













FastQC Report

Summary

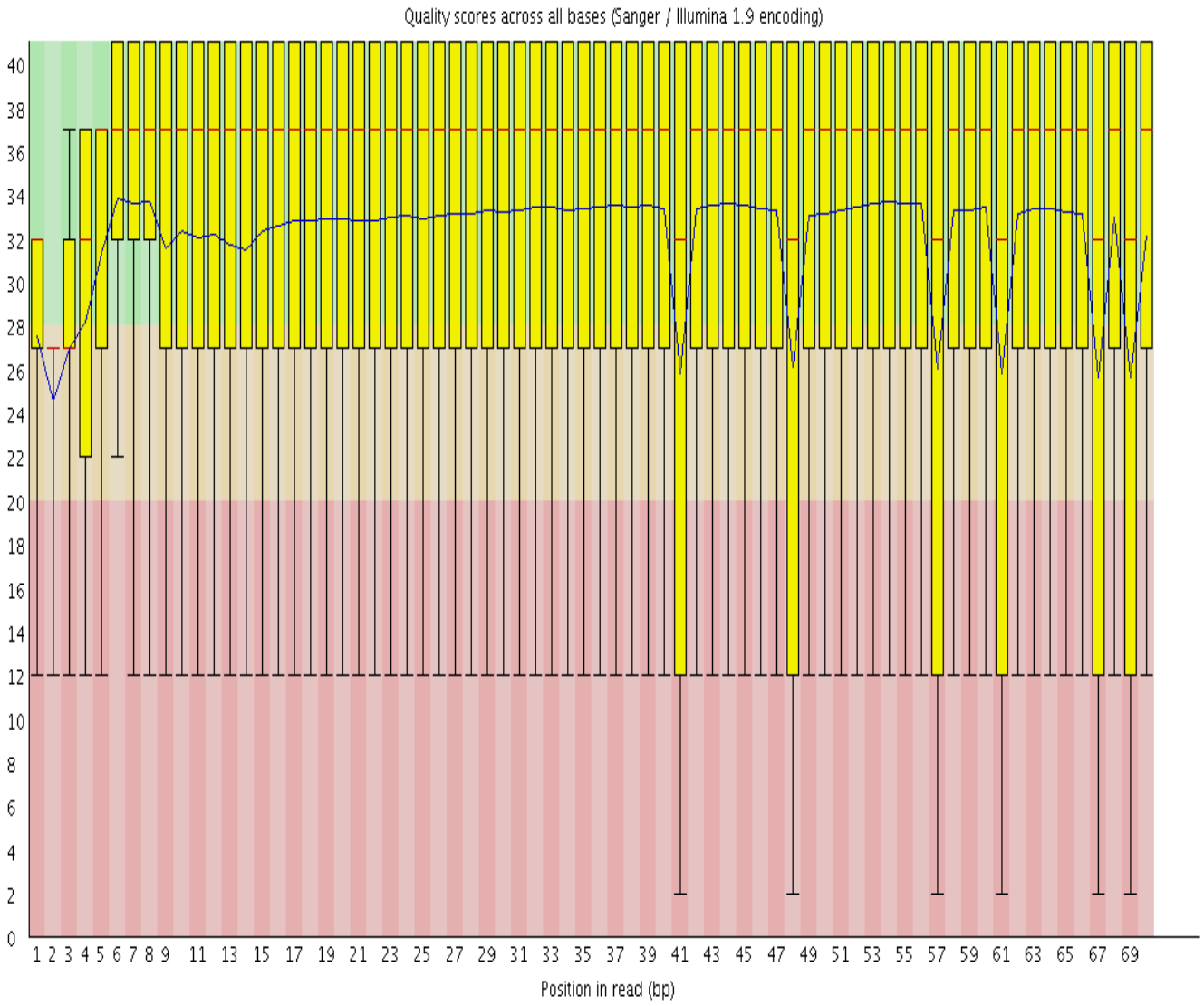
Thu 4 May 2017
AS-167496-LR-25274_R2.fastq.gz

