













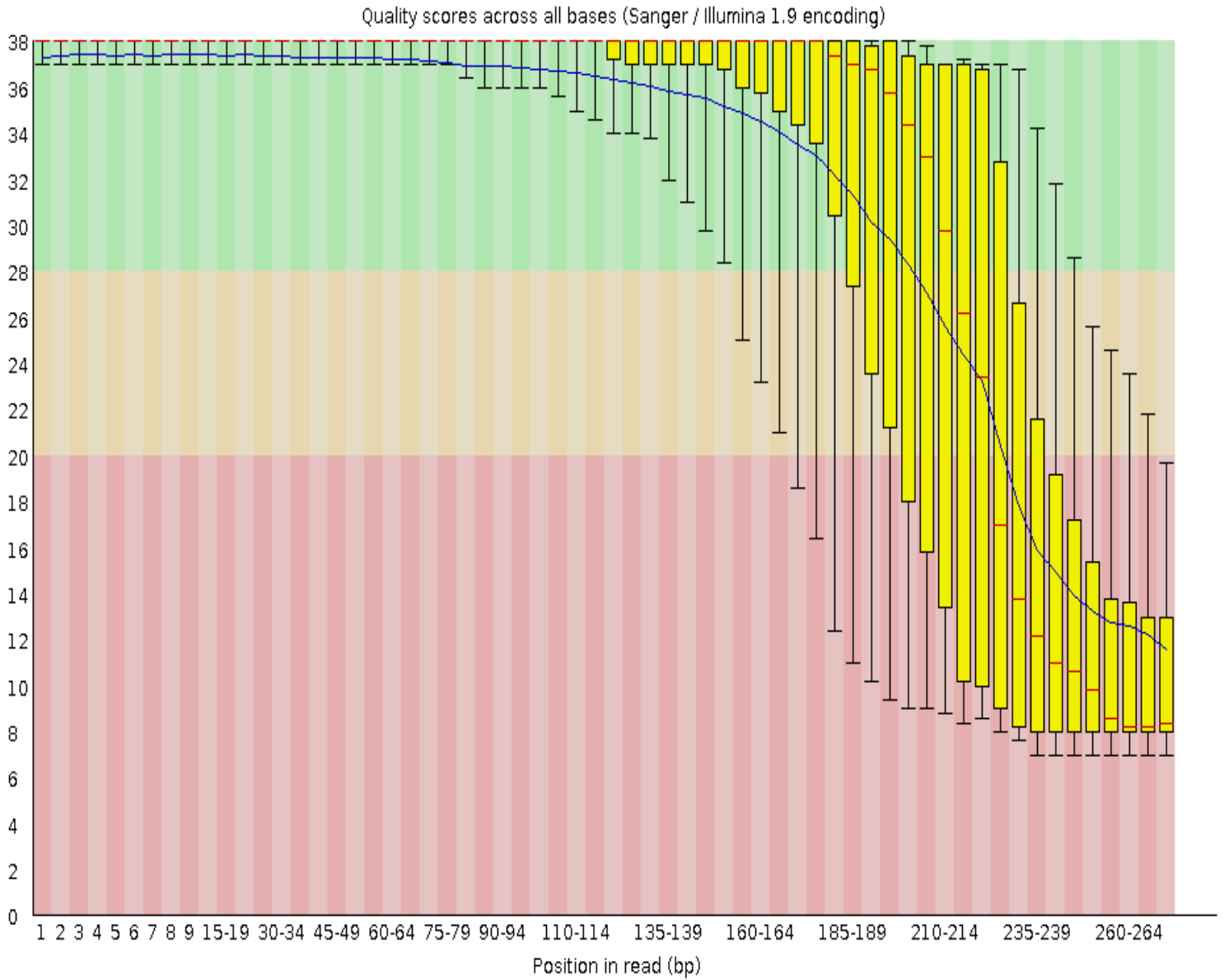
Summary

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Basic Statistics

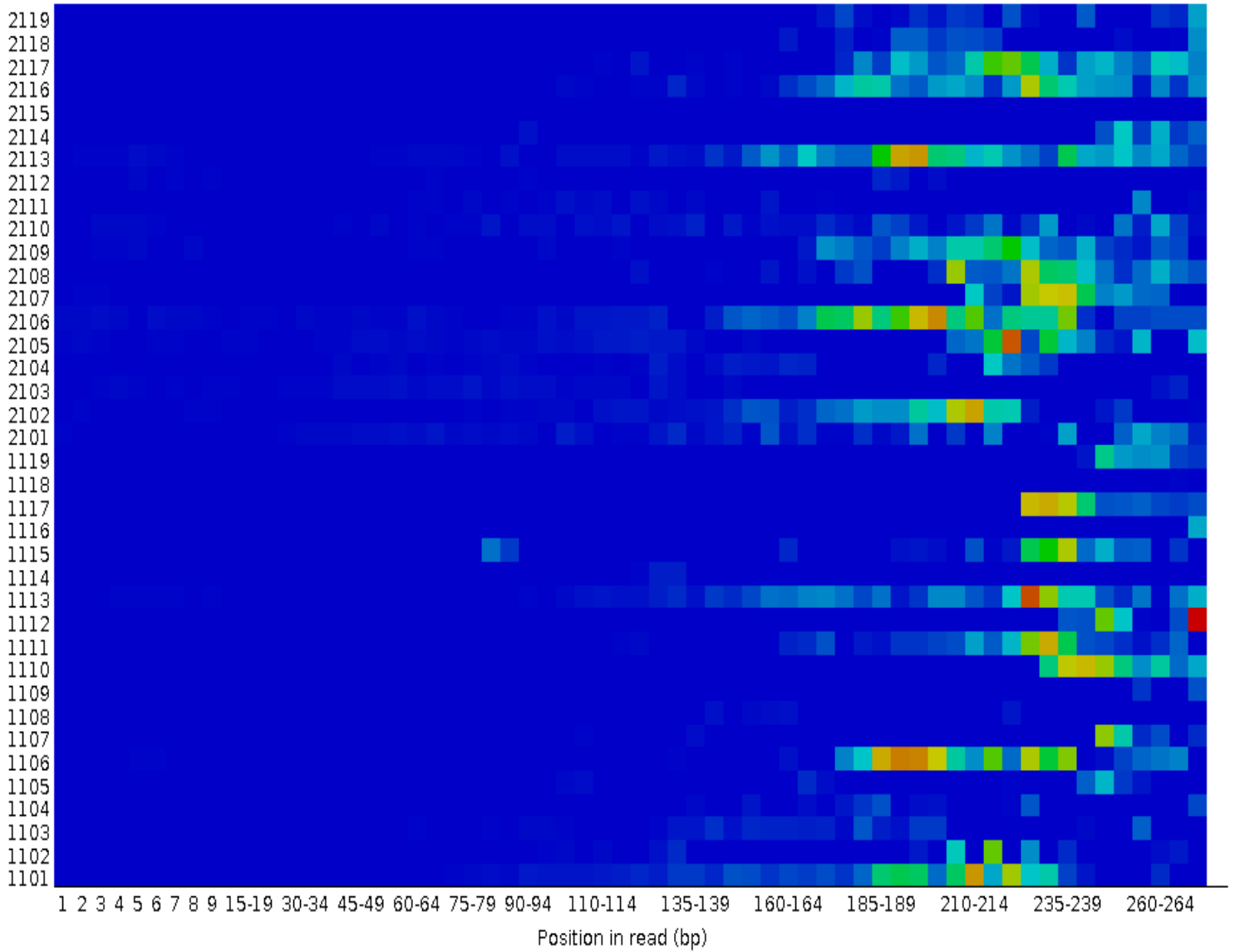
Measure	Value
Filename	R1_IJS8_mates_ICC5_SW023_S60_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	217484
Sequences flagged as poor quality	0
Sequence length	26-272
%GC	40

