












Summary

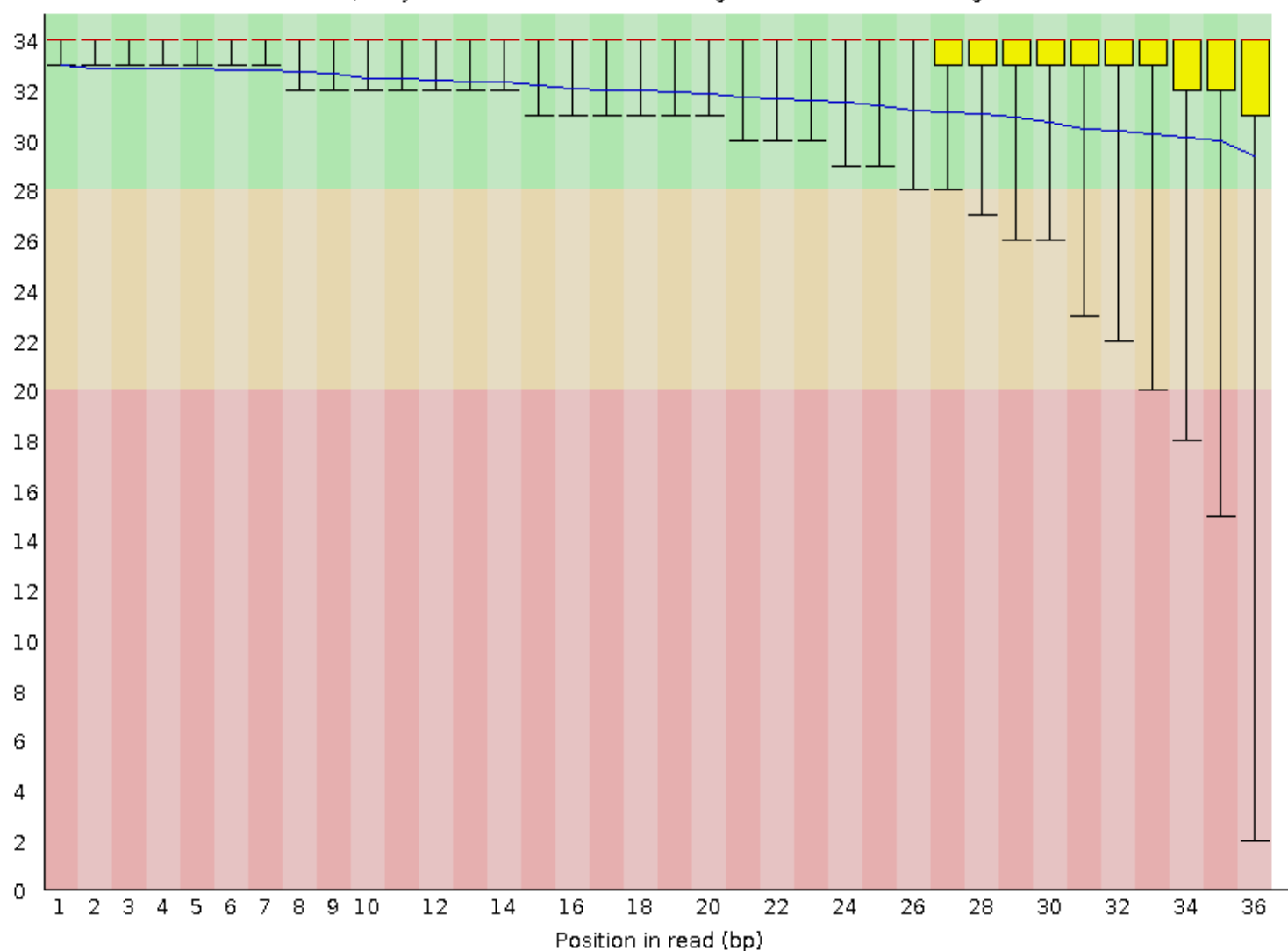
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per tile sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented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

