













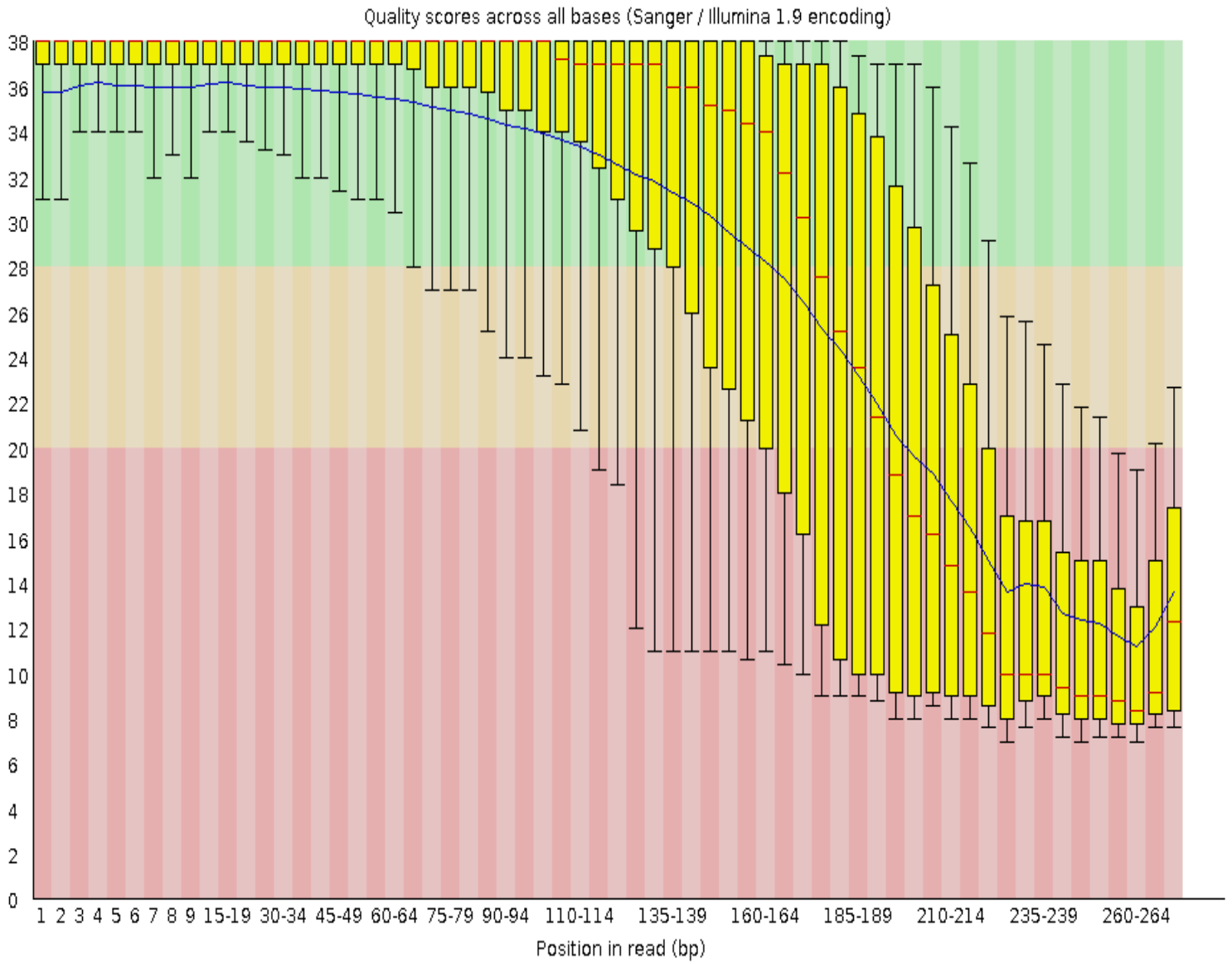
Summary

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Basic Statistics

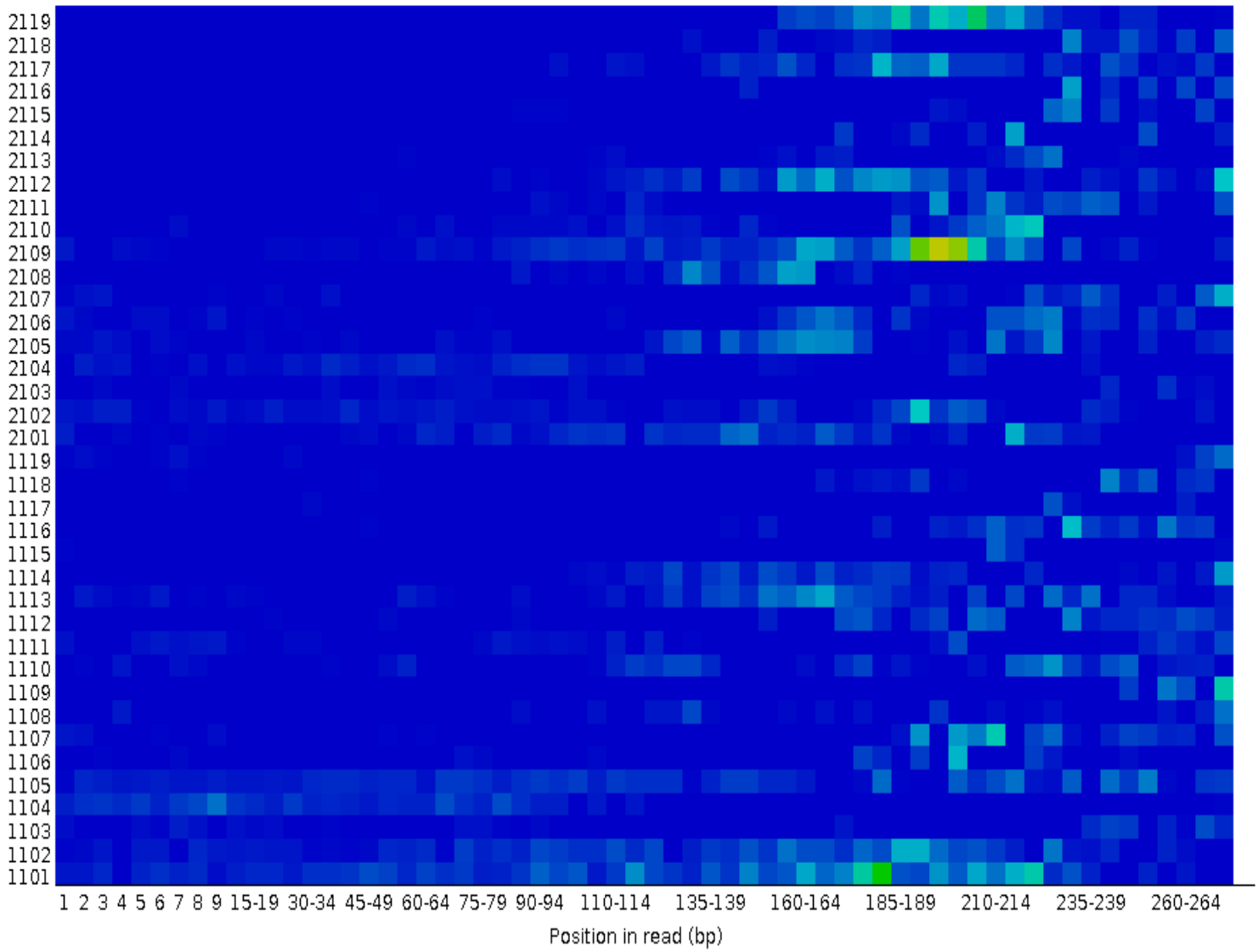
Measure	Value
Filename	lucigen_mp_dupRemoved_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	89856
Sequences flagged as poor quality	0
Sequence length	26-273
%GC	41

