

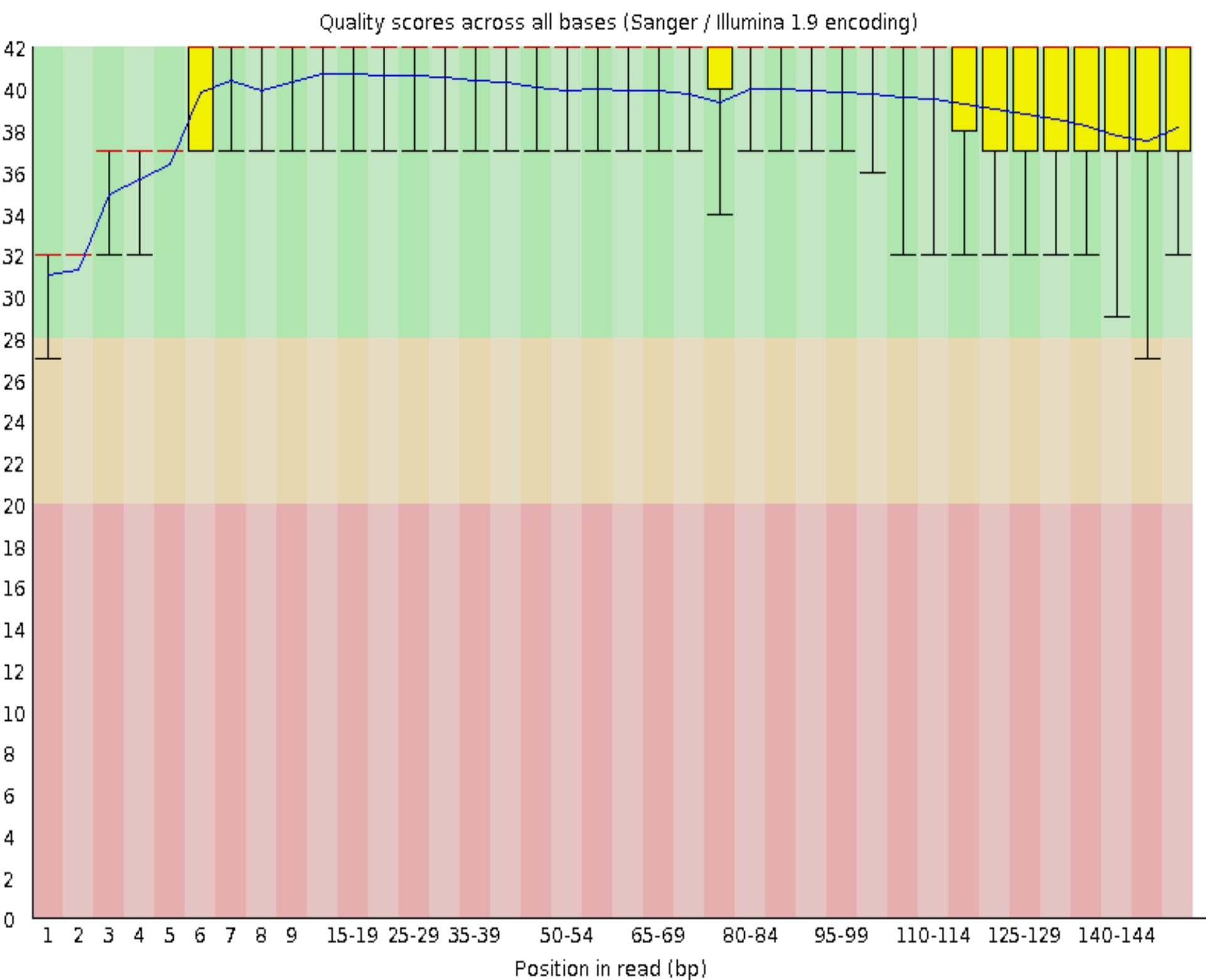
Summary

-  [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

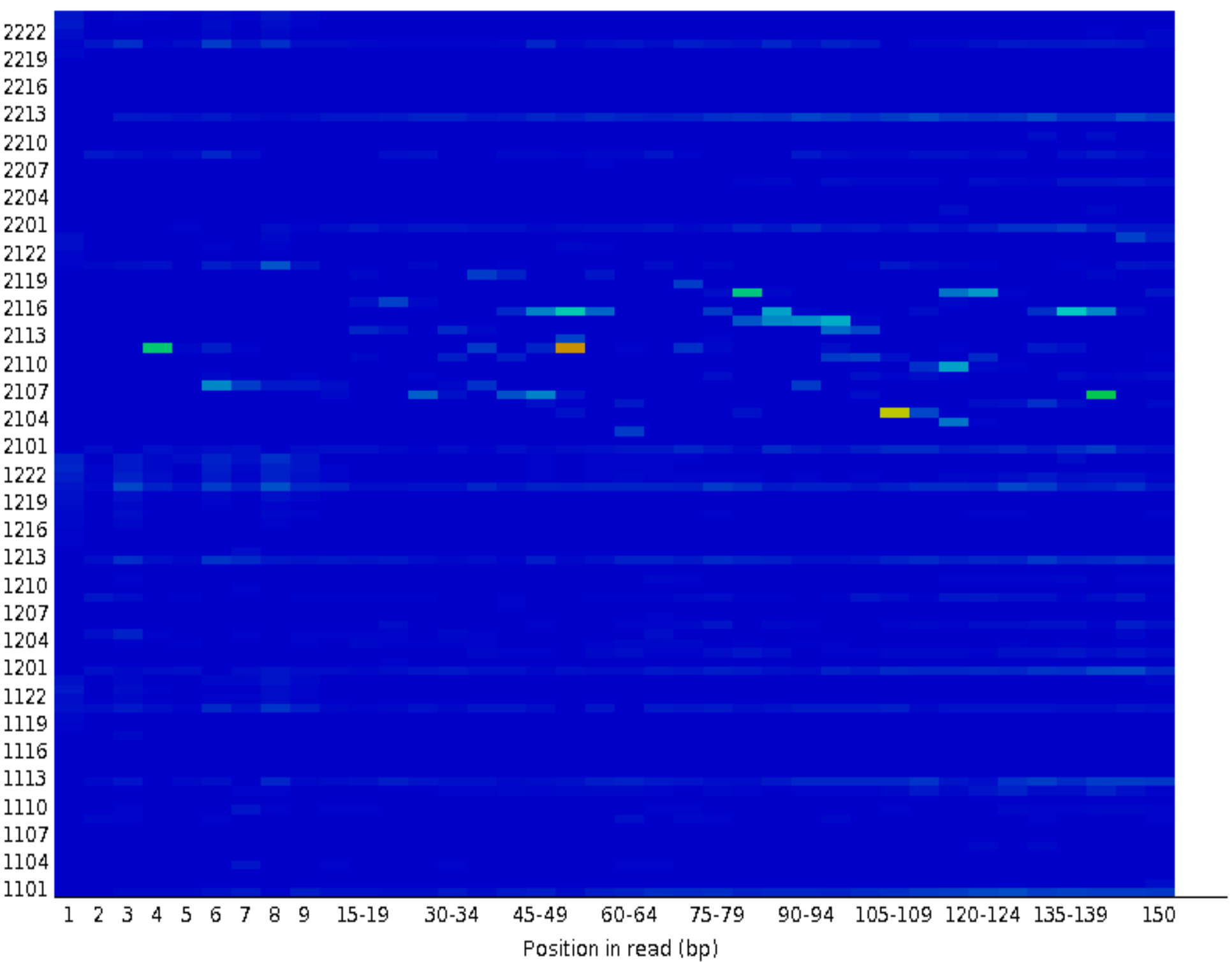
Measure	Value
Filename	IR23_L0_reverse_paired.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	20046068
Sequences flagged as poor quality	0
Sequence length	75-150
%GC	44

