













FastQC Report

Summary

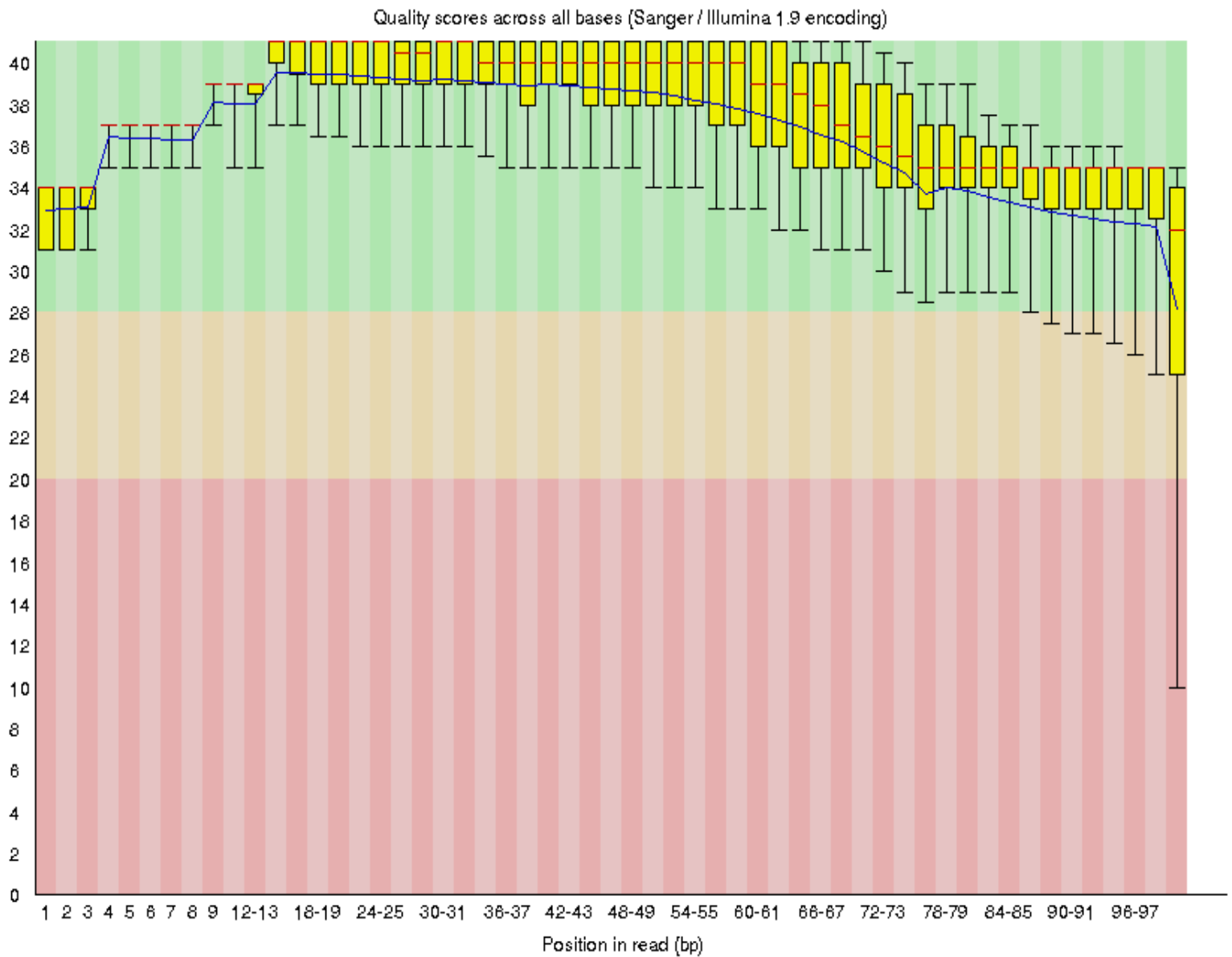
Mon 13 Apr 2015
SW018_S1_L007_R1_001.fastq

-  [Basic Statistics](#)
-  [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](#)
-  [Adapter Content](#)
-  [Kmer Content](#)

