FastQC Report

Summary

Sat 23 May 2020
E745-1.L500_SZAXPI015146-56_1_clean.fq.gz

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per tile sequence quality](#)

✅ [Per sequence quality scores](#)
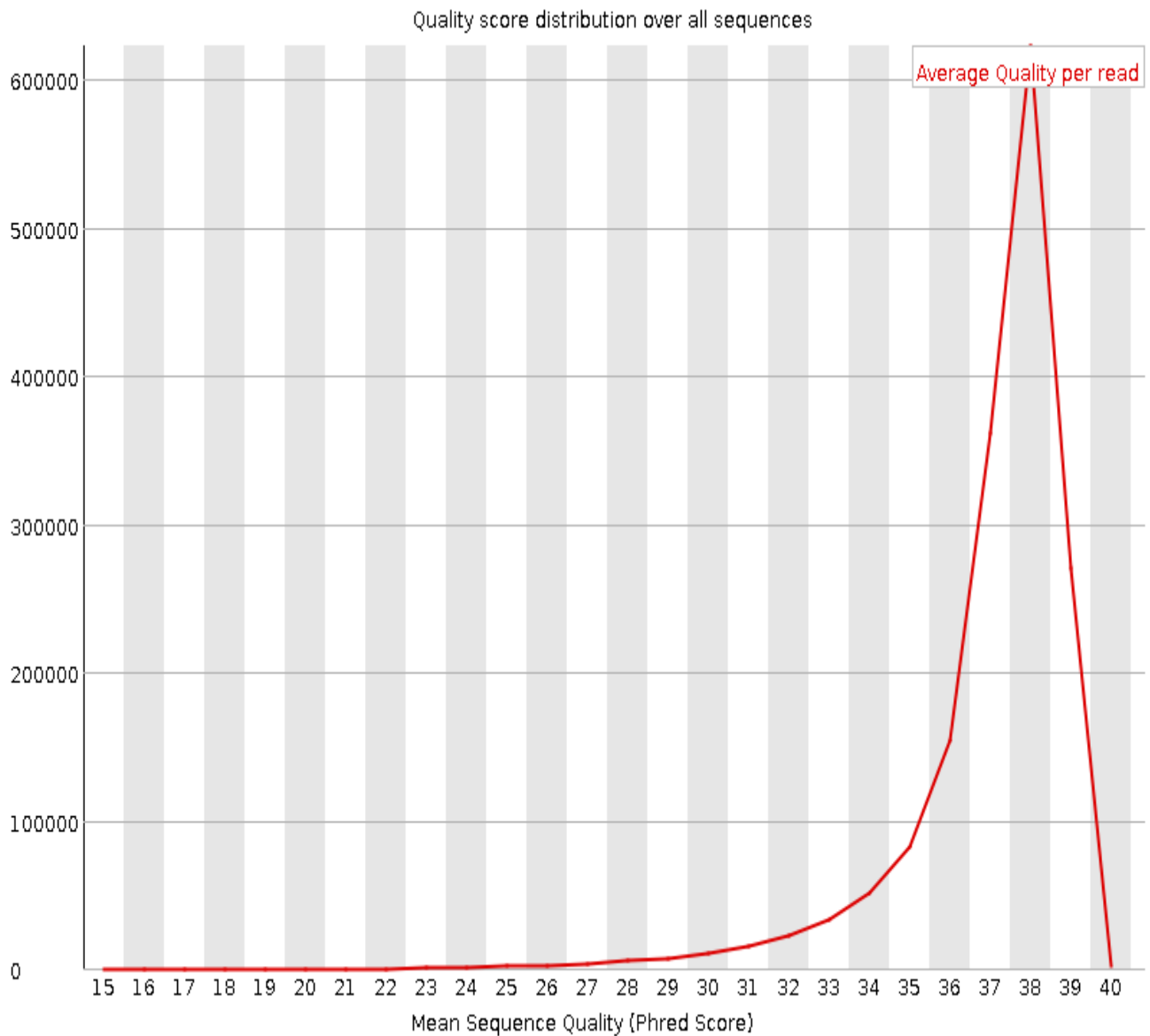
