FastQC Report

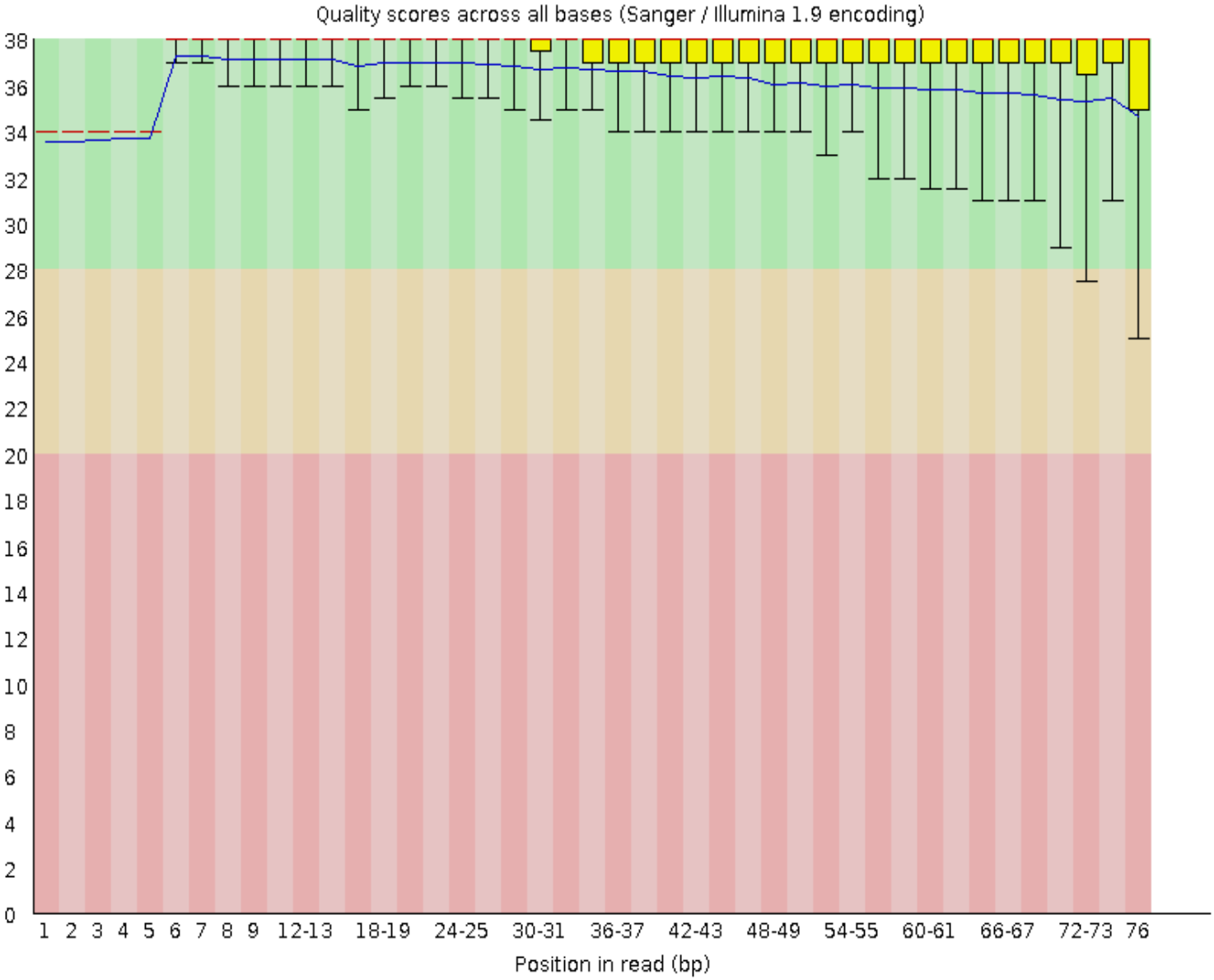
Thu 21 May 2015
skewer_42_dupRemoved_R1.fastq

