













FastQC Report

Summary

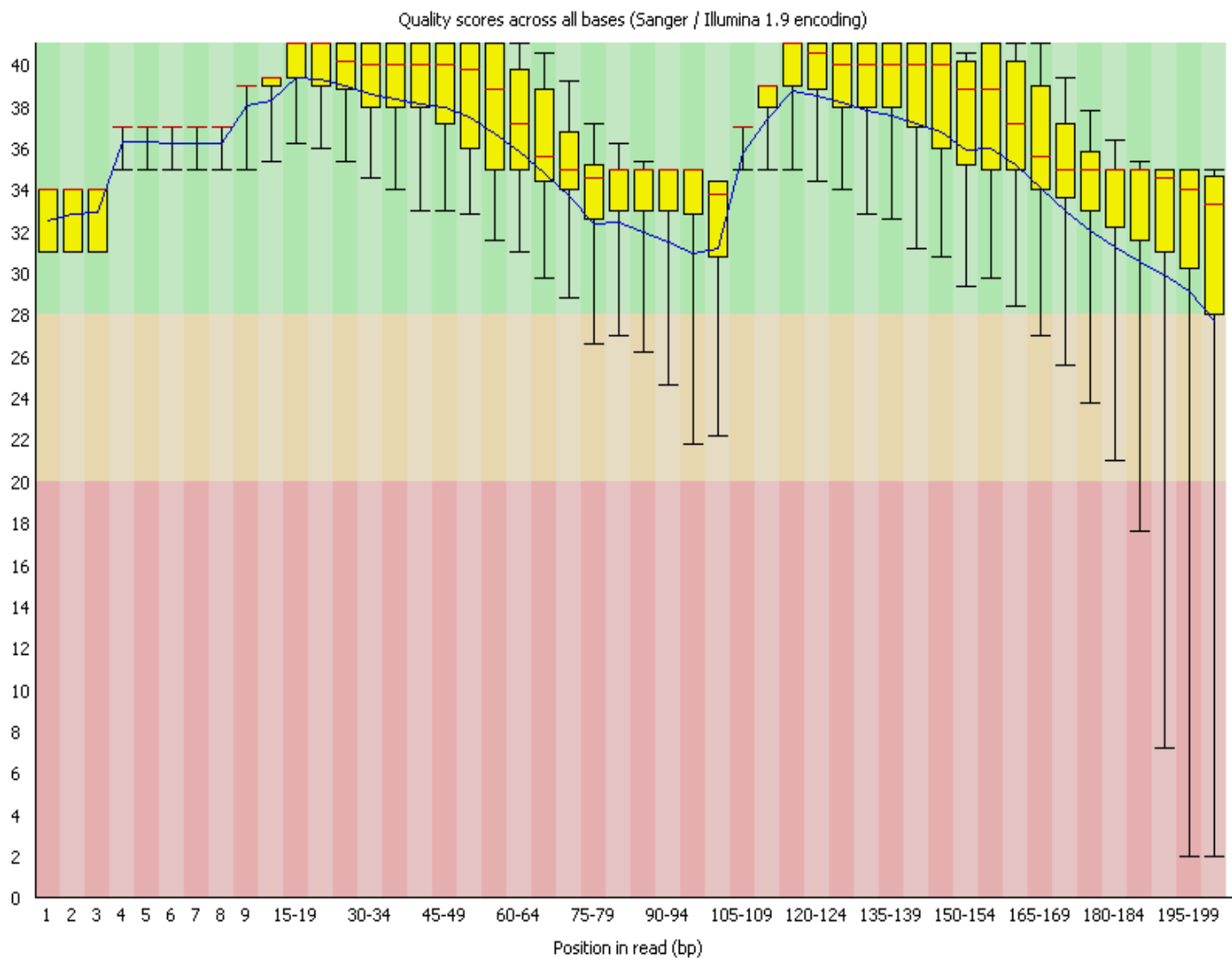
Sun 21 Sep 2014
SRR1033793.fastq

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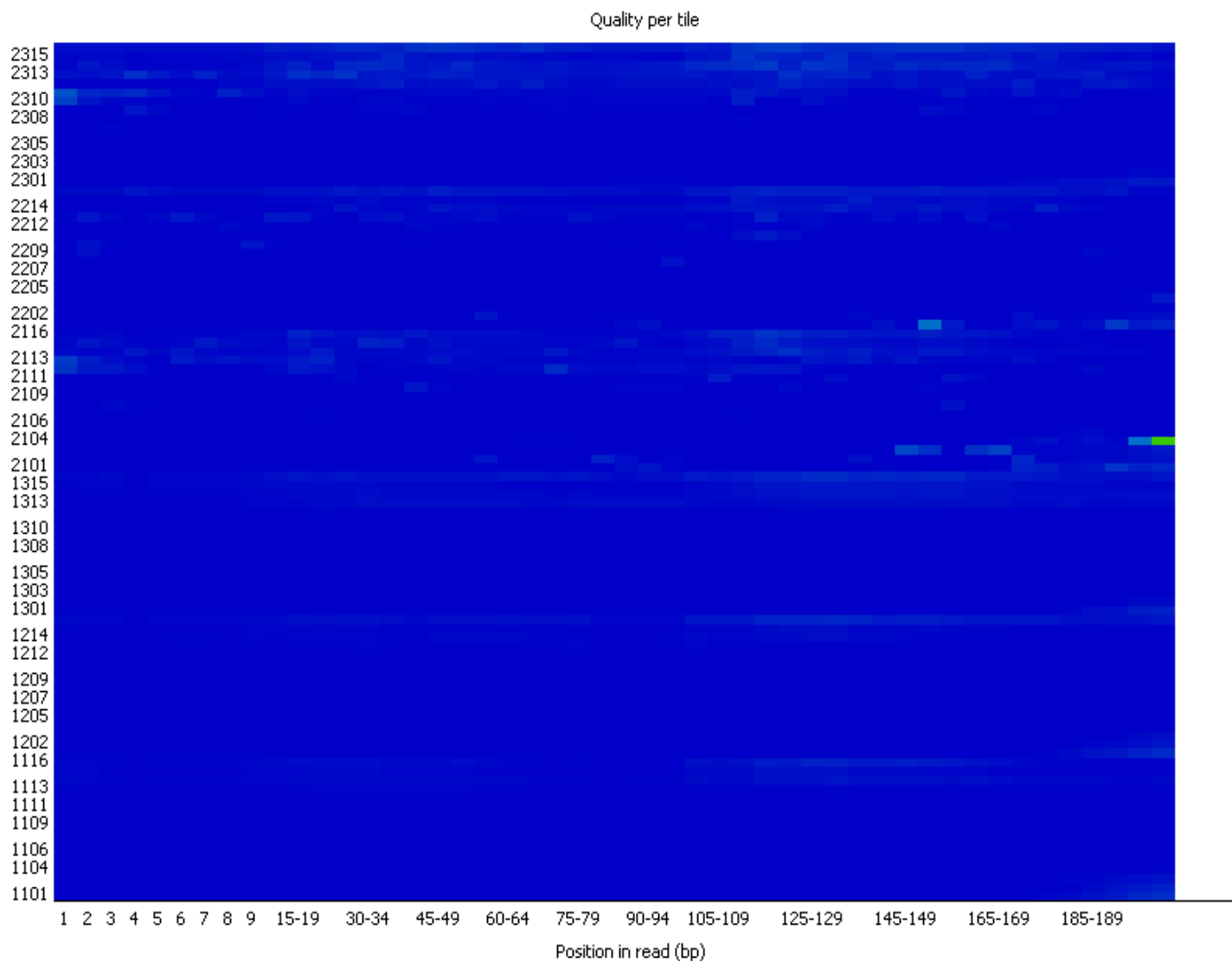
Basic Statistics

Measure	Value
Filename	SRR1033793.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	29172869
Sequences flagged as poor quality	0
Sequence length	202
%GC	53

