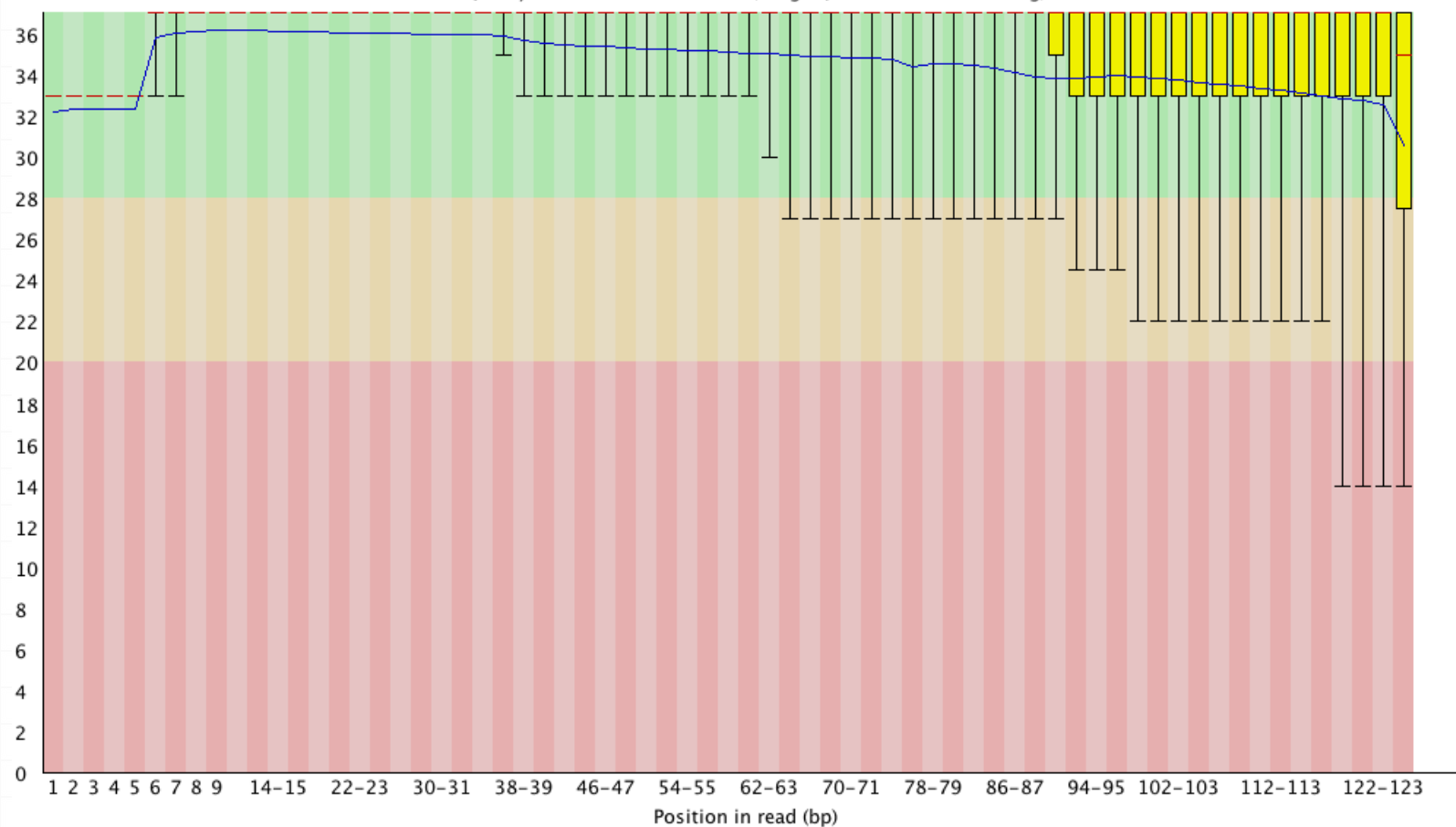


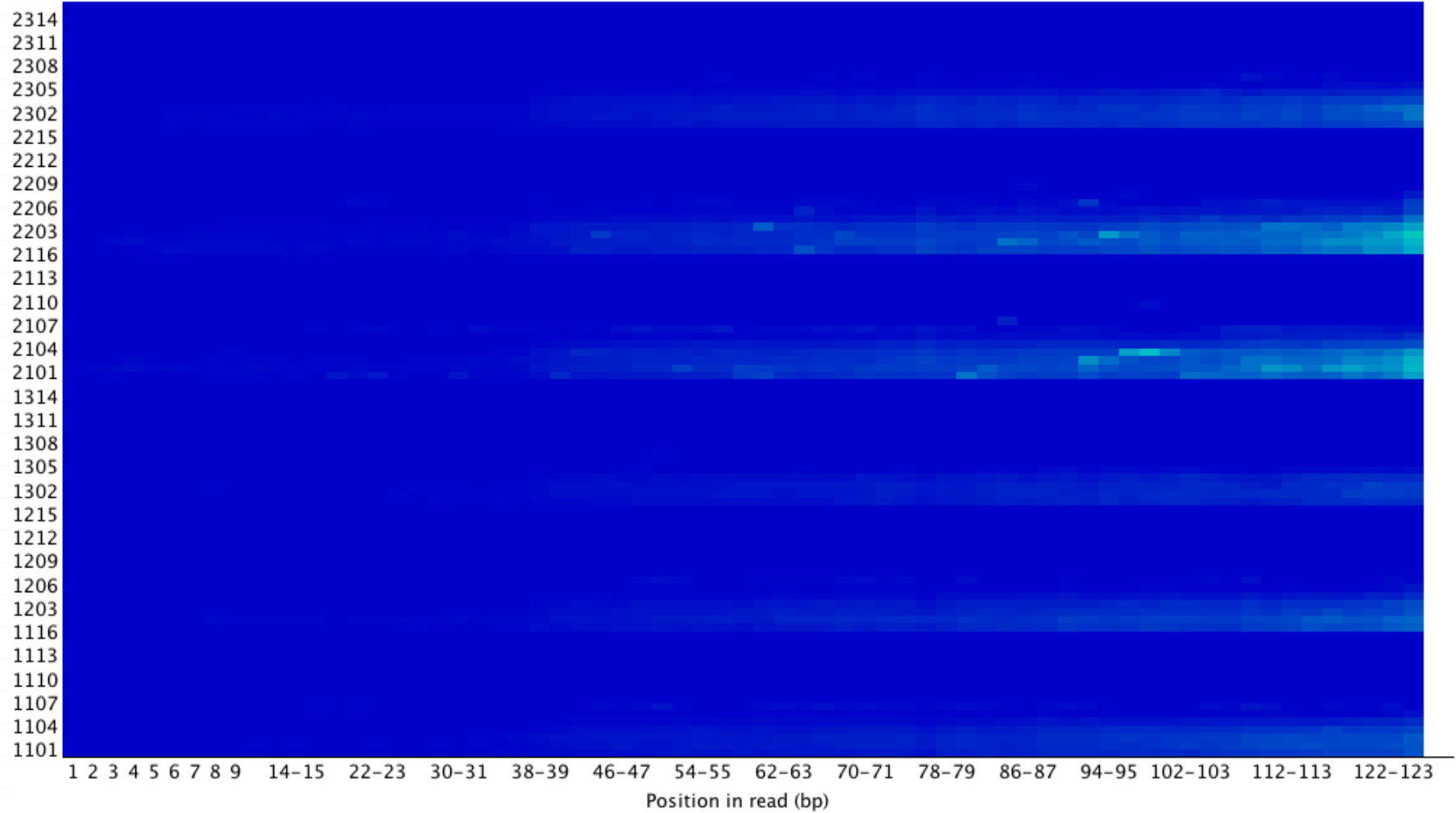
Example shotgun