Per base sequence quality



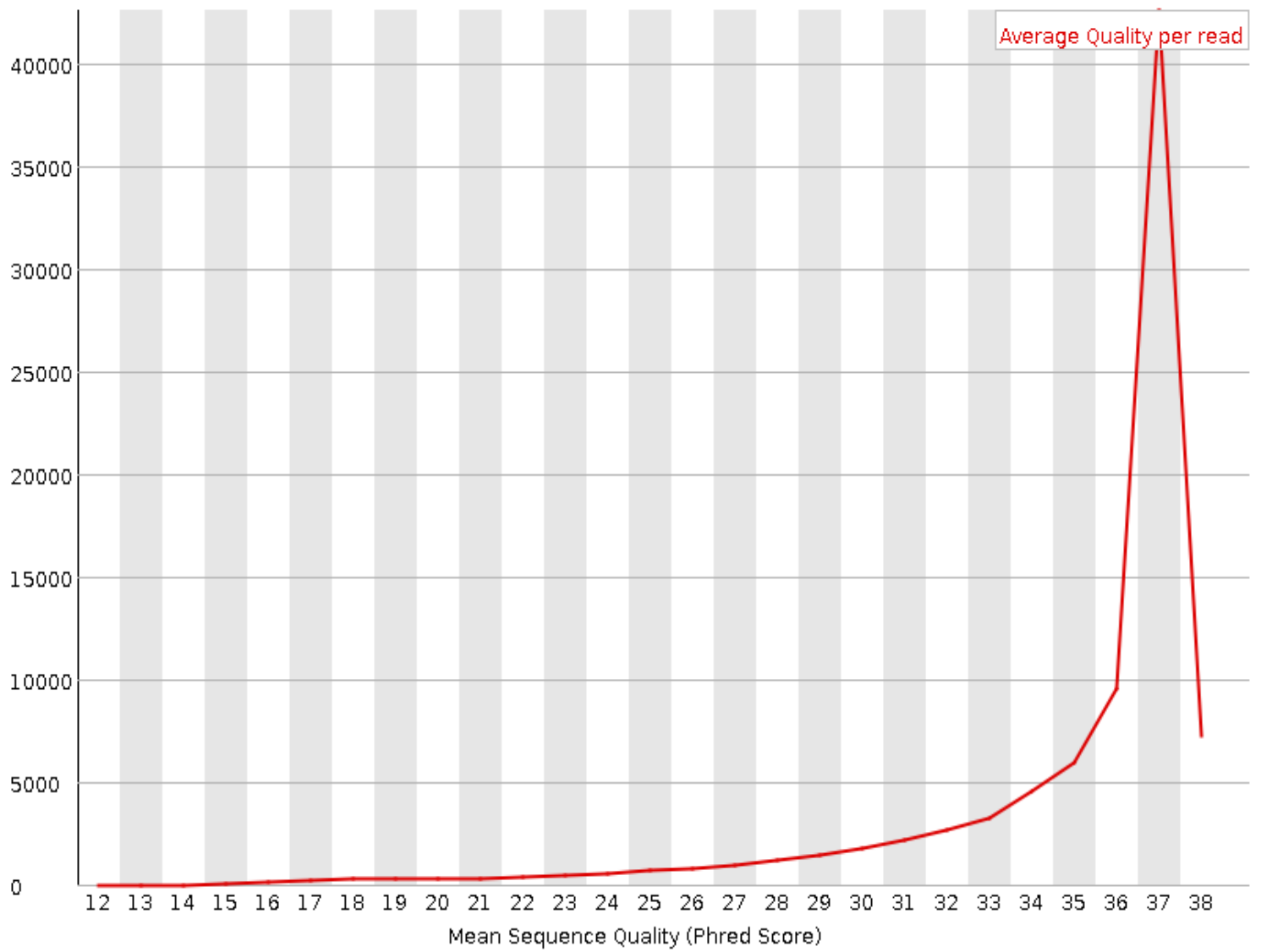
! Per tile sequence quality

Quality per tile



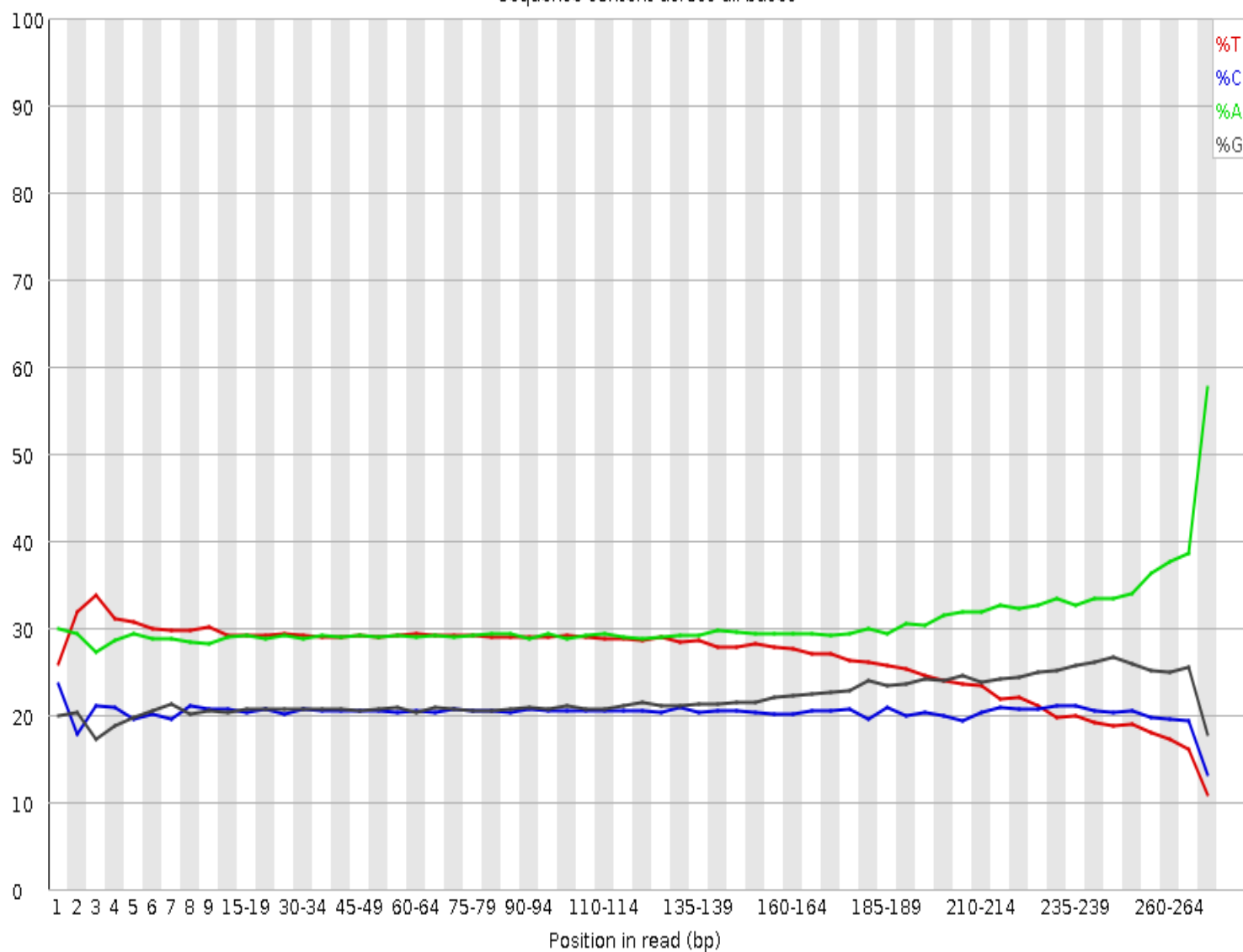
