













FastQC Report

Summary

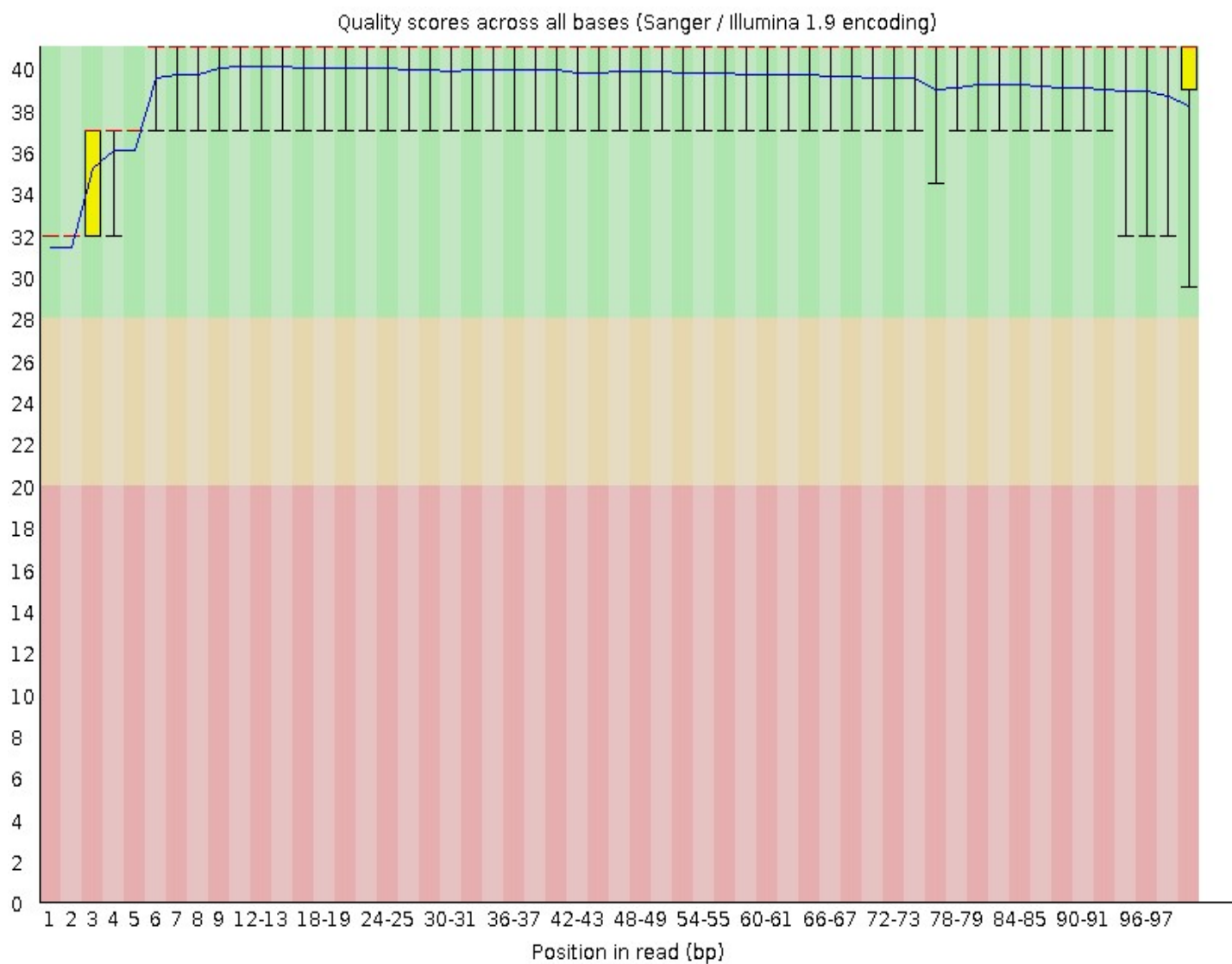
Mon 11 Sep 2023
31_4F_fox_S22_L008_R1_001.fastq.gz

