













FastQC Report

Summary

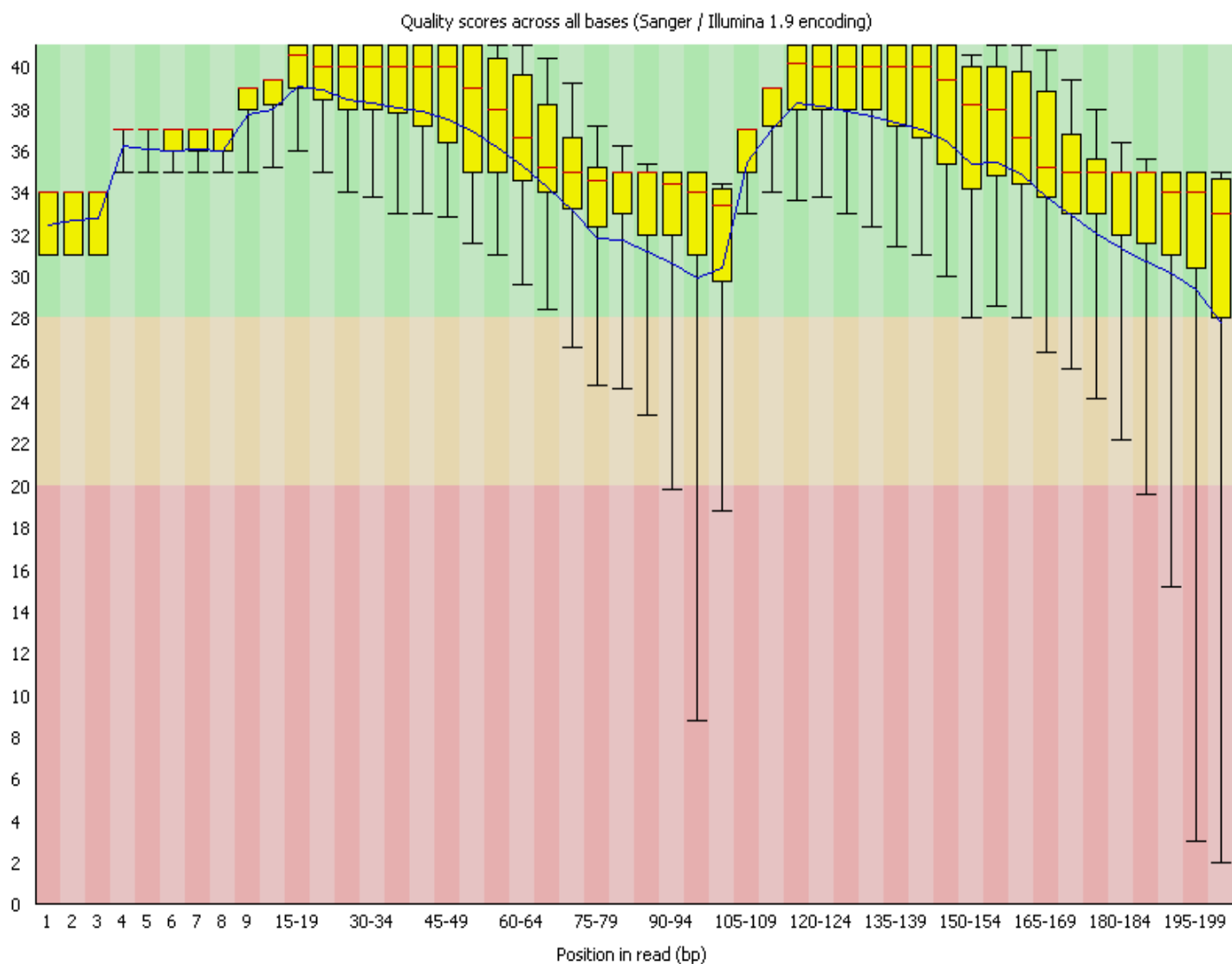
Sun 21 Sep 2014
SRR1033792.fastq

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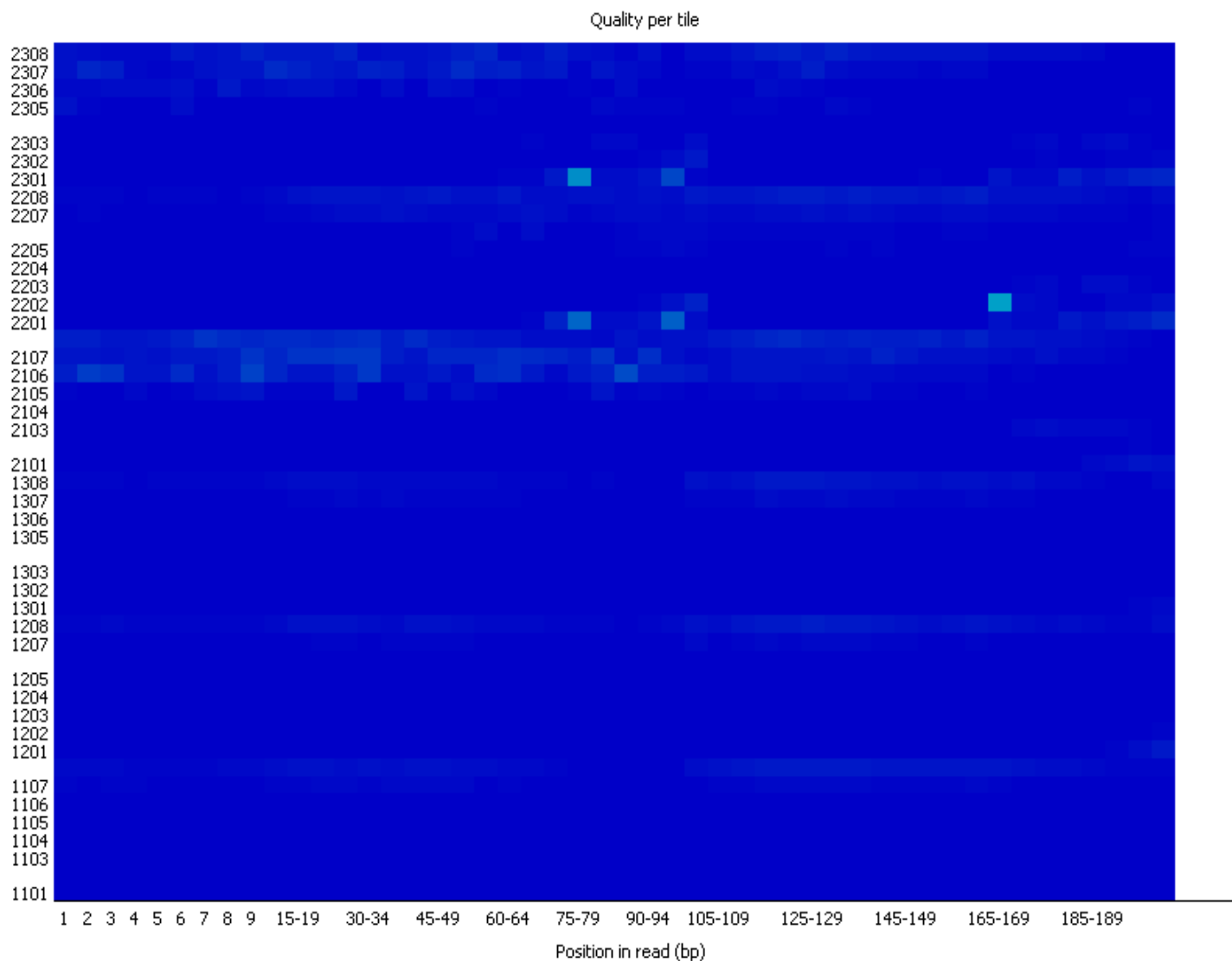
Basic Statistics

Measure	Value
Filename	SRR1033792.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	29732990
Sequences flagged as poor quality	0
Sequence length	202
%GC	52

