

FastQC Report

Summary

Wed 12 Aug 2015
Input



[Basic Statistics](#)



[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](#)



[Adapter Content](#)



[Kmer Content](#)



Basic Statistics

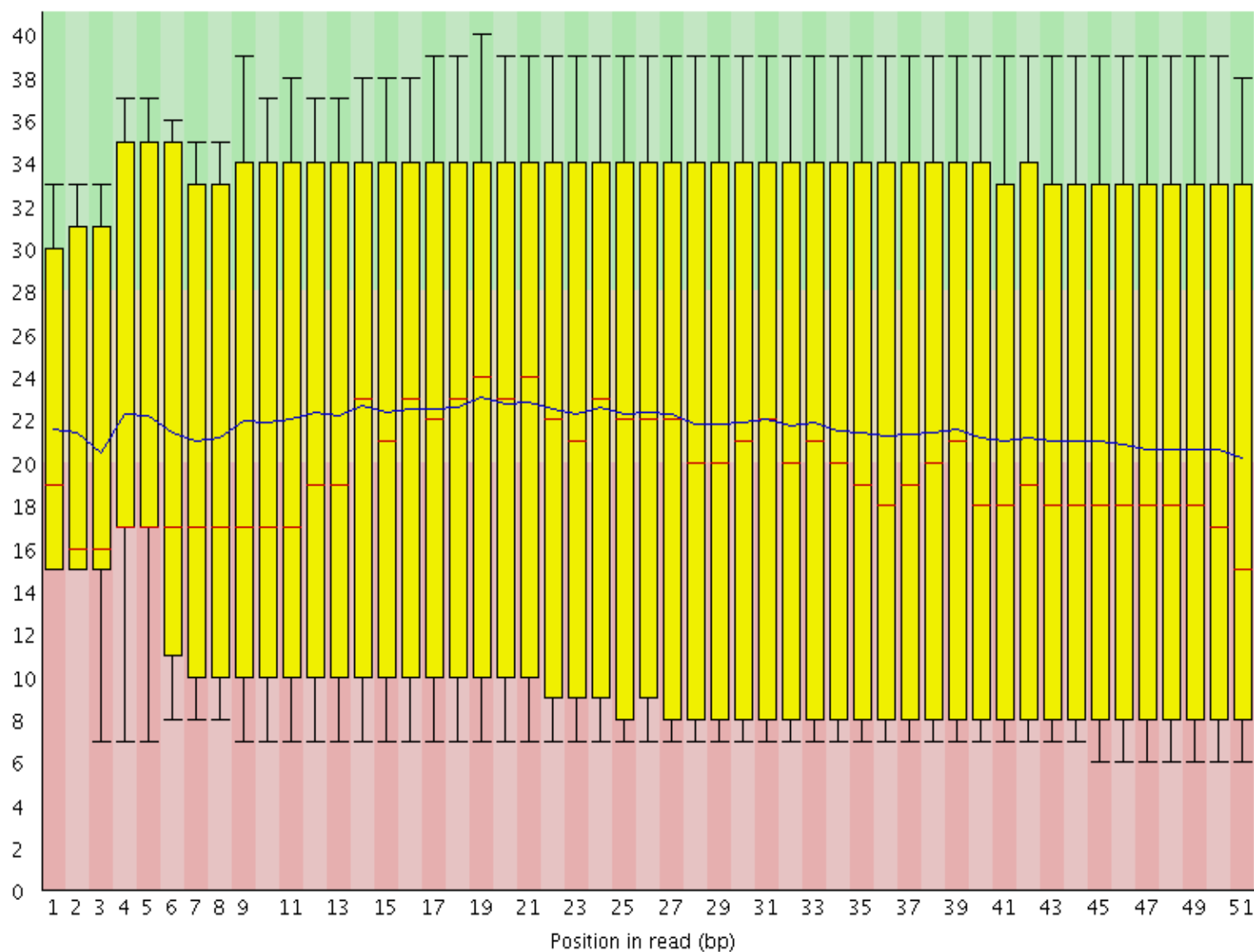
Measure

Value

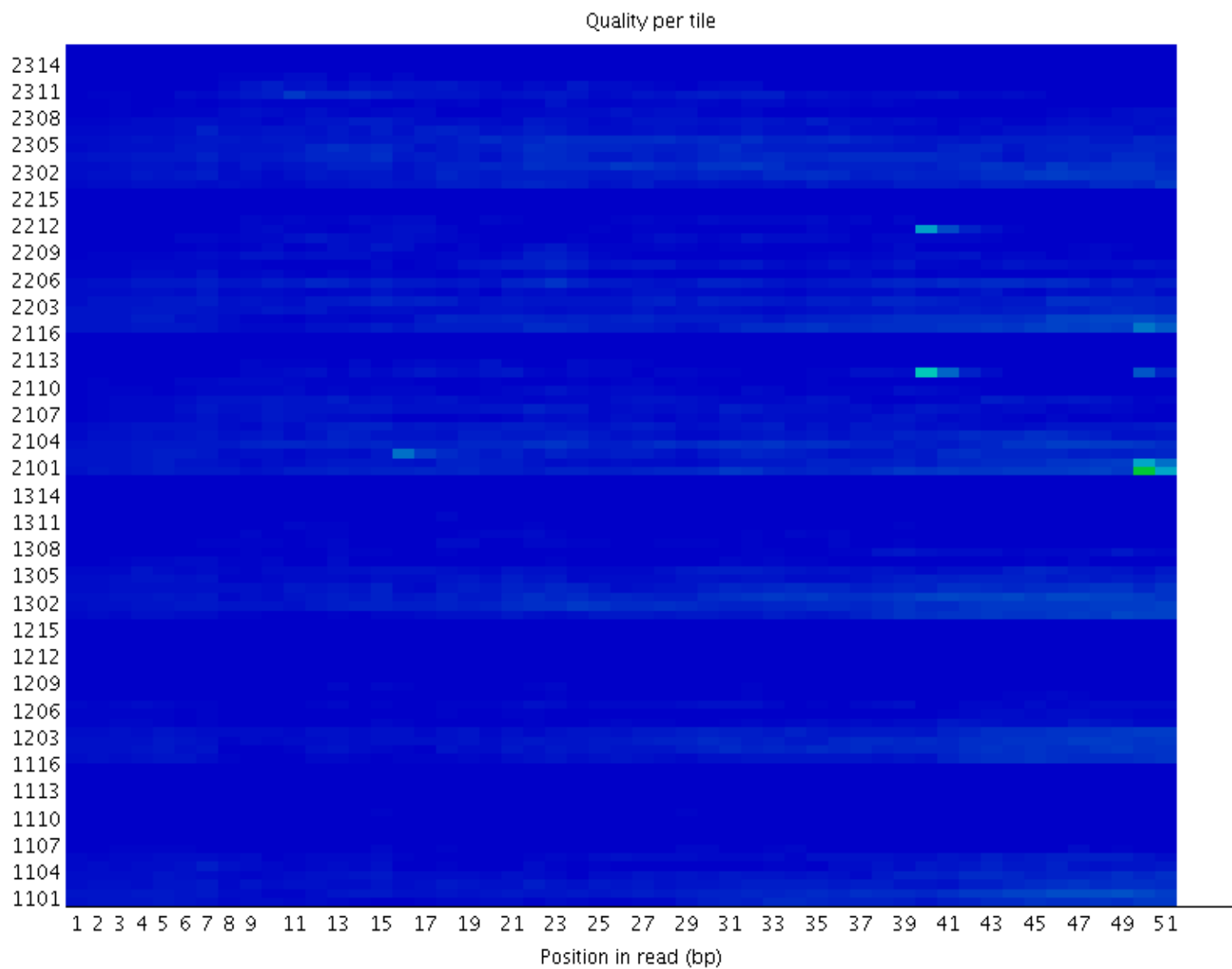
