













# FastQC Report

## Summary

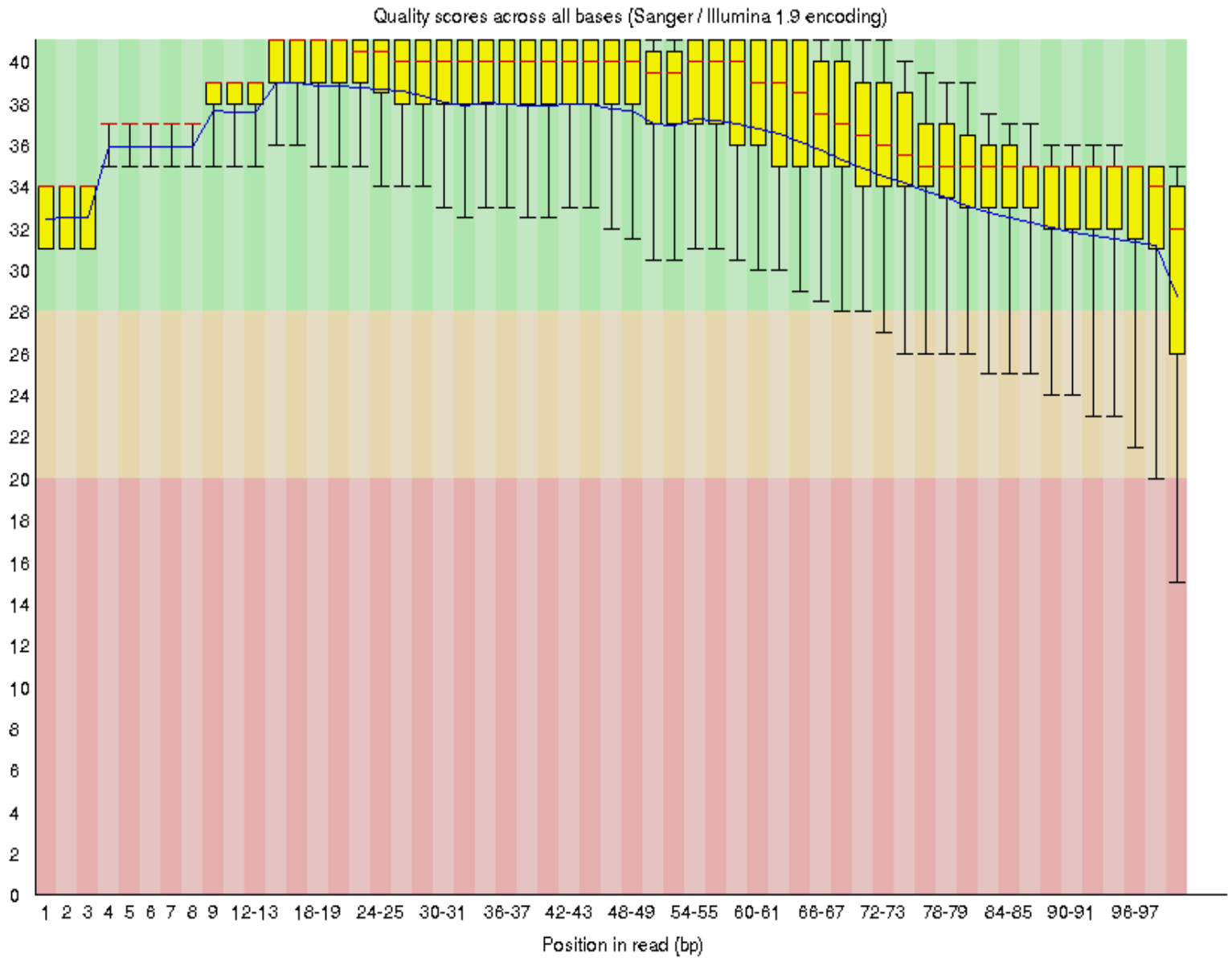
Tue 14 Apr 2015  
SW018\_S1\_L007\_R2\_001.fastq