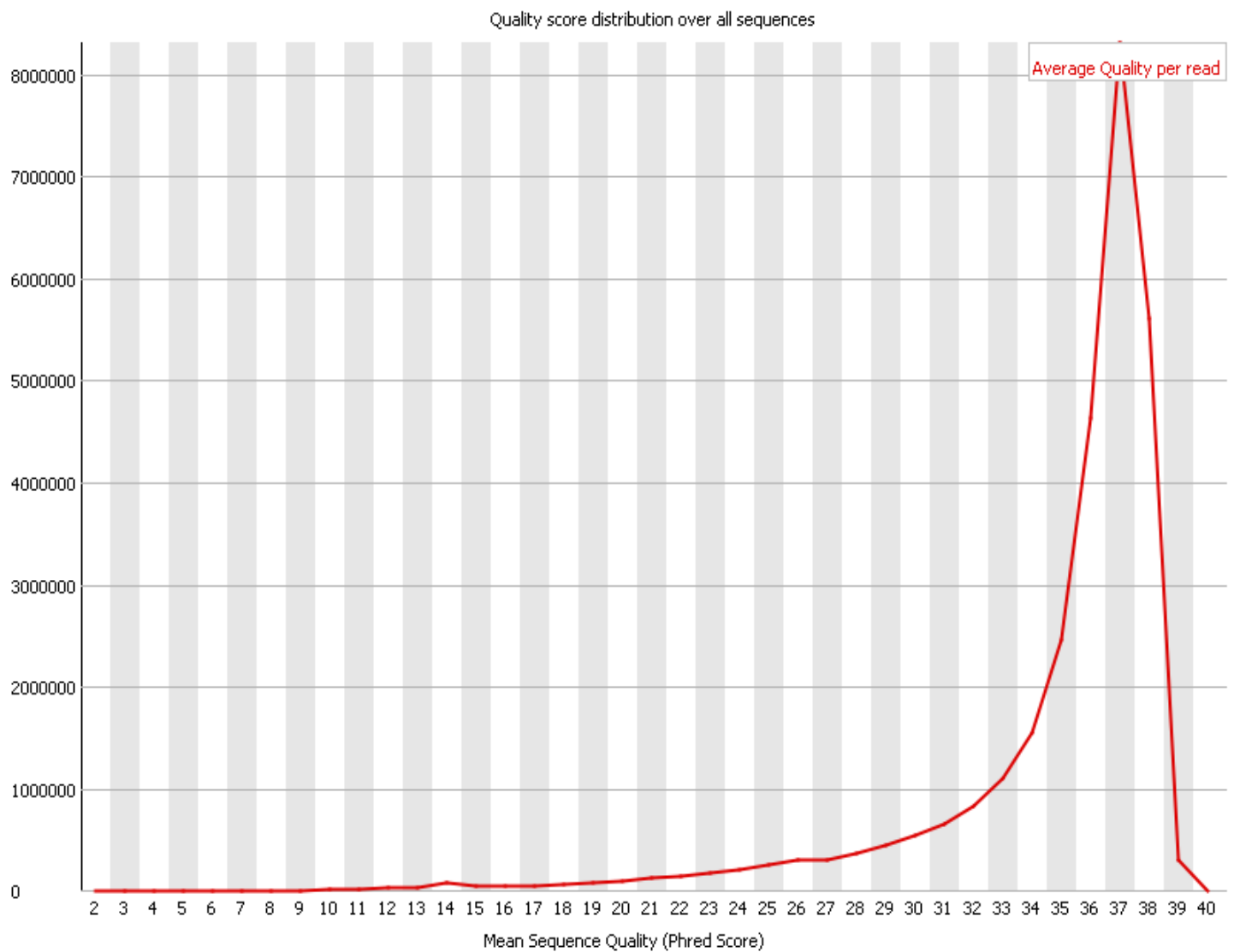
Per base sequence quality



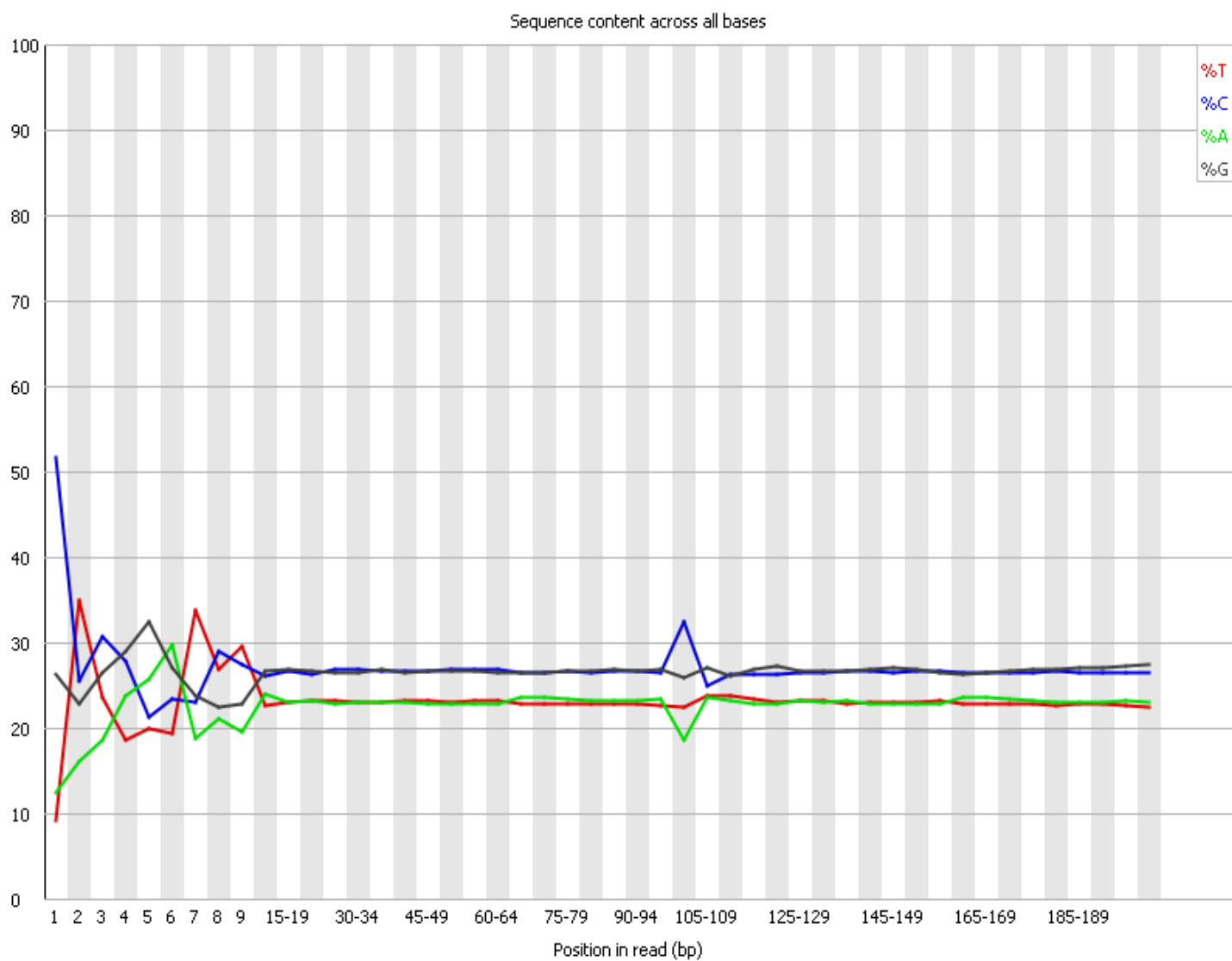
Per tile sequence quality



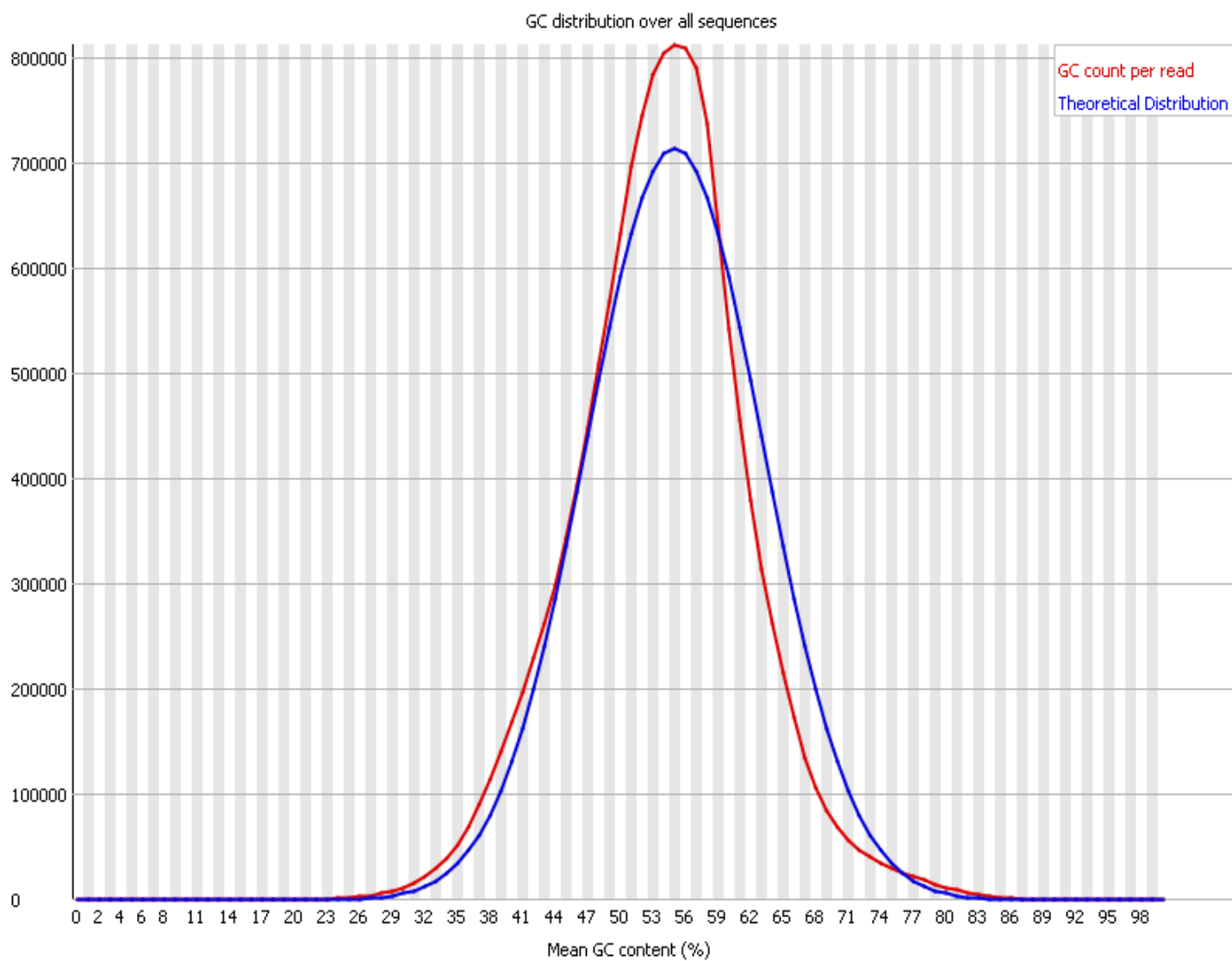
Per sequence quality scores



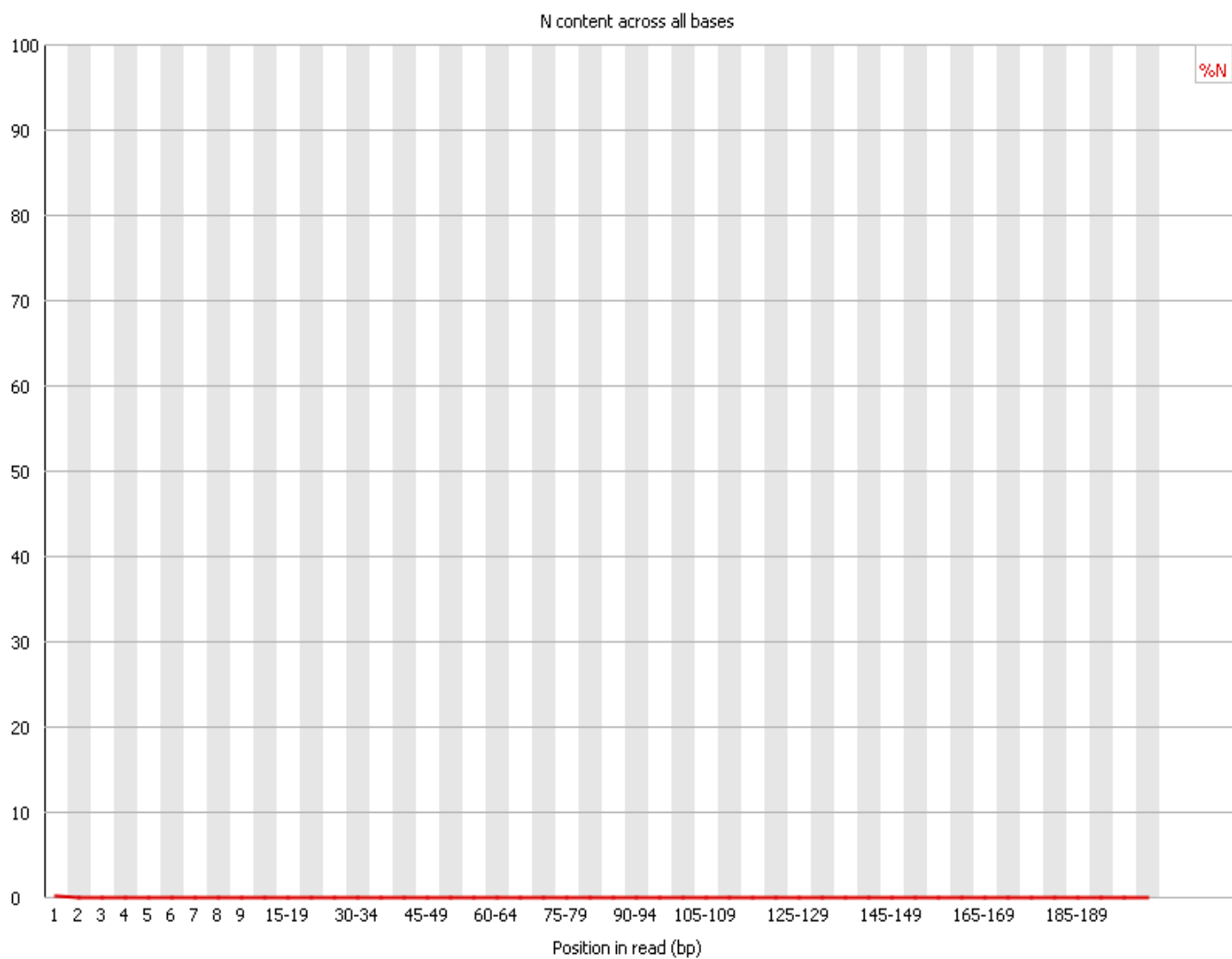
❌ Per base sequence content



