

Supplementary Information

Title

Whole genome resequencing data for three rockfish species of *Sebastes*

Authors

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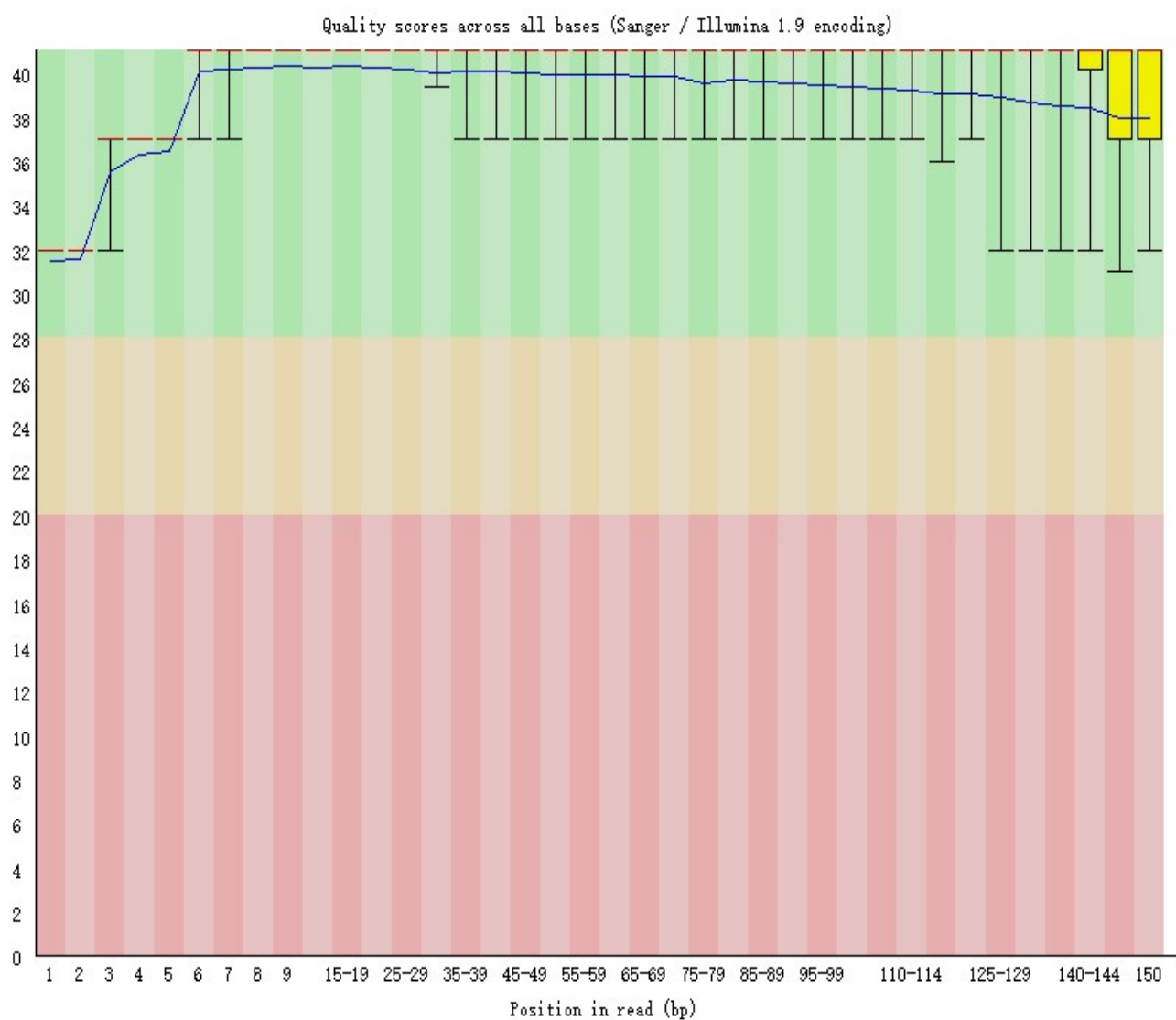
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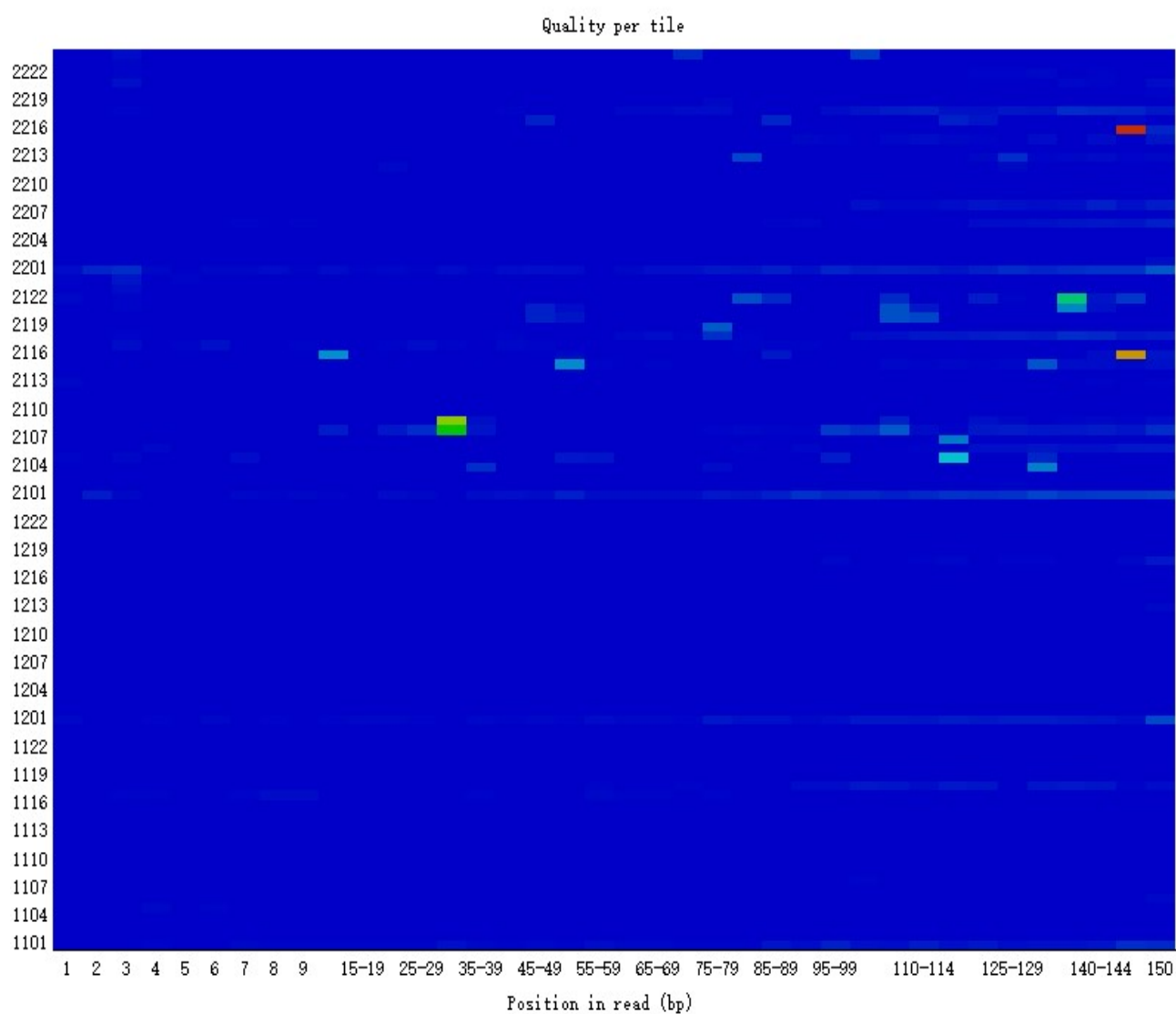
Basic Statistics

Measure	Value
Filename	SS_L4_1_clean.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	128134474
Sequences flagged as poor quality	0
Sequence length	150
%GC	40