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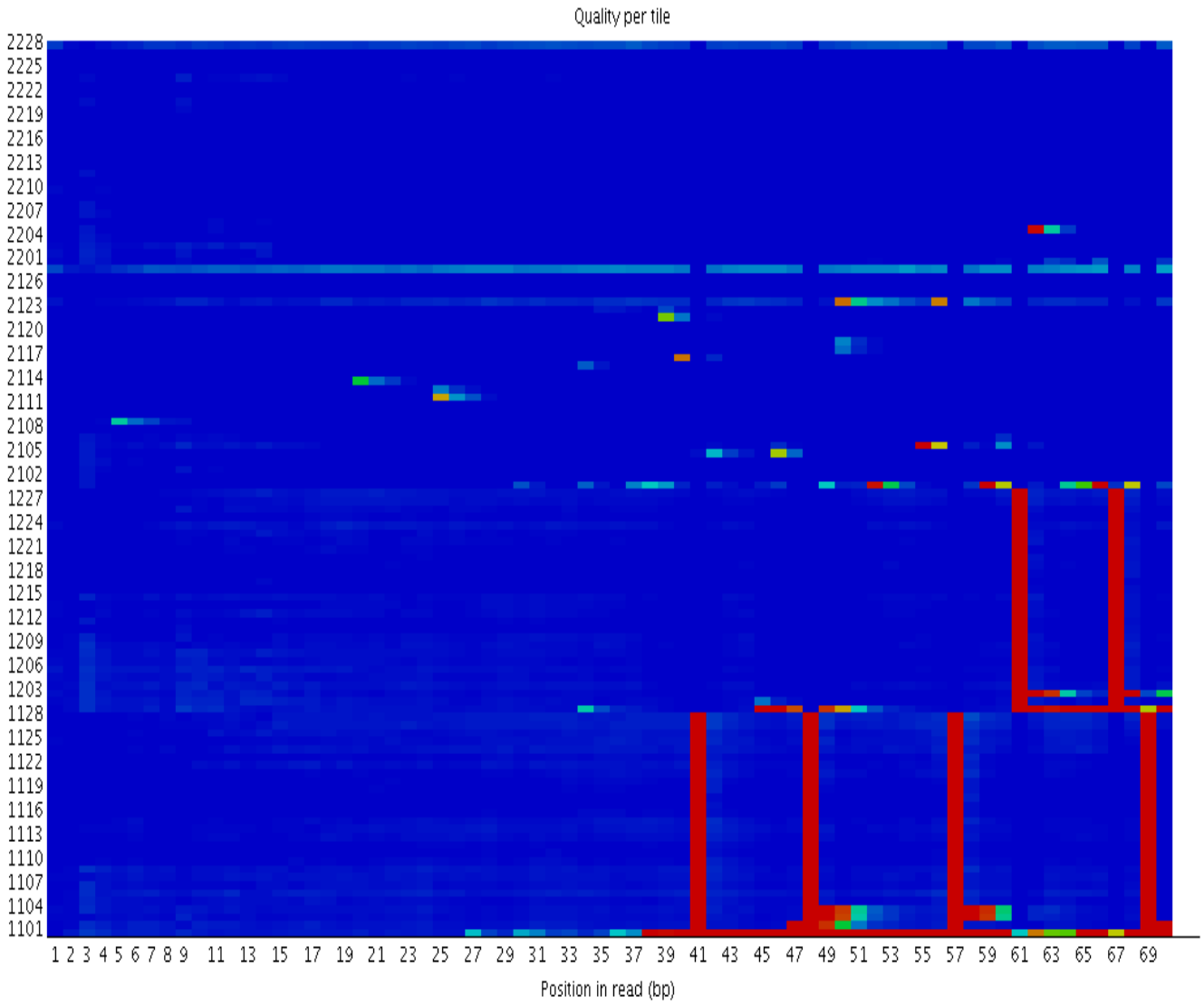
Basic Statistics

Measure	Value
Filename	AS-167496-LR-25274_R2.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	97735710
Sequences flagged as poor quality	0
Sequence length	70
%GC	51

