

FastQC Report

Summary

Sun 3 Apr 2016
18418_2#1_1.fastq

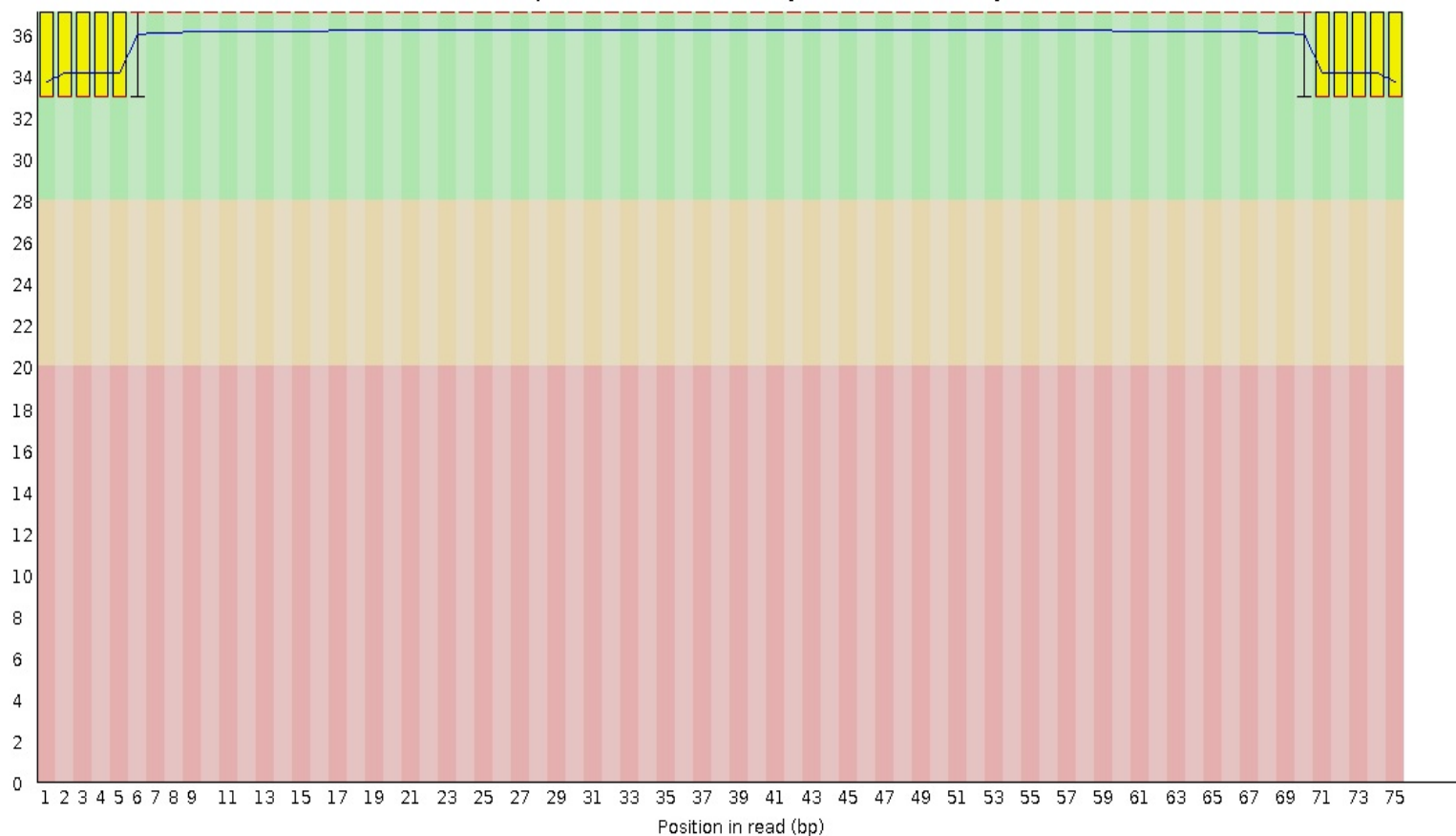
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Basic Statistics

Measure	Value
Filename	18418_2#1_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	40095362
Sequences flagged as poor quality	0
Sequence length	75
%GC	40

