






FastQC Report

Summary

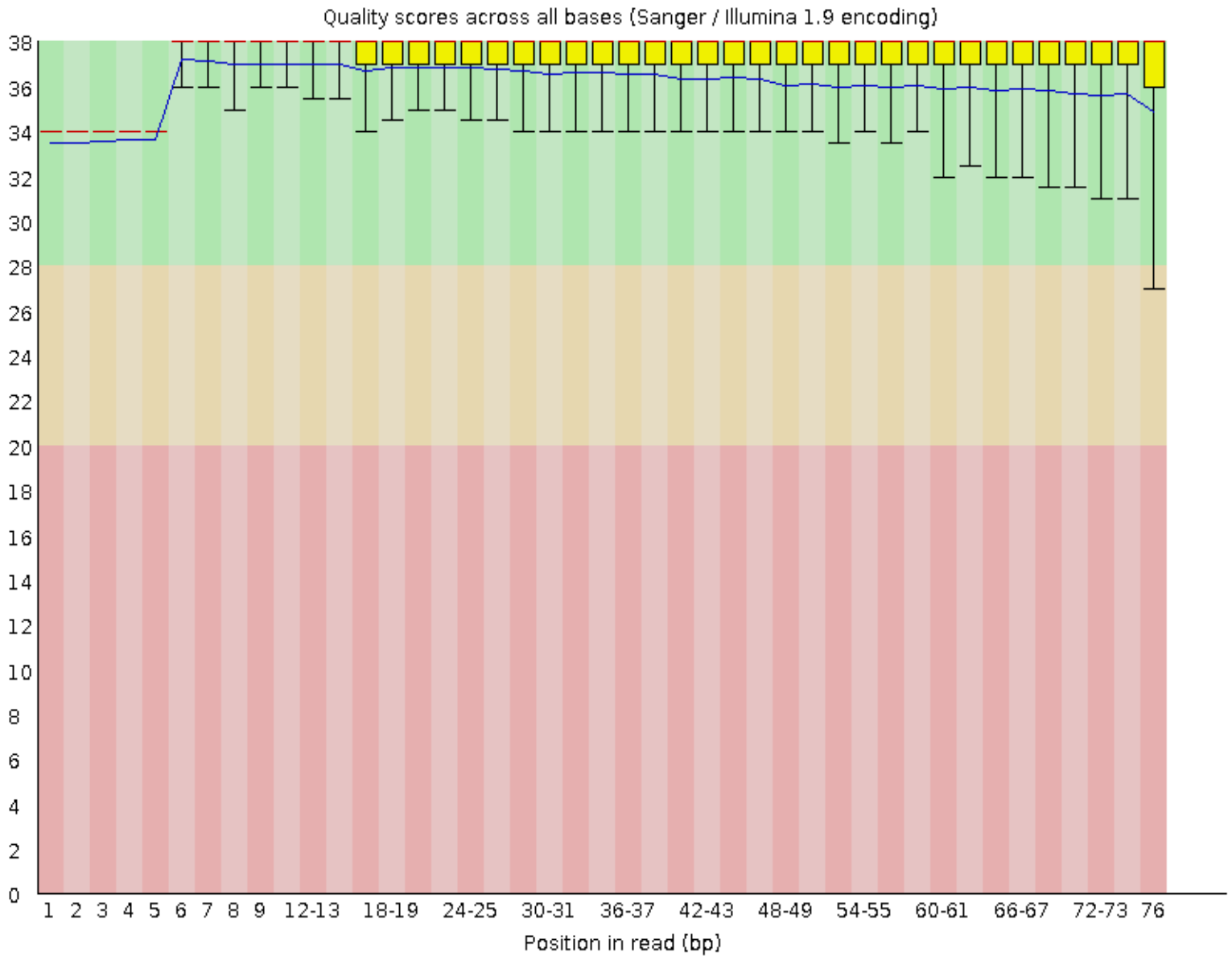
Mon 11 May 2015
SW041.r1.trimmed.fastq

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