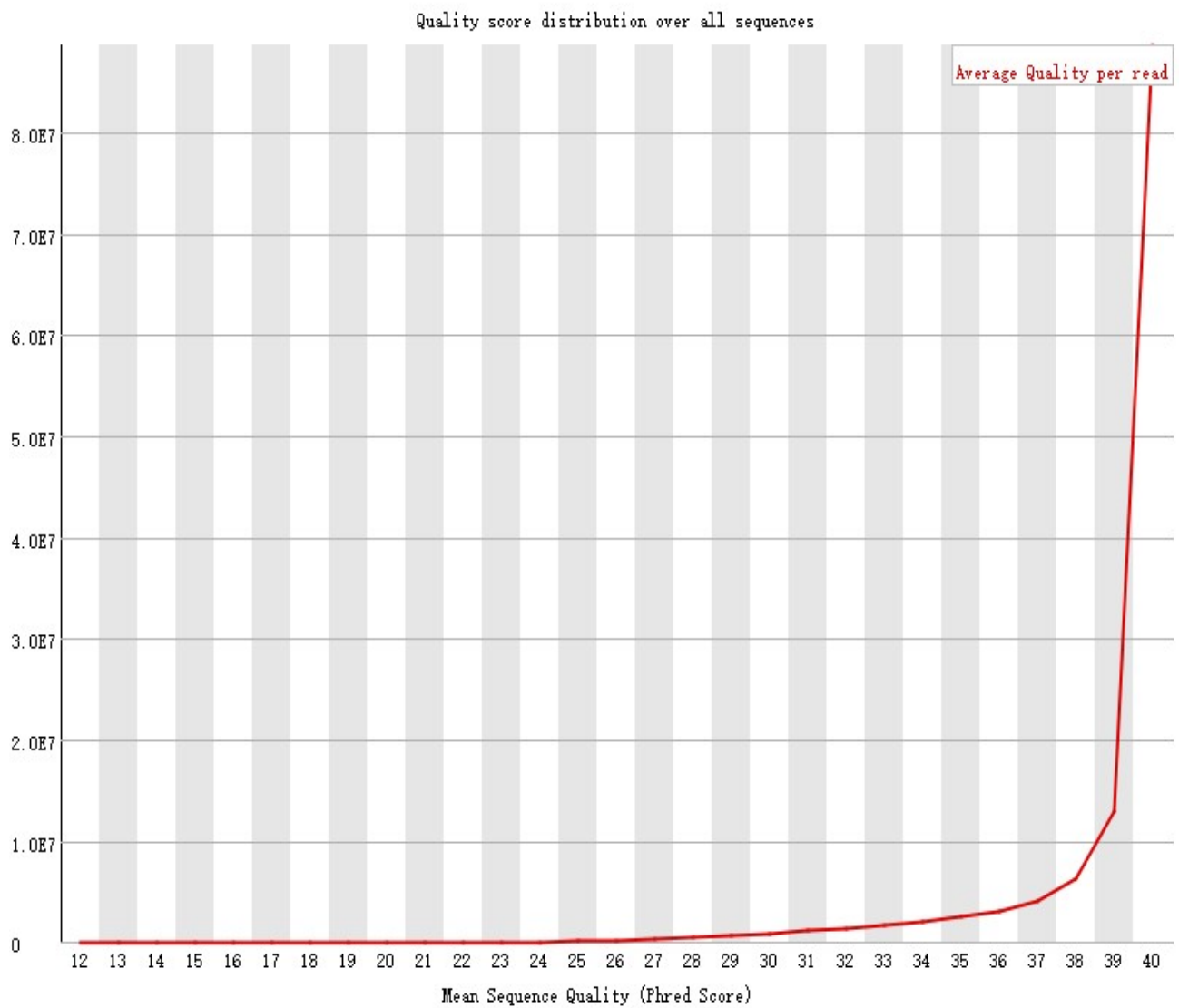
✔ Per base sequence quality



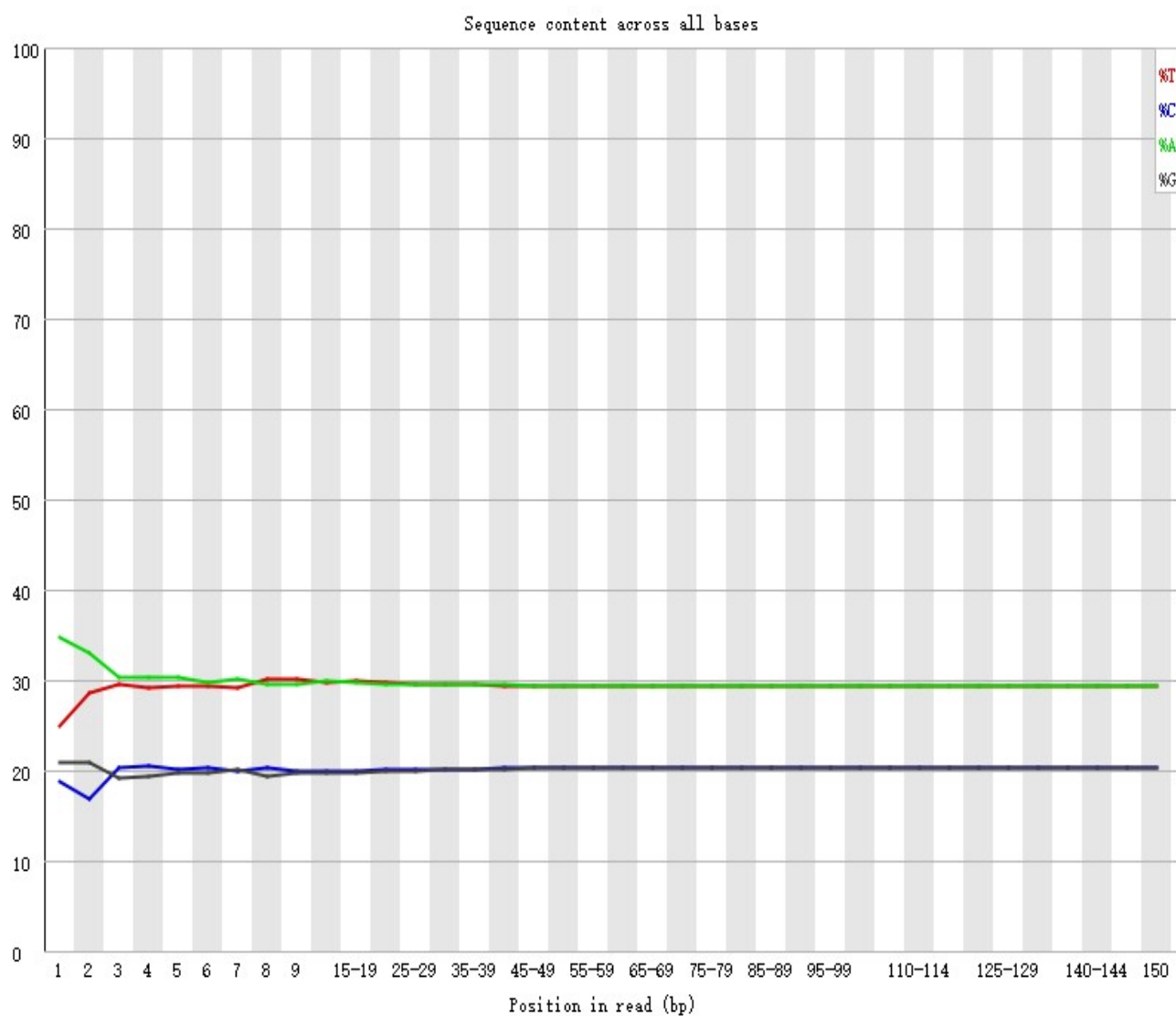
! Per tile sequence quality



✔ Per sequence quality scores

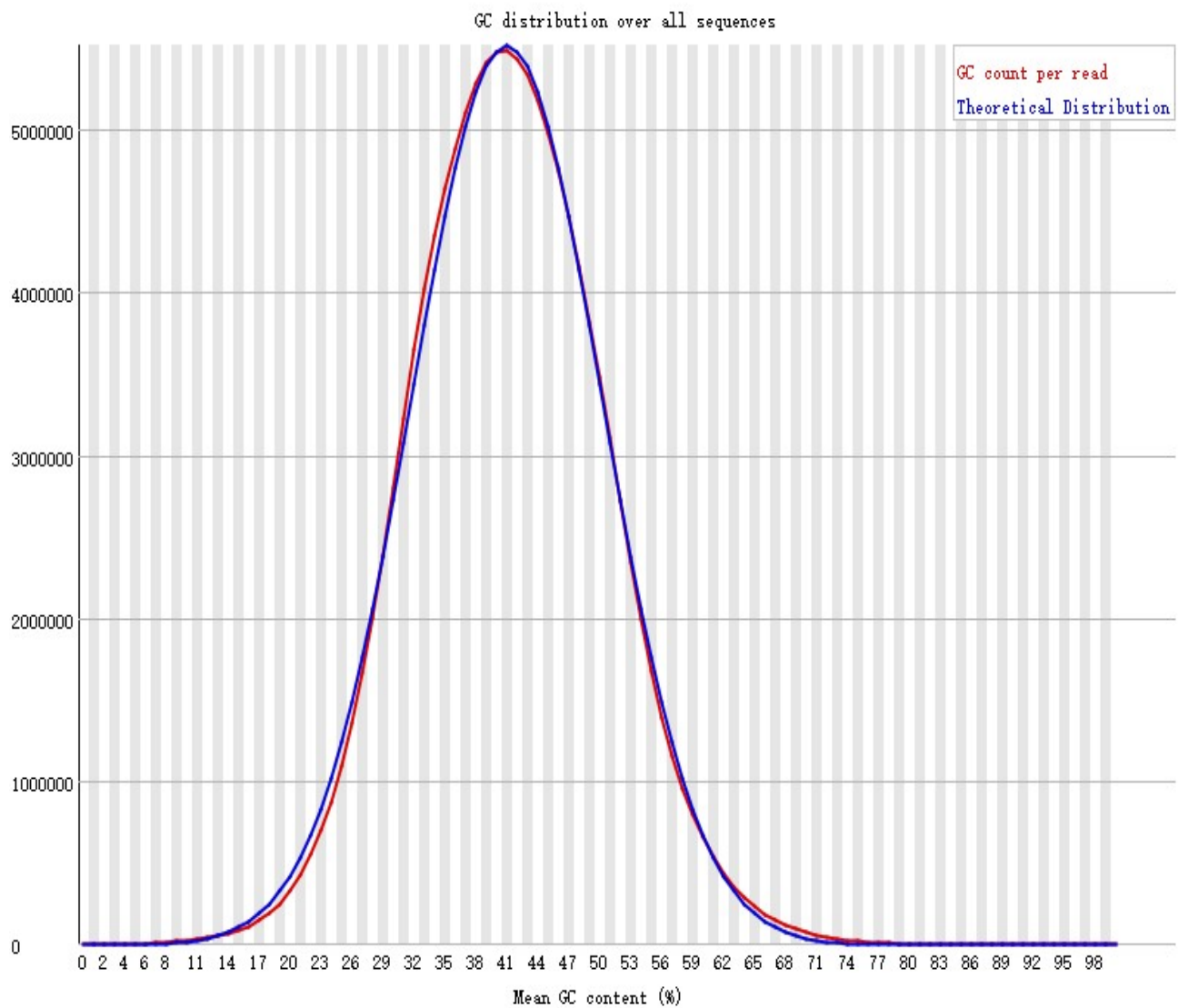


✔ Per base sequence content

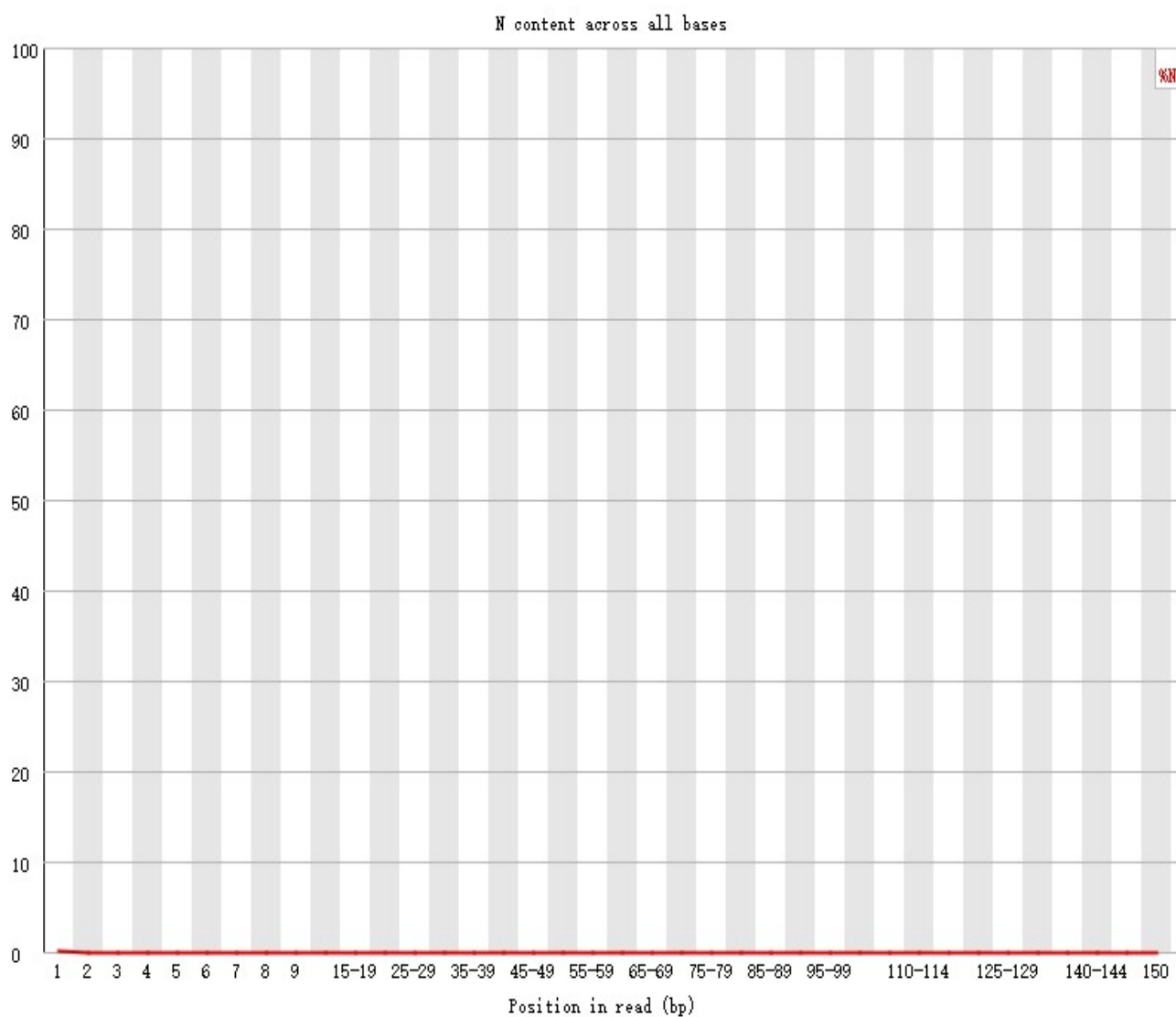




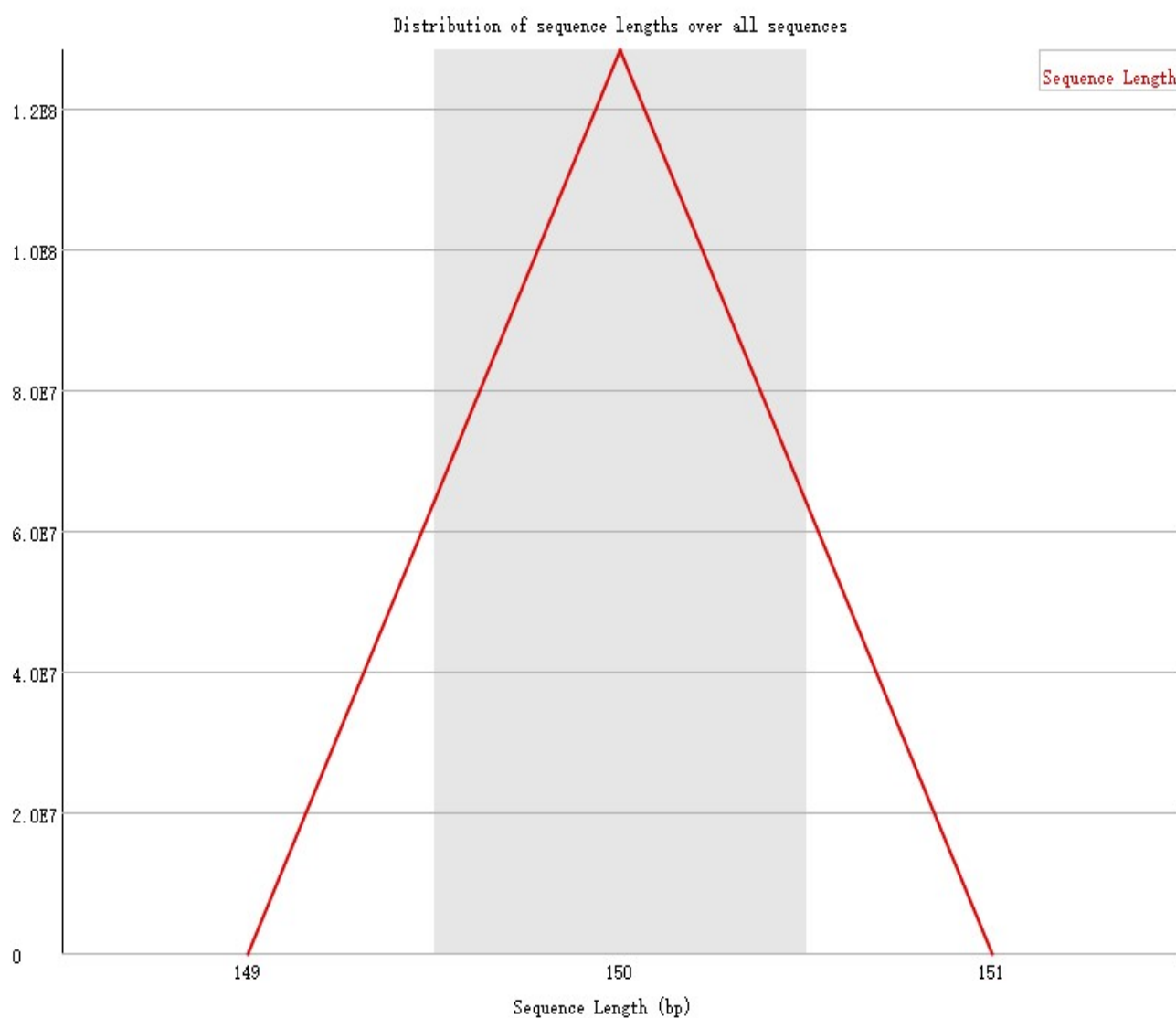
Per sequence GC content



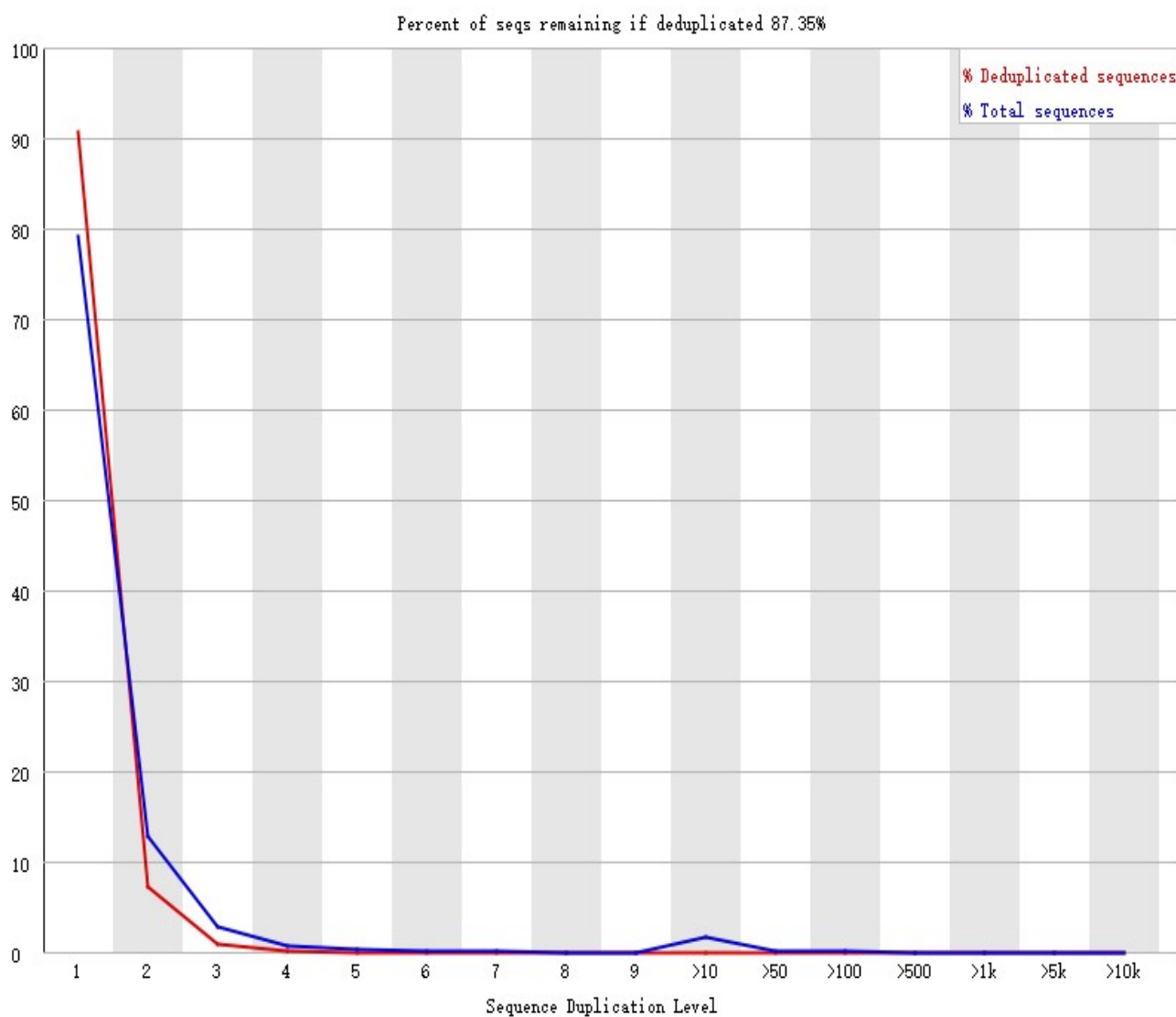
✔ Per base N content



Sequence Length Distribution



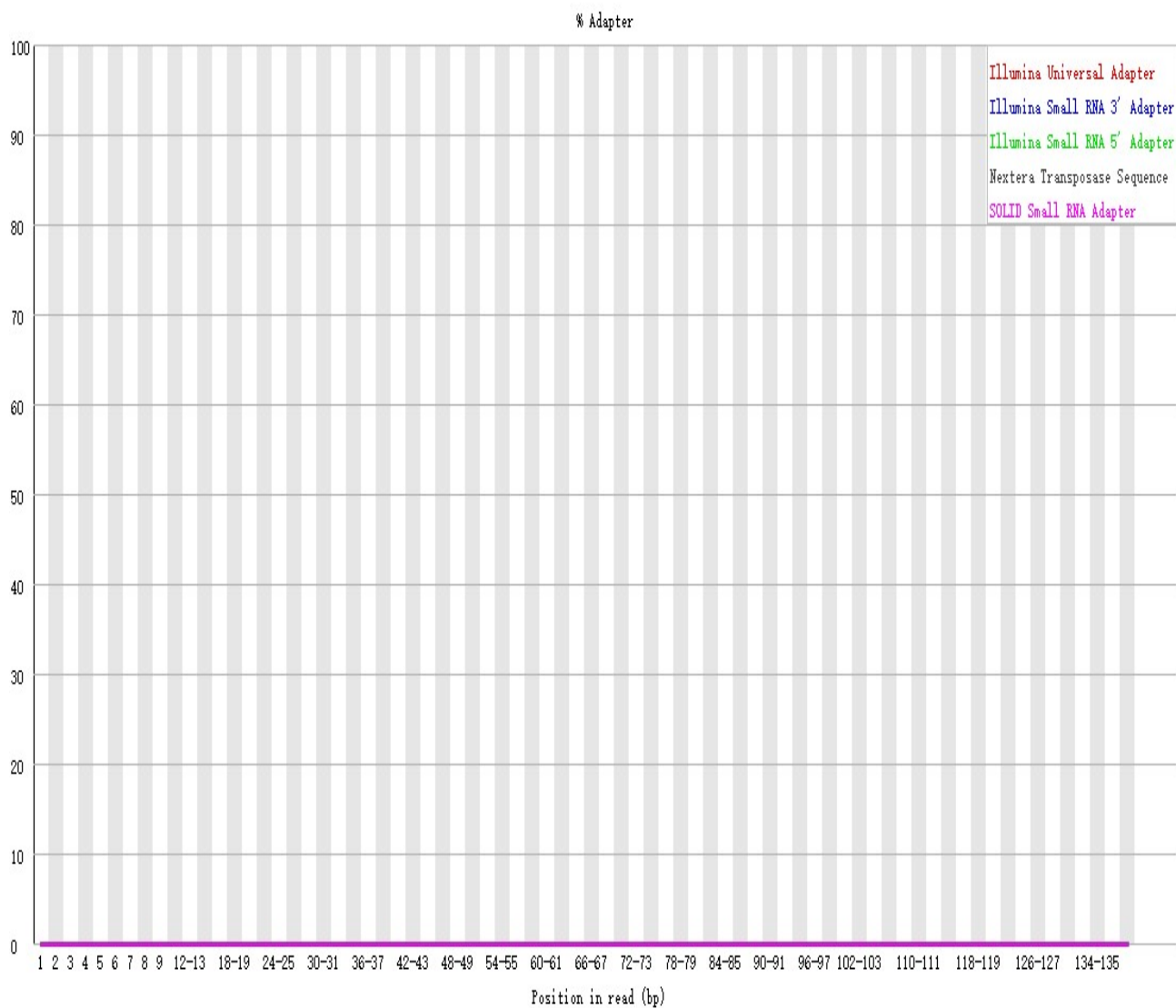
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

✓ Adapter Content



✓ Kmer Content

No overrepresented Kmers

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

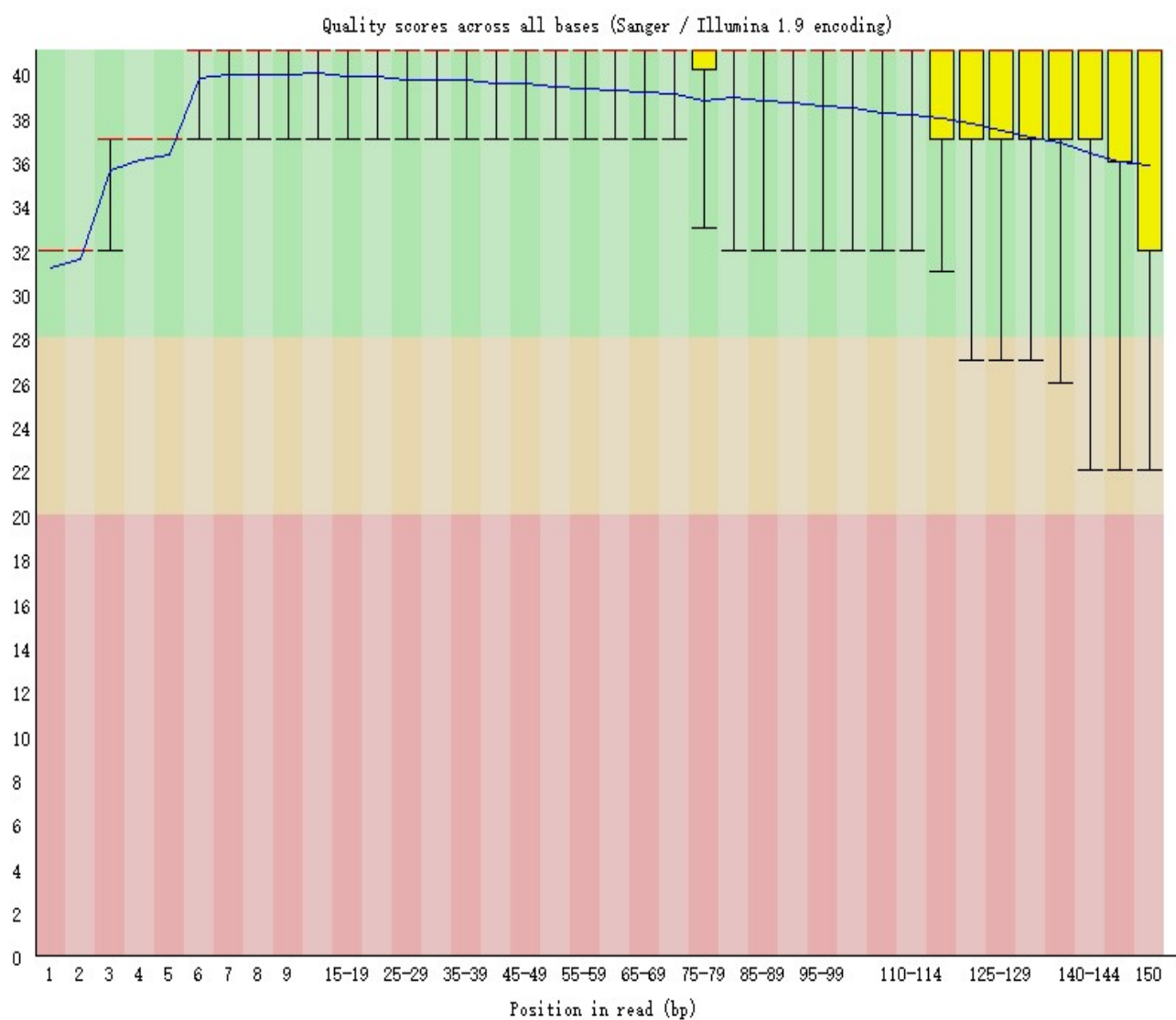
Summary

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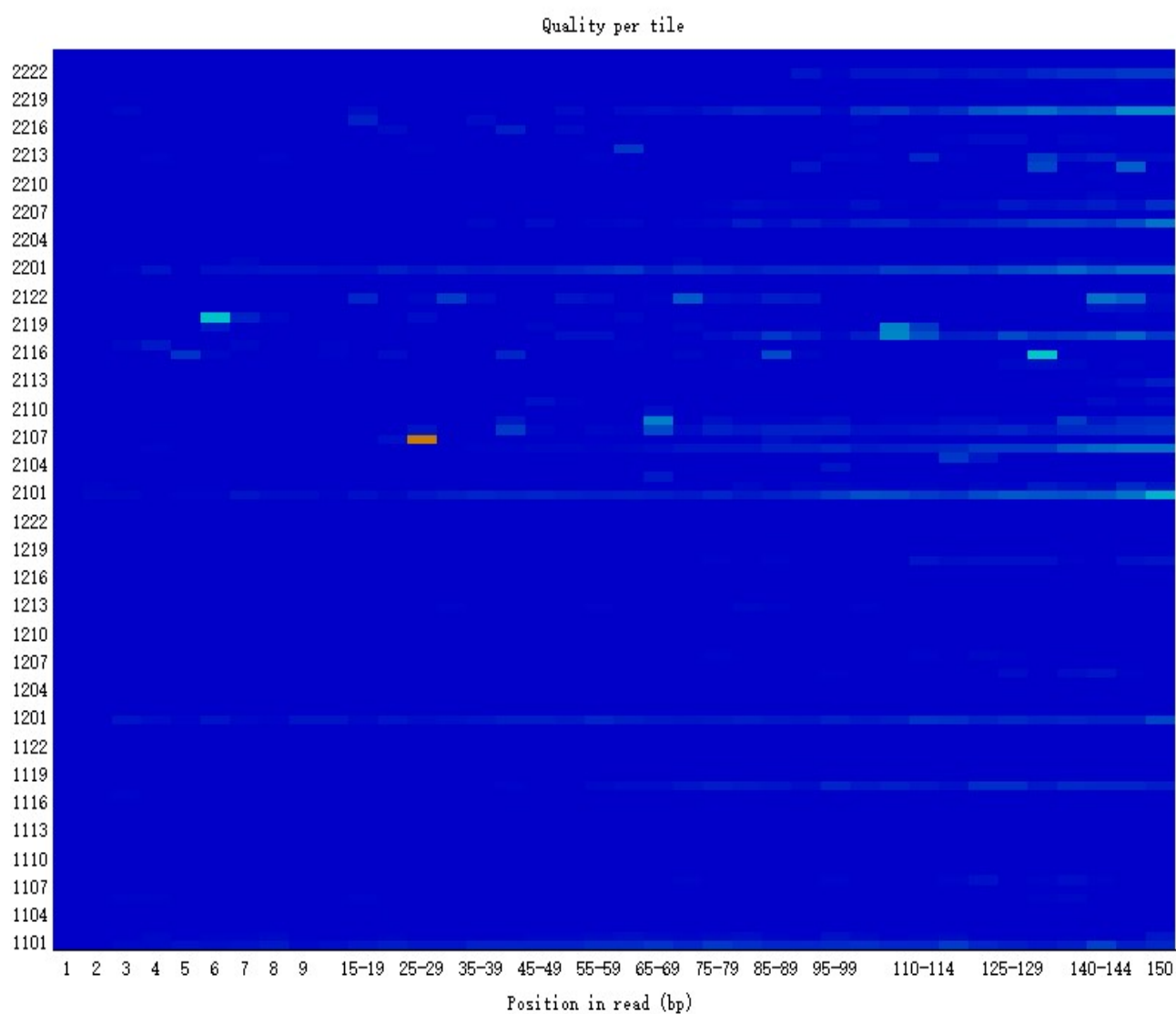
Basic Statistics

Measure	Value
Filename	SS_L4_2_clean.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	128134474
Sequences flagged as poor quality	0
Sequence length	150
%GC	40

