













FastQC Report

Summary

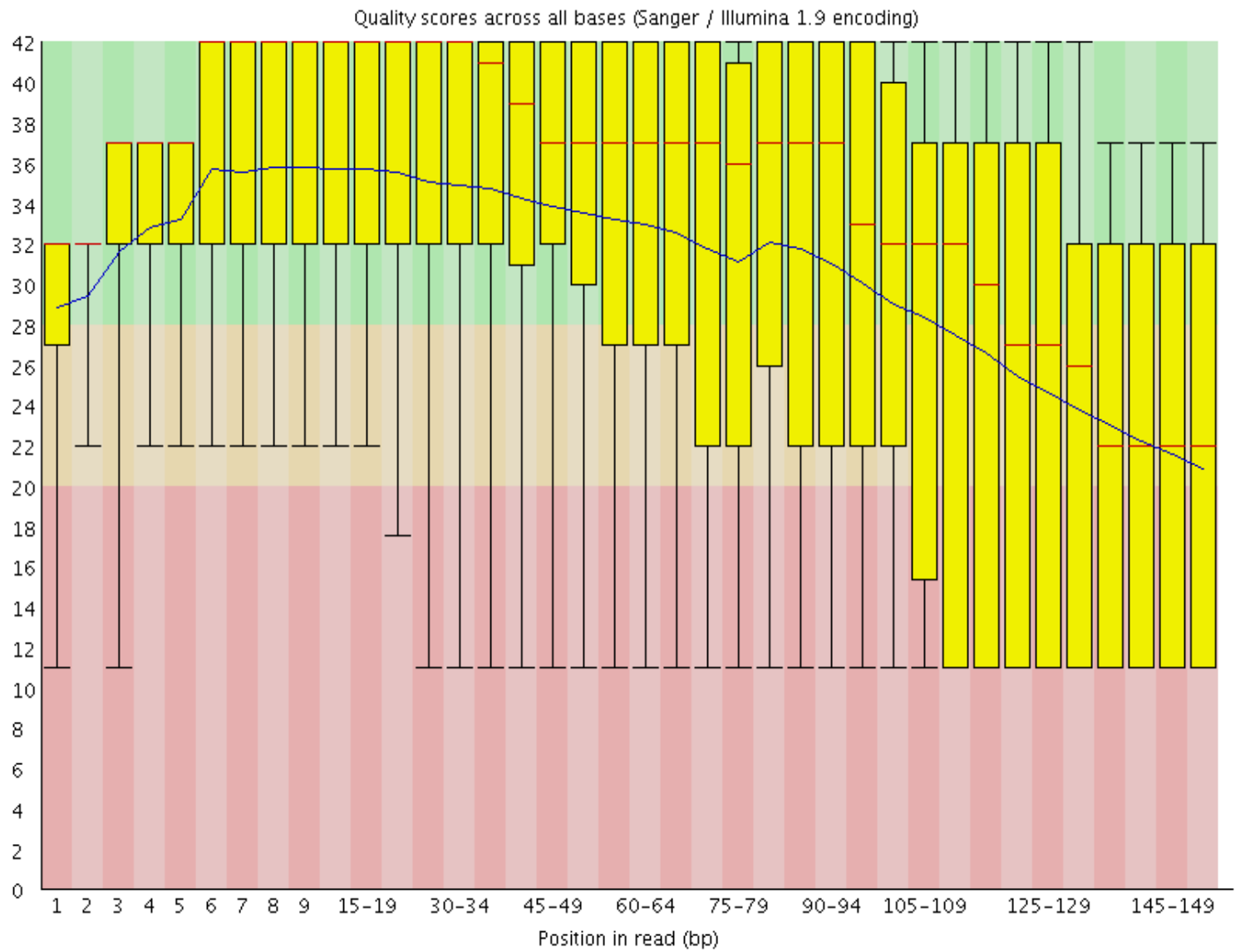
Wed 11 Apr 2018
PBA_S37_L007_R2_001.fastq

