













# FastQC Report

## Summary

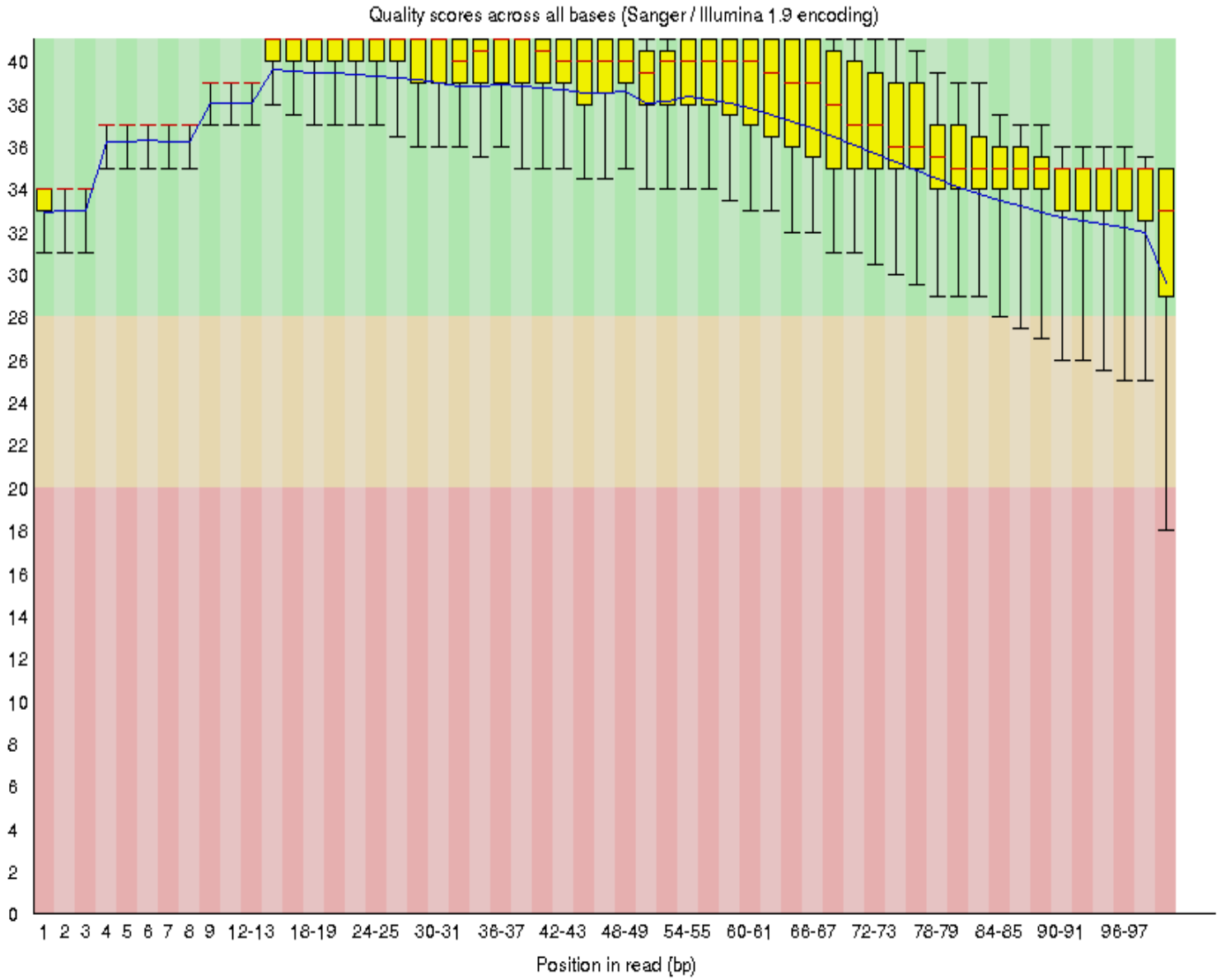
Wed 15 Apr 2015  
SW019\_S2\_L008\_R2\_001.fastq

