













# FastQC Report

## Summary

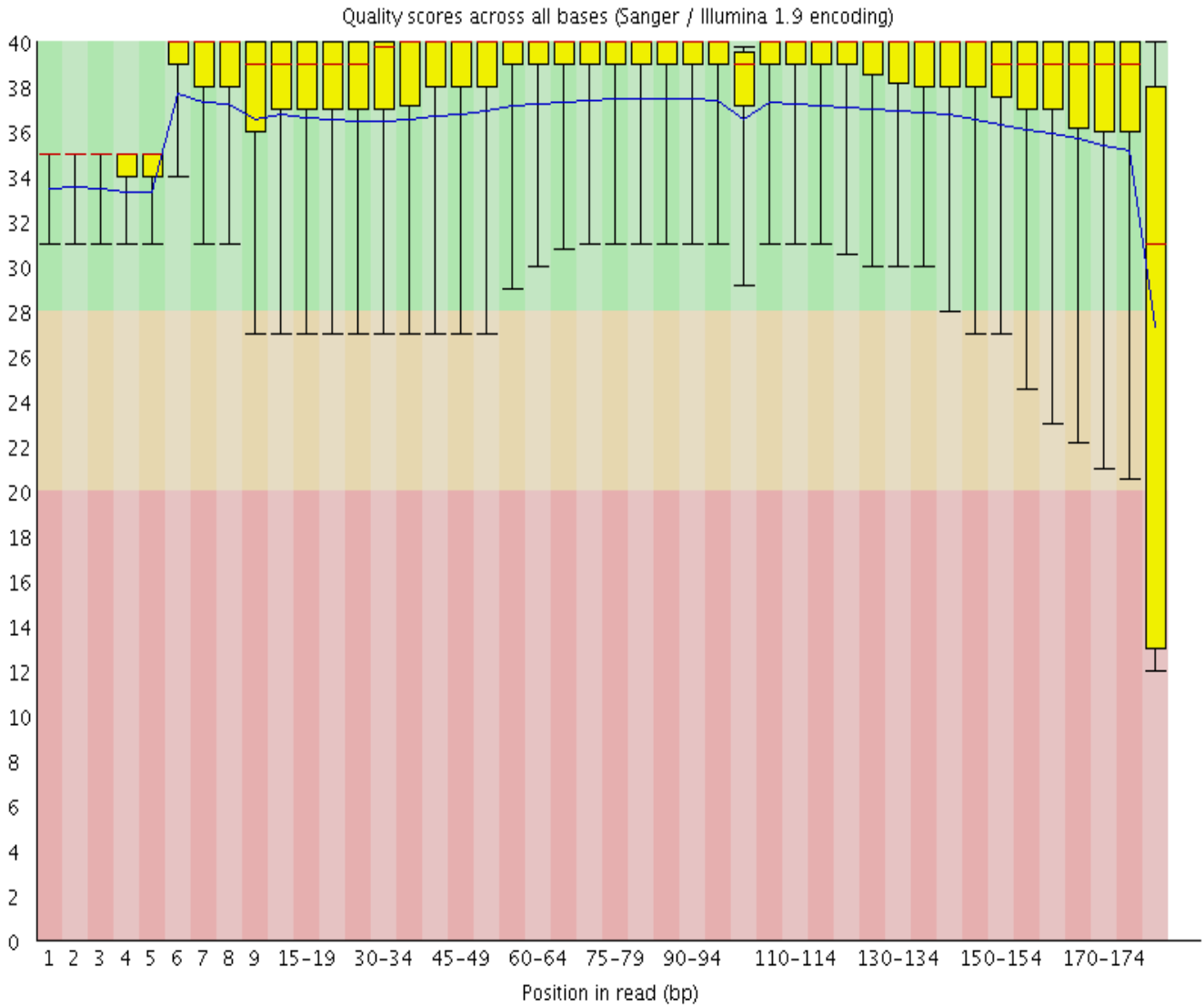
Sat 25 Mar 2017  
AS-160125-LR-22981\_R2.fastq.gz

