













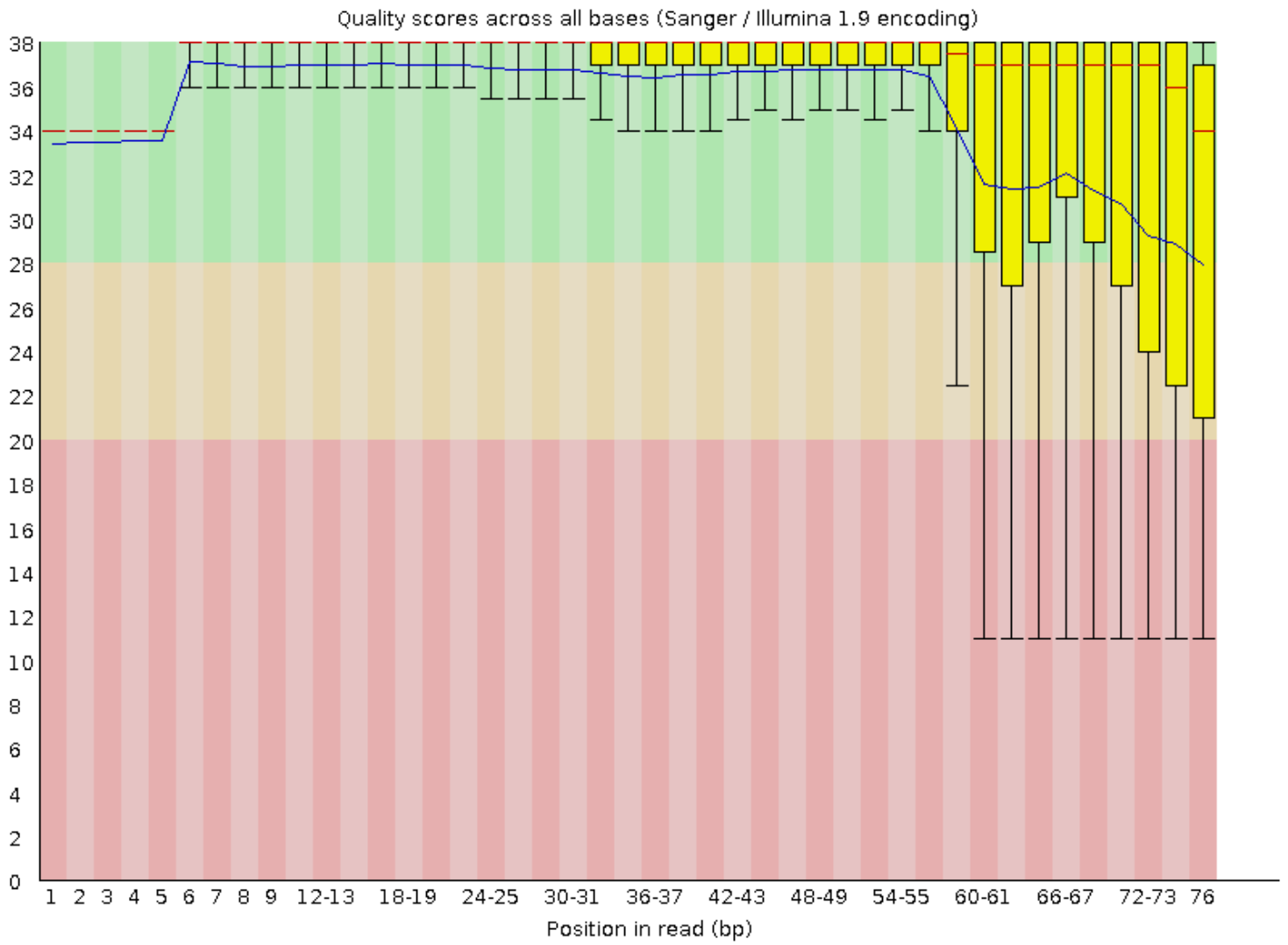
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Basic Statistics