Filename	Input
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	22077448
Sequences flagged as poor quality	0
Sequence length	51
%GC	48

✖ Per base sequence quality

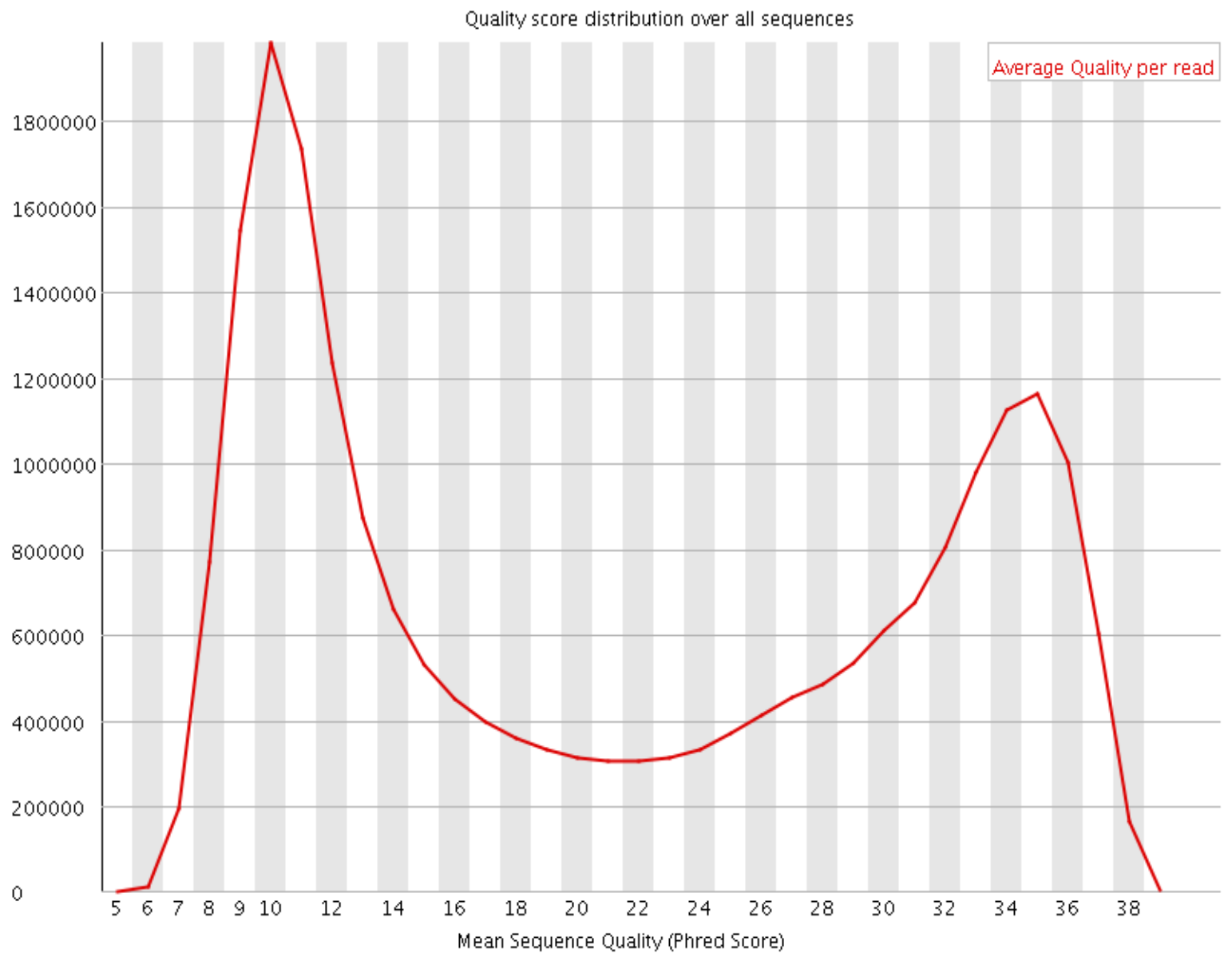
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



