

FastQC Report

Wed 28 Sep 2016

M_16_F0932_0_B_MSS1_cDNA_pool_BacteriaEnterobacter_ATCACG_L003_R1_001.fastq.gz

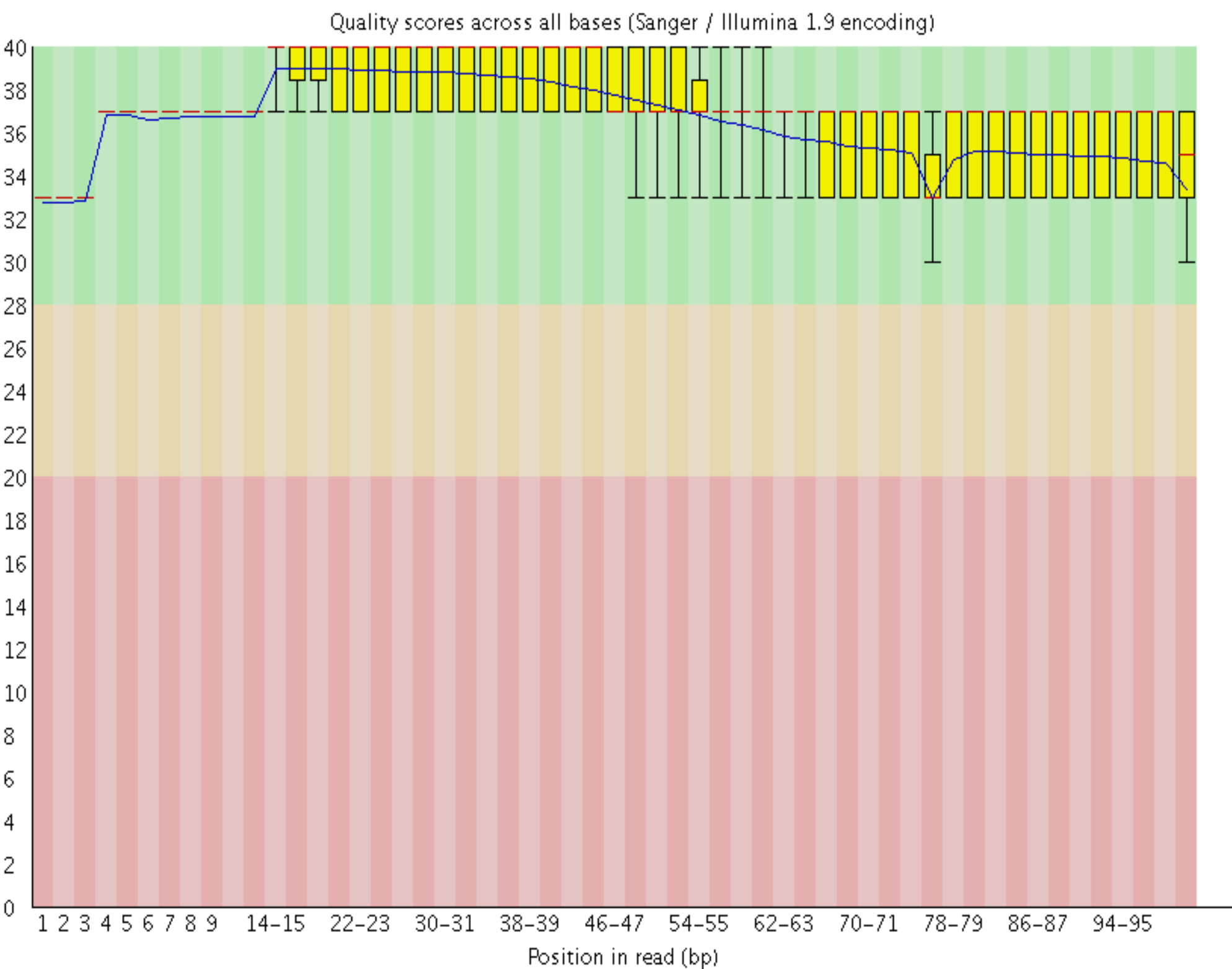
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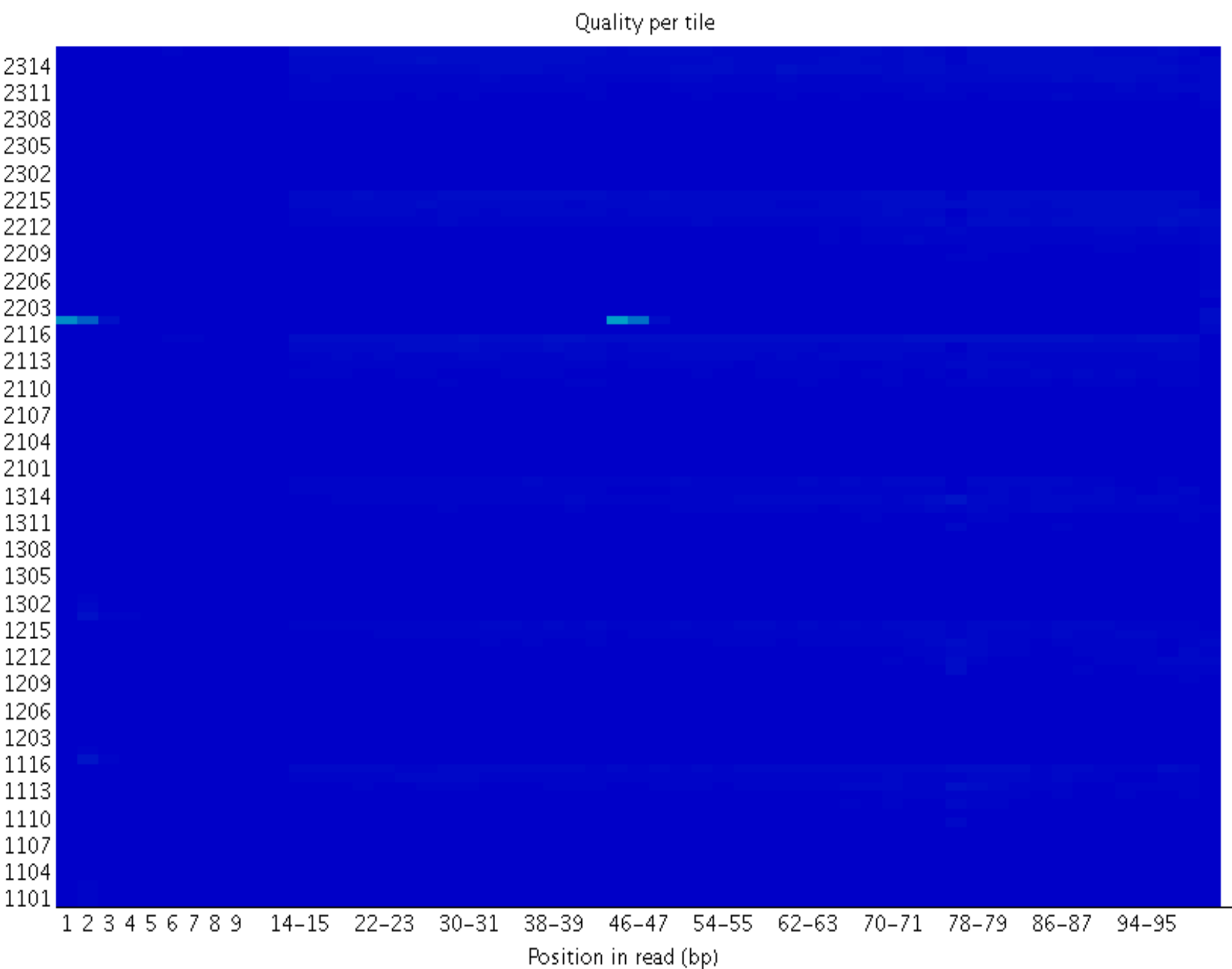
Basic Statistics

