












FastQC Report

Summary

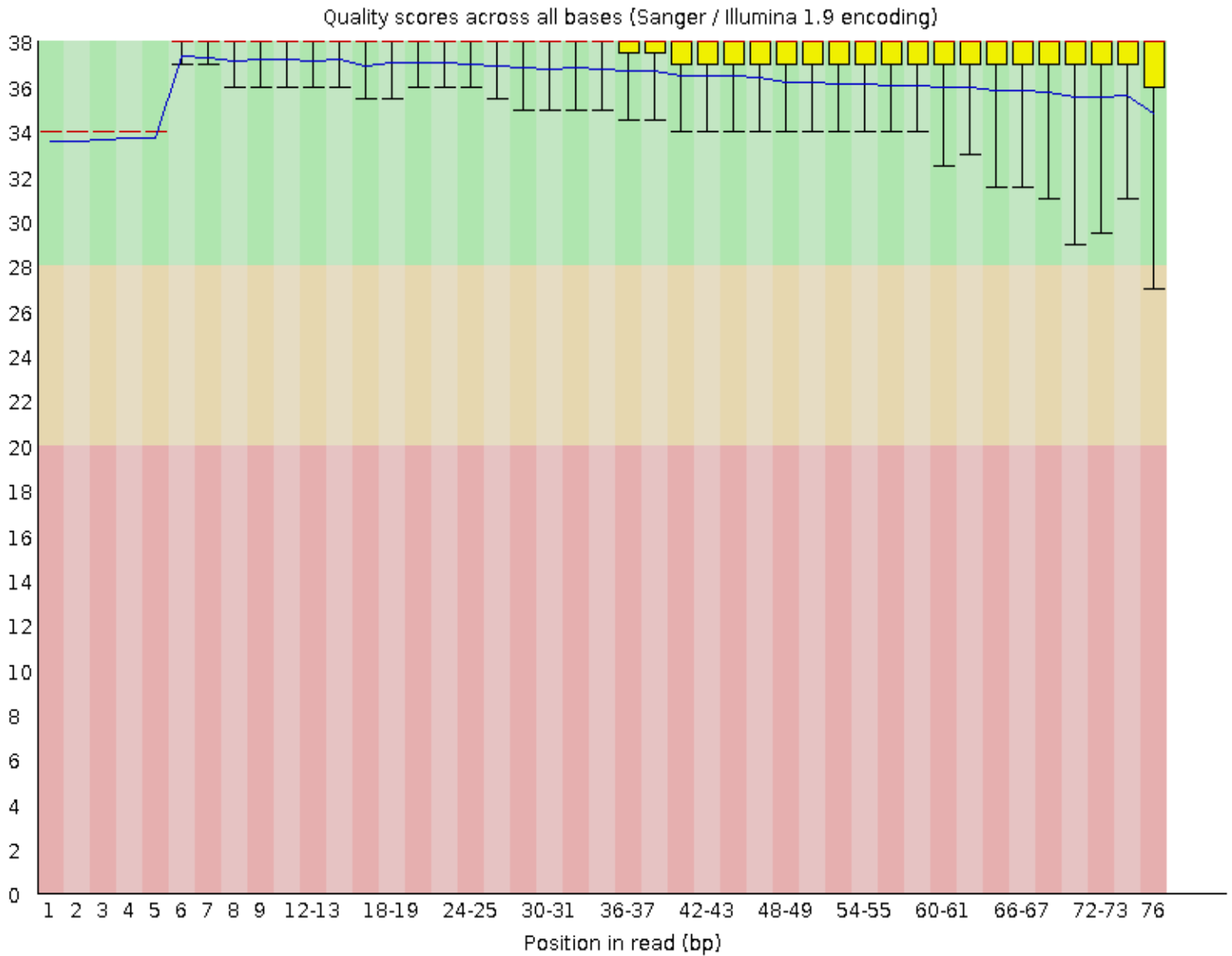
Mon 11 May 2015
SW042.r1.trimmed.fastq

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