 **Per sequence quality scores**

Quality score distribution over all sequences



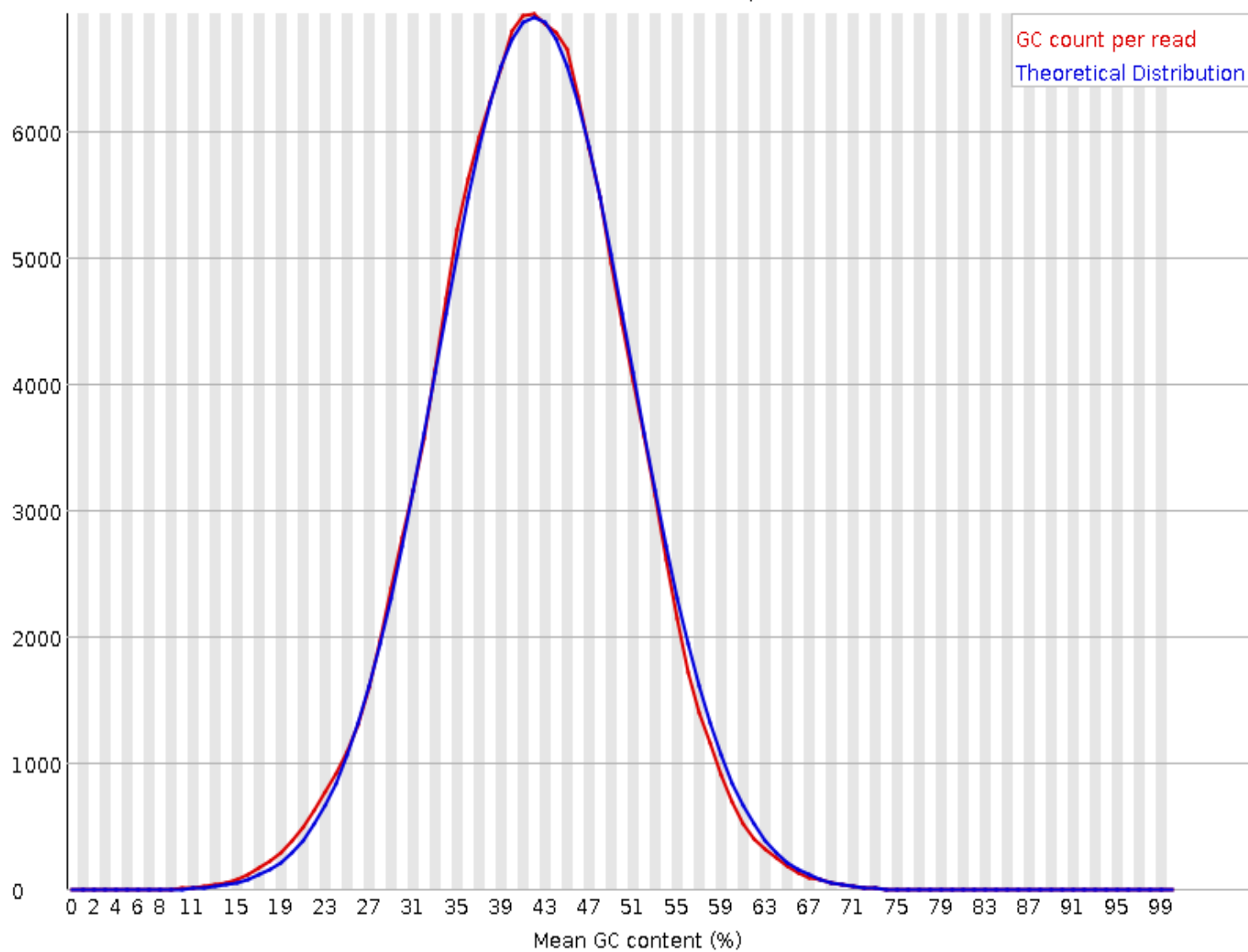
 **Per base sequence content**

Sequence content across all bases



