












## Summary

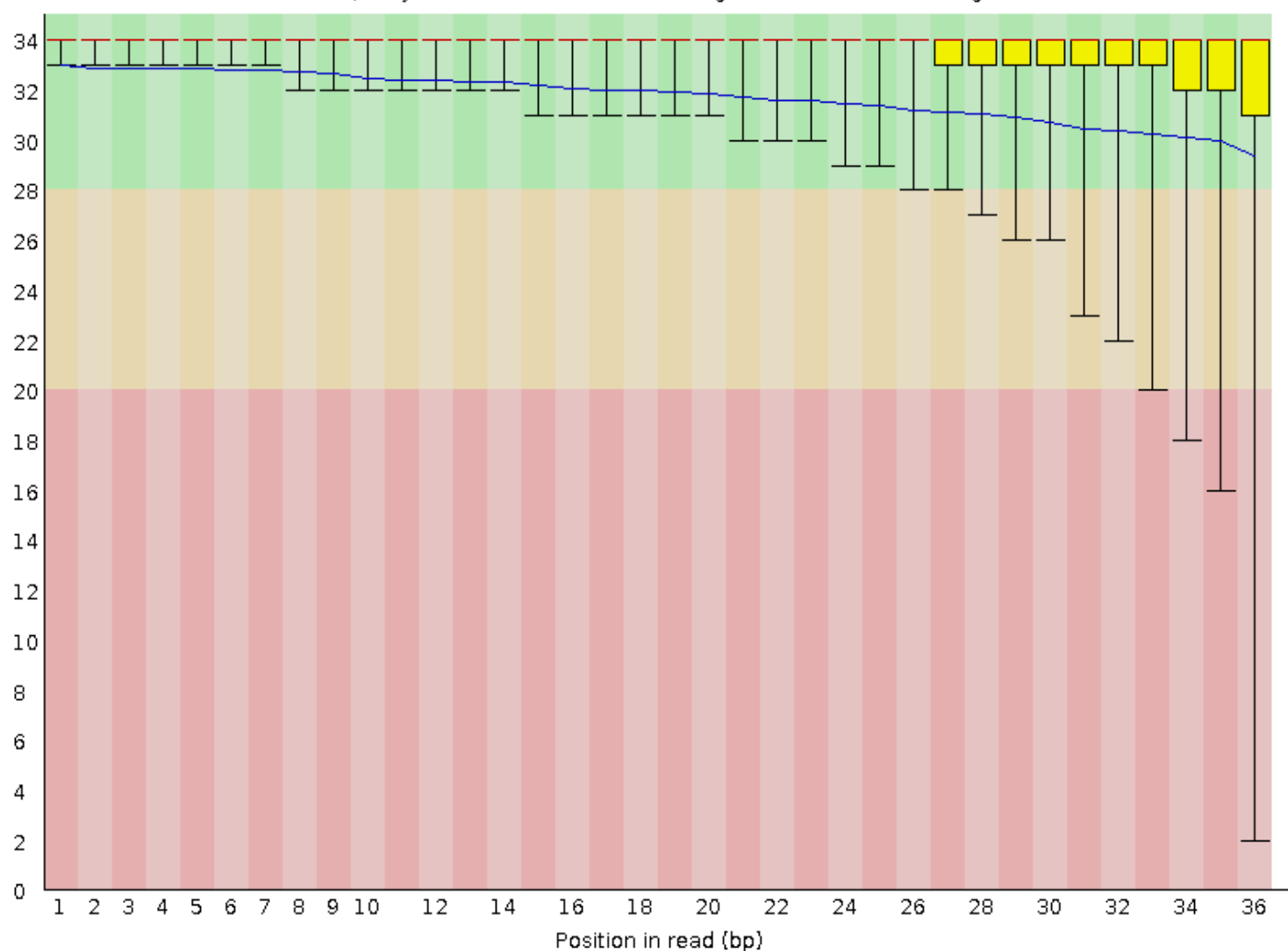
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per tile sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented sequences](#)
-  [Adapter Content](#)

