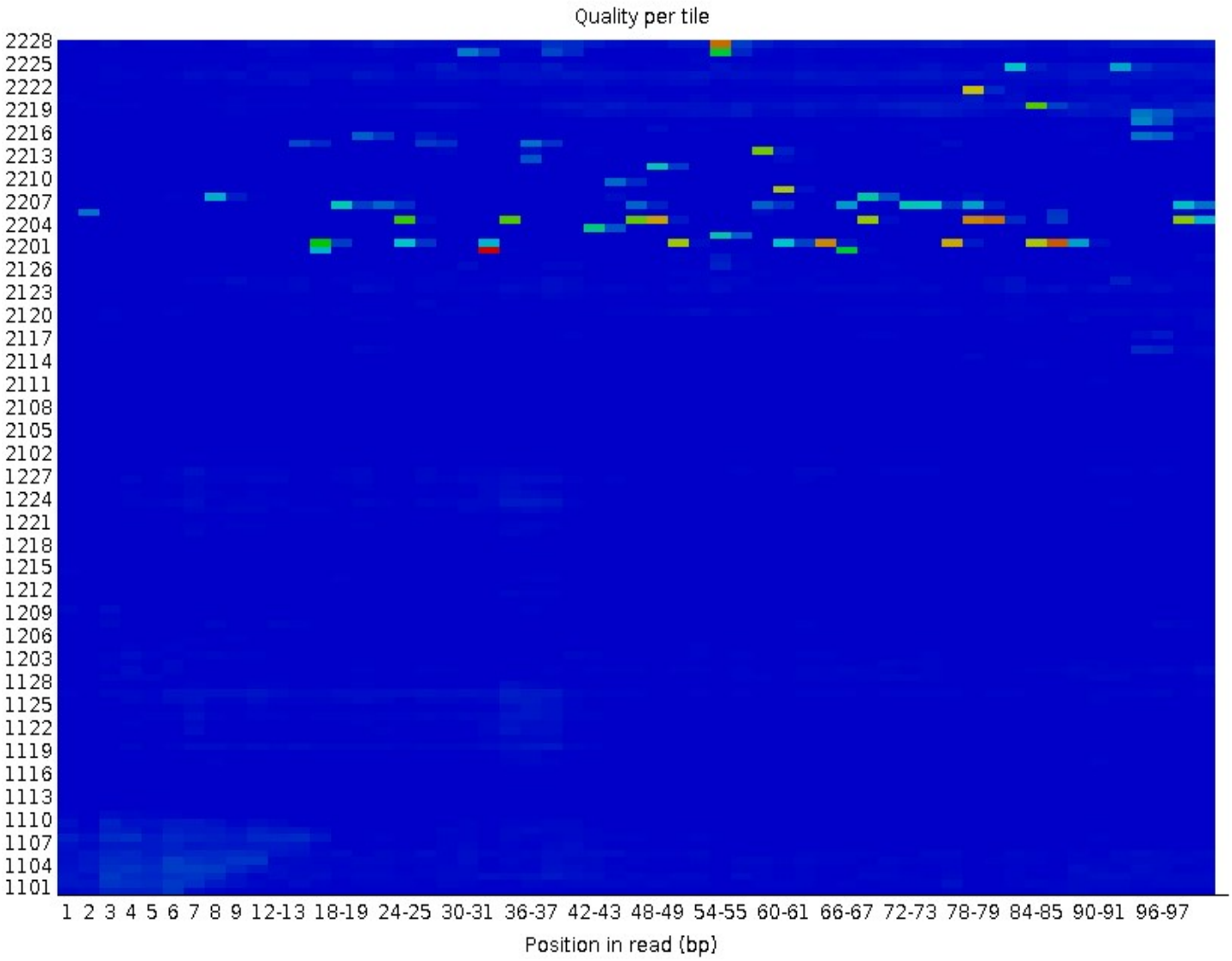
Basic Statistics

Measure	Value
Filename	31_4F_fox_S22_L008_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	3788343
Sequences flagged as poor quality	0
Sequence length	101