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## Basic Statistics

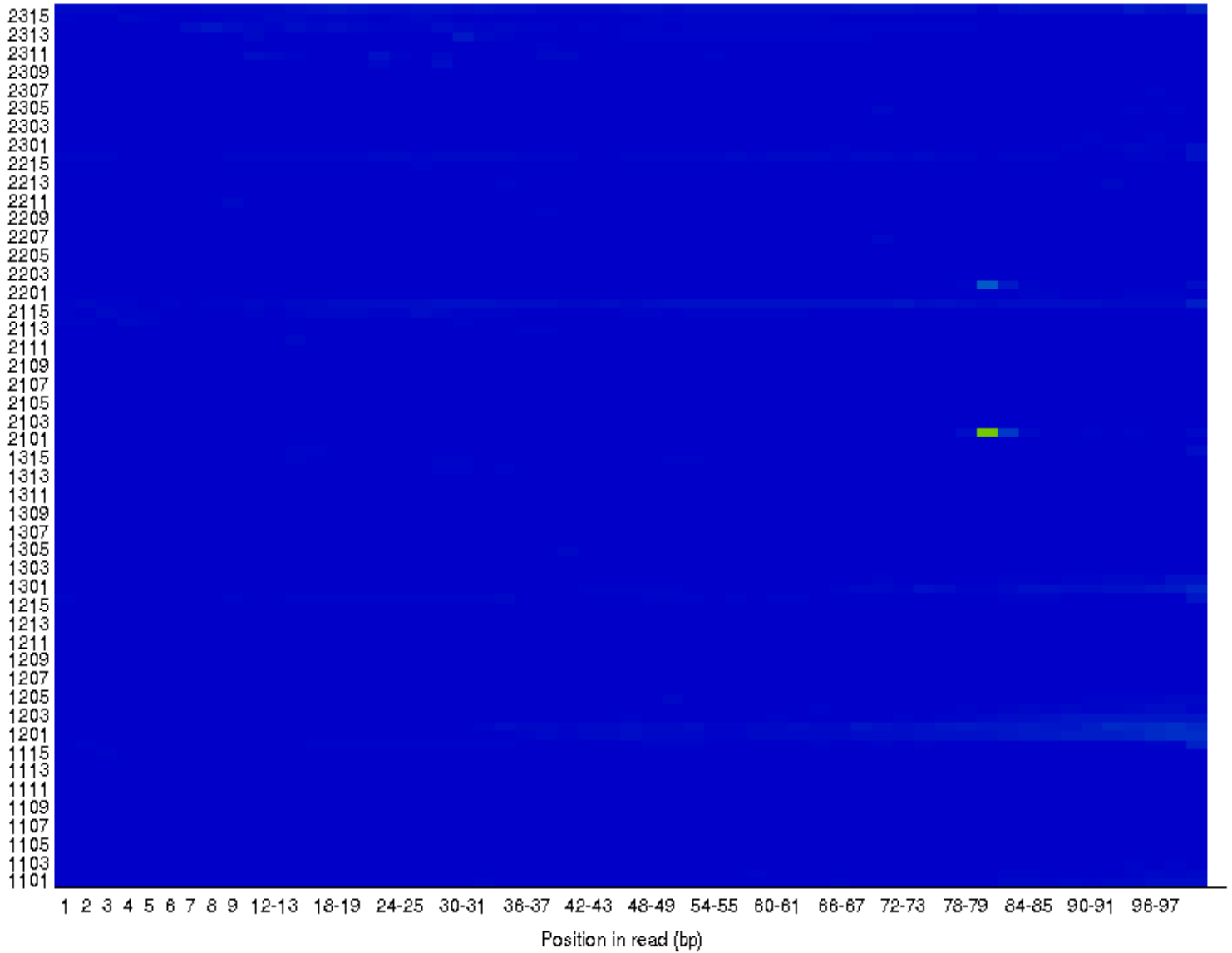
Measure	Value
Filename	SW019_S2_L008_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	98636158
Sequences flagged as poor quality	0
Sequence length	100
%GC	41