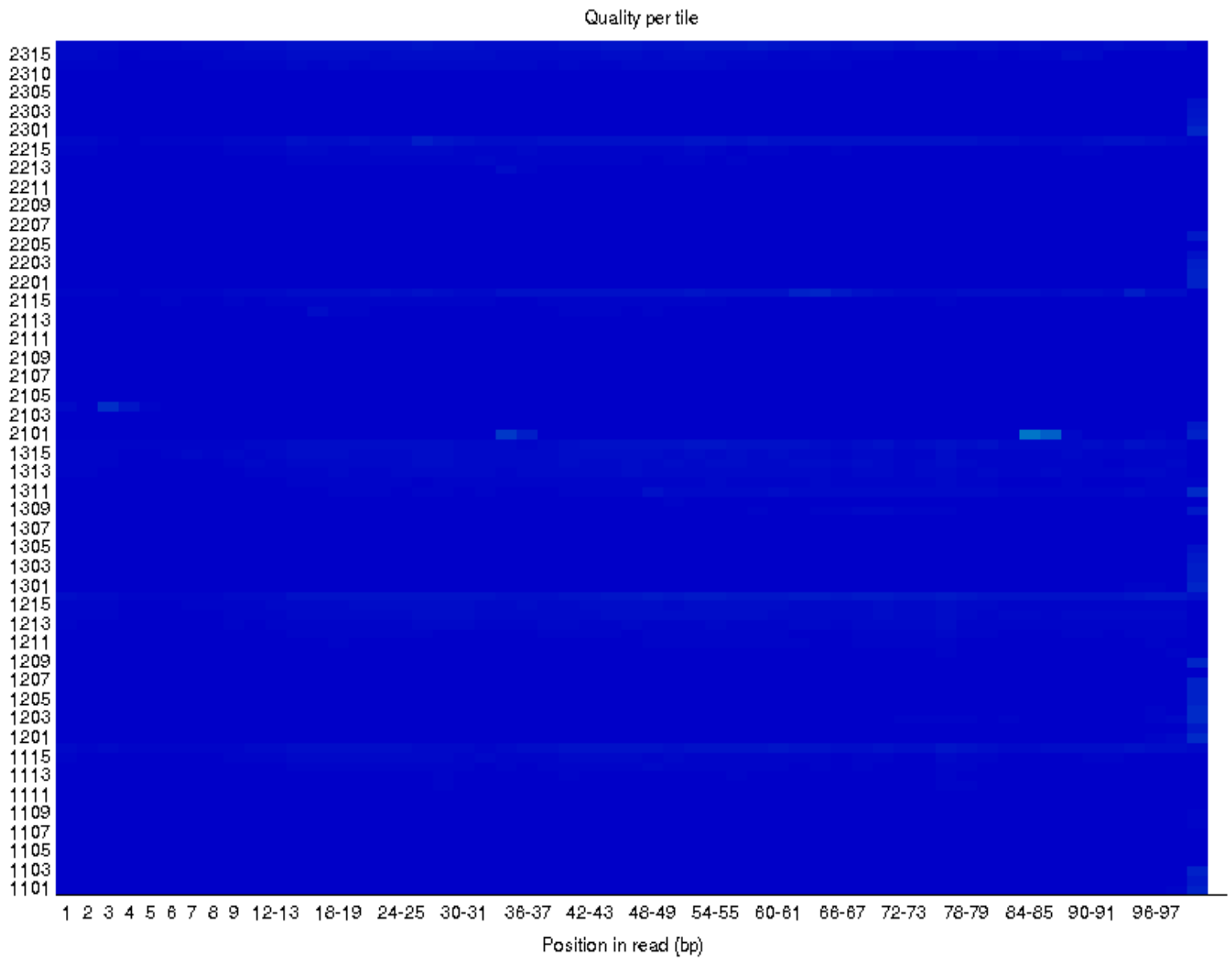
Basic Statistics

Measure	Value
Filename	SW018_S1_L007_R1_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