Measure	Value
Filename	M_16_F0932_0_B_MSS1_cDNA_pool_BacteriaEnterobacter_ATCACG_L003_R1_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	7023308
Sequences flagged as poor quality	0
Sequence length	101
%GC	53

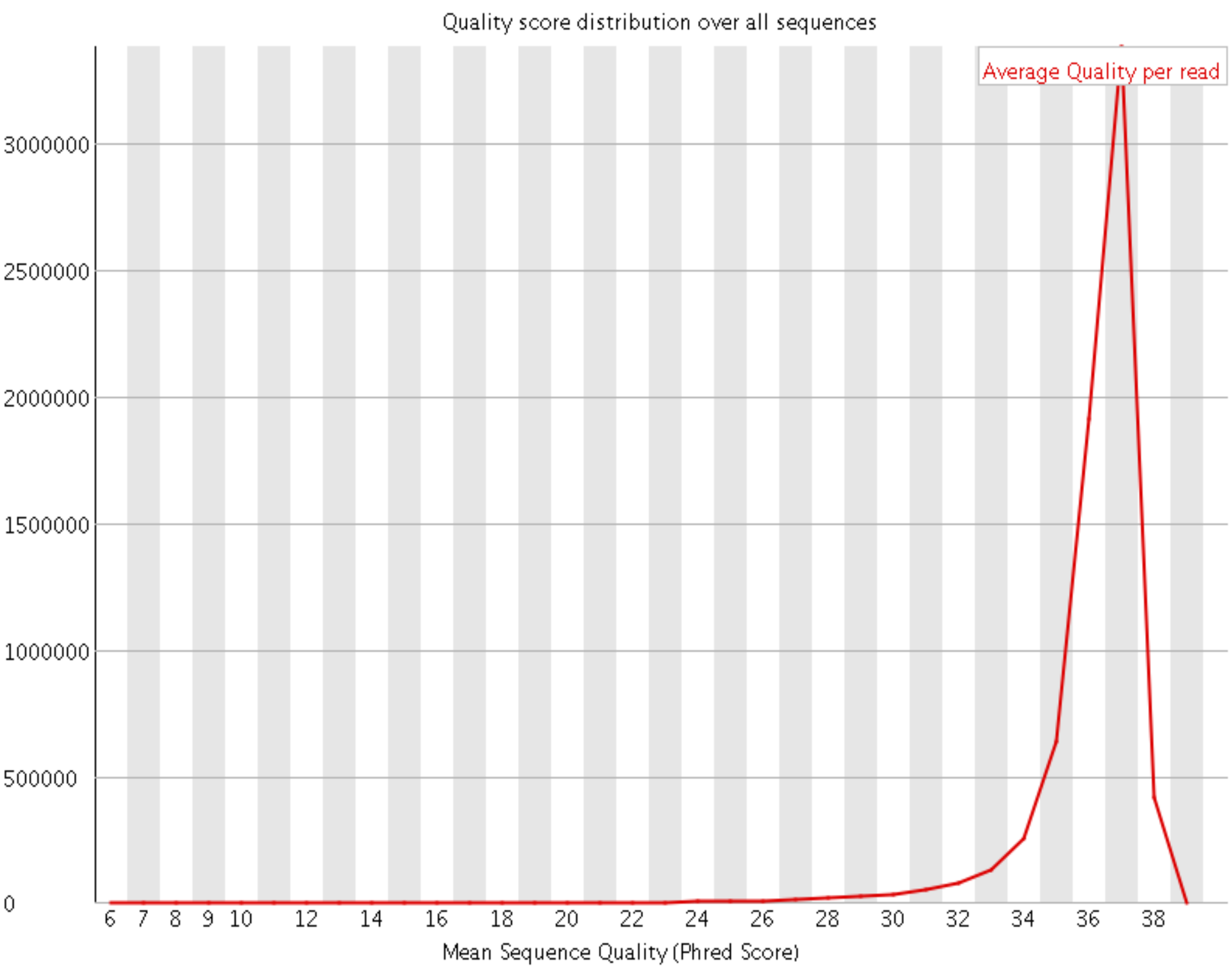
✔ Per base sequence quality



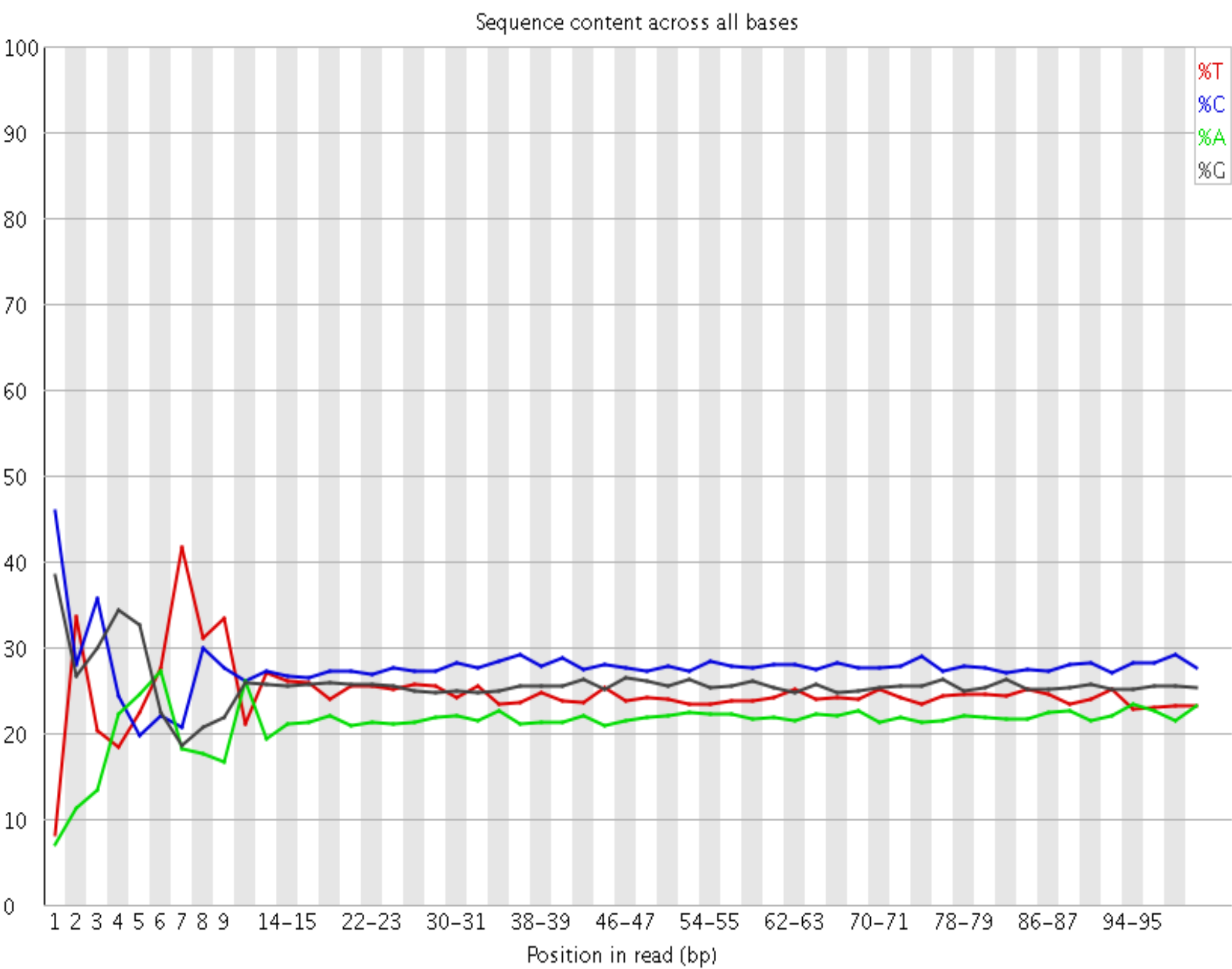