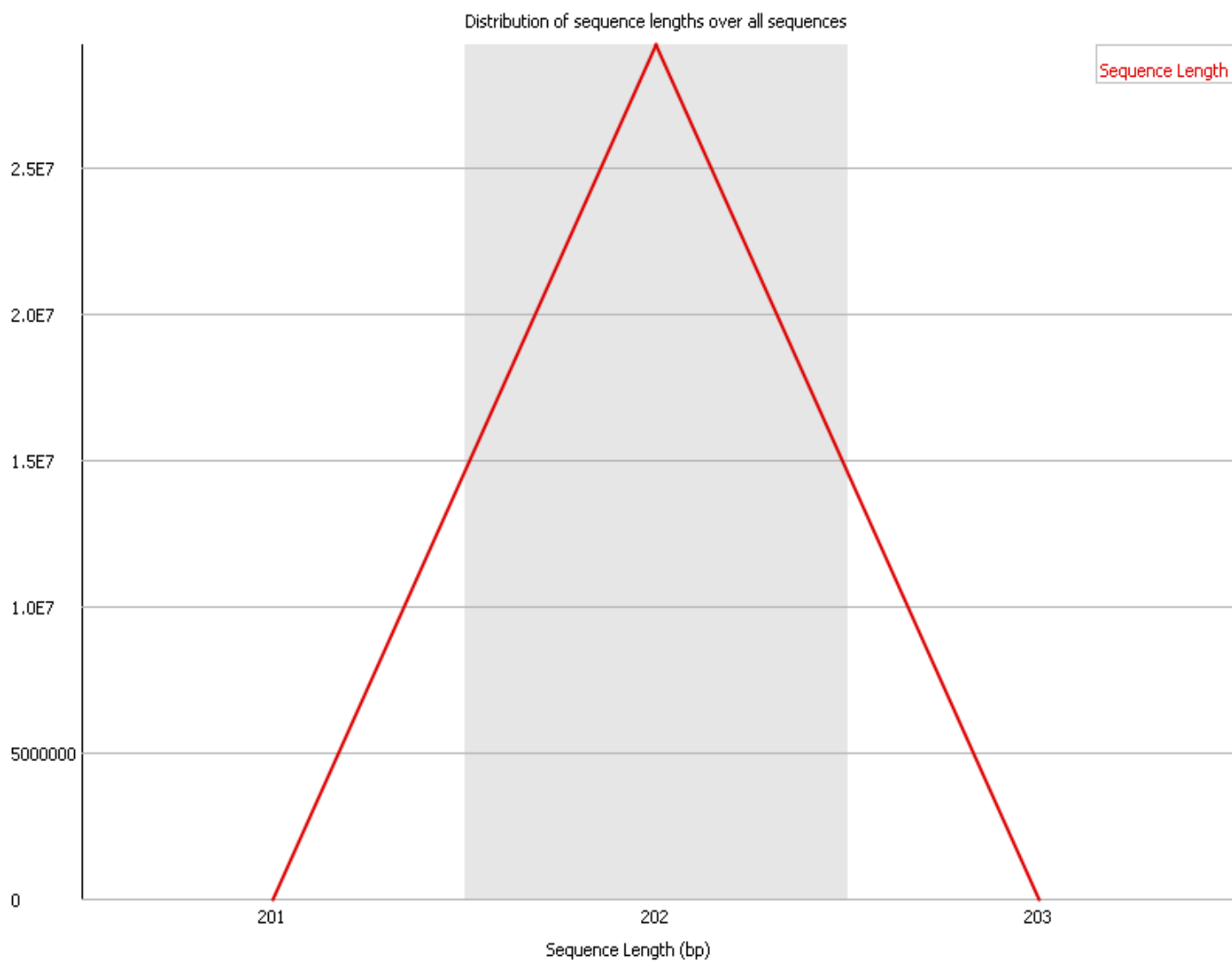
⚠ Per sequence GC content



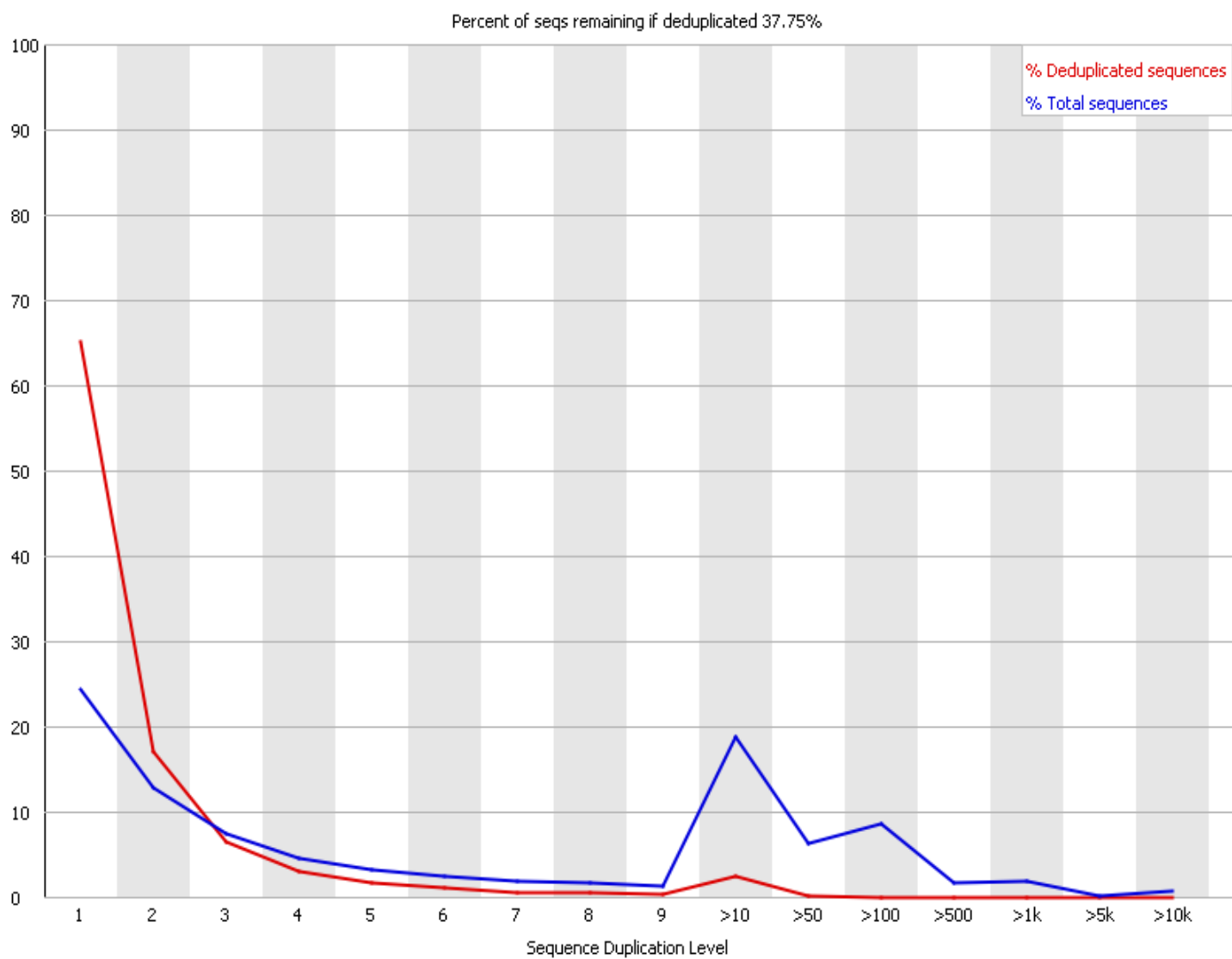
Per base N content



Sequence Length Distribution



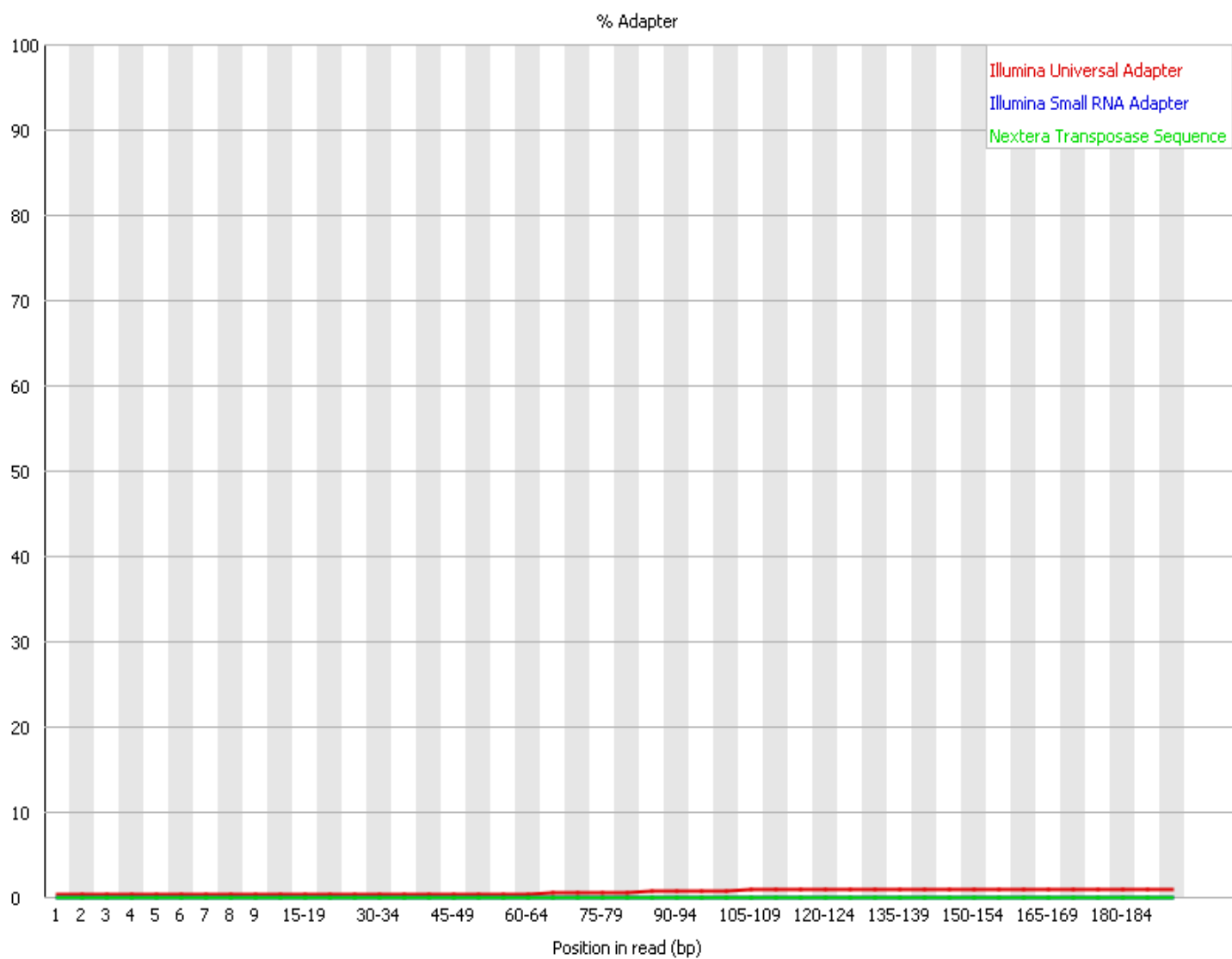
✖ Sequence Duplication Levels



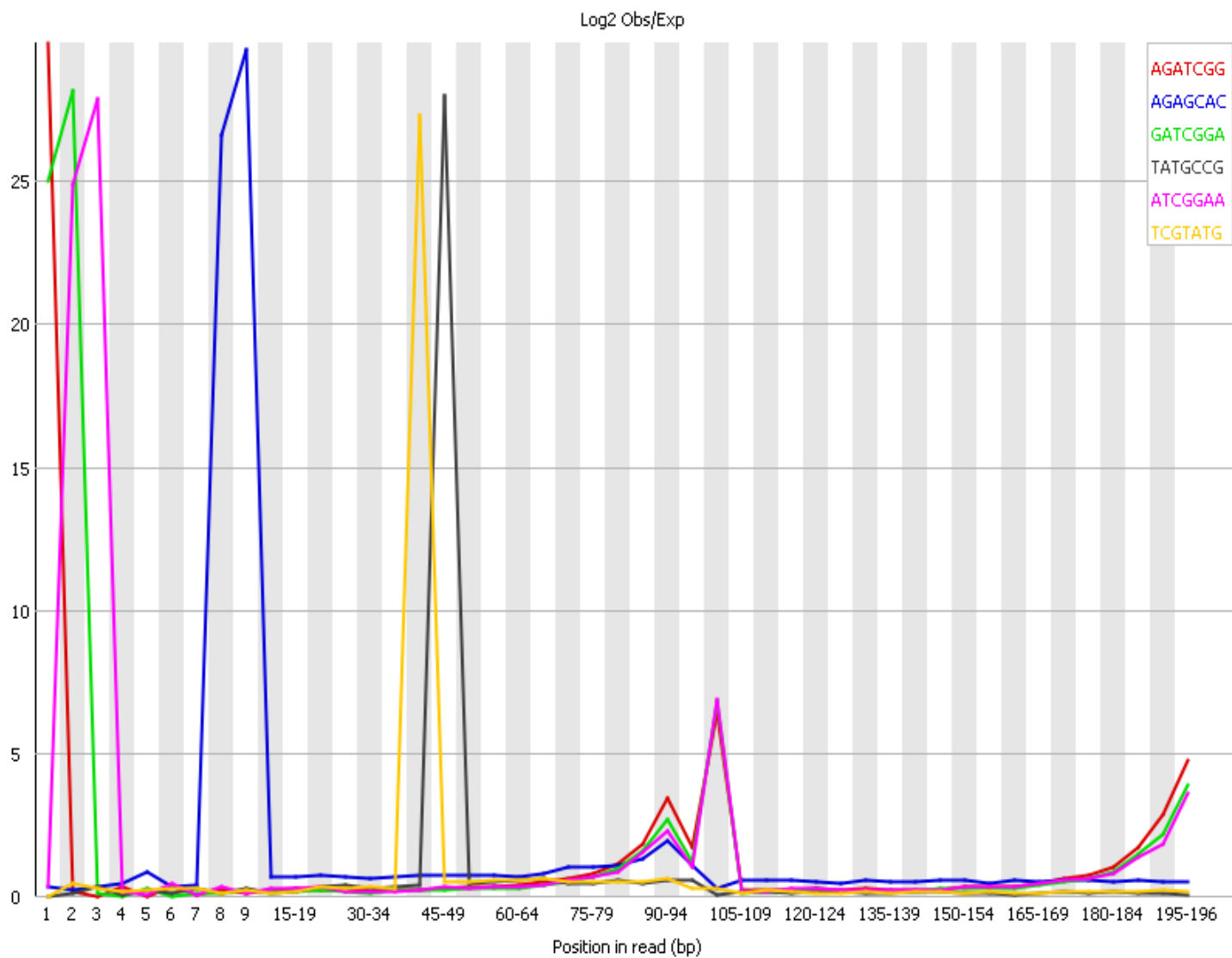