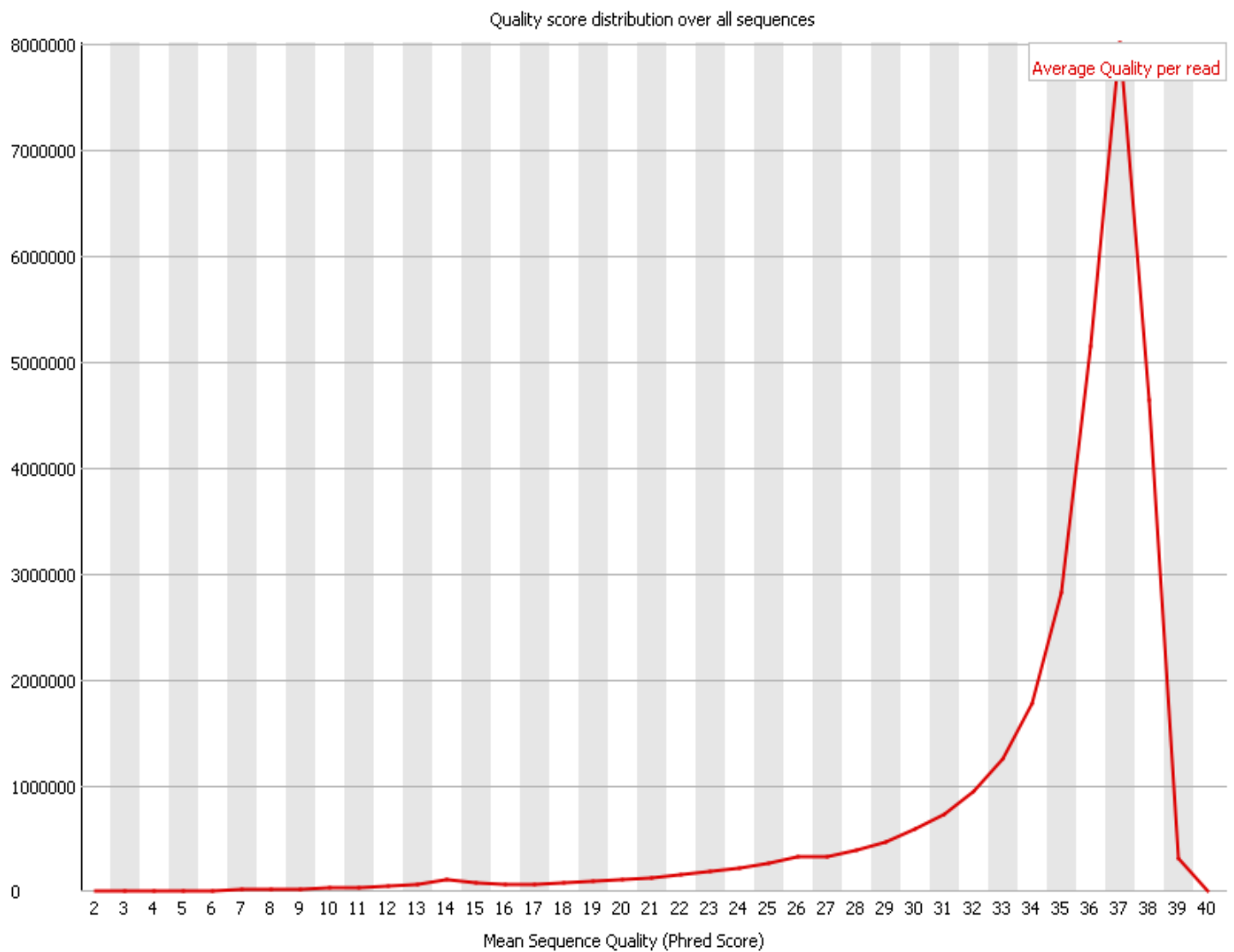
Per base sequence quality



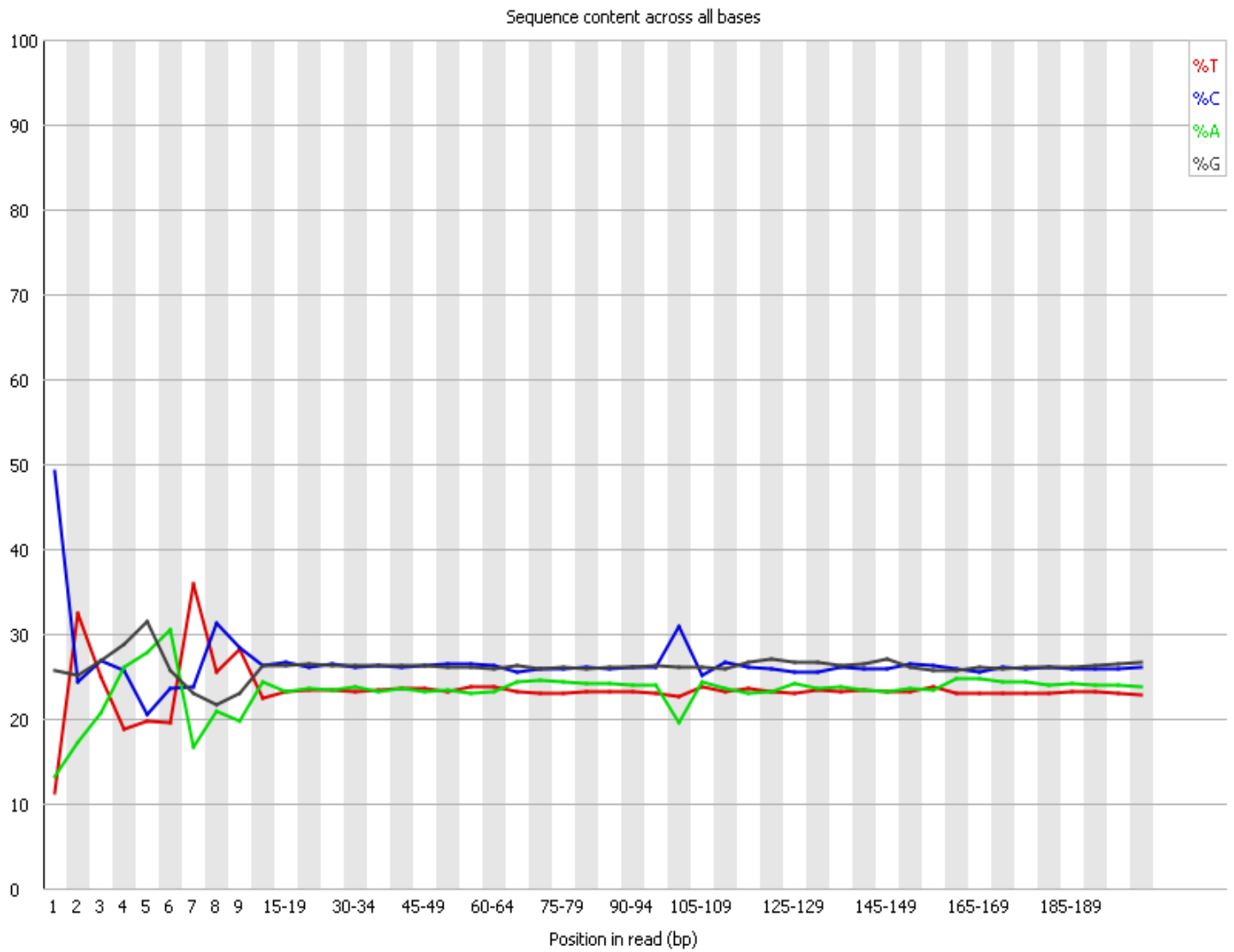
Per tile sequence quality



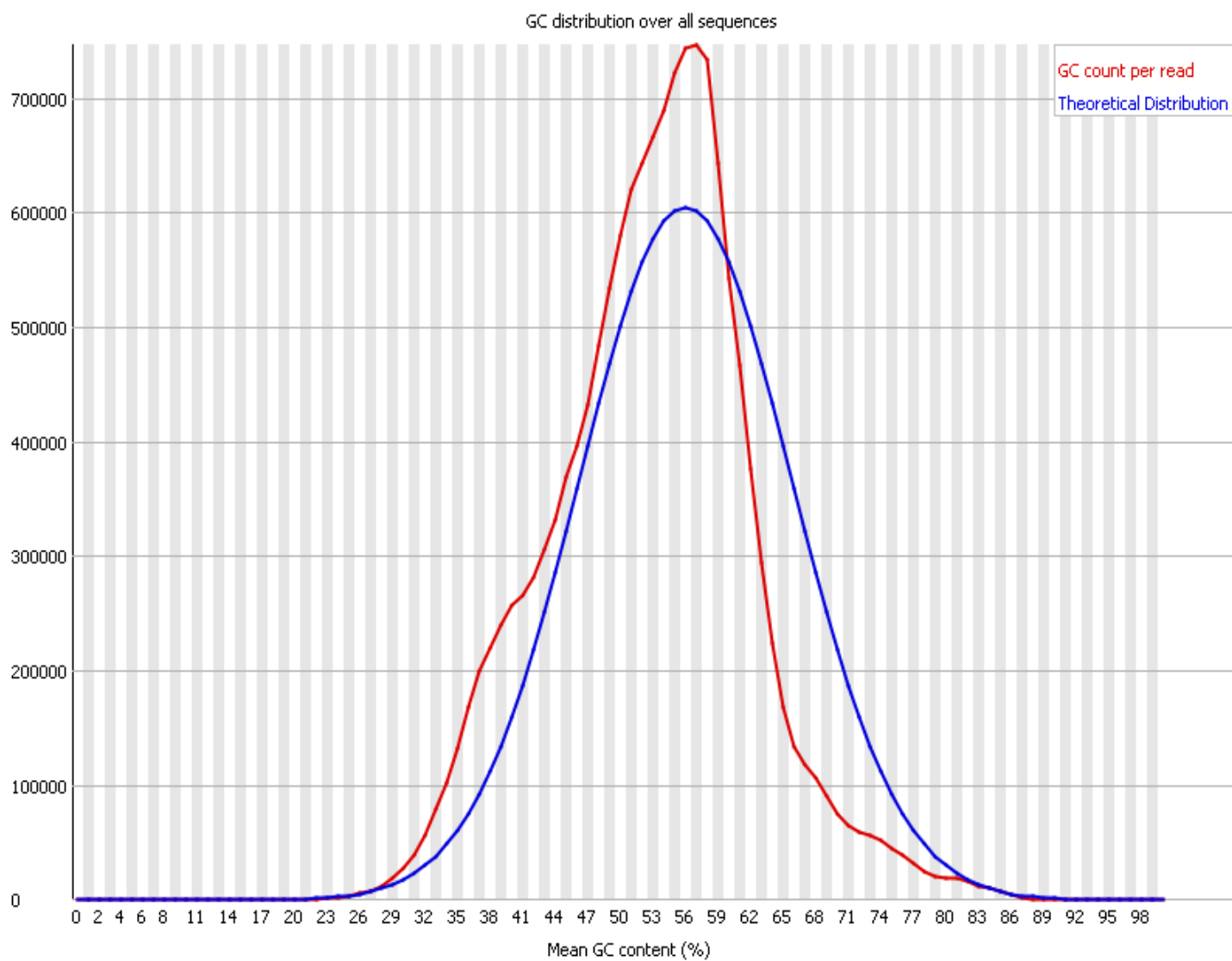
Per sequence quality scores



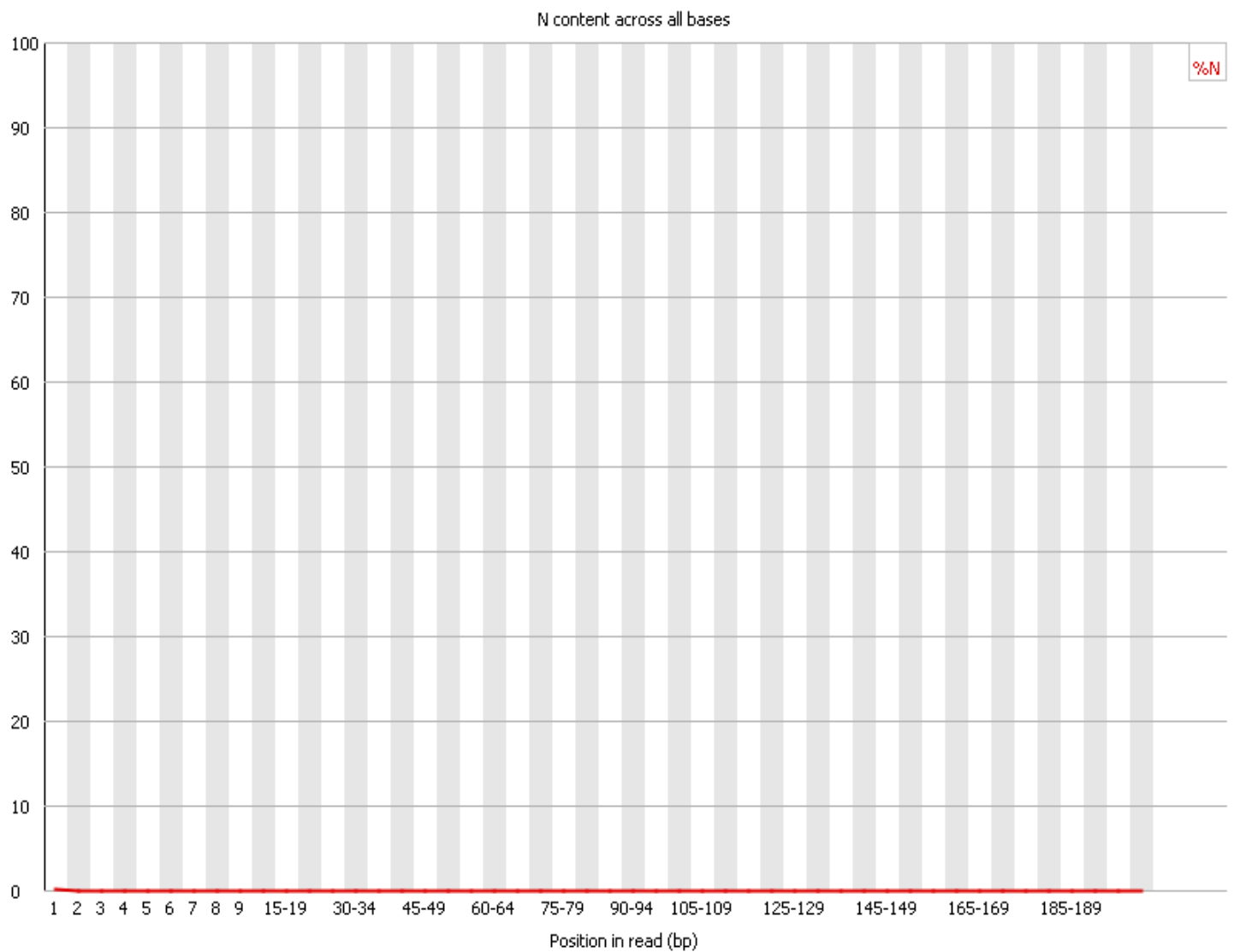
❌ Per base sequence content



