













Sun 21 Sep 2014
SRR1033796.fastq

FastQC Report

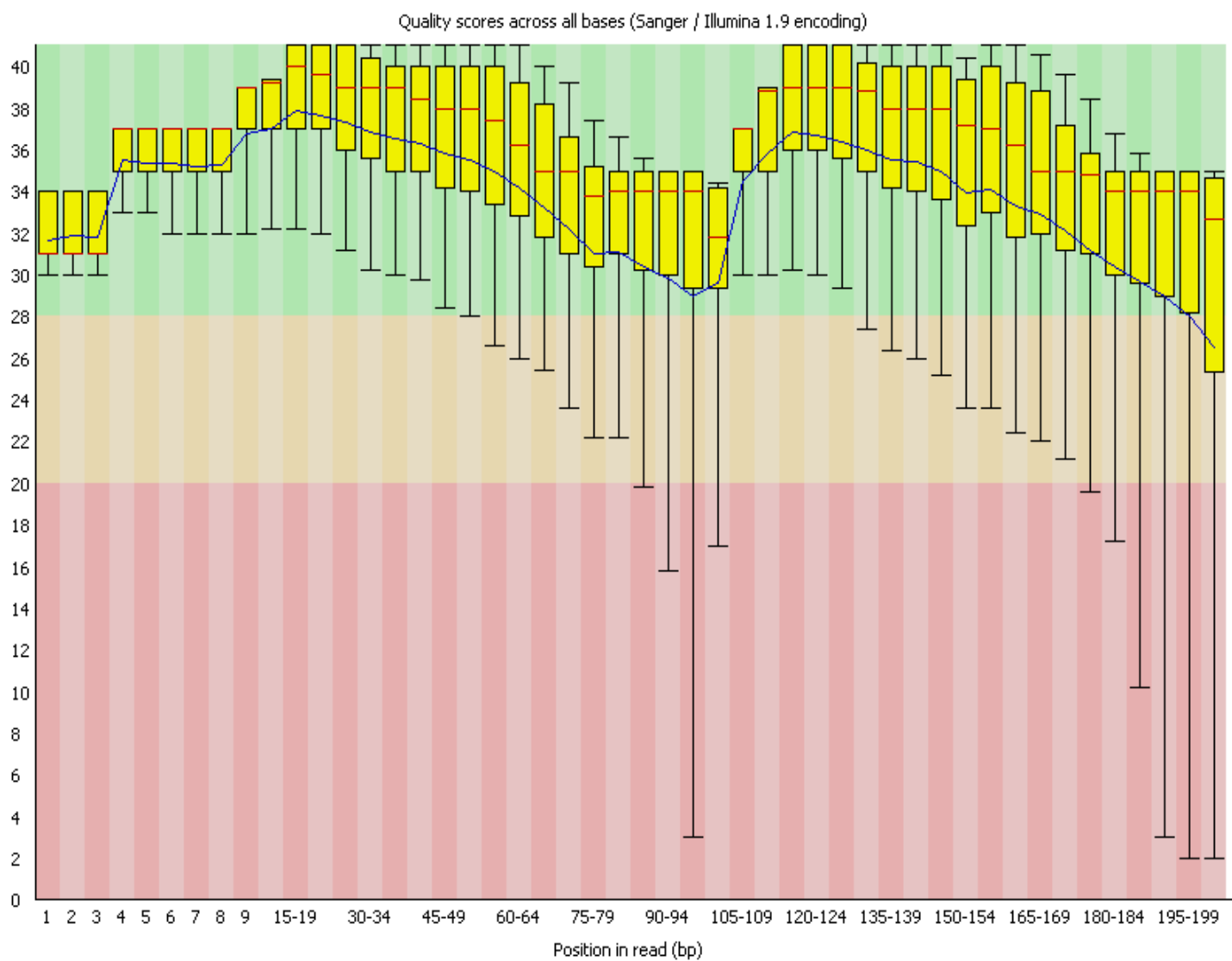
