













## Summary

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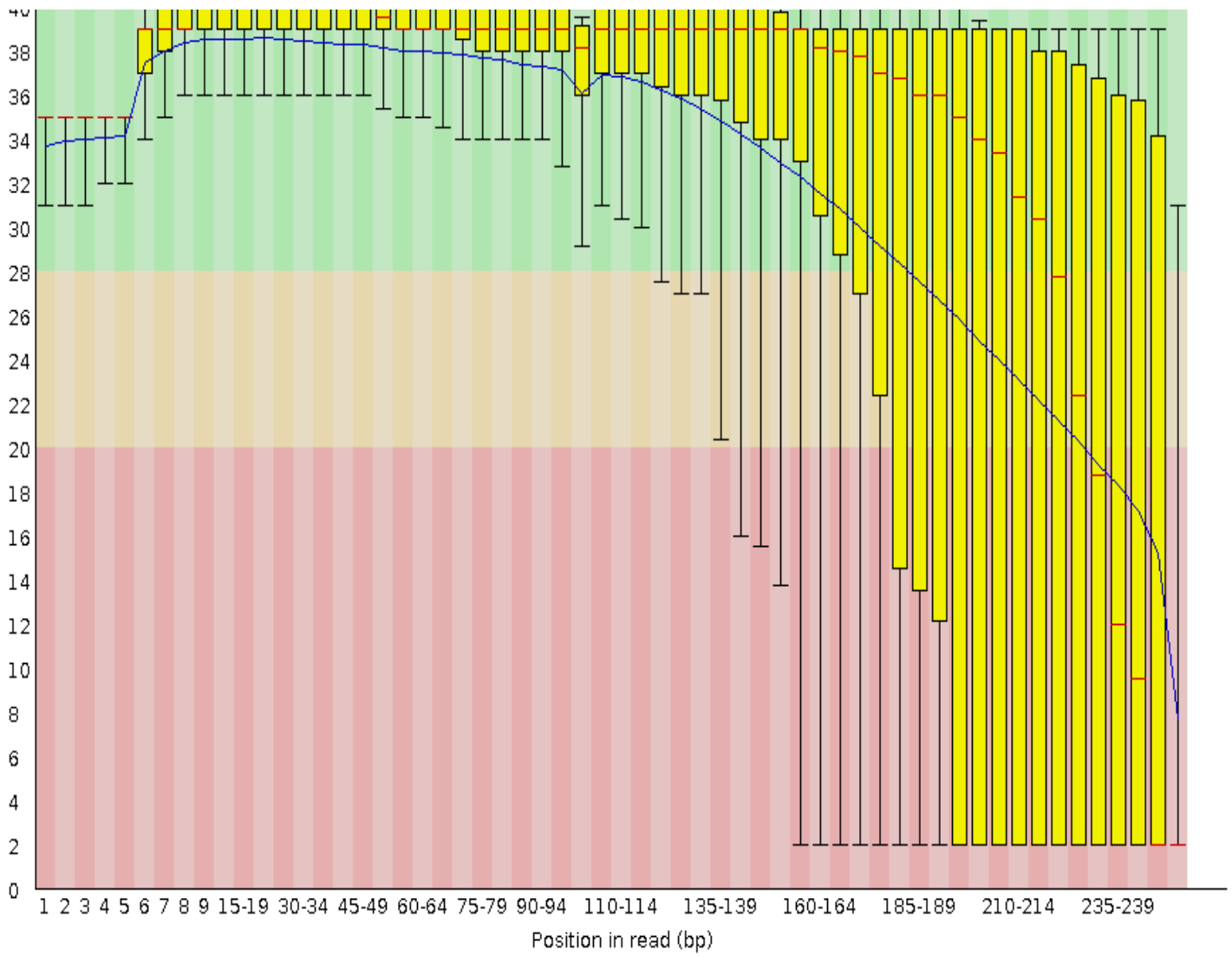
## Basic Statistics

Measure	Value
Filename	BS_tag_noAdap_pair1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	67916229
Sequences flagged as poor quality	0
Sequence length	52-250
%GC	42

