













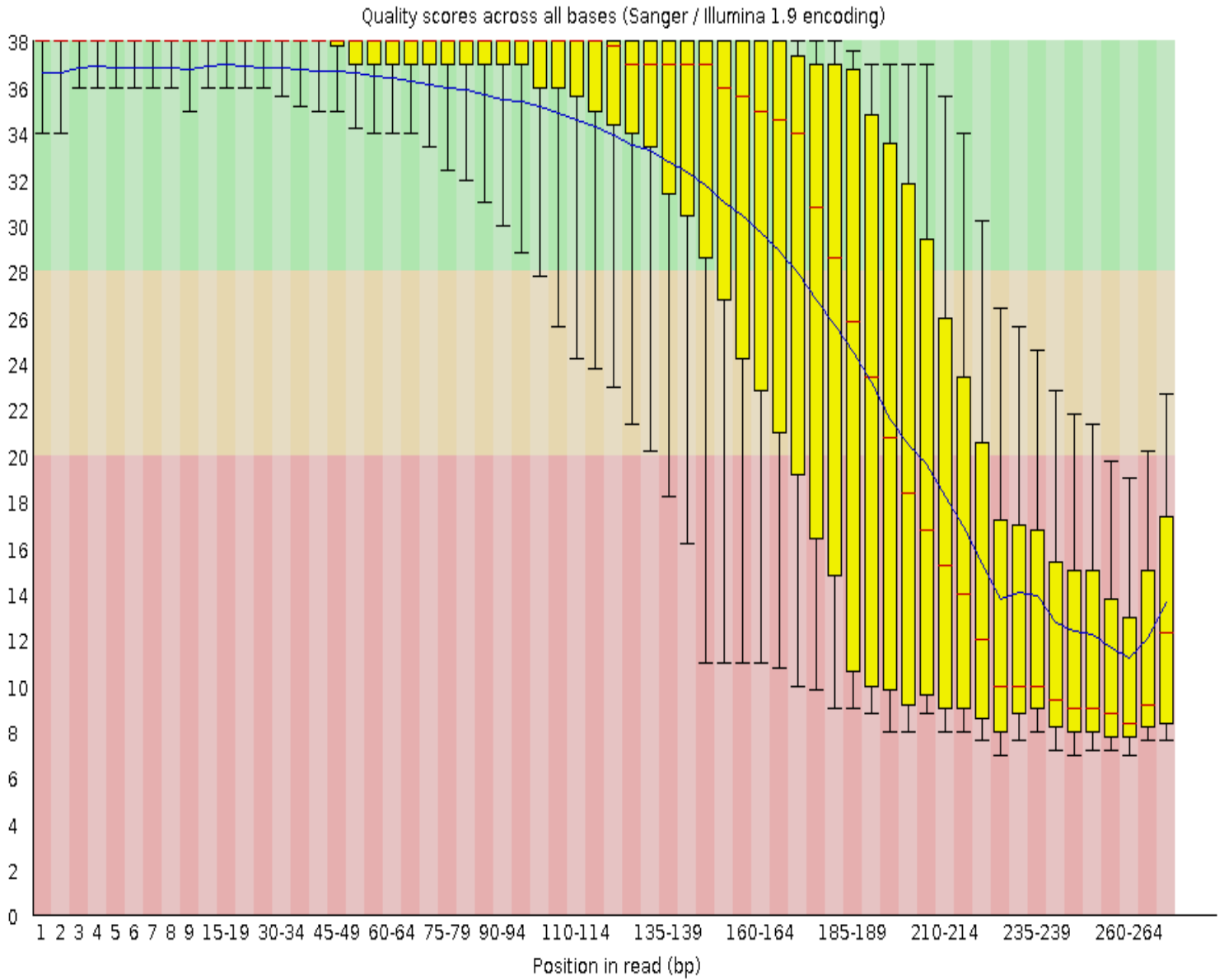
Summary

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Basic Statistics

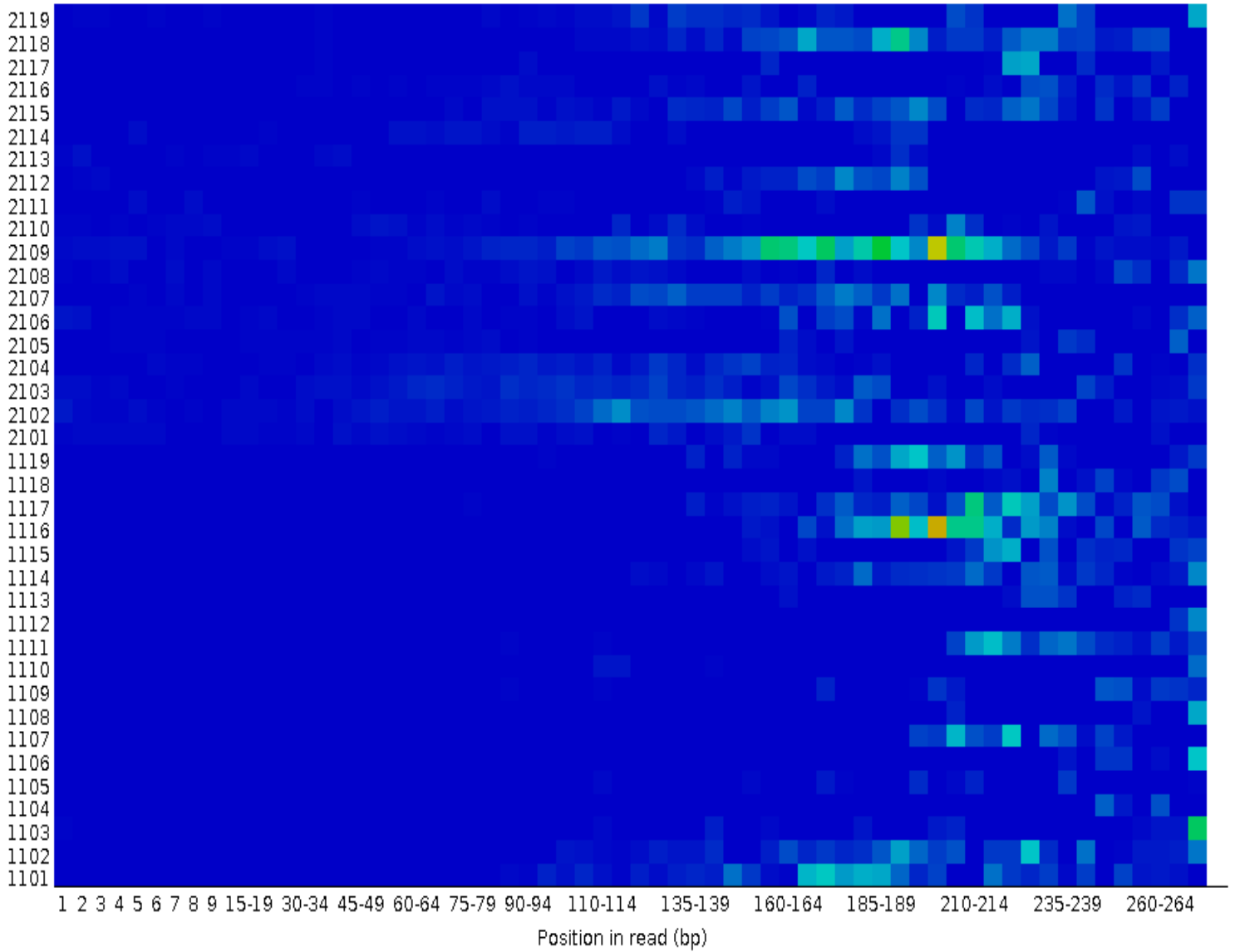
Measure	Value
Filename	R2_IJS8_mates_ICC5_SW023_S60_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	217484
Sequences flagged as poor quality	0
Sequence length	26-273
%GC	41

