













Summary

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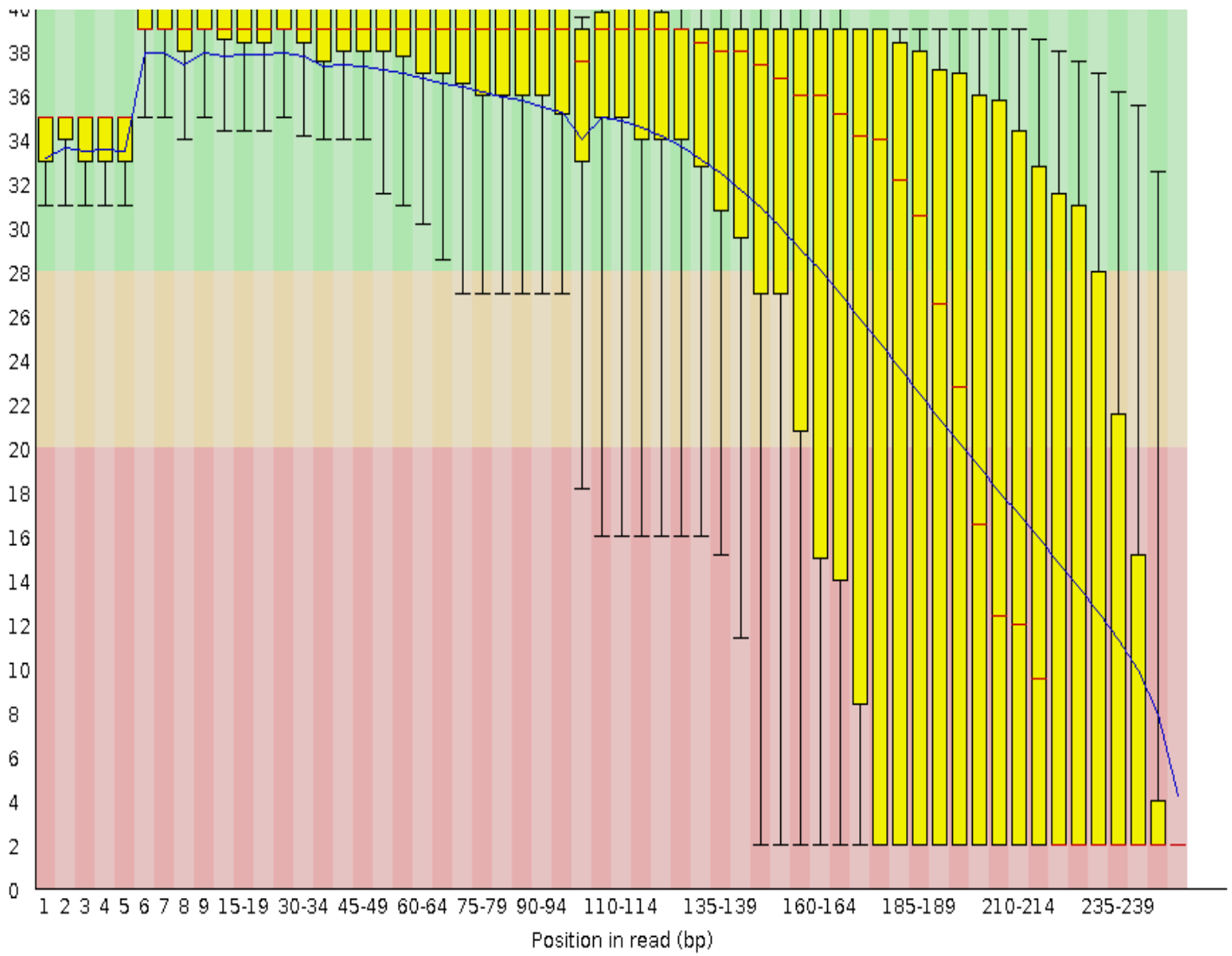
Basic Statistics

Measure	Value
Filename	BS_tag_noAdap_pair2.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	43