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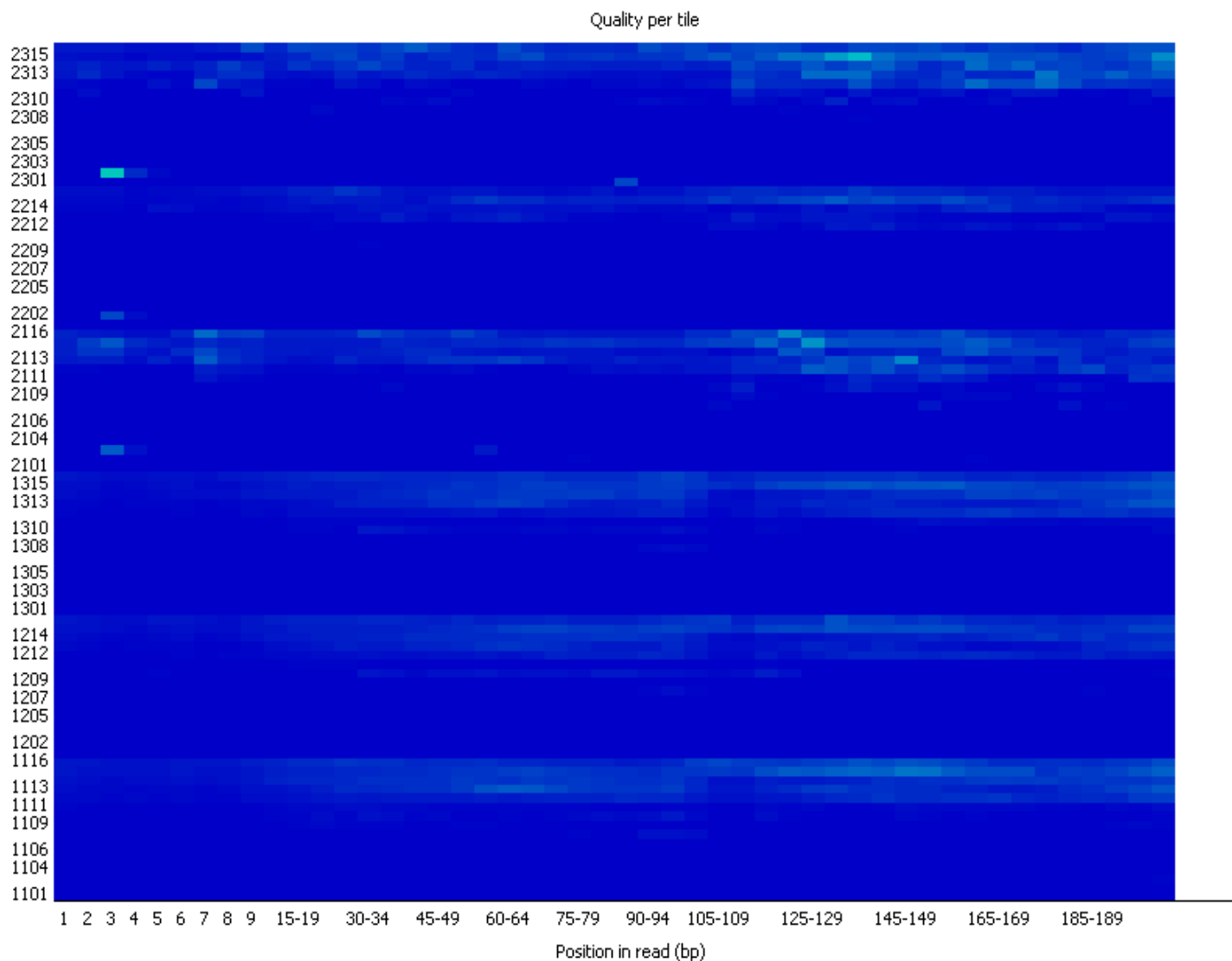
Basic Statistics

