













## Summary

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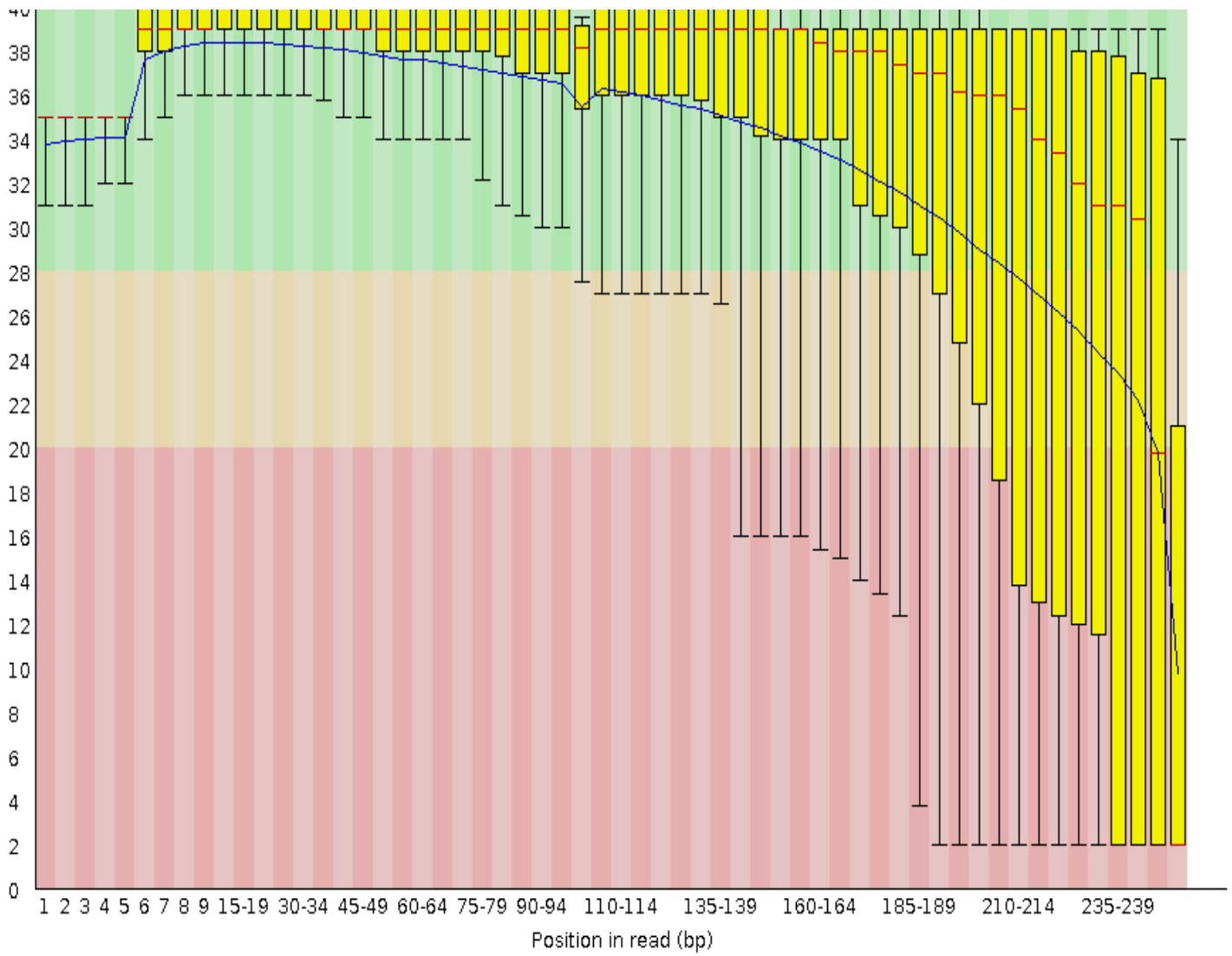
## Basic Statistics

Measure	Value
Filename	BS_MK_noAdap_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	158375348
Sequences flagged as poor quality	0
Sequence length	18-250
%GC	41

## Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

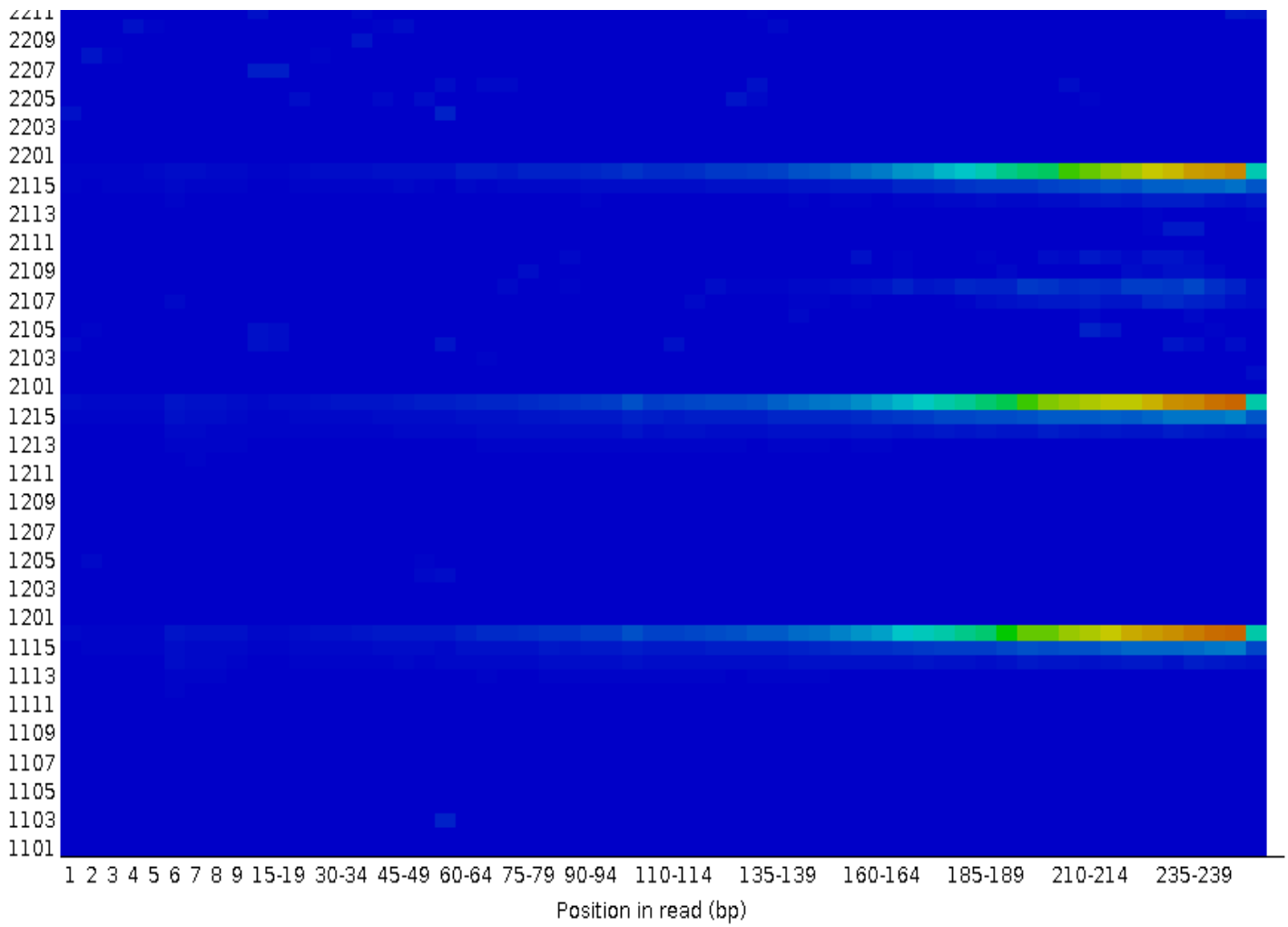




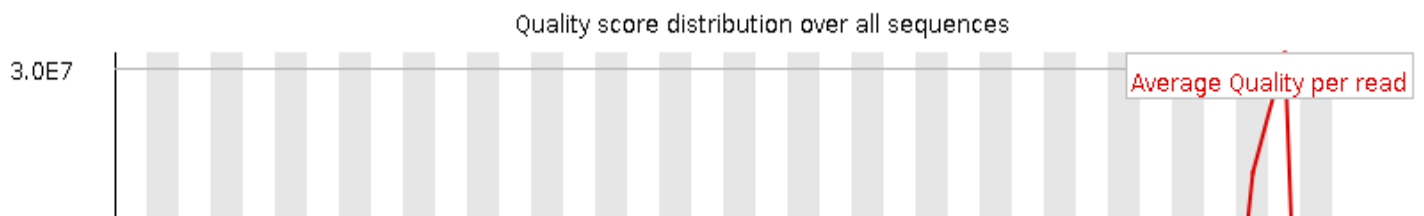
**! Per tile sequence quality**

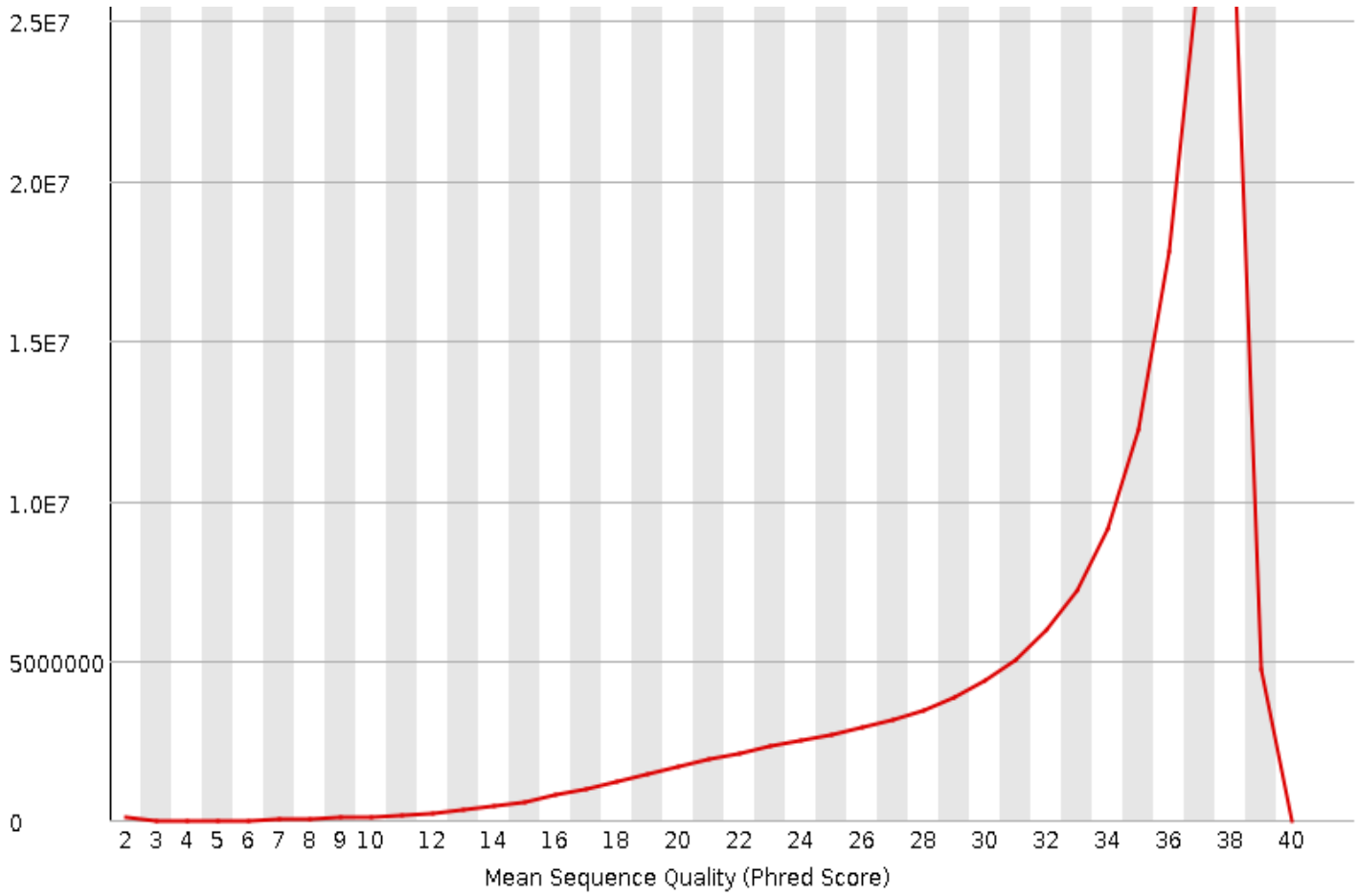
Quality per tile