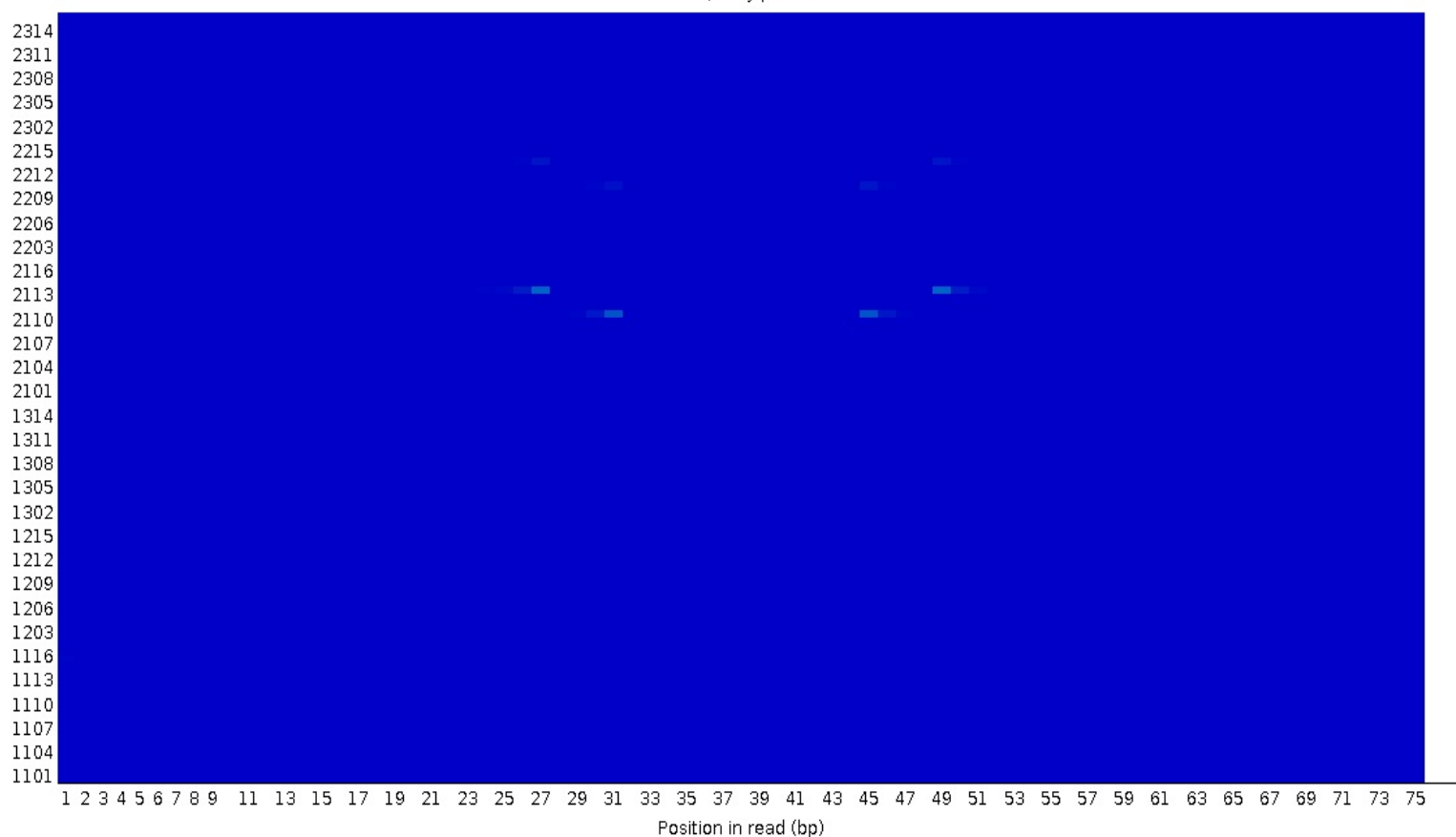
Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

