













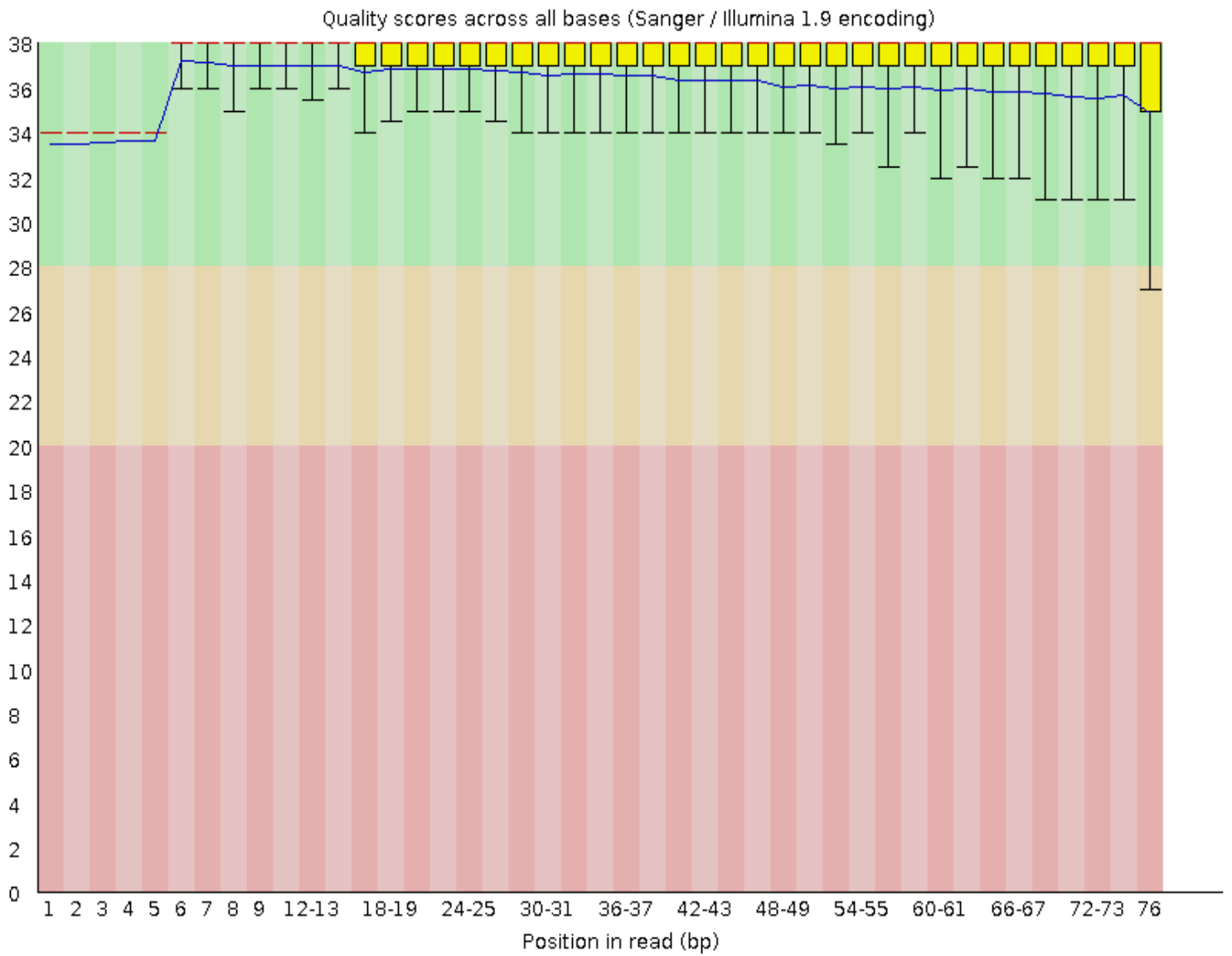
Summary

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Basic Statistics

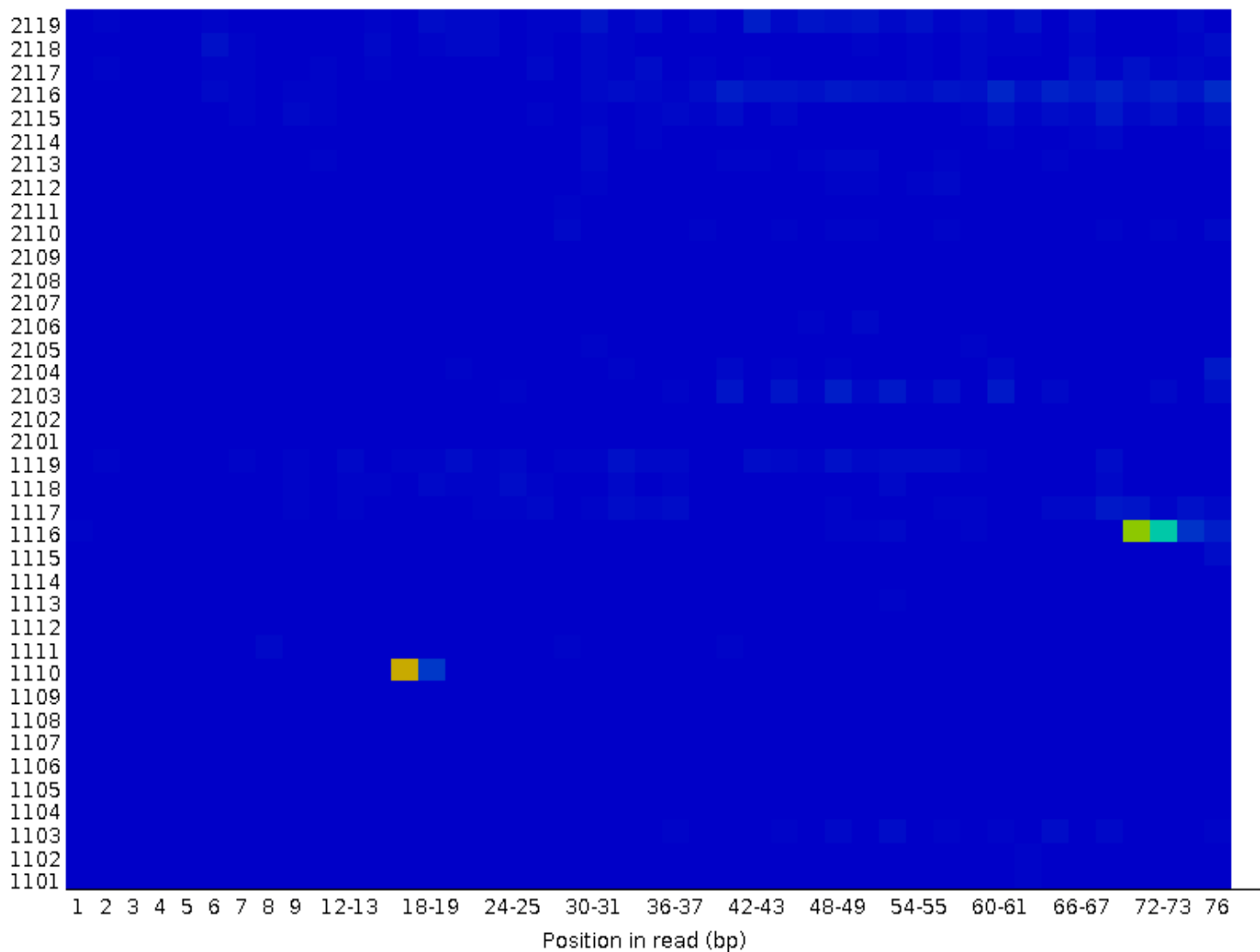
Measure	Value
Filename	skewer_run2_SW041_2-trimmed-pair1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1311142
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