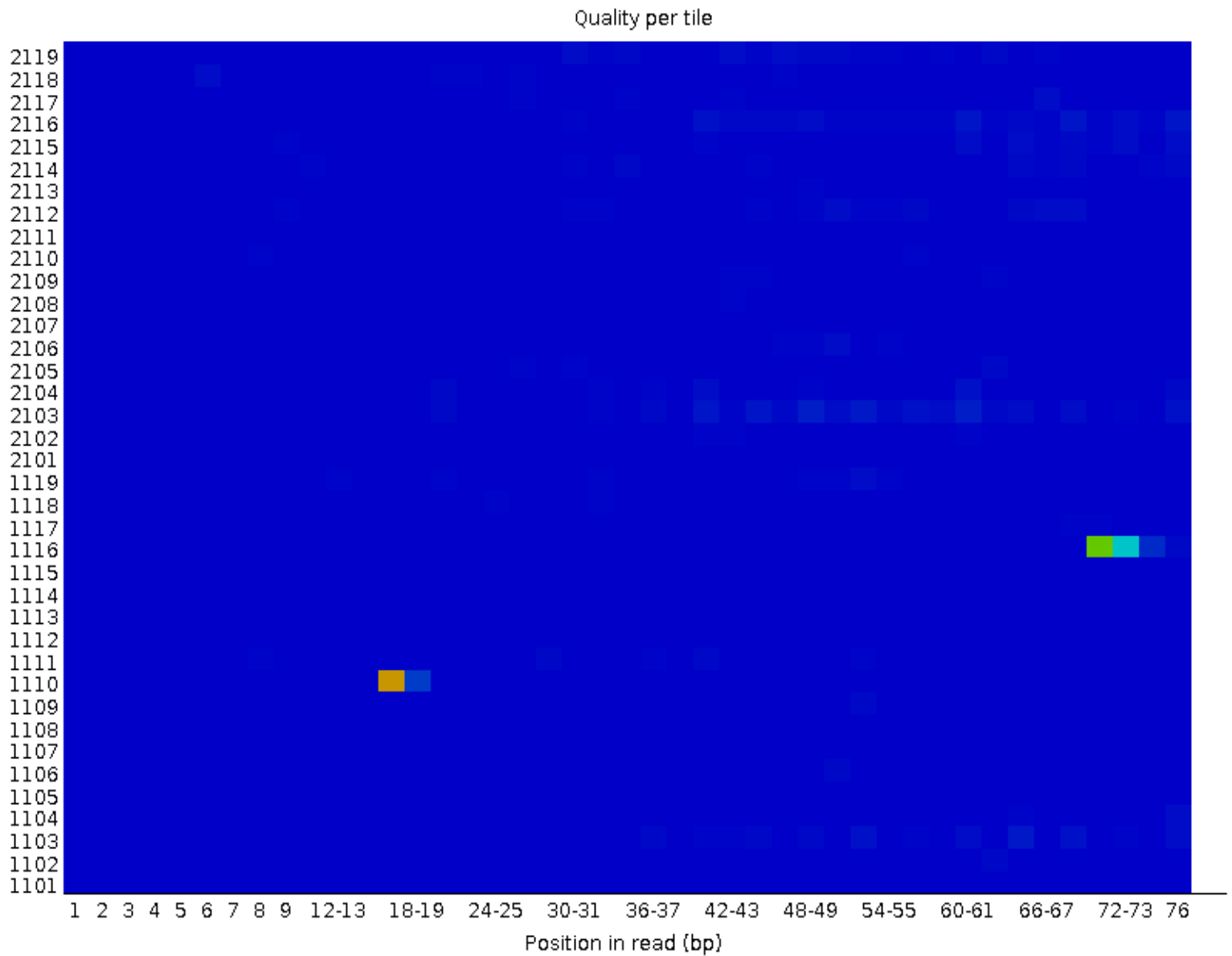
Basic Statistics

Measure	Value
Filename	SW042.r1.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