Basic Statistics

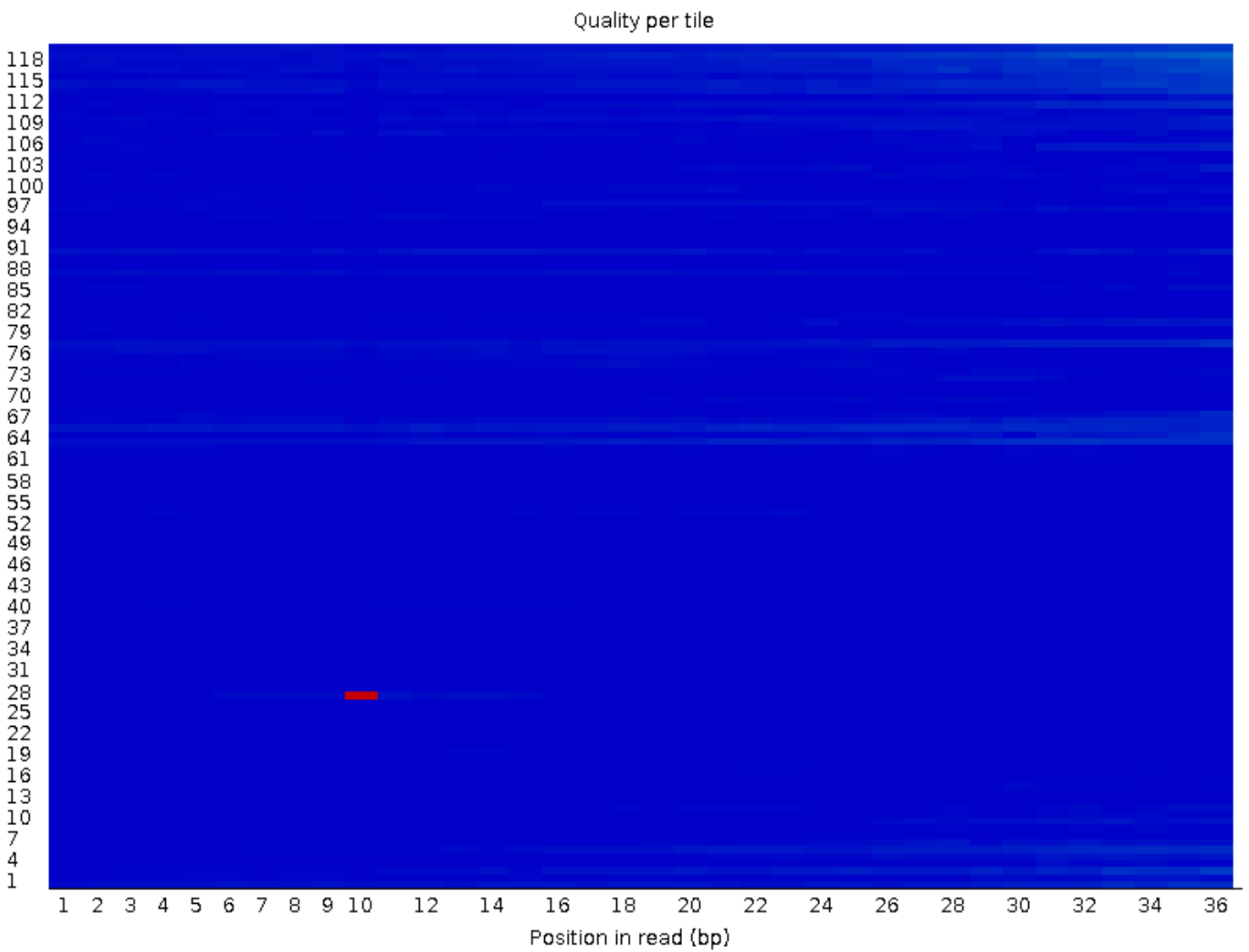
Measure	Value
Filename	ERR032071_2_REP2.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	39

