













# FastQC Report

## Summary

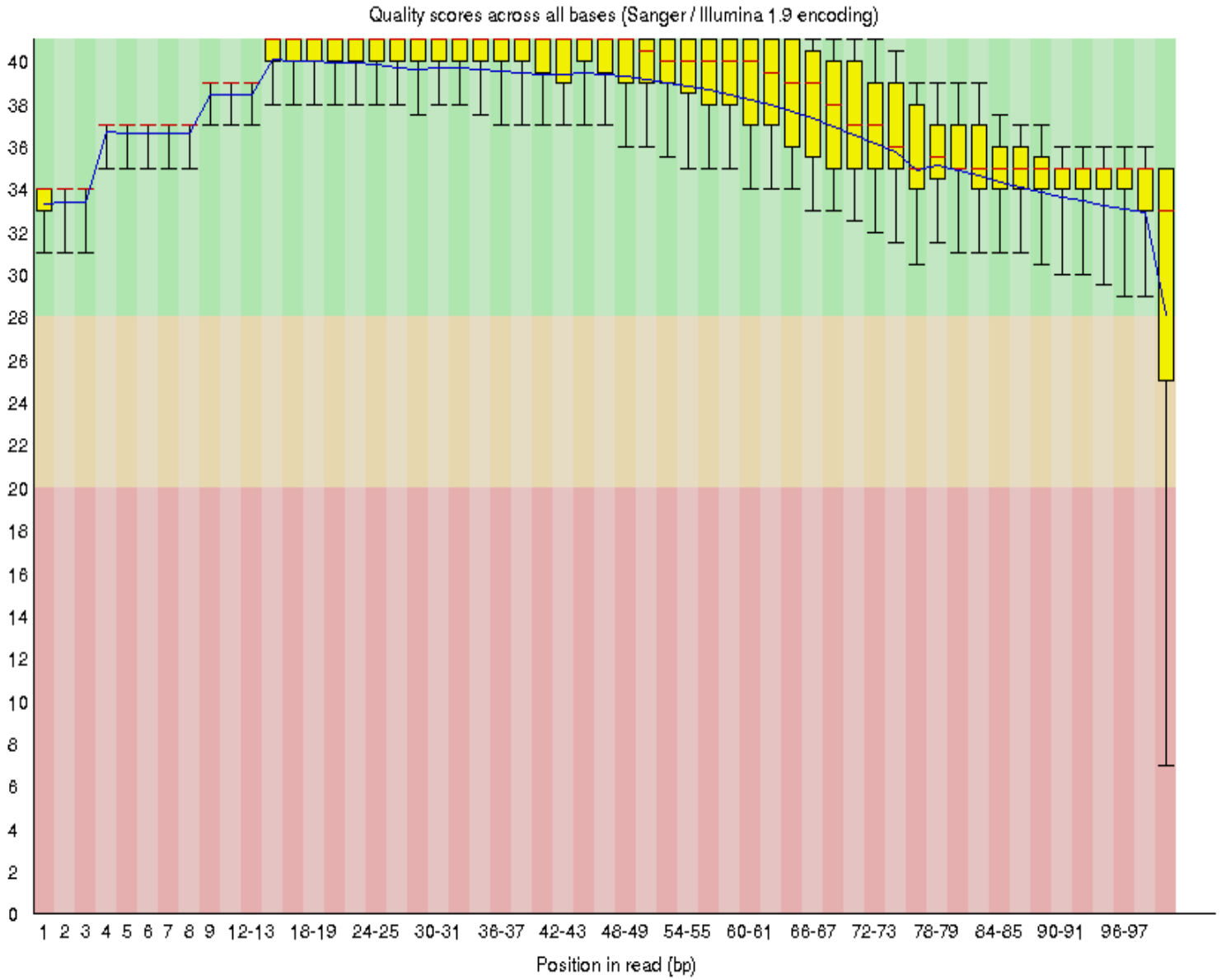
Wed 15 Apr 2015  
SW019\_S2\_L008\_R1\_001.fastq

