FastQC Report

Summary

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✅ Basic Statistics
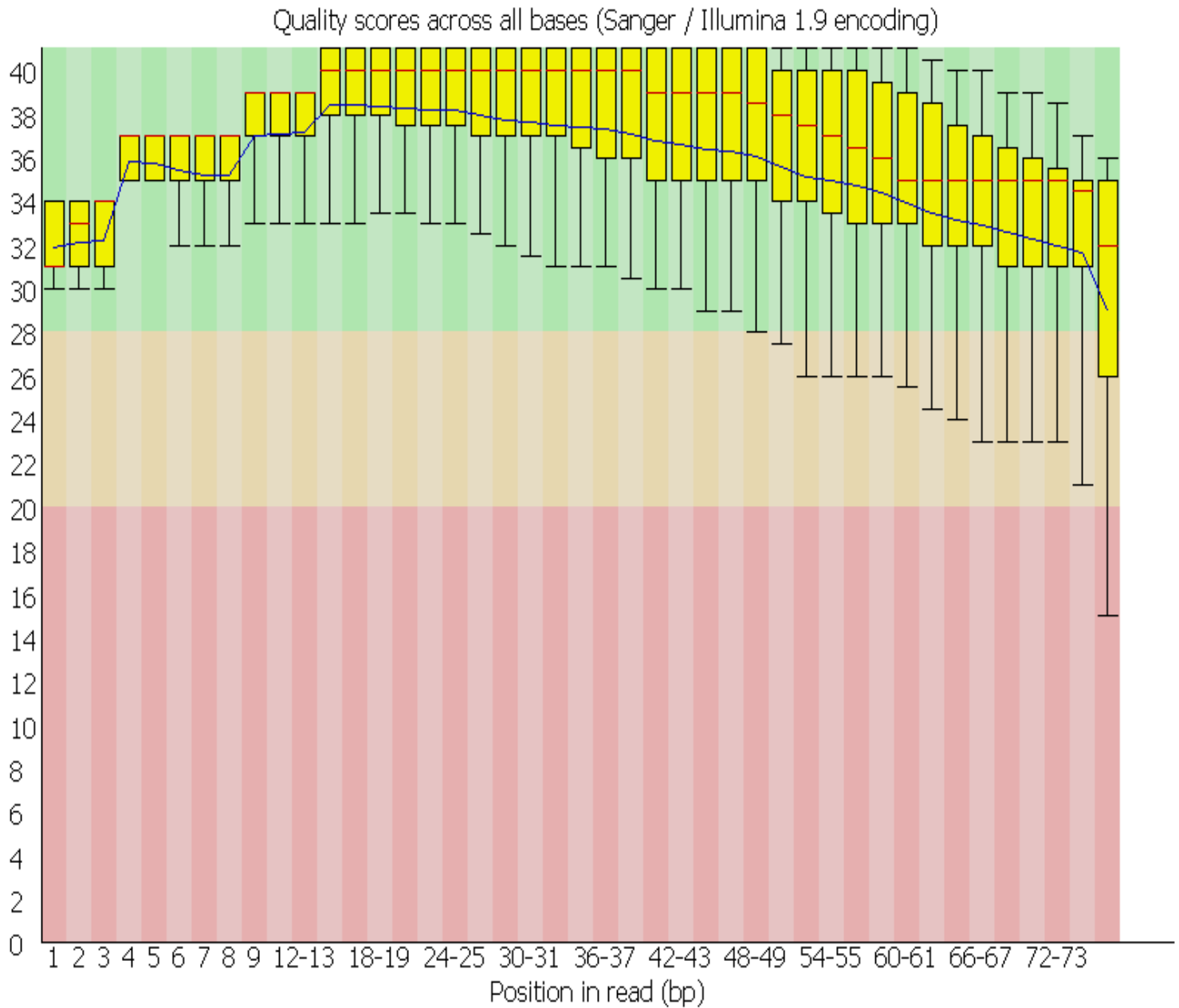
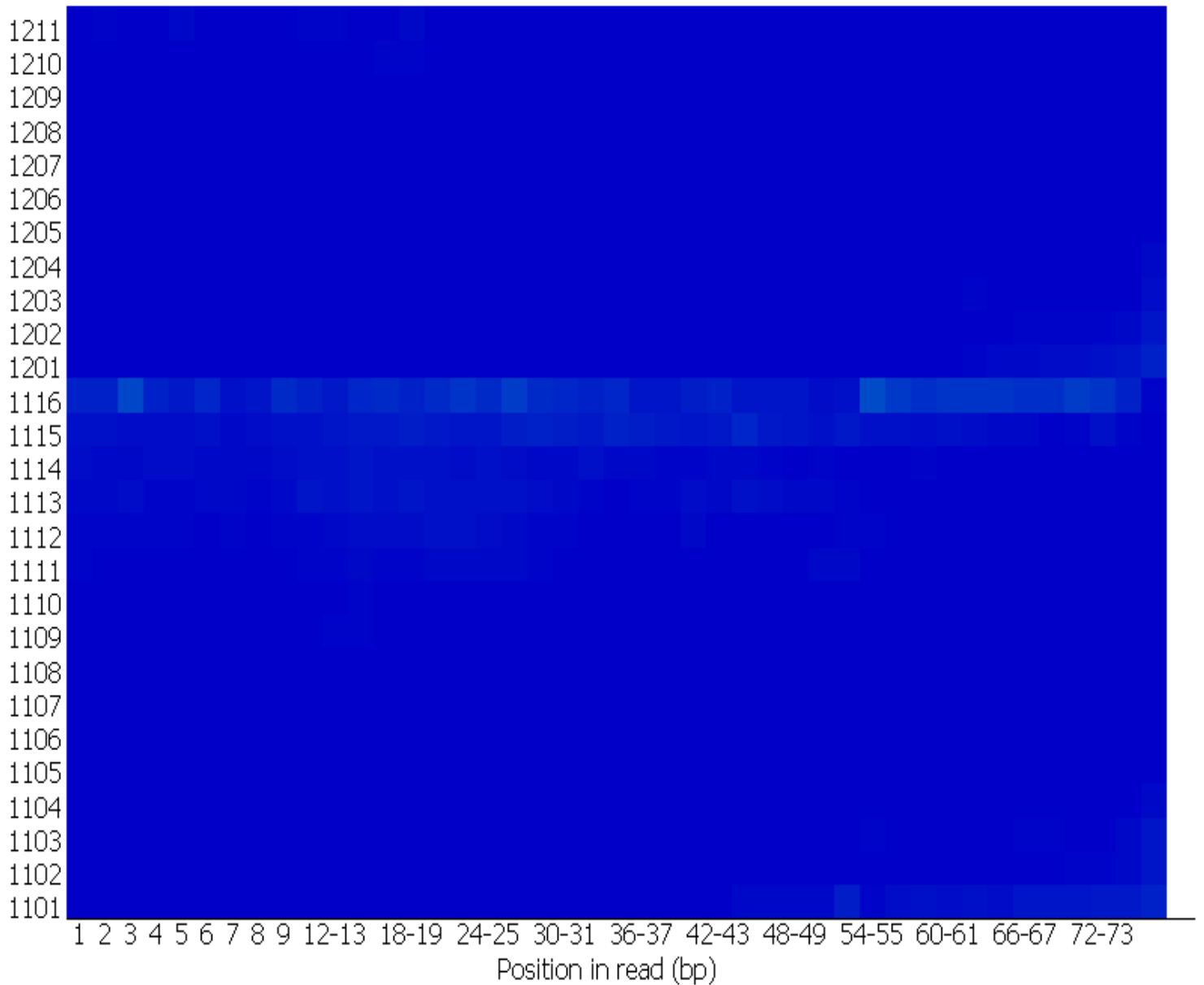| Measure	Value
Filename	totalmerge.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	42605003
Sequences flagged as poor quality	0
Sequence length	25-76
%GC	52

