

FastQC Report

Summary

Sun 3 Apr 2016
18418_2#1_2.fastq

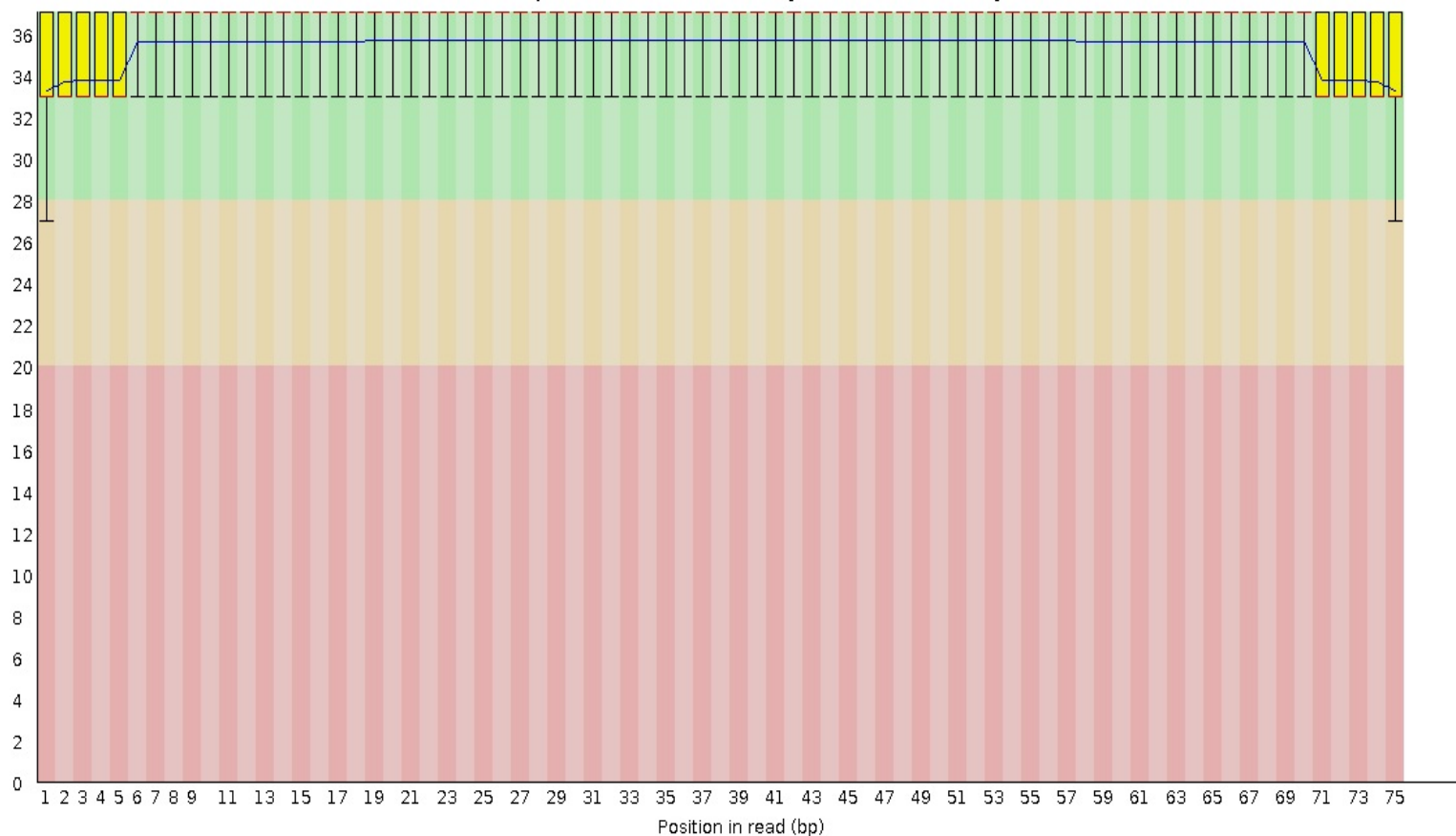
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Basic Statistics

Measure	Value
Filename	18418_2#1_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	40095362
Sequences flagged as poor quality	0
Sequence length	75
%GC	41

