













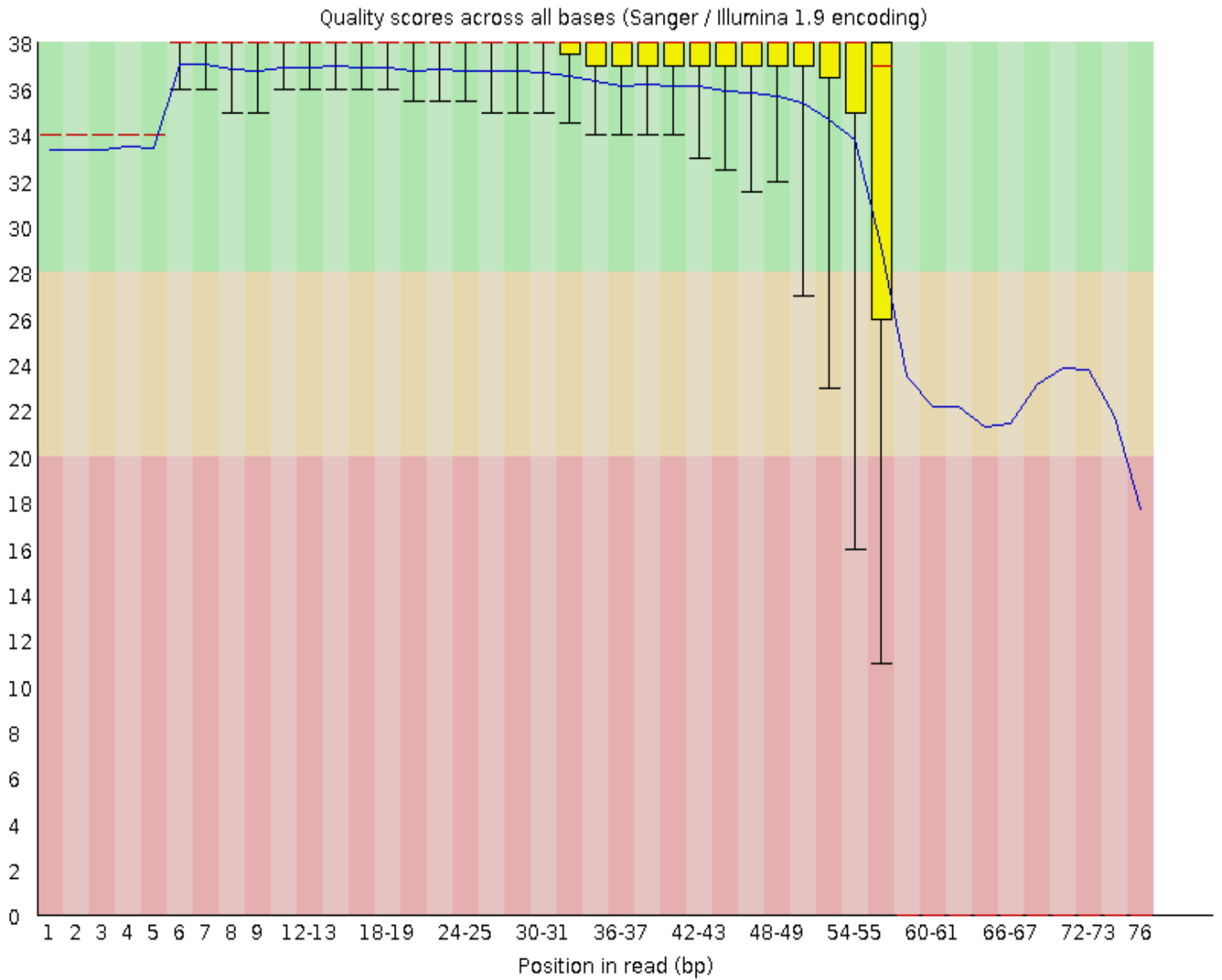
Summary

-  [Basic Statistics](#)
-  [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](#)
-  [Adapter Content](#)
-  [Kmer Content](#)