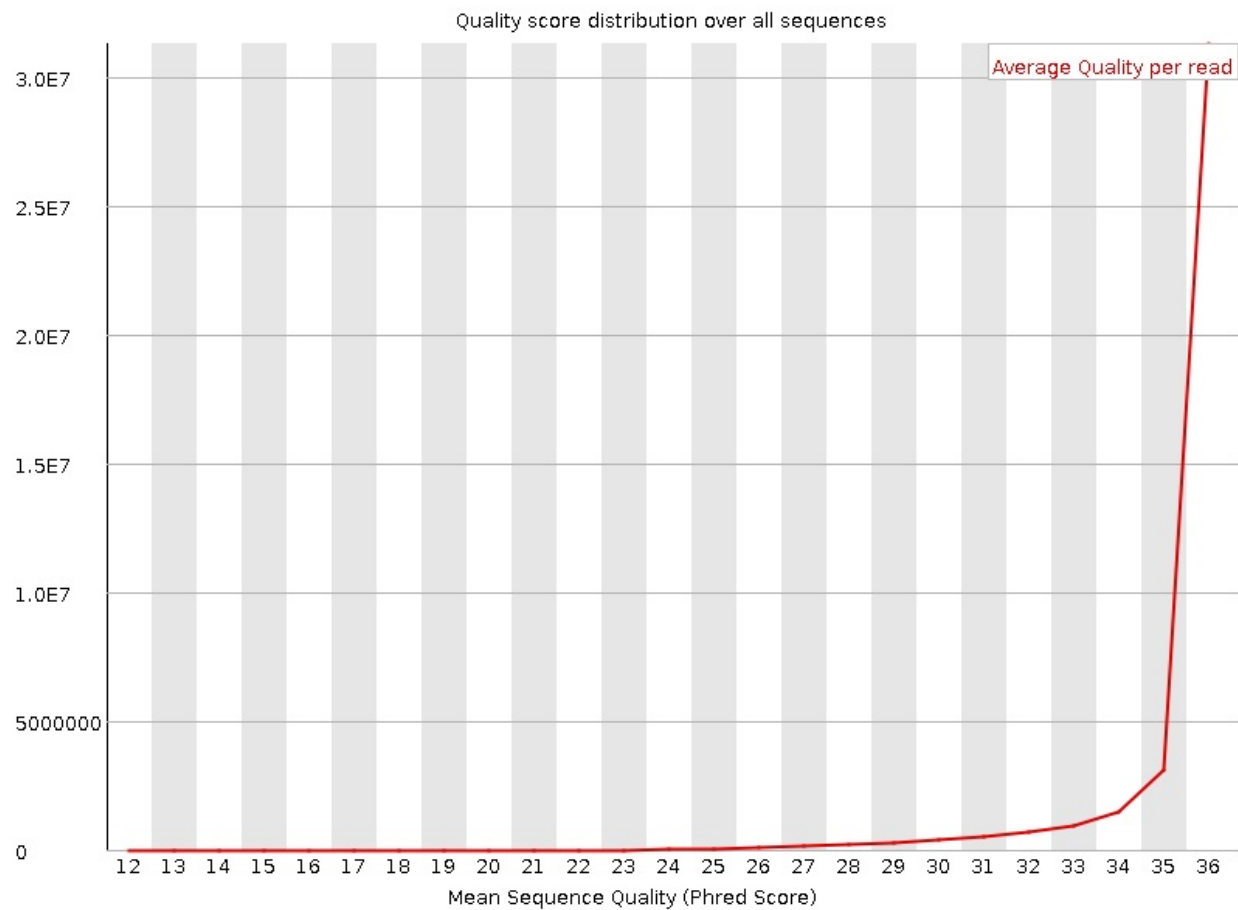


Per tile sequence quality

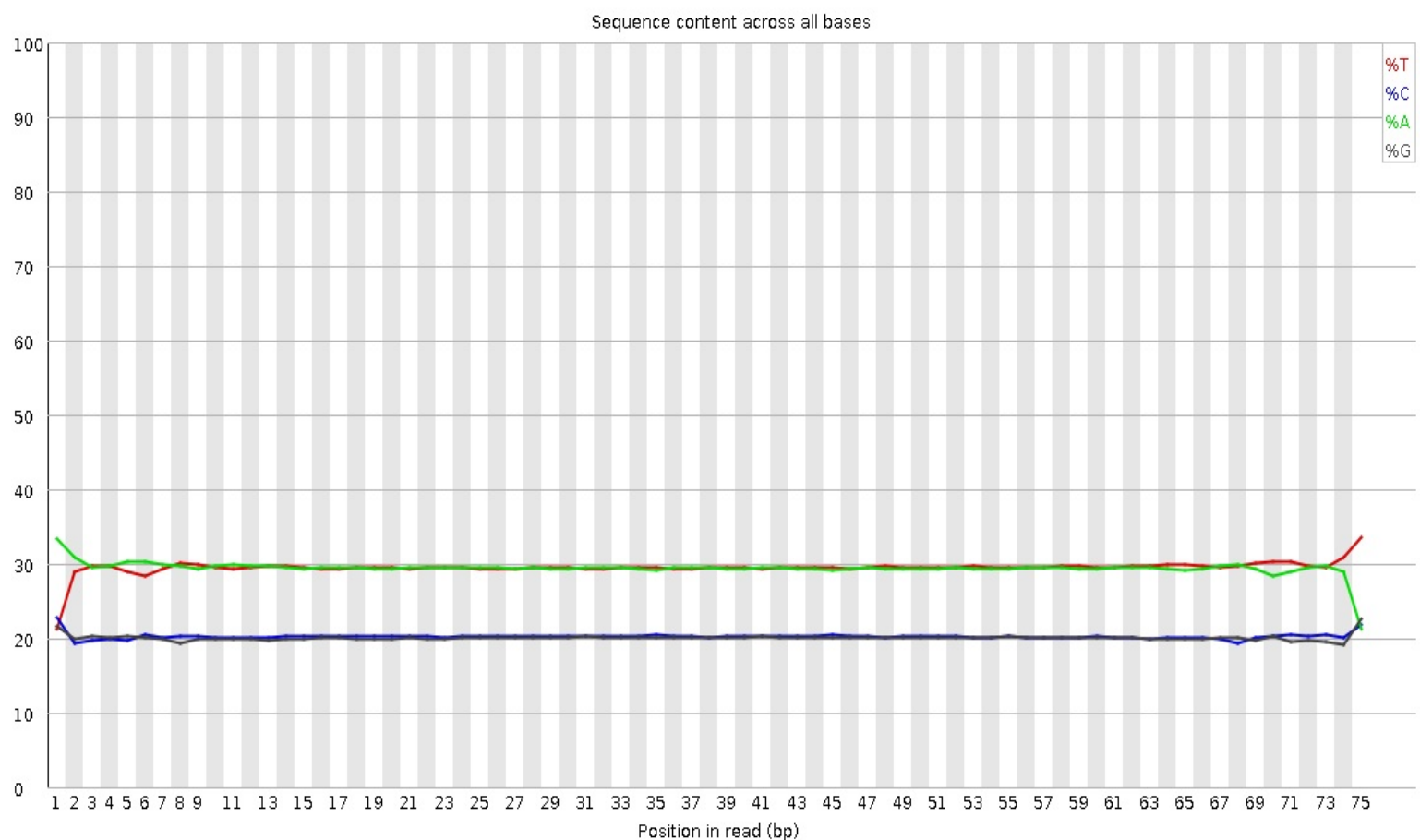
Quality per tile



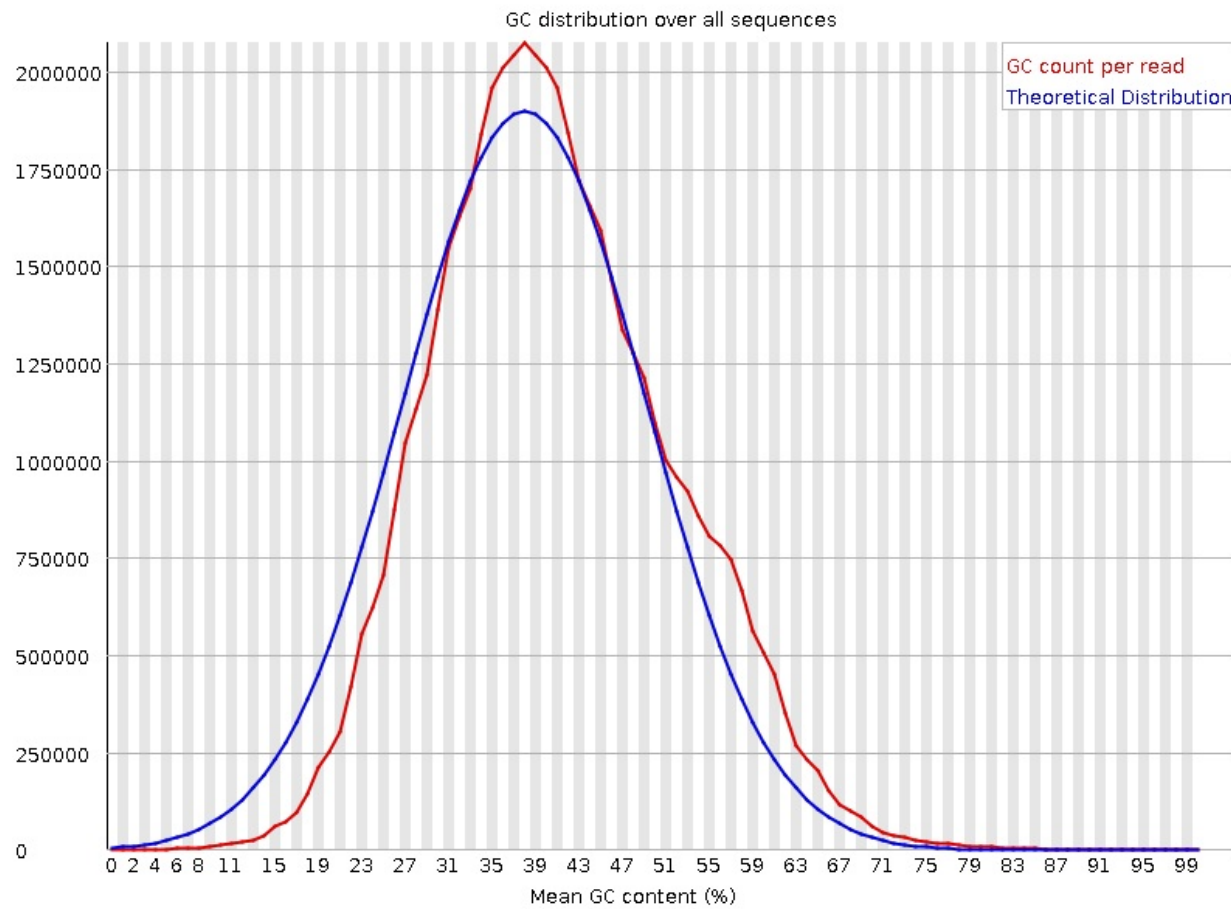
✔ Per sequence quality scores