✅ [Per base sequence content](#)
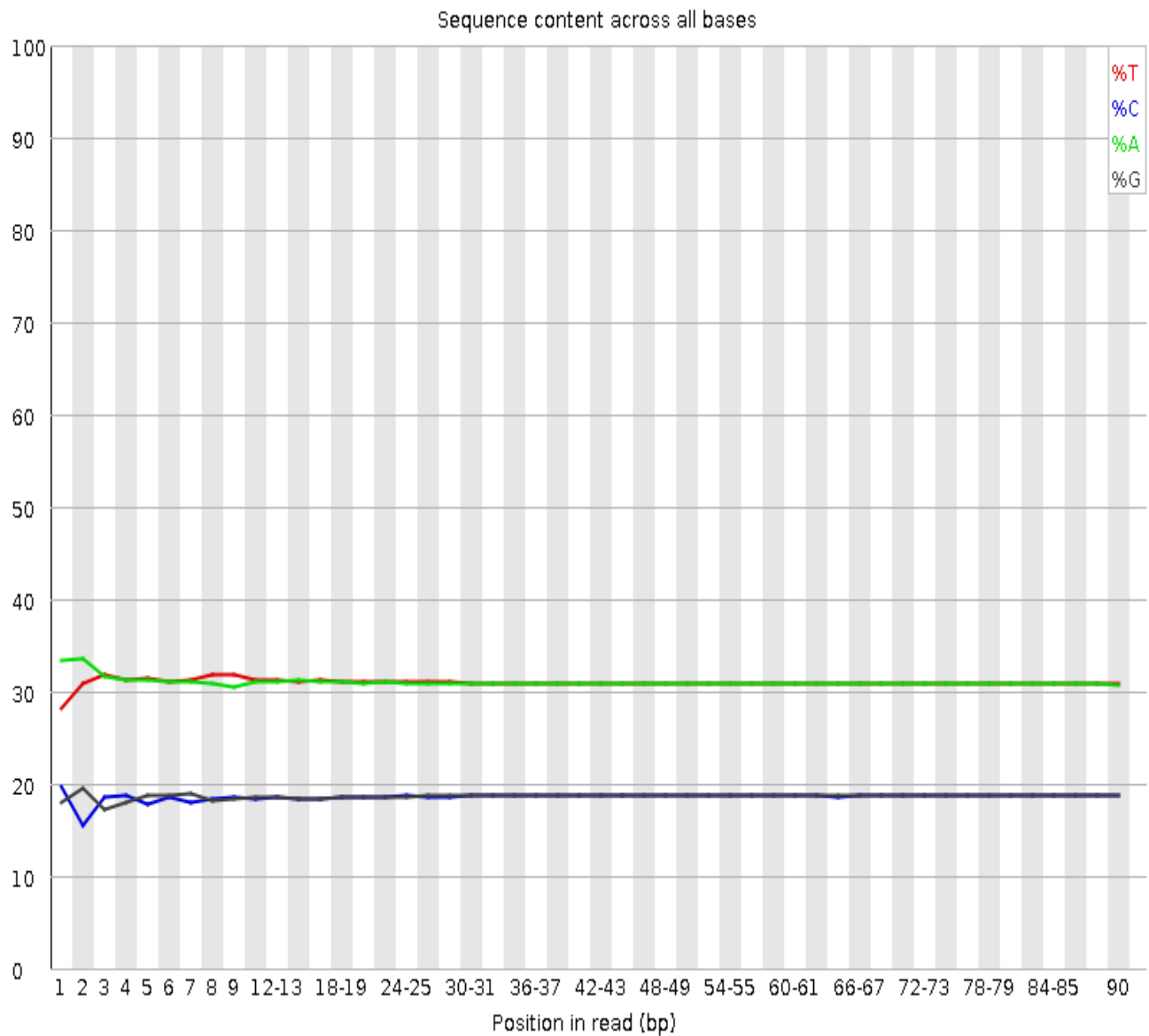
✅ [Per sequence GC content](#)