Per base sequence quality

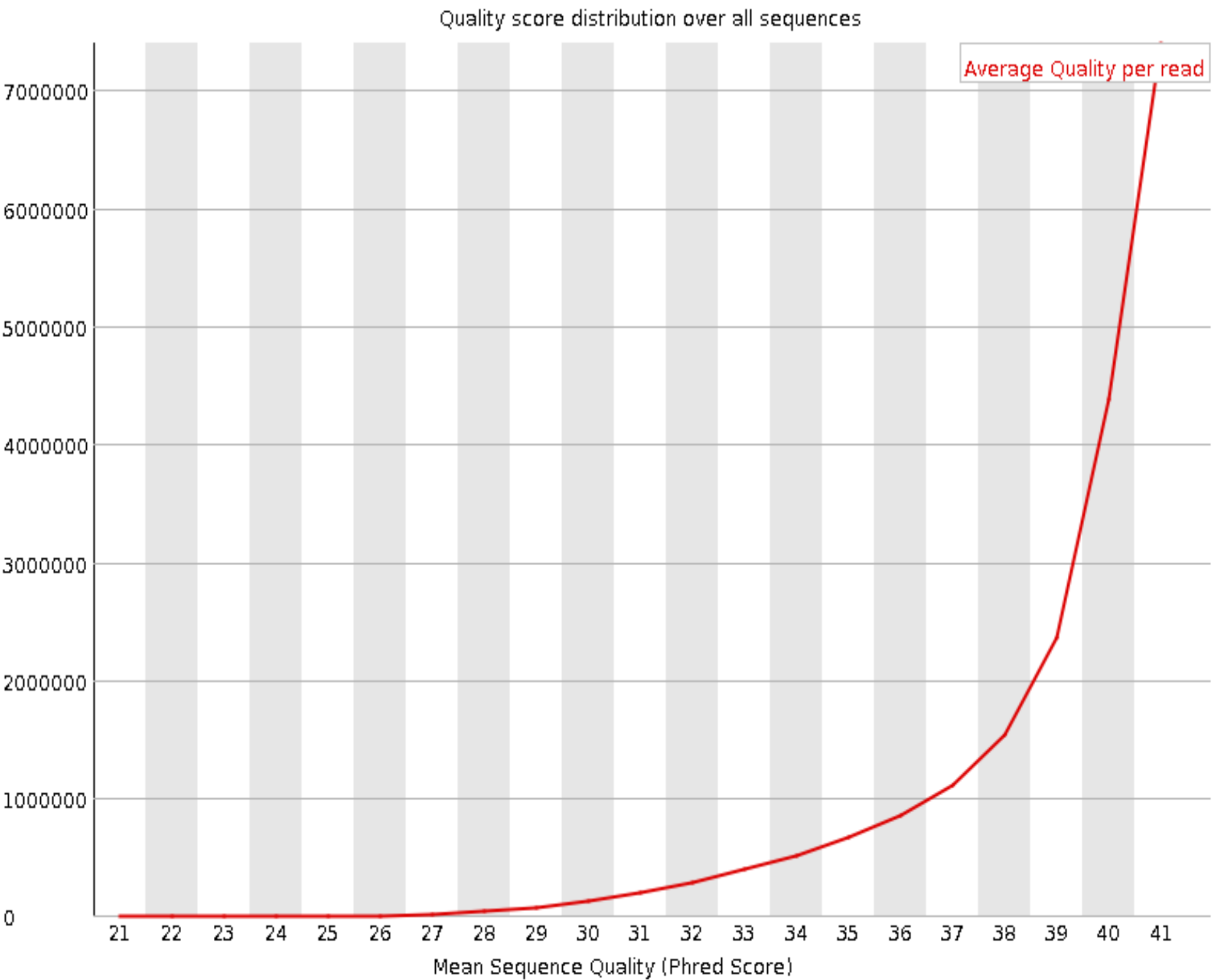


! Per tile sequence quality

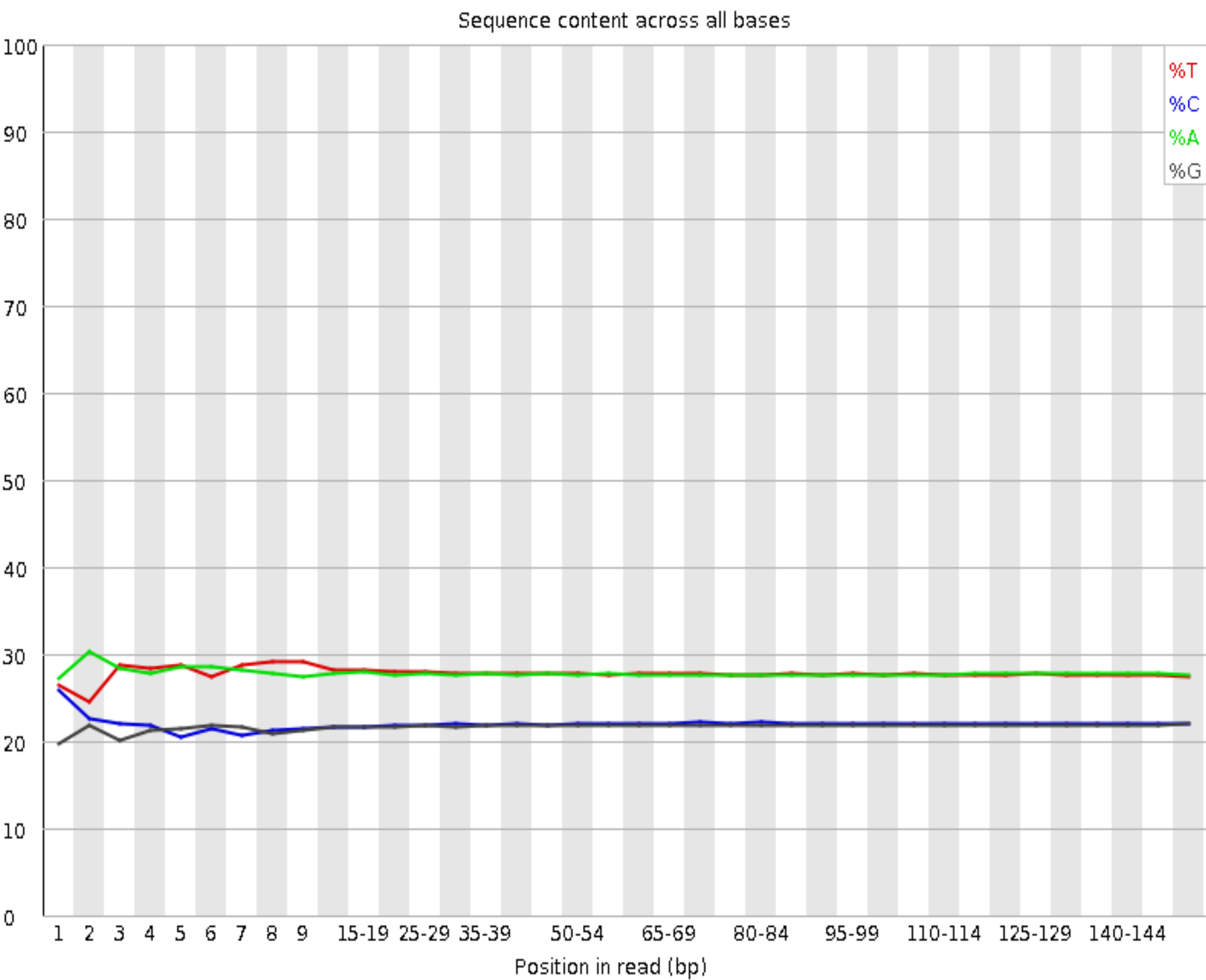
Quality per tile



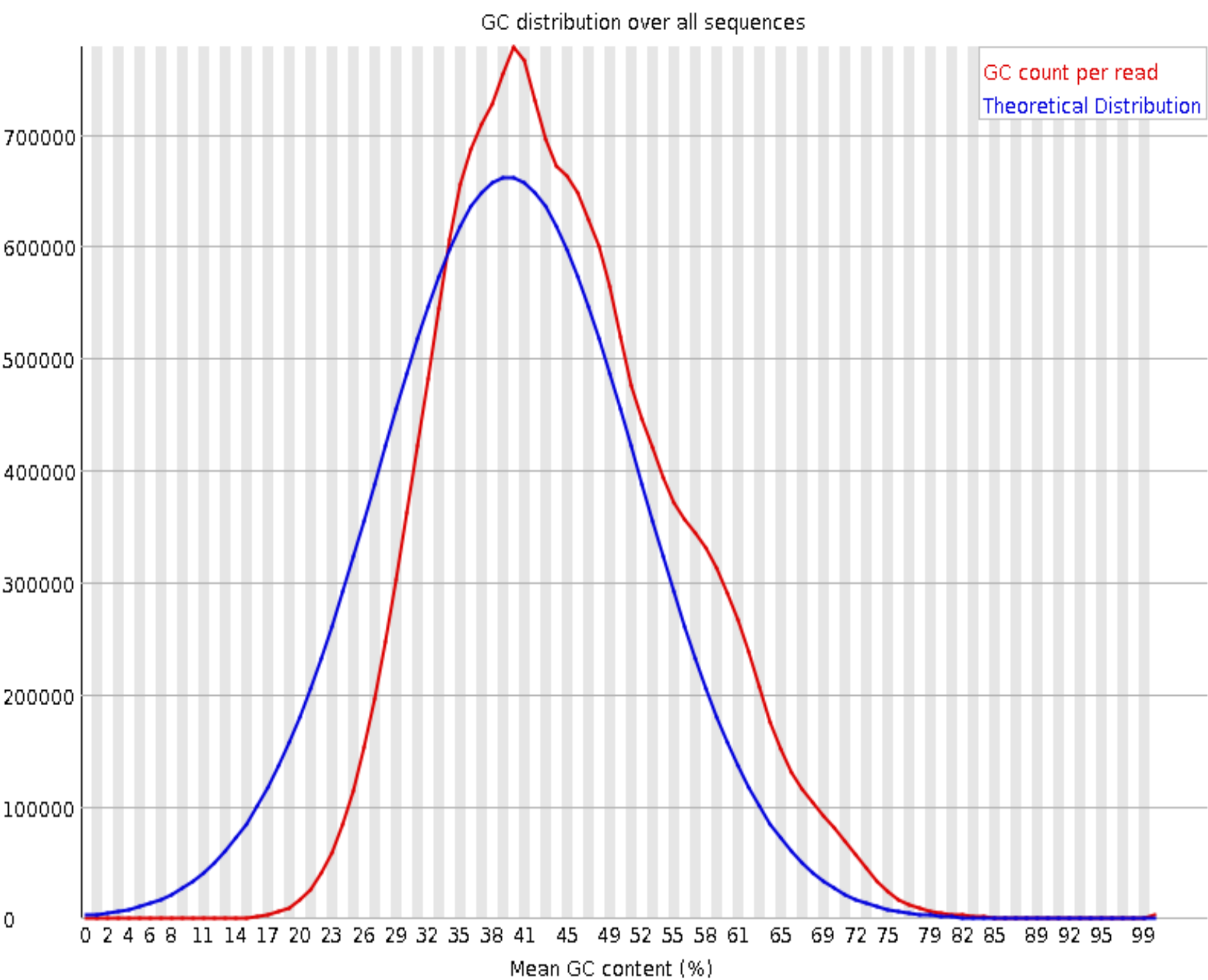
