













FastQC Report

Summary

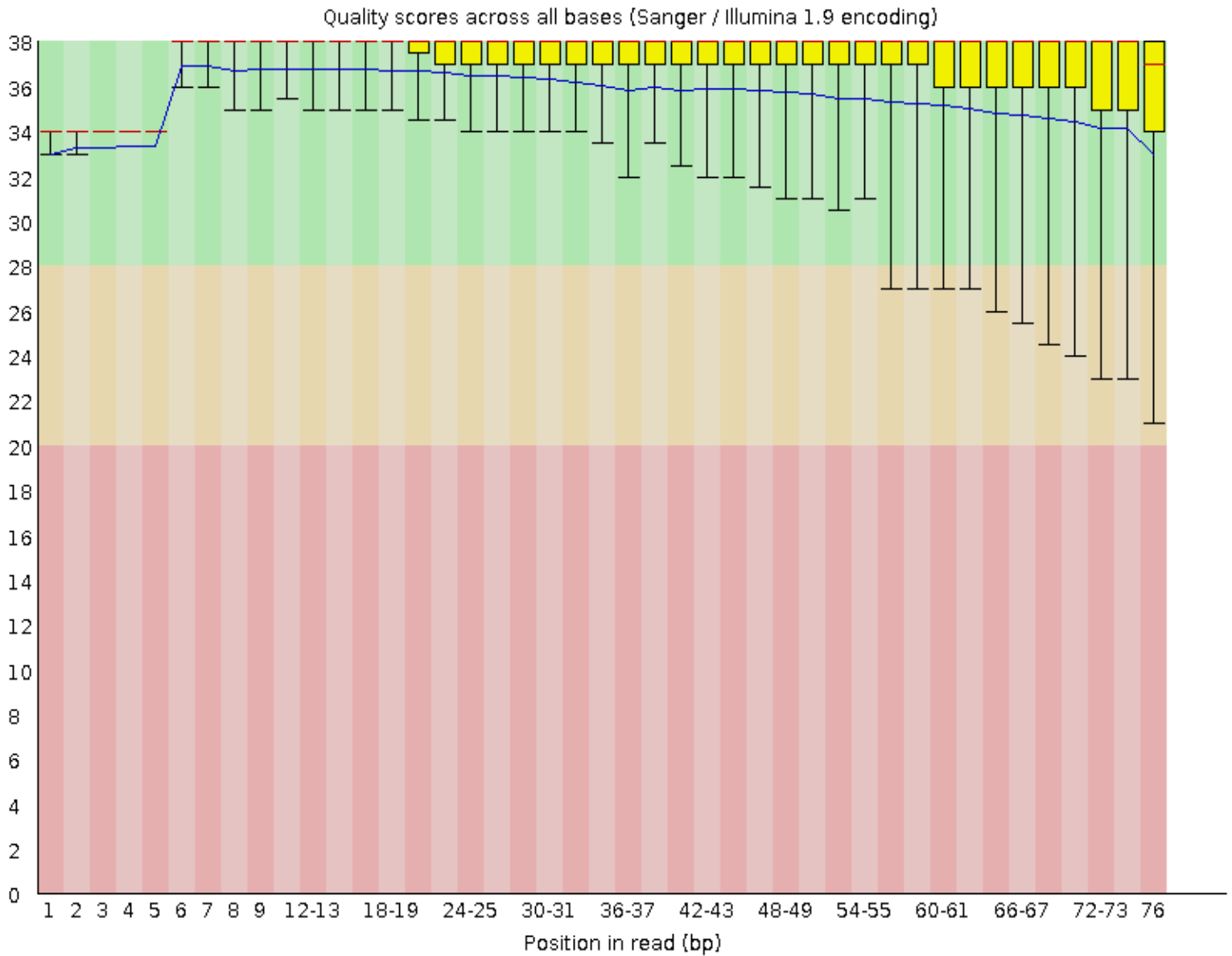
Mon 11 May 2015
SW042.r2.trimmed.fastq

-  [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](#)