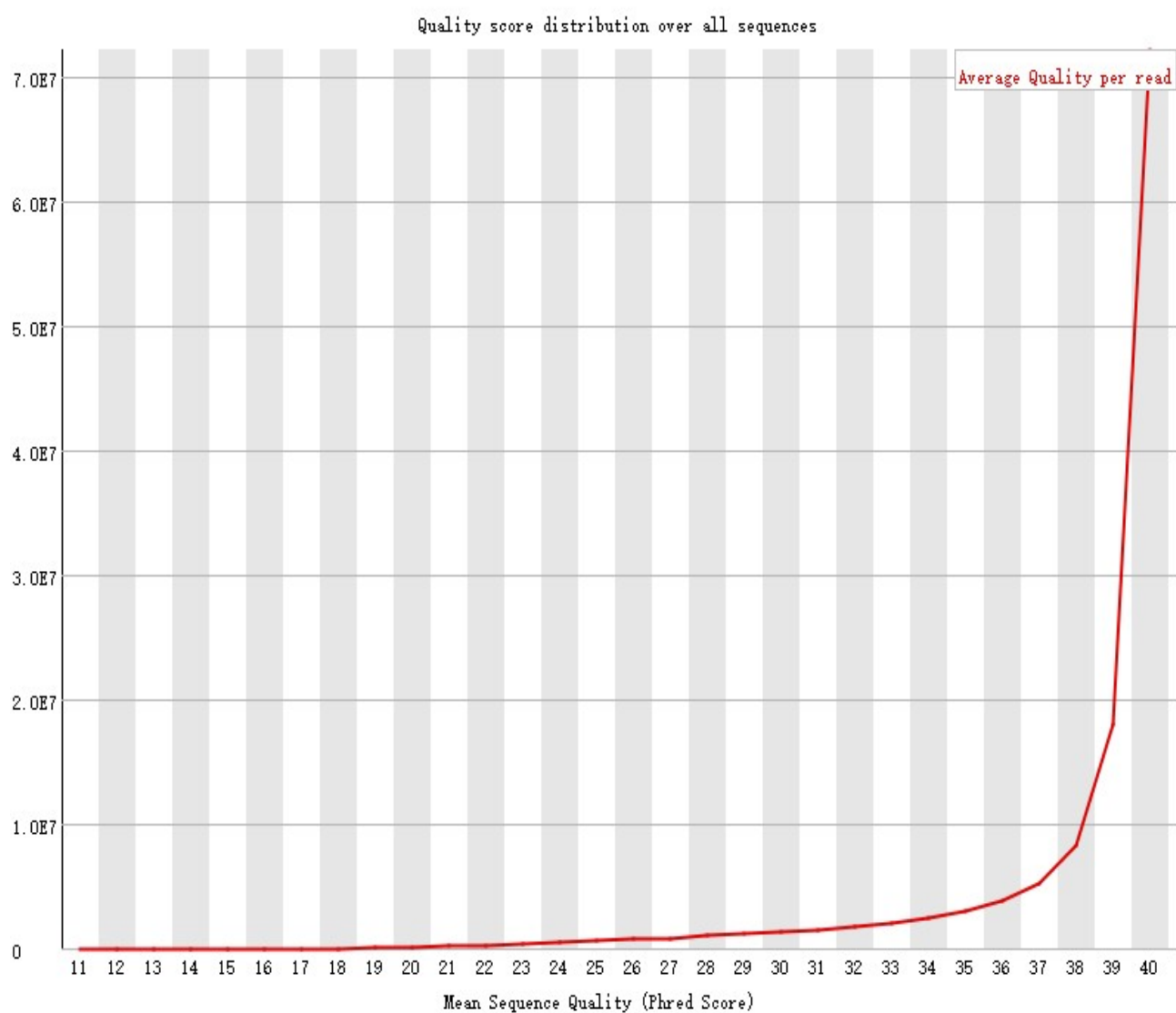
✓ Per base sequence quality



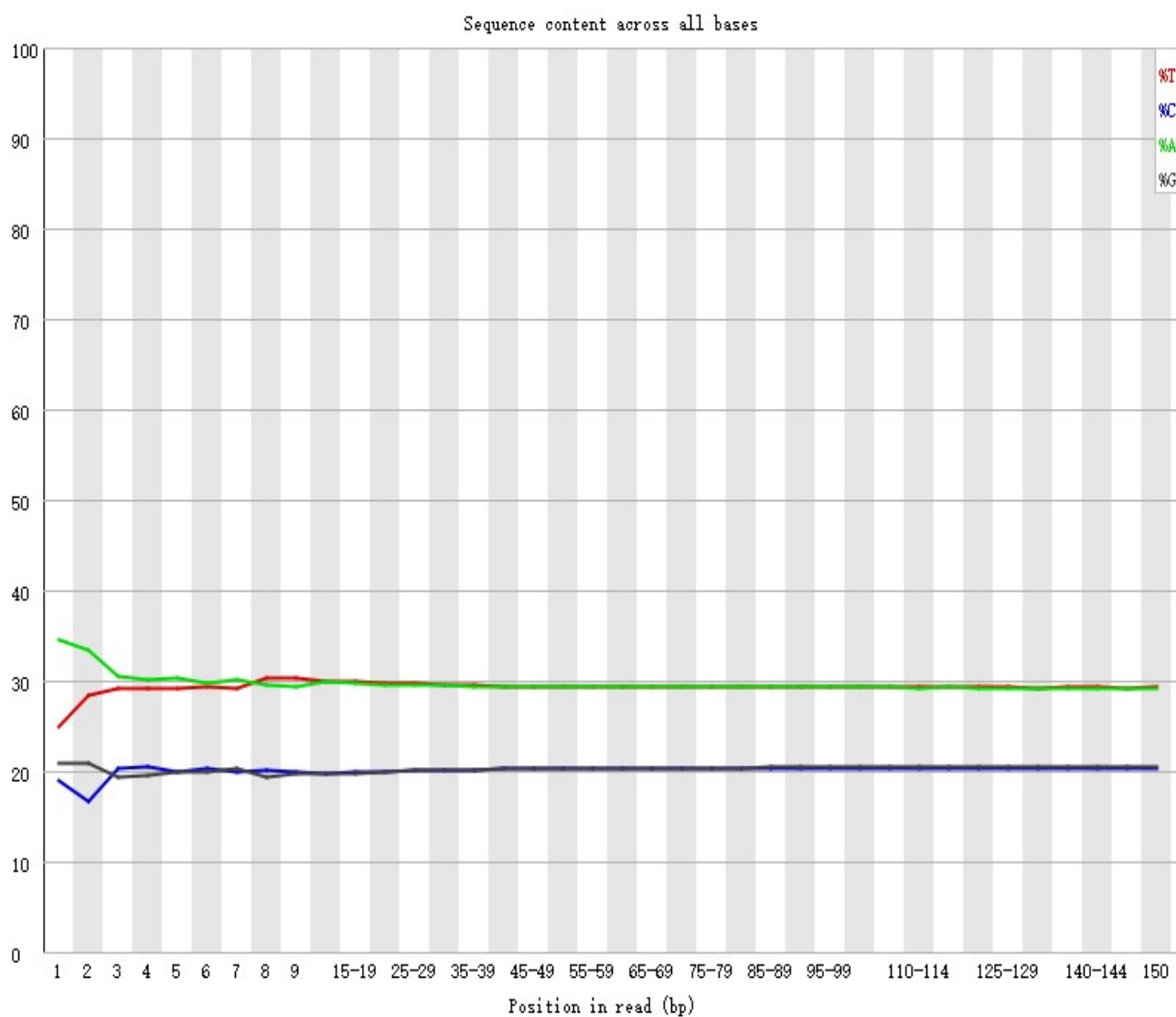
! Per tile sequence quality



✔ Per sequence quality scores

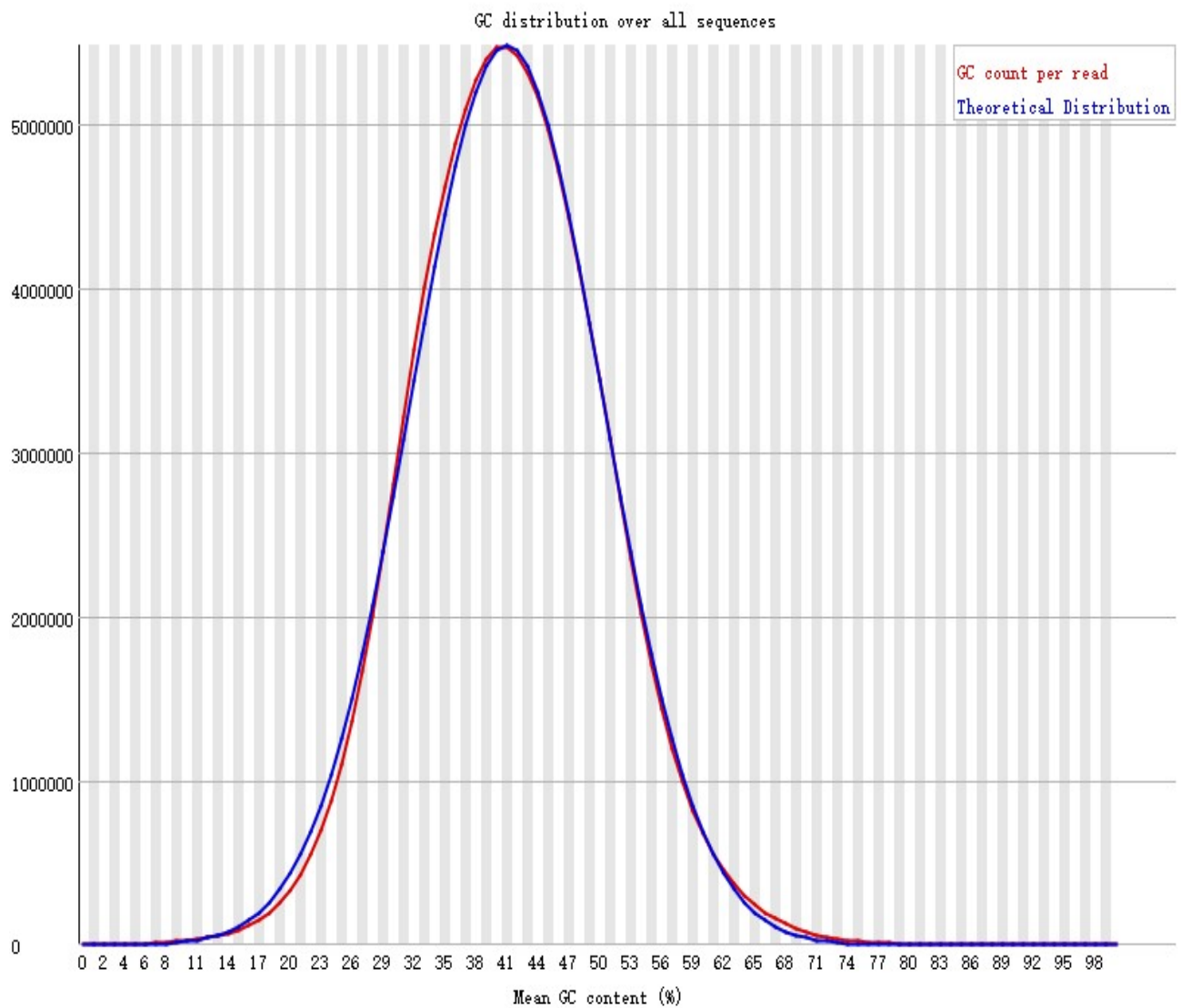


✔ Per base sequence content

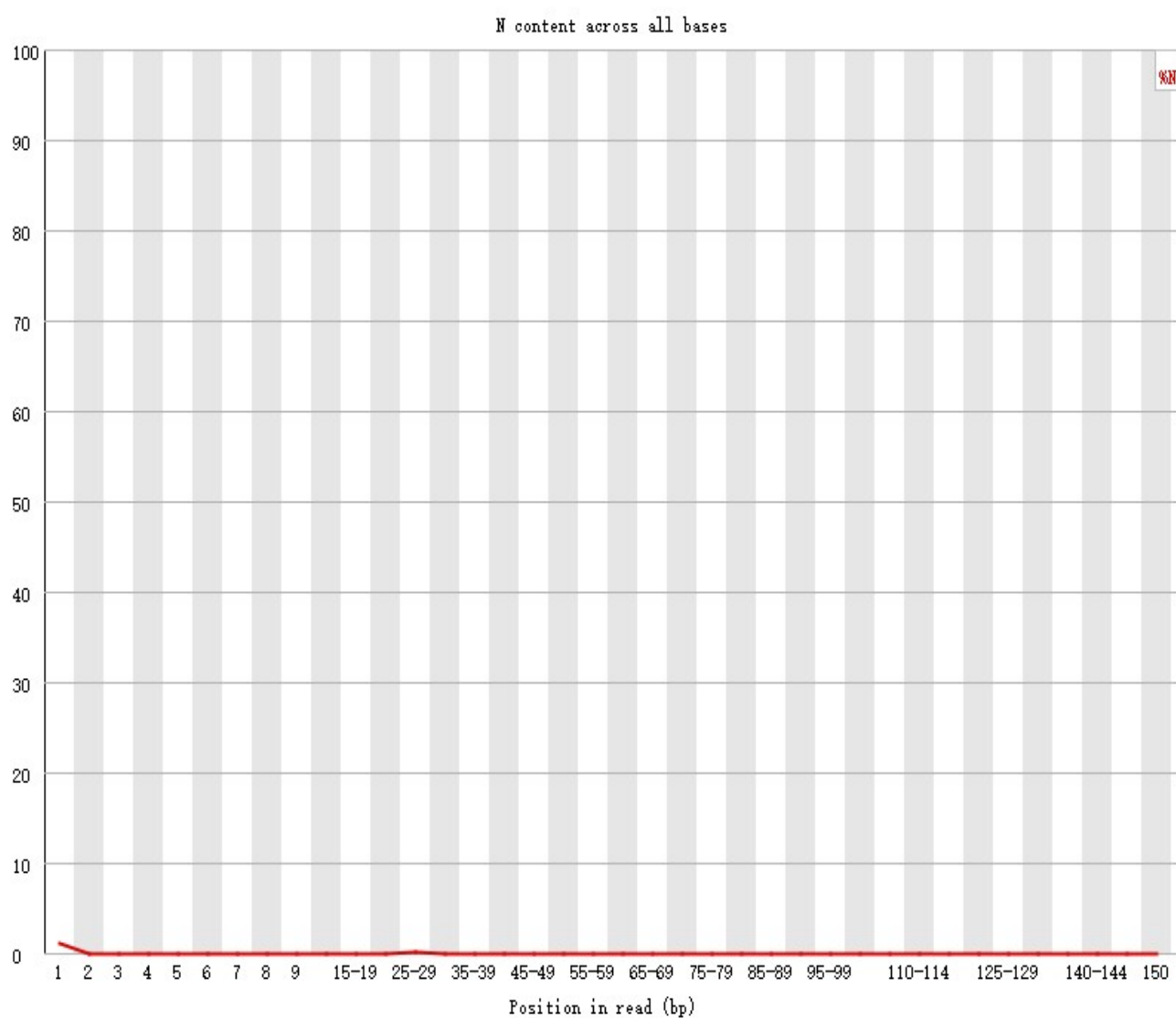




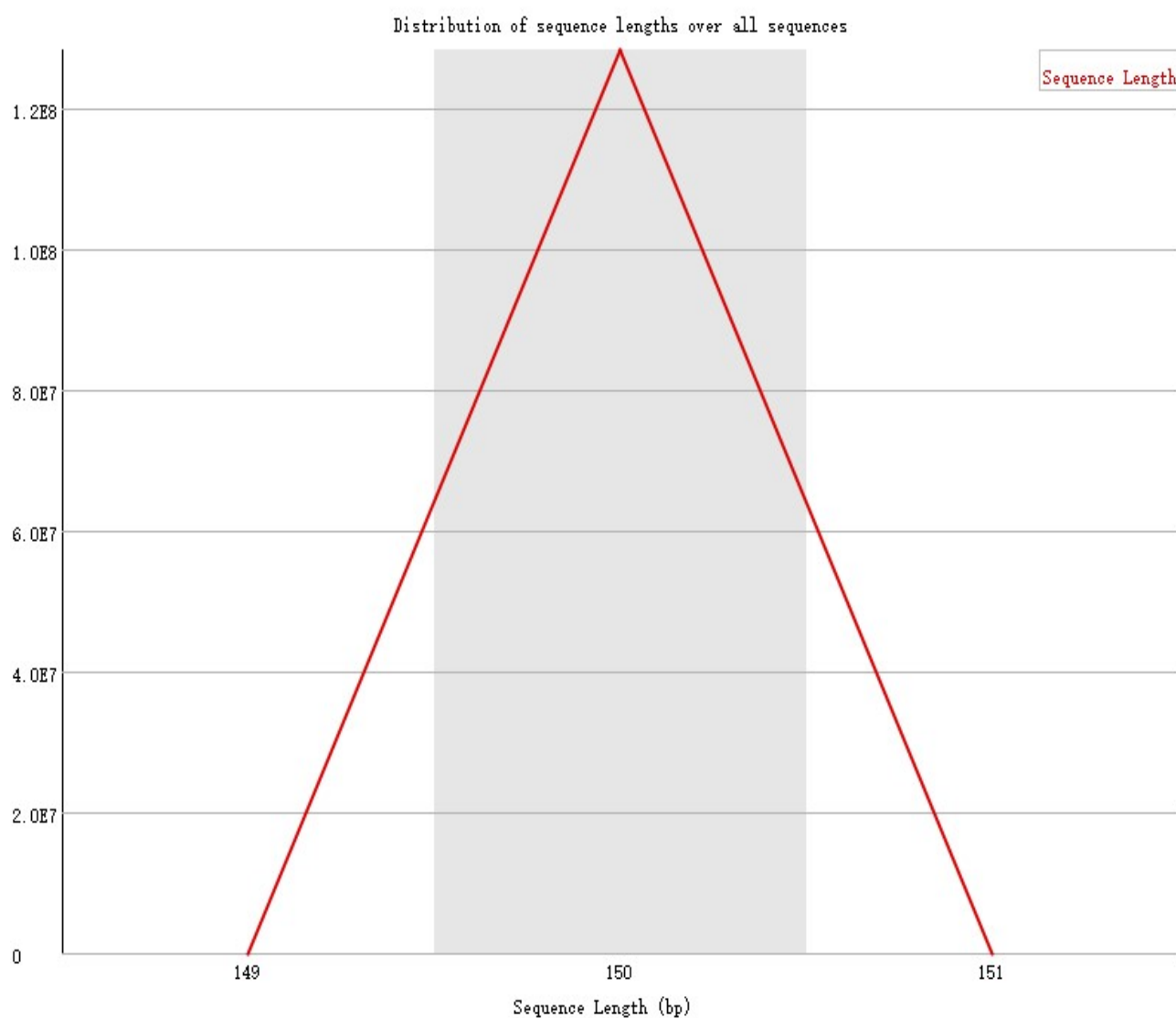
Per sequence GC content



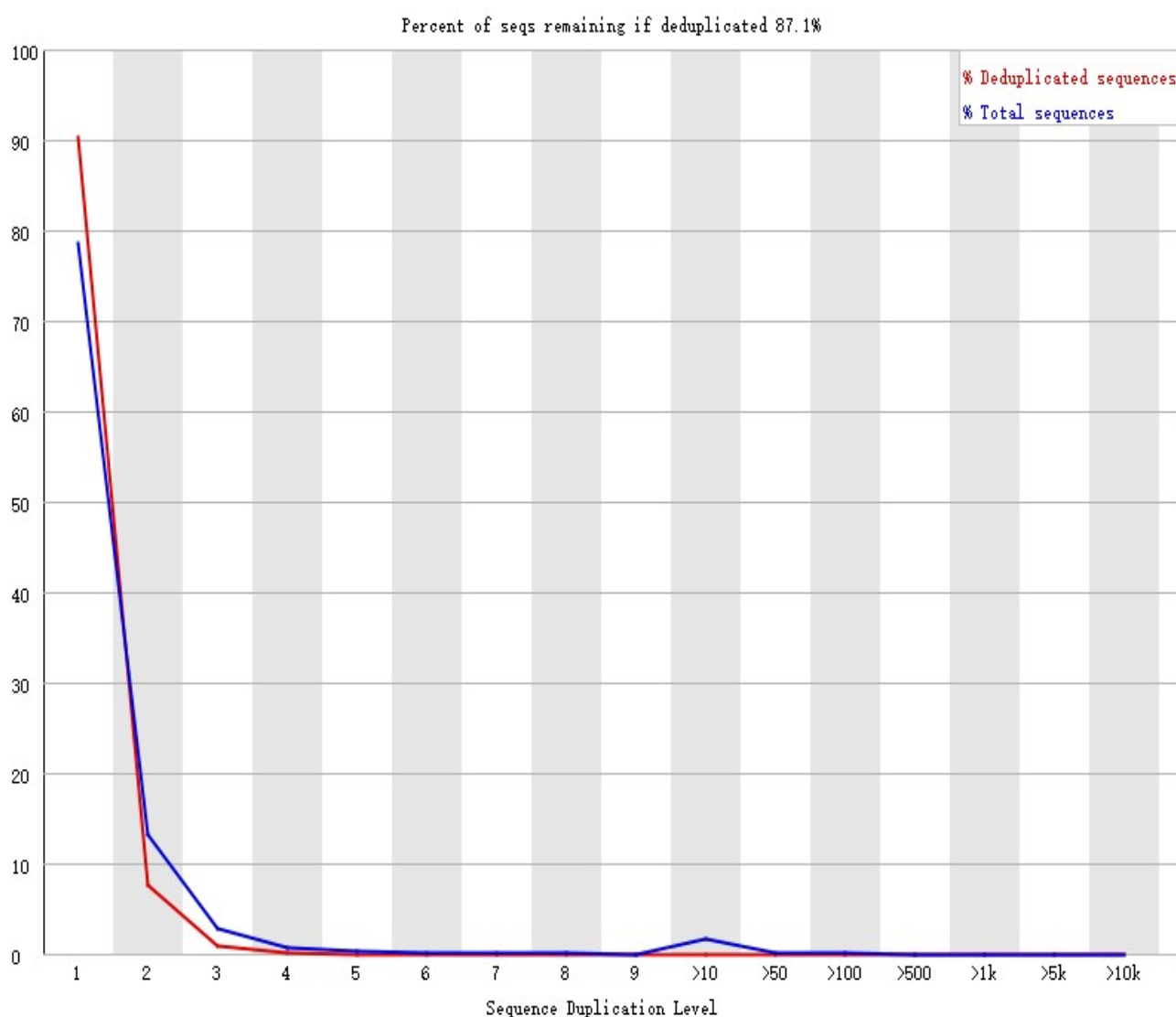
✔ Per base N content



Sequence Length Distribution



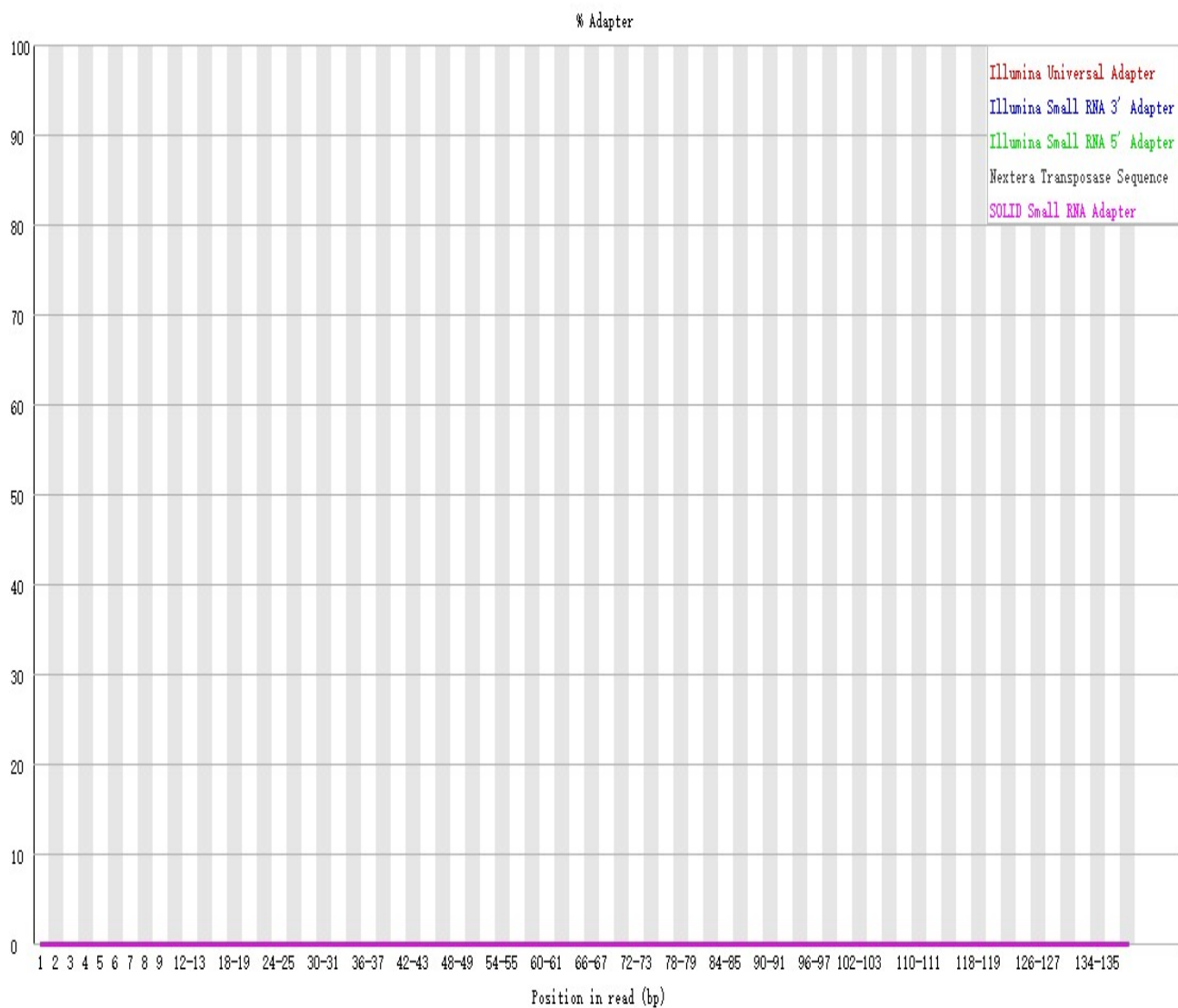
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

Adapter Content



Kmer Content

No overrepresented Kmers

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

FastQC Report

Summary

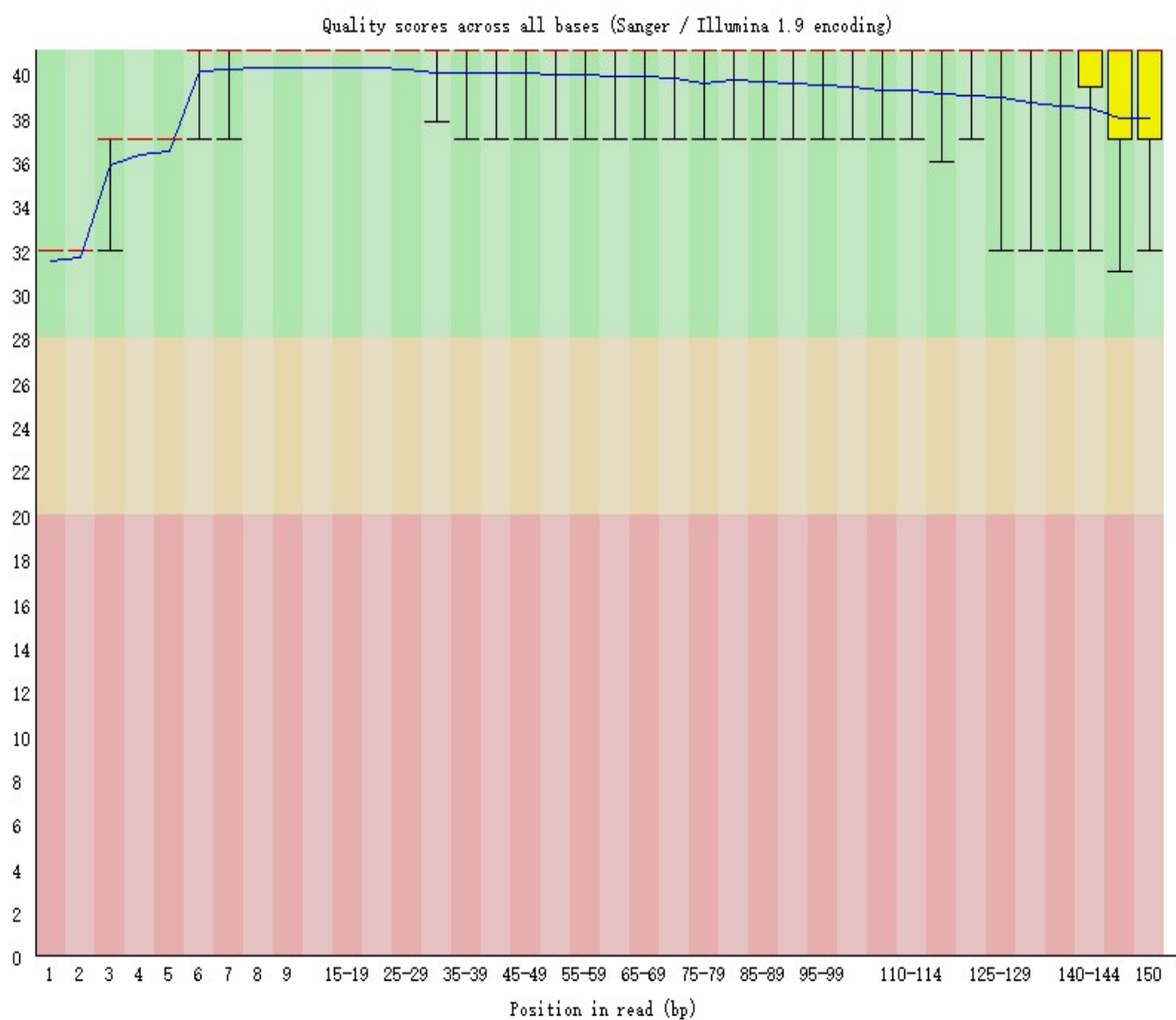
星期三 8 五月 2019
SK_L4_1_clean.fq.gz

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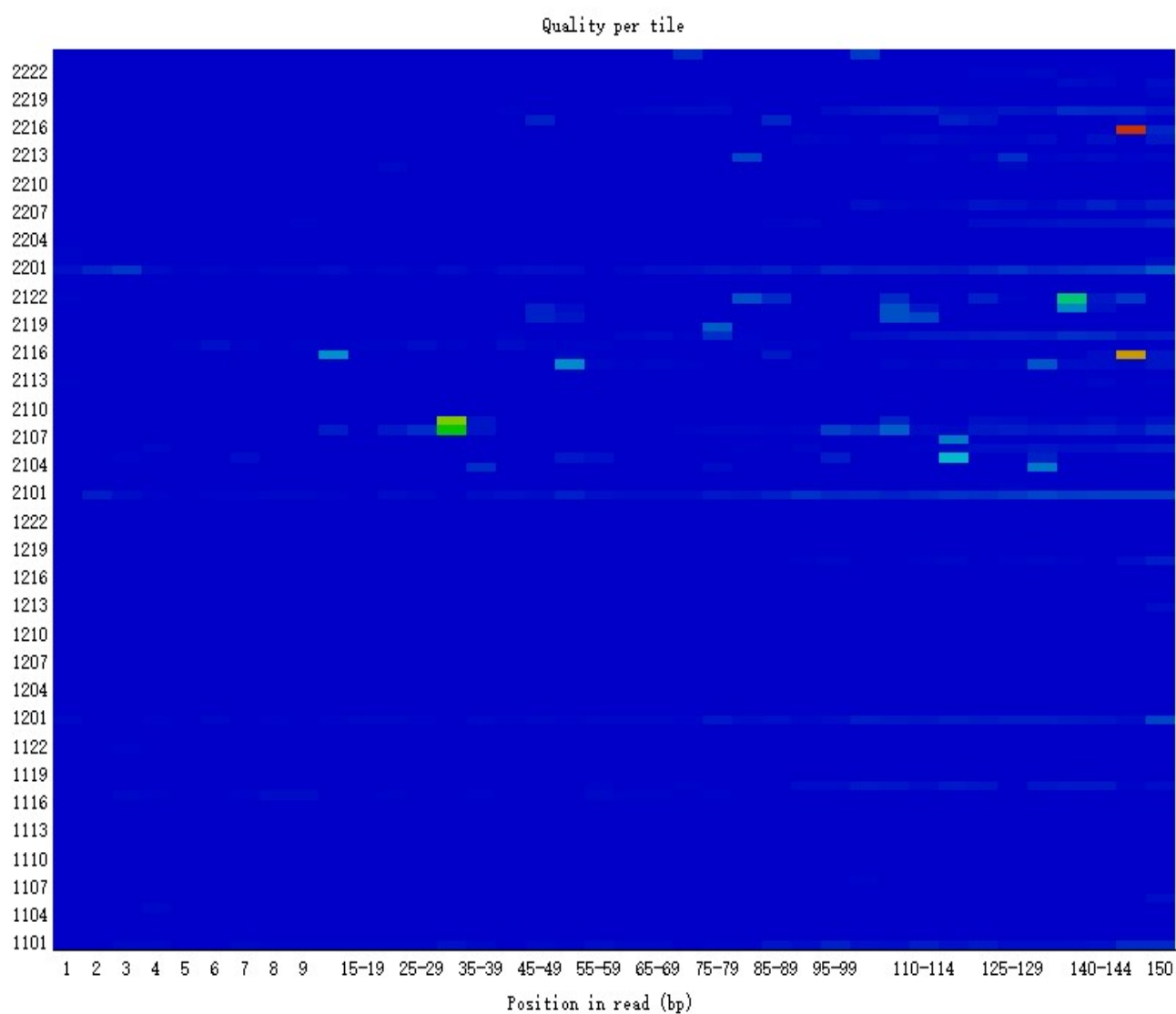
Basic Statistics