✅ Per sequence quality scores



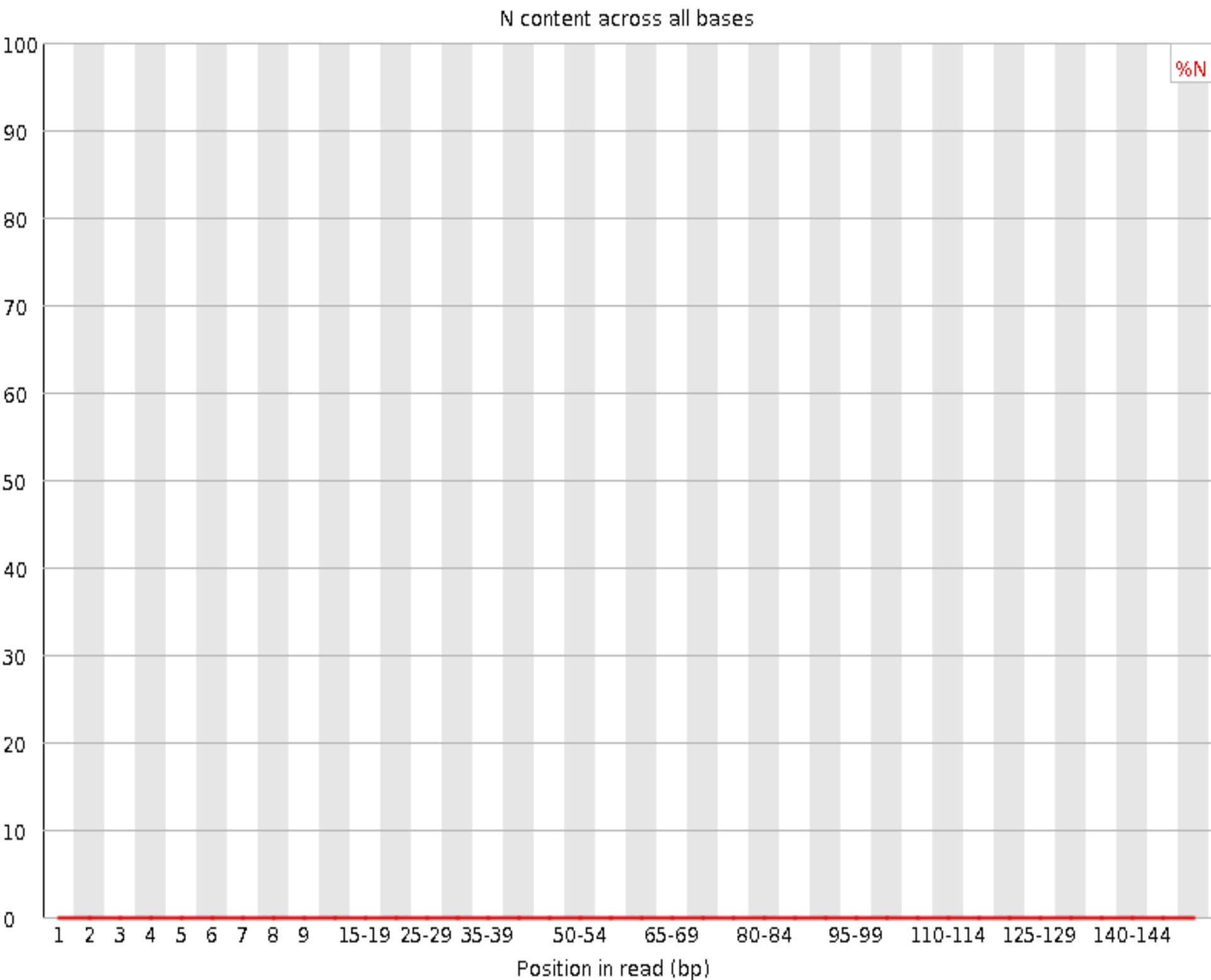
✅ Per base sequence content



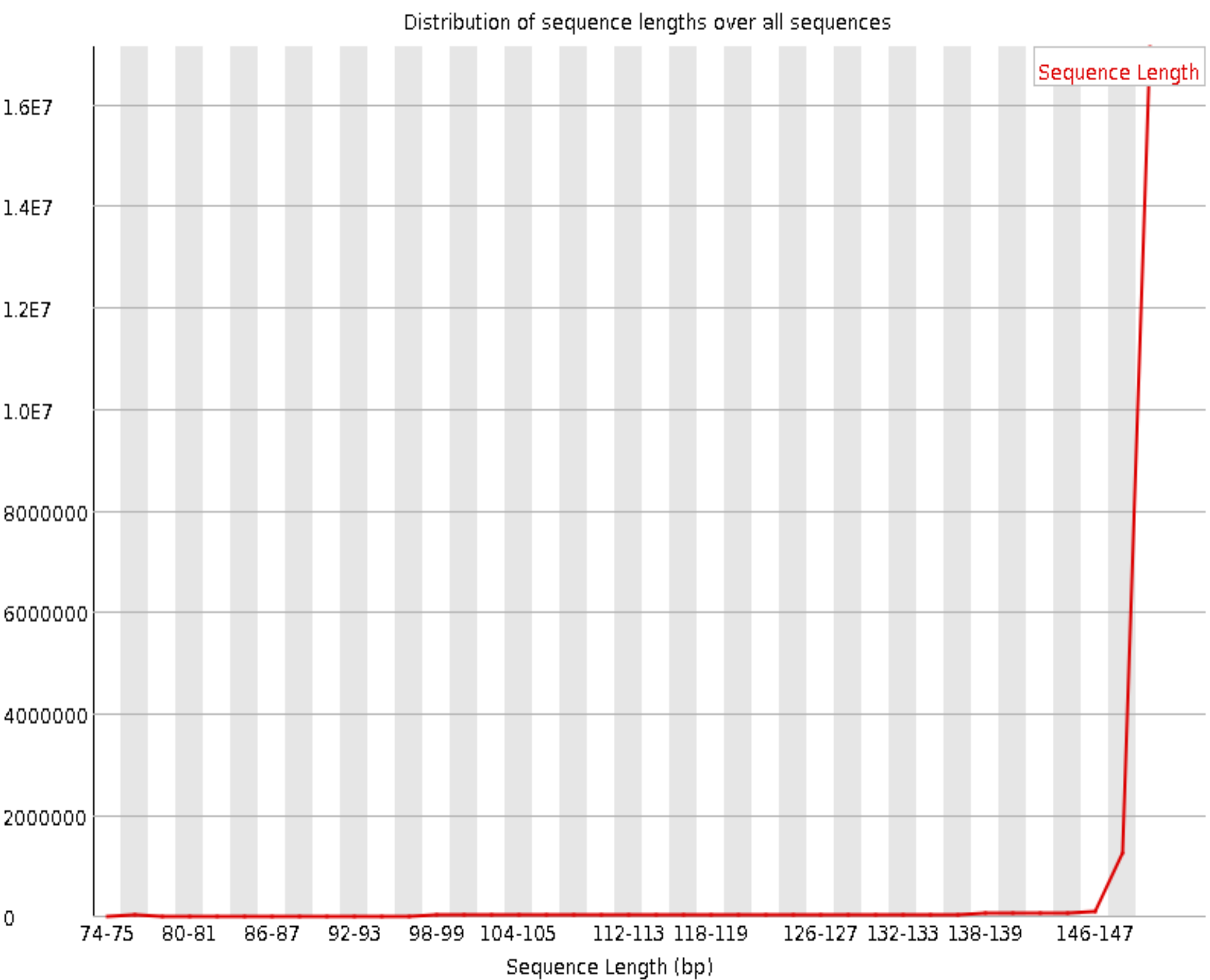
✖ Per sequence GC content