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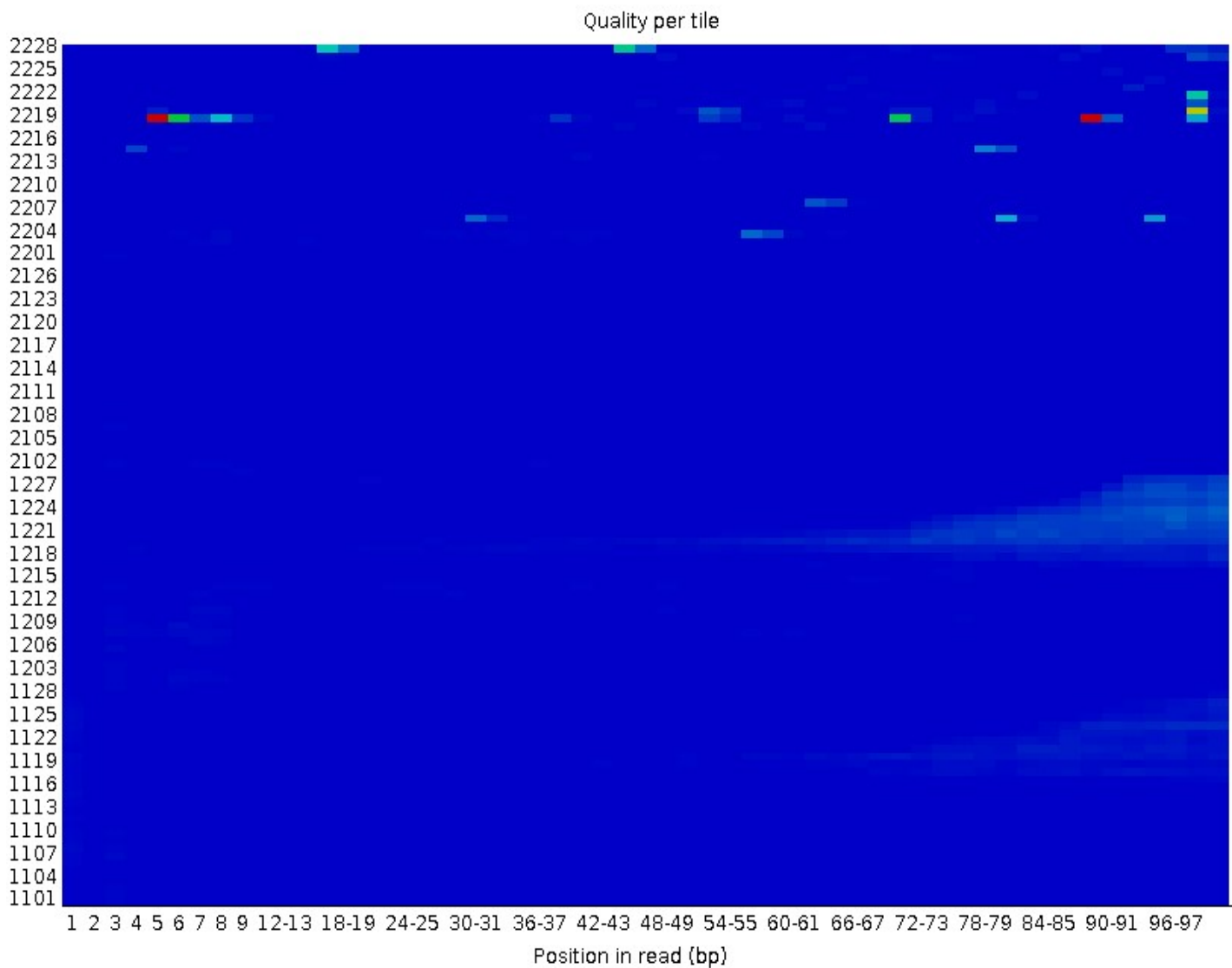
Basic Statistics

Measure	Value
Filename	31_4F_fox_S22_L008_R1_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	50