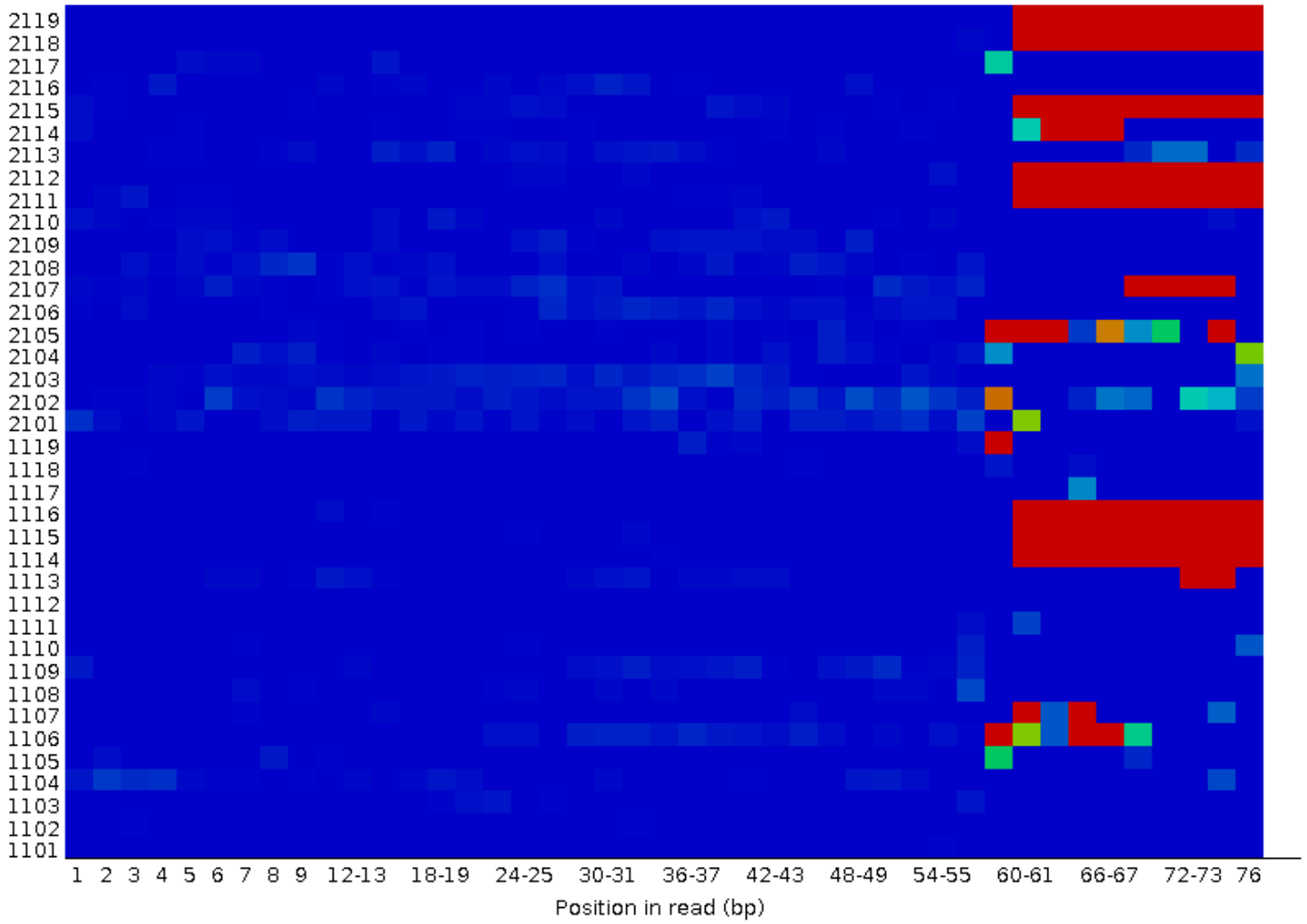
Measure	Value
Filename	skewer_SW041_2-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	27960
Sequences flagged as poor quality	0
Sequence length	28-76
%GC	44