✅ Per base sequence quality

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

Position in read (bp)

✅ Per tile sequence quality

Quality per tile

Position in read (bp)

Per sequence quality scores

Quality score distribution over all sequences
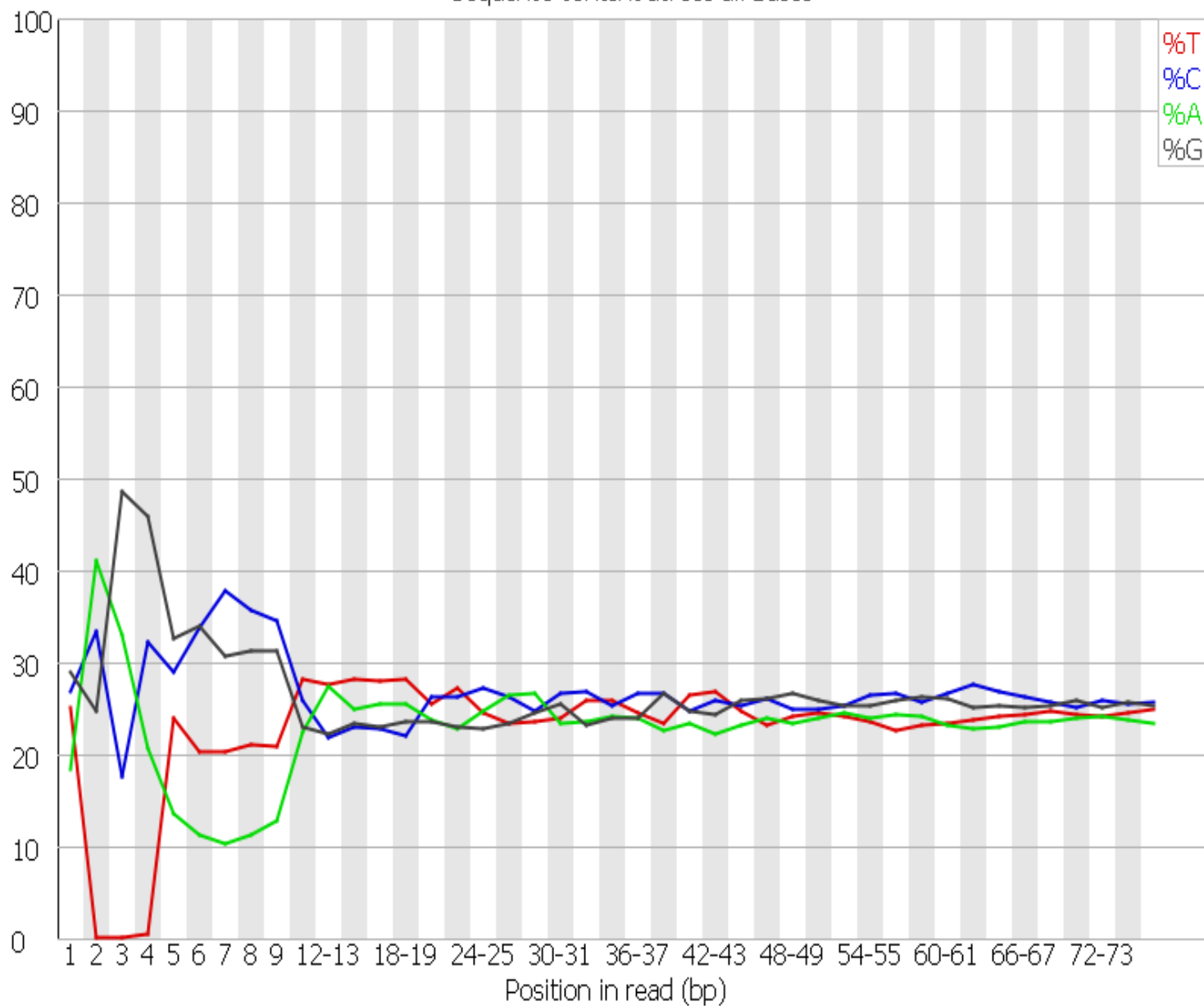
Average Quality per read