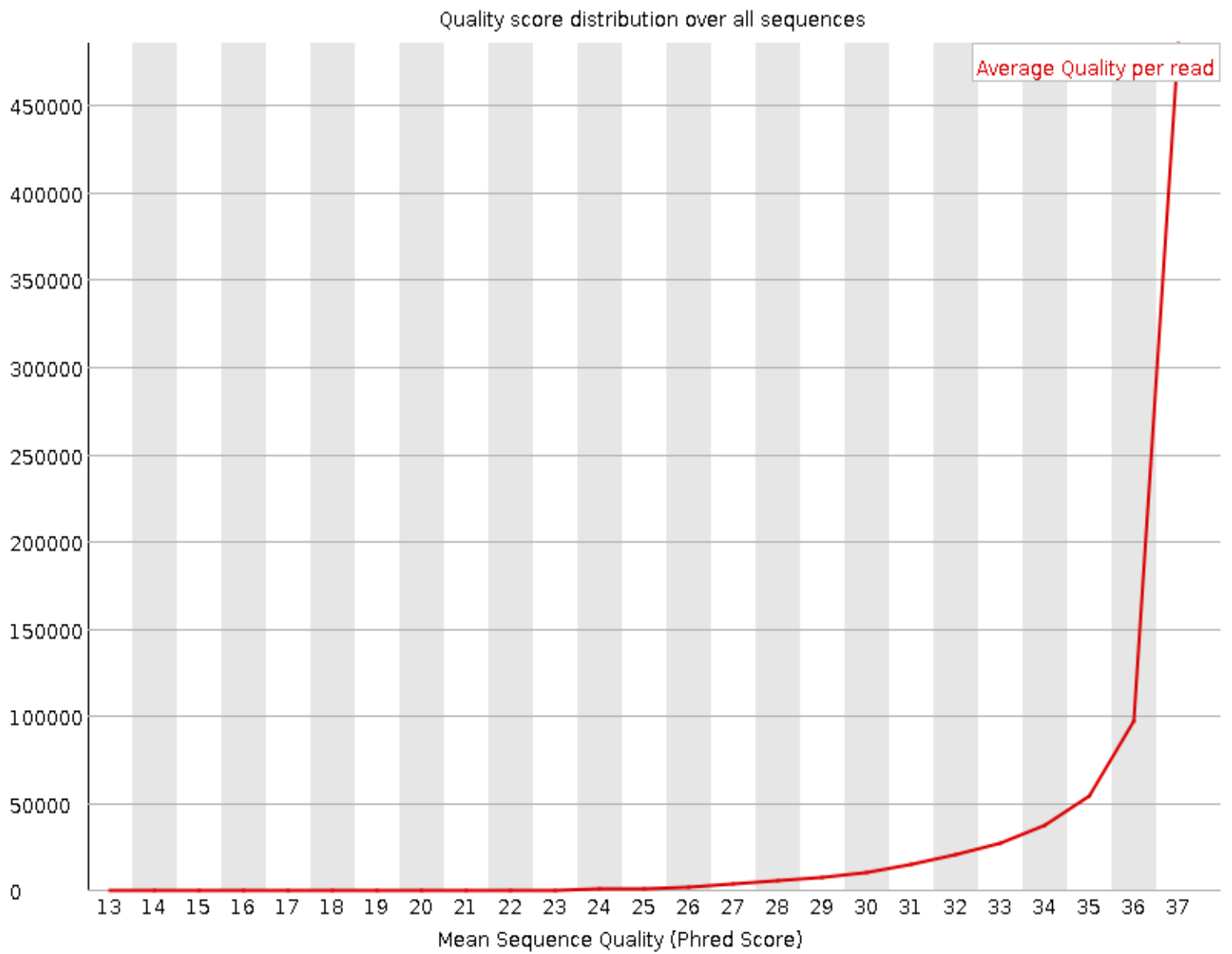
✔ Per base sequence quality



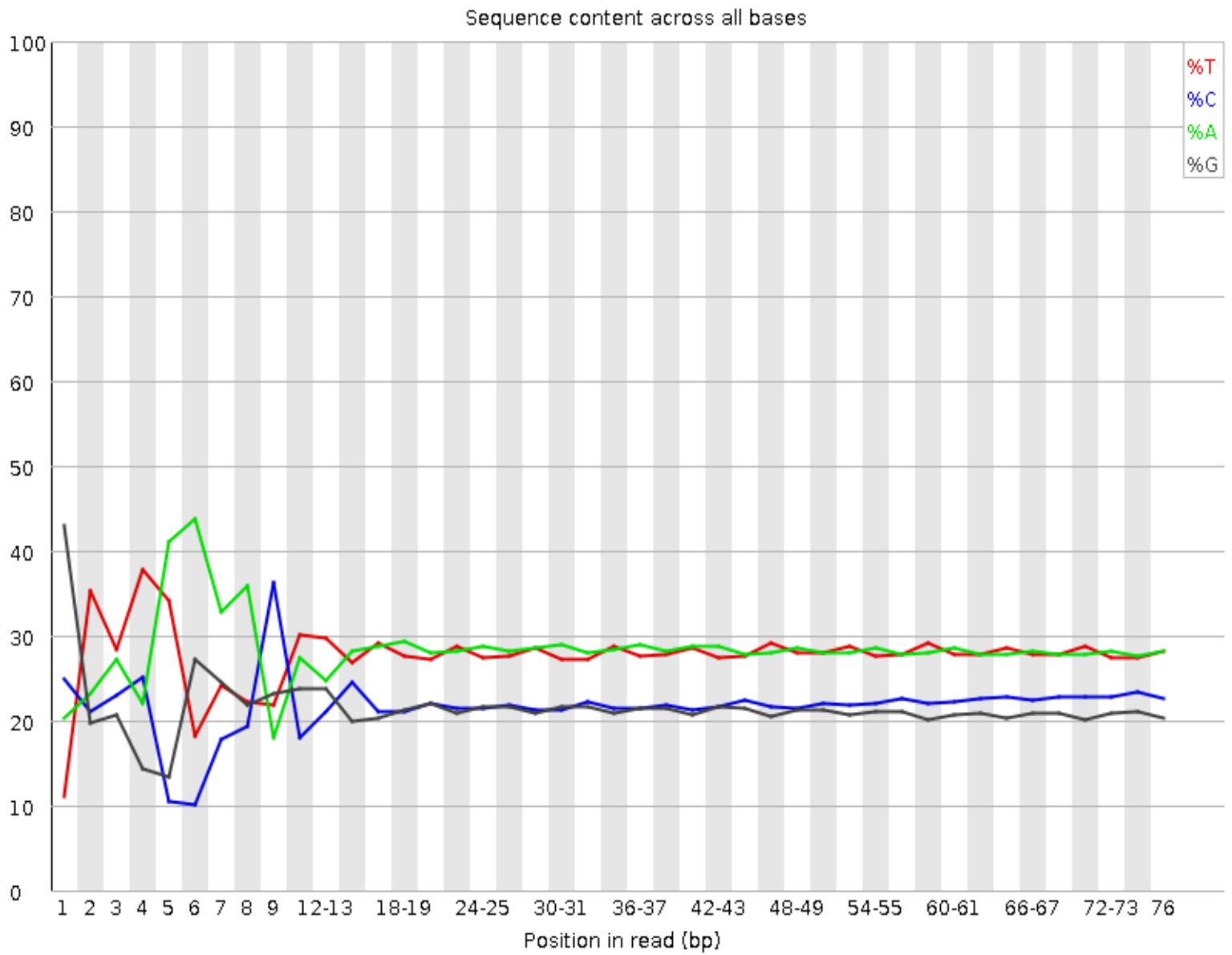
⚠ Per tile sequence quality



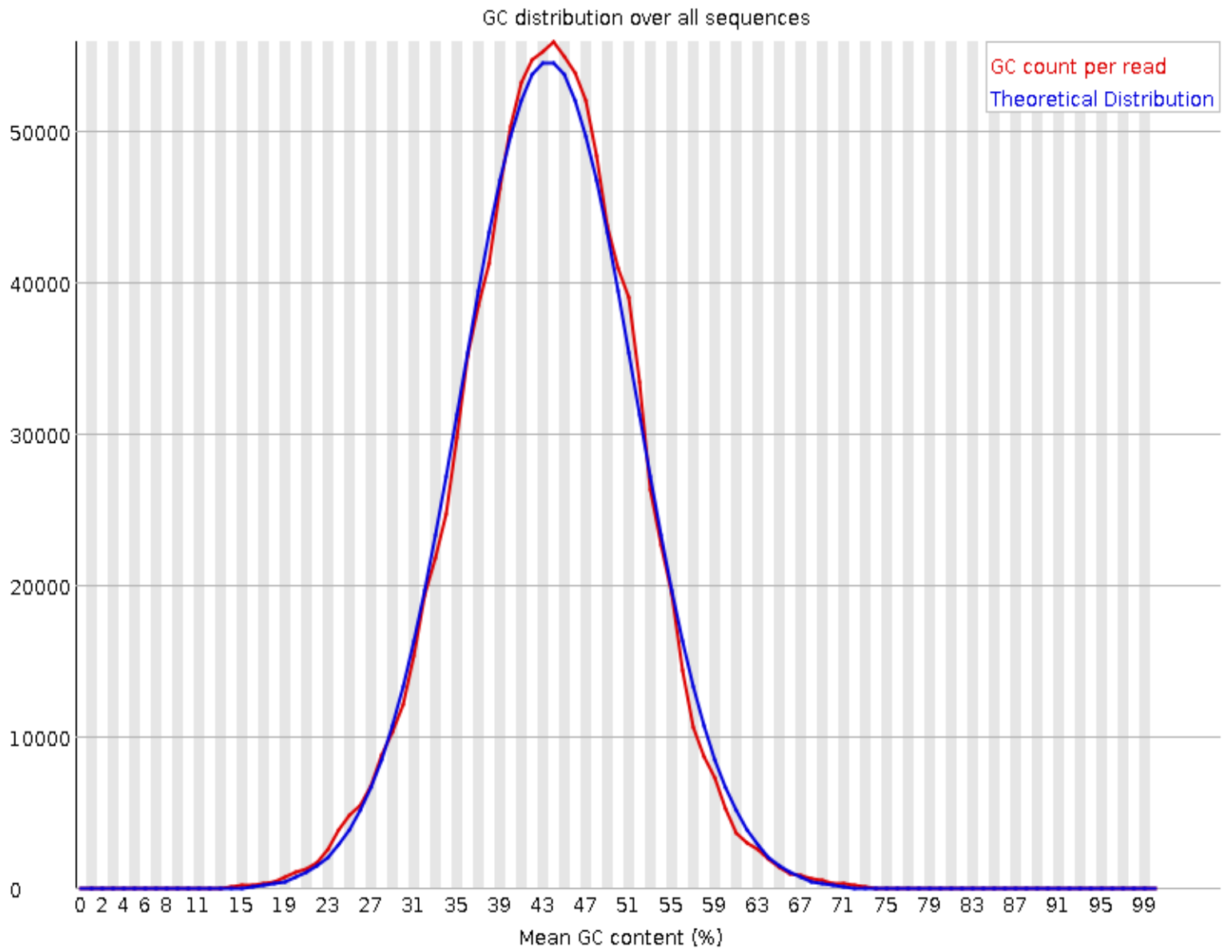
Per sequence quality scores