✔ Per tile sequence quality



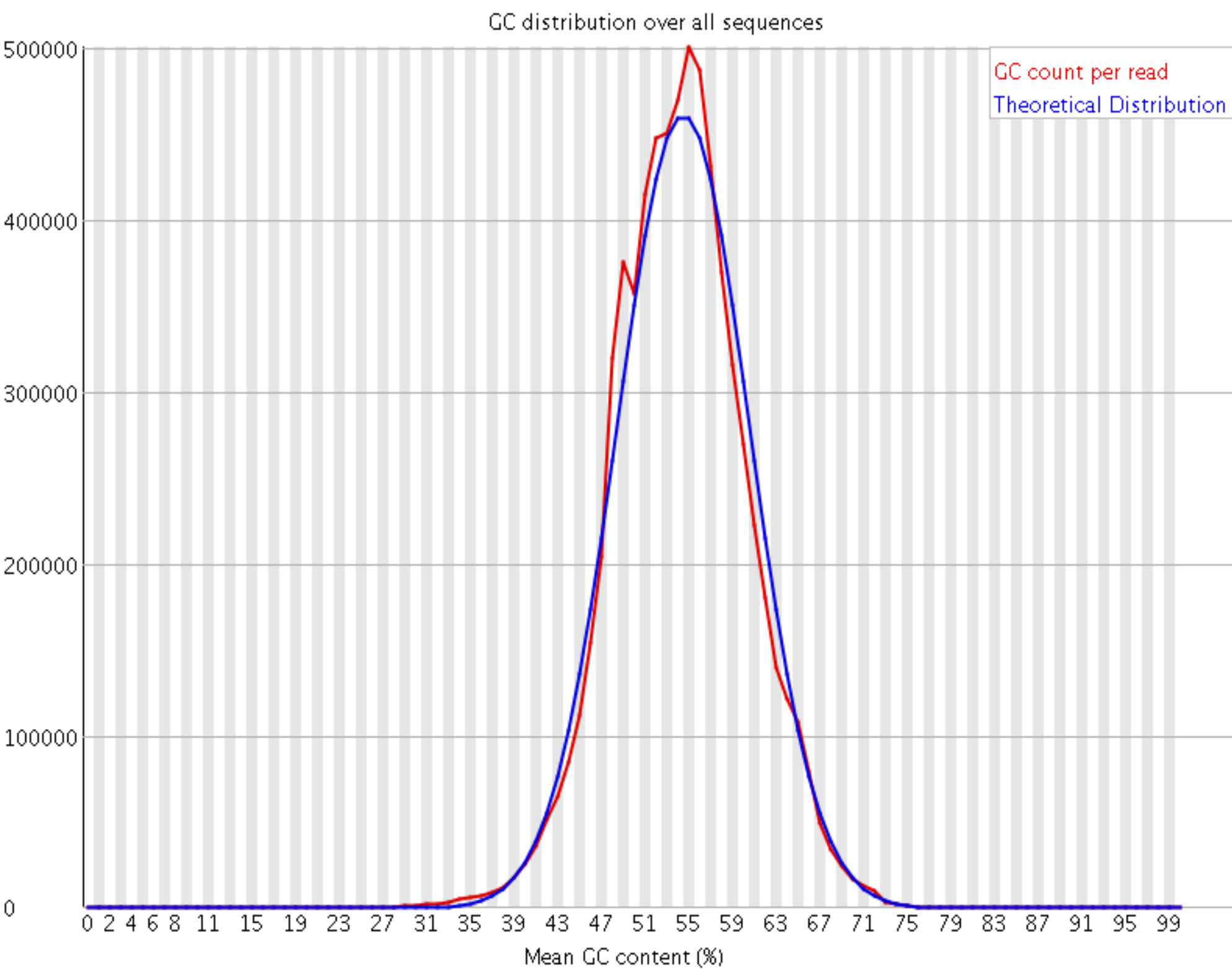
✔ Per sequence quality scores



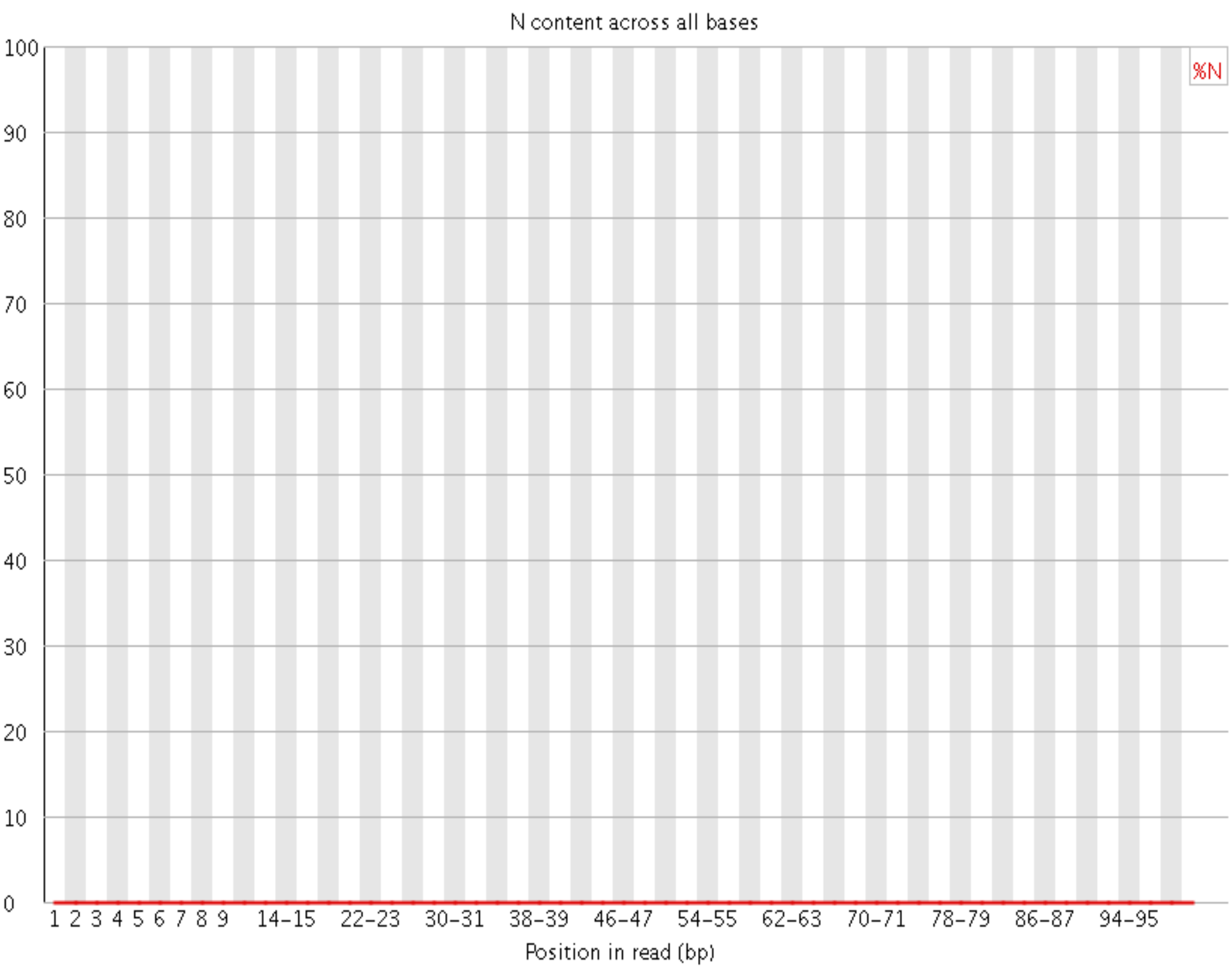
❌ Per base sequence content



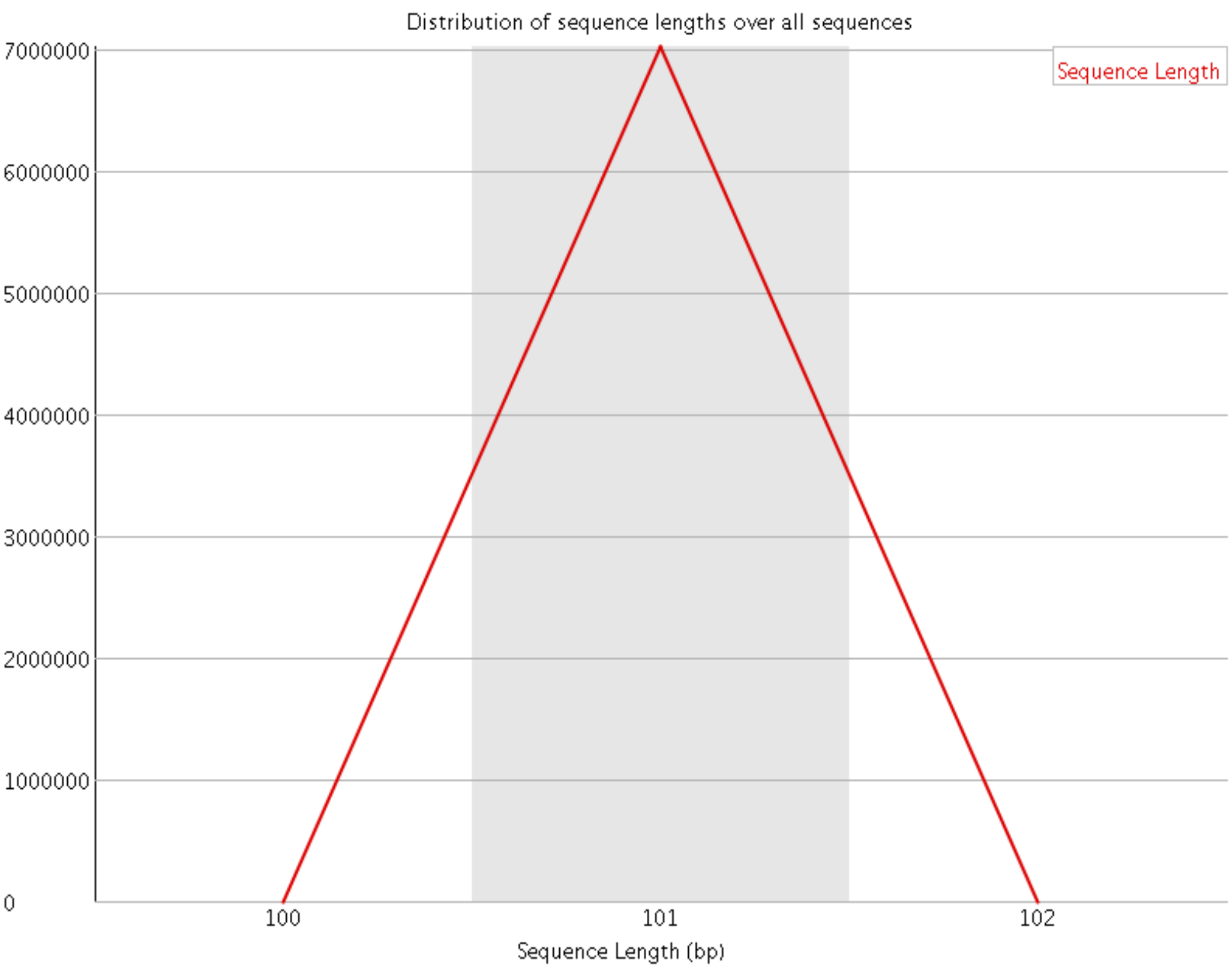
✅ Per sequence GC content



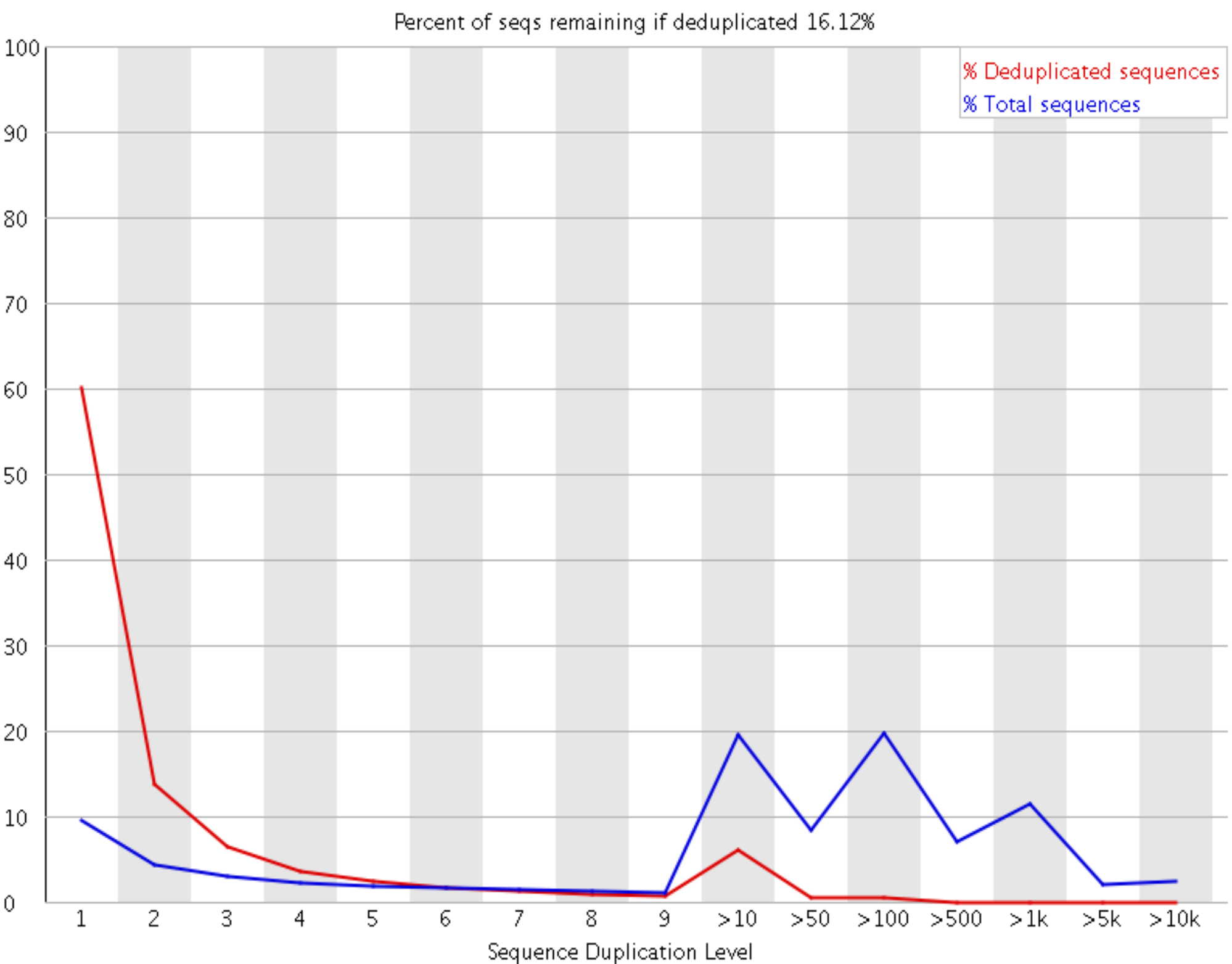
✅ Per base N content