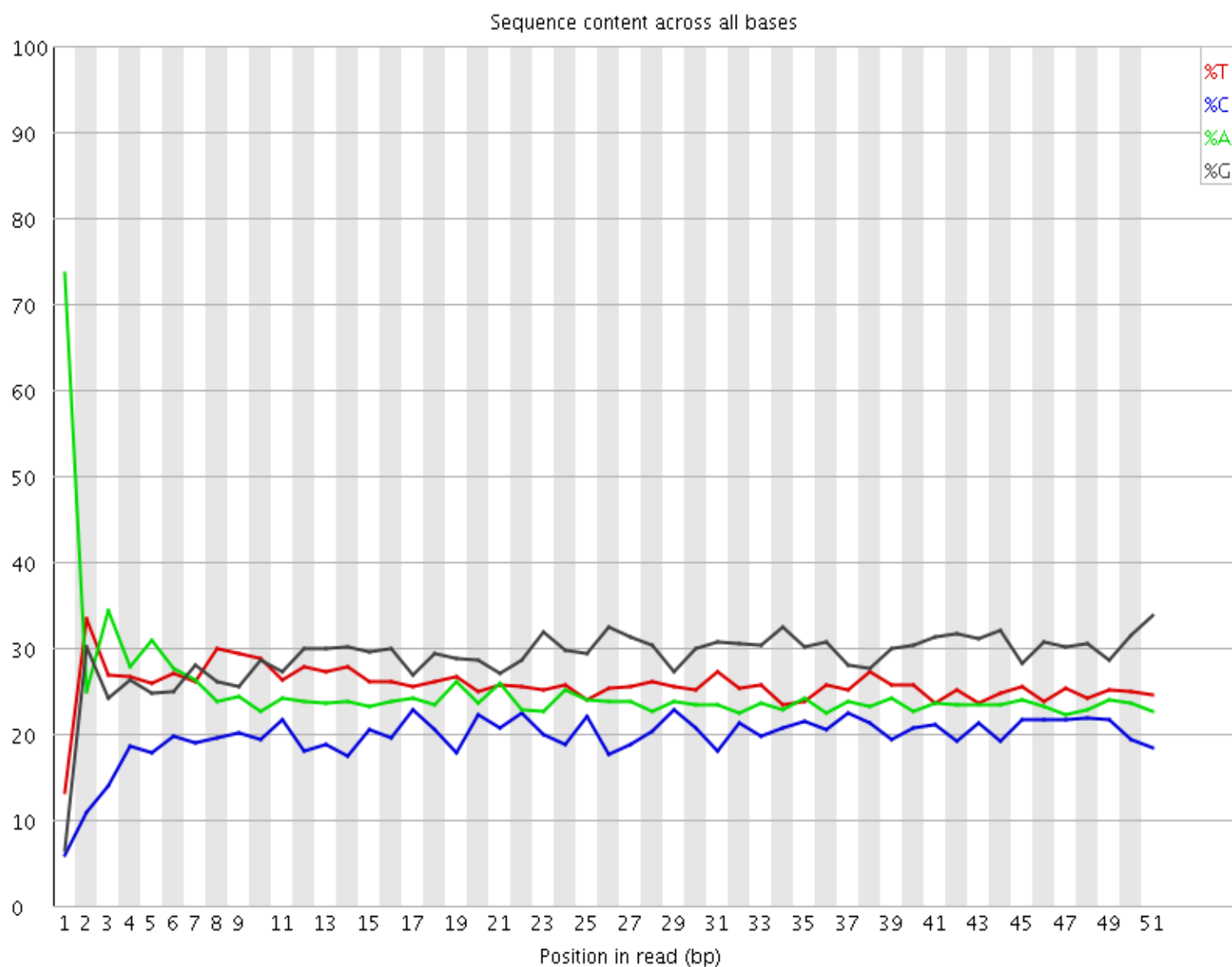
⚠ Per tile sequence quality



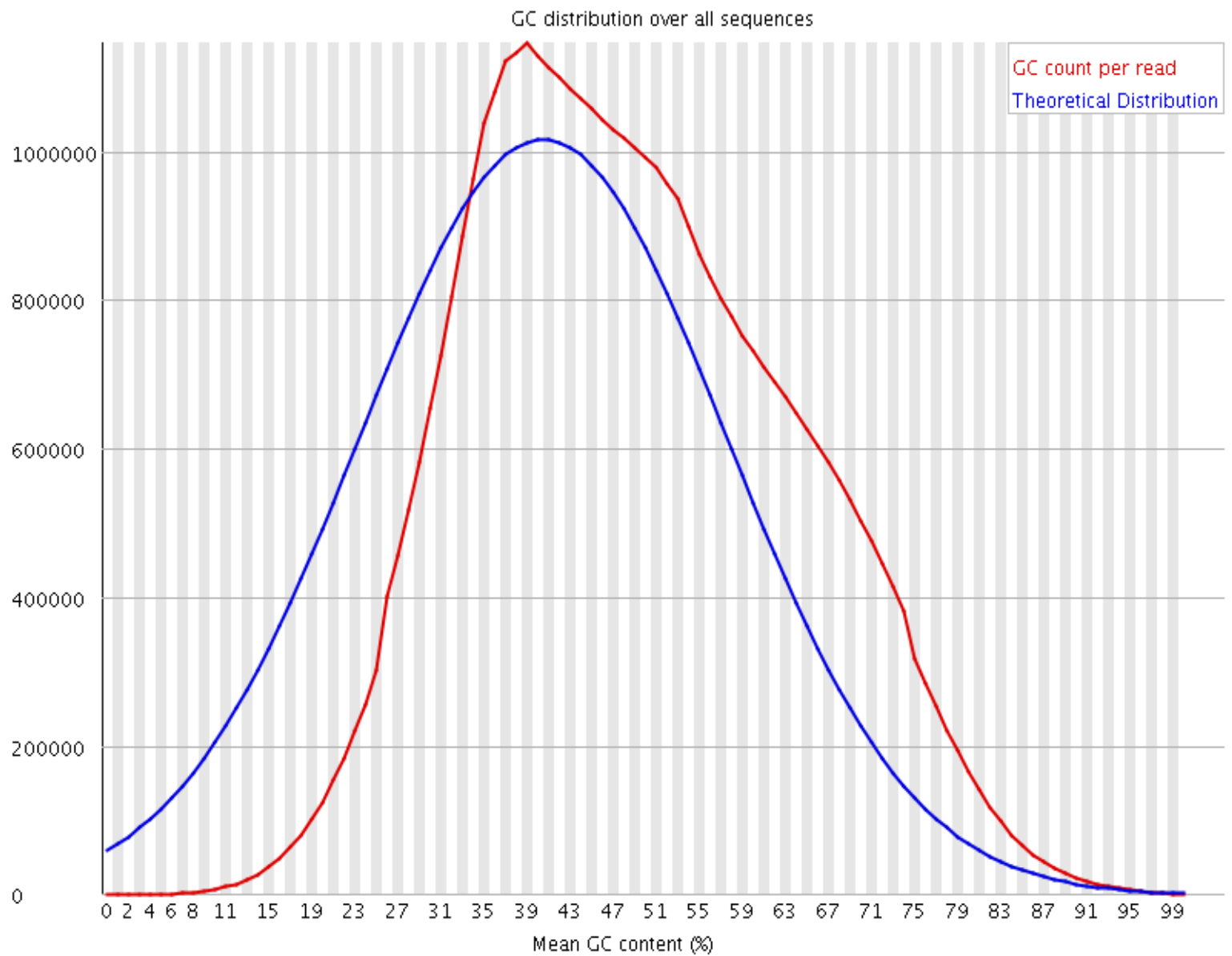