Measure	Value
Filename	SRR1033796.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	33791793
Sequences flagged as poor quality	0
Sequence length	202
%GC	50

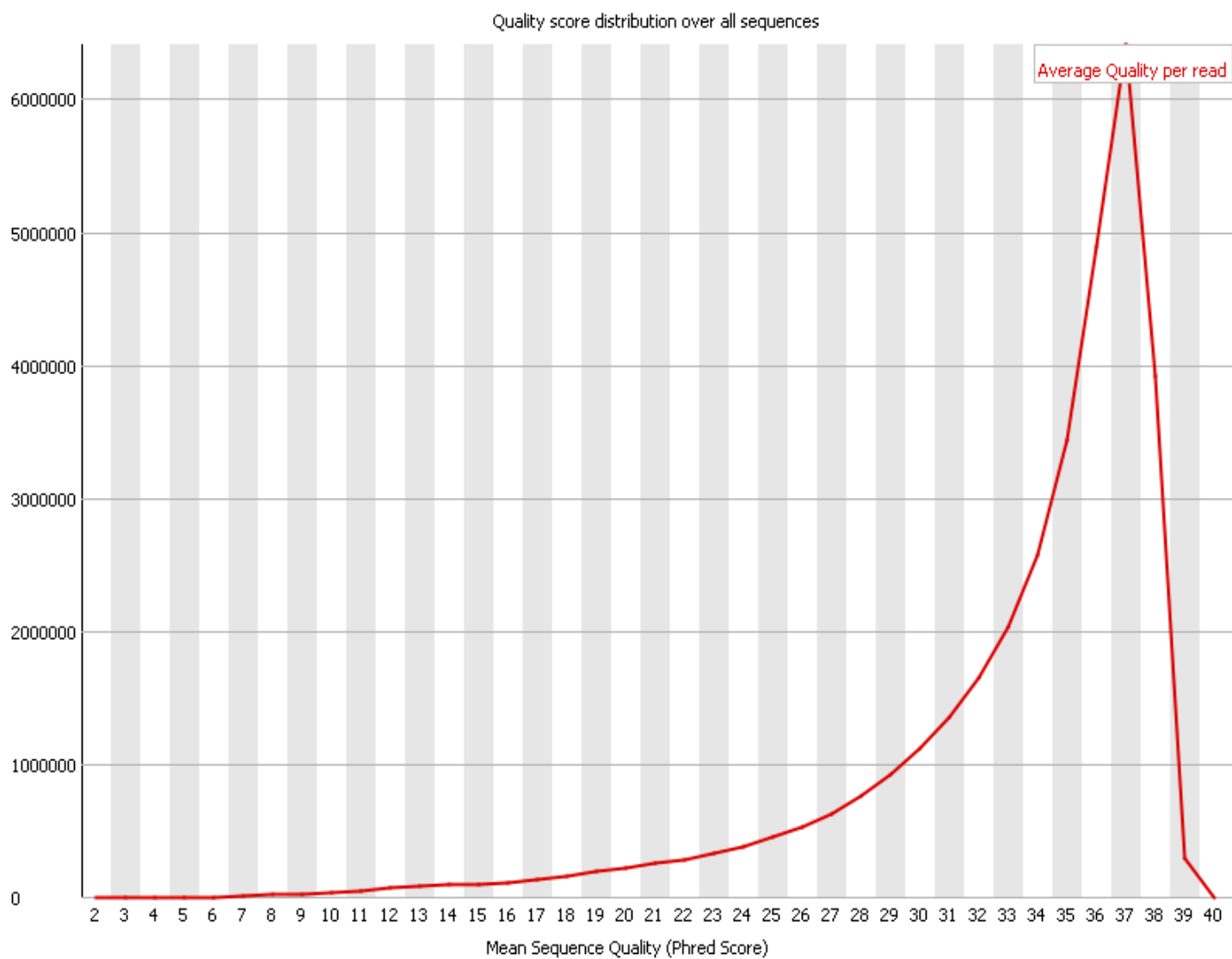
Per base sequence quality



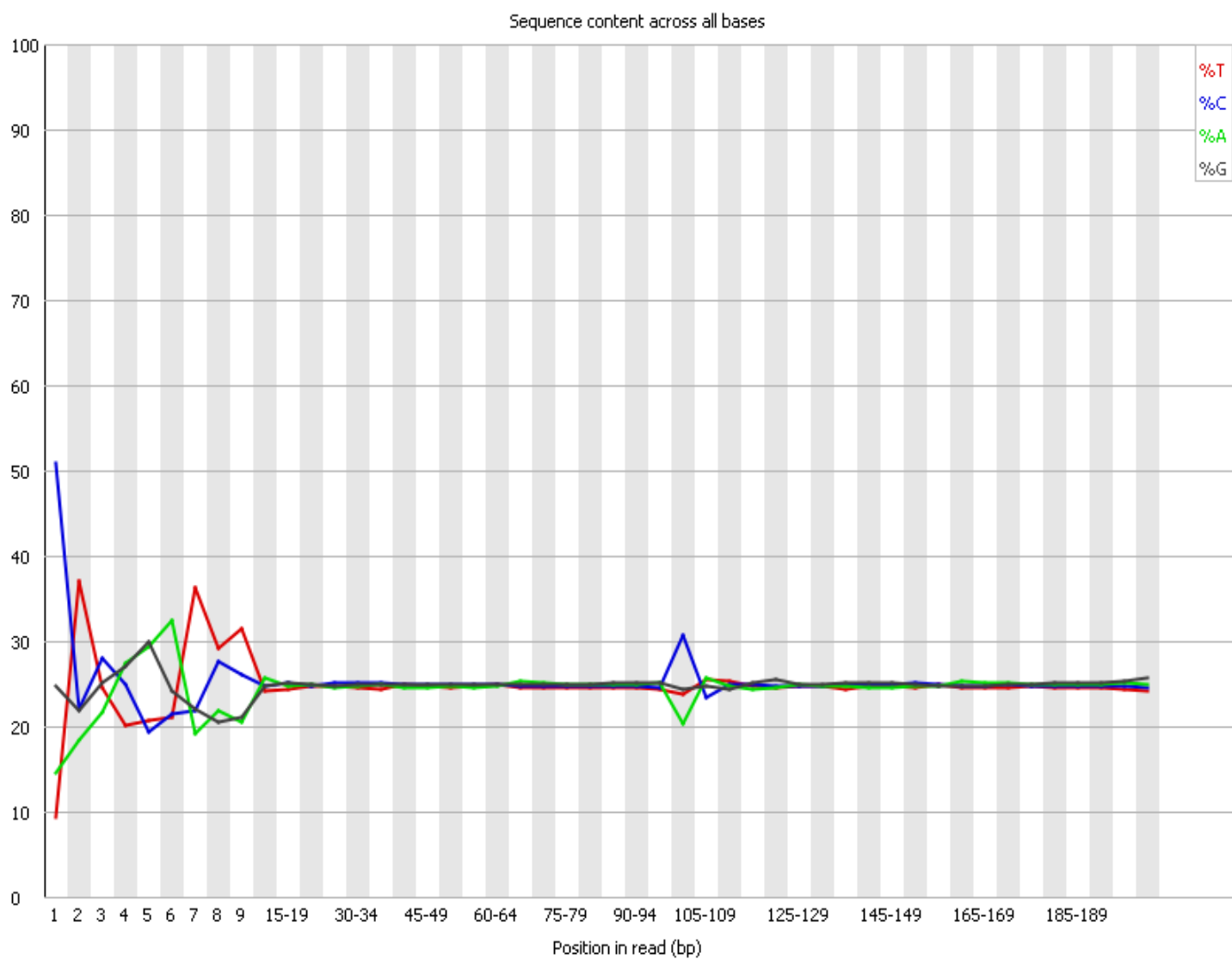
Per tile sequence quality



