













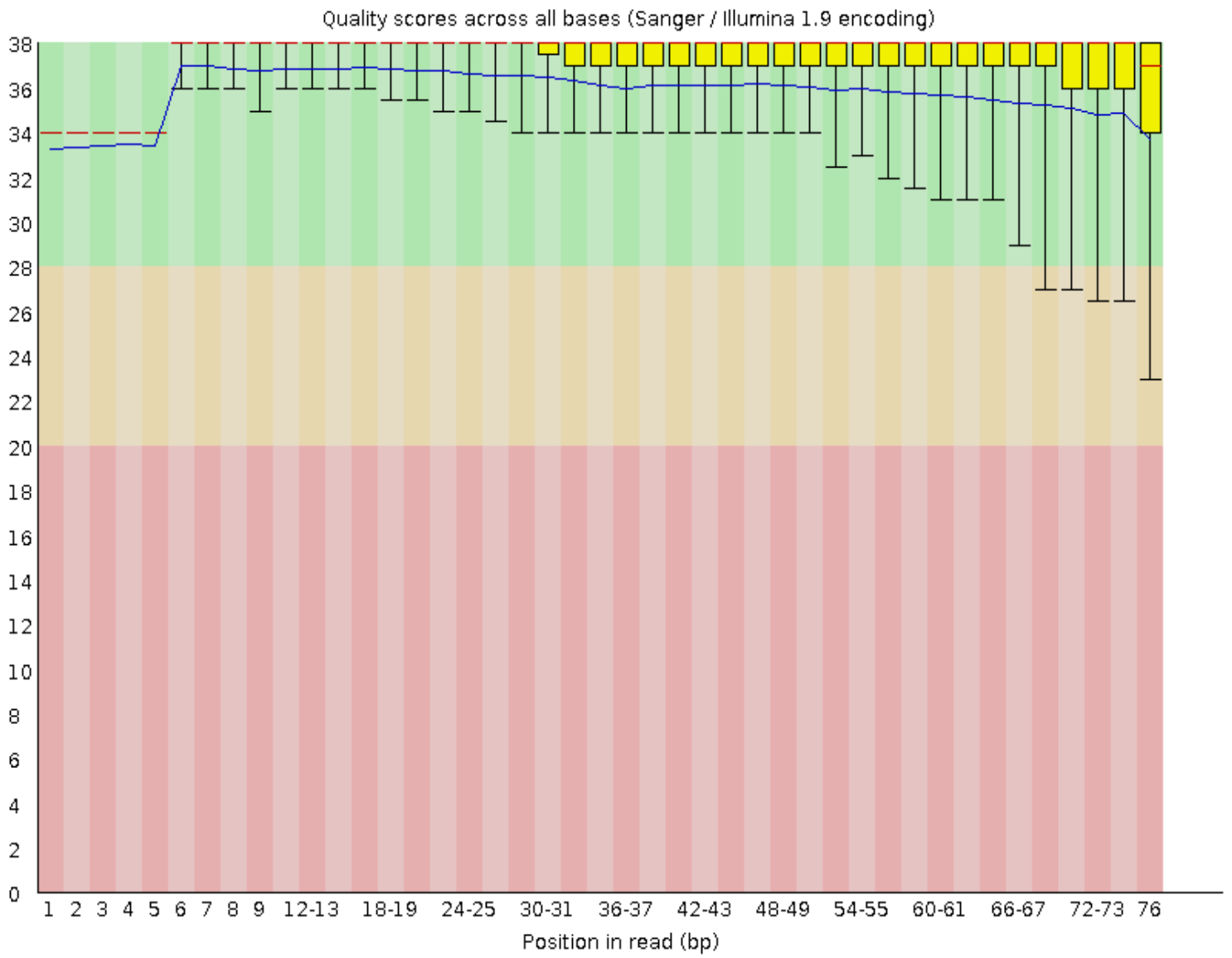
## Summary

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## Basic Statistics

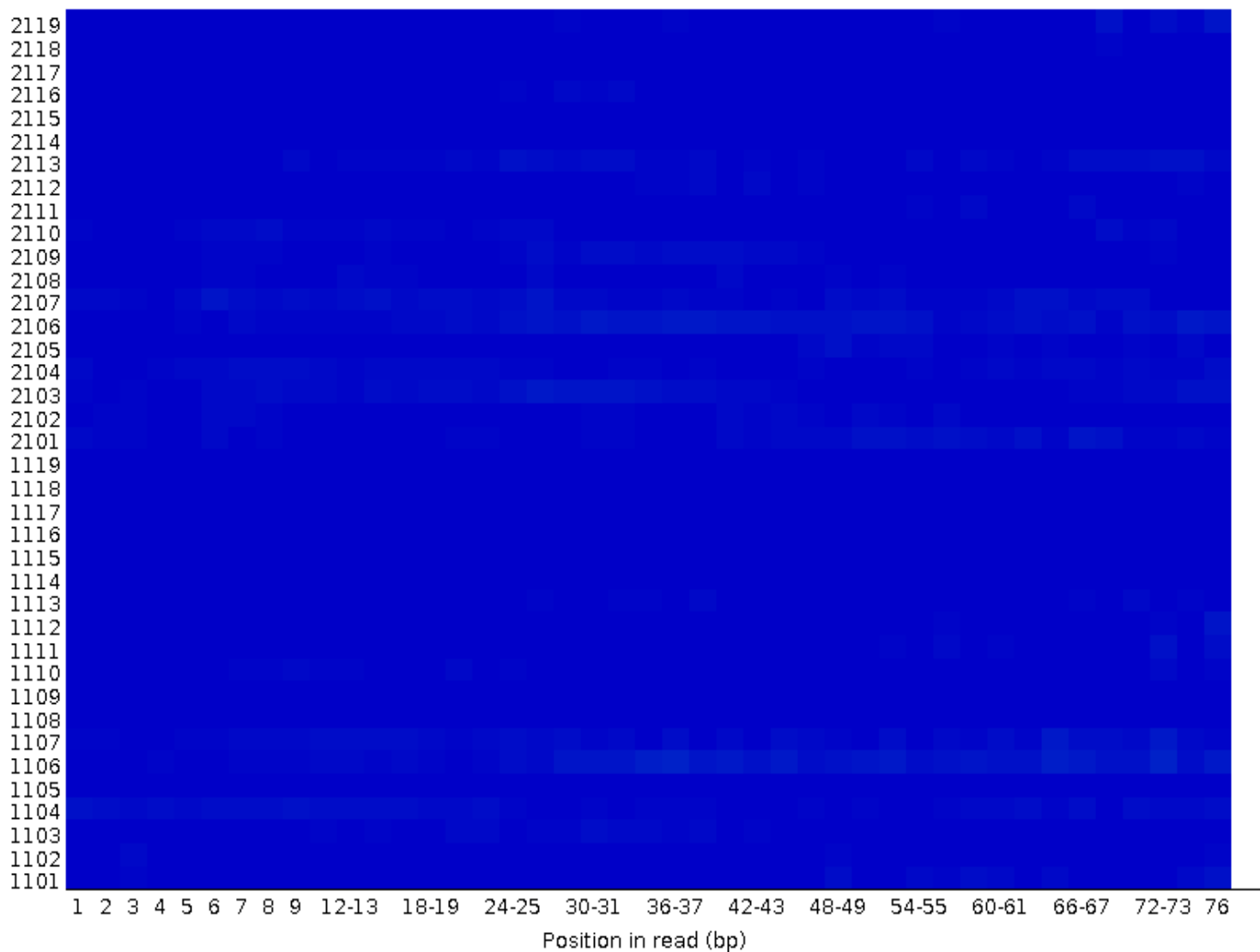
Measure	Value
Filename	skewer_run2_SW041_2-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1311142
Sequences flagged as poor quality	0
Sequence length	28-76
%GC	43