Per sequence quality scores



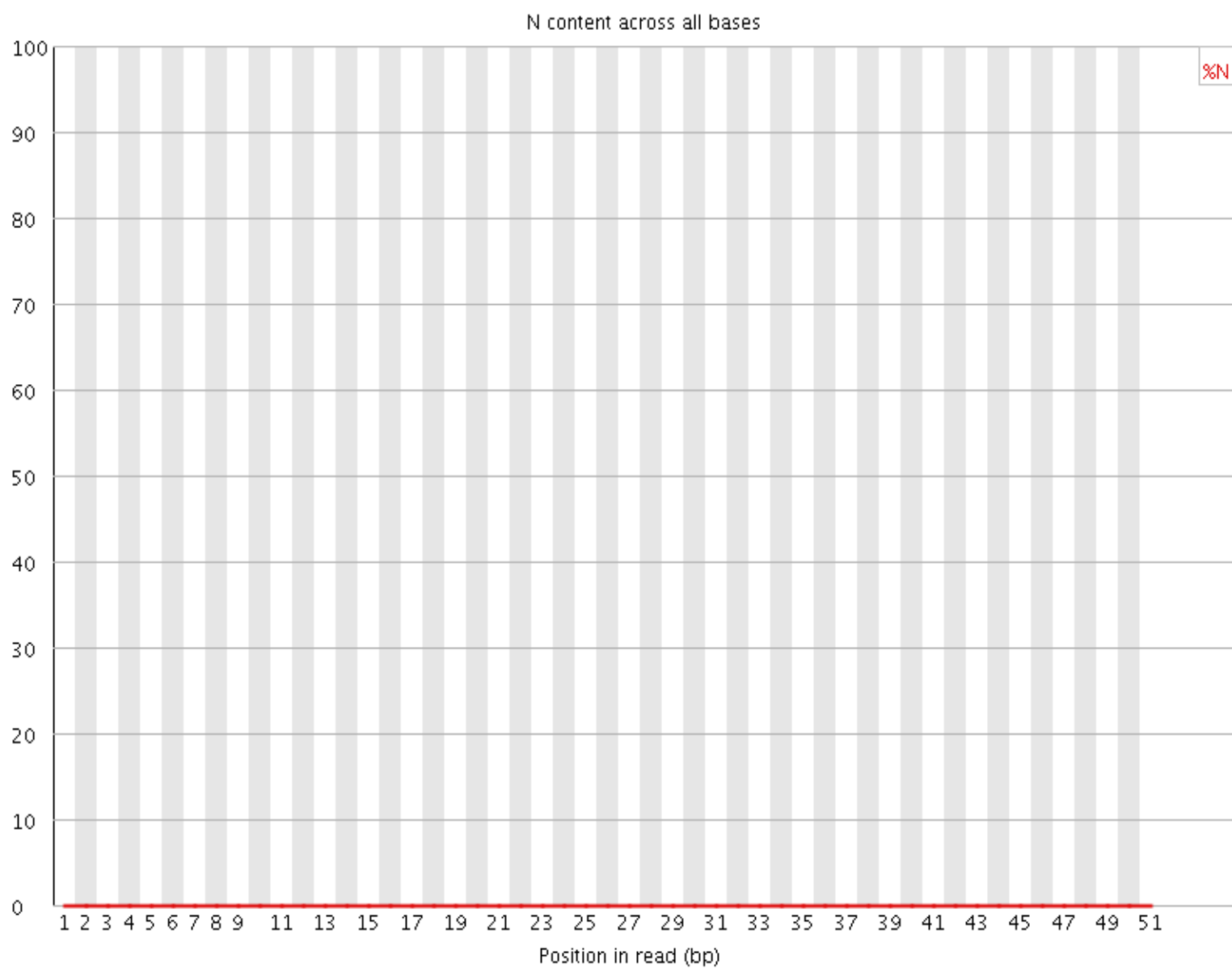