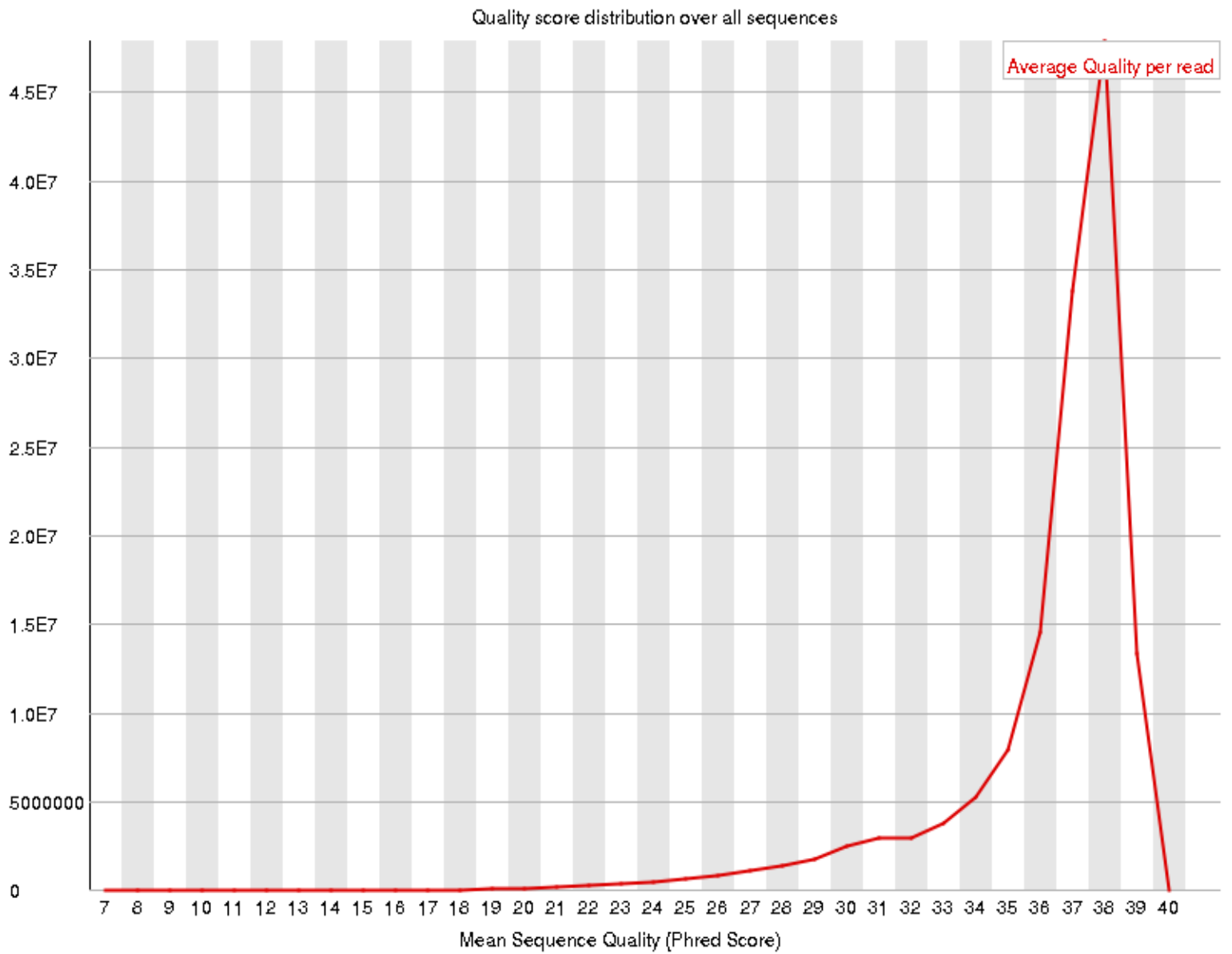
✓ Per base sequence quality



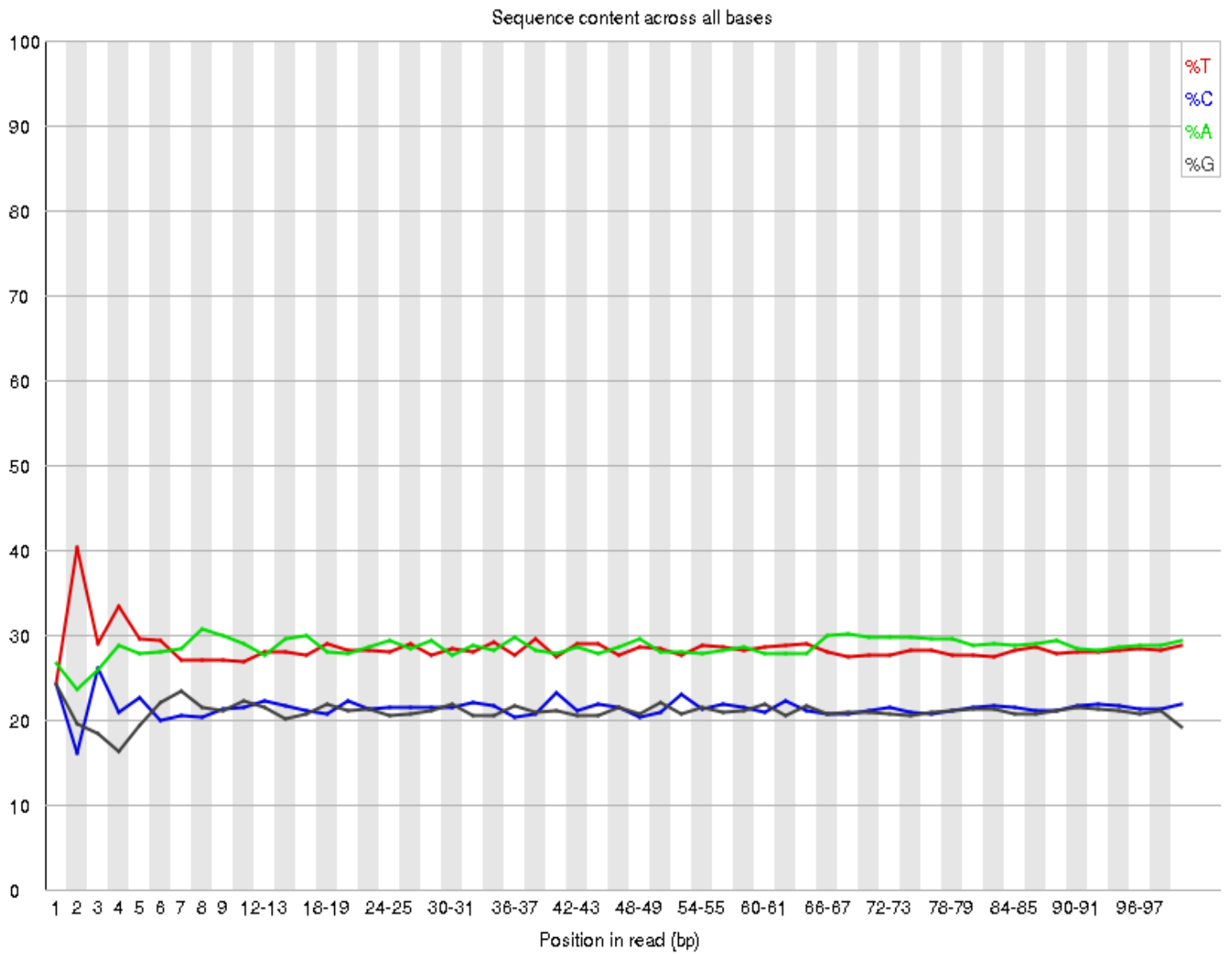
✓ Per tile sequence quality



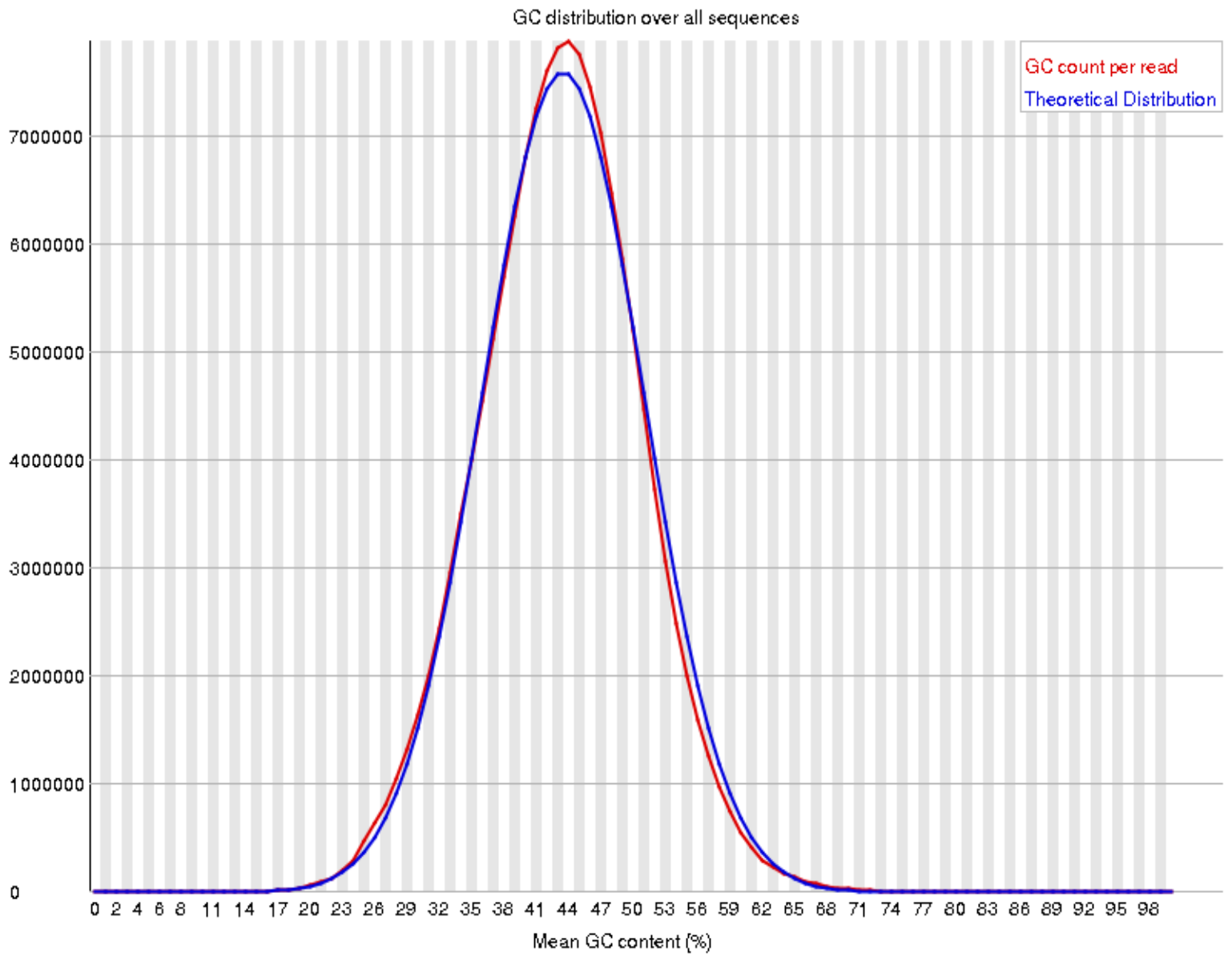
Per sequence quality scores



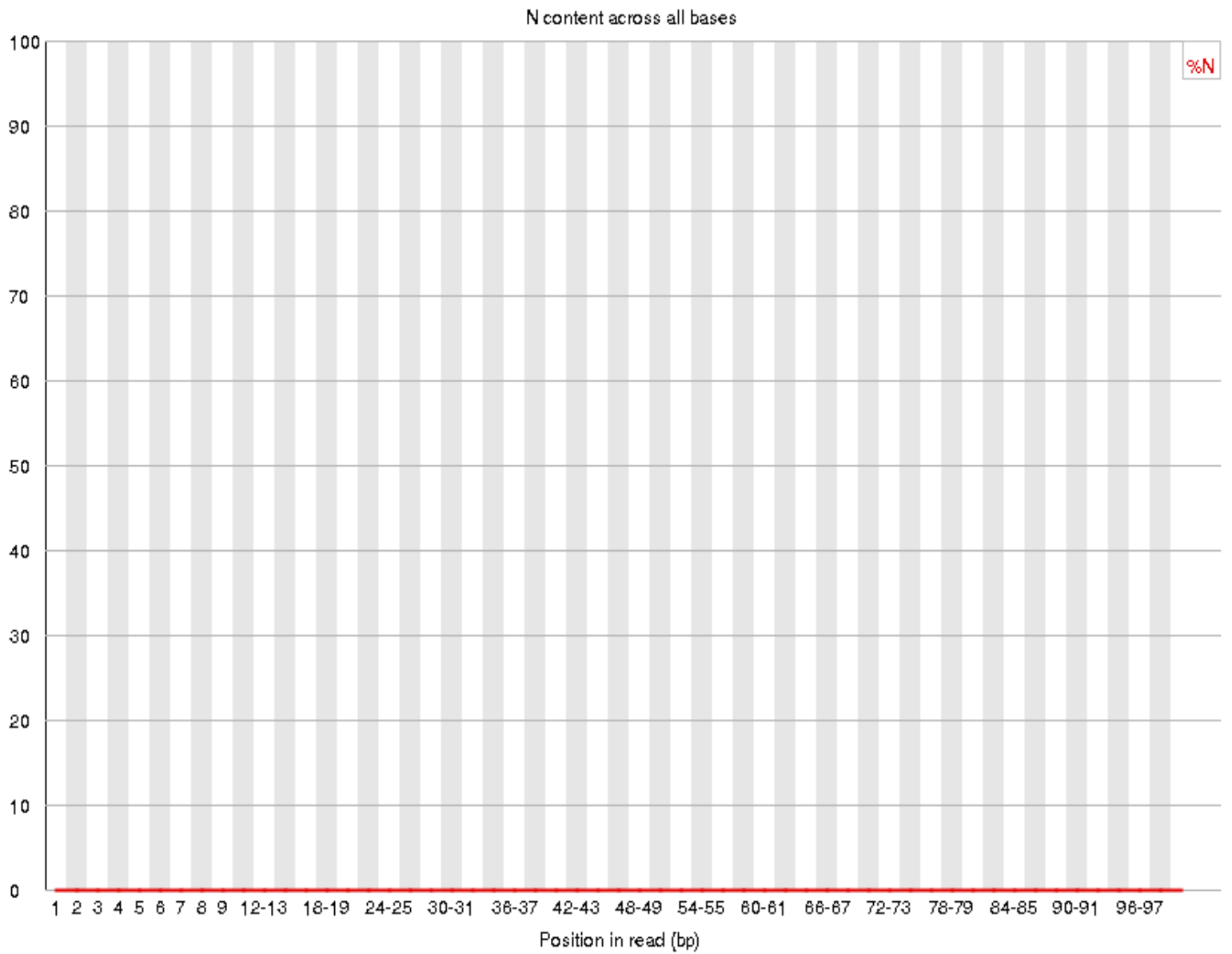