Per base sequence quality

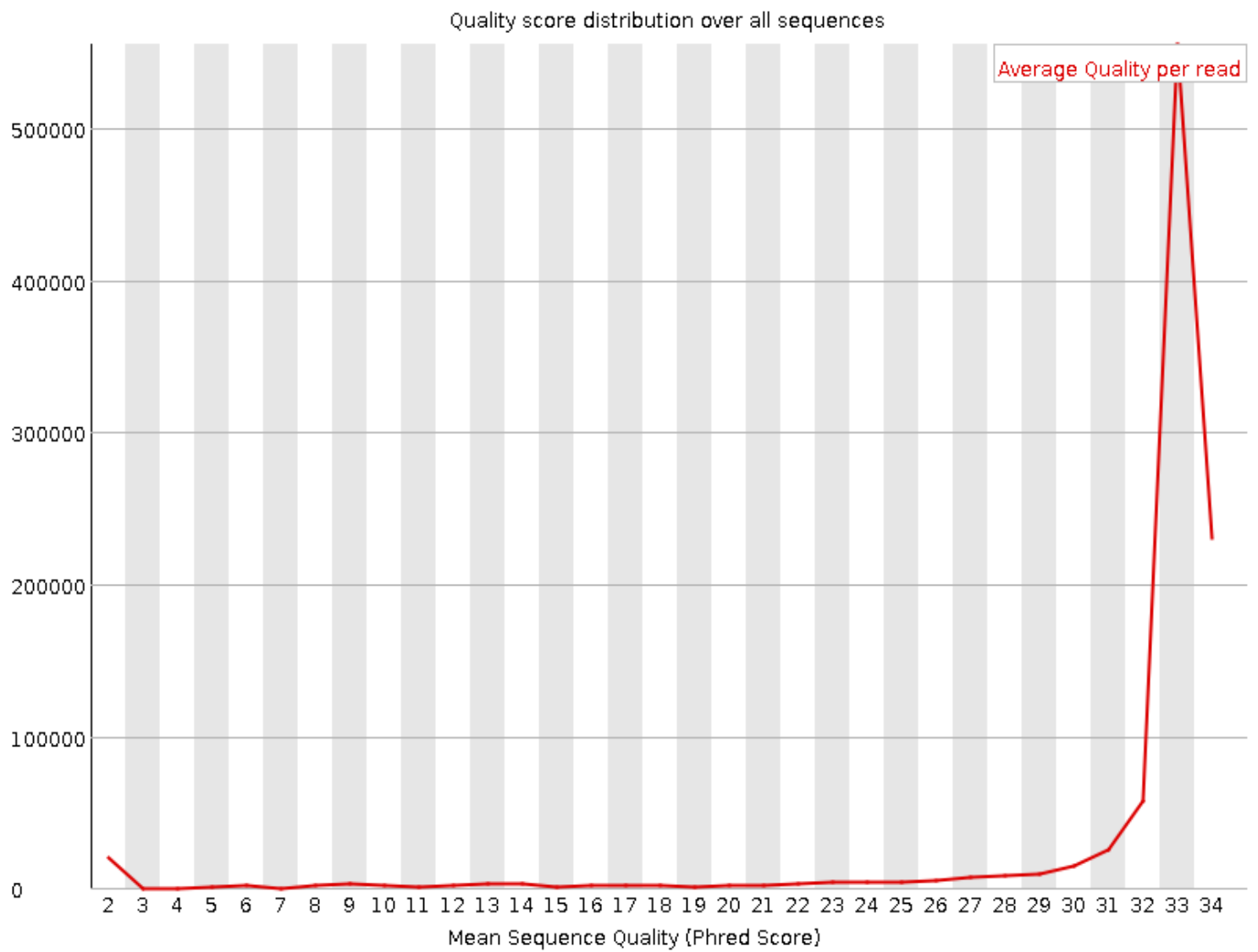
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