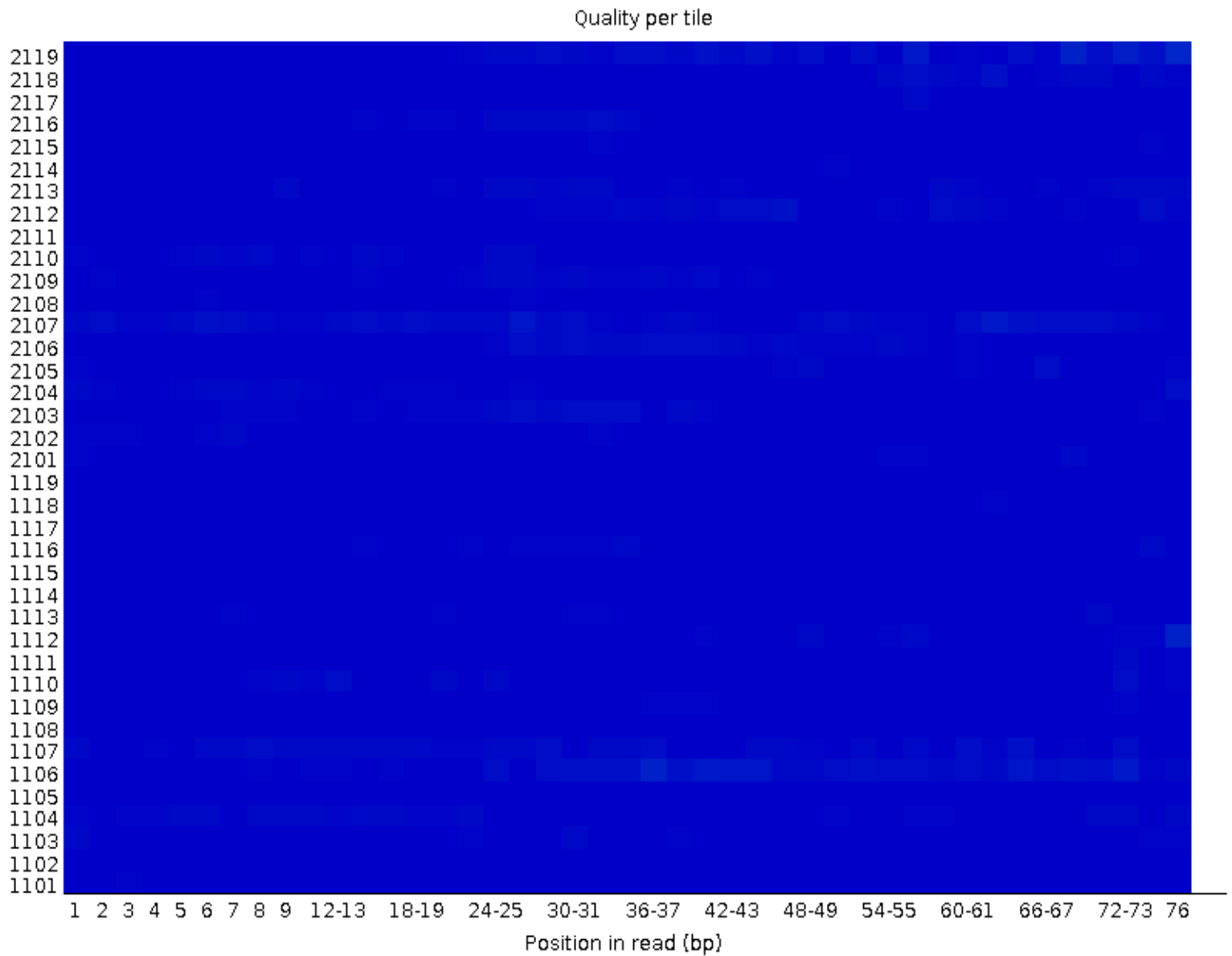
Basic Statistics

Measure	Value
Filename	SW042.r2.trimmed.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	774725
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