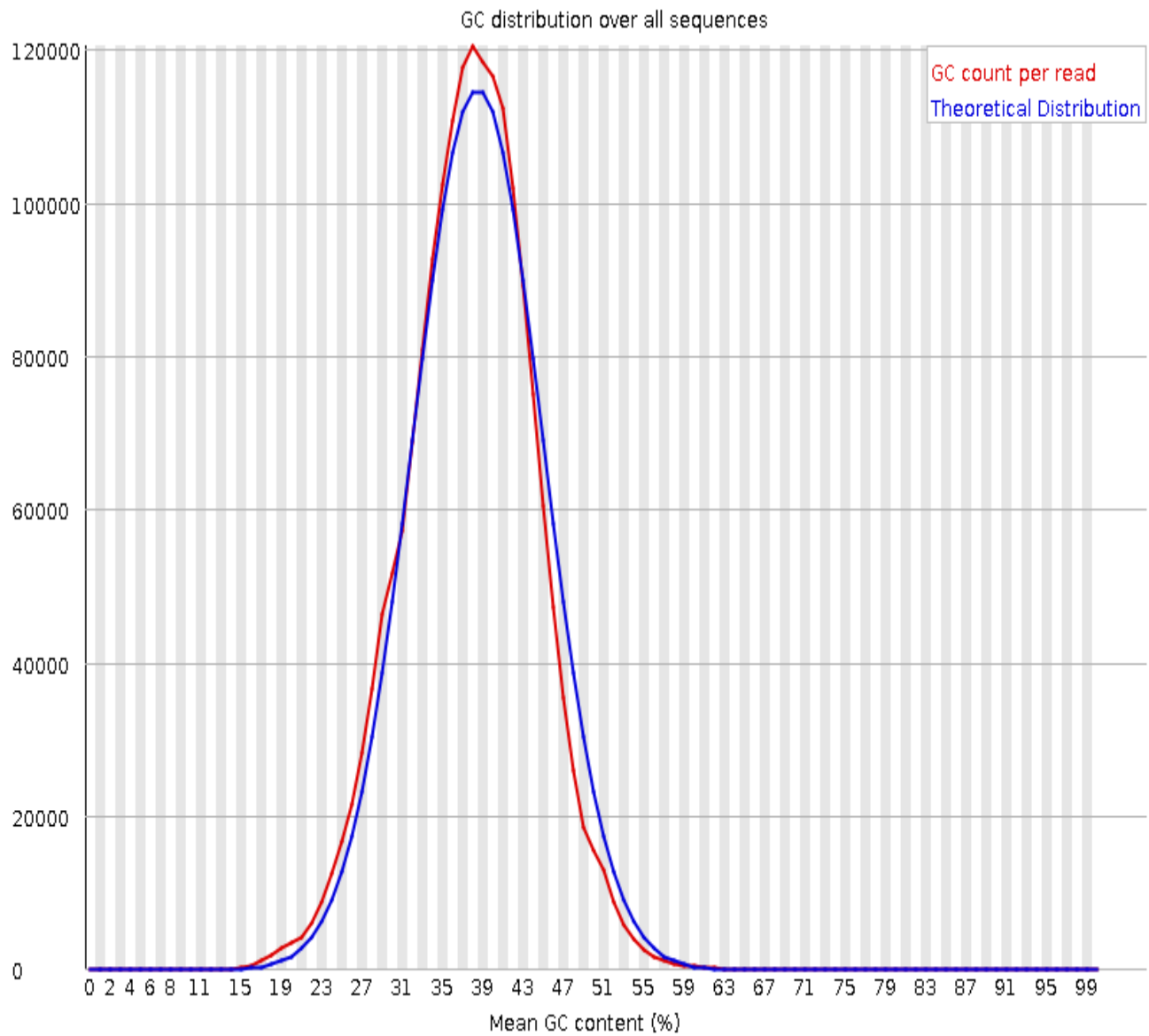
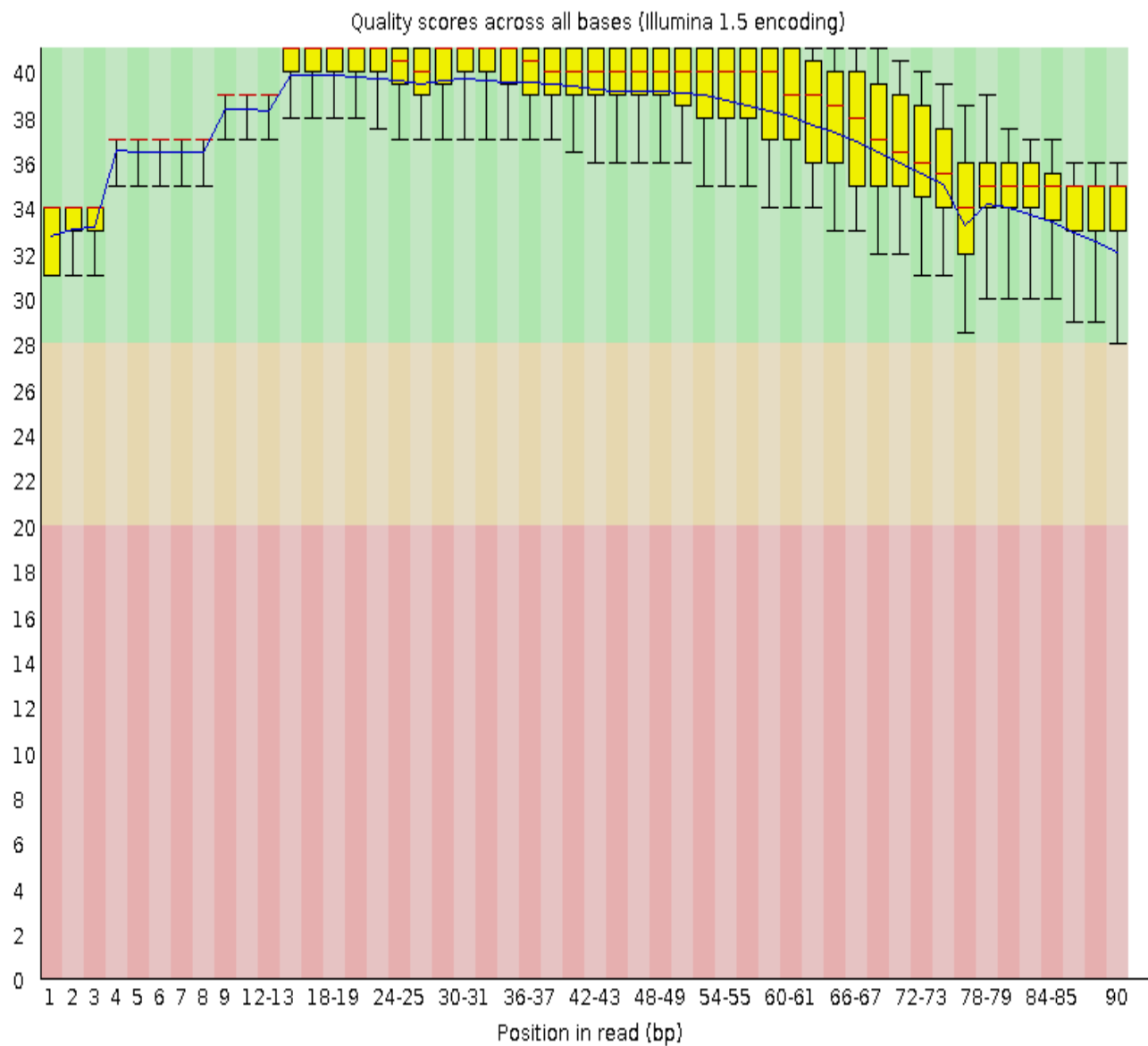✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

