FastQC Report

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Basic Statistics

Measure	Value
Filename	skewer_SW041-trimmed-pair1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2507
Sequences flagged as poor quality	0
Sequence length	49-76
%GC	43

Per base sequence quality

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

Position in read (bp)
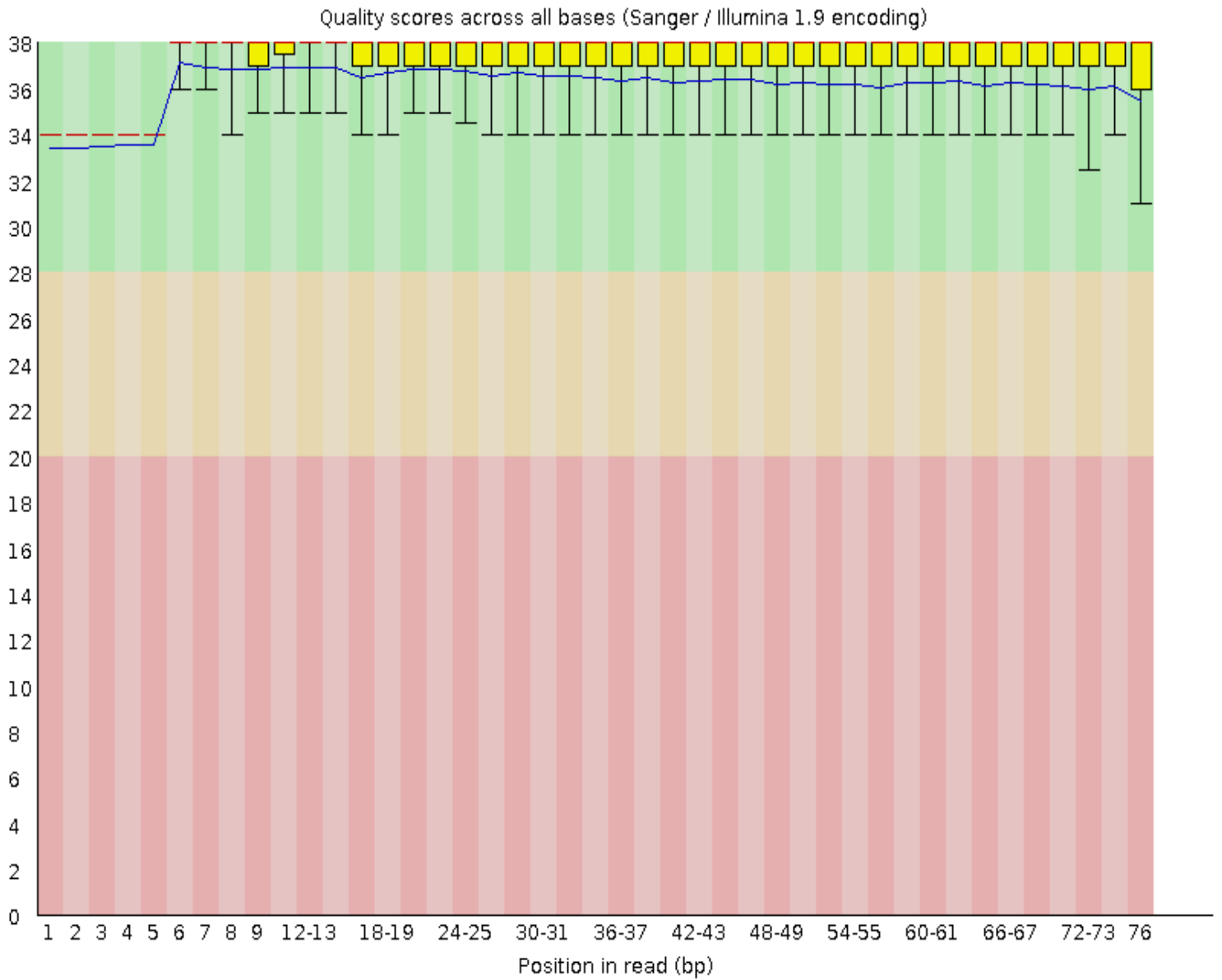
Per tile sequence quality