Basic Statistics

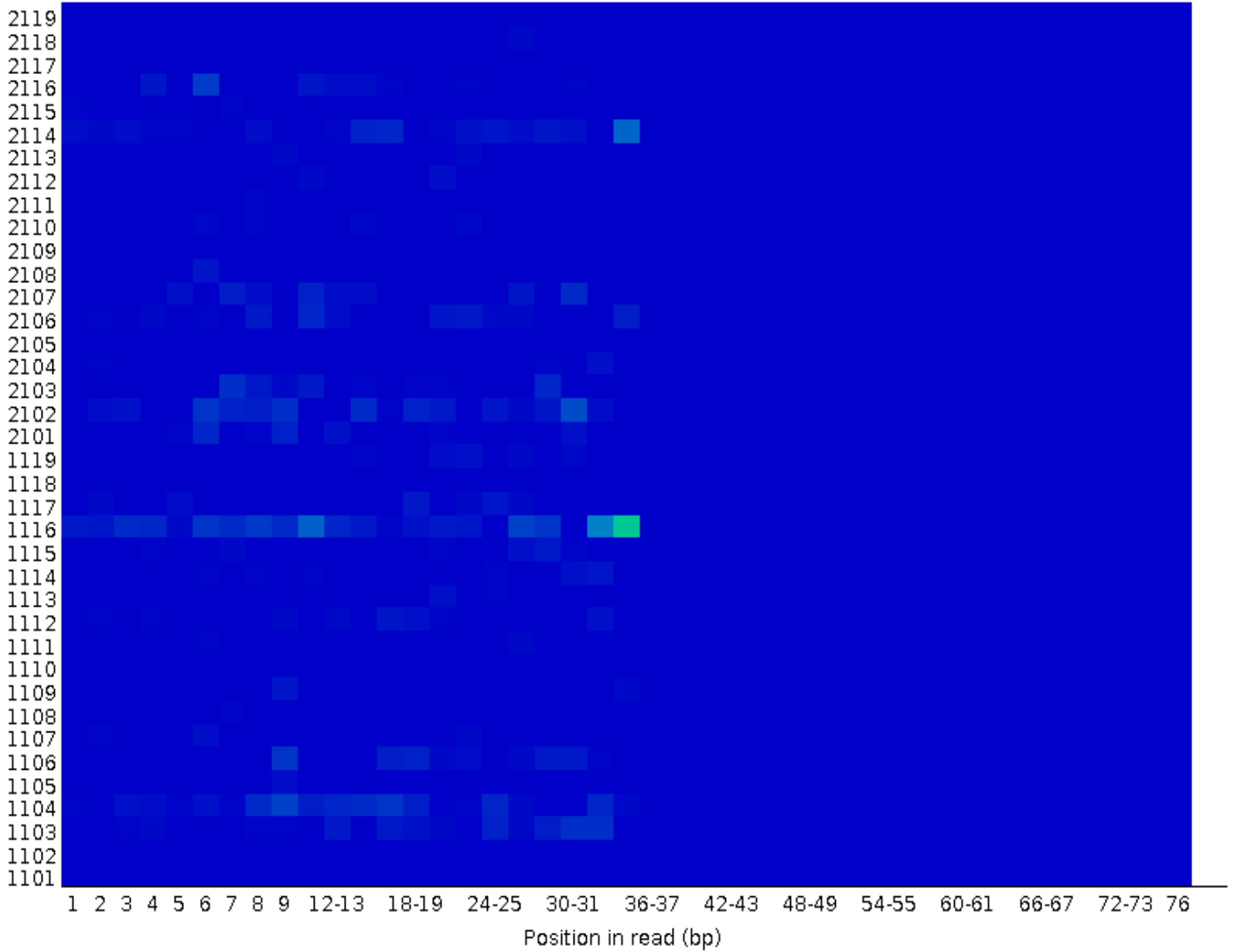
Measure	Value
Filename	skewer_SW041-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2507
Sequences flagged as poor quality	0
Sequence length	28-76
%GC	43