## Basic Statistics

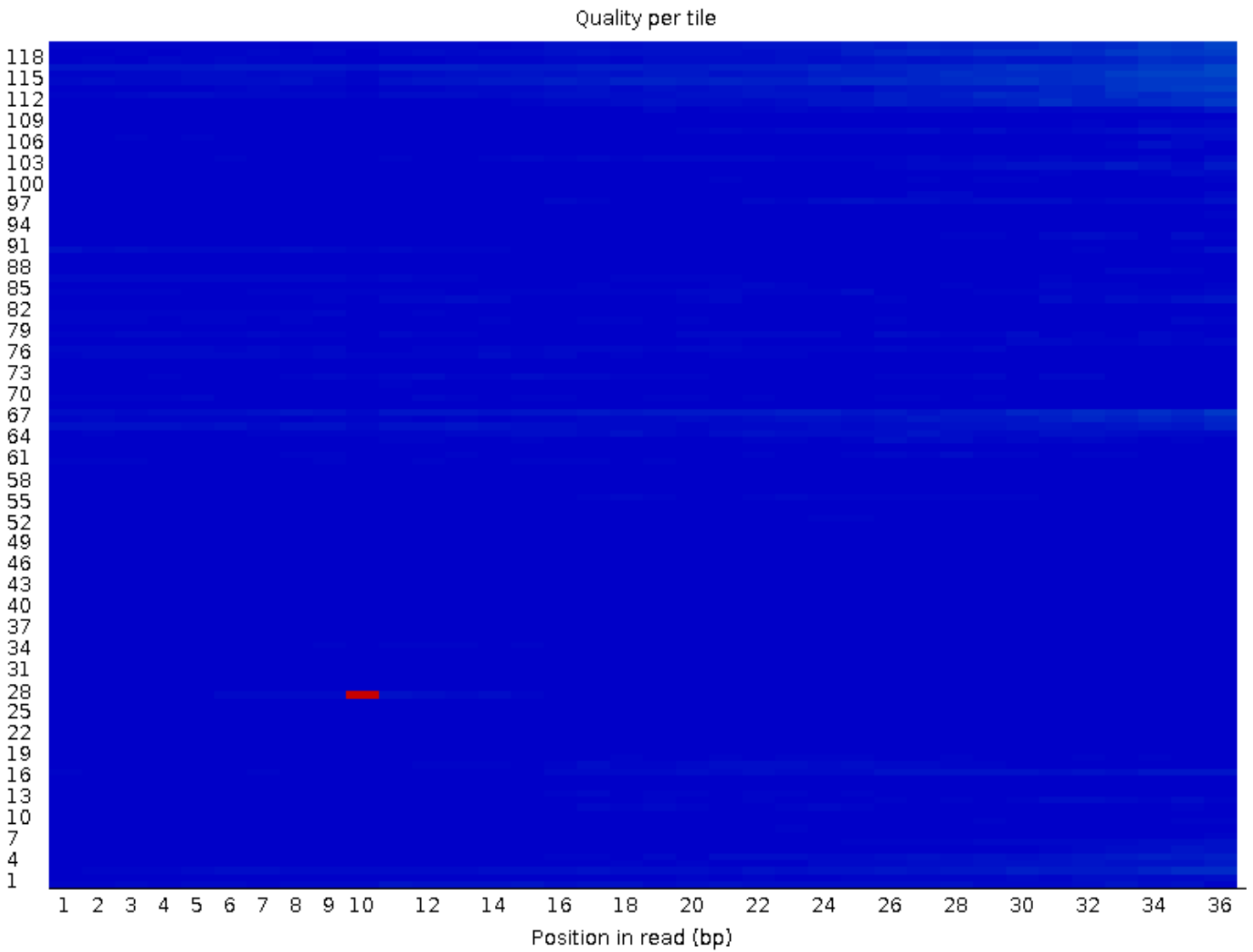
Measure	Value
Filename	ERR032071_2_REP1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	39

