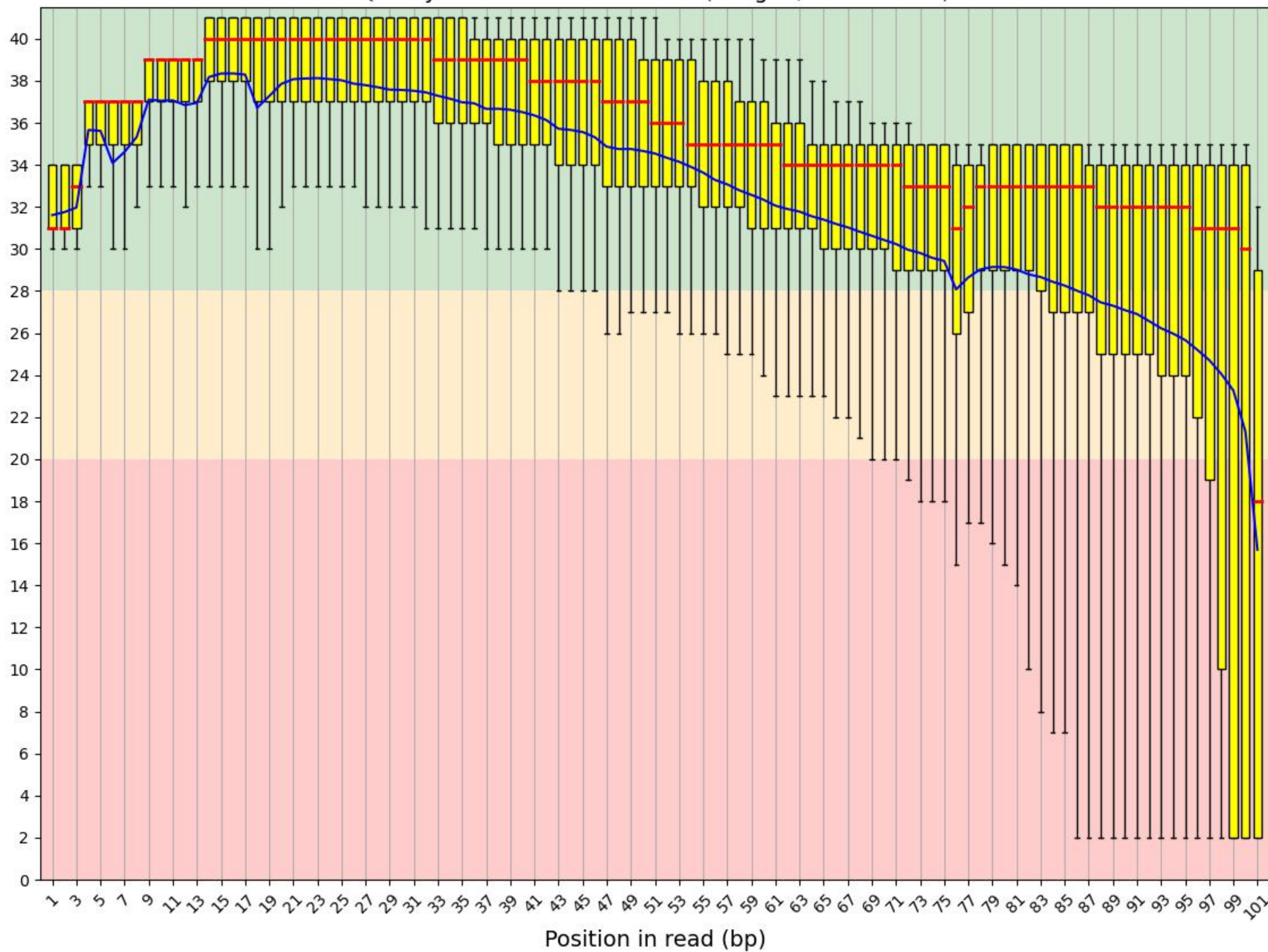
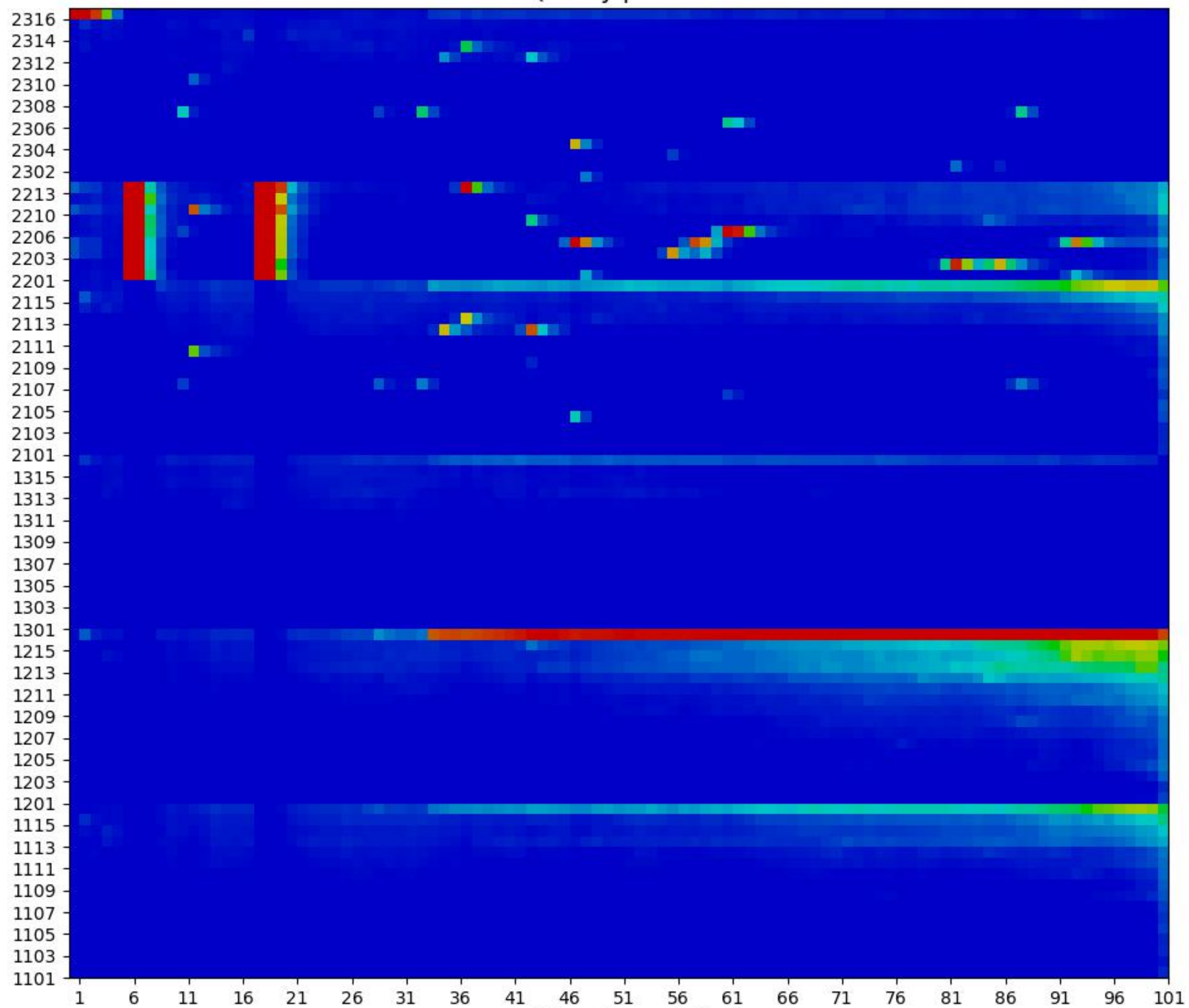


Measure	Value