## Per base sequence quality

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

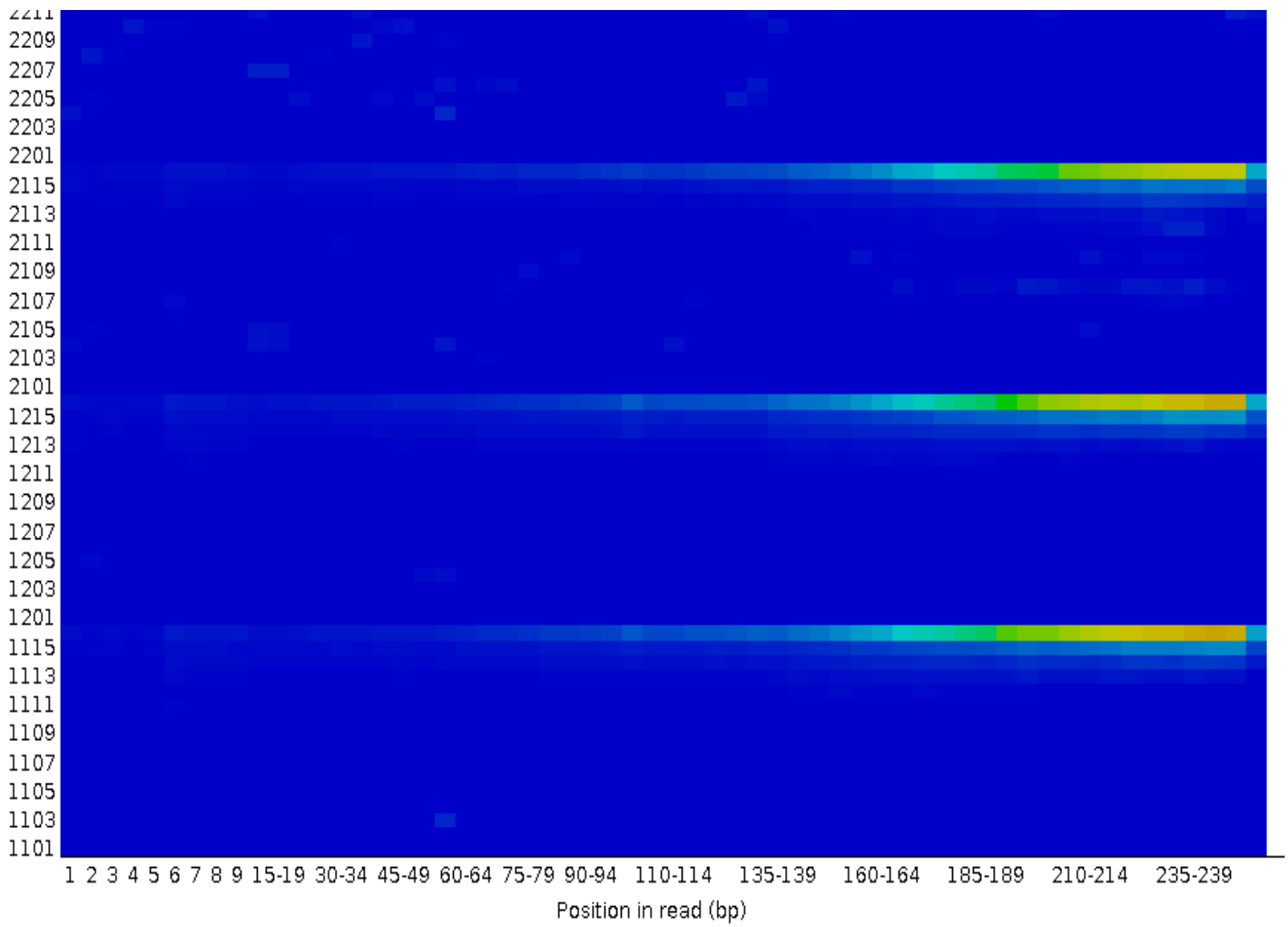




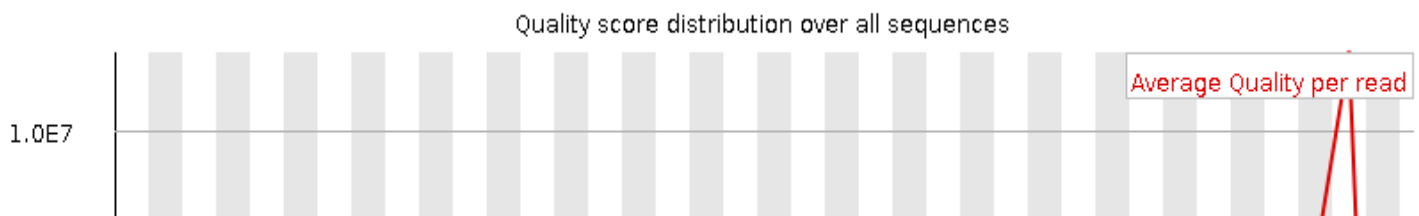
**! Per tile sequence quality**

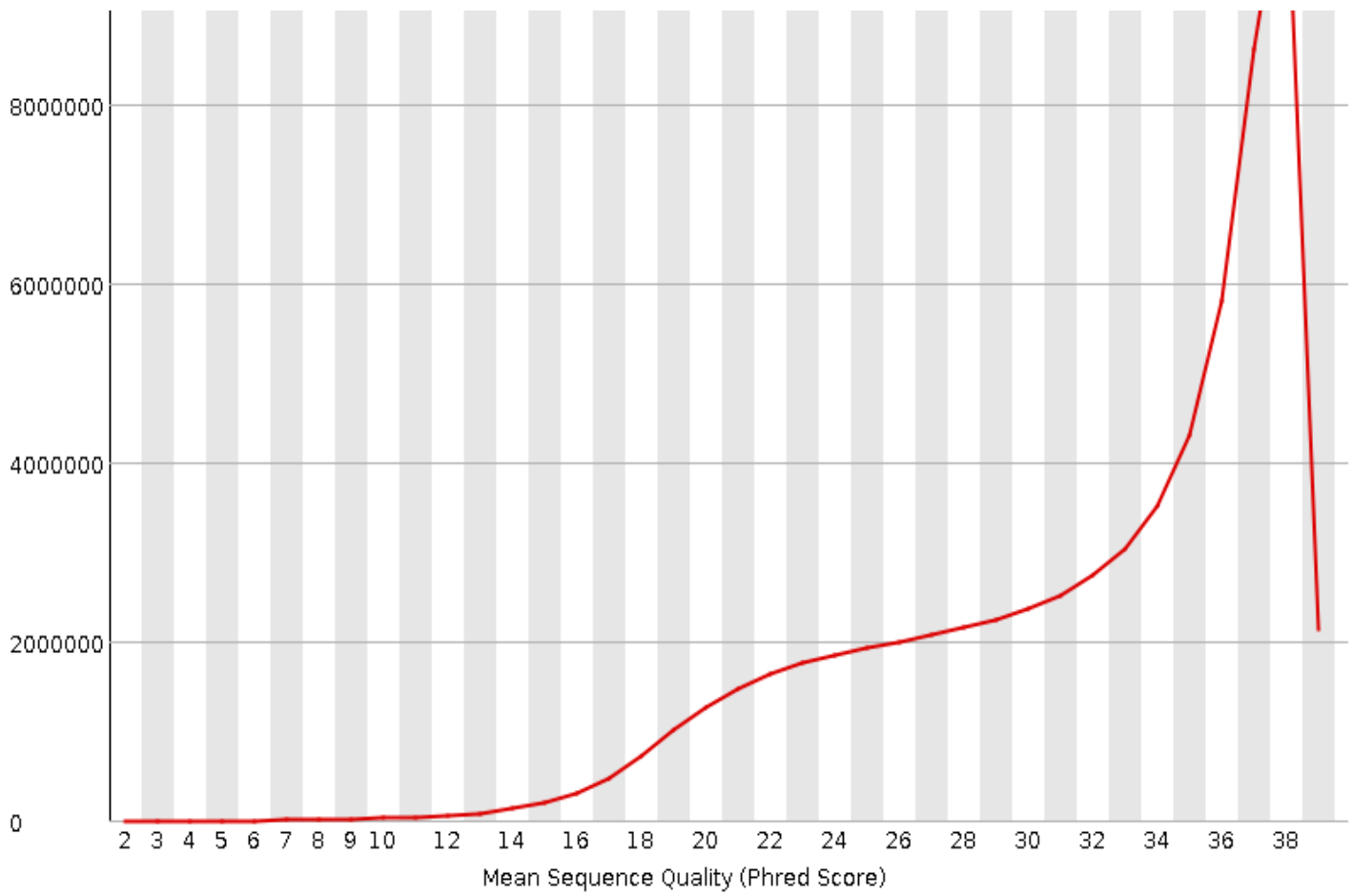
Quality per tile