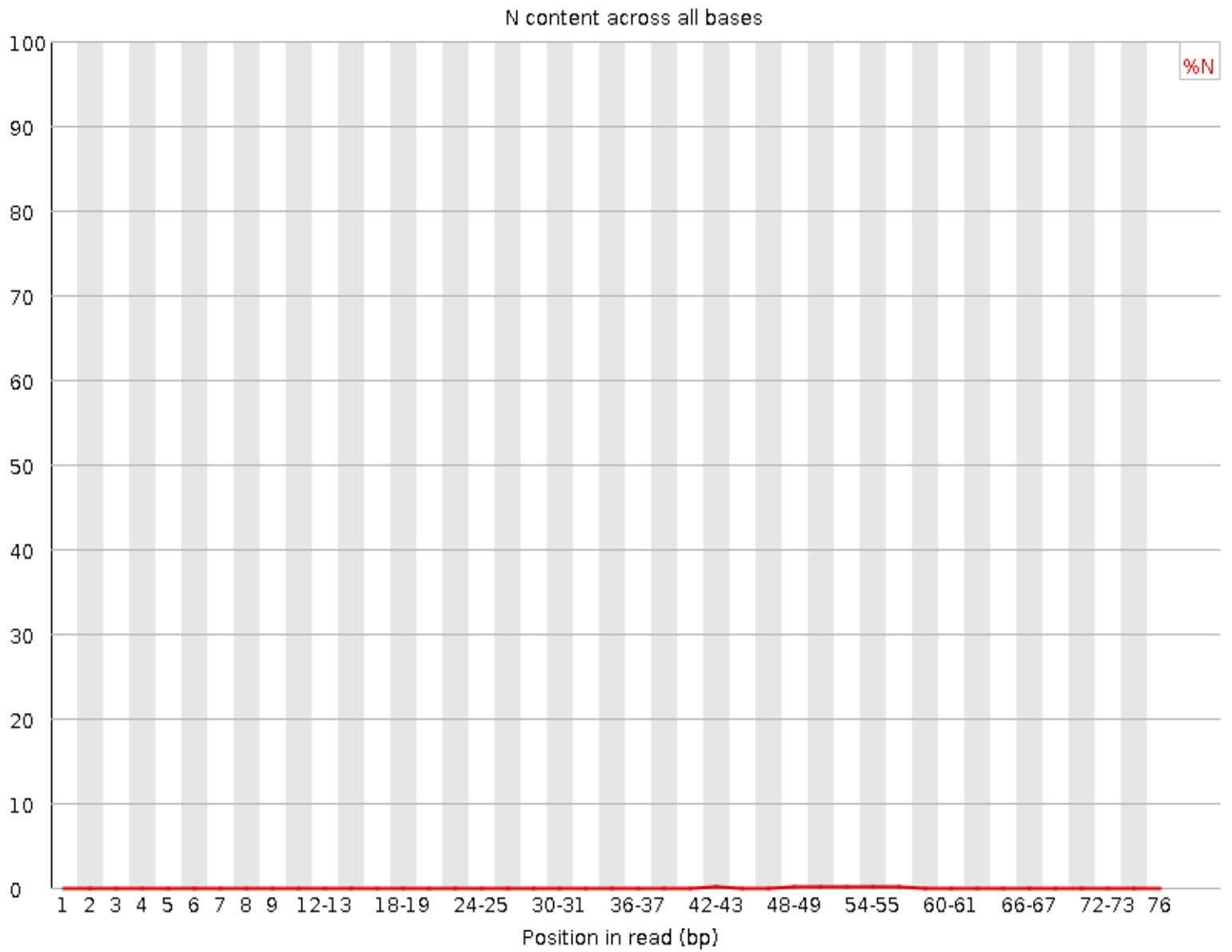
Per base sequence content



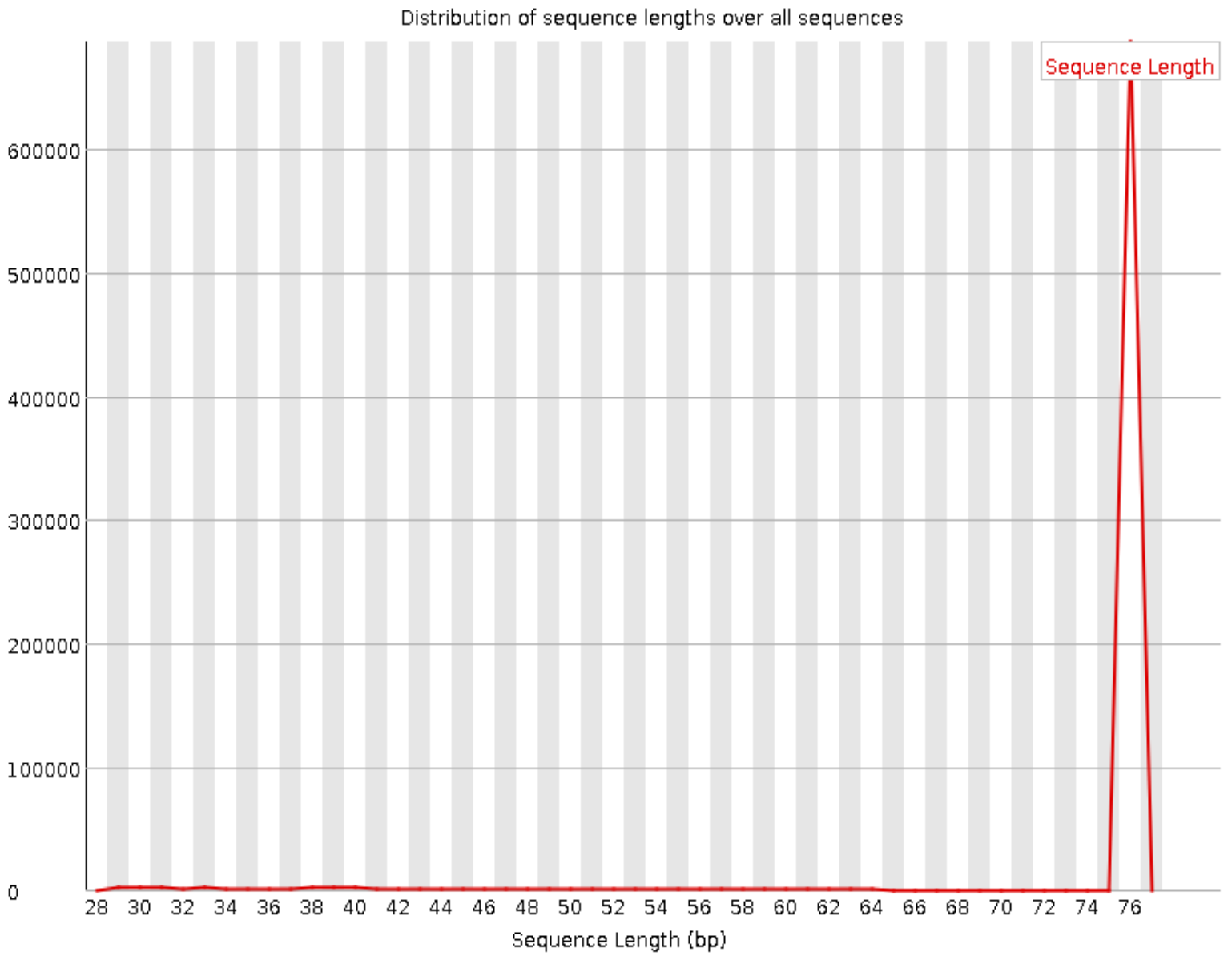
Per sequence GC content



 **Per base N content**

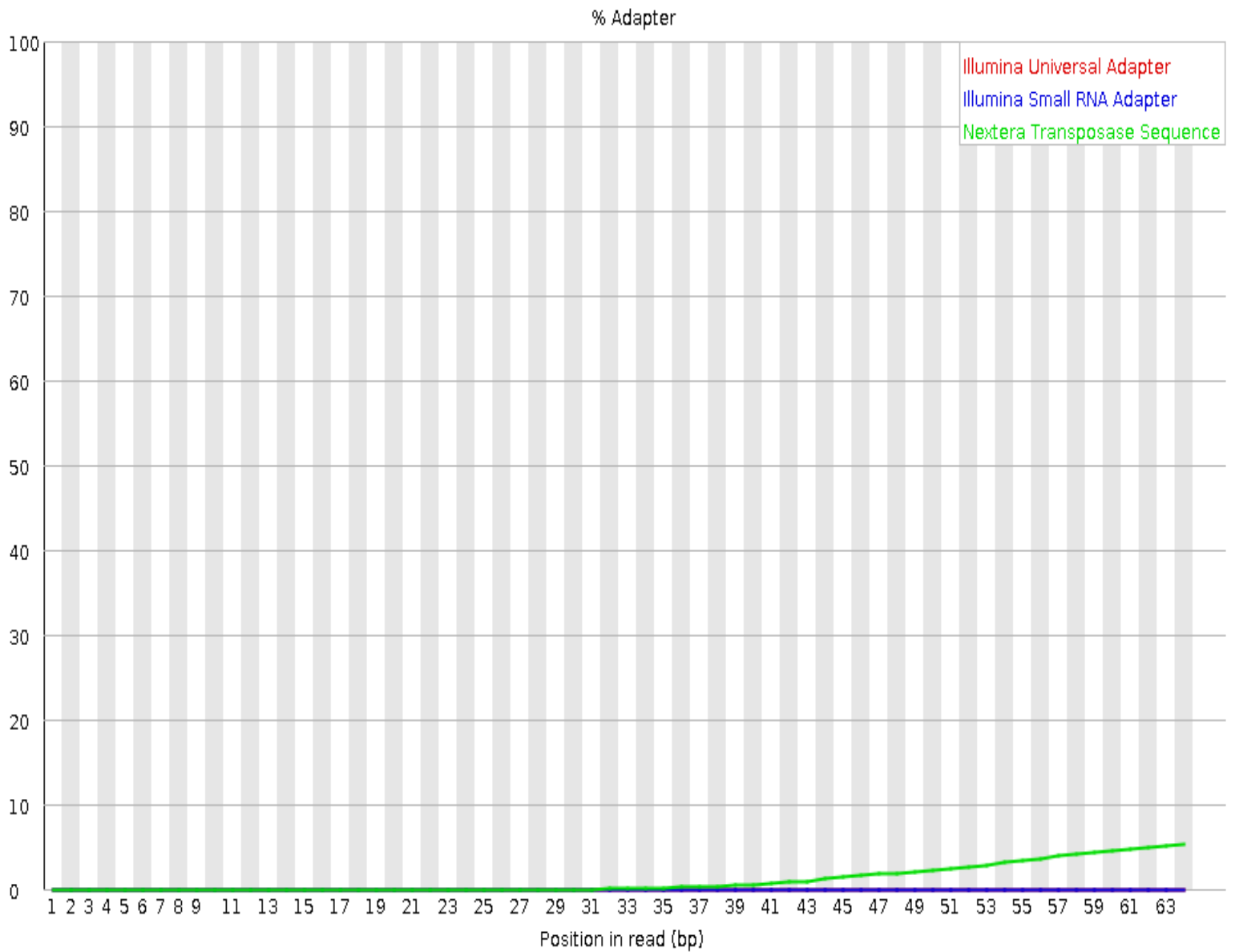


