













FastQC Report

Summary

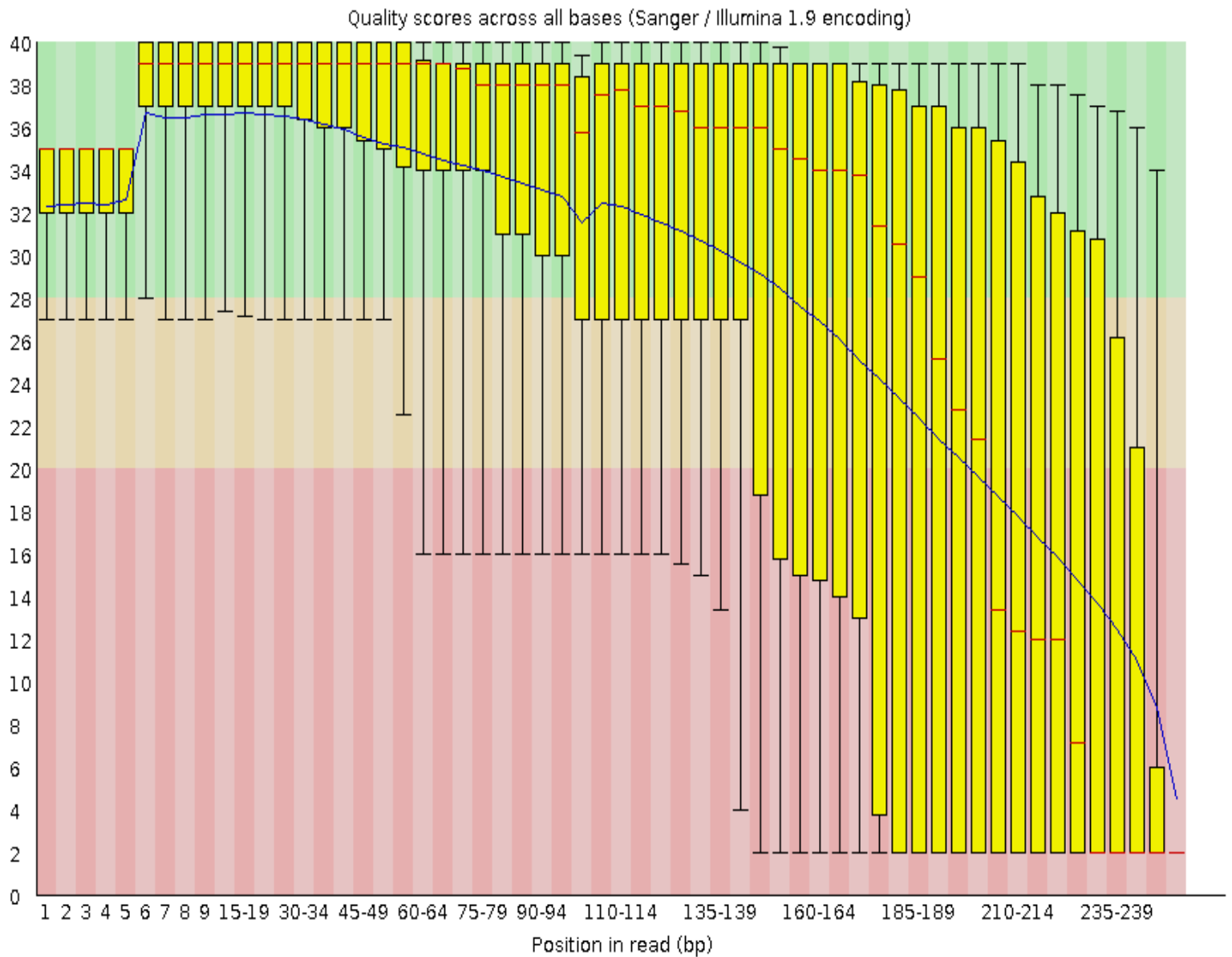
Mon 18 May 2015
BS_MK_noAdap_R2.fastq

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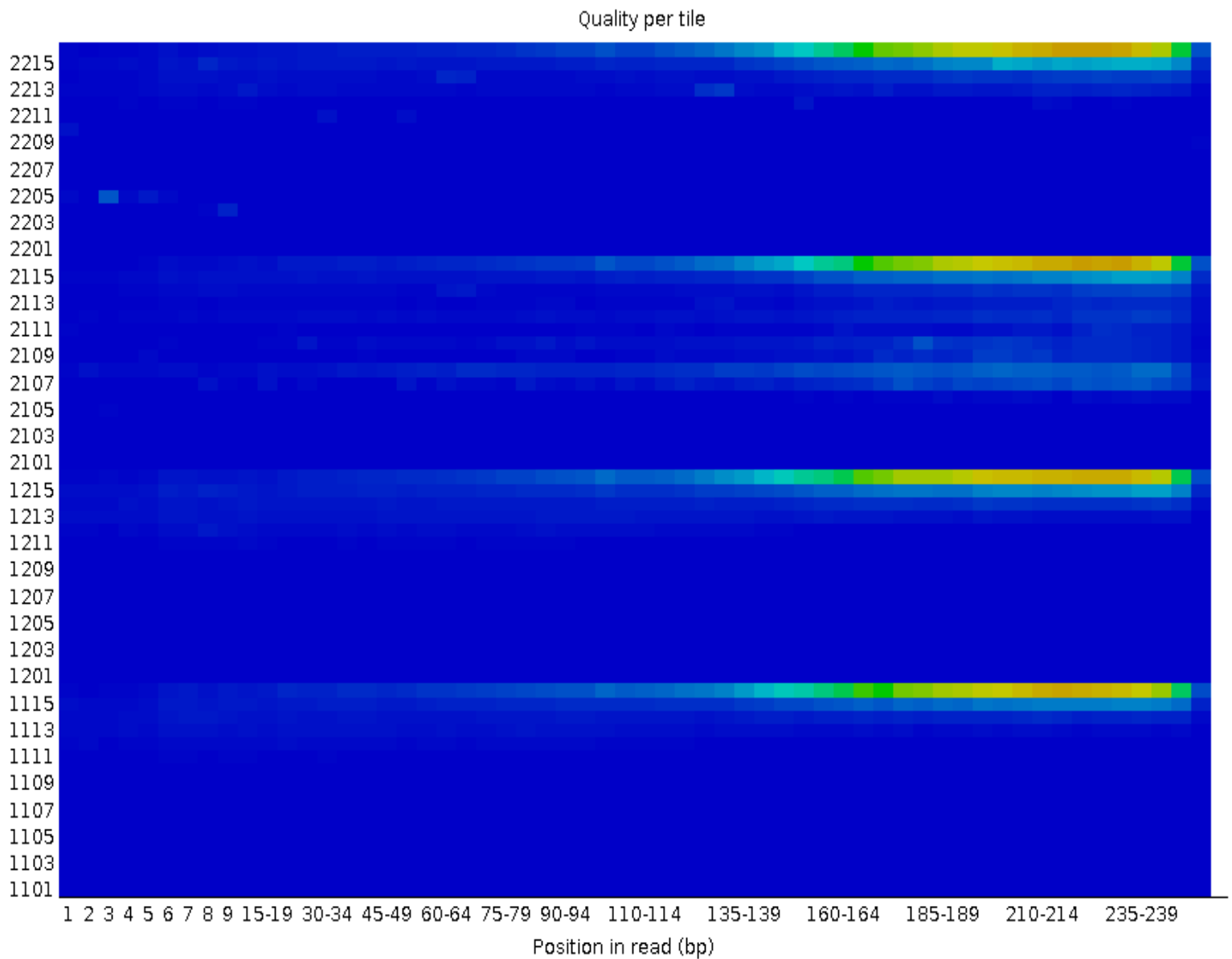
Basic Statistics

Measure	Value
Filename	BS_MK_noAdap_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	158374682
Sequences flagged as poor quality	0
Sequence length	18-250
%GC	42