Per base sequence quality



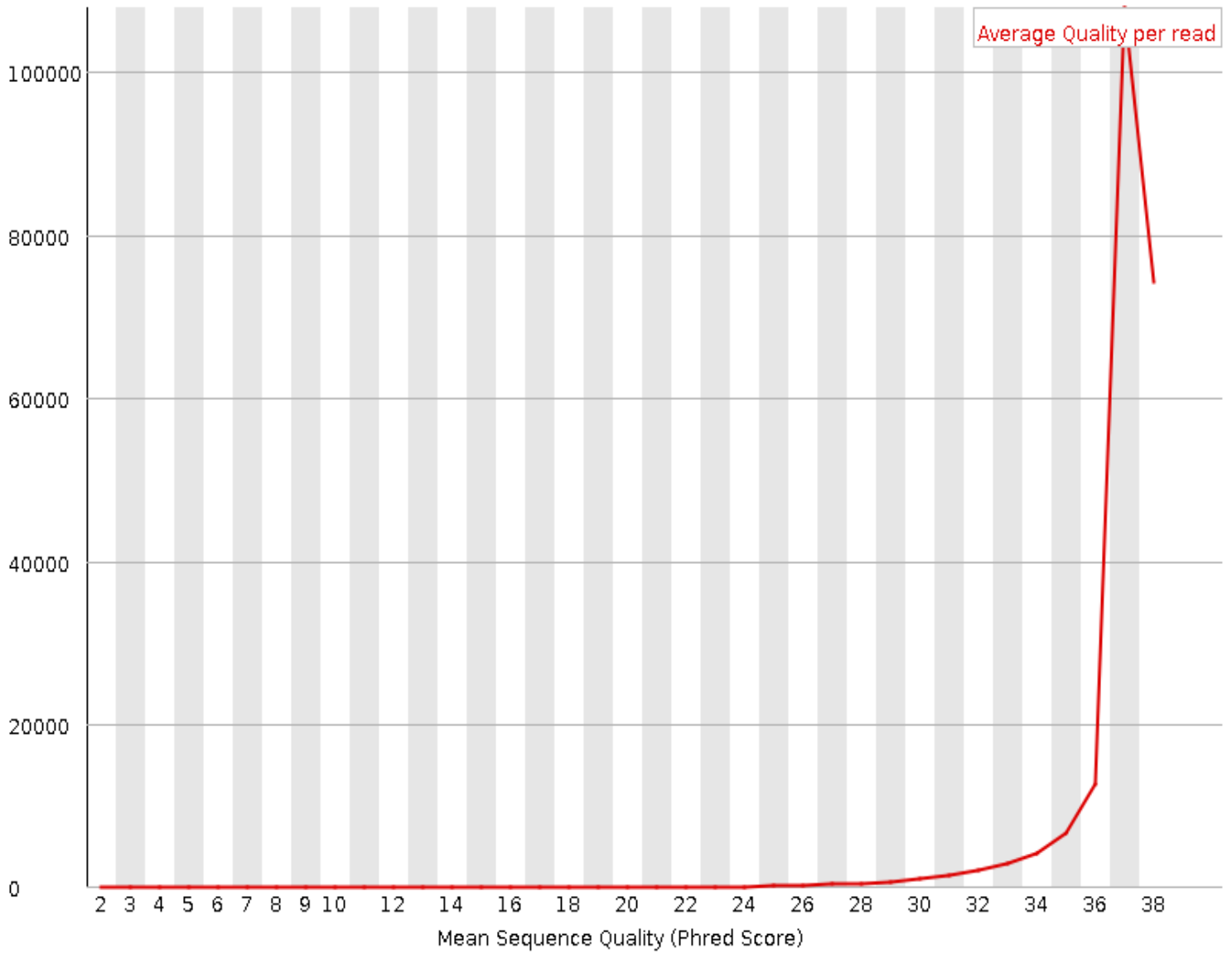
 **Per tile sequence quality**

Quality per tile