Per base sequence quality

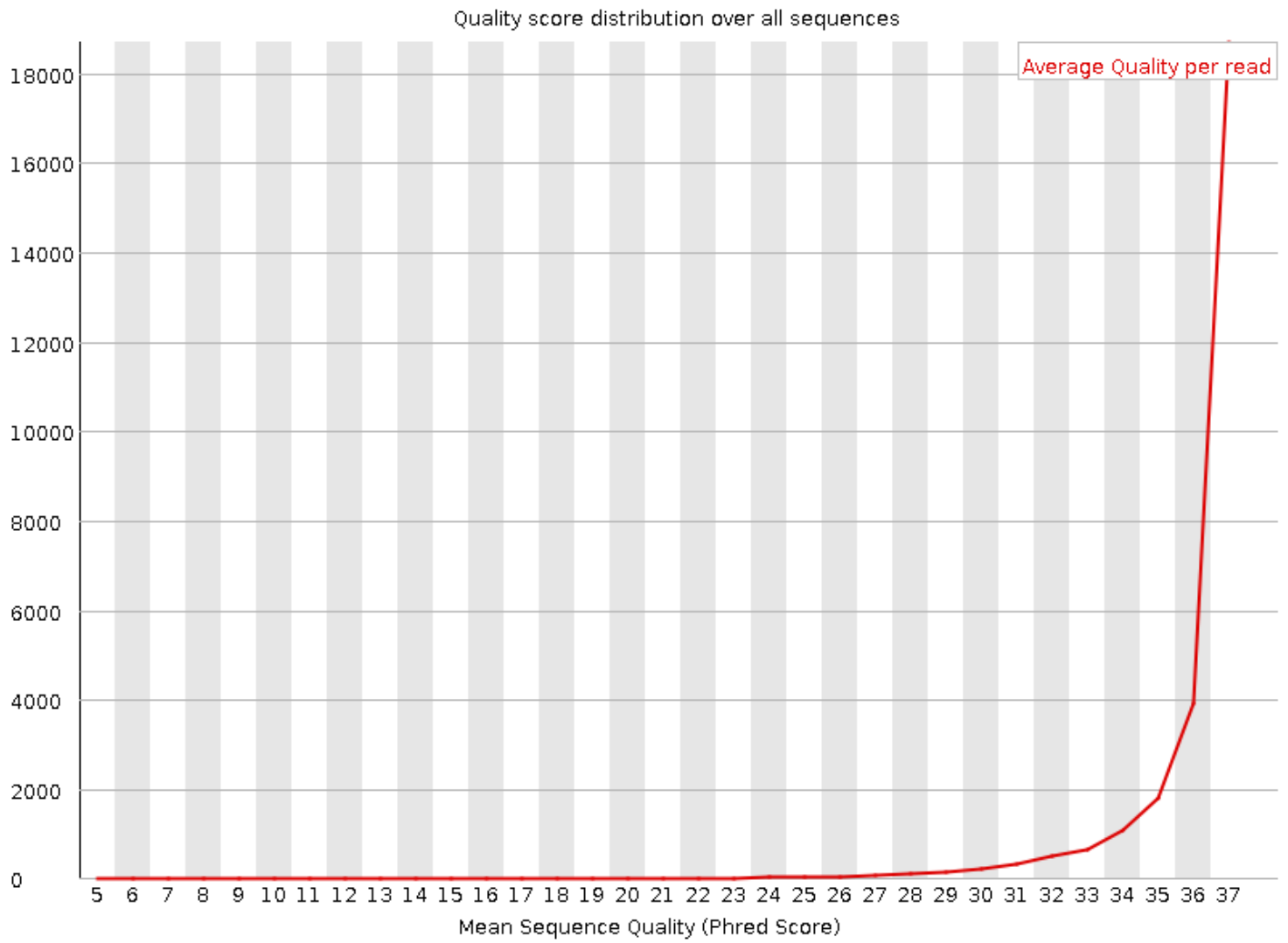


 **Per tile sequence quality**

Quality per tile

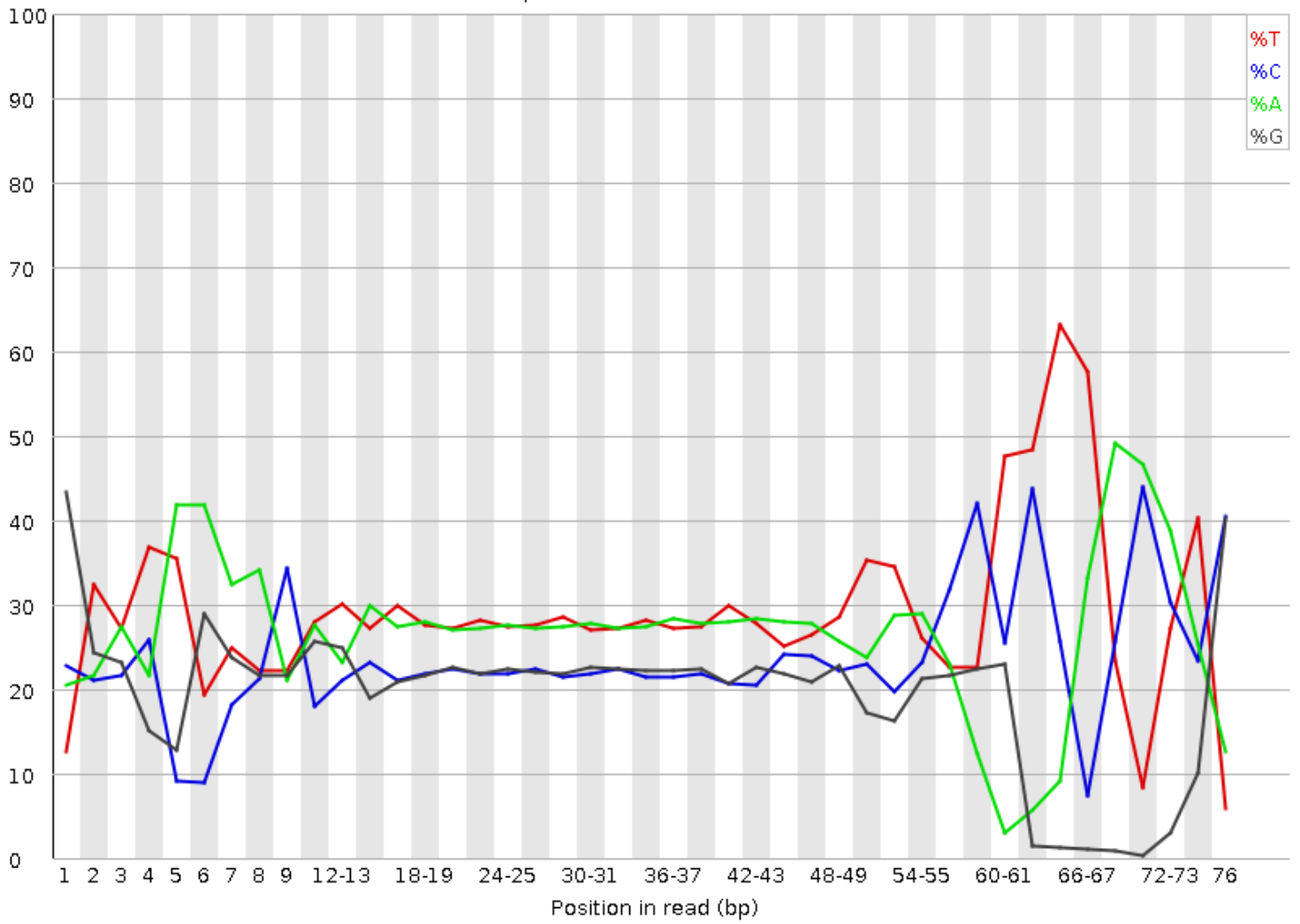