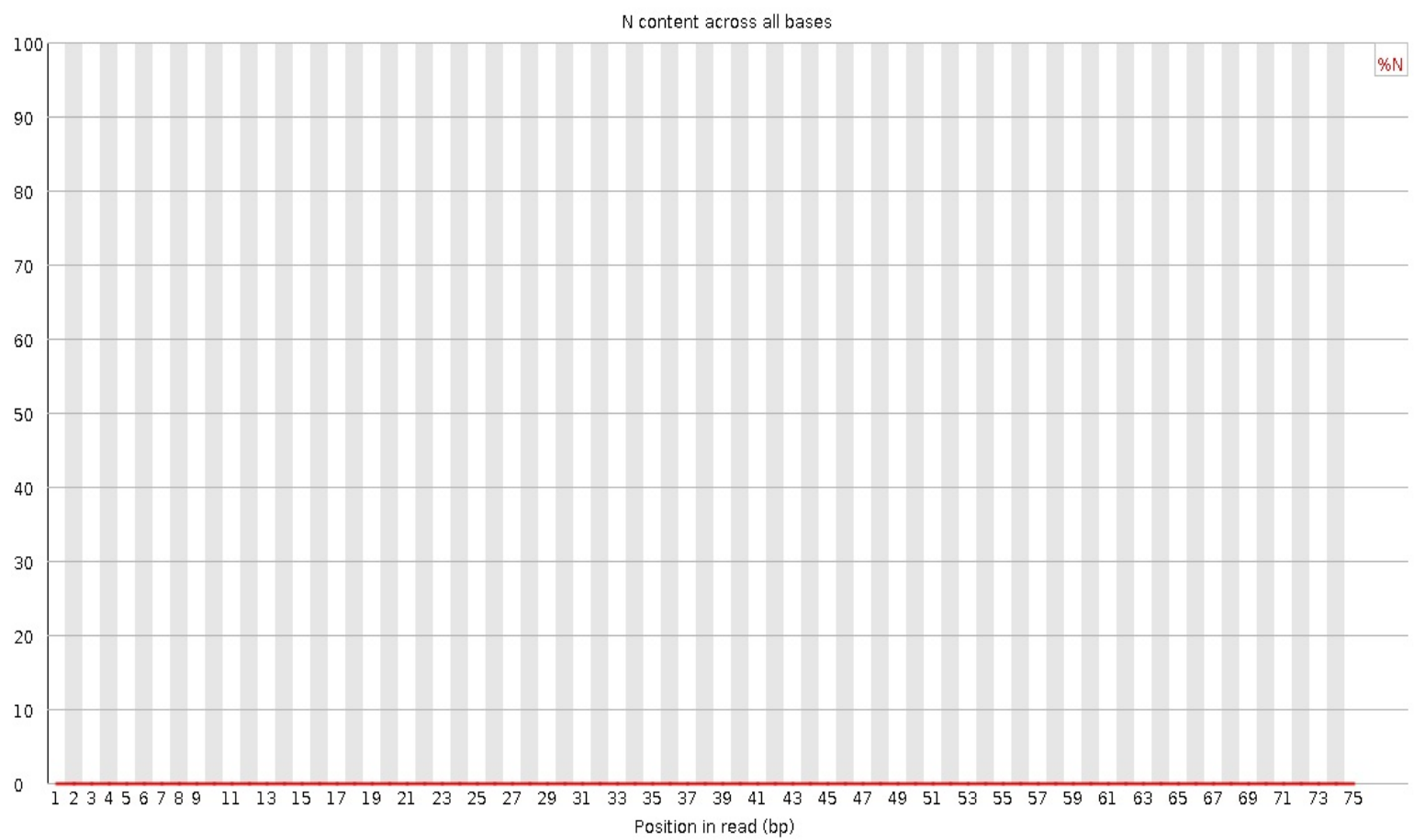
⚠ Per base sequence content



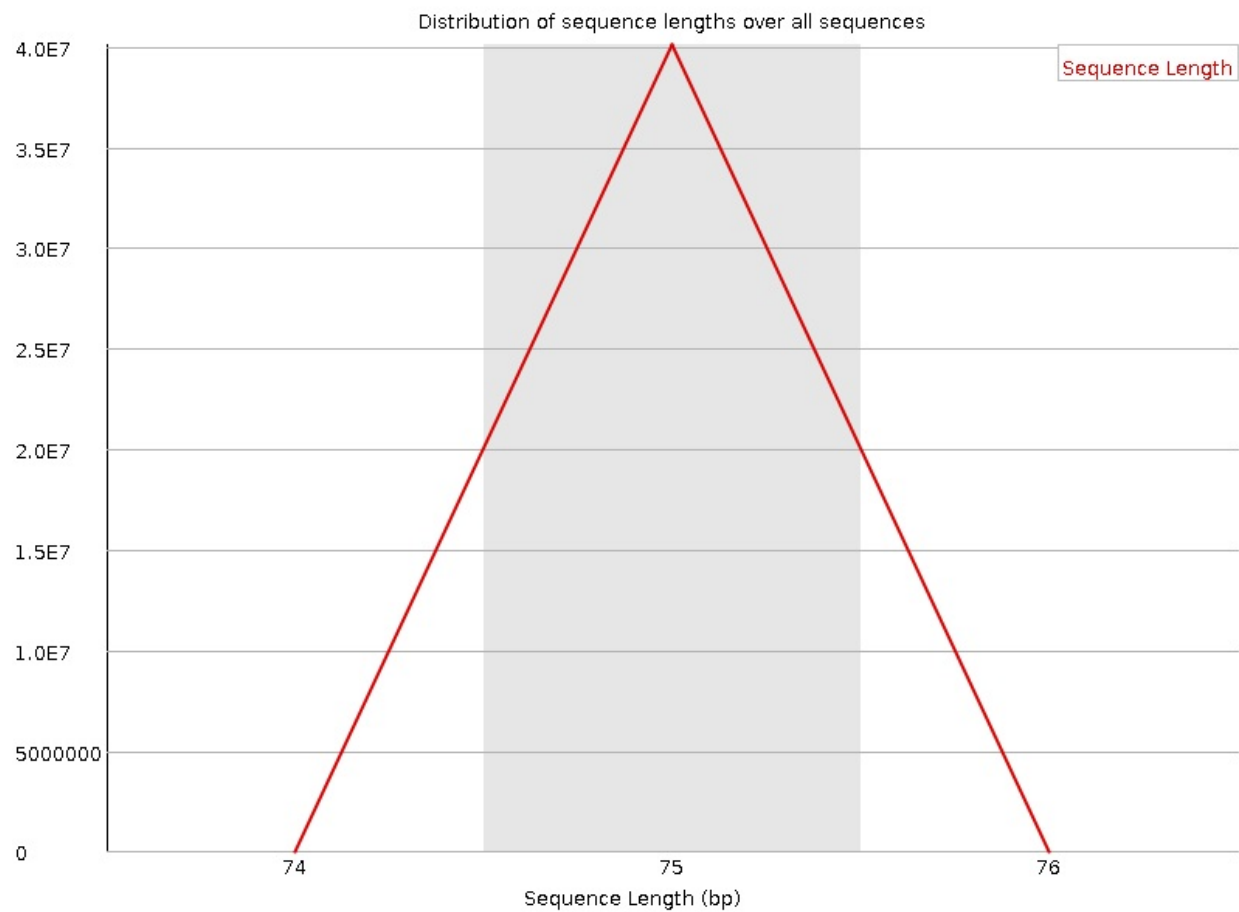
⚠ Per sequence GC content



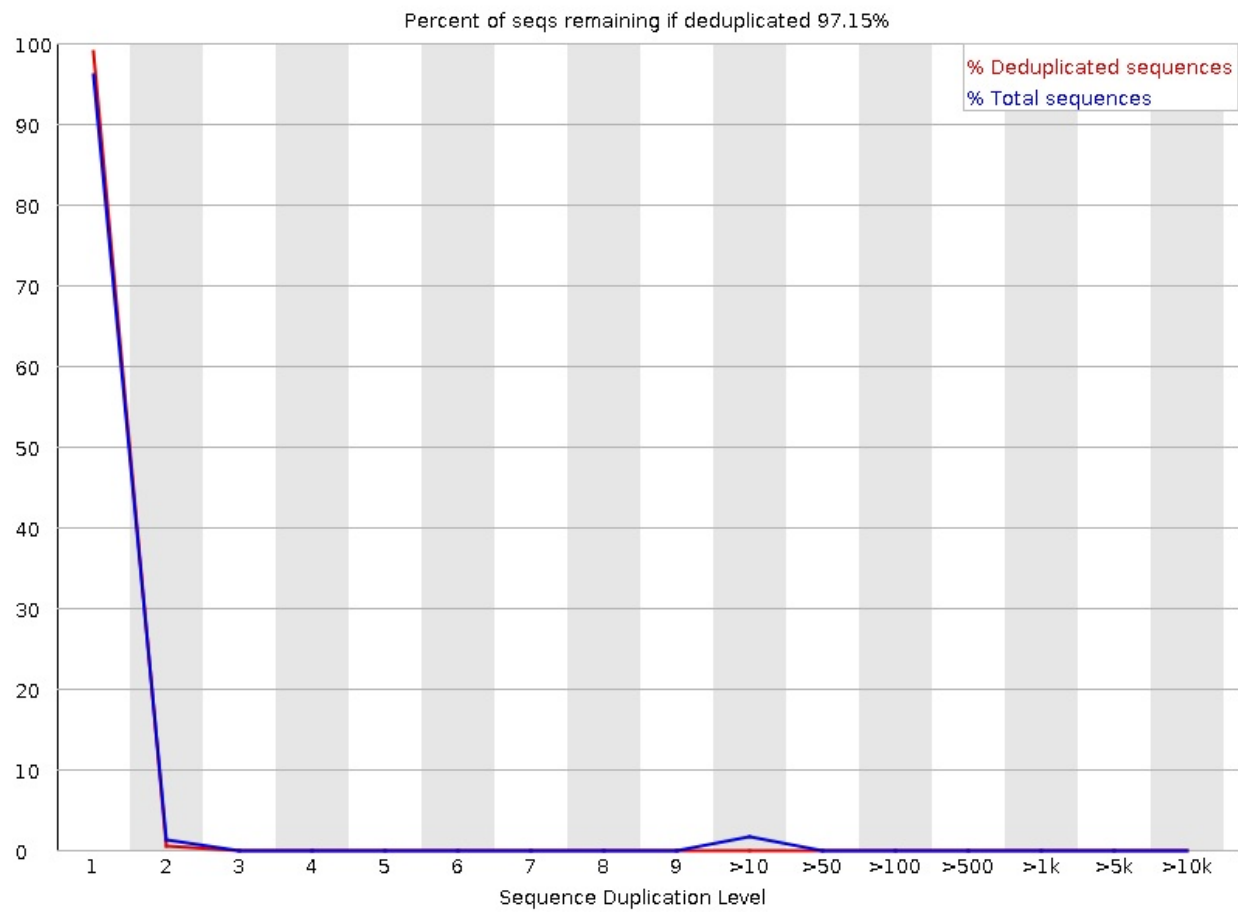
✅ Per base N content