Quality per tile

Position in read (bp)
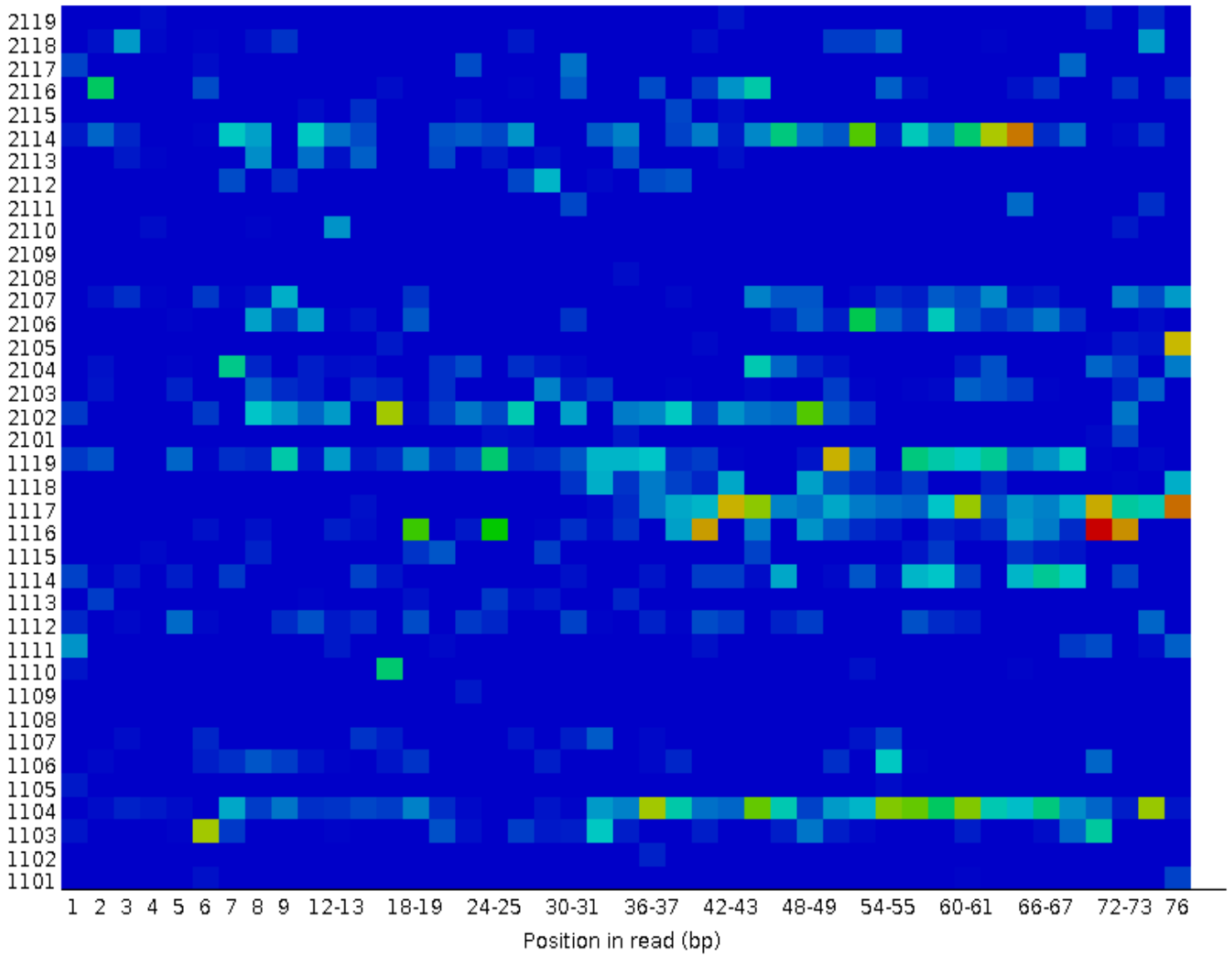
Per sequence quality scores