 **Per sequence quality scores**



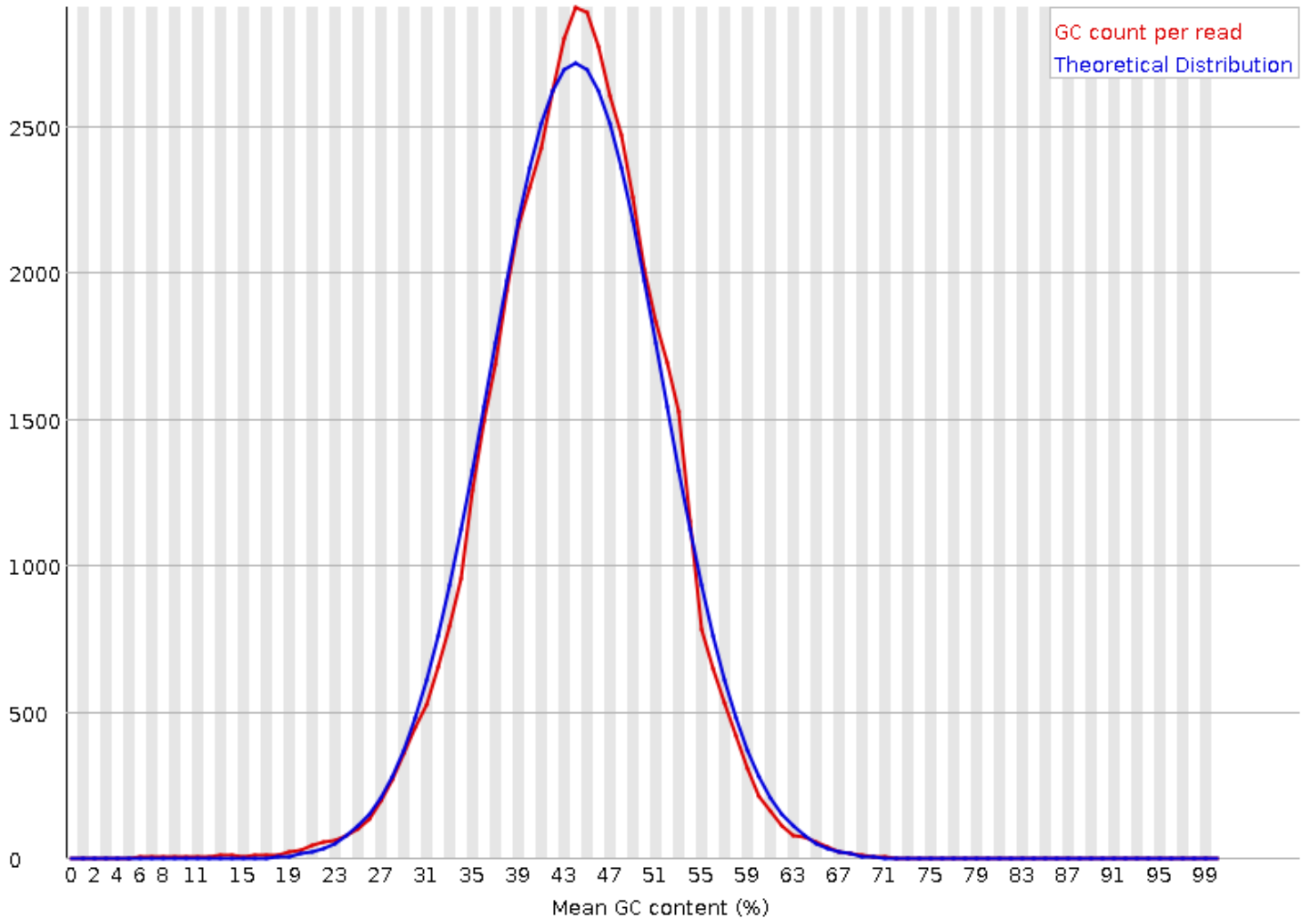
 Per base sequence content

Sequence content across all bases



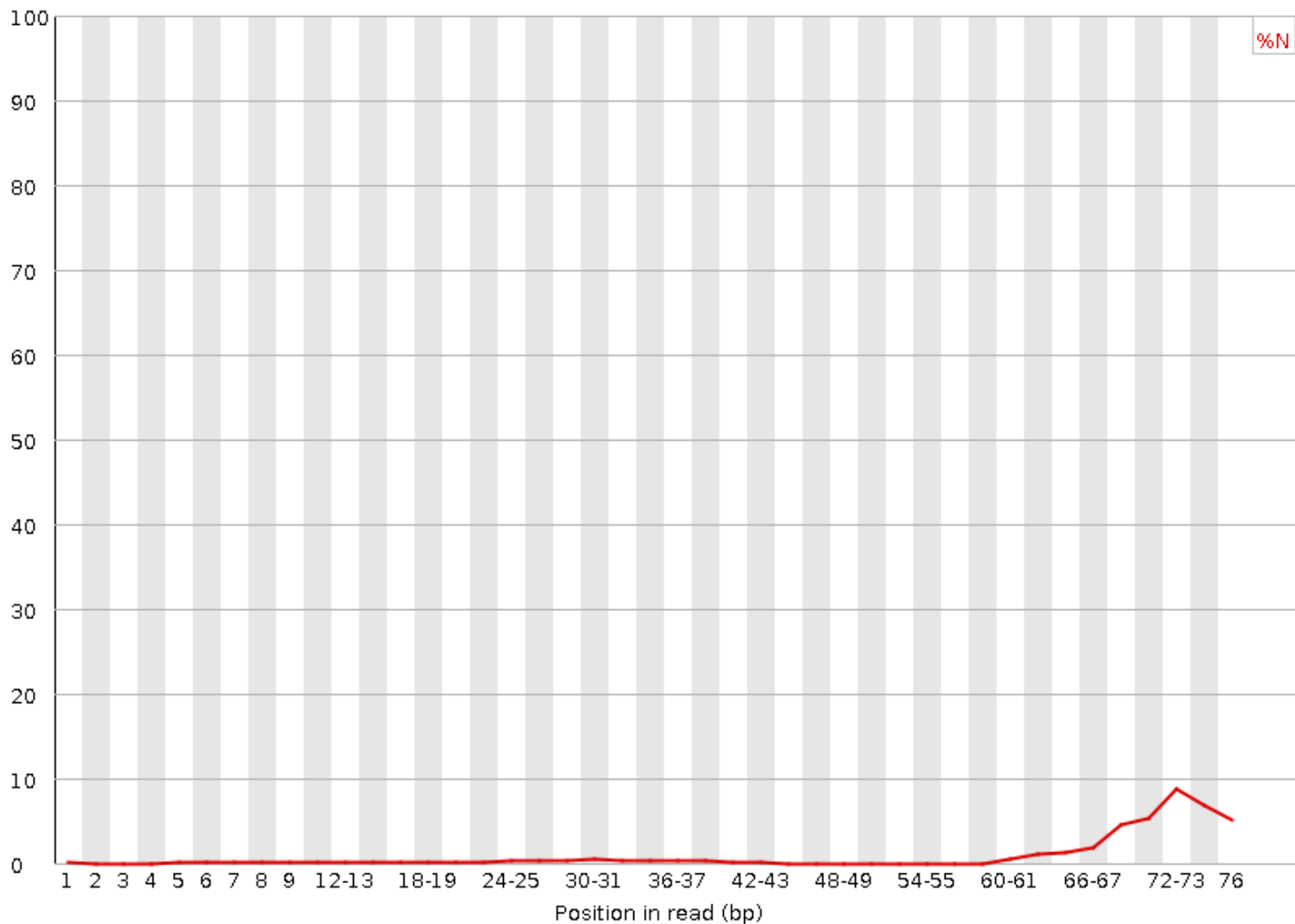