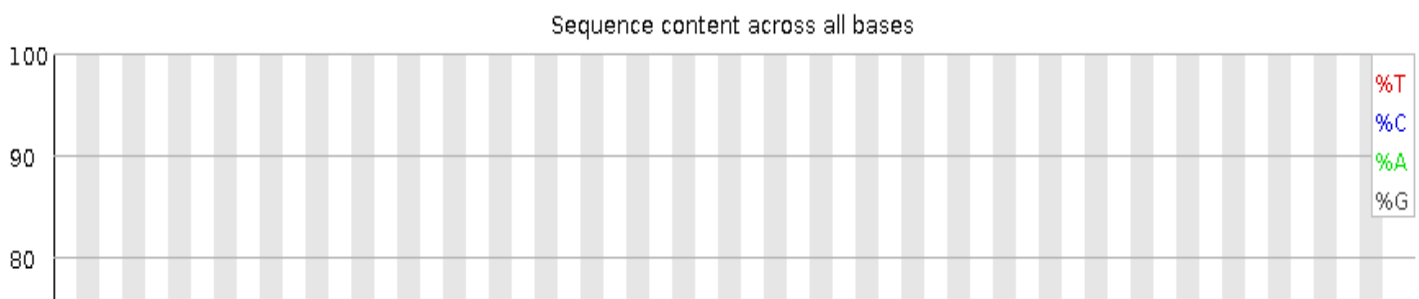


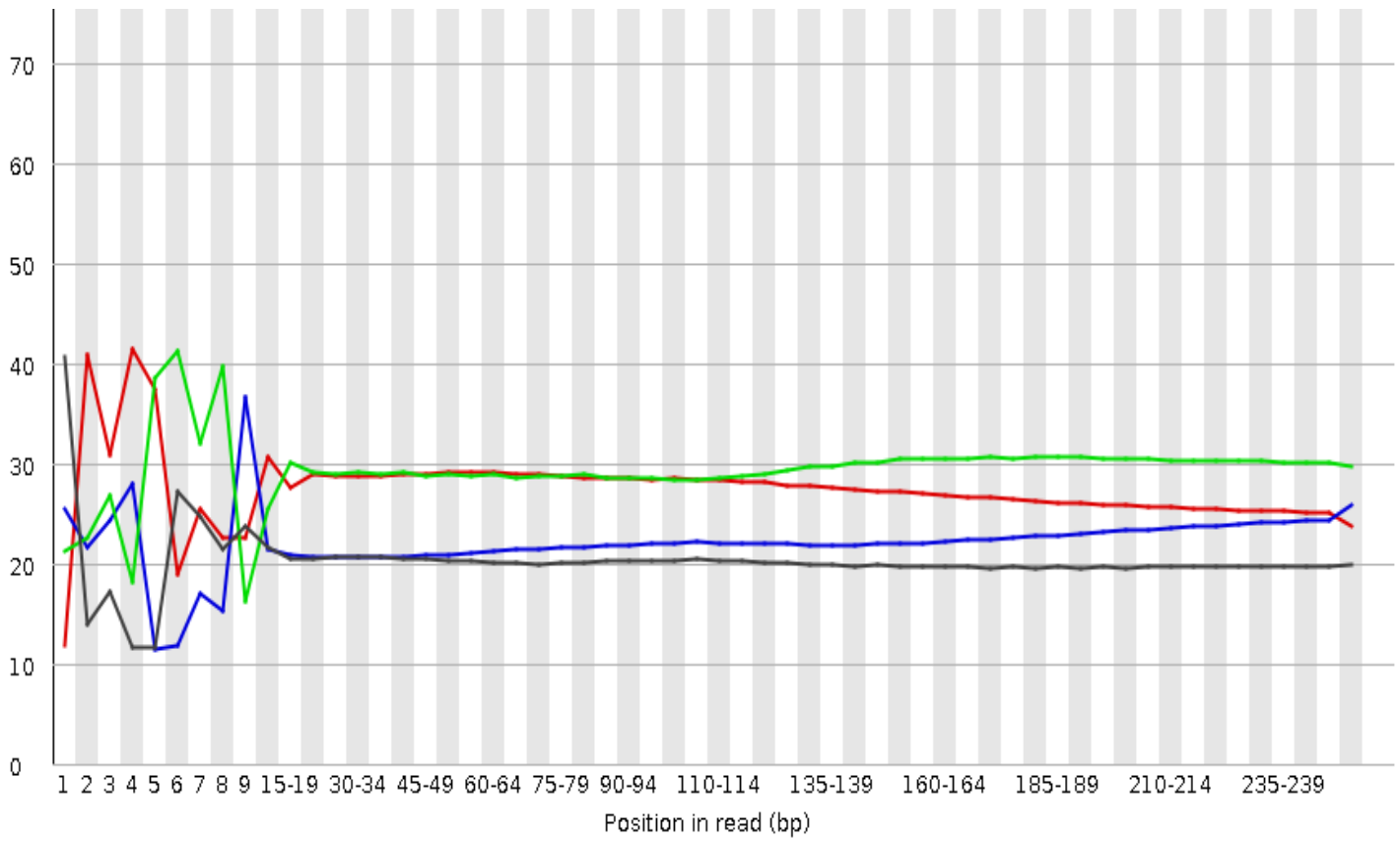
 **Per sequence quality scores**



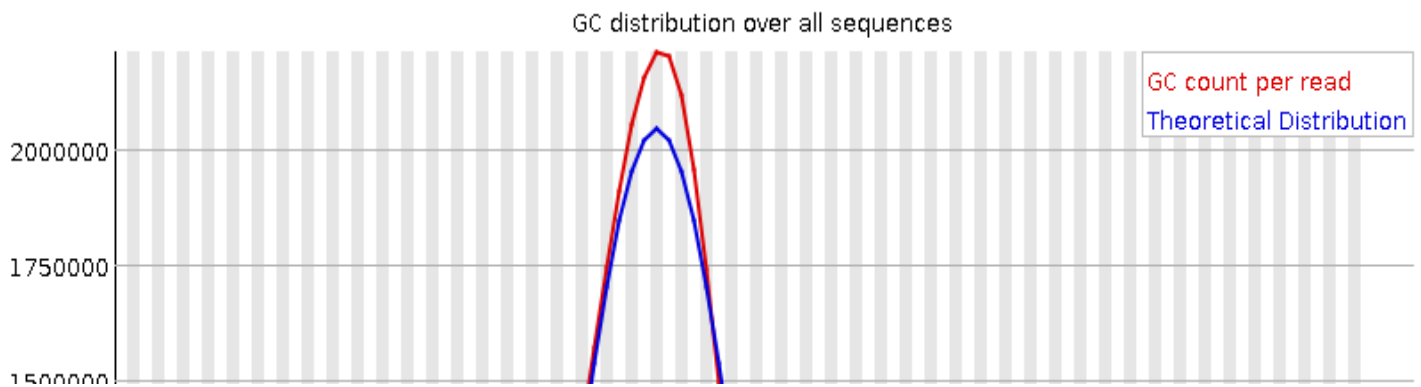


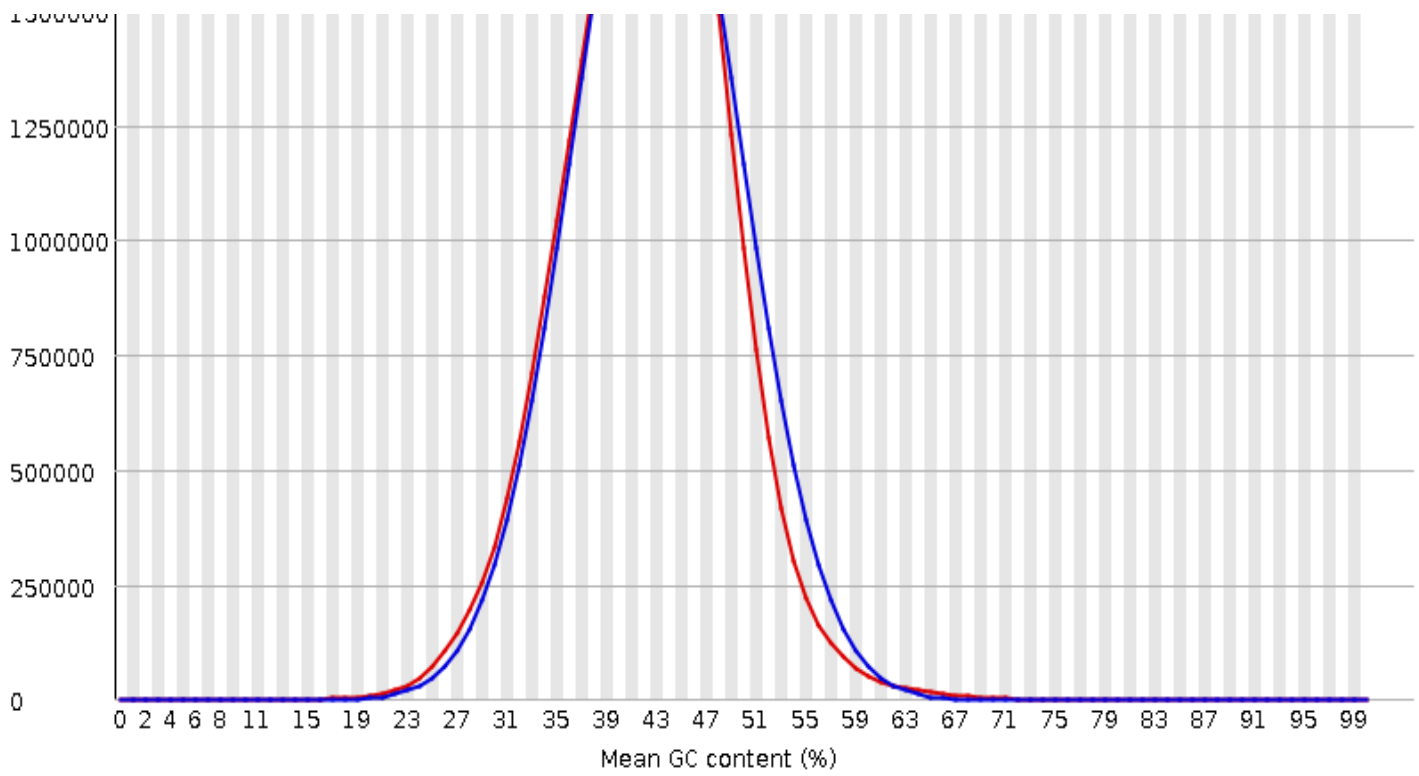
## ✖ Per base sequence content



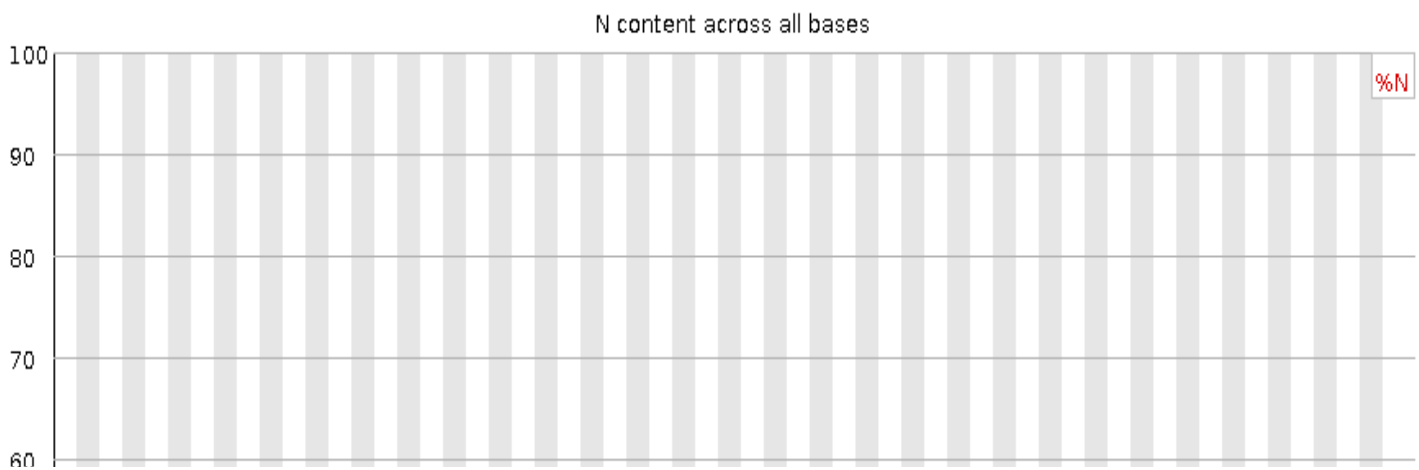