Summary

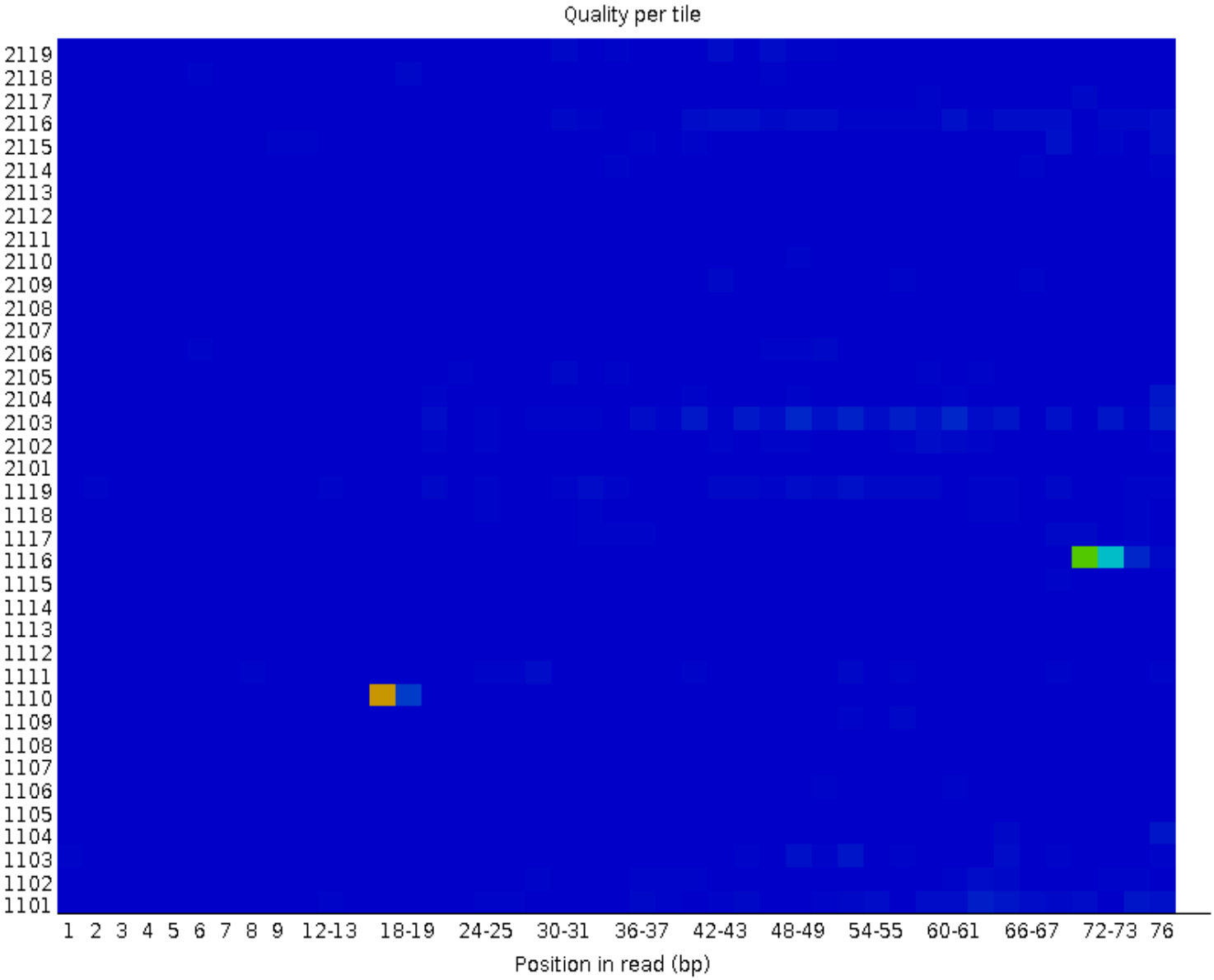
Basic Statistics

Measure	Value
Filename	skewer_42_dupRemoved_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	657883
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