%GC	51

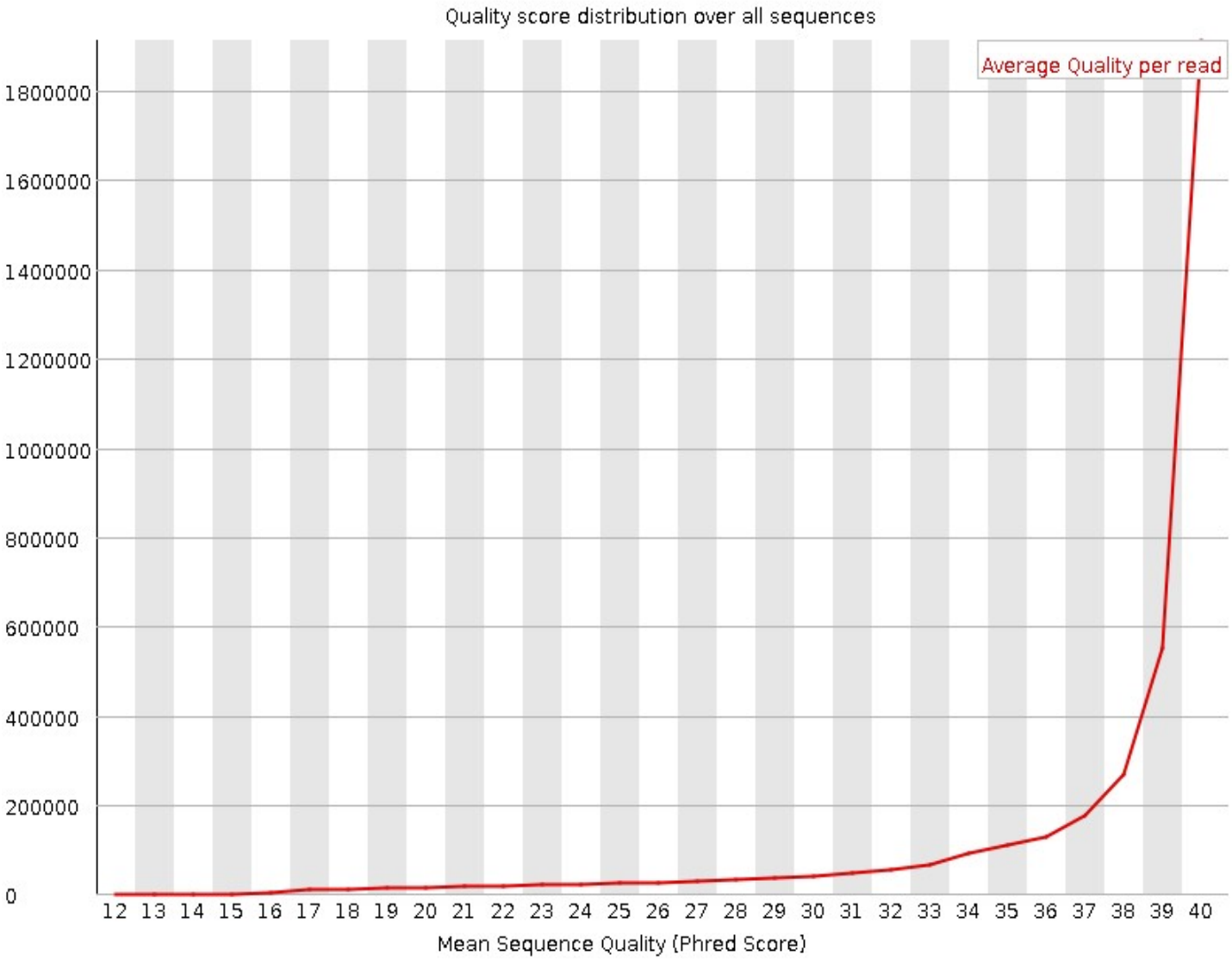
Per base sequence quality



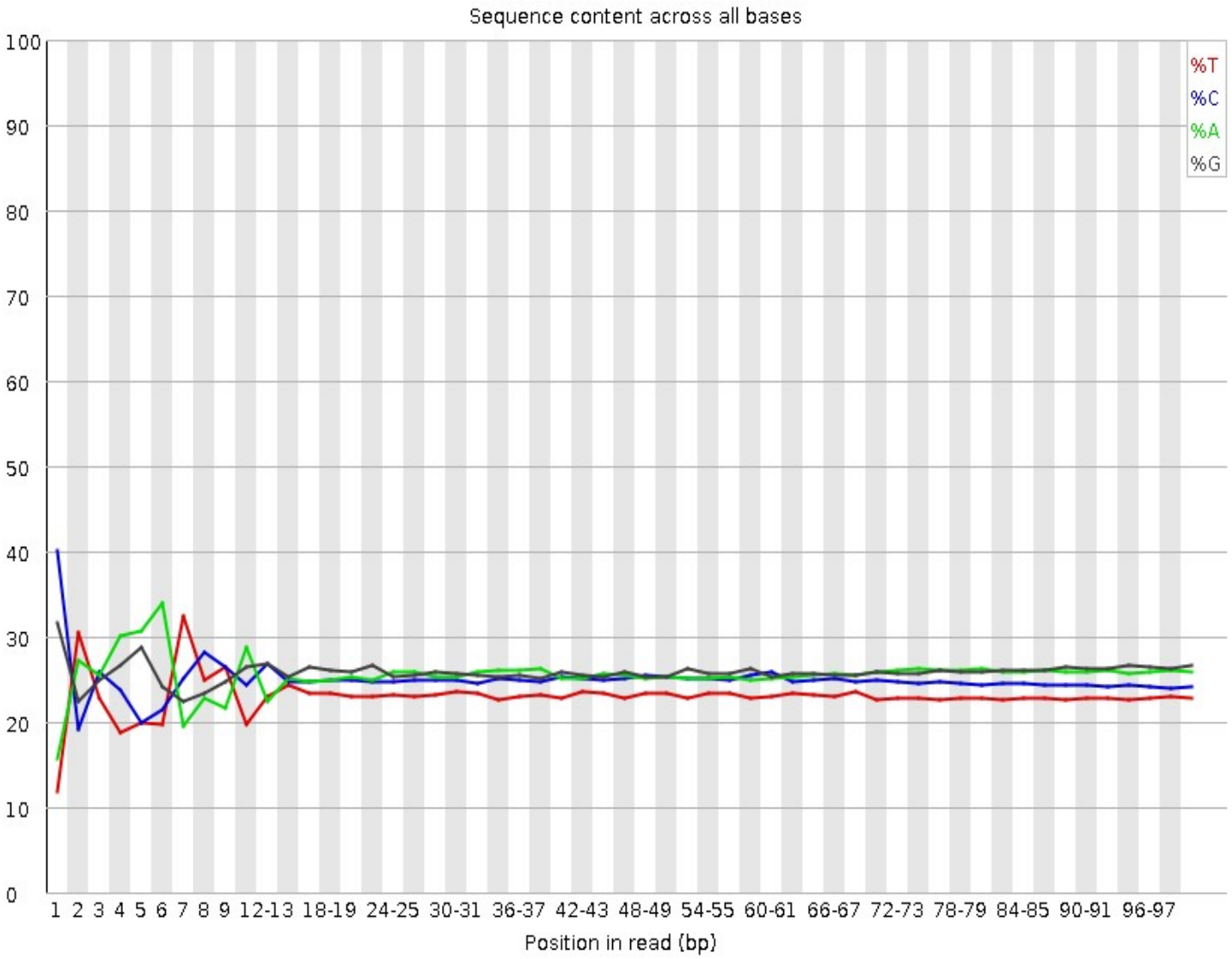
Per tile sequence quality



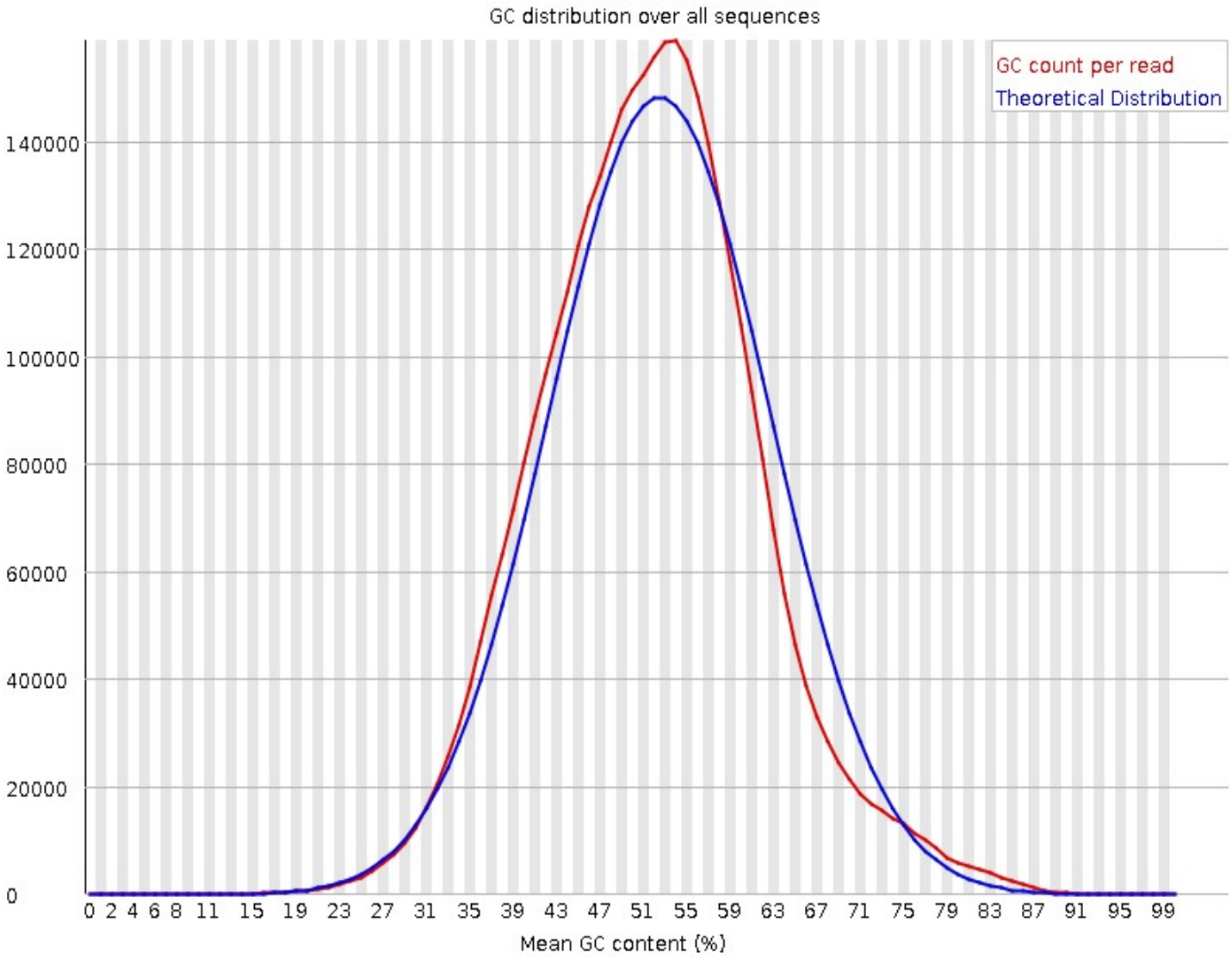
Per sequence quality scores



