

FastQC Report

Summary

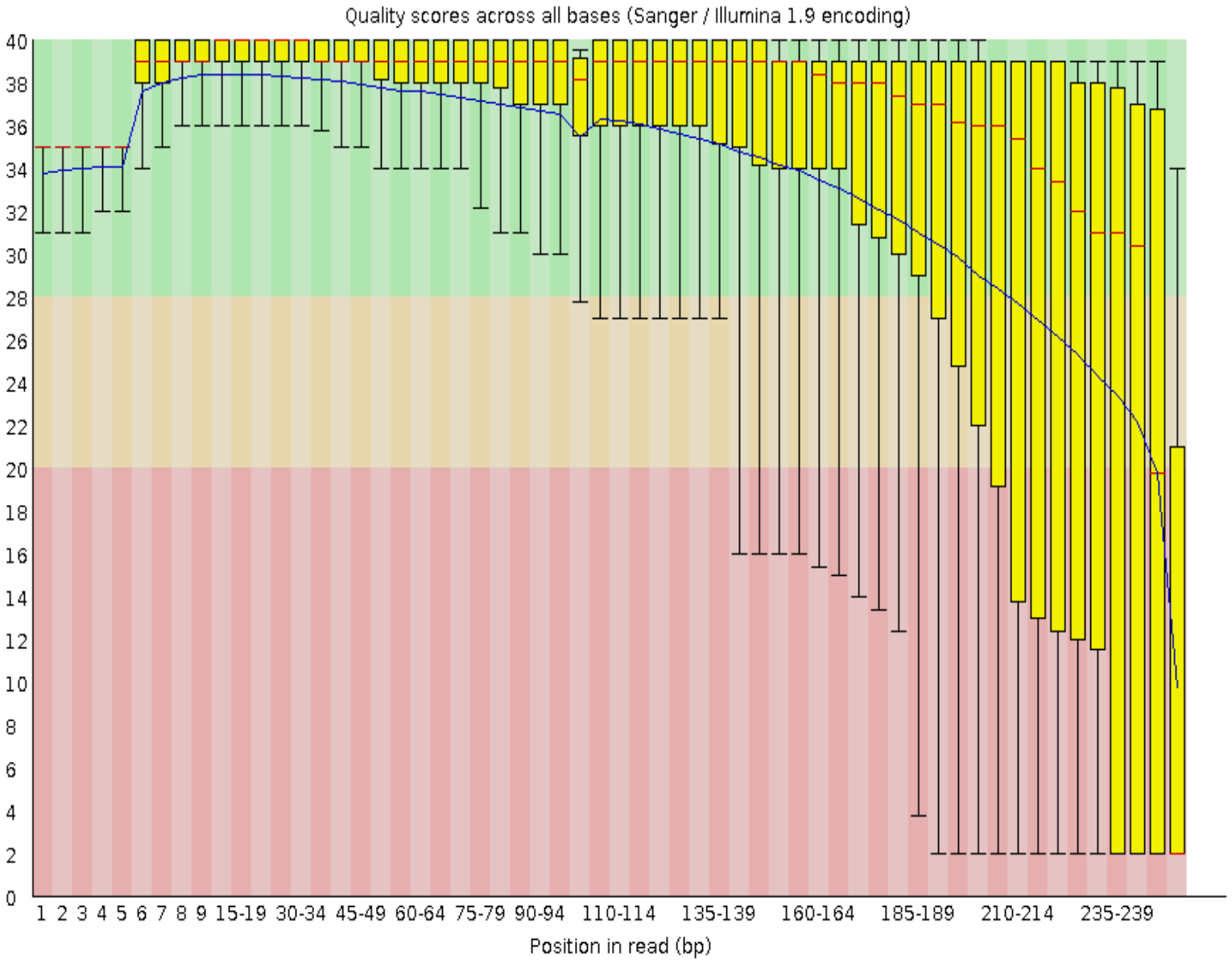
Mon 18 May 2015
BS_MK_noAdap_R1.fastq

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