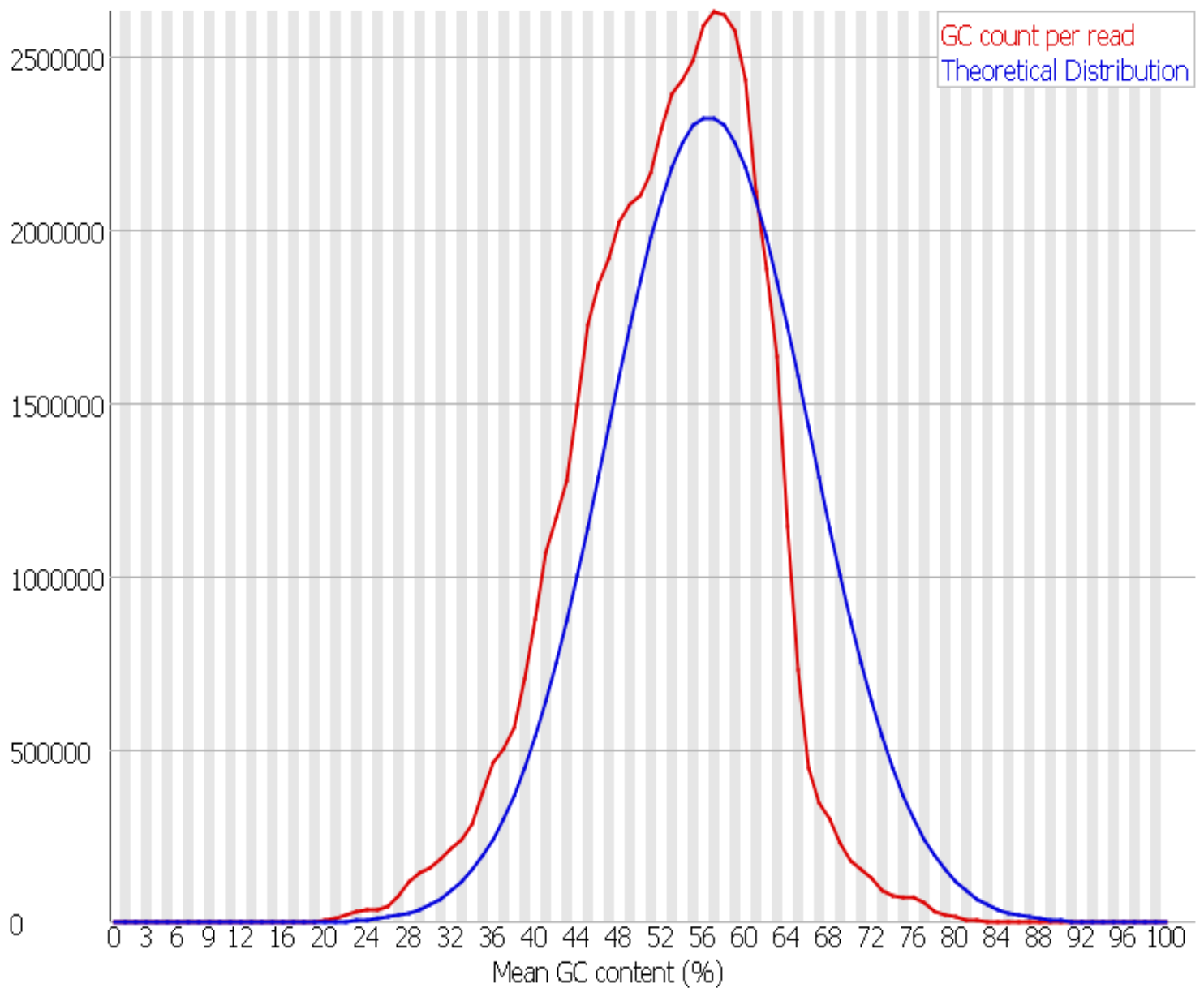Mean Sequence Quality (Phred Score)
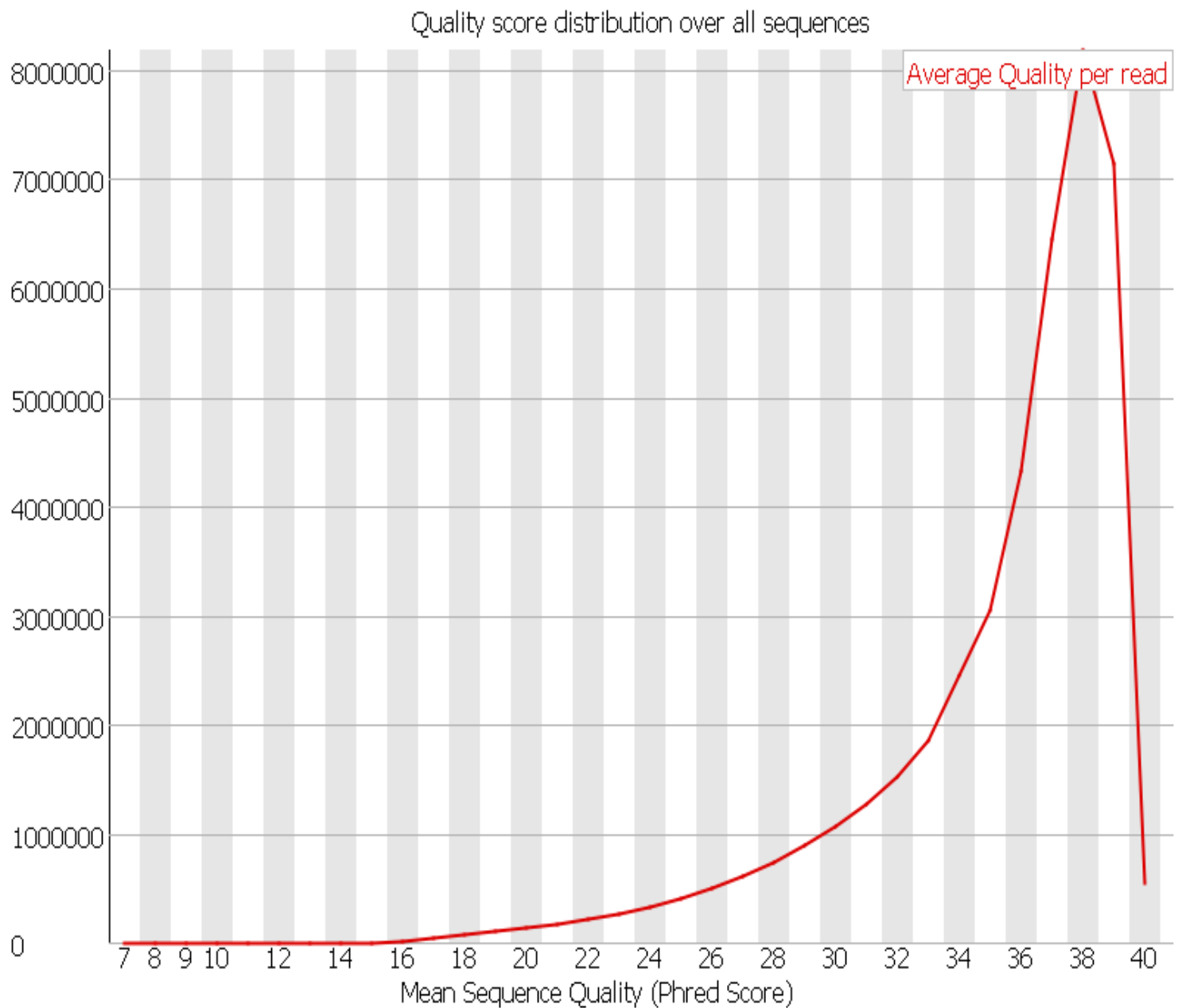