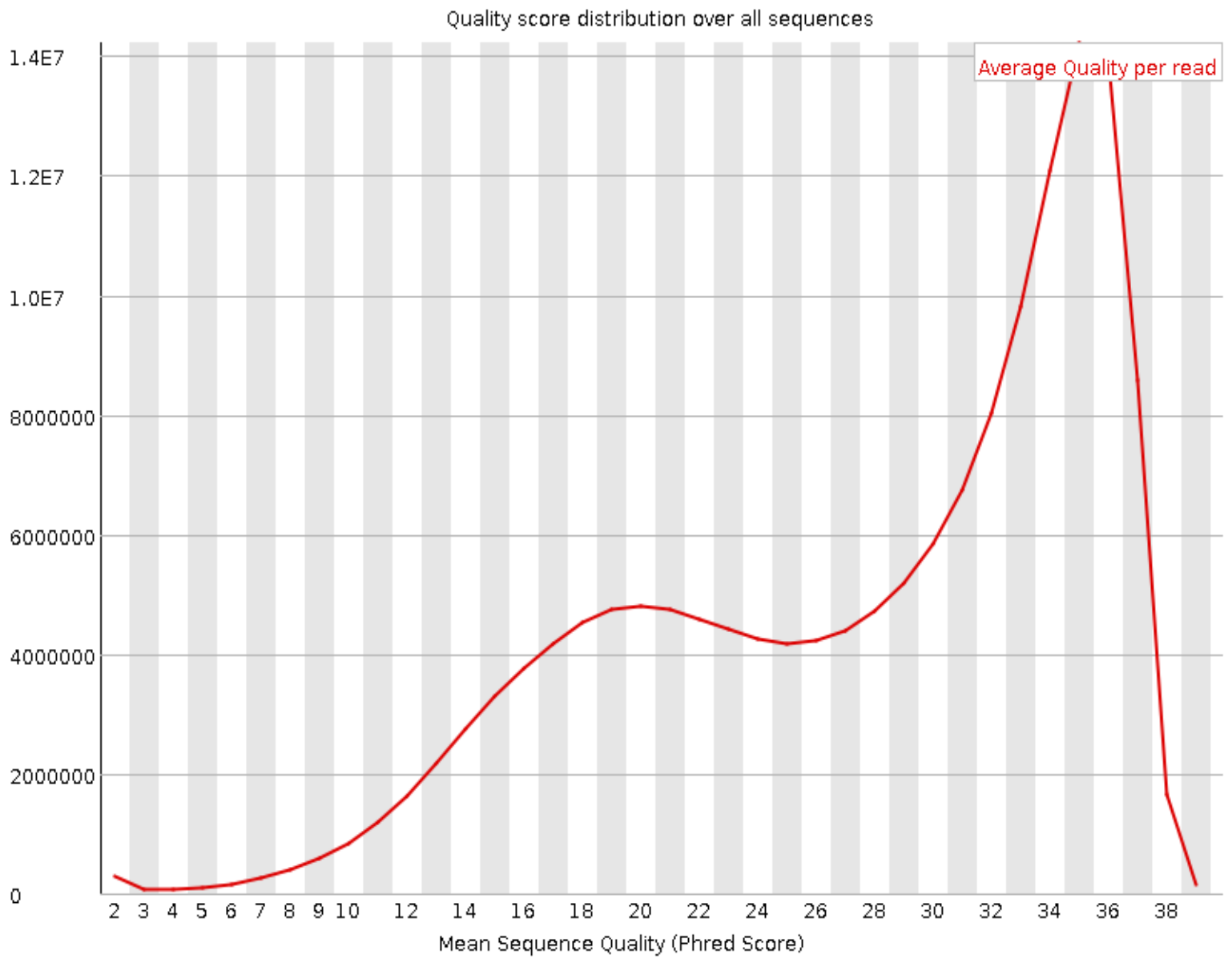
✖ Per base sequence quality



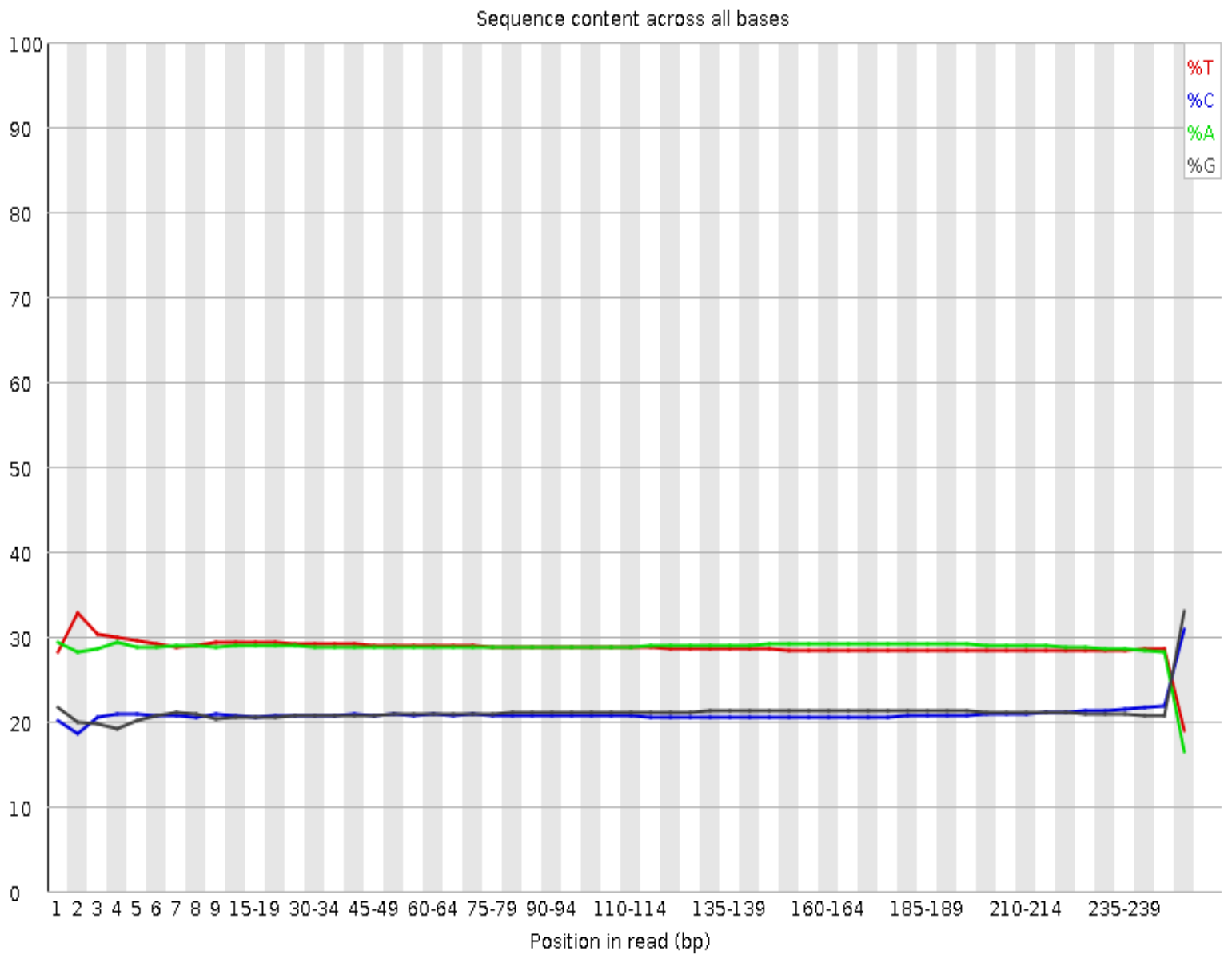
⚠ Per tile sequence quality



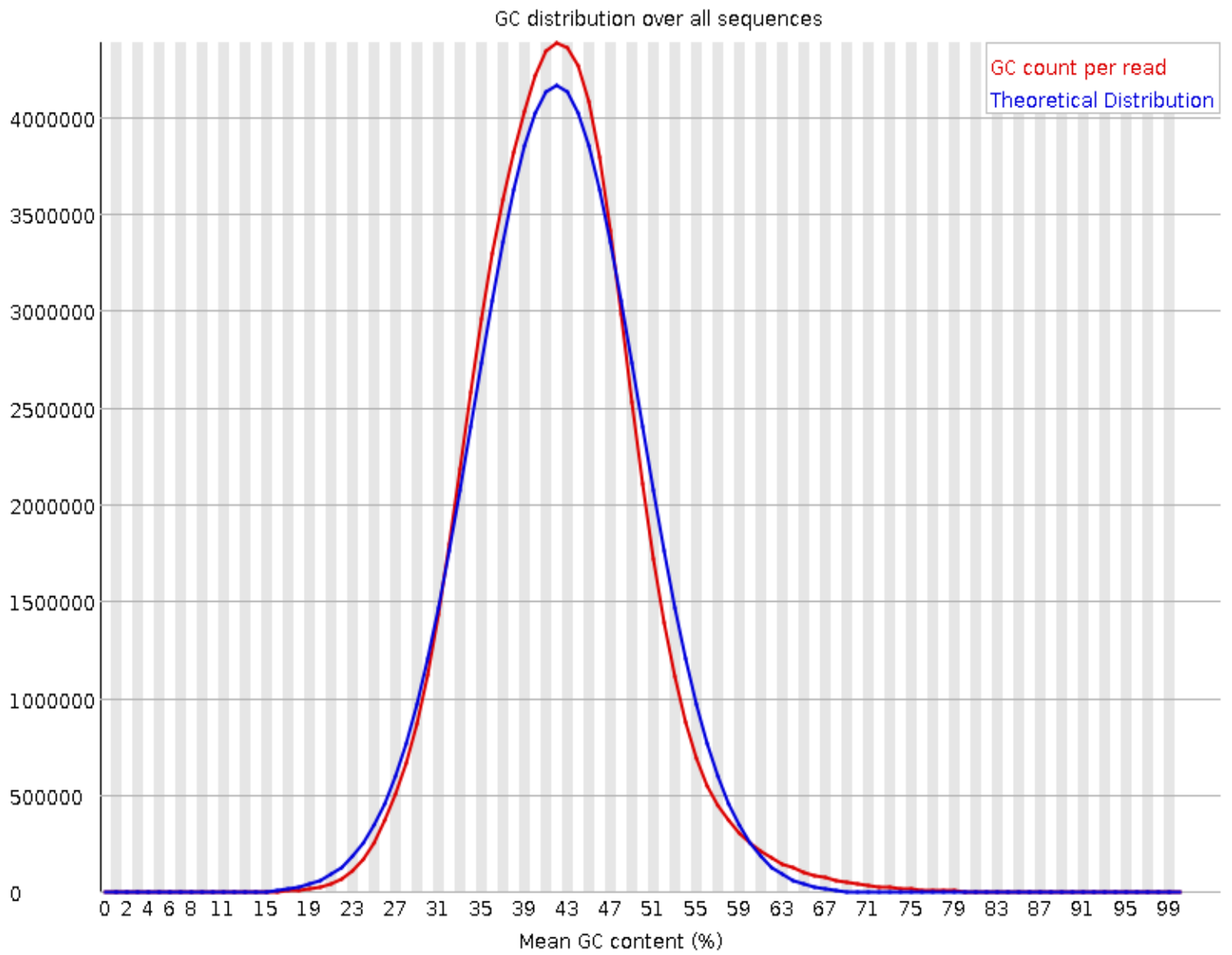
Per sequence quality scores