Quality score distribution over all sequences
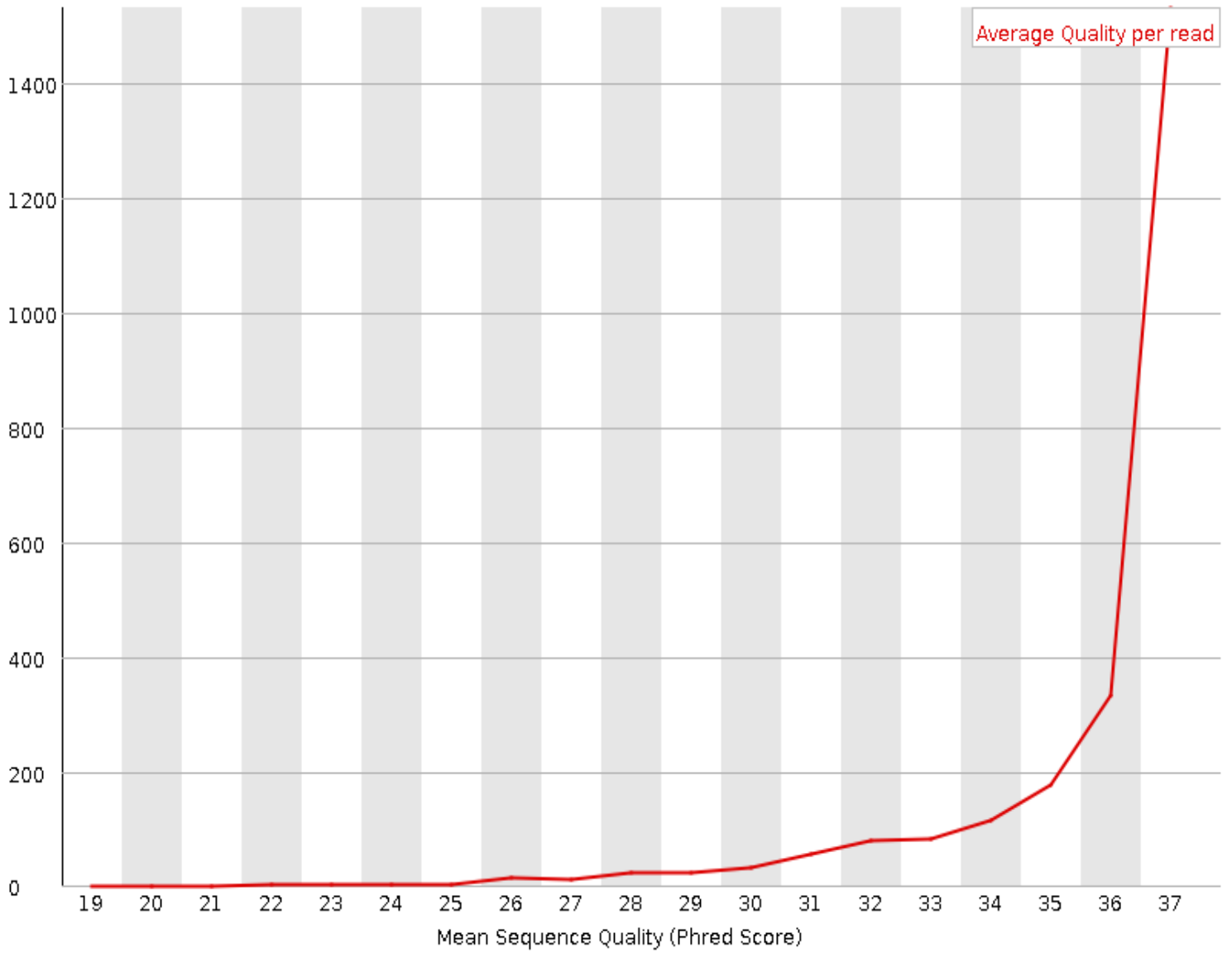