












# FastQC Report

## Summary

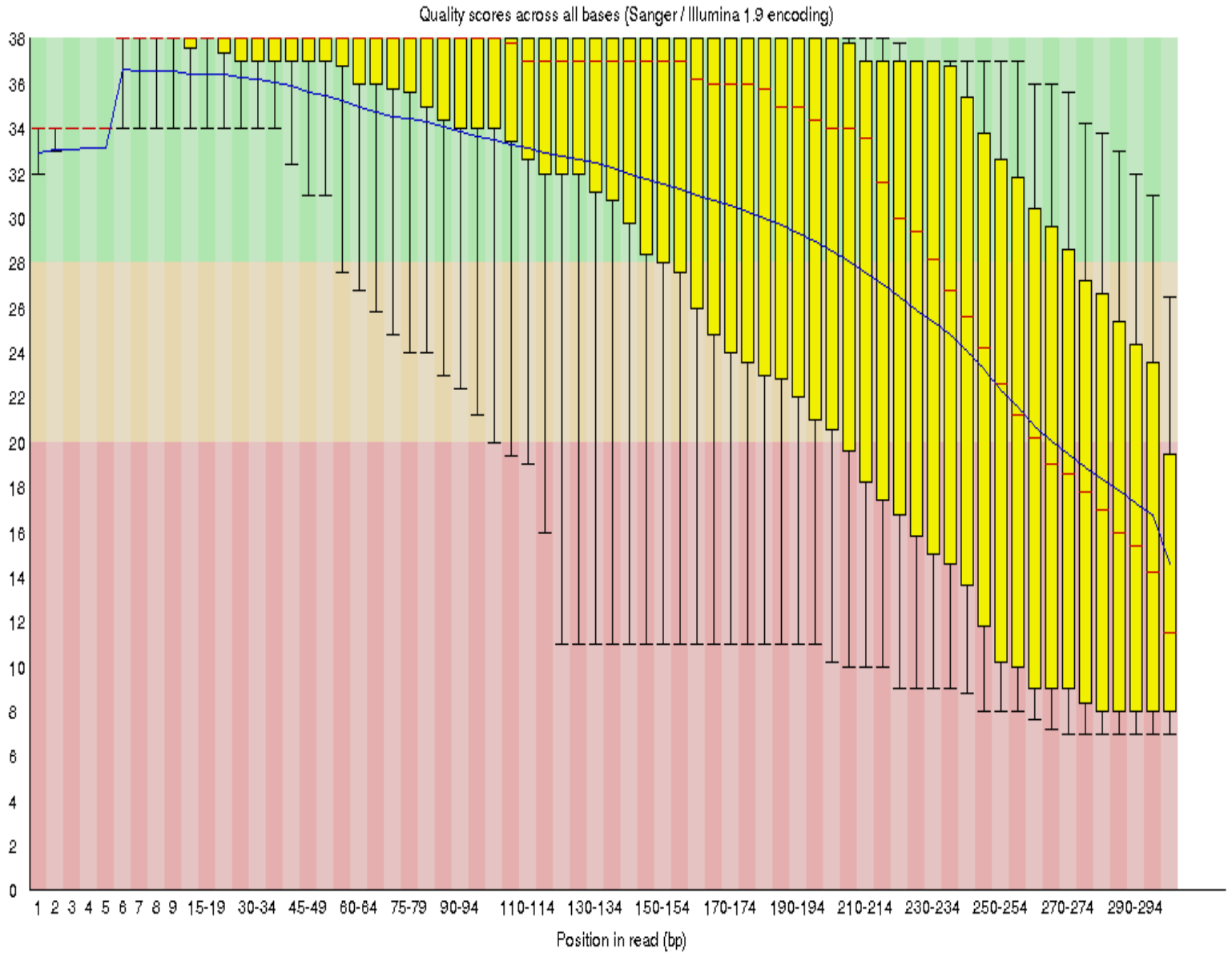
Tue 7 Apr 2015  
SW019\_S1\_L001\_R2\_001.fastq