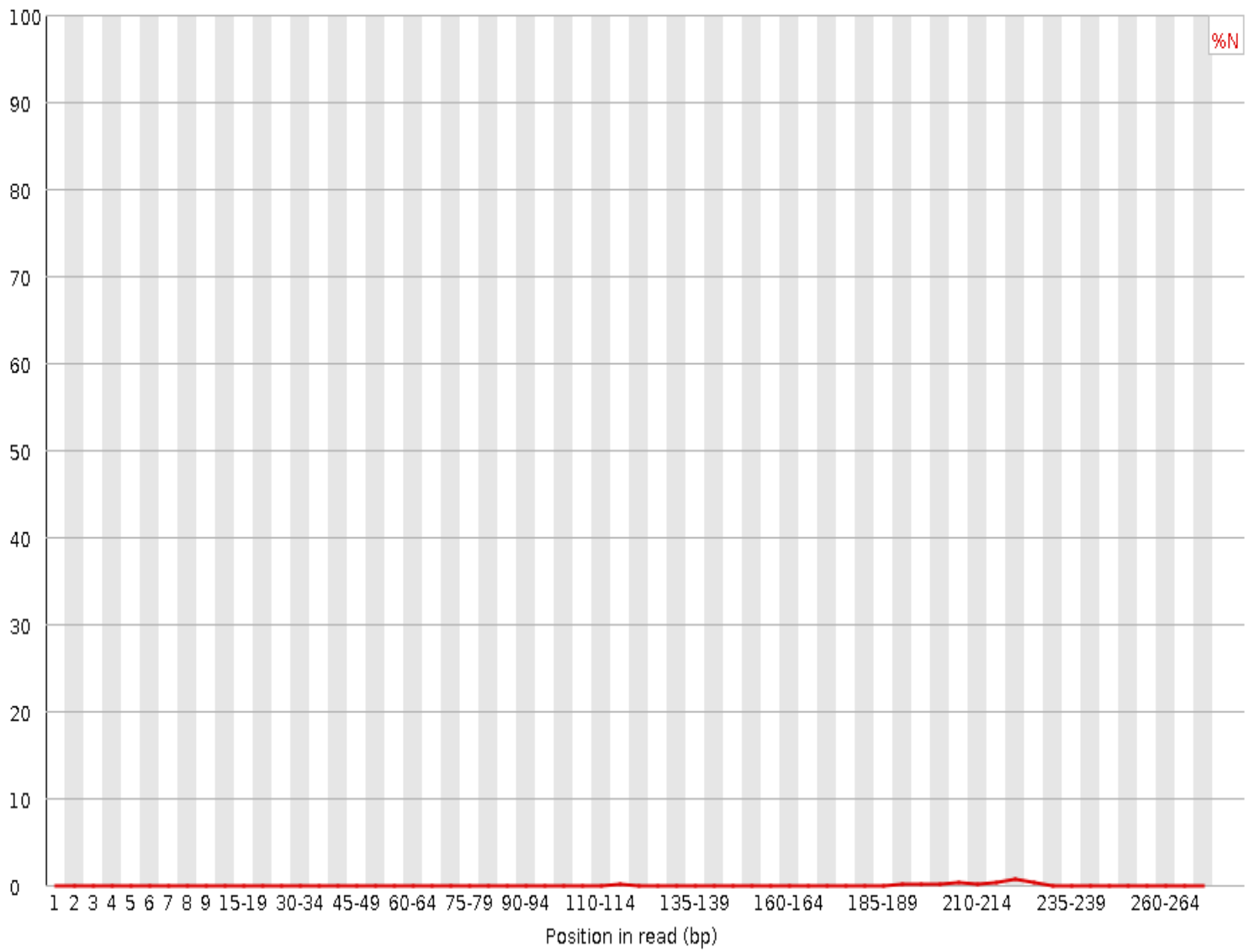
 **Per sequence GC content**

GC distribution over all sequences



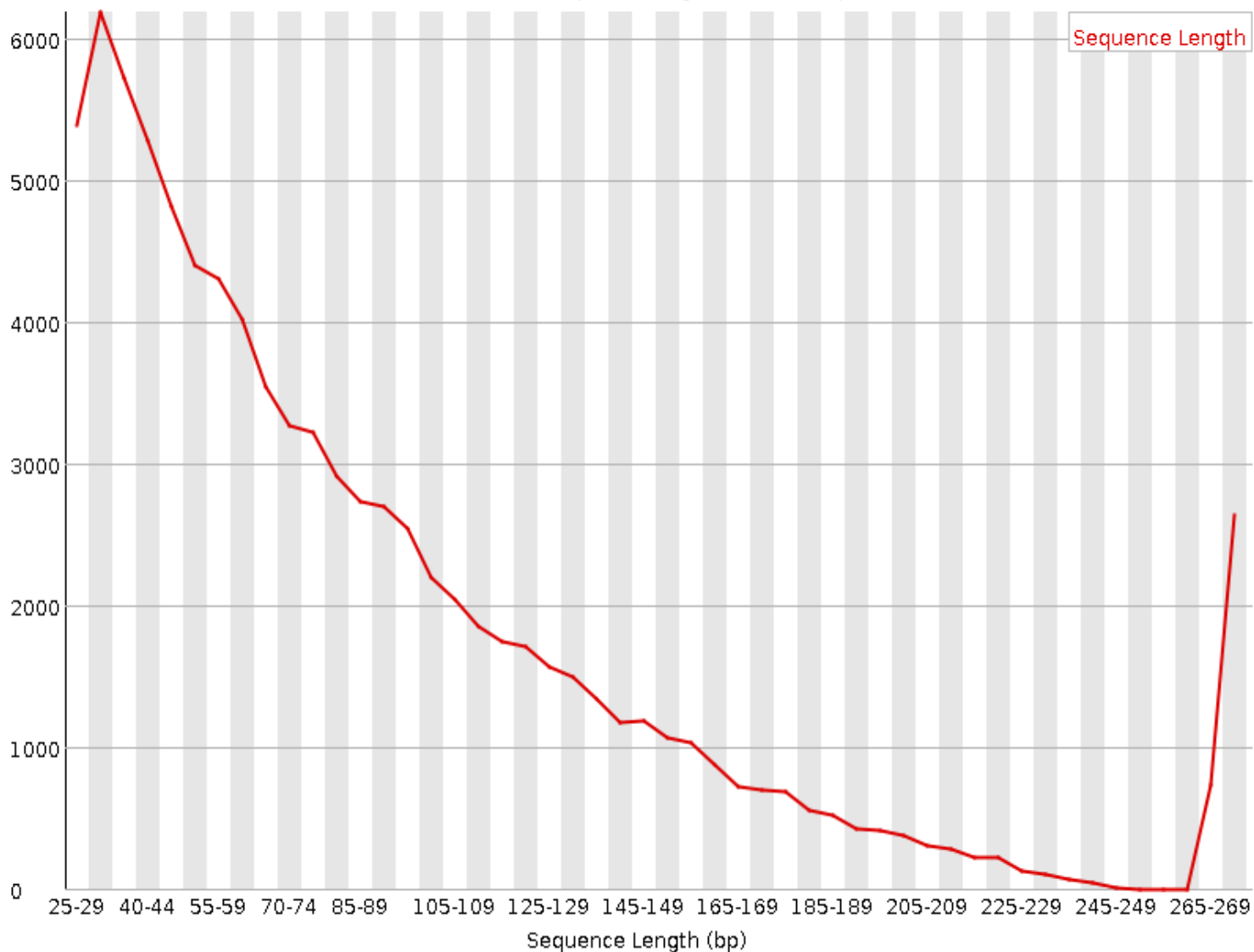
Per base N content

N content across all bases