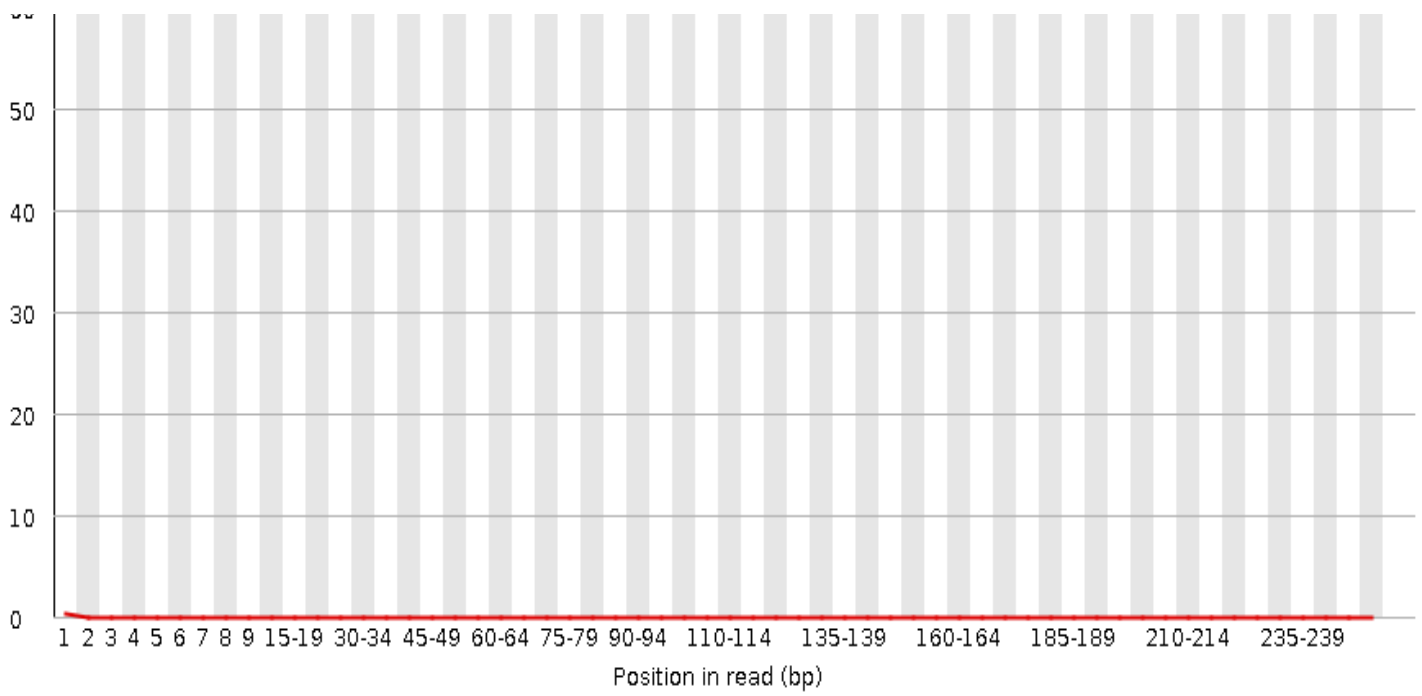
 **Per sequence GC content**



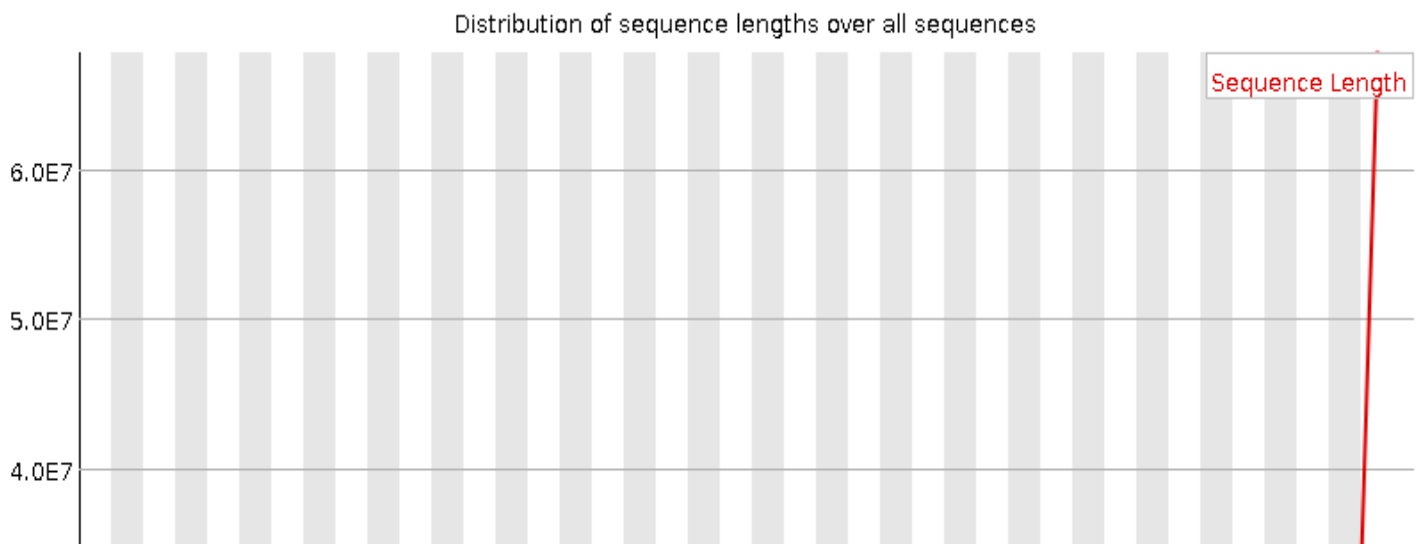


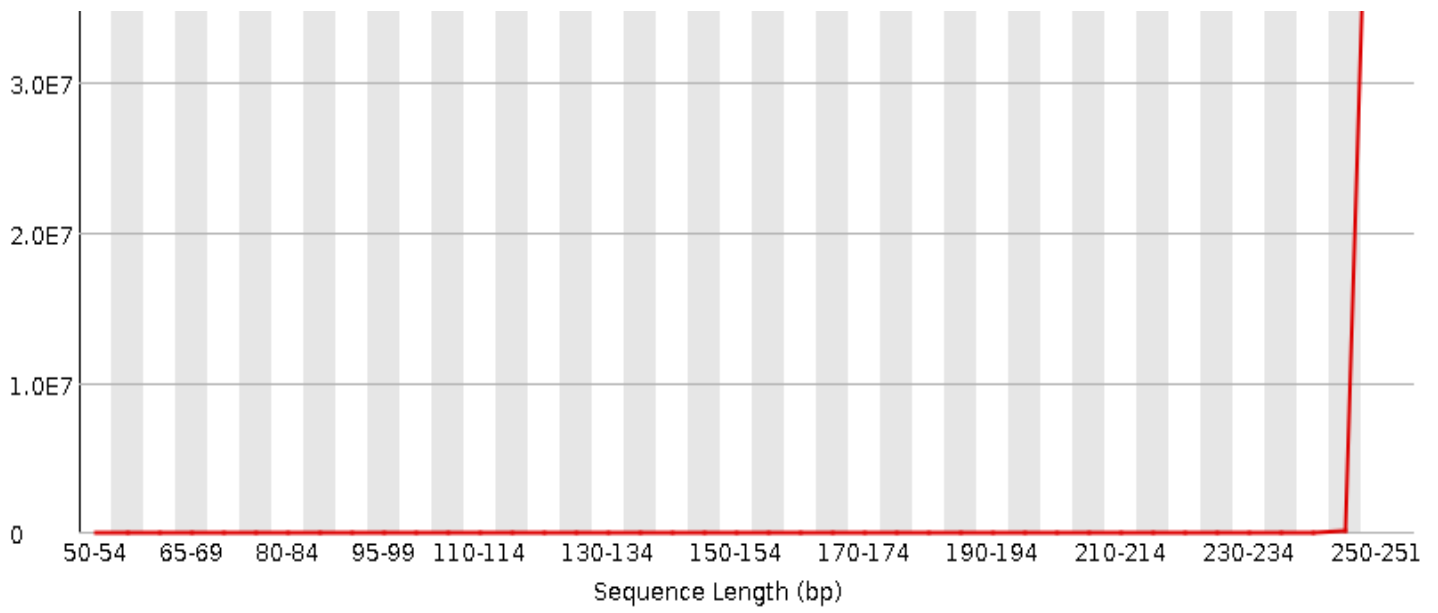
 **Per base N content**



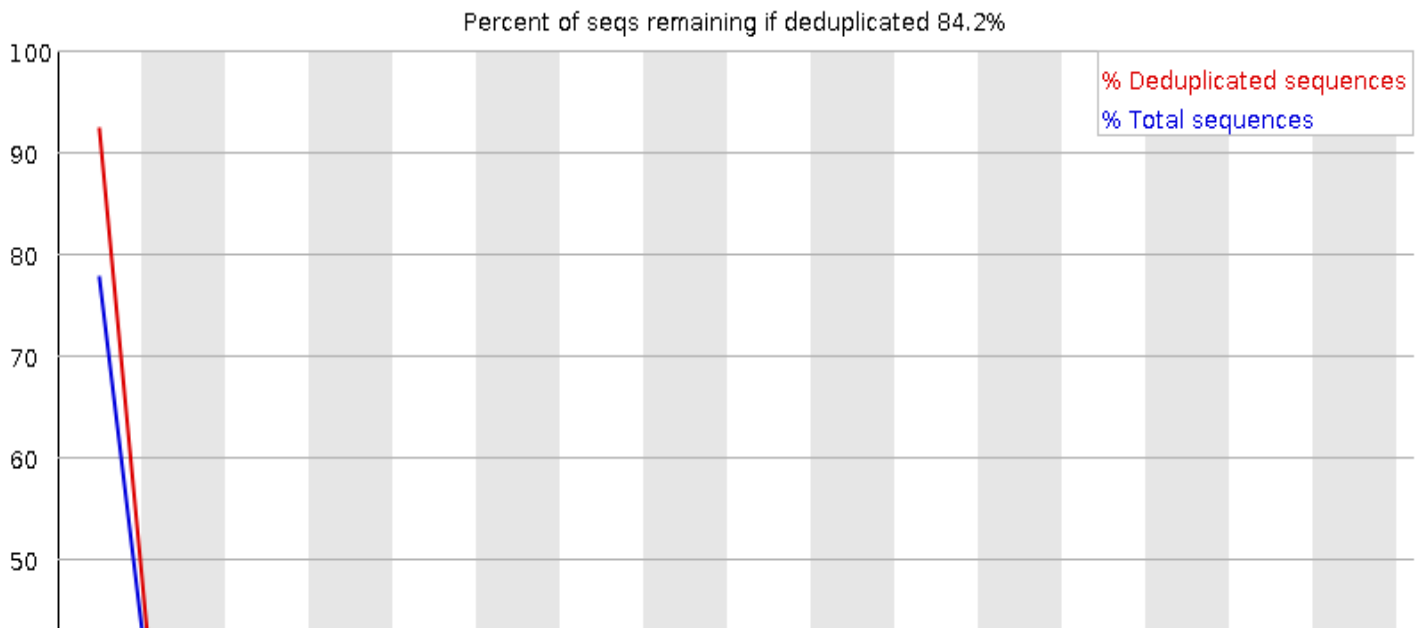