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## Basic Statistics

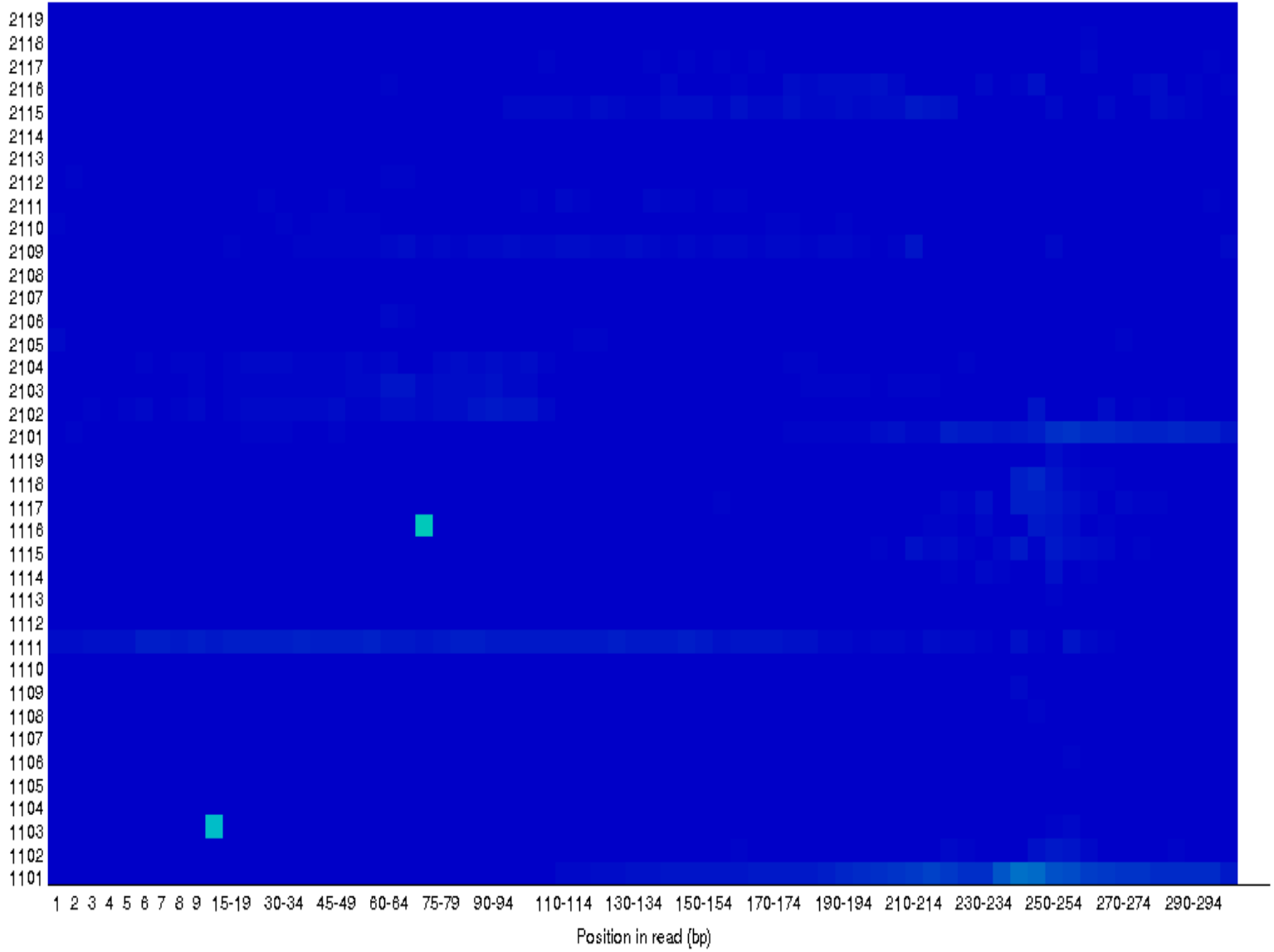
Measure	Value
Filename	SW019_S1_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	27268723
Sequences flagged as poor quality	0
Sequence length	301
%GC	41