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATG	116764	0.40024860084896	TruSeq Adapter, Index 2 (100% over 49bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACCGATGTATCTCGTATGC	98918	0.3390753237194463	TruSeq Adapter, Index 2 (100% over 50bp)

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGATCGG	85925	0.0	29.773552	1
AGAGCAC	88400	0.0	29.59132	9
GATCGGA	91670	0.0	28.11764	2
TATGCCG	35210	0.0	27.944555	45-49
ATCGGAA	92560	0.0	27.836695	3
TCGTATG	35900	0.0	27.281155	40-44
CGTATCA	20780	0.0	27.088495	150-154
CTCGTAT	36060	0.0	26.98078	40-44
TCGGAAG	102005	0.0	25.375143	4
CGGAAGA	106650	0.0	24.214888	5
TCTCGTA	40185	0.0	24.211195	40-44
AAGAGCA	108540	0.0	24.163725	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGCCGTA	23480	0.0	24.03516	145-149
GCCGTAT	23640	0.0	23.665188	145-149
ACCGATG	42145	0.0	23.356321	30-34
CCGATGT	42040	0.0	23.046398	30-34
CACCGAT	42960	0.0	22.881292	30-34
ATGCCGT	43300	0.0	22.800444	45-49
GAGCACA	107670	0.0	22.038641	9
ATCTCGT	44345	0.0	21.79412	40-44

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