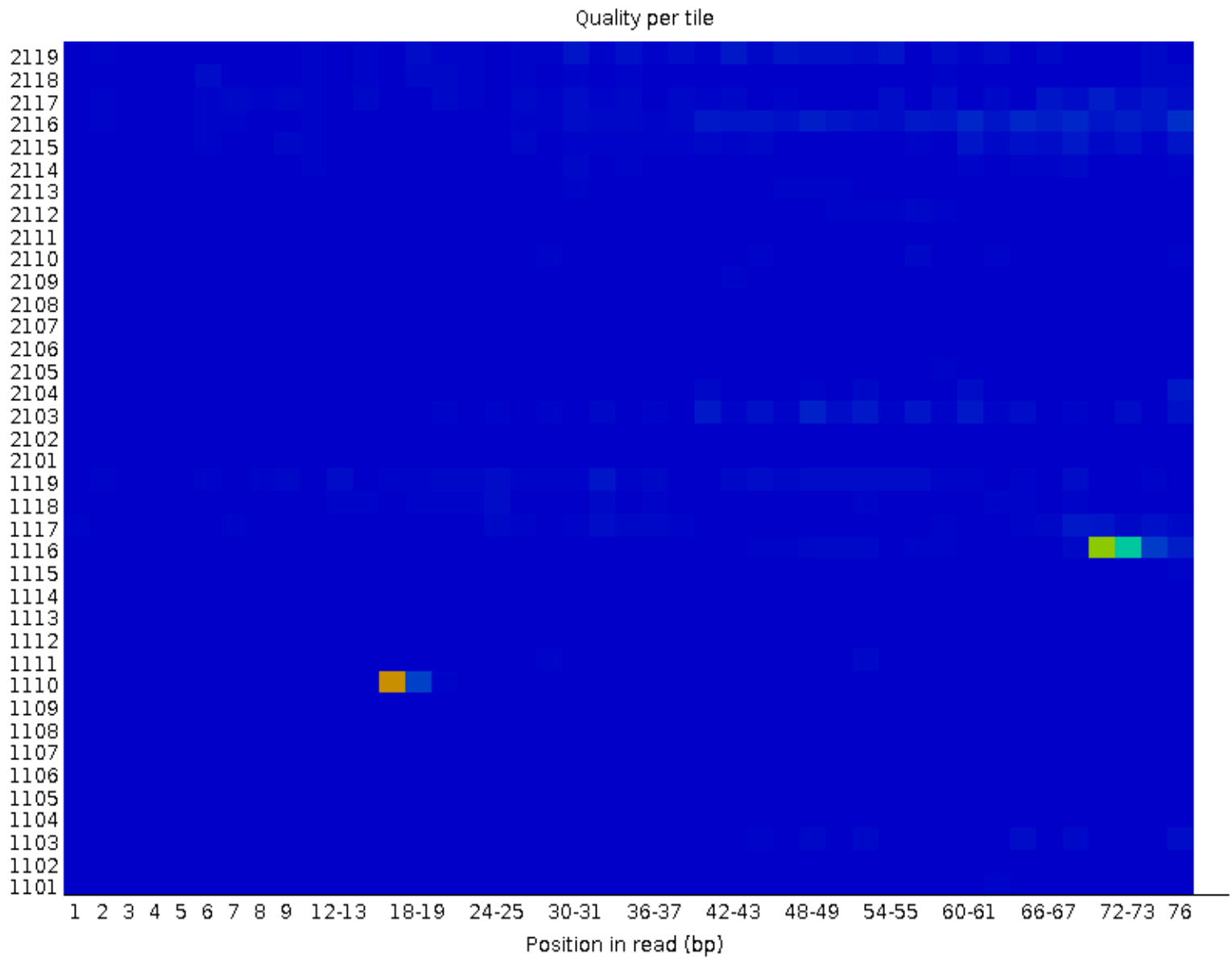
Basic Statistics

Measure	Value
Filename	SW041.r1.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