Per base sequence quality



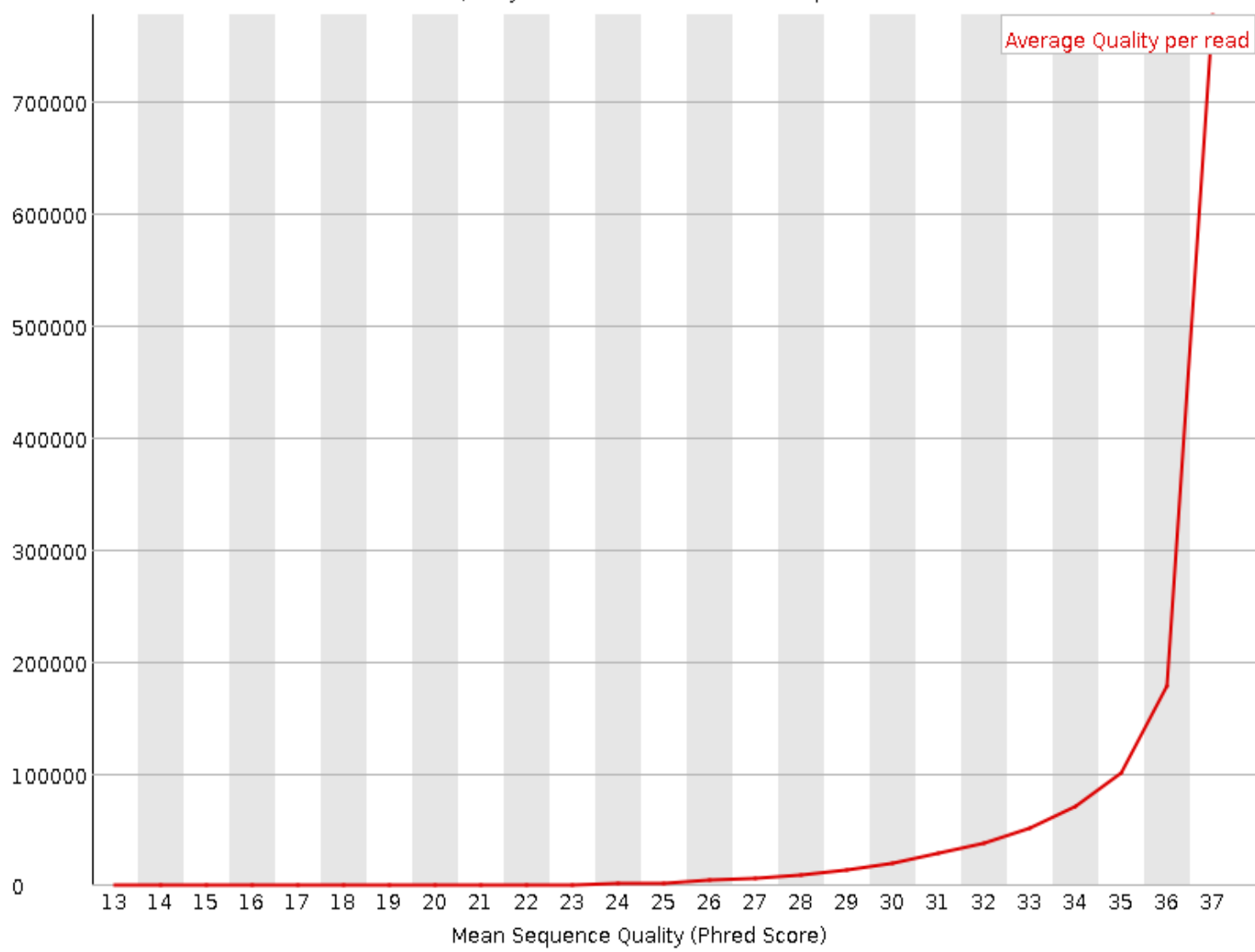
! Per tile sequence quality

Quality per tile



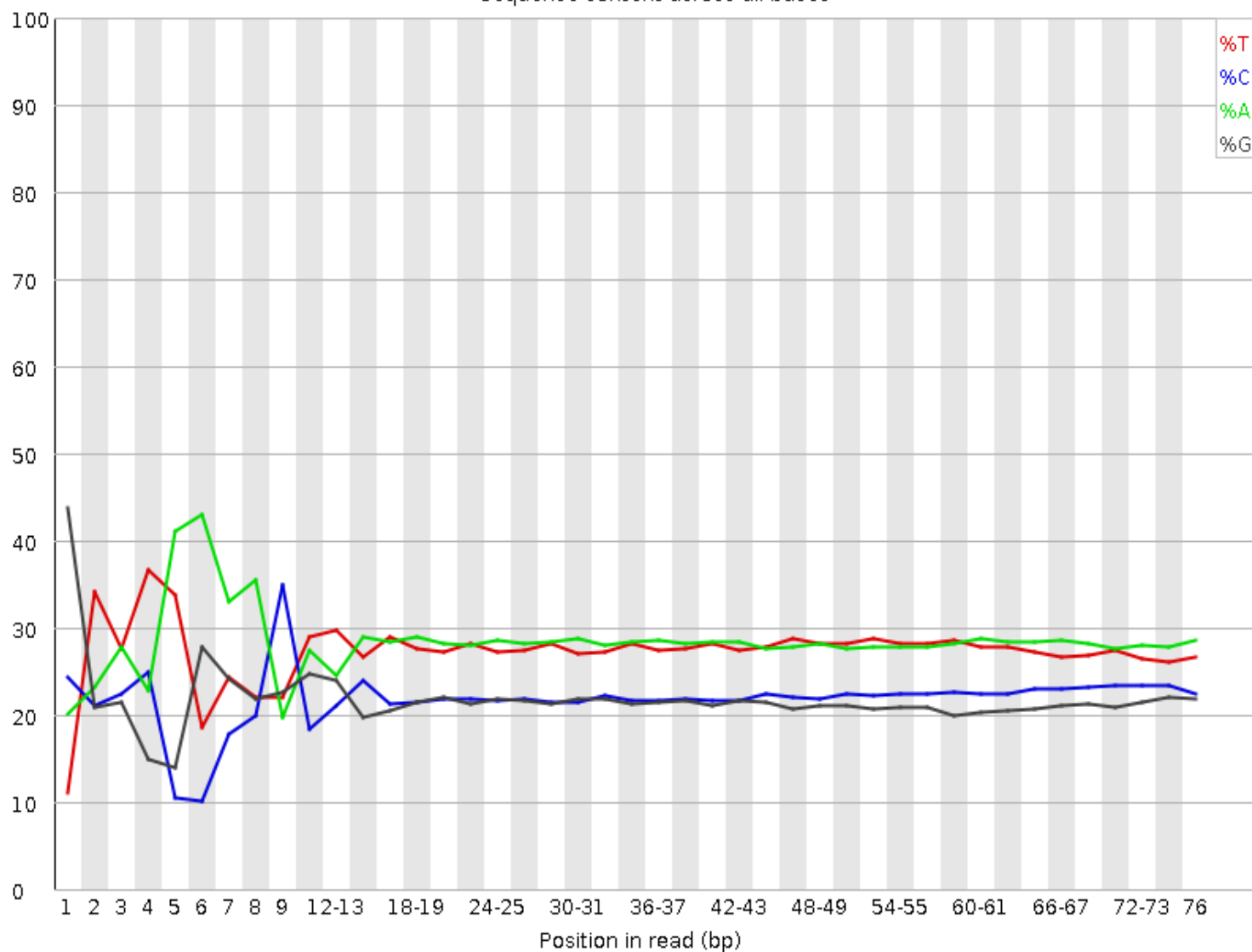
 **Per sequence quality scores**

Quality score distribution over all sequences