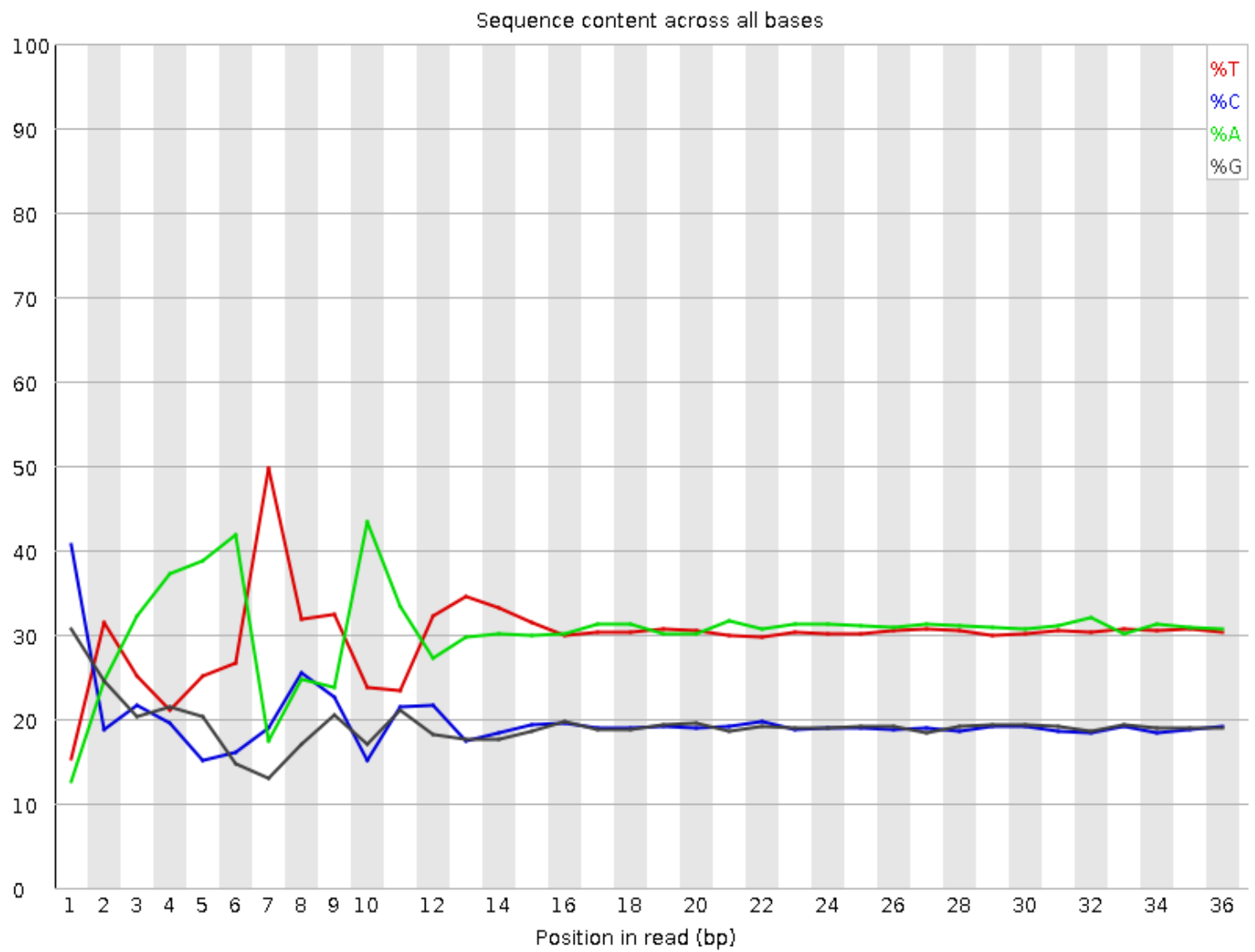
Per tile sequence quality



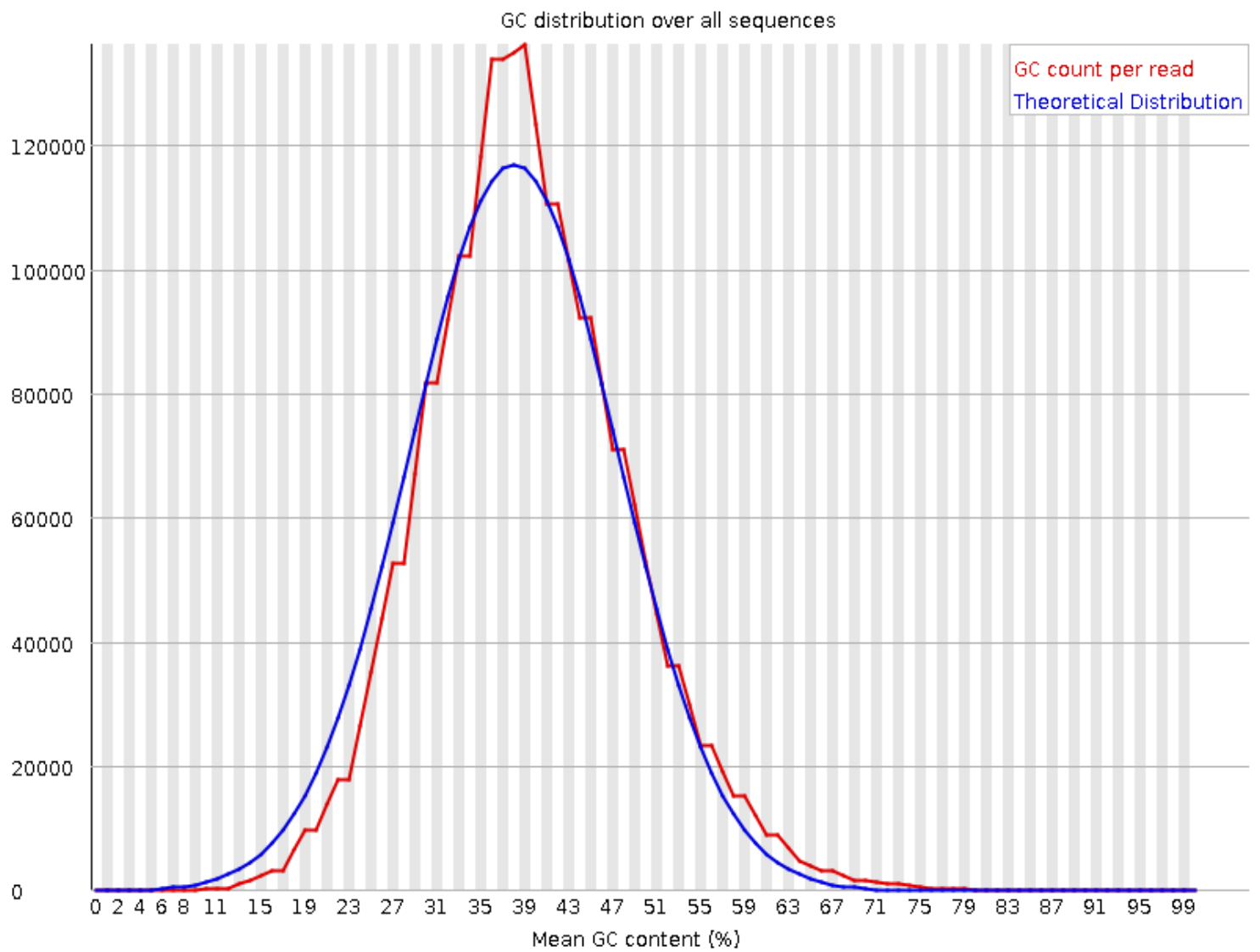
Per sequence quality scores



❌ Per base sequence content

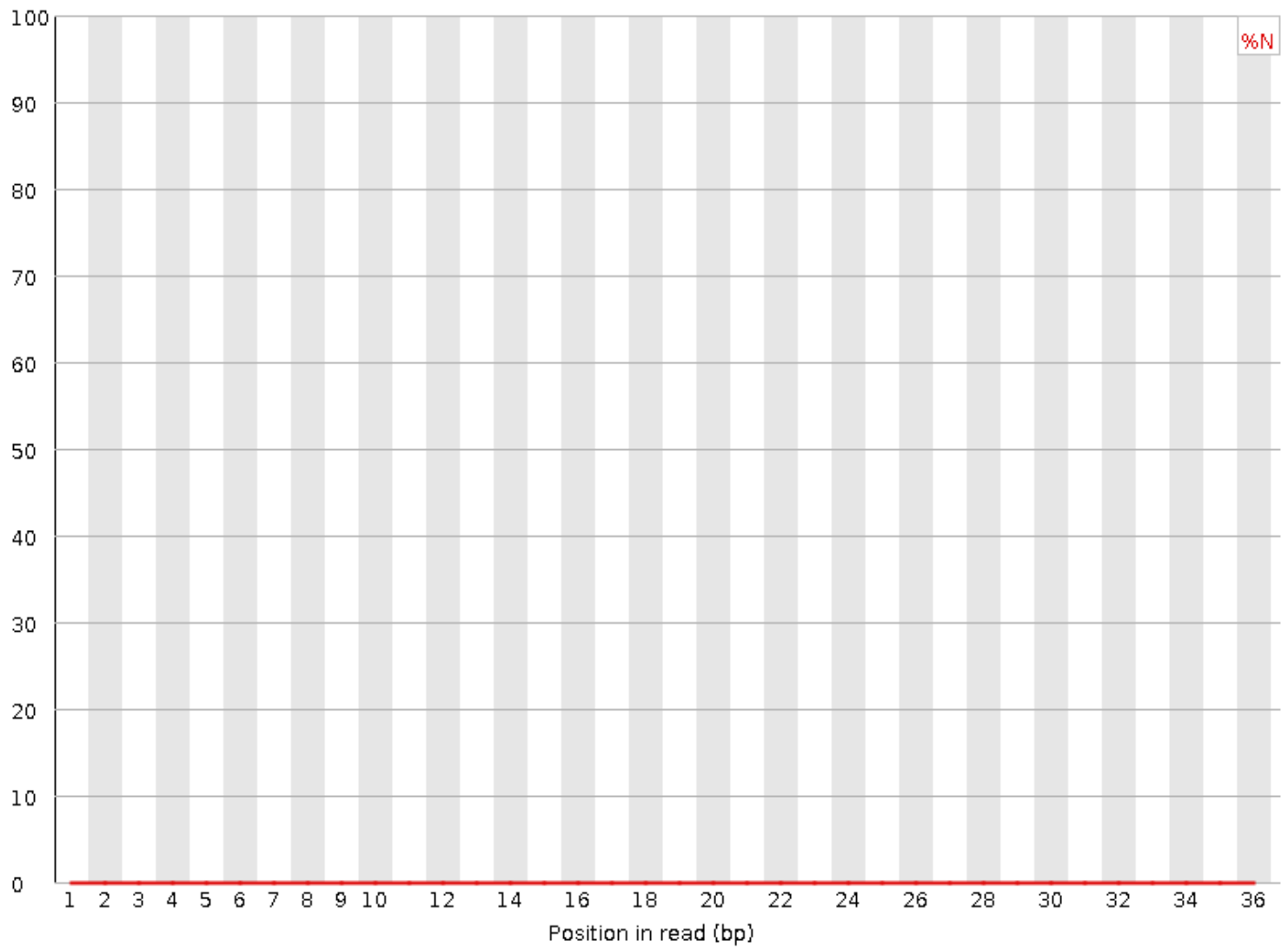


Per sequence GC content

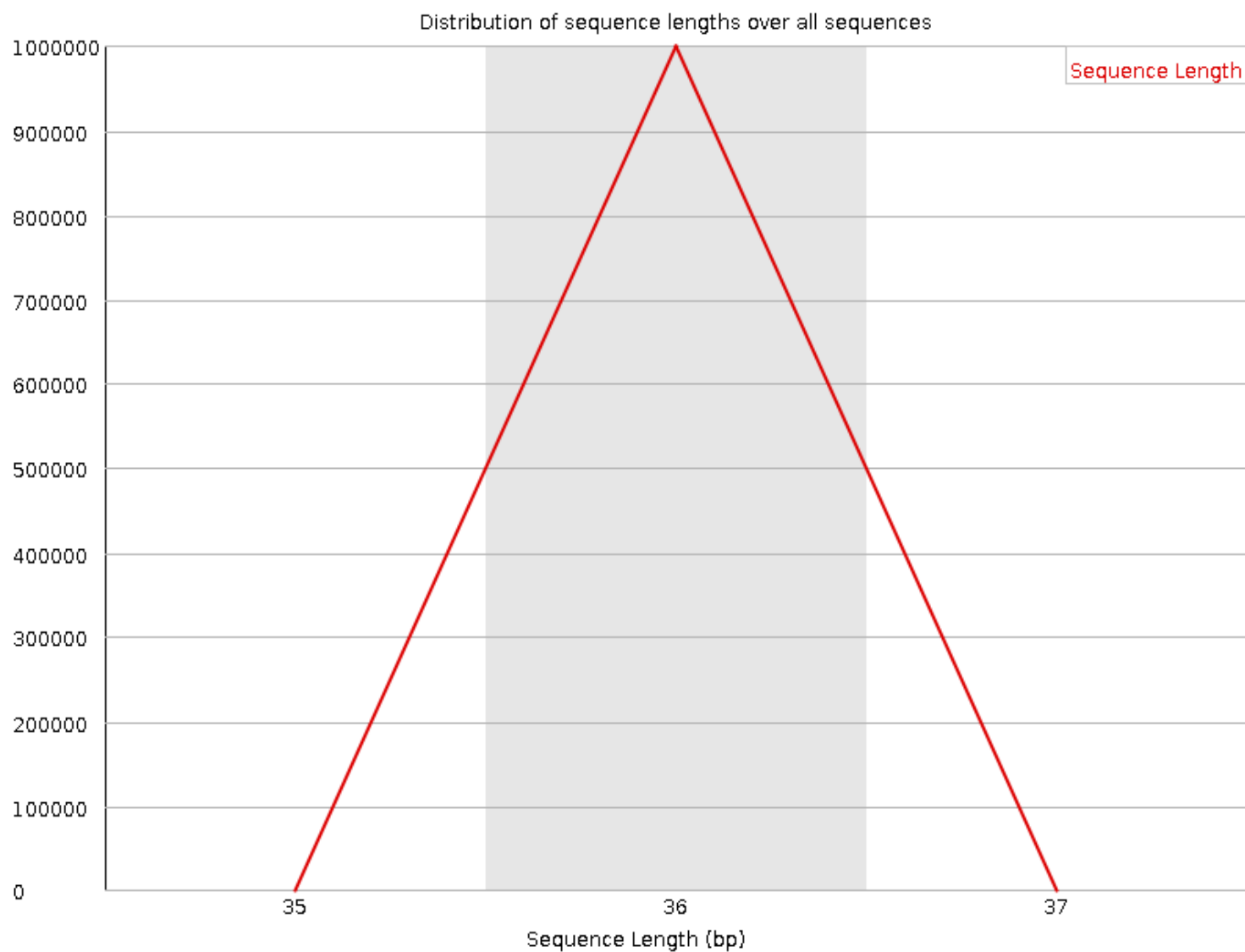


Per base N content

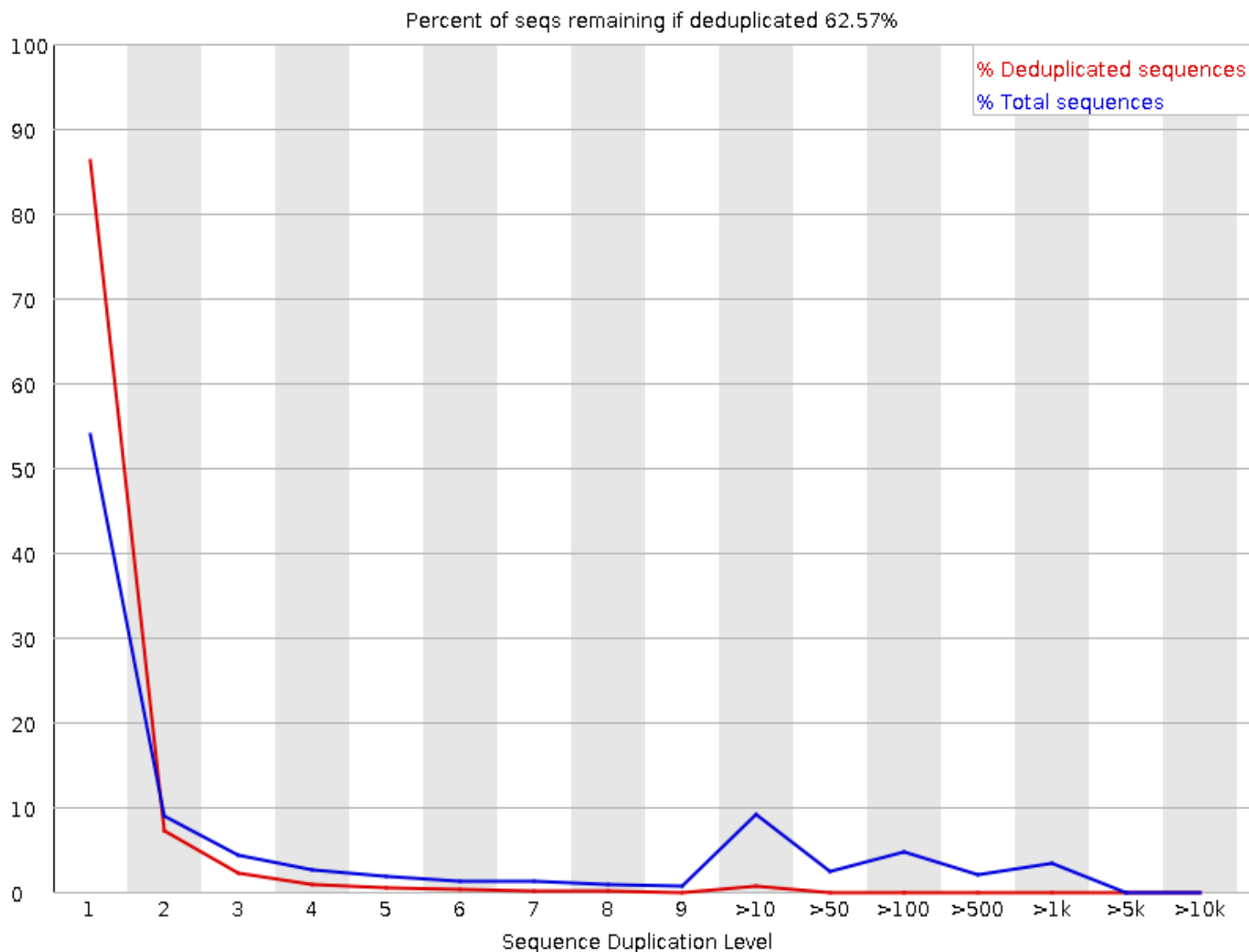
N content across all bases