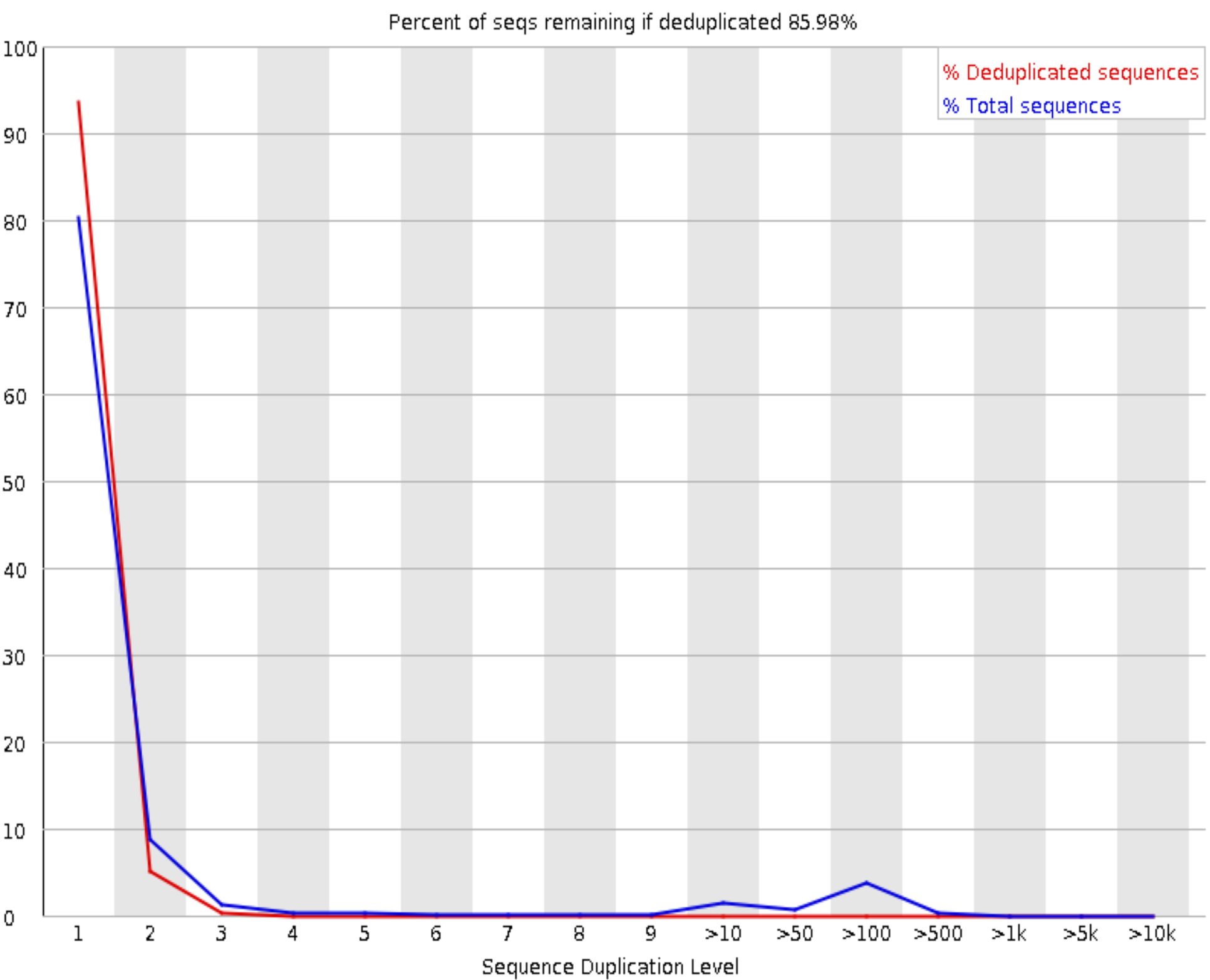
✅ Per base N content



! Sequence Length Distribution

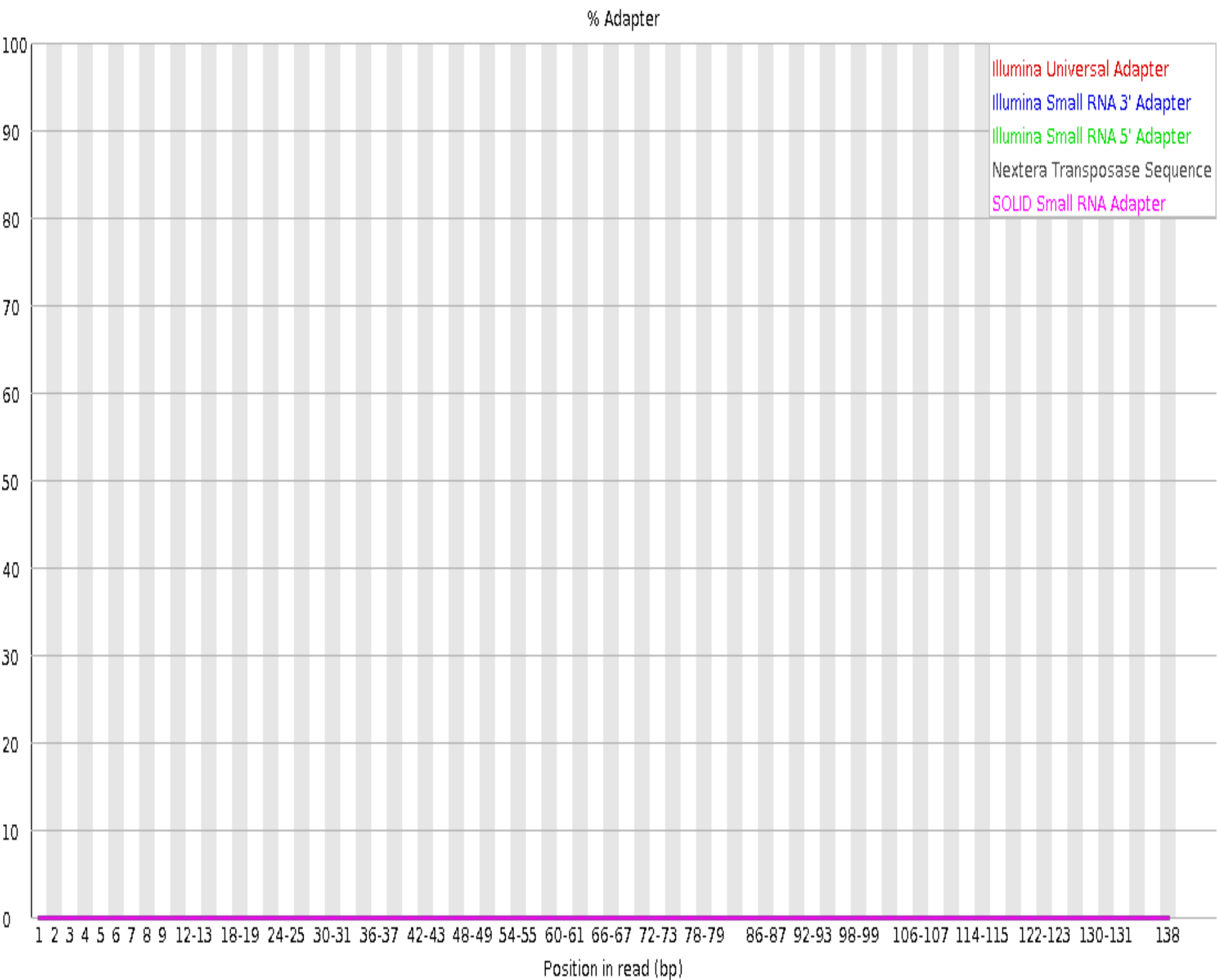


✔ Sequence Duplication Levels