Per base sequence quality

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

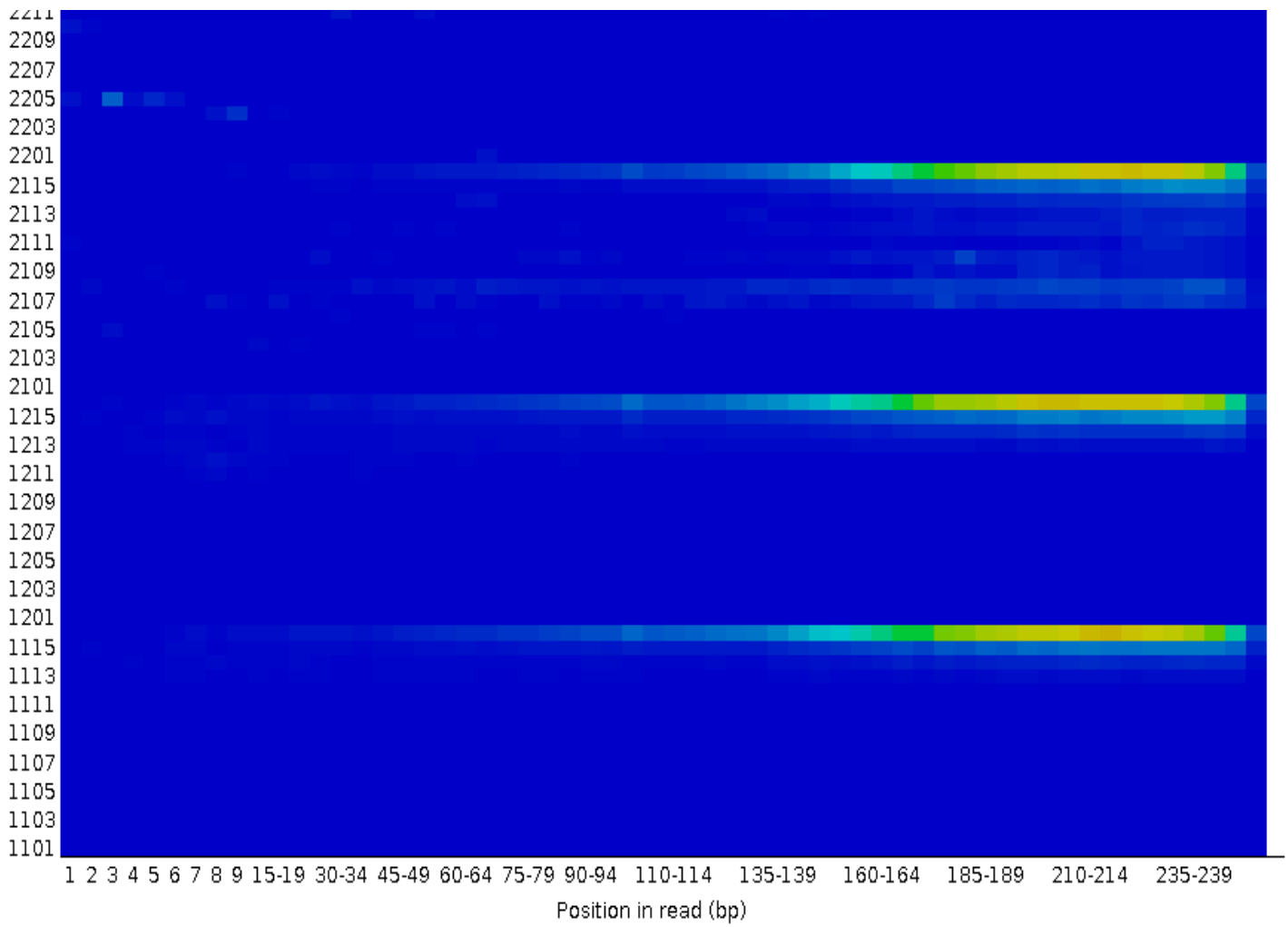