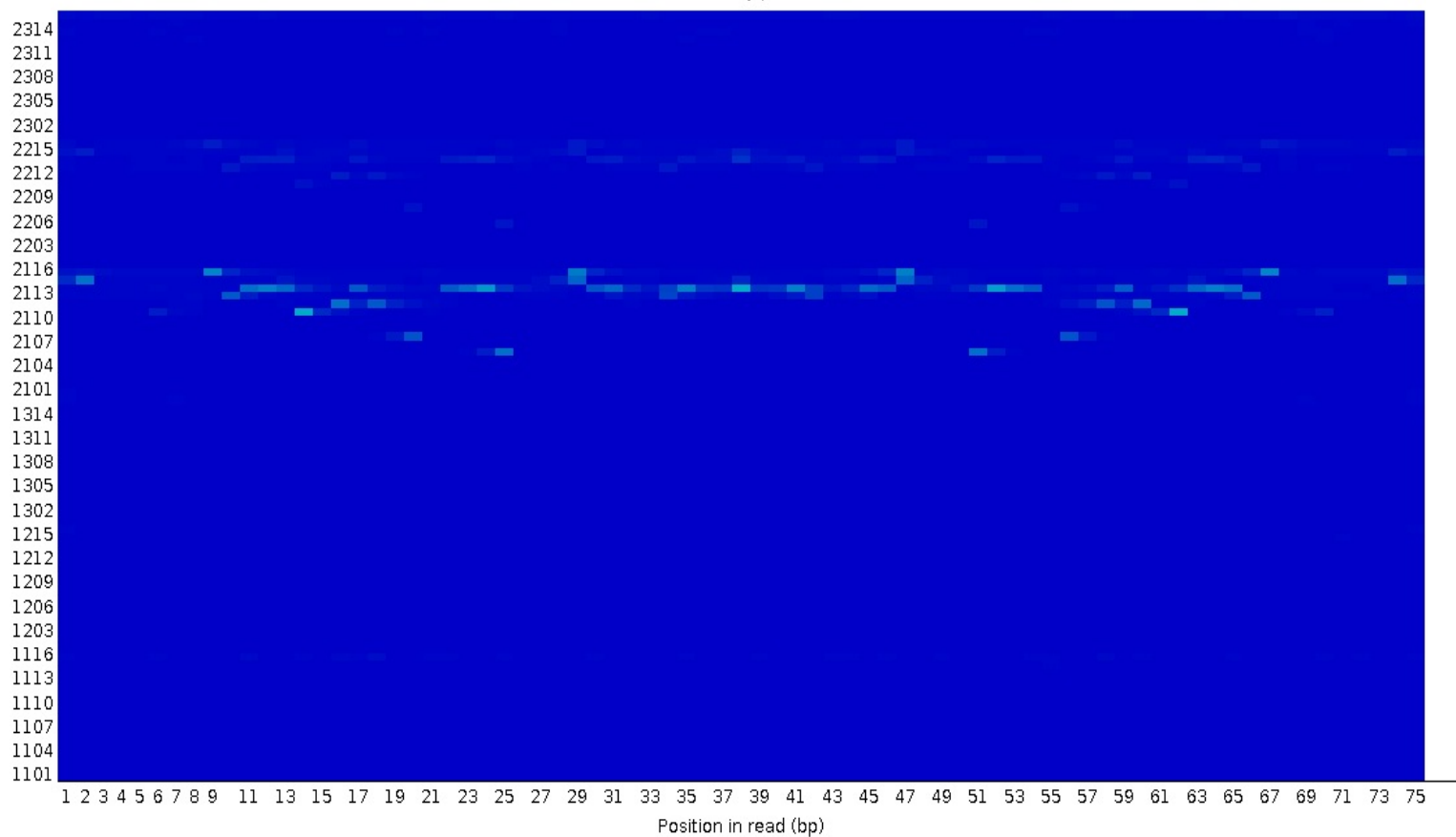
Per base sequence quality

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

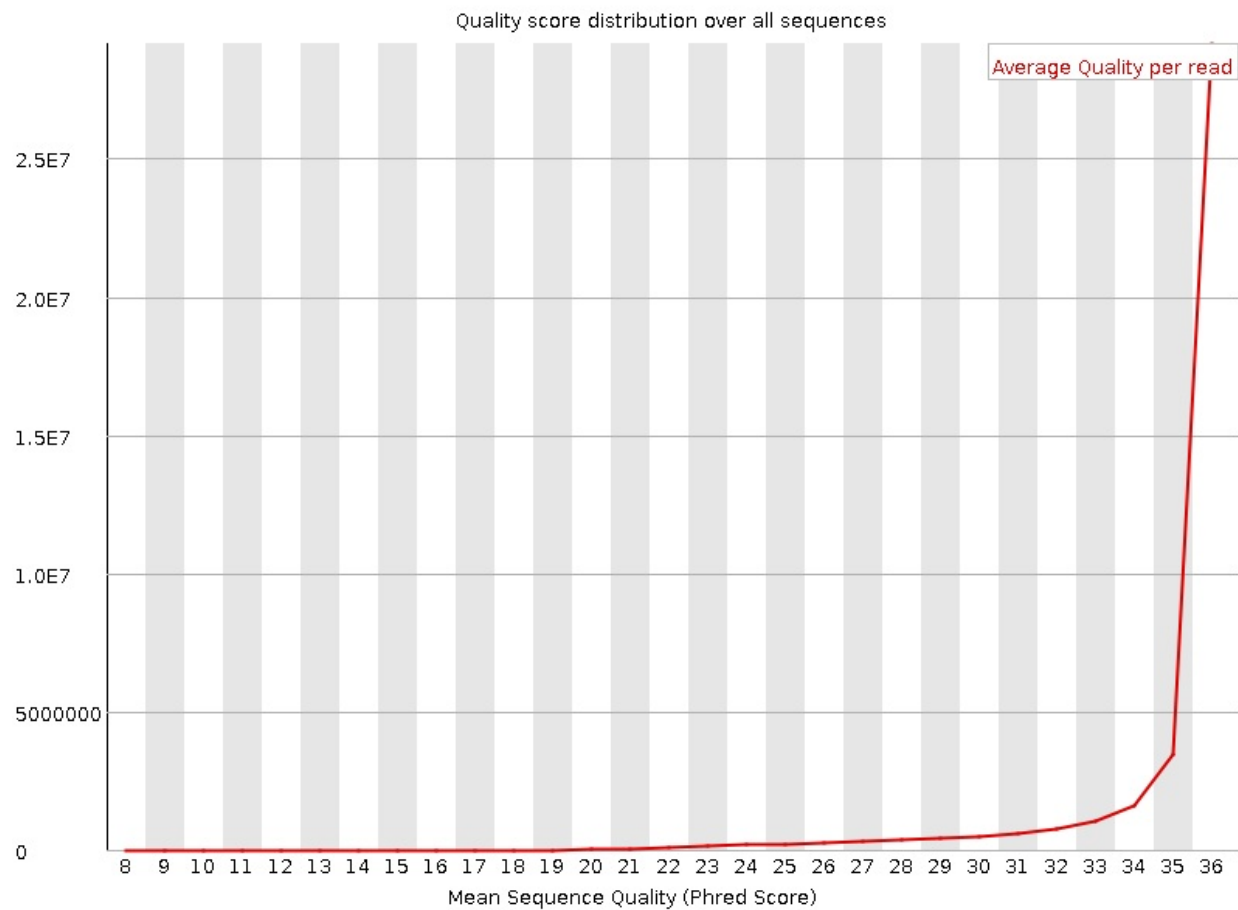


Per tile sequence quality