## Per base sequence quality

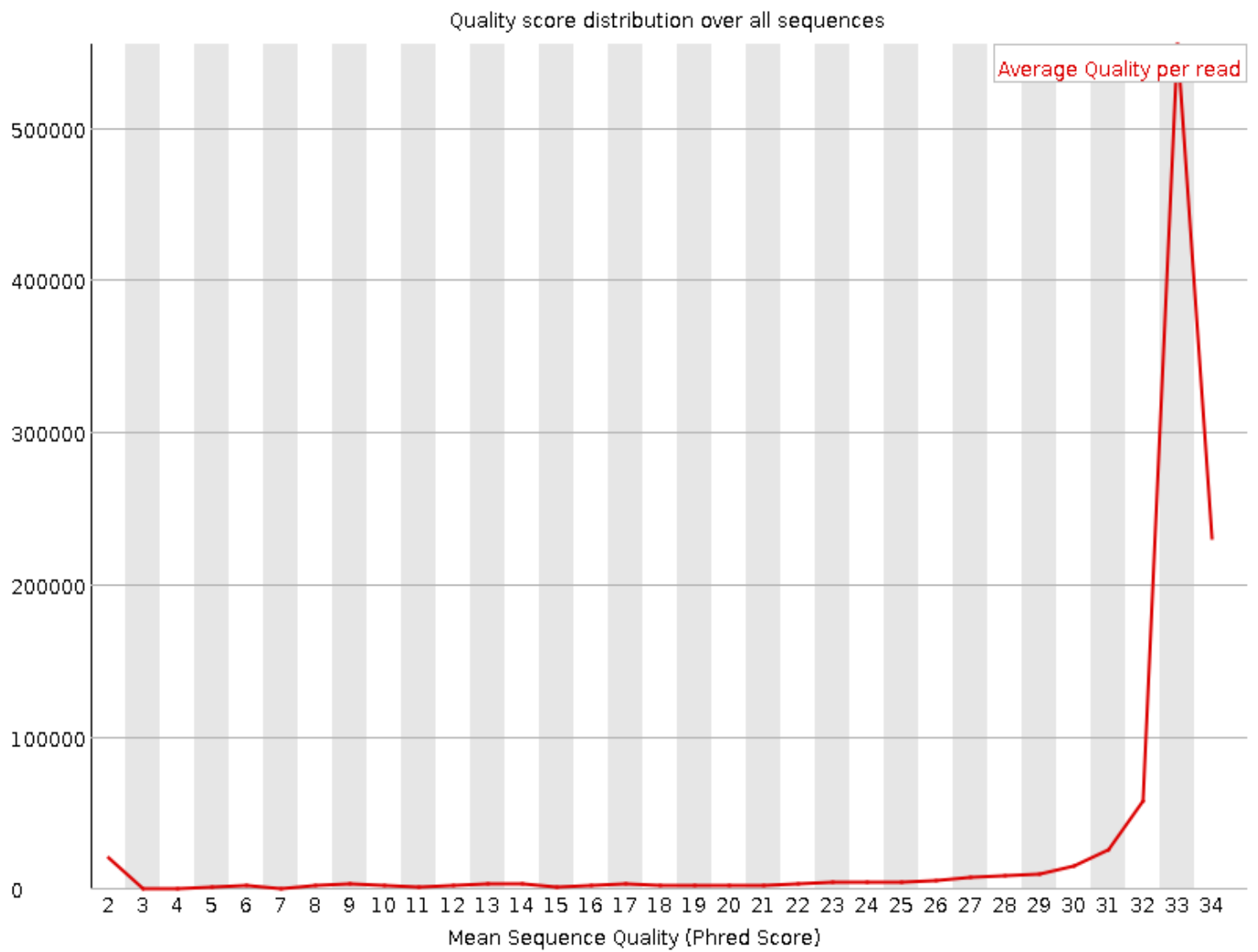
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