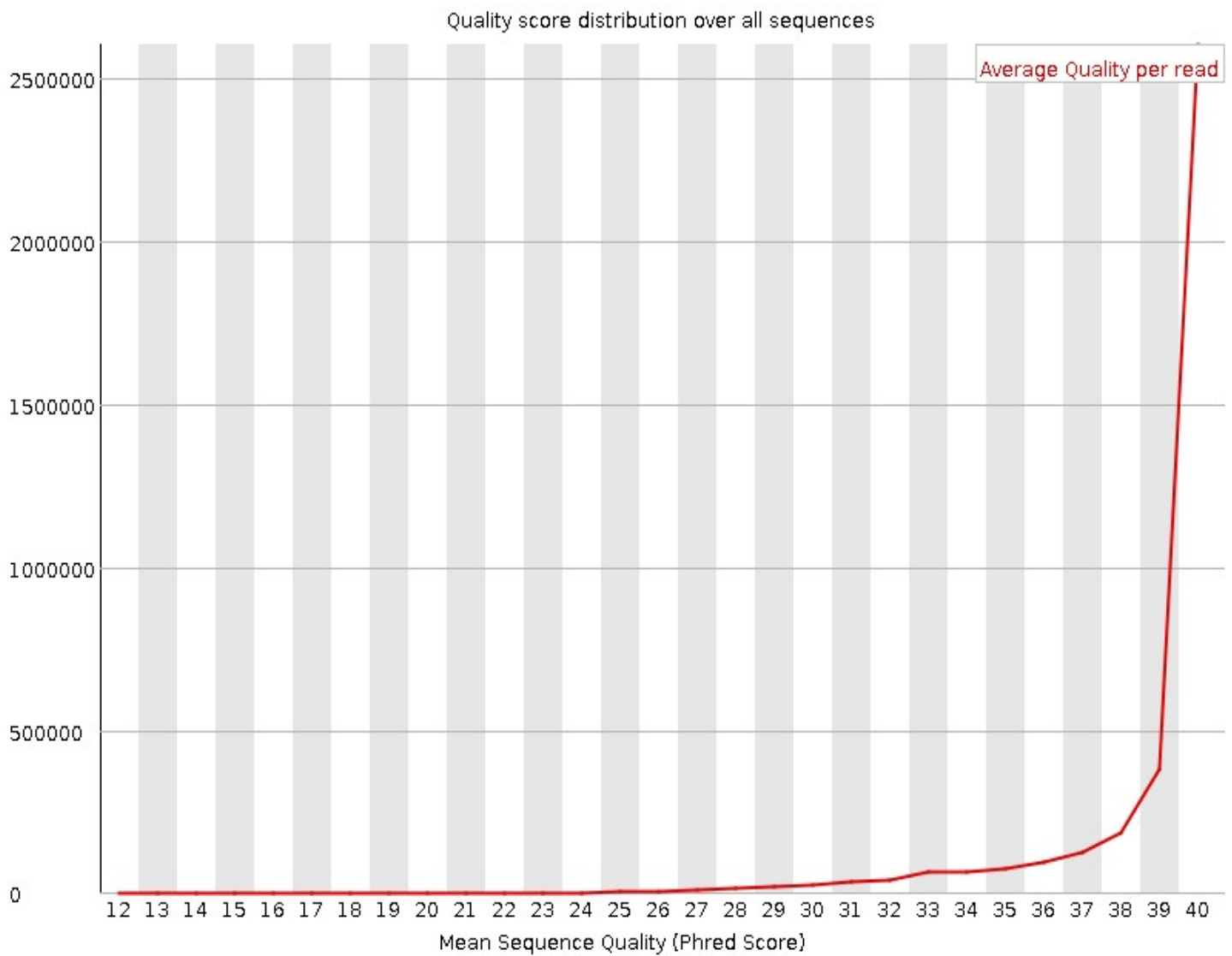
Per base sequence quality



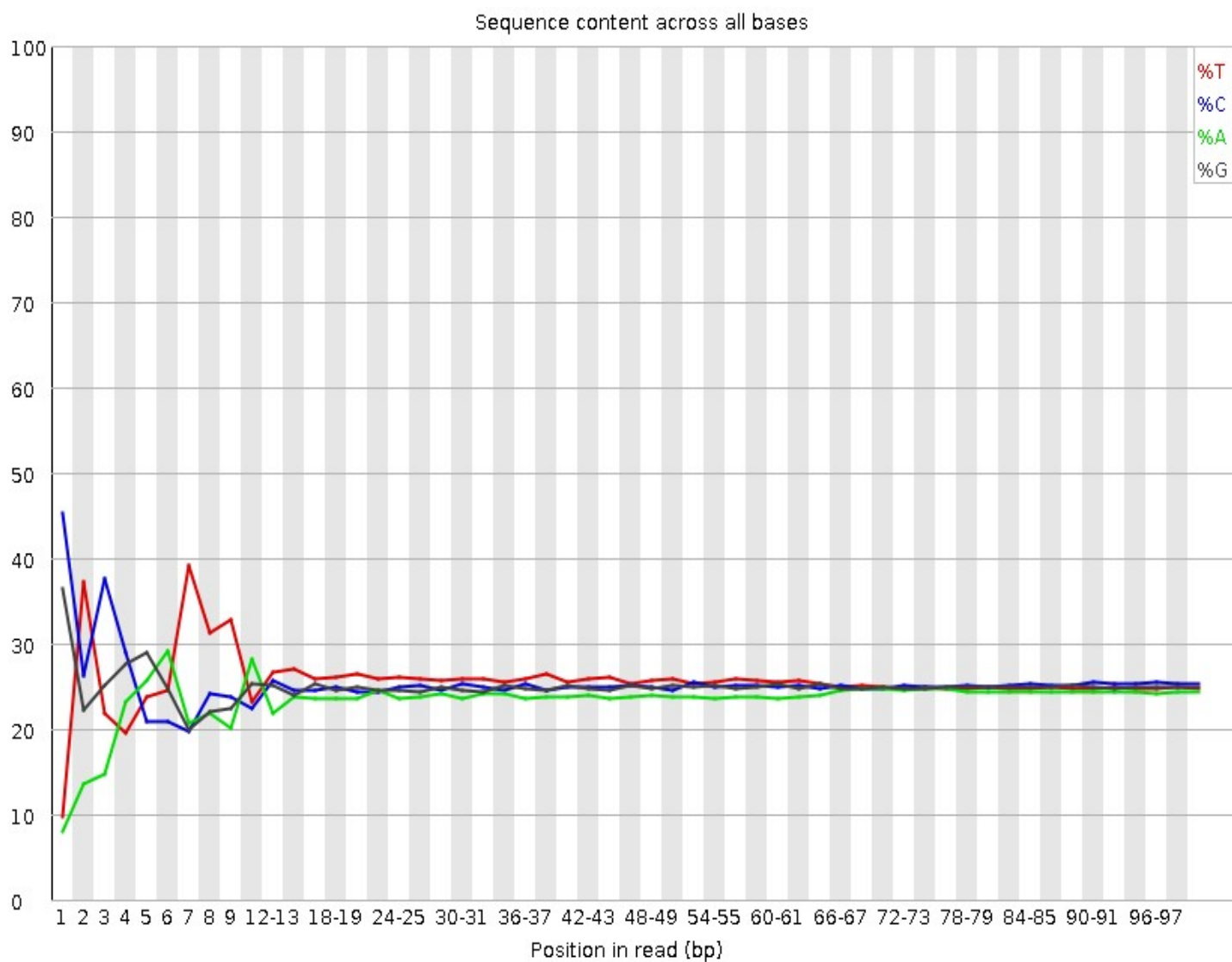
 **Per tile sequence quality**



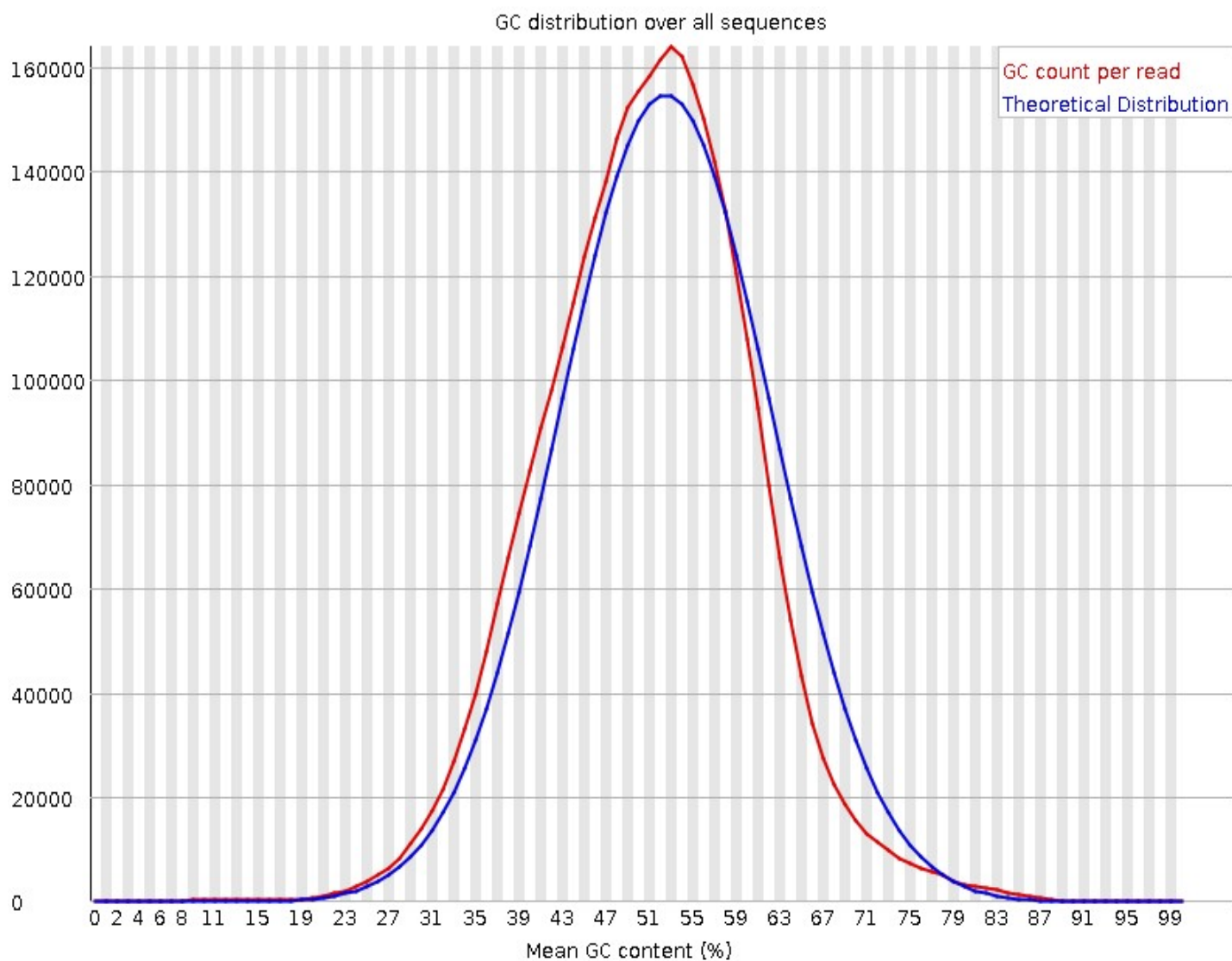
Per sequence quality scores



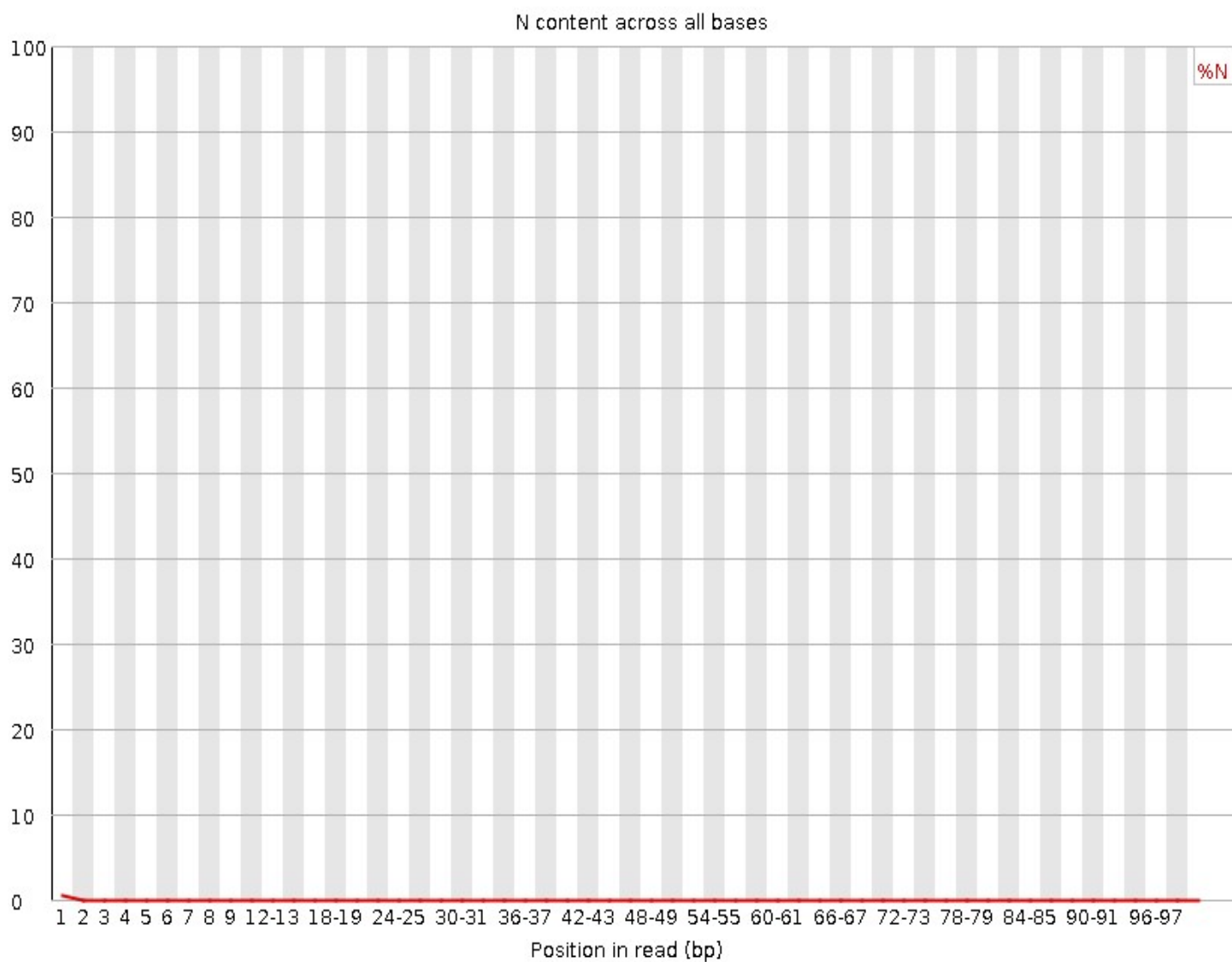