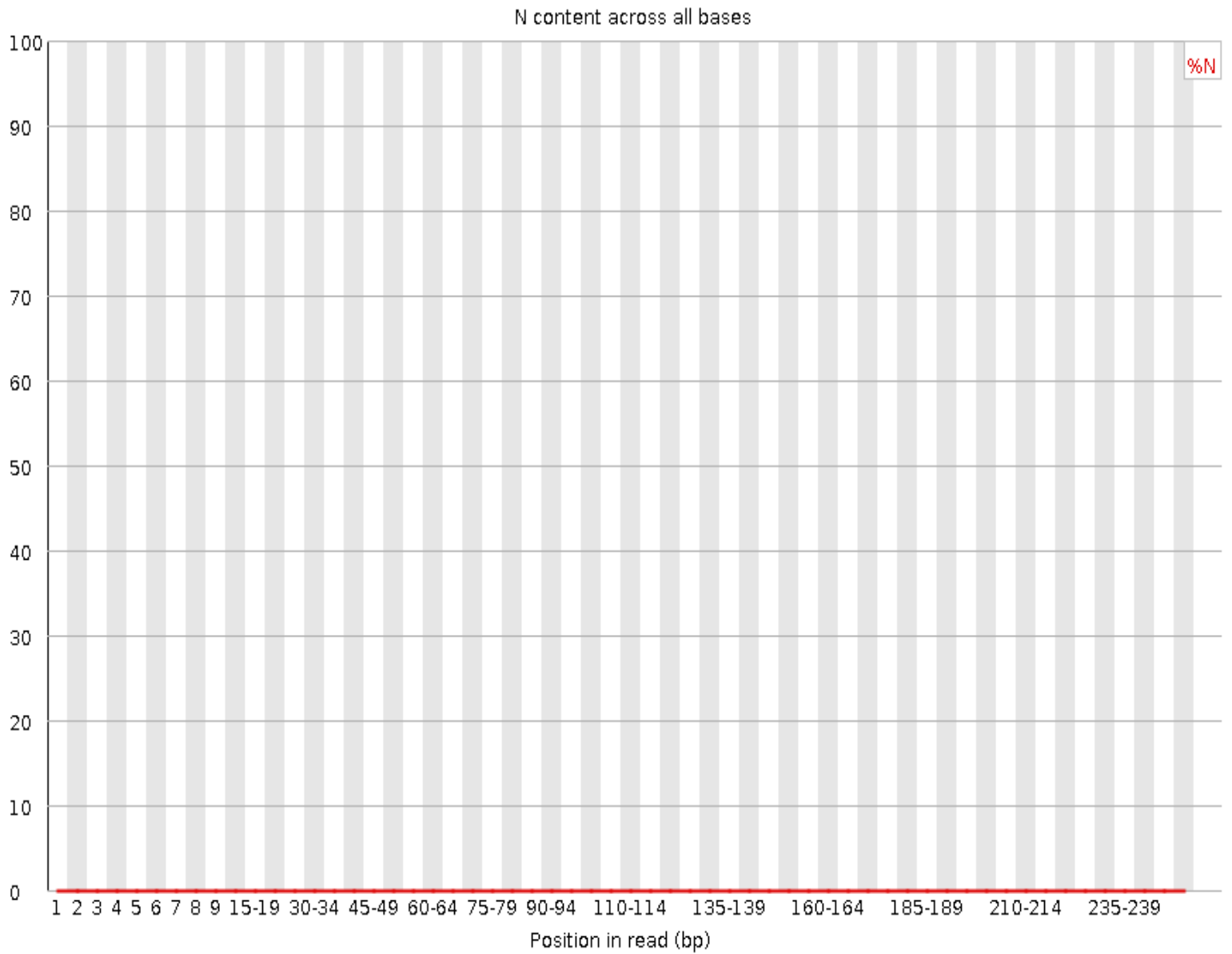
Per base sequence content



Per sequence GC content



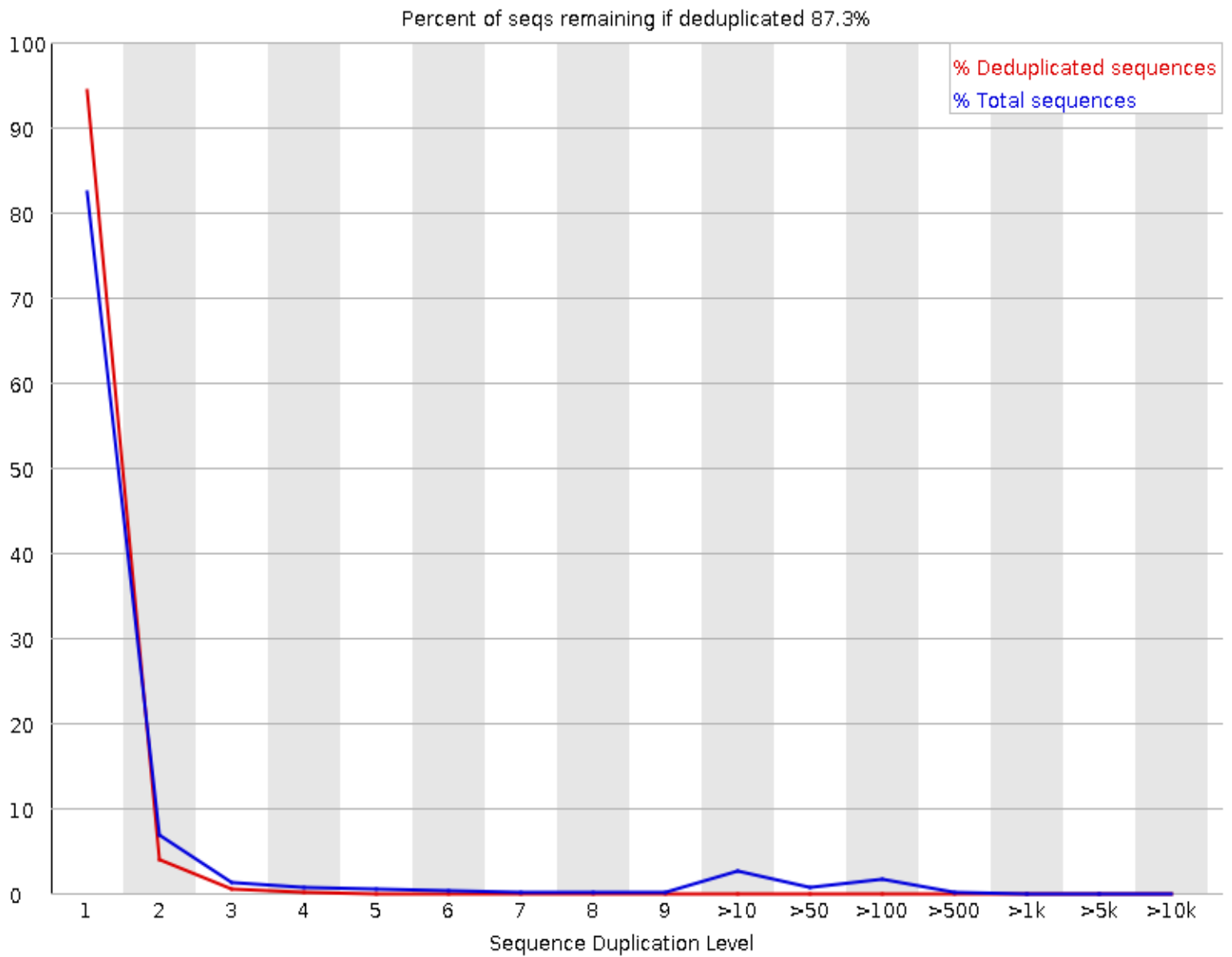
 **Per base N content**



Sequence Length Distribution



Sequence Duplication Levels