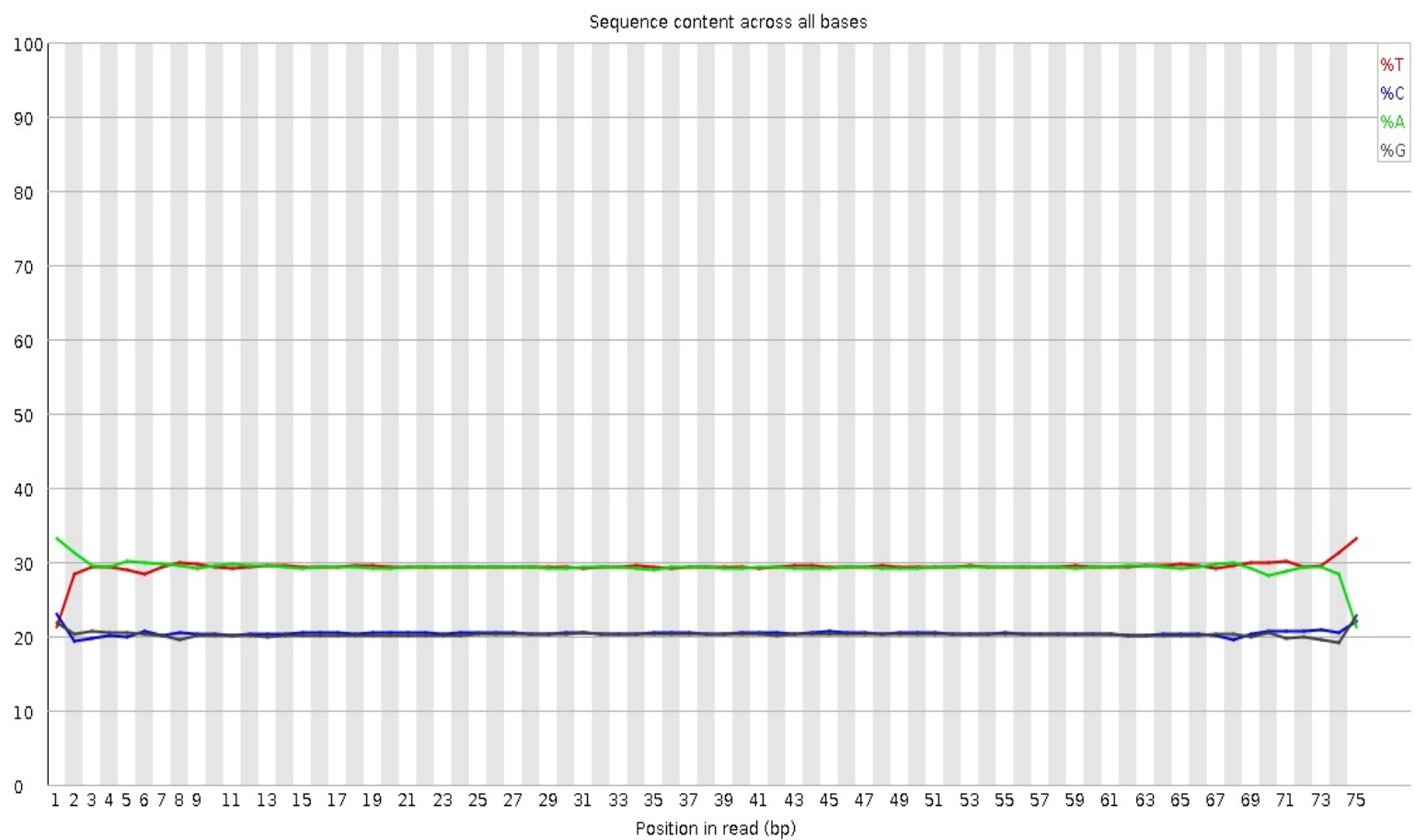
Quality per tile



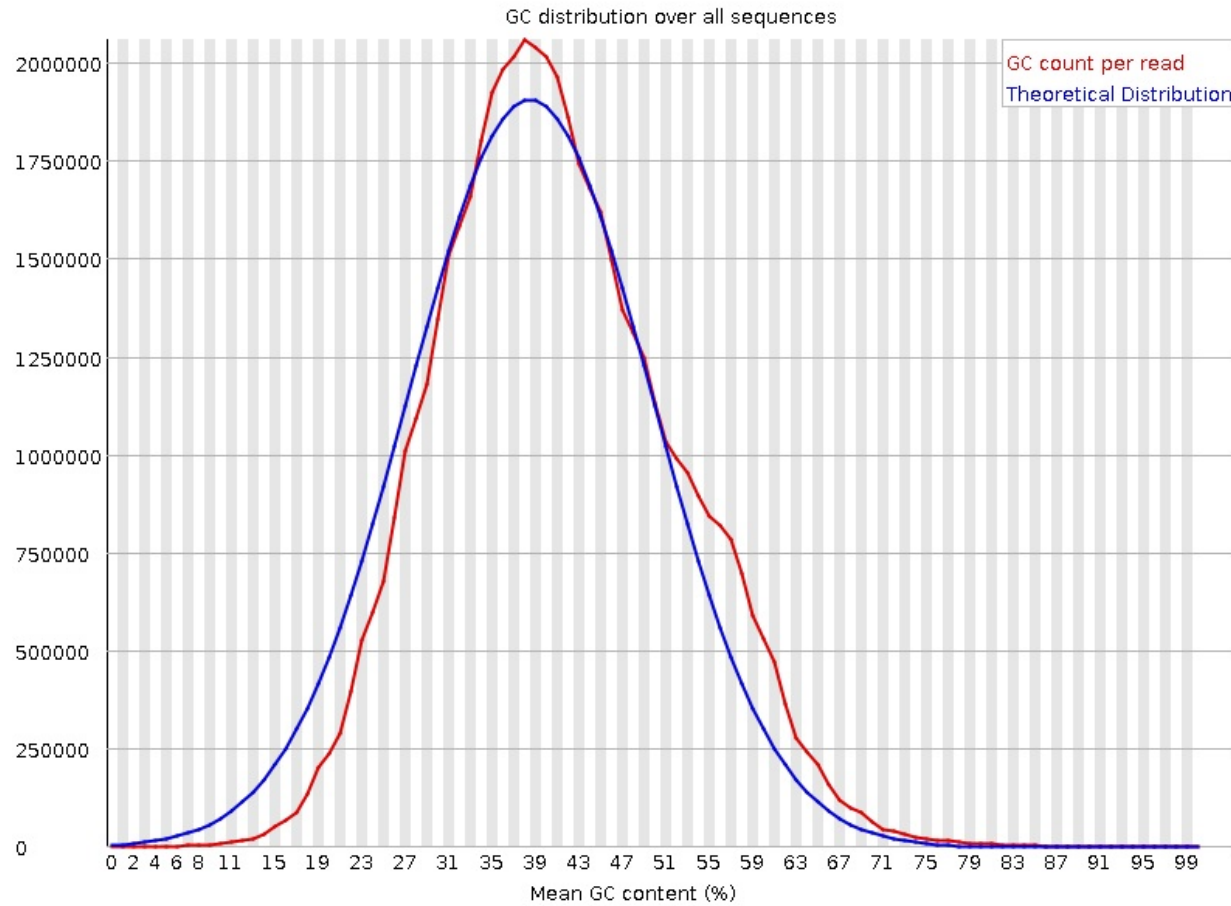
✅ Per sequence quality scores



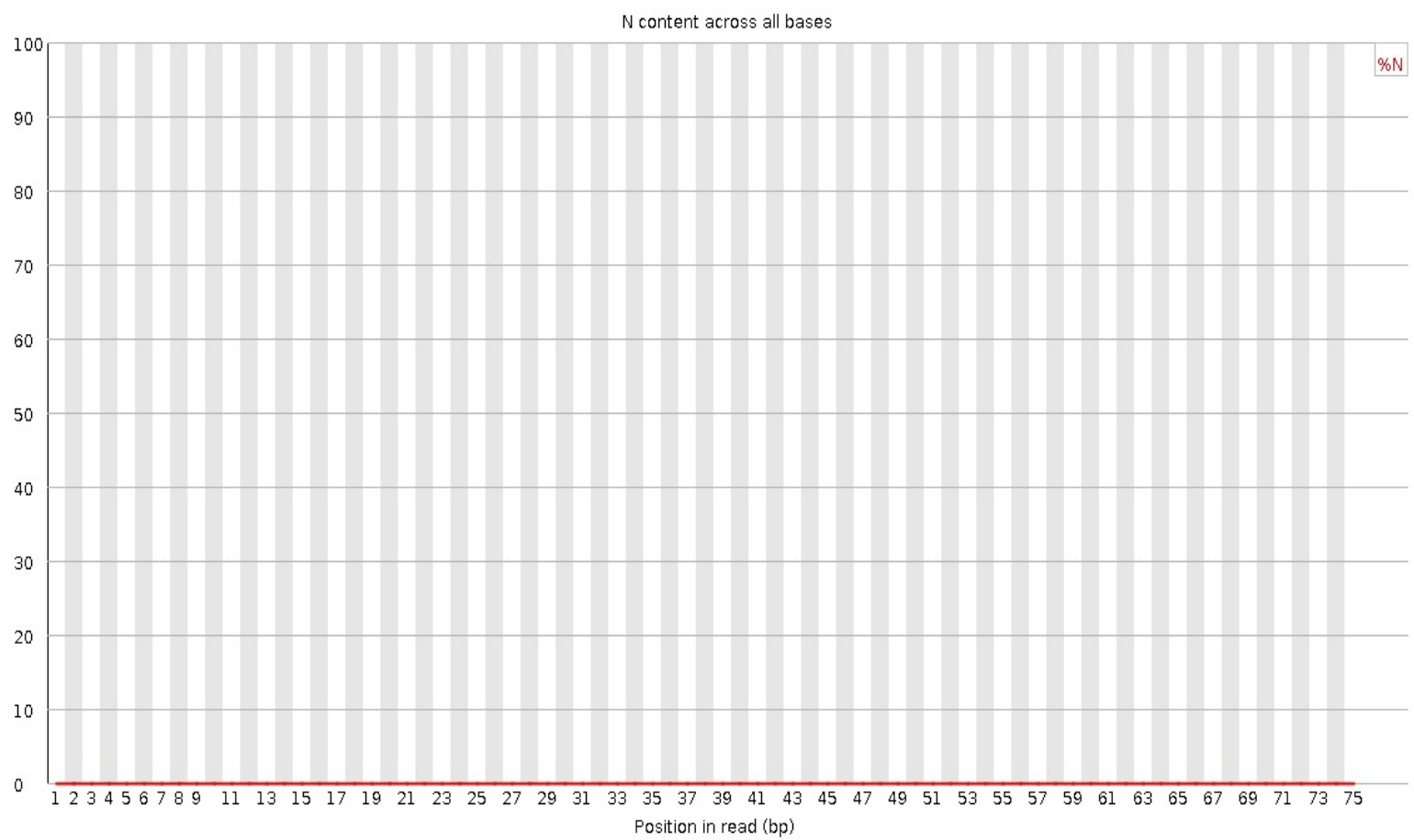
⚠️ Per base sequence content