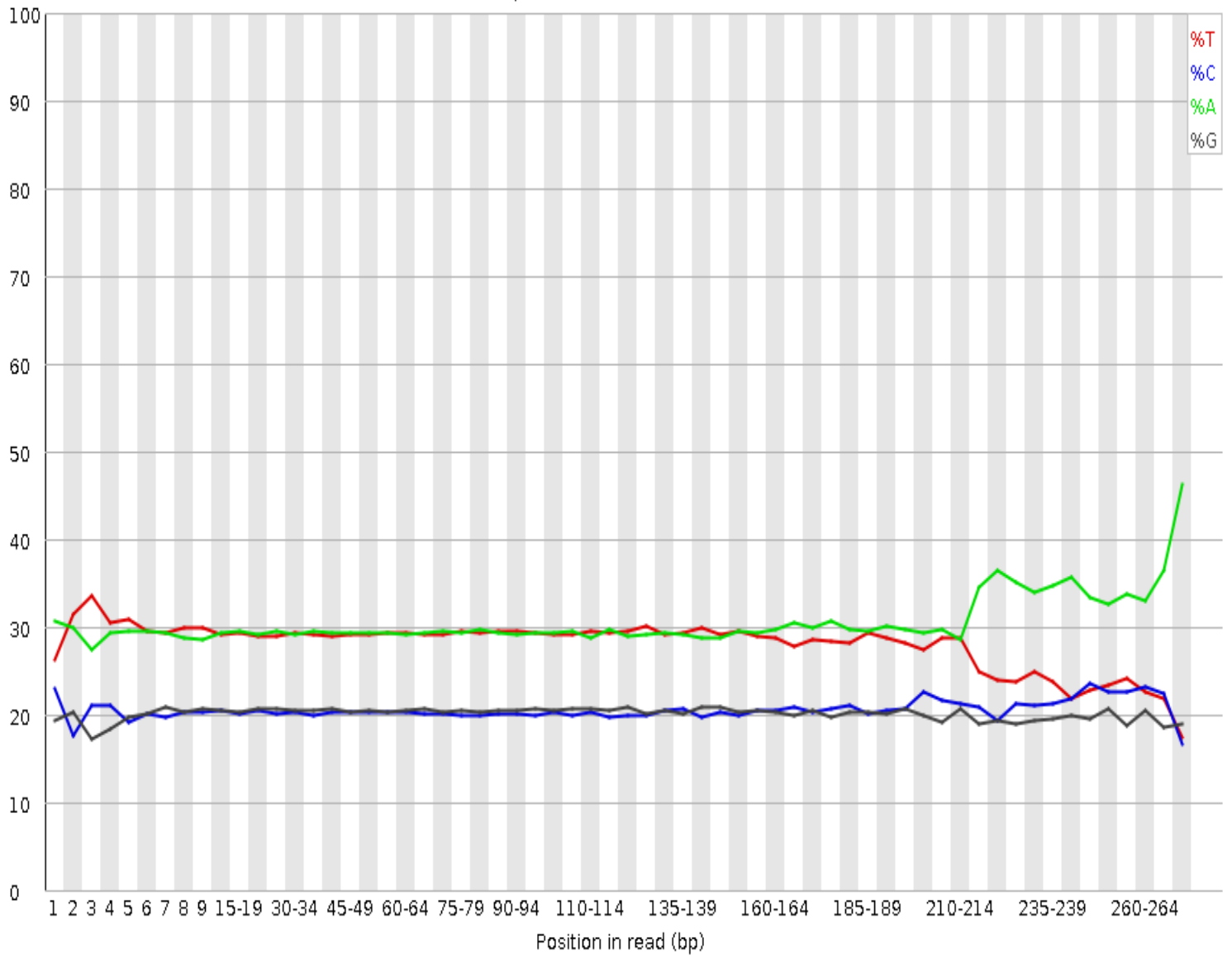
 **Per sequence quality scores**

Quality score distribution over all sequences