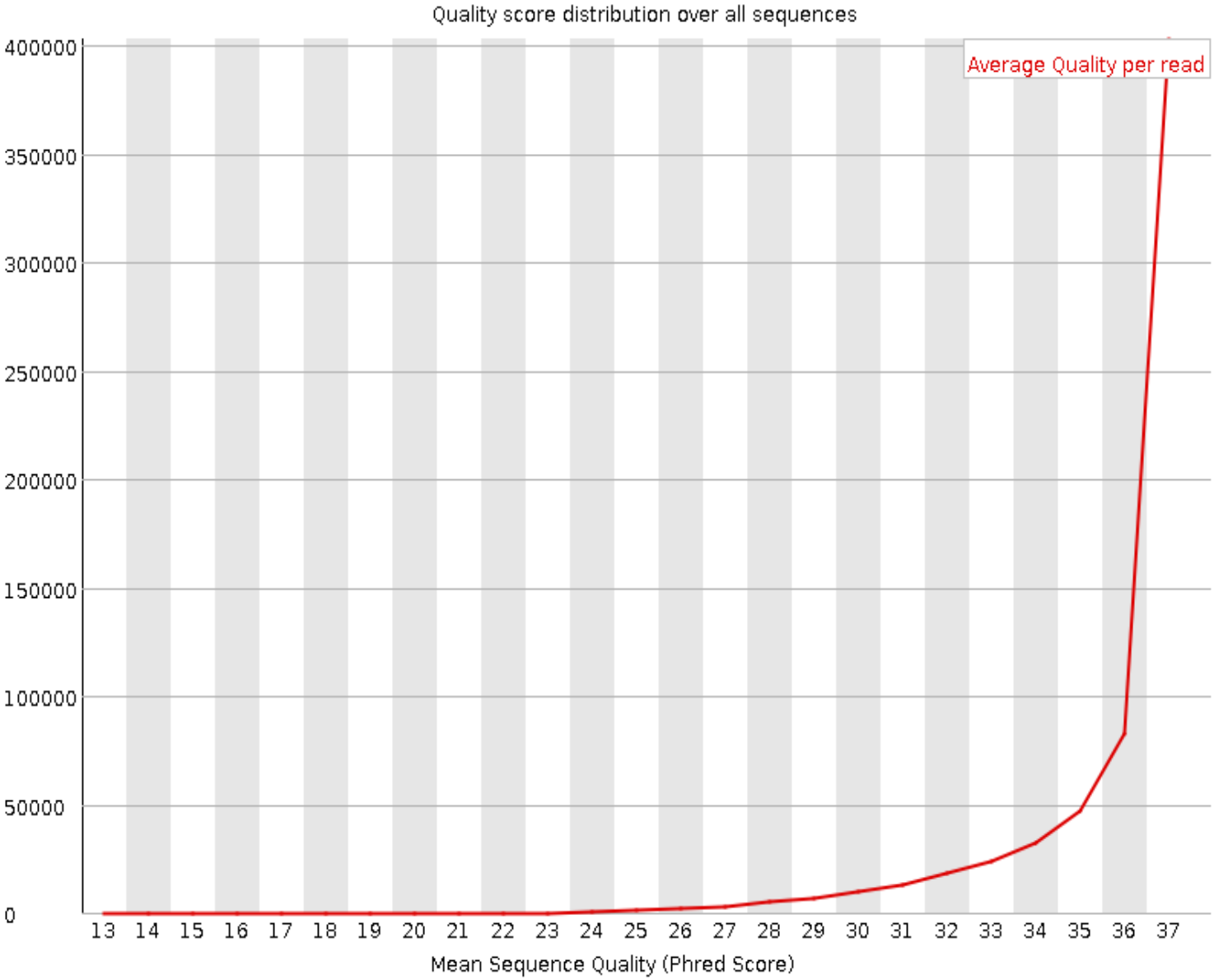
Per base sequence quality



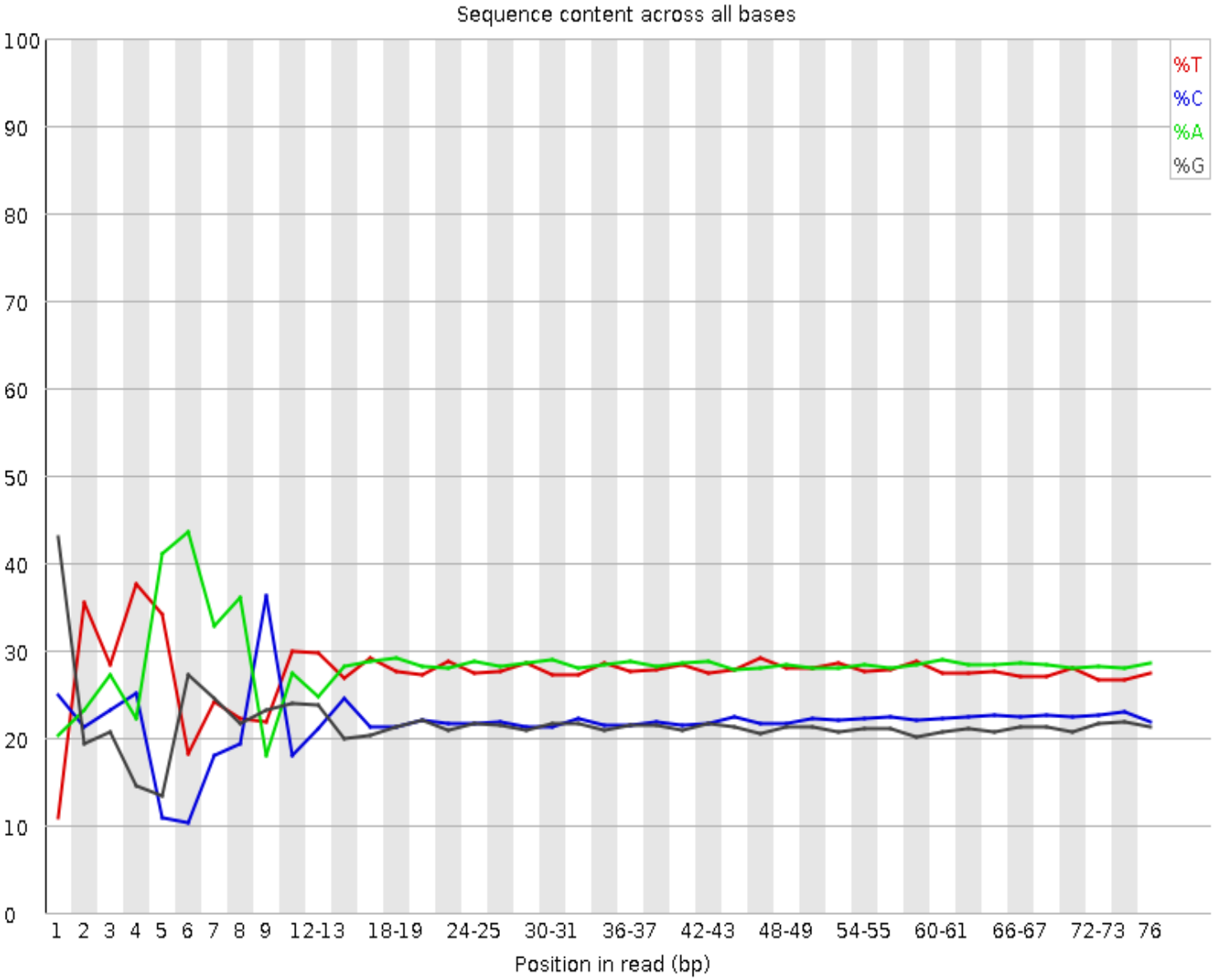
Per tile sequence quality



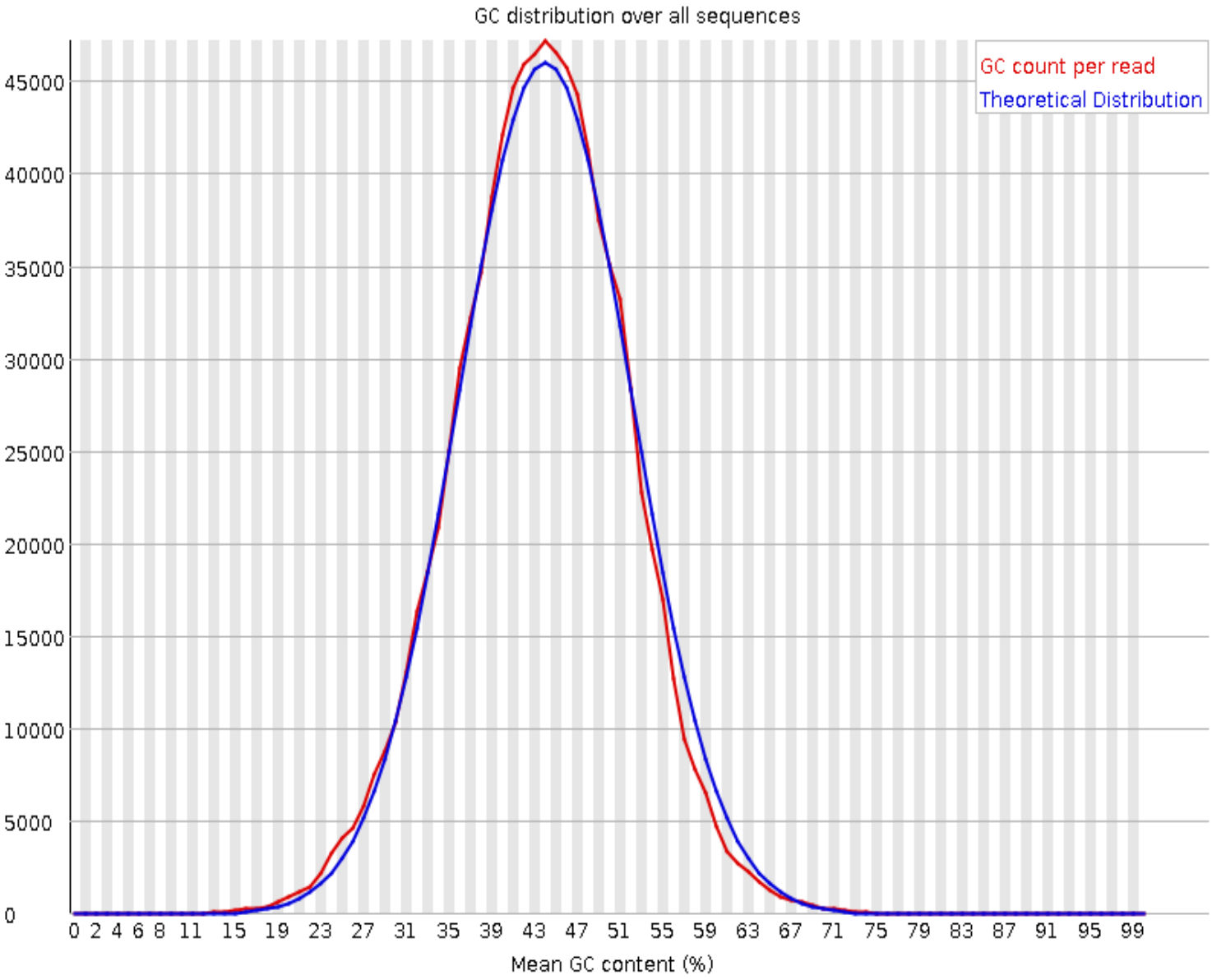
Per sequence quality scores