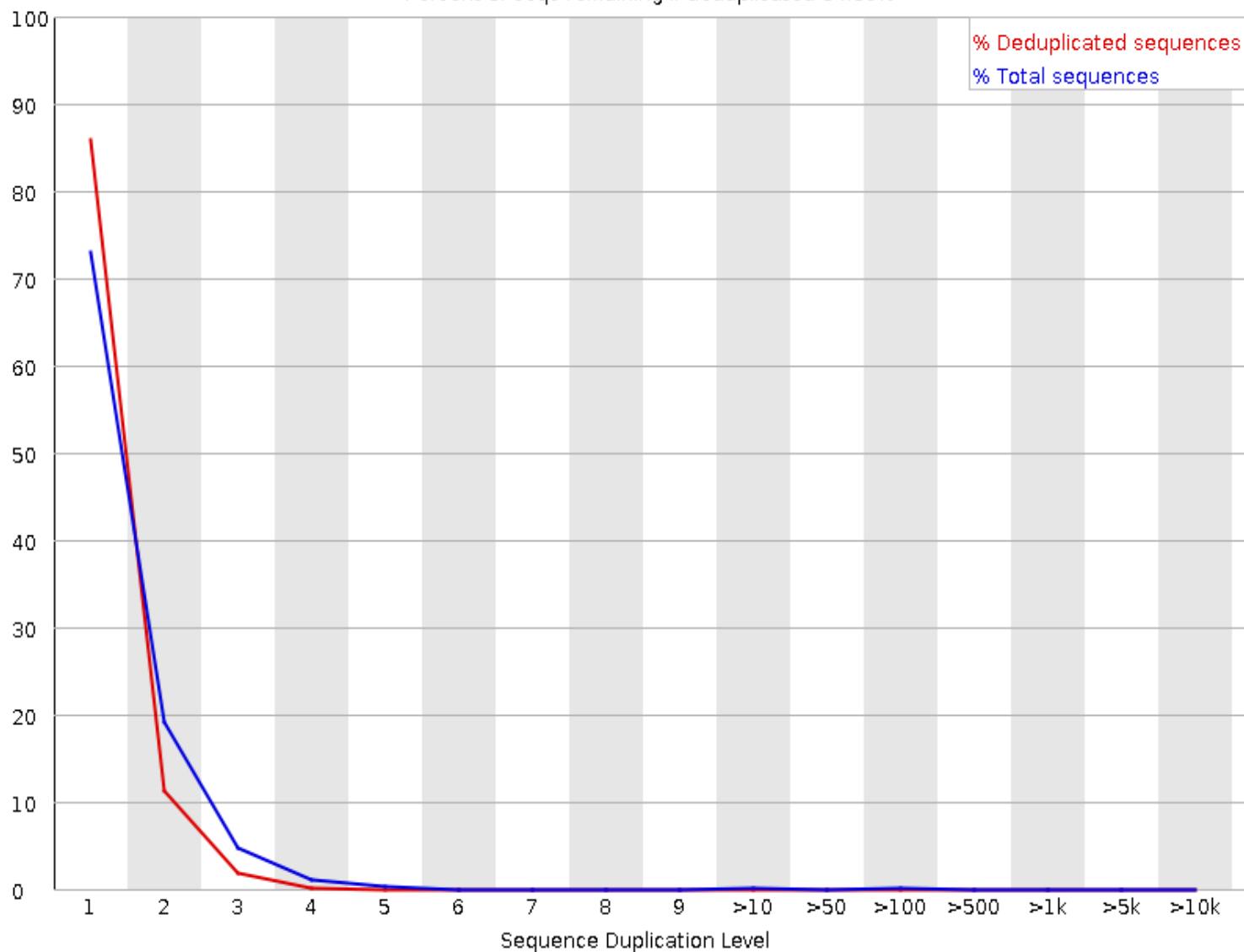
! Sequence Length Distribution

Distribution of sequence lengths over all sequences



✔ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 84.89%