❌ Per base sequence content



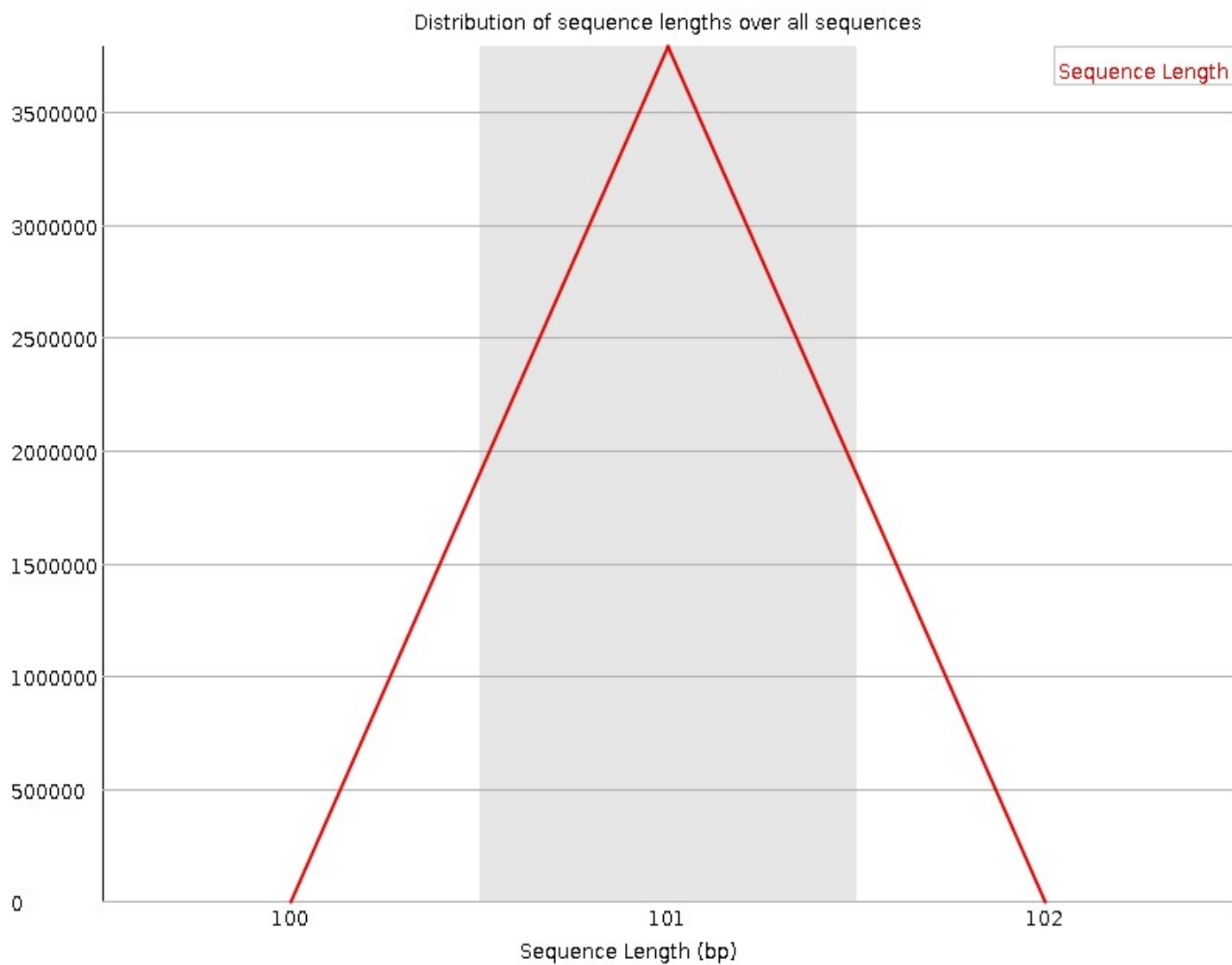
Per sequence GC content



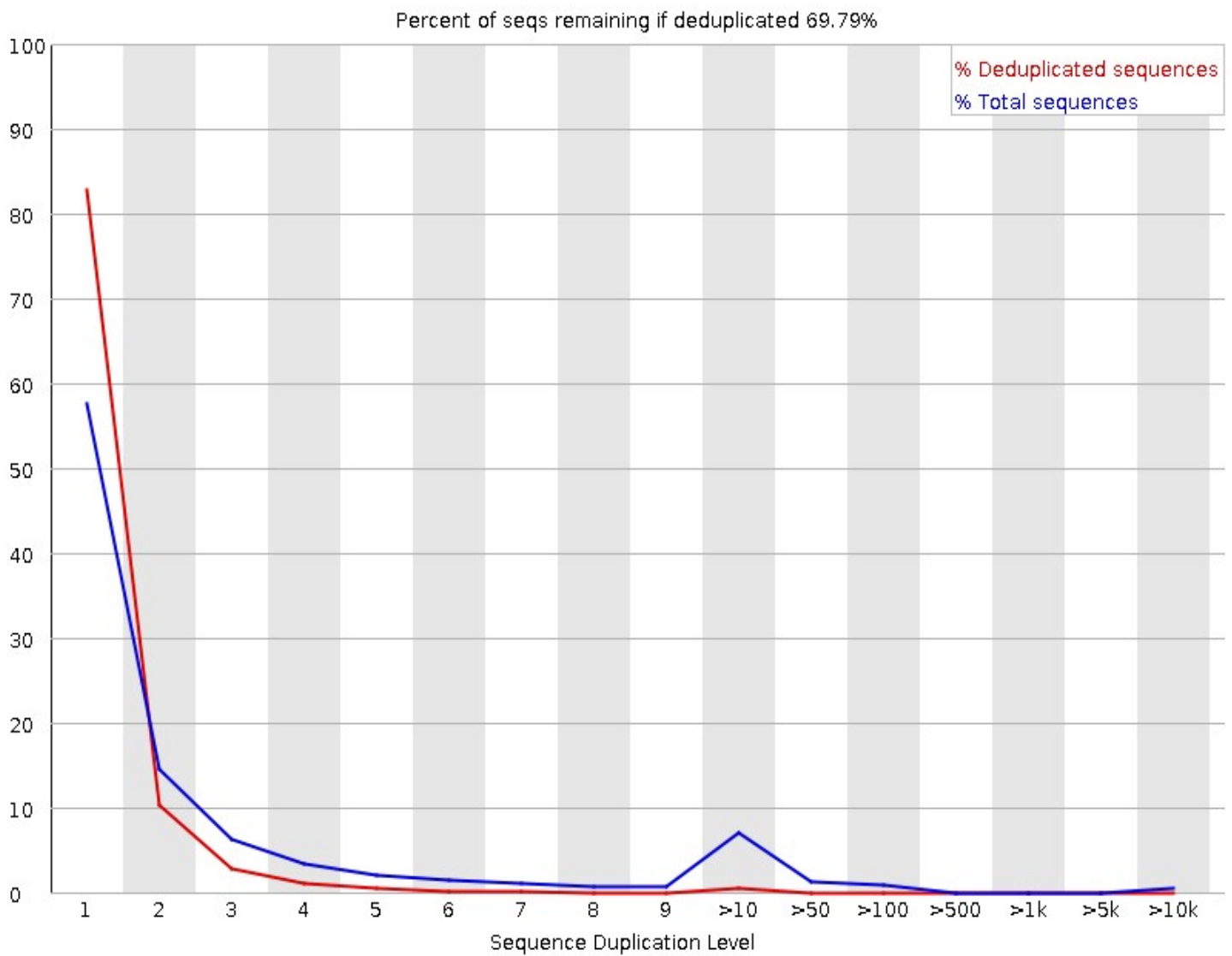
Per base N content



Sequence Length Distribution



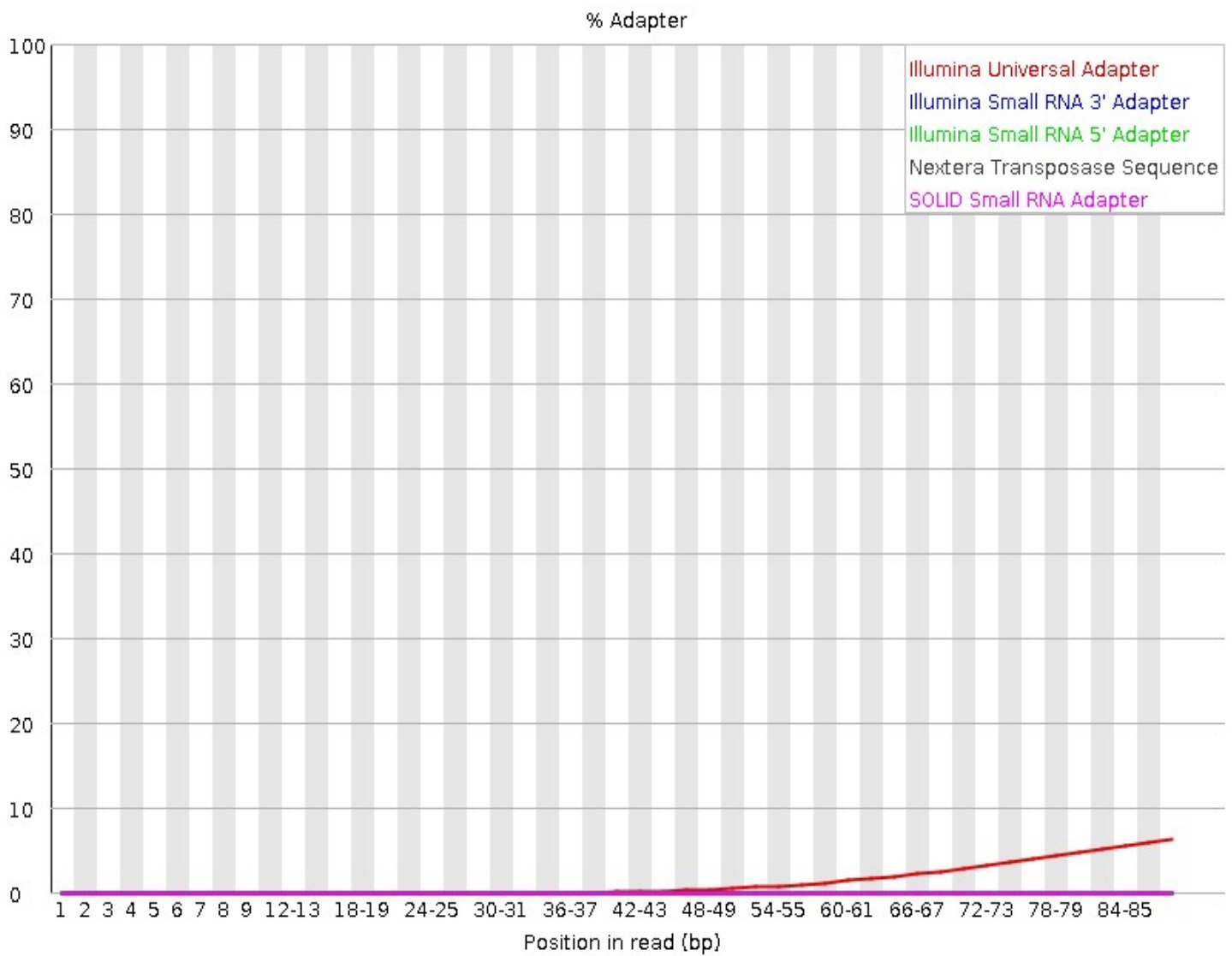
! Sequence Duplication Levels