Filename	amp_res_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	455876
Sequences flagged as poor quality	0
Sequence length	101
%GC	49.860000

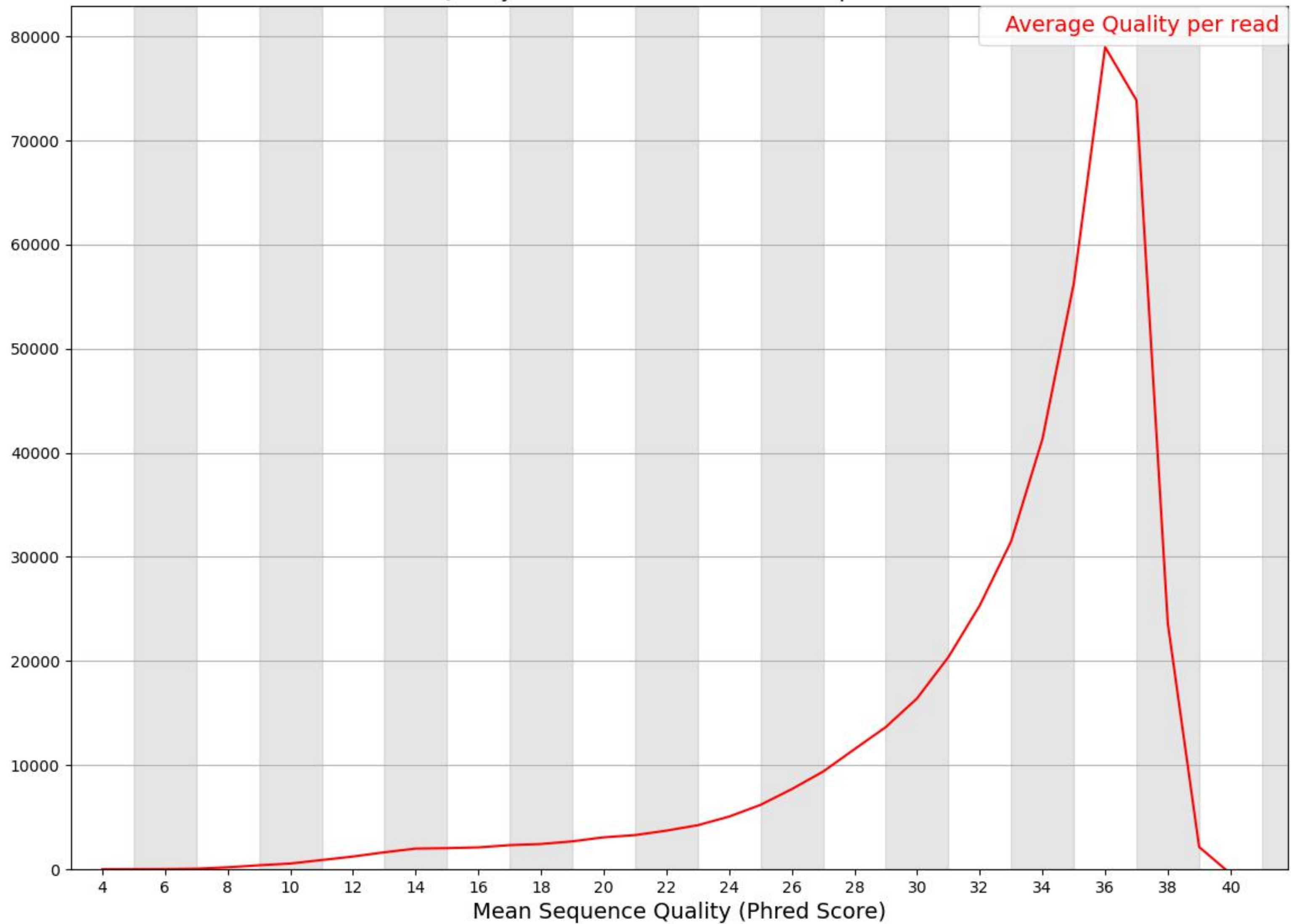
Quality scores