metagenomics data

FASTQC Summary

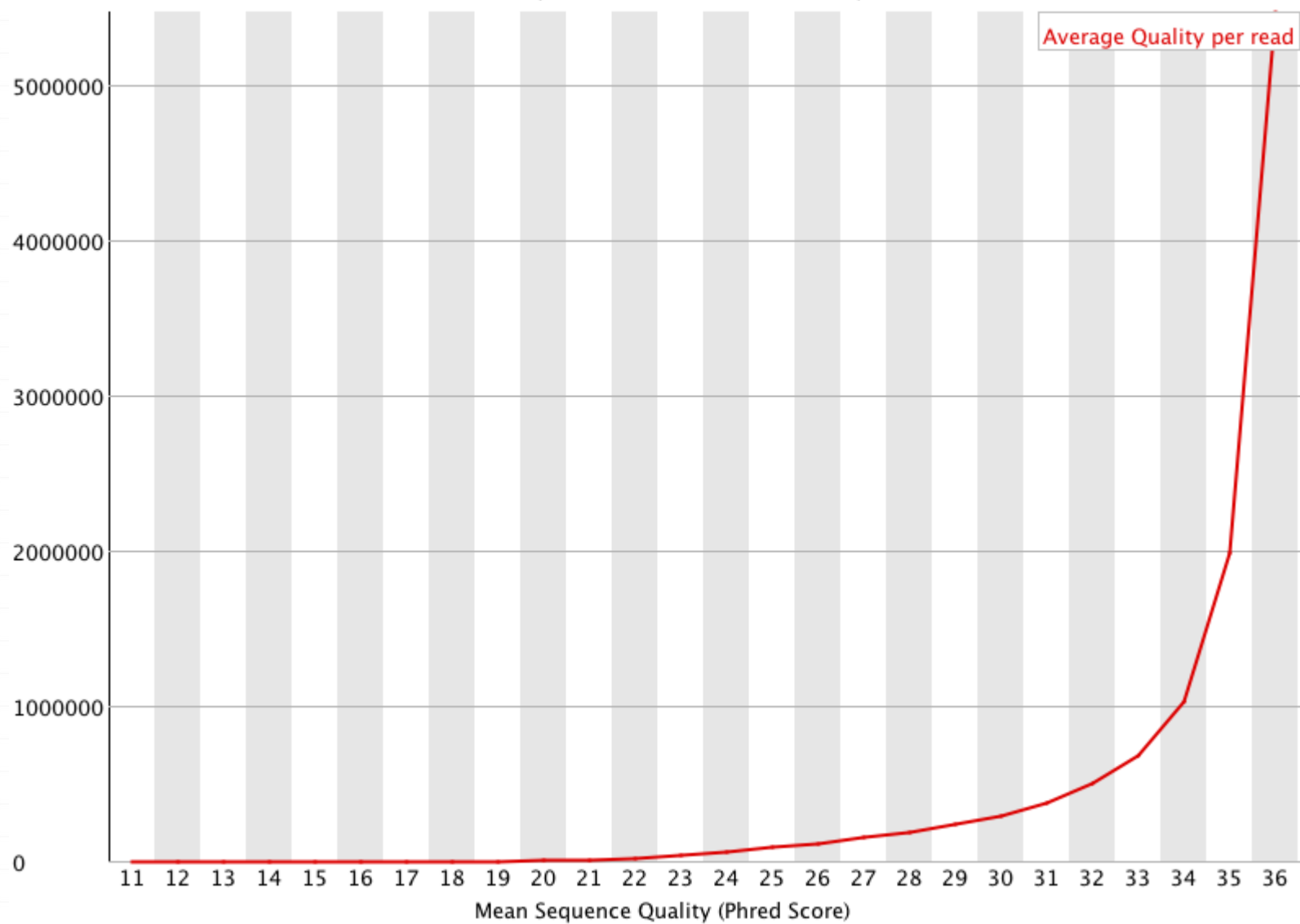