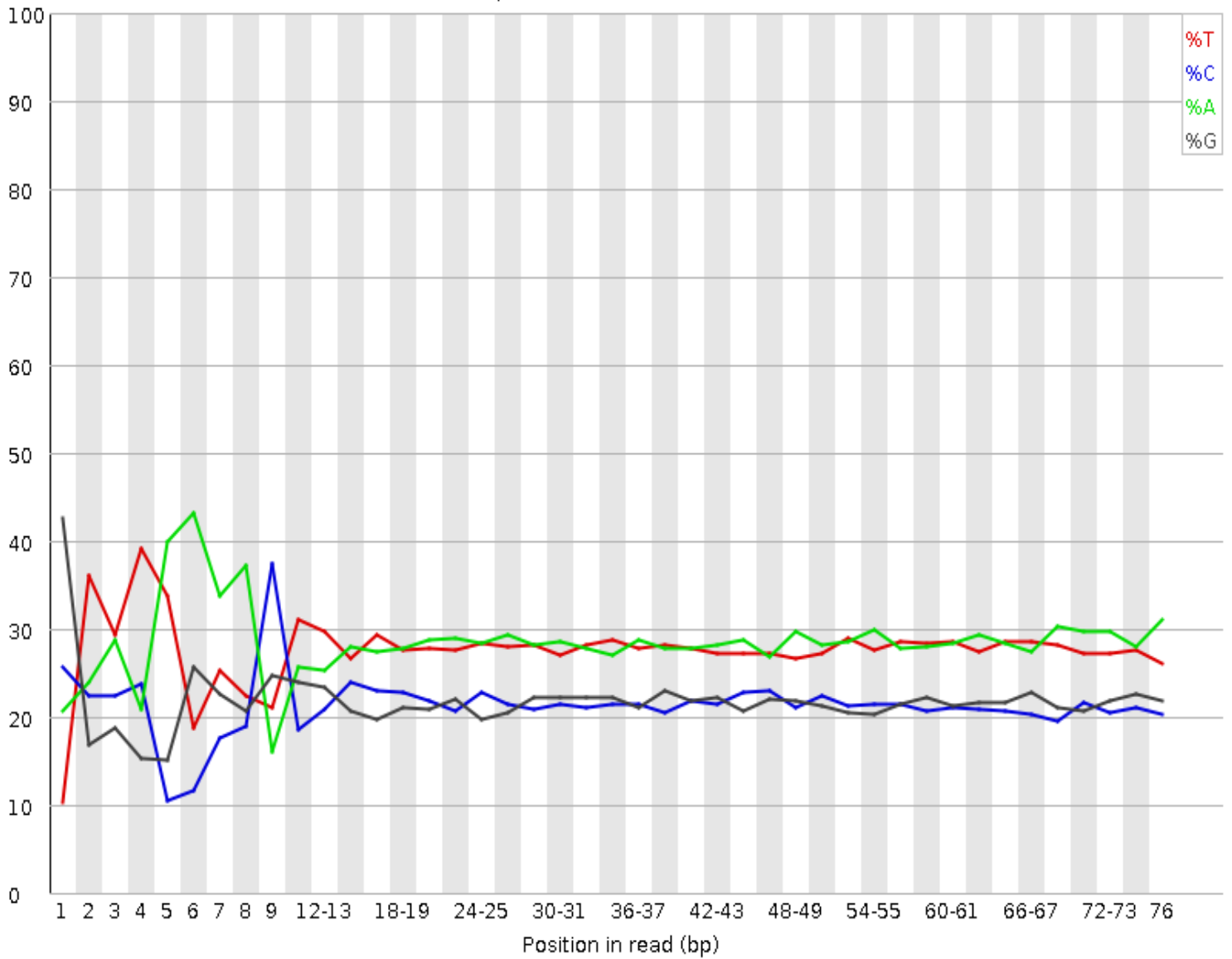
❌ **Per base sequence content**