✅ [Sequence Duplication Levels](#)

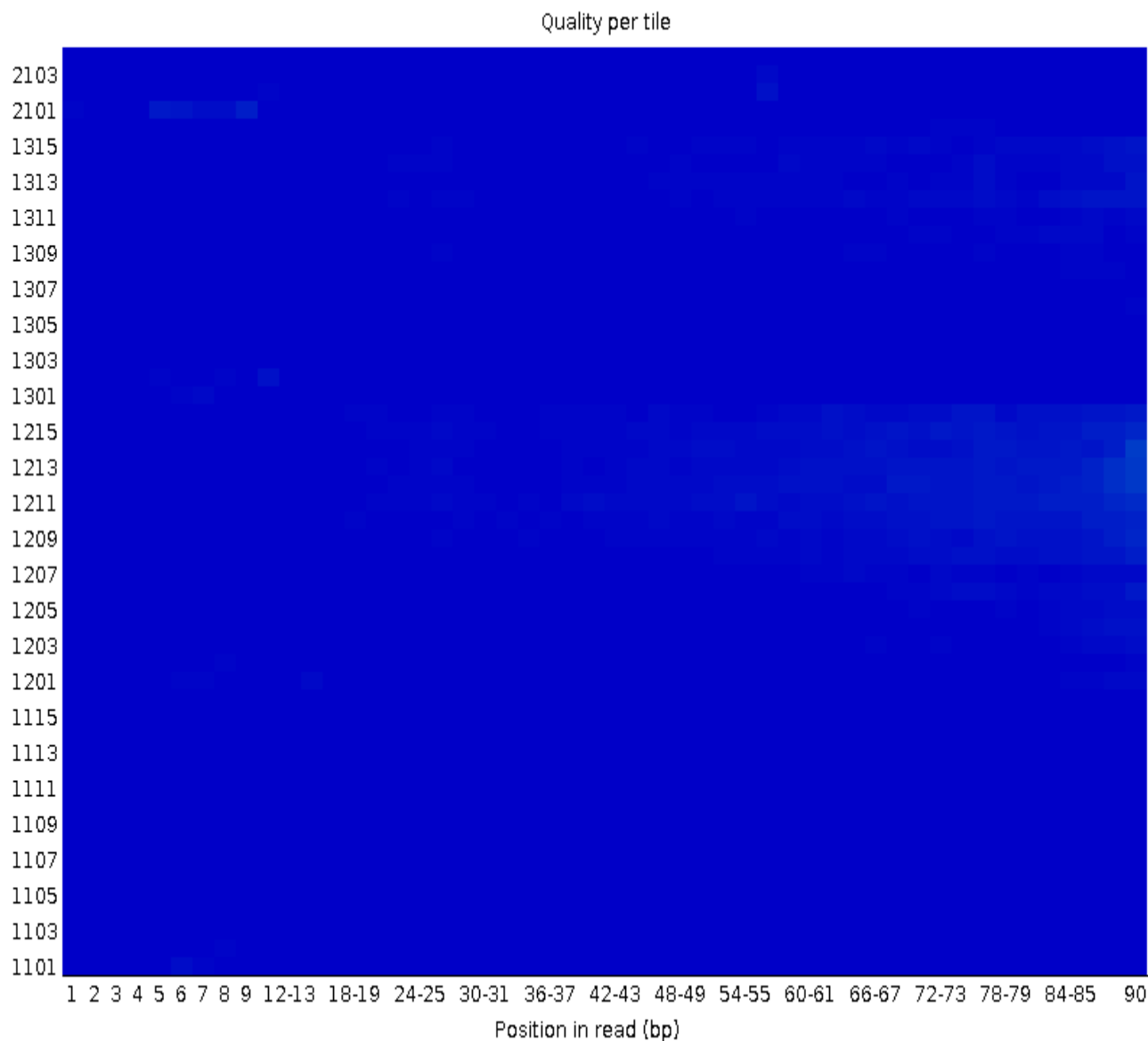✅ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