## ! Sequence Length Distribution

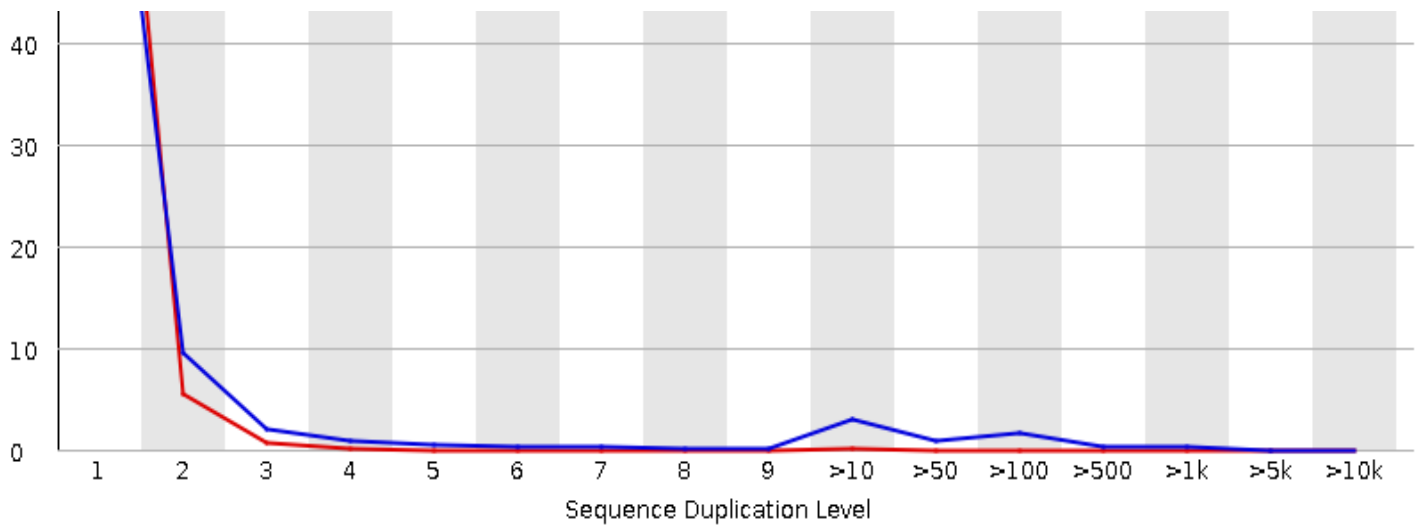




 **Sequence Duplication Levels**



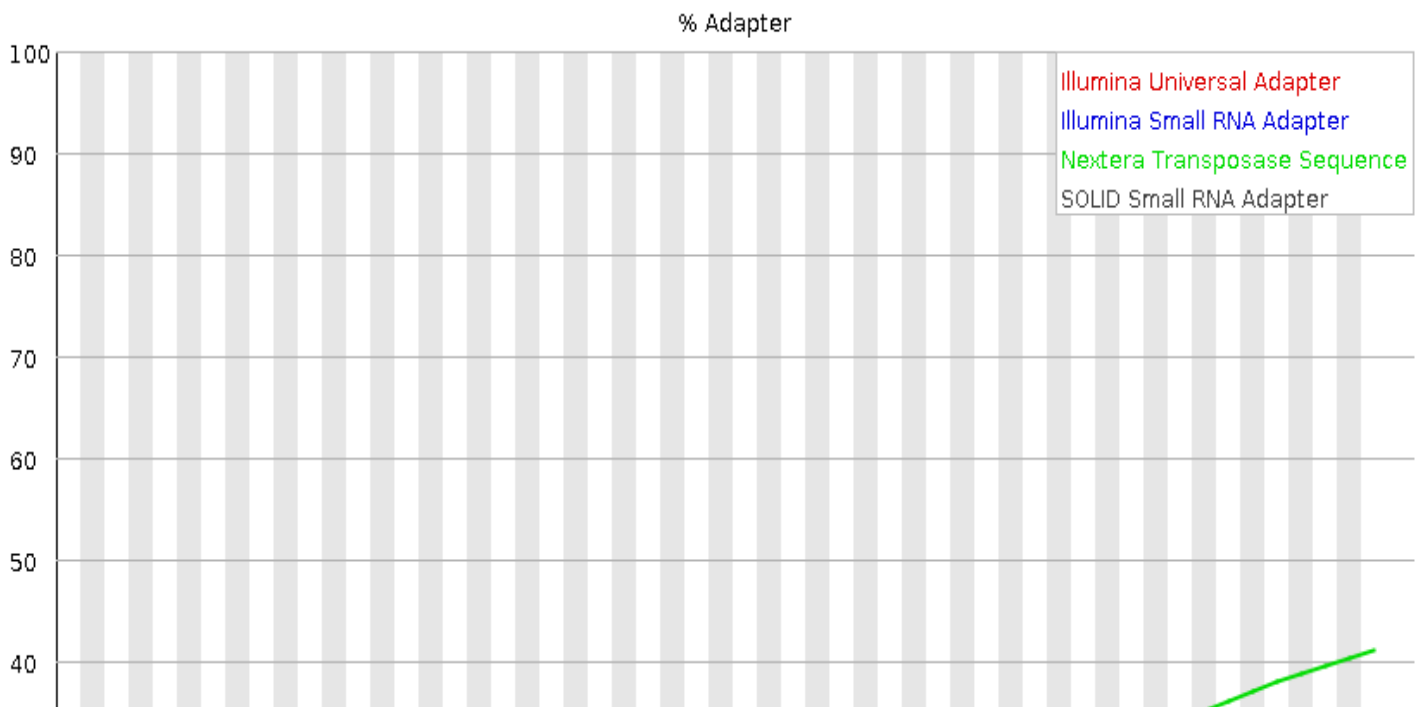


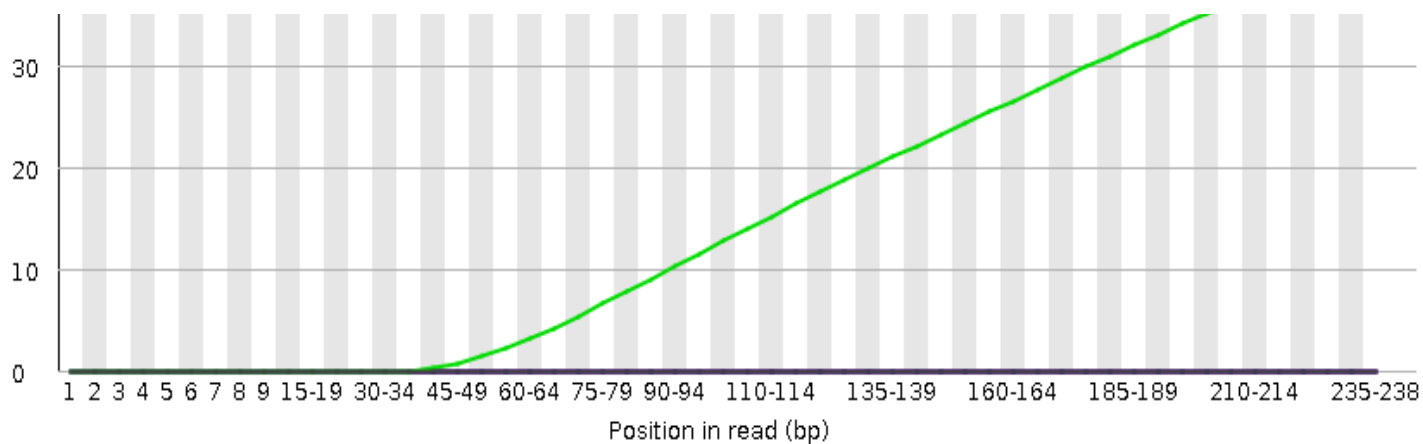


## ✔ Overrepresented sequences

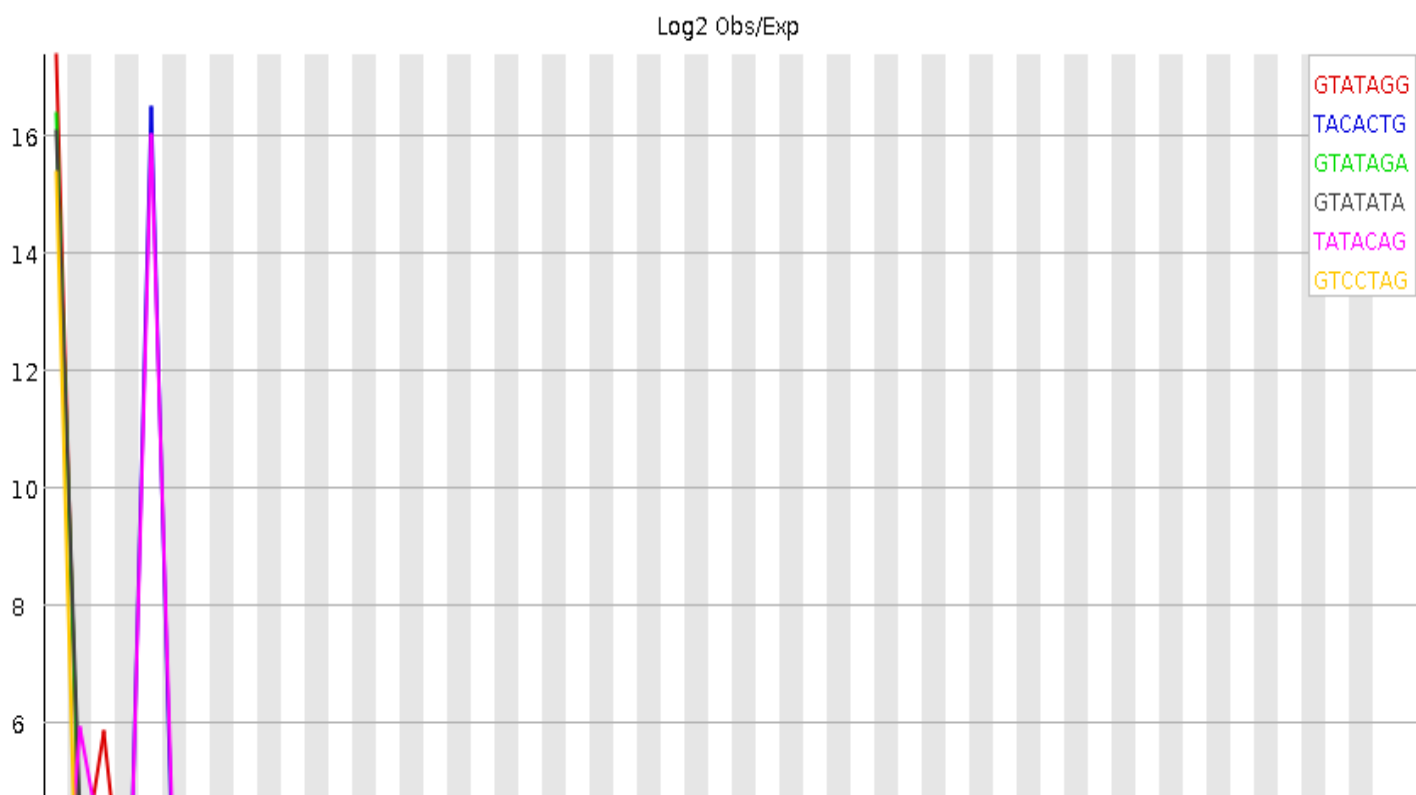