Per base sequence content



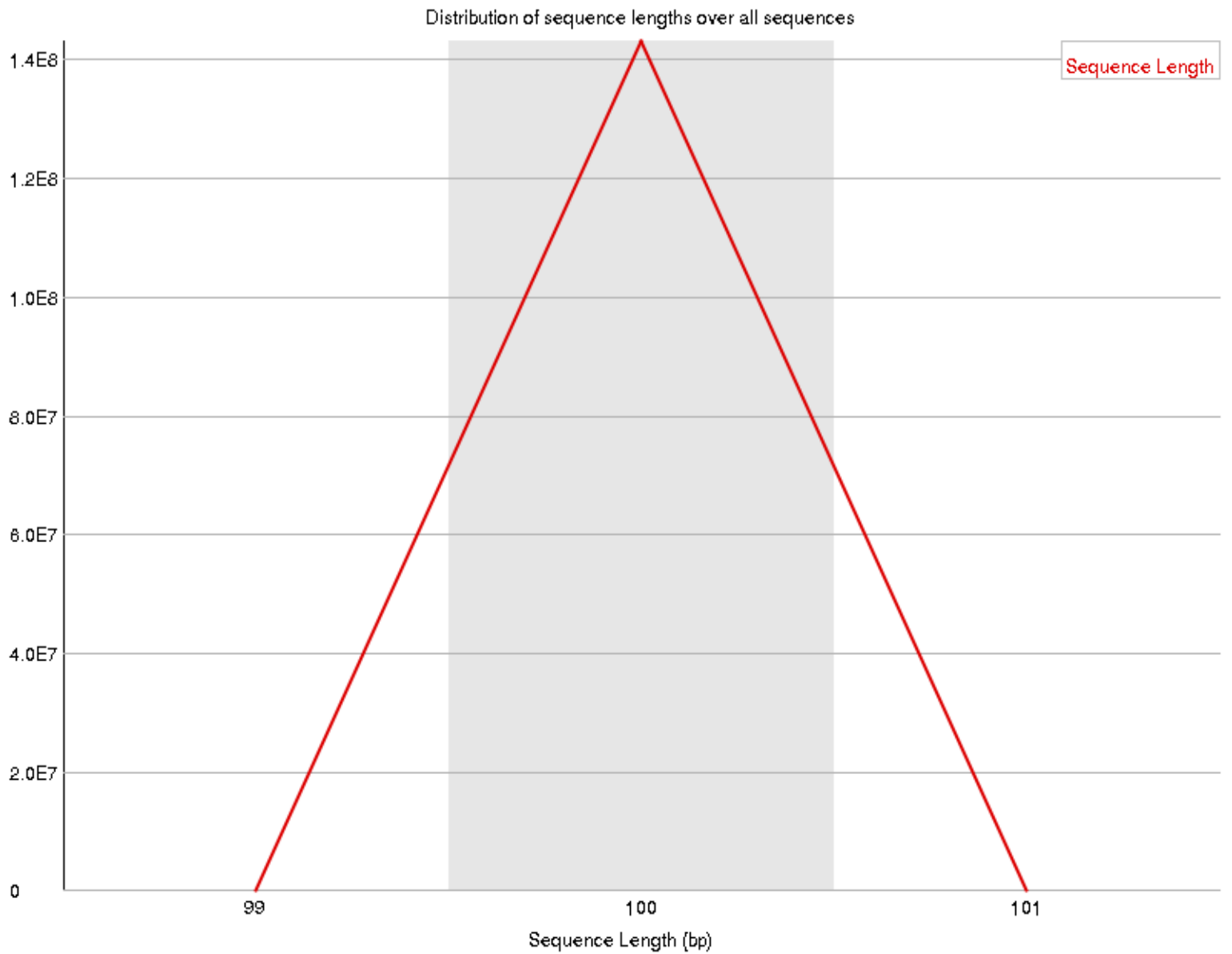
Per sequence GC content



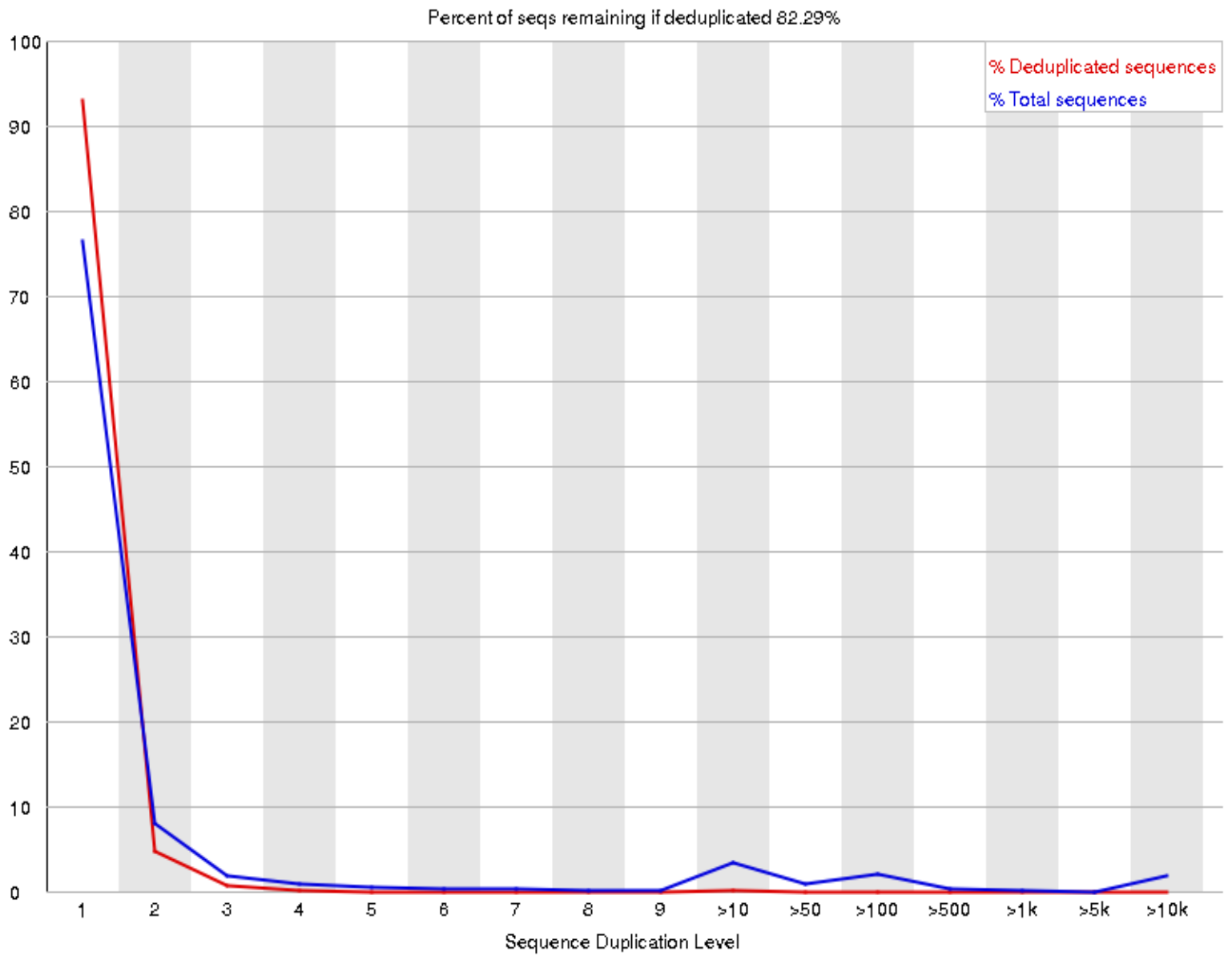
 **Per base N content**



Sequence Length Distribution



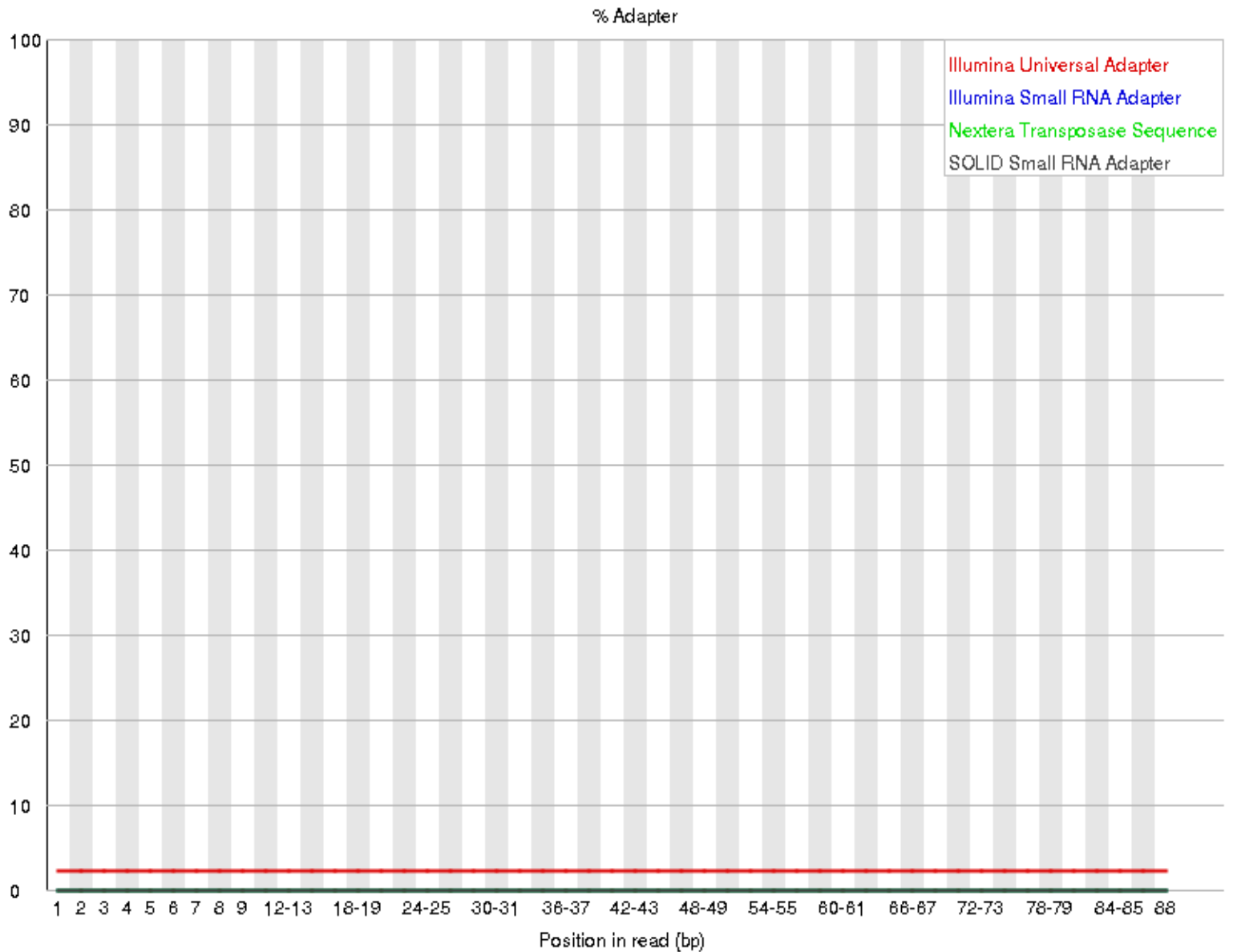