Per base sequence quality



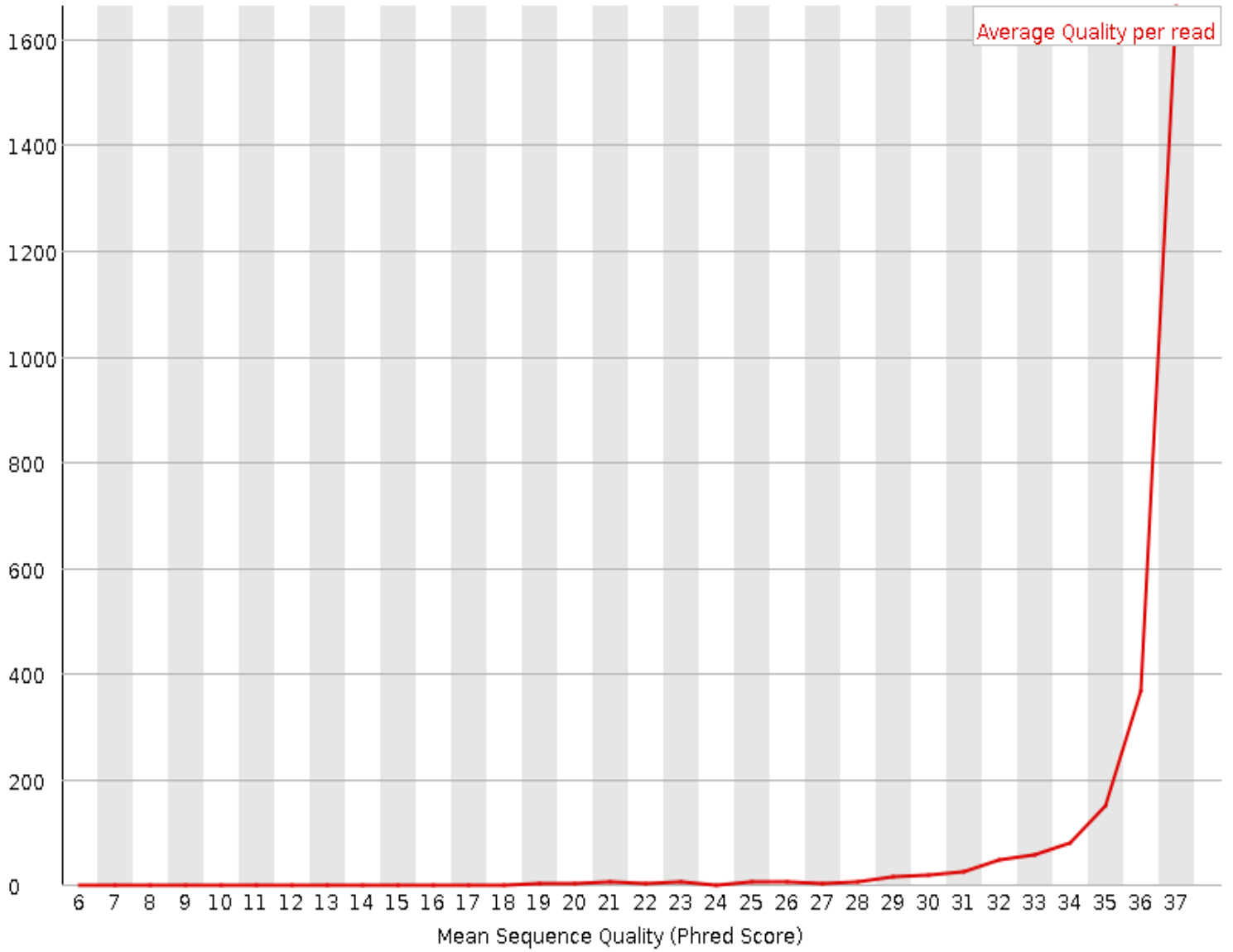
✔ **Per tile sequence quality**

Quality per tile



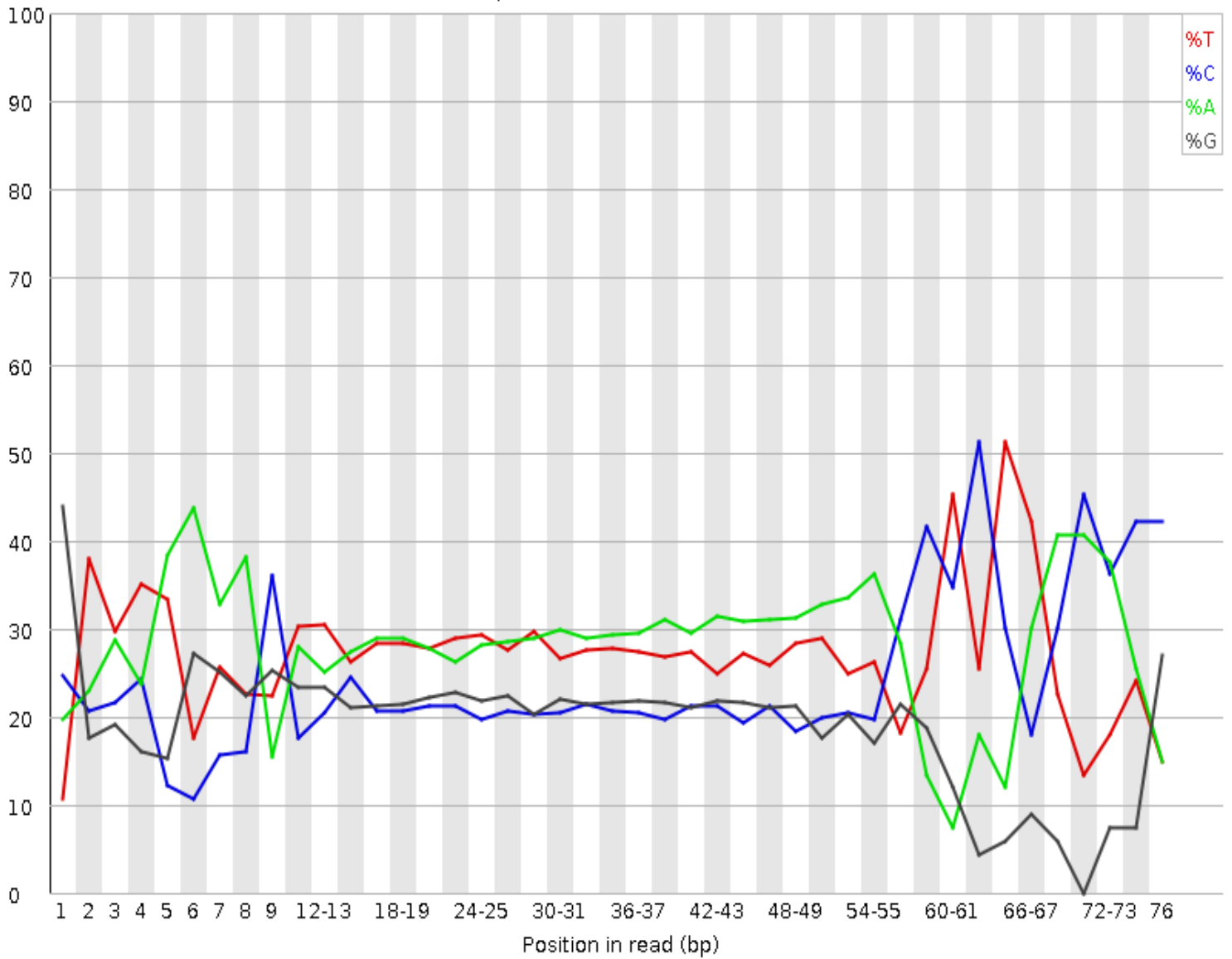