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



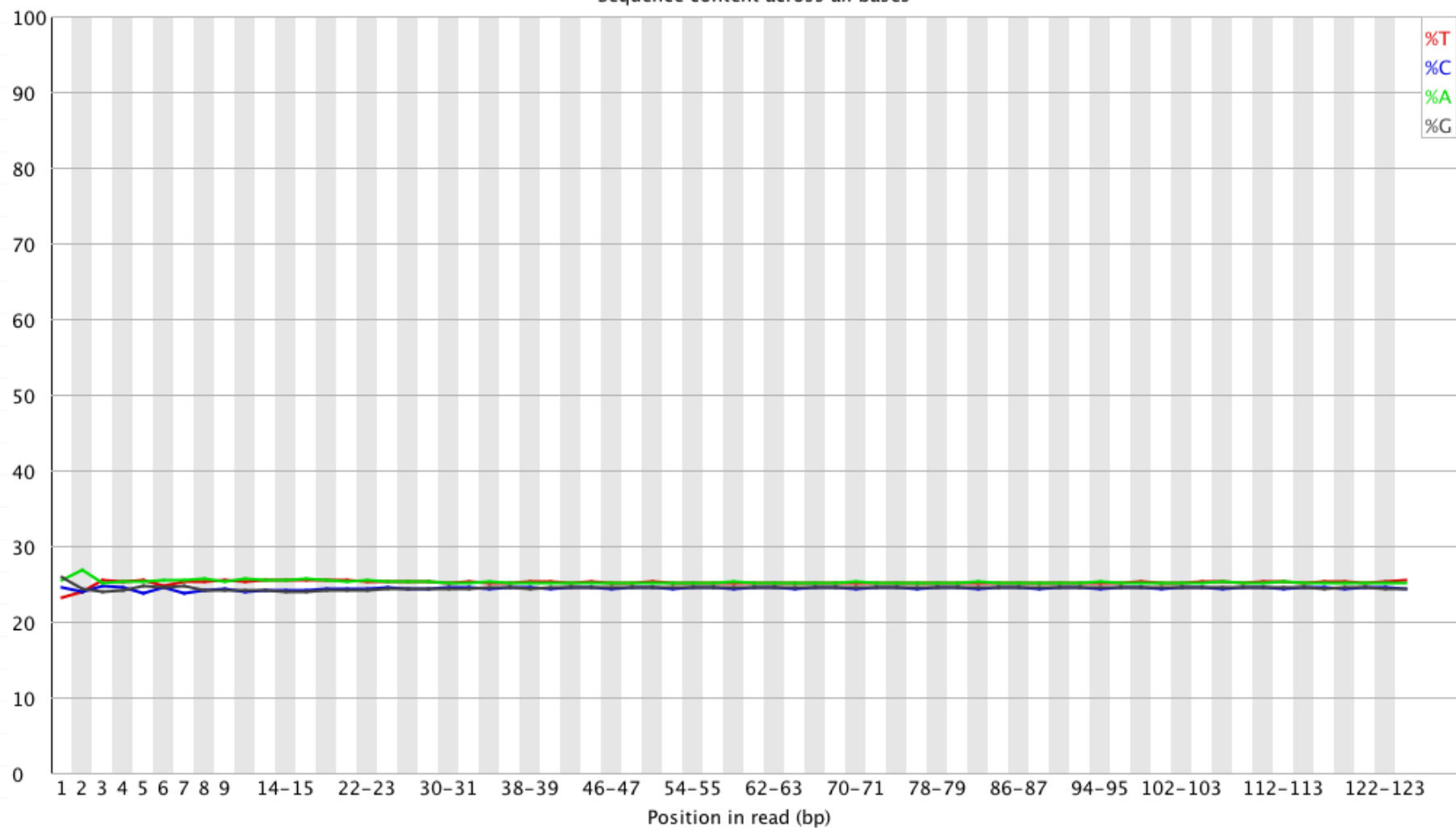
Quality per tile



