













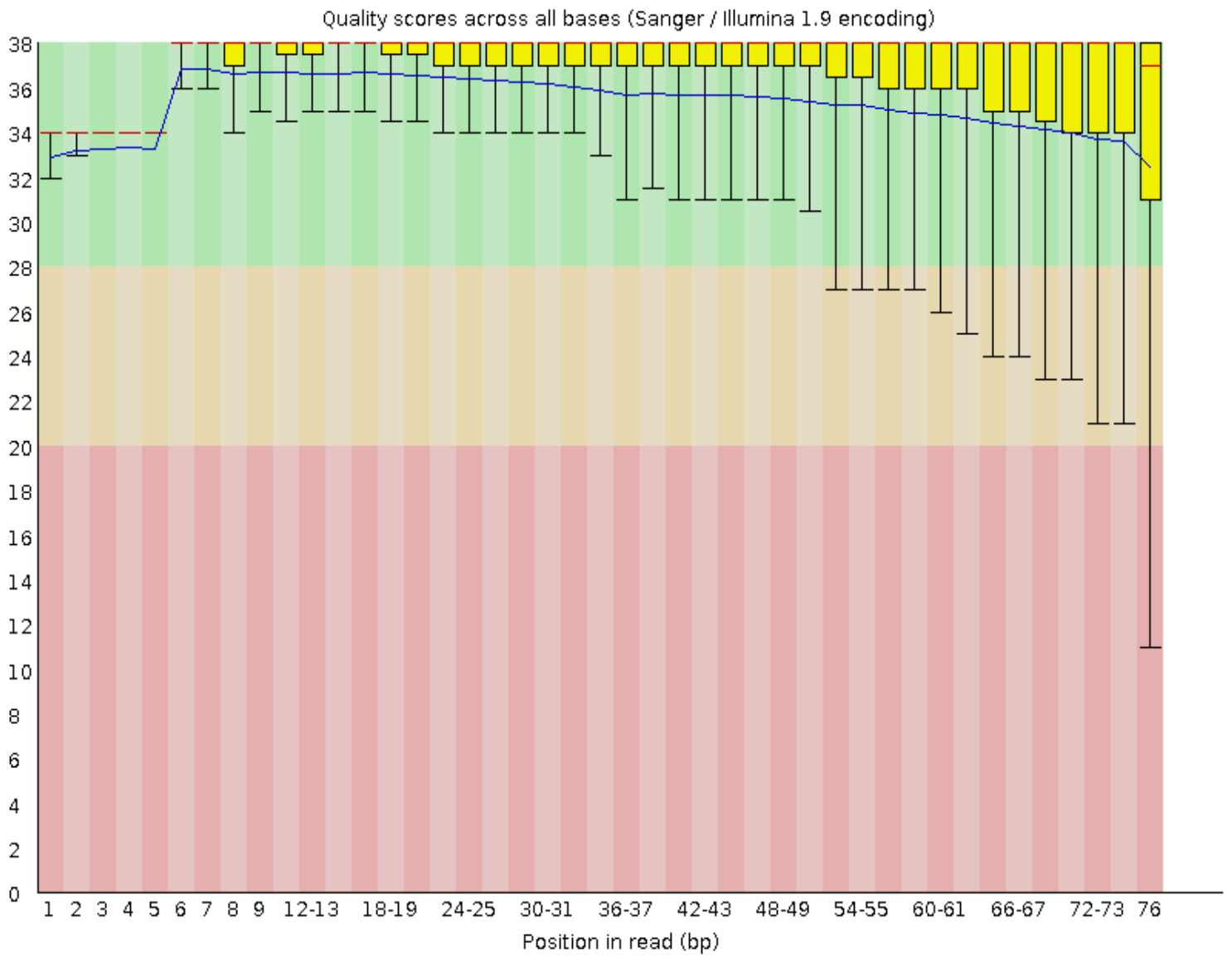
## Summary

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## Basic Statistics

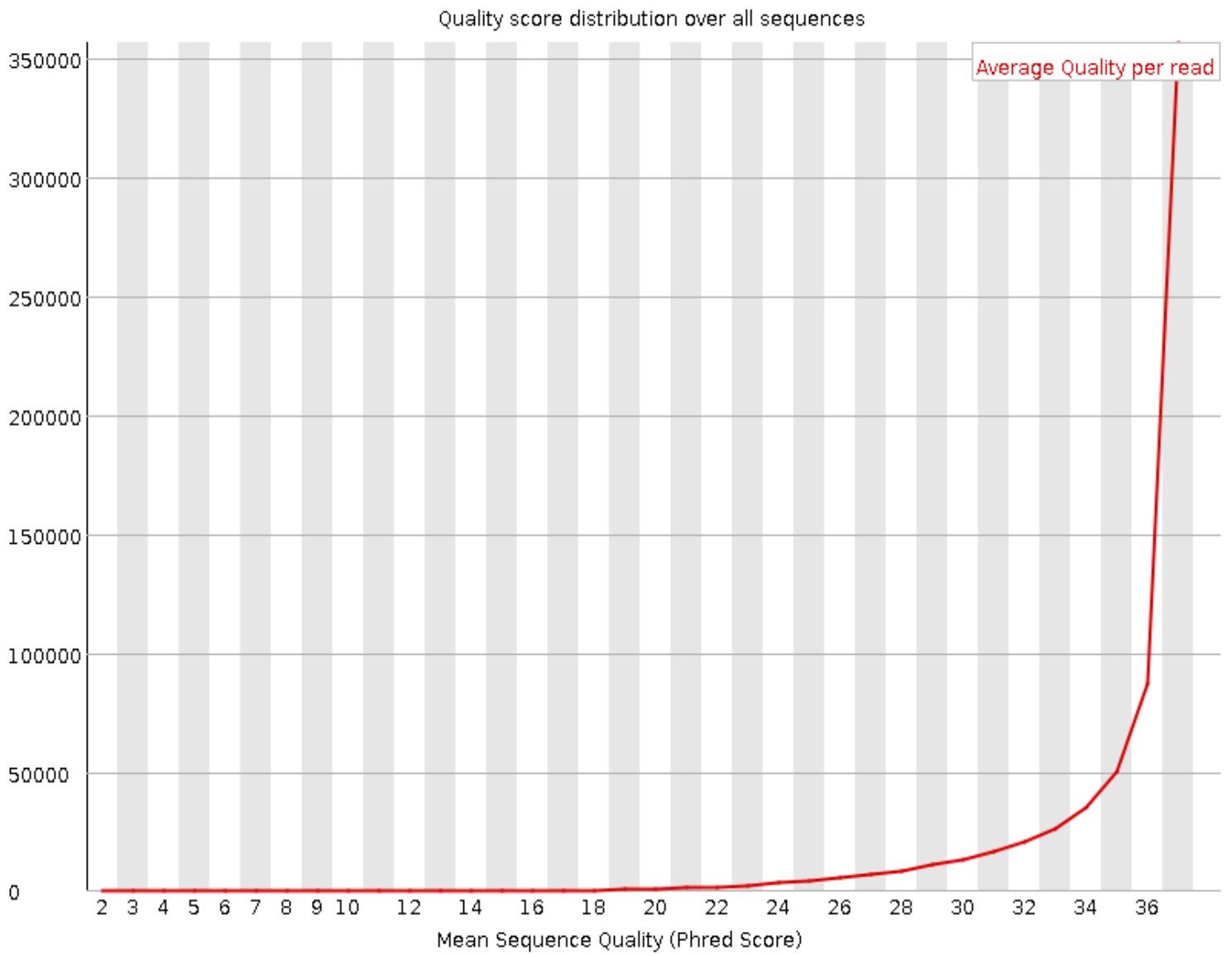
Measure	Value
Filename	skewer_42_dupRemoved_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	657883
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