Measure	Value
Filename	SK_L4_1_clean.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	137026069
Sequences flagged as poor quality	0
Sequence length	150
%GC	41

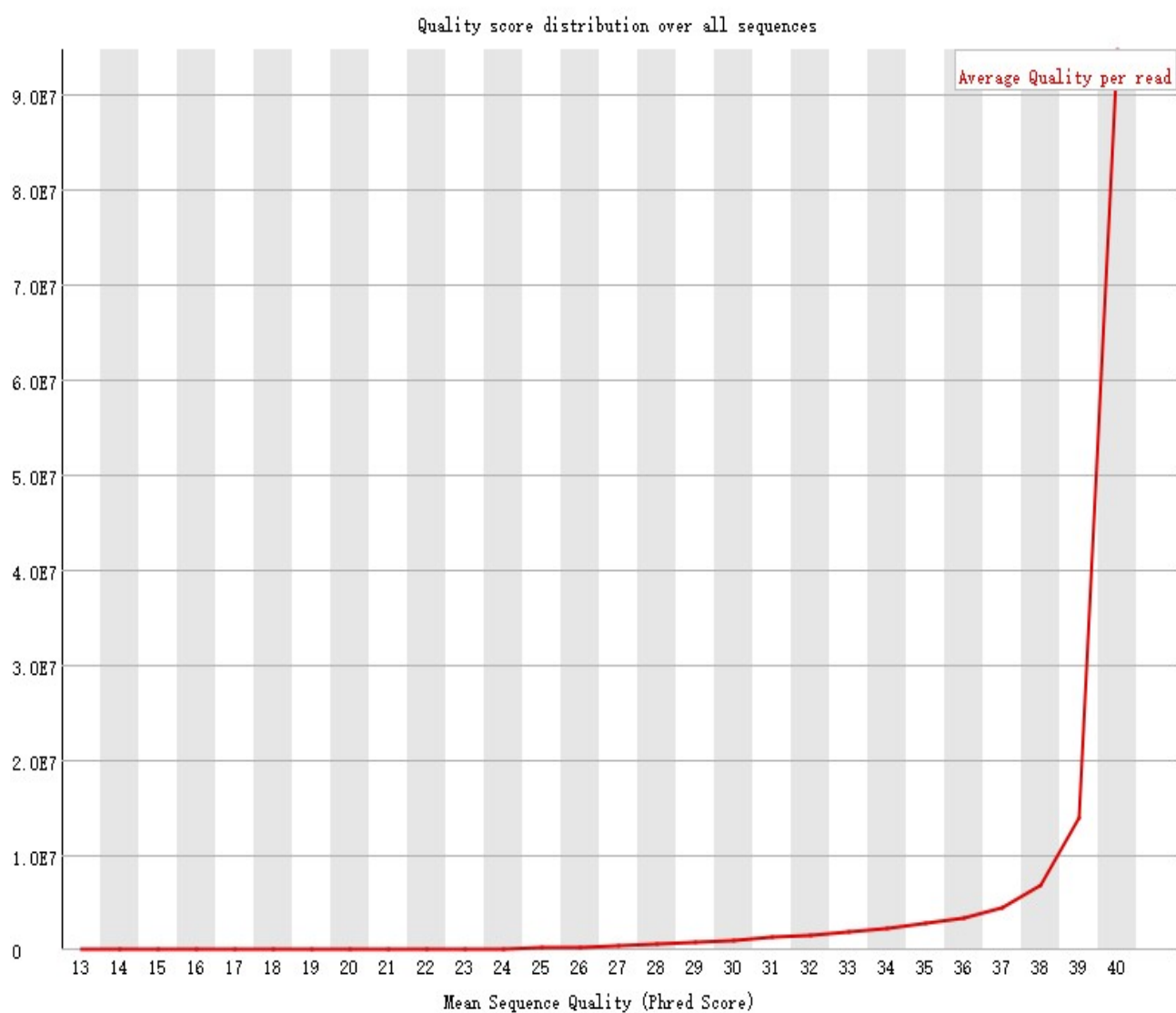
✔ Per base sequence quality



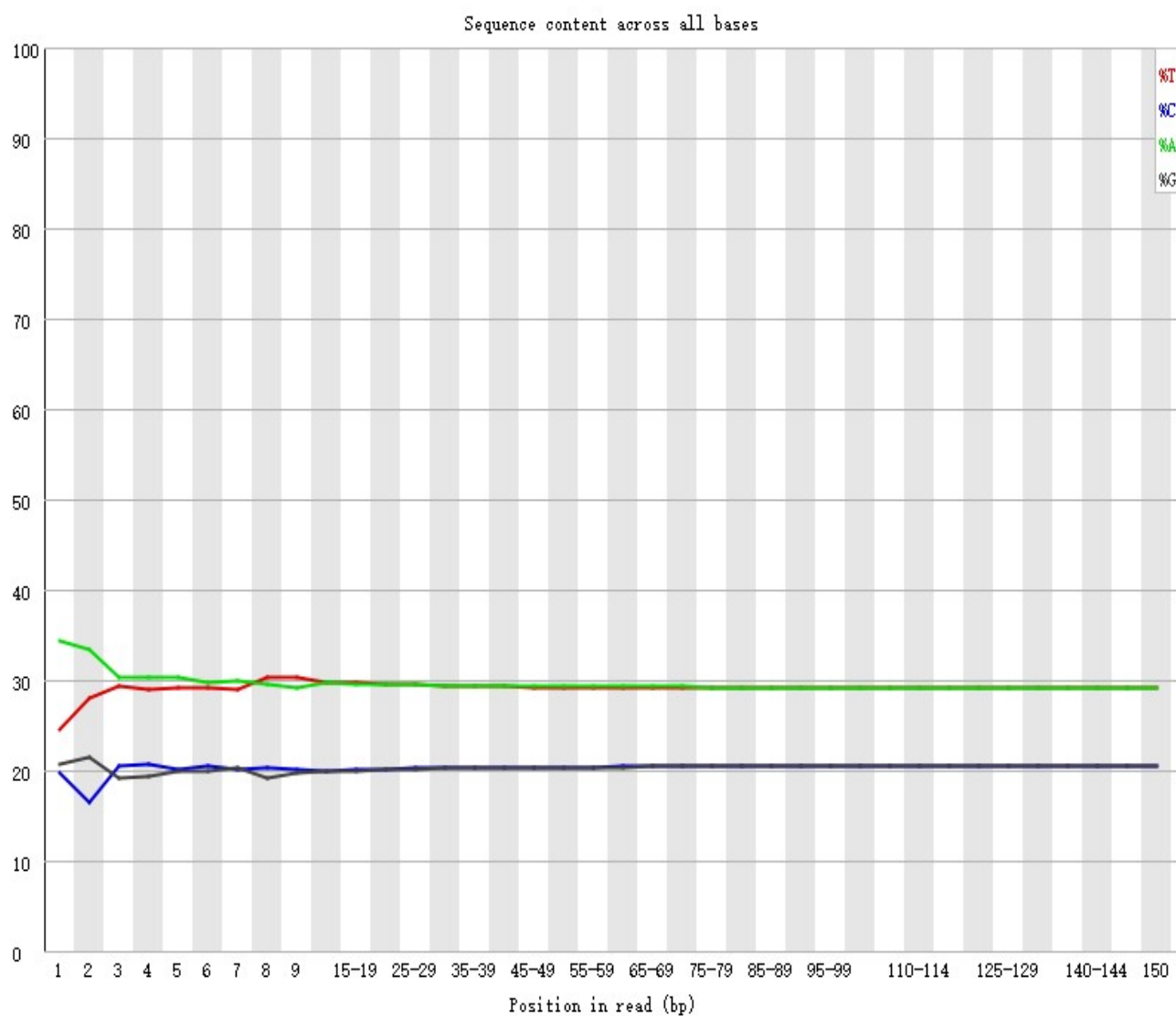
! Per tile sequence quality



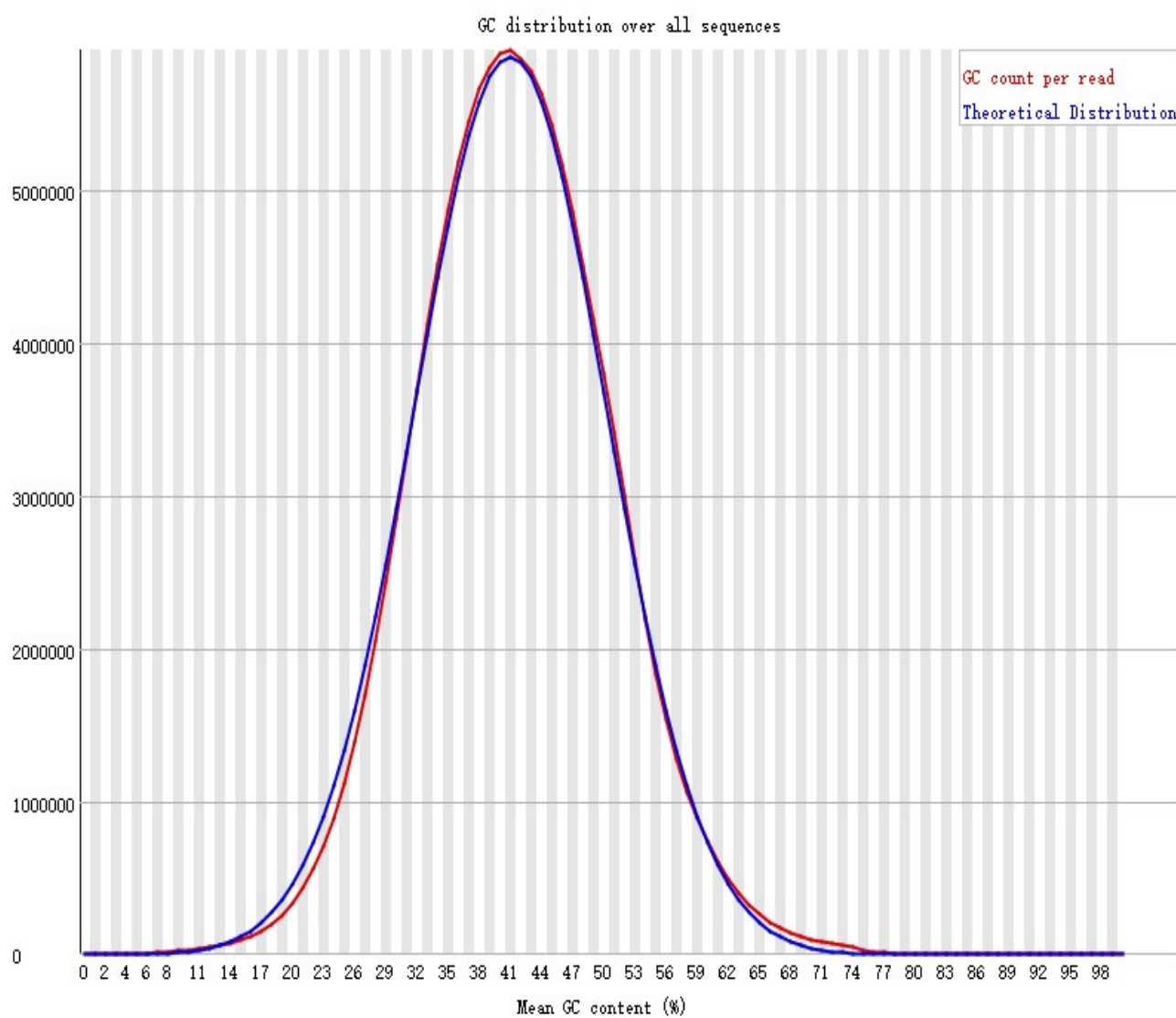
✔ Per sequence quality scores



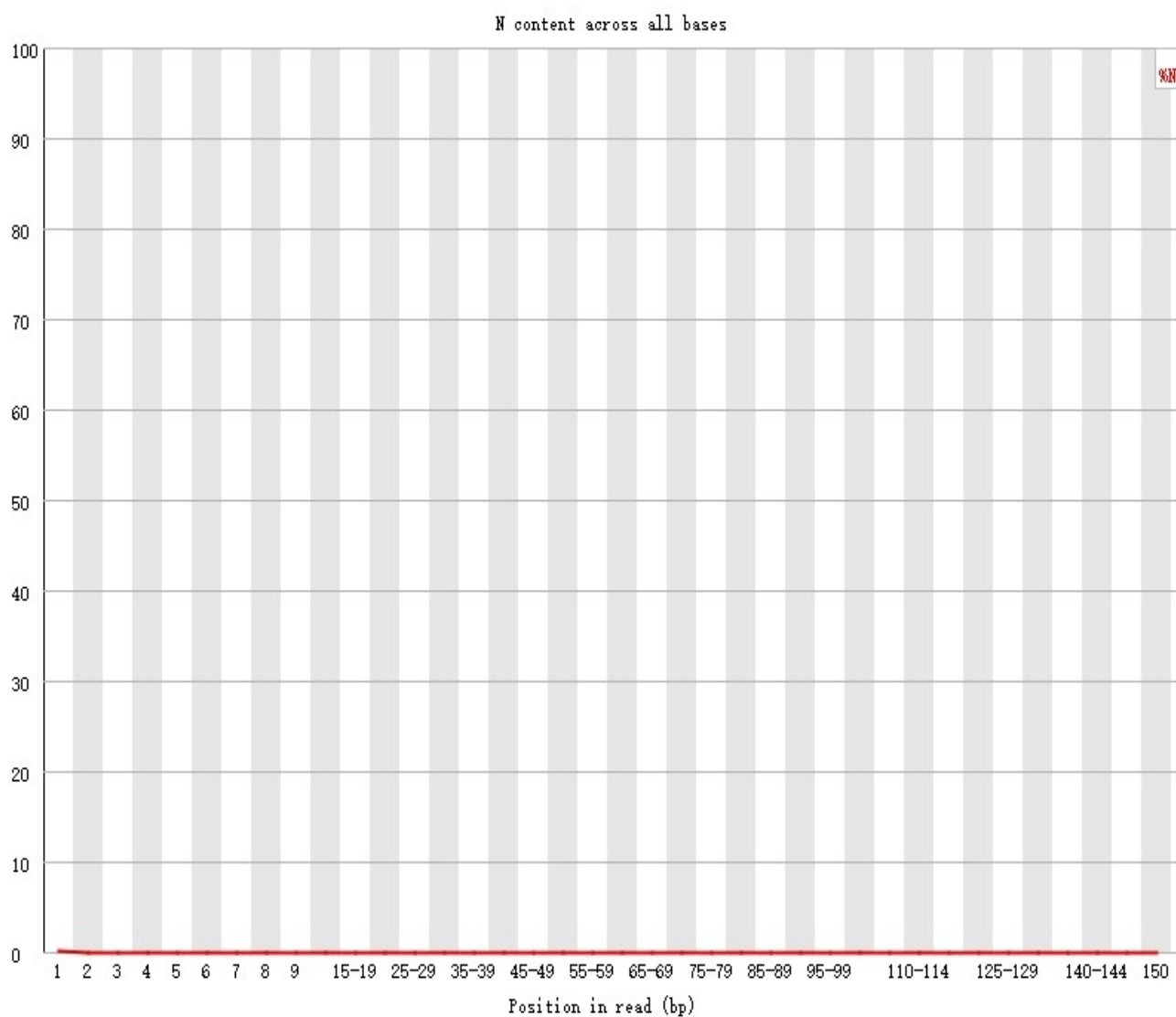
✔ Per base sequence content



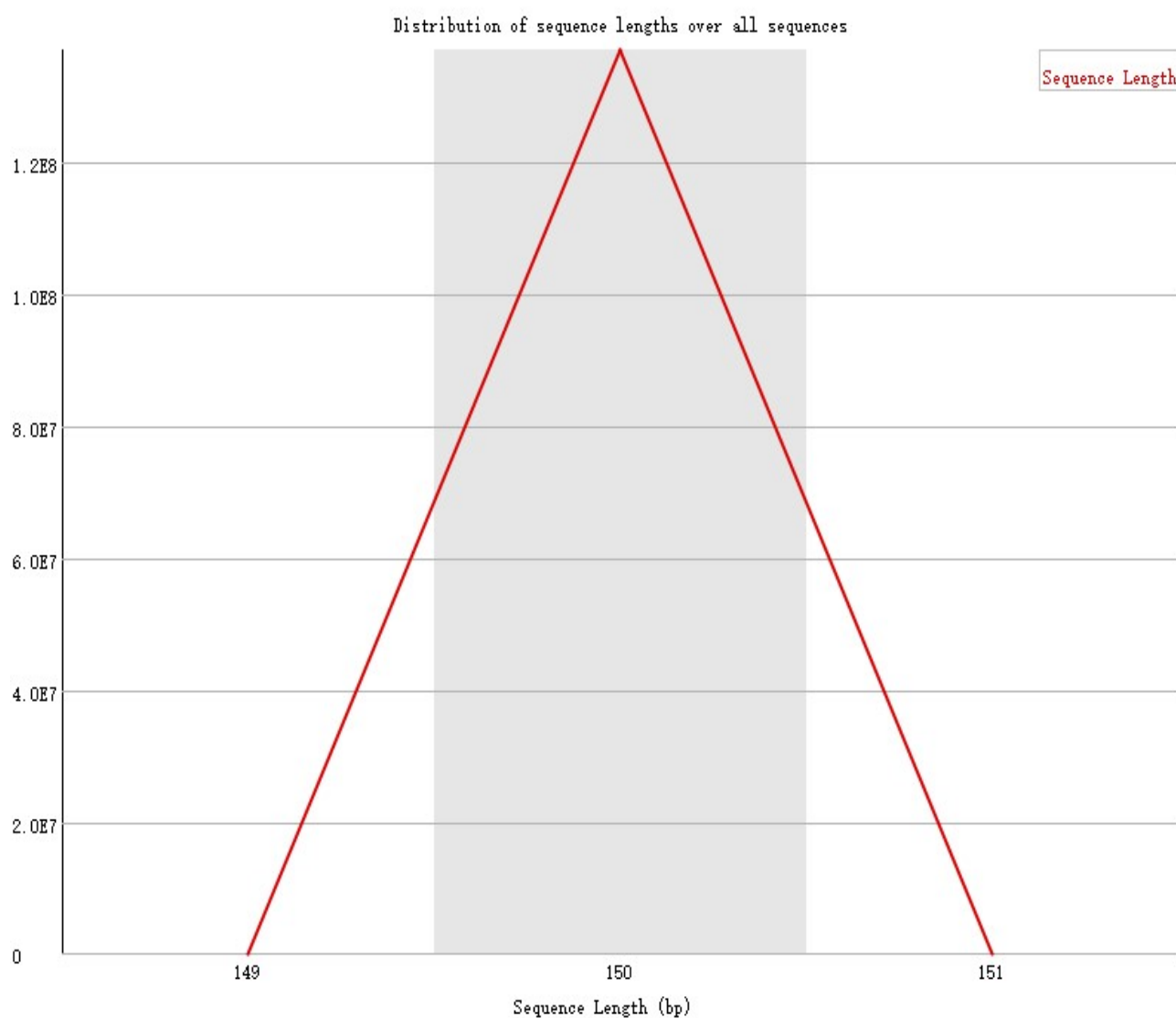
✔ Per sequence GC content



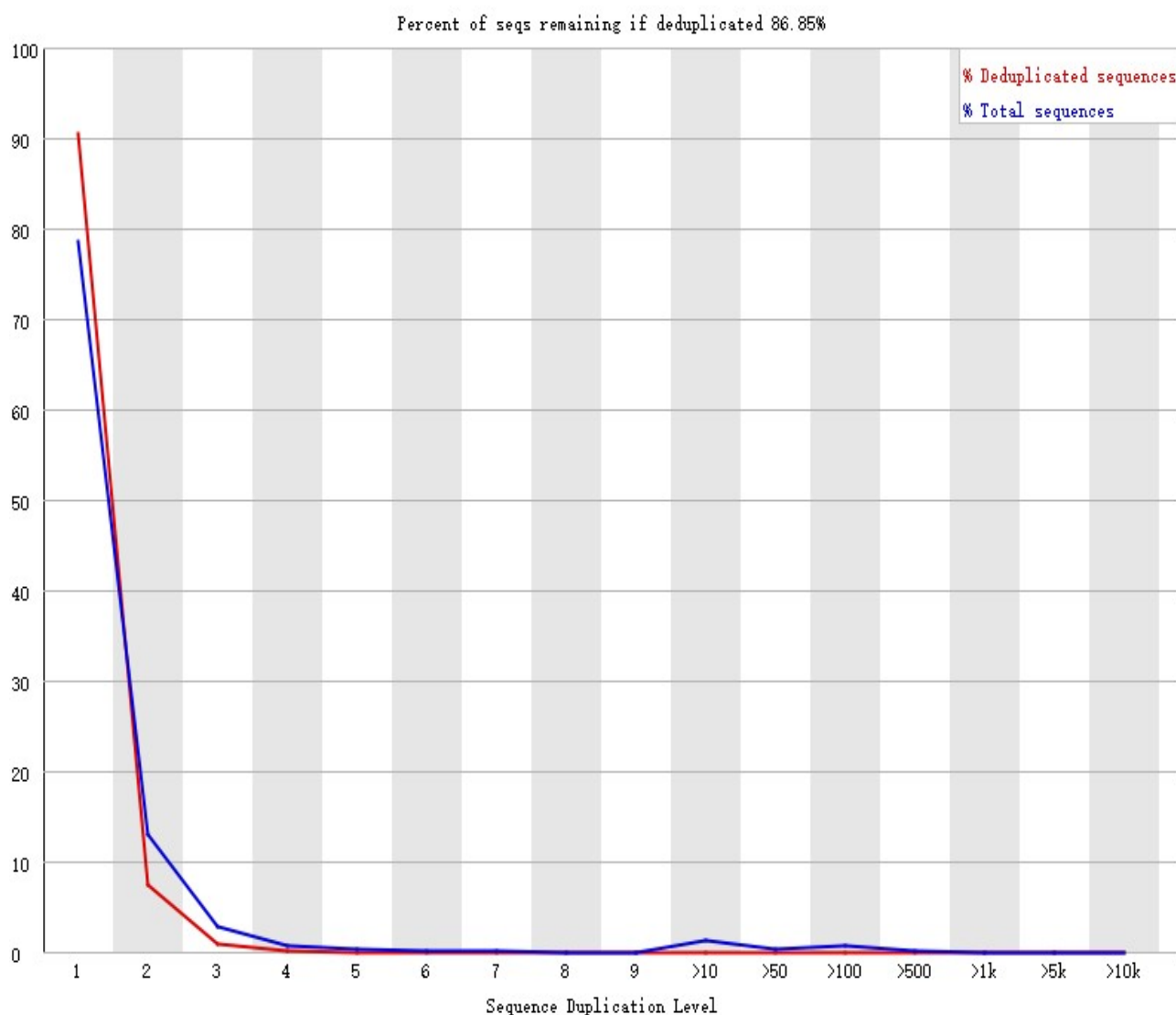
✔ Per base N content



Sequence Length Distribution



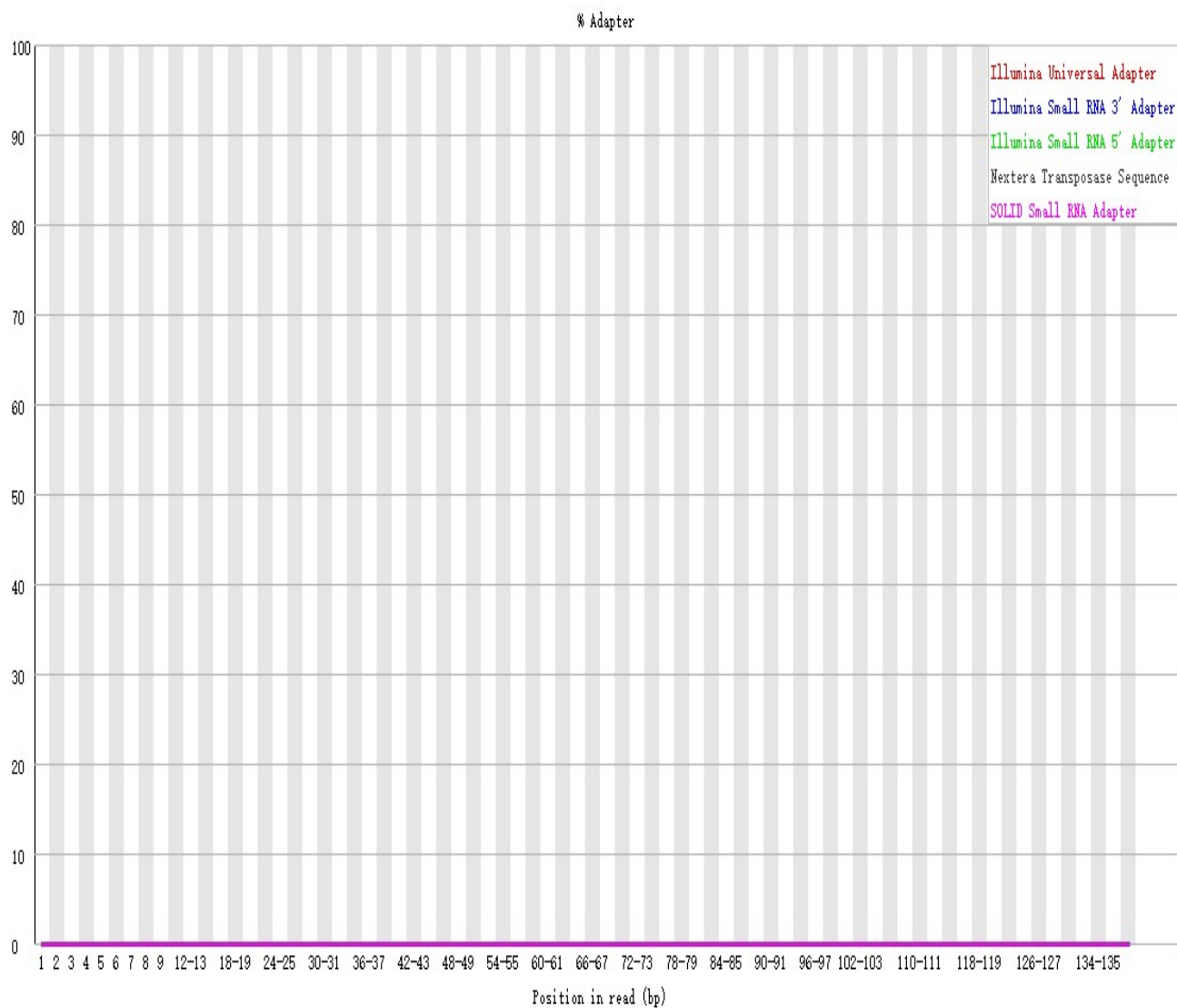
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