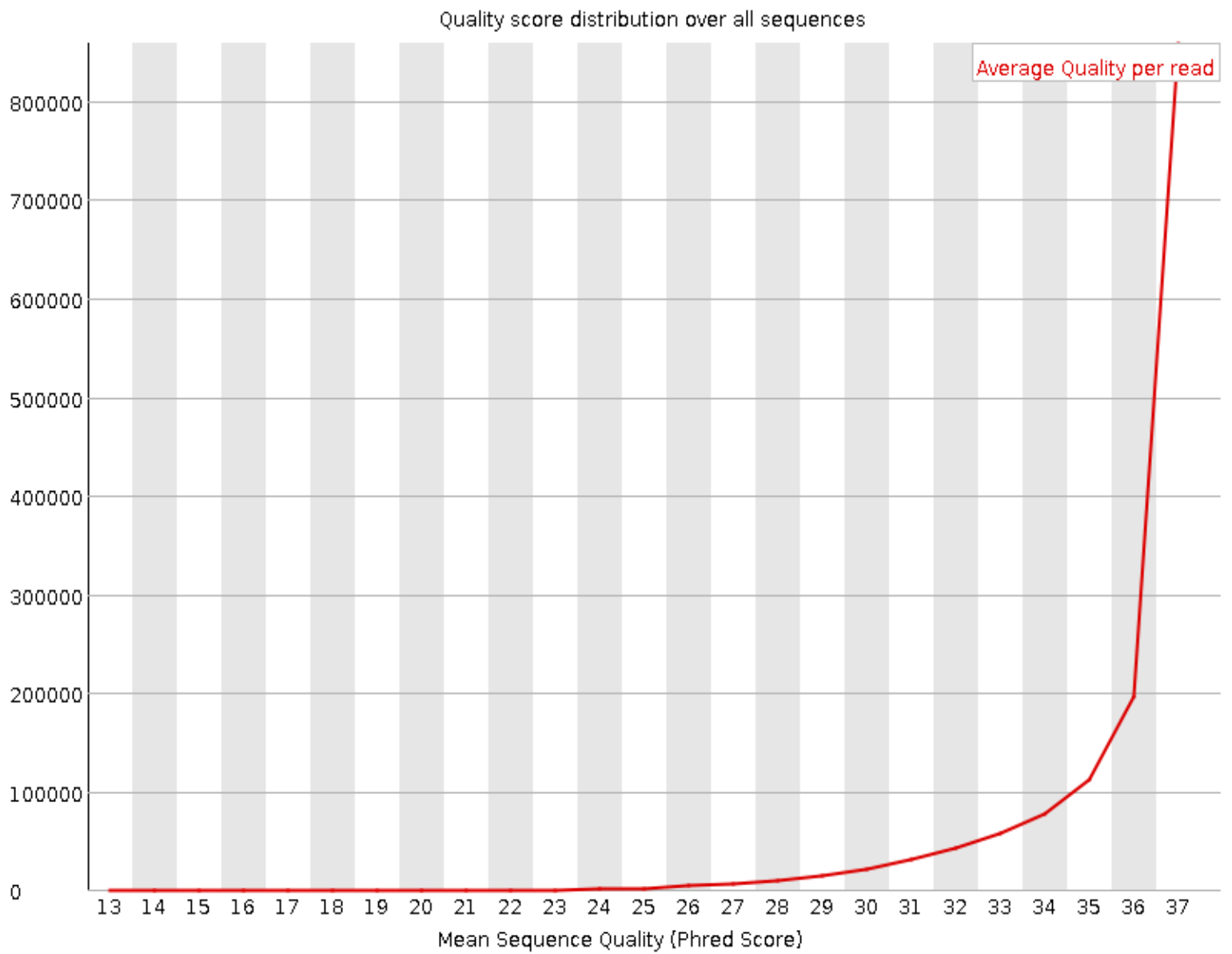
✔ Per base sequence quality



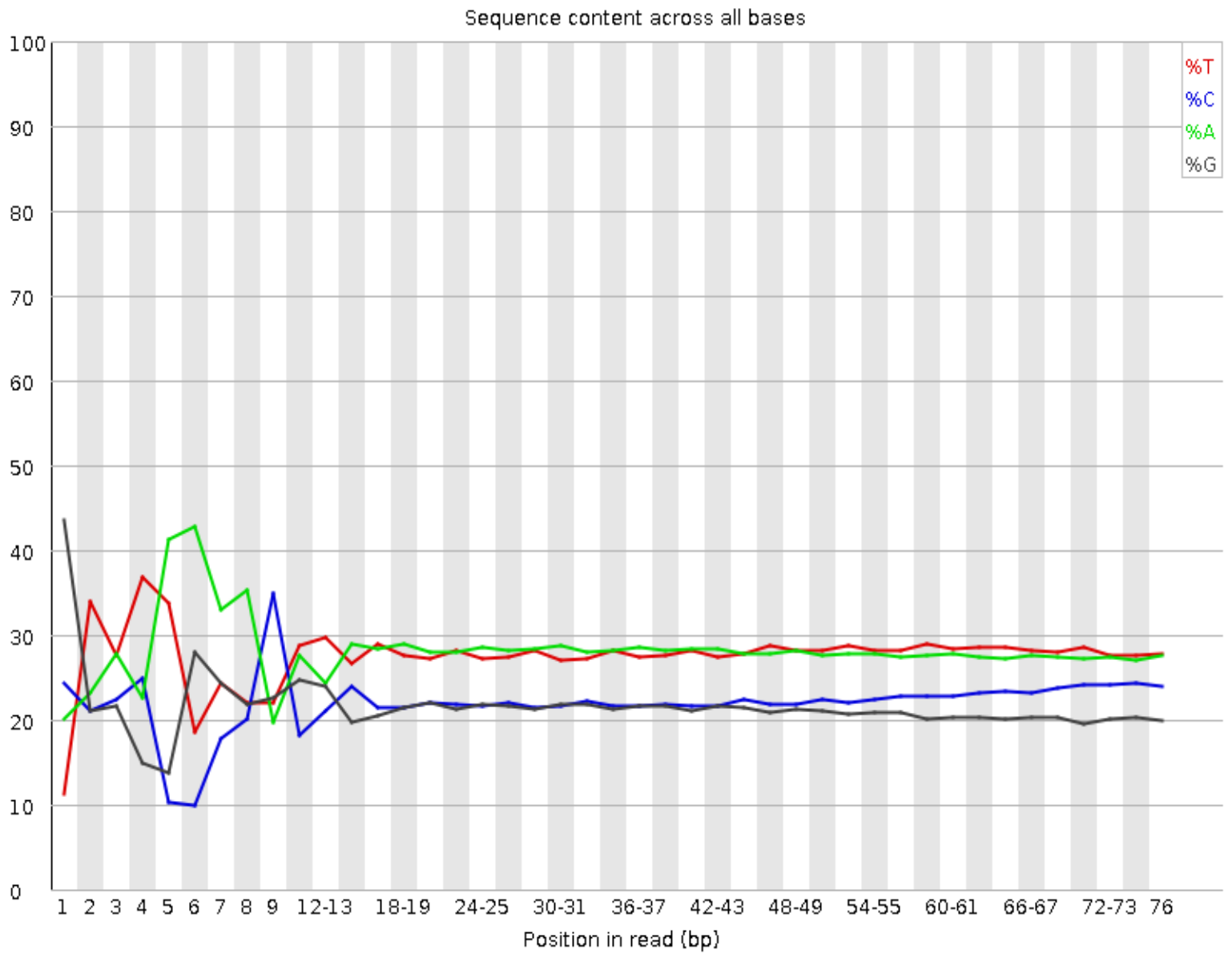
⚠ Per tile sequence quality



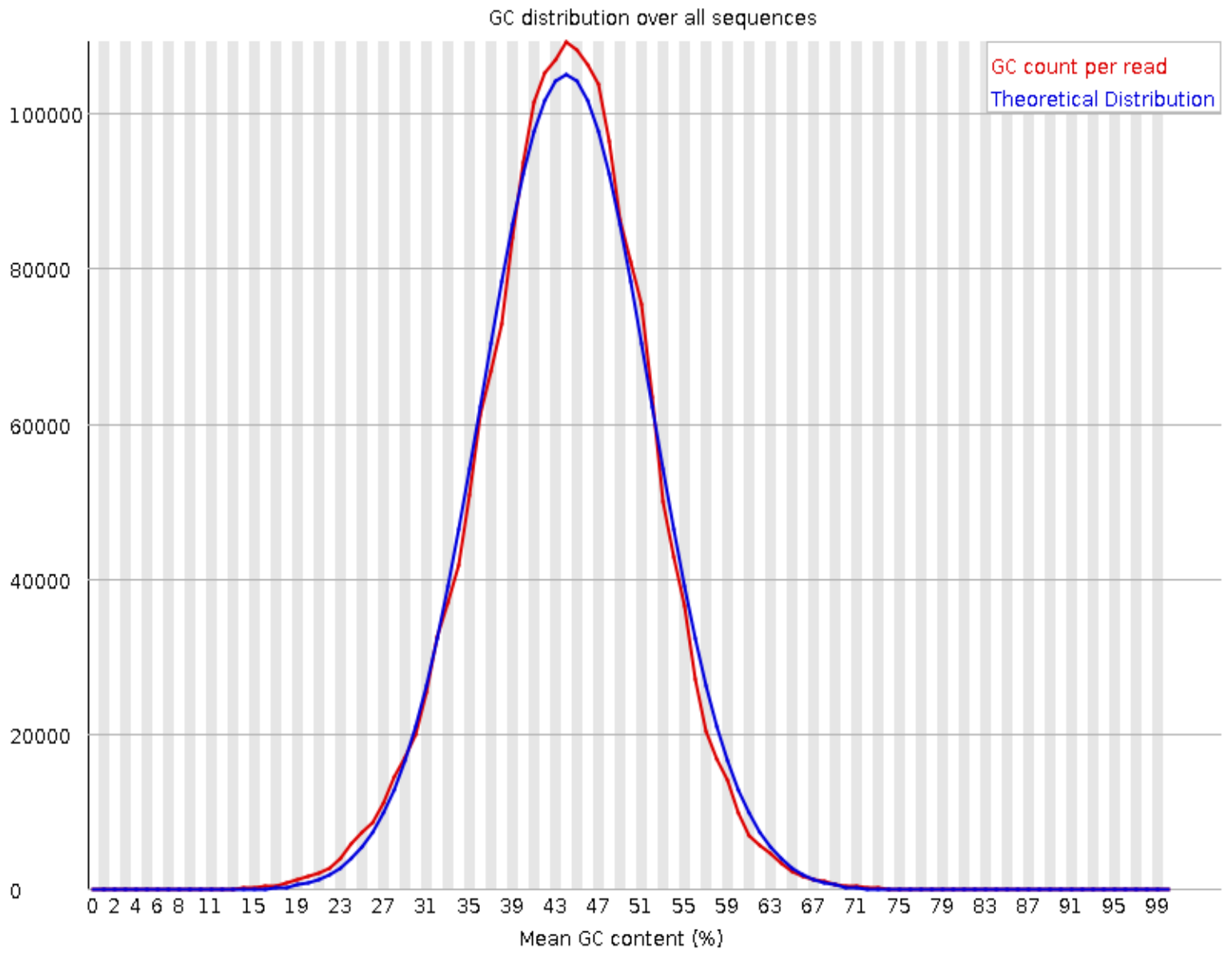
Per sequence quality scores