## Per base sequence quality

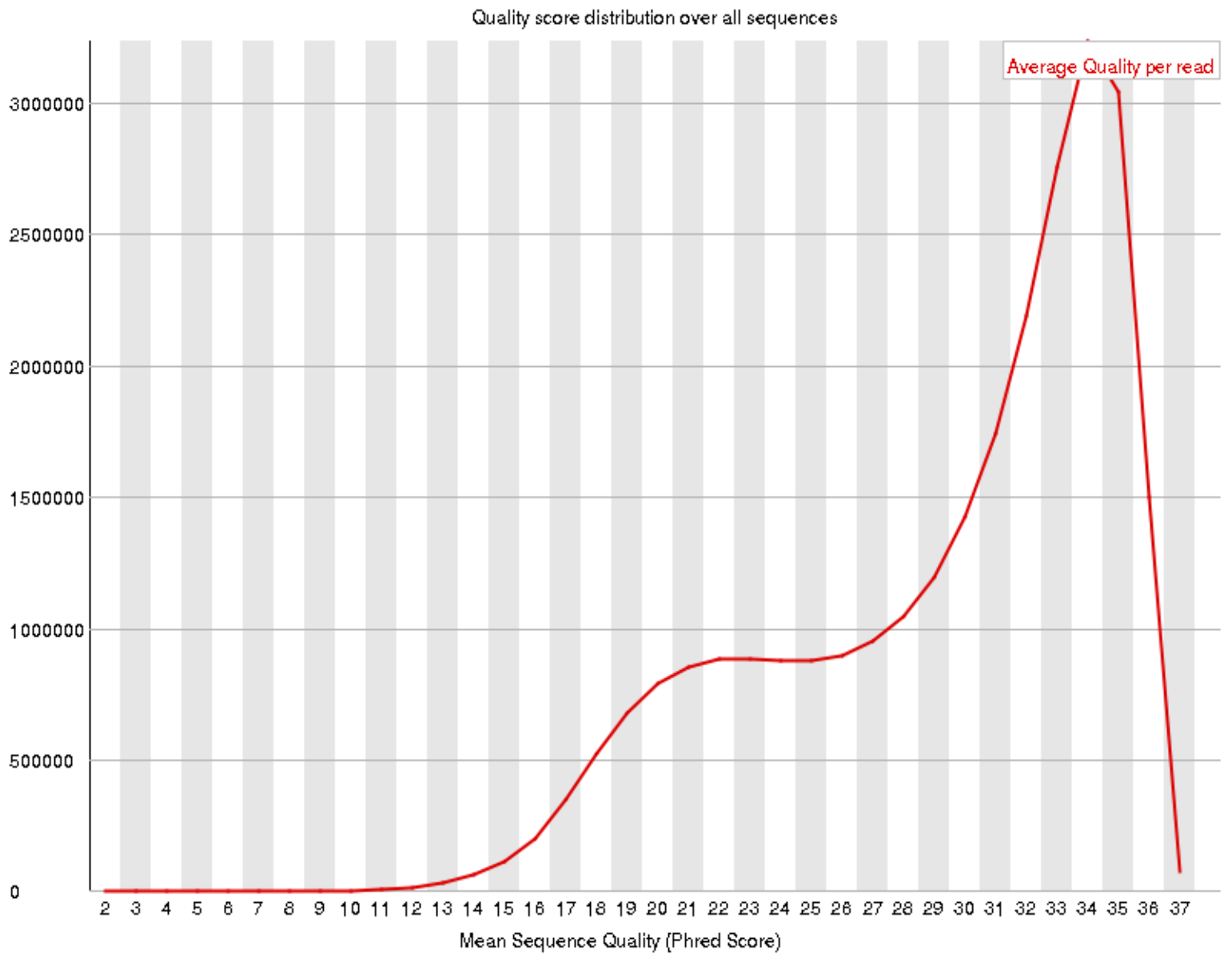


## Per tile sequence quality

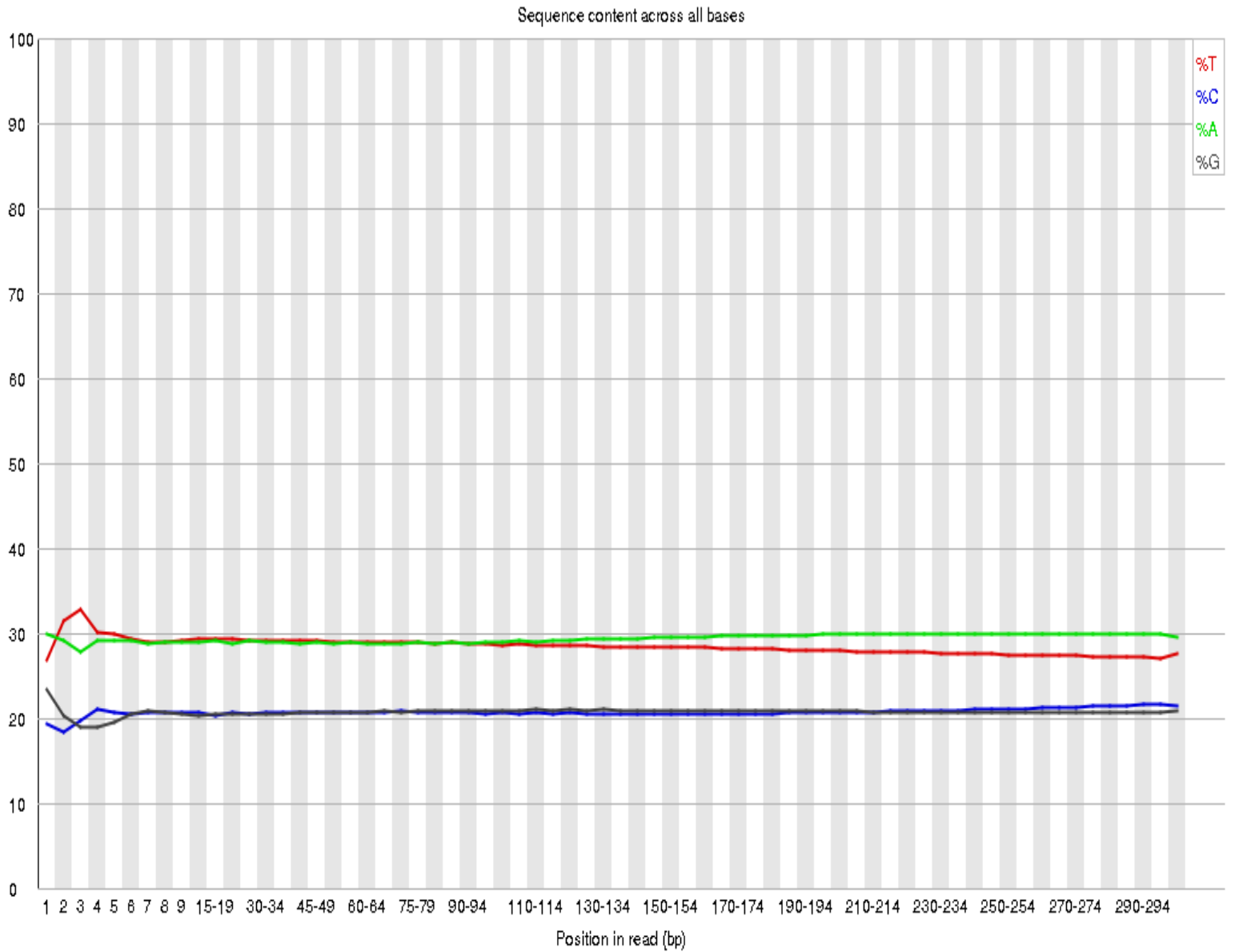
Quality per tile



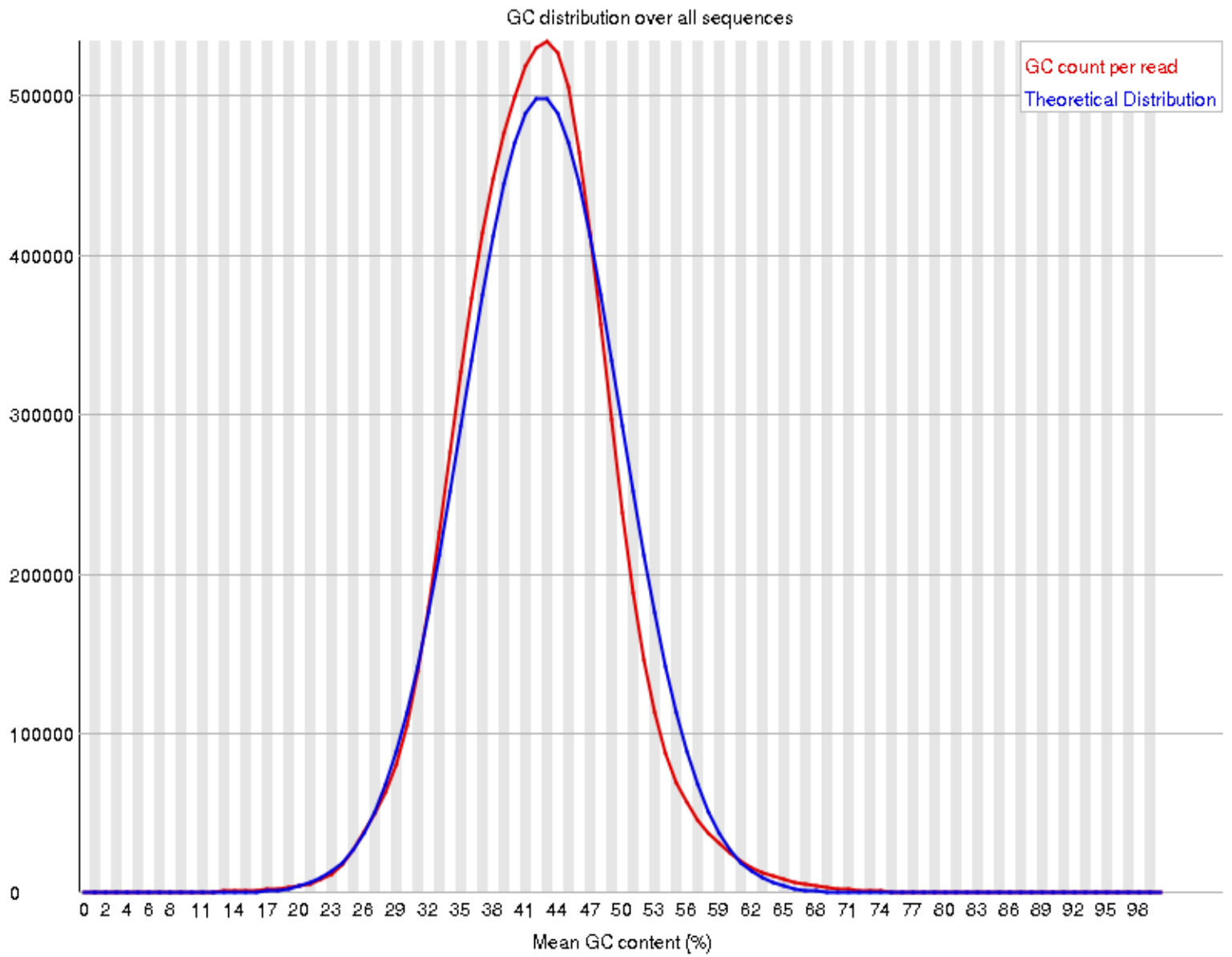