across all bases (Sanger / Illumina 1.9)



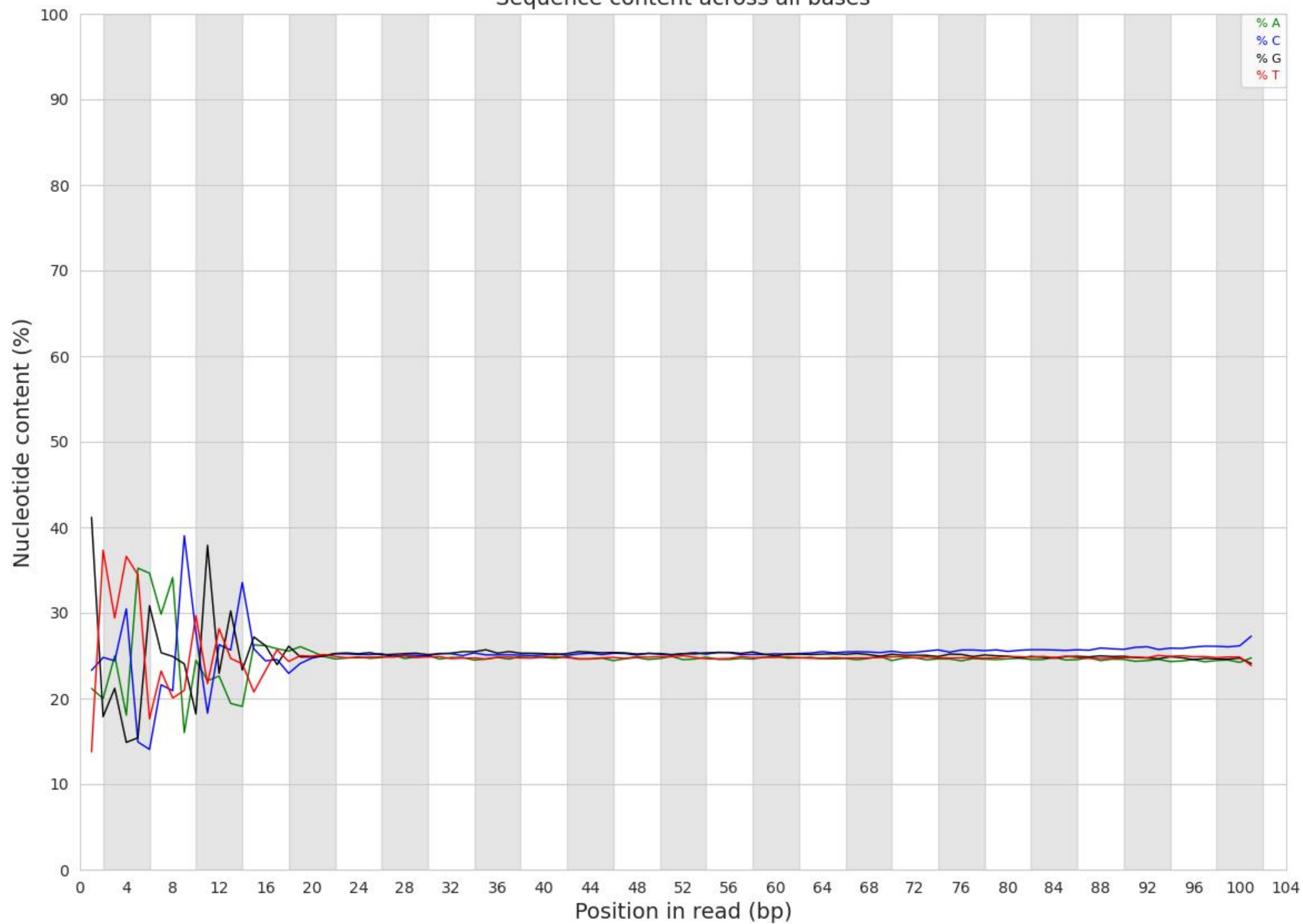
Position in read (bp)