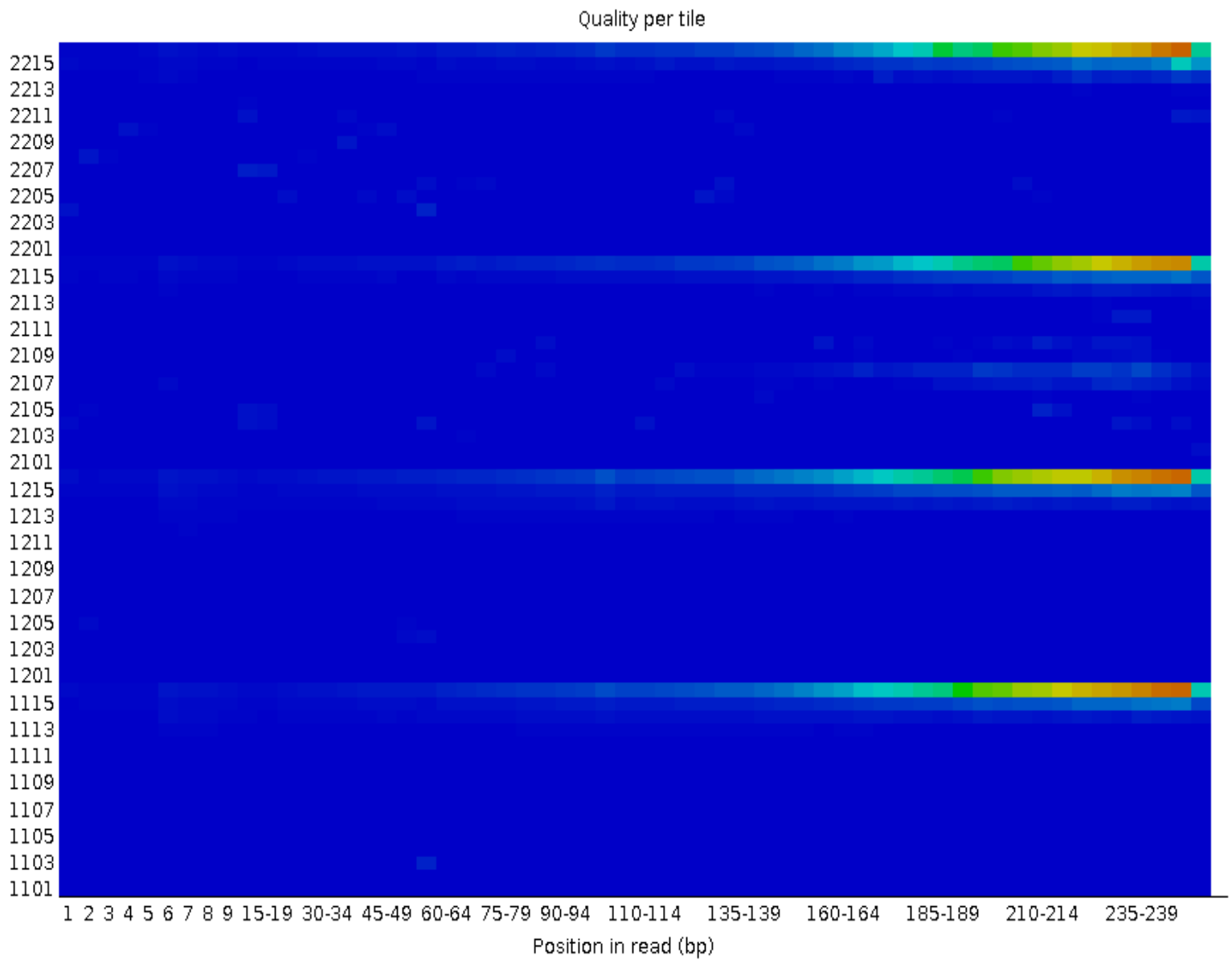
Basic Statistics

Measure	Value
Filename	BS_MK_noAdap_R1.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	41