 **Per sequence quality scores**



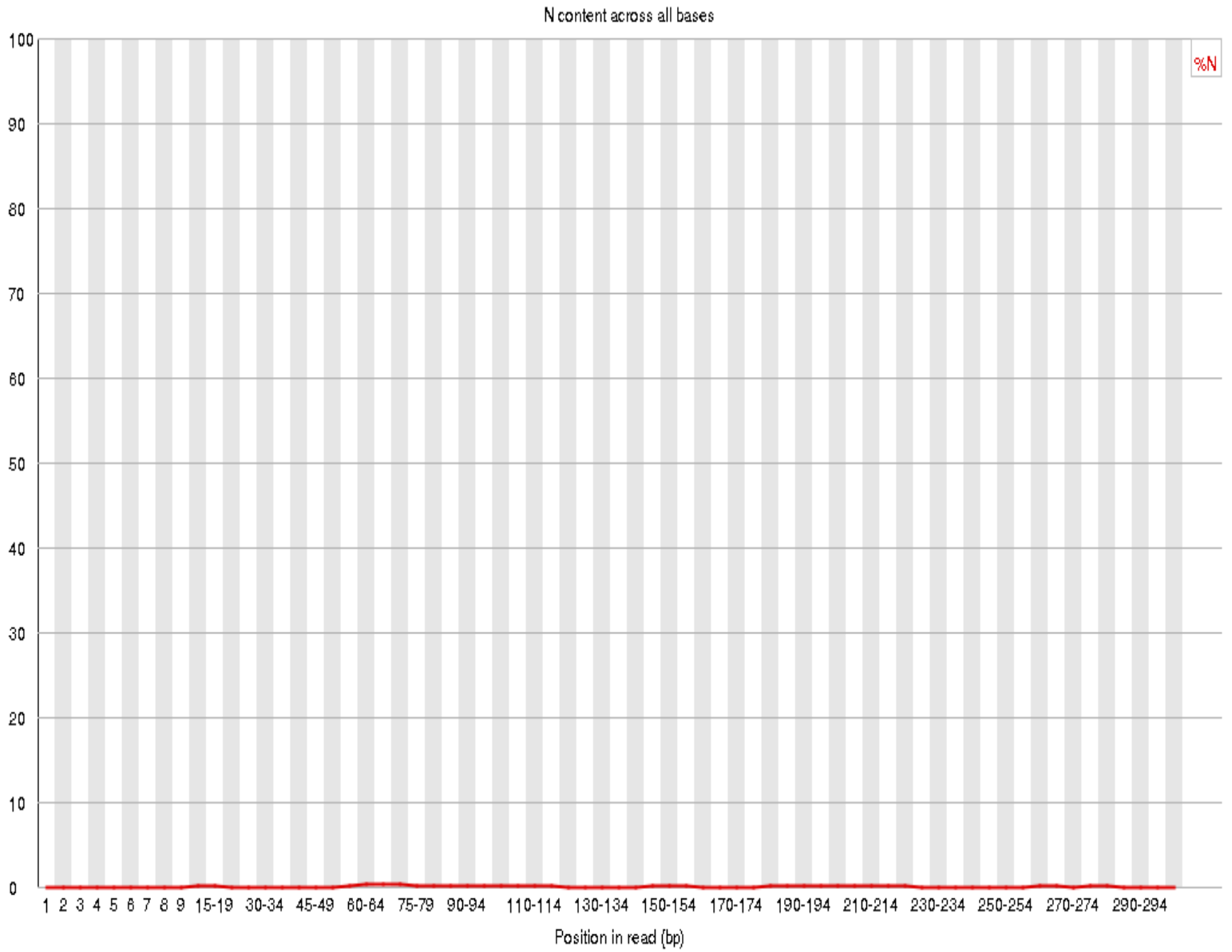
## ⚠ Per base sequence content



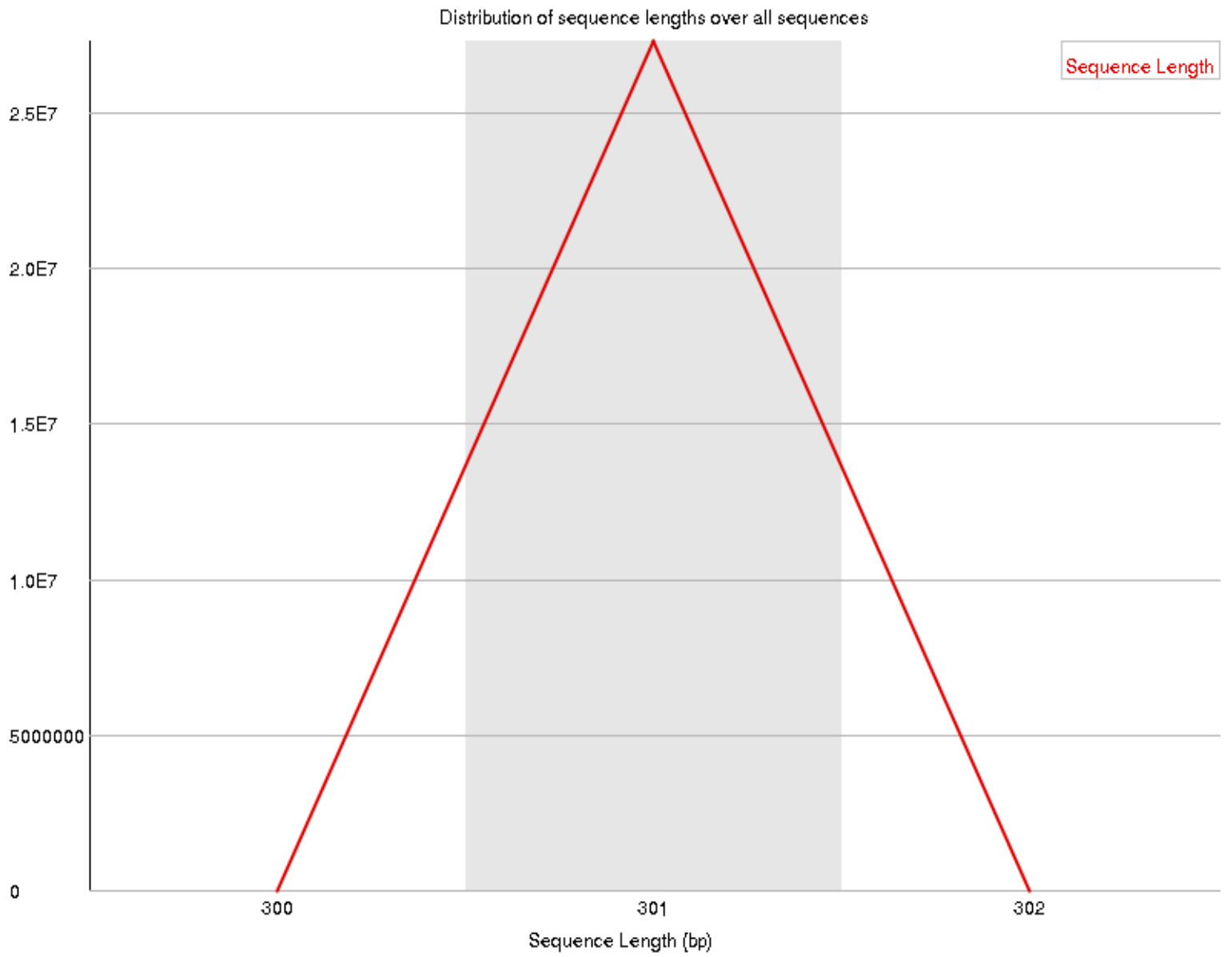
## Per sequence GC content



 **Per base N content**

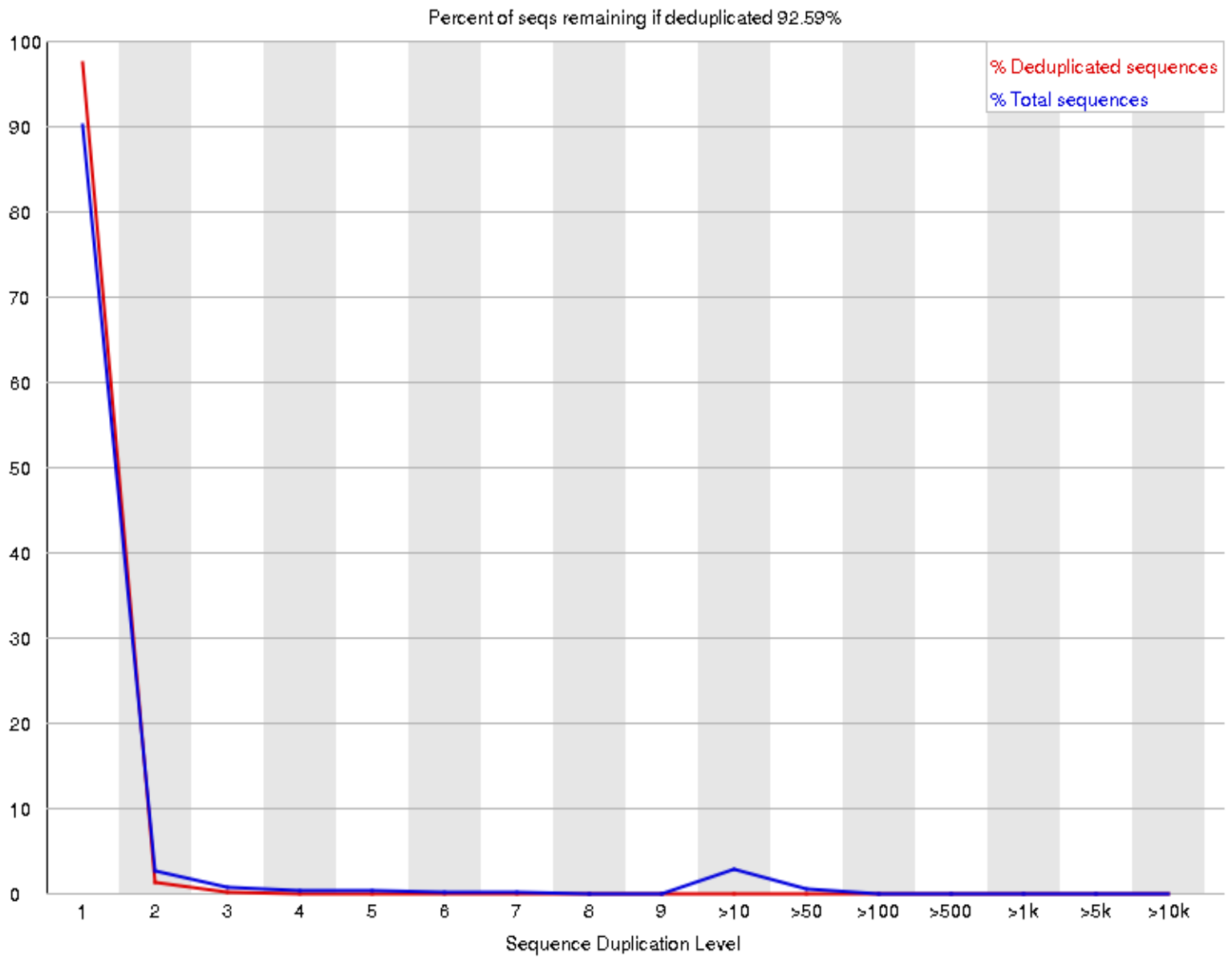