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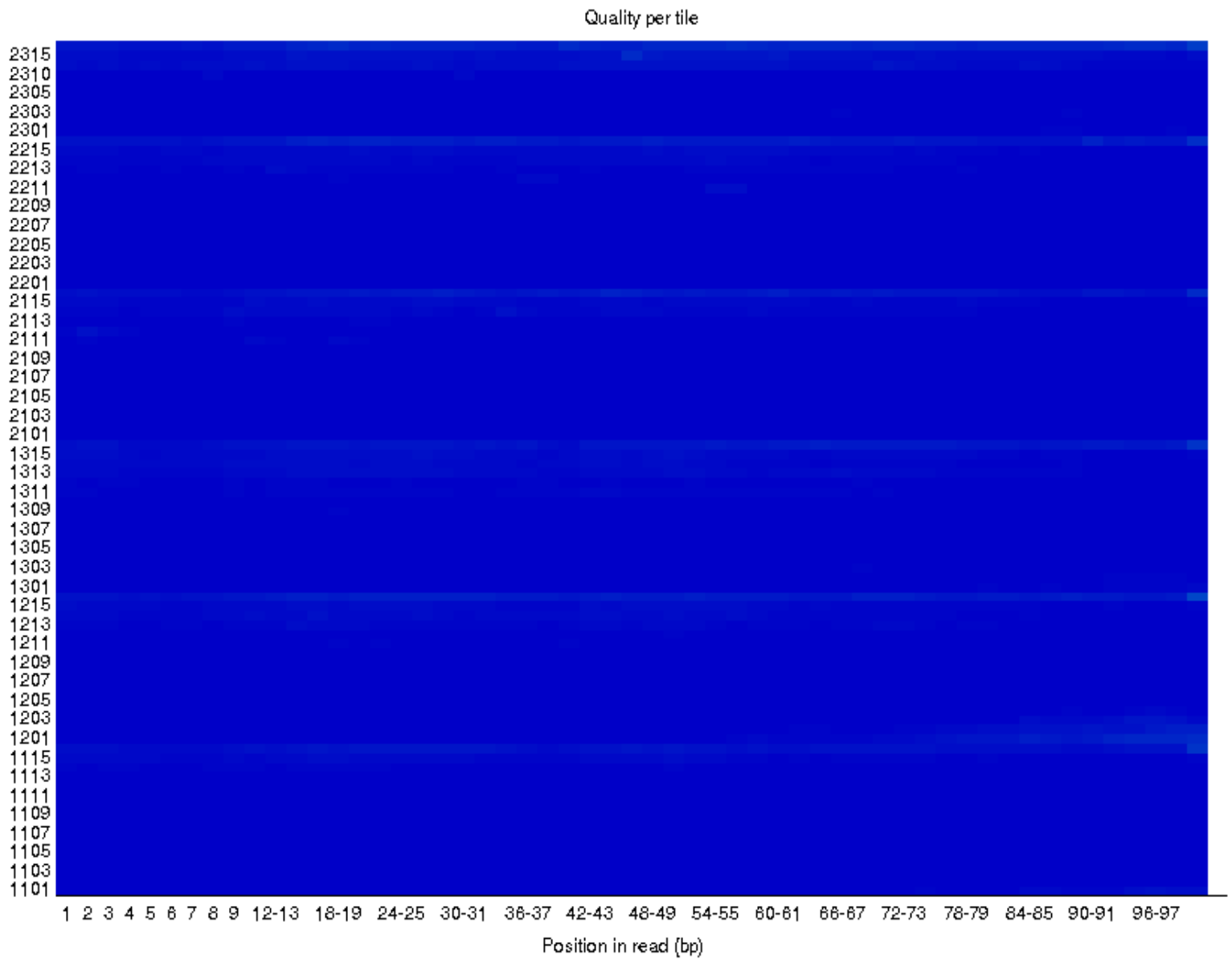
## Basic Statistics

Measure	Value
Filename	SW018_S1_L007_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	143019341
Sequences flagged as poor quality	0
Sequence length	100
%GC	42