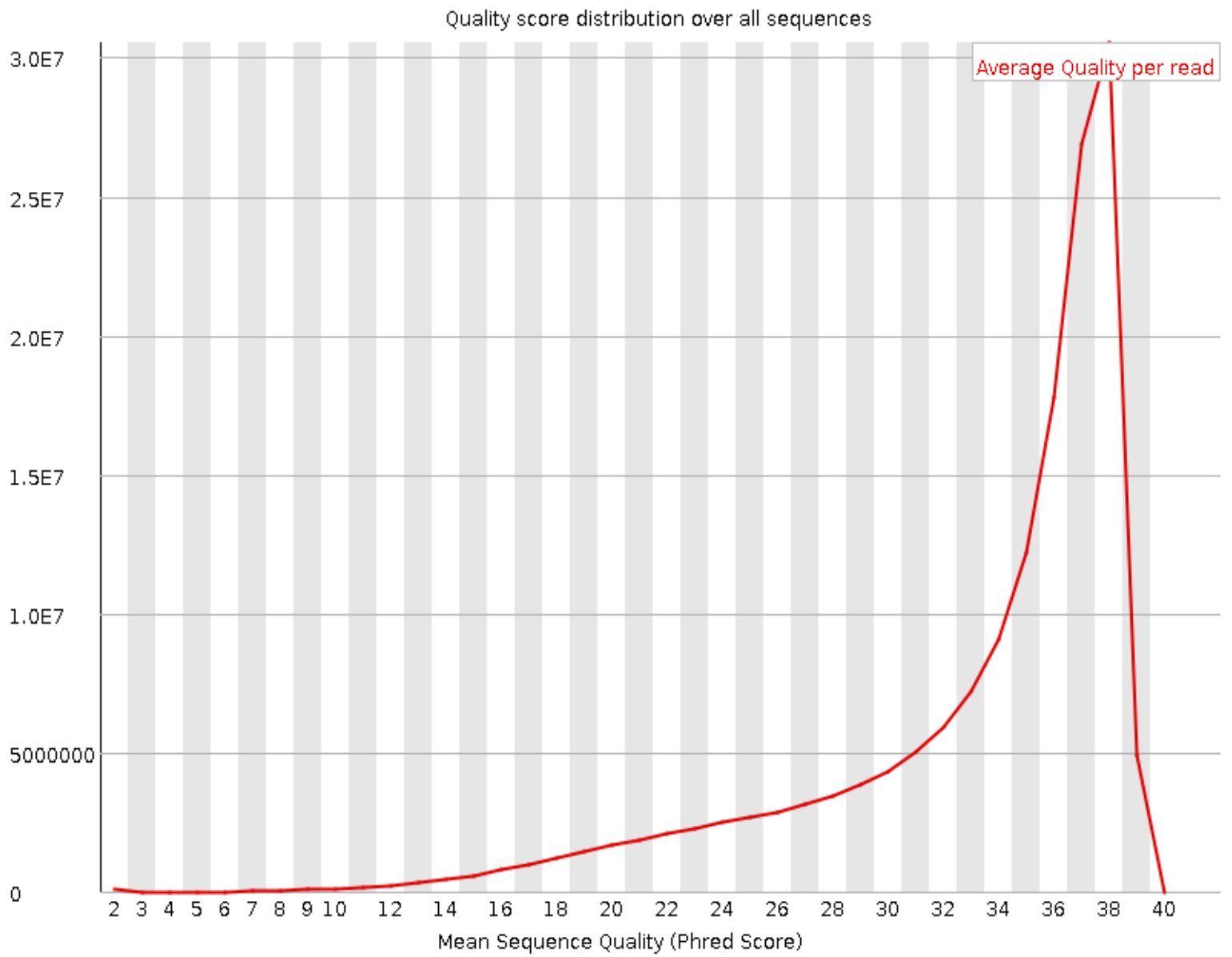
Per base sequence quality



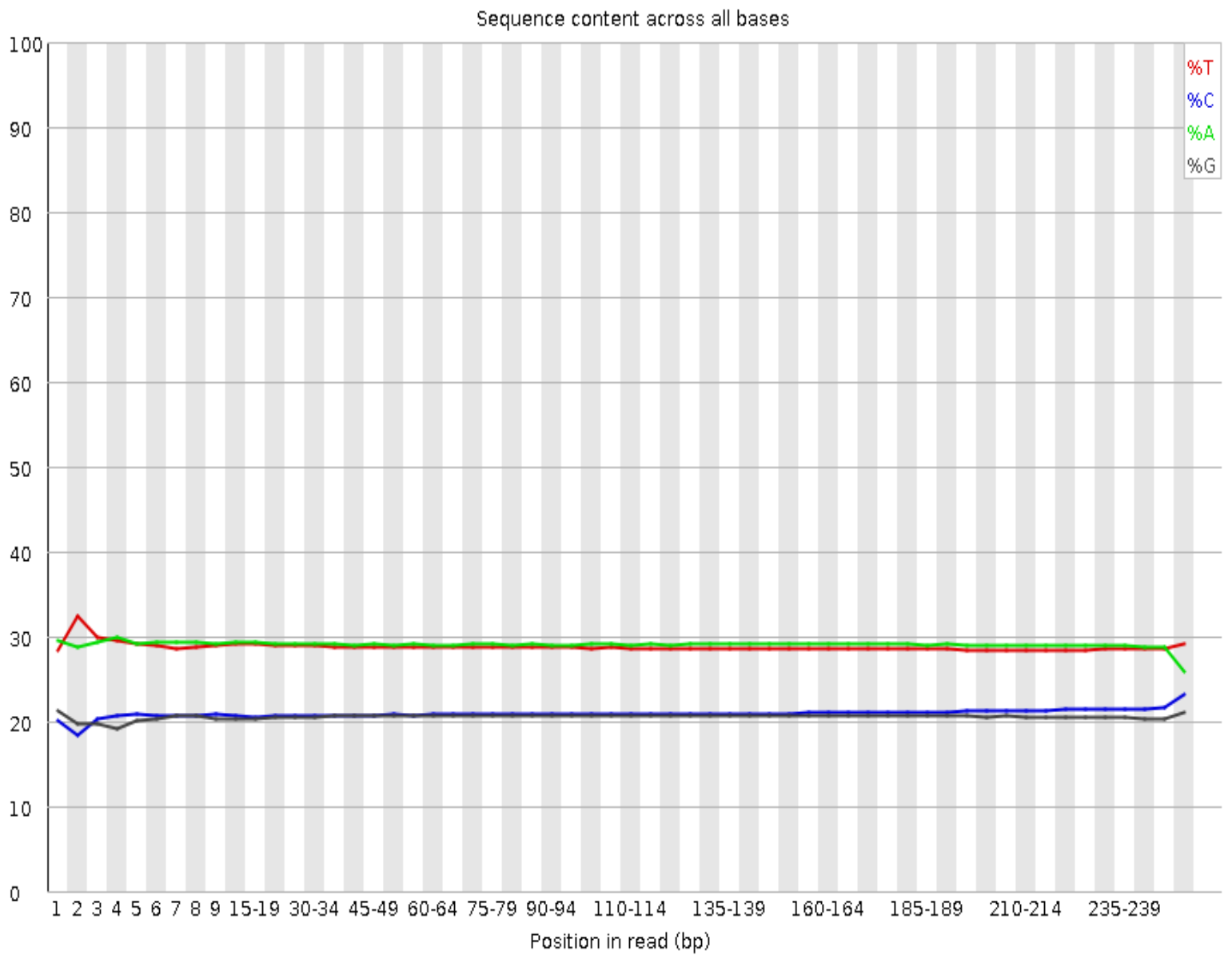
Per tile sequence quality



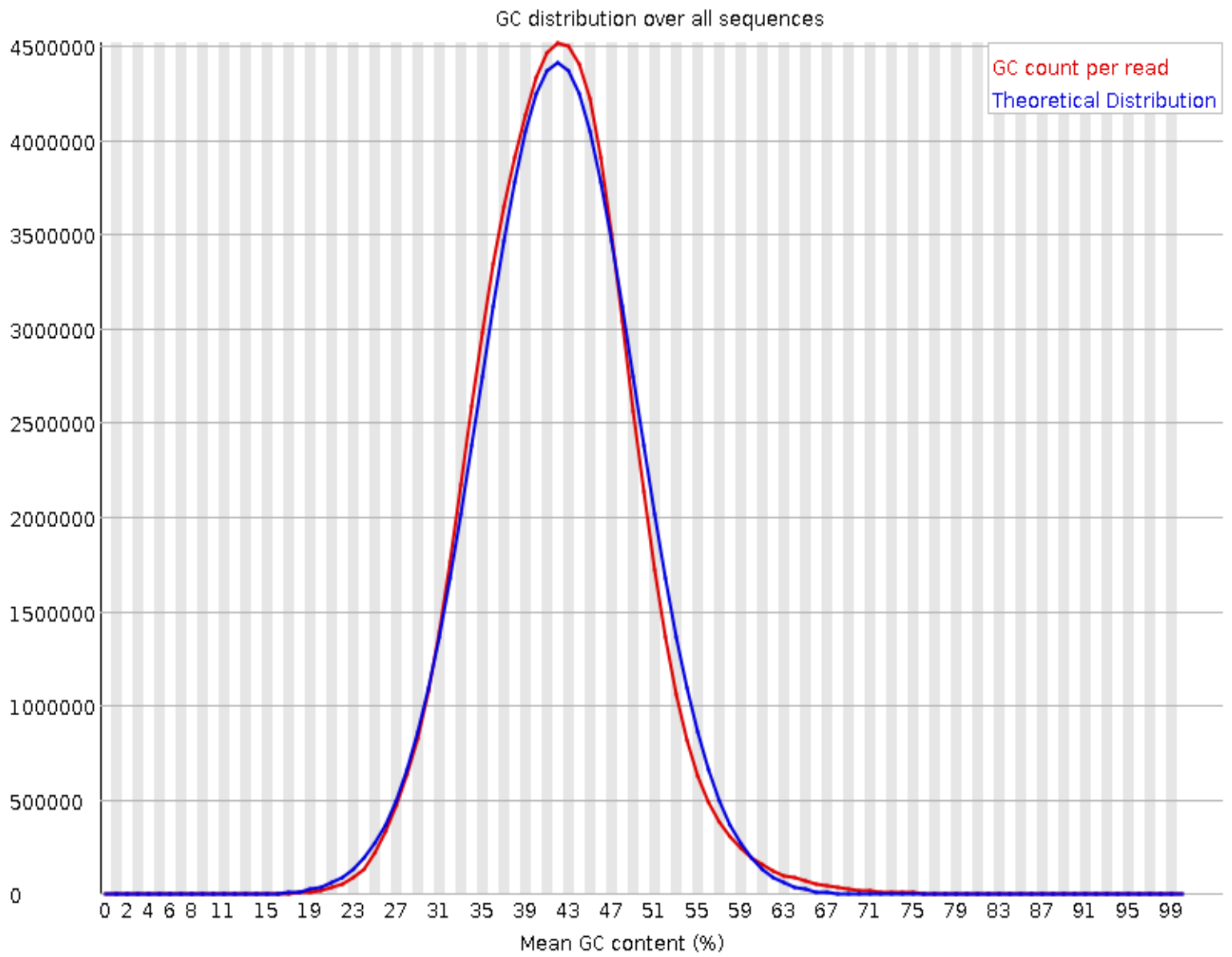
Per sequence quality scores