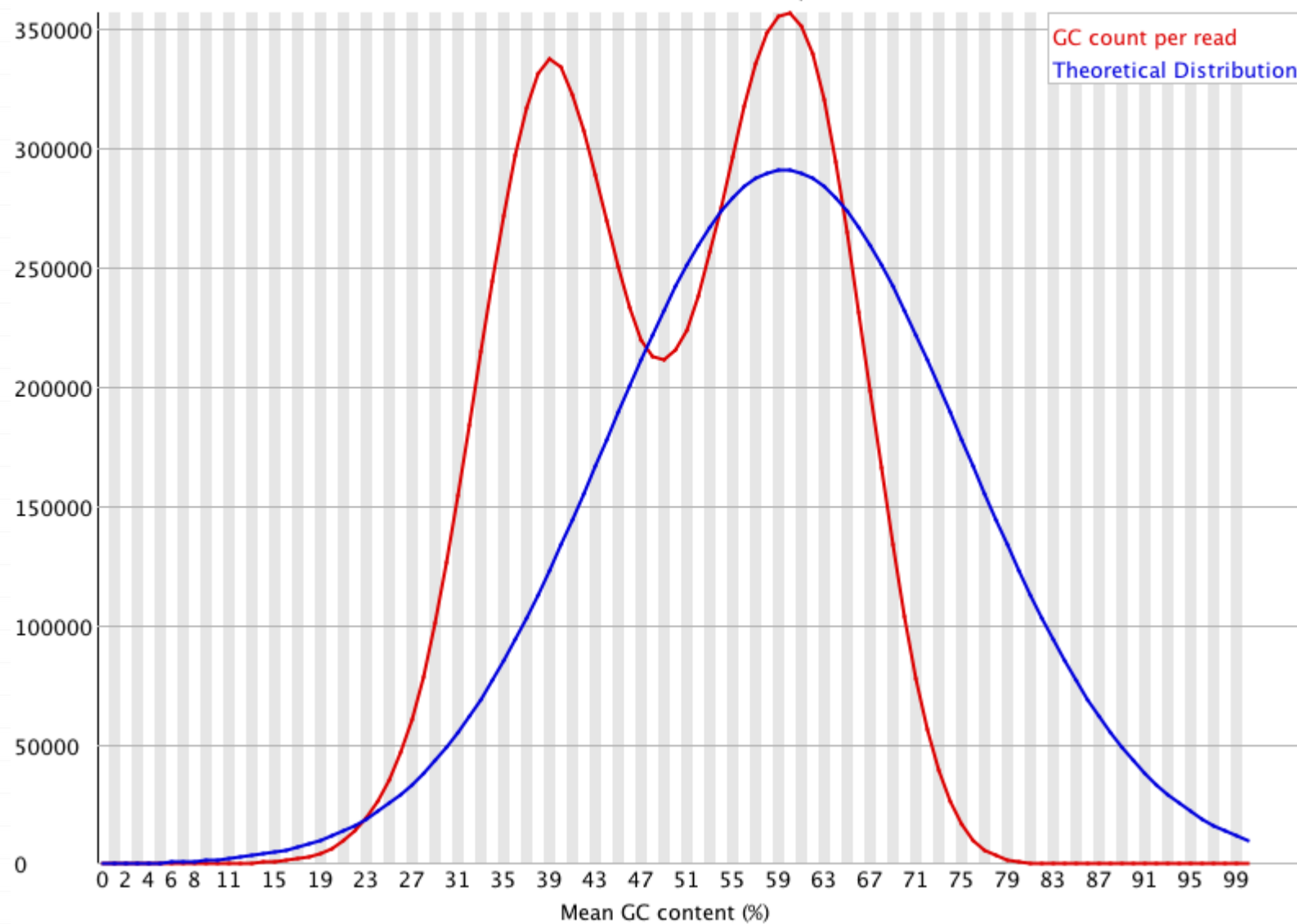
Quality score distribution over all sequences