## Per base sequence quality



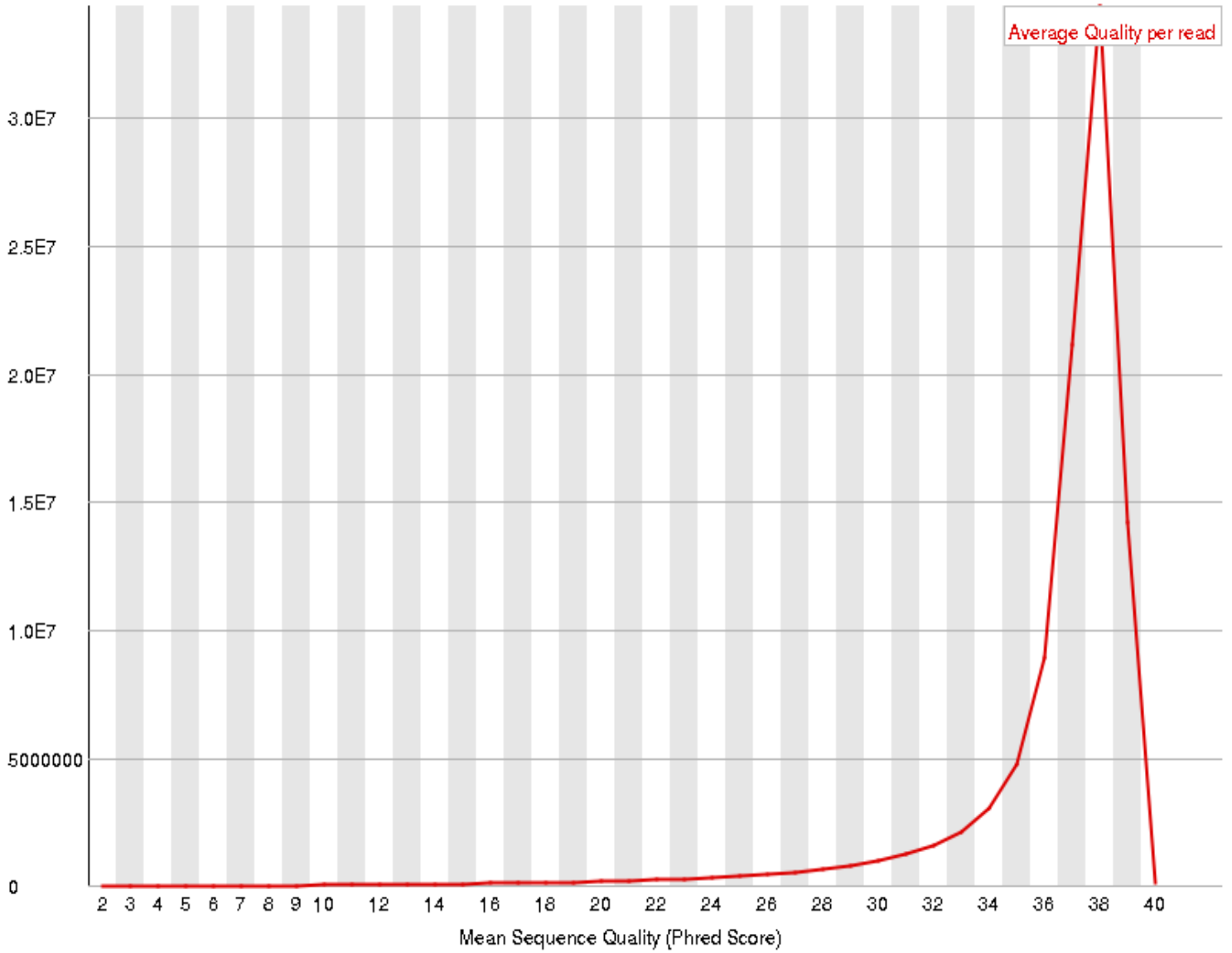
**! Per tile sequence quality**

Quality per tile



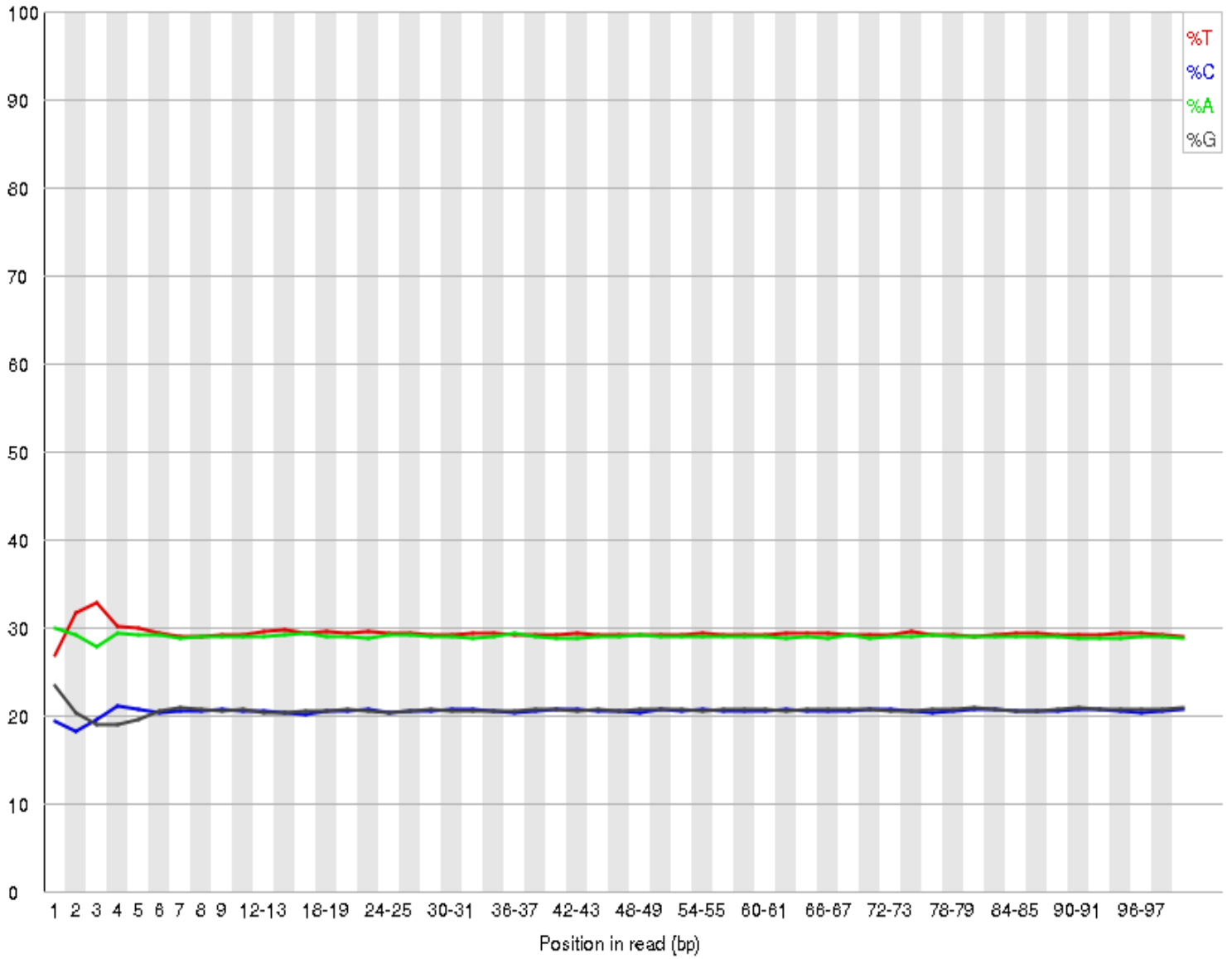
 **Per sequence quality scores**

Quality score distribution over all sequences