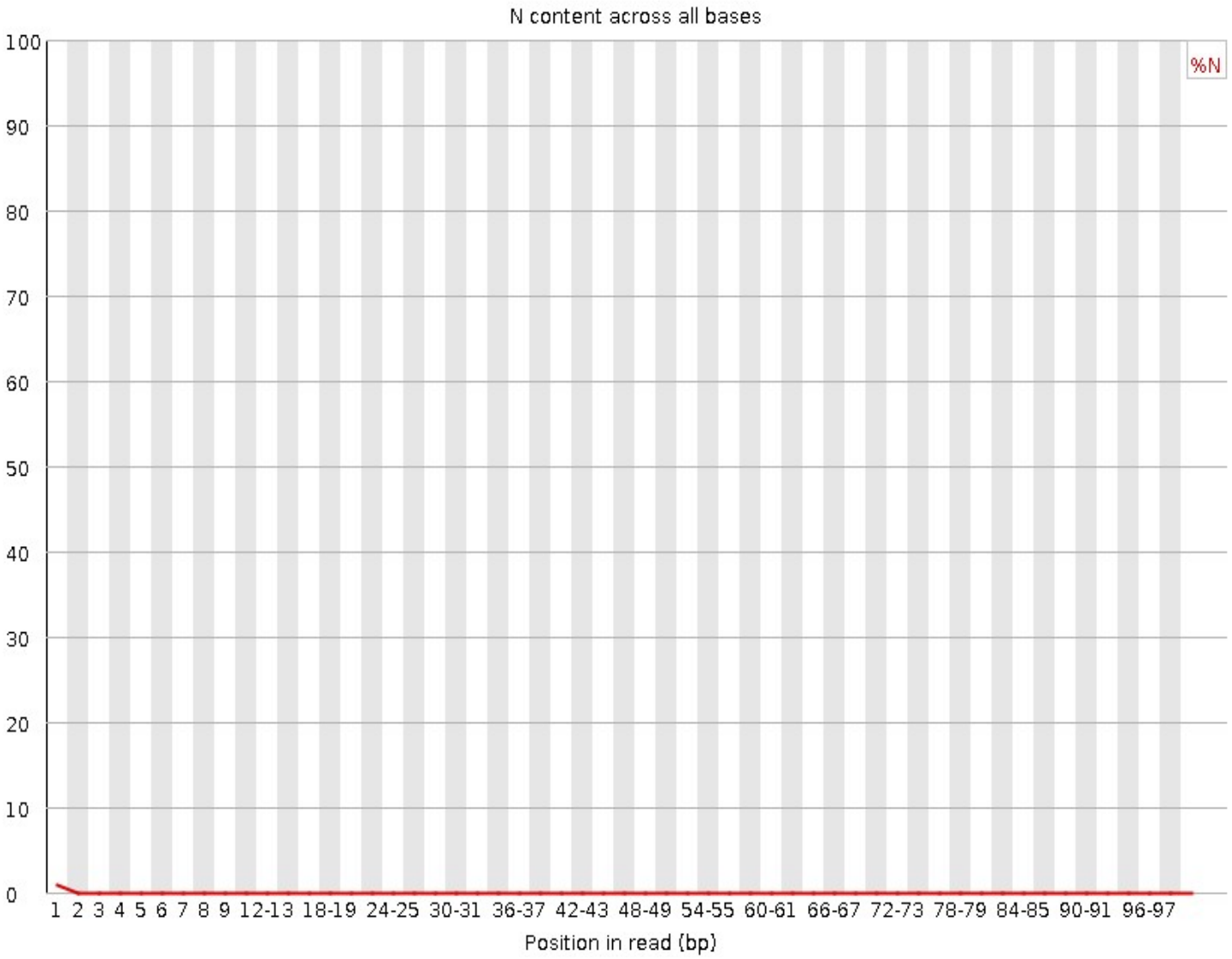
Per base sequence content



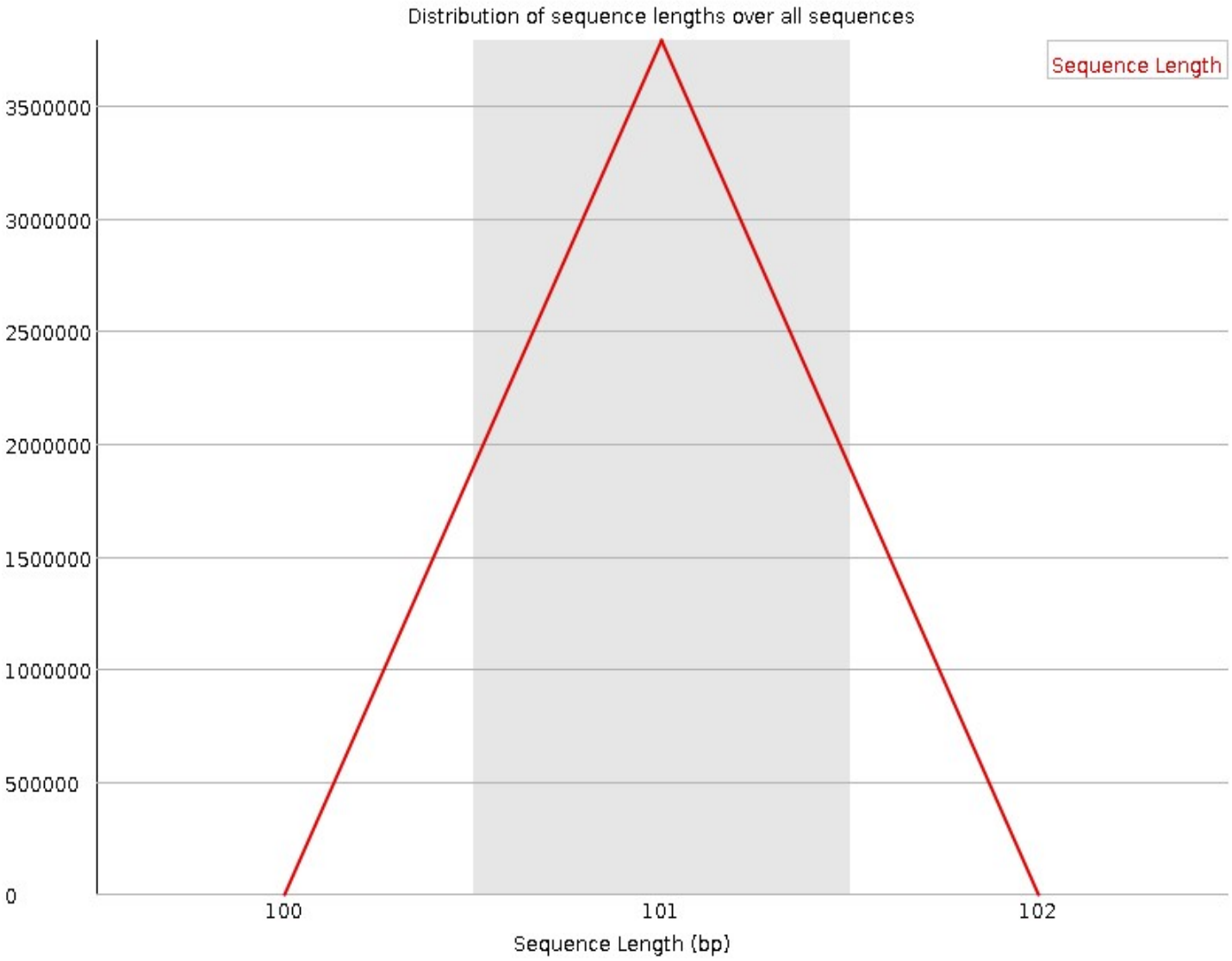
Per sequence GC content



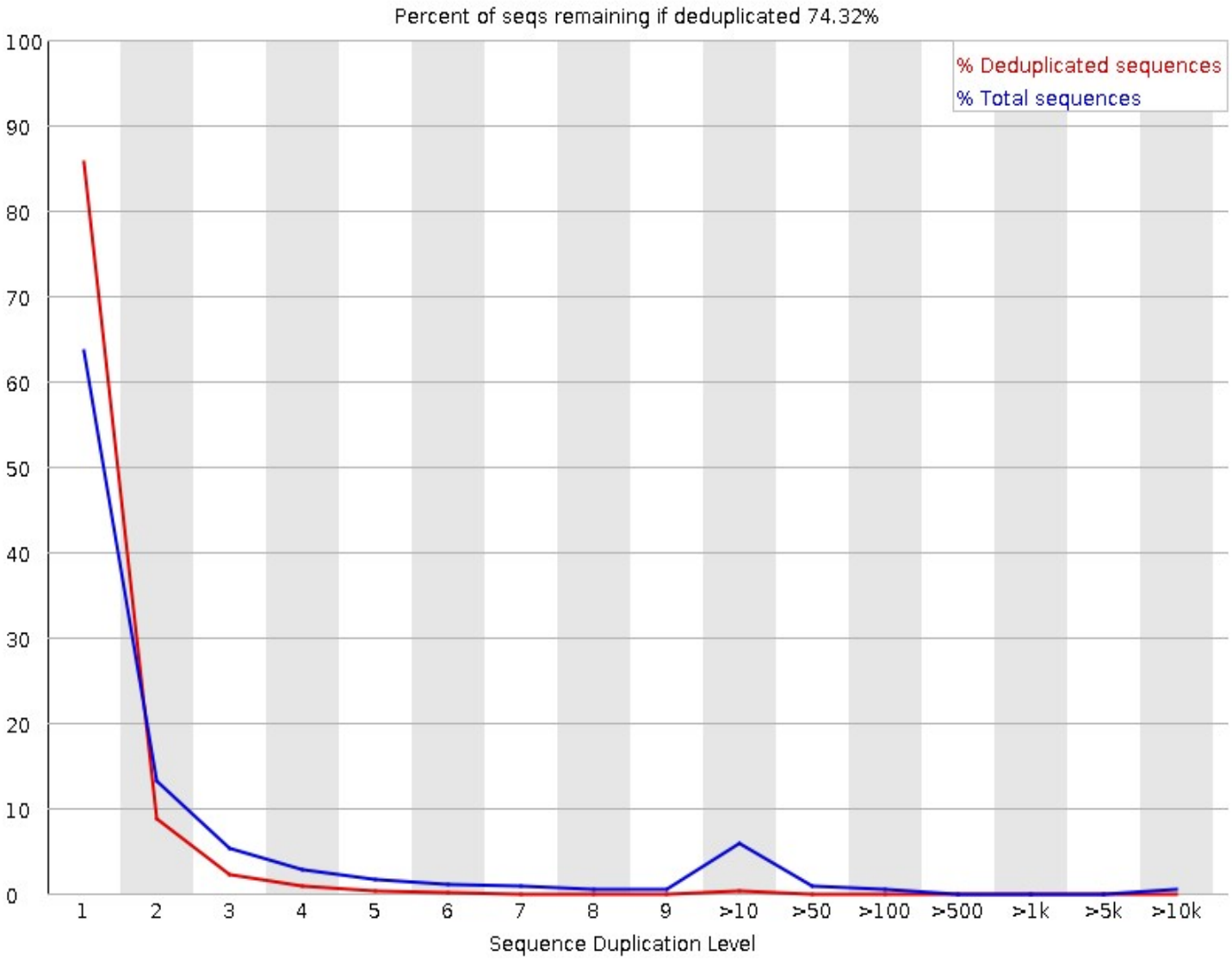
Per base N content