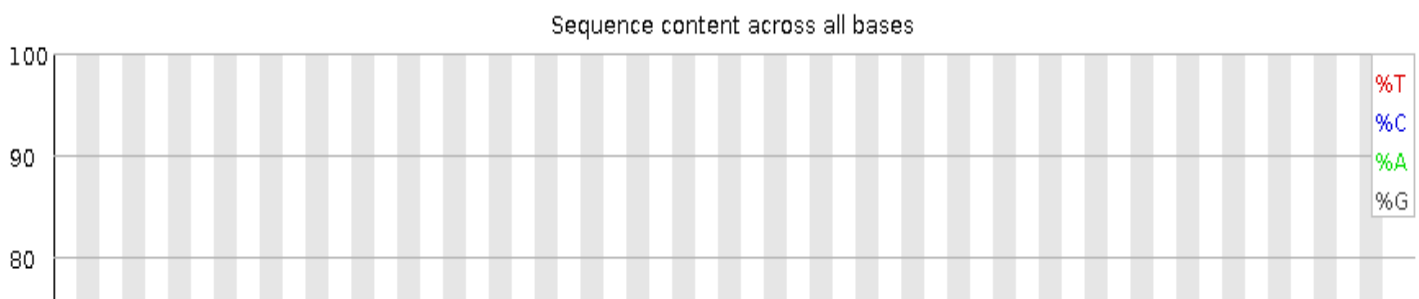


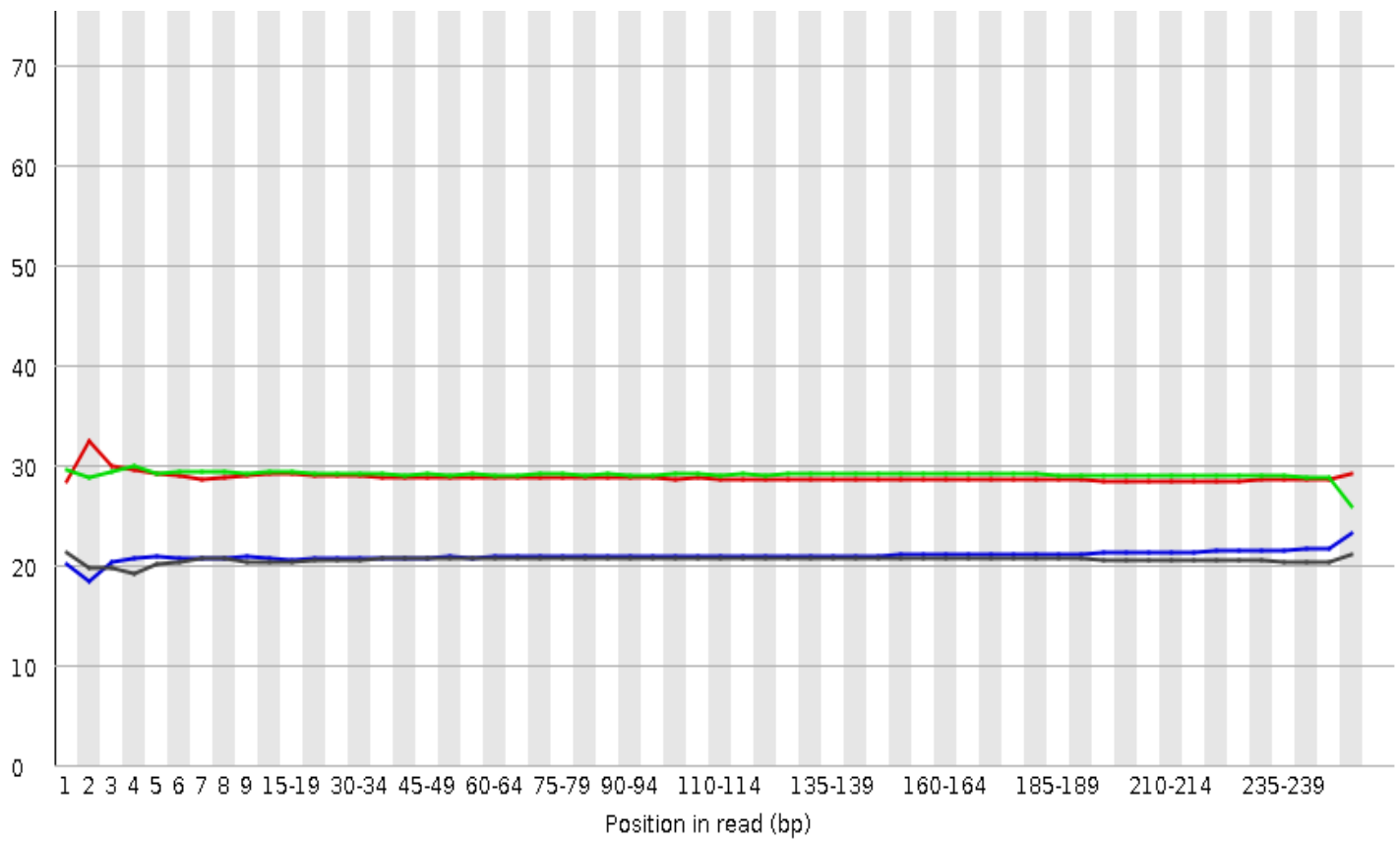
 **Per sequence quality scores**



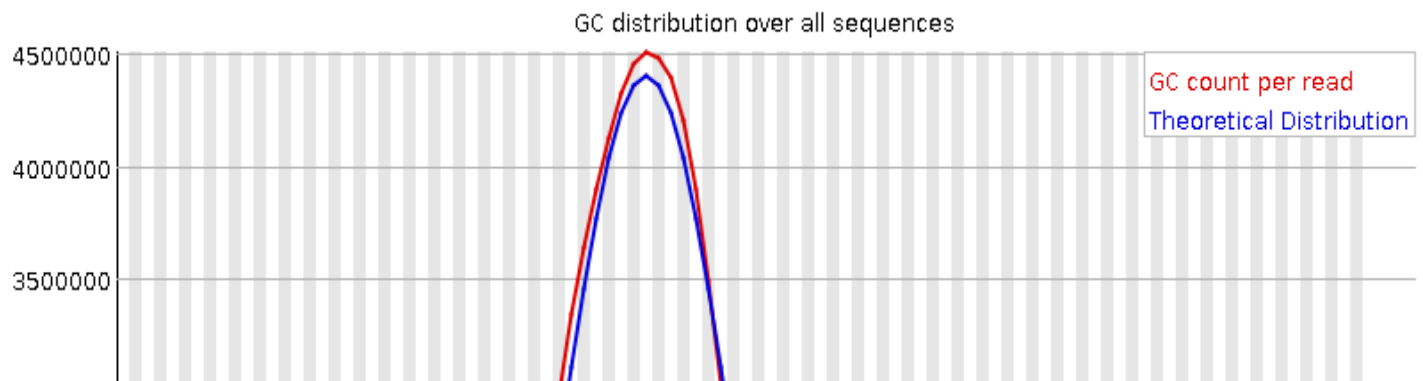


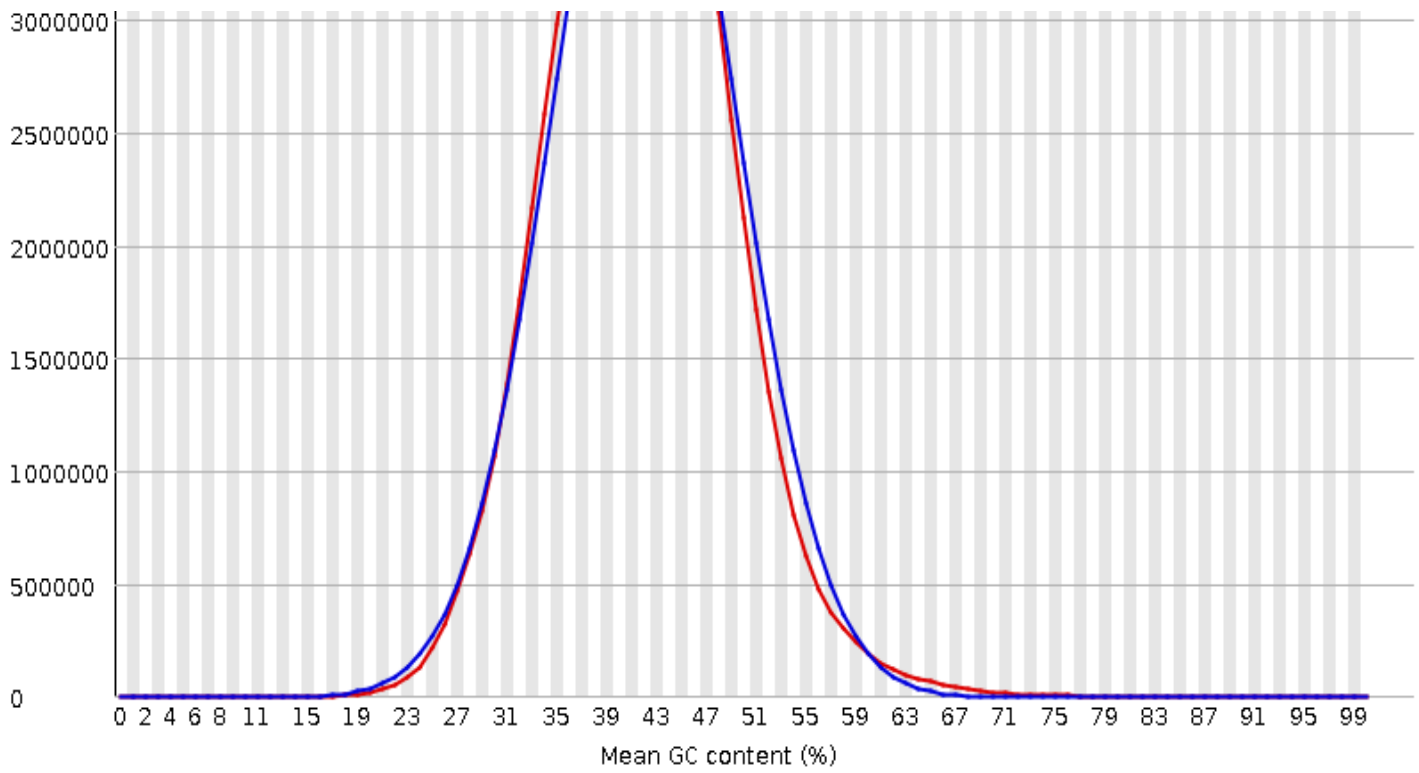
**! Per base sequence content**



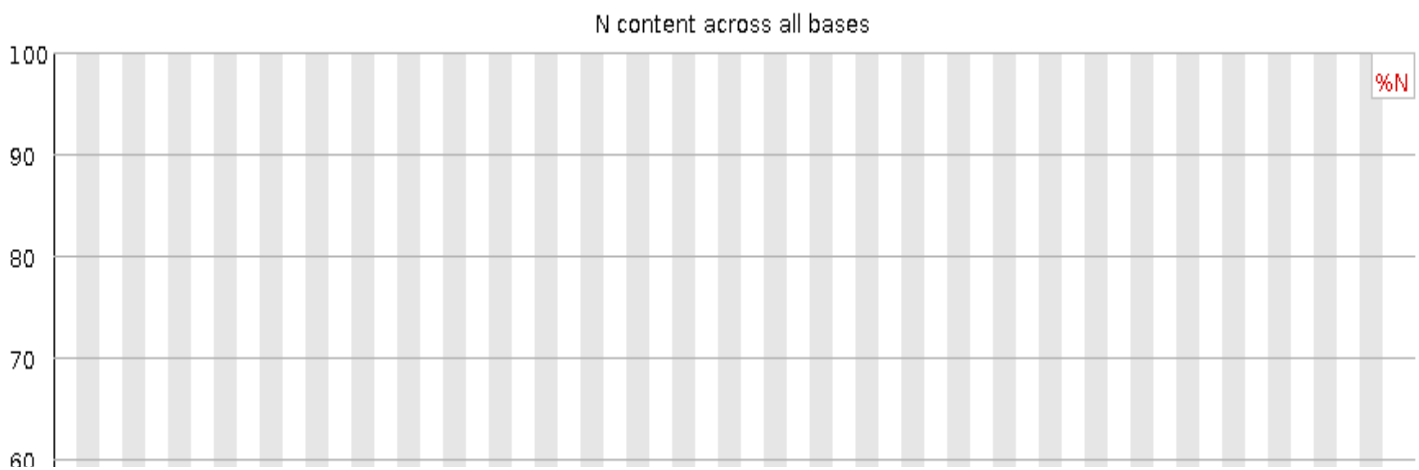