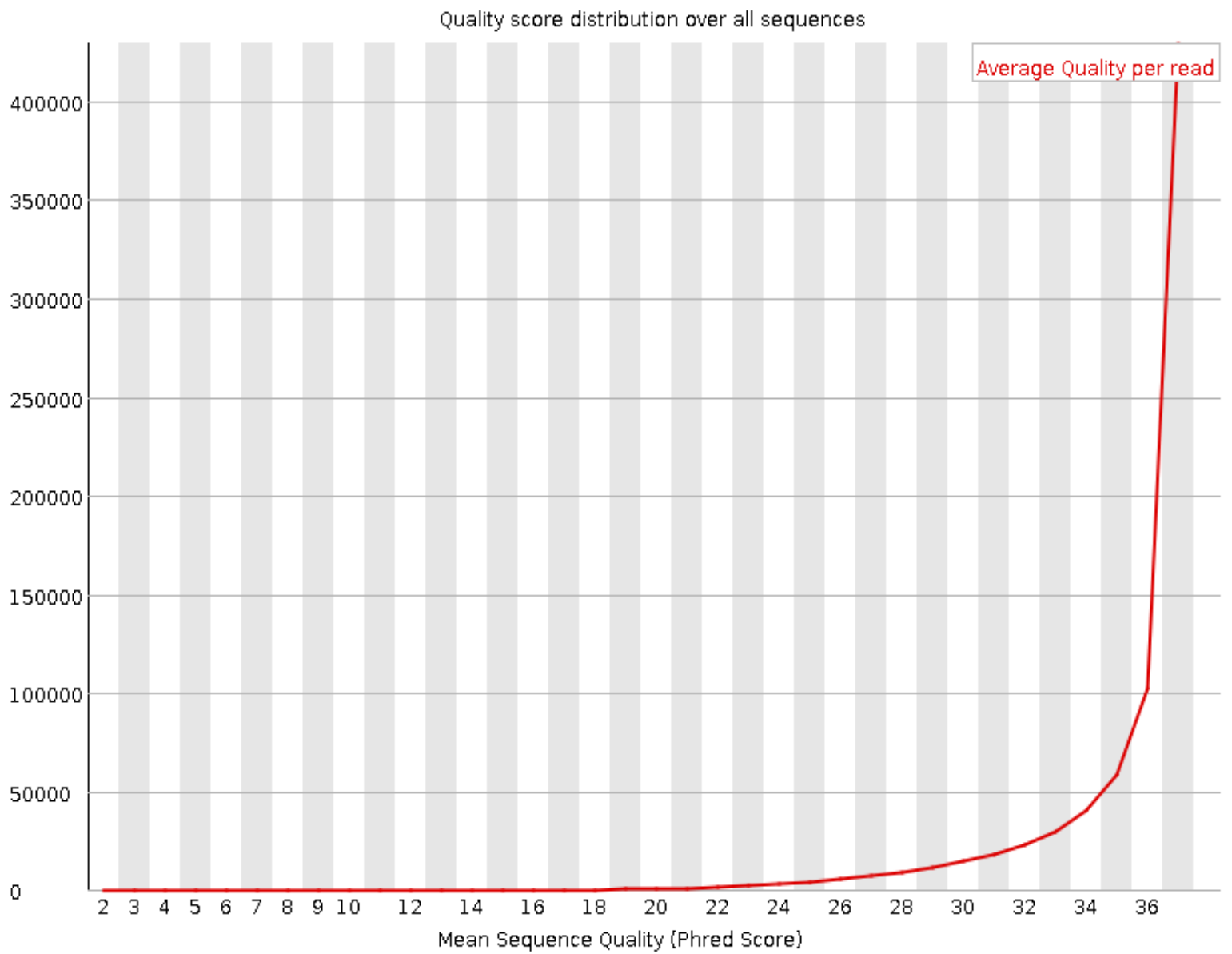
✔ Per base sequence quality



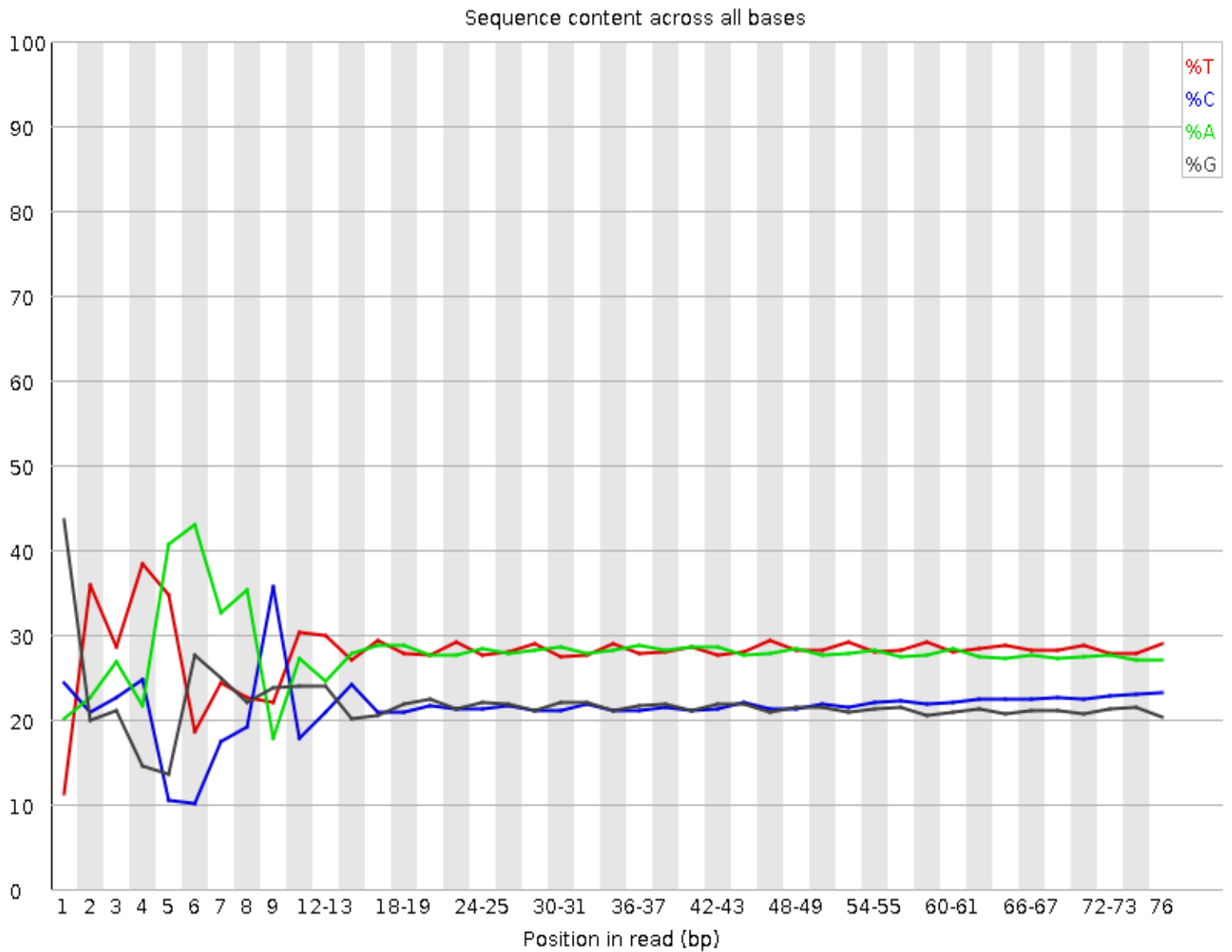
✔ Per tile sequence quality



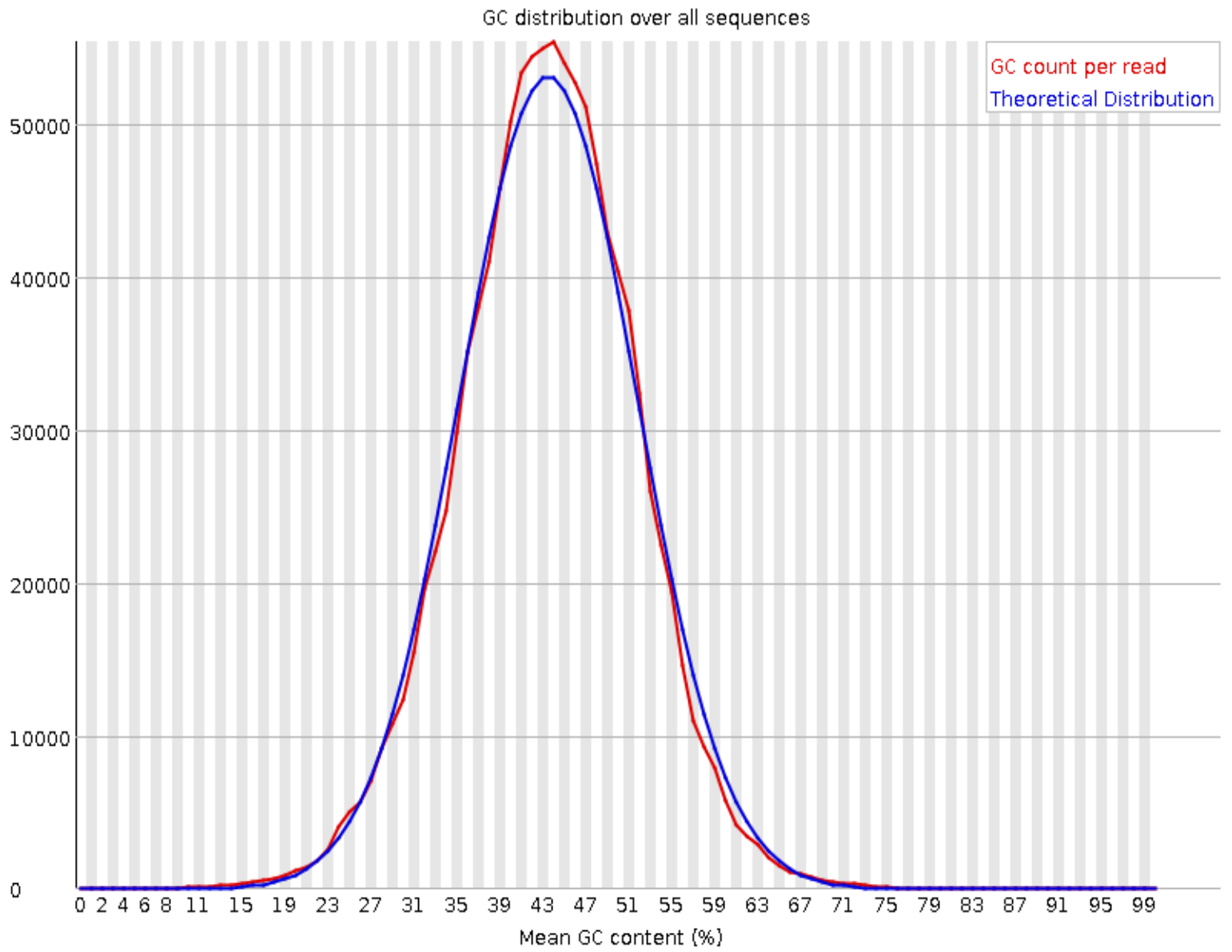