 **Per sequence quality scores**

Quality score distribution over all sequences



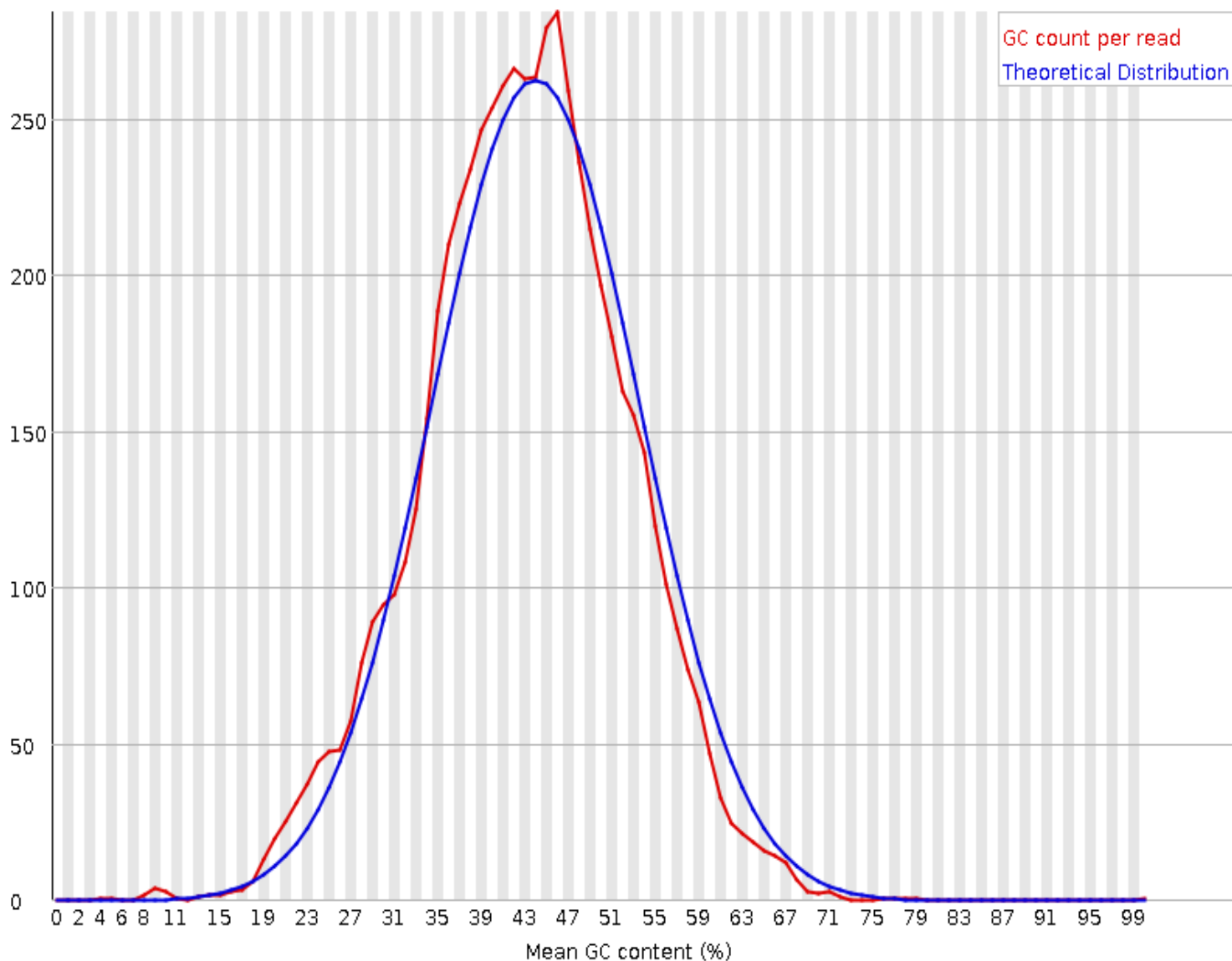
 **Per base sequence content**

Sequence content across all bases