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## Basic Statistics

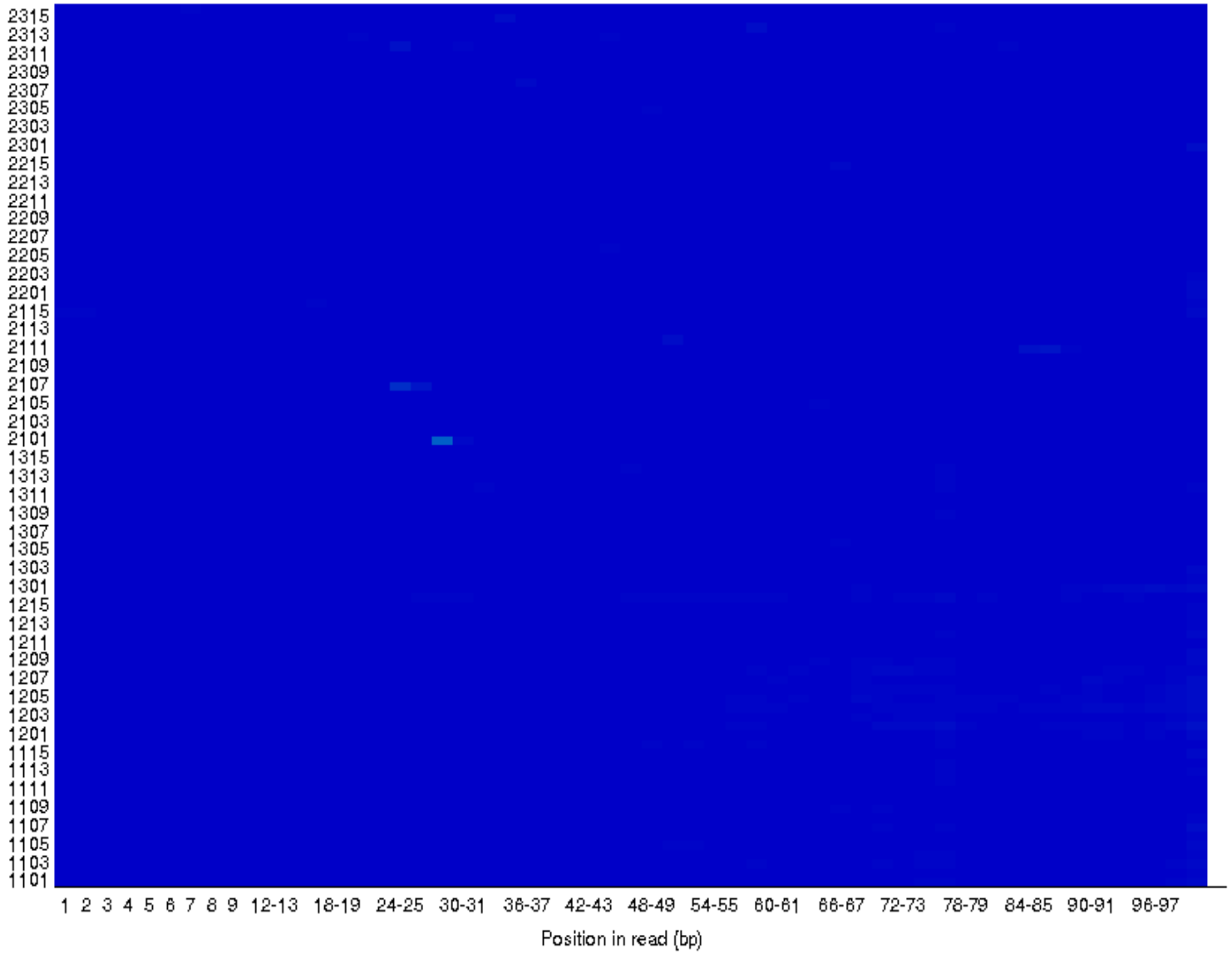
Measure	Value
Filename	SW019_S2_L008_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	98636158
Sequences flagged as poor quality	0
Sequence length	100
%GC	41