✖ Per base sequence content



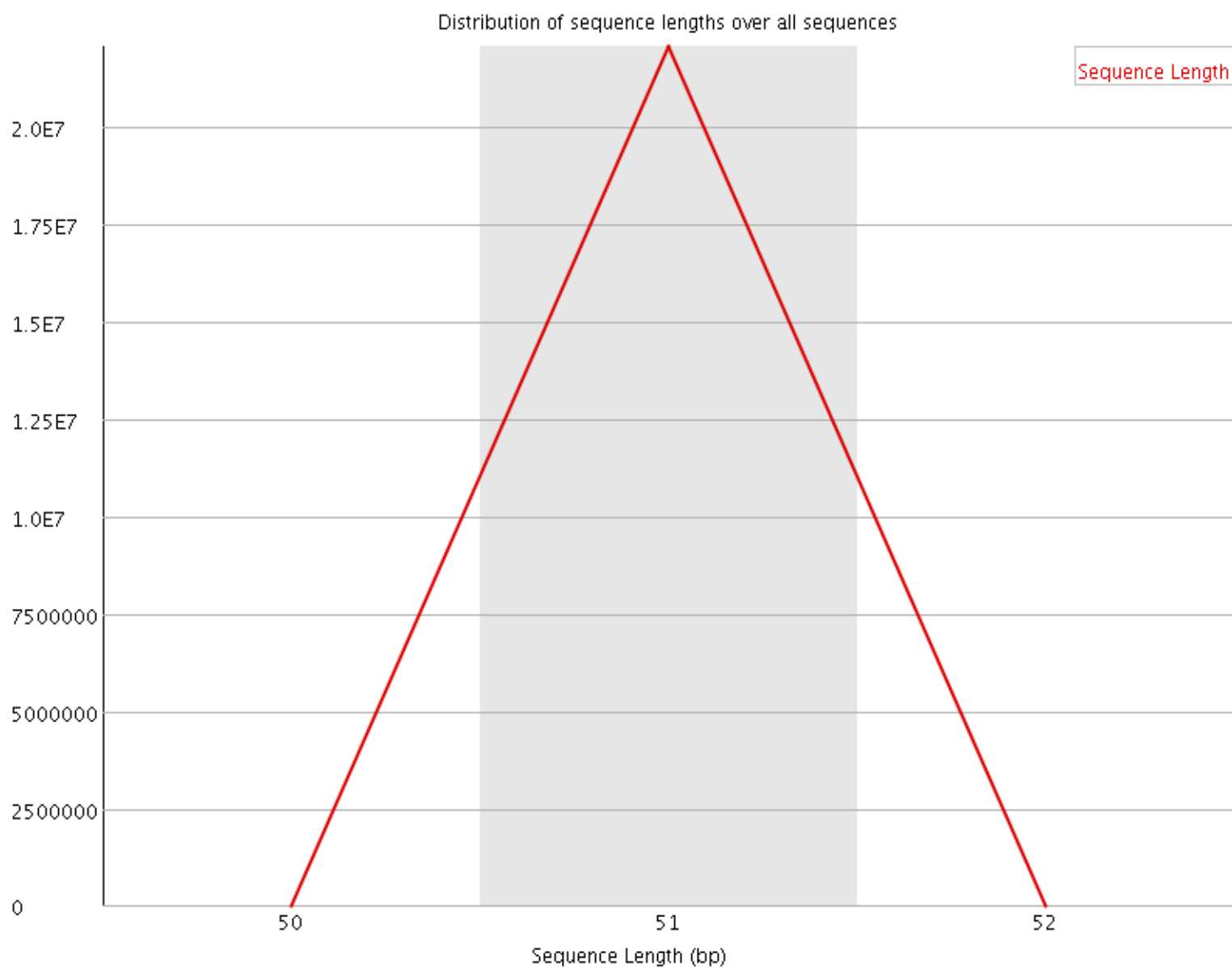
Per sequence GC content