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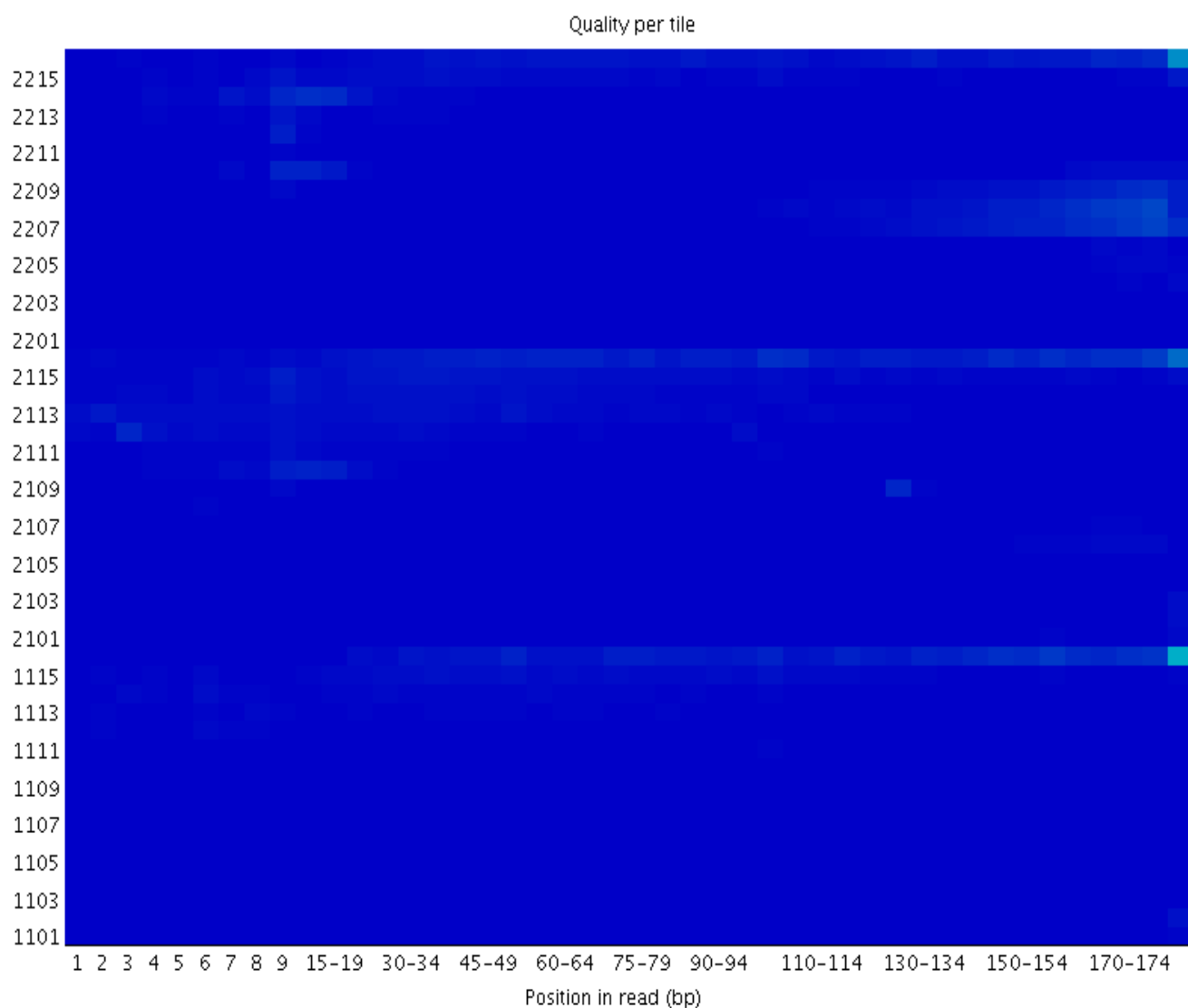
## Basic Statistics

Measure	Value
Filename	AS-160125-LR-22981_R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	23462952
Sequences flagged as poor quality	0
Sequence length	180
%GC	49