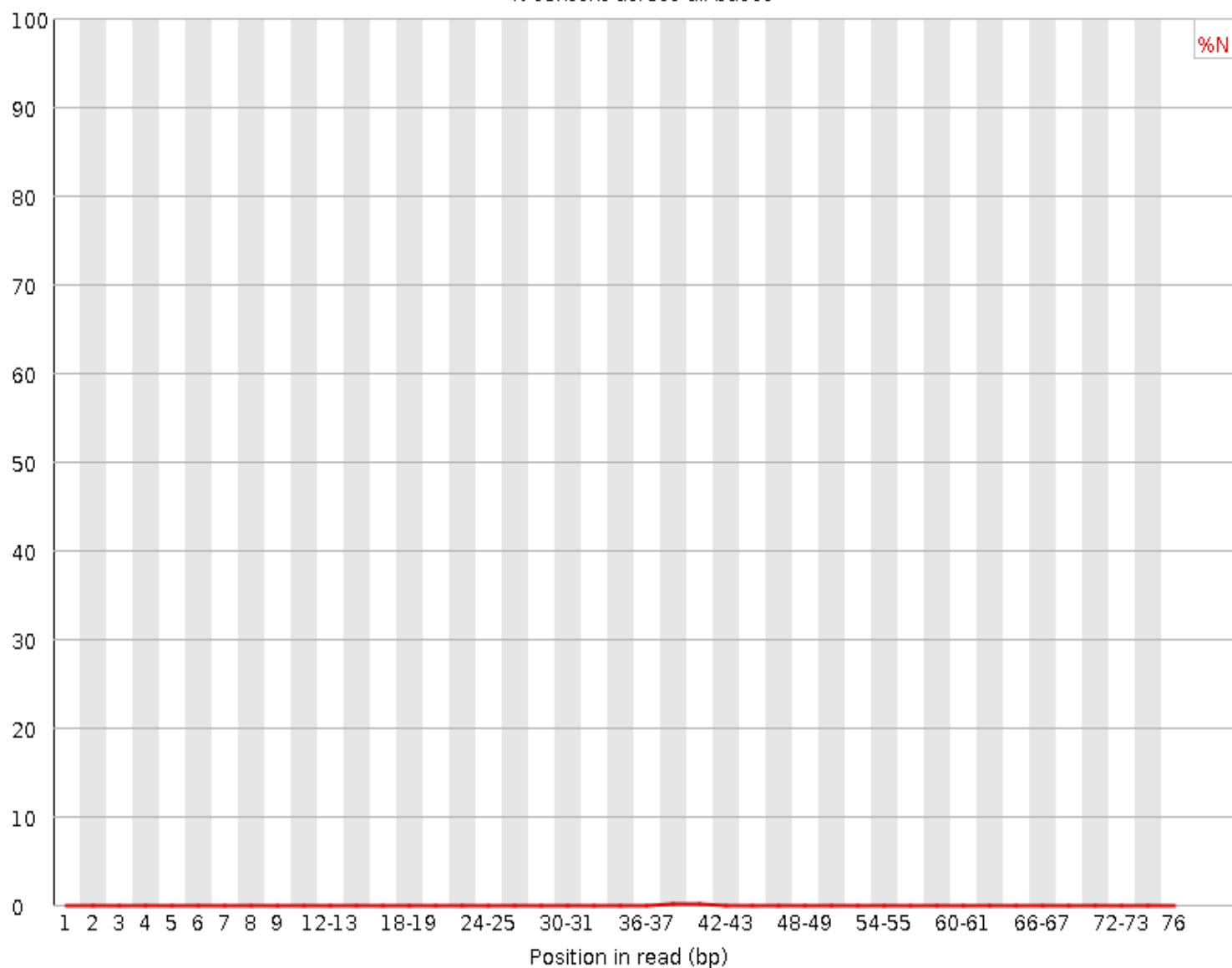
 **Per sequence GC content**

GC distribution over all sequences



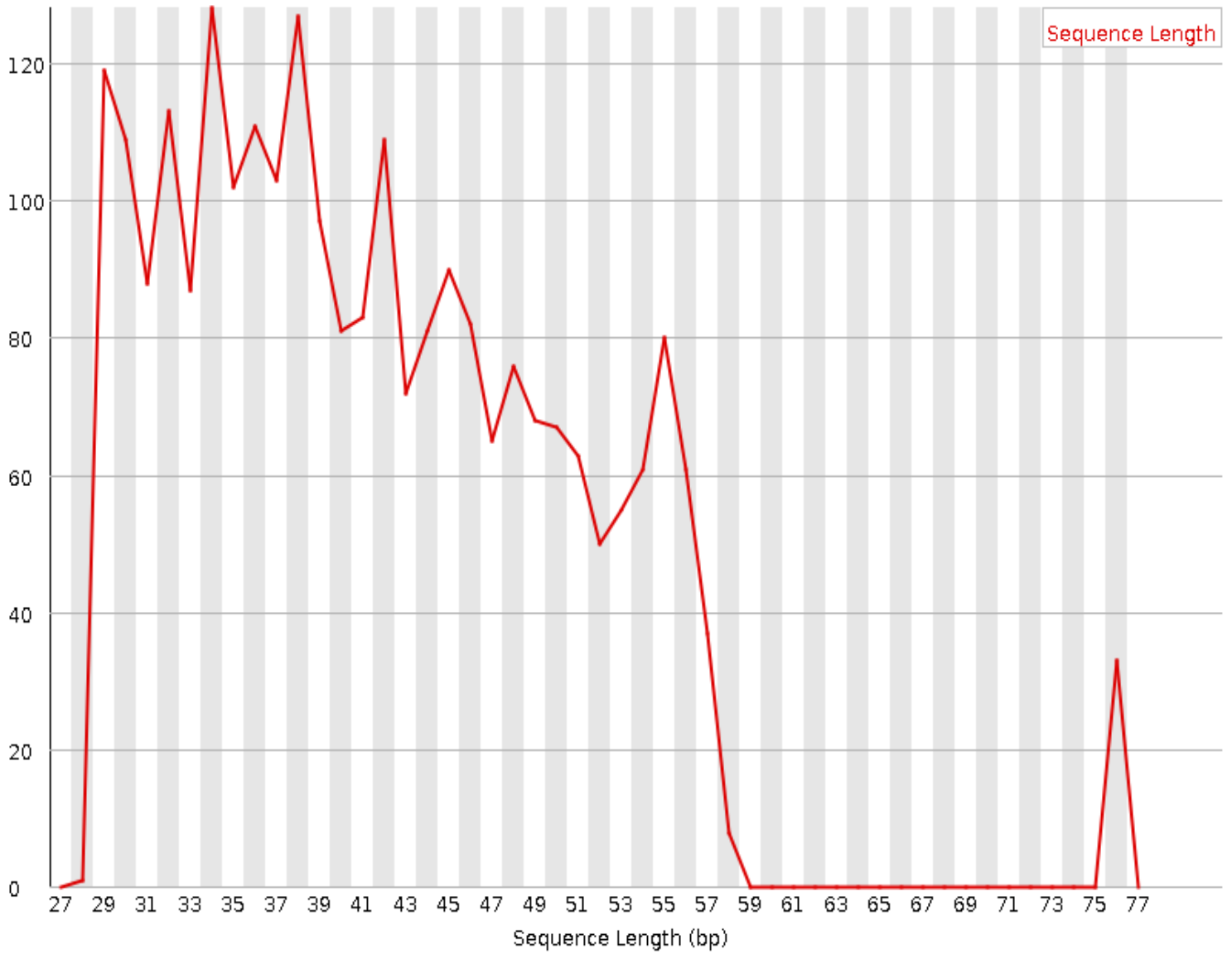