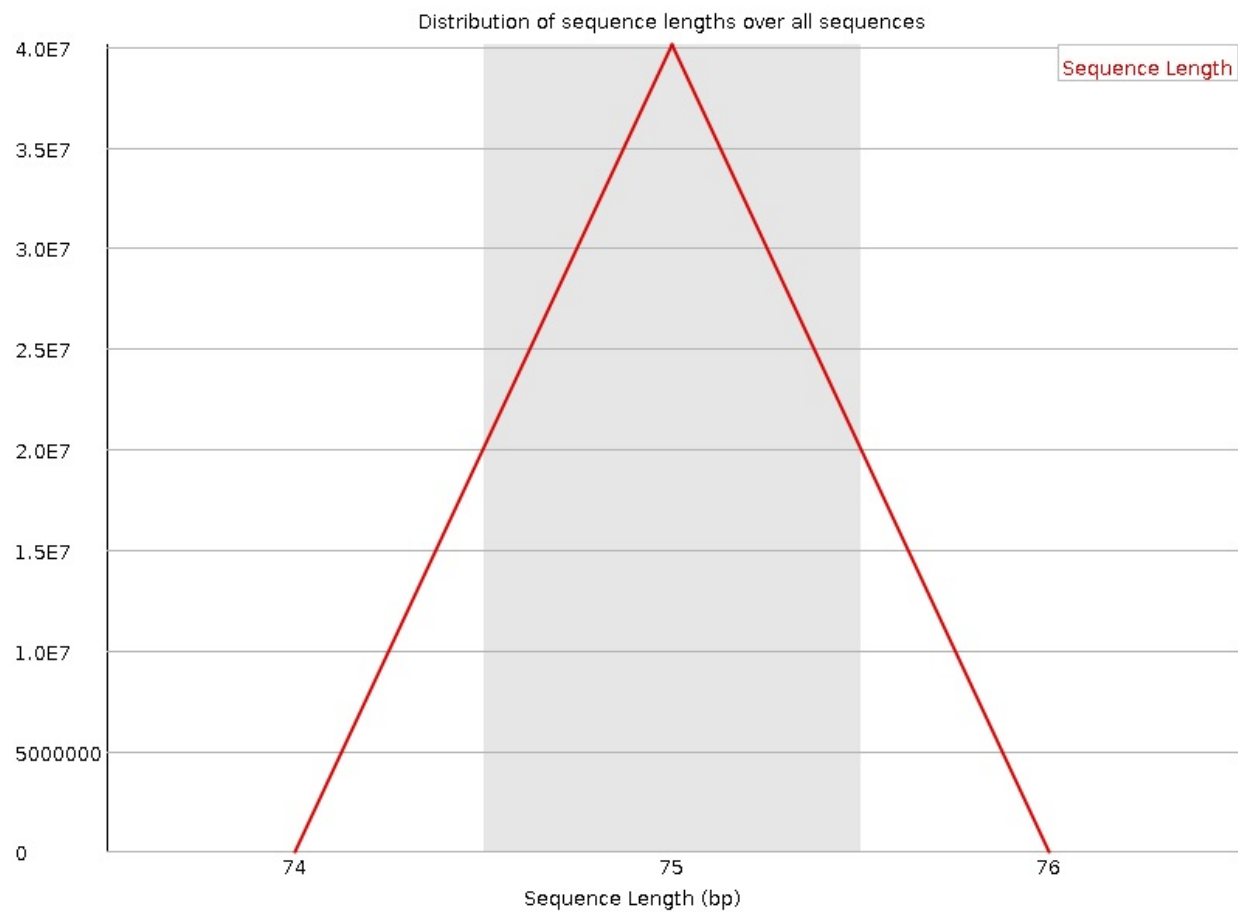
✔ Per sequence GC content



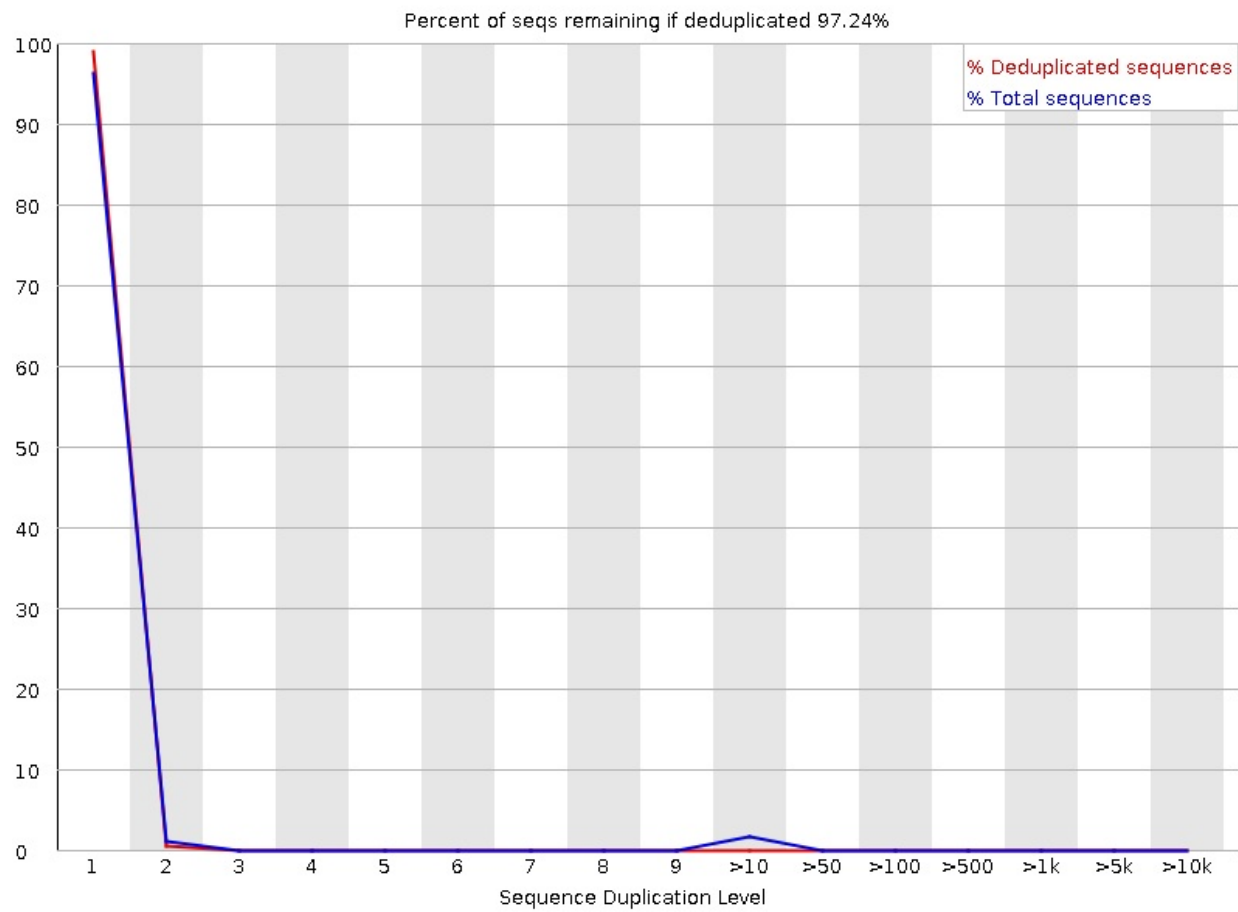
✔ Per base N content



✔ Sequence Length Distribution



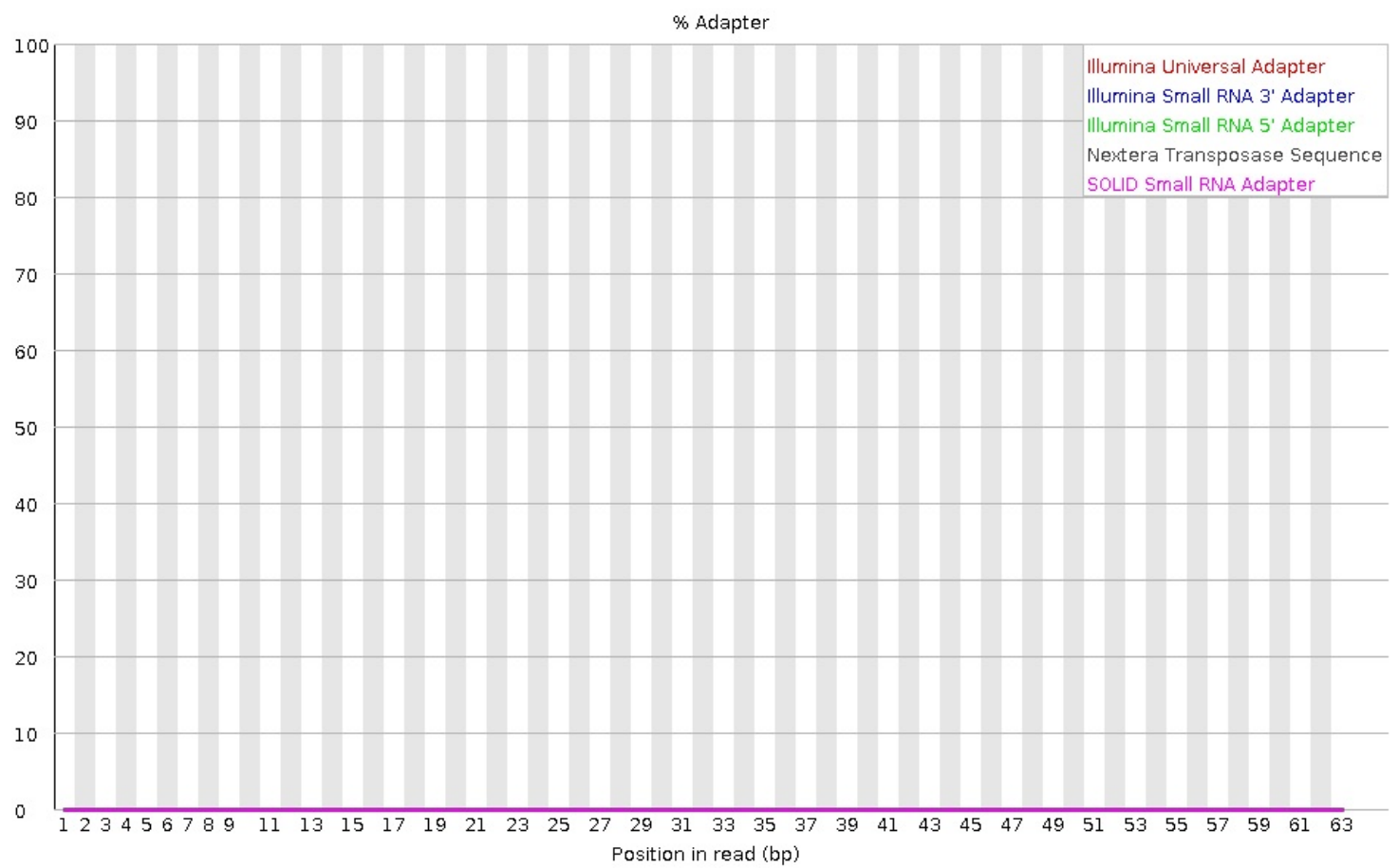
