









FastQC Report

Summary

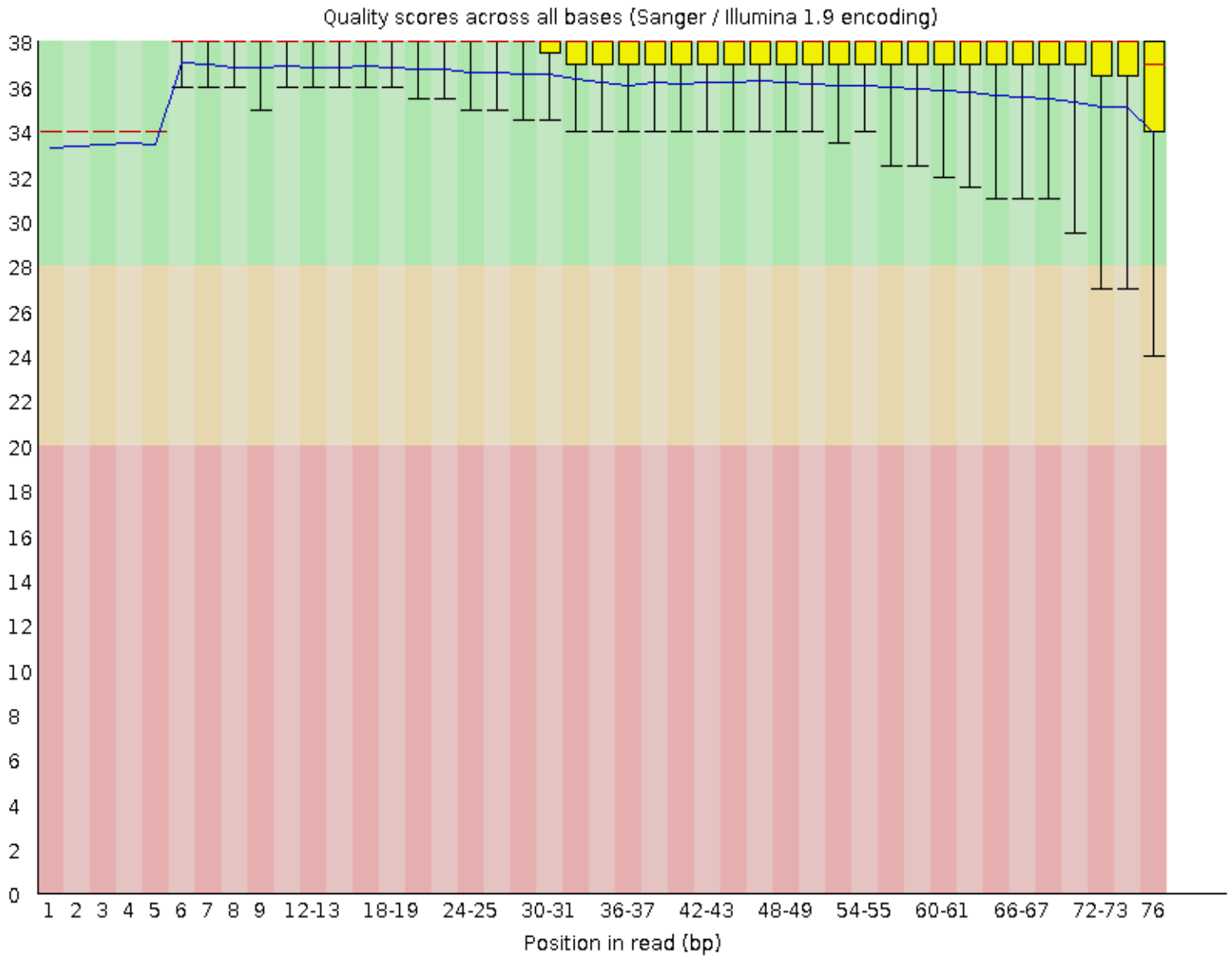
Mon 11 May 2015
SW041.r2.trimmed.fastq

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Basic Statistics