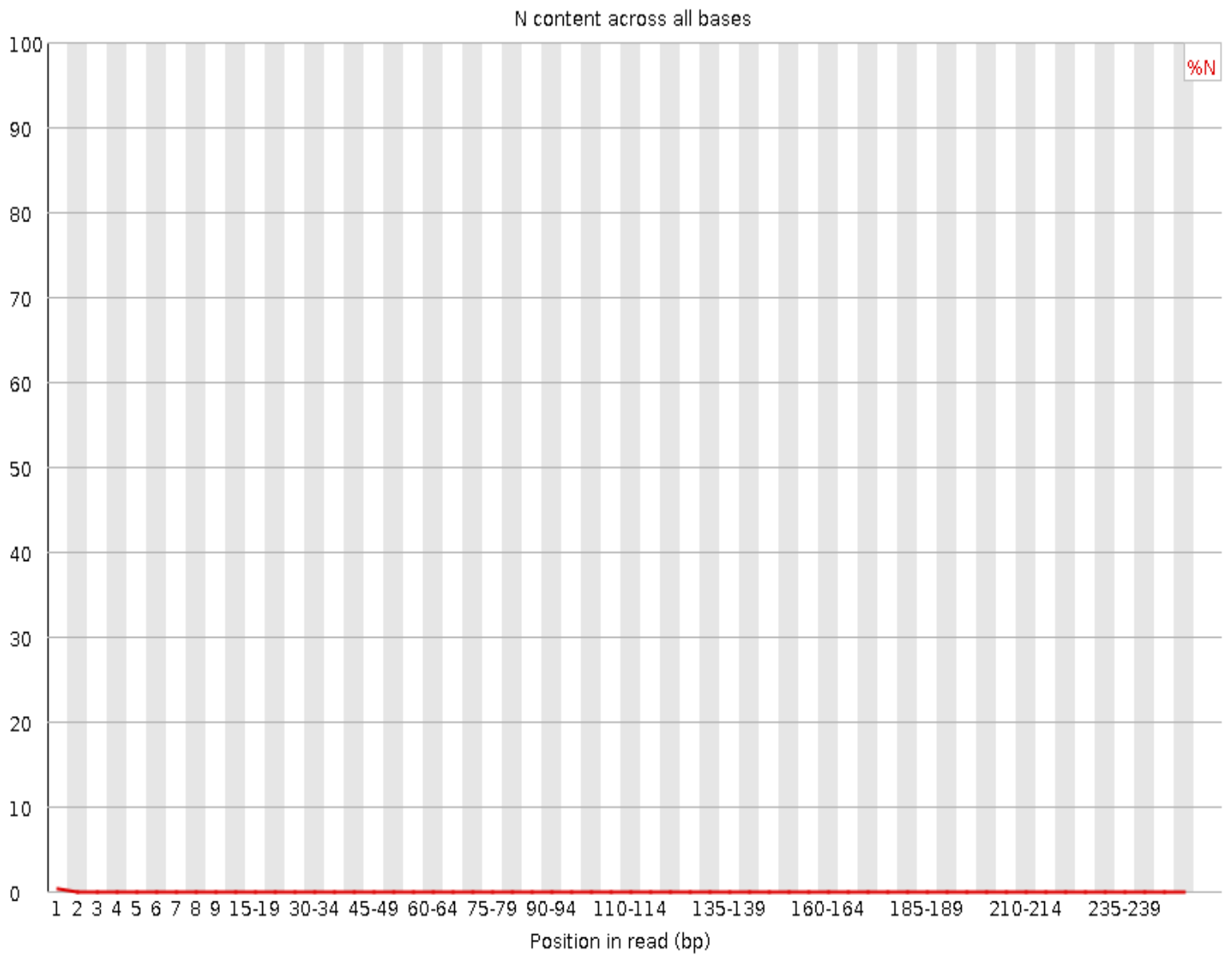
Per base sequence content



Per sequence GC content



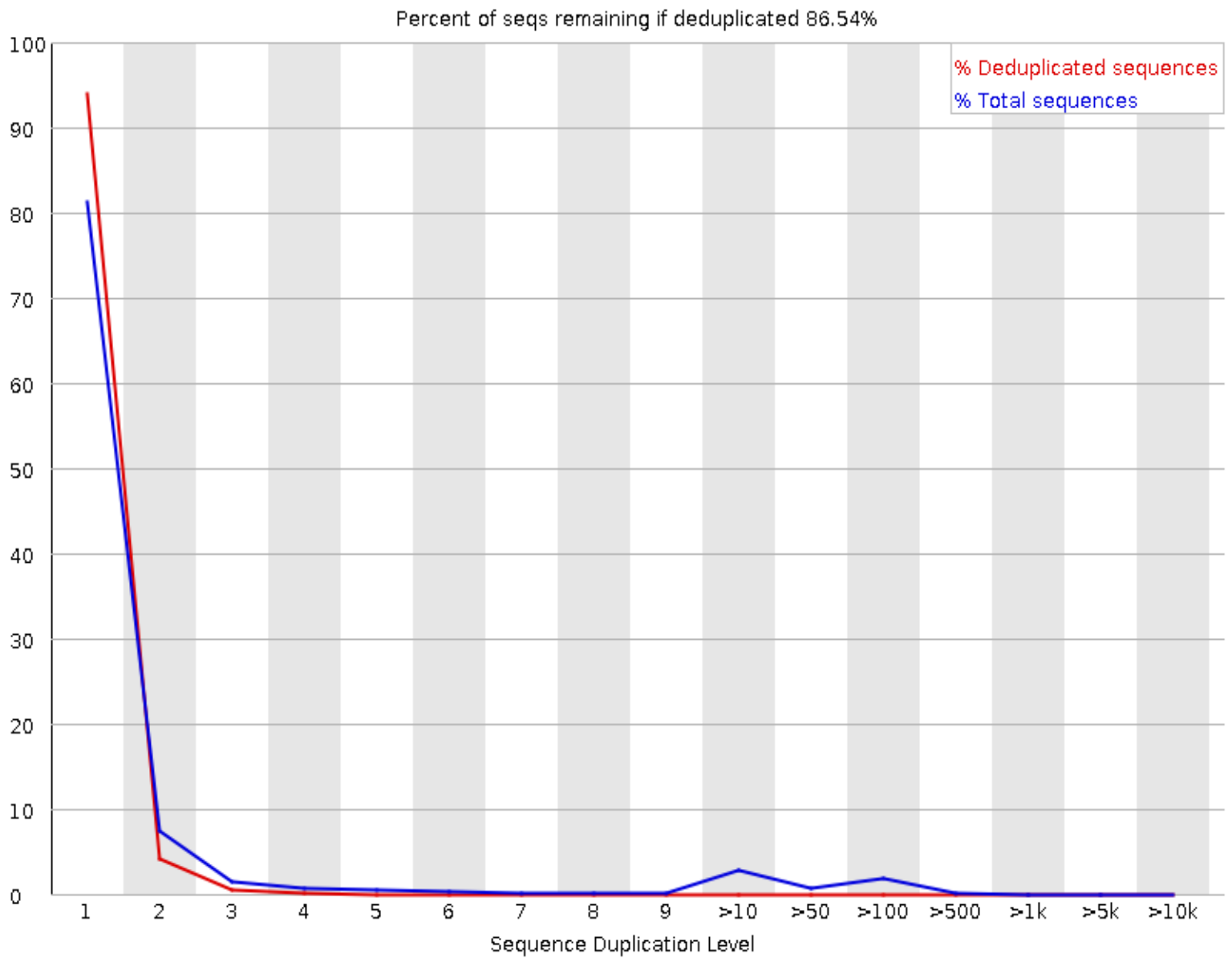
 **Per base N content**



Sequence Length Distribution



Sequence Duplication Levels