Sequence Length Distribution



! Sequence Duplication Levels



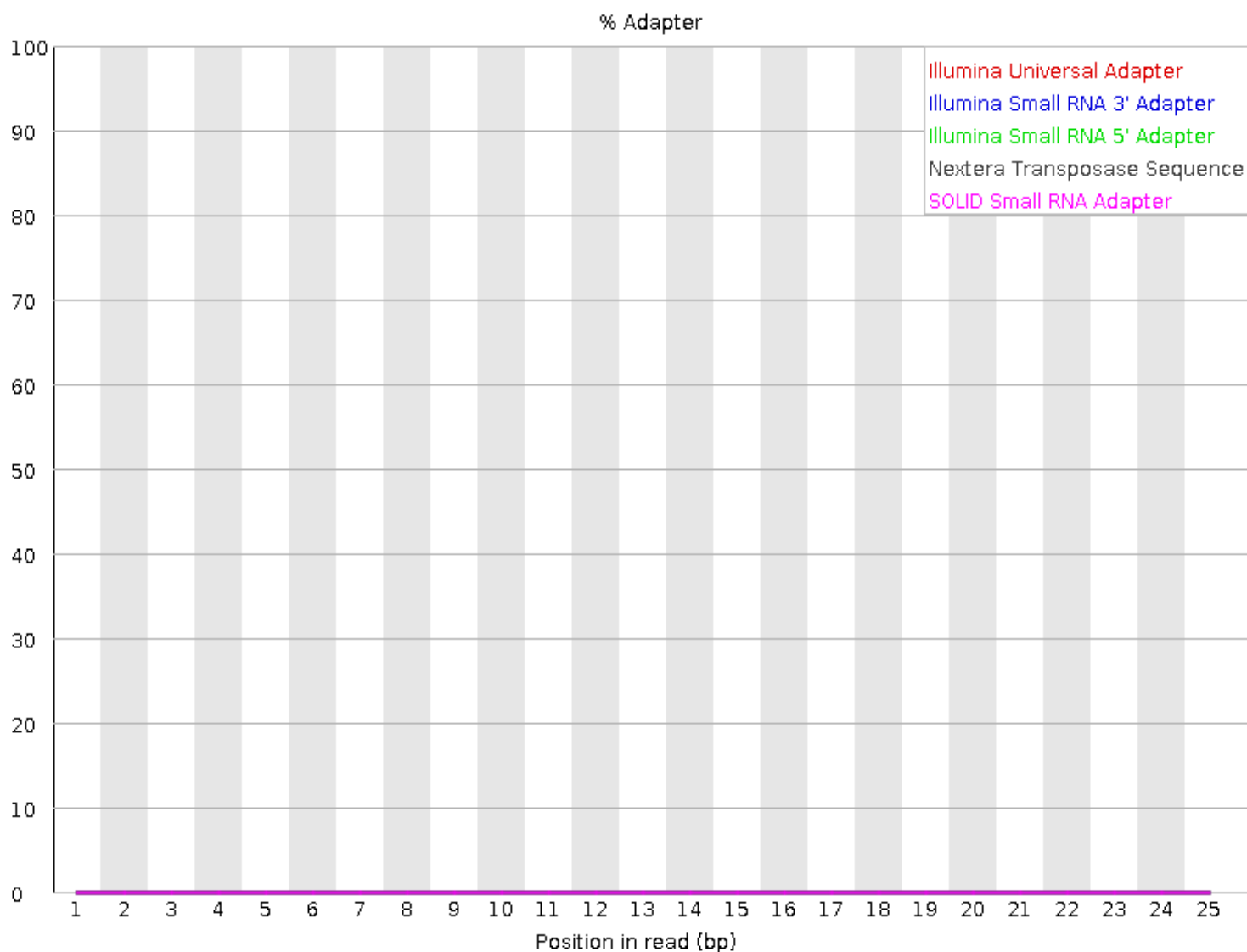
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	3265	0.3265	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	3057	0.30569999999999997	No Hit
GGGATATAGAATCTTGAGGACATATCGAAGATTTT	3006	0.3006	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	2547	0.2547	