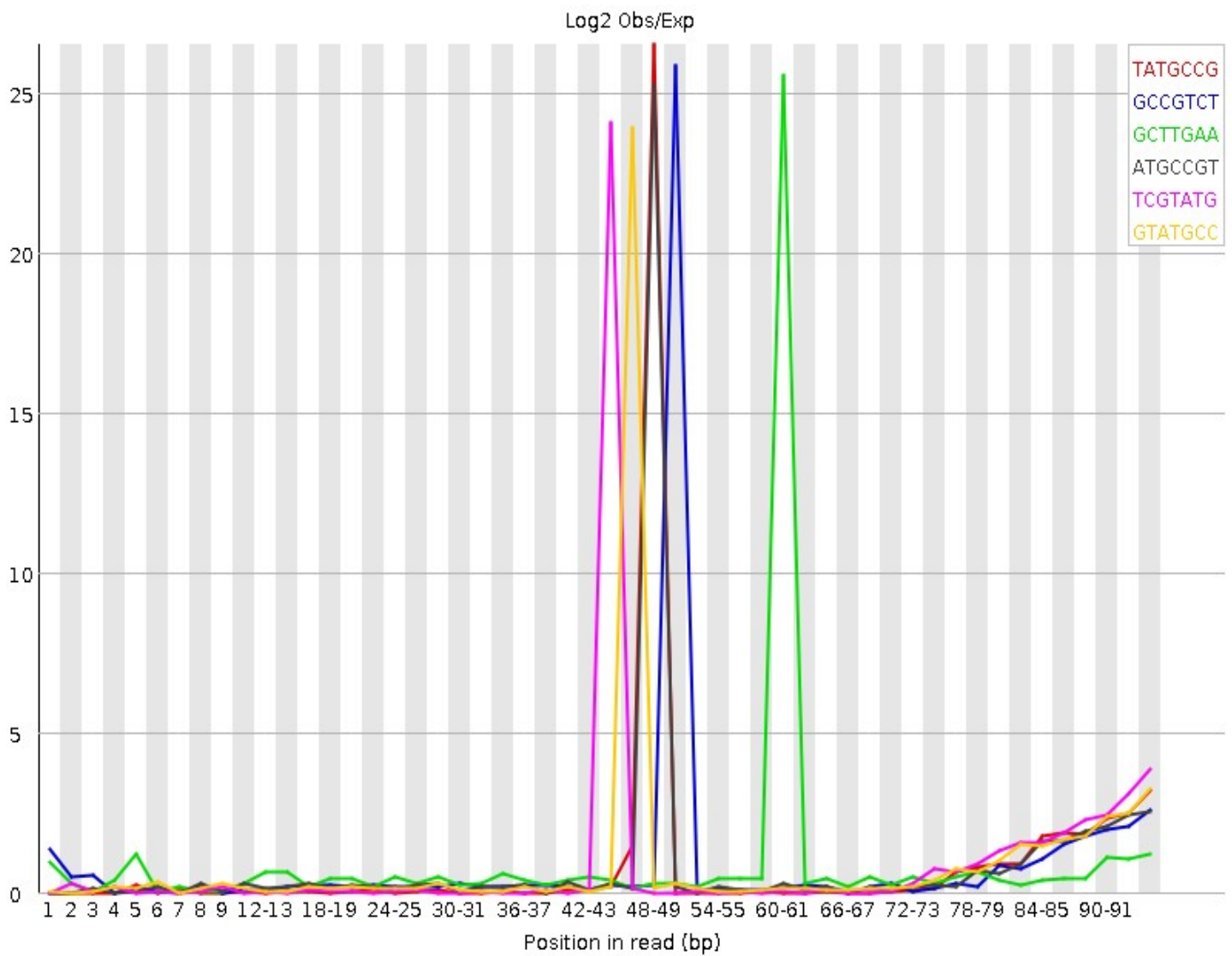
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGATCTTGCATCTCGTAT	26800	0.7074333026338956	TruSeq Adapter, Index 9 (97% over 37bp)

Adapter Content



 **Kmer Content**



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TATGCCG	5160	0.0	26.507748	48-49
GCCGTCT	5530	0.0	25.850643	50-51
GCTTGAA	5680	0.0	25.585705	60-61
ATGCCGT	5665	0.0	25.276525	48-49
TCGTATG	5990	0.0	24.102997	44-45
GTATGCC	6020	0.0	23.943752	46-47
TGCCGTC	5760	0.0	23.787748	50-51
TTGAAAA	6215	0.0	23.421442	62-63
CGTATGC	5910	0.0	23.384901	46-47
CTTGAAA	6085	0.0	22.790117	62-63
TGAAAAA	6225	0.0	22.124983	64-65
CTCGTAT	6415	0.0	21.469683	44-45

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCGTCTT	6405	0.0	21.355045	52-53
ACGTTCG	335	1.8189894E-12	21.268349	6
TGCTTGA	6760	0.0	20.725243	60-61
TCTCGTA	6605	0.0	20.564468	42-43
GAAAAAA	7300	0.0	19.842722	64-65
CGTCTTC	7460	0.0	19.289942	52-53
CGACTAT	130	0.007268825	18.396704	1
TTACGAC	340	8.931238E-10	18.161503	5

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