## Per base sequence quality



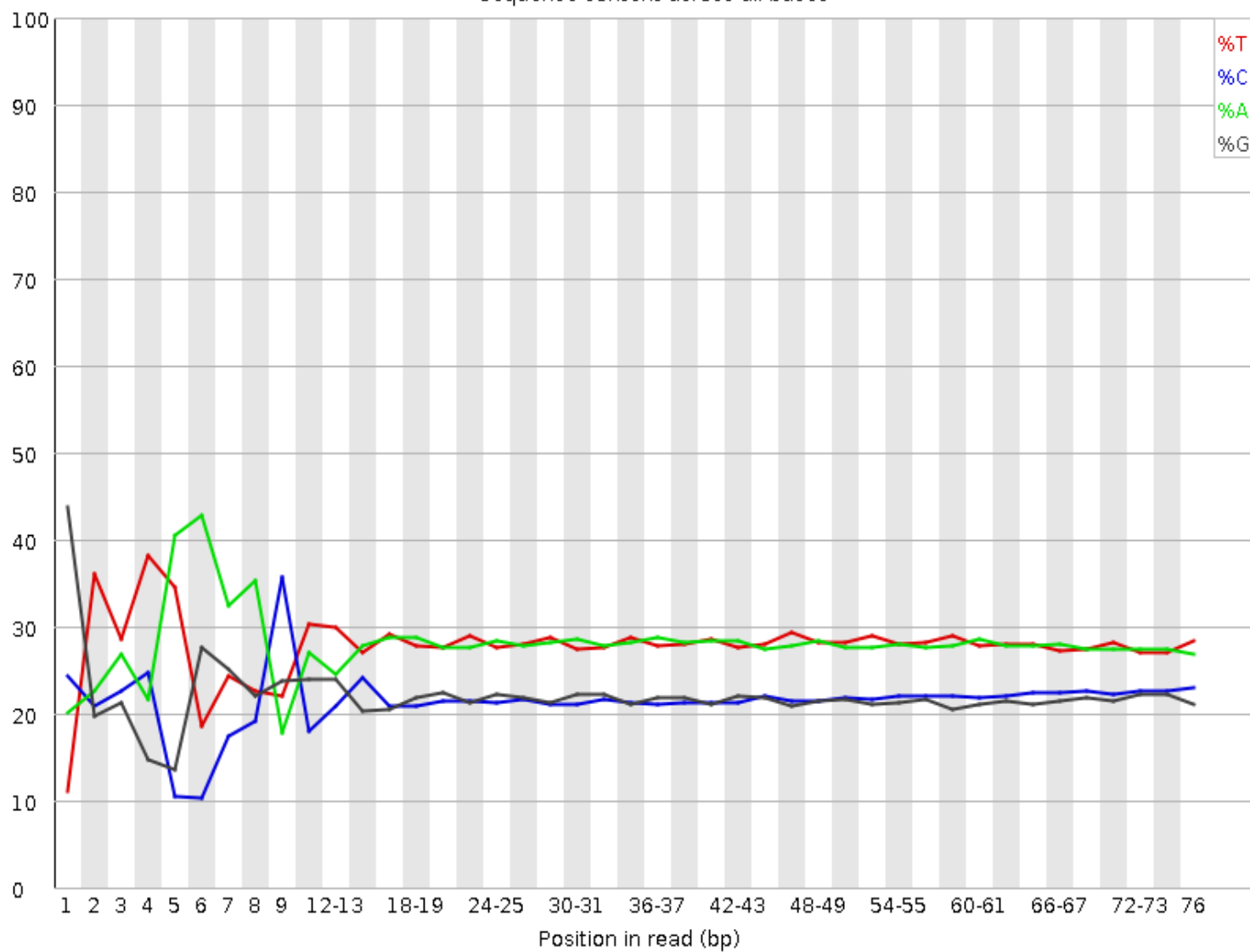
 **Per tile sequence quality**





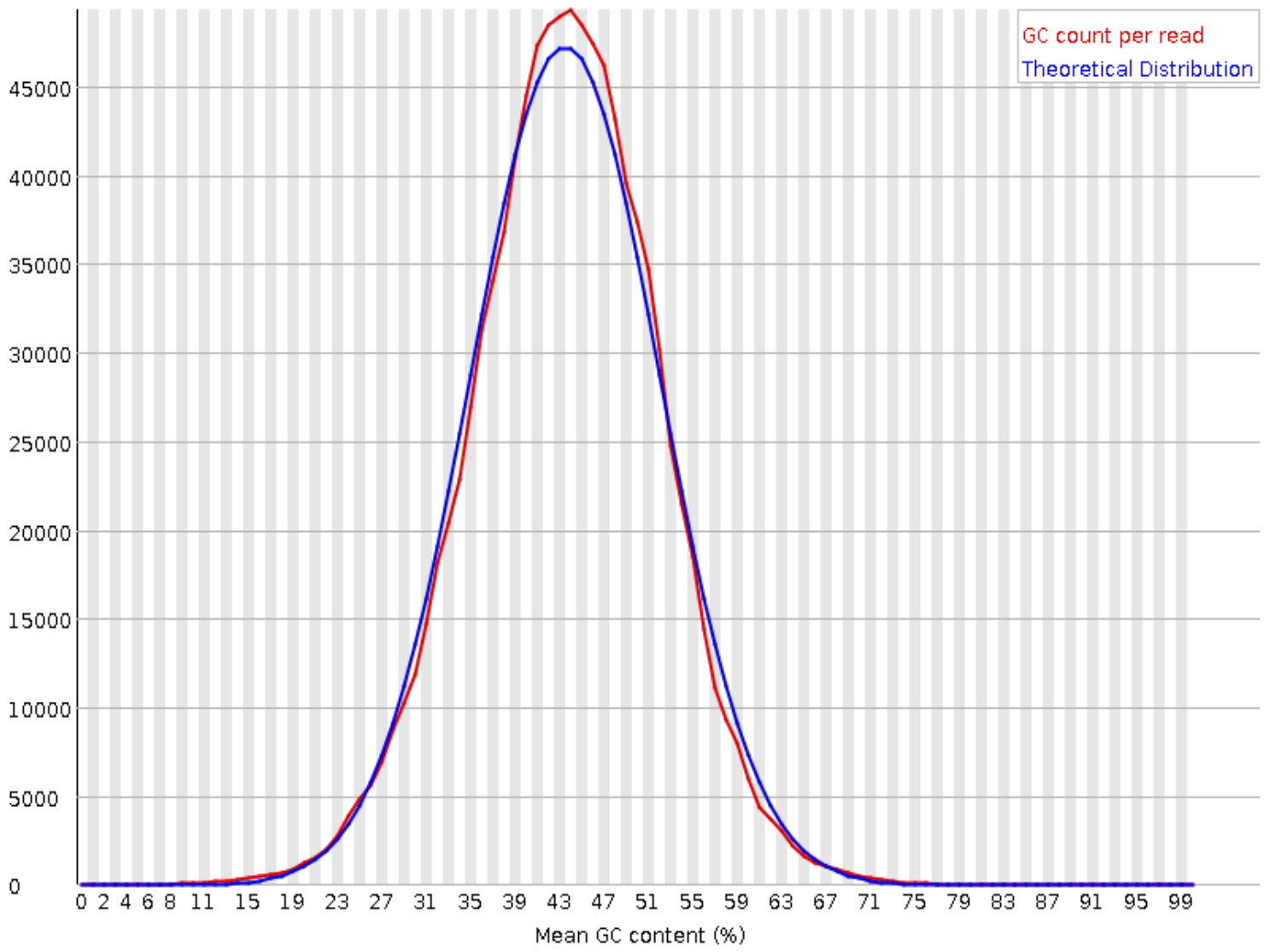
## ❌ Per base sequence content

Sequence content across all bases