✔ Sequence Duplication Levels



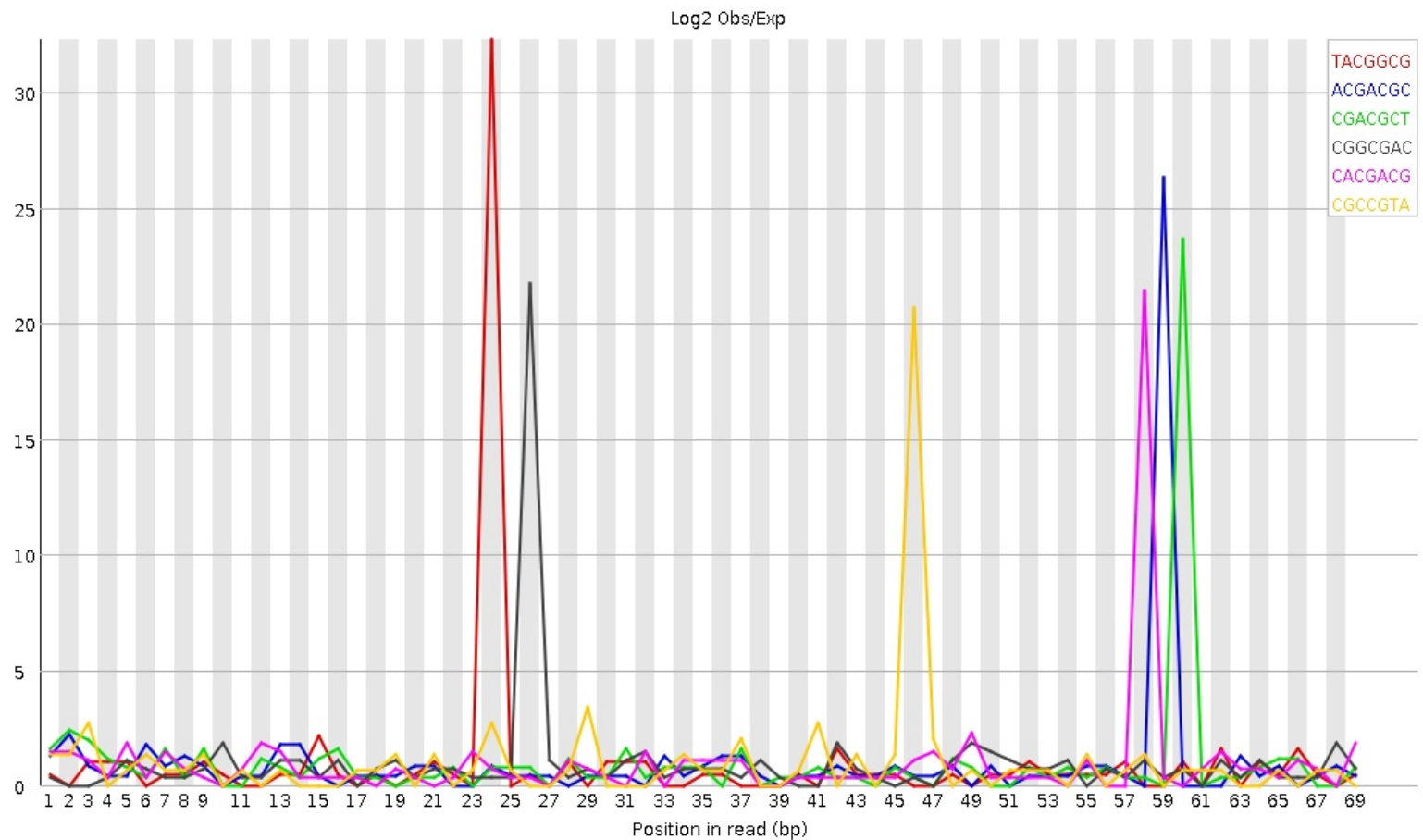
✔ Overrepresented sequences

No overrepresented sequences

✔ Adapter Content



✖ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGCG	620	0.0	32.27551	24

ACGACGC	760	0.0	26.32815	59
CGACGCT	845	0.0	23.679728	60
CGGCGAC	905	0.0	21.730438	26
CACGACG	900	0.0	21.466042	58
CGCCGTA	500	0.0	20.700481	46
ACGGCGA	995	0.0	19.764896	25
GCGTCGT	705	0.0	16.638313	11
GTCGCCG	760	0.0	14.5268345	44
GCGACCA	1590	0.0	14.321499	28
TCGCCGT	775	0.0	14.2457075	45
ATACGGC	1610	0.0	13.500635	23
CGTCGTG	880	0.0	13.329492	12
AGCGTCG	835	0.0	12.808346	10
GGCGACC	1910	0.0	12.102754	27
TCCGATC	1965	0.0	10.886198	69
GACGCTC	2290	0.0	9.641605	61
ACACGAC	2325	0.0	9.4965925	57
CGACCAC	2375	0.0	9.006728	29
GATACGG	2370	0.0	8.87981	22