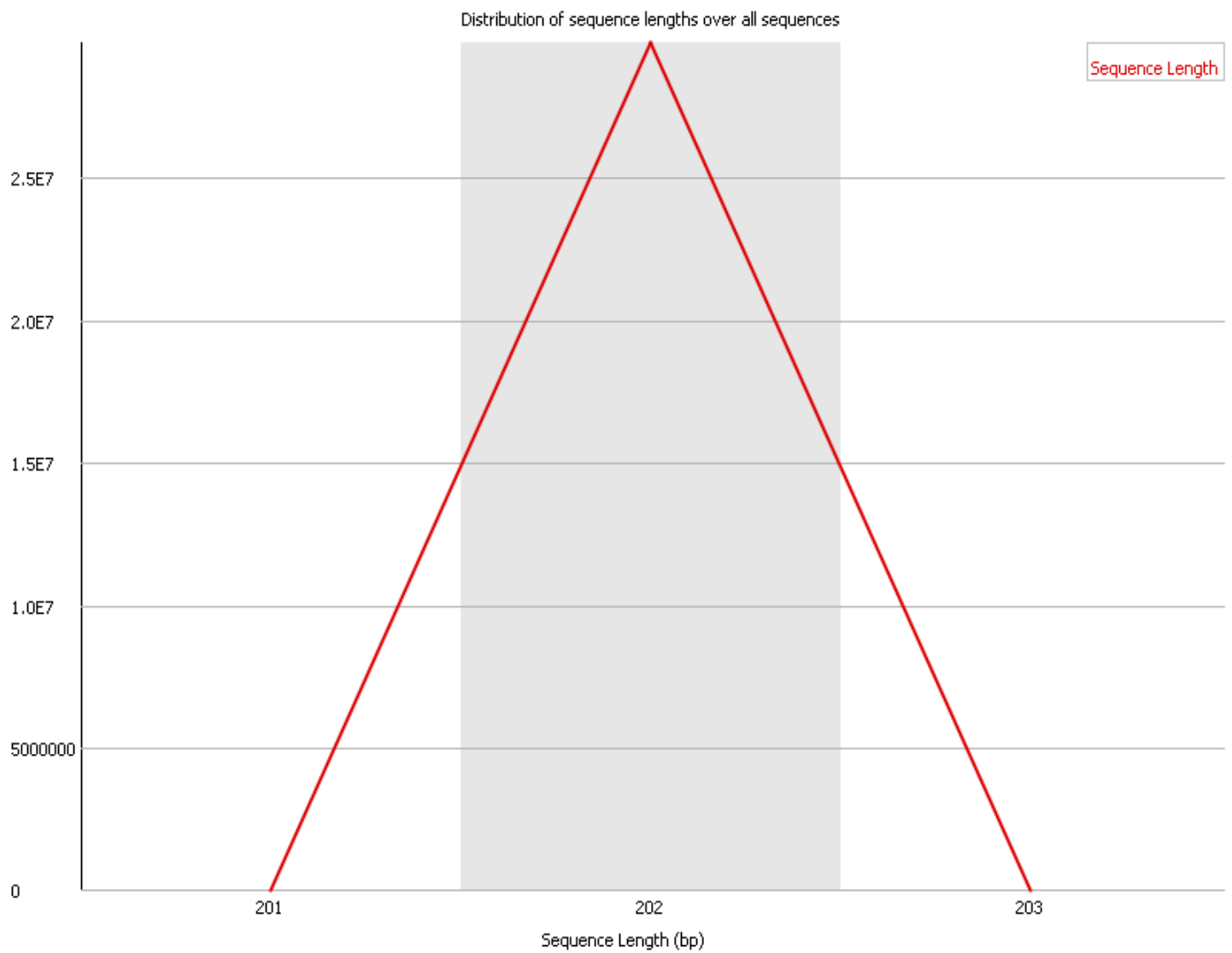
❌ Per sequence GC content



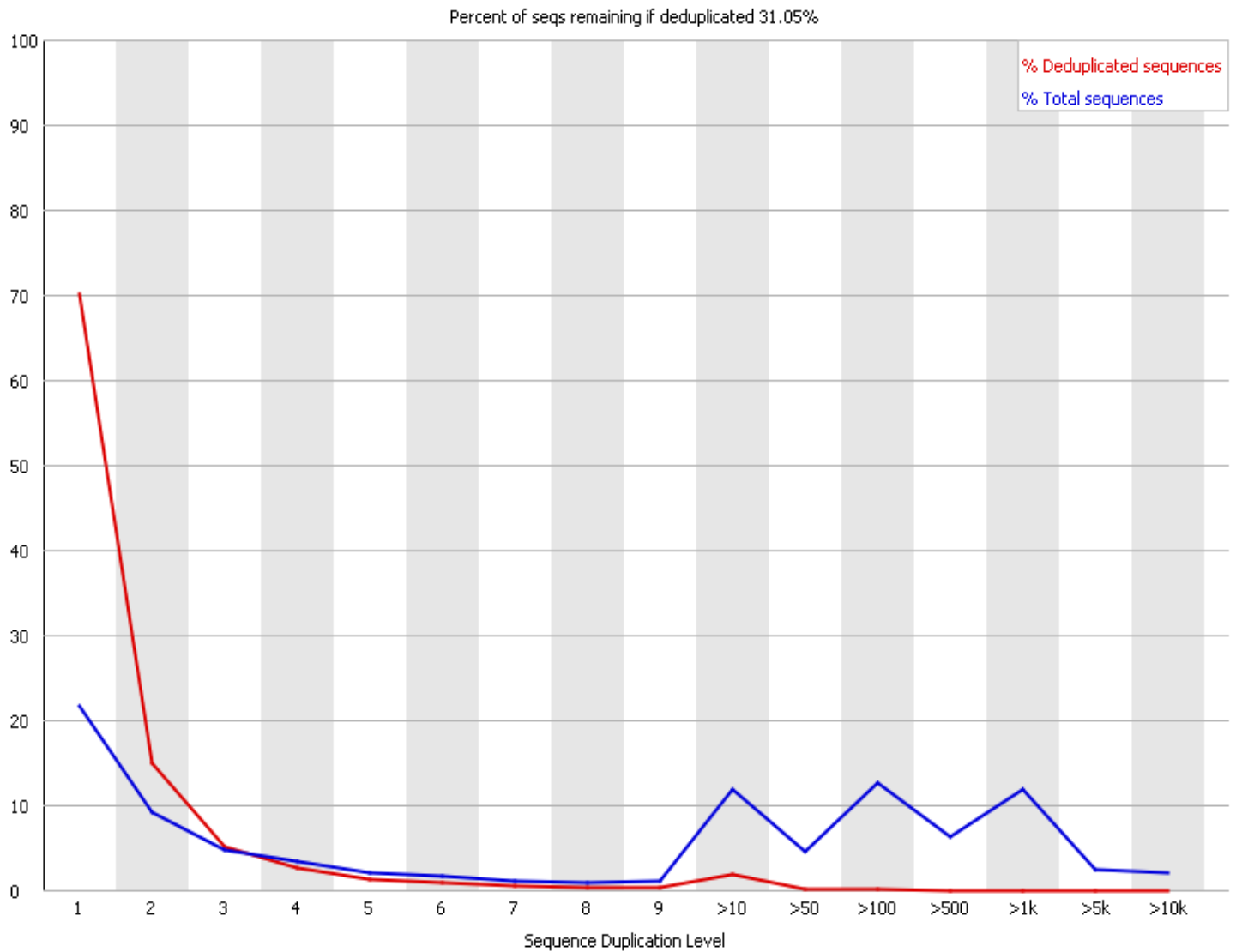
Per base N content



Sequence Length Distribution



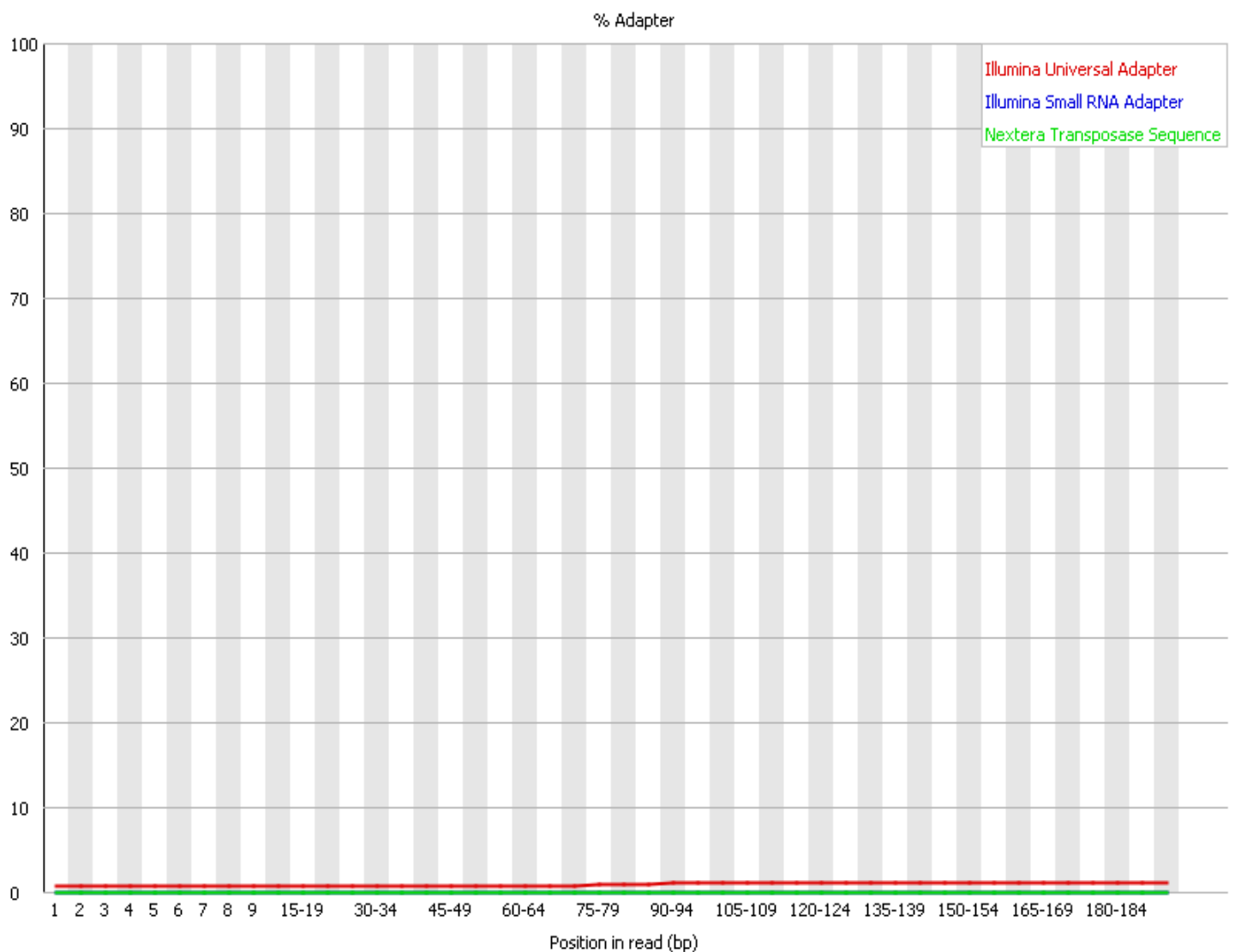
Sequence Duplication Levels



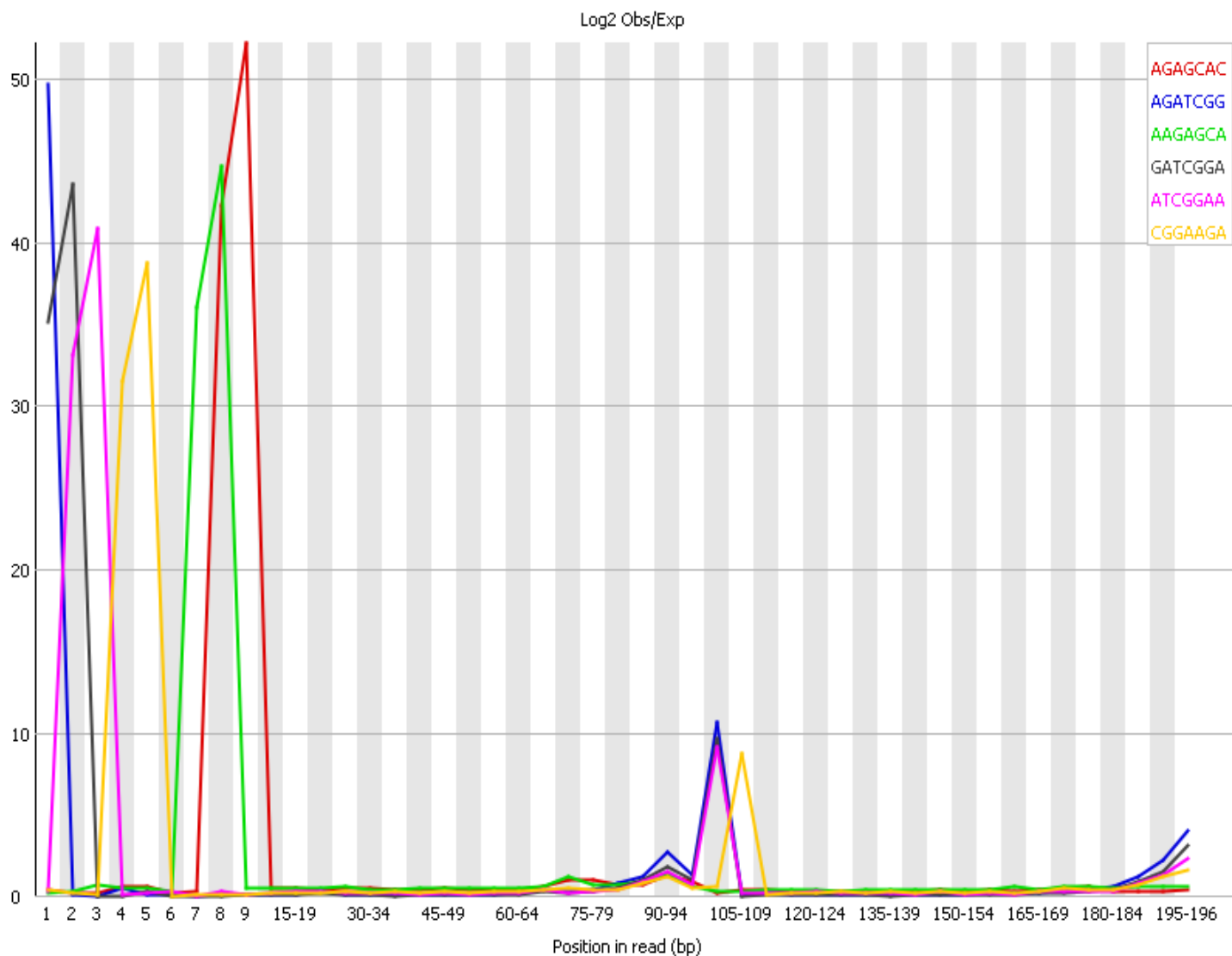