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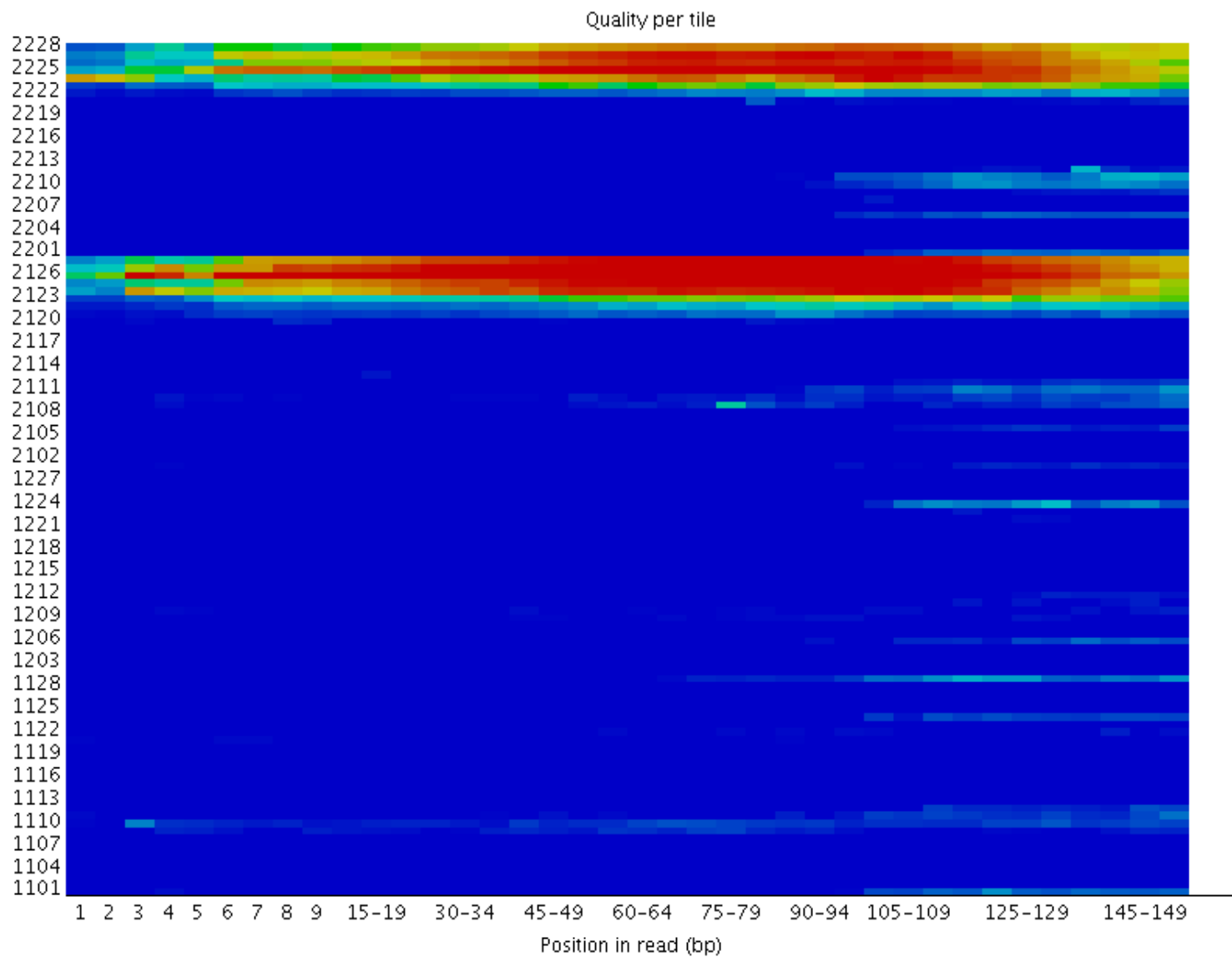
Basic Statistics

Measure	Value
Filename	PBA_S37_L007_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	32319223
Sequences flagged as poor quality	0
Sequence length	151
%GC	43