## Per base sequence quality



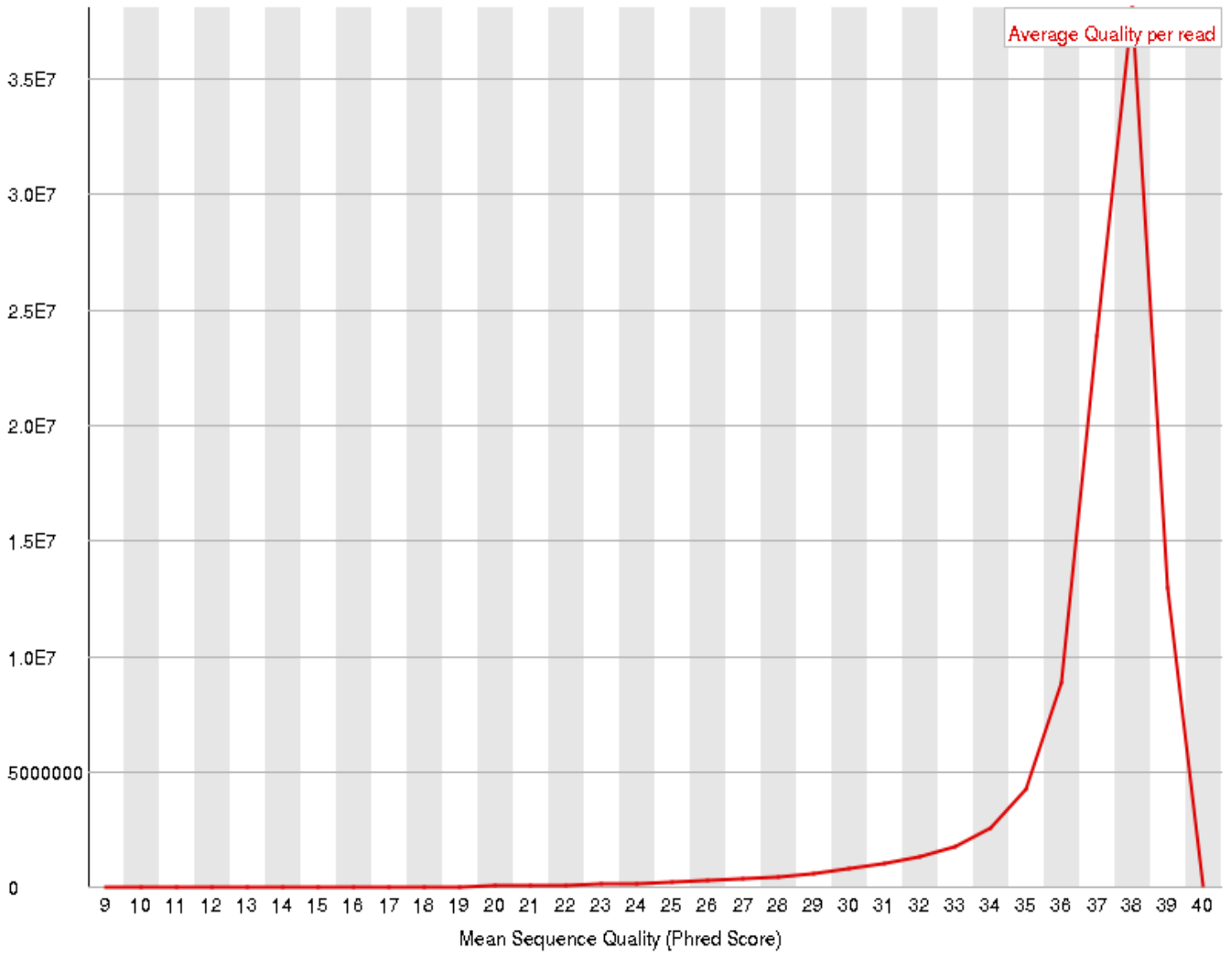
 **Per tile sequence quality**

Quality per tile



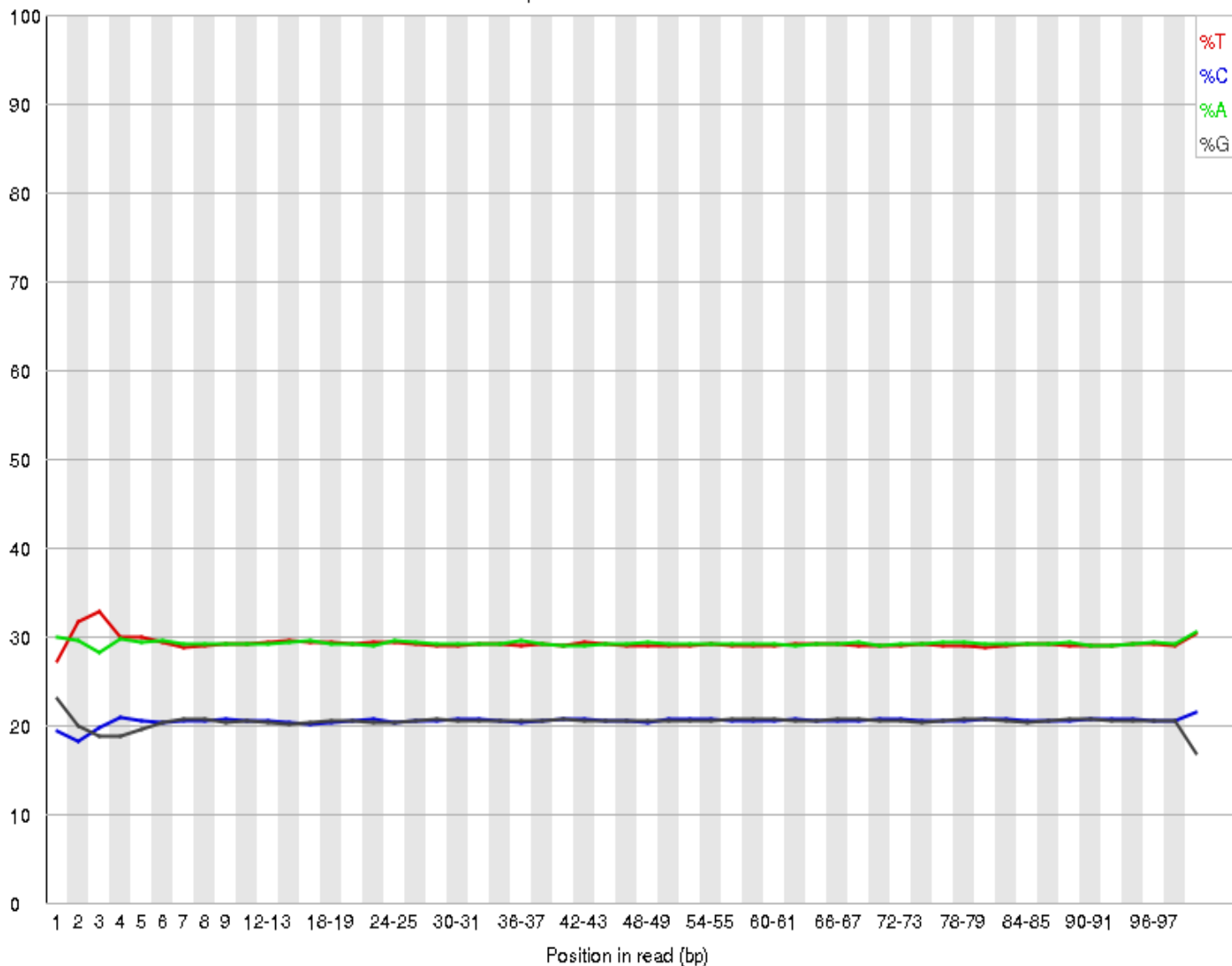
 **Per sequence quality scores**

Quality score distribution over all sequences