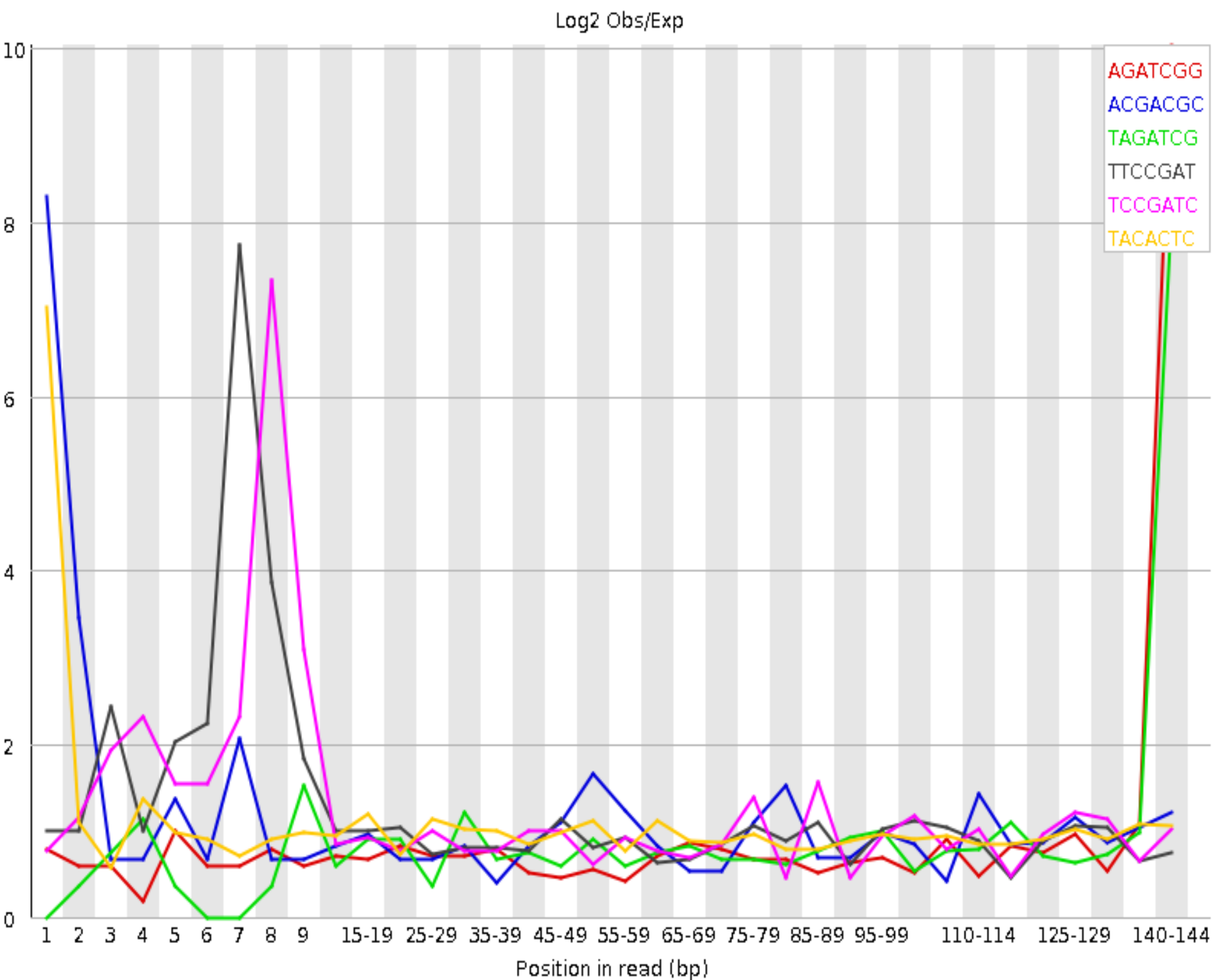


 **Overrepresented sequences**
No overrepresented sequences

 **Adapter Content**



✖ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGATCGG	3515	0.0	10.03681	140-144
ACGACGC	1020	8.11131E-5	8.318681	1
TAGATCG	1845	0.0	8.1224575	140-144
TTCCGAT	3465	0.0	7.7478647	7
TCCGATC	1830	1.06476364E-7	7.3347936	8
TACACTC	10745	0.0	7.0412655	1
GAGATCG	3605	0.0	6.668498	140-144
CTTCCGA	4970	0.0	6.3967423	6
CCGATCT	2395	1.08529985E-5	5.6047916	9
CGCTCTT	4980	0.0	5.537462	2
AAGATCG	2965	0.0	5.106927	140-144
CAGATCG	3375	0.0	5.0878167	140-144