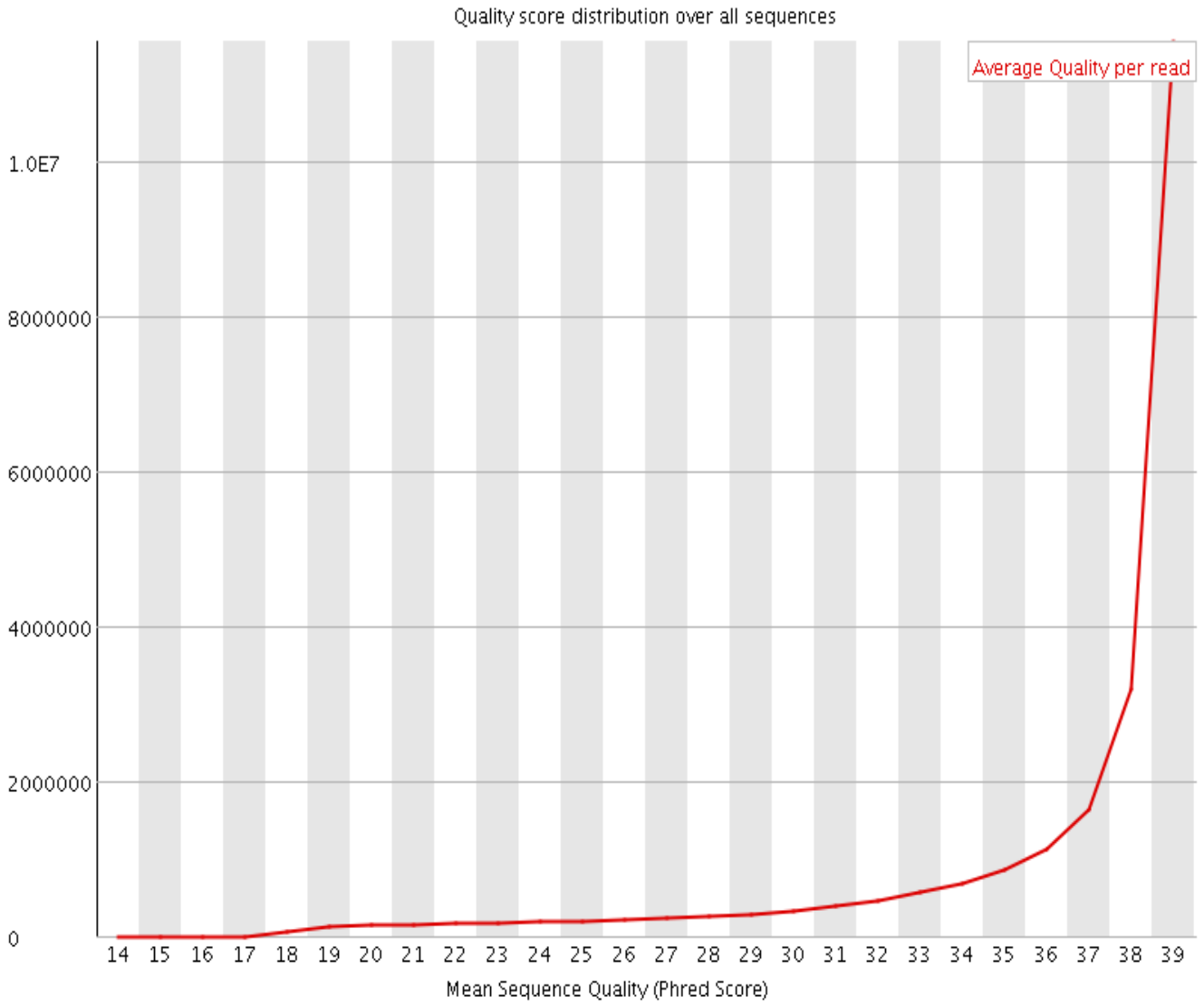
## Per base sequence quality



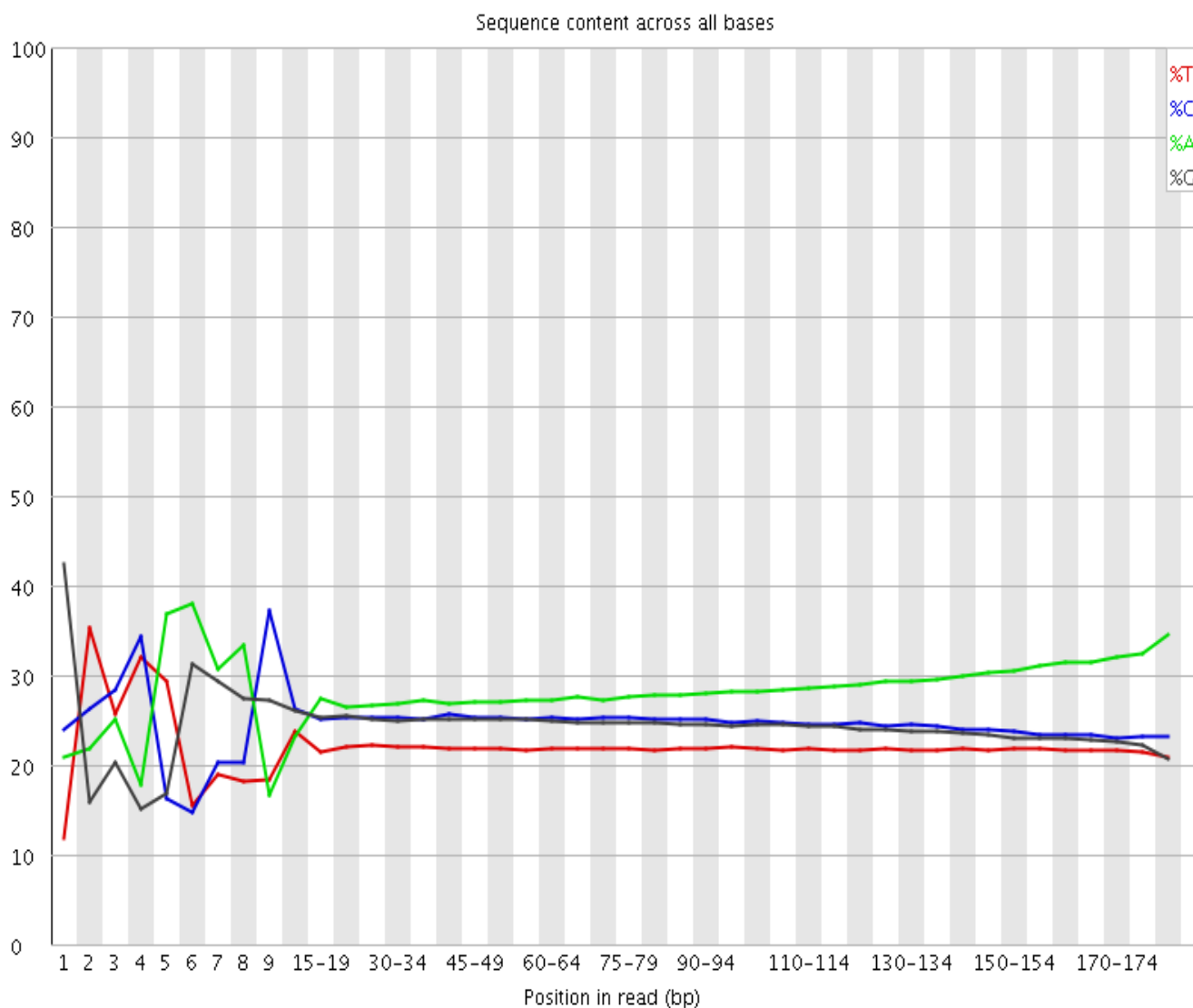
 **Per tile sequence quality**



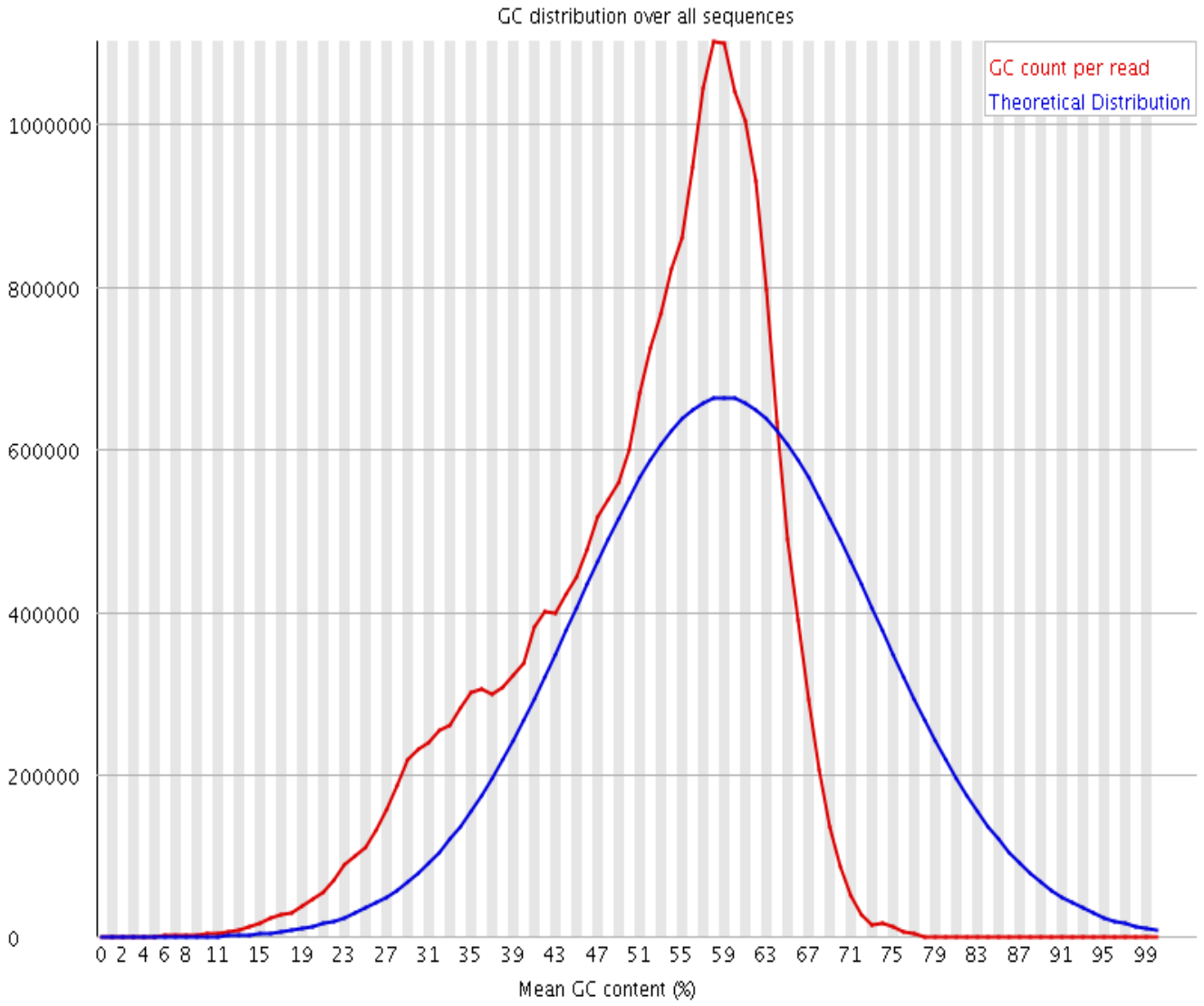
 **Per sequence quality scores**



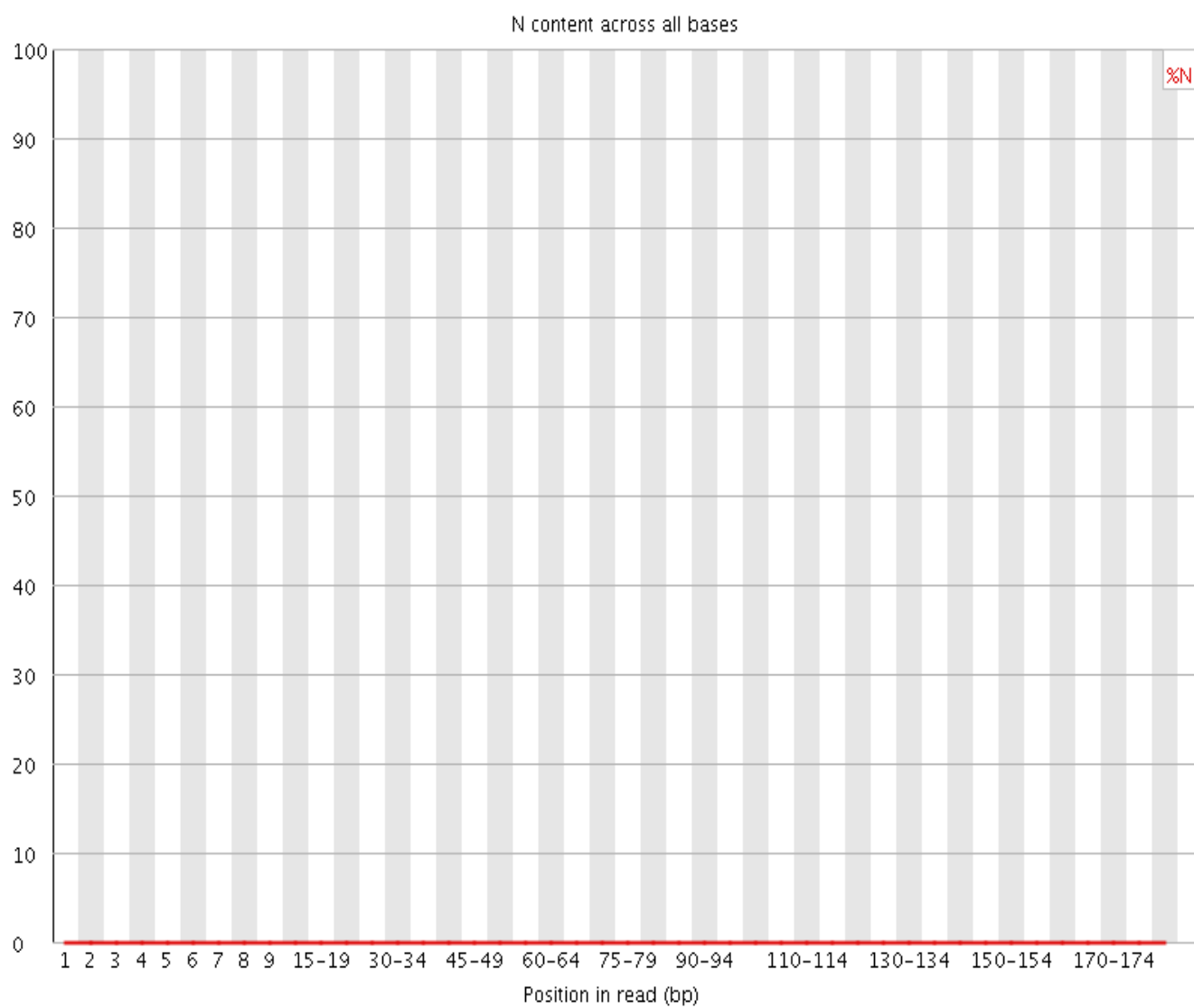