 **Per sequence quality scores**



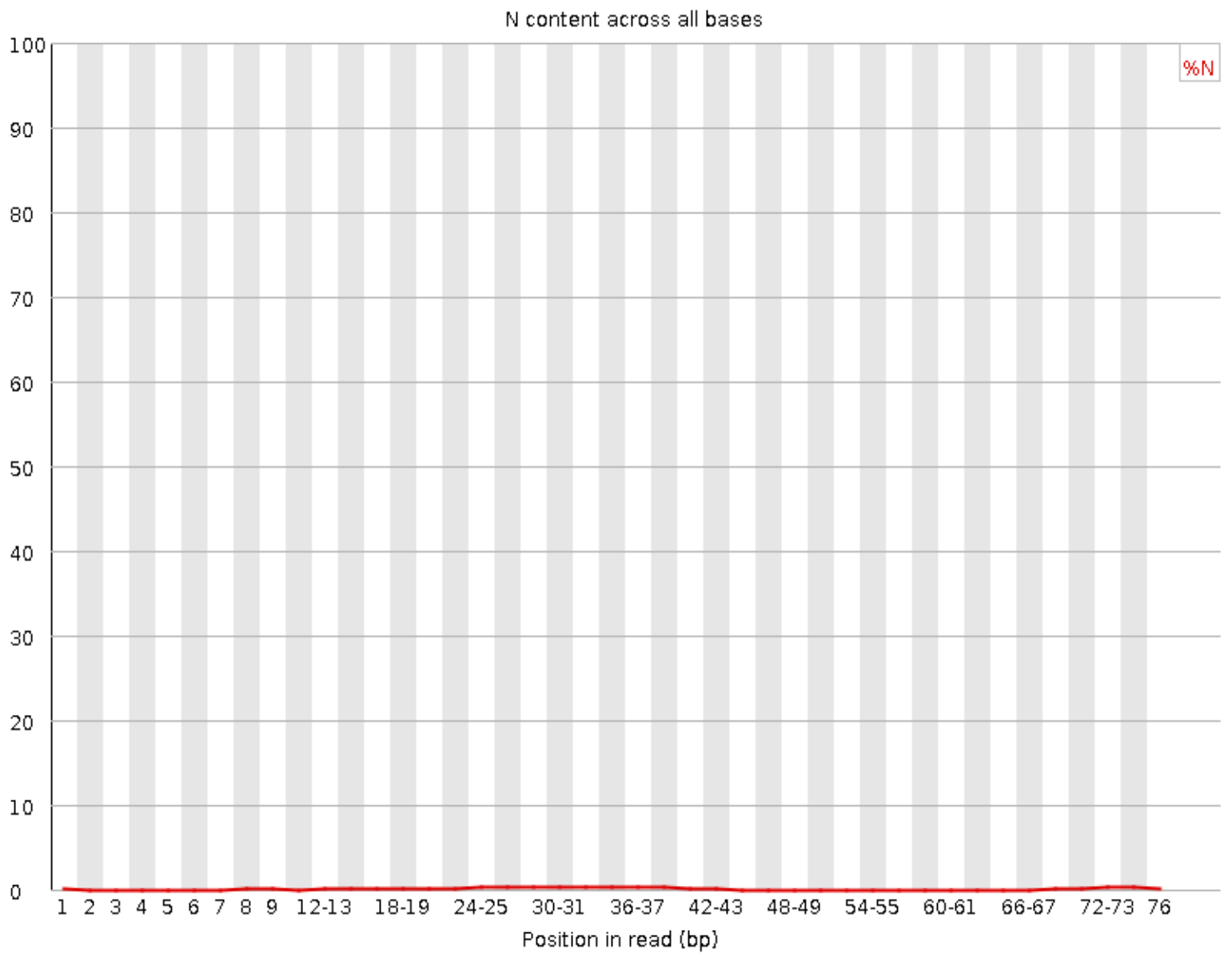
Per base sequence content



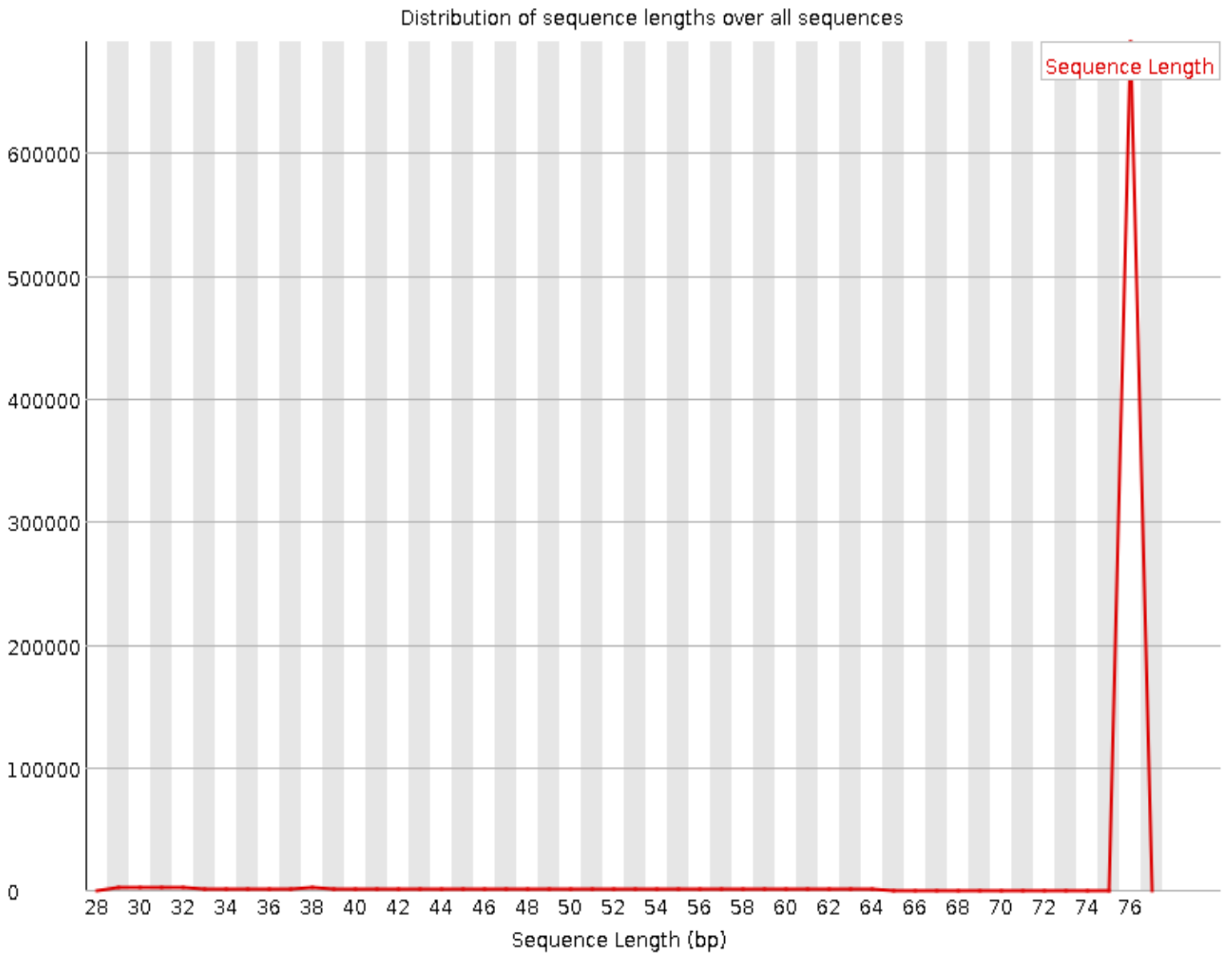
Per sequence GC content



 **Per base N content**

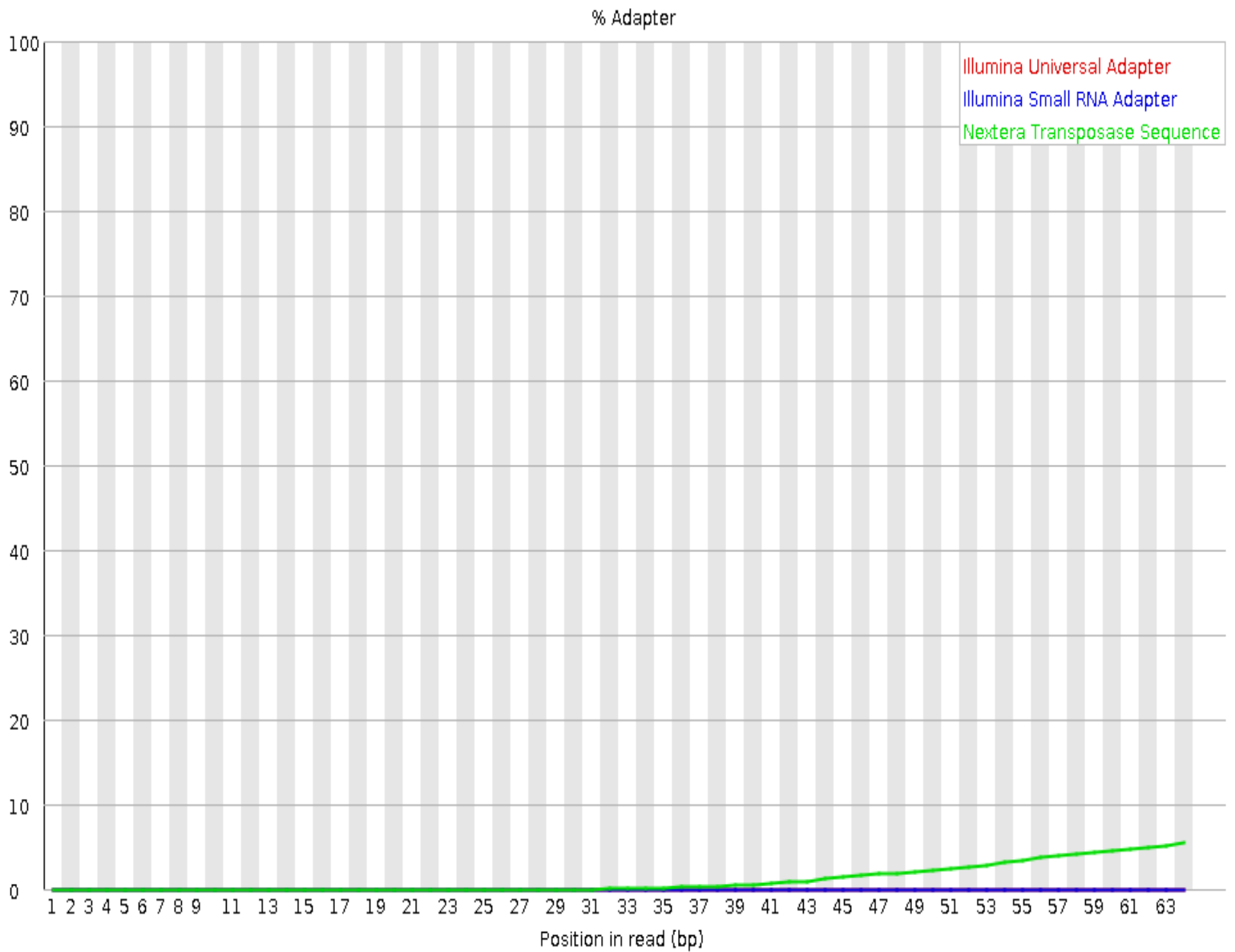