❌ **Per base sequence content**
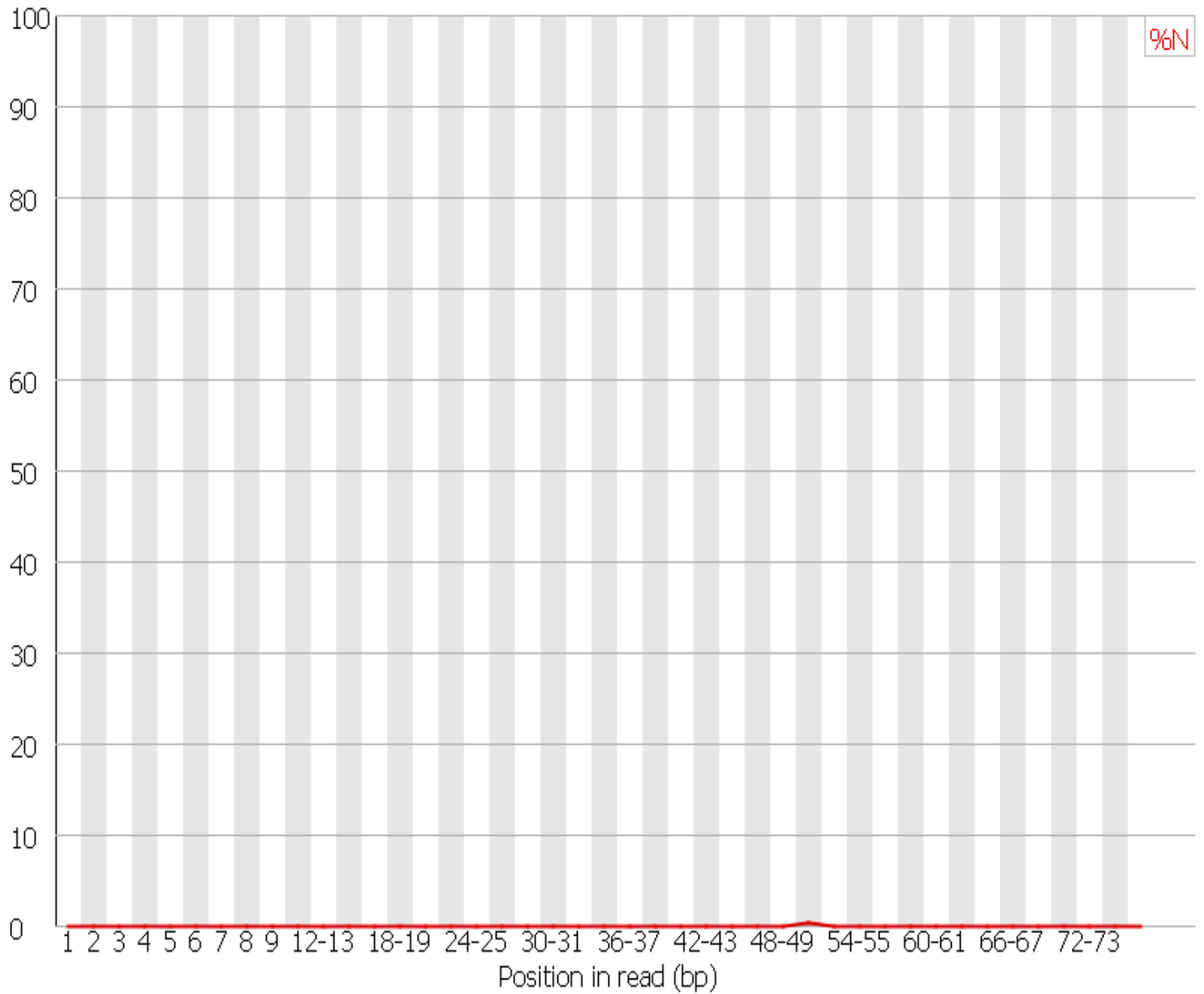
Sequence content across all bases