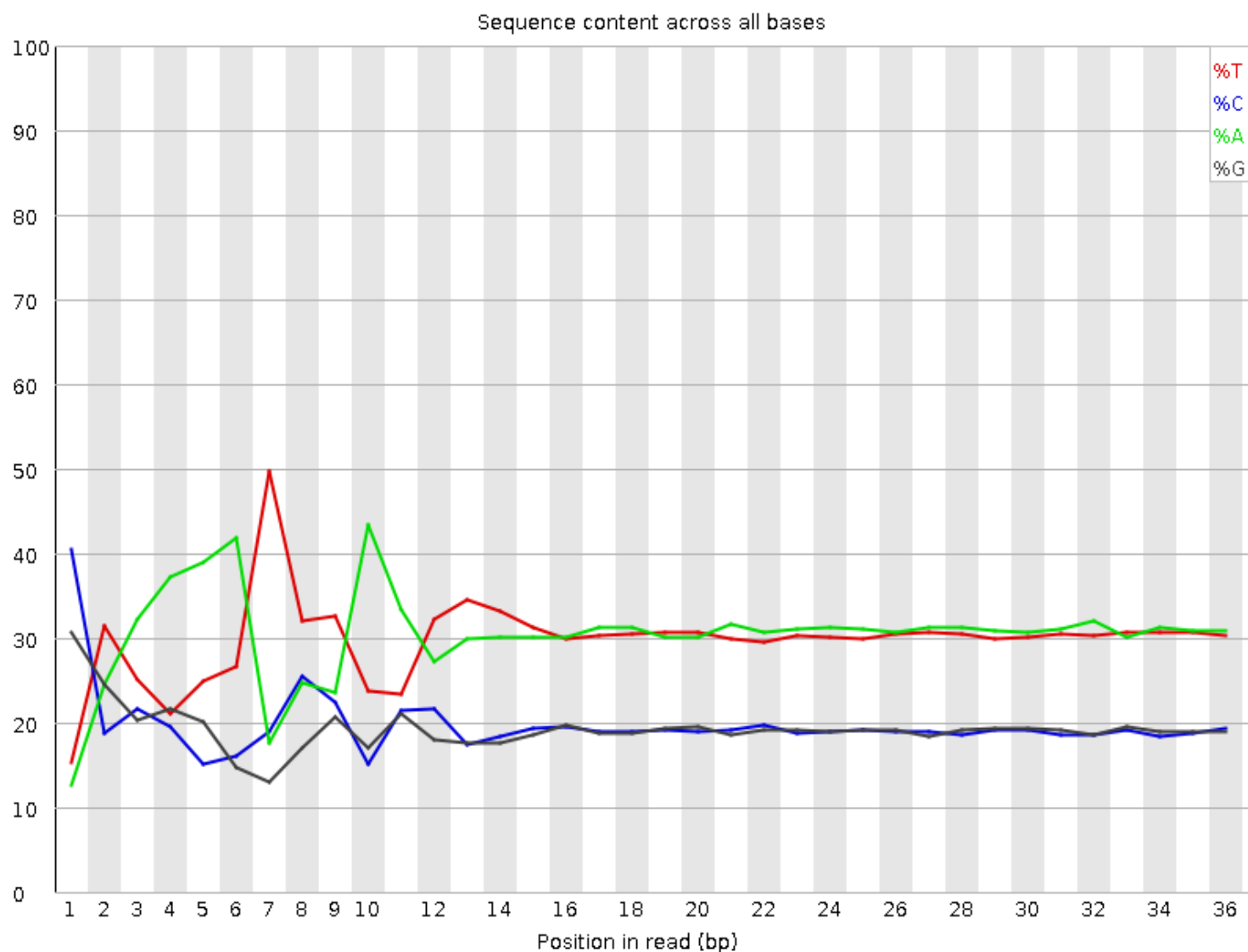
**Per tile sequence quality**



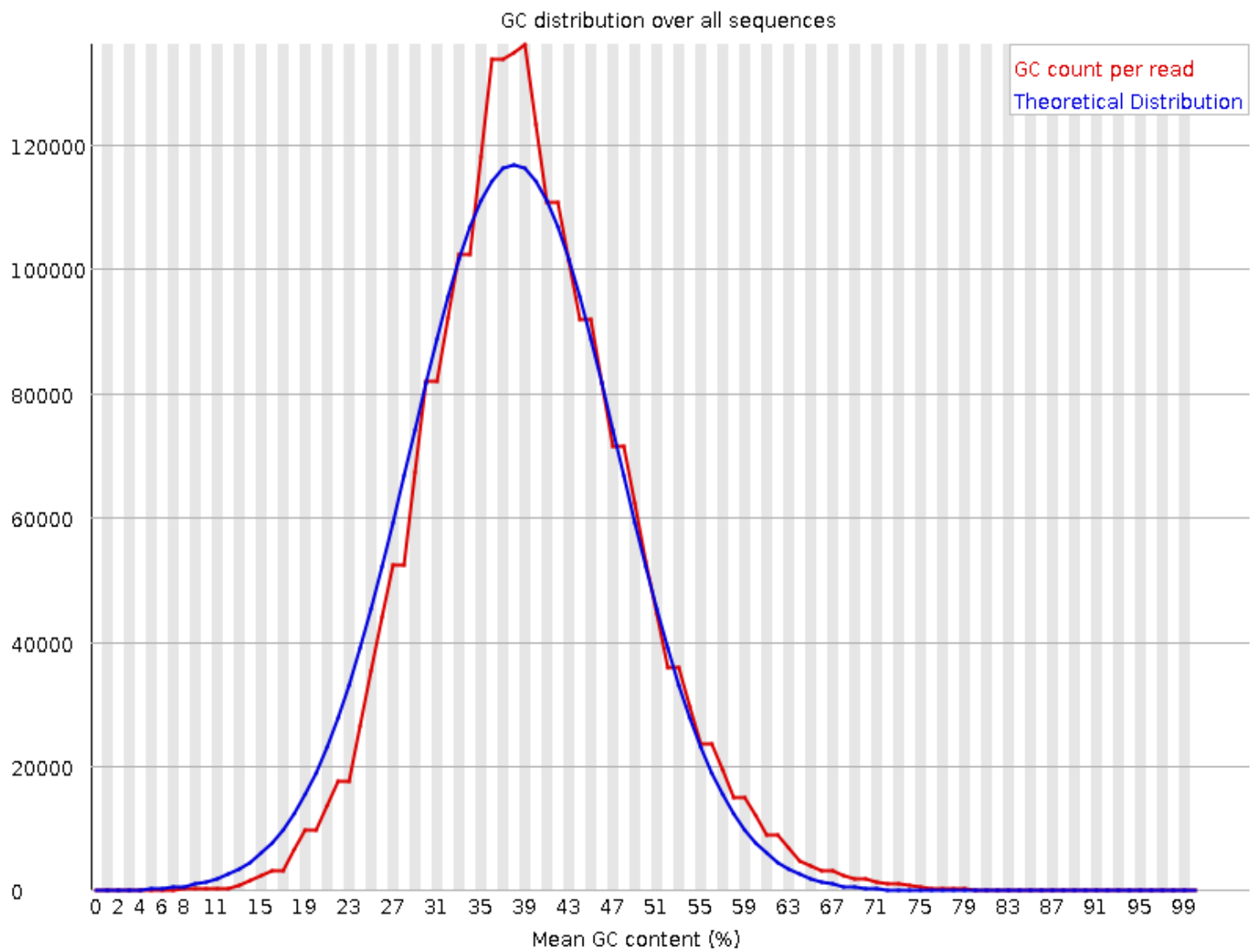
**Per sequence quality scores**



✖ Per base sequence content

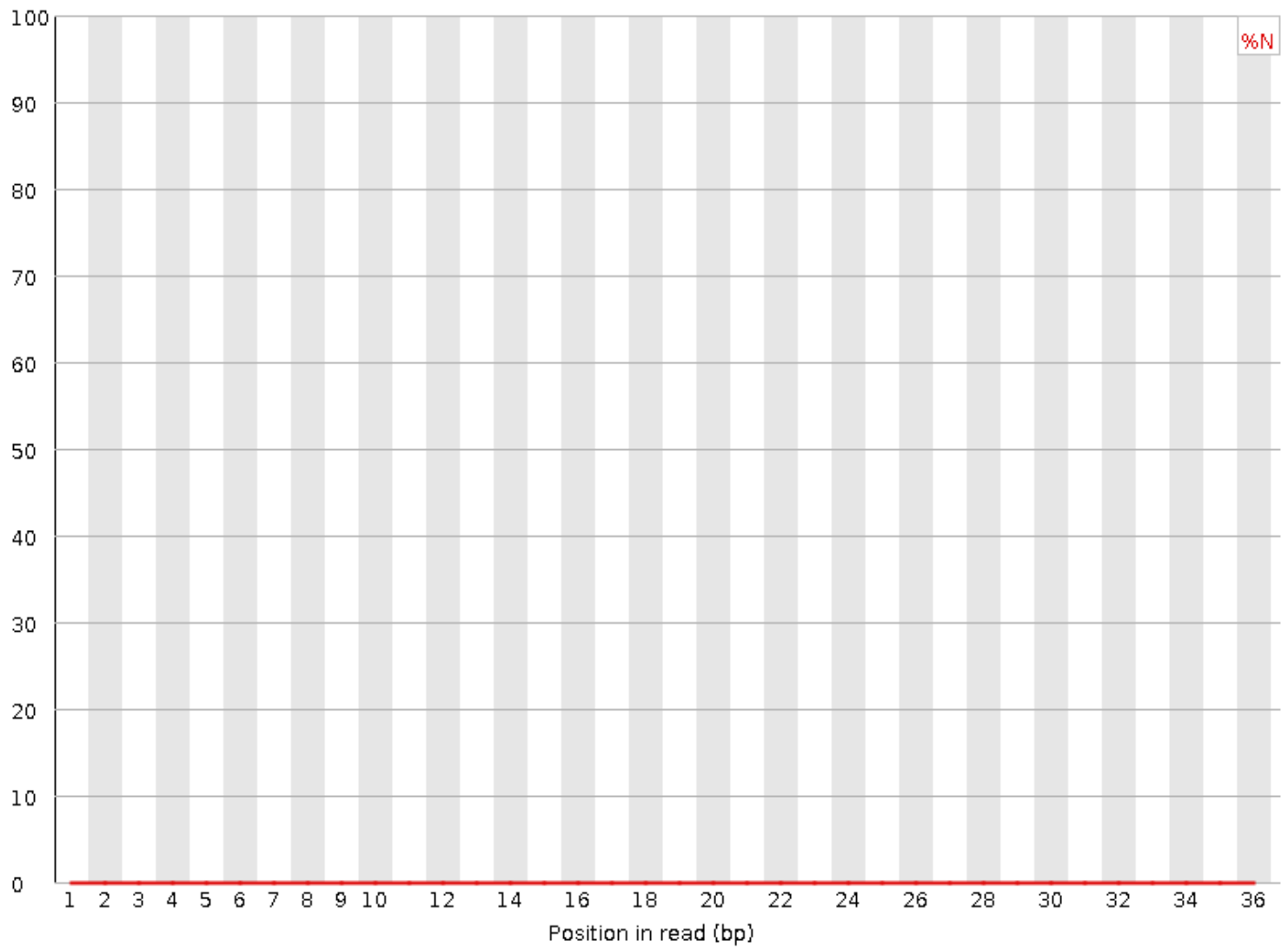


**Per sequence GC content**

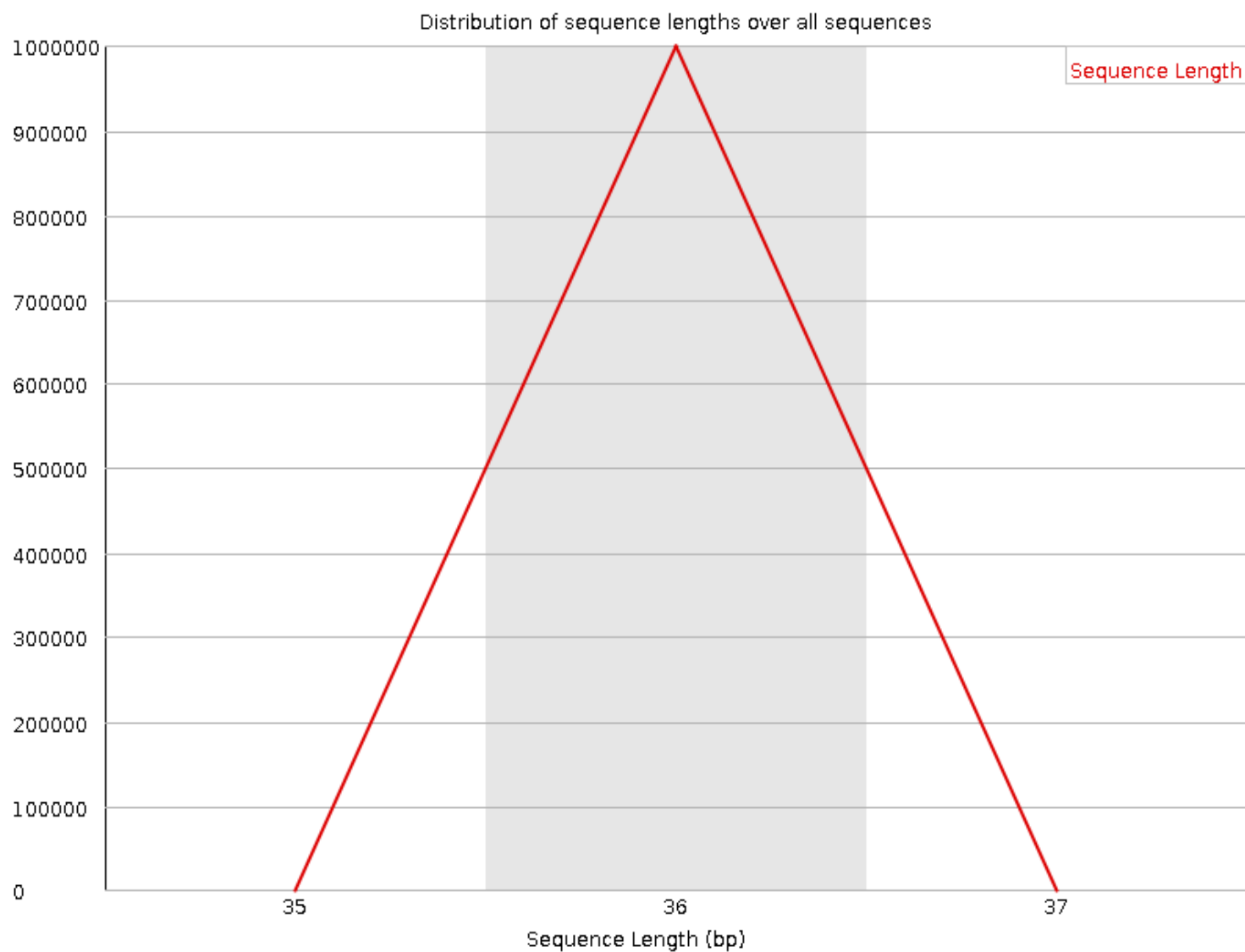


**Per base N content**

N content across all bases