✓ Adapter Content



✓ Kmer Content

No overrepresented Kmers

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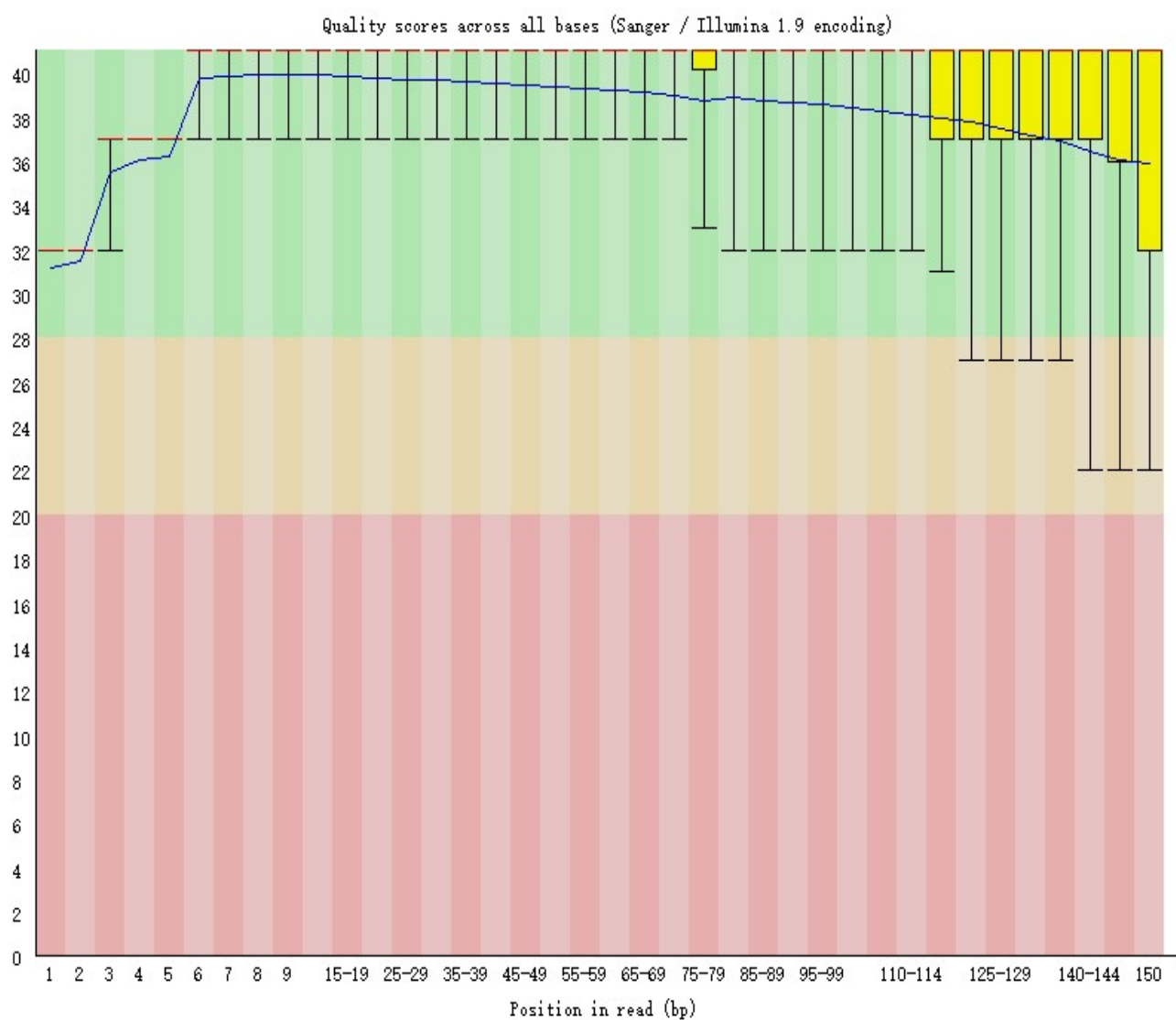
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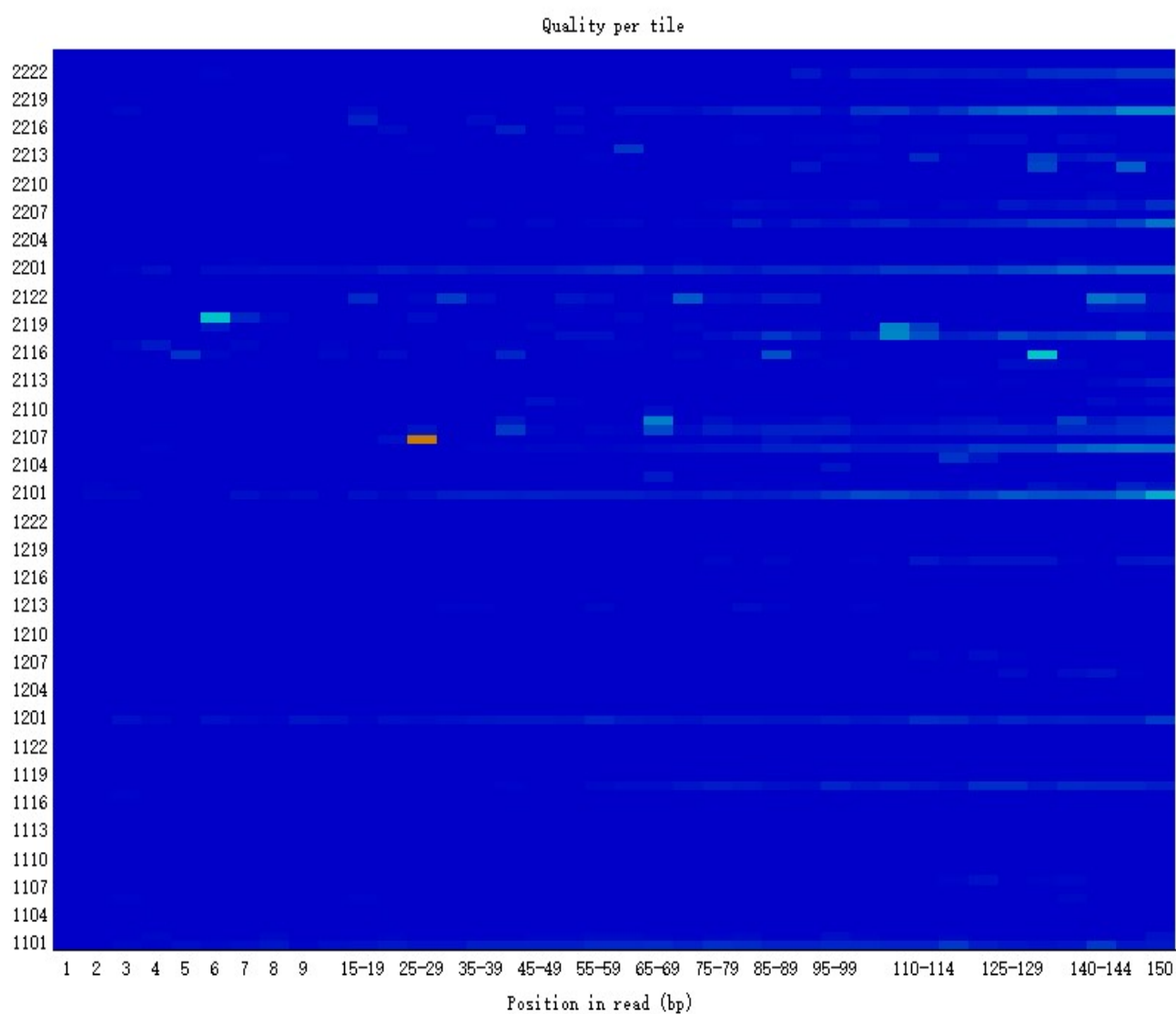
Basic Statistics

Measure	Value
Filename	SK_L4_2_clean.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	137026069
Sequences flagged as poor quality	0
Sequence length	150
%GC	41