✔ Sequence Length Distribution



❌ Sequence Duplication Levels



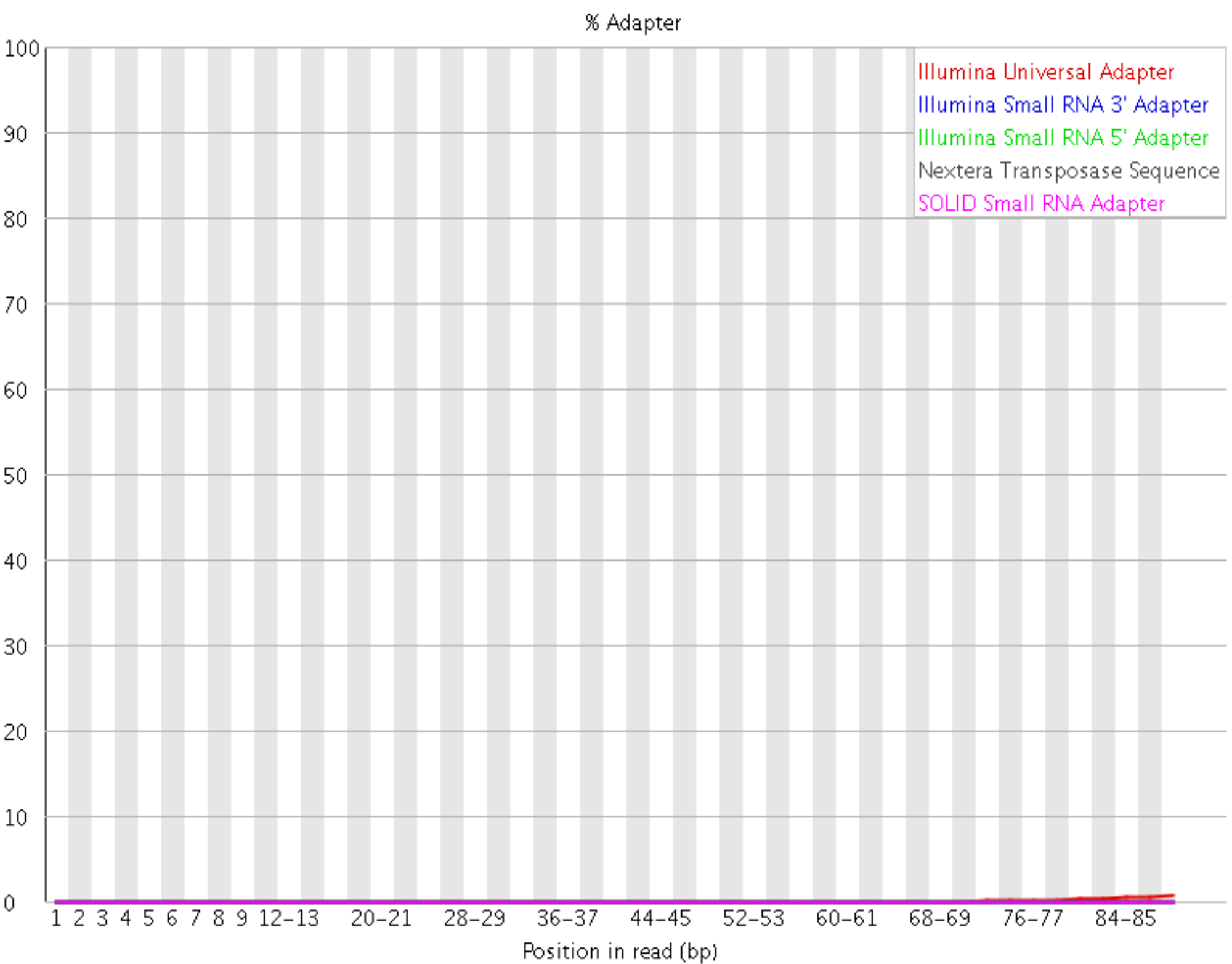
❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CTCGGTACTACATGCTTAGTCTGTCTTTACATTACCTGCCAGCTGCGAA	98187	1.3980164332818668	No Hit
CCTCGGTACTACATGCTTAGTCTGTCTTTACATTACCTGCCAGCTGCGA	20889	0.29742394894257806	No Hit
CGGTACTACATGCTTAGTCTGTCTTTACATTACCTGCCAGCTGCGAACA	20778	0.29584349710990887	No Hit
CCGGGTTCTGTCGTGGACAGTCATTCATCTAGGCCAGCAATCGCTCACTG	14168	0.2017283023897001	No Hit
GTCGTTGCTCAGCTGGTCAACTTTAGCGTTCAGAGTCTGAACGTCAGAAG	12856	0.18304764649364658	No Hit
GTGGAGCTGGCGGGAGTTGAACCCGCGTCCGAAATTCCTACATCCTCGGT	10634	0.15141013323066568	No Hit
GGCGGGAGTTGAACCCGCGTCCGAAATTCCTACATCCTCGGTACTACATG	10074	0.14343668254332573	No Hit
GCCGTACCTTGTGAACCCCTATTTGGCCTTGCTCCGGGTGGAGTTTACCG	9540	0.13583342778075516	No Hit
GTGGAGTTTACCGTGCCACGGACTGTTACCAGCCGCGCGGTGCGCTCTTA	9426	0.13421026103368955	No Hit
CTACATCCTCGGTACTACATGCTTAGTCTGTCTTTACATTACCTGCCAG	8303	0.11822064474461323	No Hit