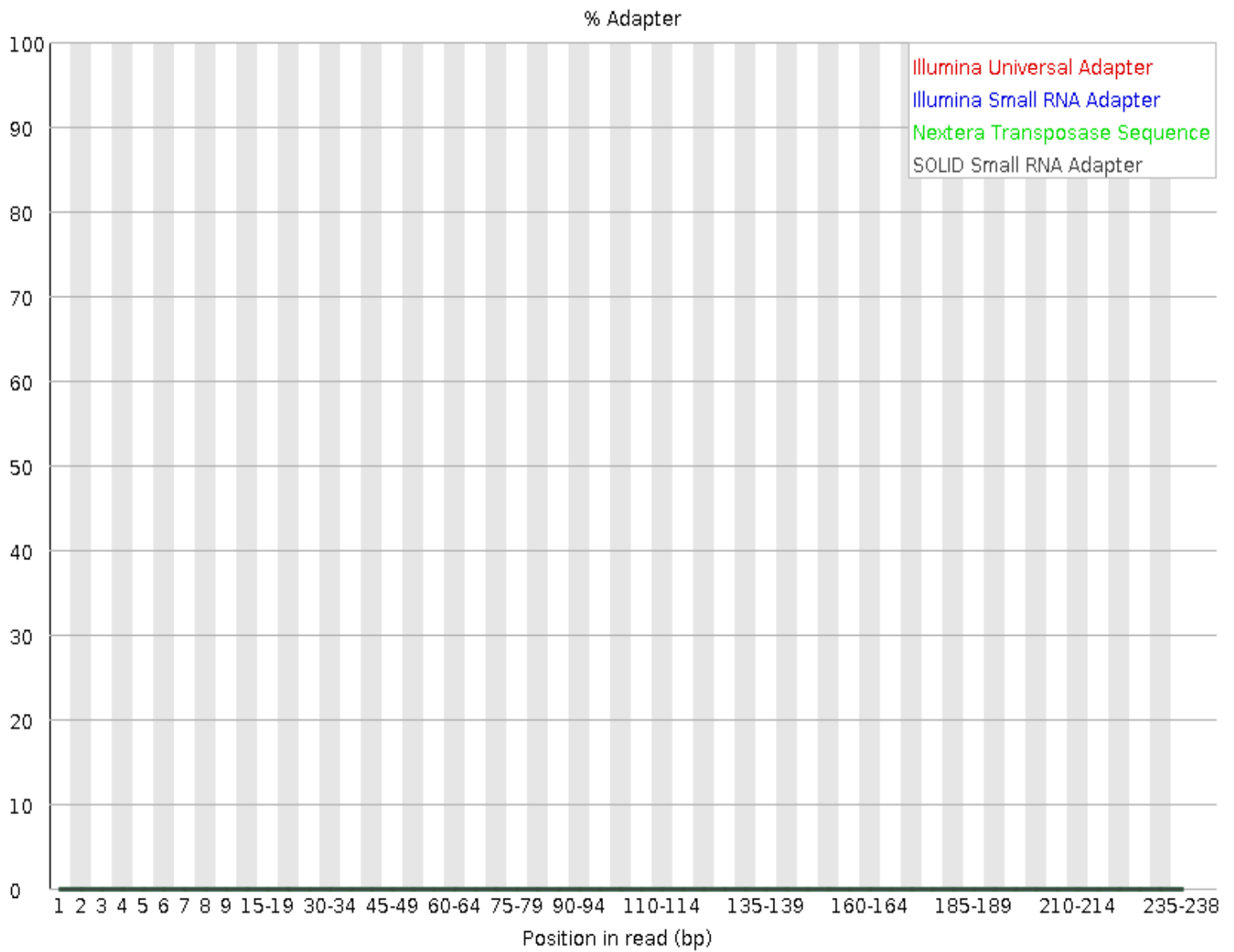


Overrepresented sequences

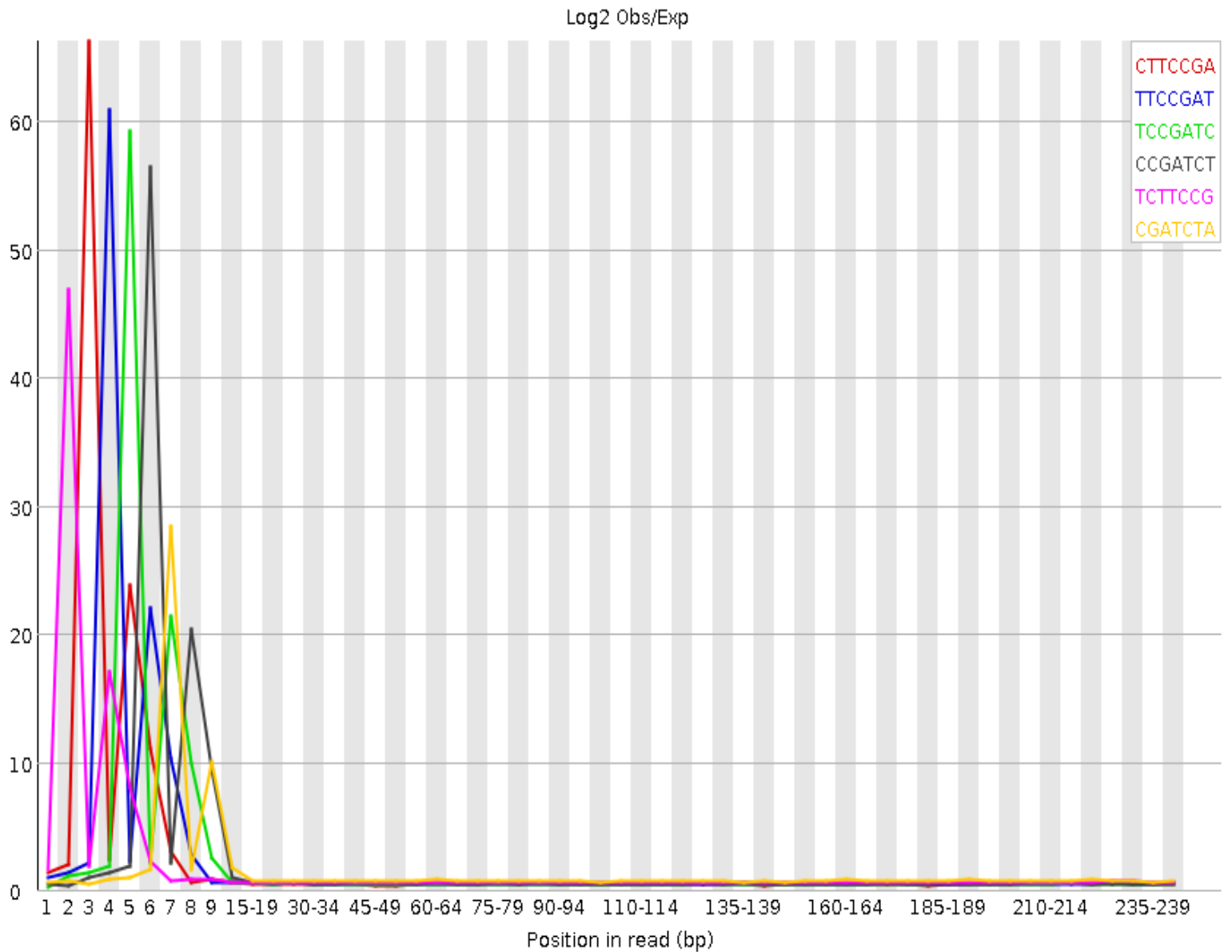
No overrepresented sequences



Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	143635	0.0	66.2239	3
TTCCGAT	156250	0.0	60.877247	4
TCCGATC	160725	0.0	59.273106	5
CCGATCT	168595	0.0	56.491806	6
TCTTCCG	203815	0.0	46.950687	2
CGATCTA	102755	0.0	28.441298	7
CGATCTT	131830	0.0	21.282585	7
CTCTTCC	483945	0.0	20.401789	1

TCGGAAG	86355	0.0	19.30245	4
ATCGGAA	100840	0.0	16.710764	3
GATCGGA	103075	0.0	16.431047	2
ACGCTCT	98425	0.0	15.963181	1
AGATCGG	113580	0.0	14.845136	1
CAAGTCG	110495	0.0	14.237549	5
GCTCTTC	252535	0.0	14.207988	2
CGATCTC	150570	0.0	13.938949	7
CGCTCTT	129680	0.0	12.215671	2
CGATCTG	175040	0.0	11.893018	7
CGGAAGA	147160	0.0	11.789873	5
AAGTCGT	136810	0.0	11.587932	6

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