Per sequence GC content
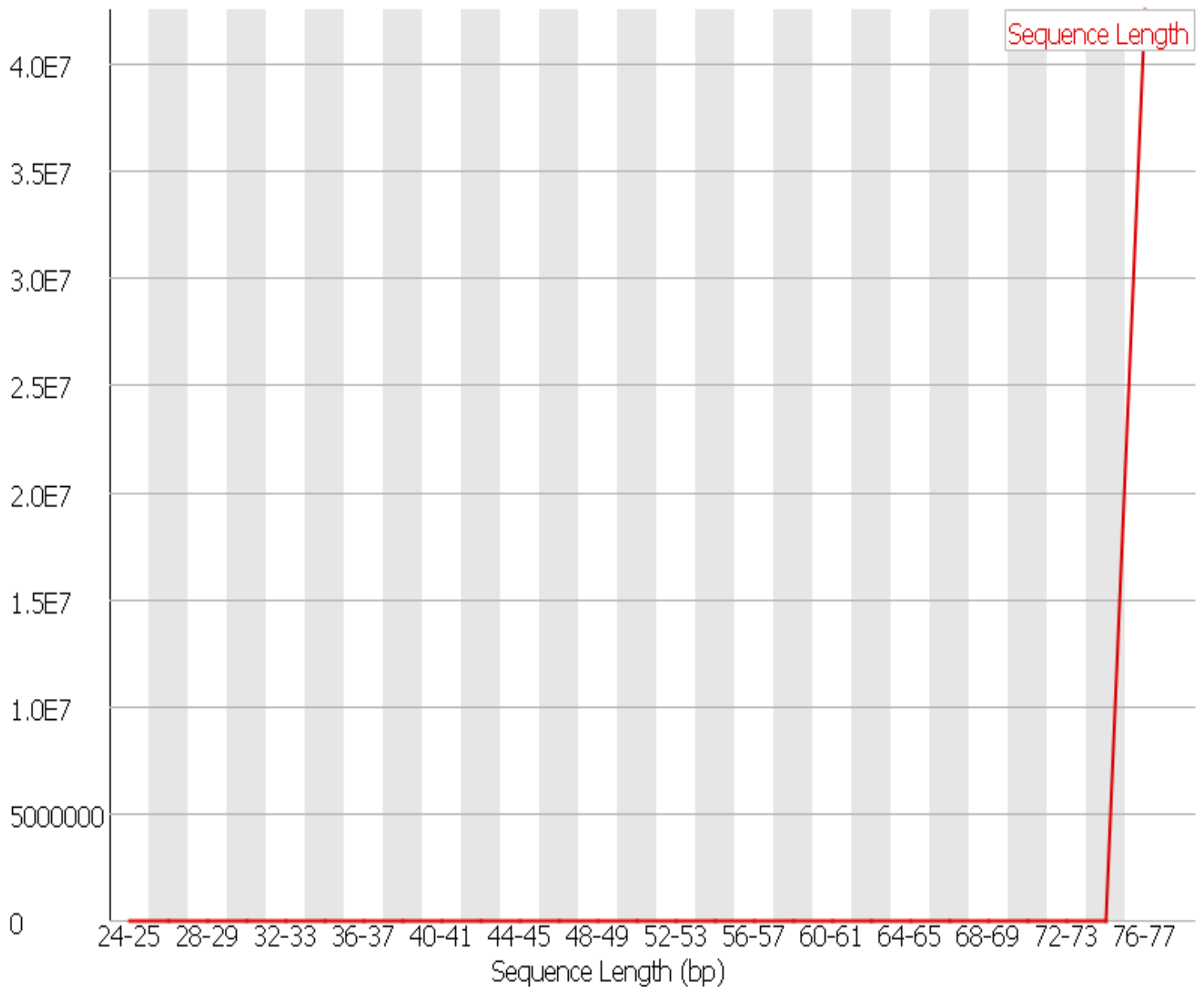
GC distribution over all sequences