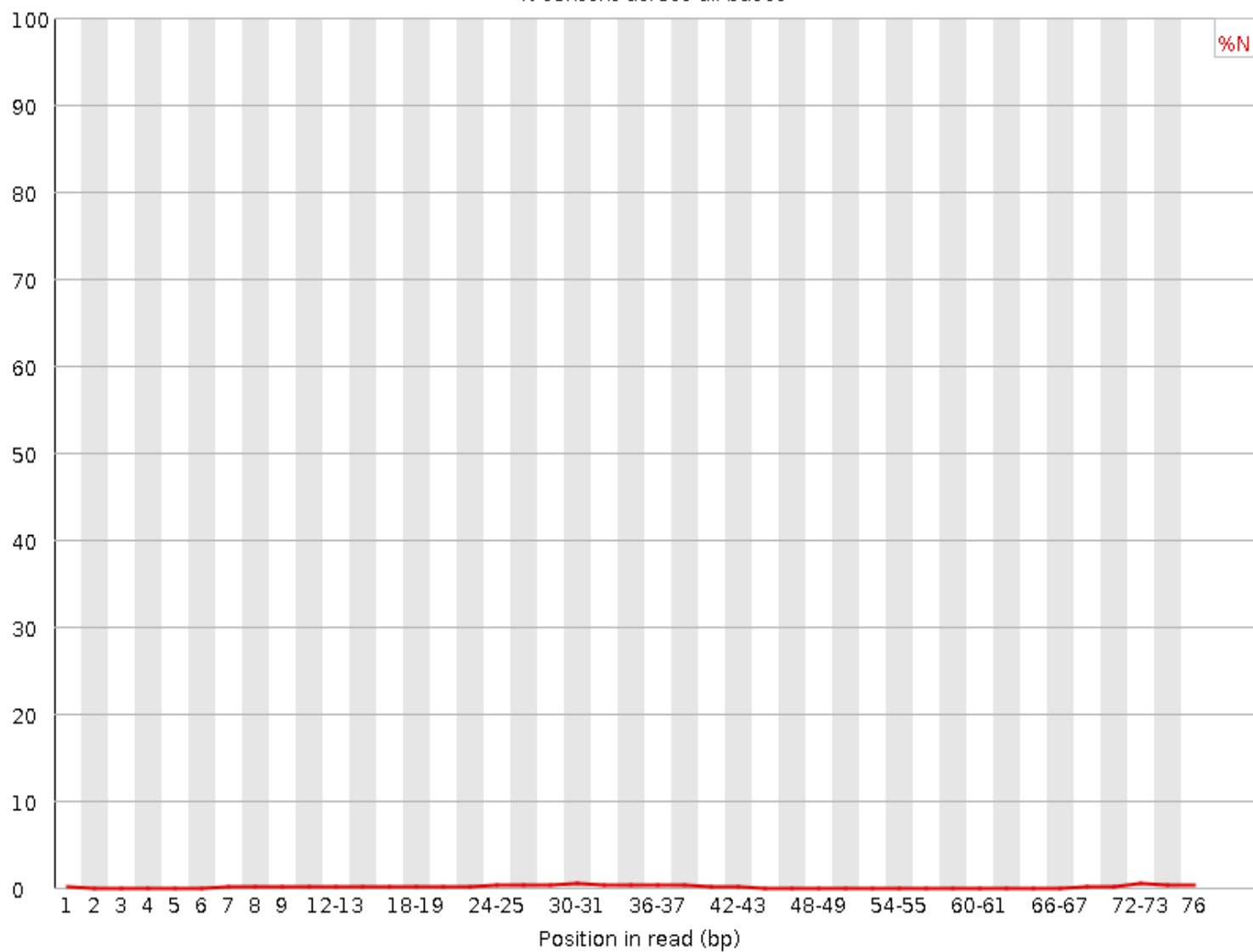
 **Per sequence GC content**

GC distribution over all sequences



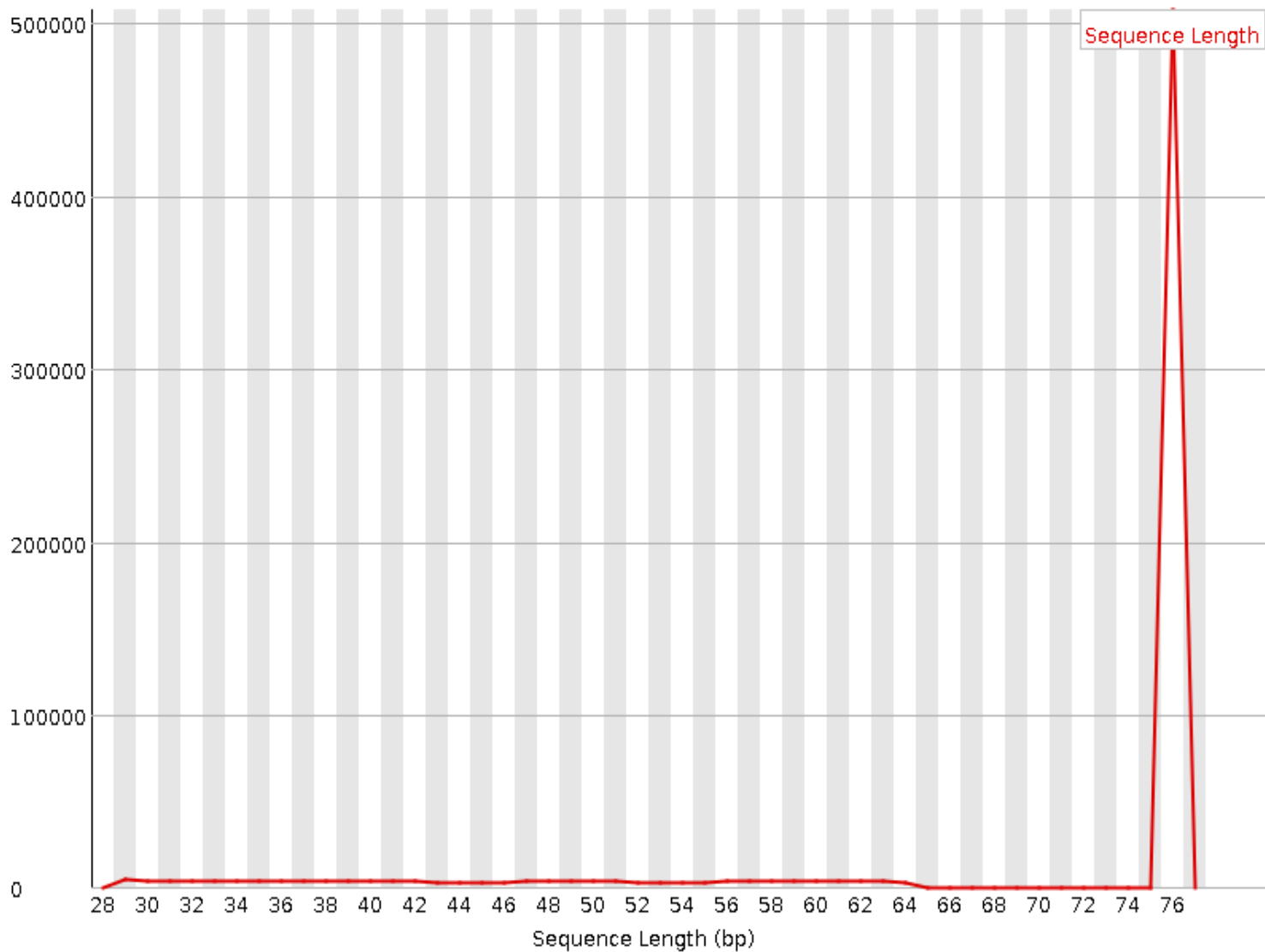
**Per base N content**

N content across all bases



## ! Sequence Length Distribution

Distribution of sequence lengths over all sequences