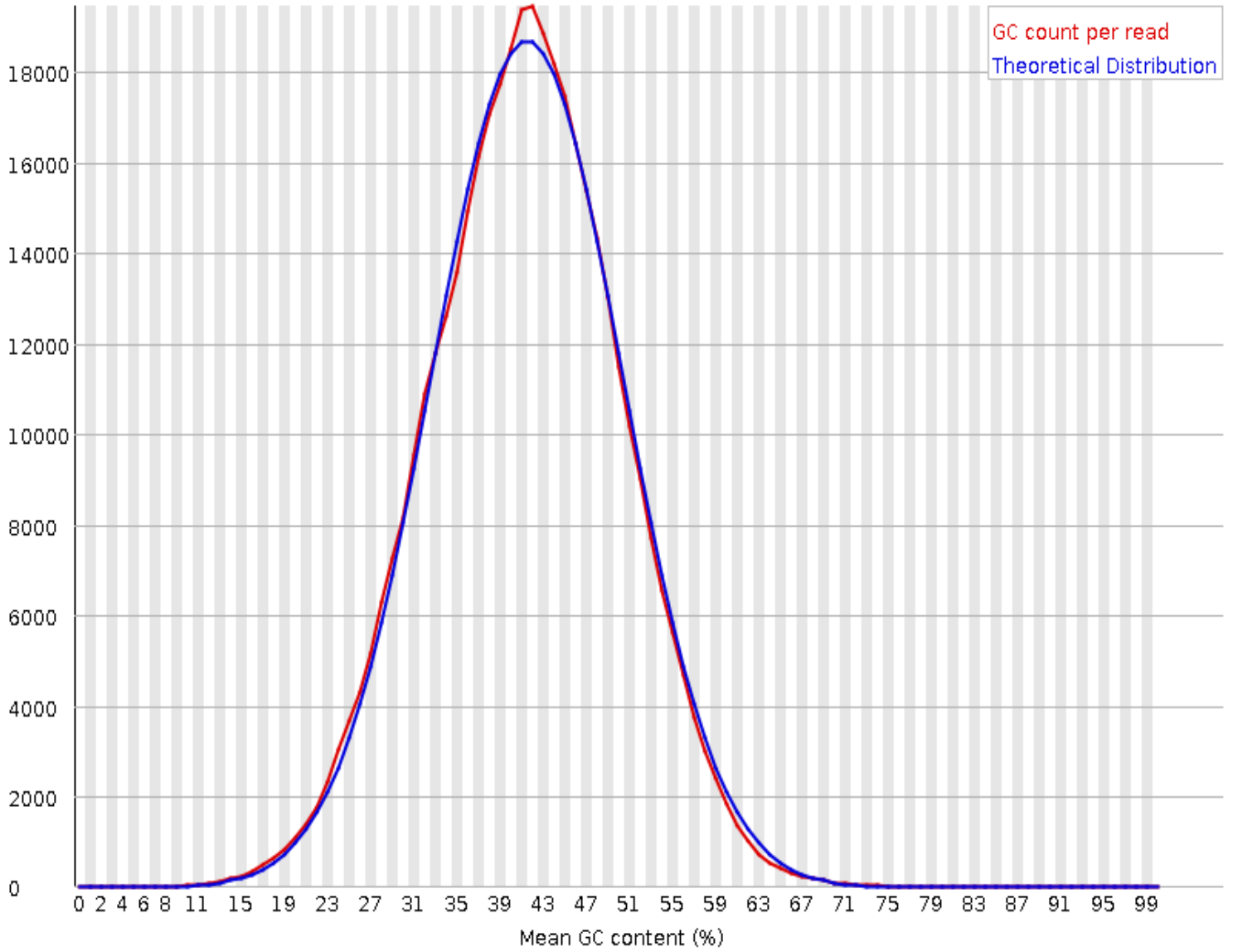
 **Per base sequence content**

Sequence content across all bases



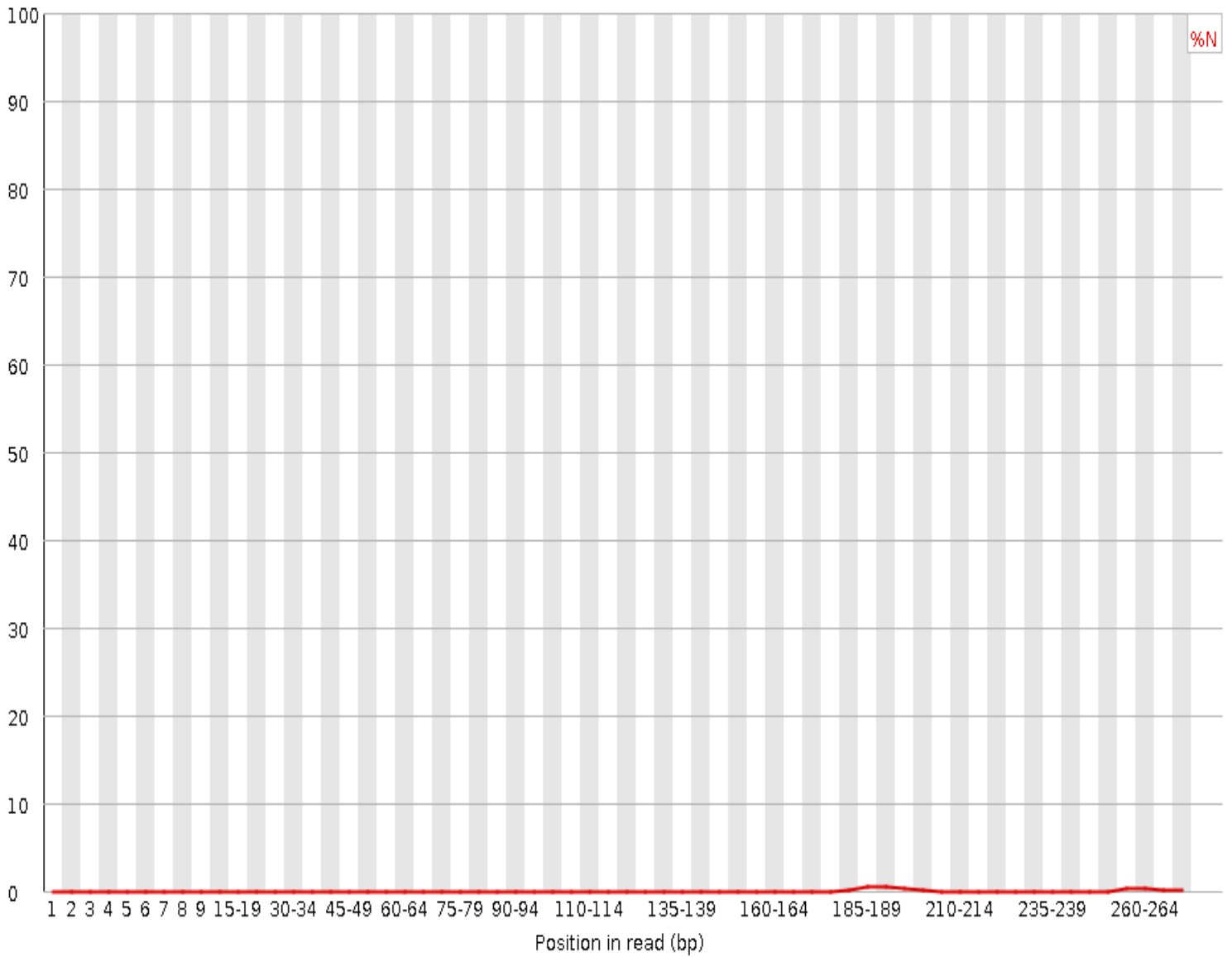