Measure	Value
Filename	E745-1.L500_SZAXPI015146-56_1_clean.fq.gz
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	1666667
Sequences flagged as poor quality	0
Sequence length	90
%GC	37

✅ Per base sequence quality

Quality scores across all bases (Illumina 1.5 encoding)

Position in read (bp)

✅ **Per tile sequence quality**

Quality per tile

Per sequence quality scores

✅ Per base sequence content

✅ Per sequence GC content
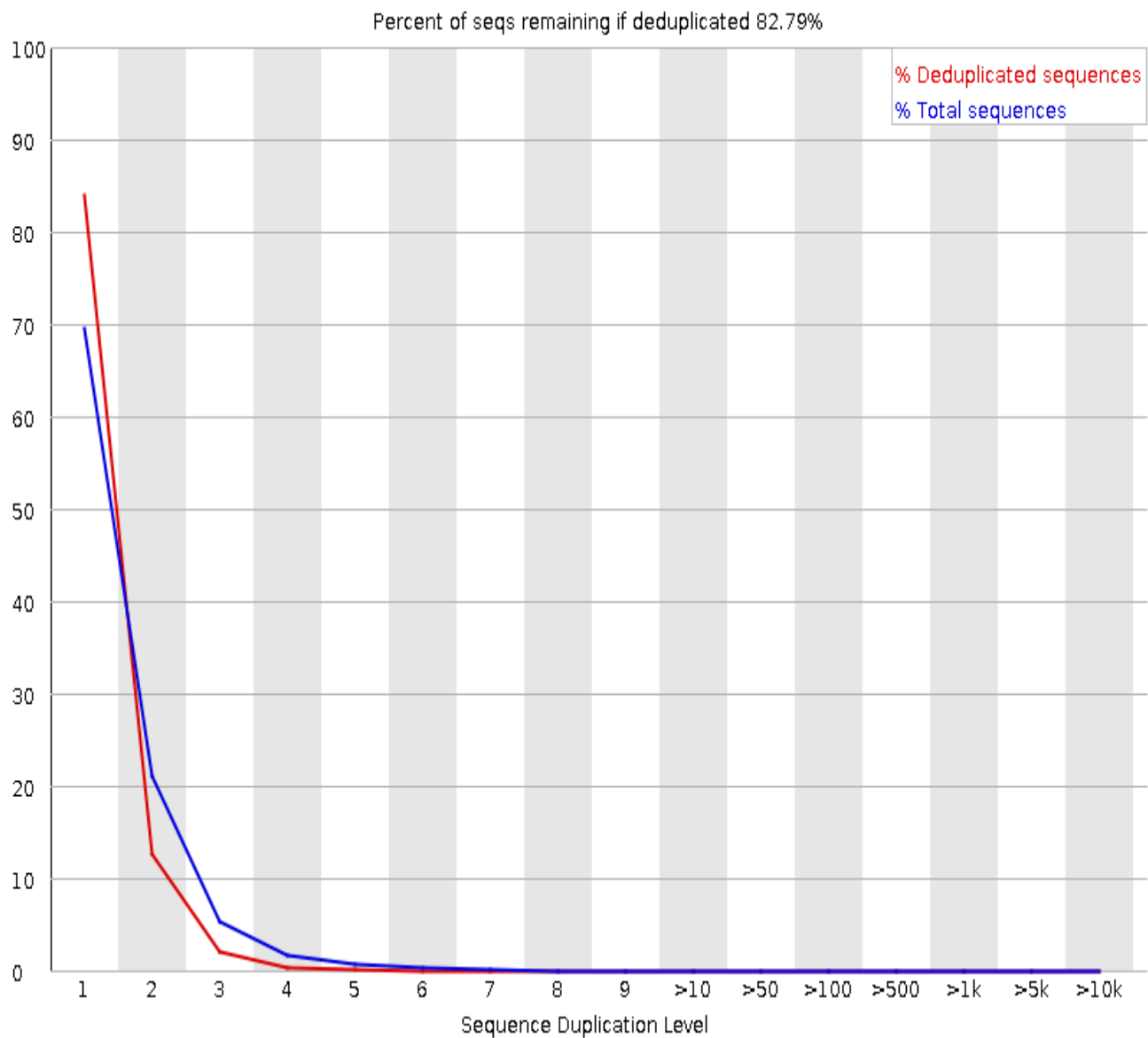
Per base N content