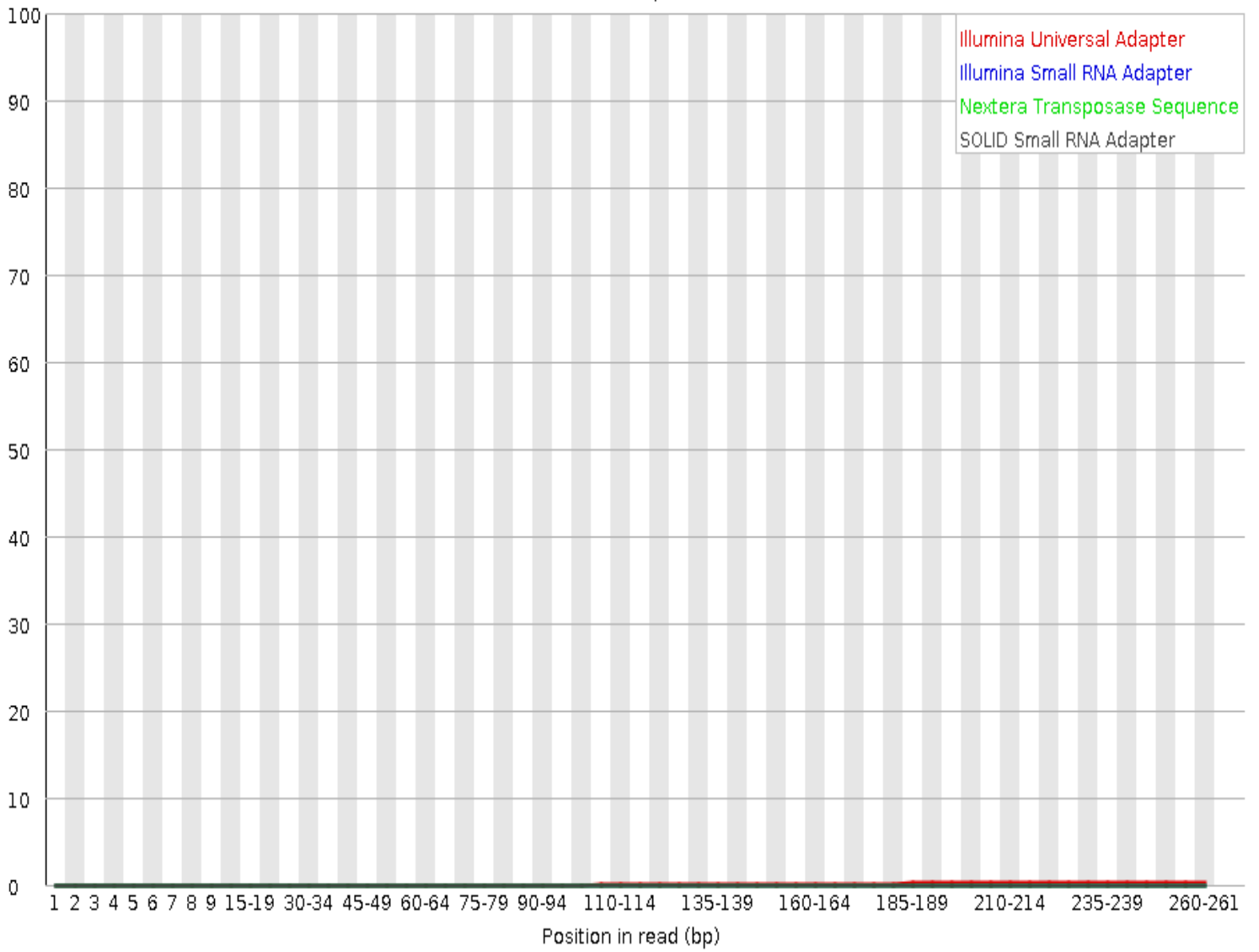


⚠ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CCATATACGTCTCCTATAGGTCTCGTATACTGCTTCCTATACGACATCAC	180	0.2003205128205128	No Hit