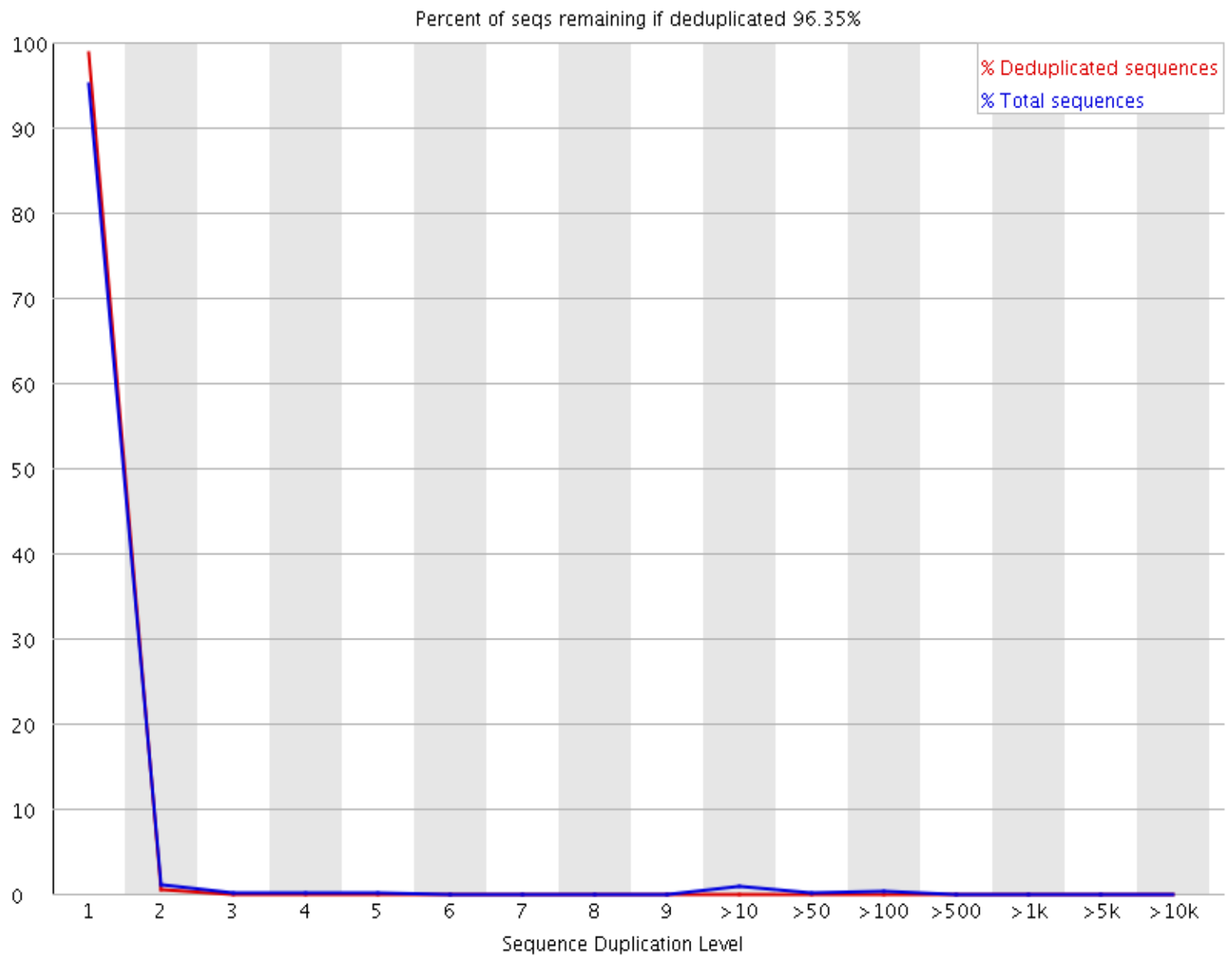
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