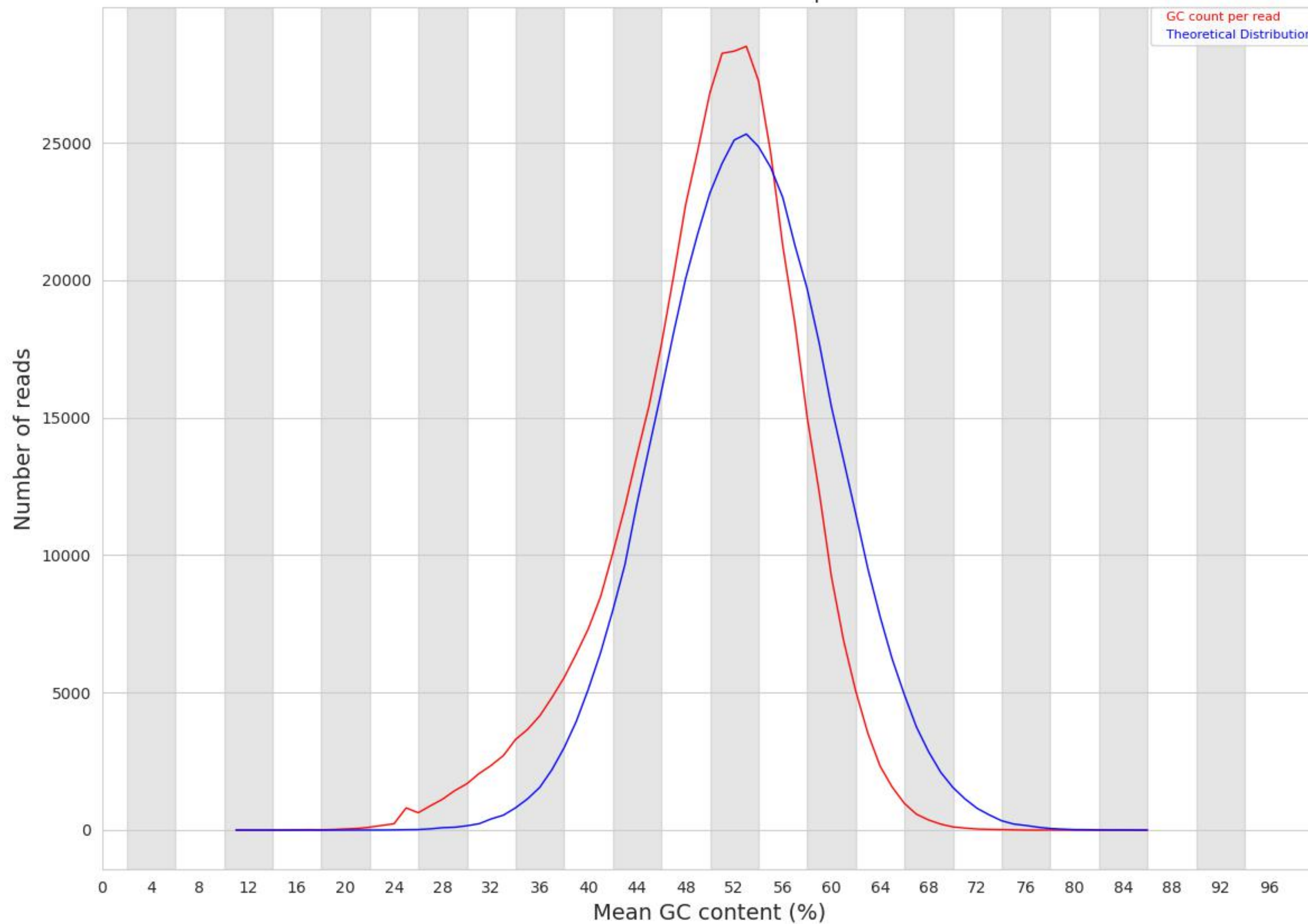
Quality score distribution over all sequences