Sequence content across all bases
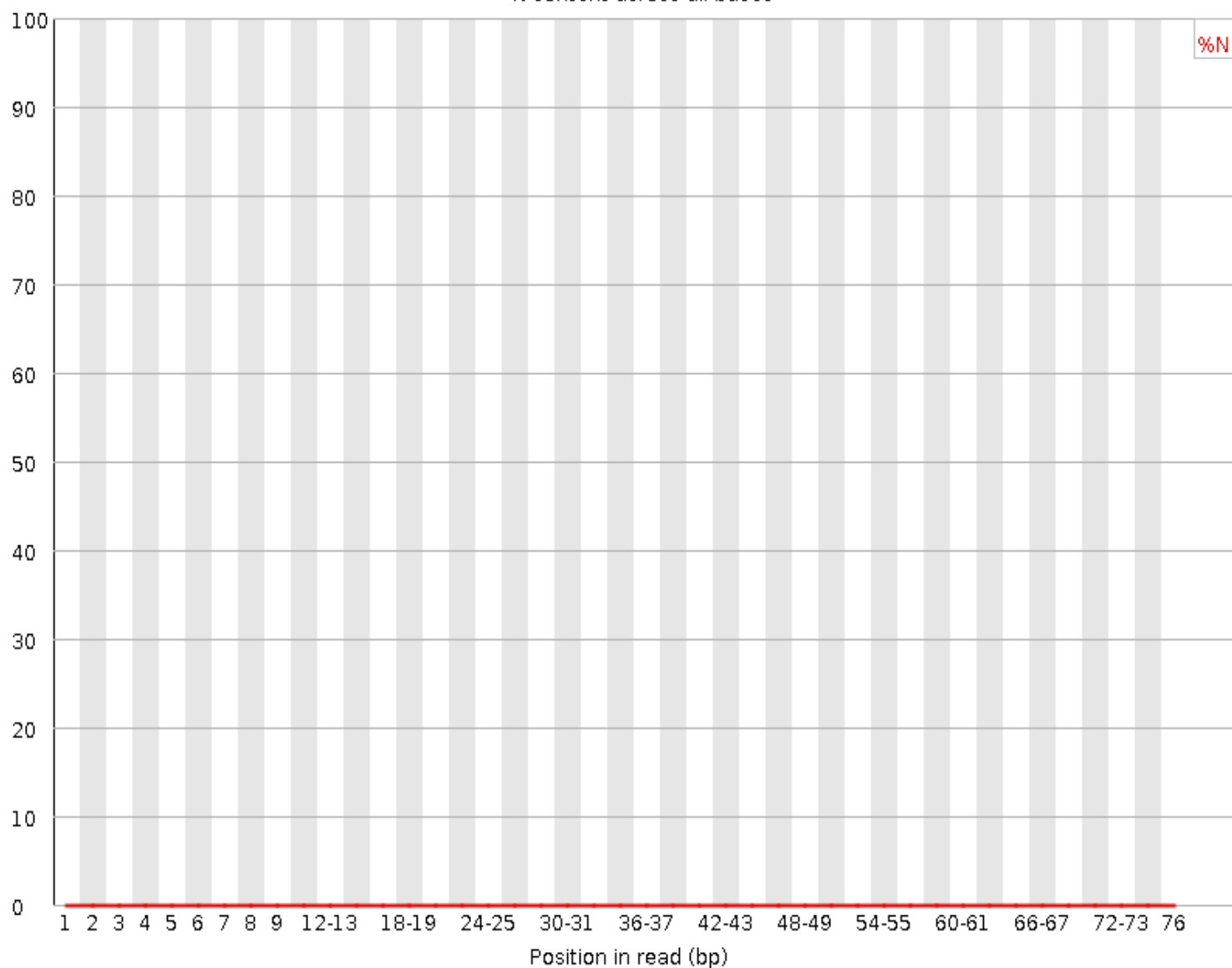
%T
%C
%A
%G