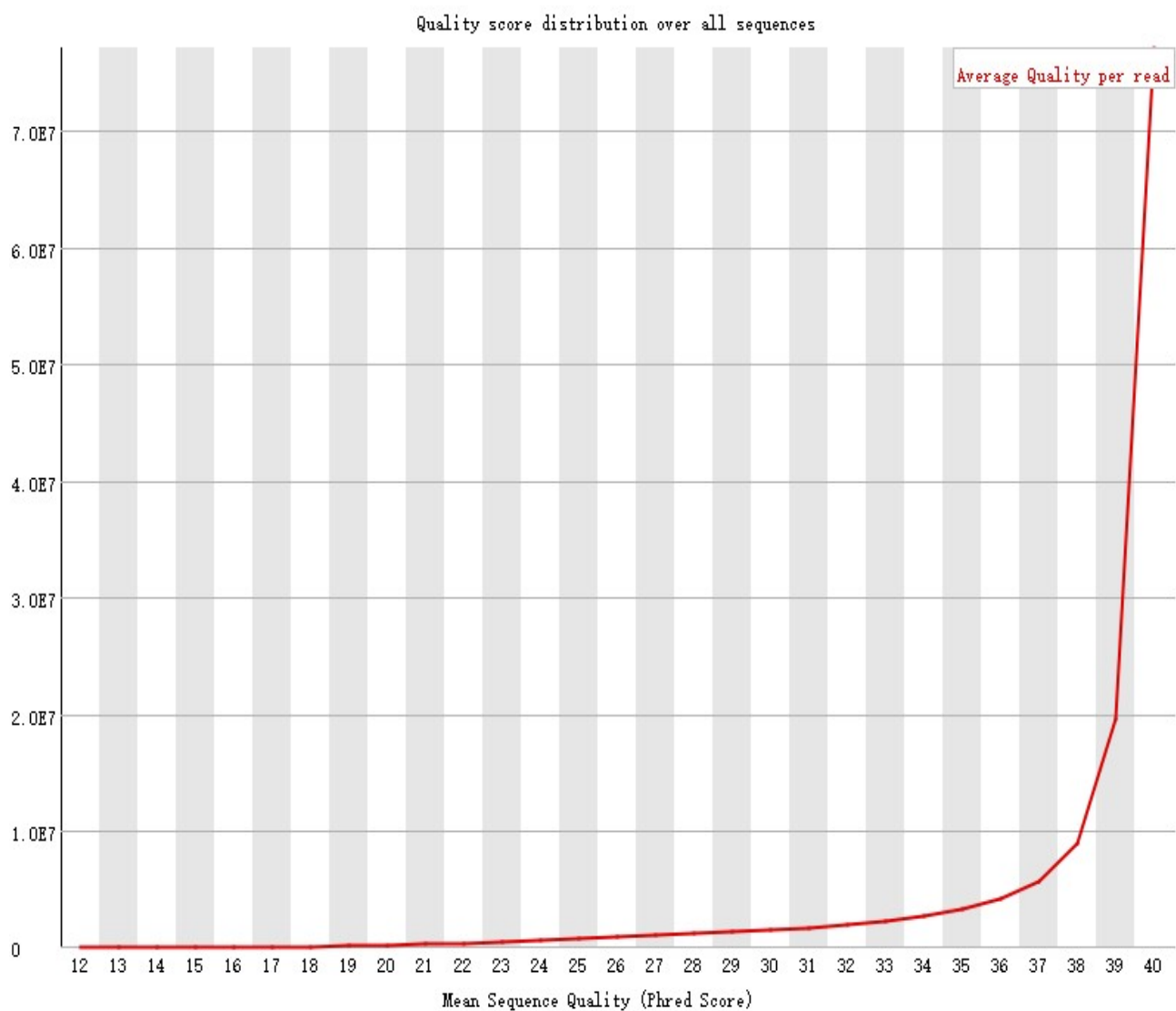
✓ Per base sequence quality



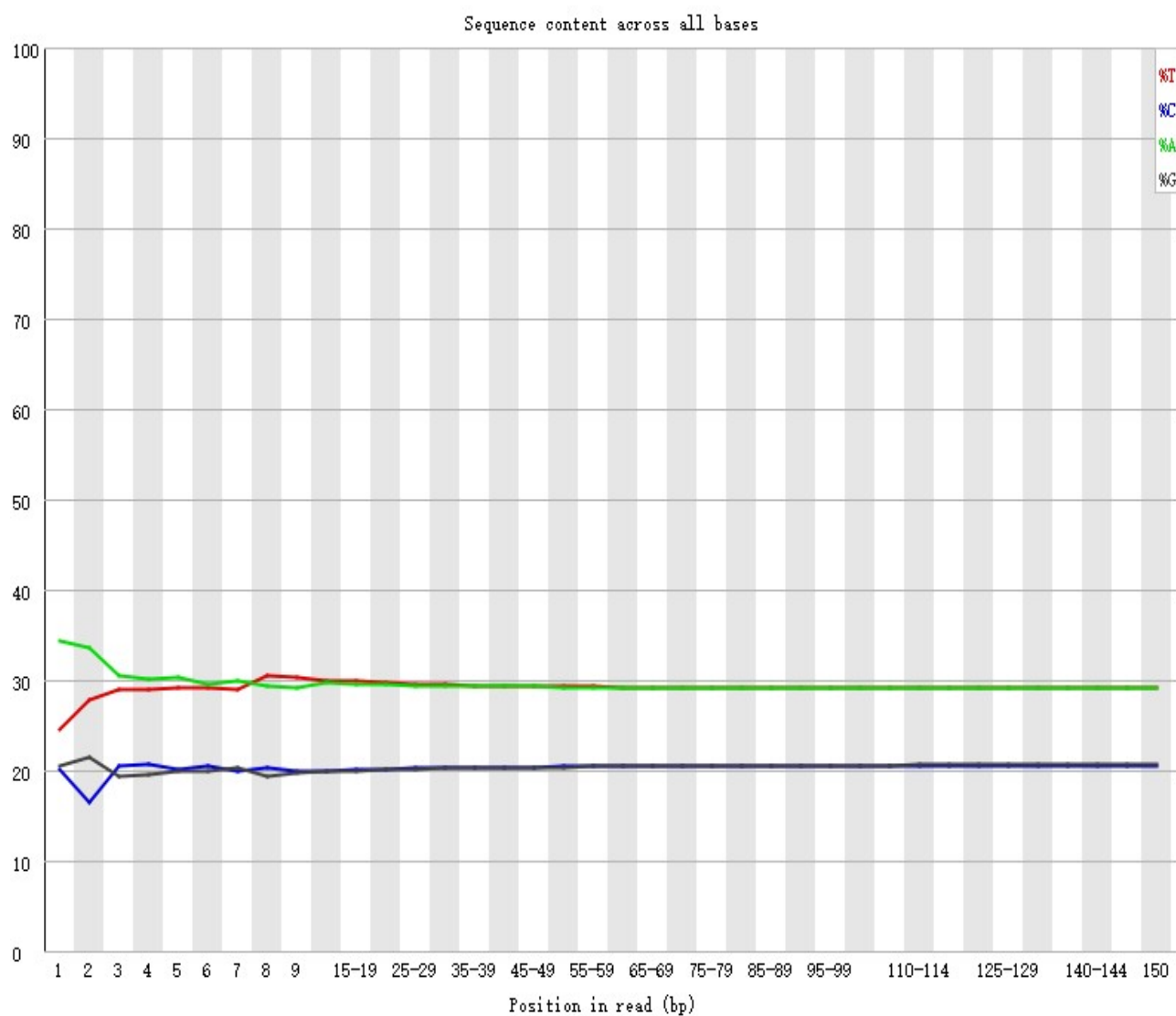
❗ Per tile sequence quality



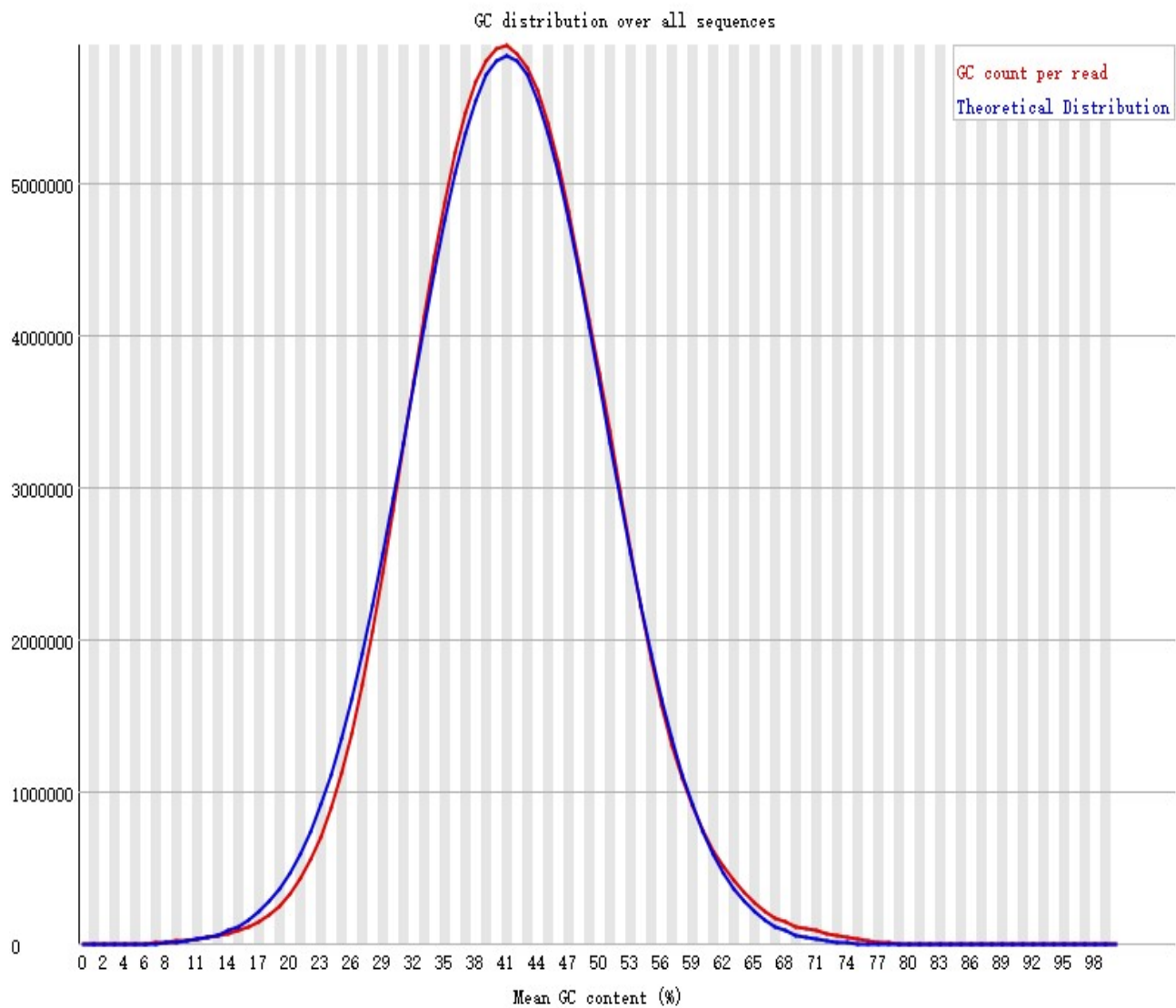
✔ Per sequence quality scores



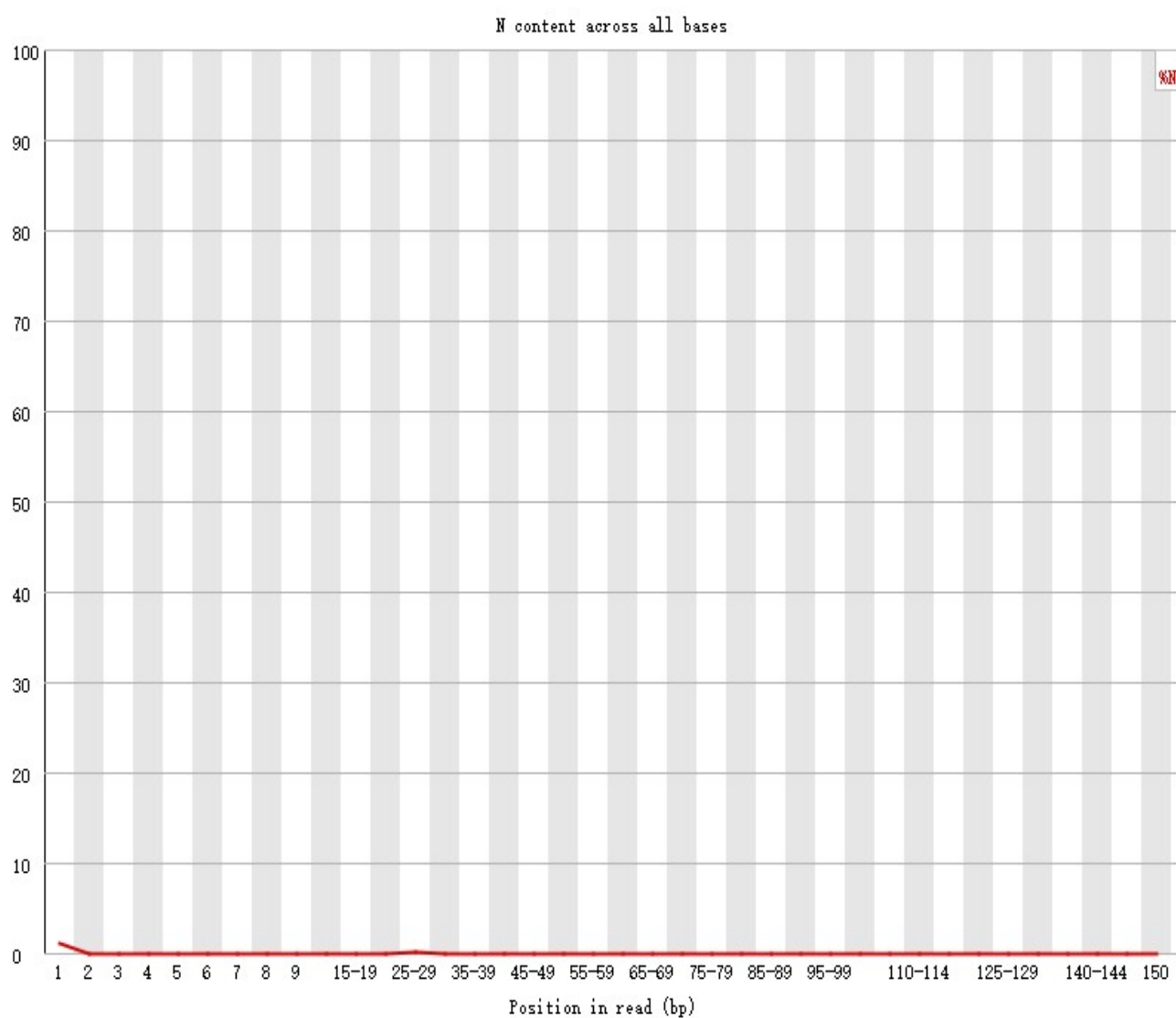
✔ Per base sequence content



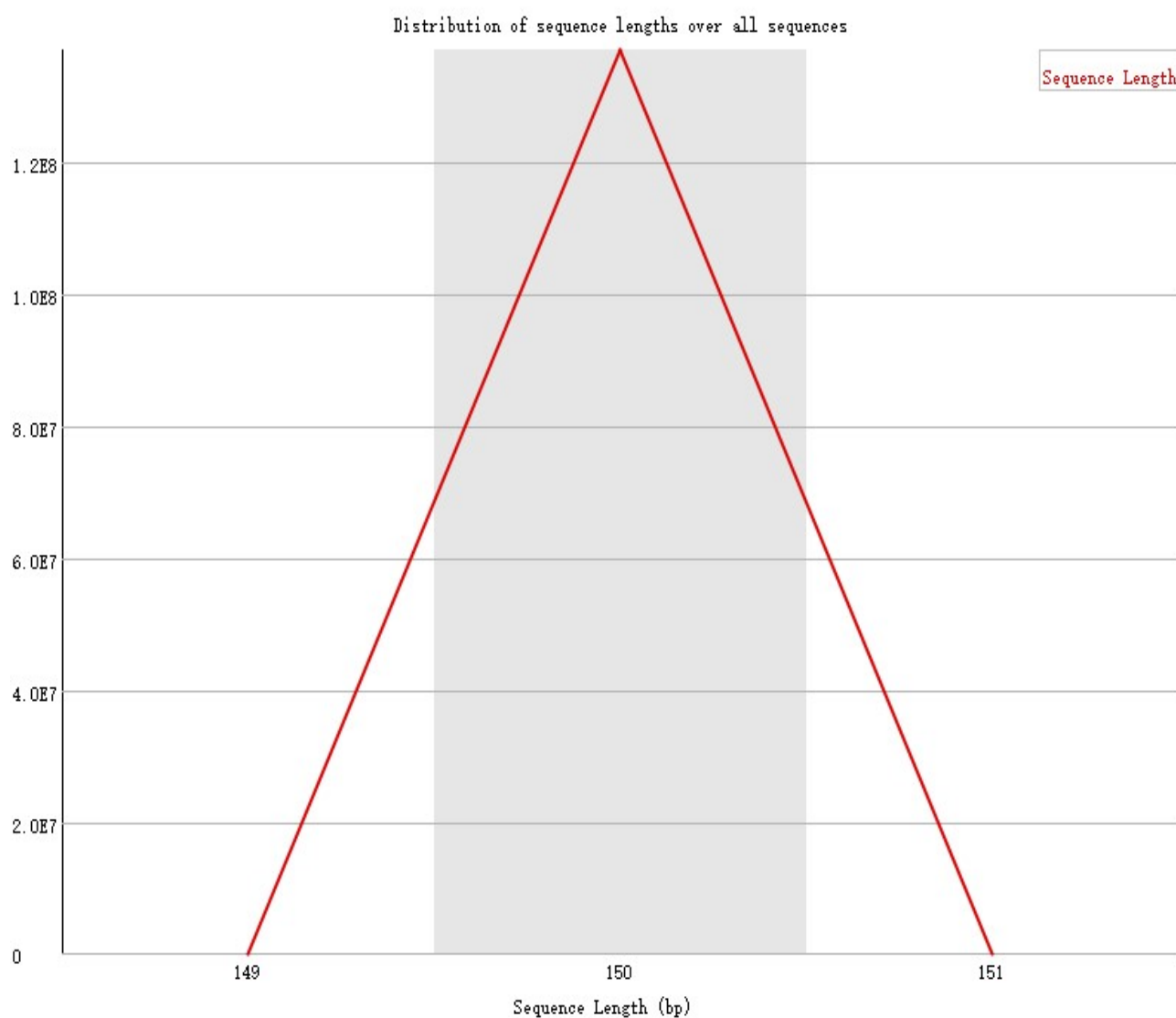
✔ Per sequence GC content



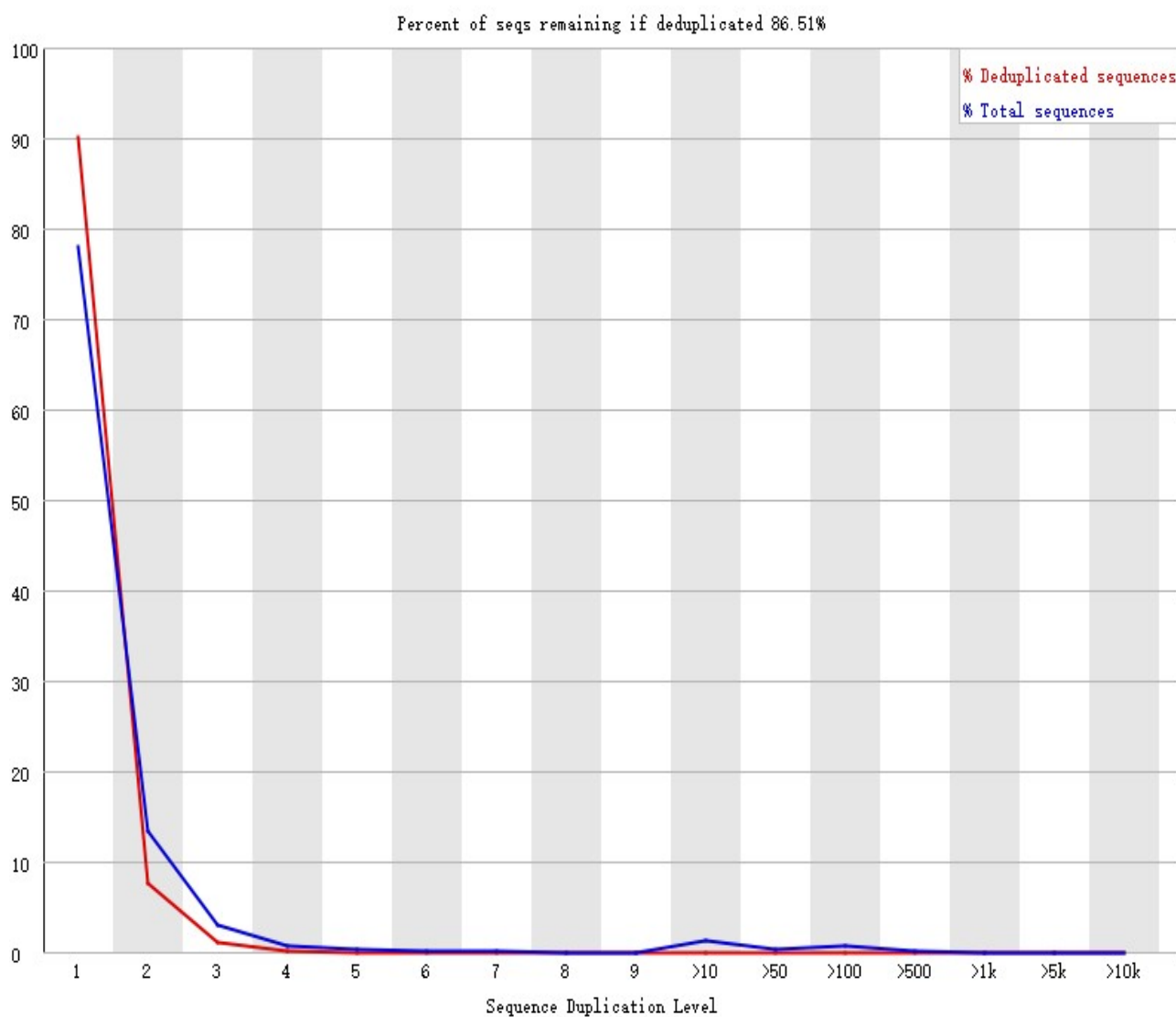
✔ Per base N content



Sequence Length Distribution



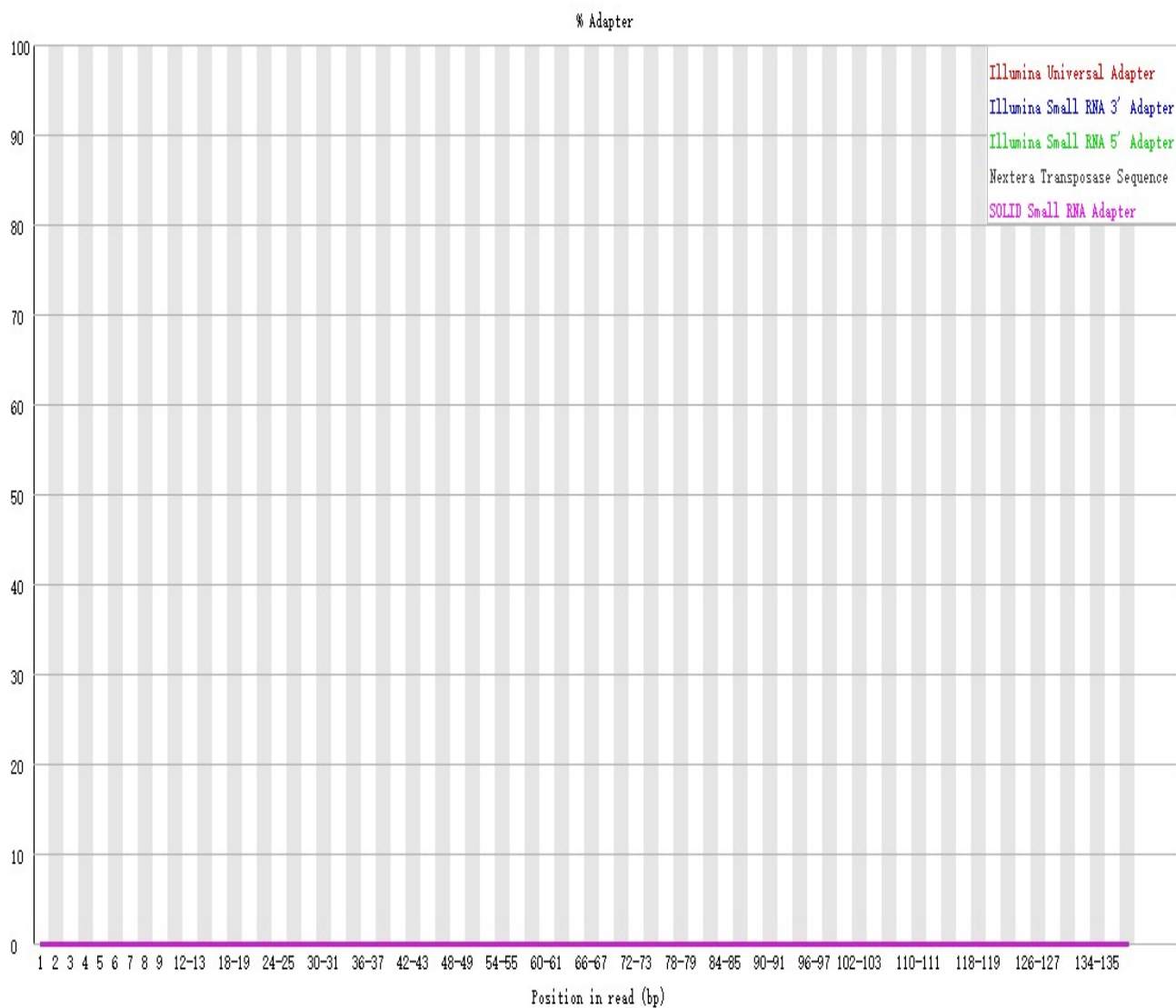
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

✓ Adapter Content



✓ Kmer Content

No overrepresented Kmers

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FastQC Report

Summary

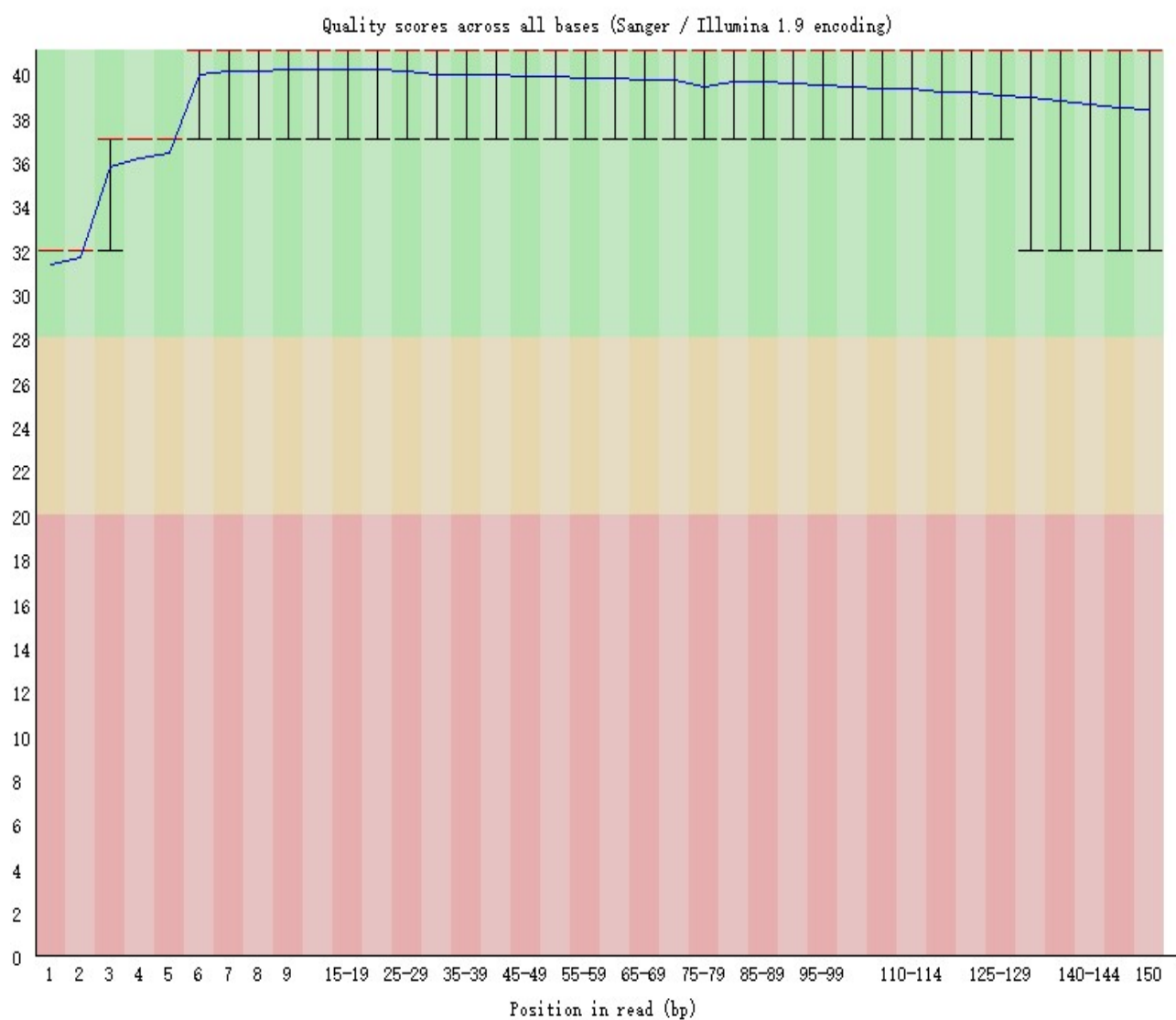
星期三 8 五月 2019
SN_1_clean.rd.fq.gz

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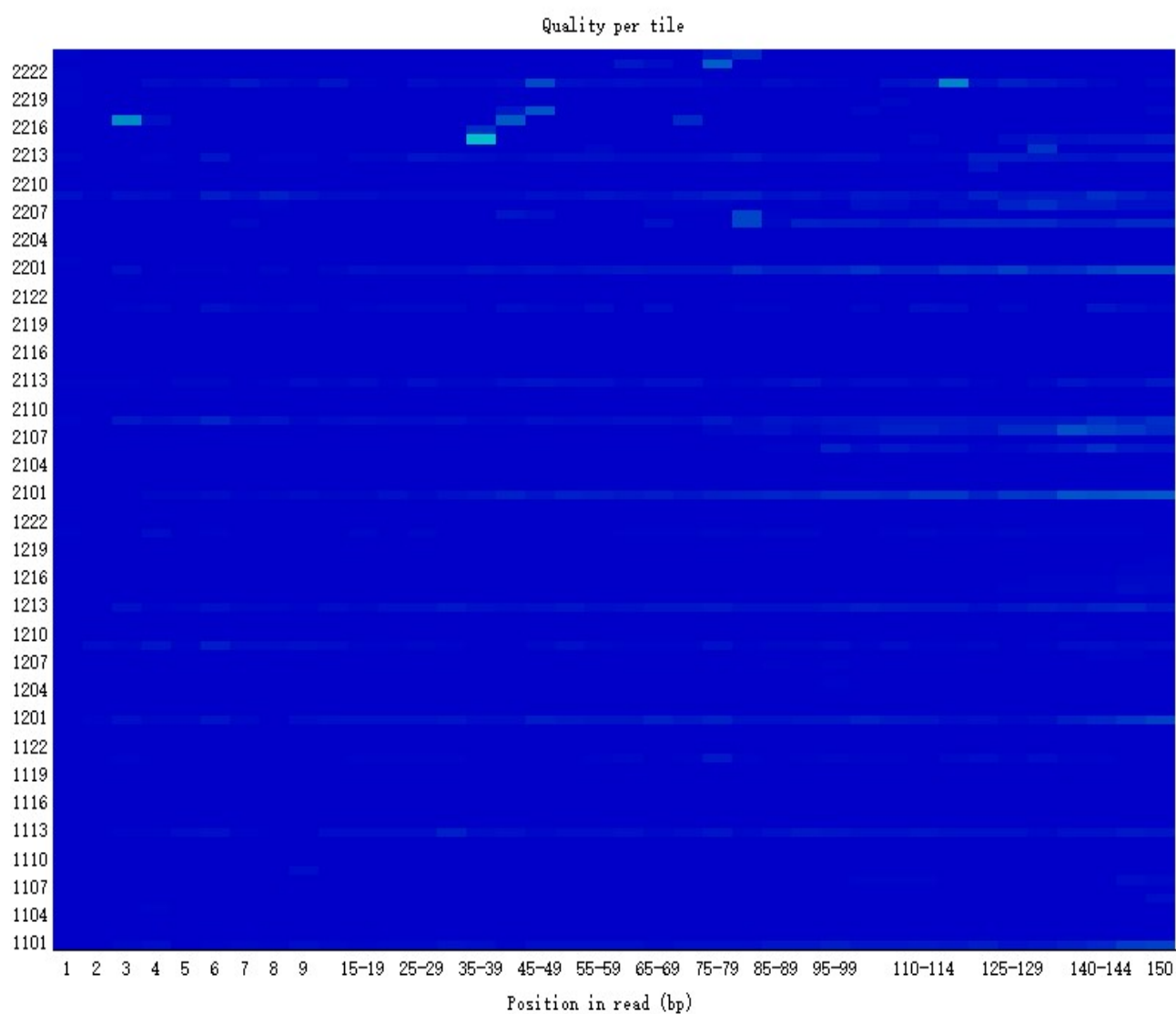
Basic Statistics

Measure	Value
Filename	SN_1_clean.rd.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	108737330
Sequences flagged as poor quality	0
Sequence length	150
%GC	41