✔ Per sequence GC content

GC distribution over all sequences

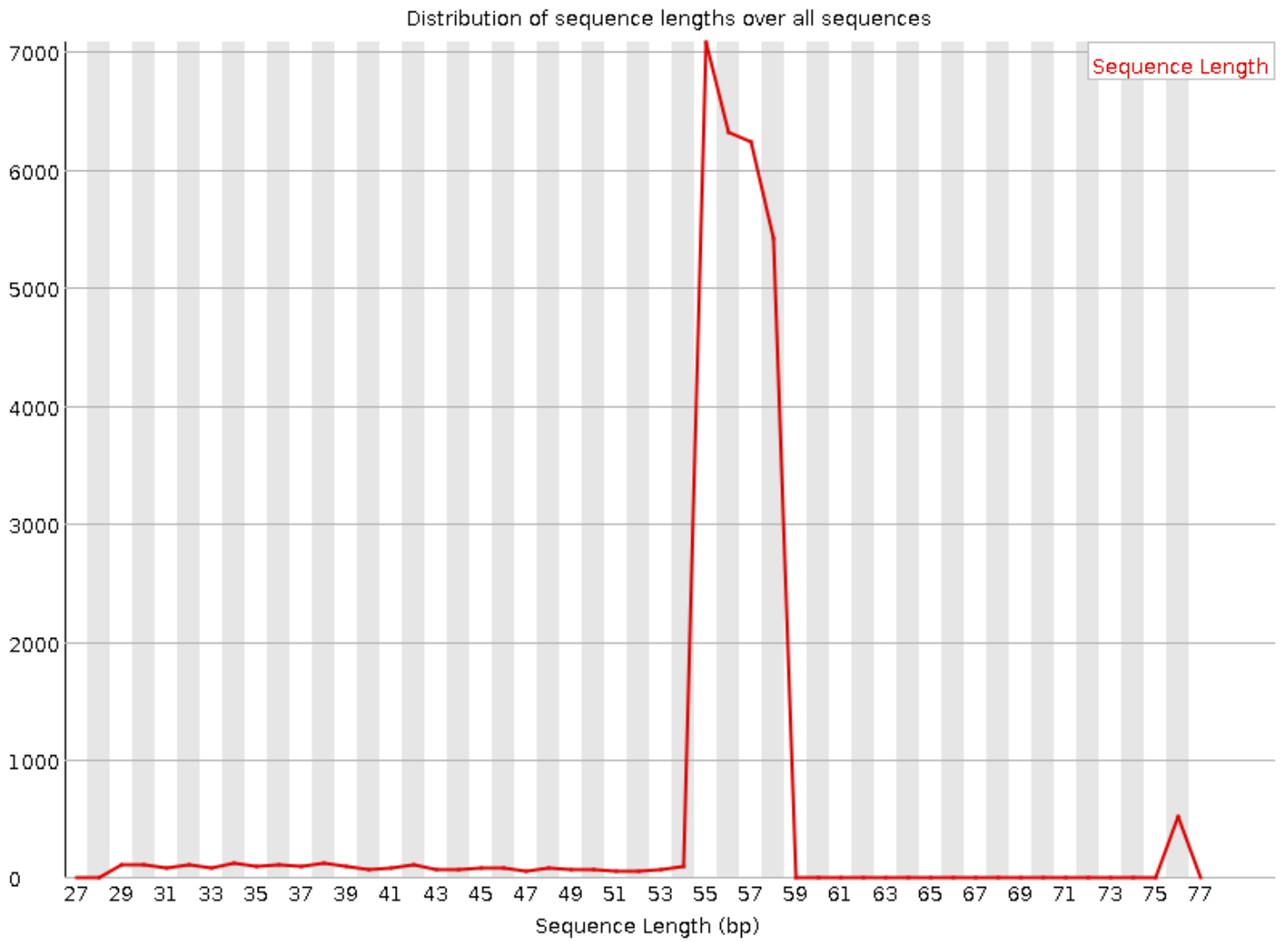


 **Per base N content**

N content across all bases