## Per base sequence quality

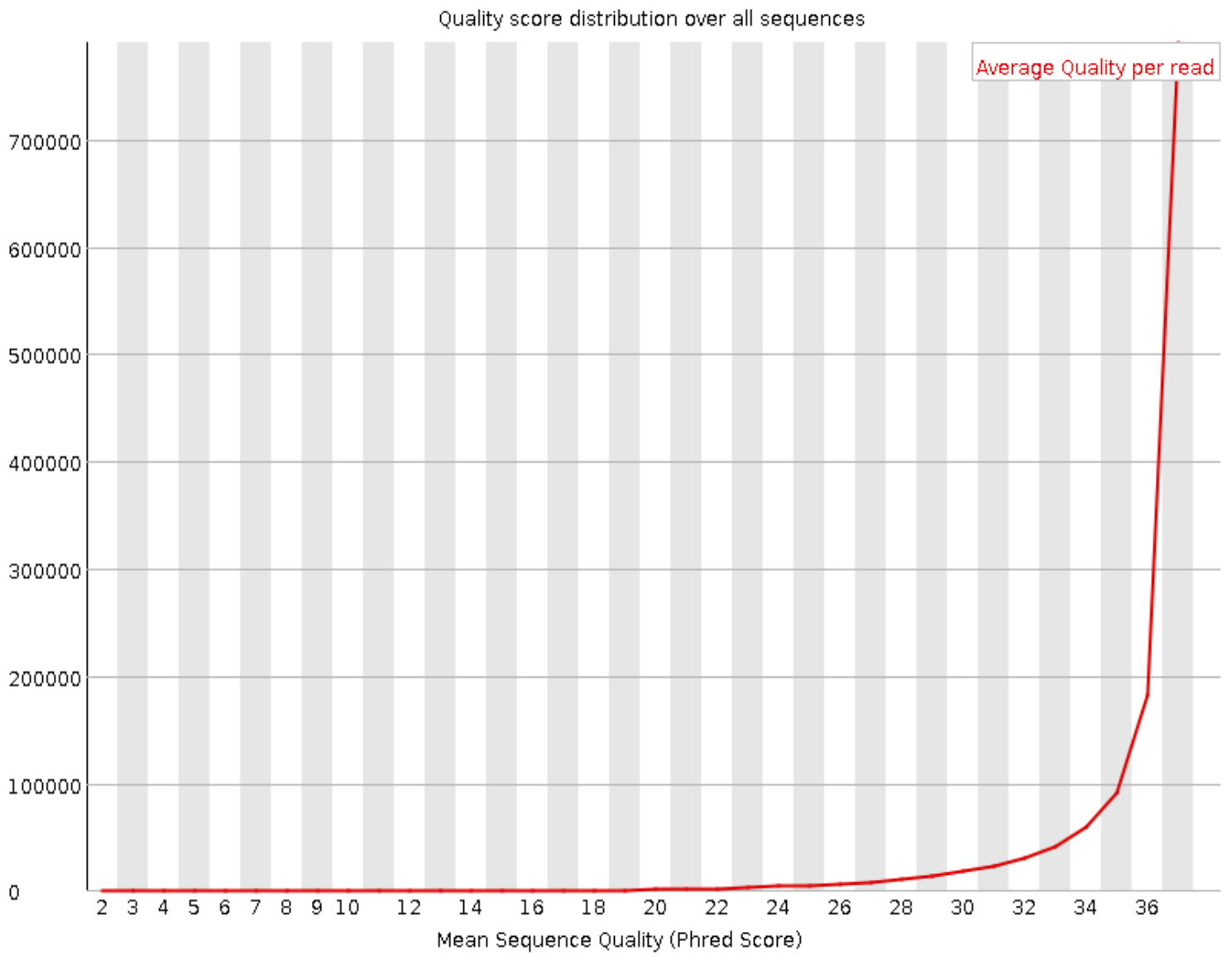


 **Per tile sequence quality**

Quality per tile

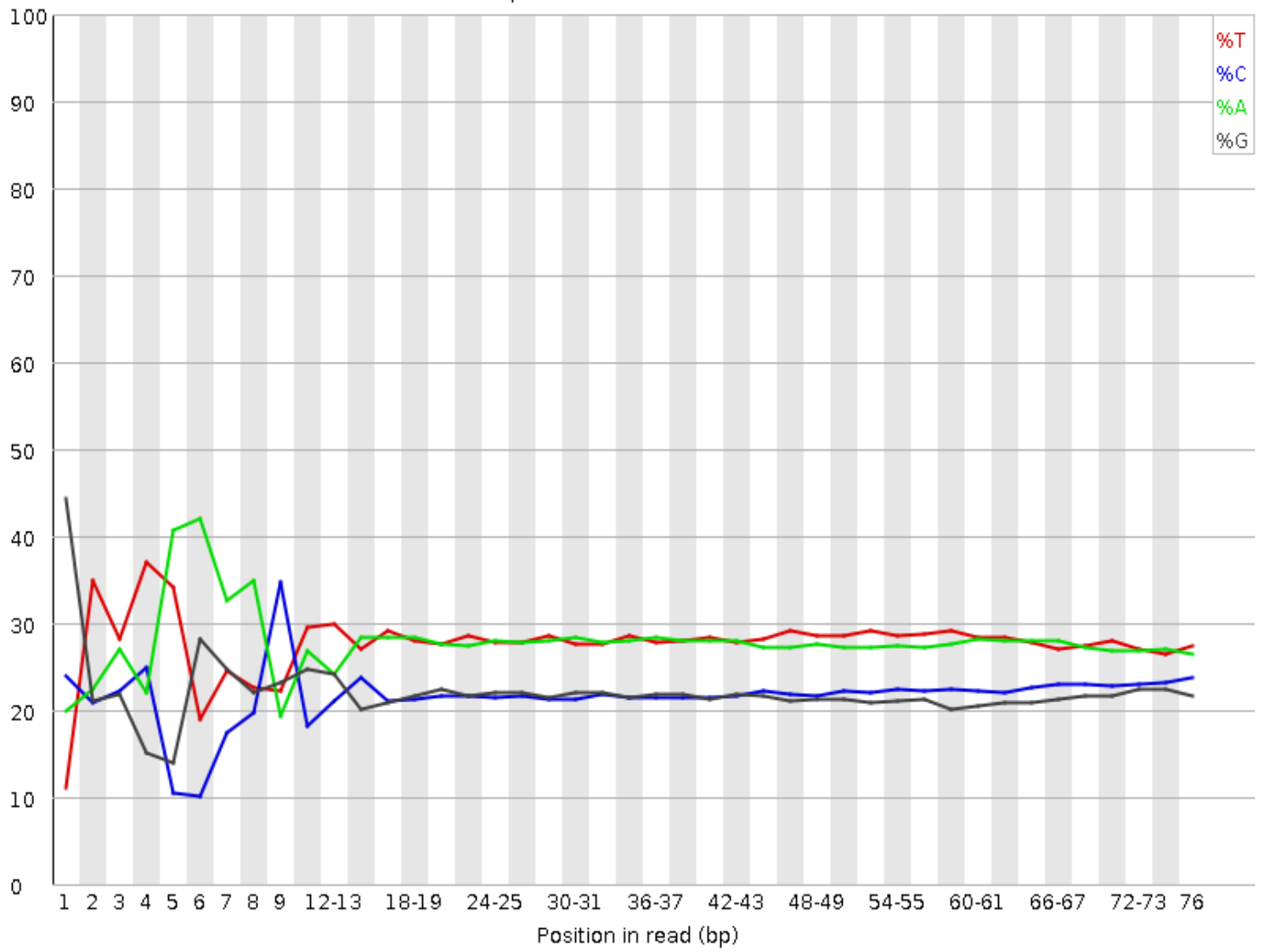


 **Per sequence quality scores**



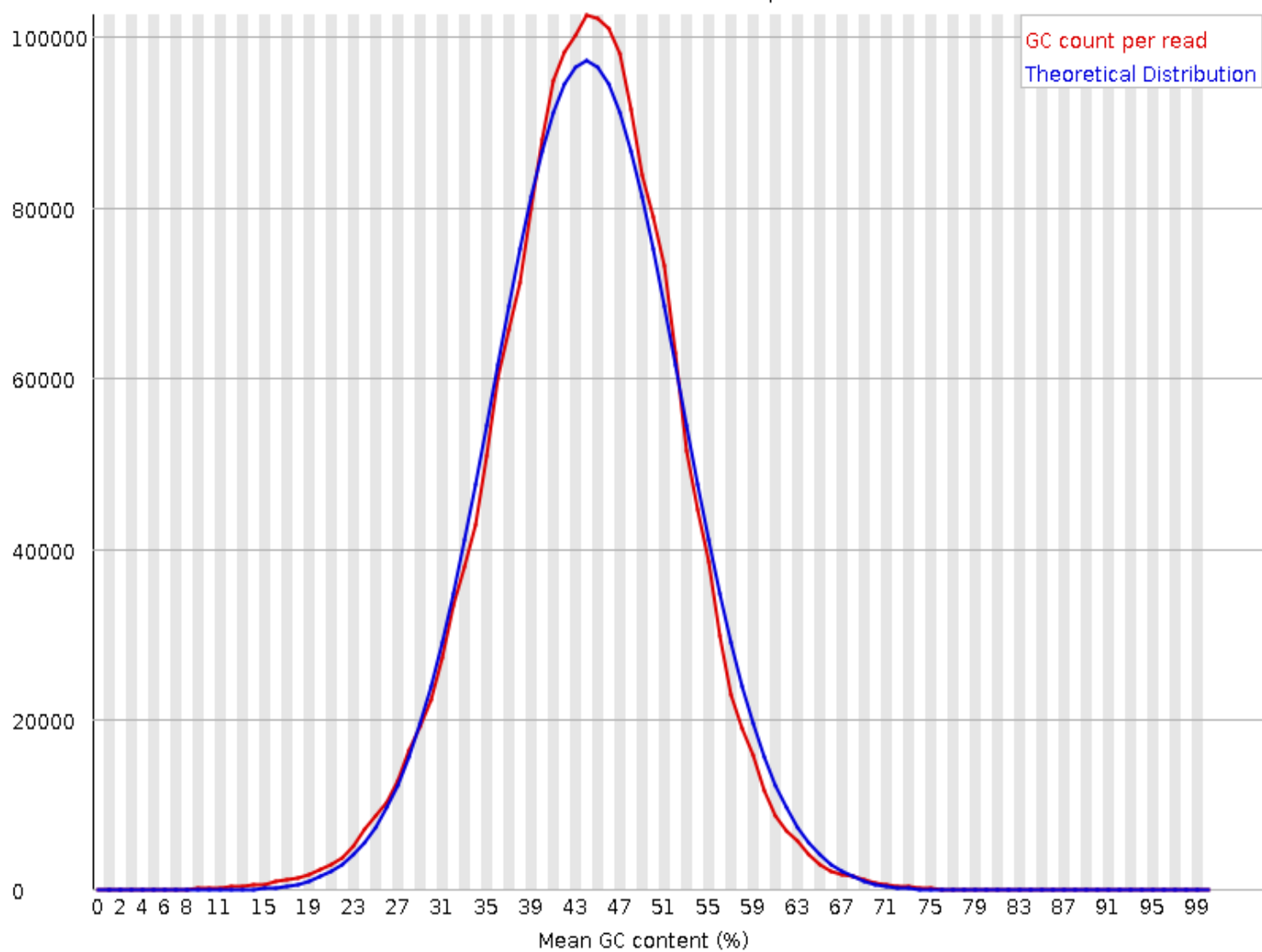