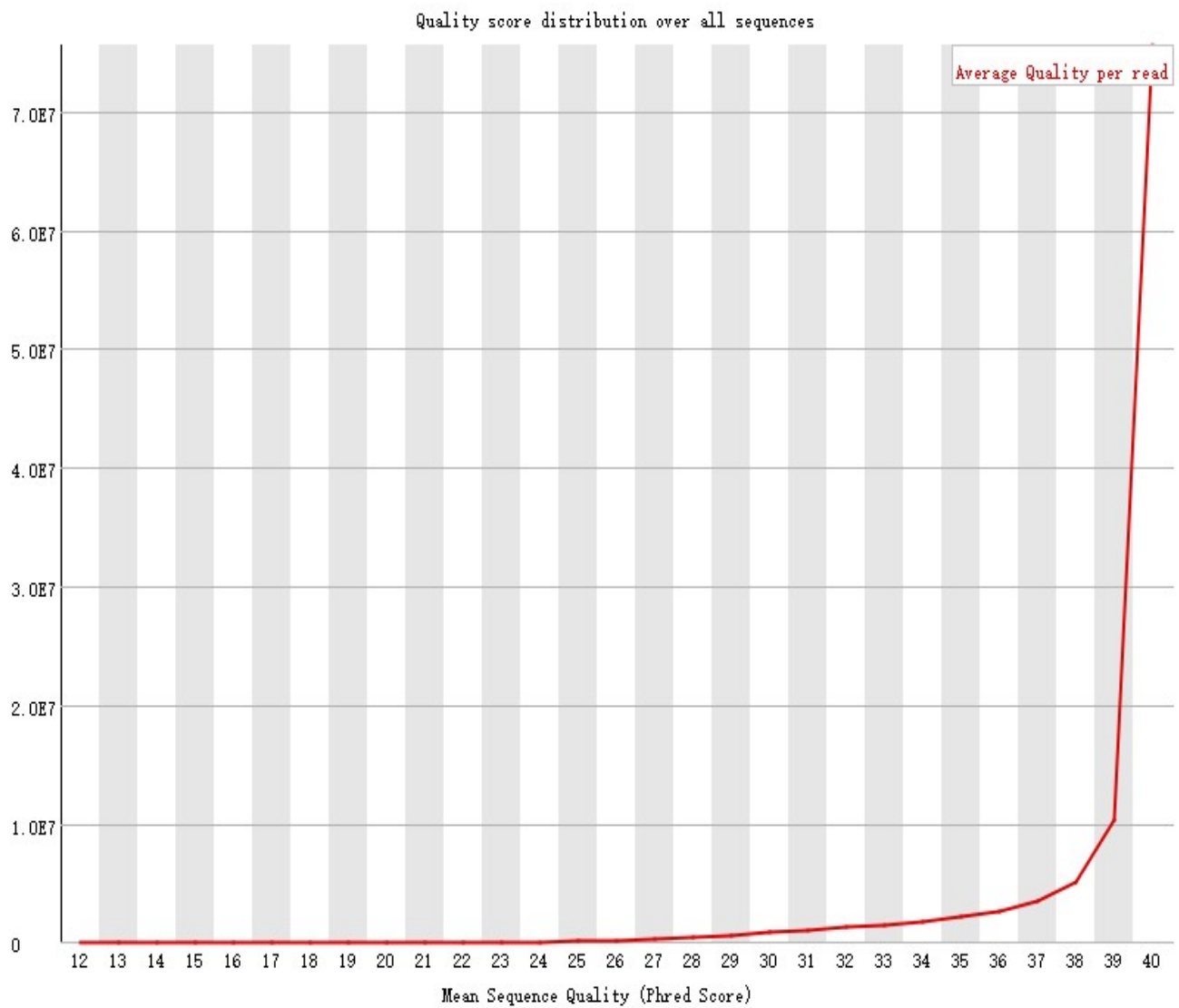
✔ Per base sequence quality



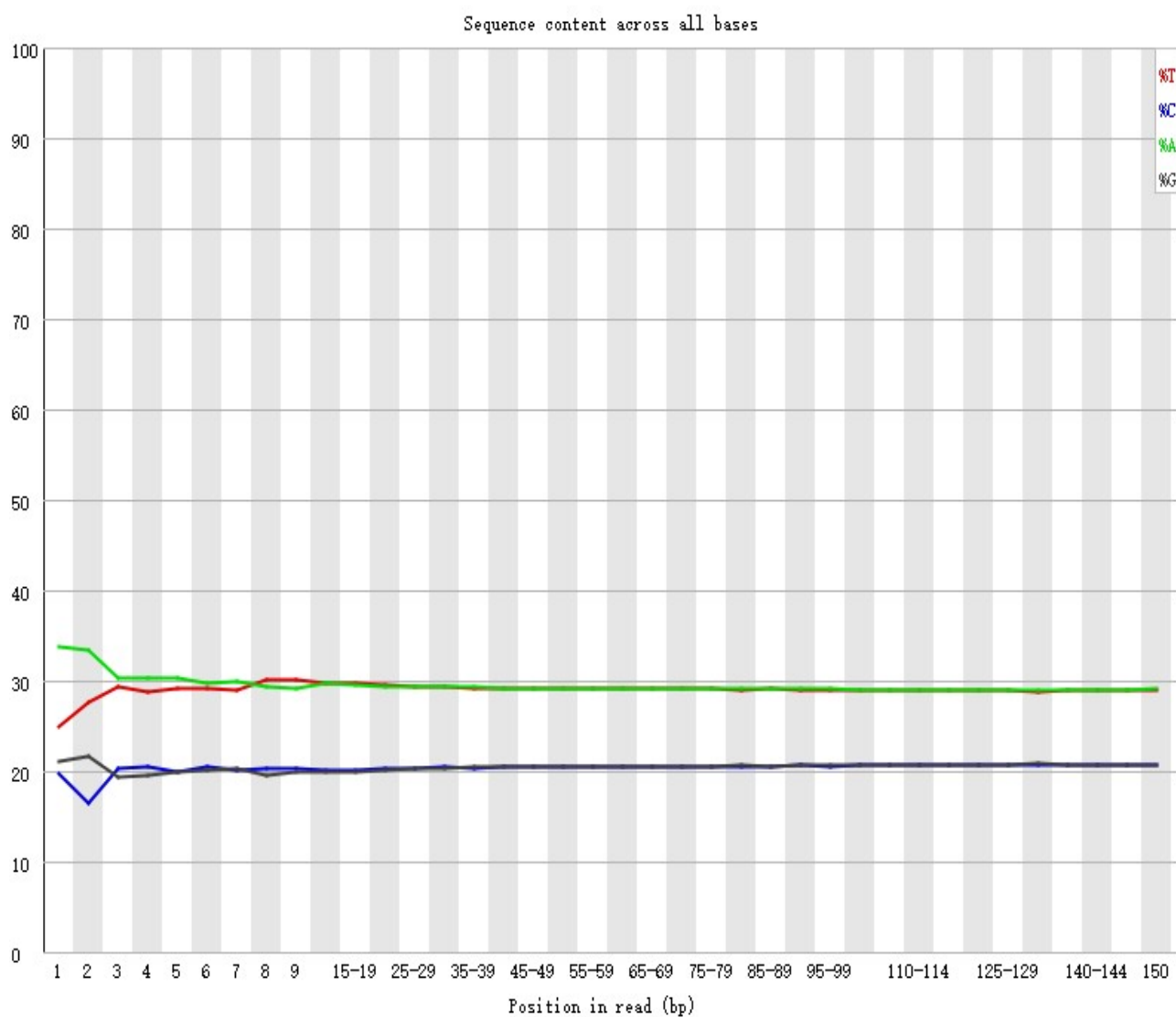
✔ Per tile sequence quality



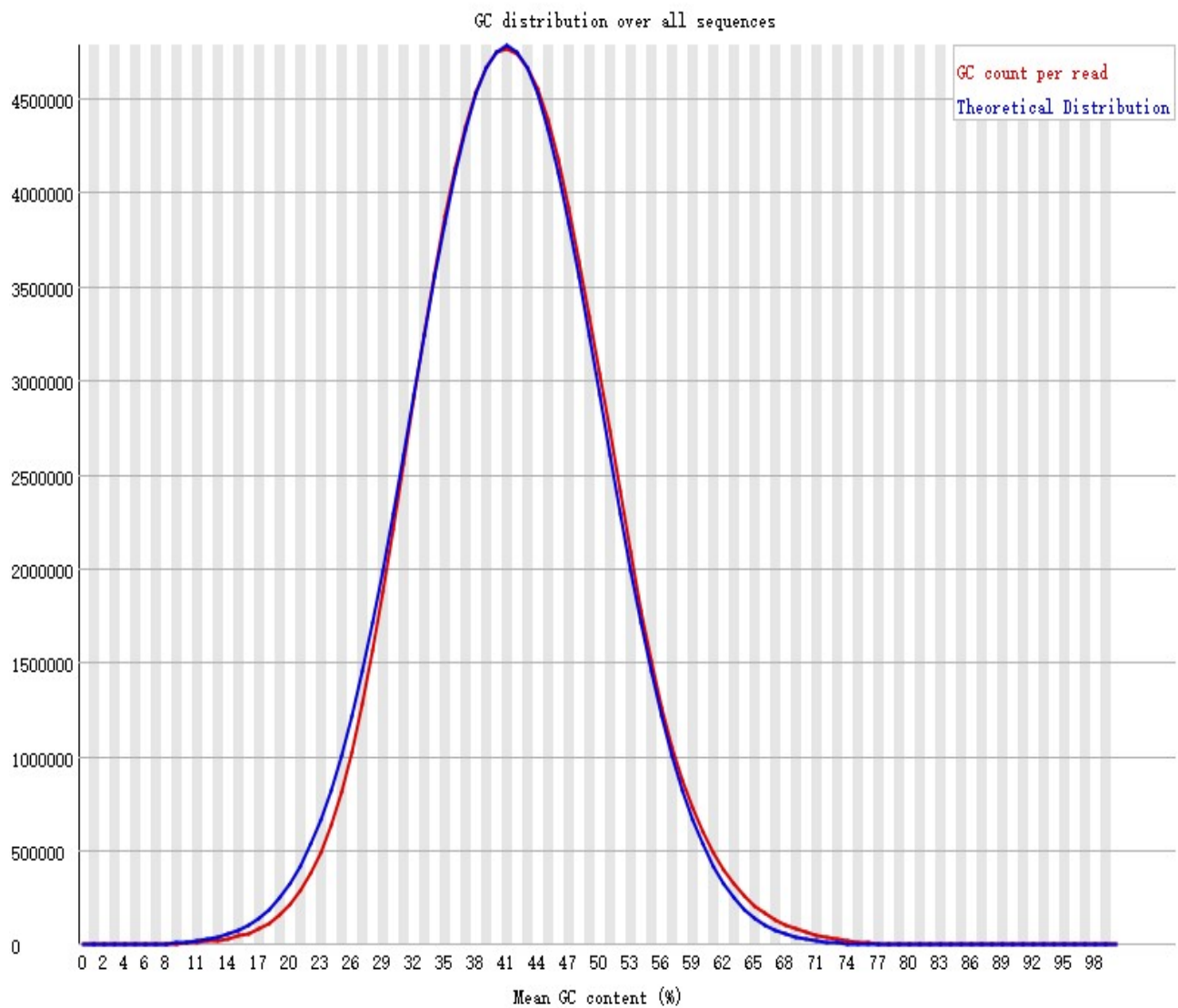
✔ Per sequence quality scores



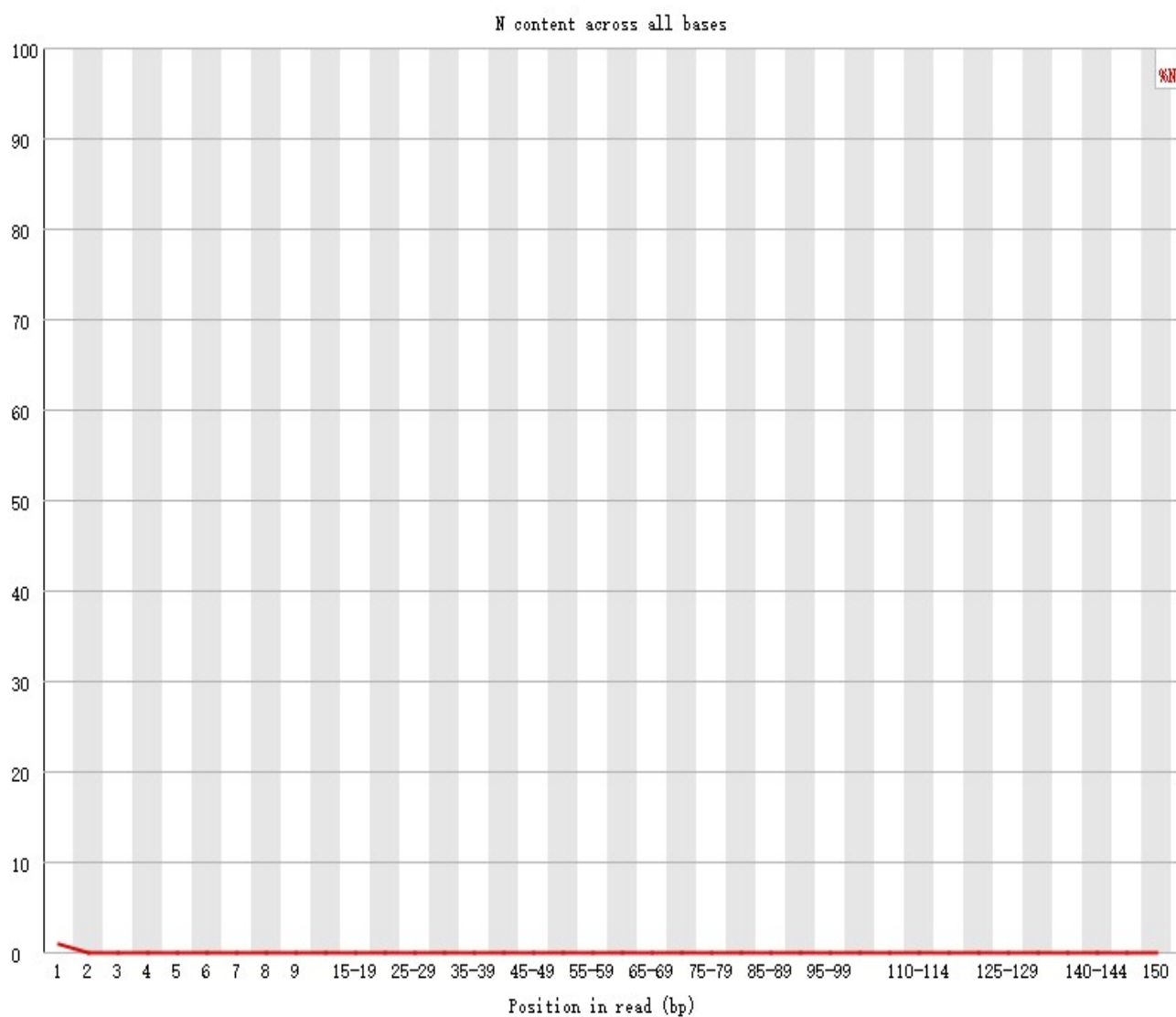
✔ Per base sequence content



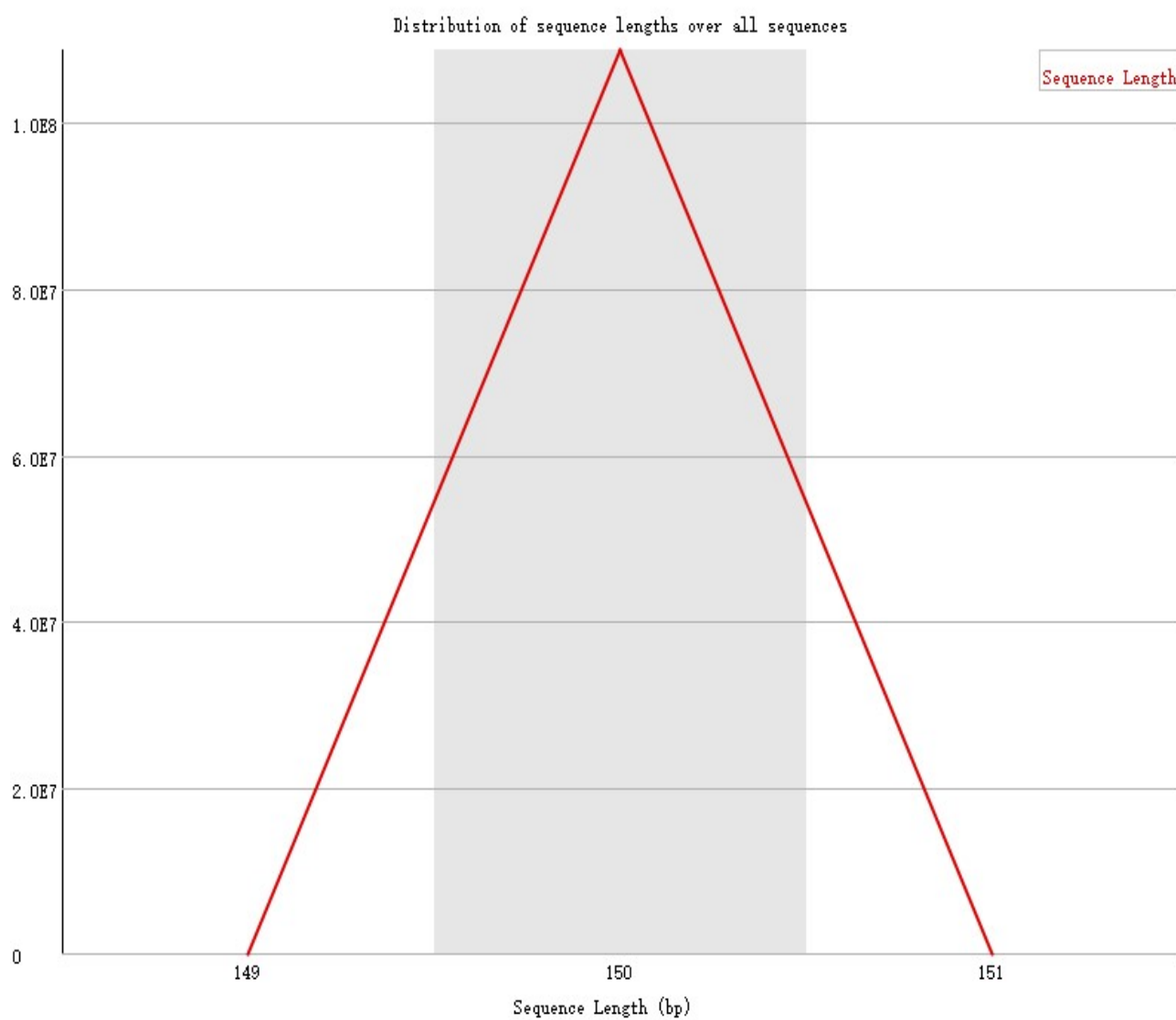
✔ Per sequence GC content



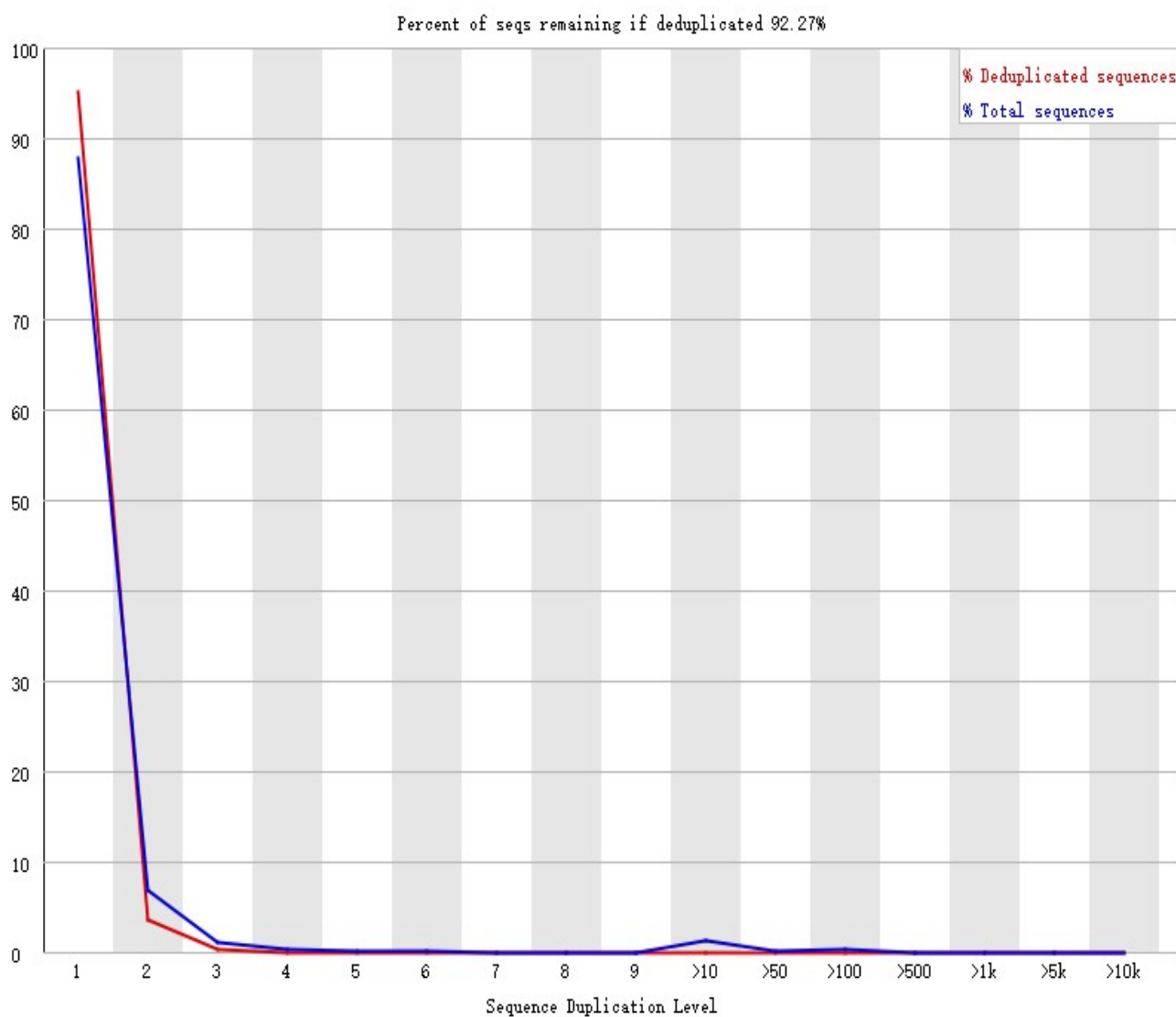
✔ Per base N content



✔ Sequence Length Distribution



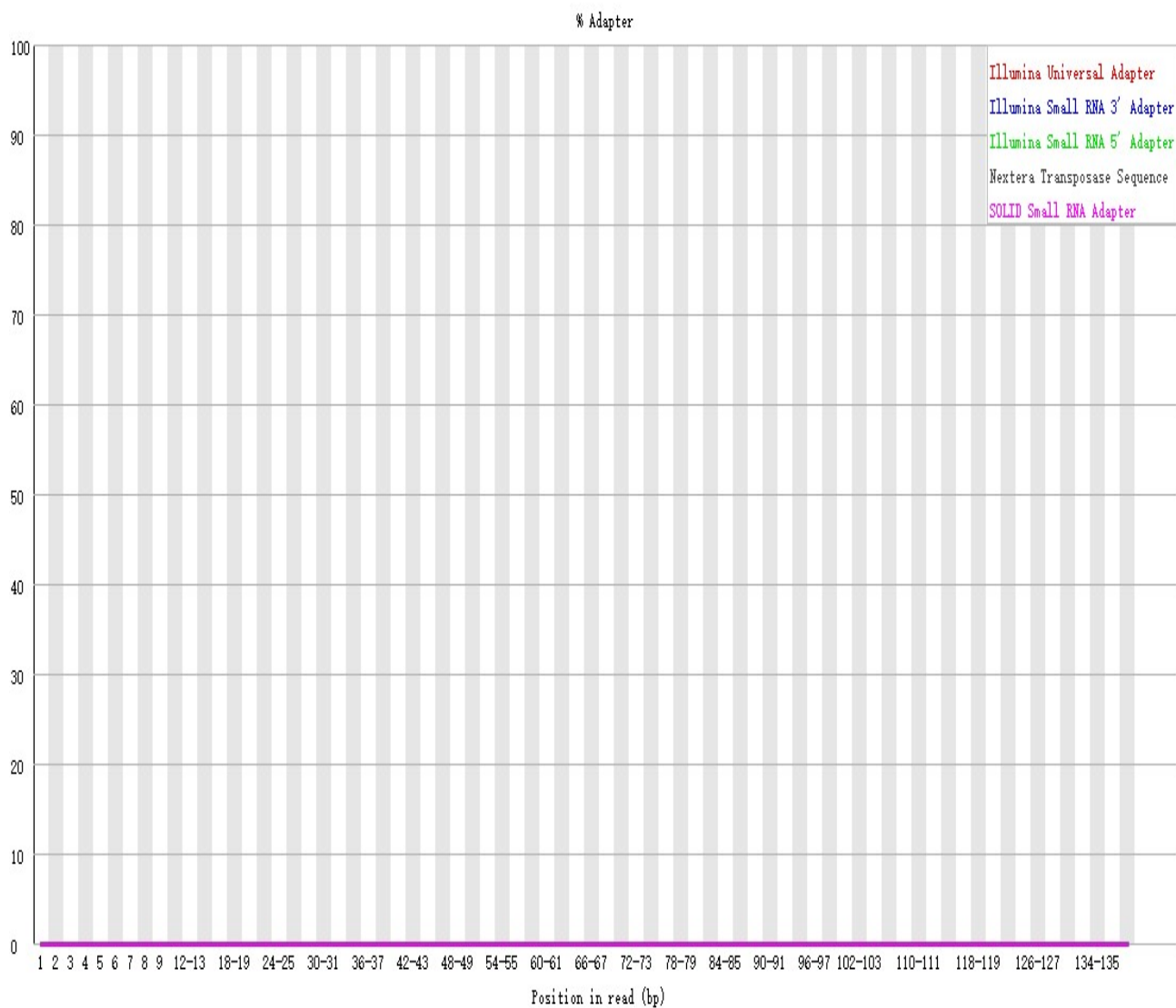
✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

✓ Adapter Content



✓ Kmer Content

No overrepresented Kmers

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

FastQC Report

Summary

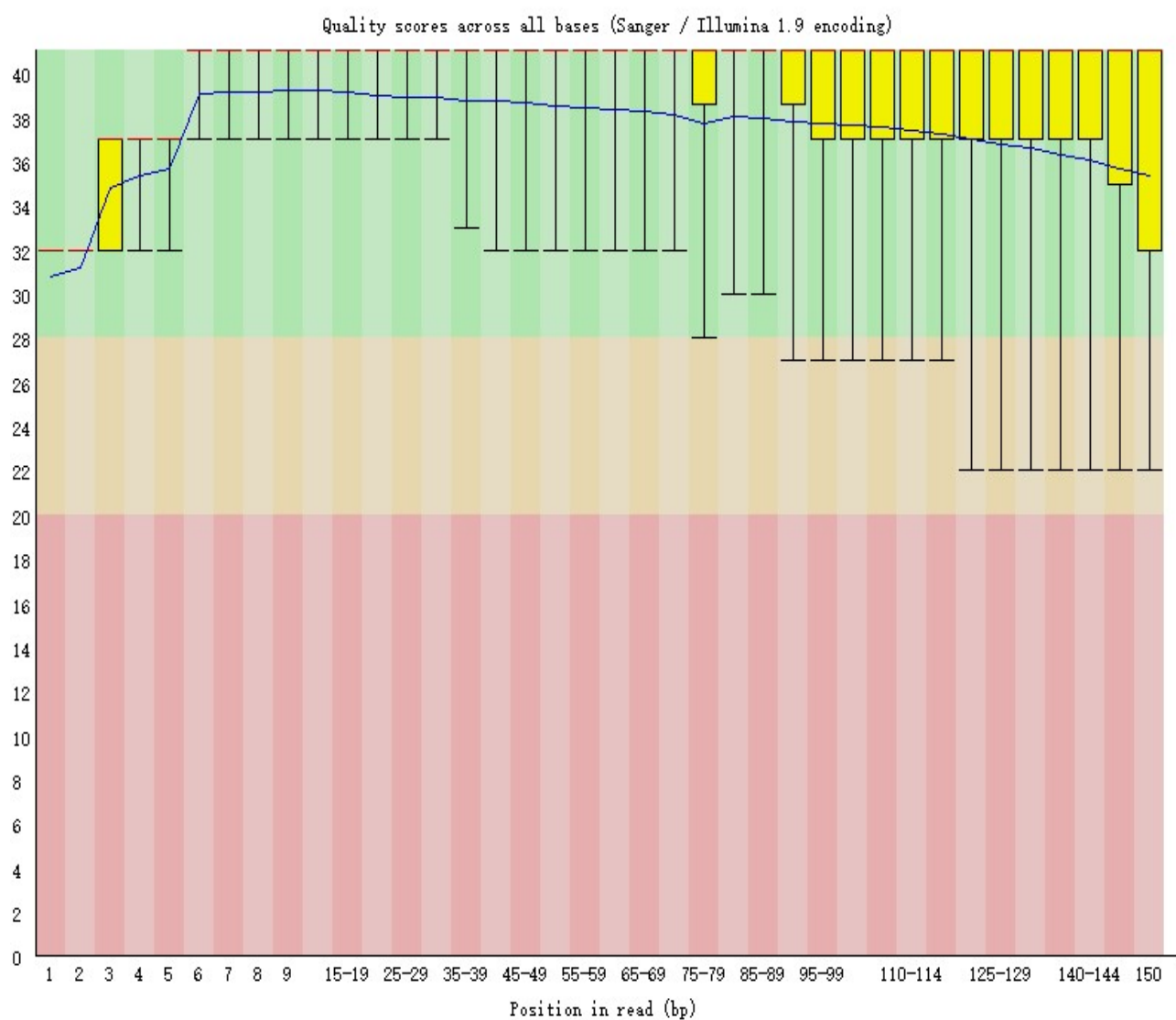
星期三 8 五月 2019
SN_2_clean.rd.fq.gz

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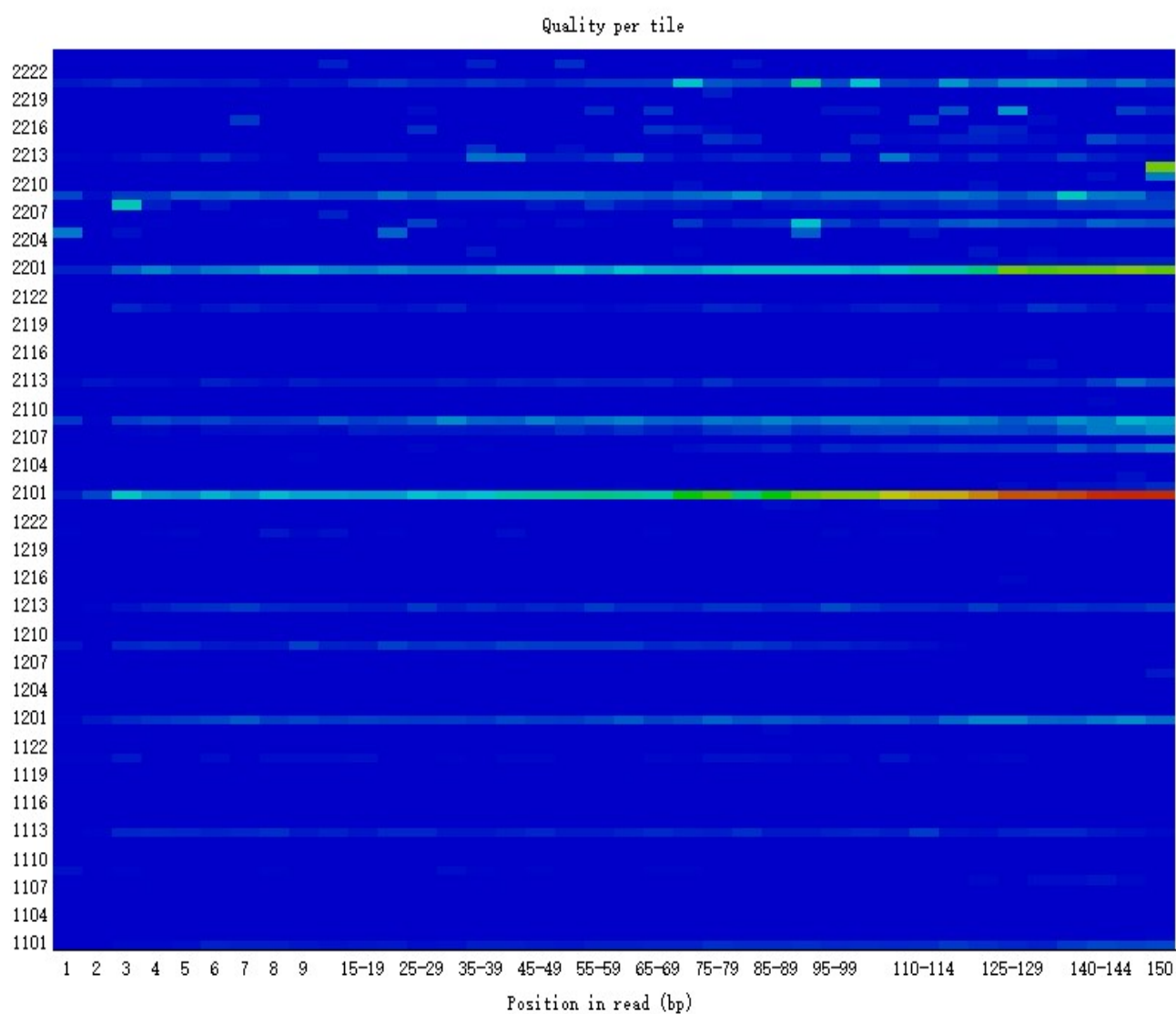
Basic Statistics