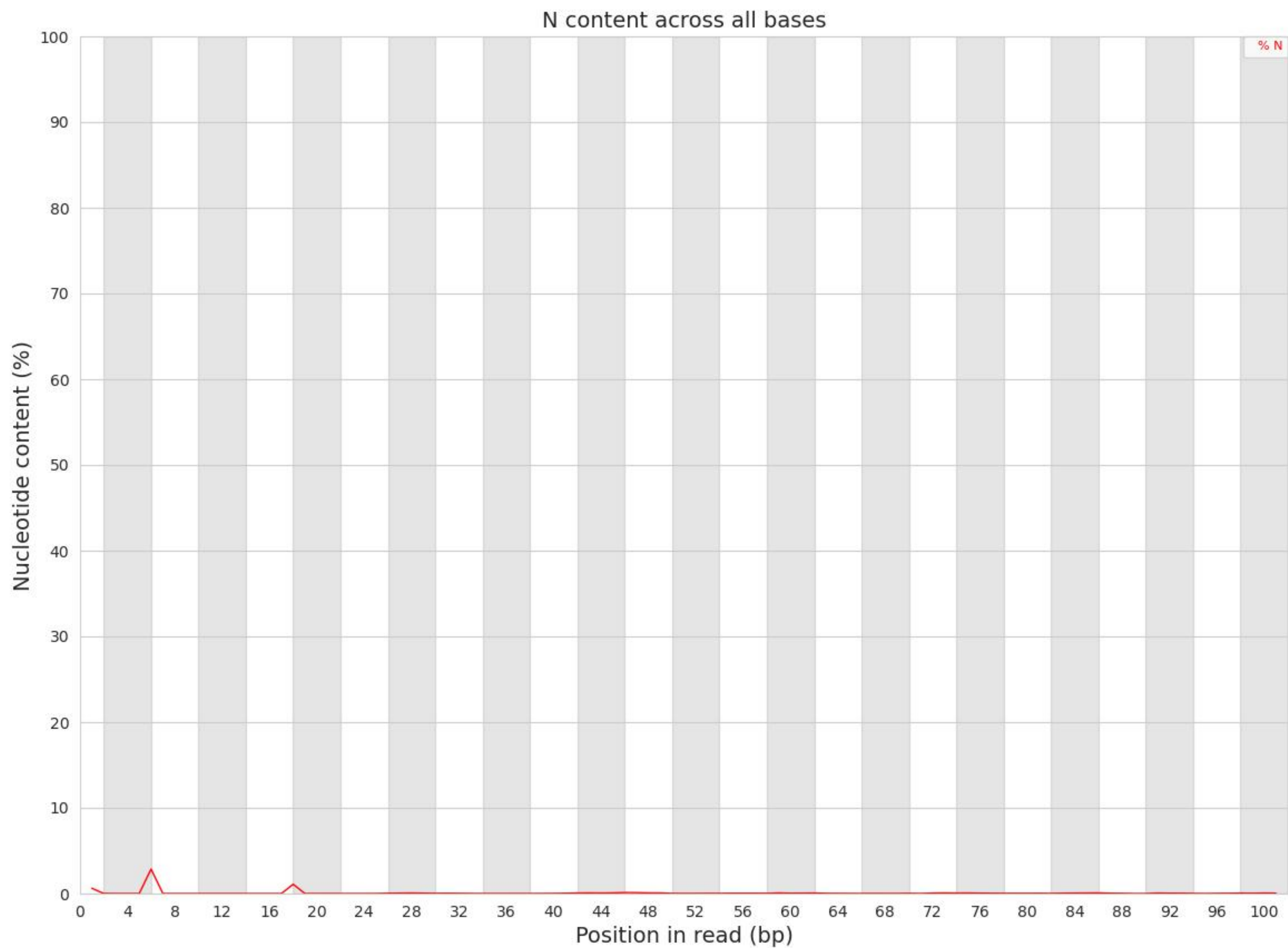


Sequence content across all bases

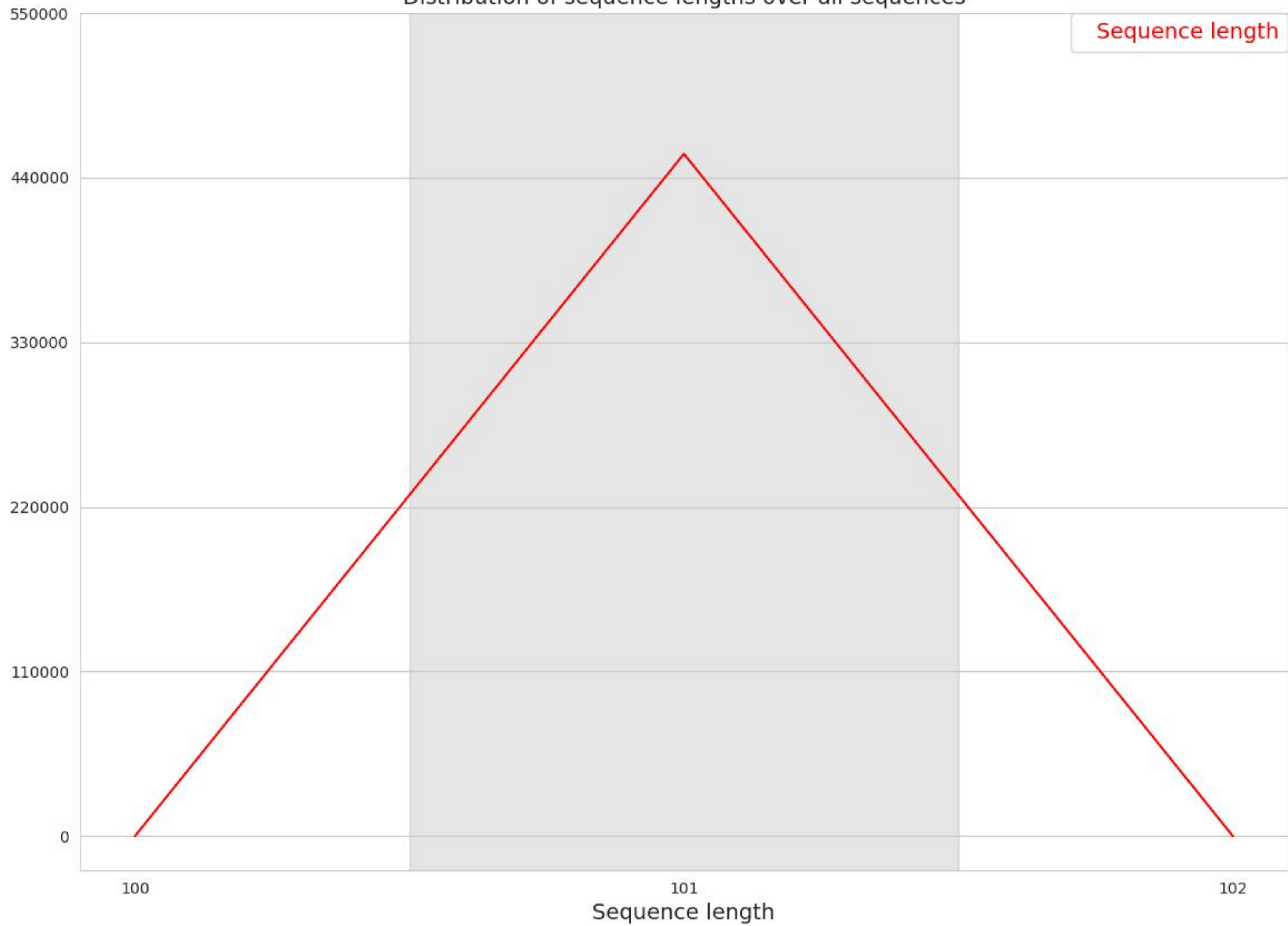