 **Per base N content**

N content across all bases



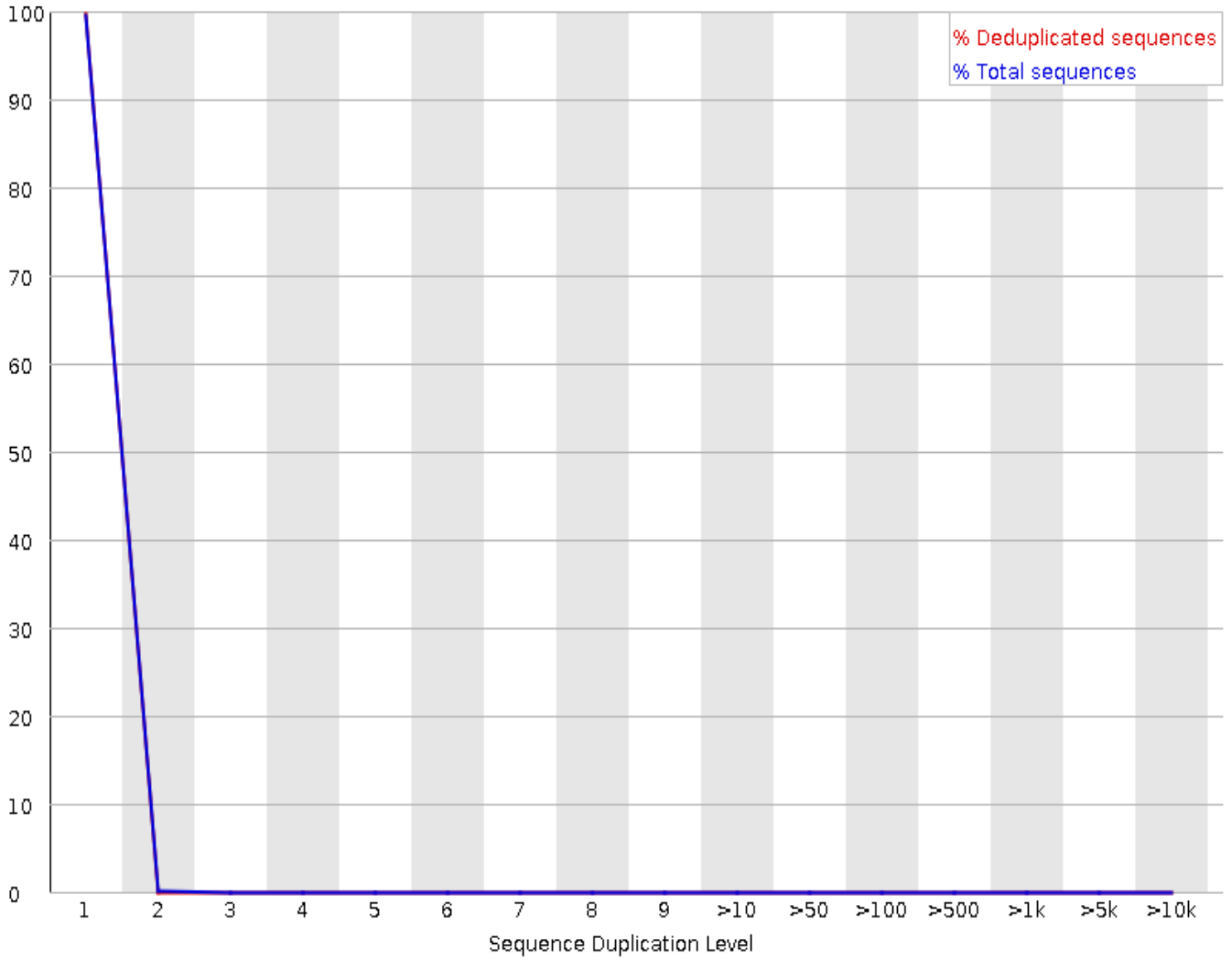
! Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99.84%