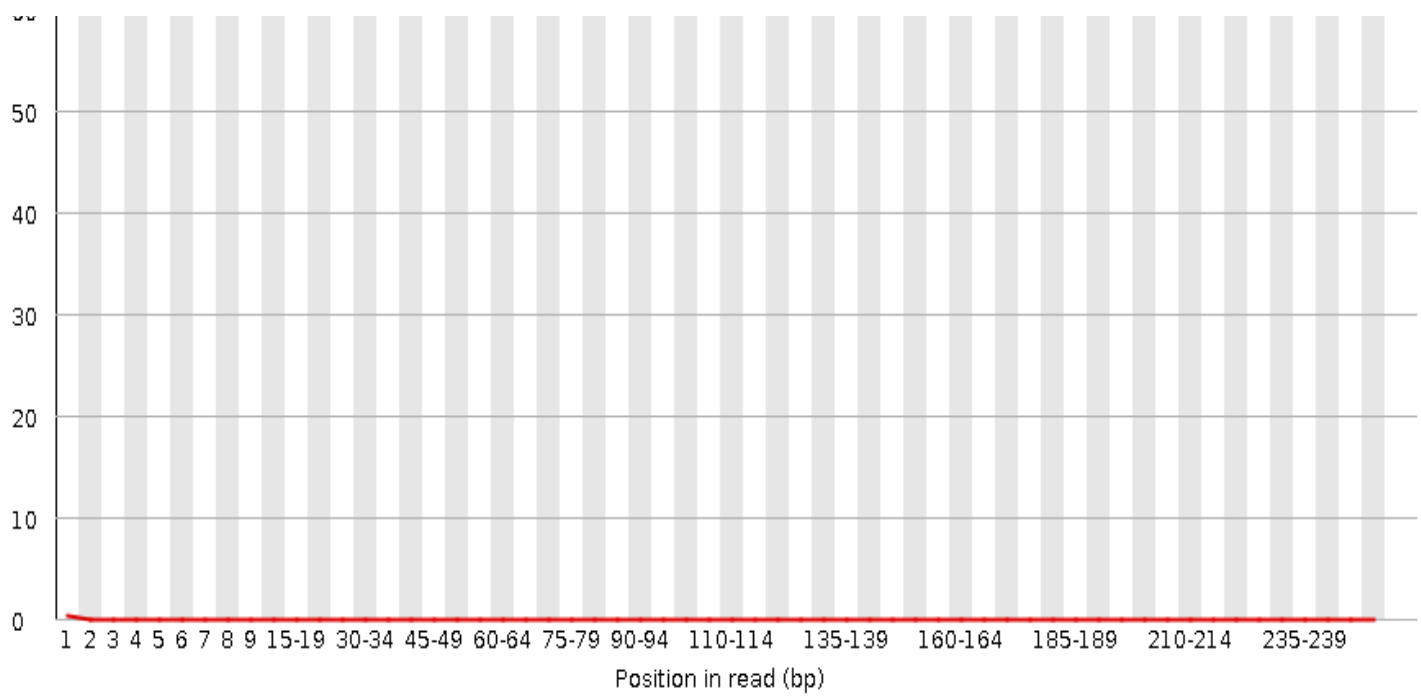
 **Per sequence GC content**



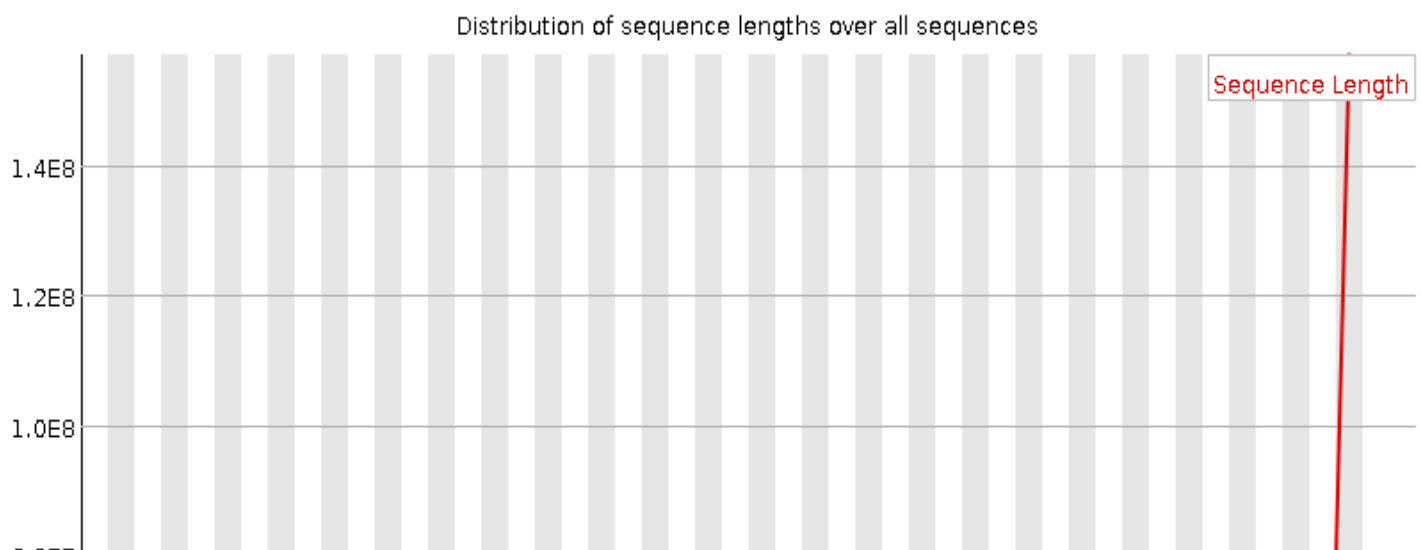


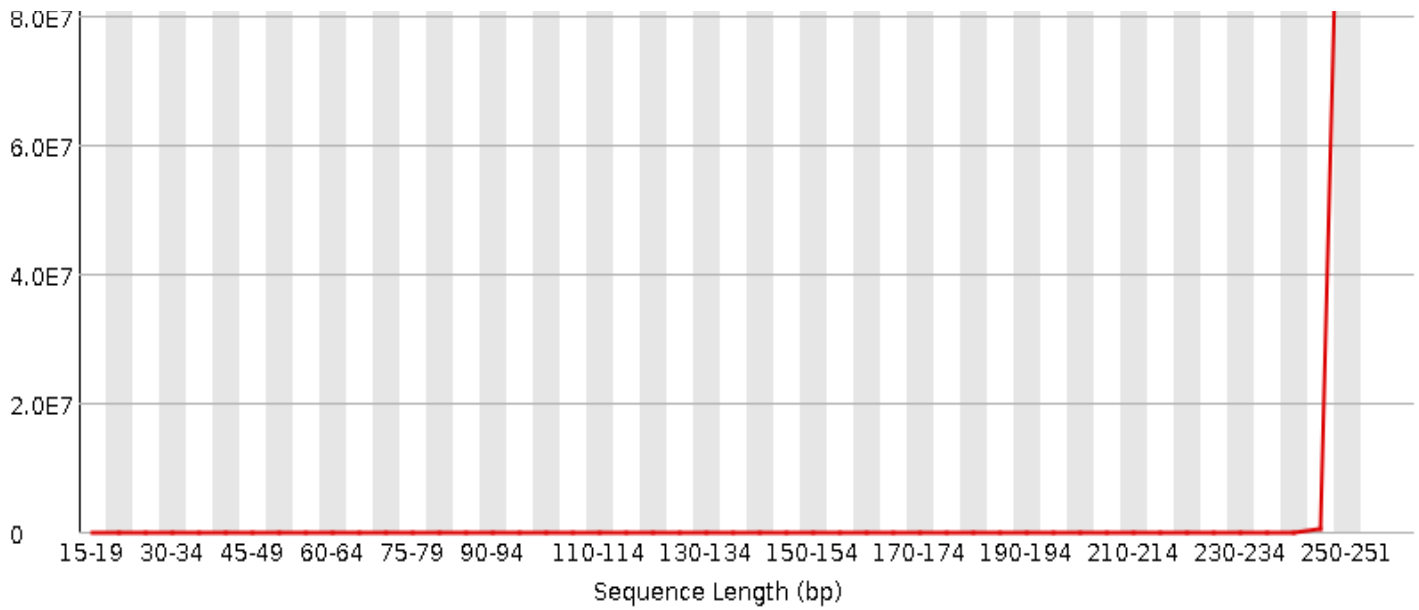
 **Per base N content**



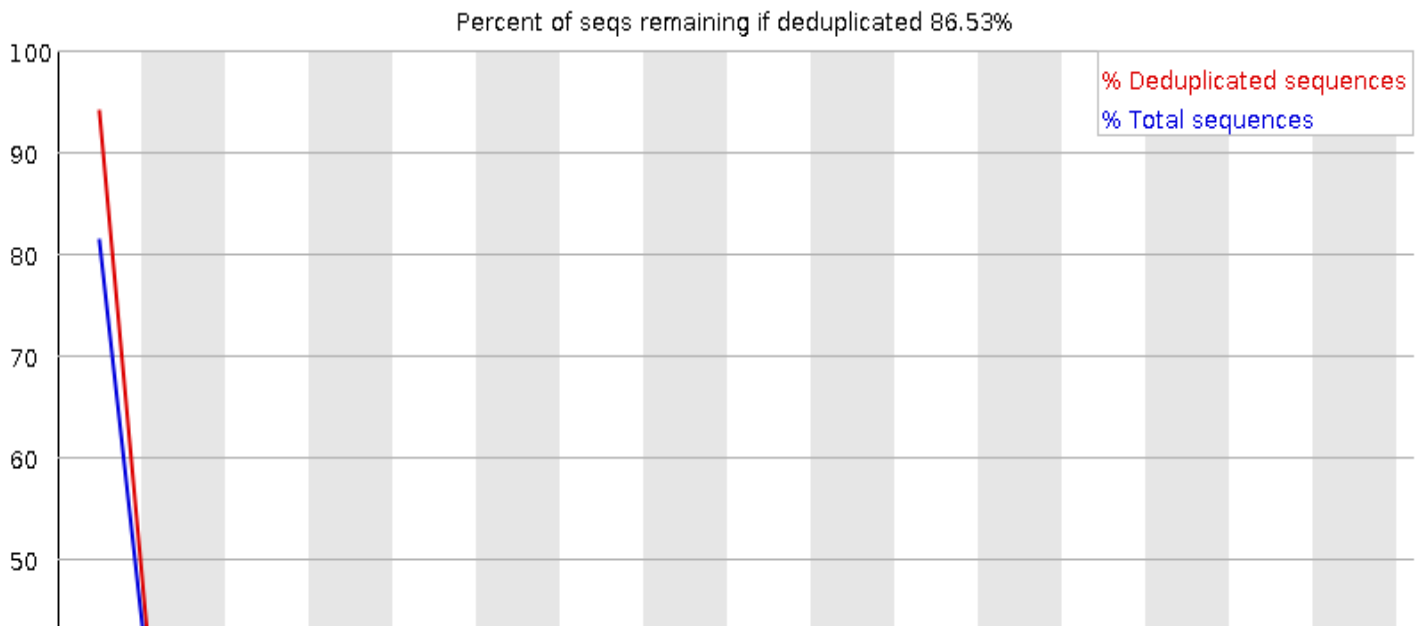