Sequence Length Distribution



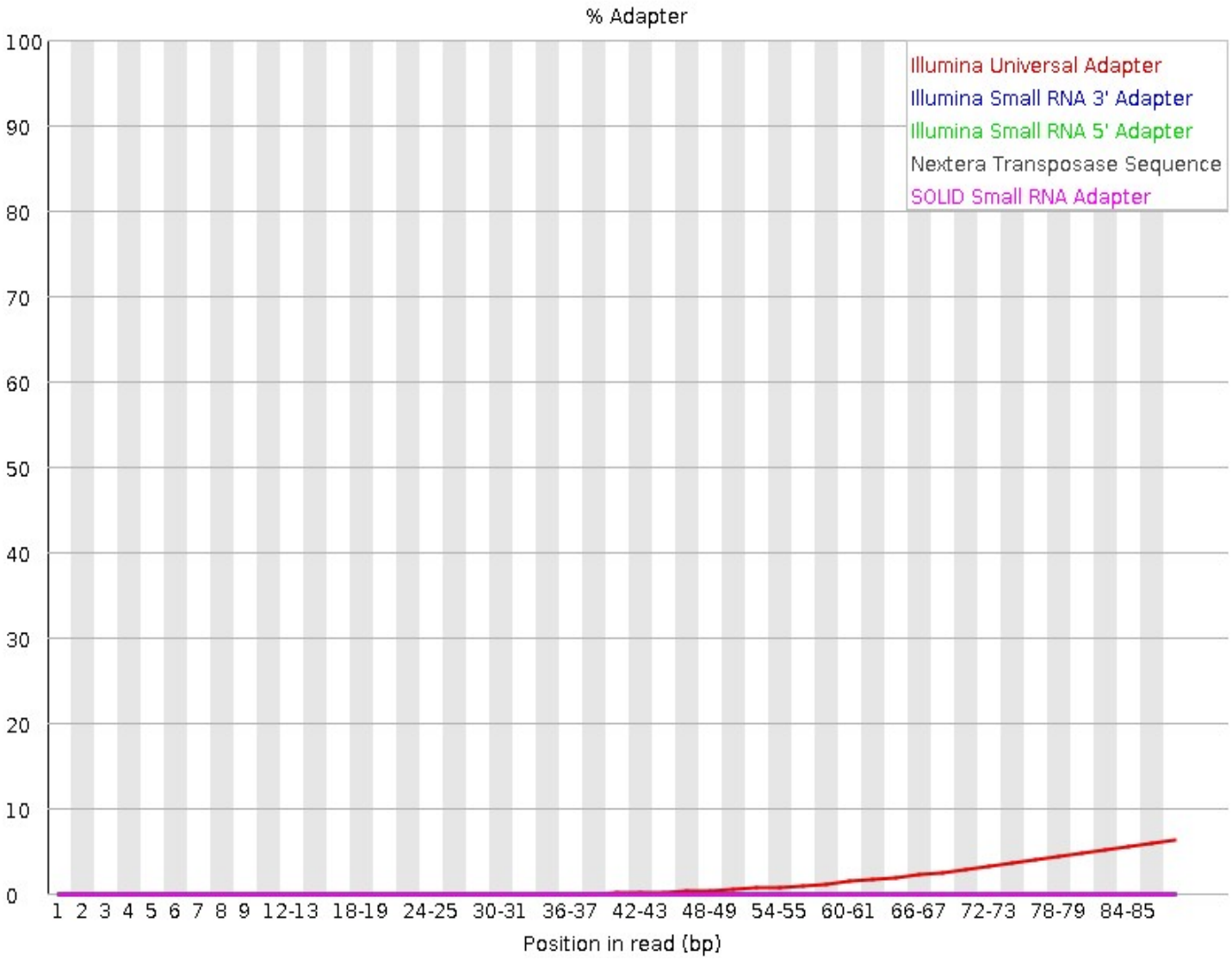
Sequence Duplication Levels



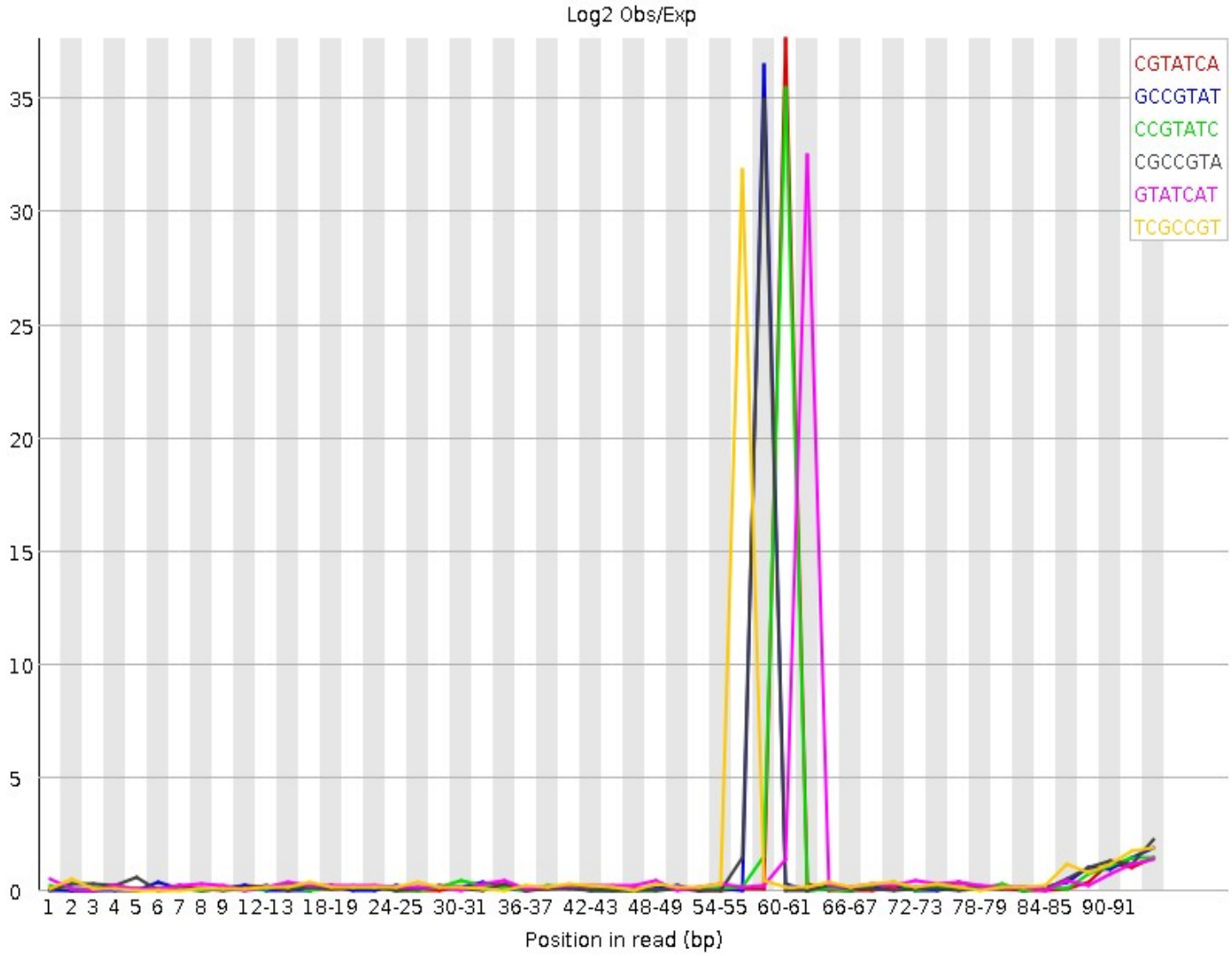
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTGCAAGATCGTGTAGATCT	27692	0.7309792170349939	Illumina Single End PCR Primer 1 (96% over 32bp)

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGTATCA	3810	0.0	37.584732	60-61
GCCGTAT	3905	0.0	36.48794	58-59
CCGTATC	3895	0.0	35.423206	60-61
CGCCGTA	3945	0.0	34.91404	58-59
GTATCAT	4280	0.0	32.45871	62-63
TCGCCGT	4475	0.0	31.840315	56-57
ATCATTA	4750	0.0	28.99703	64-65
TATCATT	5115	0.0	28.08852	62-63
GGTCGCC	5130	0.0	28.006393	54-55
GTGGTCG	5345	0.0	26.70213	52-53
GTCGCCG	5415	0.0	25.786833	56-57
TGGTCGC	5425	0.0	25.389103	54-55

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCATTAA	5825	0.0	24.624088	64-65
CATTAAA	5645	0.0	24.609968	66-67
CGGTGGT	5935	0.0	24.327753	50-51
TCTCGGT	5770	0.0	23.871038	48-49
ATCTCGG	6095	0.0	23.533274	46-47
CTCGGTG	6165	0.0	23.266068	48-49
ATTAAAA	6385	0.0	22.873539	66-67
TCGGTGG	6195	0.0	22.310064	50-51

Produced by FastQC (version 0.11.5)