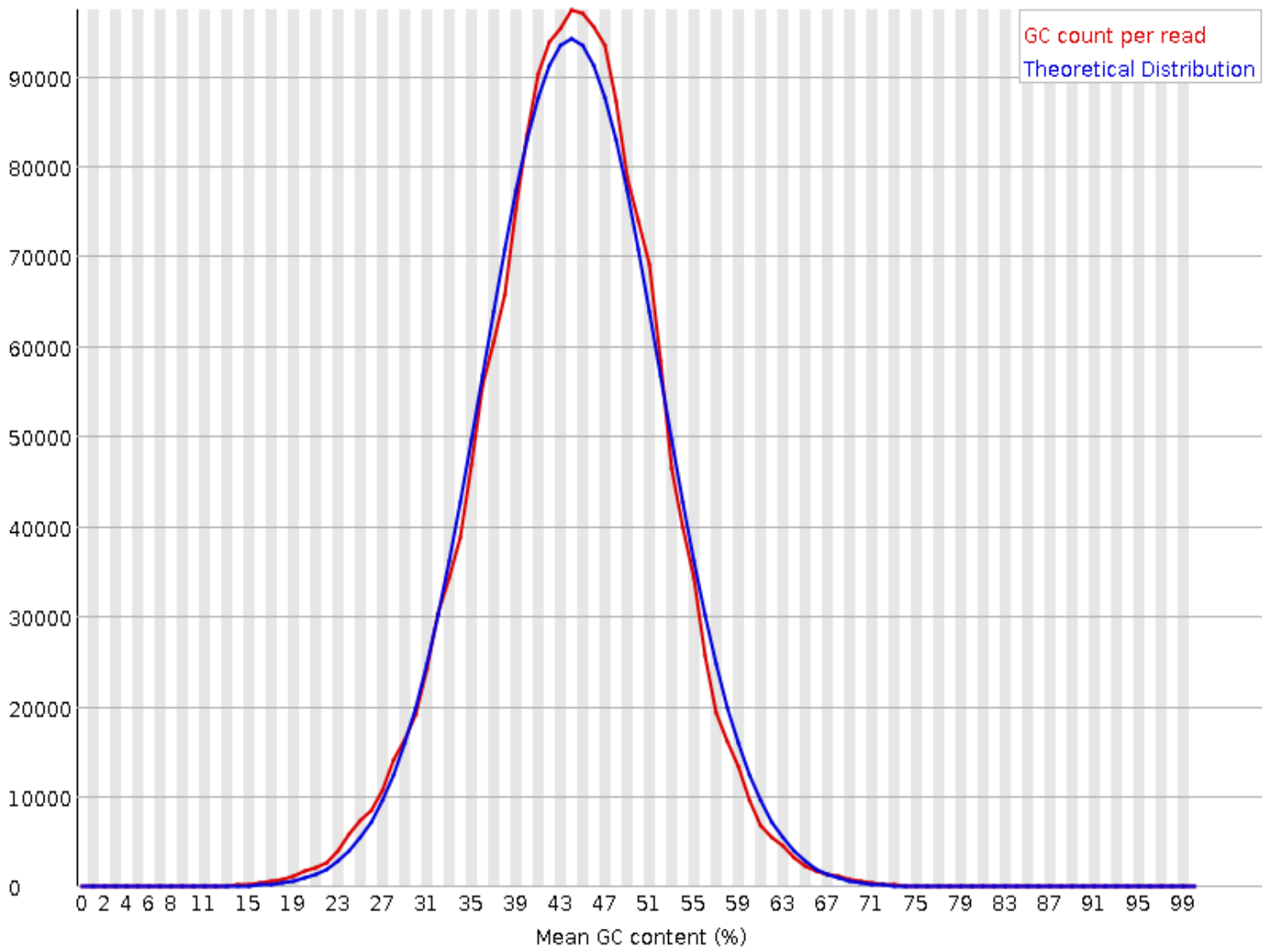
 **Per base sequence content**

Sequence content across all bases



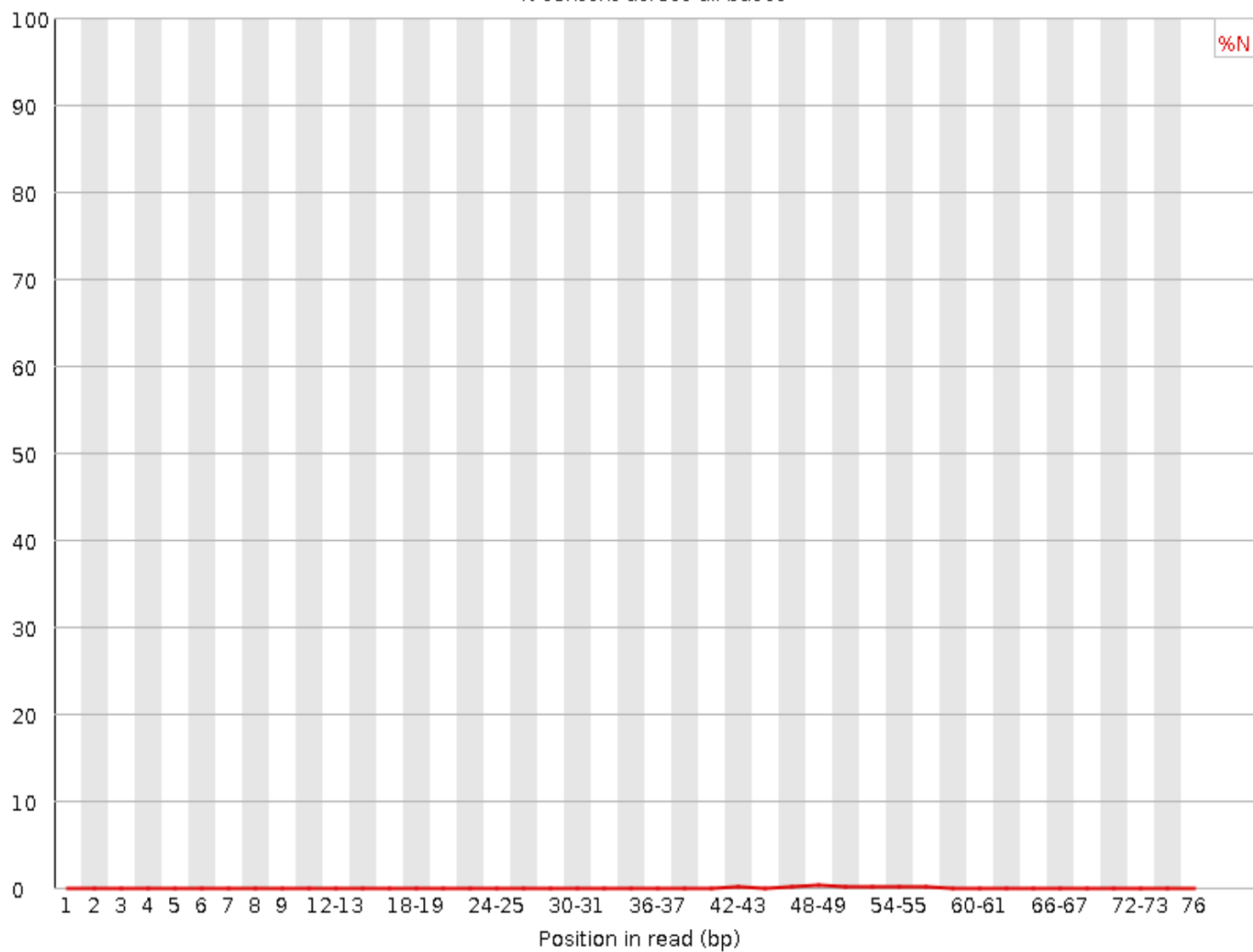
 **Per sequence GC content**

GC distribution over all sequences



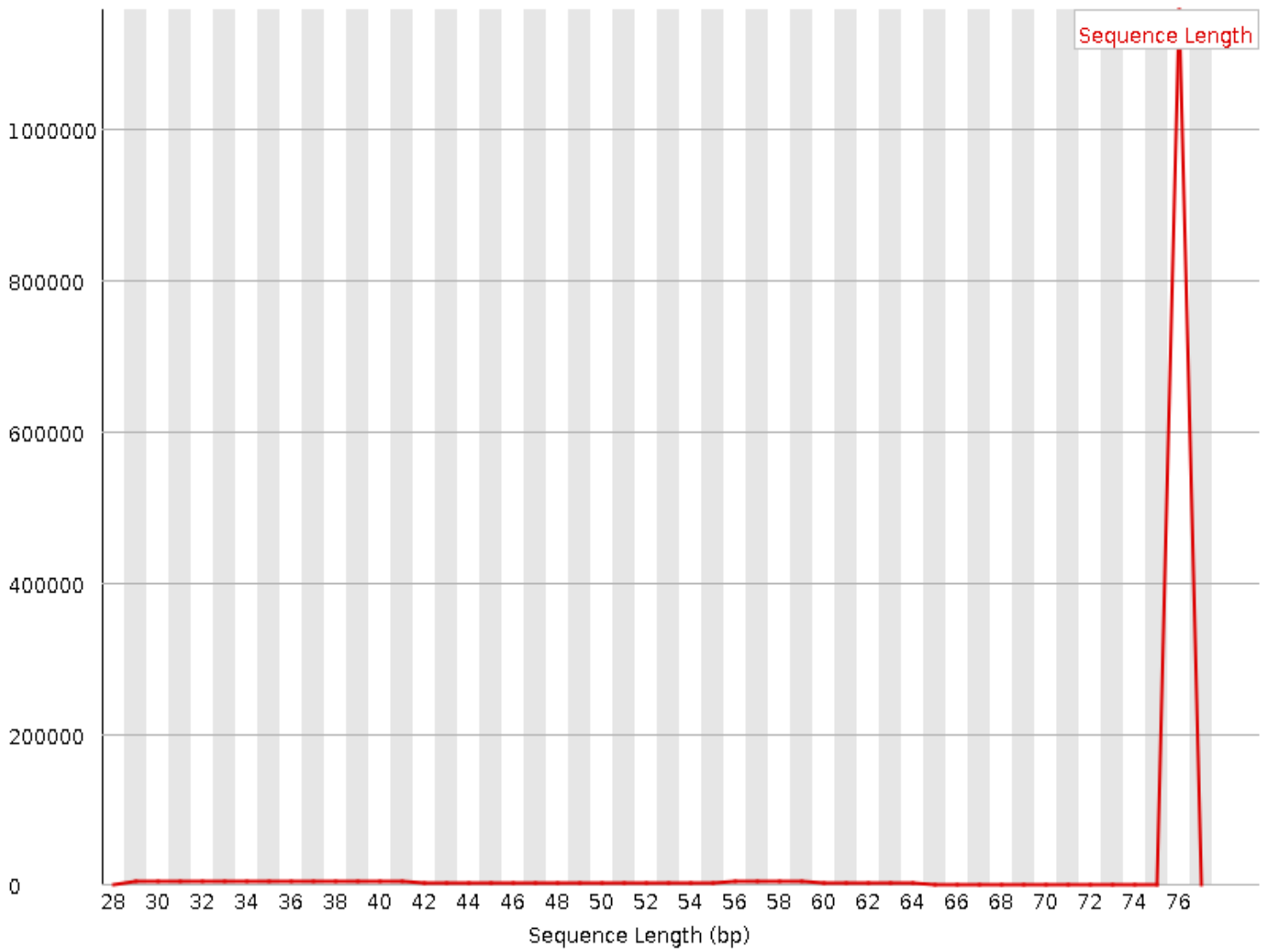