No overrepresented sequences

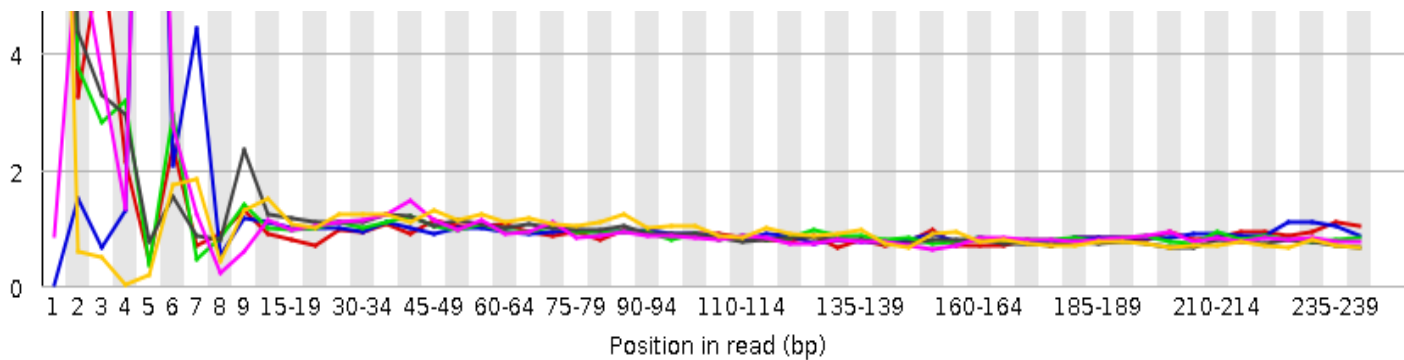
## ✘ Adapter Content





## ❌ Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTATAGG	51250	0.0	17.33505	1
TACACTG	129225	0.0	16.46555	5
GTATAGA	87005	0.0	16.337843	1
GTATATA	155415	0.0	16.04547	1
TATACAG	150640	0.0	15.994623	5
GTCCTAG	55910	0.0	15.364183	1
TATACTG	179230	0.0	15.191666	5
TATACCG	34170	0.0	15.130324	5
CTATACT	86535	0.0	14.964426	4
TTATACT	124650	0.0	14.683033	4
GTATAAG	64505	0.0	14.646772	1
GTGTAGG	78450	0.0	14.214427	1
TCTATAC	91345	0.0	14.096344	3
GTCCTAA	54615	0.0	13.843763	1
GTCTTAG	82535	0.0	13.7633	1
GTATTAG	90000	0.0	13.751808	1
GTATAAA	139180	0.0	13.7350025	1
TAGACAG	147130	0.0	13.599868	5
TACACAG	158835	0.0	13.449782	5
GTGTATA	127305	0.0	13.360569	1

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