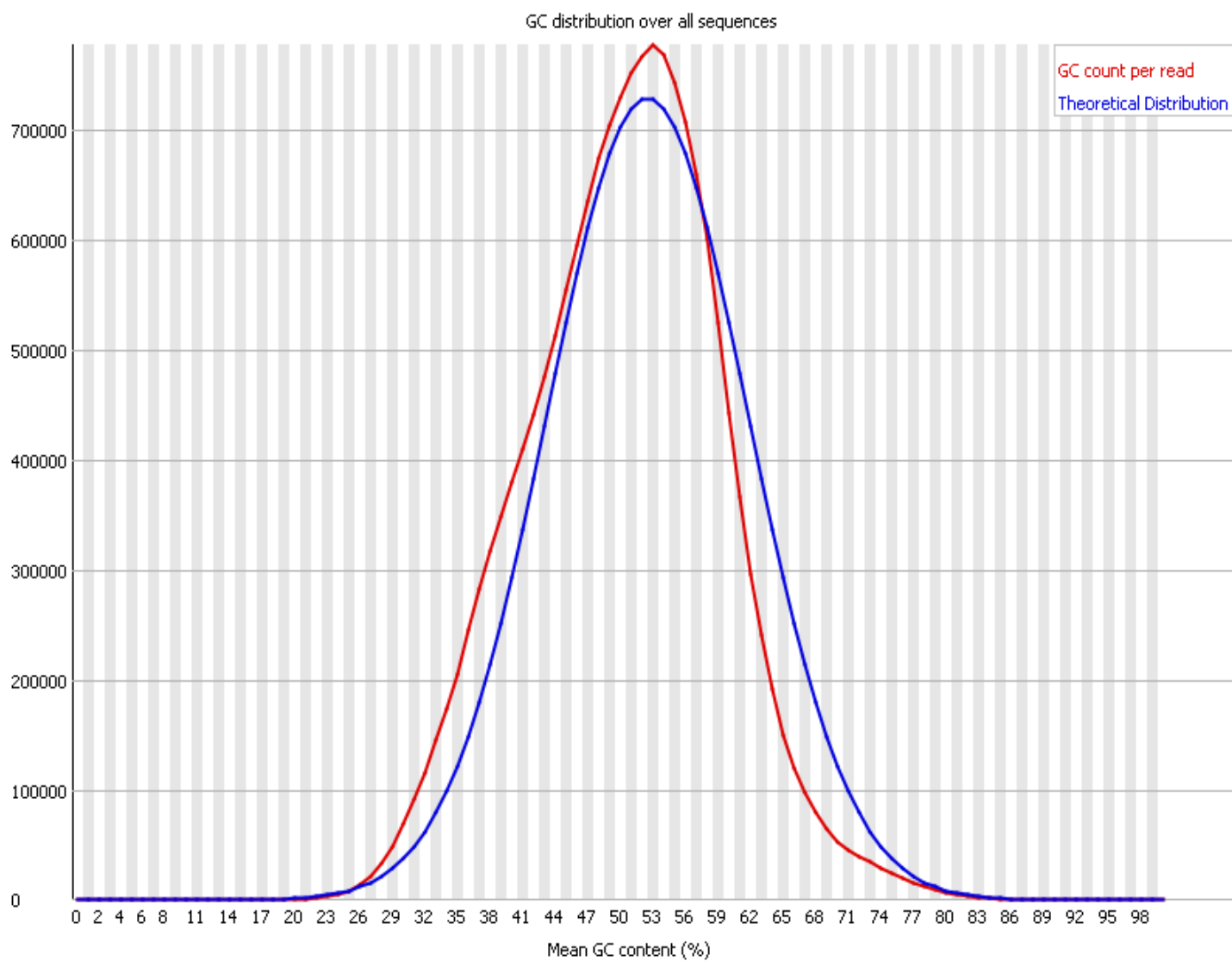
Per sequence quality scores



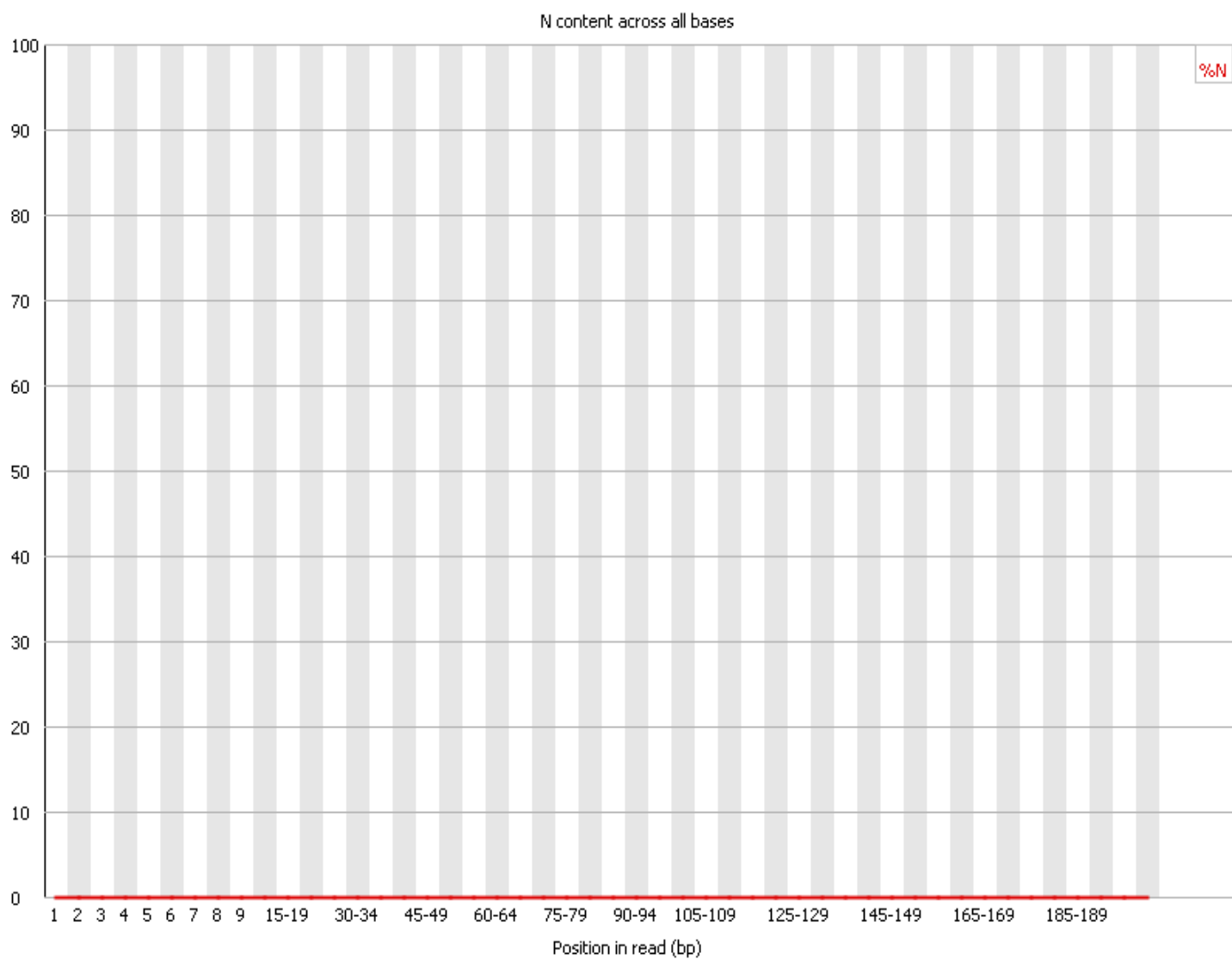
❌ Per base sequence content



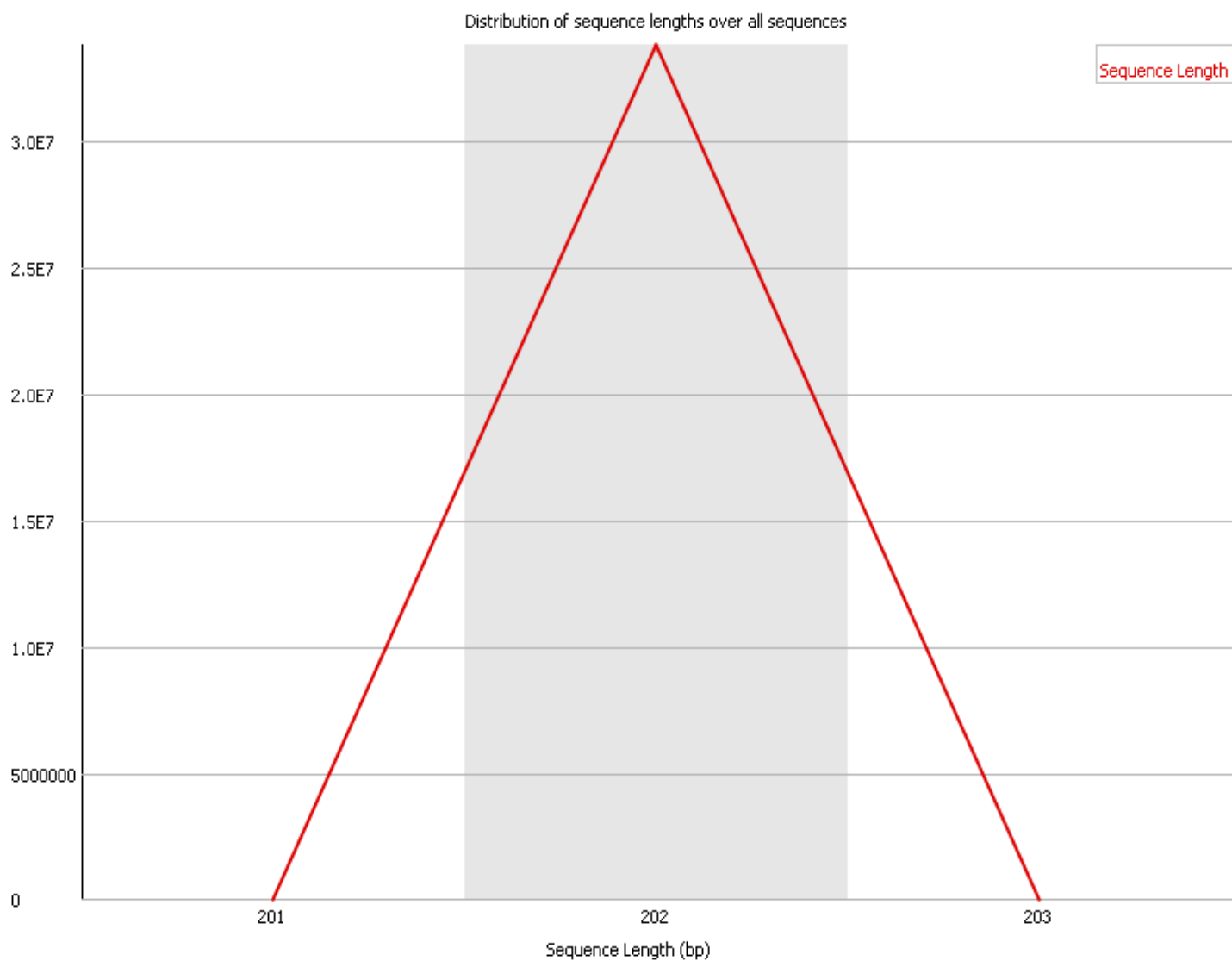
⚠ Per sequence GC content



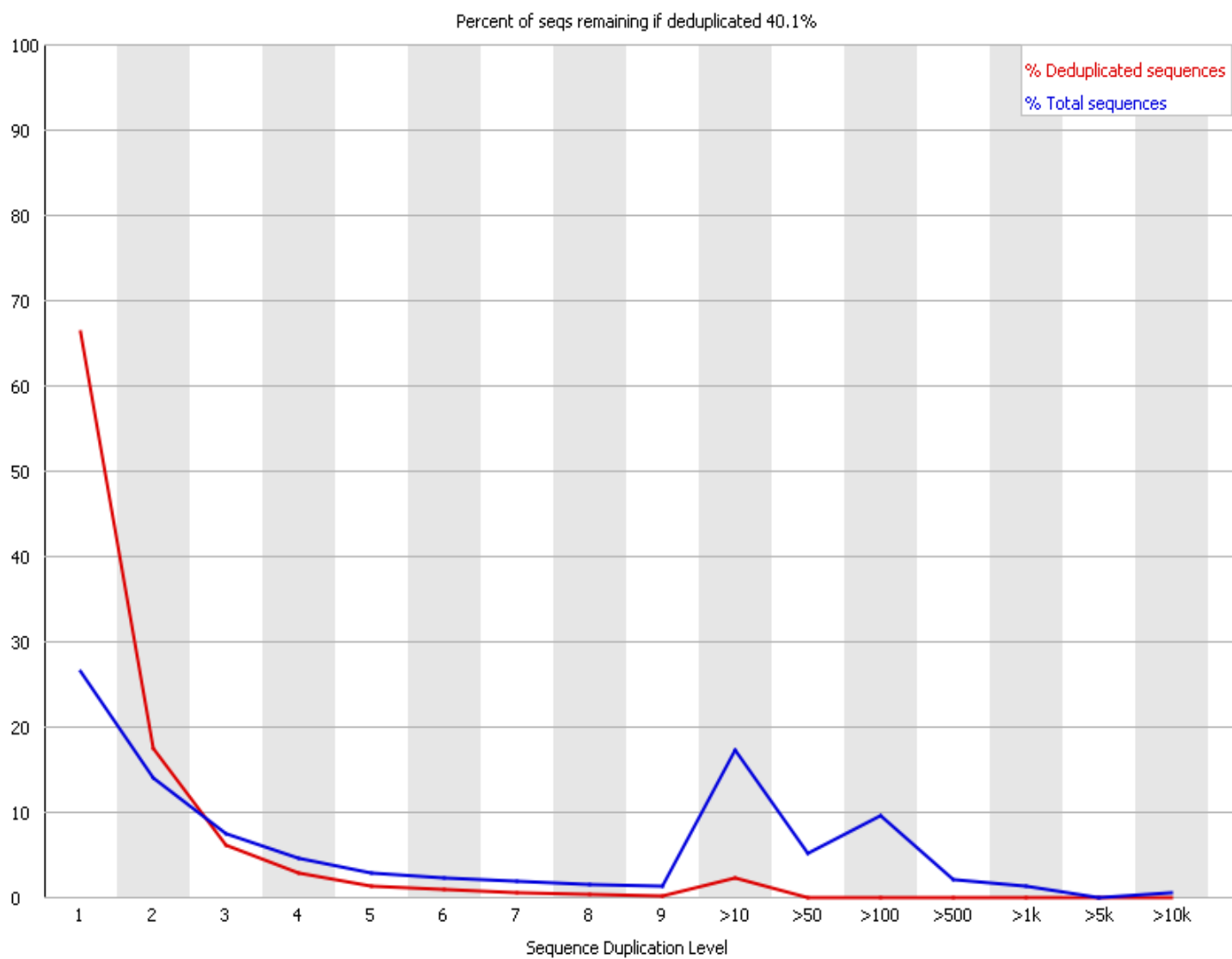
Per base N content



Sequence Length Distribution