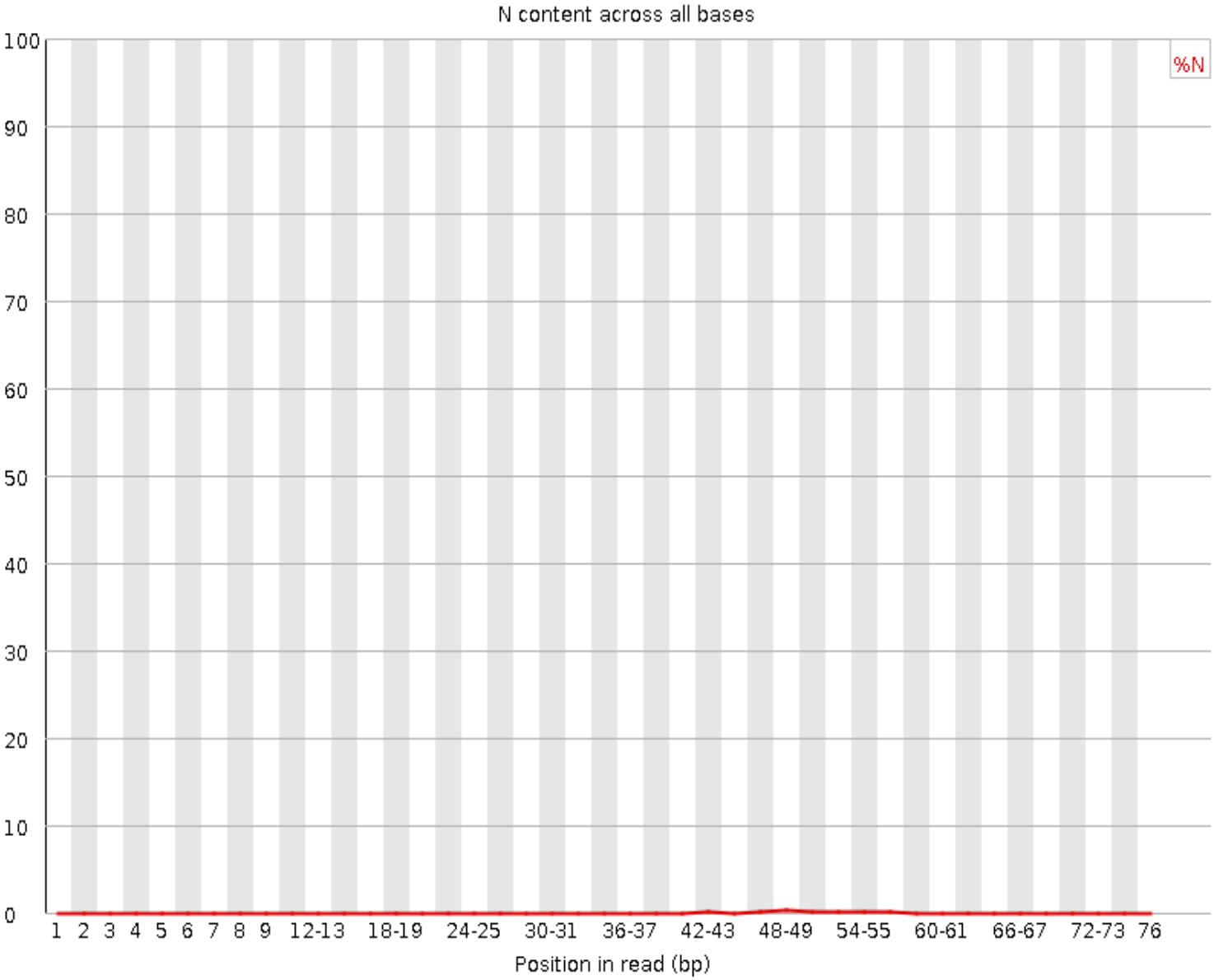
Per base sequence content



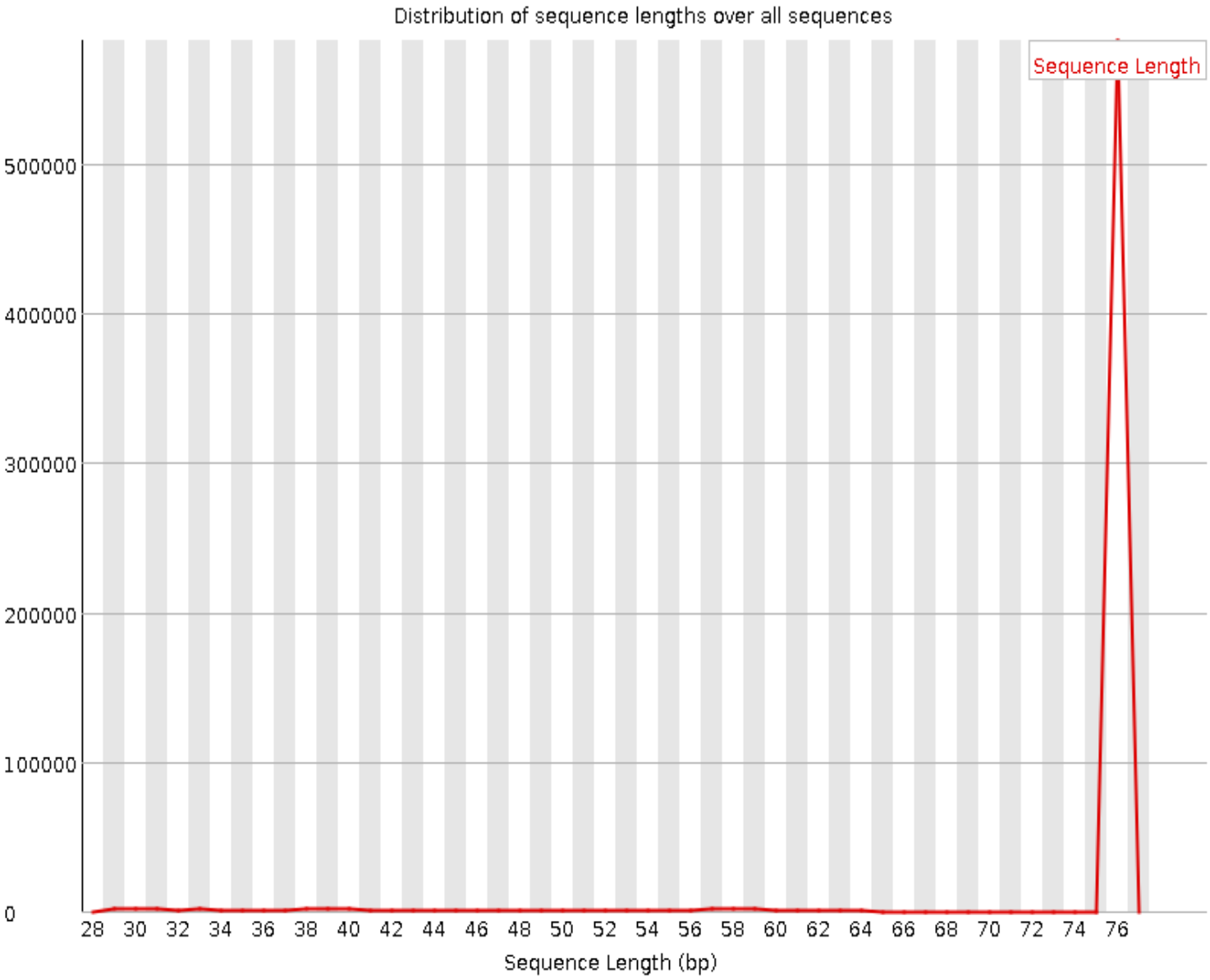
Per sequence GC content



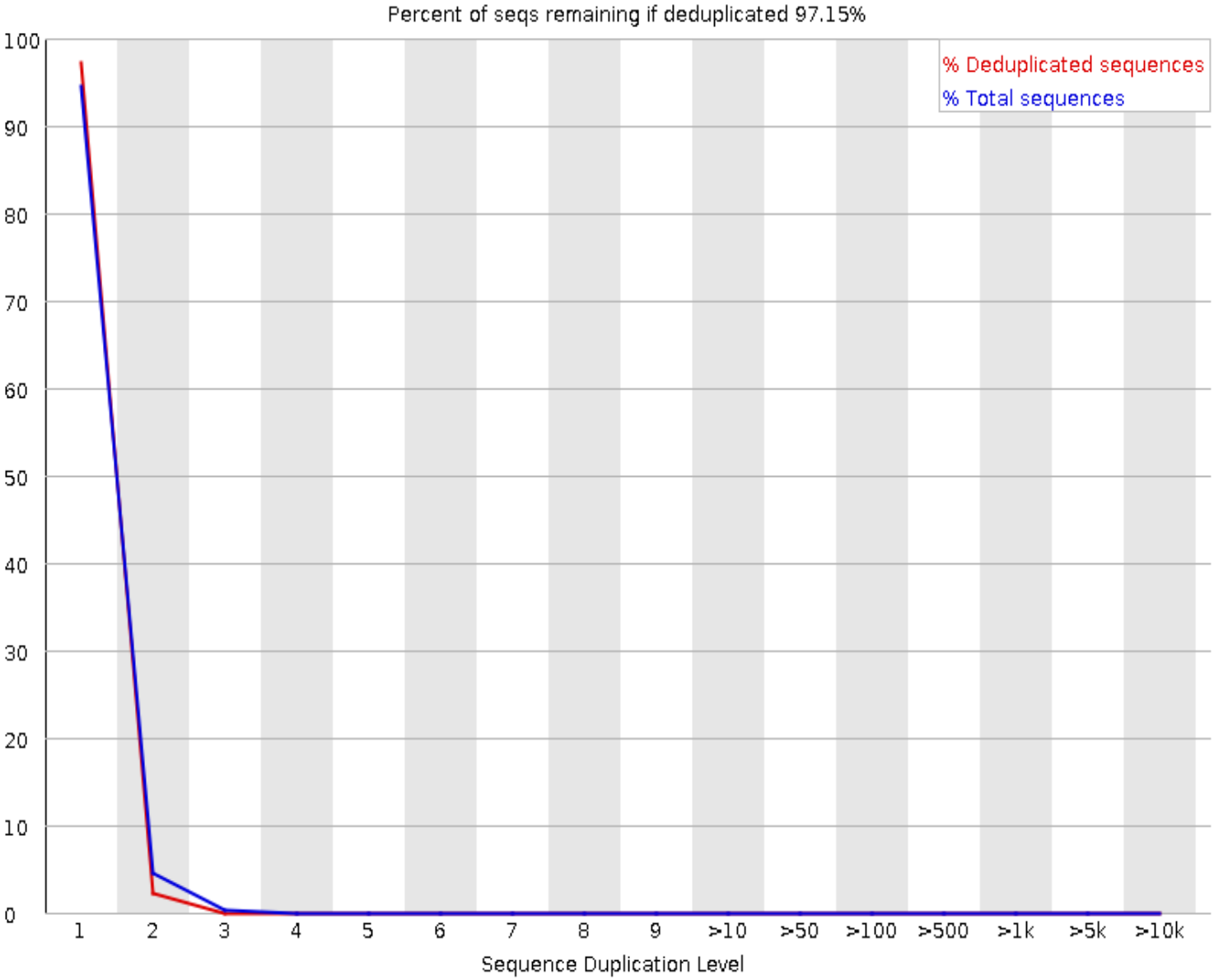
Per base N content



Sequence Length Distribution