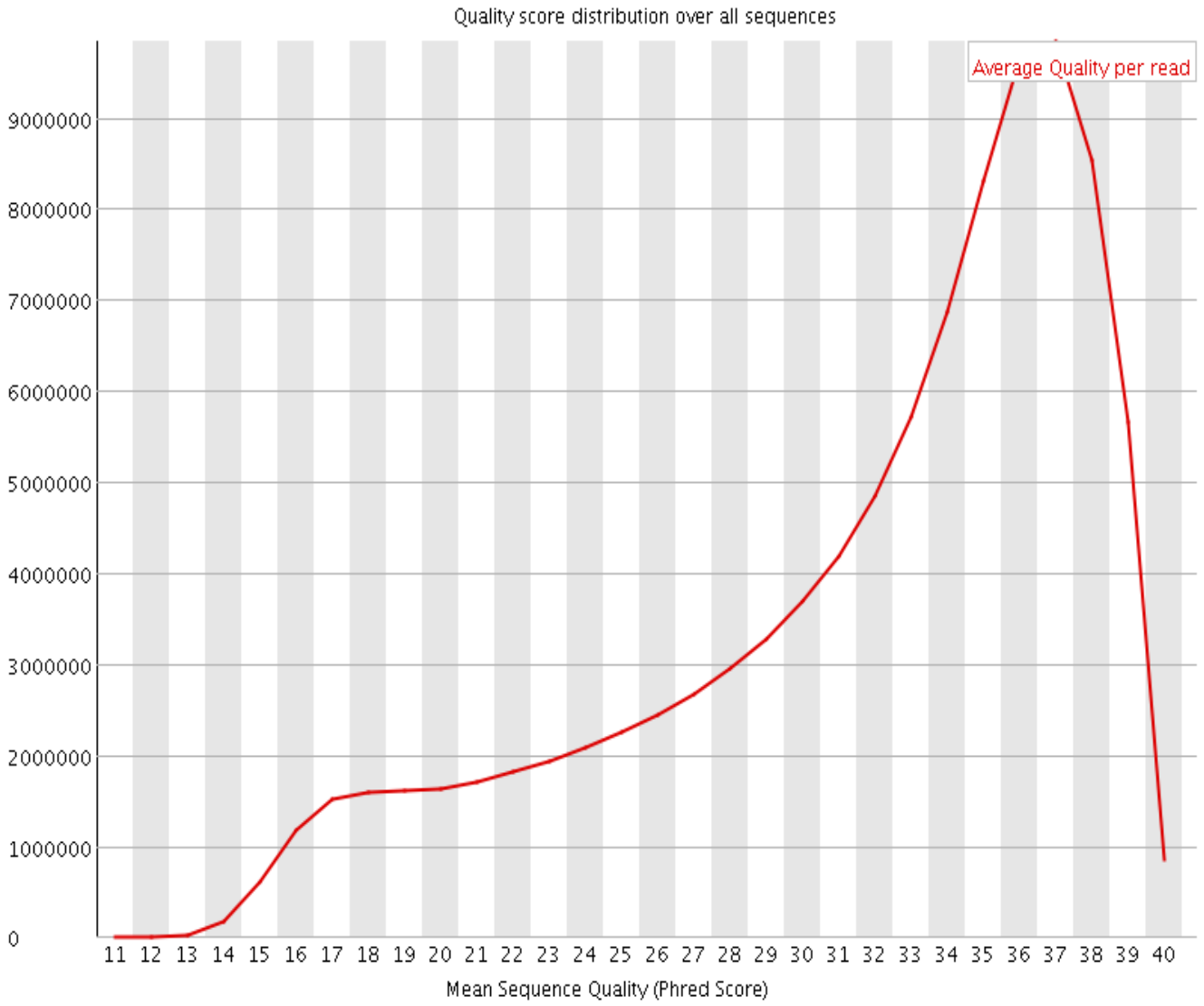
Per base sequence quality



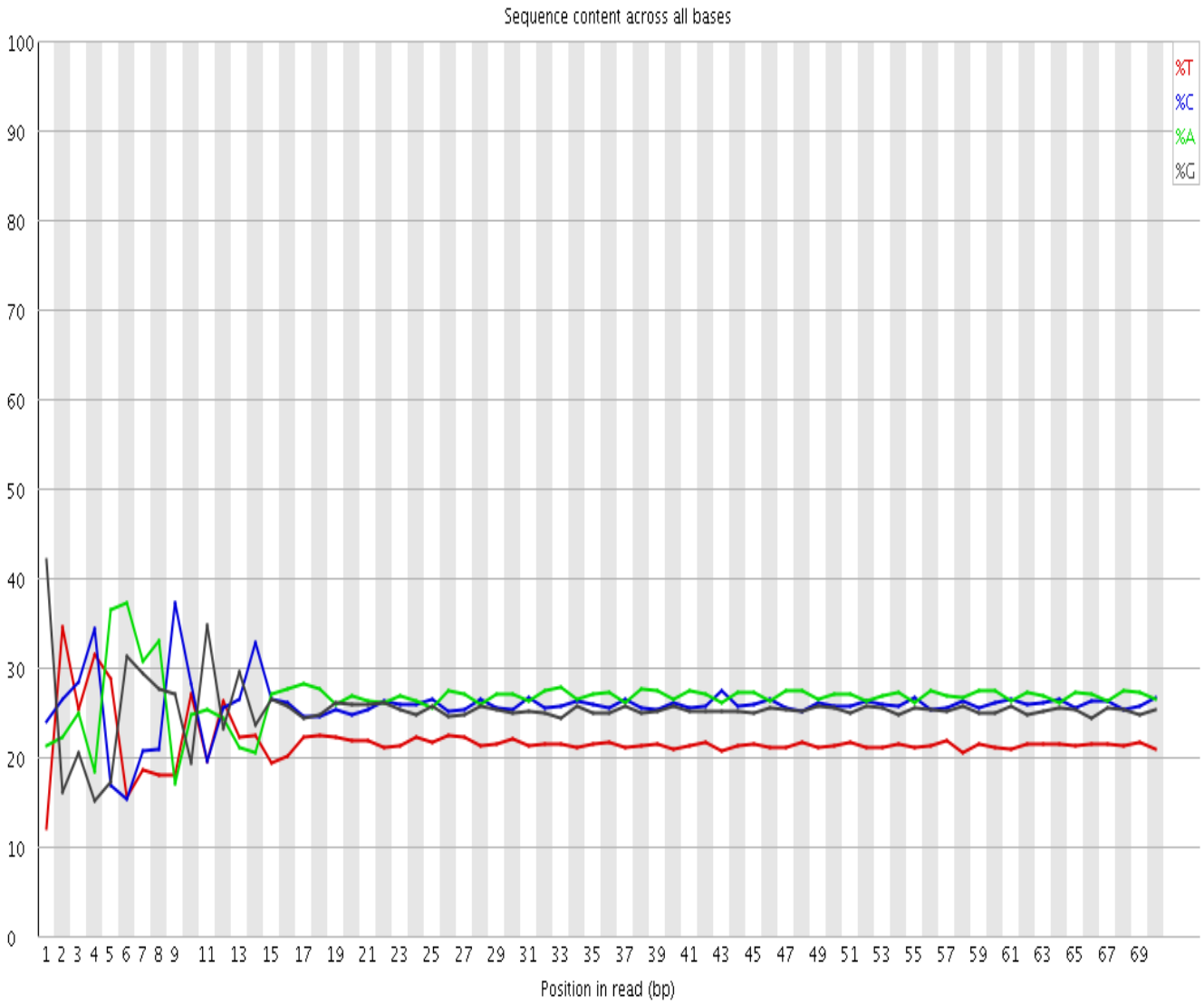
 **Per tile sequence quality**



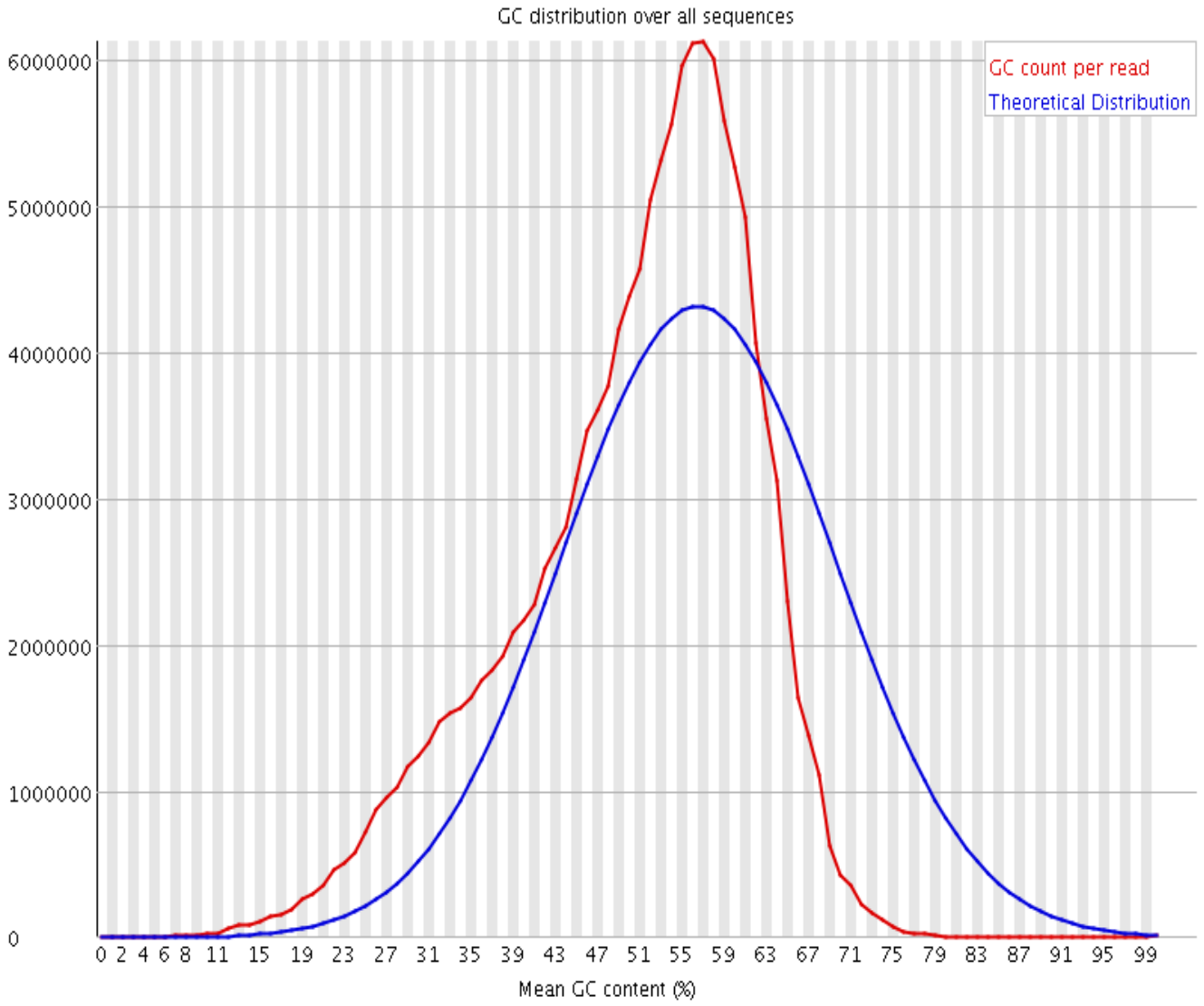
 **Per sequence quality scores**



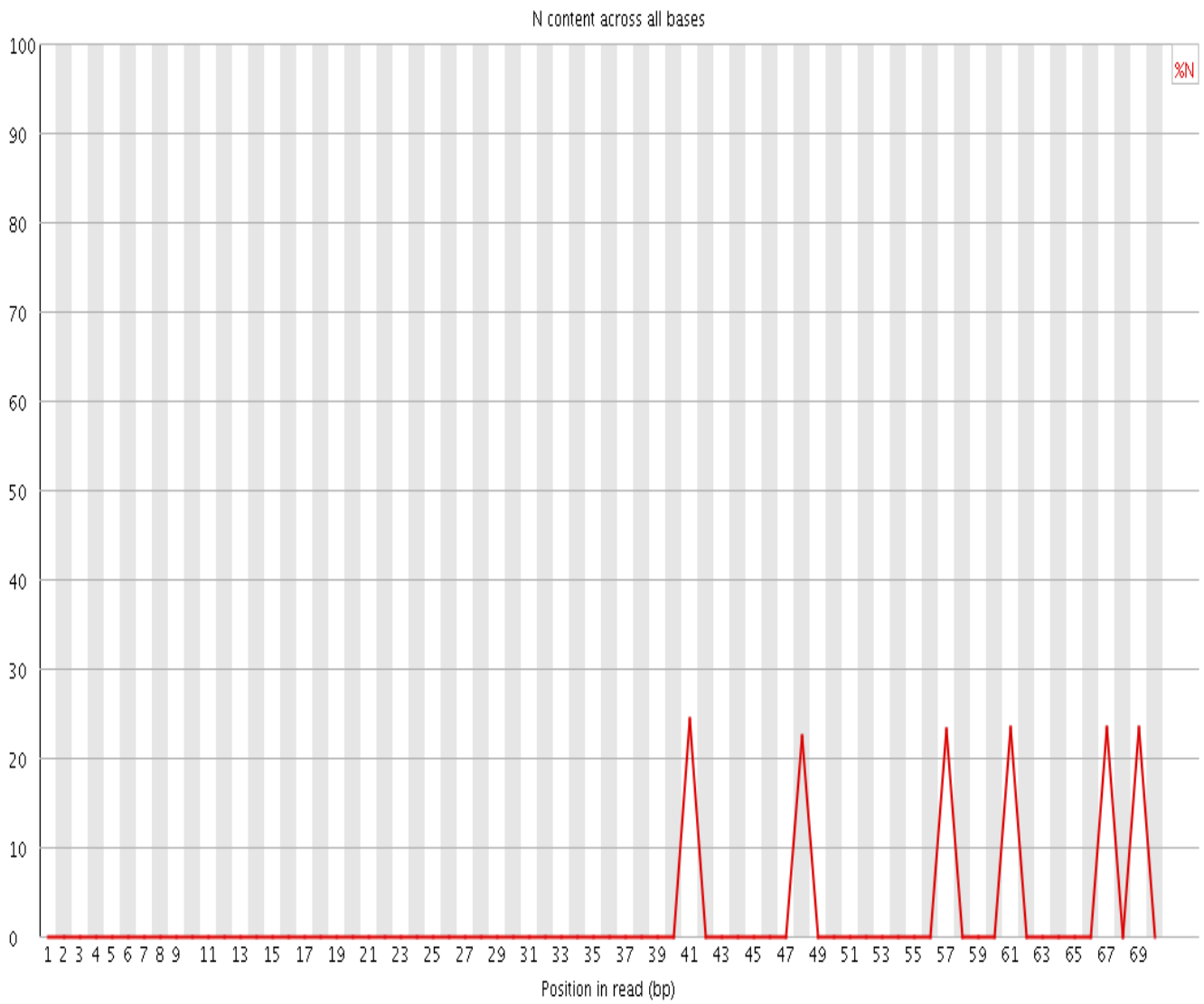