 **Per base sequence content**



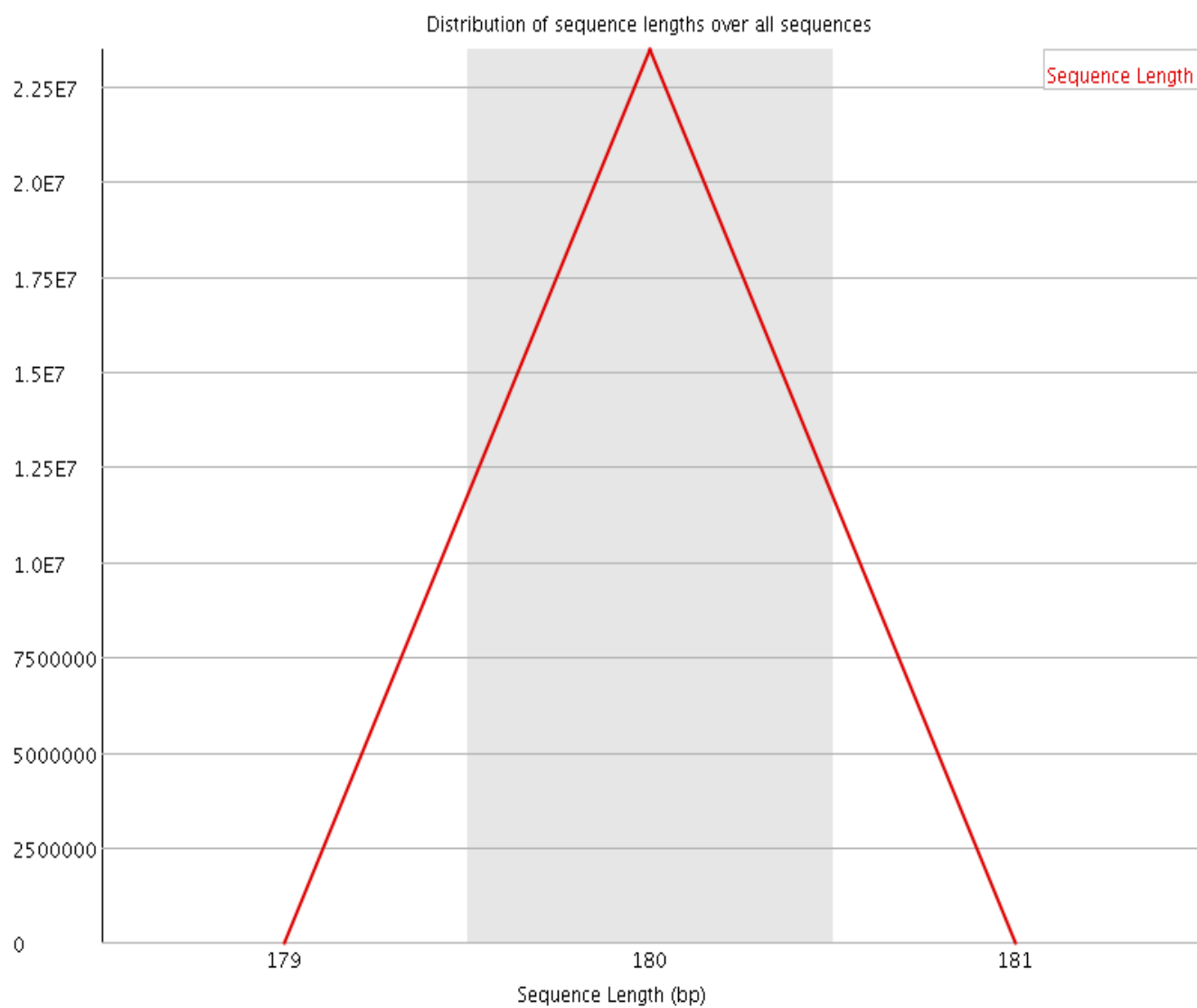
## Per sequence GC content



 **Per base N content**

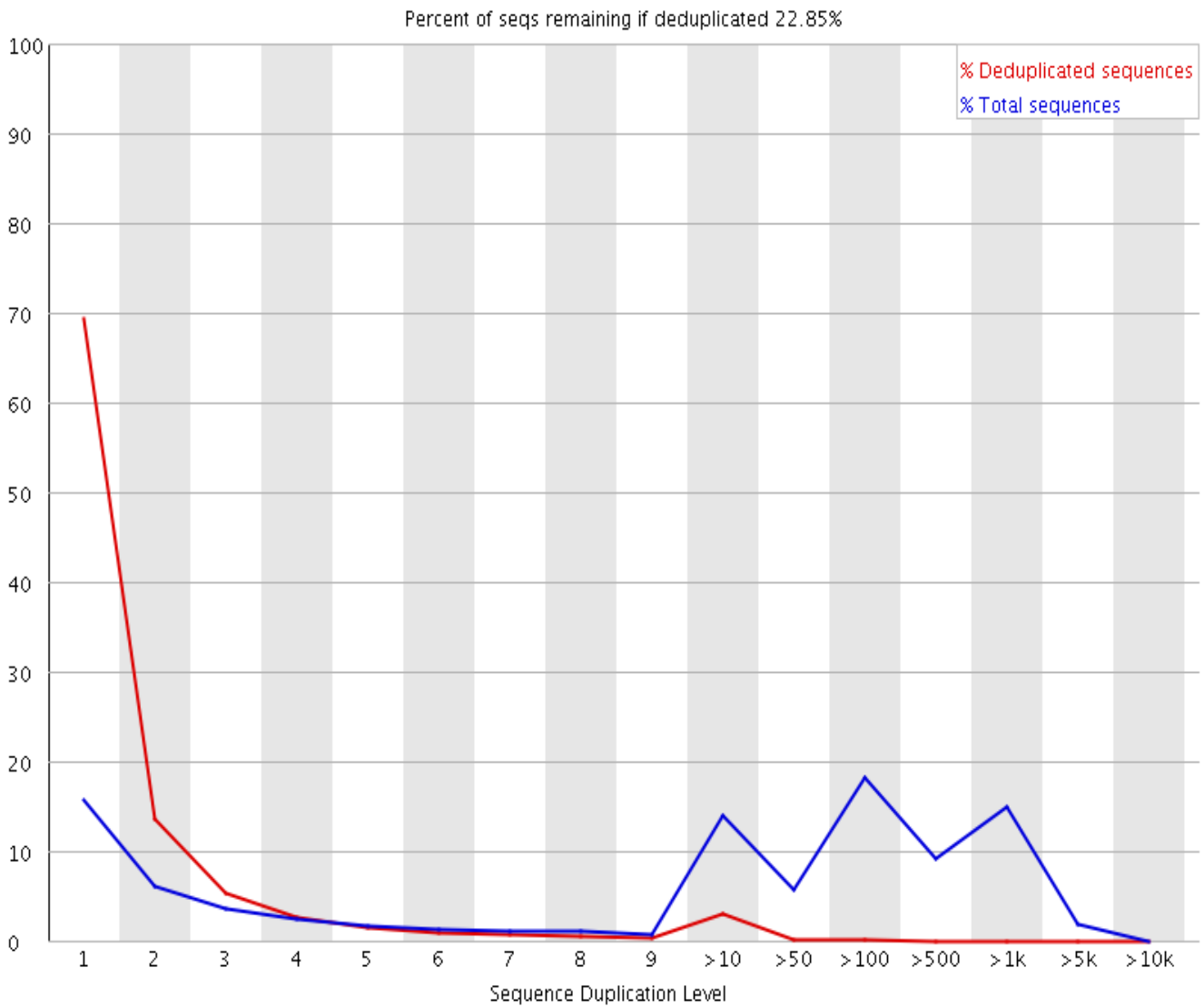