 **Per sequence GC content**

GC distribution over all sequences



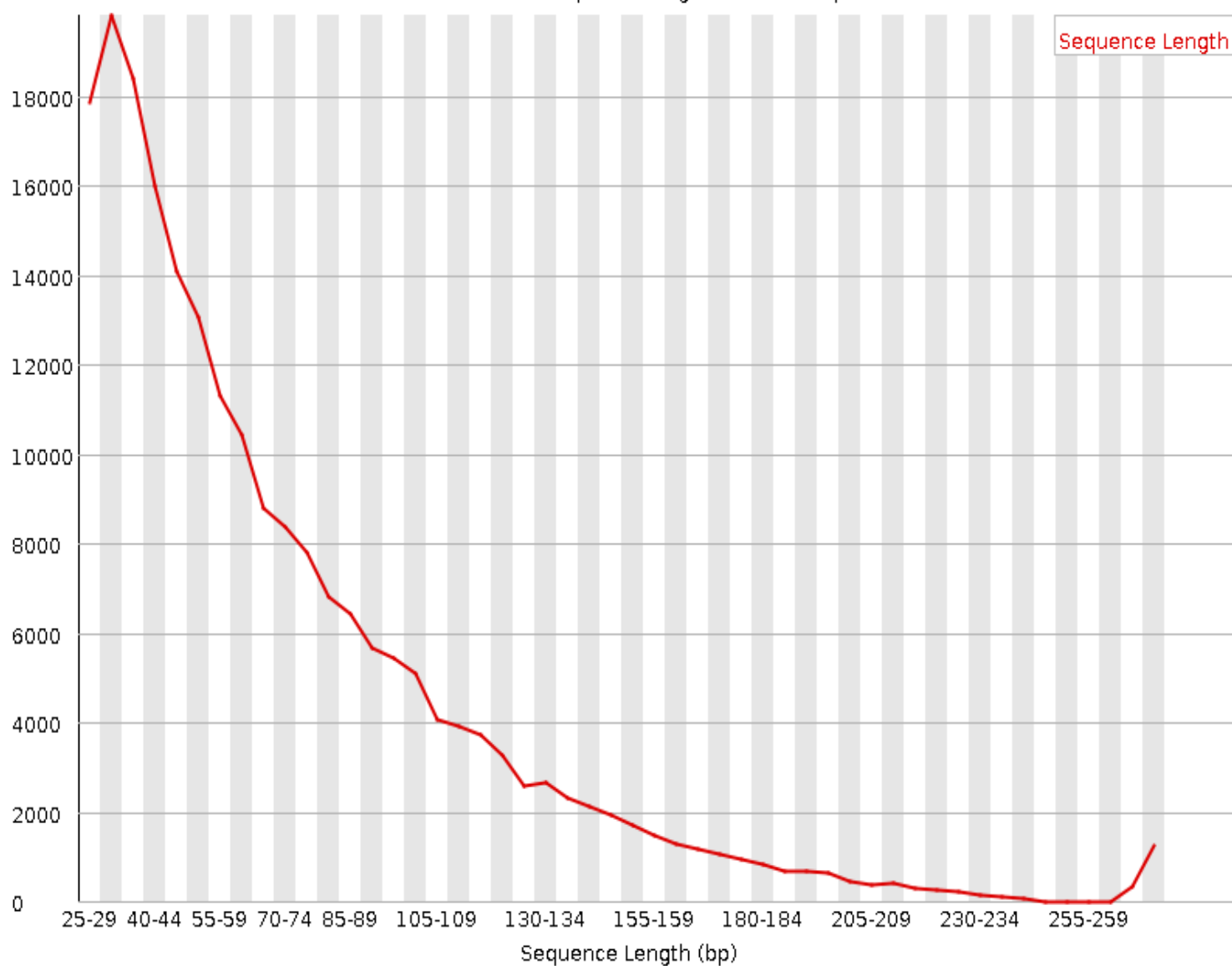
 **Per base N content**