Per base sequence content



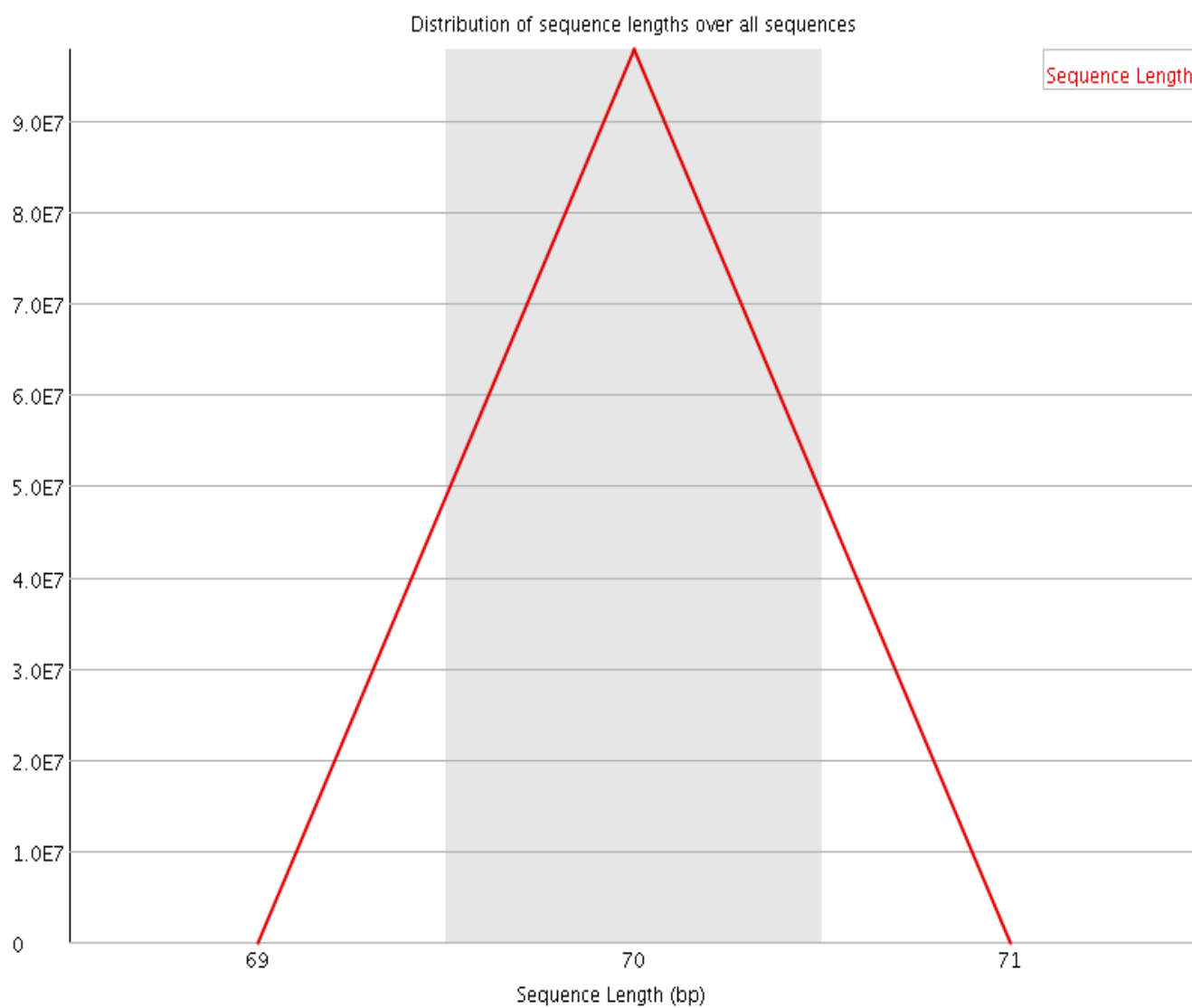
Per sequence GC content



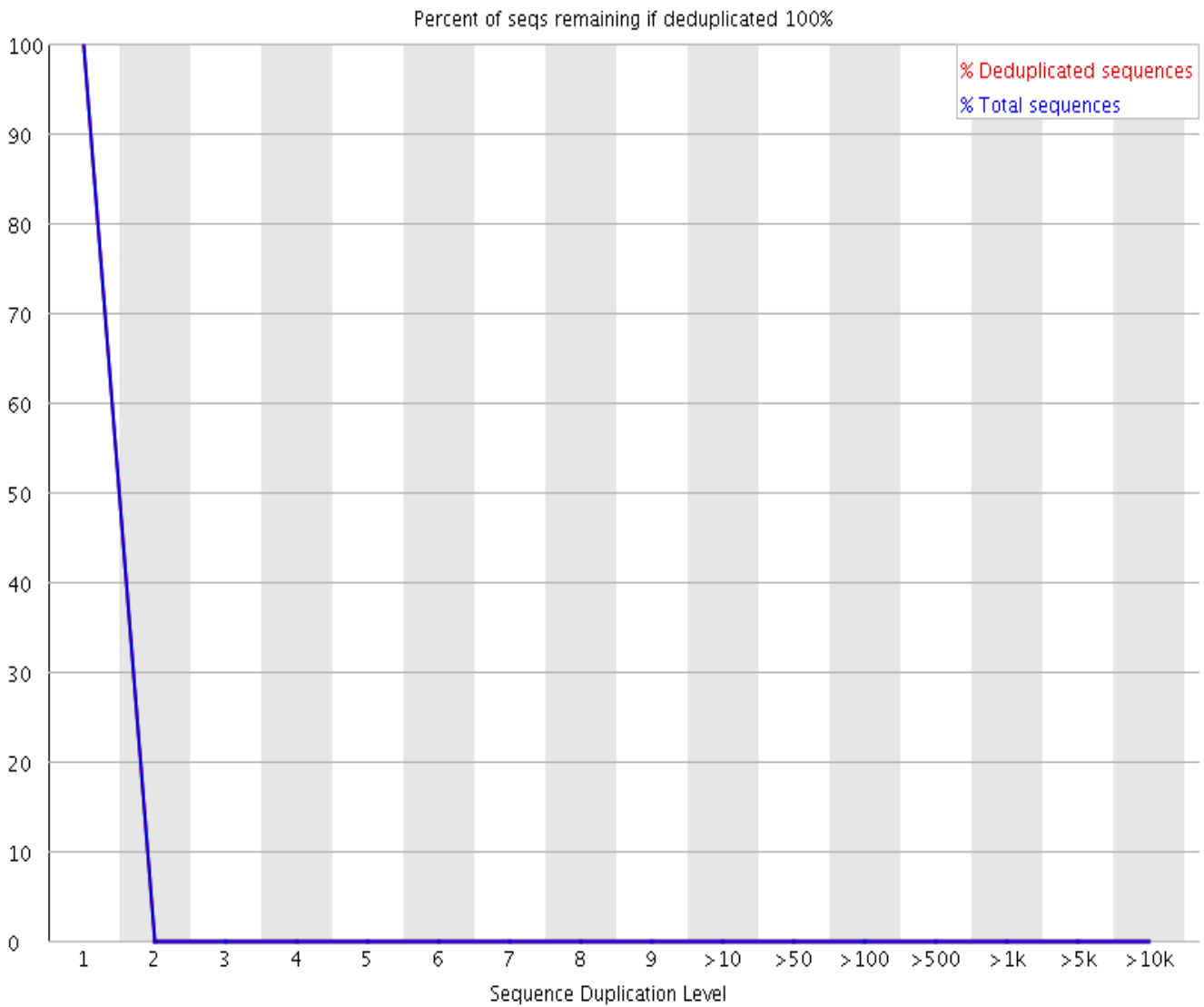
 **Per base N content**



Sequence Length Distribution