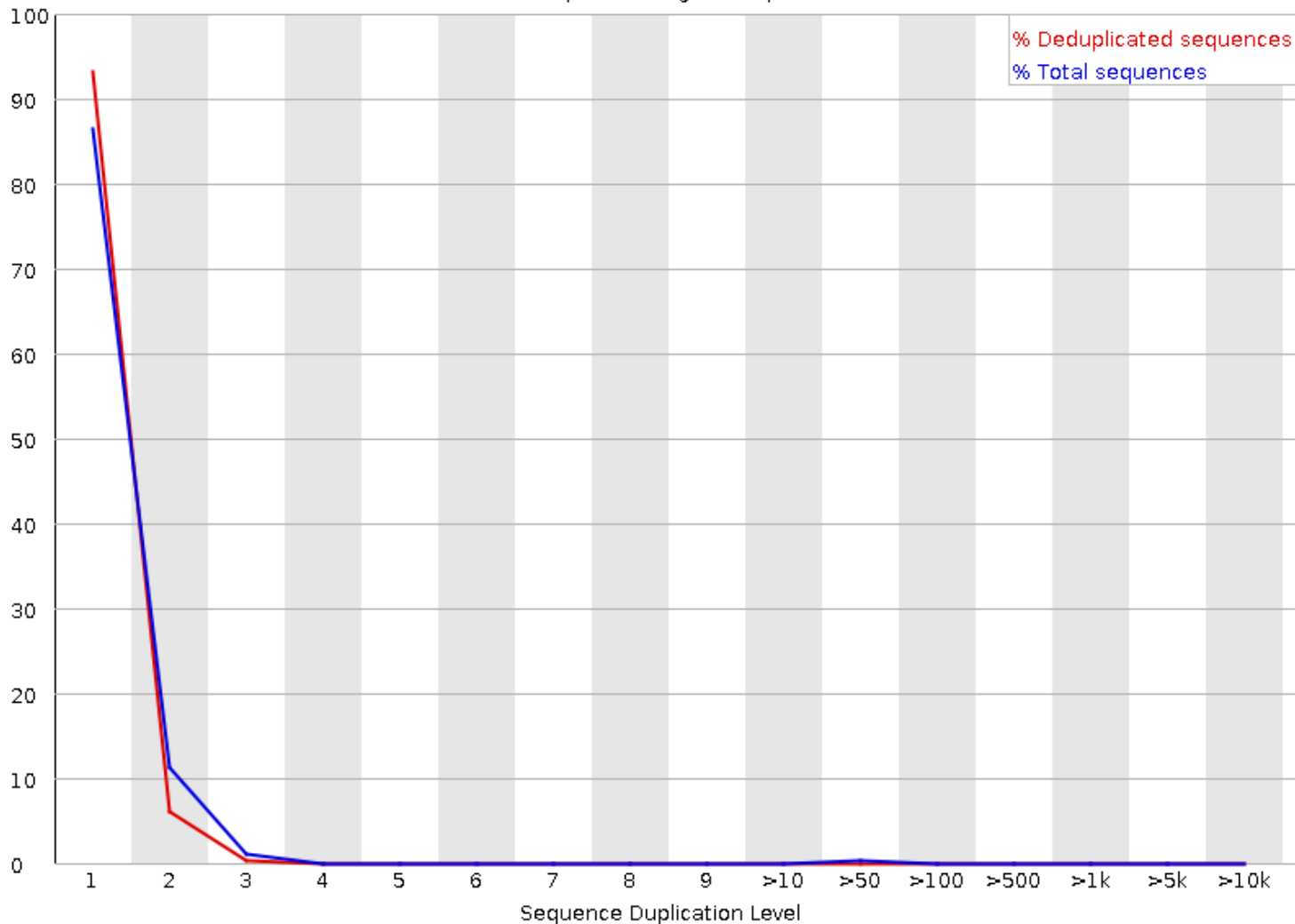


! Sequence Length Distribution



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 92.79%

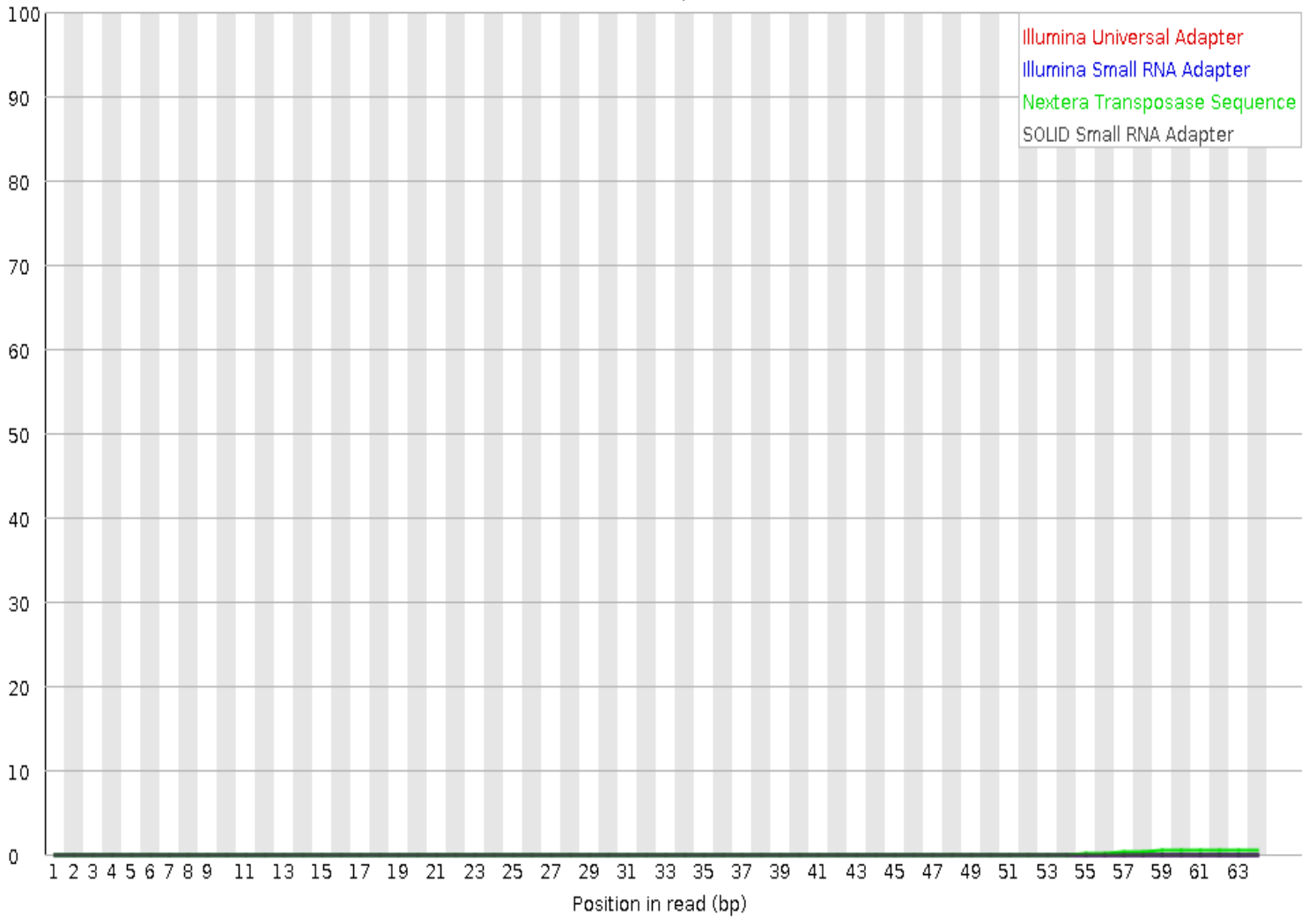


⚠ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTAACCC	80	0.28612303290414876	No Hit
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG	52	0.18597997138769673	No Hit