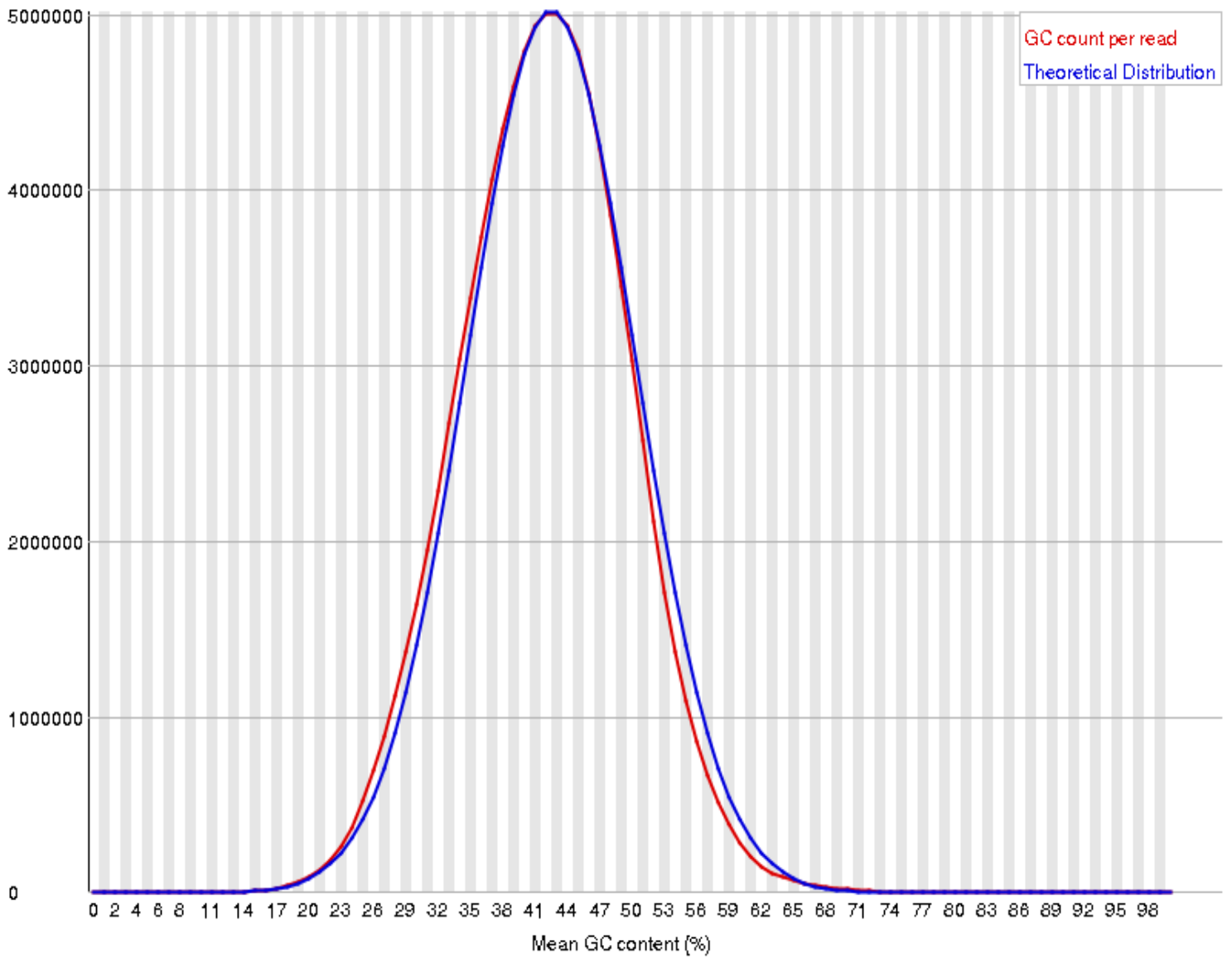
## Per base sequence content

Sequence content across all bases



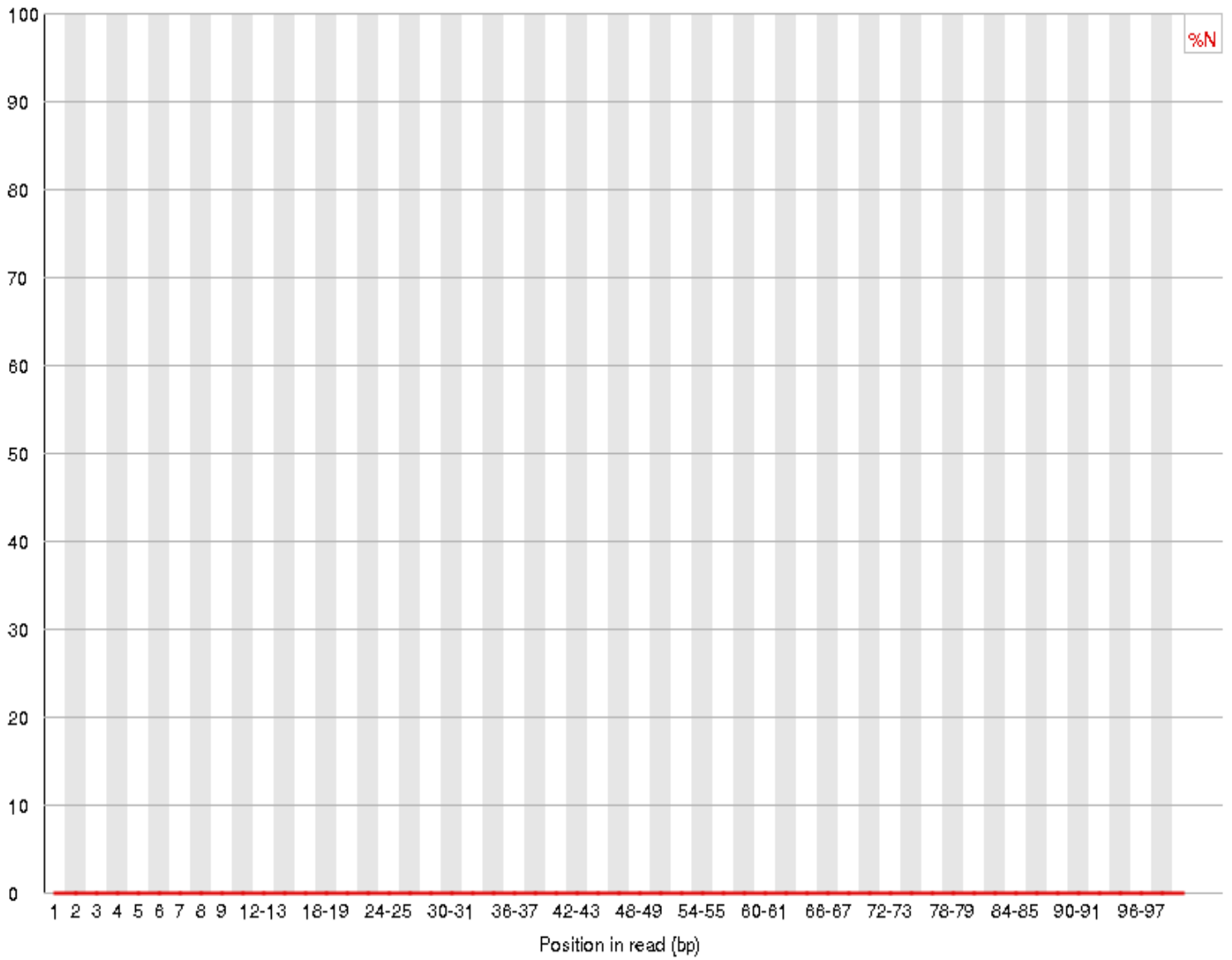
 **Per sequence GC content**

GC distribution over all sequences



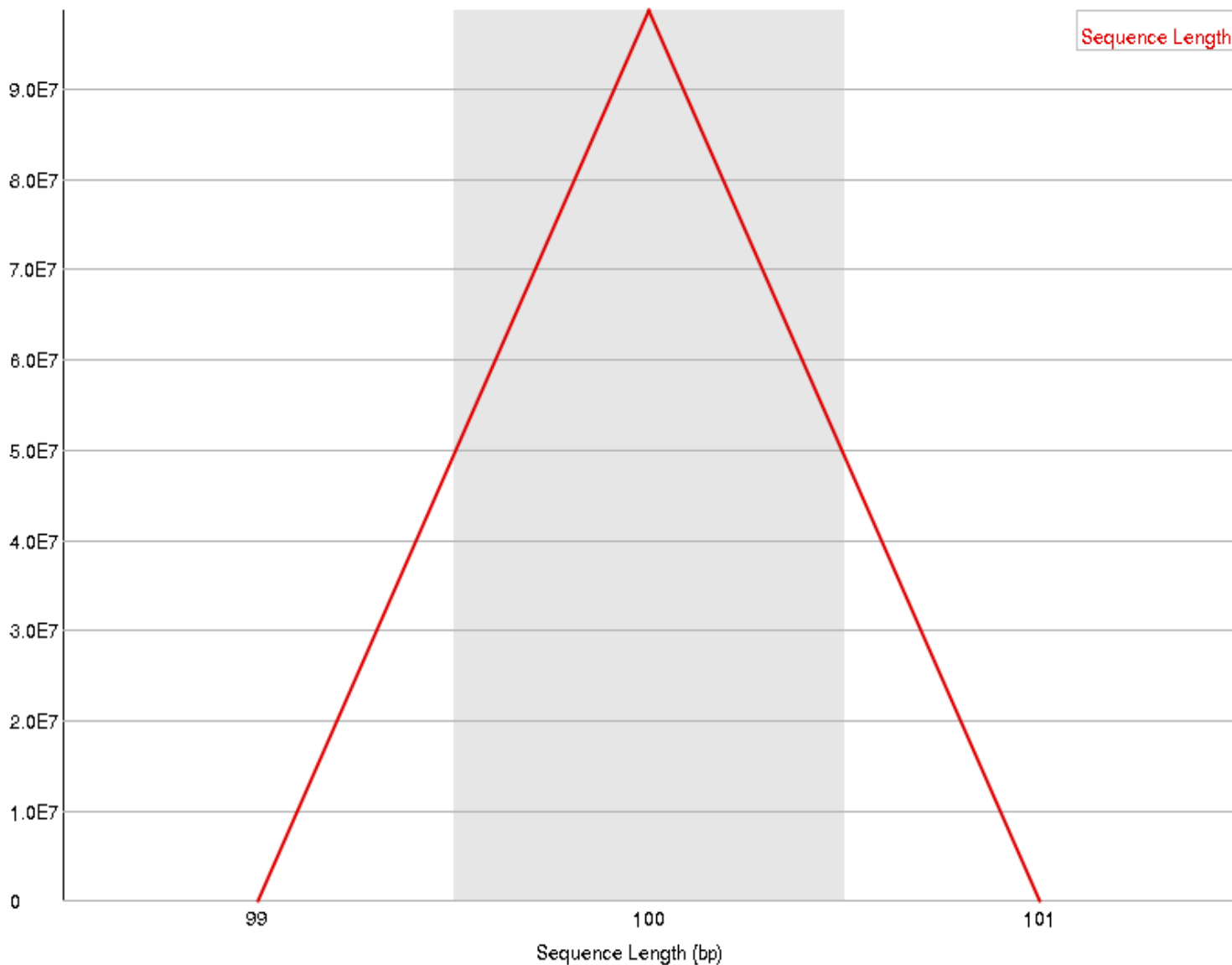