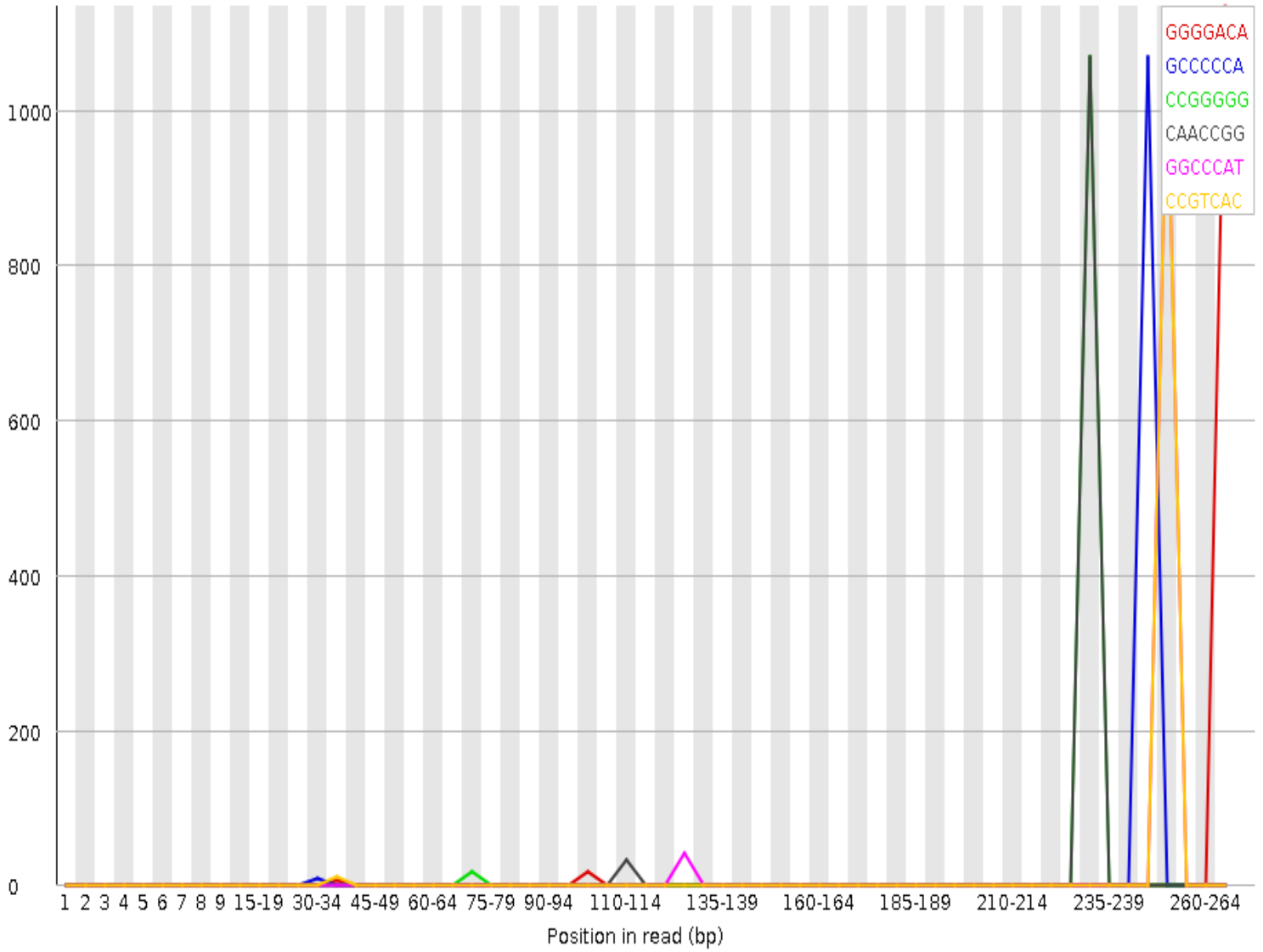
✅ Adapter Content

% Adapter



! Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
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GGGGACA	15	0.006228822	1133.3864	265-266
GCCCCCA	10	0.0070669185	1068.6213	245-249
CCGGGGG	10	0.0070669185	1068.6213	230-234
CAACCGG	10	0.0070669185	1068.6213	230-234
GGCCCAT	10	0.0070669185	1068.6213	250-254
CCGTCAC	10	0.0070669185	1068.6213	250-254
TACGCGG	10	0.0070669185	1068.6213	260-264
TACTAGC	10	0.0070669185	1068.6213	245-249
GACGCAC	10	0.0070669185	1068.6213	240-244
CCCGCGA	10	0.0070669185	1068.6213	230-234
CGGGGGG	25	2.7280583E-4	427.44858	230-234
CAACGAT	20	5.383596E-4	341.56848	225-229

CGGCGGA	15	9.3107217E-4	284.9657	235-239
AGCTACA	75	8.9940435E-4	284.9657	260-264
CGTAAGG	15	0.0017032665	233.03271	210-214
CTAACAC	10	0.0024885663	205.5041	175-179
GGGAACG	35	0.002535023	203.54695	235-239
AAGGCGT	10	0.003191194	189.13654	170-174
GATCGAG	30	0.003633237	180.68478	205-209
AAGAGGT	55	0.003633306	180.14087	220-224

Produced by [FastQC](#) (version 0.11.3)