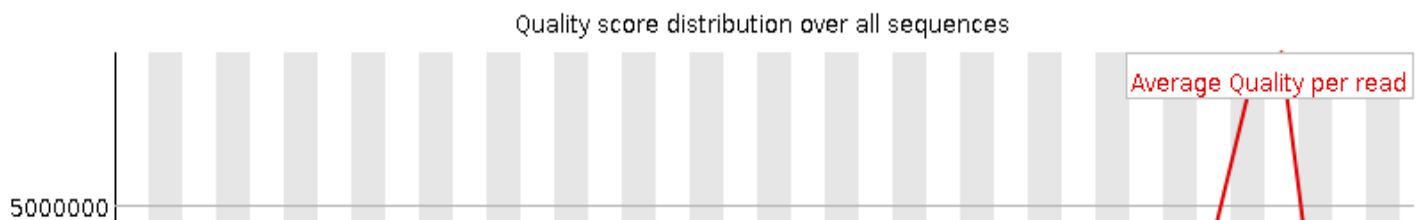
! Per tile sequence quality

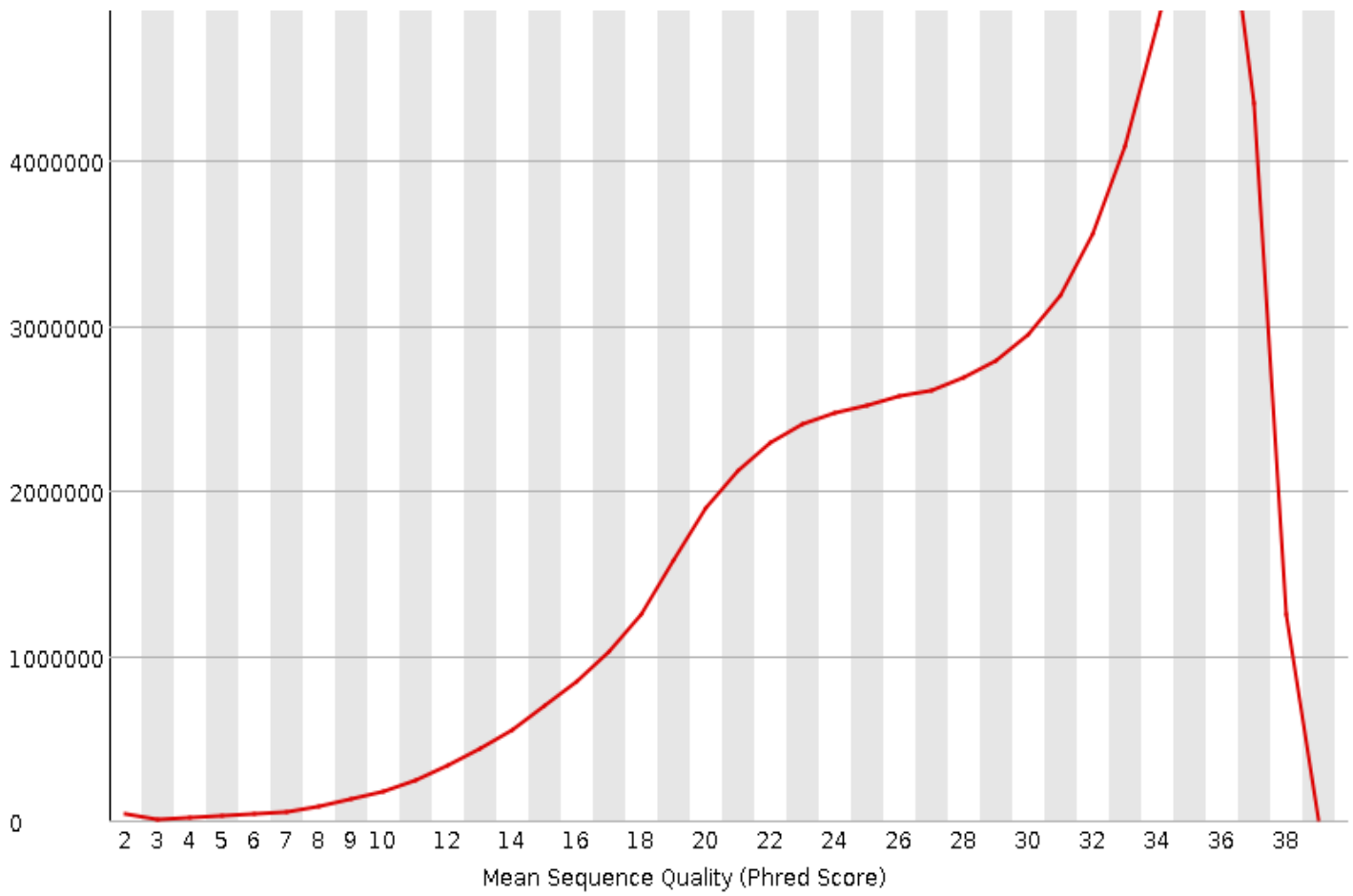
Quality per tile