✔ Sequence Length Distribution



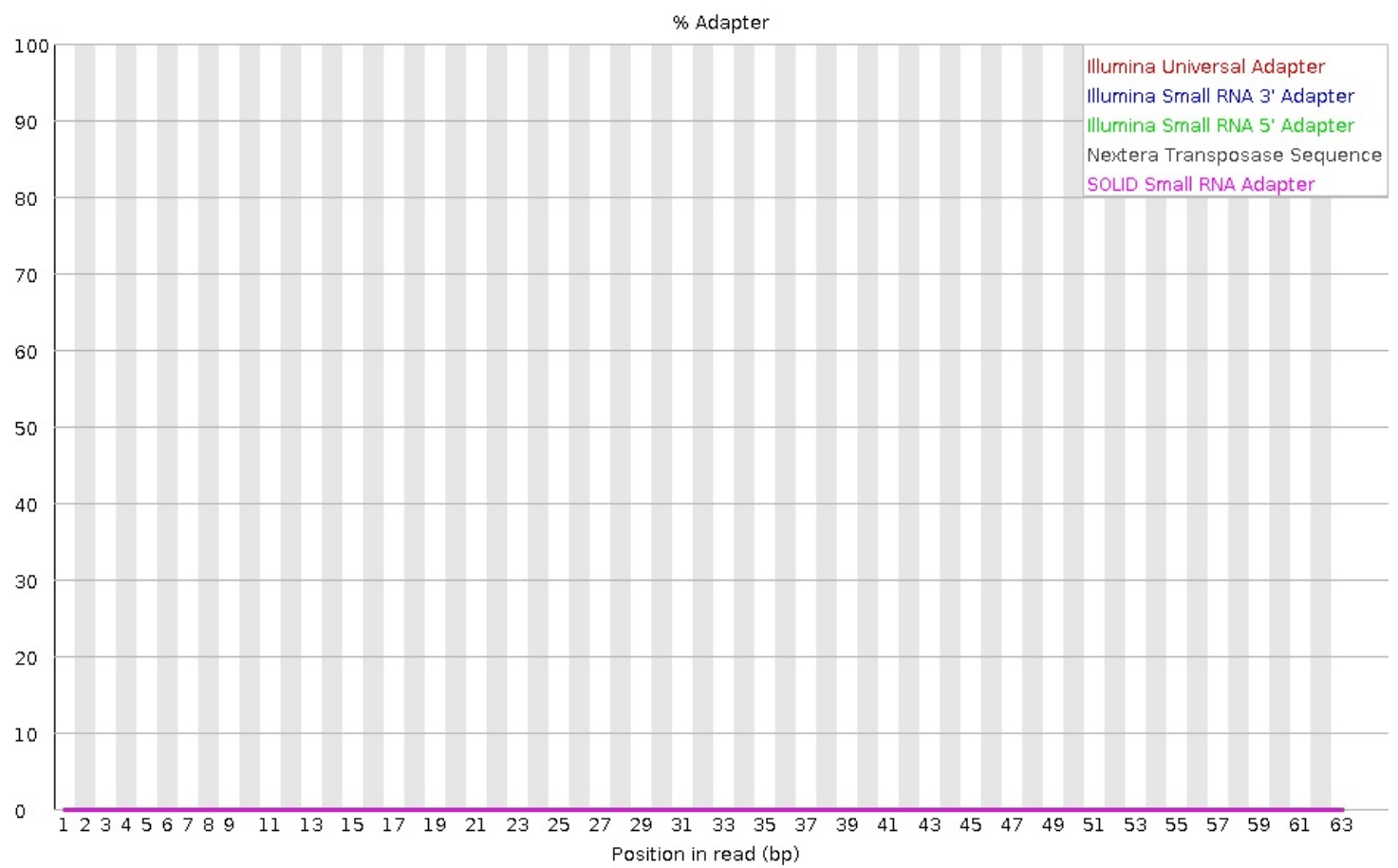
✔ Sequence Duplication Levels



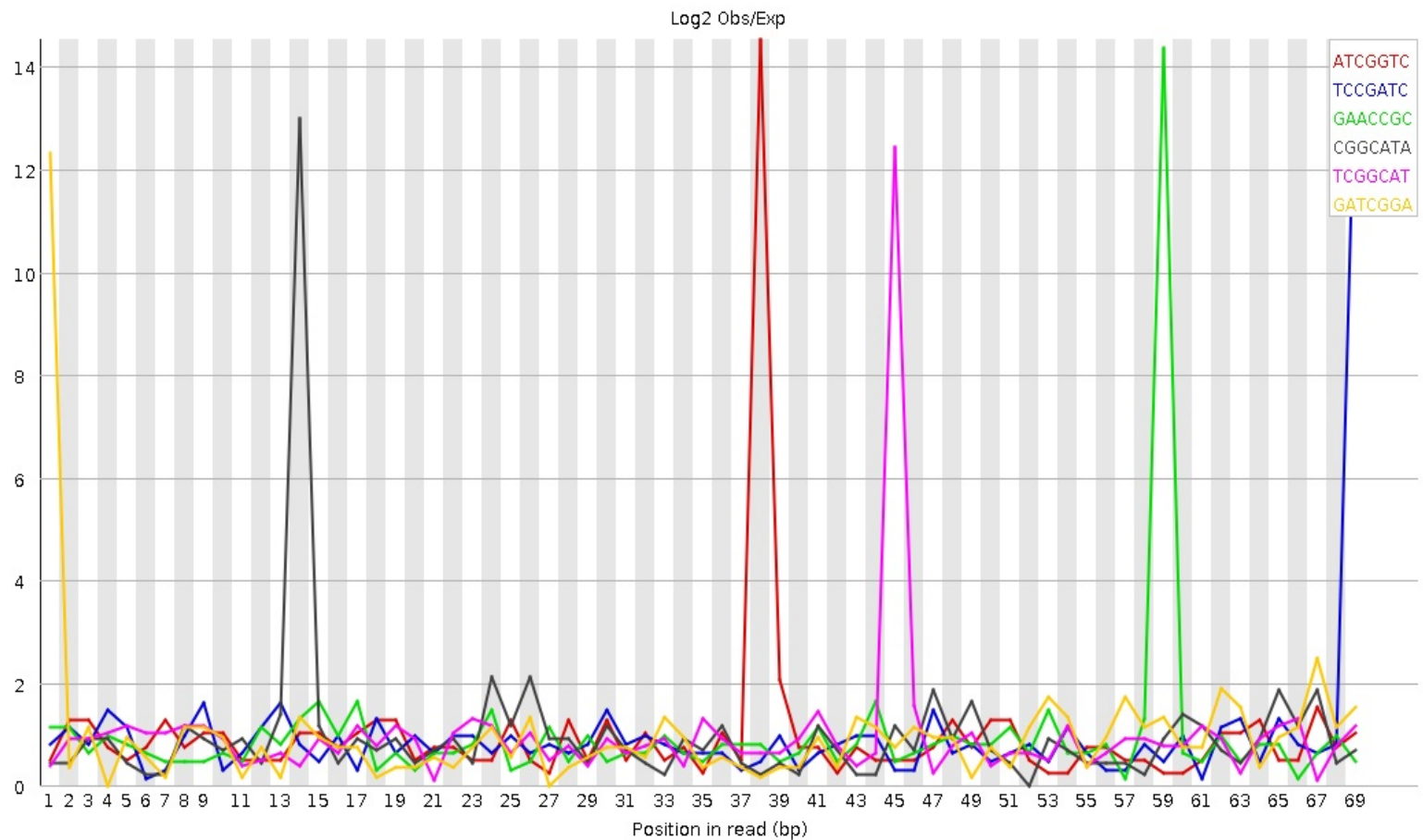
✔ Overrepresented sequences

No overrepresented sequences

✔ Adapter Content



✖ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCGGTC	1330	0.0	14.527284	38

TCCGATC	2095	0.0	14.493389	69
GAACCGC	2065	0.0	14.36663	59
CGGCATA	1460	0.0	12.996224	14
TCGGCAT	2605	0.0	12.450337	45
GATCGGA	1790	0.0	12.336171	1
GATCGGT	1680	0.0	11.911508	37
ACCGCTC	2565	0.0	11.834595	61
GCGGTTC	1920	0.0	11.498815	11
AACCGCT	2775	0.0	11.311896	60
TTCCGAT	2930	0.0	11.067755	68
TGAACCG	2940	0.0	10.795035	58
CGGCATT	3195	0.0	10.367186	46
ATGCCGA	2280	0.0	9.987669	25
CTTCCGA	3260	0.0	9.947412	67
GCATACG	1995	0.0	9.8567295	16
GAGCGGT	2460	0.0	9.535317	9
CTCGGCA	3455	0.0	9.487203	44
TACGAGA	2165	0.0	9.401747	19
CCGCTCT	3355	0.0	9.253486	62