Position in read (bp)

✅ **Per sequence GC content**
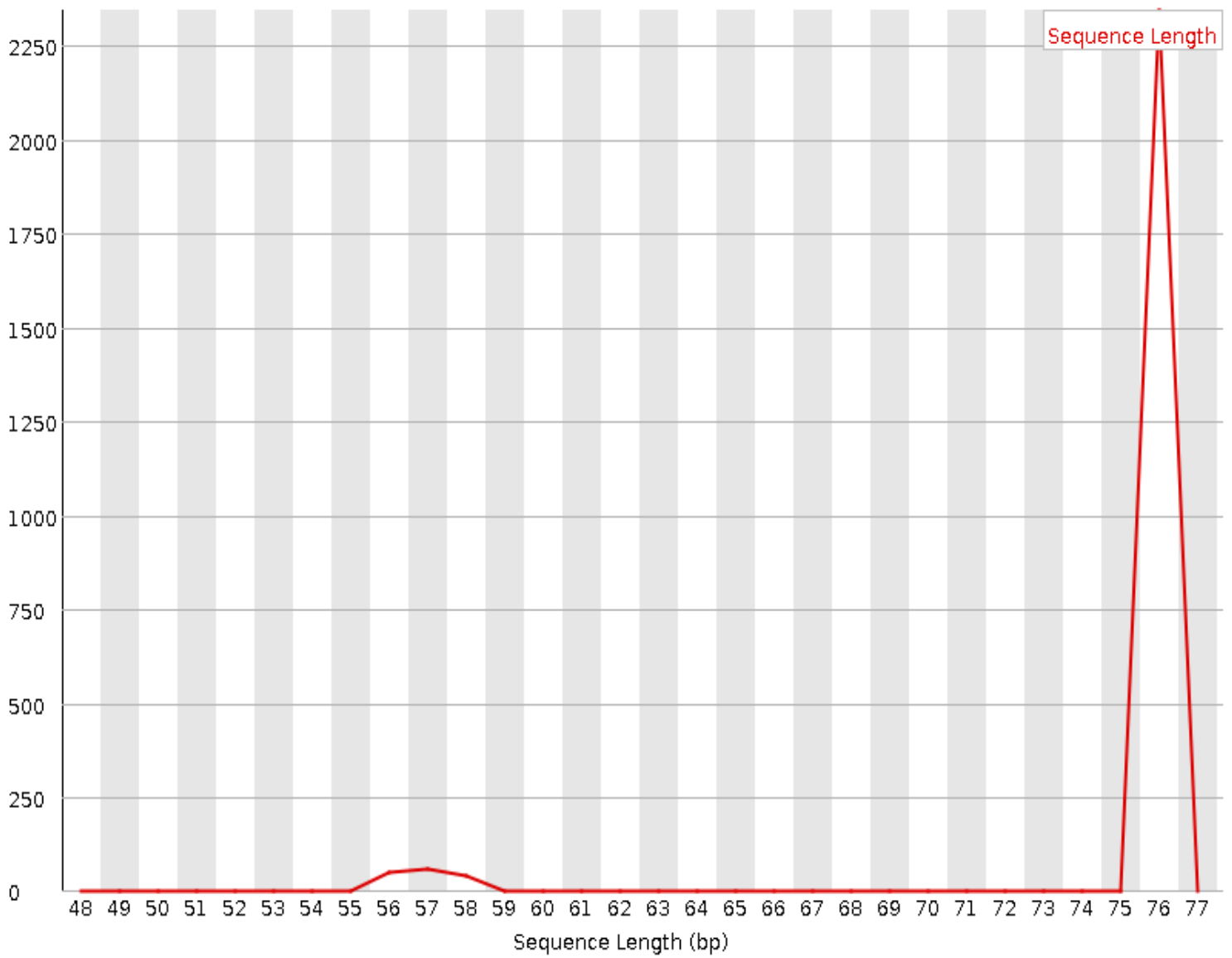
GC distribution over all sequences