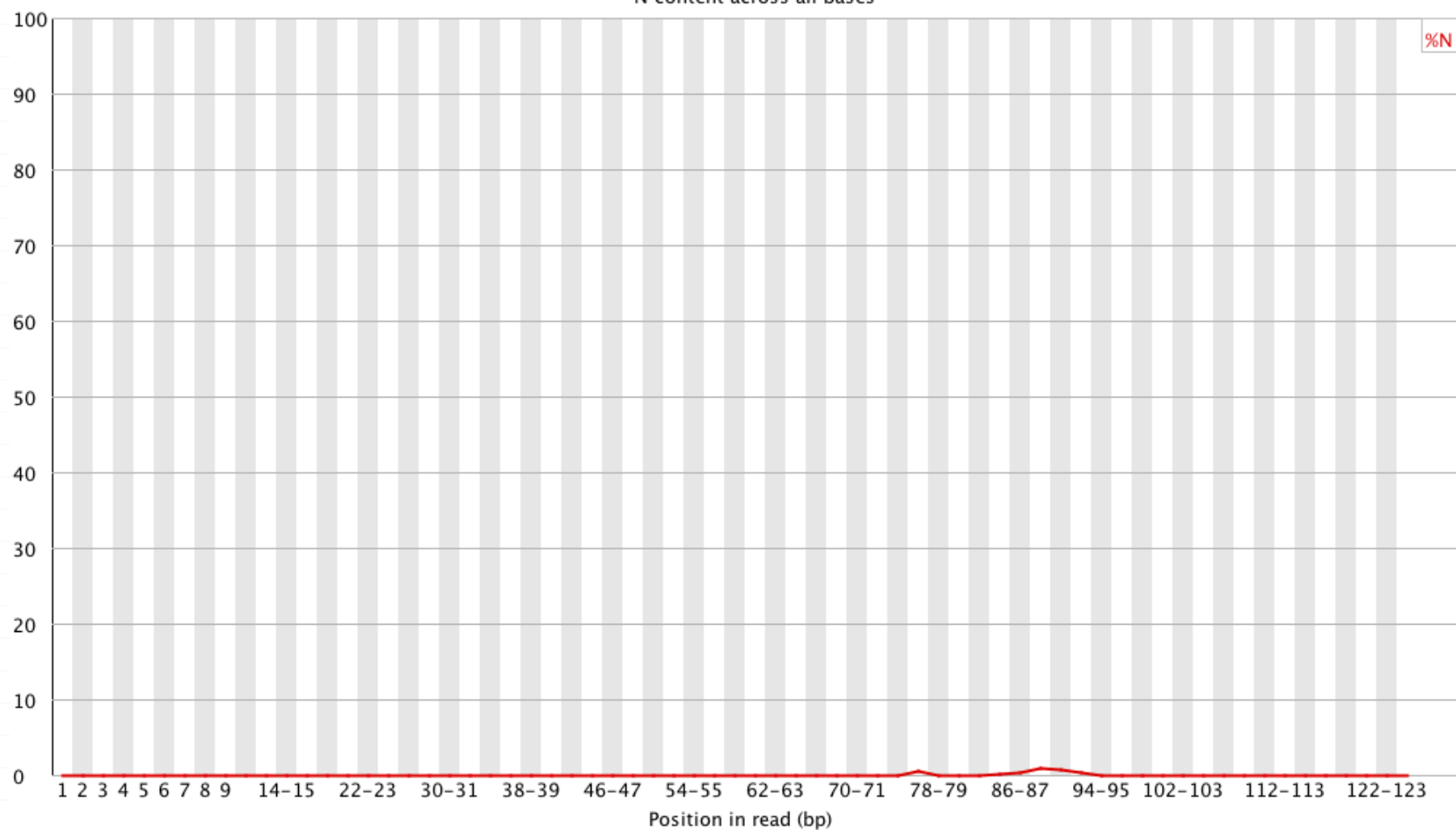
Sequence content across all bases



GC distribution over all sequences