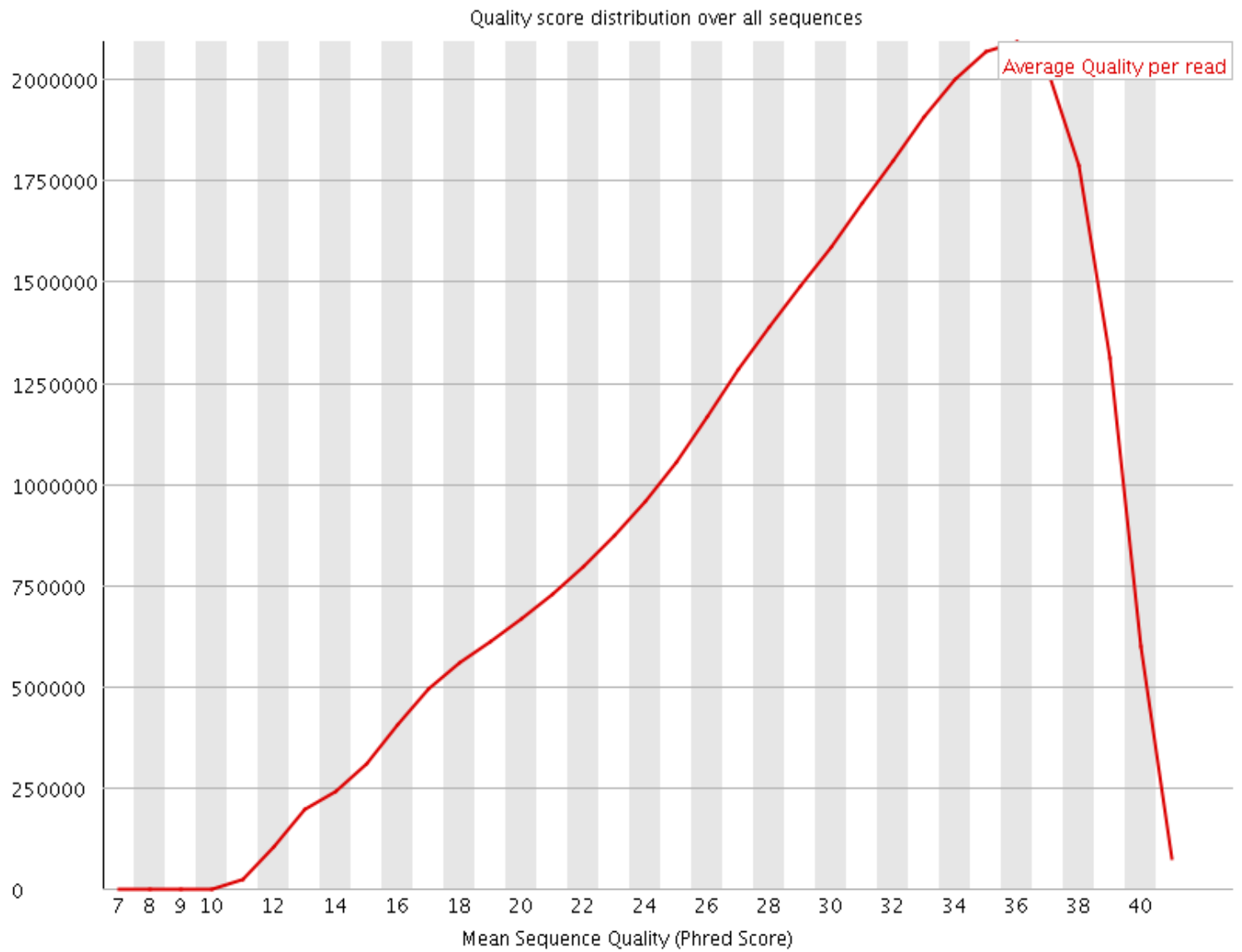
Per base sequence quality



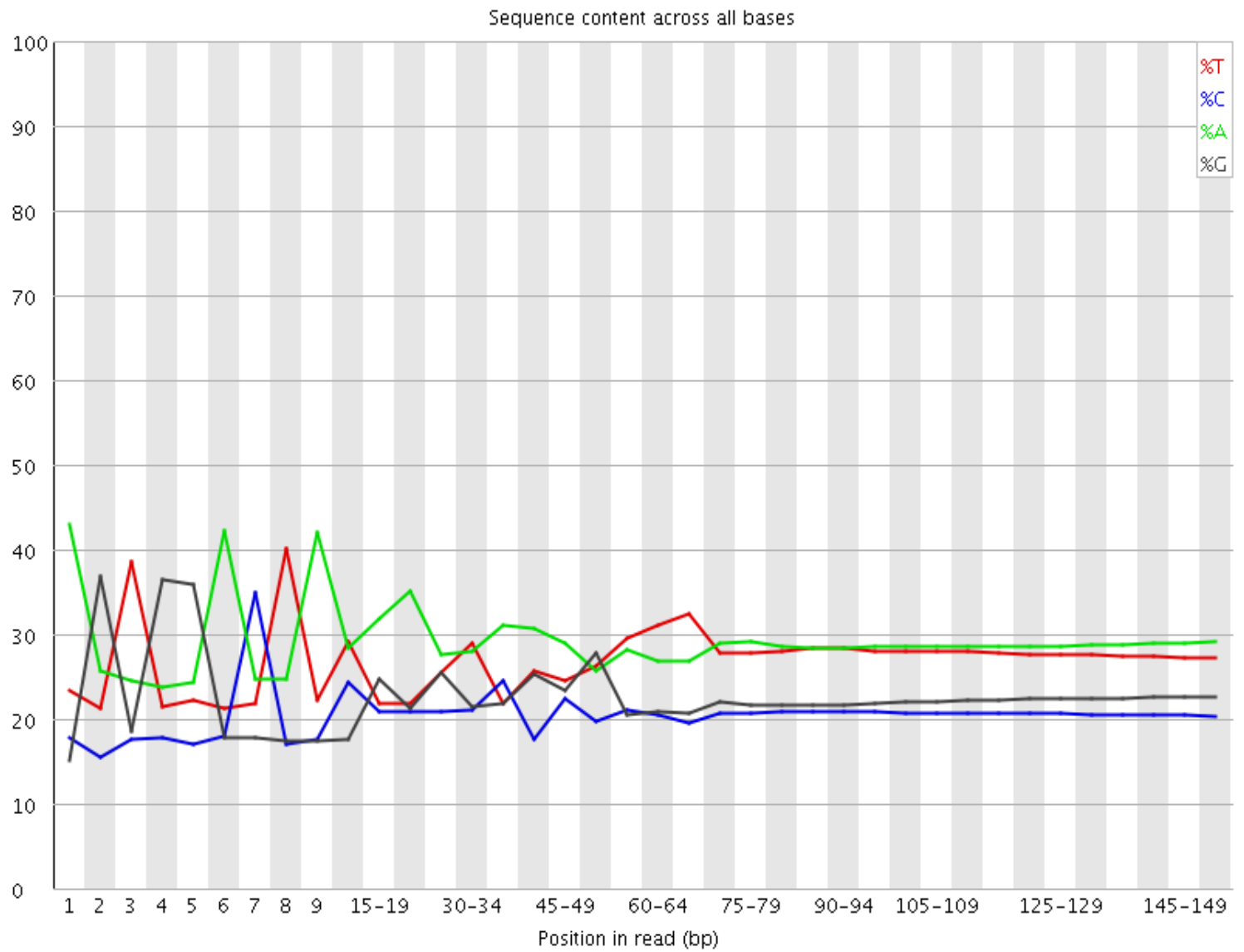
✖ Per tile sequence quality



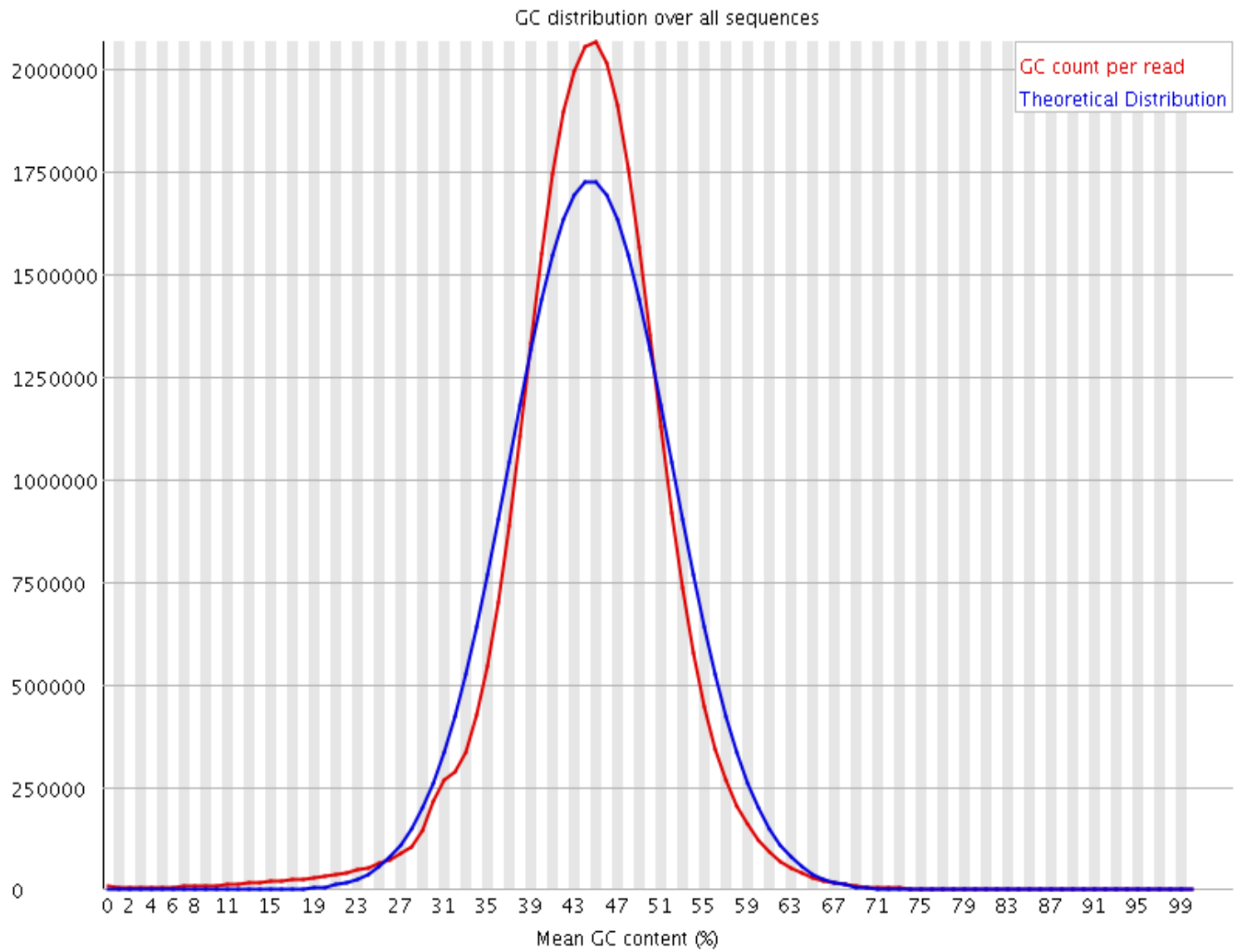
Per sequence quality scores



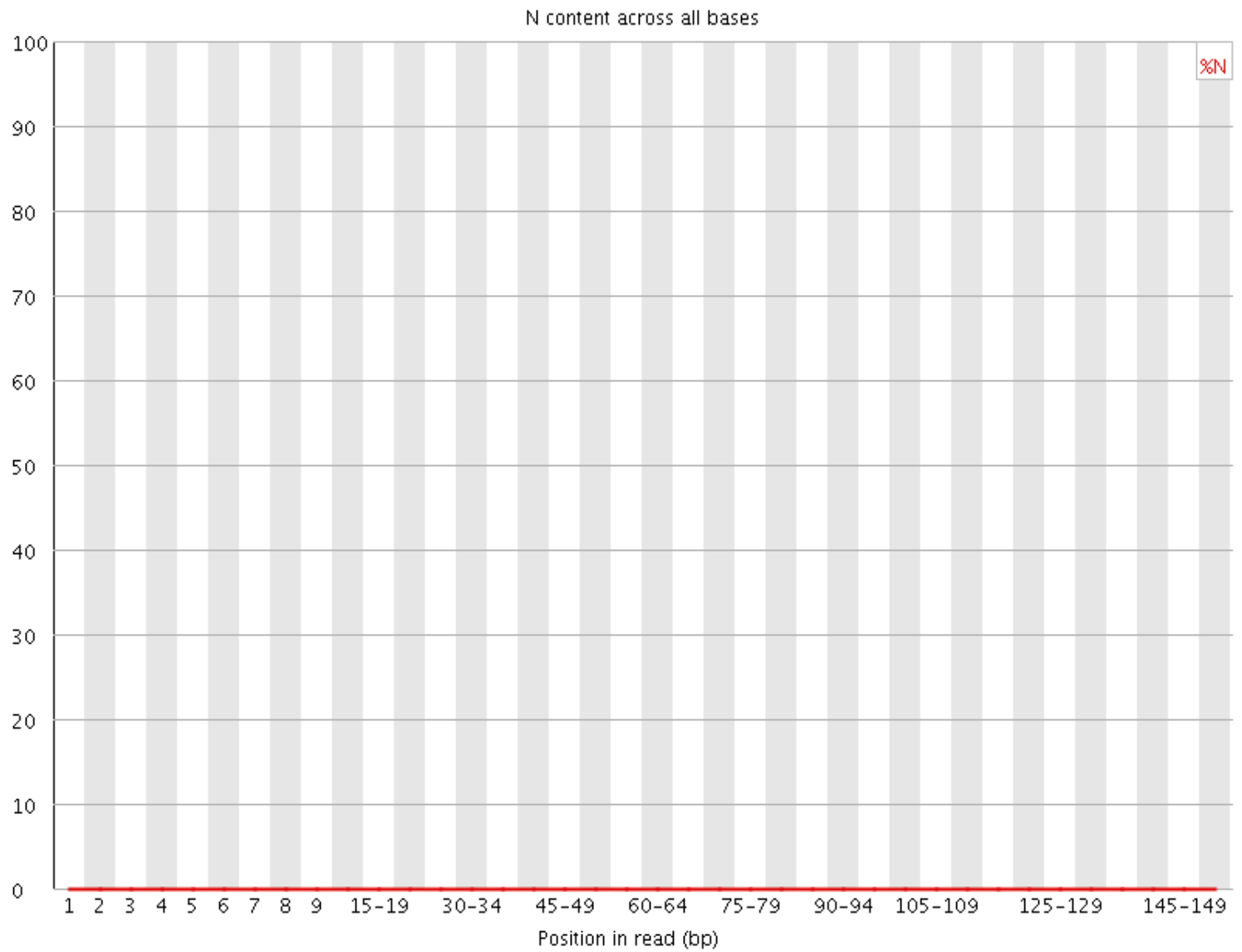
✖ Per base sequence content



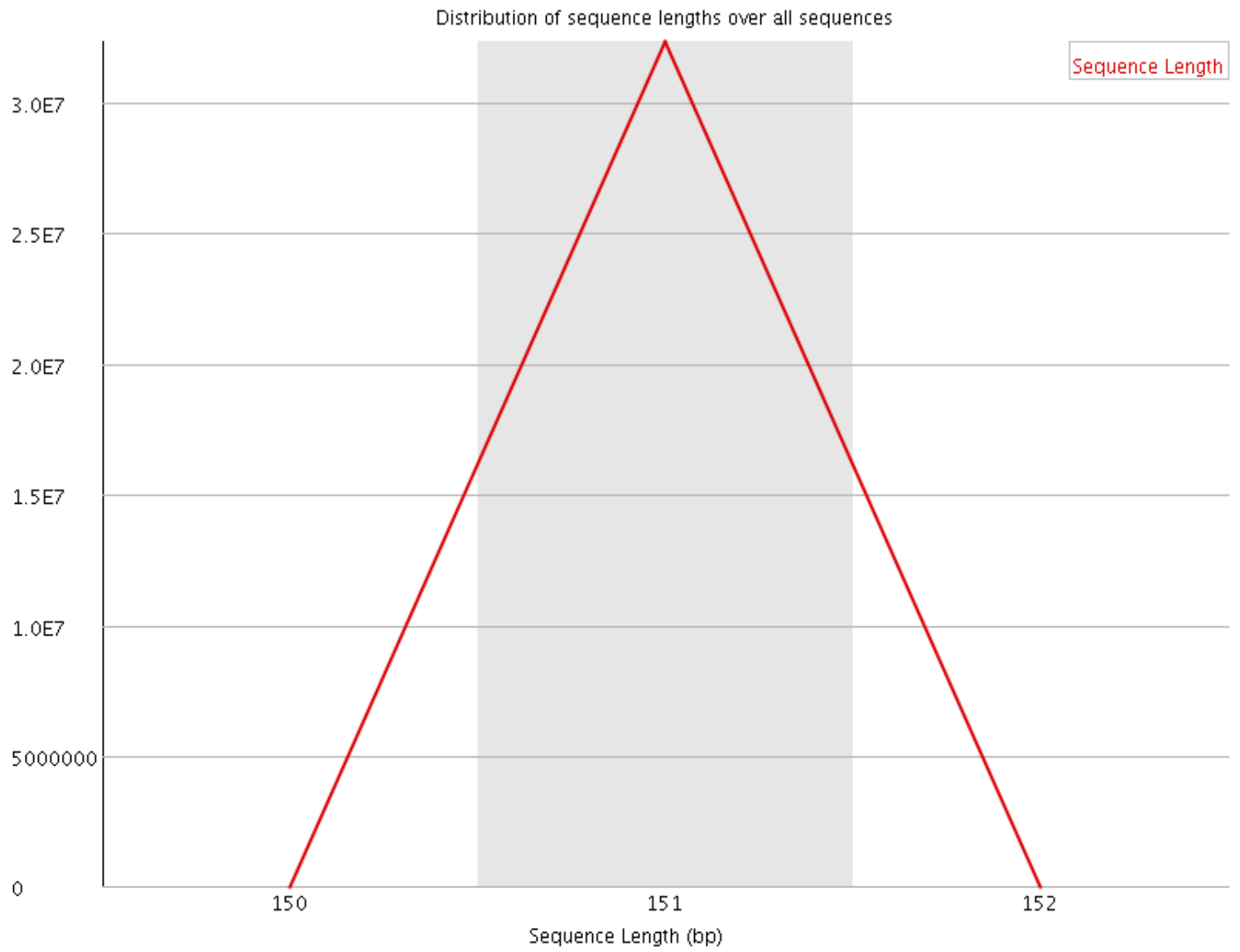
Per sequence GC content