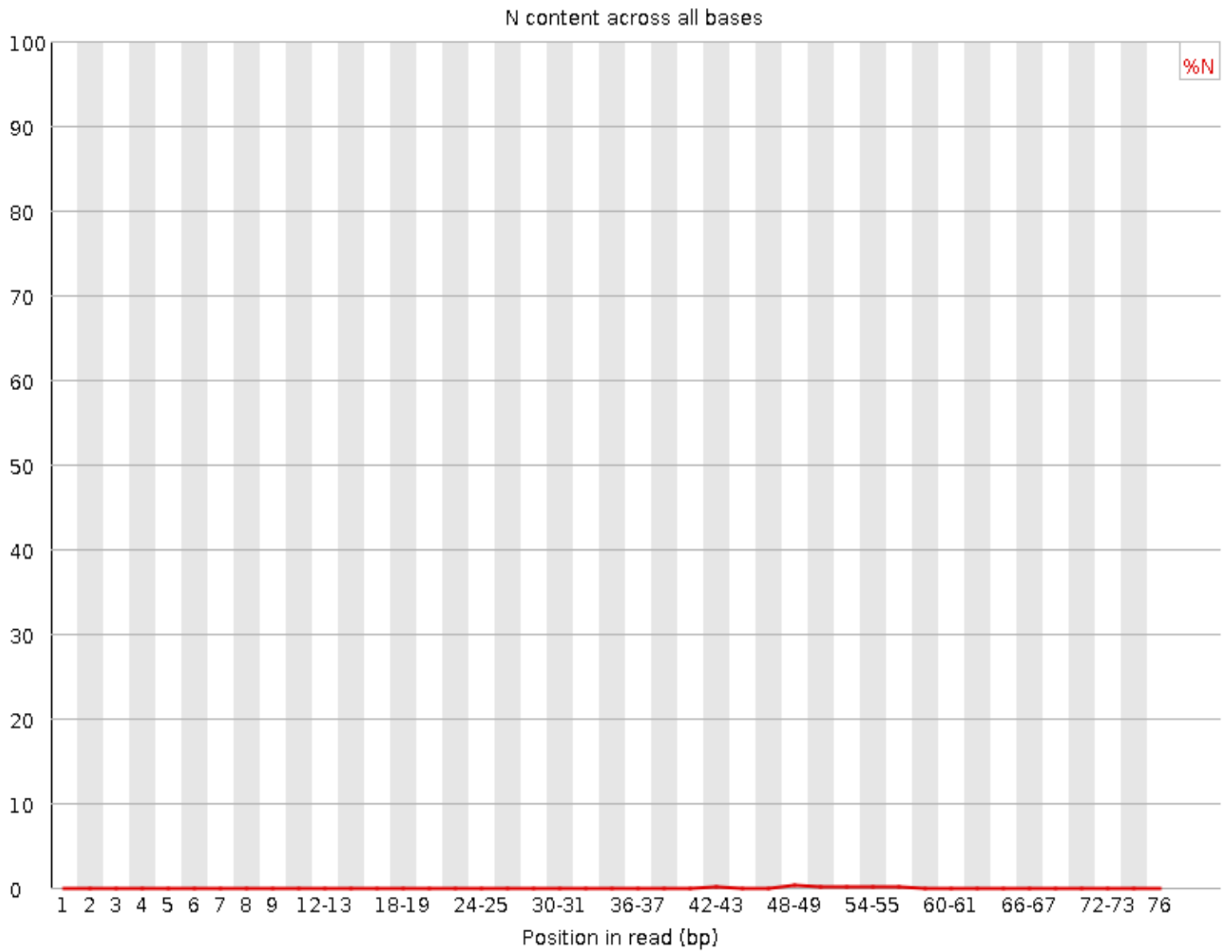
Per base sequence content



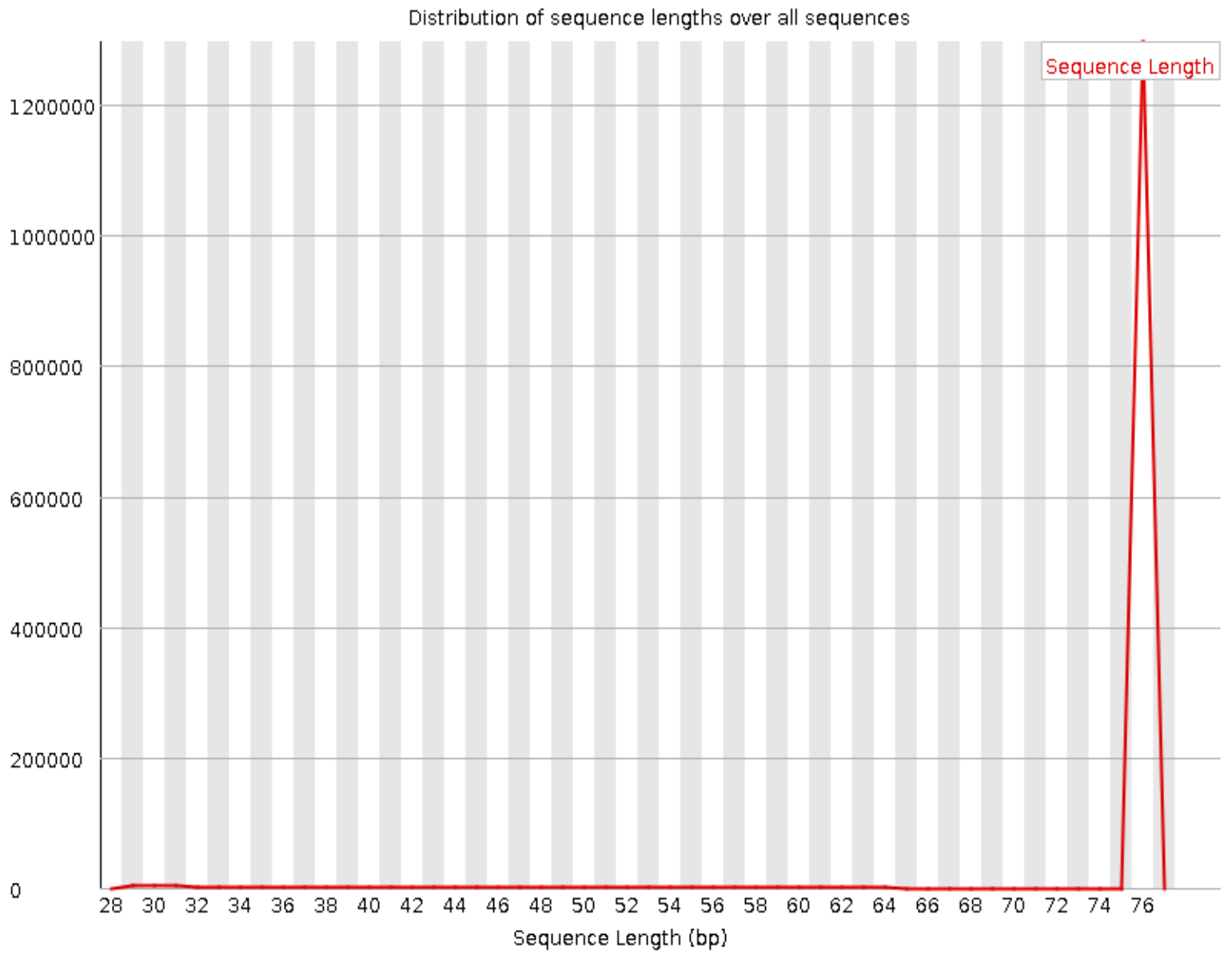
Per sequence GC content



 **Per base N content**

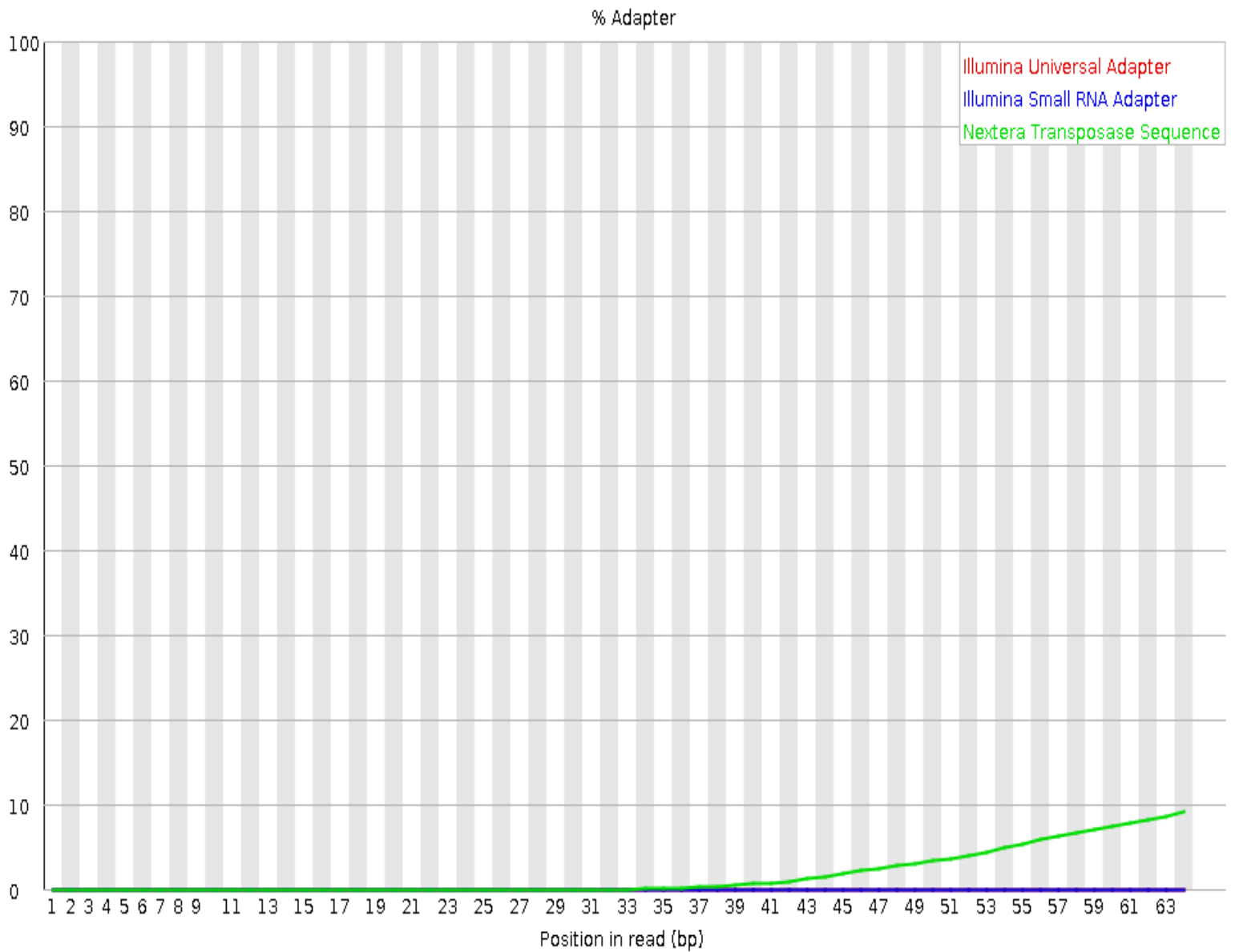


Sequence Length Distribution