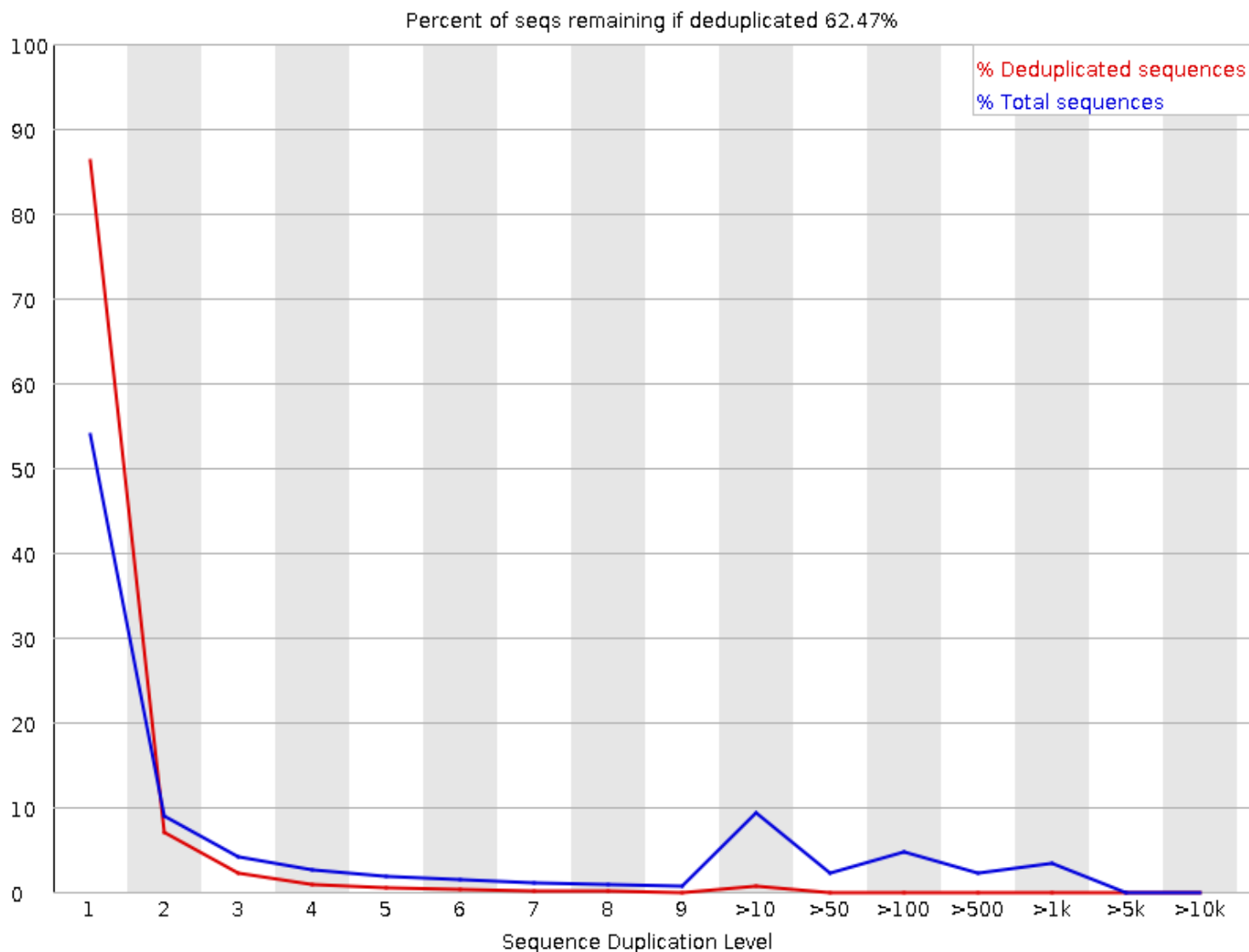


## Sequence Length Distribution



## ! Sequence Duplication Levels





## ! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	3212	0.3212	No Hit
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3088	0.3088	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	2991	0.29910000000000003	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2771	0.2771	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2447	0.2447	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1833	0.1833	No Hit
CTTGGAGGACATATCGAAGATTTTGTCTTCTACCTC	1756	0.1756	No Hit
GGAGGACATATCGAAGATTTTGTCTTCTACCTCGAT	1671	0.1671	No Hit
CGAAGATTTTGTCTTCTACCTCGATGTTGAATTGTA	1670	0.167	No Hit

Sequence	Count	Percentage	Possible Source
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1634	0.1634	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	1632	0.1632	No Hit
CTAAAGTAAGAAACACCACTAAGTTAAAACTCTCT	1609	0.1609	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1483	0.1483	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAAATCTTC	1372	0.1372	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1230	0.123	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1225	0.1225	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1201	0.1201	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1081	0.10809999999999999	No Hit
GACATATCGAAGATTTTGTCTTCTACCTCGATGTTG	1014	0.10139999999999999	No Hit



## Adapter Content