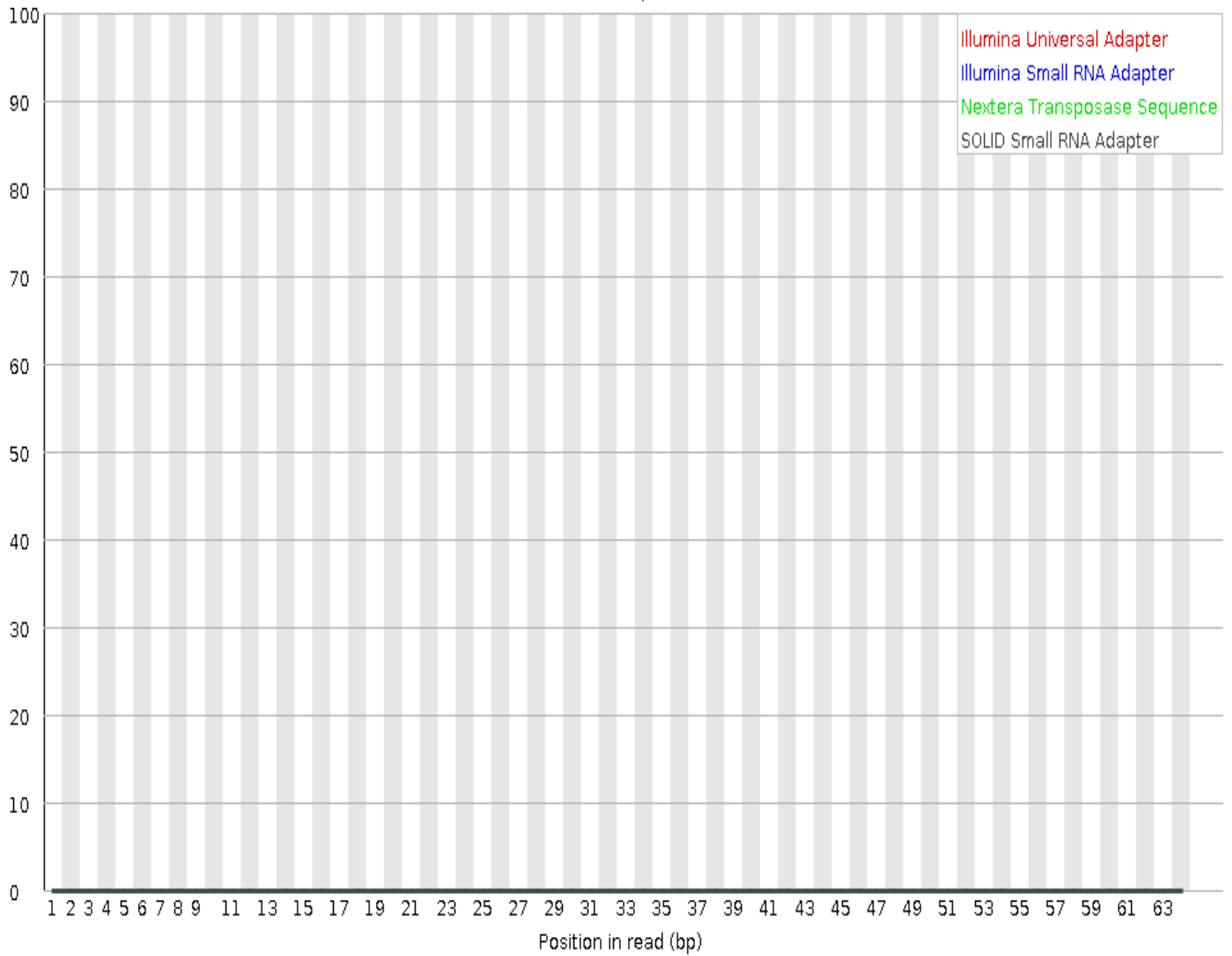


 **Overrepresented sequences**

No overrepresented sequences

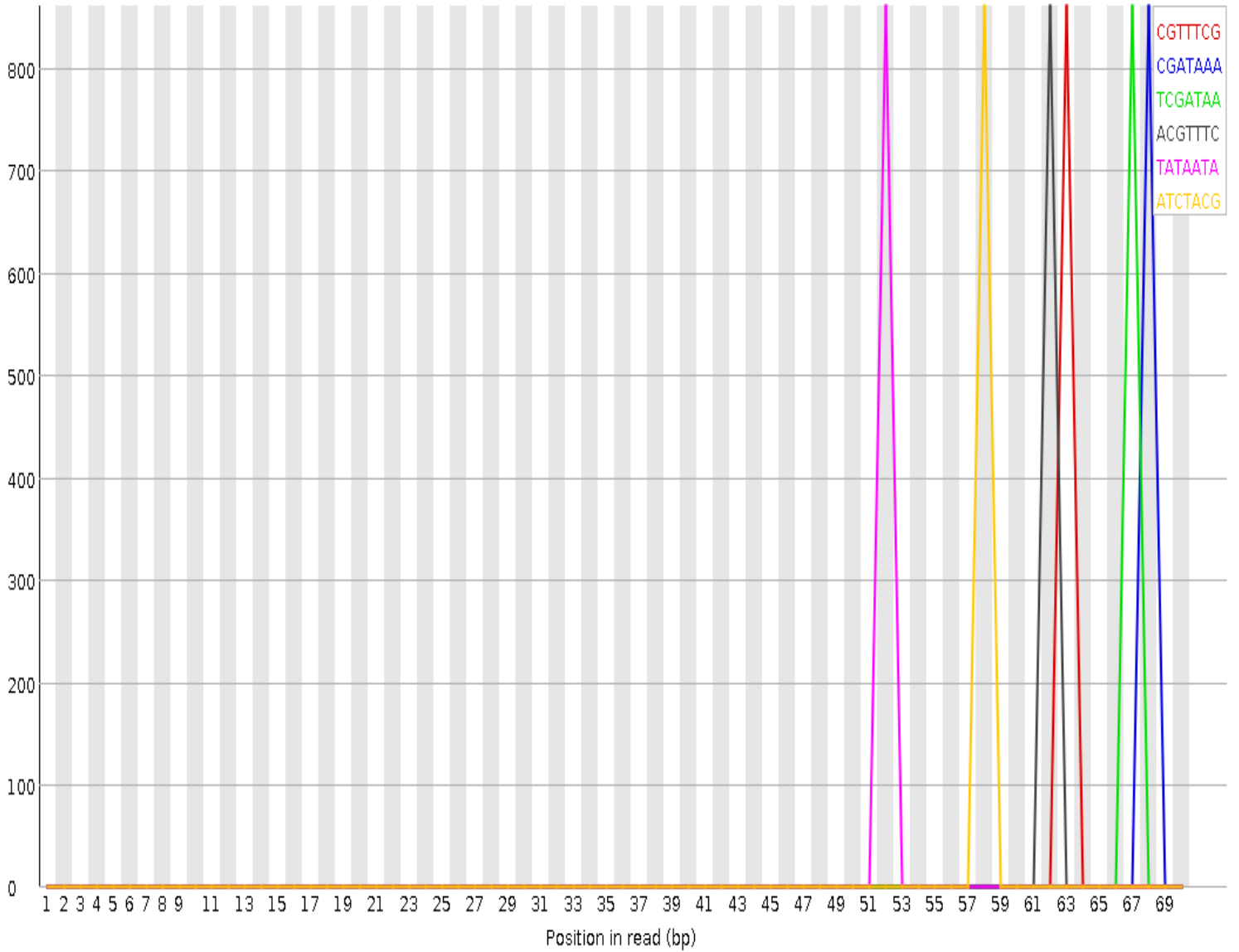
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGTTTCG	5	0.0055316943	860.5	63
CGATAAA	5	0.0055316943	860.5	68
TCGATAA	5	0.0055316943	860.5	67
ACGTTTC	5	0.0055316943	860.5	62
TATAATA	5	0.0055316943	860.5	52
ATCTACG	5	0.0055316943	860.5	58
TTCGATA	5	0.0055316943	860.5	66
GATAAAT	5	0.0055316943	860.5	69
GTTTCGA	5	0.0055316943	860.5	64
CCCACCT	5	0.0055316943	860.5	62
TCTACGT	5	0.0055316943	860.5	59

TTATAAT	5	0.0055316943	860.5	51
ATAATAT	5	0.0055316943	860.5	53
CCACCTC	5	0.0055316943	860.5	63
TACGTTT	5	0.0055316943	860.5	61
ATAAATT	5	0.0055316943	860.5	70
CACCTCA	5	0.0055316943	860.5	64
TATCTAC	5	0.0055316943	860.5	57
CACCAAC	5	0.0055316943	860.5	69
TAATATC	5	0.0055316943	860.5	54

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