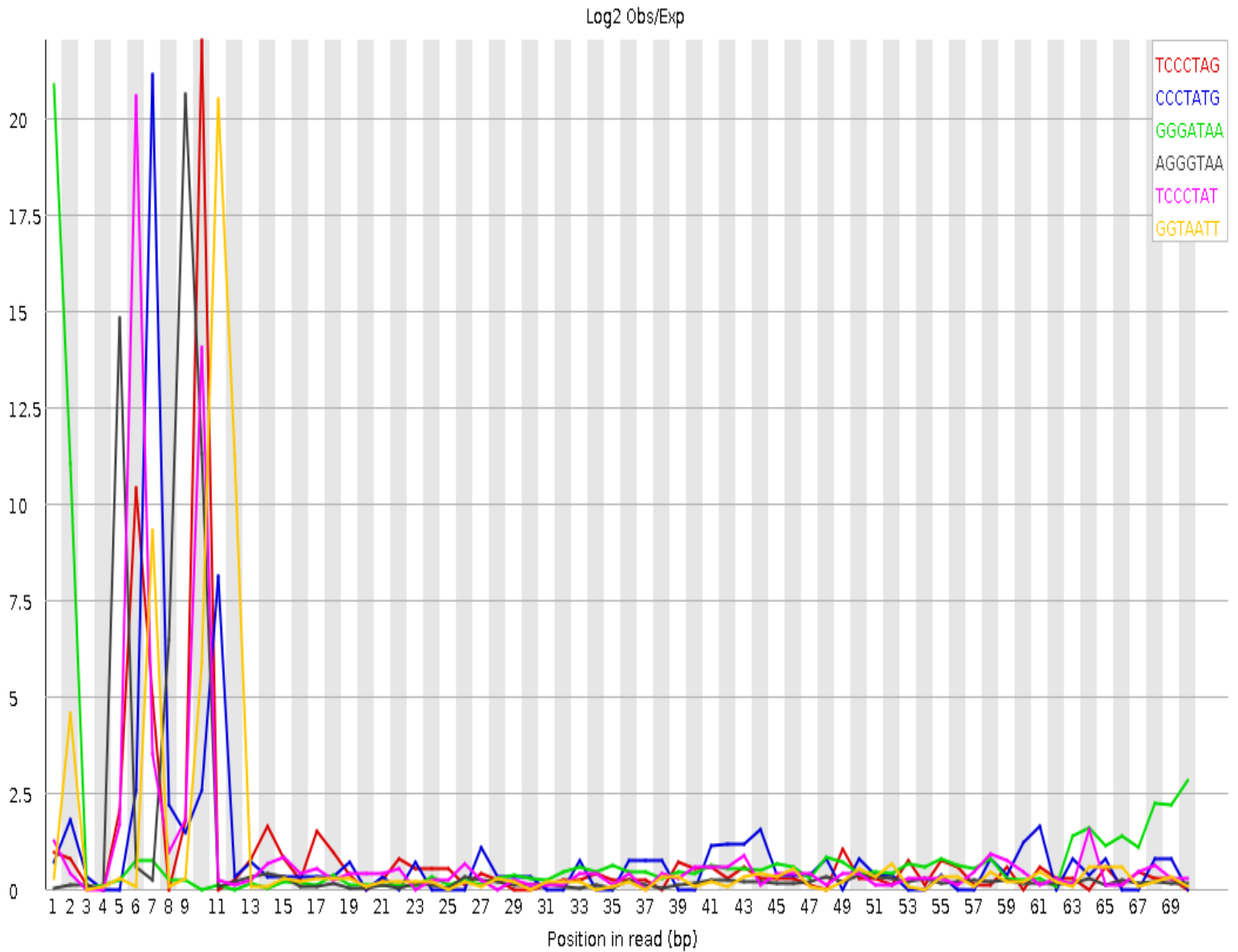


Sequence Duplication Levels

Adapter Content



Kmer Content



TCCCTAG
 CCCTATG
 GGGATAA
 AGGGTAA
 TCCCTAT
 GGTAATT

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCCCTAG	2395	0.0	21.991716	10
CCCTATG	900	0.0	21.112513	7
GGGATAA	10505	0.0	20.858673	1
AGGGTAA	10625	0.0	20.613134	9
TCCCTAT	2350	0.0	20.56874	6
GGTAATT	3110	0.0	20.472958	11
ATAACAG	11040	0.0	20.231508	4
CAGGGTA	10890	0.0	20.080917	8
ATCCCTA	7485	0.0	20.04141	9

CGGTCCG	90	0.005637958	19.223375	34
GGGTAAT	10670	0.0	19.214022	10
GATAACA	11650	0.0	18.944563	3
ATTCCTA	480	0.0	18.749952	14
GGATAAC	11725	0.0	18.73808	2
ACAGGGT	11810	0.0	18.54484	7
CCCTAGT	1095	0.0	17.961618	11
AACAGGG	12395	0.0	17.750269	6
GGTAATC	2690	0.0	17.349354	11
CTGTTAT	8875	0.0	17.316301	4
CCTGTTA	8850	0.0	17.291075	3

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