## Sequence Length Distribution



## Sequence Duplication Levels



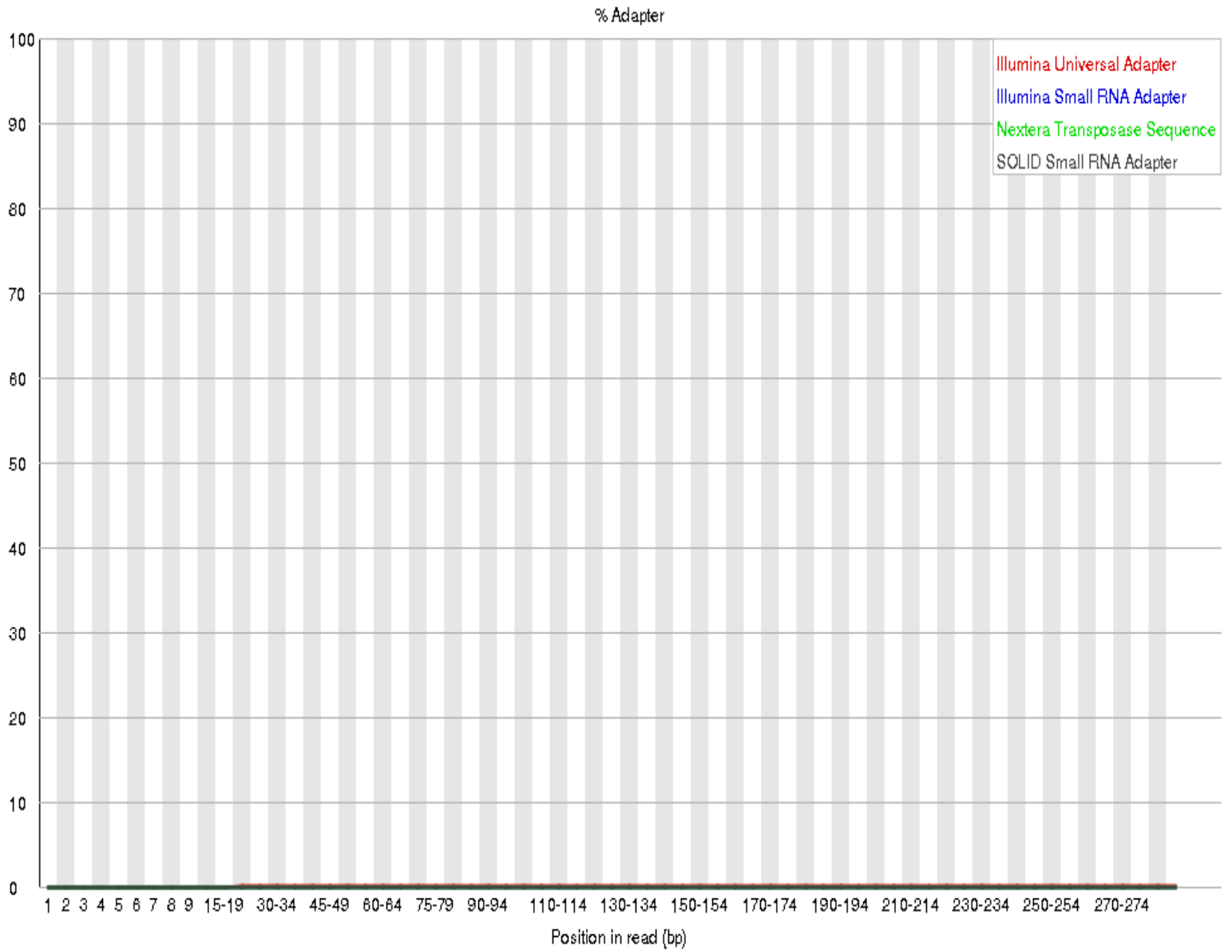


## Overrepresented sequences

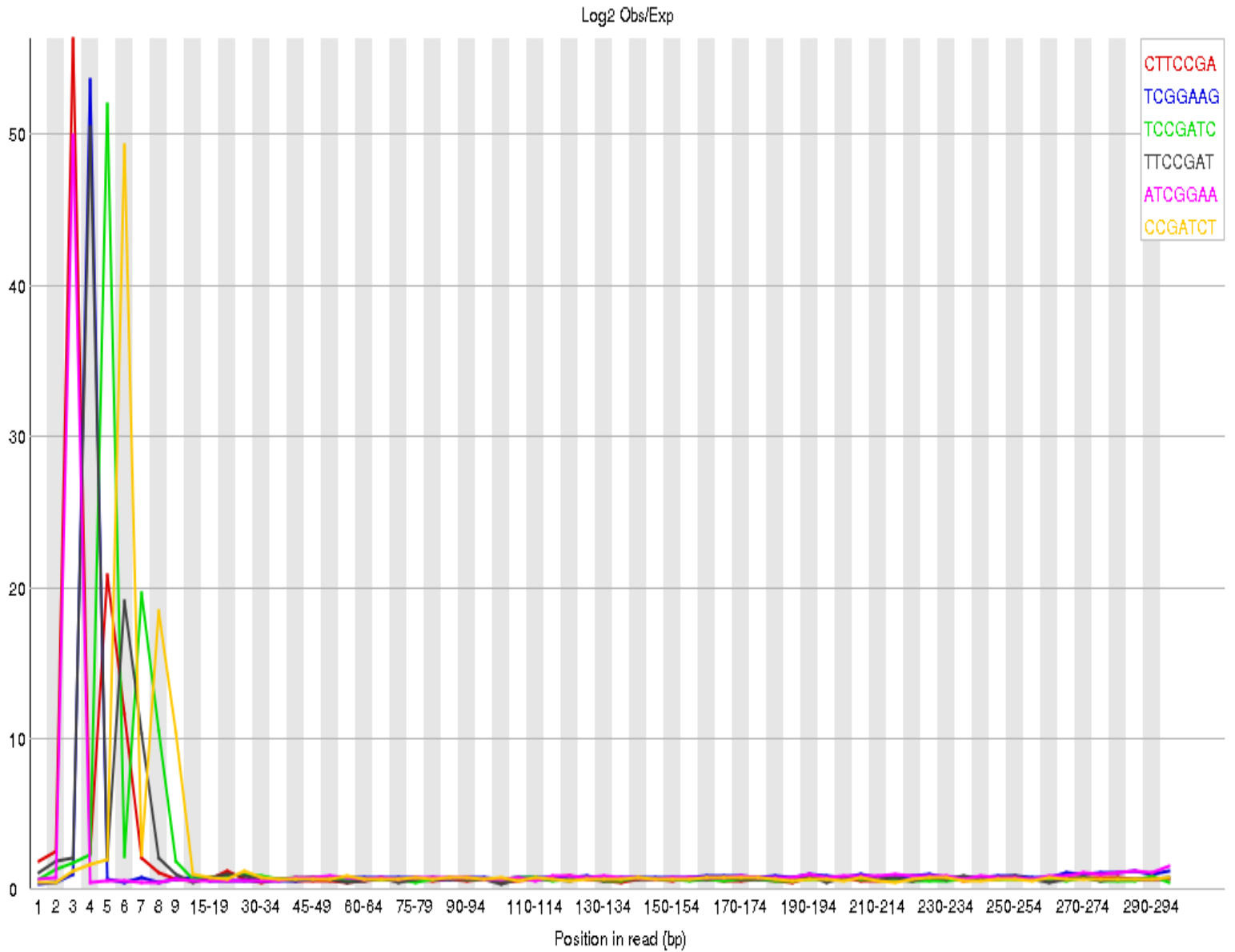
No overrepresented sequences



## Adapter Content



## Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCGA	25830	0.0	56.245663	3
TCGGAAG	30855	0.0	53.62129	4
TCCGATC	27840	0.0	52.016403	5
TTCCGAT	28530	0.0	50.503345	4
ATCGGAA	33310	0.0	49.940838	3
CCGATCT	29370	0.0	49.2569	6
GATCGGA	33645	0.0	49.22524	2
AGATCGG	35290	0.0	47.06803	1

TCTTCCG	37780	0.0	39.040398	2
CGGAAGA	46065	0.0	35.24636	5
GAAGAGC	64885	0.0	25.61453	7
CGATCTA	20960	0.0	22.514668	7
CTCTTCC	87675	0.0	17.499624	1
AAGAGCG	41260	0.0	16.048435	8
CGATCTT	27155	0.0	15.694766	7
GGAAGAG	109385	0.0	15.193862	6
ACGCTCT	20515	0.0	14.727741	1
AGAGCGT	31610	0.0	12.363805	9
GCTCTTC	49995	0.0	11.405819	2
CGCTCTT	27265	0.0	11.132785	2

Produced by [FastQC](#) (version 0.11.3)