Per base sequence quality



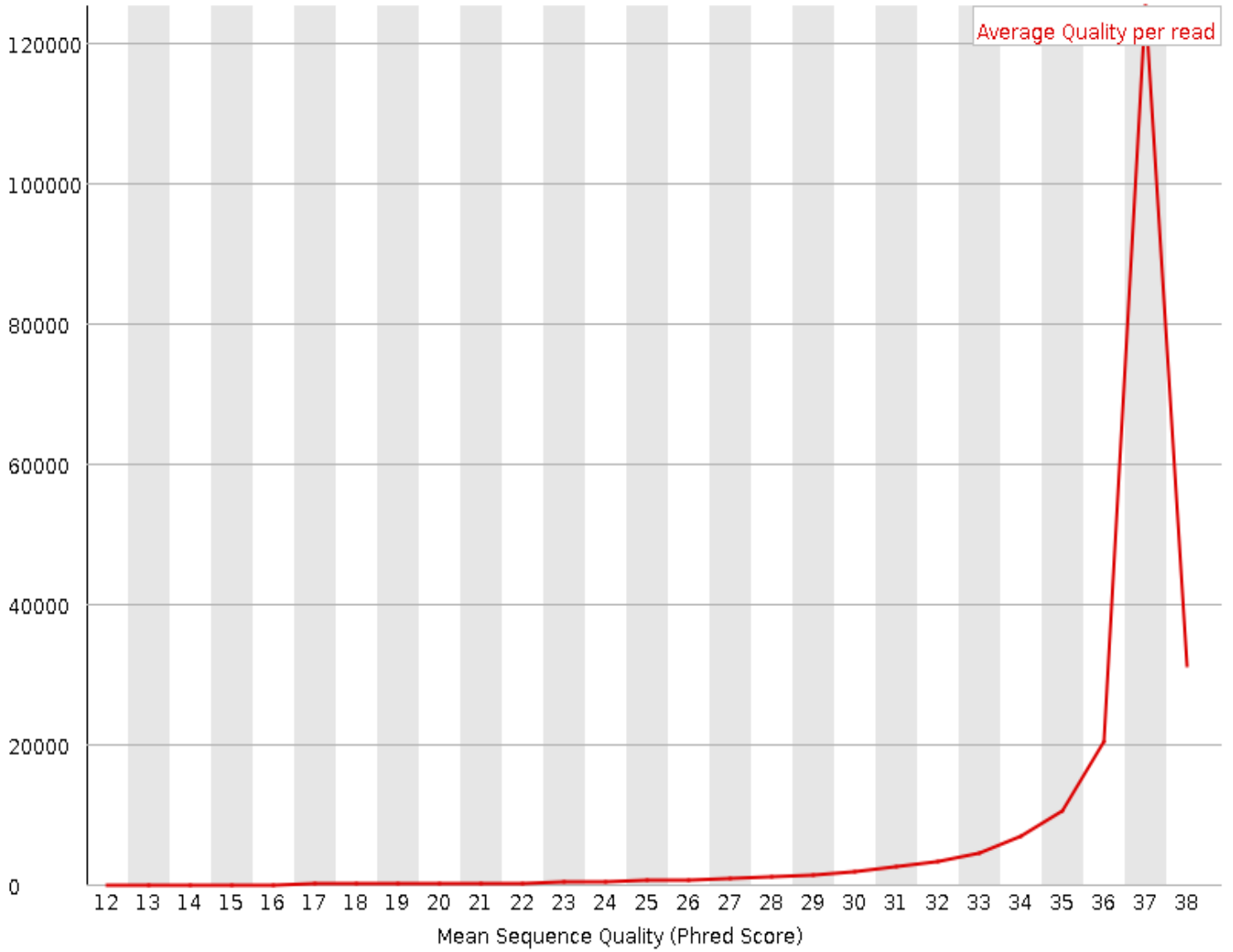
! Per tile sequence quality

Quality per tile



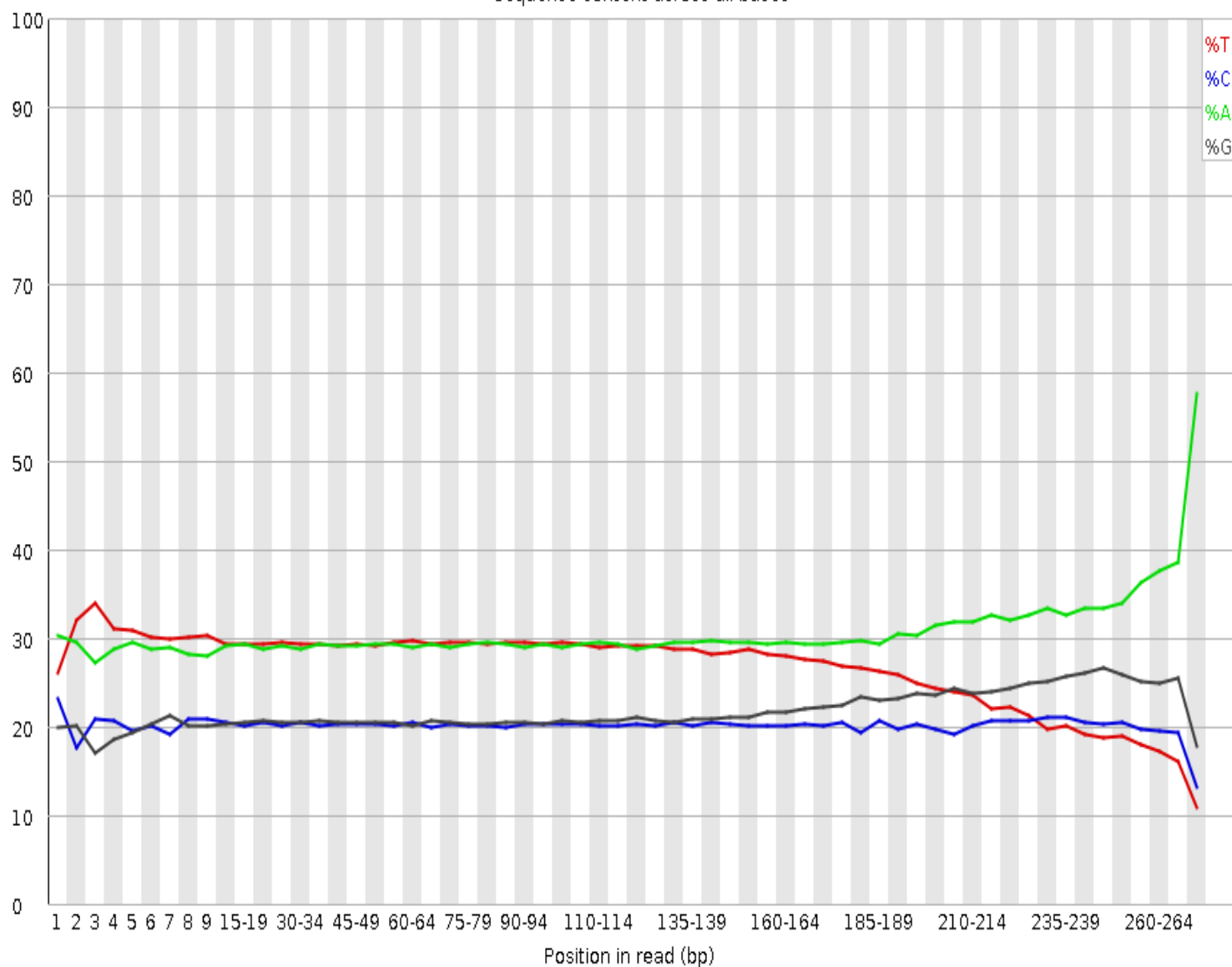
 **Per sequence quality scores**

Quality score distribution over all sequences



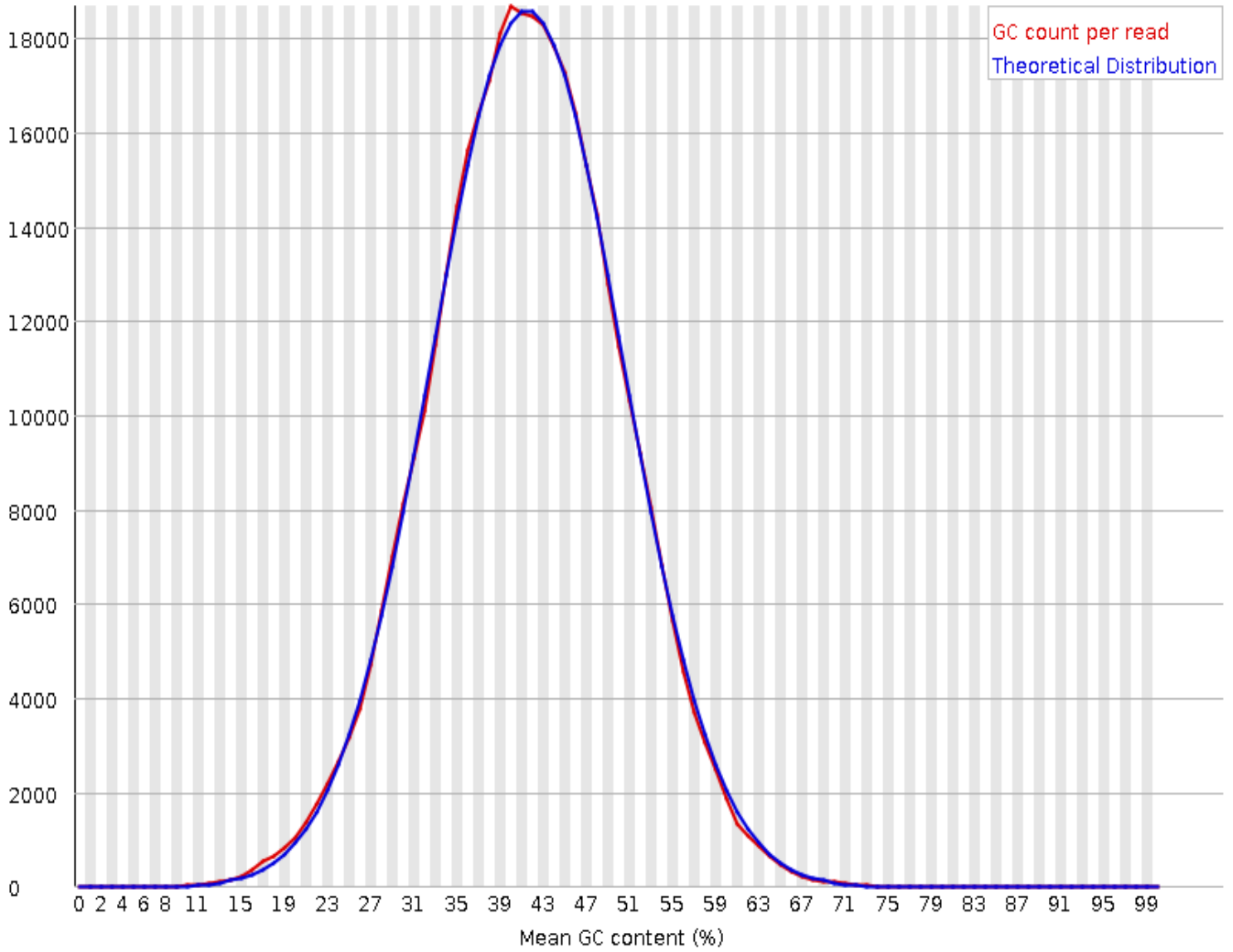