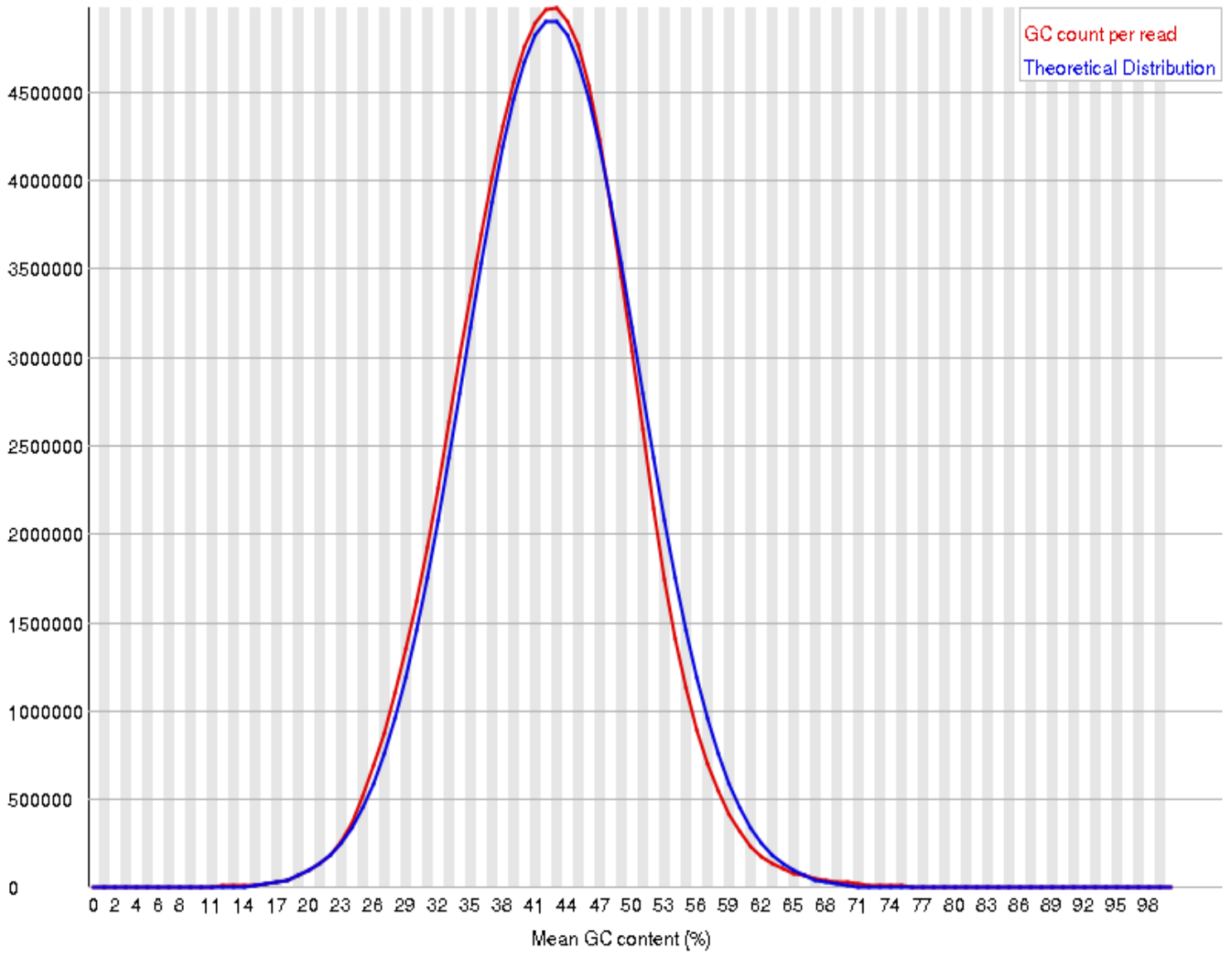
## Per base sequence content

Sequence content across all bases



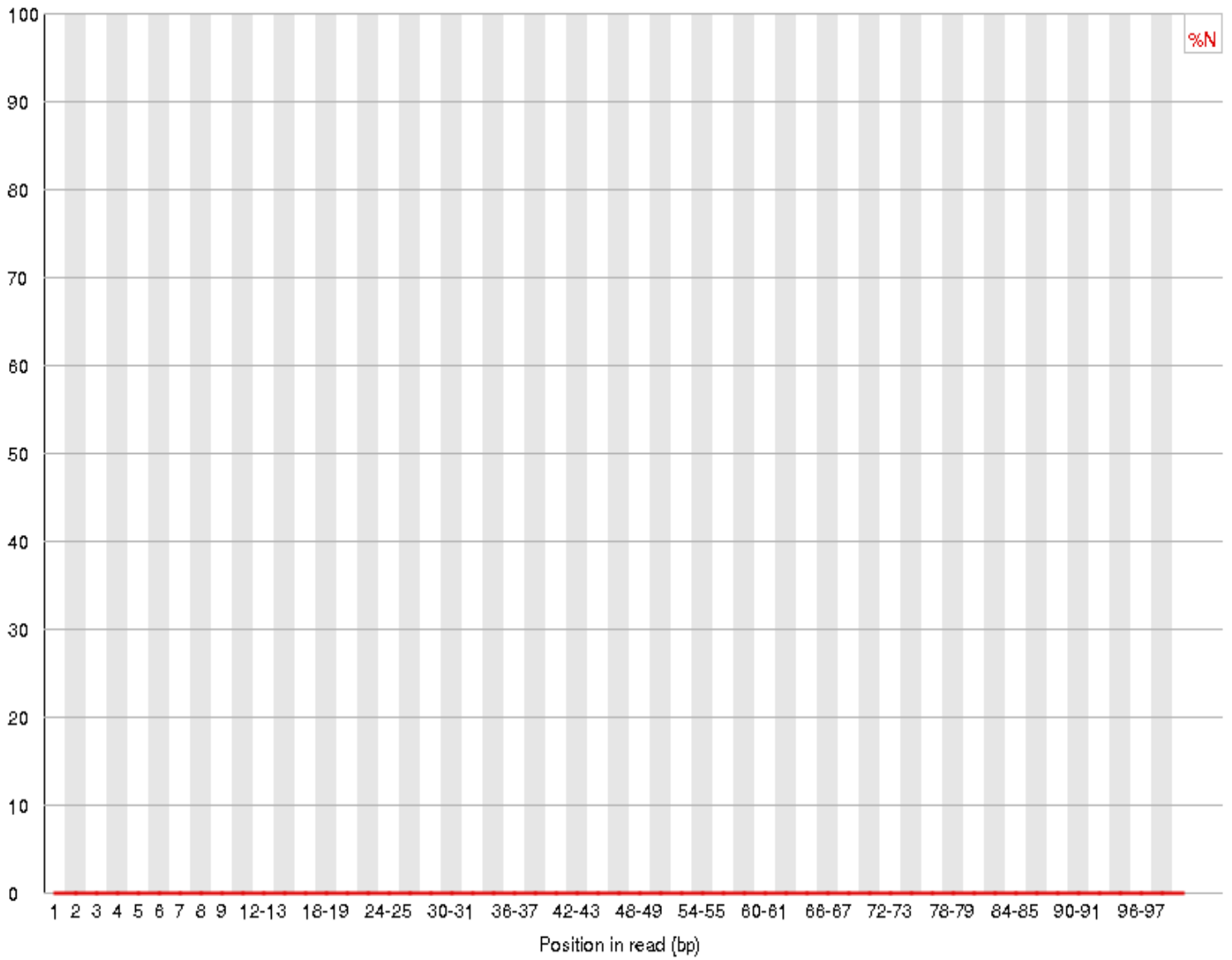
 **Per sequence GC content**

GC distribution over all sequences



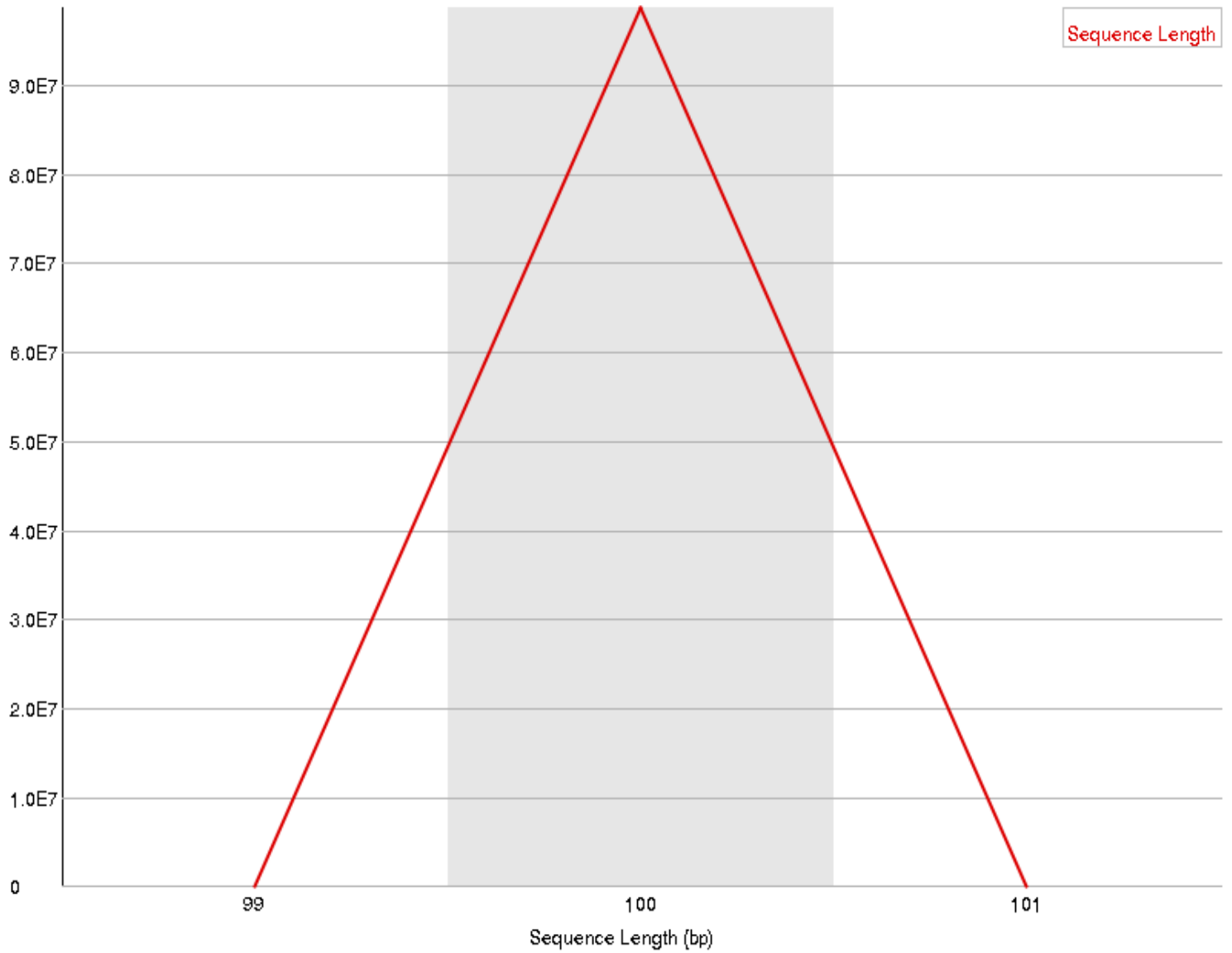