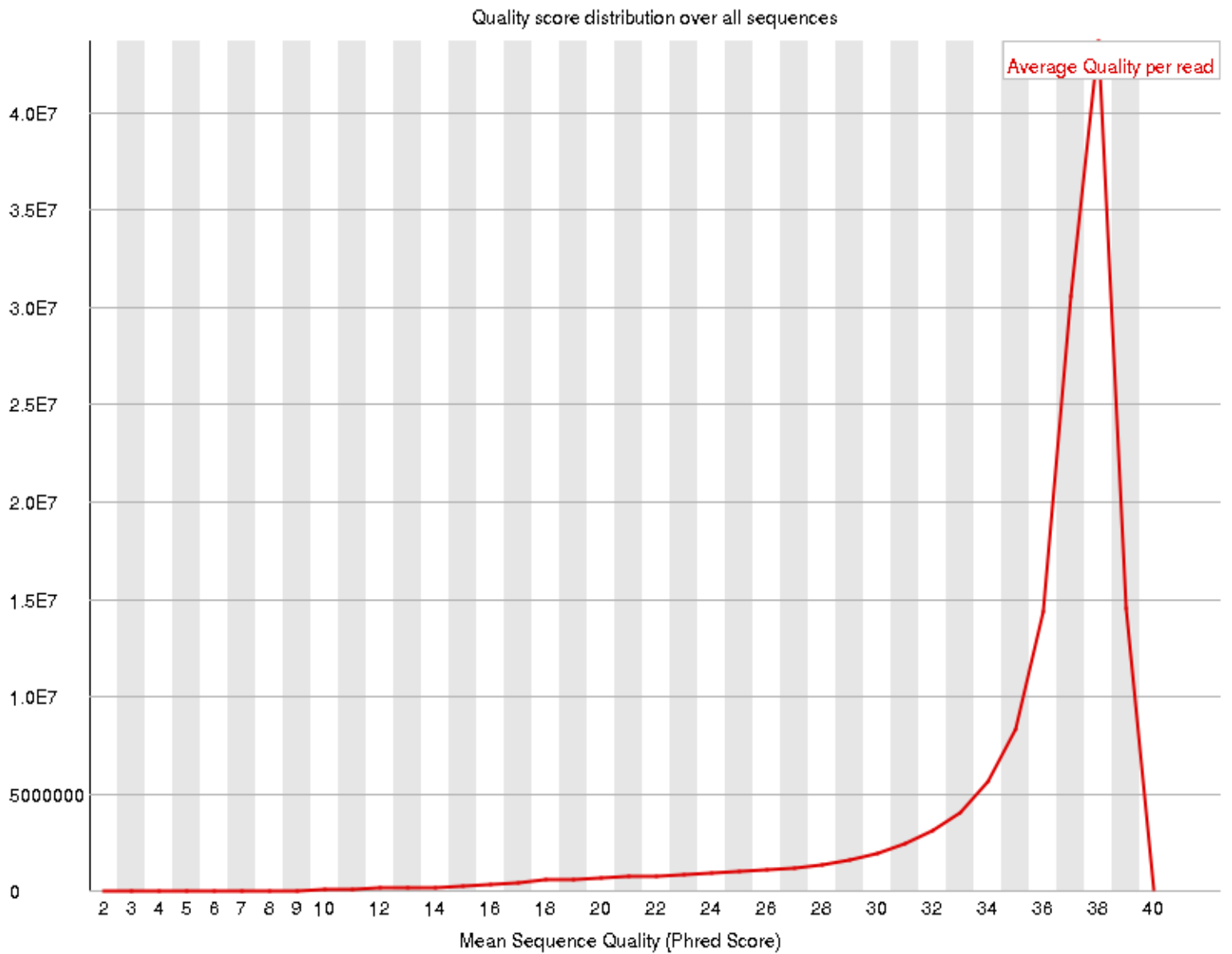
## ✓ Per base sequence quality



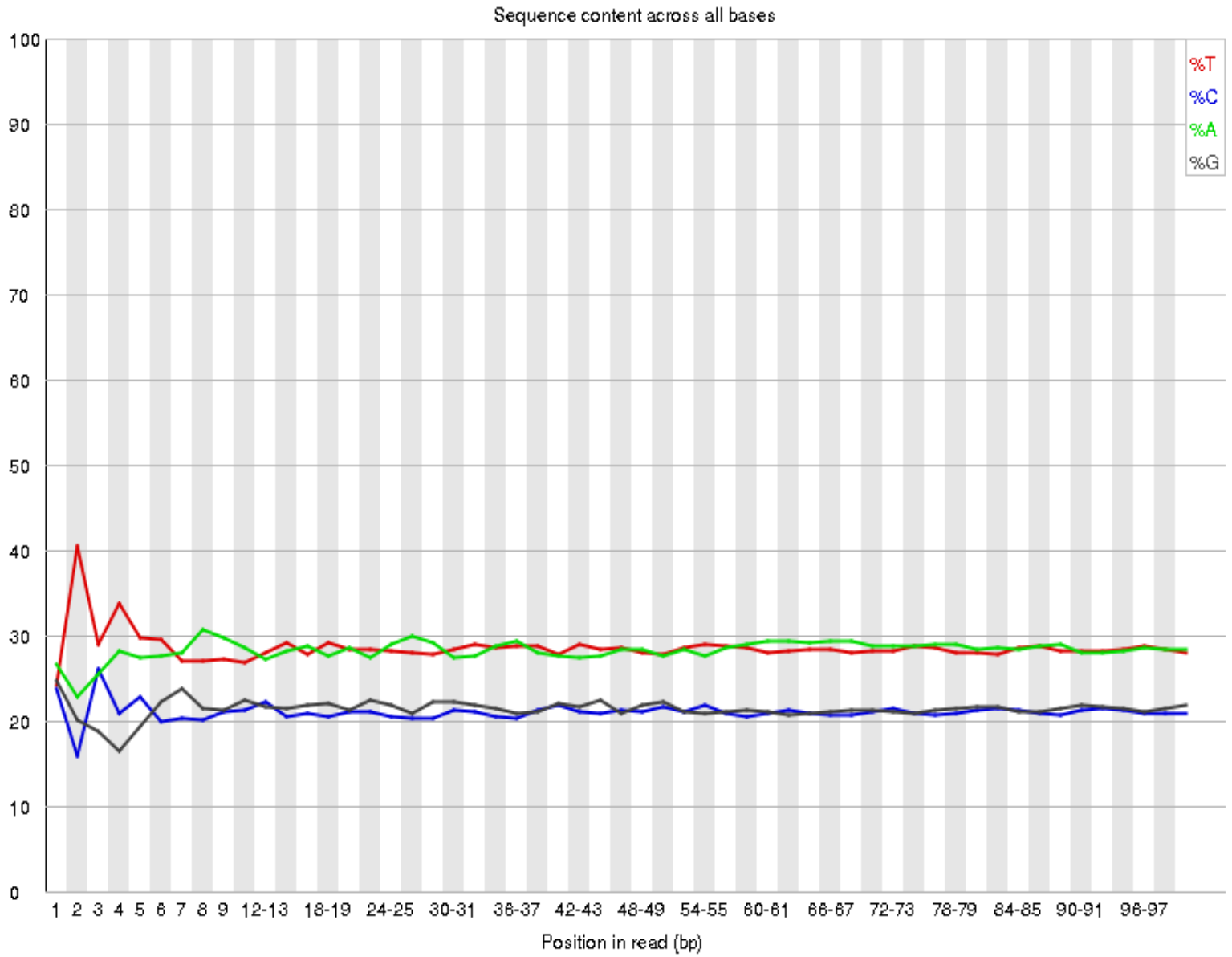
## ✓ Per tile sequence quality



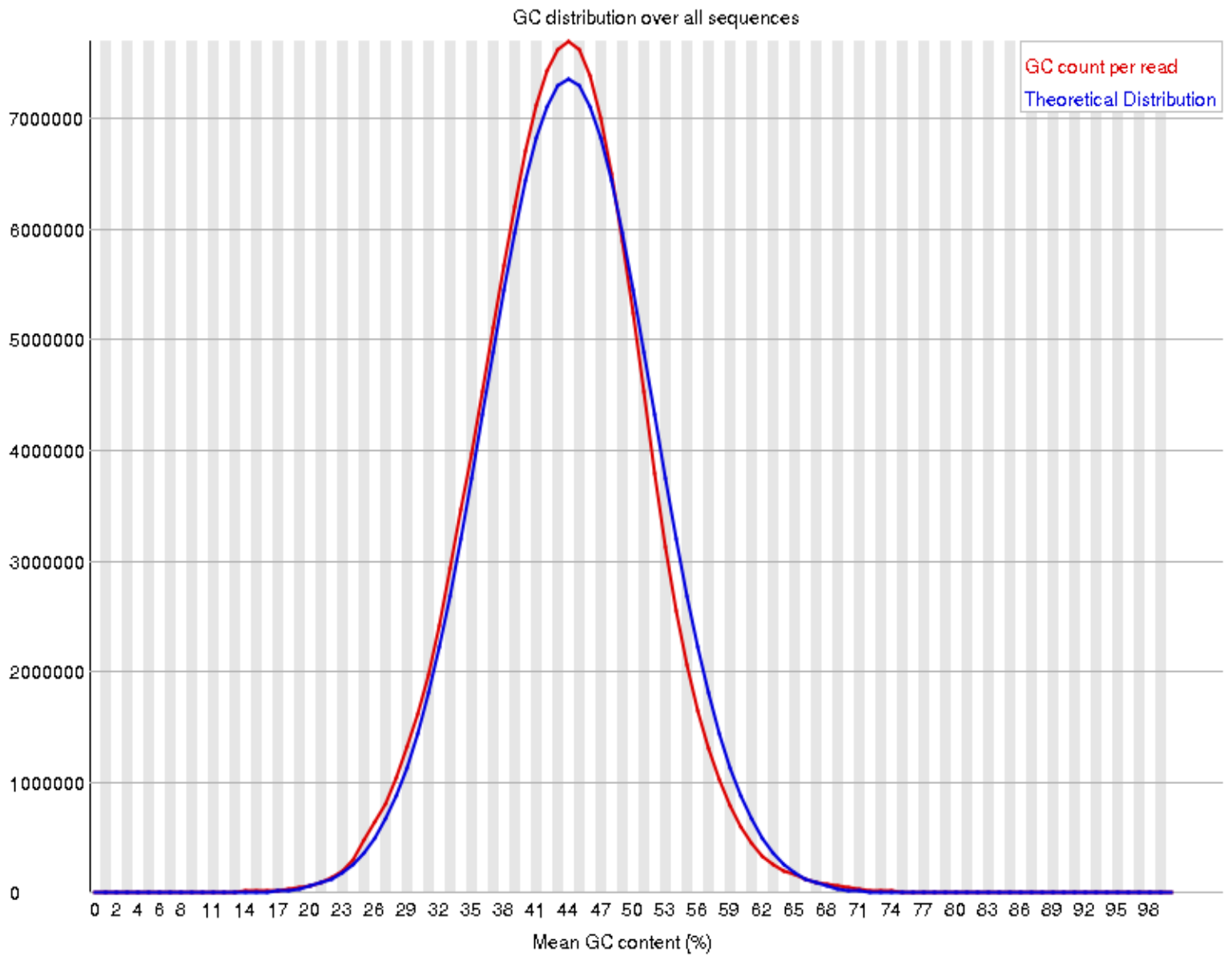
## Per sequence quality scores



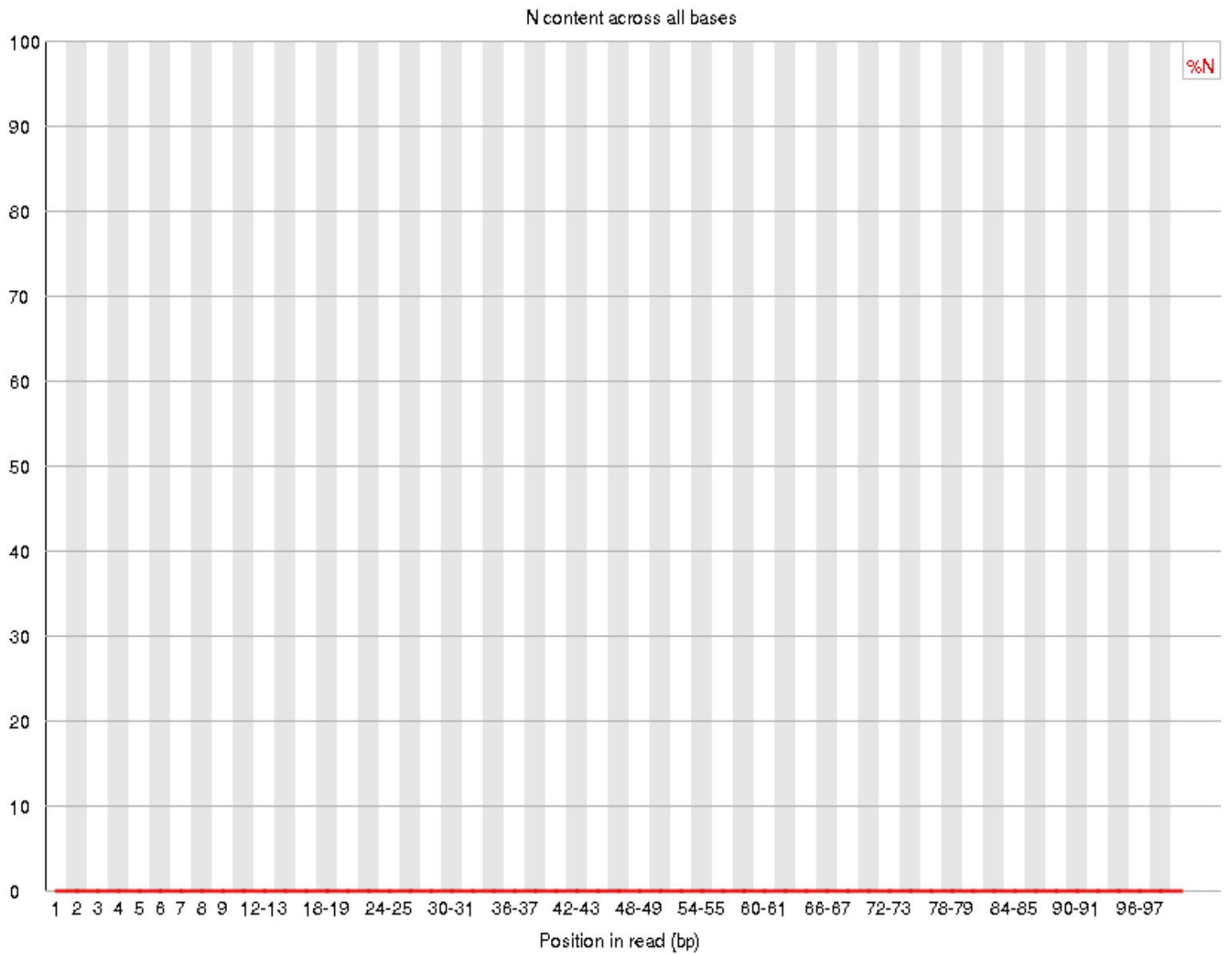