N content across all bases

✅ Sequence Length Distribution
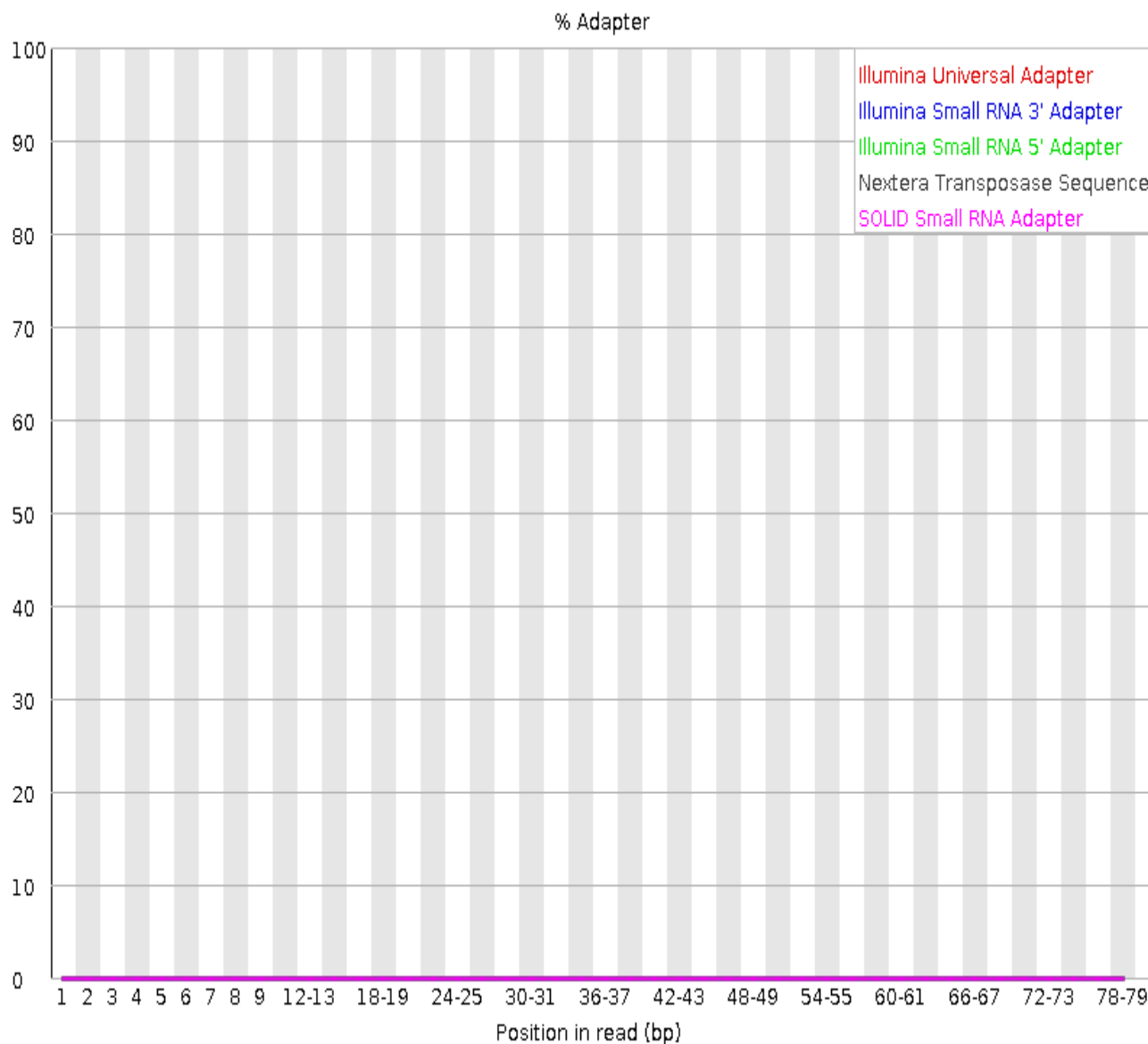
✅ Sequence Duplication Levels

✅Overrepresented sequences

No overrepresented sequences

✅Adapter Content

Produced by [FastQC](version 0.11.8) **(version 0.11.8)**