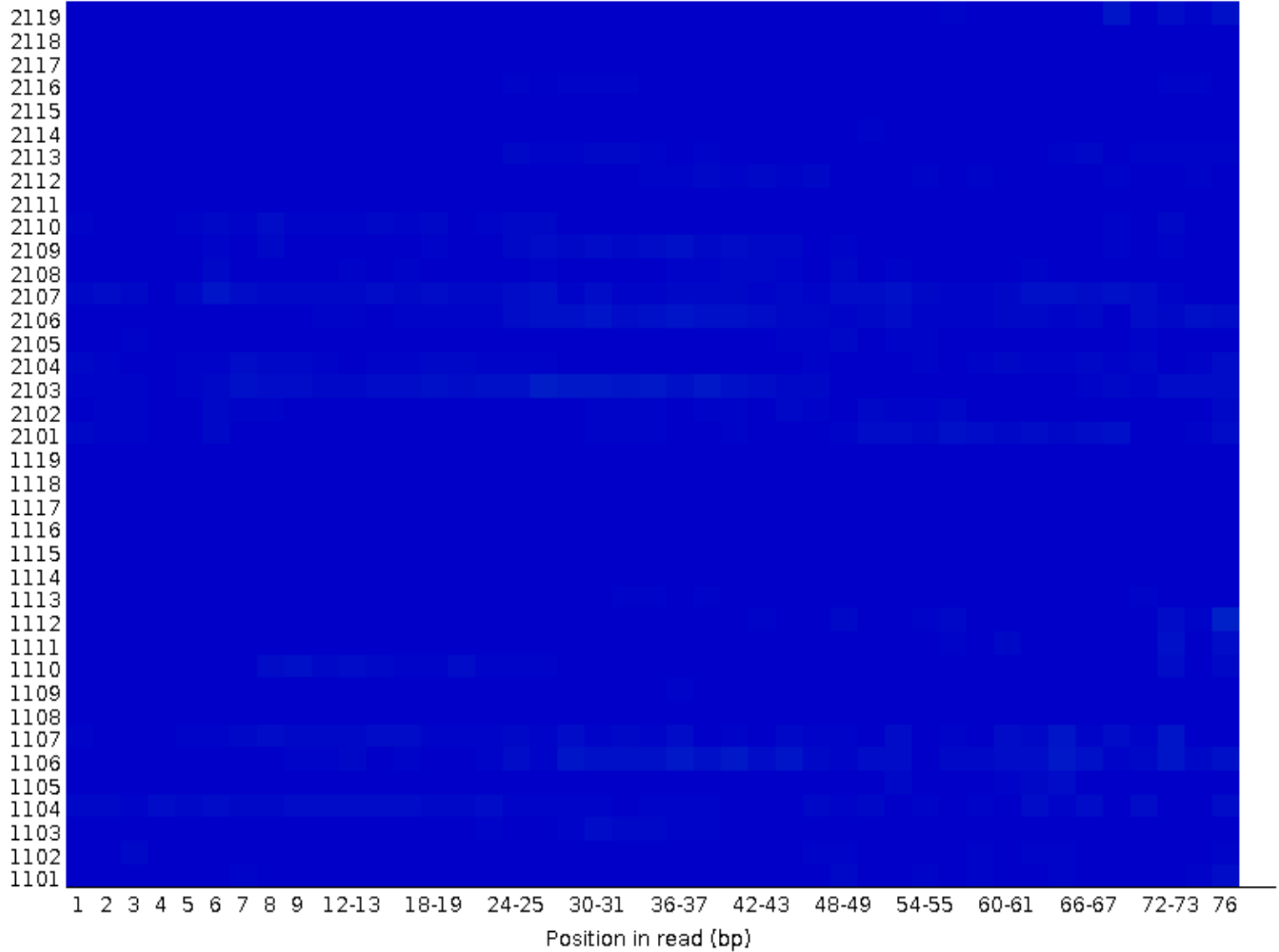
Measure	Value
Filename	SW041.r2.trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1449494
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