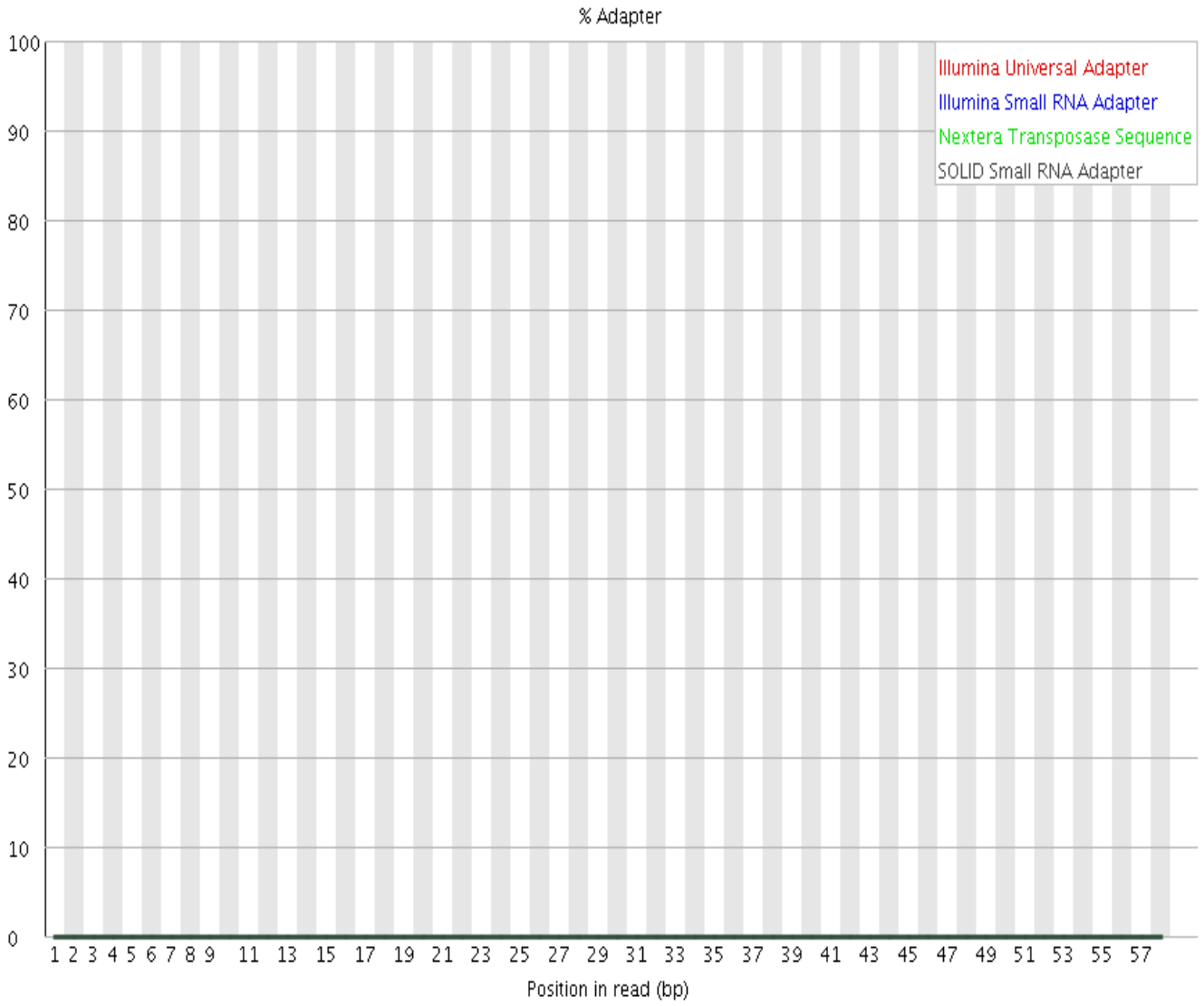


Sequence Duplication Levels

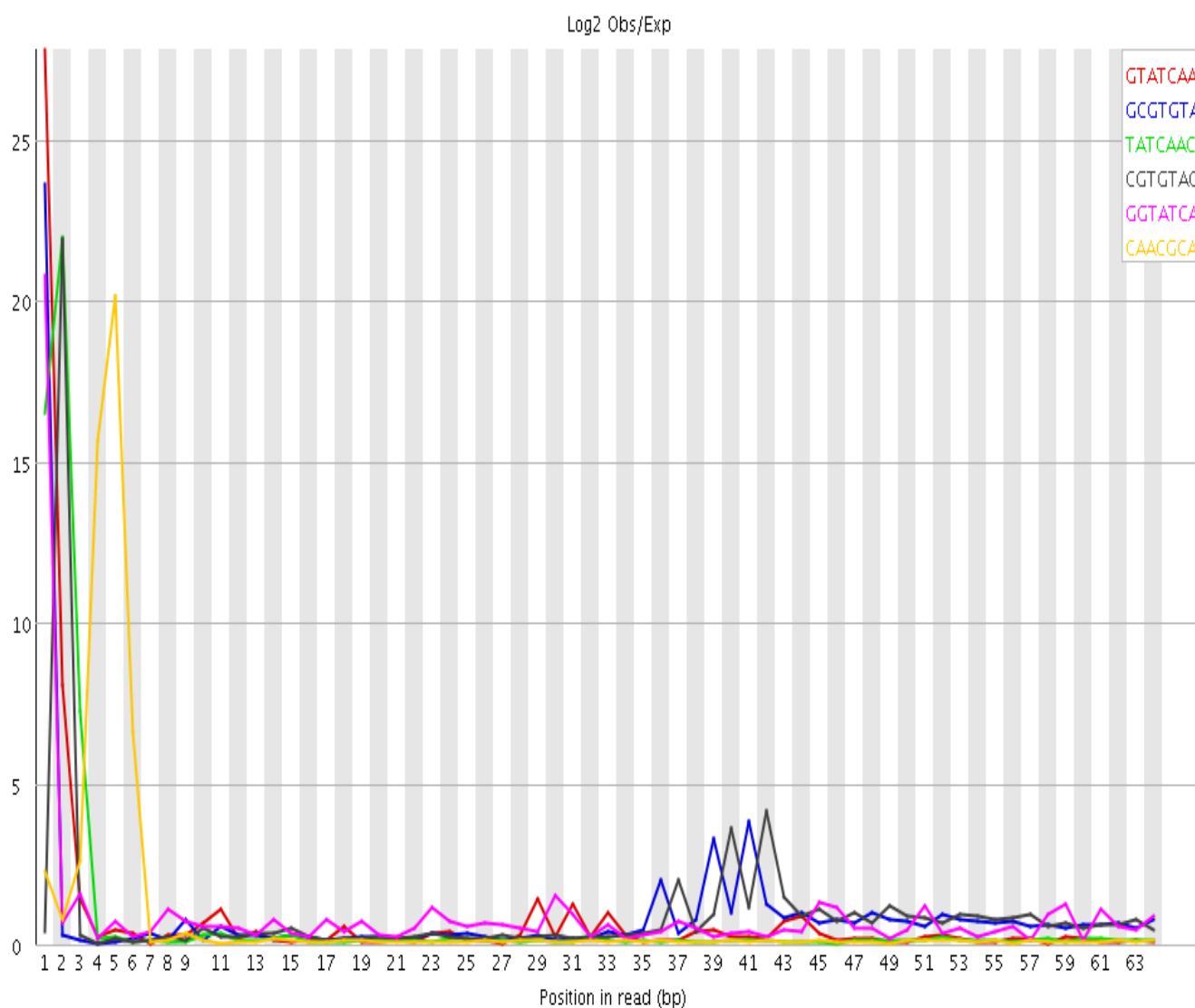


 **Overrepresented sequences**
 No overrepresented sequences

 **Adapter Content**



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTATCAA	133145	0.0	27.781467	1
GCGTGTA	40035	0.0	23.658514	1
TATCAAC	154640	0.0	22.000942	2
CGTGTAG	36395	0.0	21.912285	2
GGTATCA	52825	0.0	20.794472	1
CAACGCA	162910	0.0	20.188671	5
GTGTAGA	41405	0.0	19.885506	3
TCAACGC	167510	0.0	19.727934	4
GTAGATC	38850	0.0	19.27582	5
TAGATCT	38125	0.0	18.744879	6
AGATCTC	41175	0.0	17.472443	7
AACGCAG	190390	0.0	17.219028	6
CGTATCA	29505	0.0	16.407385	23
GCCGTAT	30595	0.0	15.611992	21

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	199350	0.0	15.521938	9
AGAGTGA	187765	0.0	15.452279	11
ATCAACG	220210	0.0	15.3771515	3
CGCAGAG	212995	0.0	15.163353	8
CAGAGTG	199095	0.0	14.98393	10
TAGTGTC	20960	0.0	14.411579	37

Produced by [FastQC](#) (version 0.11.4)