Per base N content
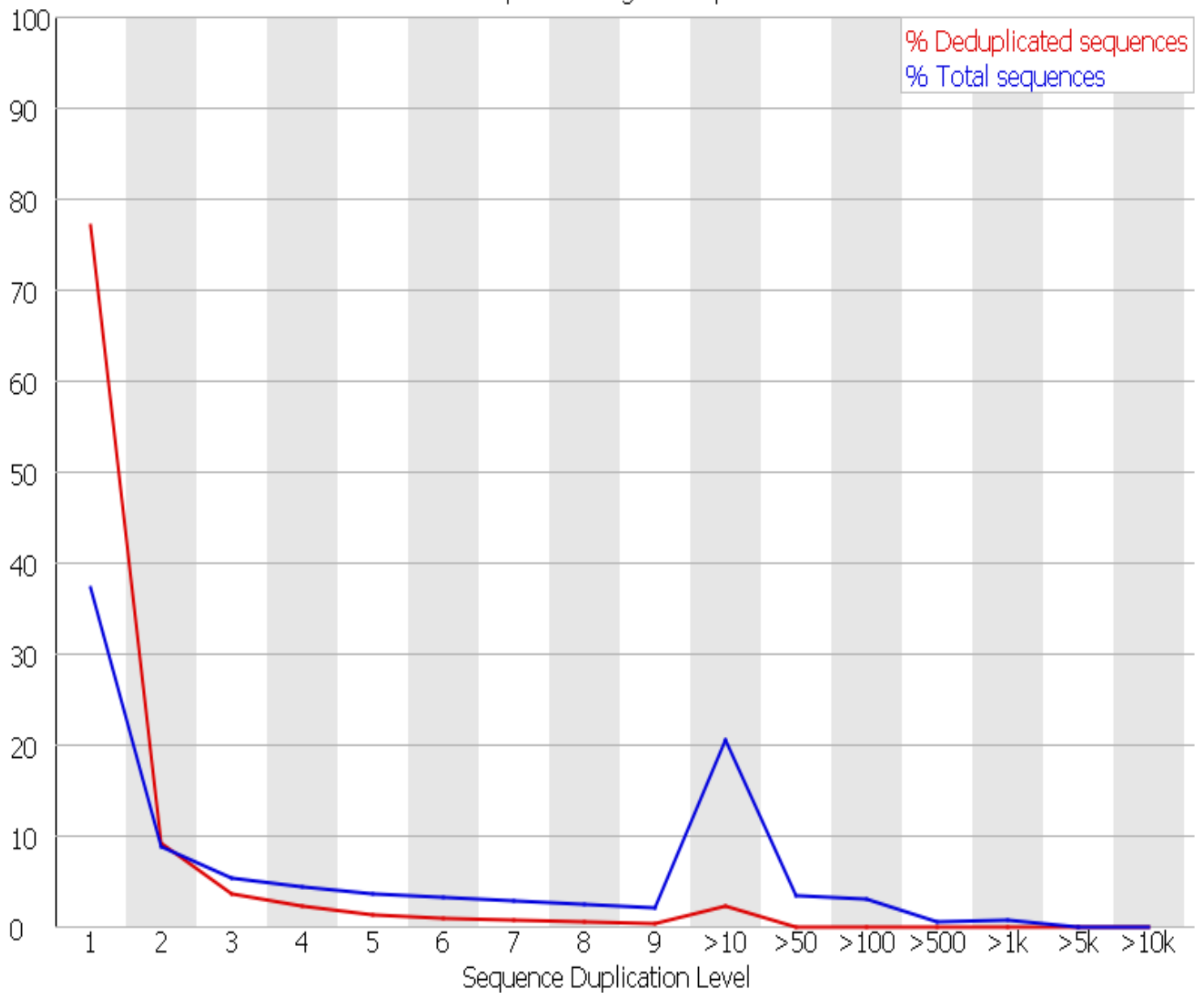
N content across all bases