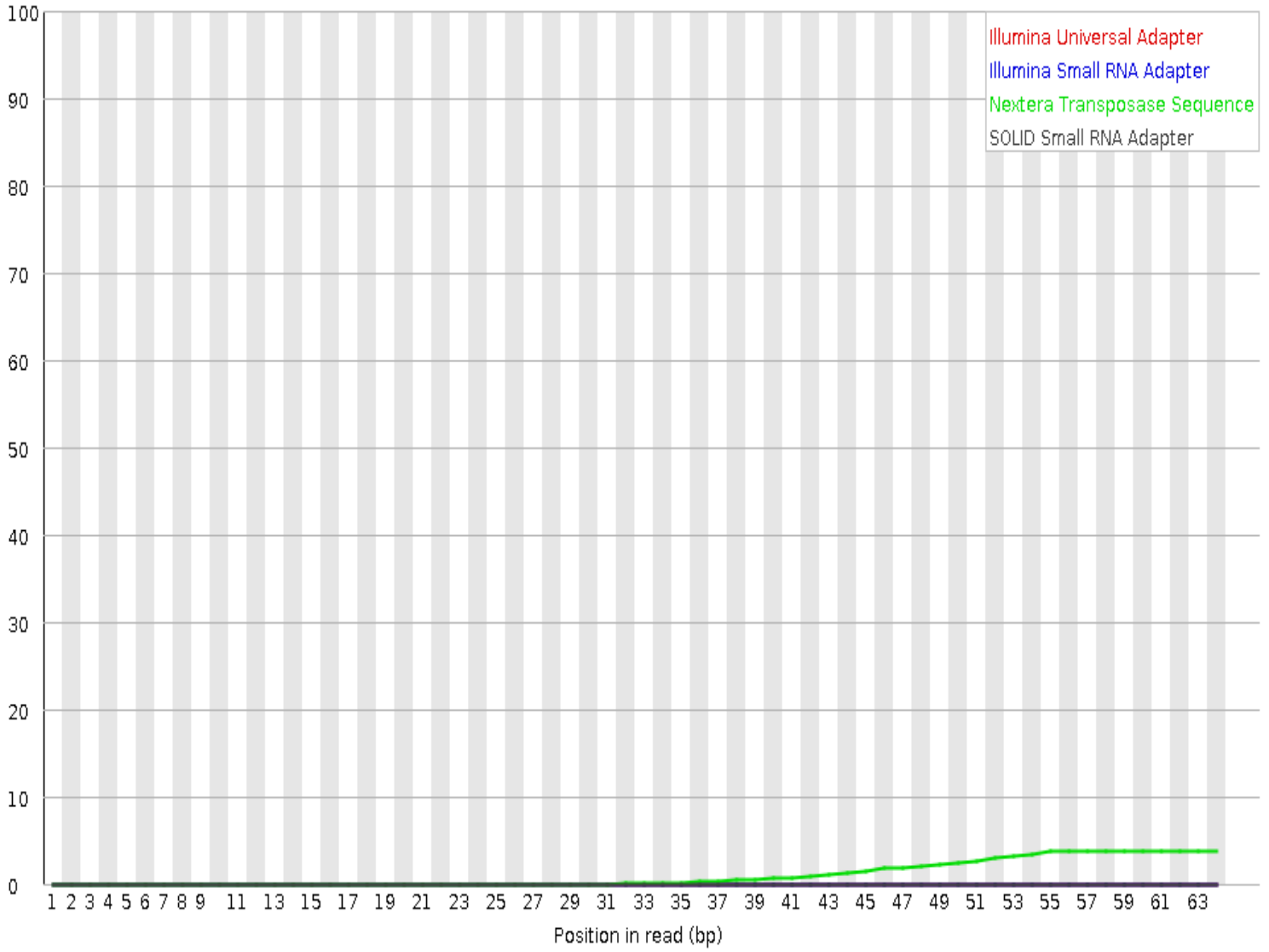


## Sequence Duplication Levels



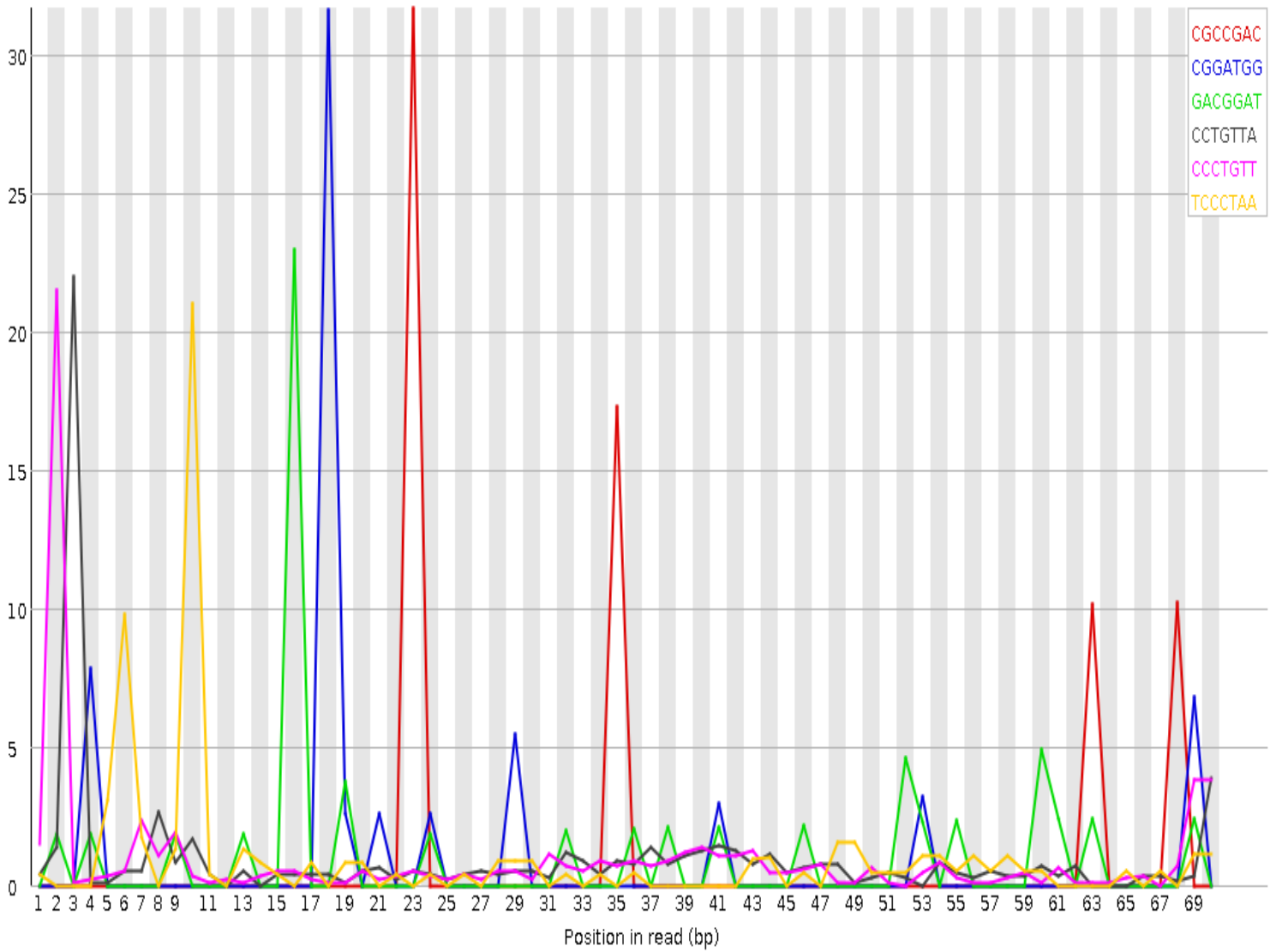


% Adapter



## ! Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGCCGAC	40	0.0039562234	31.656017	23
CGGATGG	120	5.456968E-12	31.600405	18
GACGGAT	165	3.4924597E-10	22.966324	16
CCTGTTA	2195	0.0	21.996464	3
CCCTGTT	2245	0.0	21.501644	2
TCCCTAA	705	0.0	21.054071	10
GCGCAGT	75	0.0033430322	21.038013	6
GGGATAA	2950	0.0	20.648928	1
AGACGGA	200	1.72804E-10	20.529285	15
ACGGATG	200	1.72804E-10	20.524586	17
GGGCTCT	170	1.1941665E-8	20.483305	23
AGTCGTG	260	1.8189894E-10	20.450445	65
ACCCTGT	2440	0.0	19.790821	1

AGGGATA	2145	0.0	19.569807	1
CTGTTAT	2510	0.0	19.361675	4
AAGACGG	180	2.3645043E-8	19.301037	14
ATCCCTA	2405	0.0	19.171898	9
CGTGTAG	280	4.674803E-10	19.055635	68
TTTTCCG	85	0.006801677	18.606949	19
ATAACAG	3360	0.0	18.5961	4

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