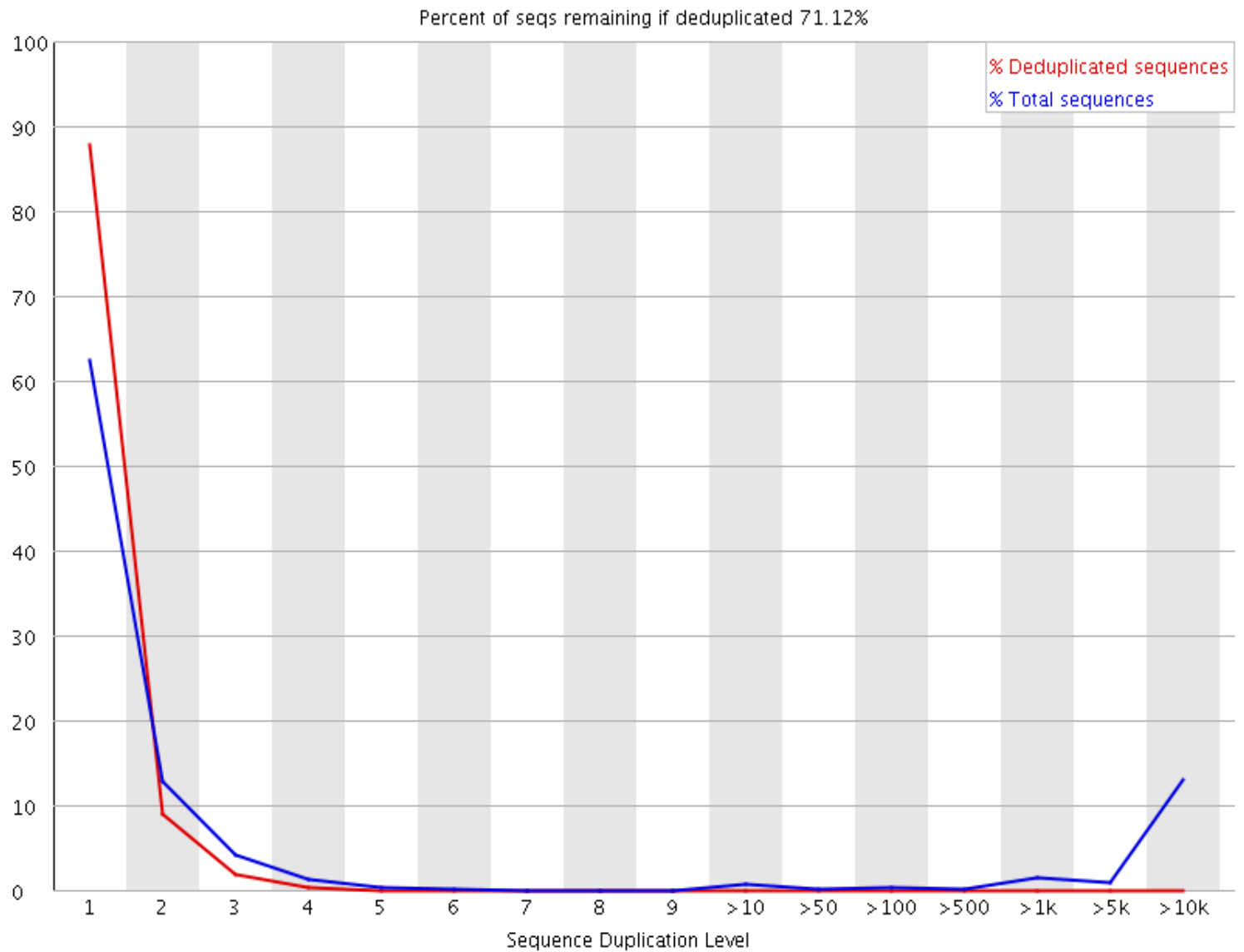
Per base N content



Sequence Length Distribution



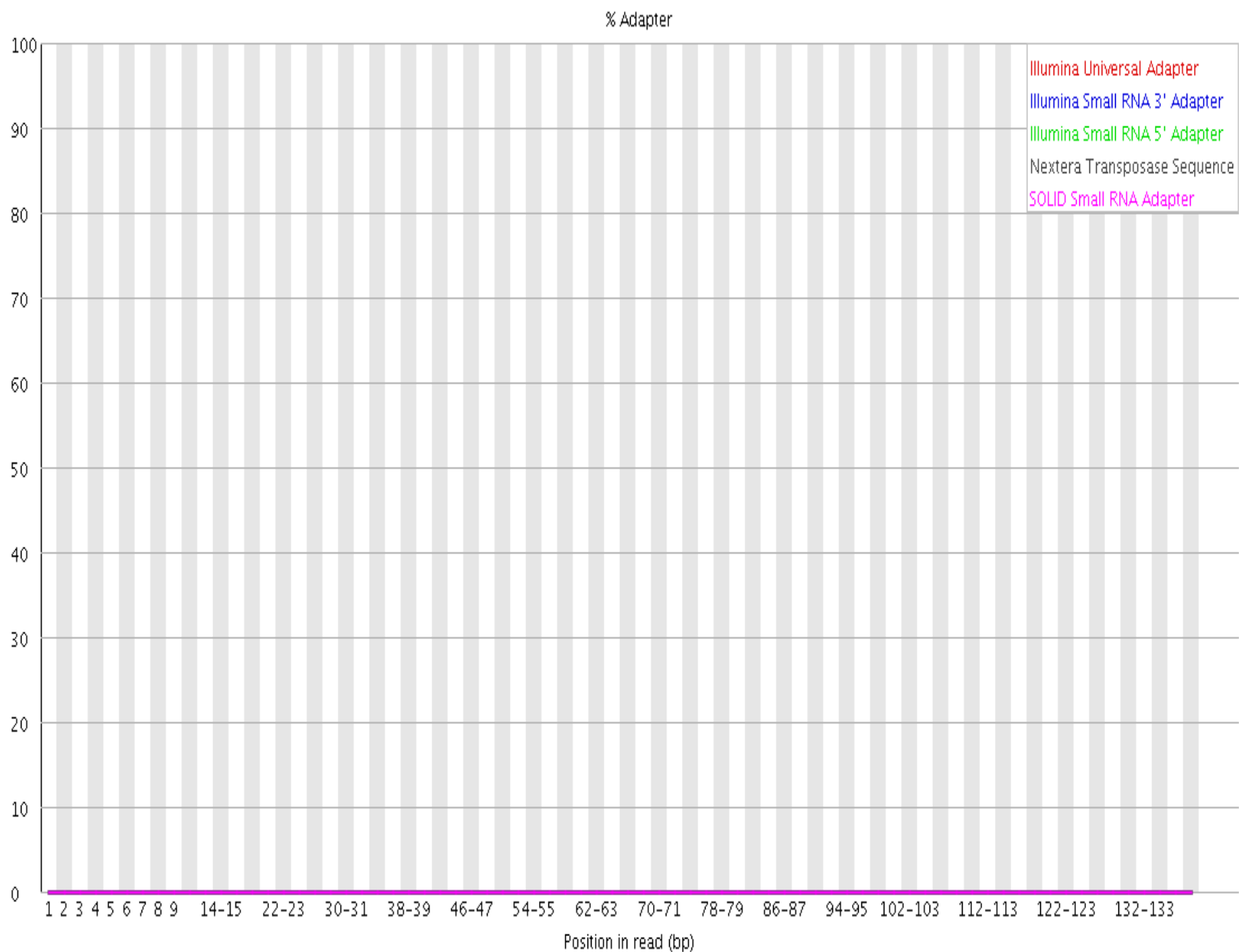
Sequence Duplication Levels



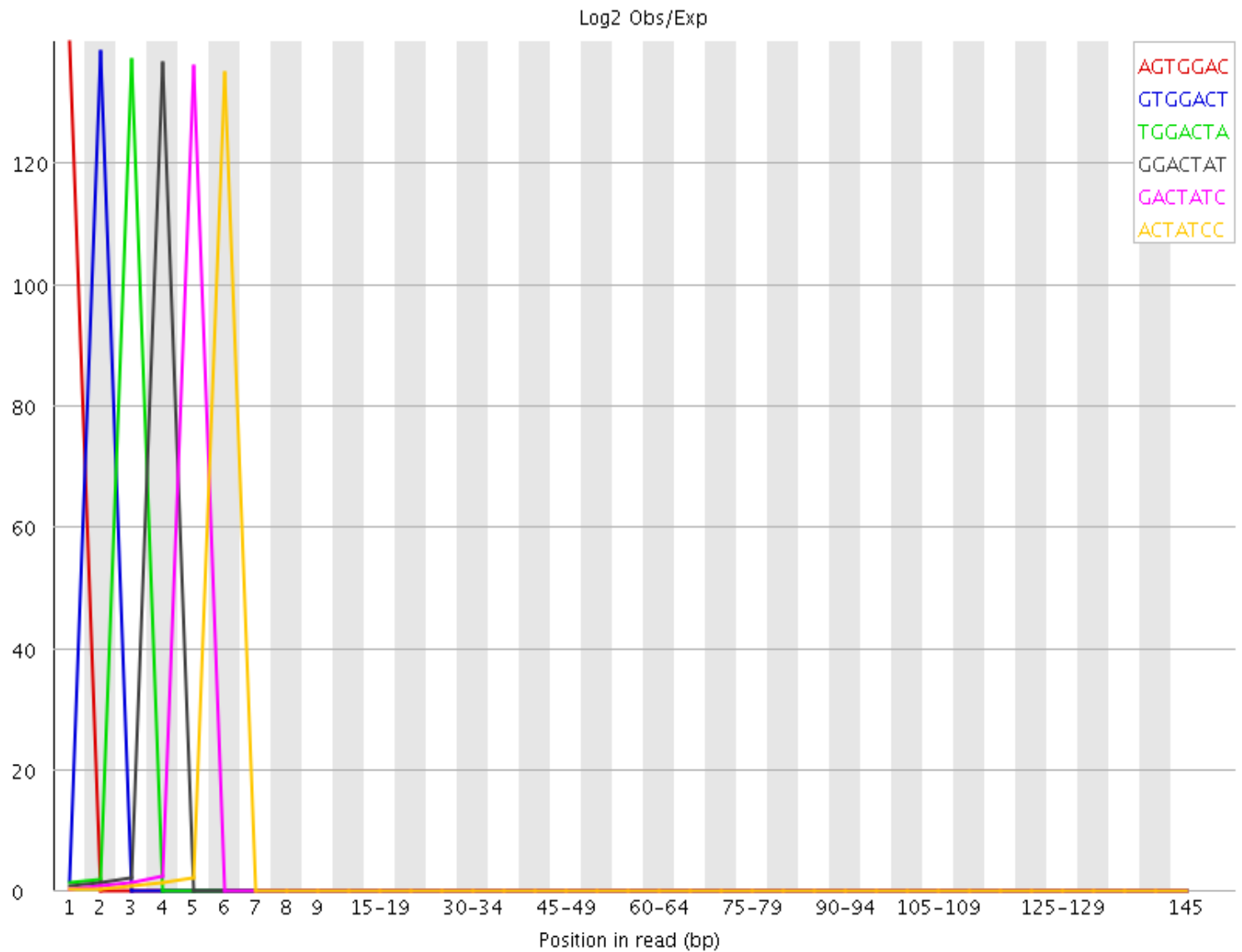
✖ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGAGTACATGG	1978924	6.123055619251738	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGAGTCGCAGT	1676091	5.186049800764084	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGATTACATGG	46576	0.1441123754738782	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCGAGTCGCAGTC	34727	0.10744998417814686	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGATTCGCAGT	34444	0.10657434431514644	No Hit

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGTGGAC	578920	0.0	139.78726	1
GTGGACT	585220	0.0	138.23163	2
TGGACTA	588895	0.0	136.9578	3
GGACTAT	593960	0.0	136.42706	4
GACTATC	590125	0.0	135.96223	5
ACTATCC	587470	0.0	134.86871	6
CTATCCA	597725	0.0	132.82771	7
TATCCAT	610885	0.0	129.48206	8
ATCCATG	619085	0.0	127.89115	9
CGGACTA	8435	0.0	39.10773	3
GCGGACT	10070	0.0	33.19004	2
GACTATA	19980	0.0	31.532661	5
ACTATAC	18250	0.0	29.95331	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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GGACTAT	593960	0.0	136.42706	4
GACTATC	590125	0.0	135.96223	5
ACTATCC	587470	0.0	134.86871	6
CTATCCA	597725	0.0	132.82771	7
TATCCAT	610885	0.0	129.48206	8
ATCCATG	619085	0.0	127.89115	9
CGGACTA	8435	0.0	39.10773	3
GCGGACT	10070	0.0	33.19004	2
GACTATA	19980	0.0	31.532661	5
ACTATAC	18250	0.0	29.95331	6

AGCGGAC	12095	0.0	28.112747	1
TGAACGC	622590	0.0	26.669287	10-14
ATGAACG	627480	0.0	26.55758	10-14
GGCCTAT	13015	0.0	25.847	4
CATGAAC	635520	0.0	25.808174	10-14
CGCAAAG	643760	0.0	25.606897	15-19
ACTATCA	36100	0.0	25.505444	6

Produced by [FastQC](#) (version 0.11.5)