 **Per base sequence content**

Sequence content across all bases



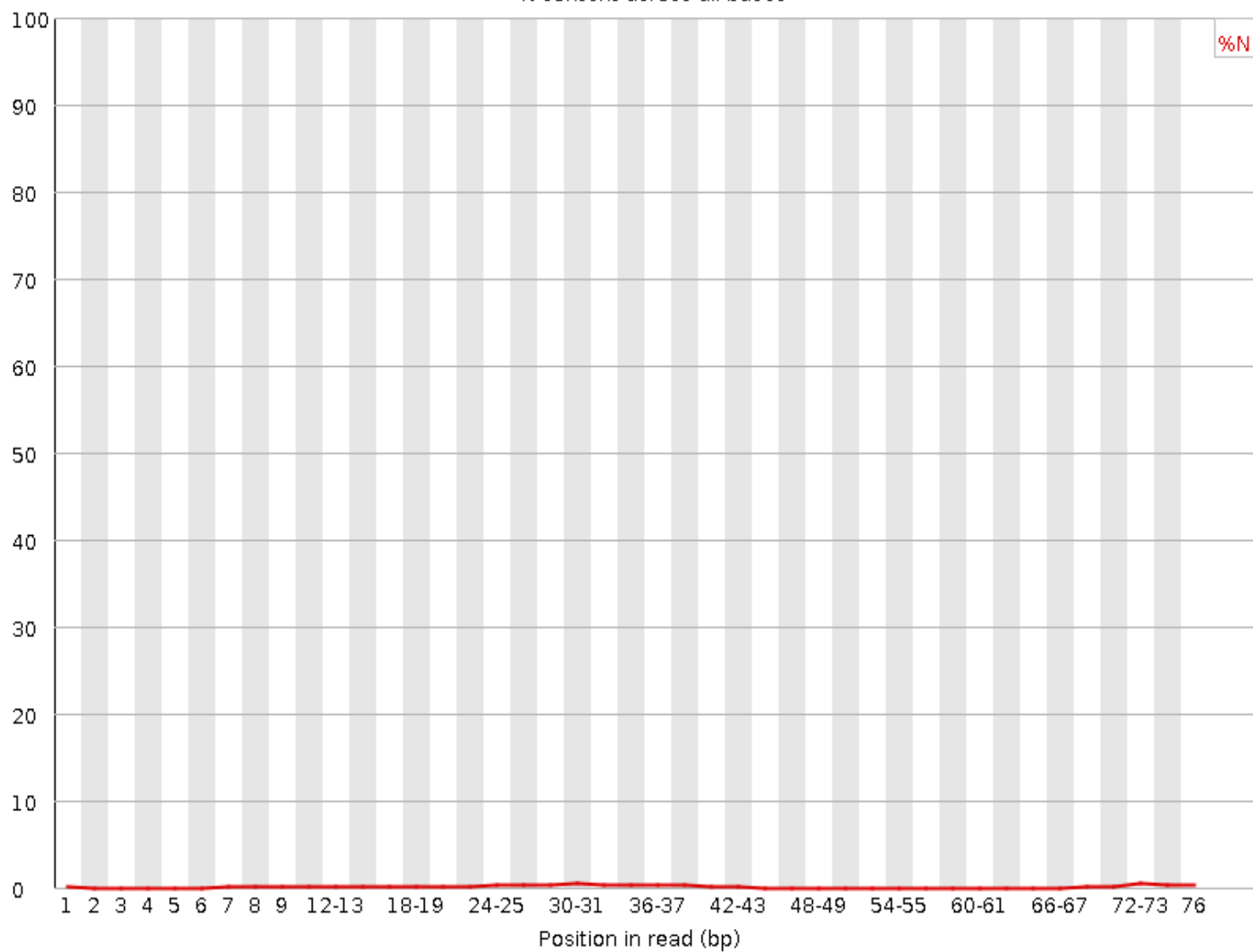
**Per sequence GC content**

GC distribution over all sequences



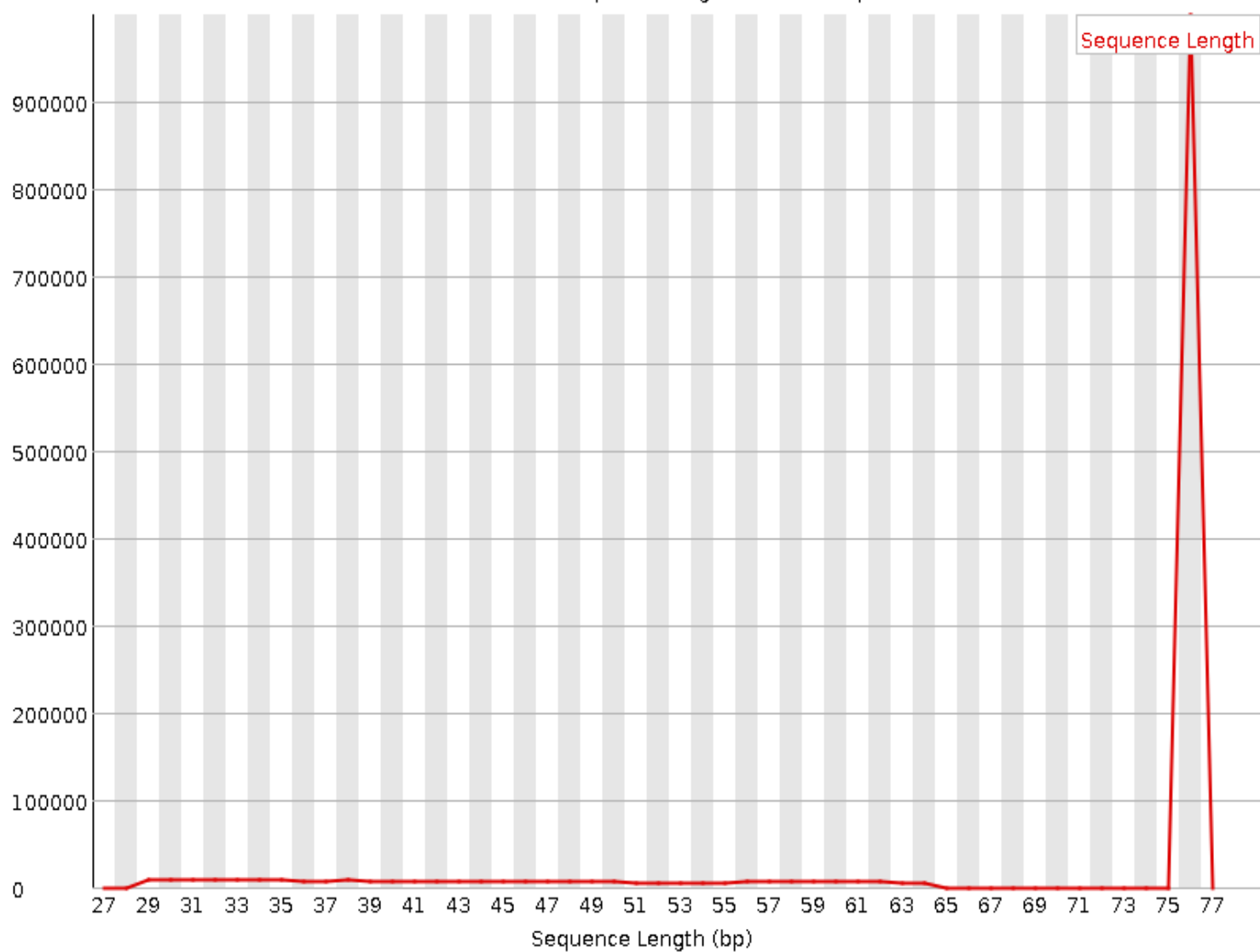
 **Per base N content**

N content across all bases