Sequence Duplication Levels



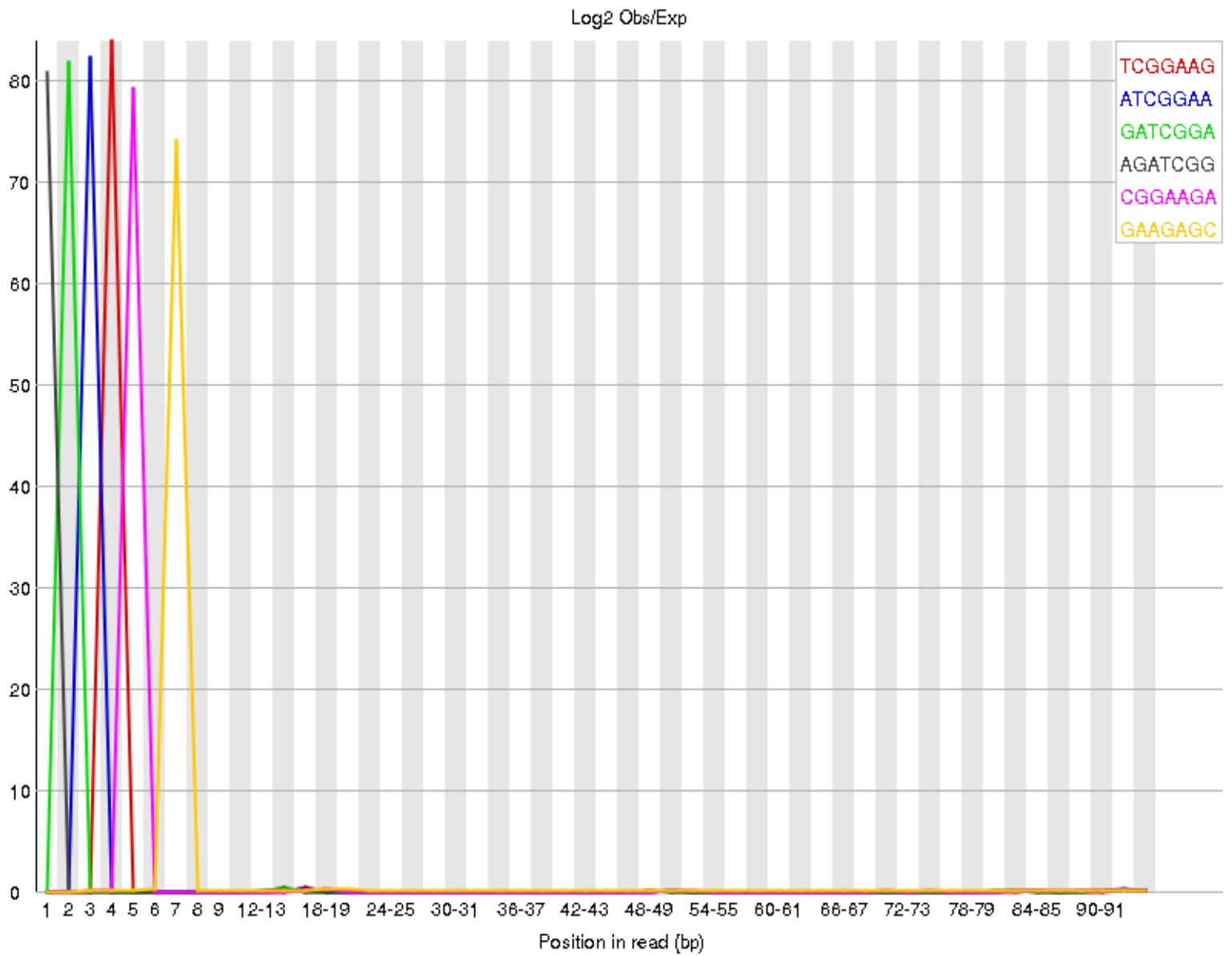
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTAGTTCCATCTCGTAT	2637049	1.8438408270948472	TruSeq Adapter, Index 10 (97% over 38bp)

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	393425	0.0	83.77254	4
ATCGGAA	401260	0.0	82.24104	3
GATCGGA	402755	0.0	81.83779	2
AGATCGG	407805	0.0	80.862564	1
CGGAAGA	415850	0.0	79.20886	5
GAAGAGC	444645	0.0	73.96697	7
AGAGCAC	373320	0.0	71.69977	9
GGAAGAG	509765	0.0	64.716255	6

AAGAGCA	447620	0.0	62.980602	8
TATGCCG	310195	0.0	41.71756	48-49
CGTATGC	313305	0.0	41.33026	46-47
ATGCCGT	318075	0.0	40.89091	48-49
GCCGTCT	318990	0.0	40.74908	50-51
TGCCGTC	321415	0.0	40.147	50-51
GAACTCC	330225	0.0	39.78145	22-23
TCTCGTA	327420	0.0	39.39103	42-43
GCACACG	335910	0.0	39.257057	12-13
TAGTTCC	335910	0.0	38.8918	34-35
CACGTCT	342465	0.0	38.646175	14-15
GTATGCC	339210	0.0	38.513374	46-47

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