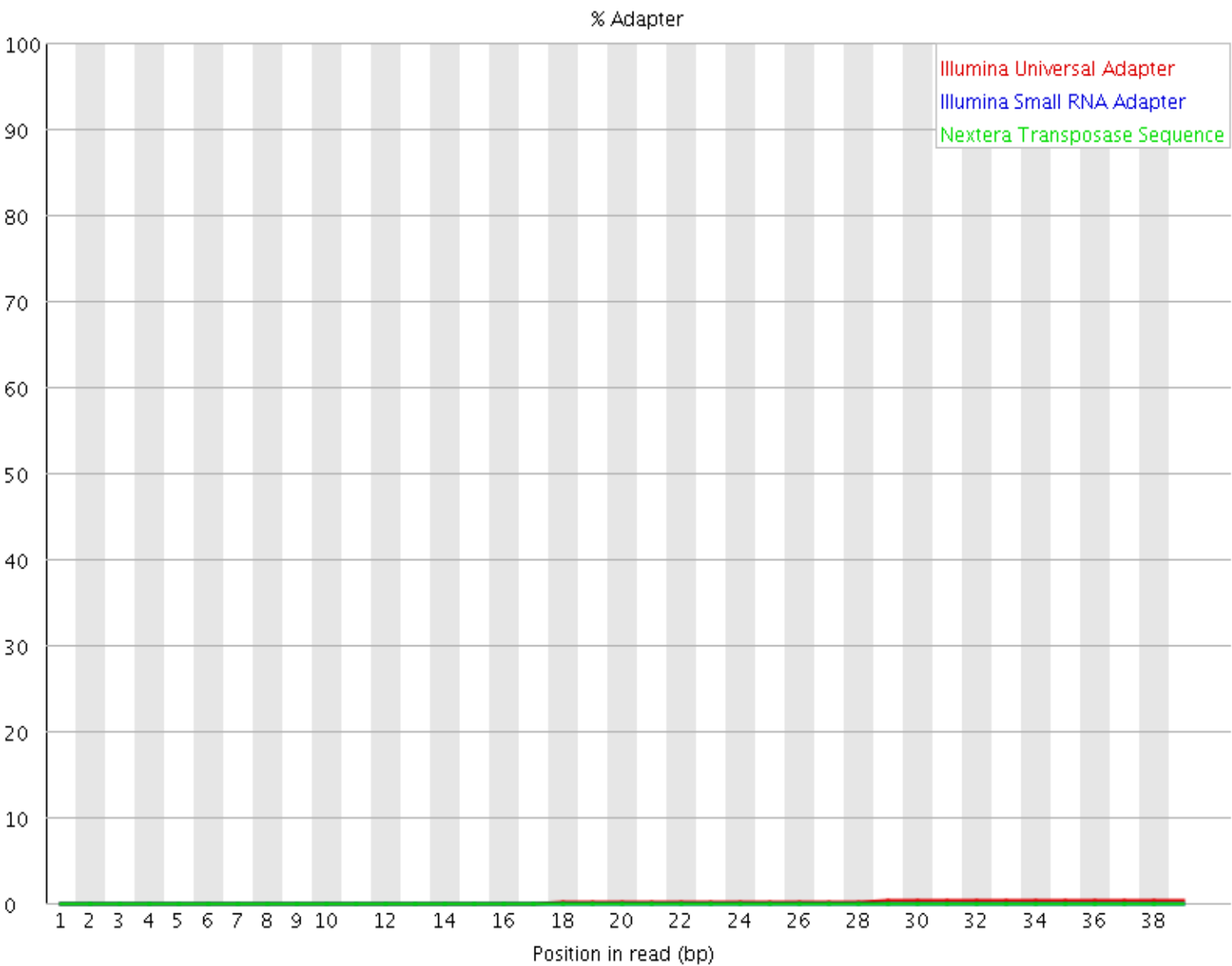


Overrepresented sequences

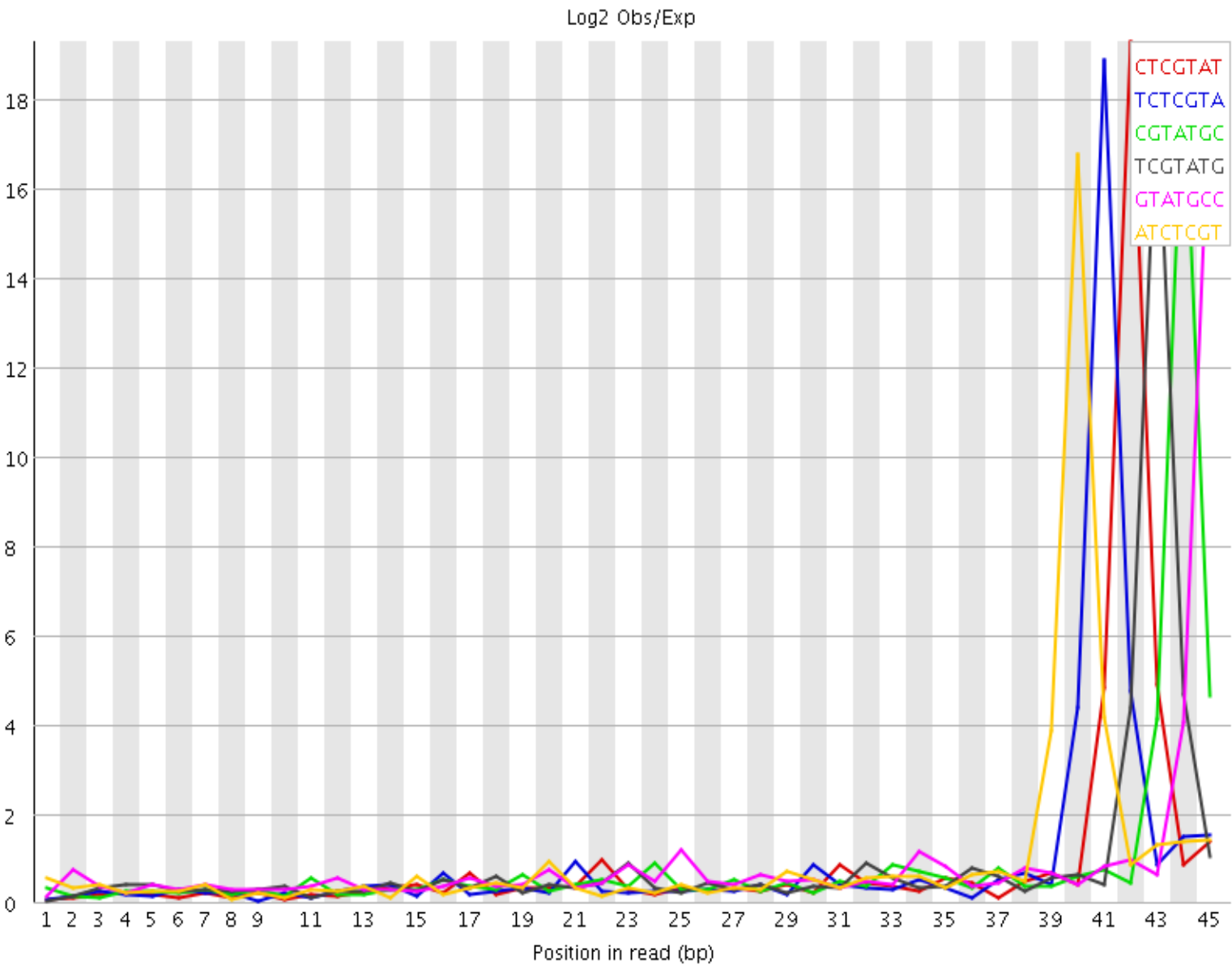
No overrepresented sequences



Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTCGTAT	9260	0.0	19.292496	42
TCTCGTA	9400	0.0	18.88578	41
CGTATGC	9485	0.0	18.83476	44
TCGTATG	9810	0.0	18.348473	43
GTATGCC	9655	0.0	18.340004	45
ATCTCGT	10750	0.0	16.786173	40
CACGATC	7485	0.0	15.539616	36
CGATCTC	7745	0.0	15.453254	38
ACGATCT	7510	0.0	15.398014	37

TCACGAT	7850	0.0	14.817073	35
GATCTCG	8345	0.0	14.55943	39
ATCACGA	7890	0.0	14.314562	34
AATCGGA	2520	0.0	13.855995	1
CATCACG	8760	0.0	13.483806	33
CATCTCG	3830	0.0	13.217847	39
CAGTCAC	15010	0.0	11.317592	27
CTTAGGC	4785	0.0	11.143552	33
CCAGTCA	15680	0.0	10.790946	26
TCCAGTC	17385	0.0	10.52201	25
ATATTCG	2020	0.0	10.482938	1

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