 **Per base N content**

N content across all bases



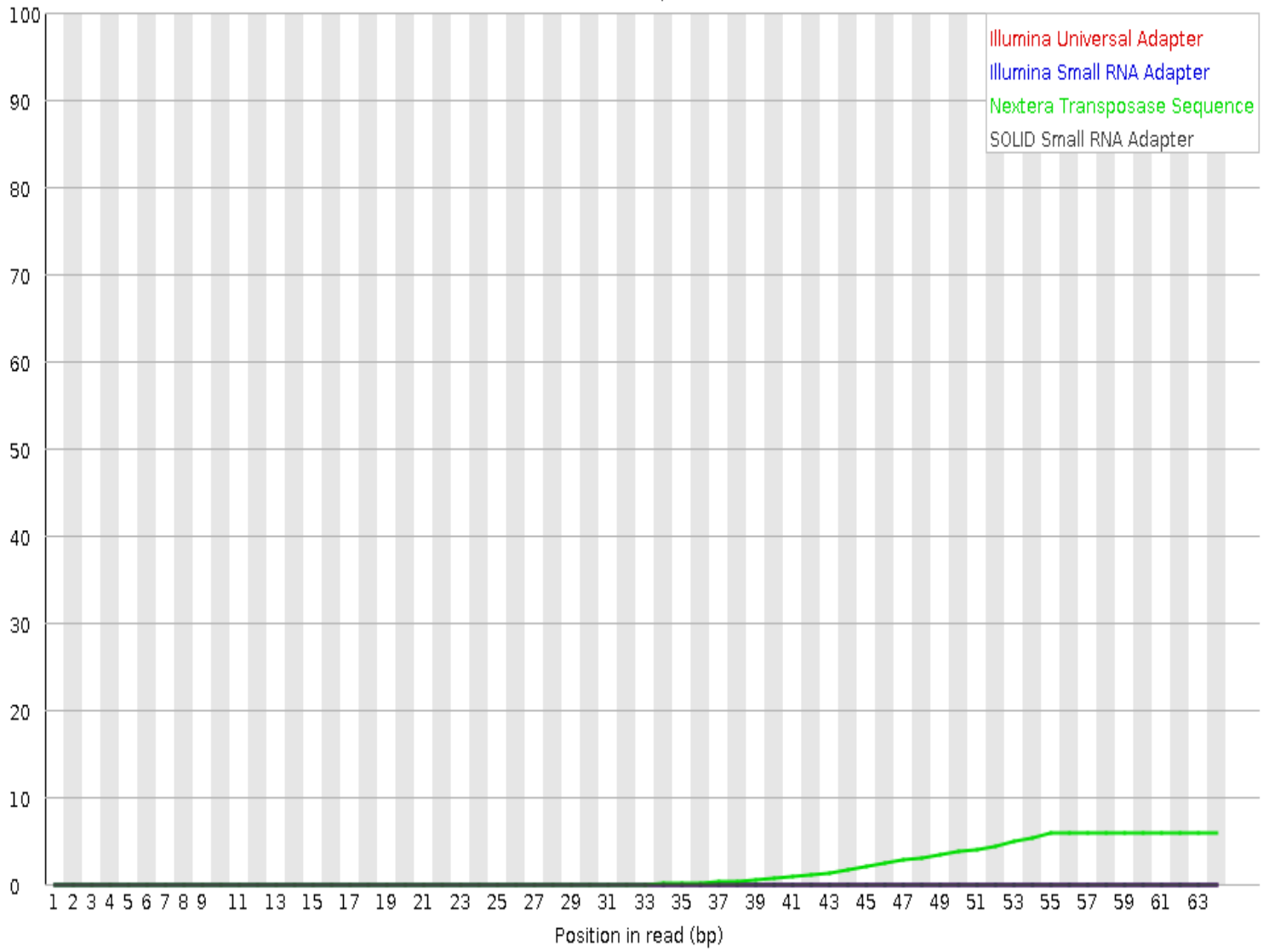
! Sequence Length Distribution

Distribution of sequence lengths over all sequences



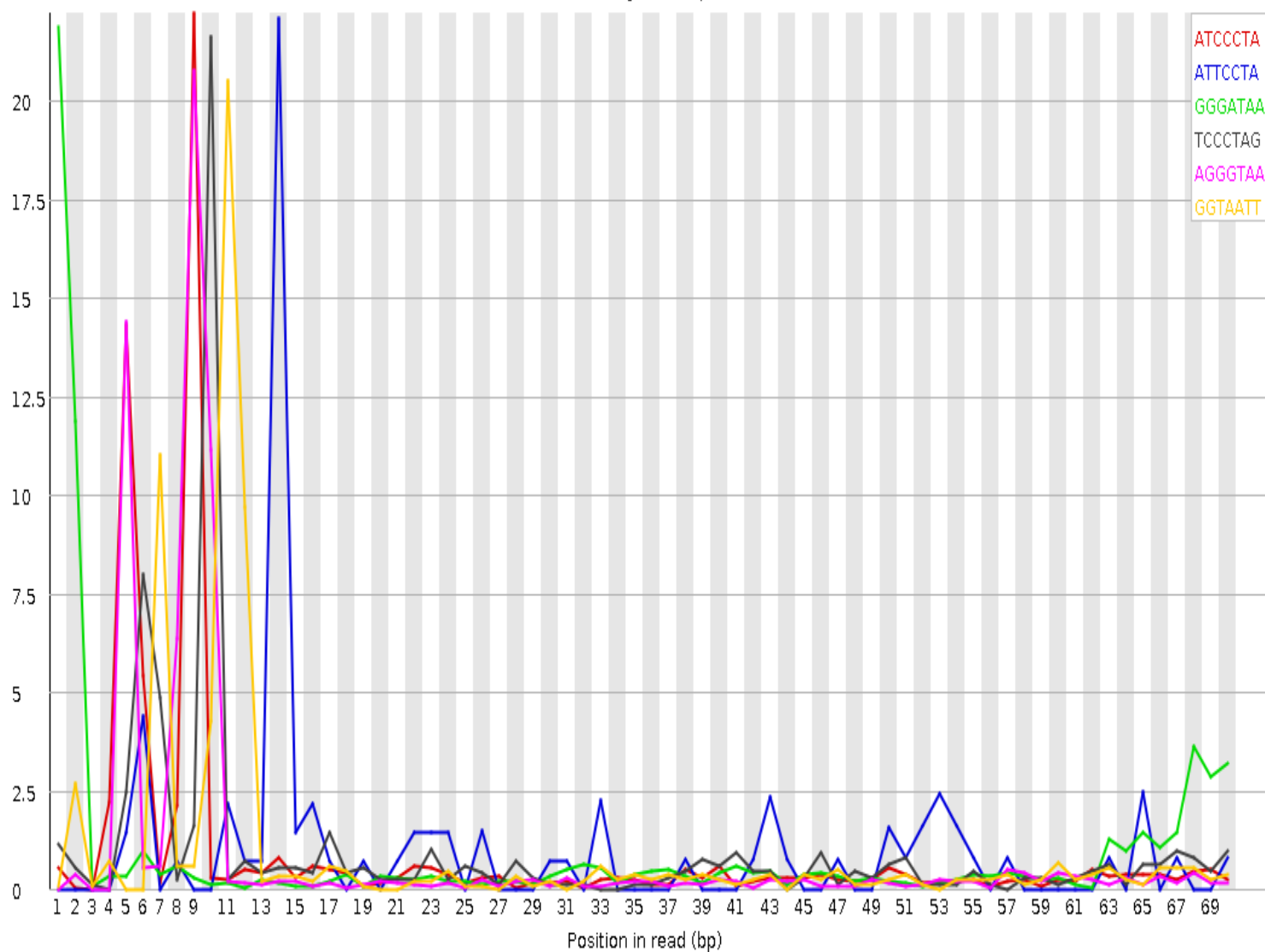
Sequence Duplication Levels

% Adapter



 **Kmer Content**

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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ATCCCTA	6405	0.0	22.20169	9
ATTCCTA	450	0.0	22.09566	14
GGGATAA	8695	0.0	21.888004	1
TCCCTAG	2240	0.0	21.604921	10
AGGGTAA	9160	0.0	20.771328	9
GGTAATT	2700	0.0	20.502207	11
GTTATTC	520	0.0	20.398325	11
ATAACAG	9495	0.0	20.386806	4
CCTGTTA	7100	0.0	20.261856	3
CAGGGTA	9475	0.0	20.220713	8
TCCCTAA	2055	0.0	19.83998	10
CCCTGTT	7385	0.0	19.749224	2
GGATAAC	9840	0.0	19.672775	2

GATAACA	9880	0.0	19.52603	3
ACAGGGT	9975	0.0	19.406527	7
CTGTTAT	7415	0.0	19.355663	4
TATCCCT	7405	0.0	19.337778	8
ACCCTGT	7605	0.0	19.139435	1
GGGTAAT	9200	0.0	19.023655	10
CGACCGT	115	8.323114E-4	18.789106	45

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