 **Per base sequence content**

Sequence content across all bases



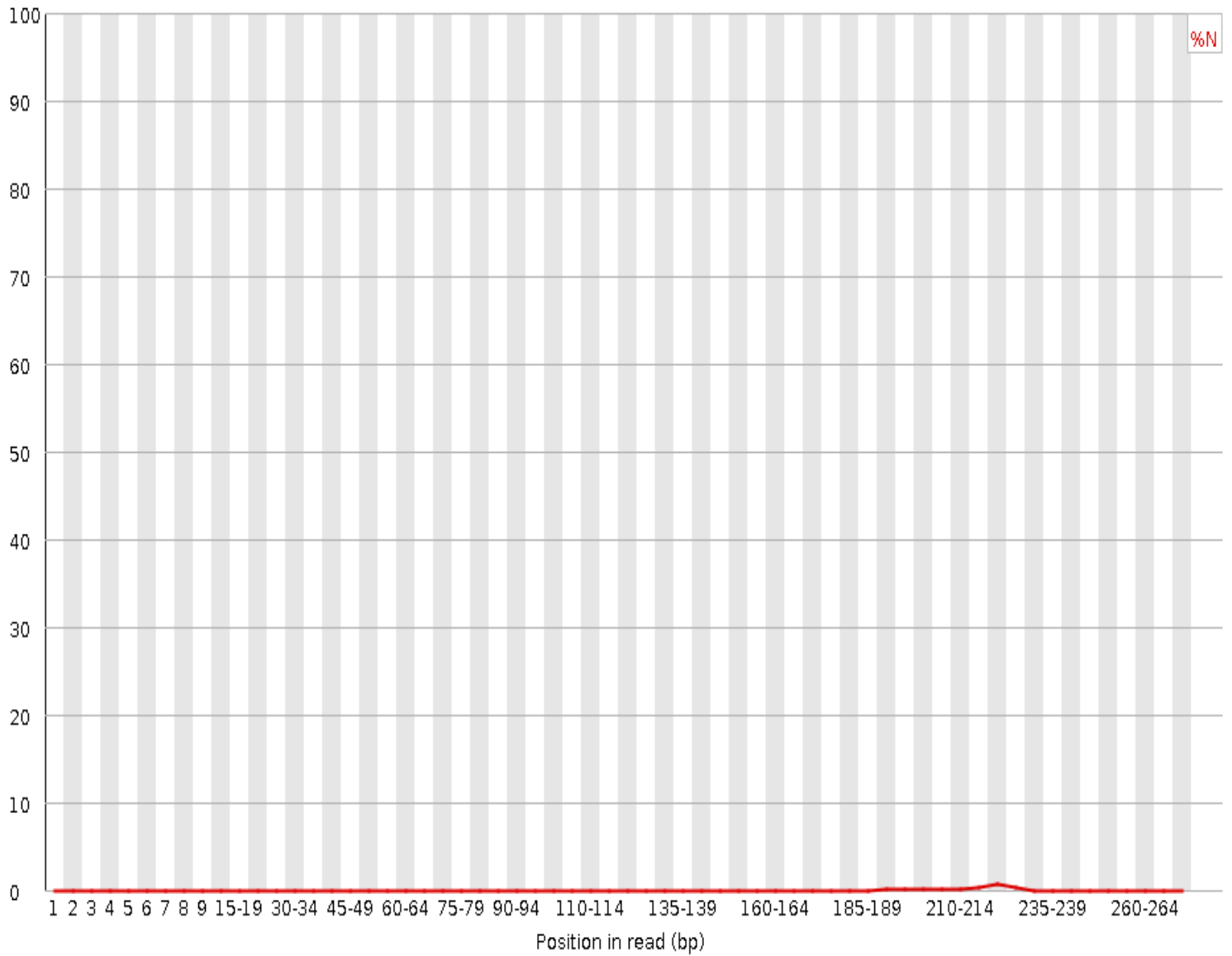
 **Per sequence GC content**

GC distribution over all sequences



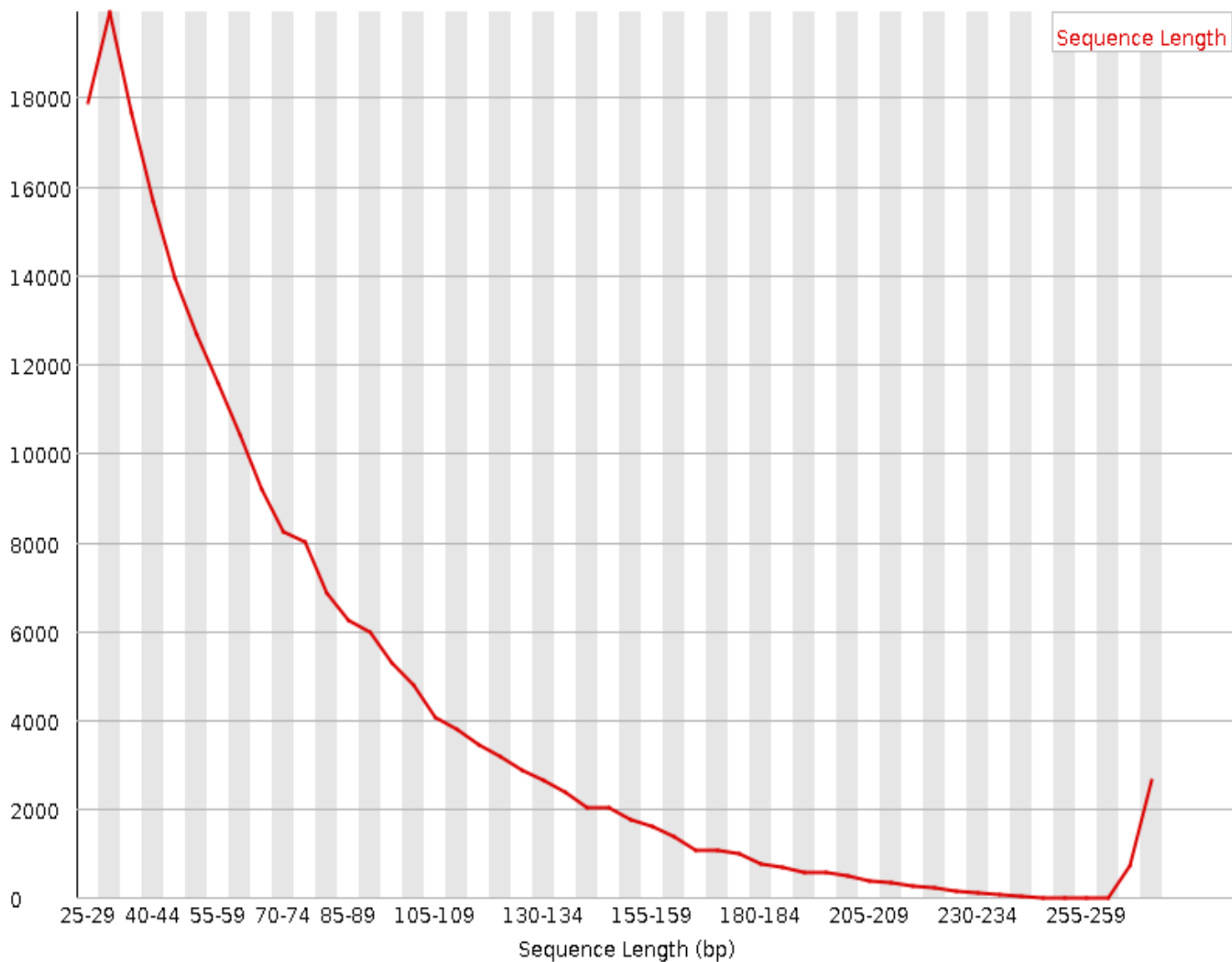
 **Per base N content**

N content across all bases



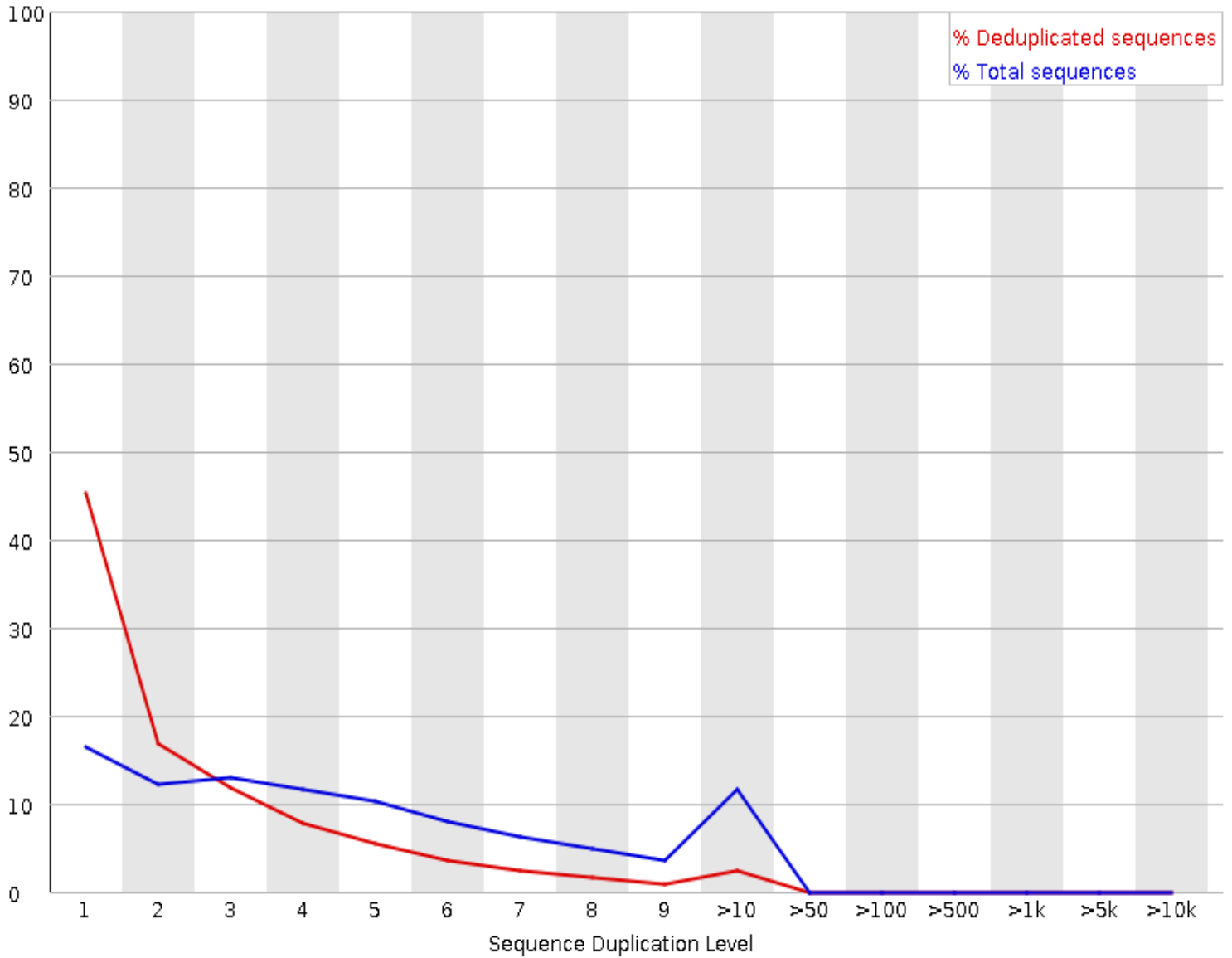
Sequence Length Distribution