## Per base sequence content



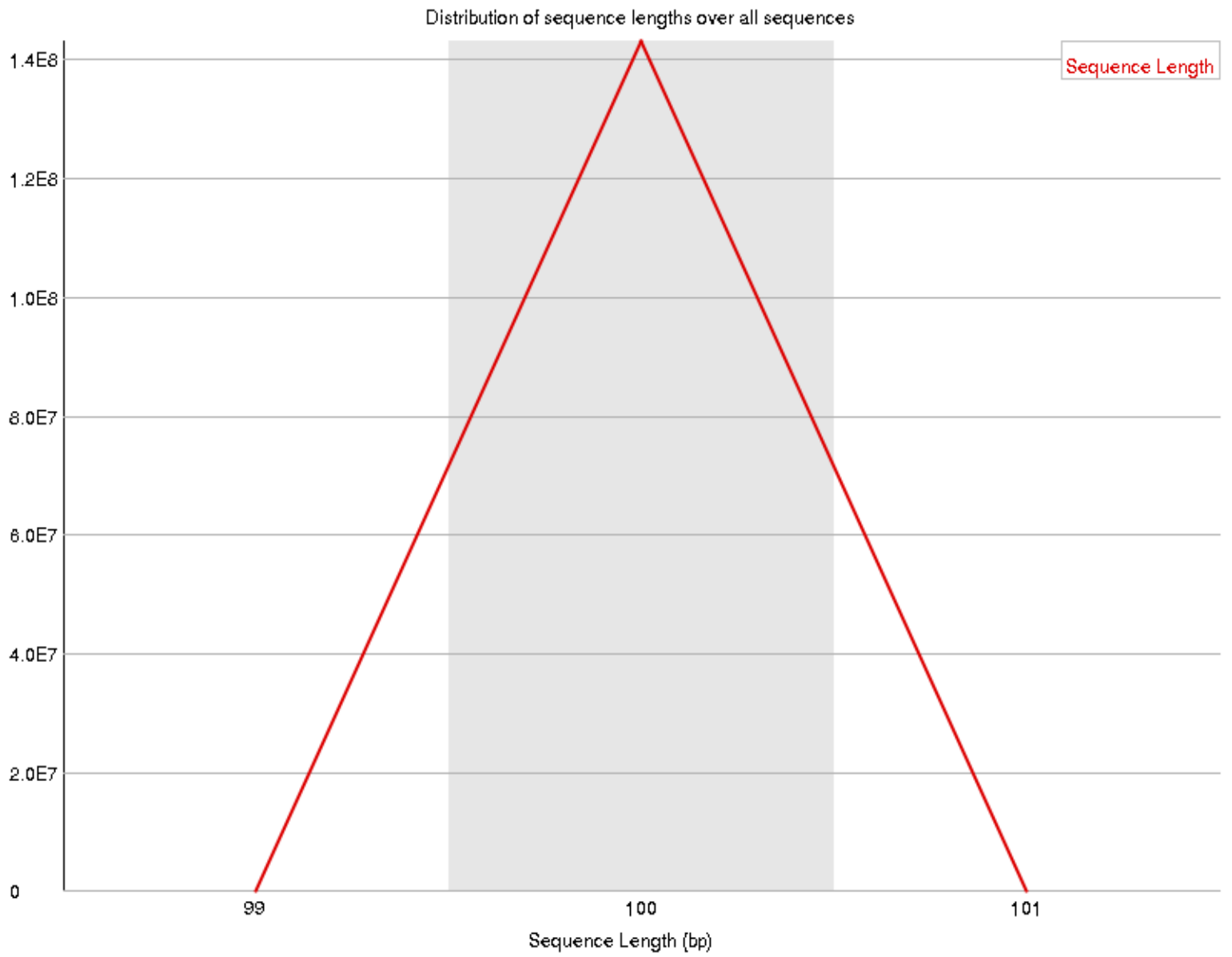
 **Per sequence GC content**



 **Per base N content**

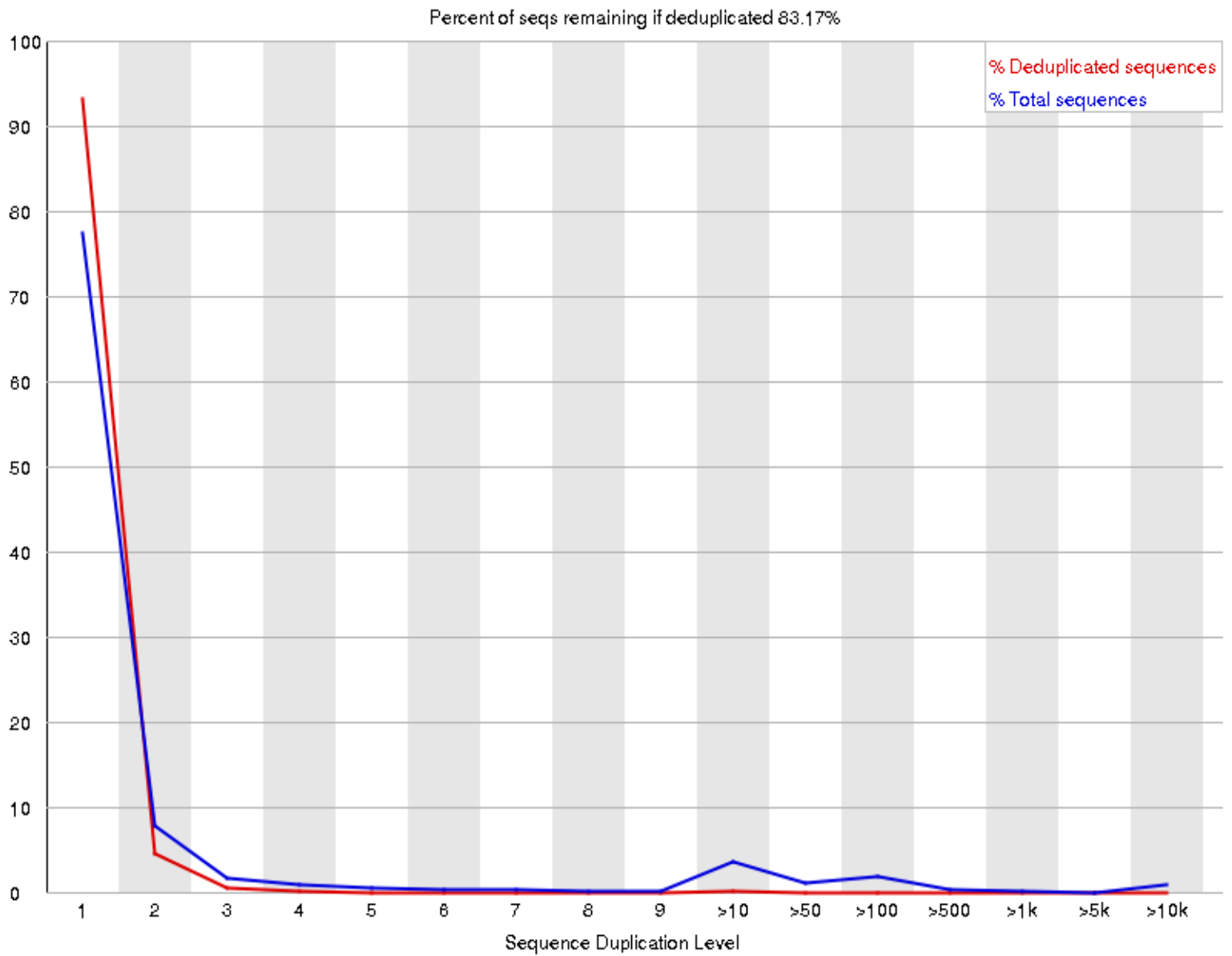


## Sequence Length Distribution



## Sequence Duplication Levels