N content across all bases



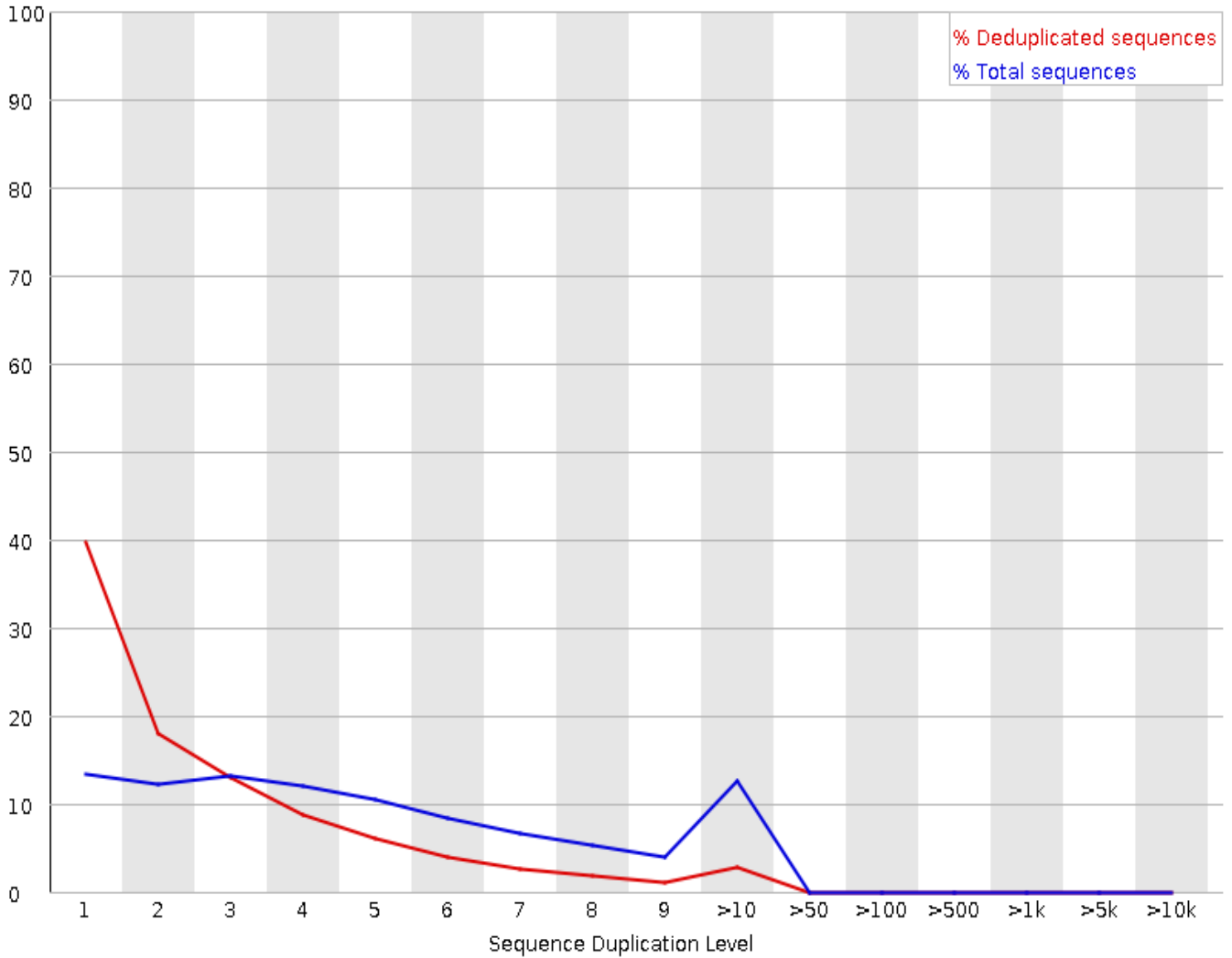
! Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 33.91%