 **Per base N content**

N content across all bases



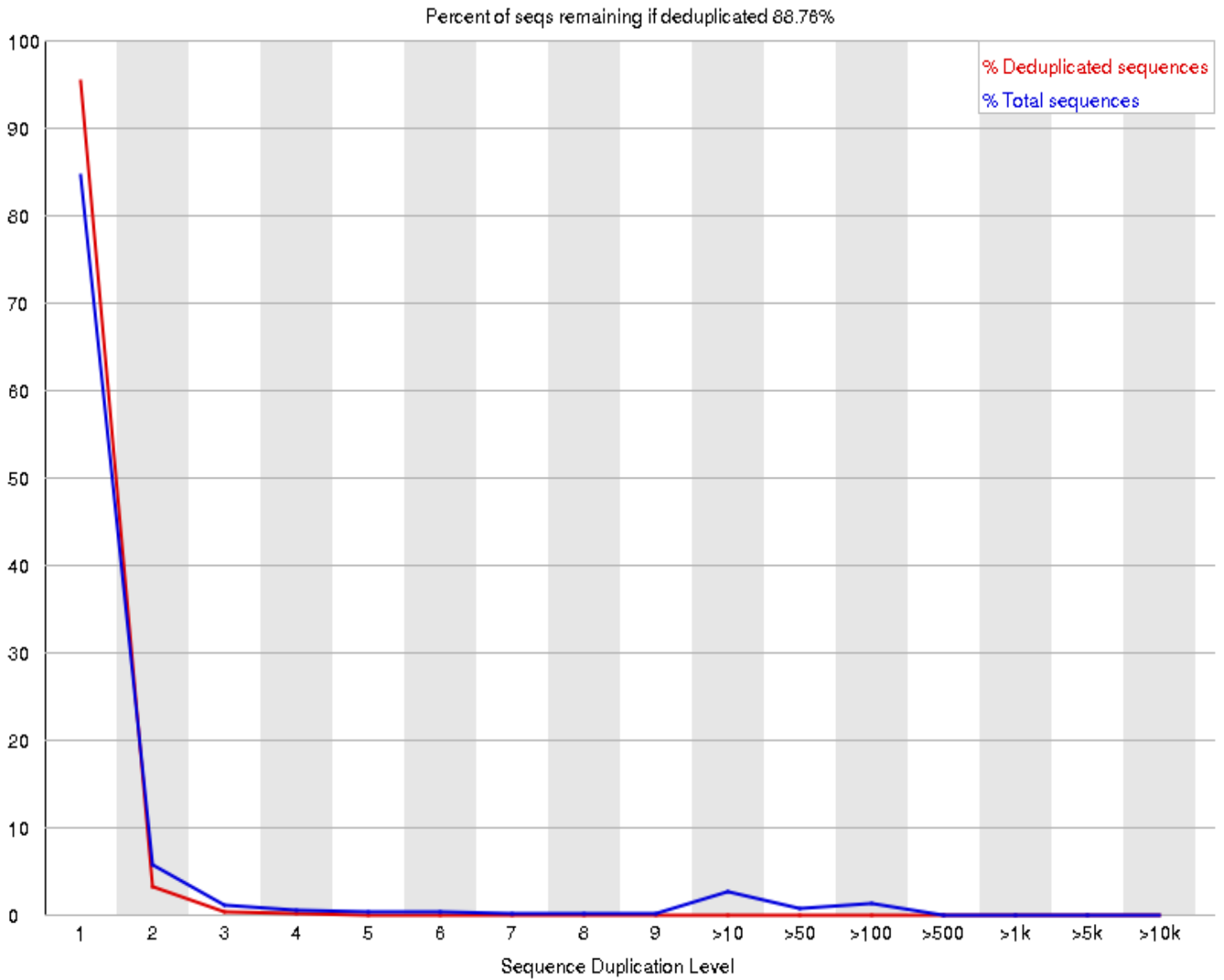
## Sequence Length Distribution

Distribution of sequence lengths over all sequences



## Sequence Duplication Levels



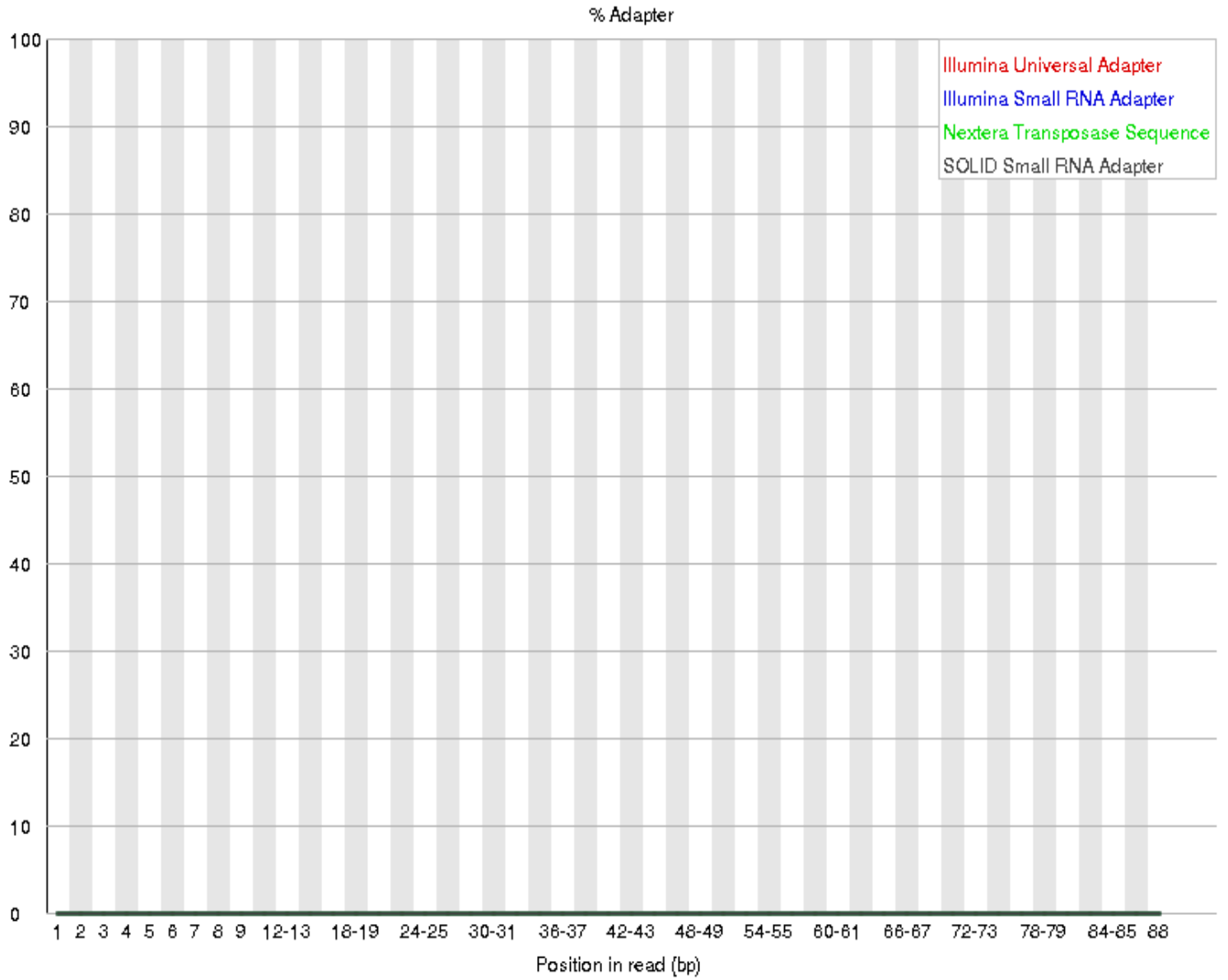