Sequence Length Distribution

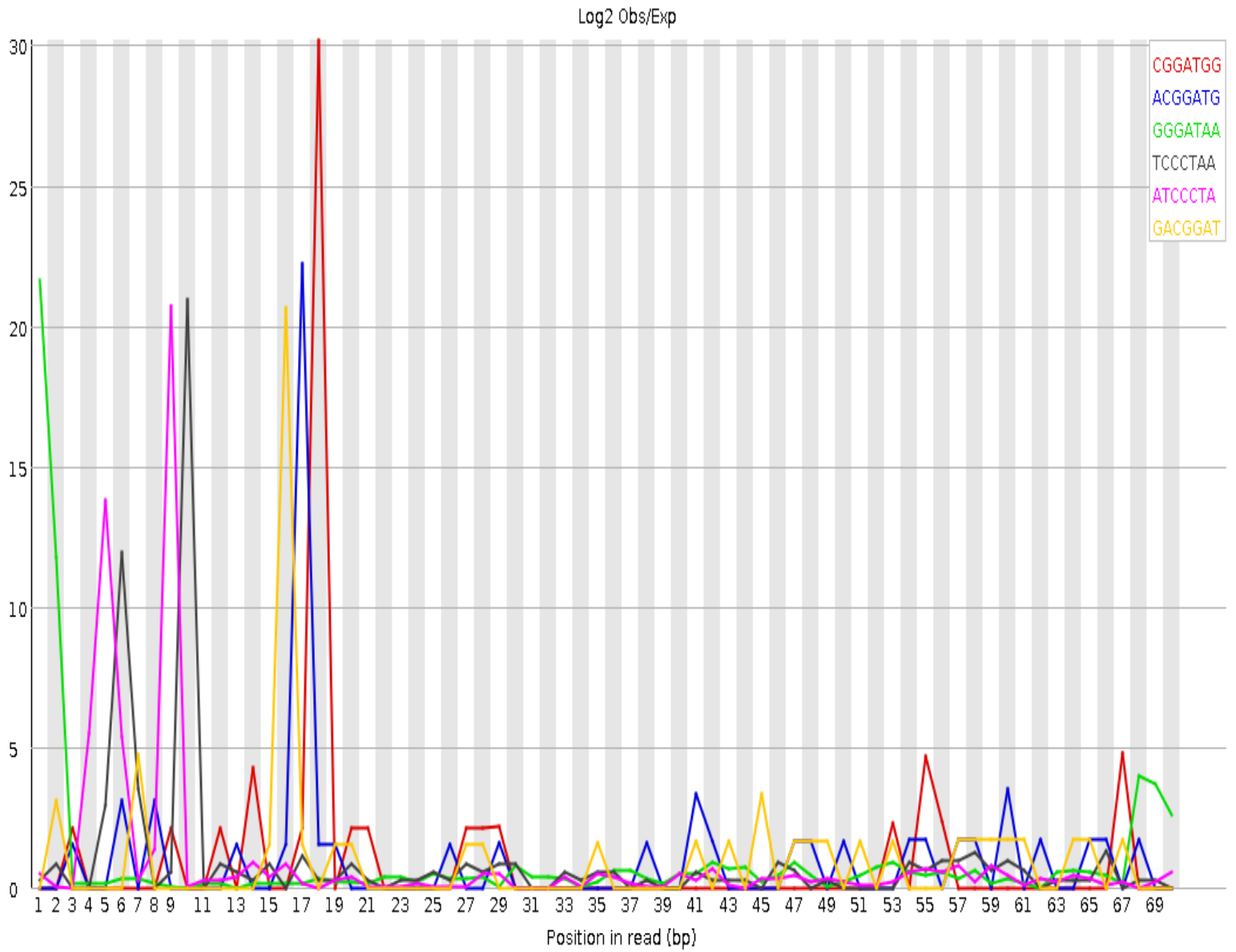


Sequence Duplication Levels

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGGATGG	155	0.0	30.167513	18
ACGGATG	210	7.2759576E-12	22.252083	17
GGGATAA	3785	0.0	21.67954	1
TCCCTAA	1115	0.0	20.956232	10
ATCCCTA	3060	0.0	20.726318	9
GACGGAT	210	1.5825208E-10	20.659973	16
GGGCTCT	230	2.3646862E-11	20.357977	23
CAGGGTA	3960	0.0	20.057993	8
ATAACAG	4100	0.0	19.935139	4

AGGGTAA	3955	0.0	19.91845	9
GGGTAAT	3990	0.0	19.576408	10
CCTGTTA	3310	0.0	19.552881	3
CCCTGTT	3385	0.0	19.313017	2
CCCTATG	295	0.0	19.22365	7
GGATAAC	4315	0.0	19.170067	2
GATAACA	4285	0.0	19.074463	3
ACCCTGT	3450	0.0	18.757004	1
AAGACGG	250	8.0035534E-11	18.695381	14
GCTTAAG	125	1.1253555E-4	18.692959	11
CTGTTAT	3470	0.0	18.555166	4

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