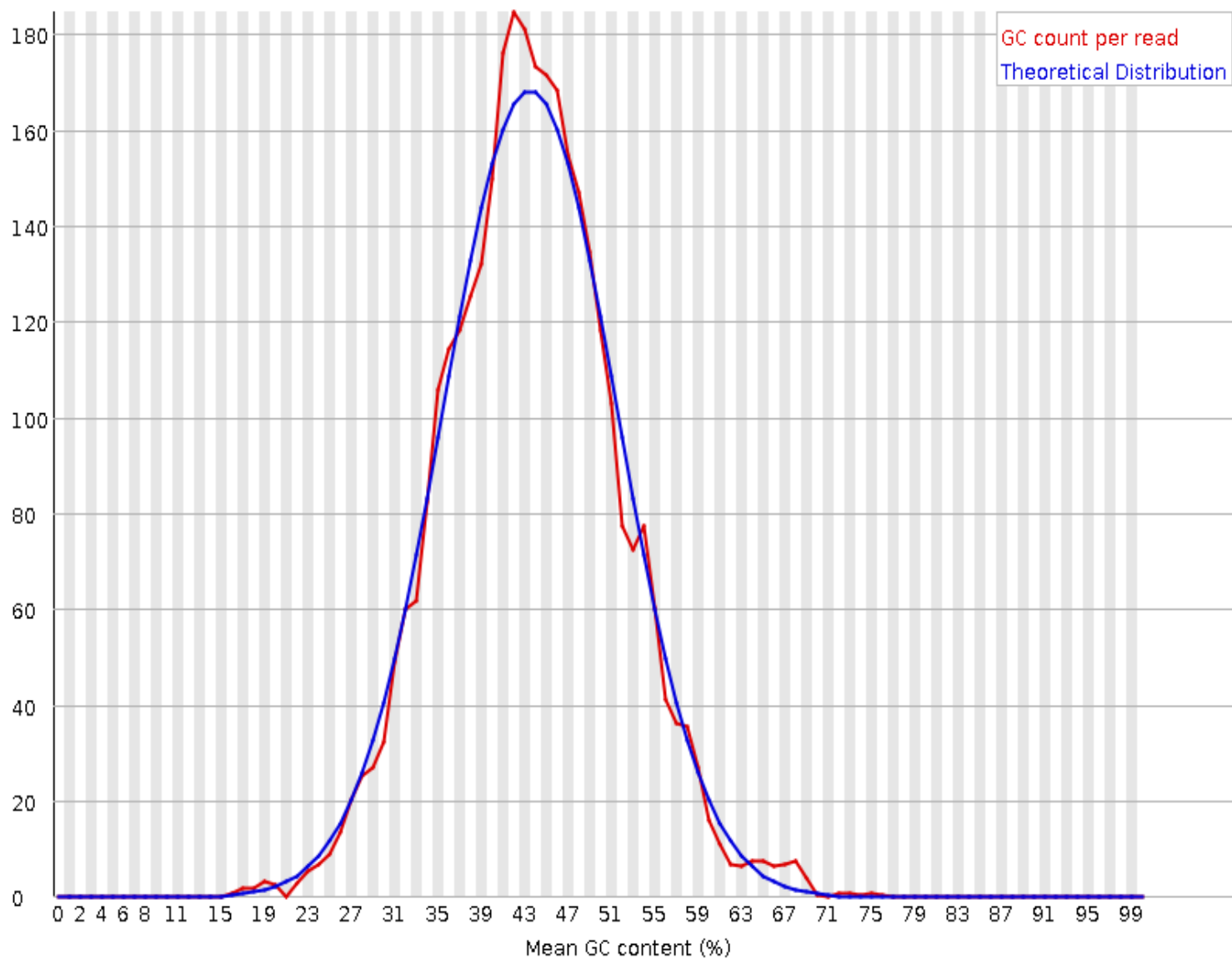
Per base N content
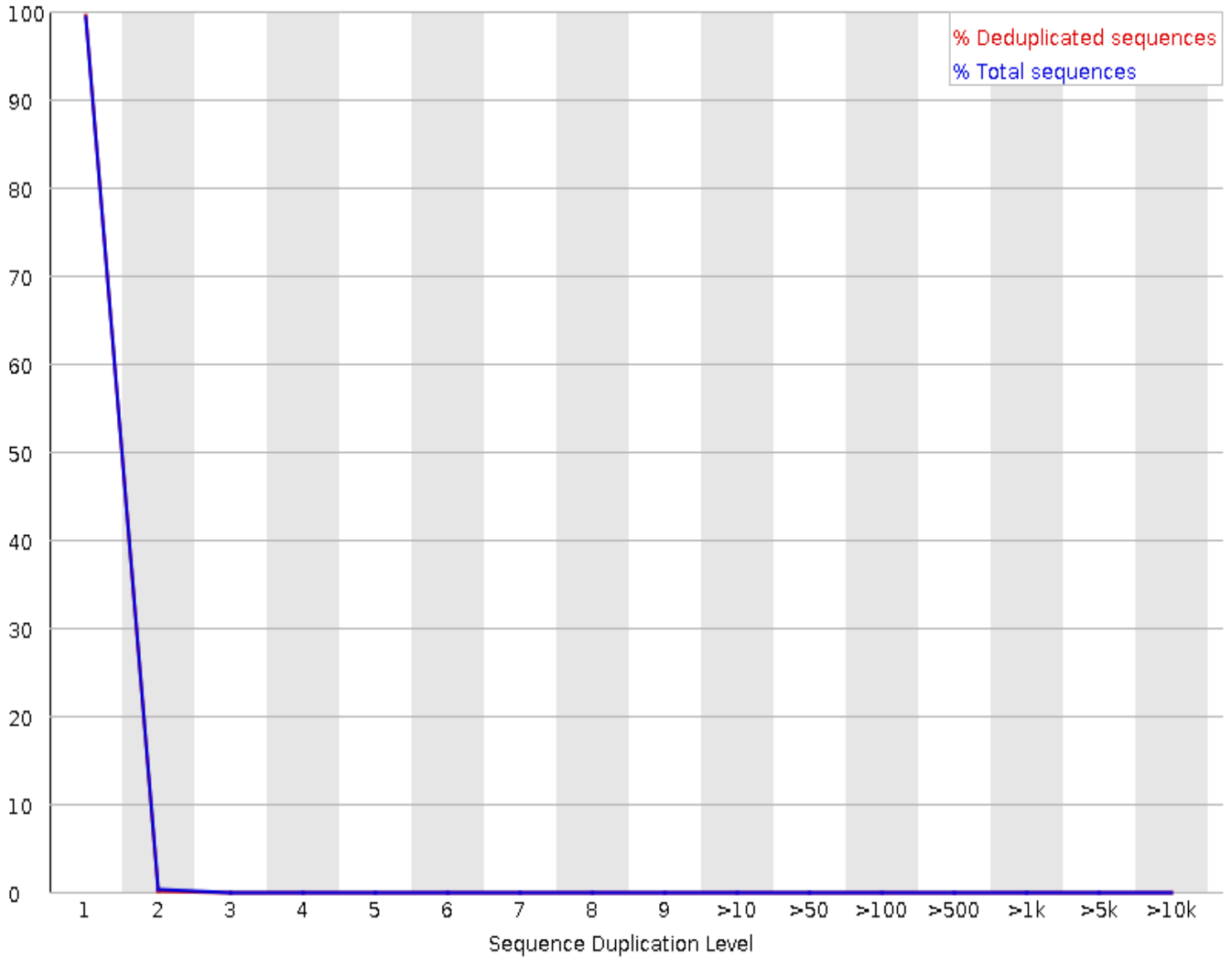
N content across all bases