## Overrepresented sequences

No overrepresented sequences

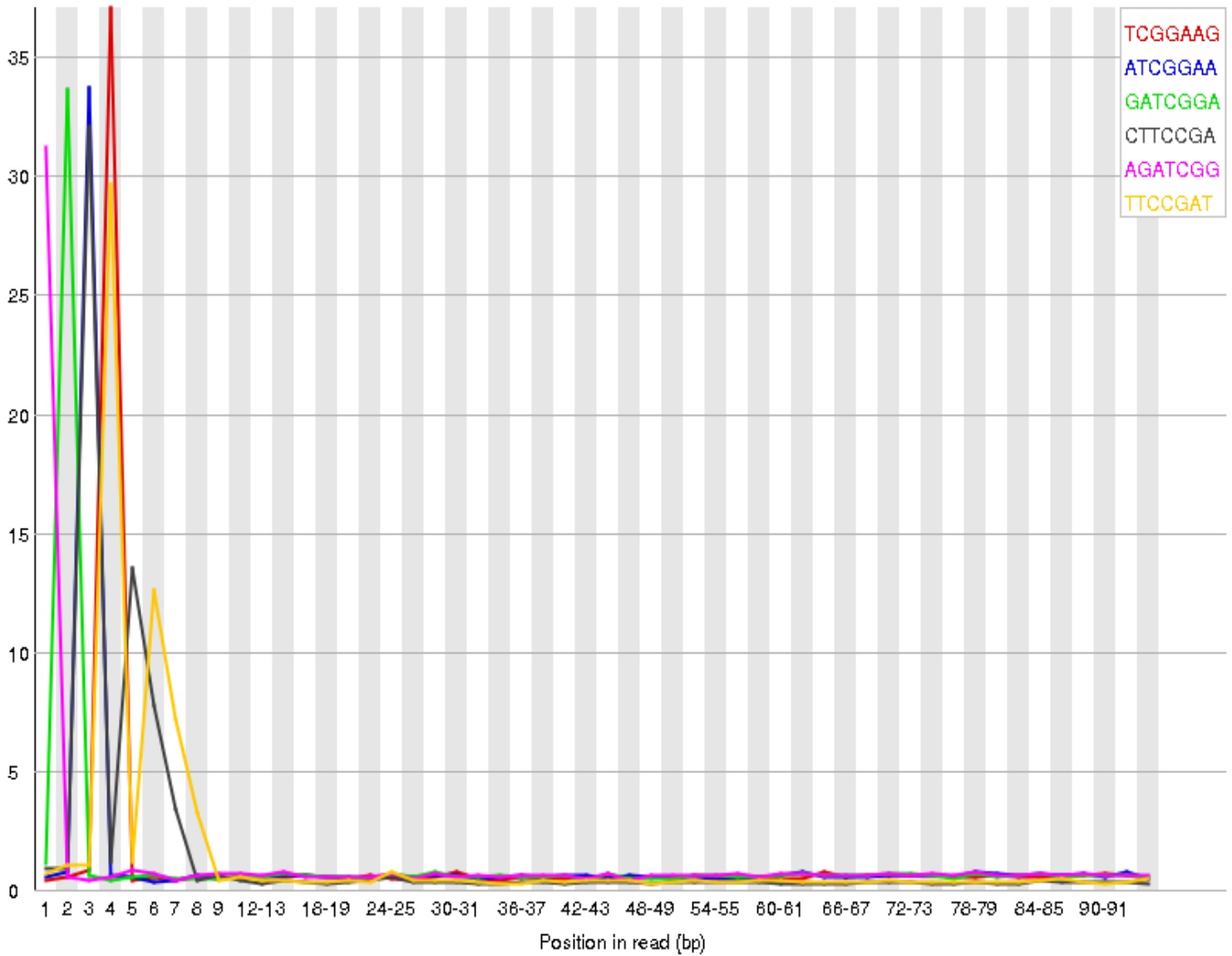


## Adapter Content



## Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	33825	0.0	37.023273	4
ATCGGAA	37185	0.0	33.728436	3
GATCGGA	37170	0.0	33.666775	2
CTTCGGA	52445	0.0	32.077045	3
AGATCGG	40075	0.0	31.220497	1
TTCCGAT	56610	0.0	29.625711	4
TCCGATC	56990	0.0	29.48576	5
CCGATCT	58950	0.0	28.47366	6
CGGAAGA	47830	0.0	26.280695	5
TCTTCCG	66375	0.0	25.628723	2
GAAGAGC	69105	0.0	18.516283	7
CGATCTA	29855	0.0	17.48689	7

ACGCTCT	26180	0.0	15.175937	1
CTCTTCC	127135	0.0	13.901948	1
CGATCTT	37110	0.0	12.4727125	7
CGCTCTT	32985	0.0	12.137969	2
GGAAGAG	108830	0.0	12.085648	6
GCTCTTC	68235	0.0	10.908647	2
CGATCTC	39815	0.0	9.253052	7
CGATCTG	45405	0.0	9.045308	7

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