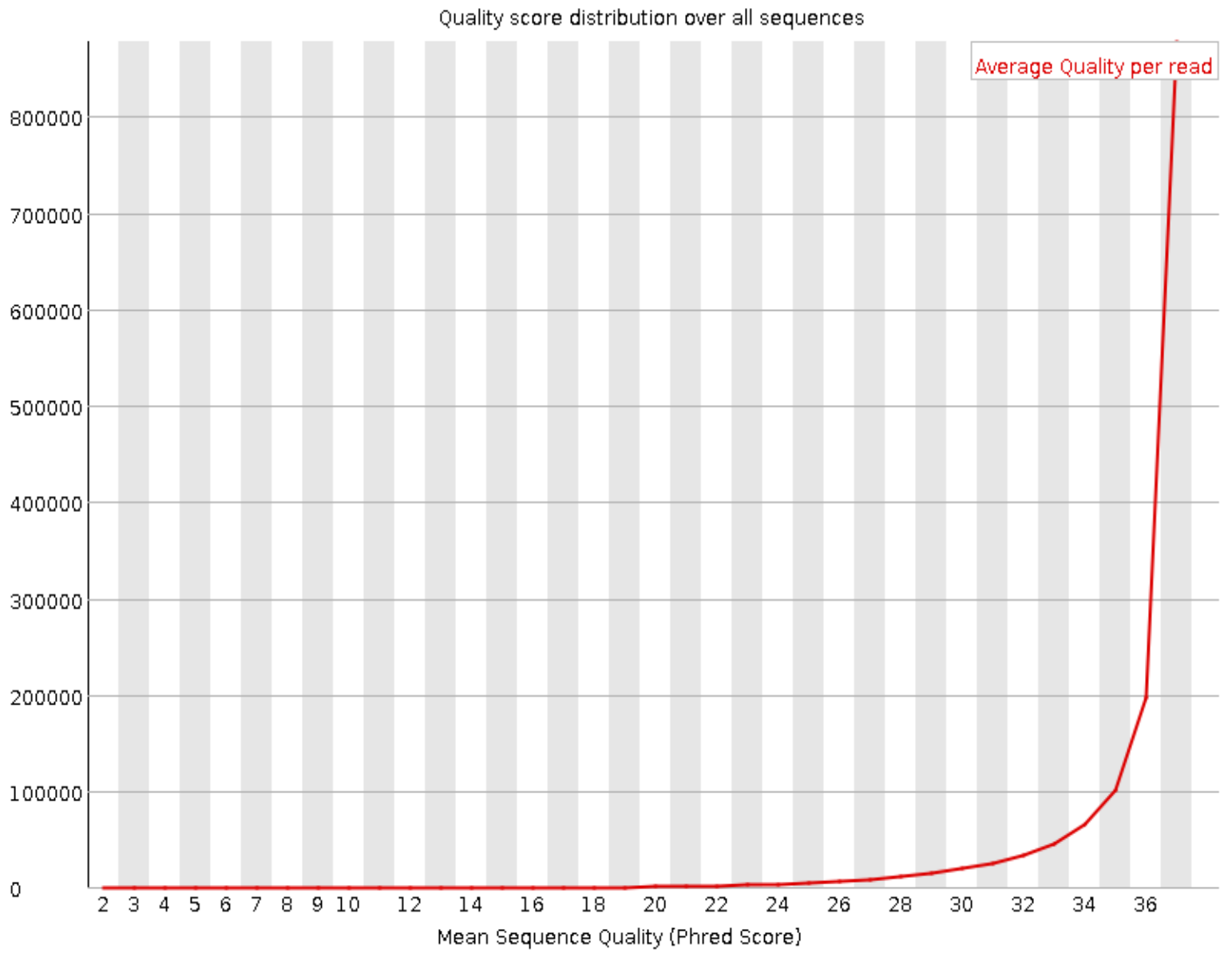
✔ Per base sequence quality



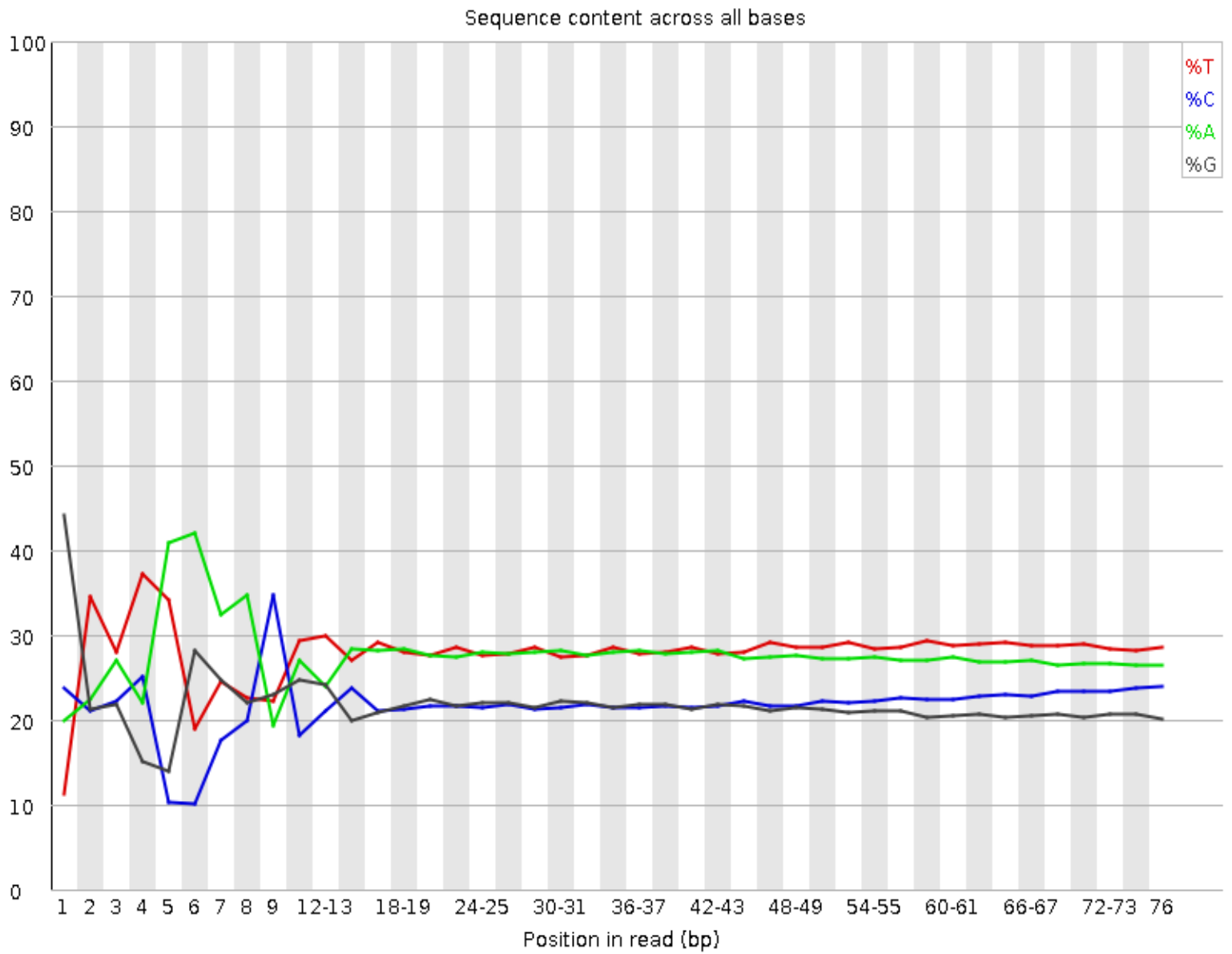
✔ Per tile sequence quality

Quality per tile

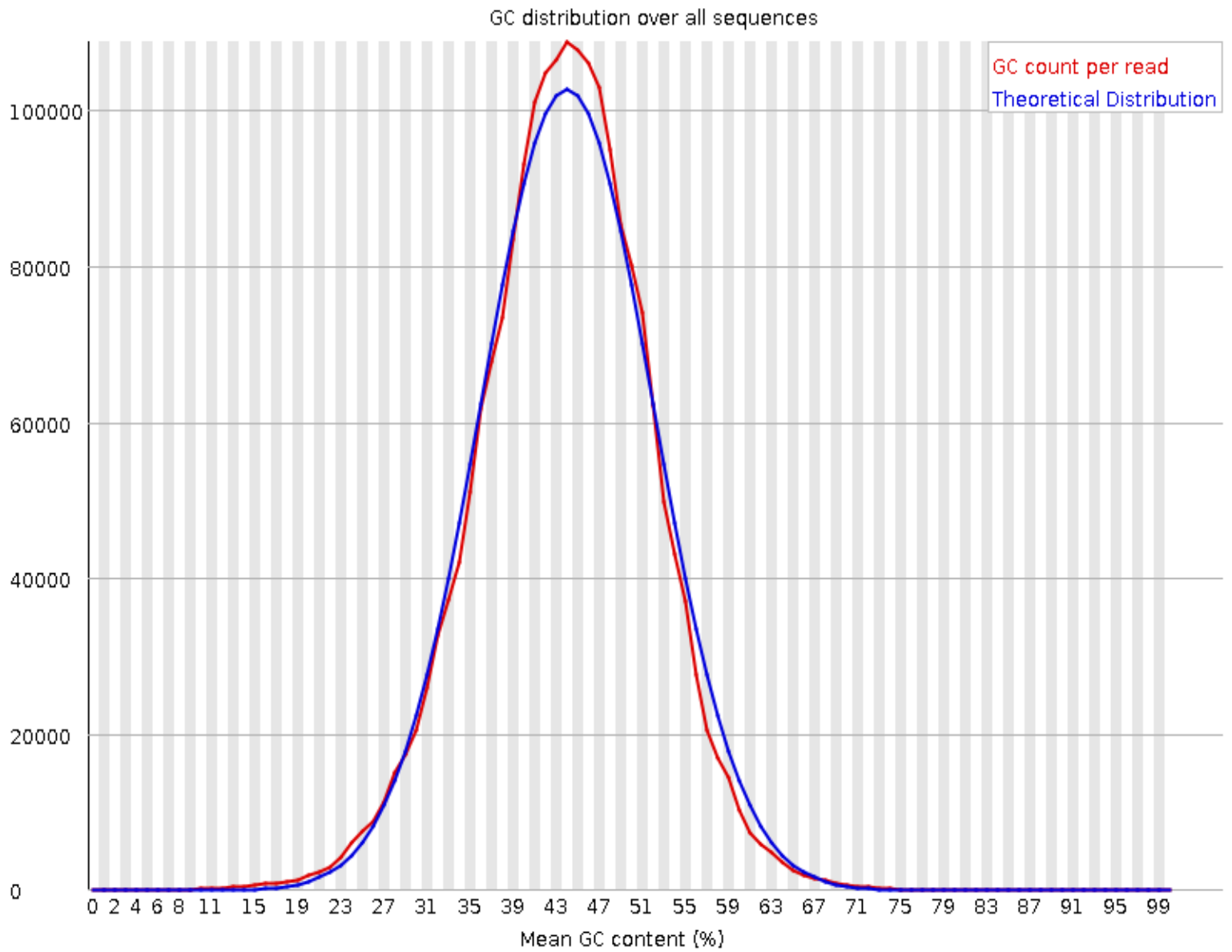