Distribution of sequence lengths over all sequences



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 36.63%

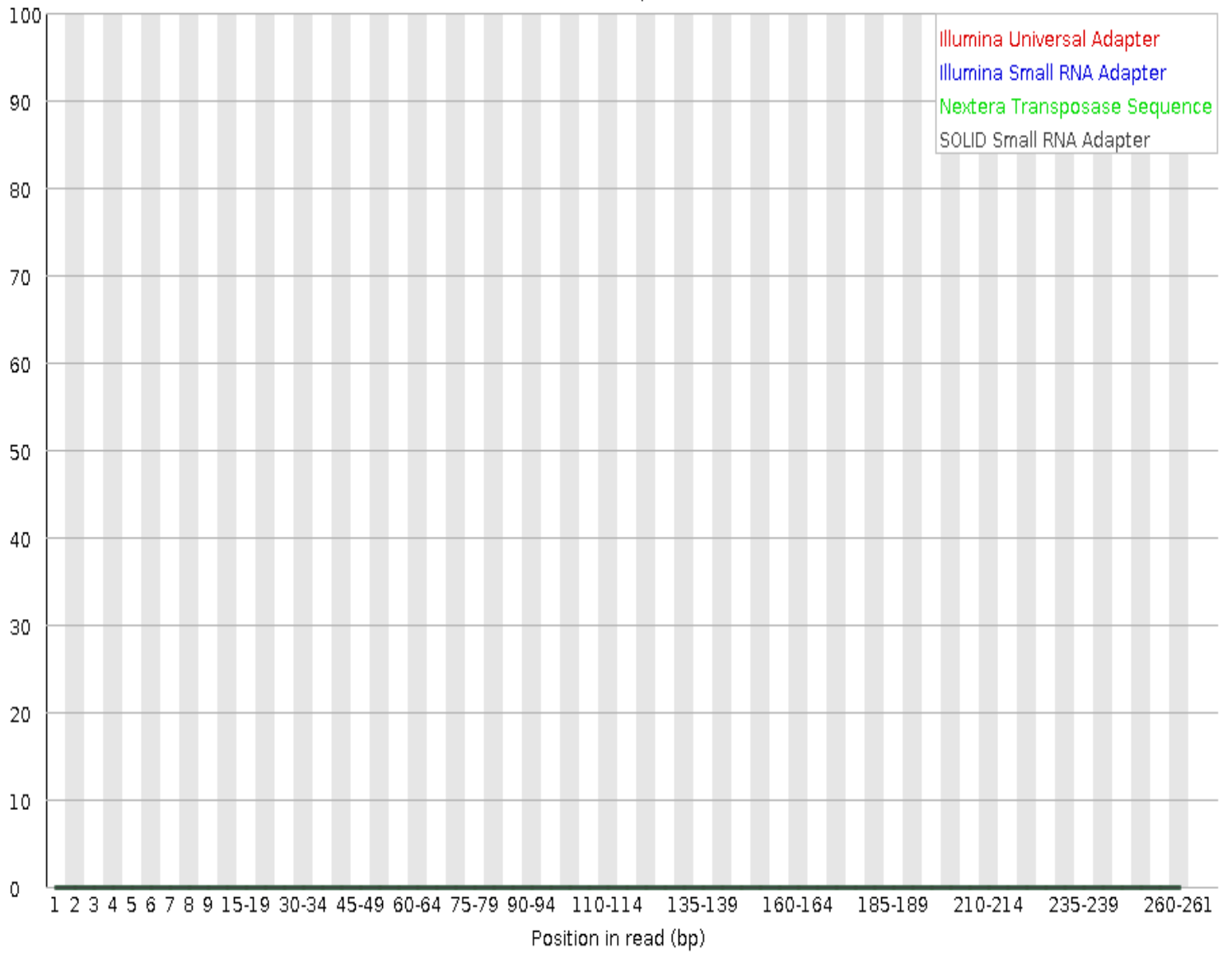


 **Overrepresented sequences**

No overrepresented sequences

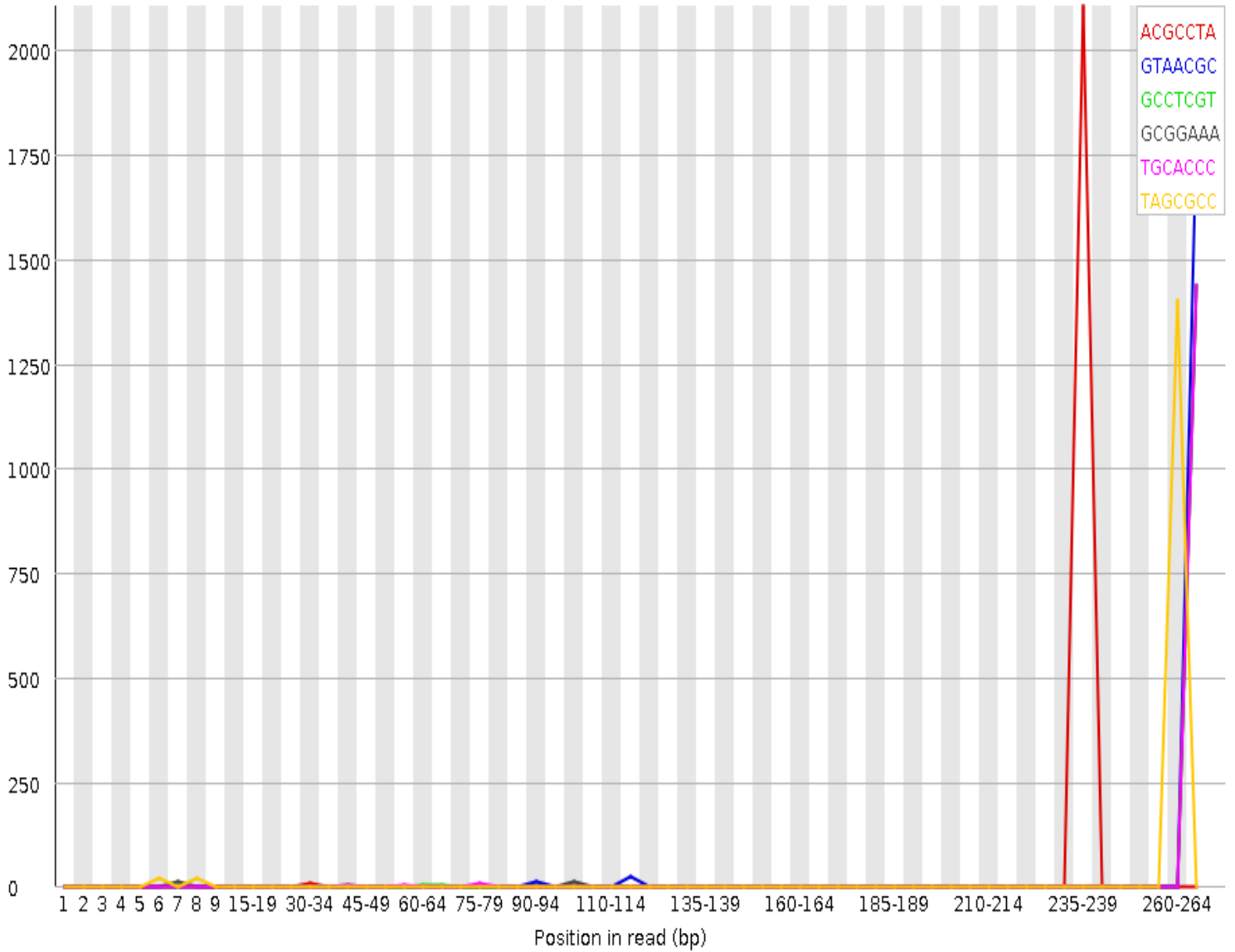
 **Adapter Content**

% Adapter



Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGCCTA	10	0.0018237033	2103.9072	235-239
GTAACGC	20	0.0024768016	1796.0183	265-266
GCCTCGT	25	0.0038696614	1436.8146	265-266
GCGGAAA	25	0.0038696614	1436.8146	265-266
TGCACCC	25	0.0038696614	1436.8146	265-266
TAGCGCC	15	0.004102701	1402.6047	260-264
GTCTAGG	15	0.004102701	1402.6047	240-244
CGTGGGG	30	0.0055718203	1197.3456	265-266
AGTACGG	35	1.3660634E-5	1152.8258	225-229
CGCGAGG	20	0.007292568	1051.9536	250-254
CGGGGCA	20	0.007292568	1051.9536	230-234

TGCGCAC	20	0.007292568	1051.9536	245-249
TTCGGAT	20	0.007292568	1051.9536	230-234
CGATCGT	20	0.007292568	1051.9536	240-244
TATCGGG	20	0.007292568	1051.9536	230-234
CGCCGTG	35	0.0075831967	1026.2961	265-266
GGTCGTA	20	0.007935548	1008.7226	225-229
CGTAAAG	15	0.009273468	935.0698	195-199
ACCCTAG	40	0.009903709	898.00916	265-266
CGTCCGG	25	0.0079448875	841.56287	260-264

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