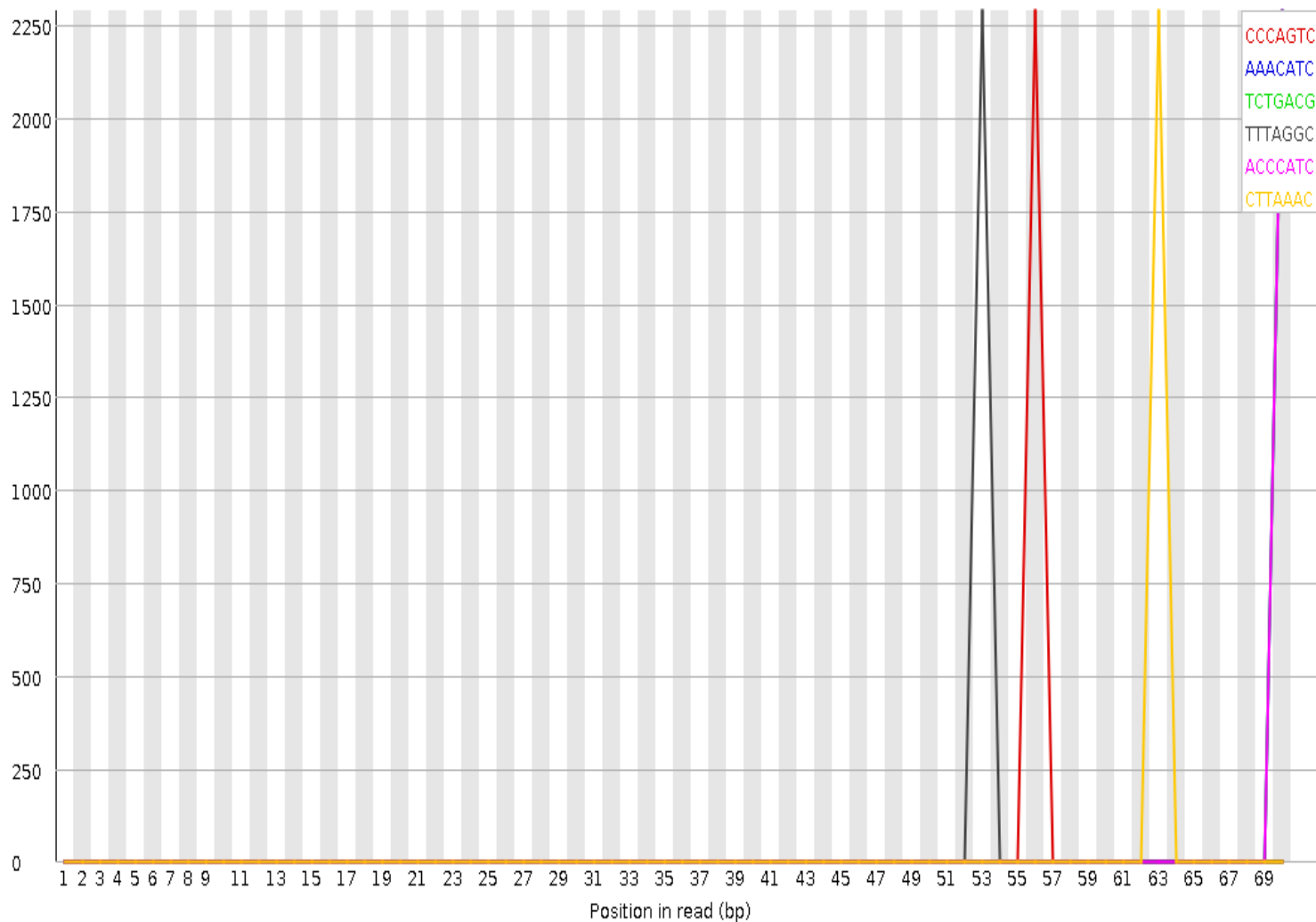
✅ Adapter Content

% Adapter



! Kmer Content

Log2 Obs/Exp



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCCAGTC	5	0.001434637	2287.5835	56
AACATC	5	0.001434637	2287.5835	70
TCTGACG	10	1.3932986E-6	2287.5835	70
TTTAGGC	5	0.001434637	2287.5835	53
ACCCATC	5	0.001434637	2287.5835	70
CTTAAAC	5	0.001434637	2287.5835	63
ATACCCA	5	0.001434637	2287.5835	68
AGTCCCT	5	0.001434637	2287.5835	59
TAGGCTG	5	0.001434637	2287.5835	55
ACATCTG	35	1.4551915E-11	1307.1906	70
TTGTCTC	10	0.0057371547	1143.7917	57
GTGTCTC	10	0.0057371547	1143.7917	59
GTCACTT	20	1.1140915E-5	1143.7917	61
CAGTCCC	10	0.0057371547	1143.7917	58
CTATAGC	10	0.0057371547	1143.7917	53

TAAACAT	10	0.0057371547	1143.7917	69
TAAACAC	10	0.0057371547	1143.7917	65
CACATCT	40	2.7284841E-11	1143.7917	69
TATACCC	10	0.0057371547	1143.7917	67
CCAGTCC	10	0.0057371547	1143.7917	57

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