## Sequence Length Distribution



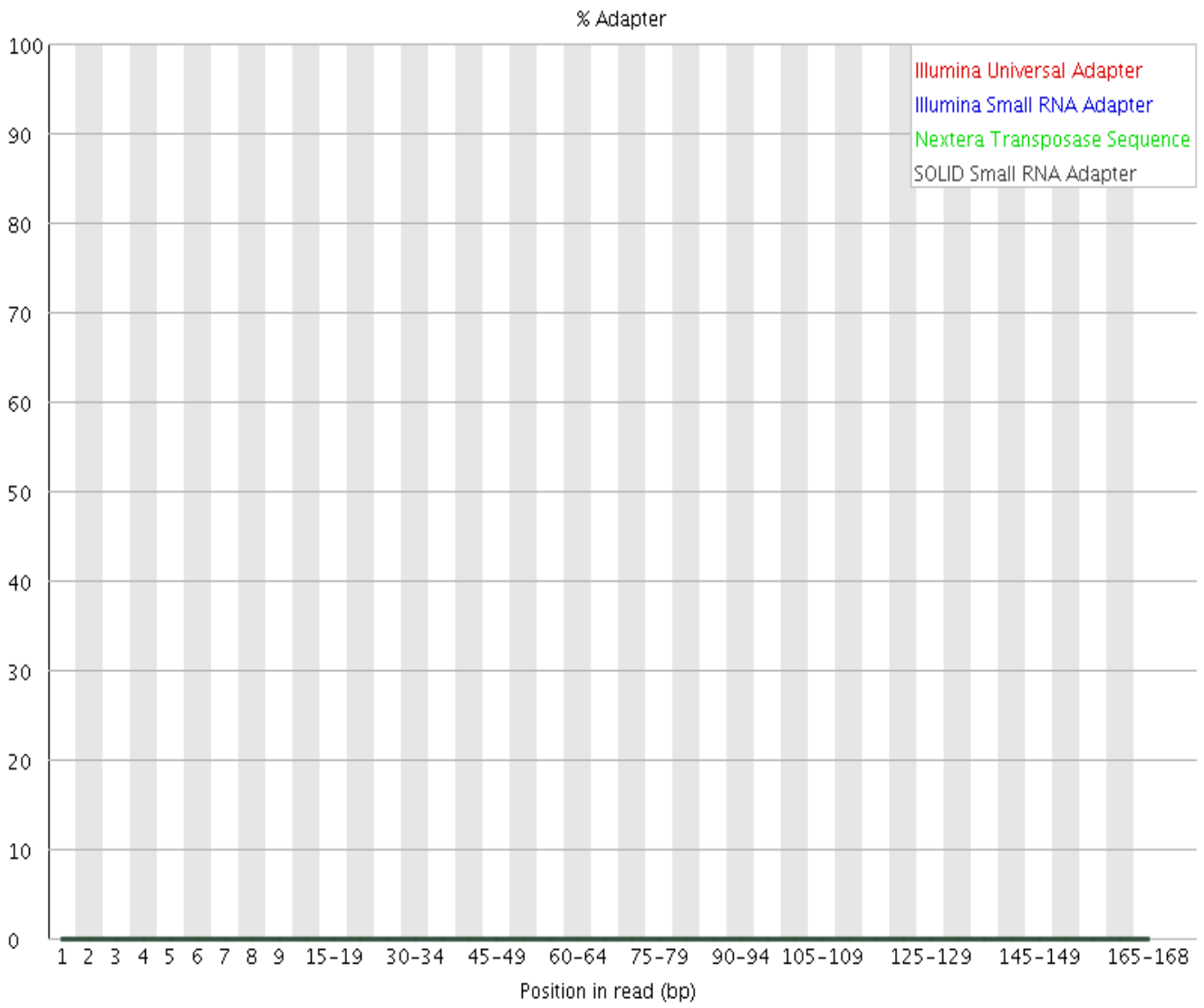
## Sequence Duplication Levels



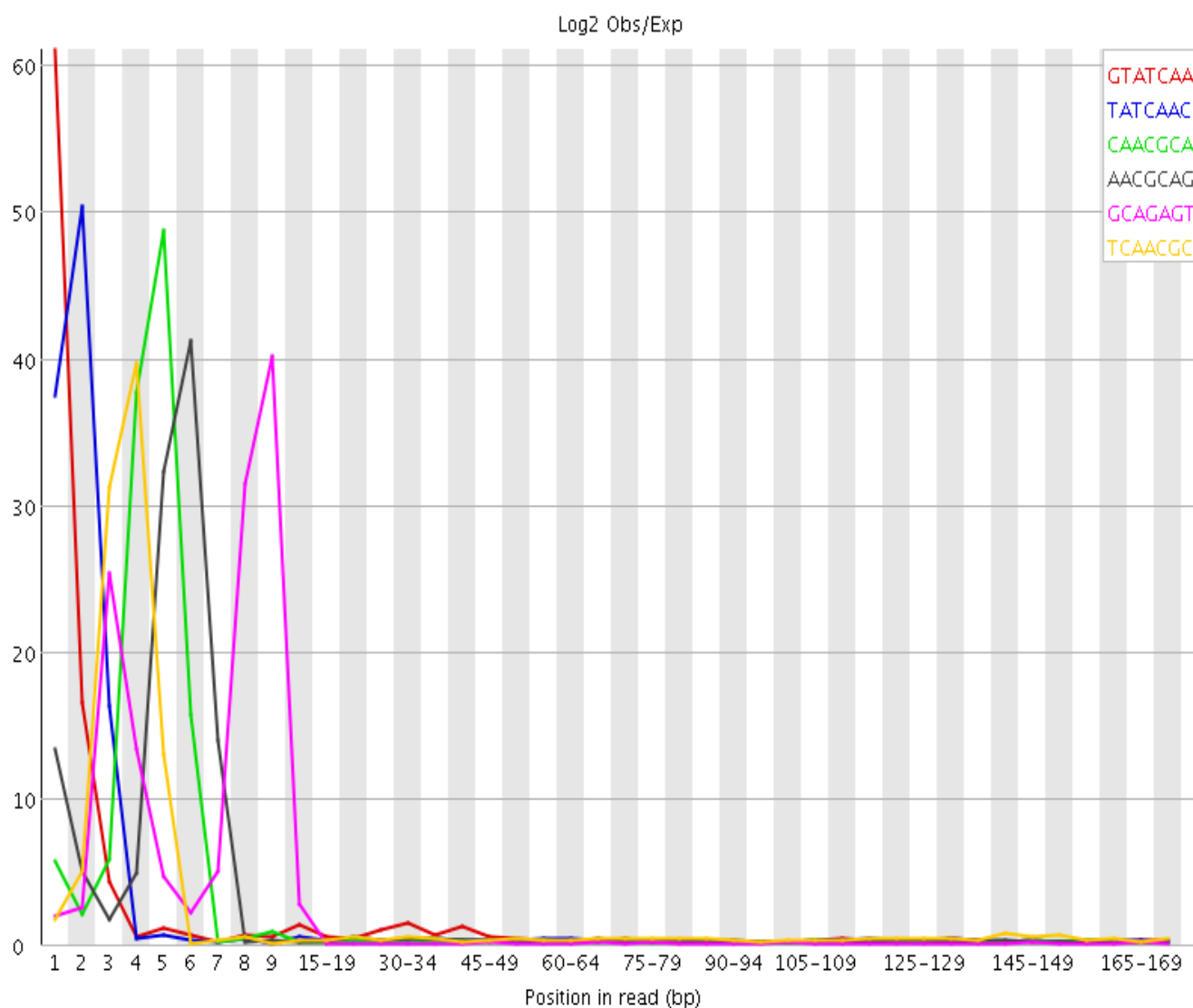


 **Overrepresented sequences**  
 No overrepresented sequences

 **Adapter Content**



## Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTATCAA	43145	0.0	61.023277	1
TATCAAC	45635	0.0	50.38804	2
CAACGCA	45705	0.0	48.728745	5
AACGCAG	53885	0.0	41.234615	6
GCAGAGT	51835	0.0	40.203728	9
TCAACGC	56650	0.0	39.682728	4
CGCAGAG	54845	0.0	39.45006	8
ACGCAGA	67725	0.0	32.178635	7
GAGTGAA	57595	0.0	31.573196	1
CAGAGTG	51200	0.0	31.117329	9
AGTGAAT	64210	0.0	27.952776	2
TGAATGG	69435	0.0	26.41317	2
GTGAATG	70560	0.0	26.1294	1
GGTATCA	28450	0.0	25.842323	1

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCAACG	89570	0.0	25.554926	3
AGAGTGA	46995	0.0	24.713745	5
ATGGGGG	12360	0.0	23.228	3
GAATGGG	80445	0.0	22.310871	3
AATGGGG	46380	0.0	21.833893	6
ATGGGGC	26945	0.0	20.95477	3

Produced by [FastQC](#) (version 0.11.4)