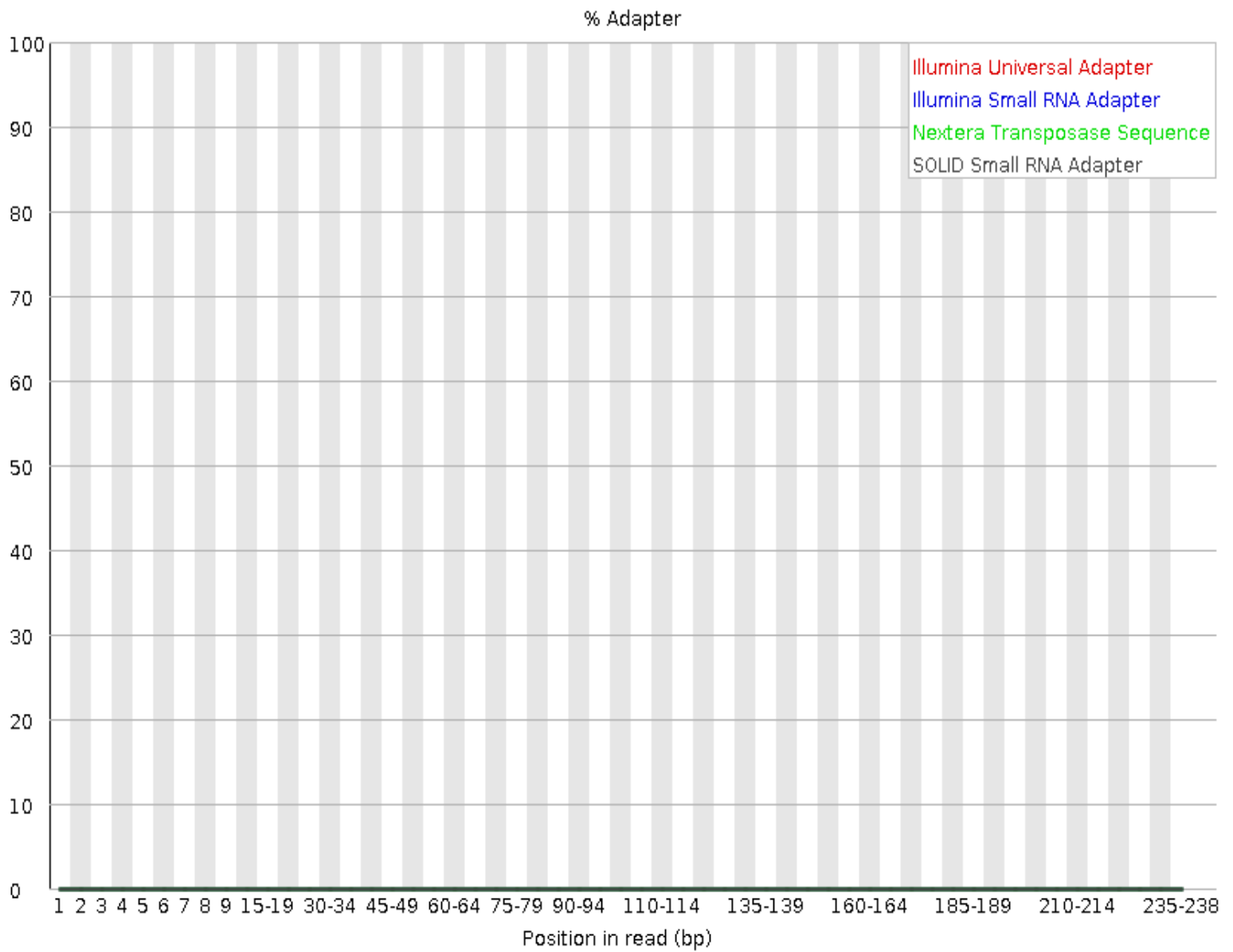


Overrepresented sequences

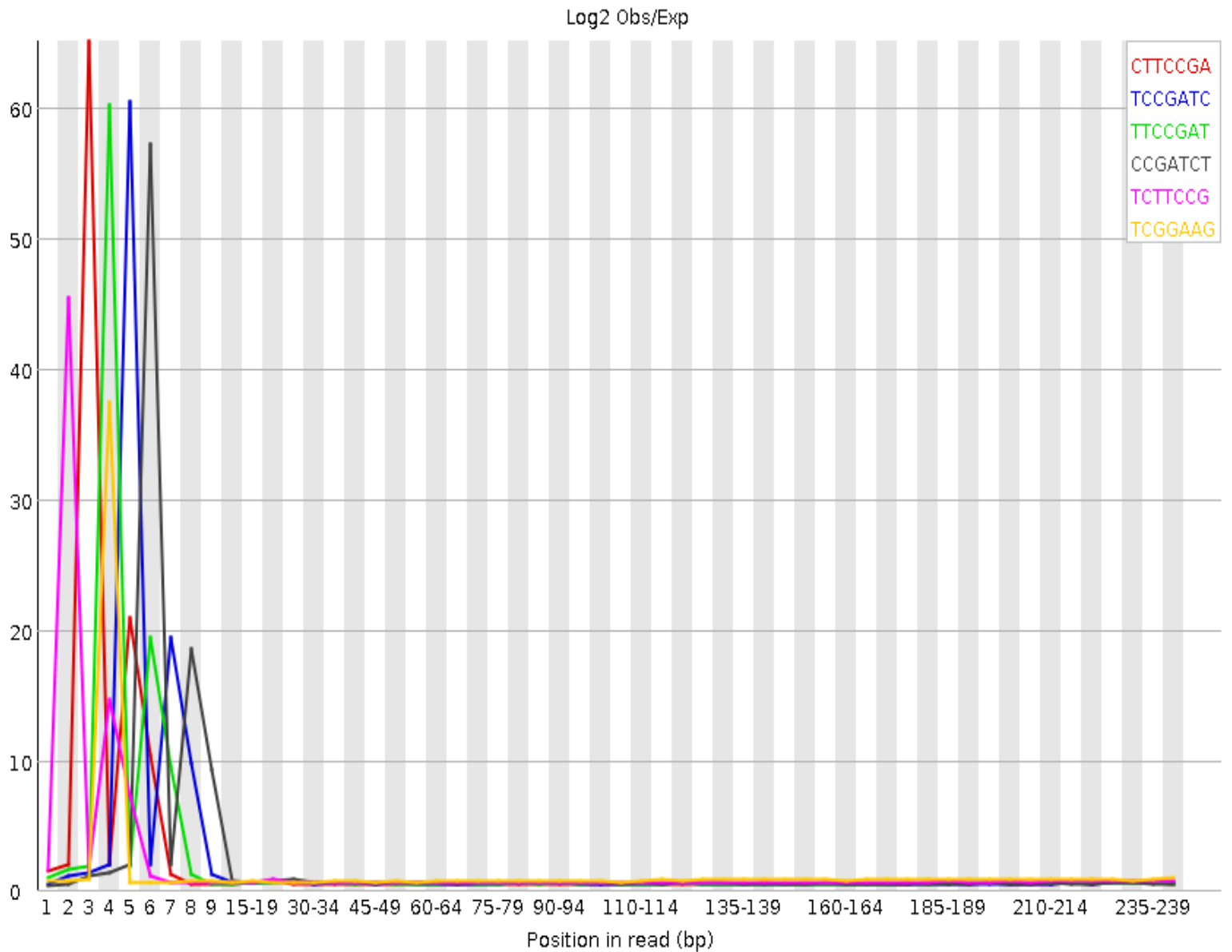
No overrepresented sequences



Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	144400	0.0	65.05692	3
TCCGATC	154445	0.0	60.480114	5
TTCCGAT	155530	0.0	60.214745	4
CCGATCT	162685	0.0	57.19979	6
TCTTCCG	208445	0.0	45.518627	2
TCGGAAG	110290	0.0	37.528744	4
ATCGGAA	120005	0.0	34.358017	3
GATCGGA	120405	0.0	34.28055	2

AGATCGG	133740	0.0	31.094324	1
CGATCTA	103160	0.0	27.983278	7
CGGAAGA	177415	0.0	23.782608	5
CTCTTCC	481270	0.0	20.34482	1
CGATCTT	135660	0.0	19.420763	7
GAAGAGC	266540	0.0	16.186306	7
ACGCTCT	101195	0.0	14.303666	1
CAAGTCG	112860	0.0	14.108764	5
CGATCTC	148945	0.0	13.665078	7
CGATCTG	168820	0.0	12.770591	7
GCTCTTC	252535	0.0	12.59454	2
GTCGTCA	141200	0.0	11.542871	8

Produced by [FastQC](#) (version 0.11.3)