## ! Sequence Length Distribution

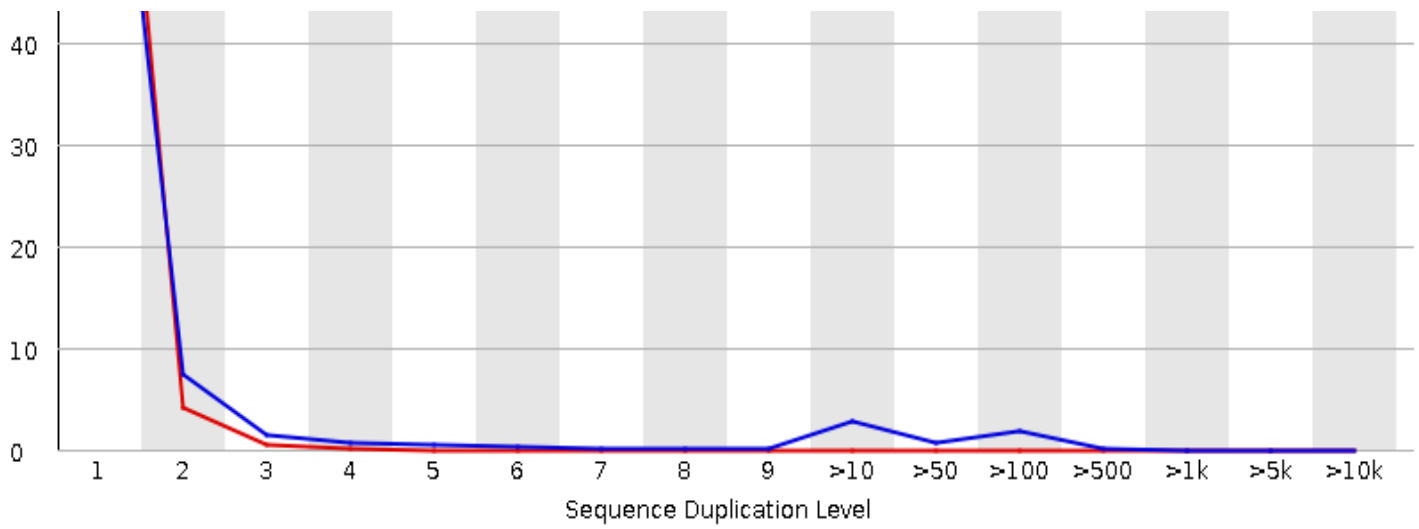




## ✔ Sequence Duplication Levels



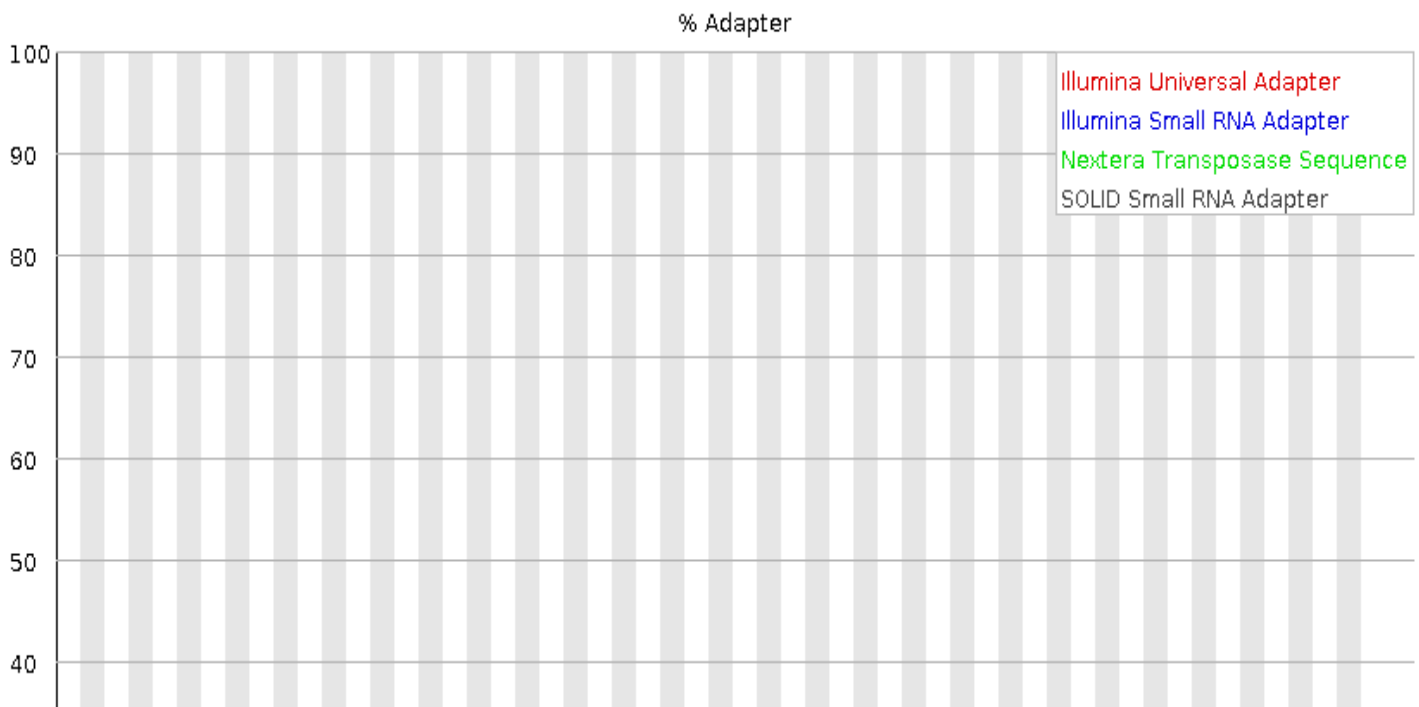




## ✔ Overrepresented sequences

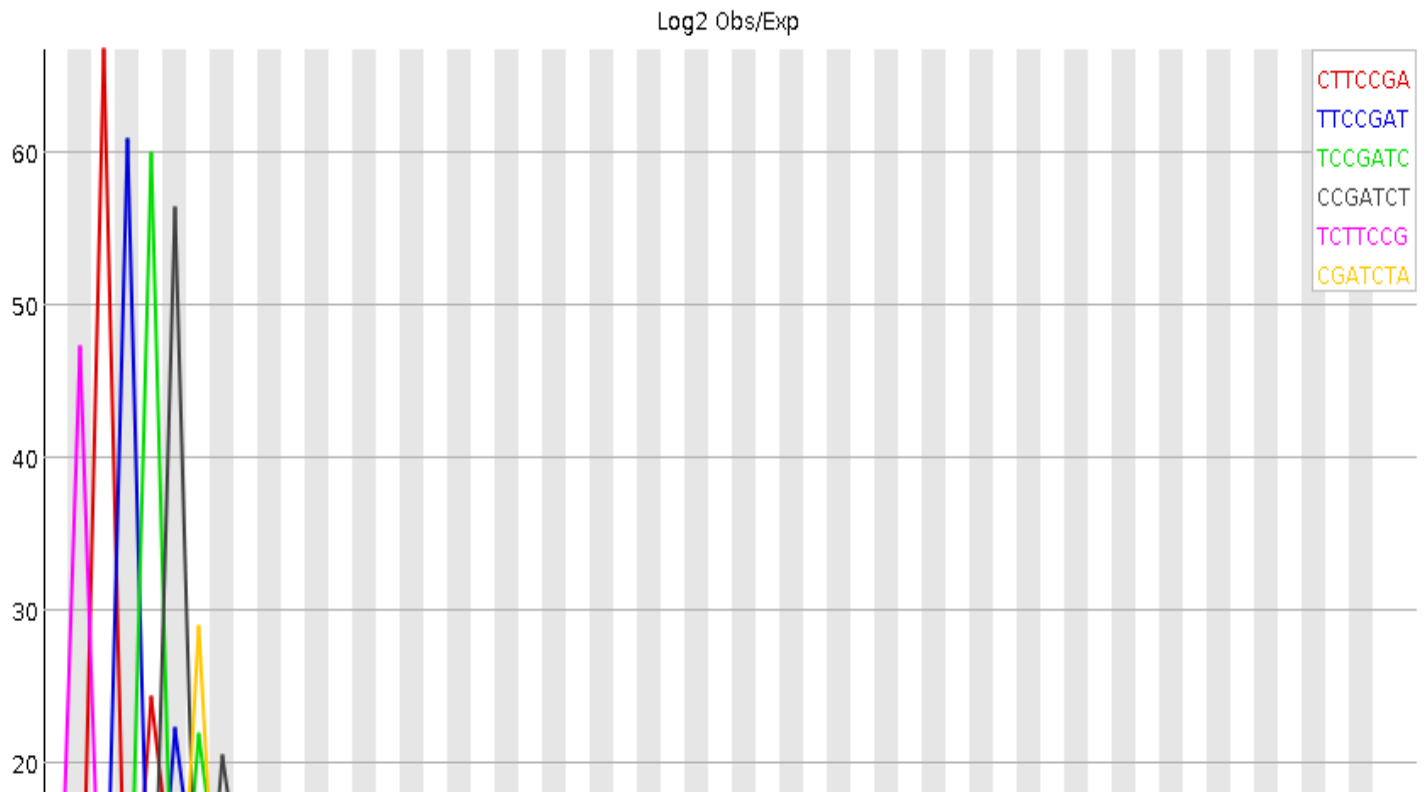
No overrepresented sequences