 **Per base N content**

N content across all bases



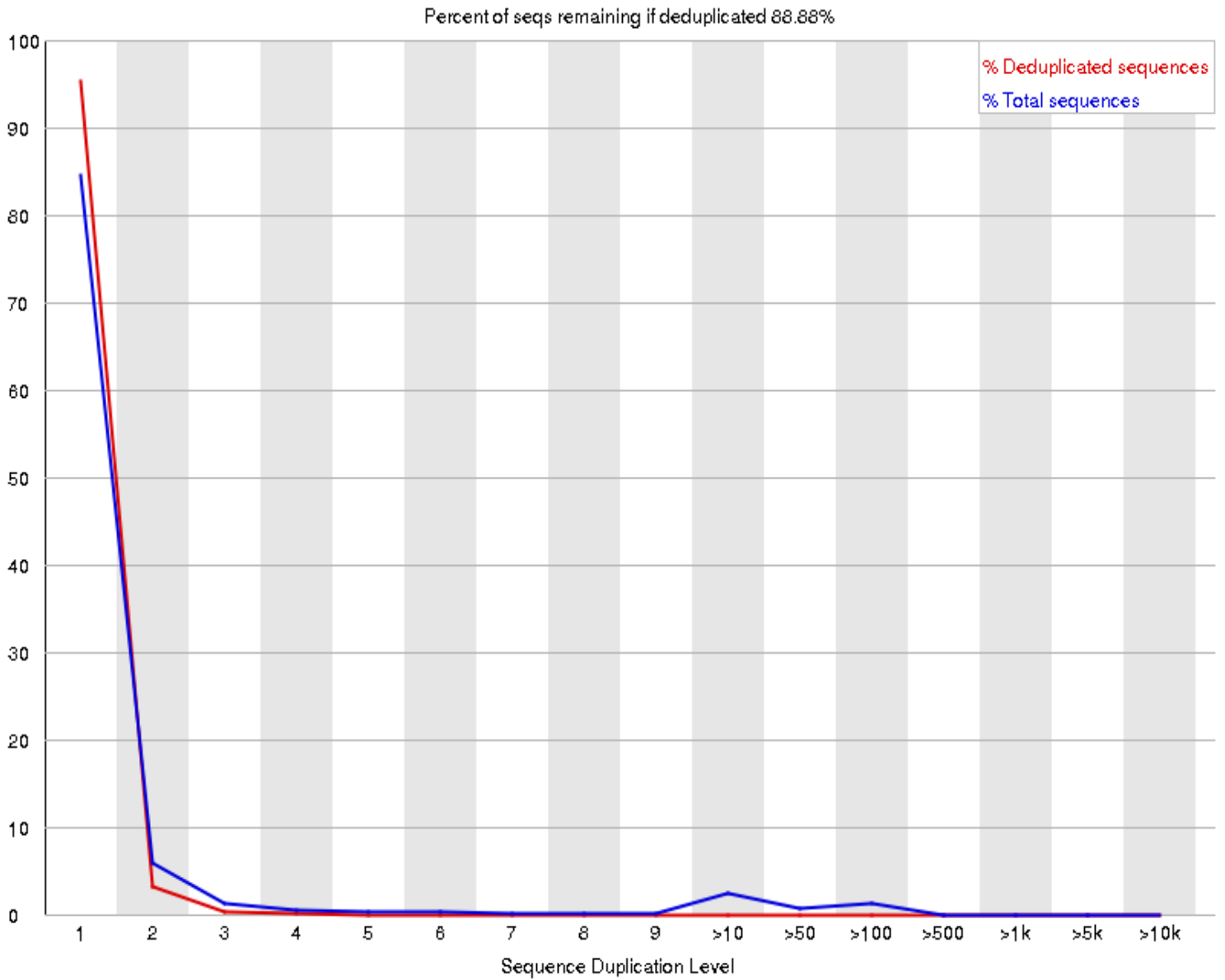
## Sequence Length Distribution

Distribution of sequence lengths over all sequences



## Sequence Duplication Levels

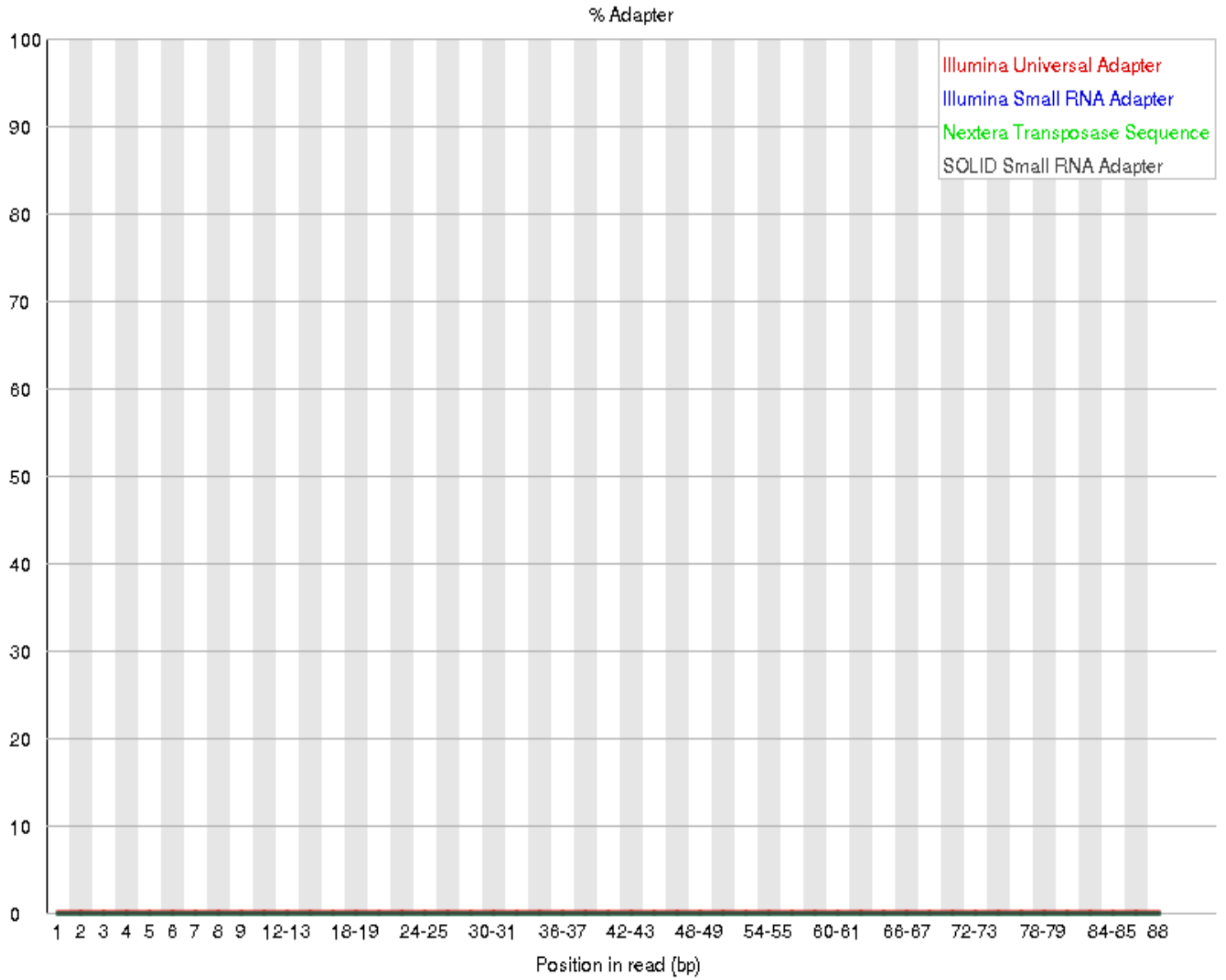




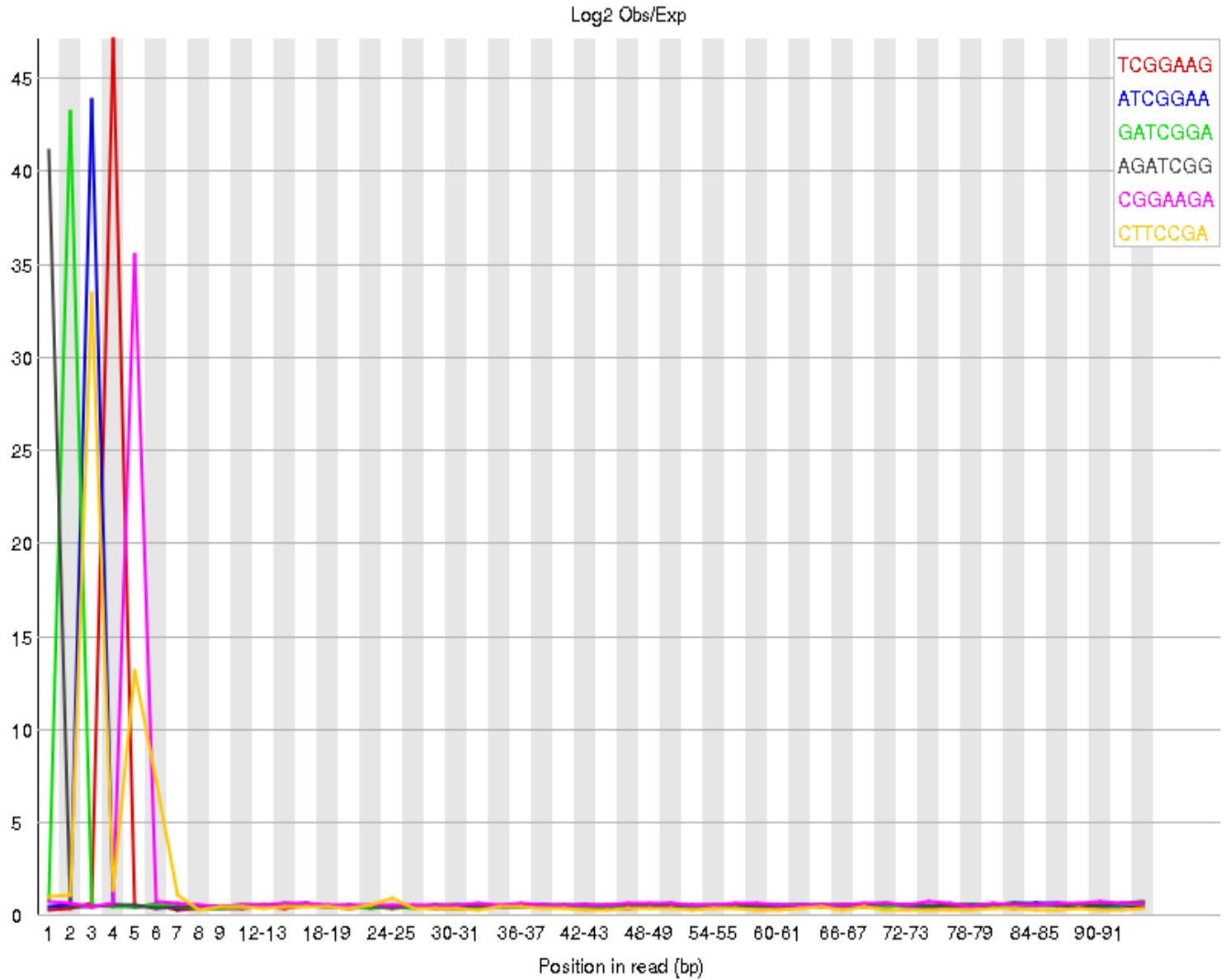
 **Overrepresented sequences**

No overrepresented sequences

 **Adapter Content**



## Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	42280	0.0	47.055843	4
ATCGGAA	45525	0.0	43.804966	3
GATCGGA	46240	0.0	43.212006	2
AGATCGG	48740	0.0	41.12628	1
CGGAAGA	56245	0.0	35.512196	5
CTTCGGA	51420	0.0	33.426674	3
TTCCGAT	55025	0.0	31.49295	4
TCCGATC	55955	0.0	31.009537	5
CCGATCT	57860	0.0	29.912022	6
TCTTCCG	65220	0.0	26.57195	2
GAAGAGC	76810	0.0	26.283108	7
AAGAGCG	38375	0.0	21.136011	8

CGATCTA	29770	0.0	17.853113	7
GGAAGAG	118180	0.0	17.424122	6
AGAGCGT	28890	0.0	16.669424	9
ACGCTCT	25670	0.0	14.189326	1
CTCTTCC	128170	0.0	14.146915	1
CGATCTT	36555	0.0	12.945322	7
AGCGTCG	14380	0.0	12.269932	10-11
GCGTCGT	14465	0.0	11.697054	12-13

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