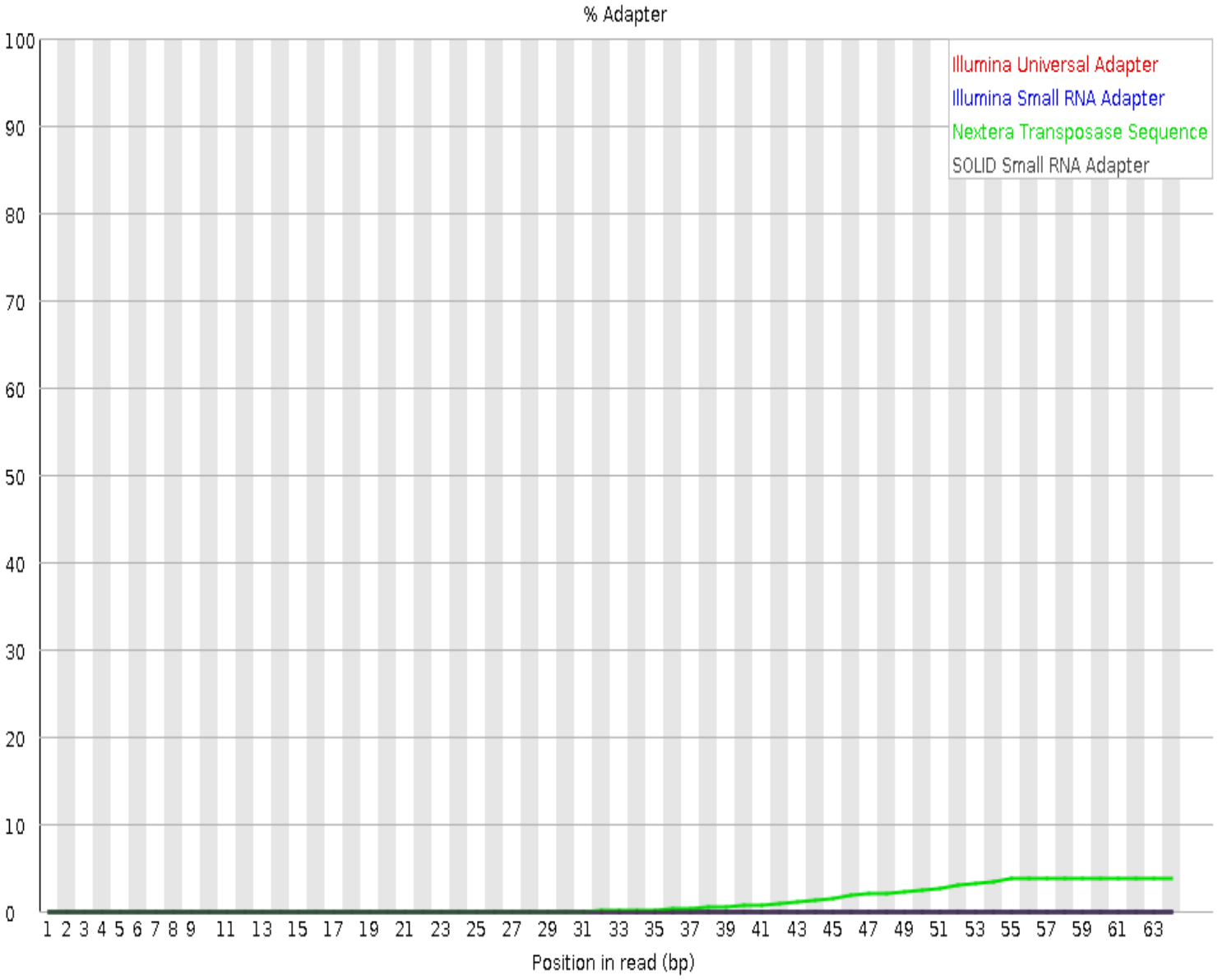
Sequence Duplication Levels



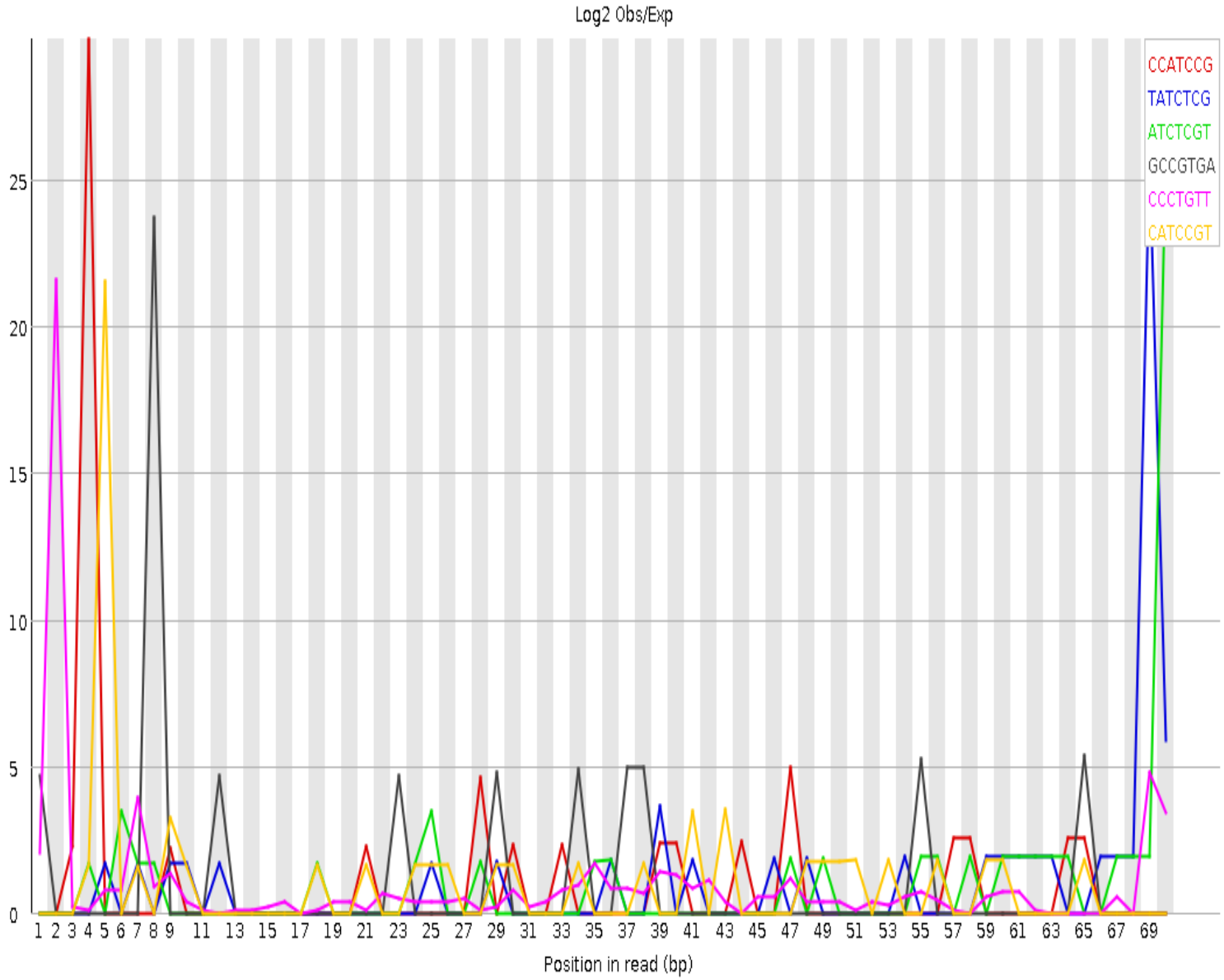
Overrepresented sequences

No overrepresented sequences

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCATCCG	145	1.8189894E-12	29.75243	4
TATCTCG	190	7.2759576E-12	25.77622	69
ATCTCGT	190	7.2759576E-12	25.773996	70
GCCGTGA	70	0.0016731899	23.700256	8
CCCTGTT	2410	0.0	21.618708	2
CATCCGT	200	8.913048E-11	21.568874	5
ATCCGTC	200	8.913048E-11	21.567234	6
CCTGTTA	2435	0.0	21.124178	3
TAGGTCG	110	4.4070548E-5	21.116379	5
ATTCCTA	190	1.0950316E-9	20.956017	14
ATCCCTA	2495	0.0	20.613049	9

GGGATAA	3260	0.0	20.570555	1
ACCCTGT	2560	0.0	20.359724	1
CTGTTAT	2640	0.0	19.609556	4
AGGGTAA	3380	0.0	19.24068	9
CAGGGTA	3460	0.0	18.987604	8
ATAACAG	3520	0.0	18.94962	4
TCCCTAG	825	0.0	18.90275	10
TATCCCT	2790	0.0	18.55246	8
GGGTAAT	3300	0.0	18.400019	10

Produced by FastQC (version 0.11.3)