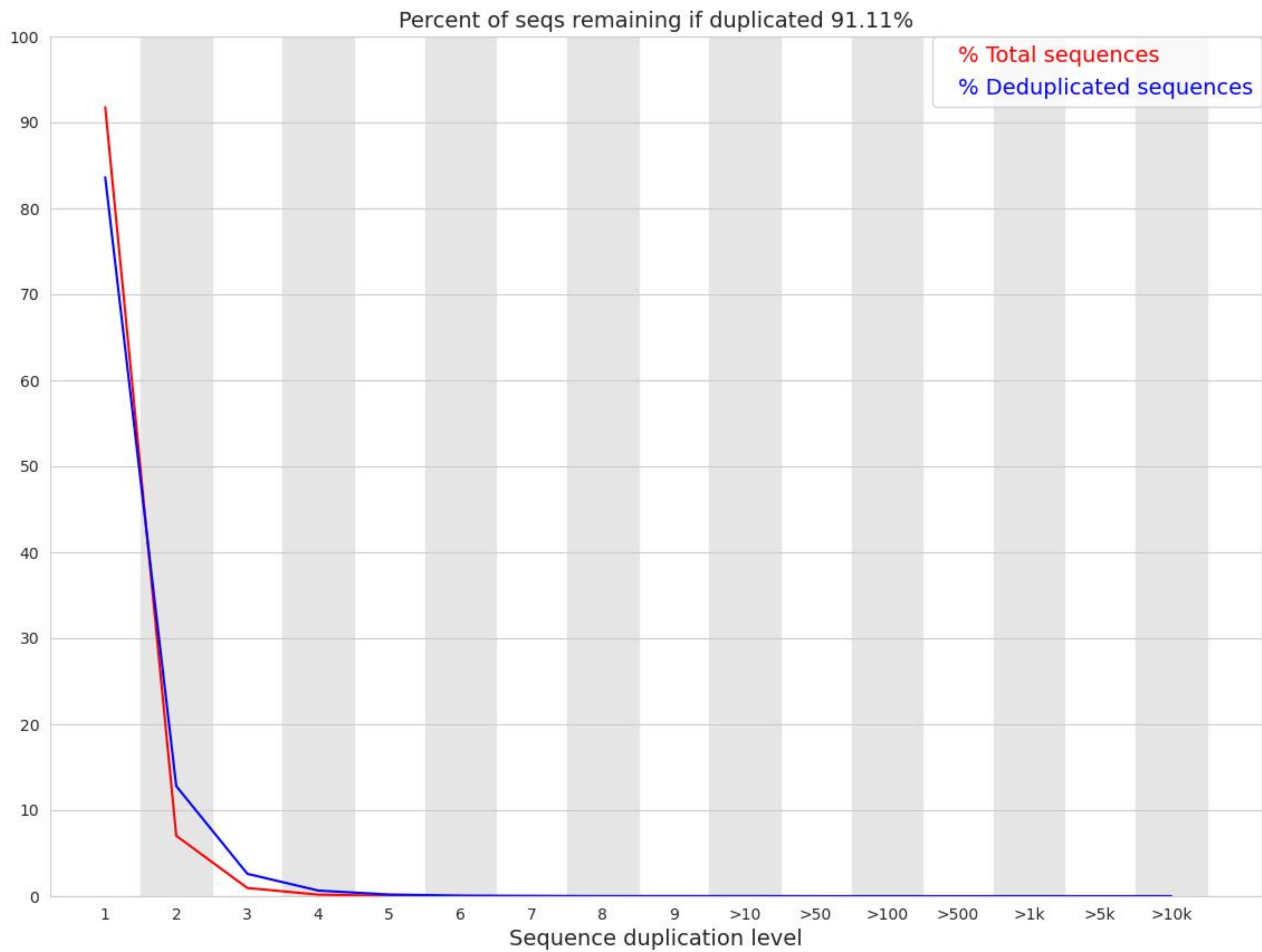
GC distribution over all sequences





Distribution of sequence lengths over all sequences





Overrepresented sequences

No overrepresented sequences