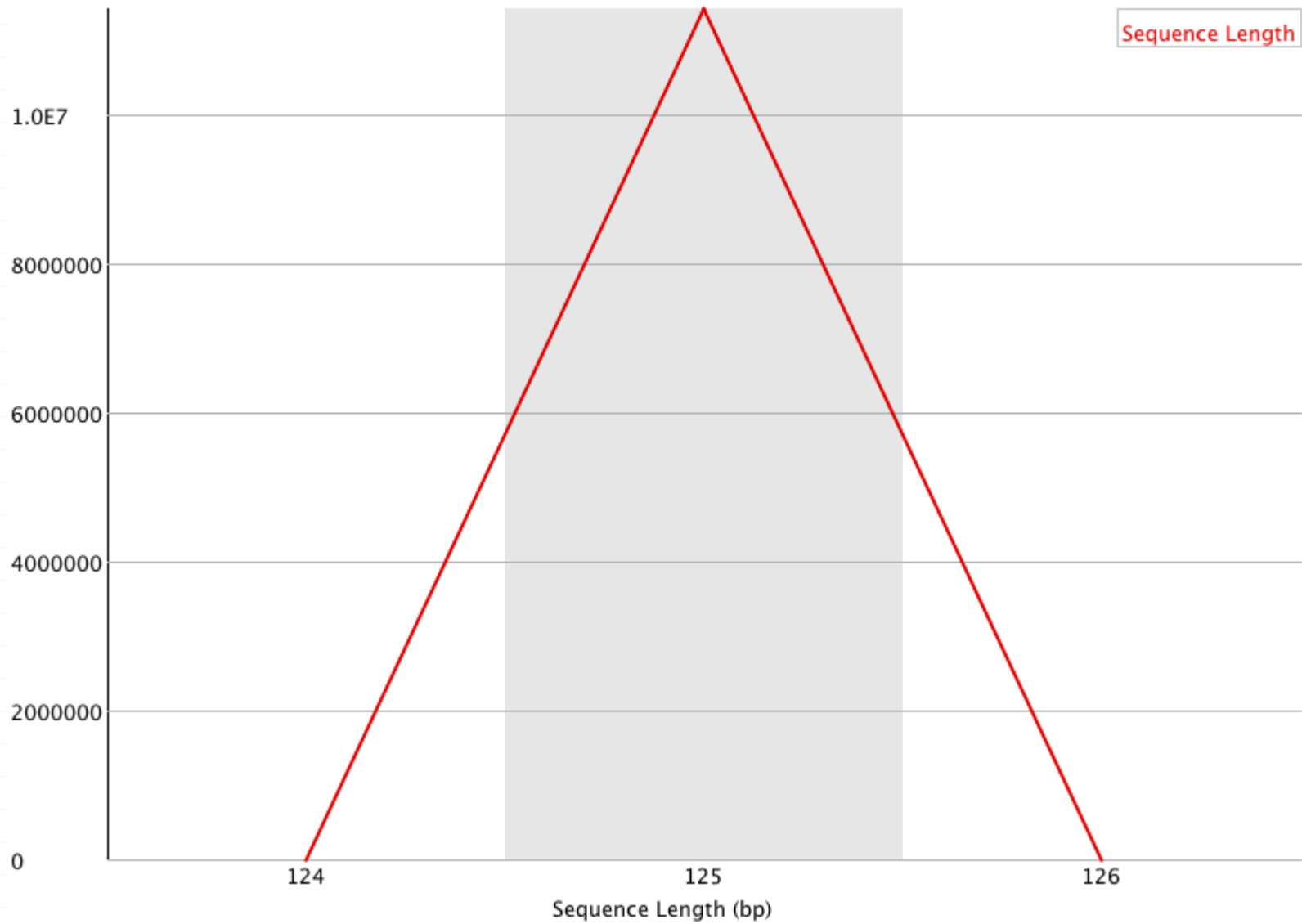


N content across all bases

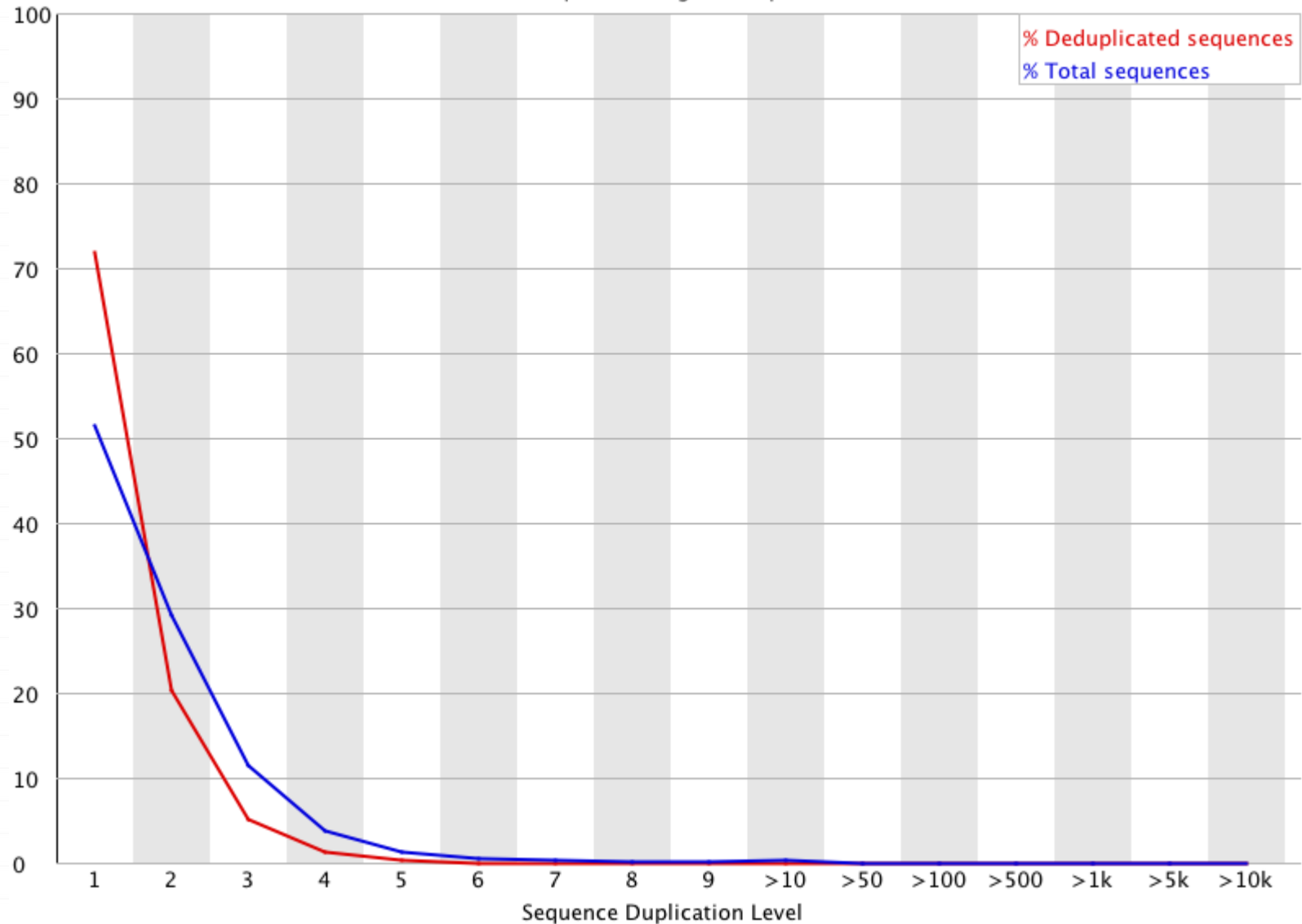