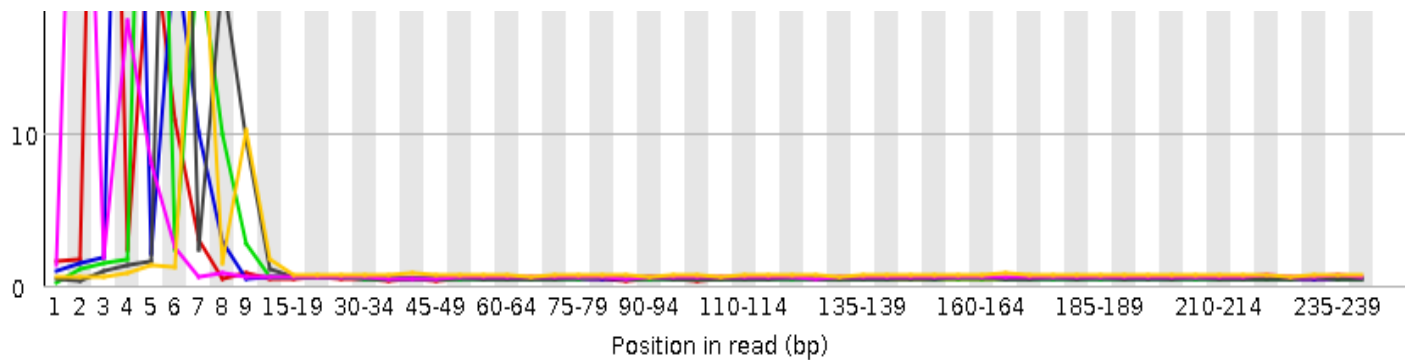
## ✔ Adapter Content





## Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	145275	0.0	66.53125	3
TTCCGAT	158720	0.0	60.672935	4
TCCGATC	161410	0.0	59.76742	5
CCGATCT	171095	0.0	56.192036	6
TCTTCCG	206080	0.0	47.1668	2
CGATCTA	103390	0.0	28.848629	7
CGATCTT	133475	0.0	21.242126	7
CTCTTCC	482765	0.0	20.687376	1
TCGGAAG	87670	0.0	19.198708	4
ATCGGAA	101300	0.0	16.880007	3
GATCGGA	103775	0.0	16.489159	2
ACGCTCT	99995	0.0	15.826003	1
AGATCGG	114580	0.0	14.762171	1
GCTCTTC	251205	0.0	14.641771	2
CAAGTCG	111400	0.0	14.289115	5
CGATCTC	152860	0.0	13.018867	7
CGATCTG	175100	0.0	12.512958	7
CGCTCTT	131175	0.0	12.2556925	2
GTCGTCA	134680	0.0	11.710667	8
AAGTCGT	137630	0.0	11.689735	6

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