⚠ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTA	216331	0.727579029219732	TruSeq Adapter, Index 14 (97% over 44bp)
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAGTTCCGTATCTCGTAT	179322	0.6031078609988434	TruSeq Adapter, Index 14 (97% over 44bp)
CCCACAGCAGCTTCCGGAGGCCTGGATGTGATGGCATCACAGAAGAGACC	45637	0.1534894405170822	No Hit

✓ Adapter Content



✗ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGAGCAC	94040	0.0	52.15453	9
AGATCGG	99070	0.0	49.67305	1
AAGAGCA	110340	0.0	44.70754	8
GATCGGA	113160	0.0	43.53235	2
ATCGGAA	120495	0.0	40.857967	3
CGGAAGA	126585	0.0	38.783916	5
TCGGAAG	128105	0.0	38.430824	4
GAGCACA	120015	0.0	33.403694	9
CGTATCA	31275	0.0	32.493824	150-154
TATCTCG	53830	0.0	32.45879	40-44
TATGCCG	54200	0.0	32.396587	45-49
CGCCGTA	31755	0.0	32.22546	145-149

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCCGTAT	55050	0.0	31.917267	35-39
CGTATGC	56400	0.0	31.254519	45-49
TCGTATG	57415	0.0	30.691751	45-49
GTTCCGT	58435	0.0	30.148872	35-39
TTCCGTA	62055	0.0	28.465927	35-39
ACACGTC	62640	0.0	28.35637	10-14
GTATGCC	62890	0.0	28.281605	45-49
GCCGTCT	61760	0.0	28.199509	50-54

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