Sequence Length Distribution

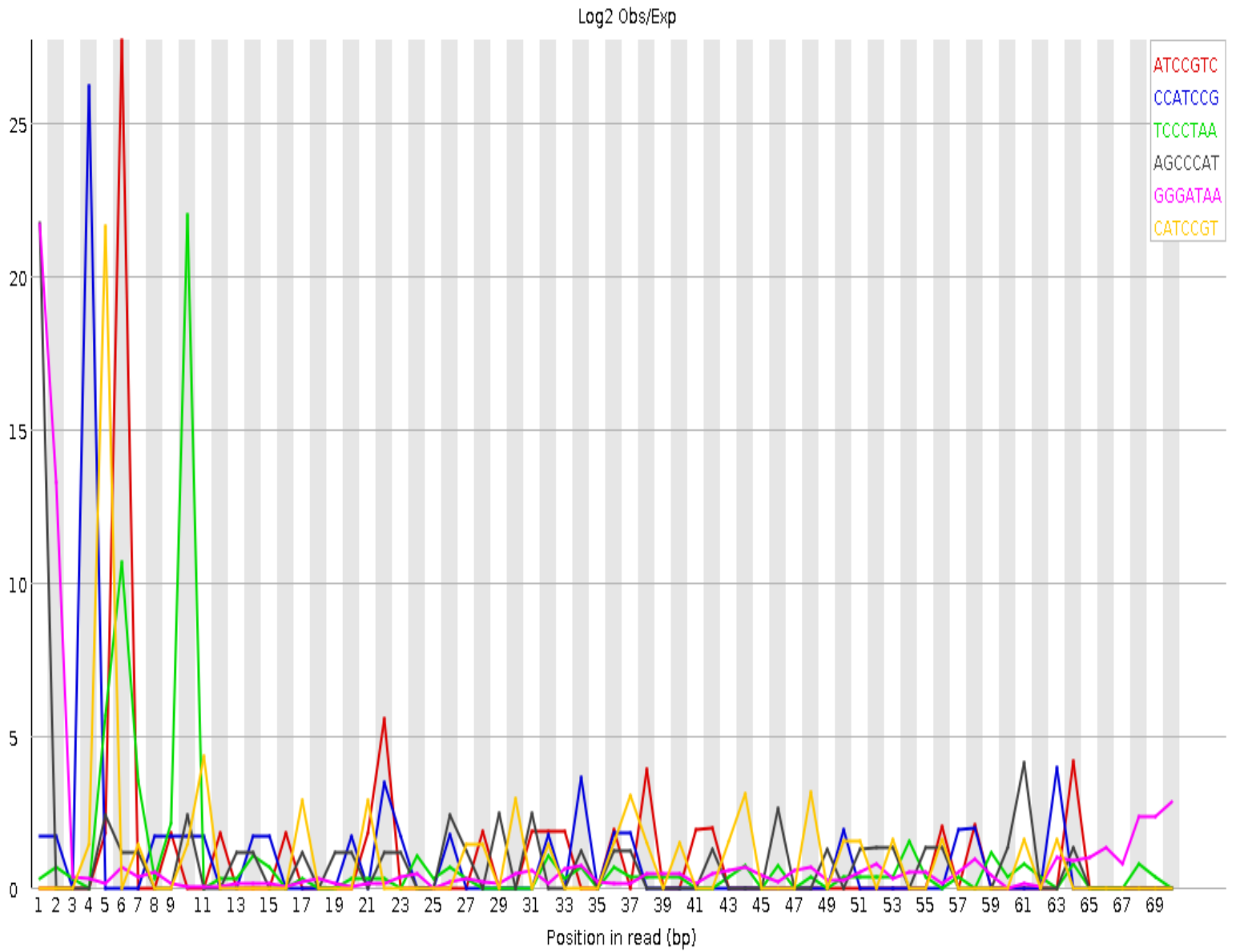


Sequence Duplication Levels

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCGTC	180	0.0	27.700655	6
CCATCCG	190	0.0	26.24442	4
TCCCTAA	935	0.0	22.042017	10
AGCCCAT	275	0.0	21.768847	1
GGGATAA	4080	0.0	21.682884	1
CATCCGT	230	1.8189894E-12	21.680172	5
CCGTCTT	235	1.8189894E-12	21.217524	8
CCGGATA	95	3.9256838E-4	21.005026	1
AGGGTAA	4170	0.0	20.964811	9

ATCCCTA	3025	0.0	20.658735	9
CCCTTAG	145	7.522867E-7	20.642872	1
CCCTGTT	3240	0.0	20.62426	2
TCCGTCT	260	0.0	20.455868	7
CTGTTAT	3165	0.0	20.376394	4
CCTGTTA	3205	0.0	20.227114	3
ACCCTGT	3320	0.0	20.135088	1
CCCTATG	365	0.0	20.035543	7
CAGGGTA	4385	0.0	20.012697	8
GGATAAC	4530	0.0	19.59478	2
GGTAAT	4145	0.0	19.487362	10

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