⚠️ Sequence Length Distribution

Distribution of sequence lengths over all sequences

✅ Sequence Duplication Levels
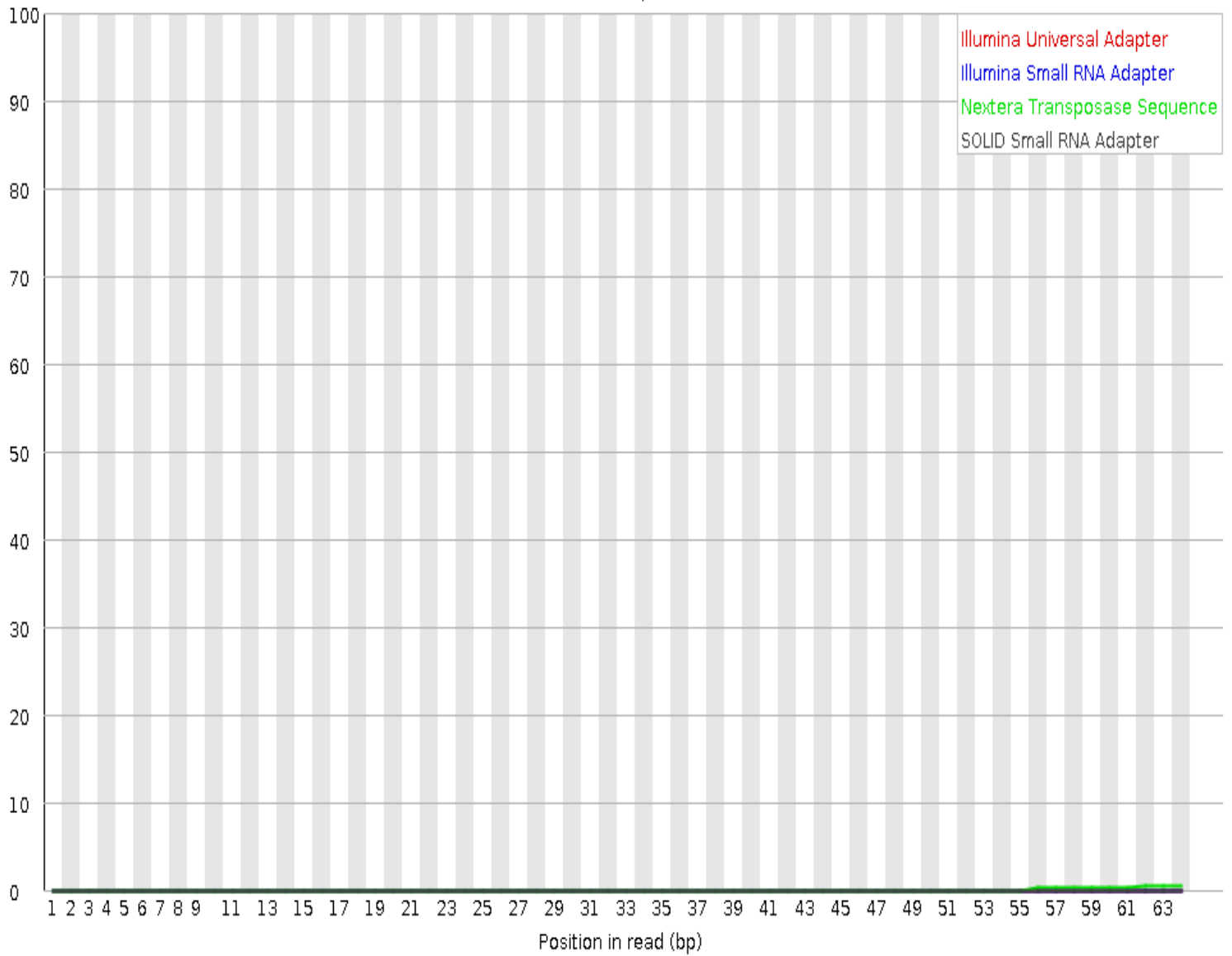
Percent of seqs remaining if deduplicated 99.76%

% Deduplicated sequences
% Total sequences

Sequence Duplication Level

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

% Adapter

- Illumina Universal Adapter
- Illumina Small RNA Adapter
- Nextera Transposase Sequence
- SOLID Small RNA Adapter

Position in read (bp)

✅ Kmer Content

No overrepresented Kmers

Produced by FastQC (version 0.11.3)