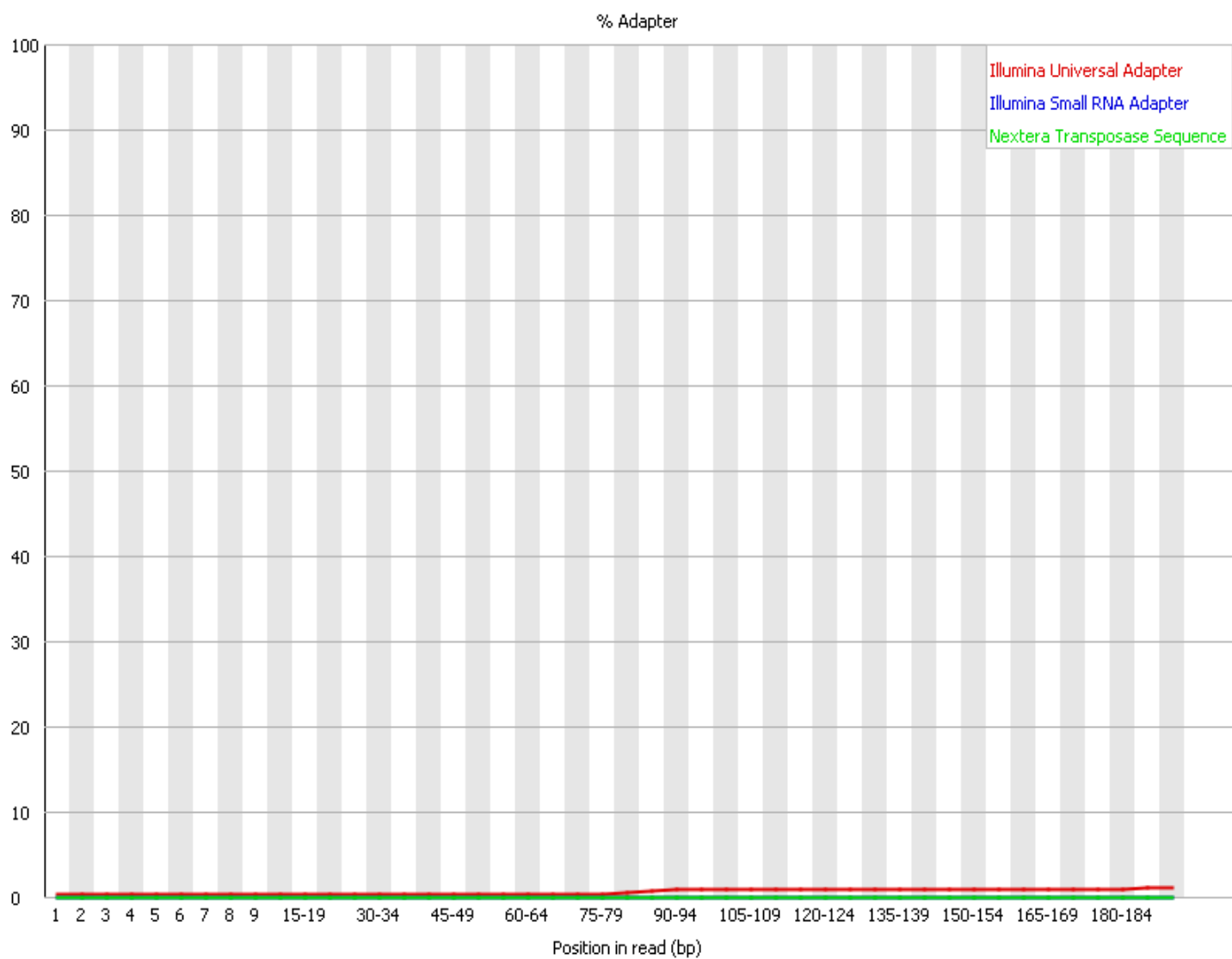
✖ Sequence Duplication Levels



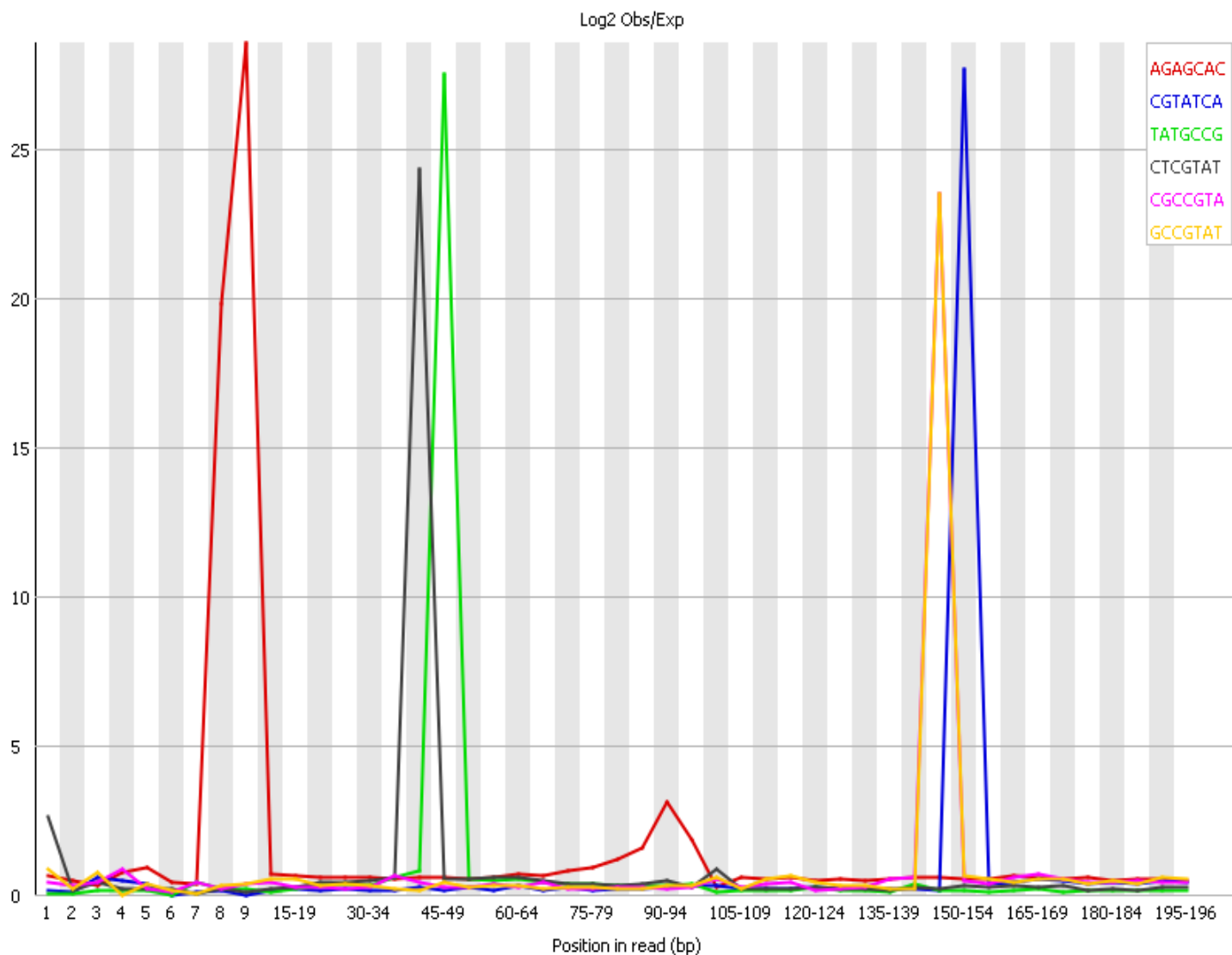
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATATCTCGTATG	119234	0.3528489891021764	TruSeq Adapter, Index 6 (100% over 49bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACGCCAATATCTCGTATGC	77832	0.2303281154687471	TruSeq Adapter, Index 6 (100% over 50bp)

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGAGCAC	100695	0.0	28.518702	9
CGTATCA	20790	0.0	27.688478	150-154
TATGCCG	34670	0.0	27.503523	45-49
CTCGTAT	39395	0.0	24.32847	40-44
CGCCGTA	24585	0.0	23.485035	145-149
GCCGTAT	24615	0.0	23.480299	145-149
TCGTATG	41620	0.0	23.263283	40-44
CGCCAAT	41080	0.0	23.124882	30-34
ATCGGAA	126720	0.0	22.385487	3
TCTCGTA	42160	0.0	22.323908	40-44
GATCGGA	128510	0.0	22.104258	2
CCGTATC	25285	0.0	22.068567	150-154

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGGAAGA	130450	0.0	21.909096	5
AAGAGCA	133380	0.0	21.87539	8
ACGCCAA	44620	0.0	21.479069	30-34
AGATCGG	134145	0.0	21.148005	1
AGTCACG	44705	0.0	21.114077	25-29
ATGCCGT	45730	0.0	21.023083	45-49
TCGGAAG	137050	0.0	20.87713	4
ATCTCGT	45765	0.0	20.582537	40-44

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