## ! Sequence Length Distribution

Distribution of sequence lengths over all sequences

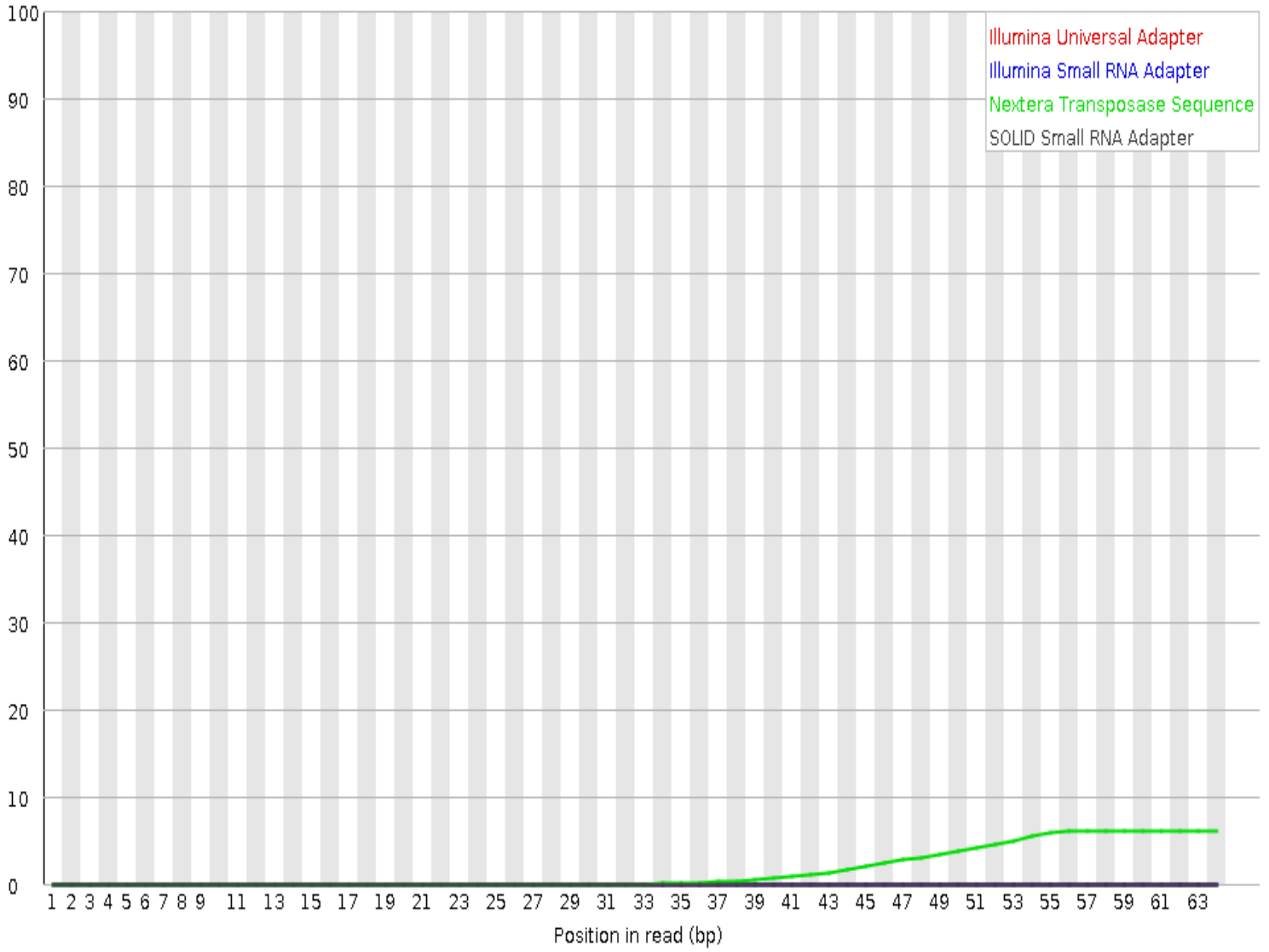


## Sequence Duplication Levels



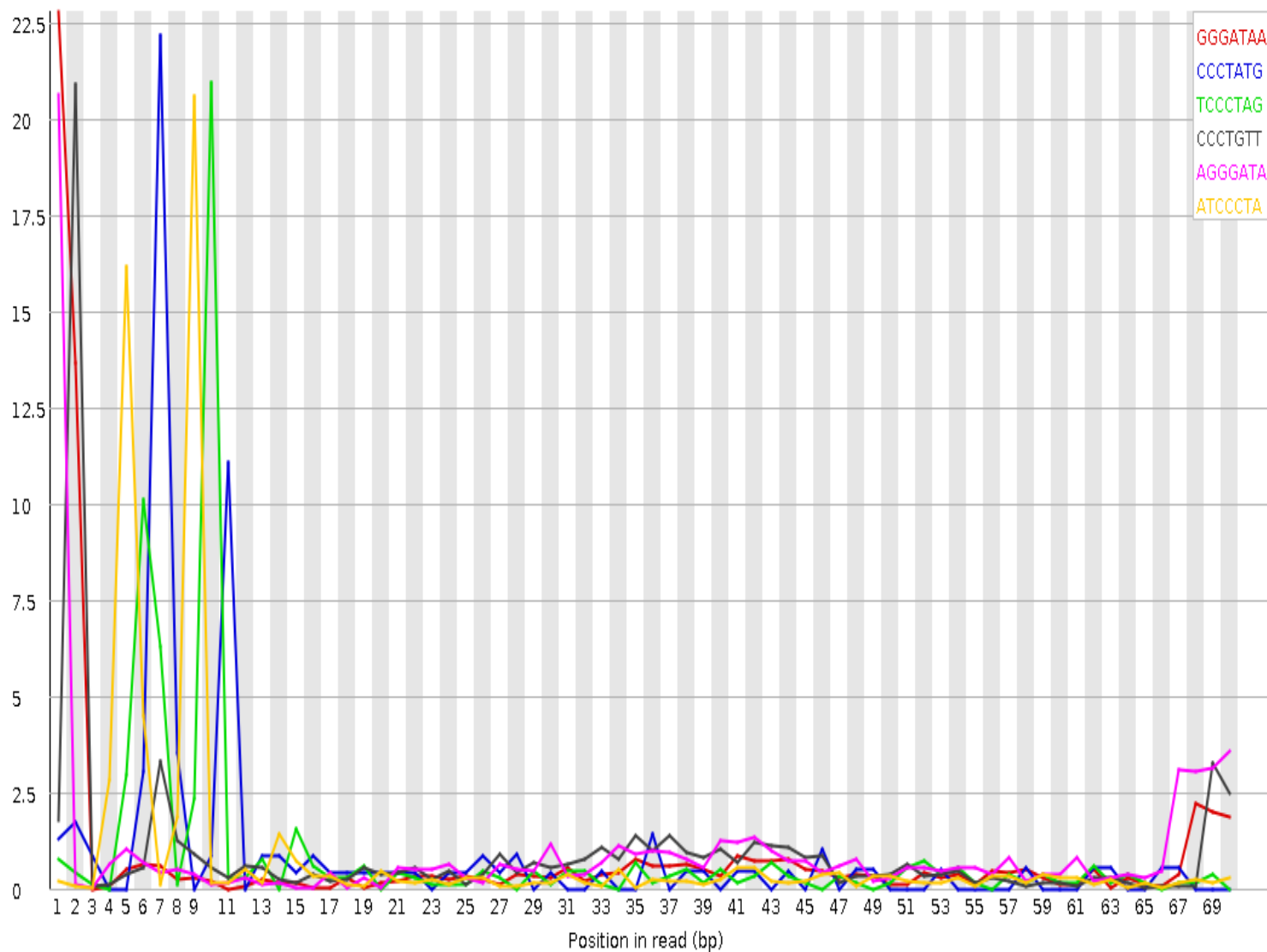


% Adapter



 **Kmer Content**

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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GGGATAA	7310	0.0	22.797293	1
CCCTATG	705	0.0	22.203465	7
TCCCTAG	1970	0.0	20.998077	10
CCCTGTT	6345	0.0	20.9222	2
AGGGATA	4700	0.0	20.661074	1
ATCCCTA	6230	0.0	20.623749	9
ACCCTGT	6480	0.0	20.49651	1
ATAACAG	8245	0.0	20.354658	4
CCTGTTA	6390	0.0	20.333885	3
GGATAAC	8355	0.0	19.936012	2
TCCCTAT	1960	0.0	19.48694	6
GATAACA	8650	0.0	19.292309	3
AGGGTAA	8680	0.0	19.098875	9

TCCCTAA	1970	0.0	19.08916	10
CAGGGTA	8730	0.0	19.05472	8
CTGTTAT	6810	0.0	19.034563	4
CCTATGC	470	0.0	18.663042	8
ACAGGGT	9060	0.0	18.34874	7
AACAGGG	9340	0.0	17.966265	6
GGTAATT	2480	0.0	17.943556	11

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