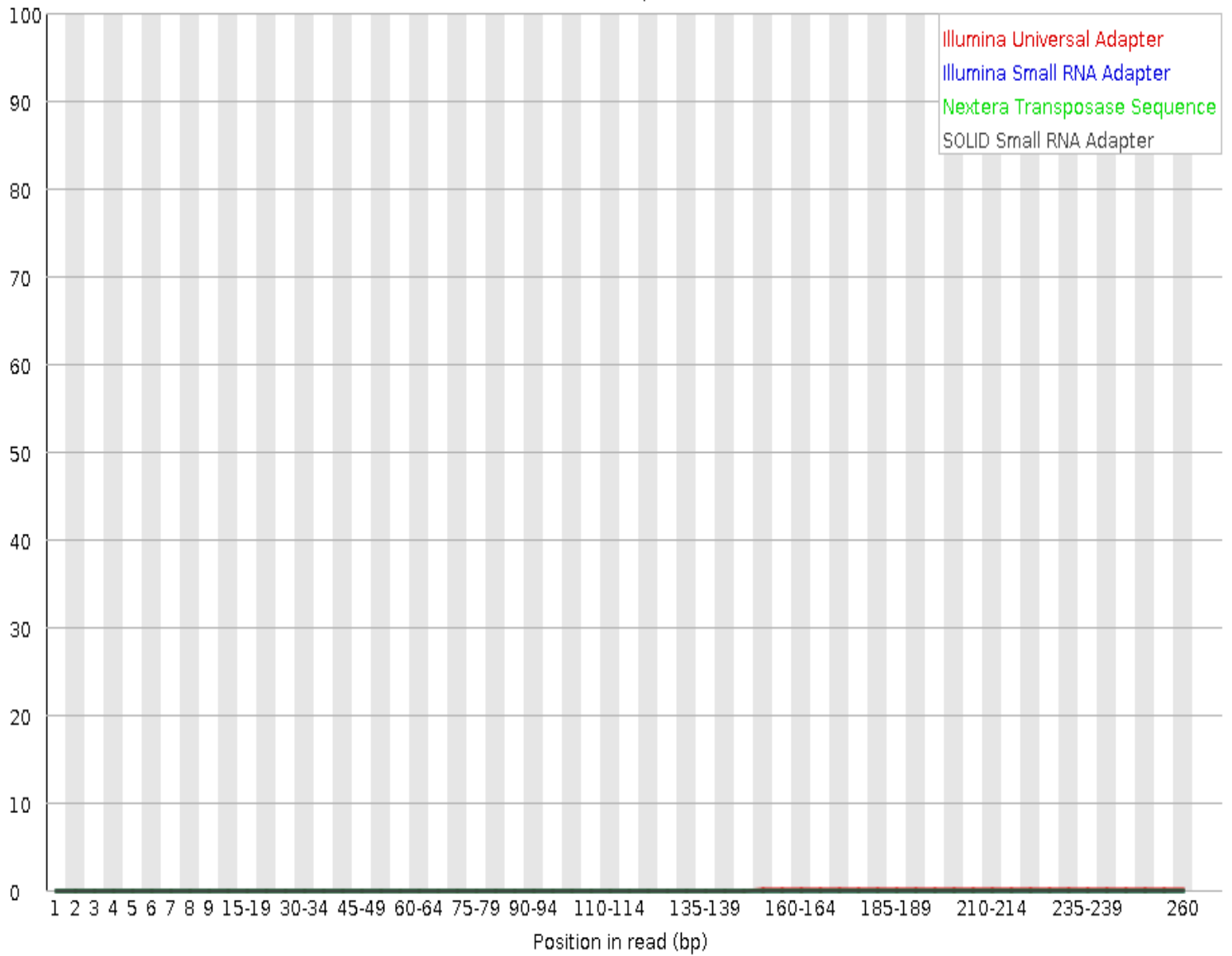


 **Overrepresented sequences**

No overrepresented sequences

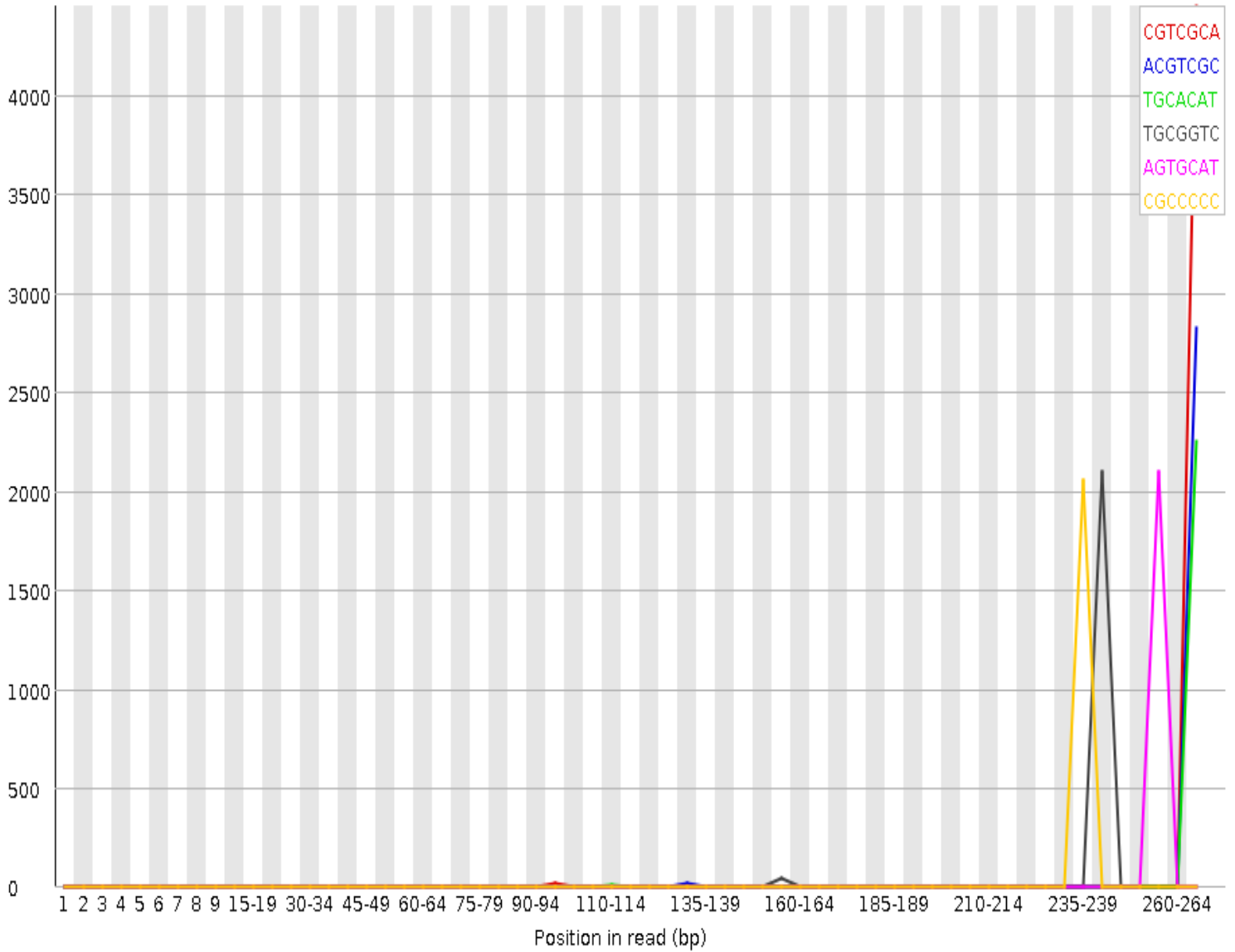
 **Adapter Content**

% Adapter



! Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGTCGCA	15	3.9523913E-4	4447.6816	265-266
ACGTCGC	40	9.4896986E-4	2822.5674	265-266
TGCACAT	50	0.0014826914	2258.0537	265-266
TCGGTC	25	0.001796256	2096.7642	240-244
AGTCAT	25	0.001796256	2096.7642	255-259
CGCCCC	5	0.001929834	2052.7764	235-239
GTACCC	30	0.0025864558	1747.3035	240-244
ATAGTGC	30	0.0025864558	1747.3035	245-249
CCCGCA	30	0.0025864558	1747.3035	245-249
ACCCCG	10	0.002650271	1747.3035	240-244
CGCAAGT	10	0.0029102273	1667.8806	230-234

ACGCAAG	15	0.0029267692	1658.4578	230-234
CCGTCCC	10	0.0029771156	1649.1404	195-199
AGGCCCG	15	0.0033406338	1553.1587	215-219
CCTATAA	35	0.0035202461	1497.6887	260-264
TTCGATT	35	0.0035202461	1497.6887	260-264
ATCGCGT	10	0.0040715896	1411.2837	190-194
CCGTGAC	5	0.004170567	1397.8429	220-224
AGGGGGC	35	0.004050948	1397.8429	230-234
CTAGTAA	85	0.004284229	1328.2668	265-266

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