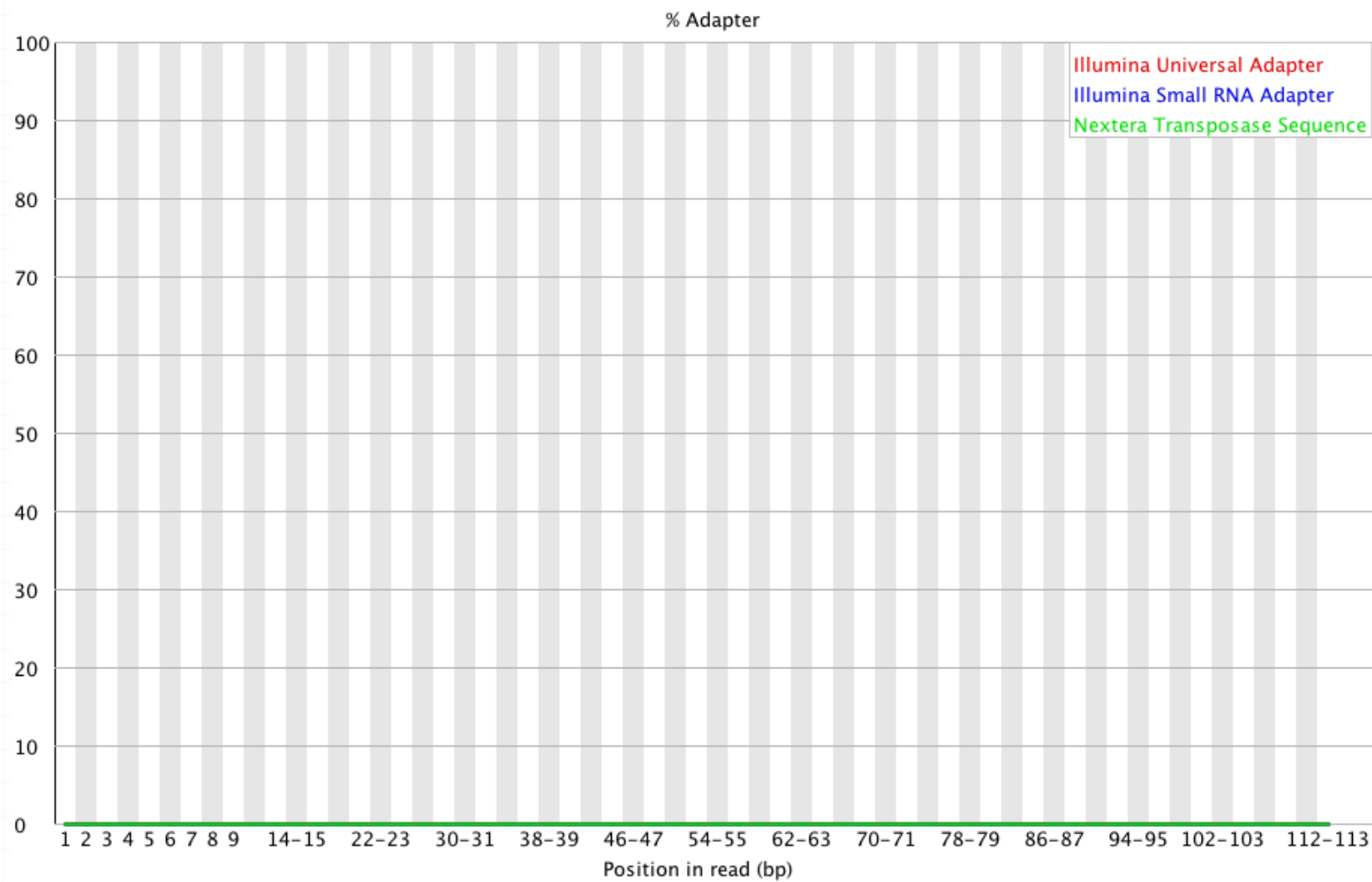
Distribution of sequence lengths over all sequences

Sequence Length



Percent of seqs remaining if deduplicated 71.75%





Log2 Obs/Exp