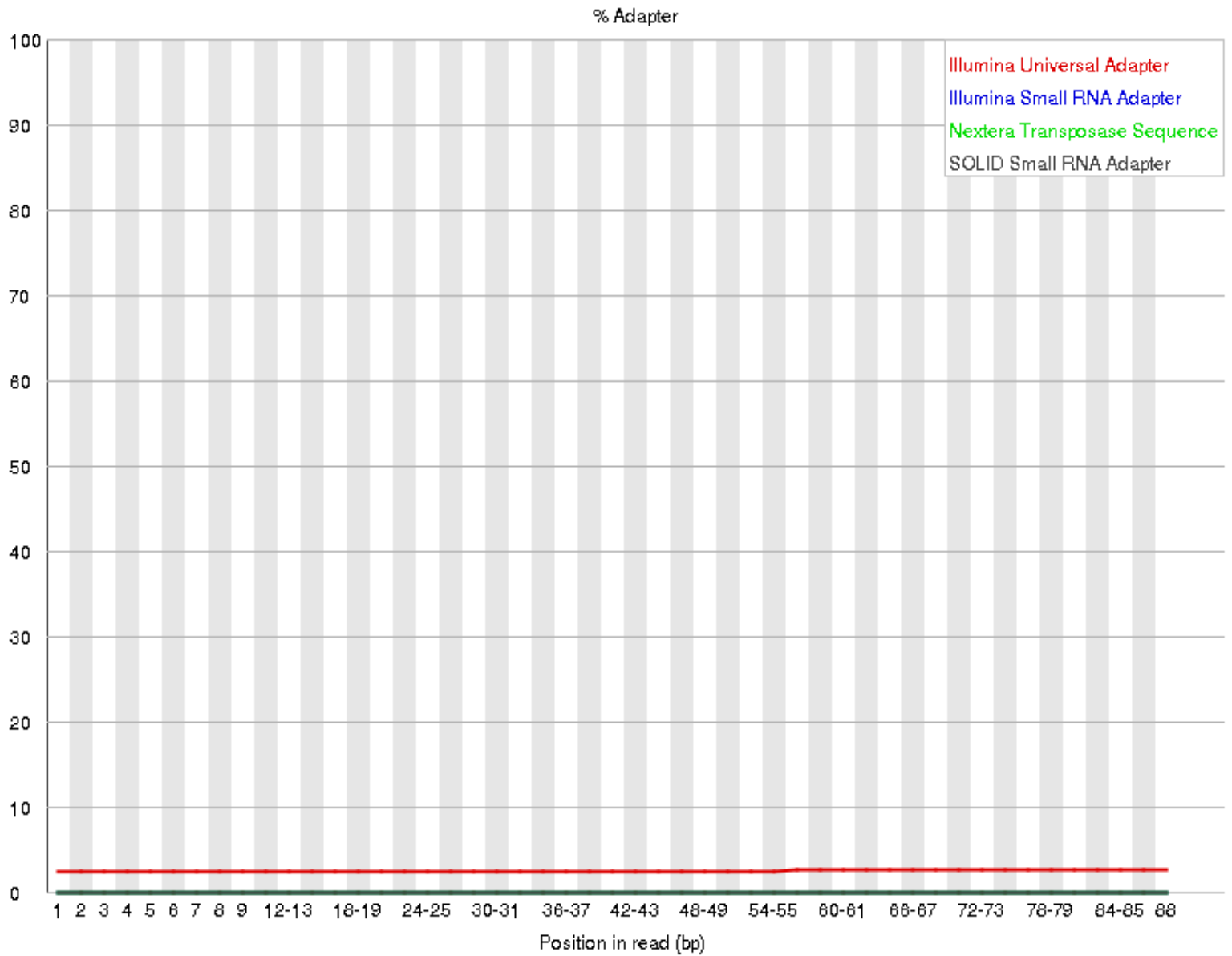




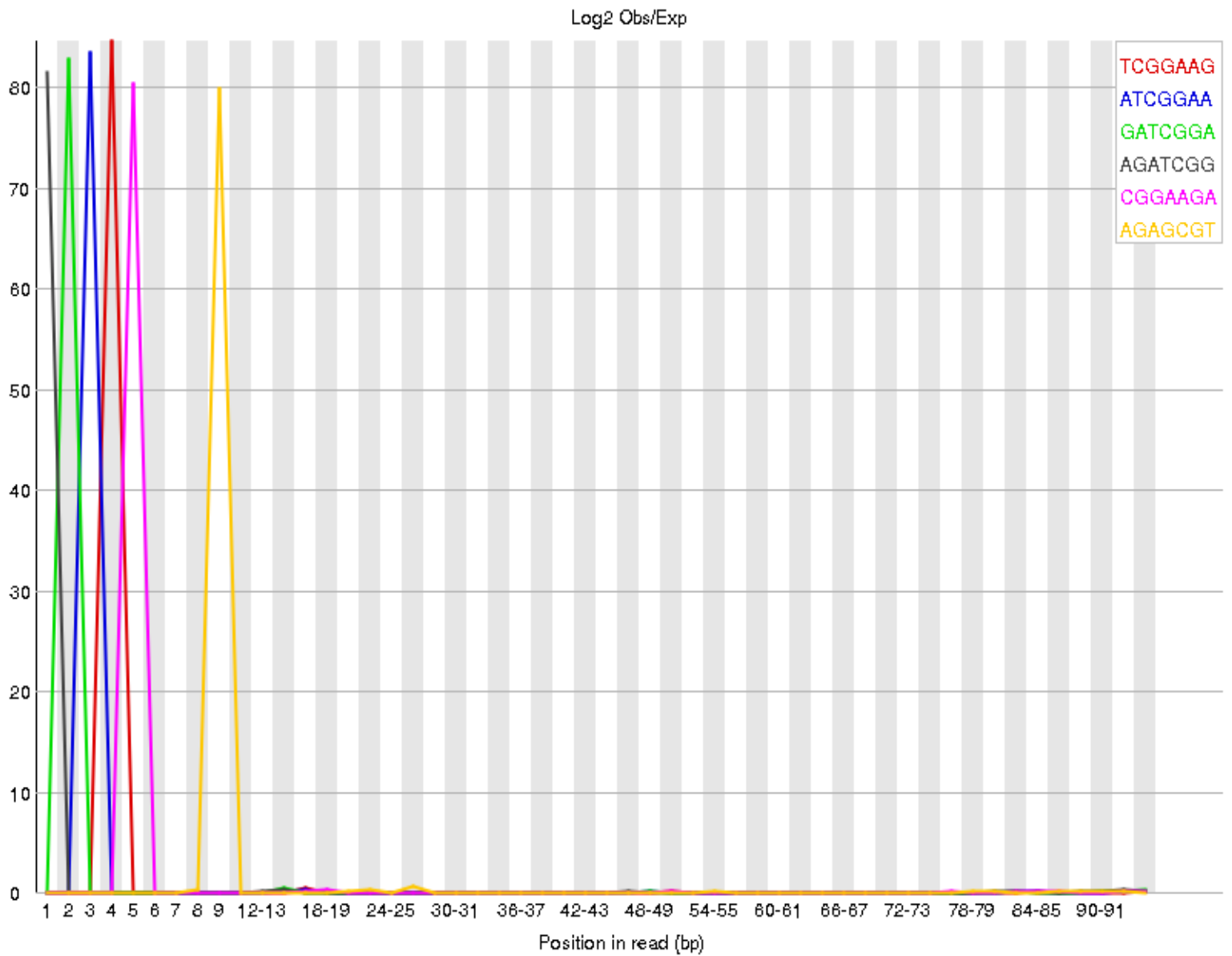
## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAGATCTCGGTGGTCGCC	925185	0.6468950237996133	Illumina Single End PCR Primer 1 (100% over 50bp)

## ✓ Adapter Content



## ✗ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	426665	0.0	84.48367	4
ATCGGAA	432840	0.0	83.43929	3
GATCGGA	436705	0.0	82.8059	2
AGATCGG	443985	0.0	81.55533	1
CGGAAGA	447775	0.0	80.37105	5
AGAGCGT	340610	0.0	79.81413	9
AAGAGCG	368650	0.0	77.7458	8
GAAGAGC	475055	0.0	75.47971	7
GGAAGAG	545930	0.0	66.05819	6

AGCGTCG	304610	0.0	42.809742	10-11
GCGTCGT	302635	0.0	42.476933	12-13
GAGCGTC	315995	0.0	41.618294	10-11
CGTCGTG	310155	0.0	41.513702	12-13
CGTGTAG	313205	0.0	40.23951	16-17
GTCGCCG	167970	0.0	39.512432	44-45
GGTCGCC	168255	0.0	39.505558	44-45
TCGTGTA	326075	0.0	38.73328	14-15
ATCTCGG	204860	0.0	38.170208	36-37
TCGGTGG	208845	0.0	38.104267	38-39
CGCCGTA	147250	0.0	37.725086	46-47

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