⚠ Sequence Length Distribution

Distribution of sequence lengths over all sequences

❌ **Sequence Duplication Levels**
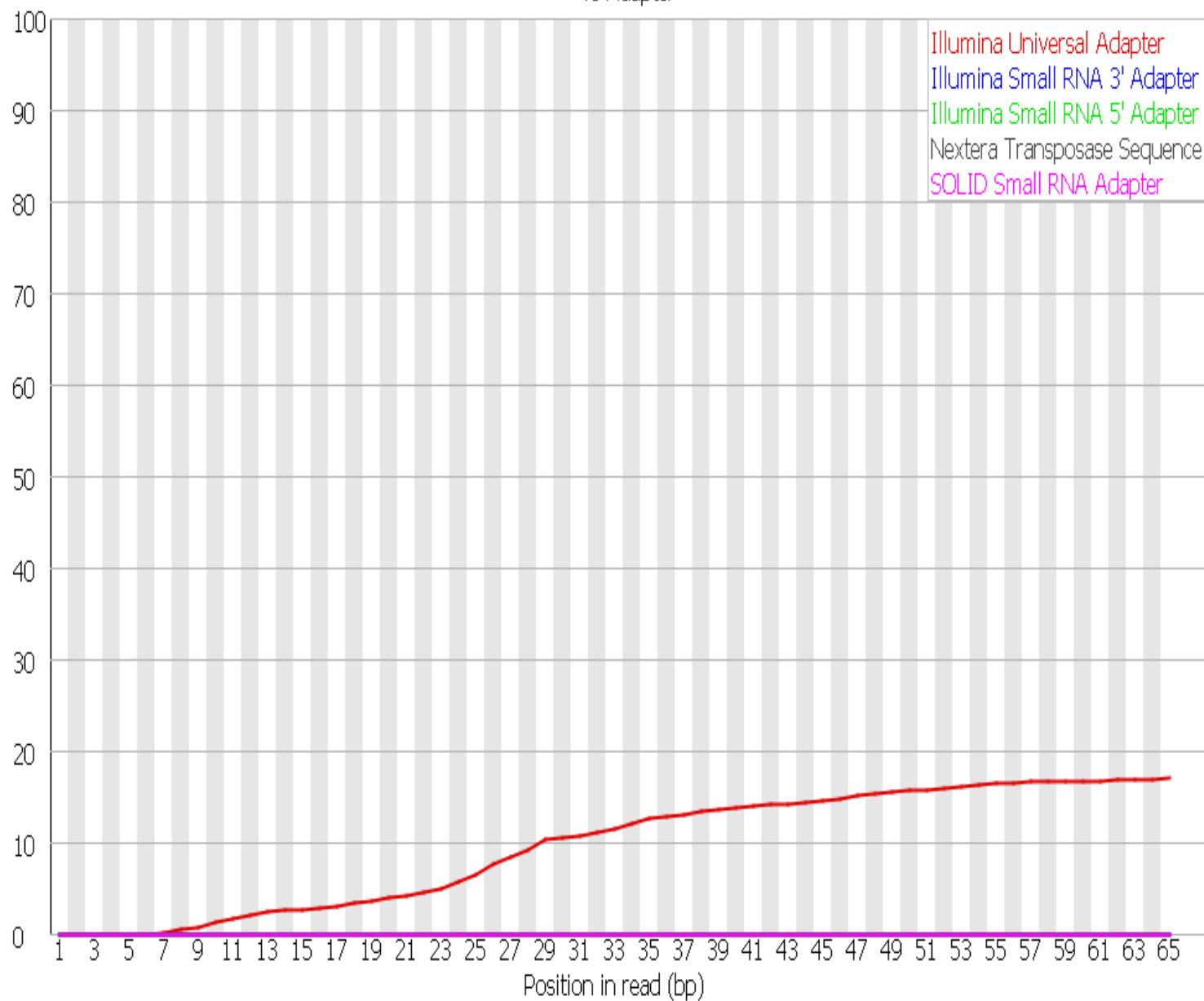
Percent of seqs remaining if deduplicated 48.38%

% Deduplicated sequences
% Total sequences

Sequence Duplication Level

✅ **Overrepresented sequences**

No overrepresented sequences

❌ **Adapter Content**

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