 **Per sequence quality scores**



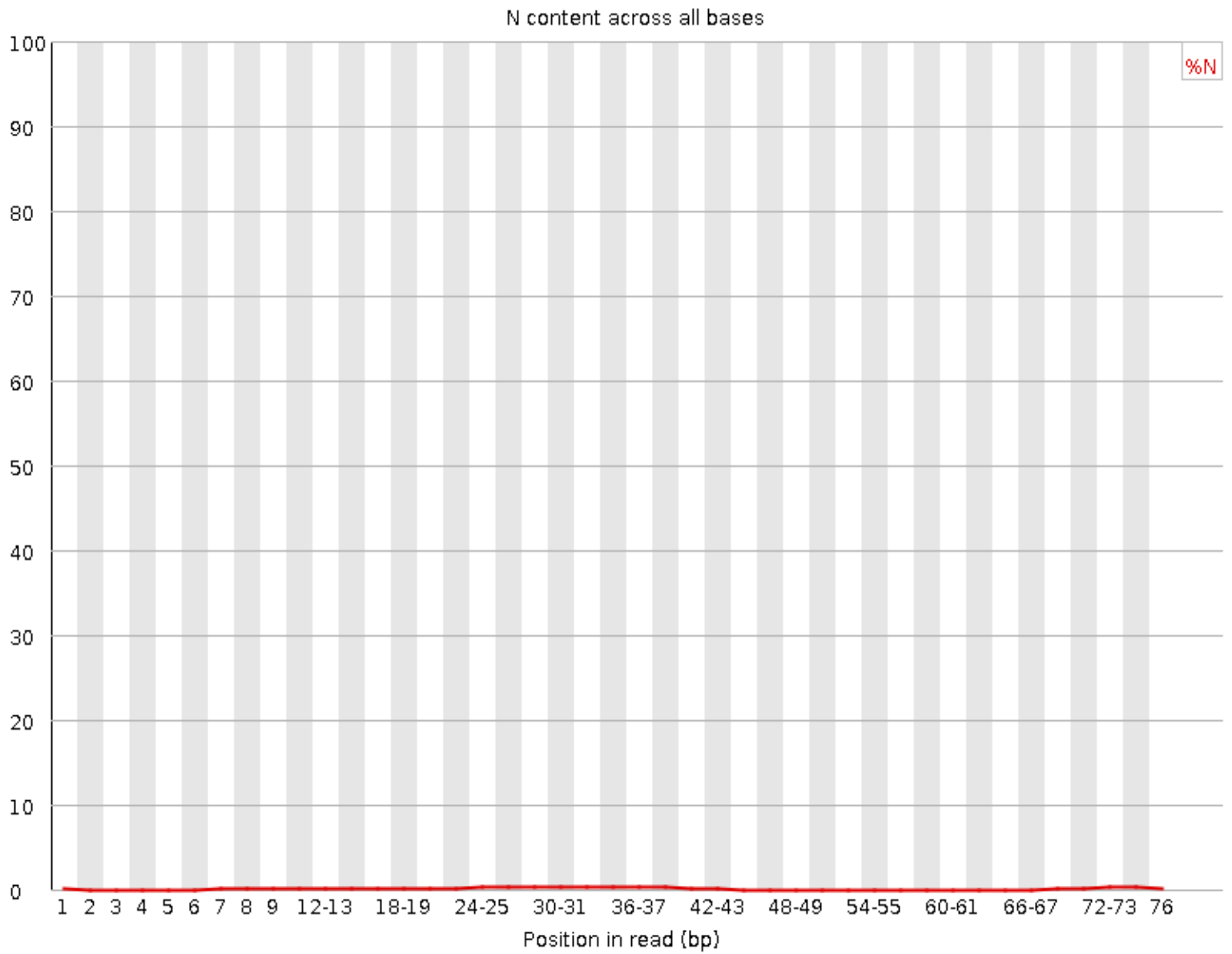
Per base sequence content



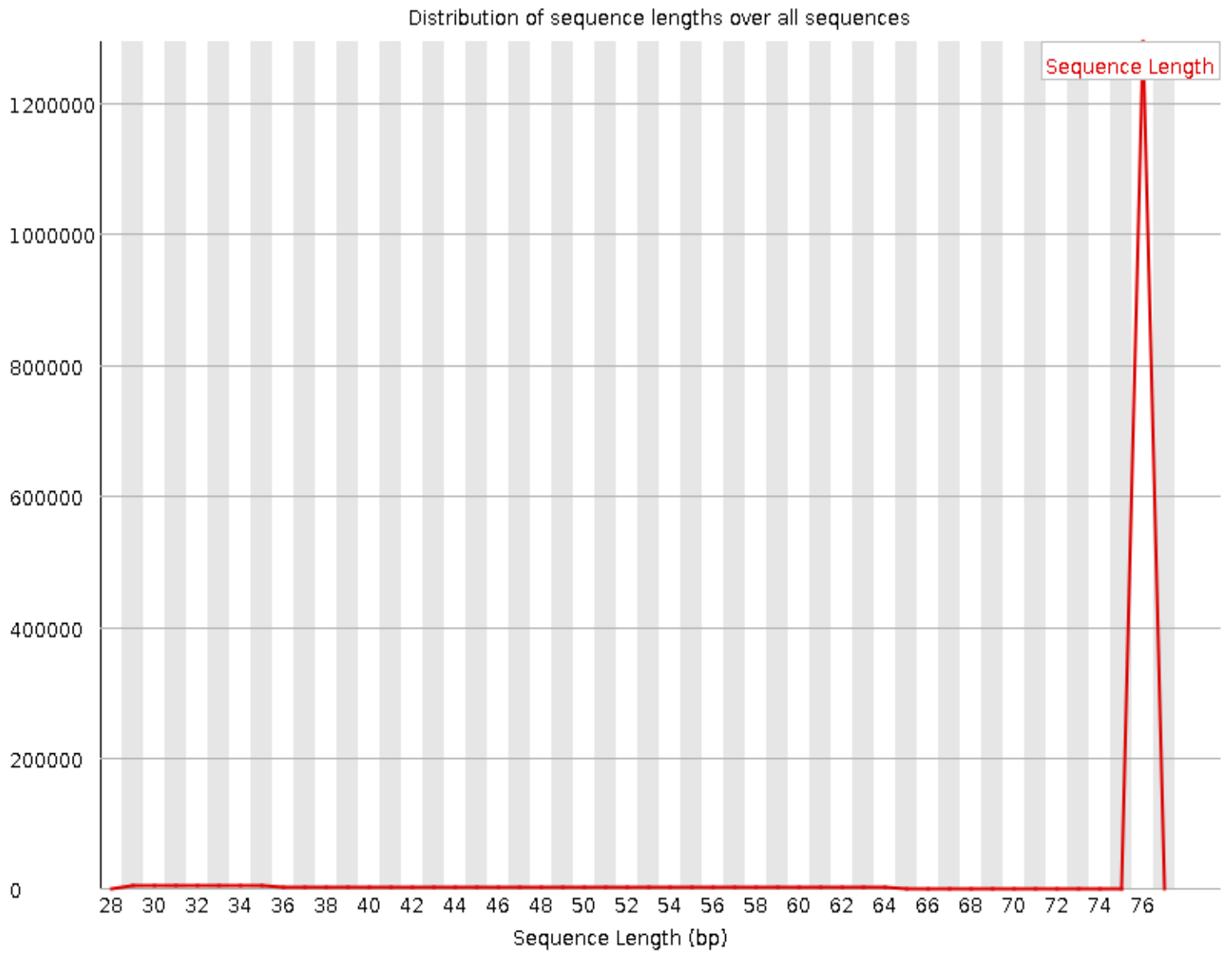
 **Per sequence GC content**



 **Per base N content**