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2389	0.2389	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1881	0.18810000000000002	No Hit
CTTGGAGGACATATCGAAGATTTTGTCTTCTACCTC	1718	0.17179999999999998	No Hit
CGAAGATTTTGTCTTCTACCTCGATGTTGAATTGTA	1691	0.1691	No Hit
GGAGGACATATCGAAGATTTTGTCTTCTACCTCGAT	1657	0.16570000000000001	No Hit

Sequence	Count	Percentage	Possible Source
AAATAACTAAAGTAAGAAACACCACTAAGTTAAAAA	1640	0.164	No Hit
CTAAAGTAAGAAACACCACTAAGTTAAAACTCTCT	1619	0.1619	No Hit
GTTATTTCAAGGACGAAAAGACCCTAGAGAGTTTTT	1614	0.1614	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1538	0.15380000000000002	No Hit
CTACAATTCAACATCGAGGTAGAAAACAAATCTTC	1355	0.1355	No Hit
CCTATCTTTAACTACAATTCAACATCGAGGTAGAAA	1280	0.128	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1217	0.1217	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1125	0.11249999999999999	No Hit
CAAGGACGAAAAGACCCTAGAGAGTTTTTAACTTAG	1036	0.1036	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1035	0.1035	No Hit
GACATATCGAAGATTTTGTCTTCTACCTCGATGTTG	1025	0.10250000000000001	No Hit



Adapter Content



Produced by [FastQC](#) (version 0.11.7)