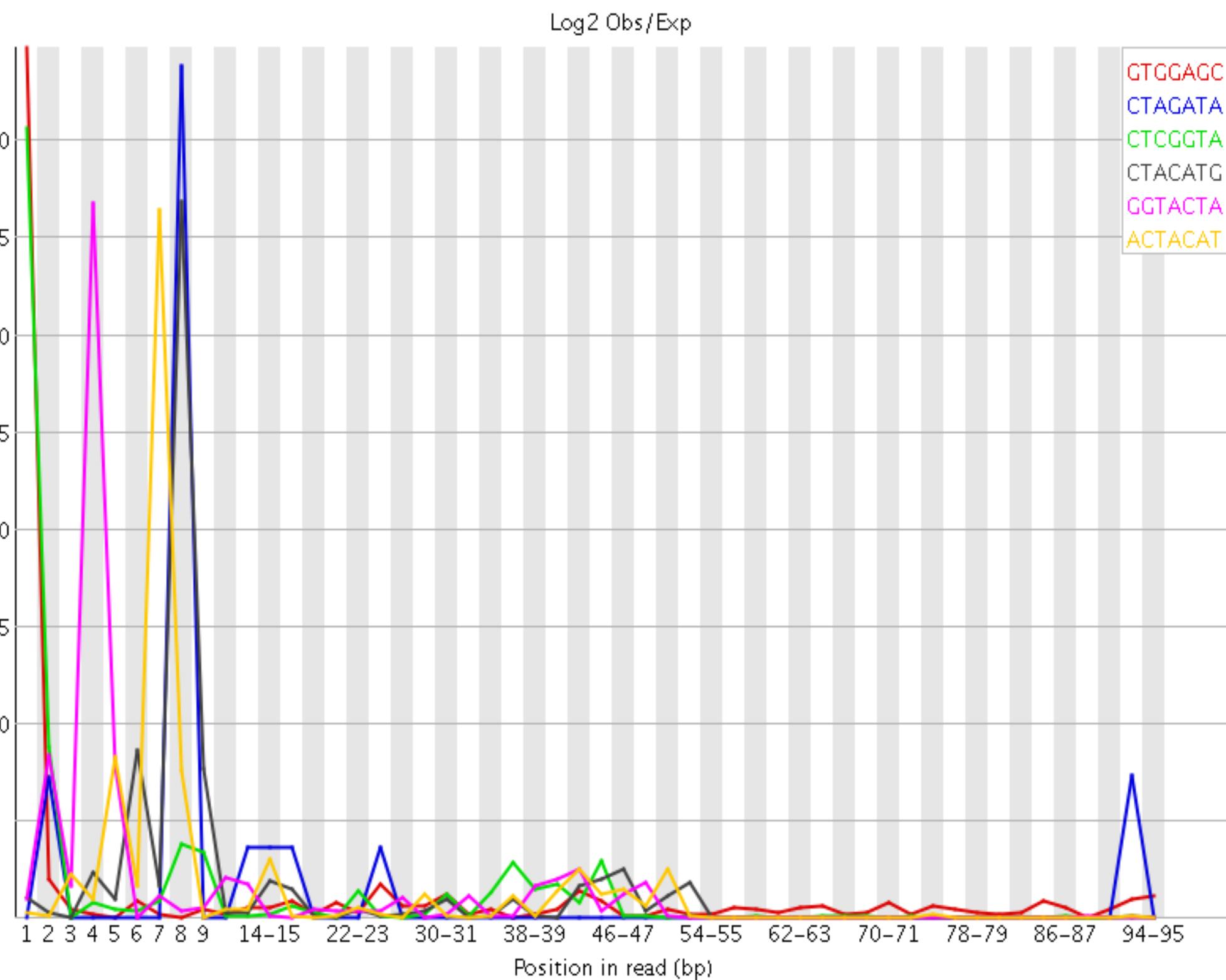
CCTACATCCTCGGTACTACATGCTTAGTCTGTCTTTACATTCACCTGCCA	7920	0.11276737400666467	No Hit
GCTGGCGGGAGTTGAACCCGCGTCCGAAATTCCTACATCCTCGGTACTAC	7644	0.10883760188218998	No Hit
GGTAAATGTACAGGAAGTGAAAAGGGTAGCGTTGCTACCGTGGTCTGAAT	7362	0.1048223999289224	No Hit
CAGACGCTGGTTAGCGCGAGCTGCGTCGTCTTTAGCAGCCTGAACGTCAG	7257	0.10332737792504613	No Hit
GCCTGATTAGTTTTTAACGCTTCAACCCCAGGCAGGGCATCCACGCGATCT	7087	0.10090686610924651	No Hit
ATTAGTTTTTAACGCTTCAACCCCAGGCAGGGCATCCACGCGATCTCTTTT	7082	0.10083567458525243	No Hit



Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTGGAGC	2115	0.0	44.71121	1
CTAGATA	65	2.594299E-6	43.838734	8
CTCGGTA	23065	0.0	40.66936	1
CTACATG	26120	0.0	36.873543	8
GGTACTA	26145	0.0	36.78405	4
ACTACAT	26505	0.0	36.409607	7
TACATGC	26620	0.0	36.25257	9
CGGTACT	26480	0.0	36.067085	3
GTACTAC	27060	0.0	35.662846	5
TAGGCTA	645	0.0	35.342854	8
TACTACA	27985	0.0	34.433155	6
TCGGTAC	29045	0.0	32.800205	2
AACCCCG	960	0.0	29.682686	9
CTCCGAT	870	0.0	27.856377	1
TGTCTTA	410	0.0	27.799973	2

TAGACTA	105	6.918749E-5	27.138264	5
TTAGGCT	900	0.0	26.91211	7
CCTCTAG	435	0.0	26.766542	94-95
GGGTTCT	5810	0.0	26.075434	3
TGGGATG	510	0.0	26.073832	2