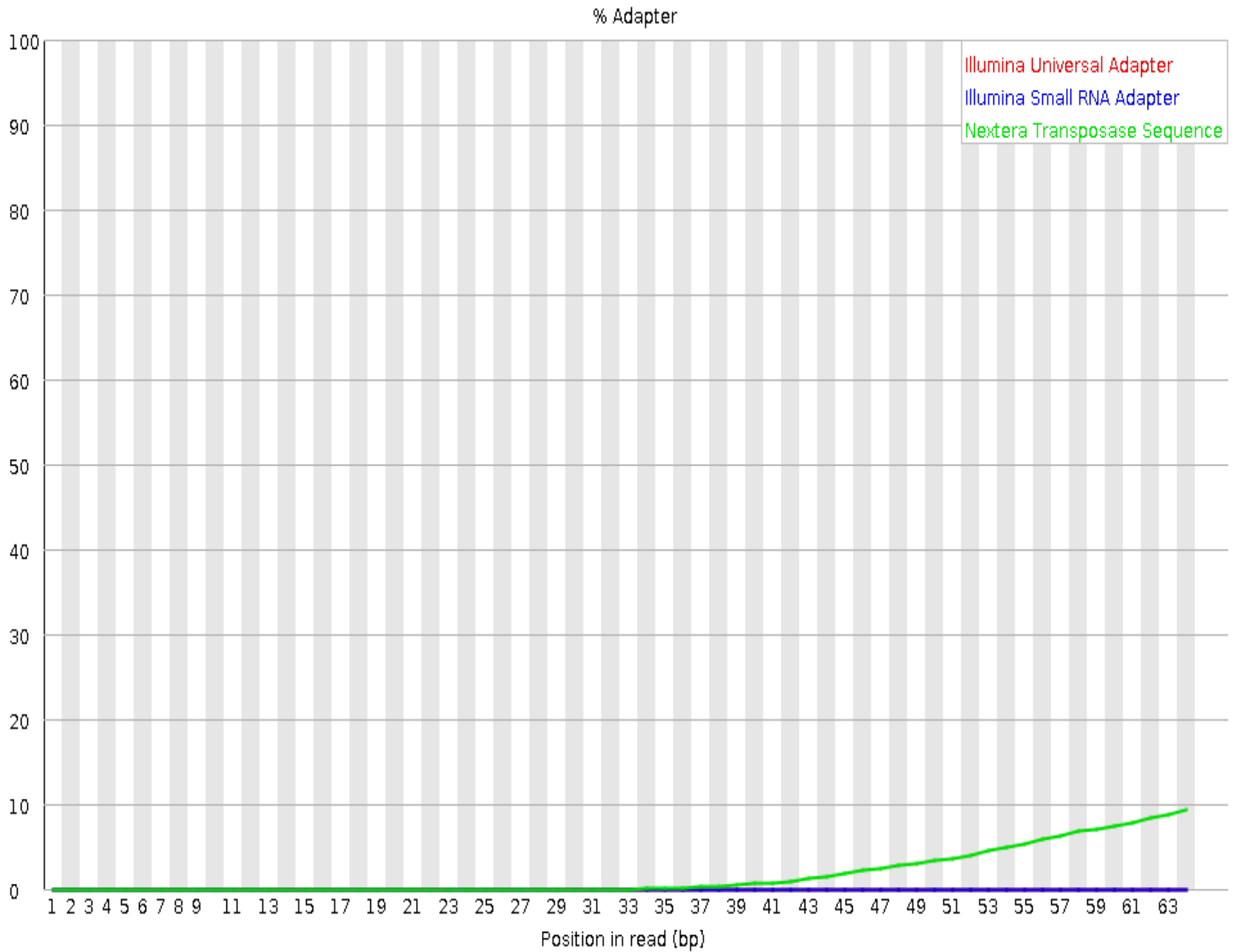


Sequence Length Distribution

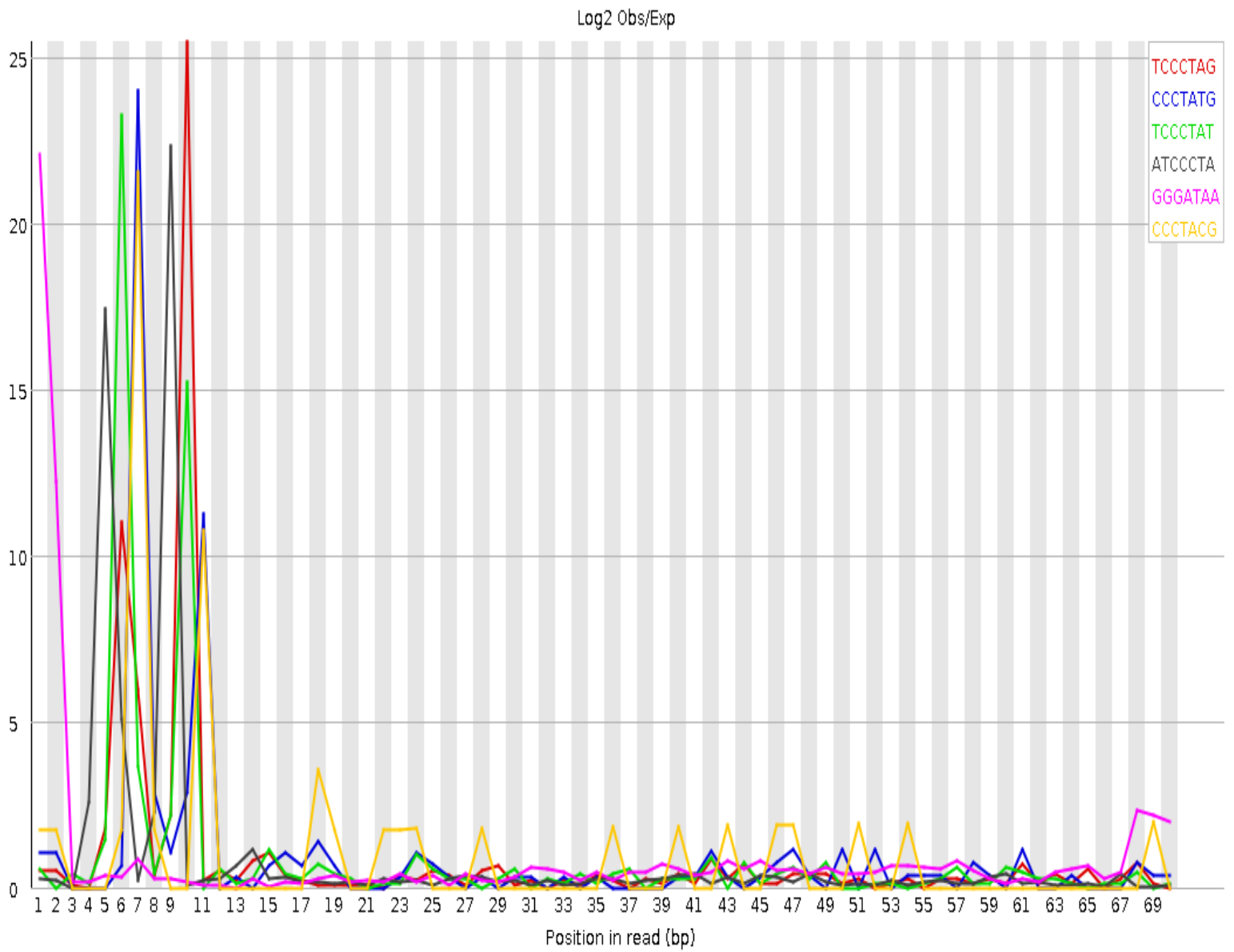


Sequence Duplication Levels

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCCCTAG	2380	0.0	25.489286	10
CCCTATG	915	0.0	24.02373	7
TCCCTAT	2245	0.0	23.289268	6
ATCCCTA	7700	0.0	22.380154	9
GGGATAA	9825	0.0	22.145144	1
CCCTACG	185	7.512426E-10	21.603647	7
ATAACAG	10475	0.0	20.984201	4
CCCTAGA	960	0.0	20.83259	11
CCCTGTT	8780	0.0	20.51777	2

CCTGTTA	8780	0.0	20.217863	3
CTGTTAT	8835	0.0	20.20509	4
AGGGTAA	10610	0.0	20.16893	9
CAGGGTA	10690	0.0	20.10736	8
GGATAAC	11025	0.0	19.813112	2
CCCTAGT	970	0.0	19.58693	11
ACCCTGT	9155	0.0	19.580412	1
TATCCCT	9045	0.0	19.490374	8
GATAACA	11265	0.0	19.453478	3
ACAGGGT	11530	0.0	18.862595	7
GGTAAT	11035	0.0	18.697414	10

Produced by [FastQC](#) (version 0.11.2)