Measure	Value
Filename	SN_2_clean.rd.fq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	108737330
Sequences flagged as poor quality	0
Sequence length	150
%GC	41

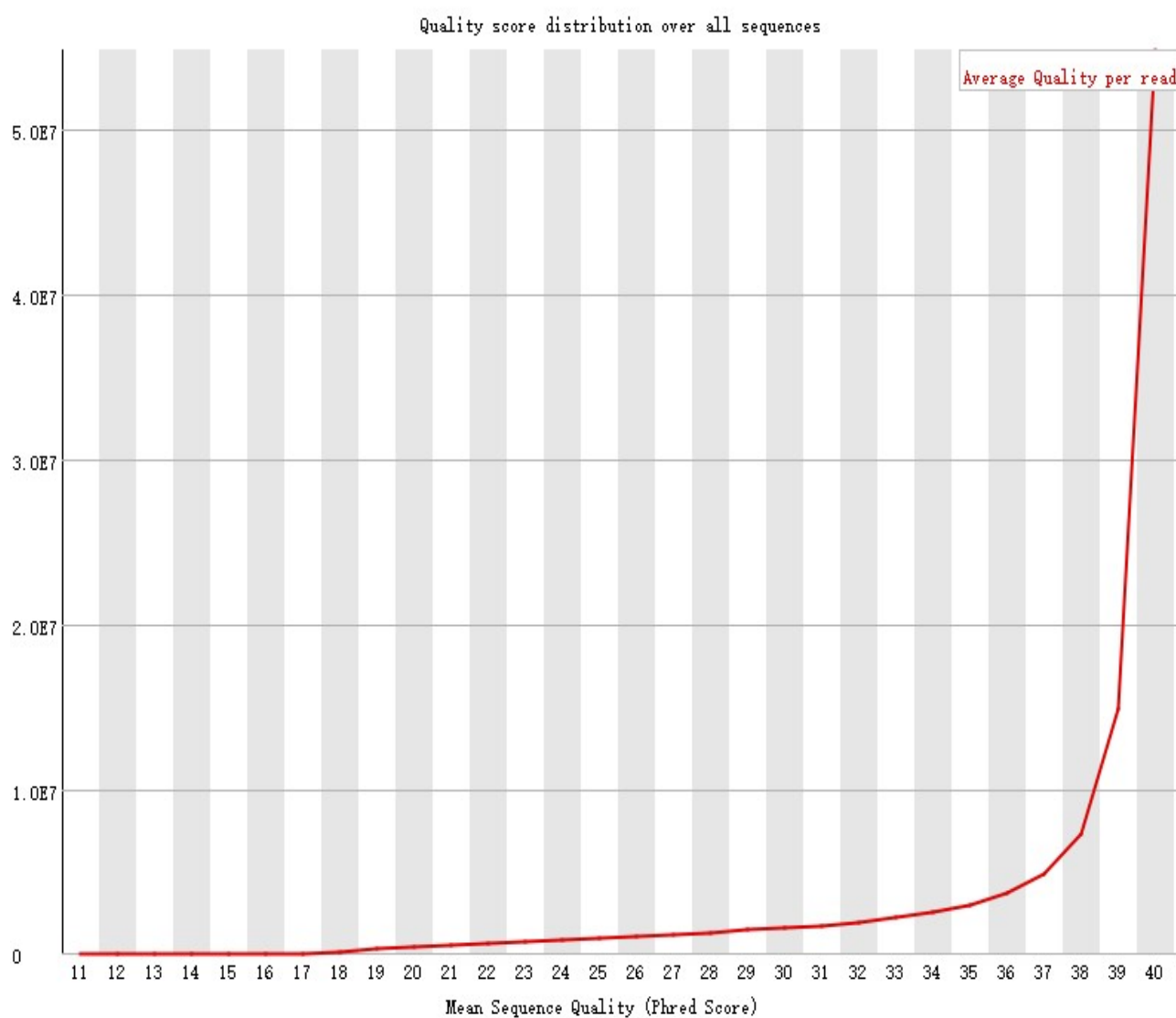
✓ Per base sequence quality



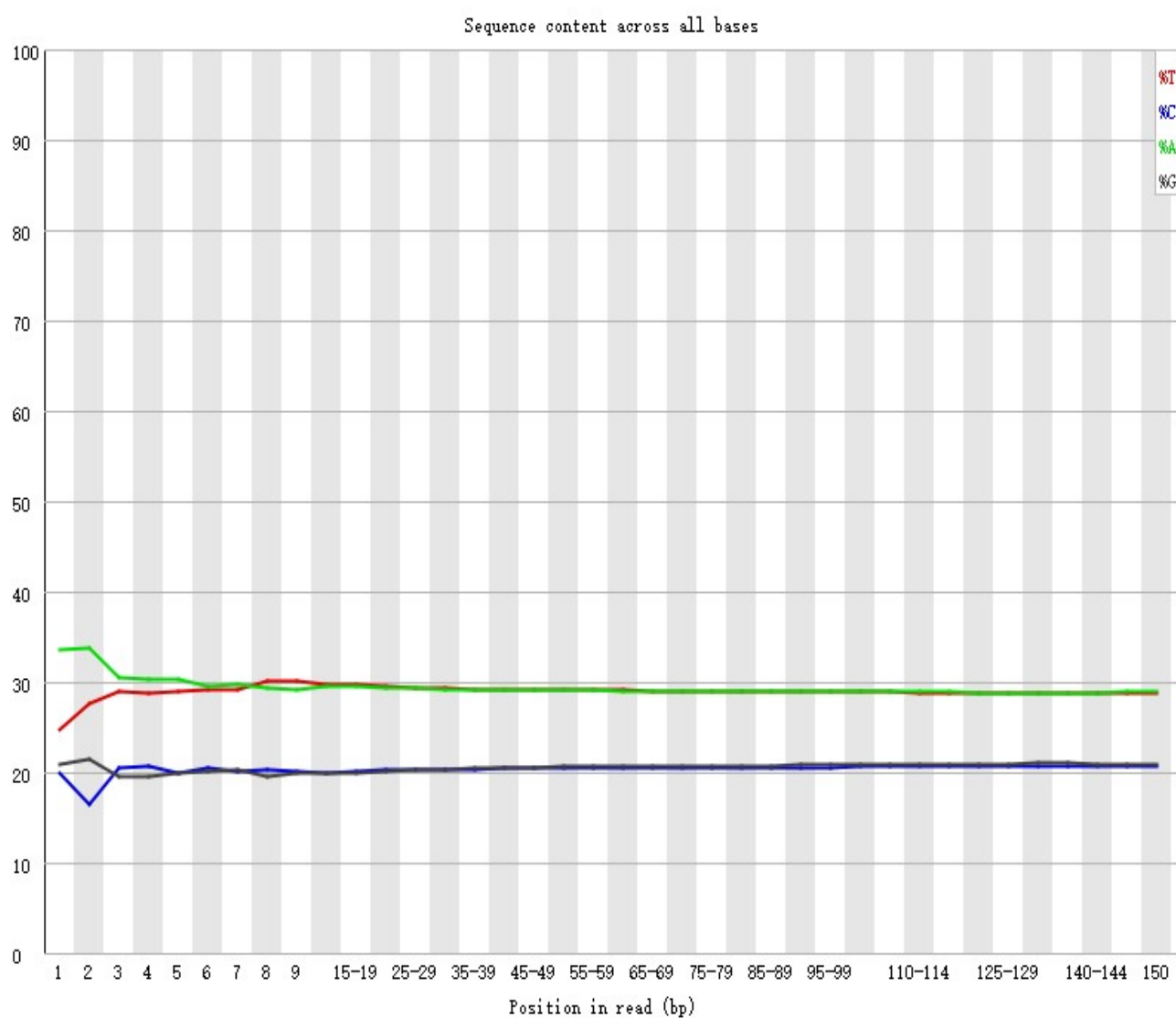
! Per tile sequence quality



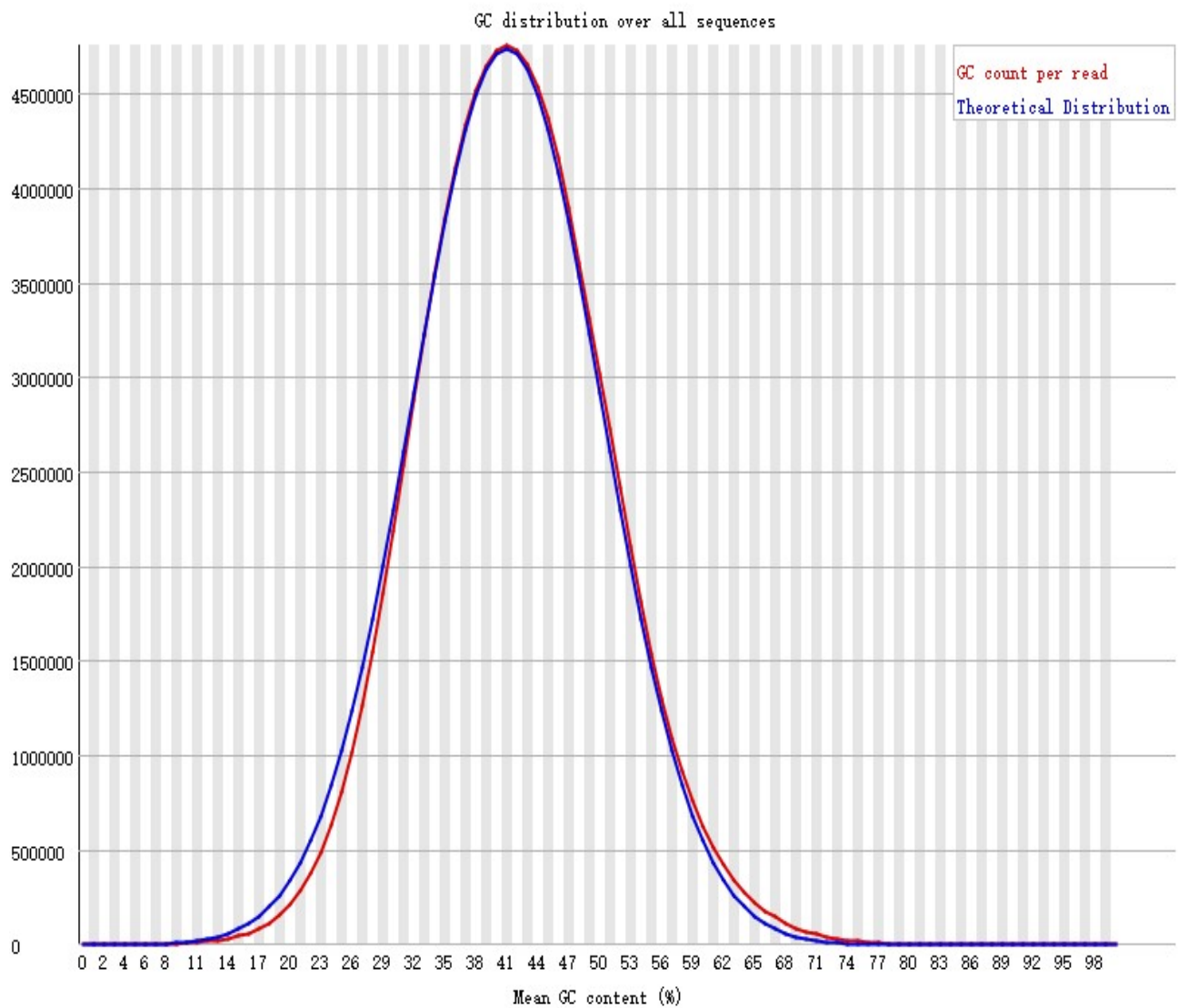
✔ Per sequence quality scores



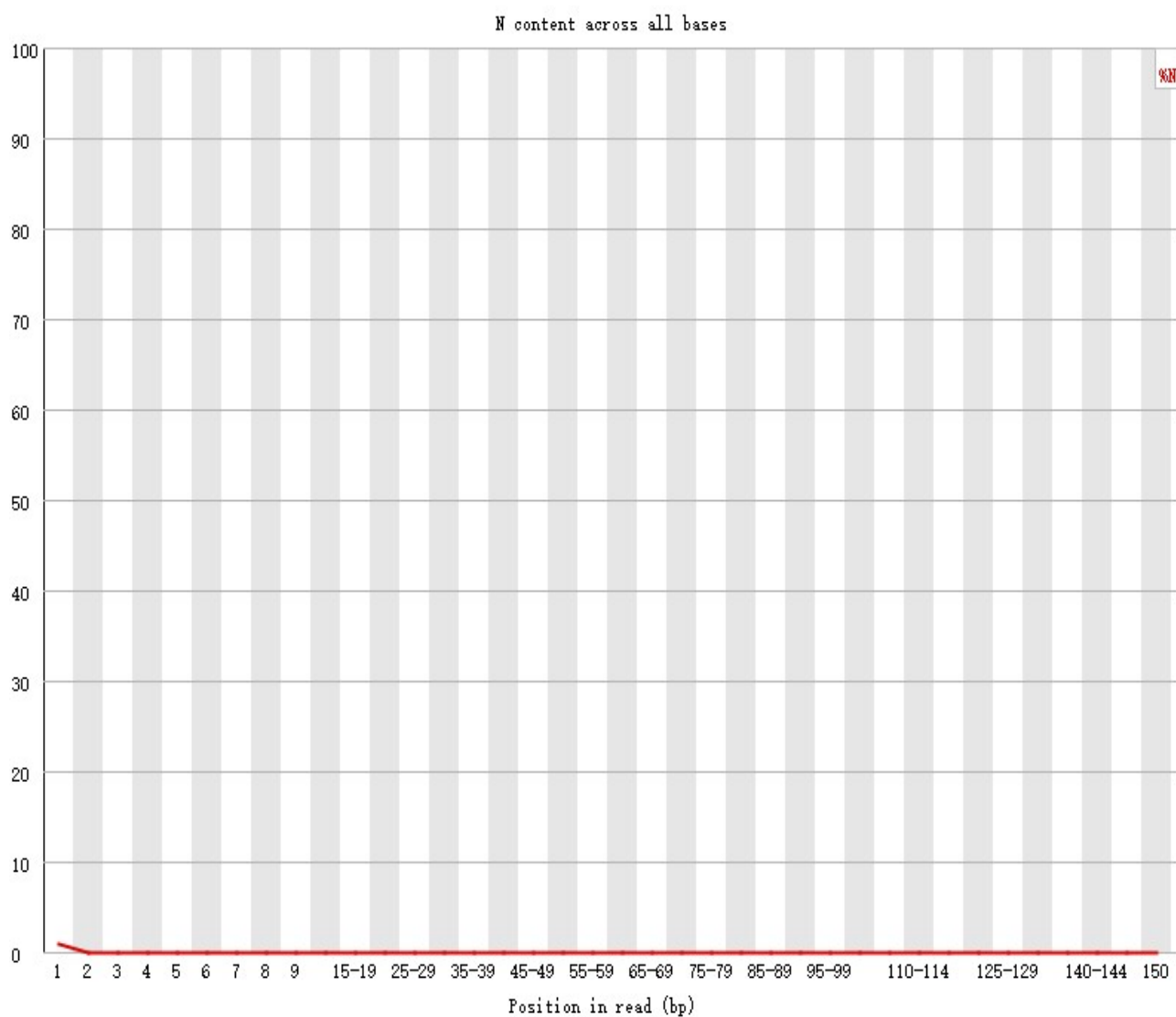
✔ Per base sequence content



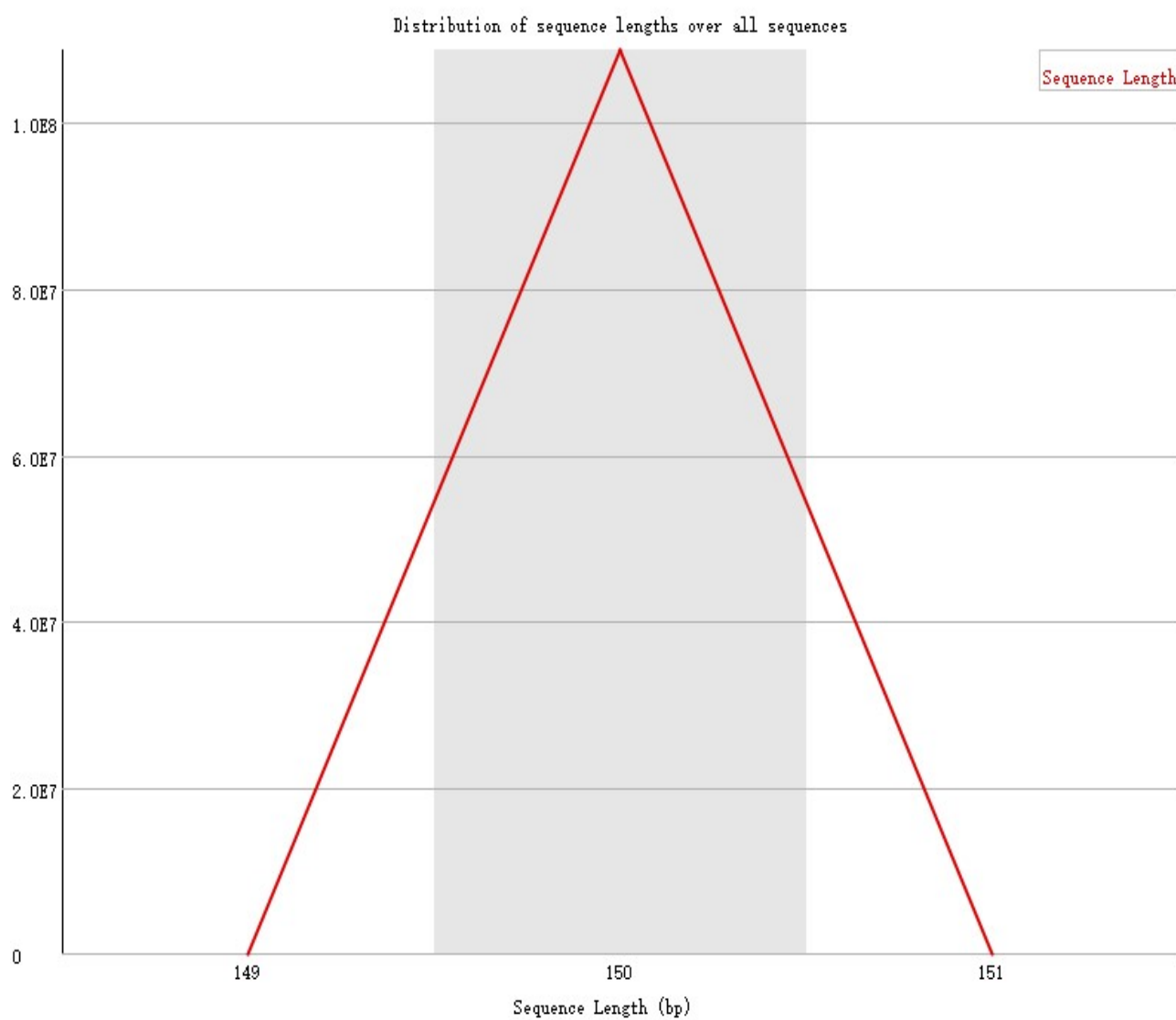
✔ Per sequence GC content



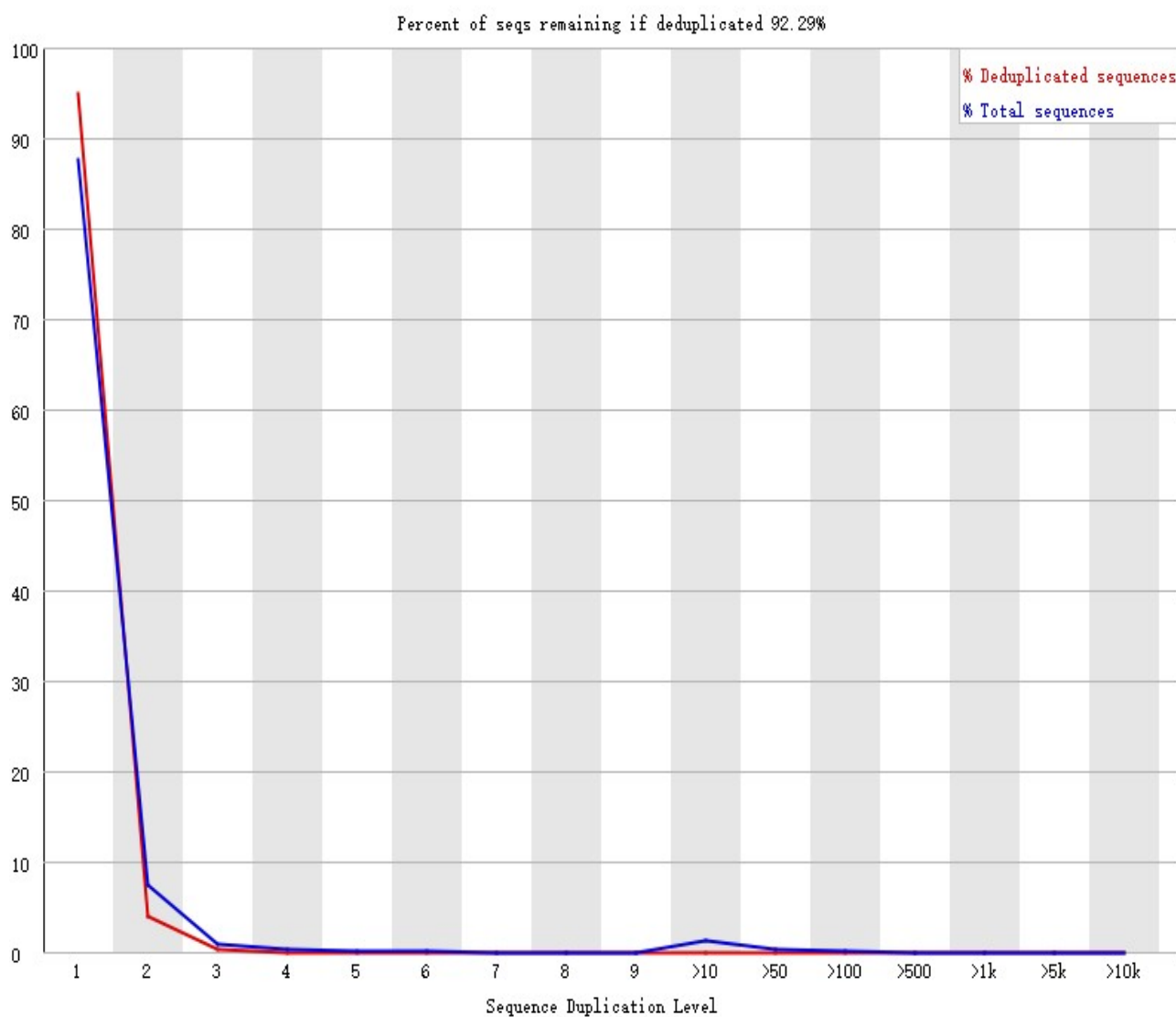
✔ Per base N content



✔ Sequence Length Distribution



✔ Sequence Duplication Levels



✔ Overrepresented sequences

No overrepresented sequences

✓ Adapter Content