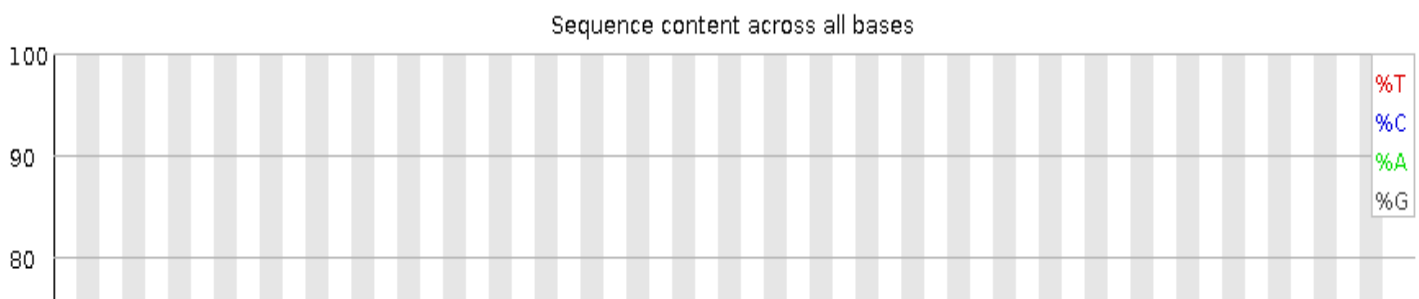


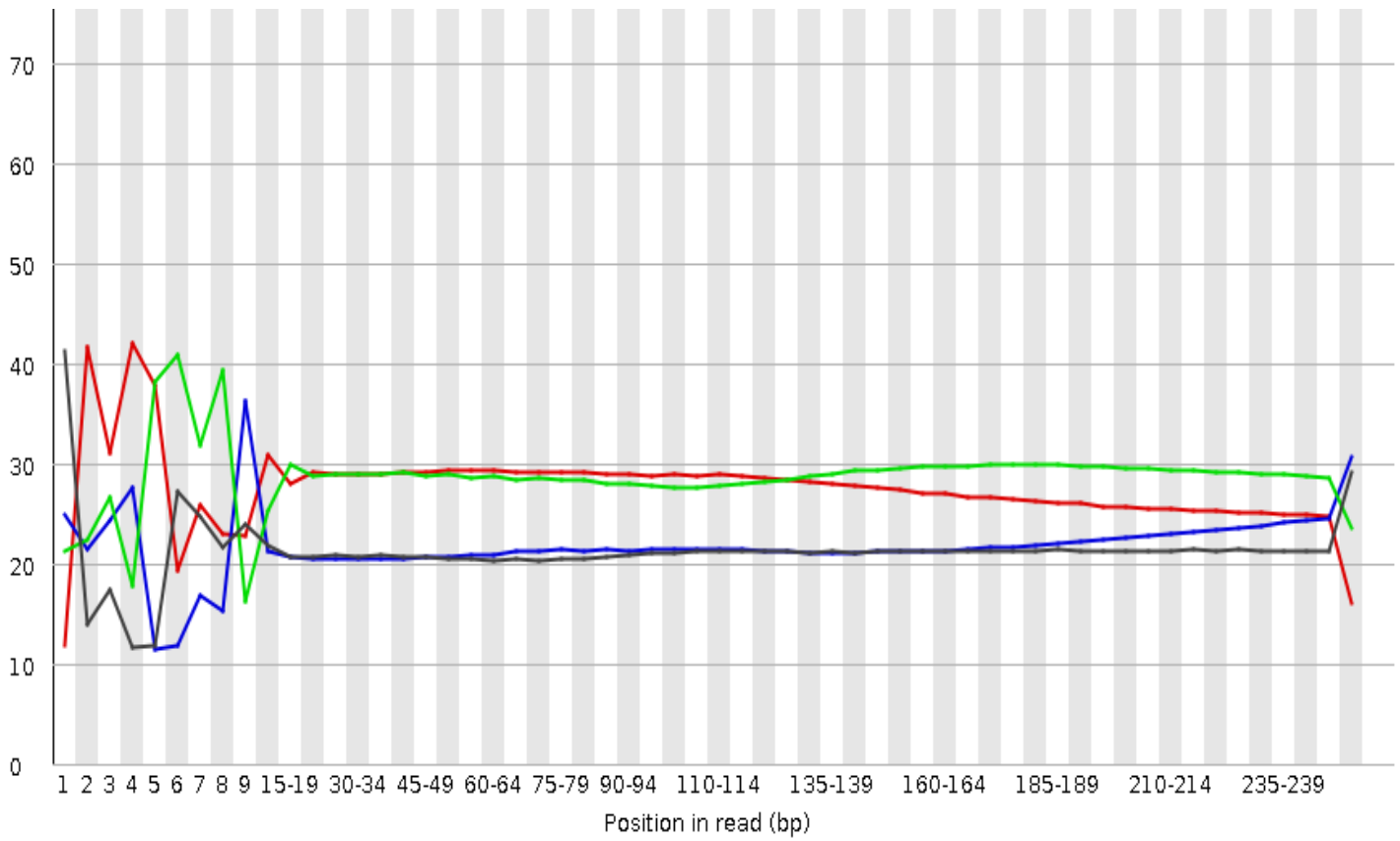
 **Per sequence quality scores**



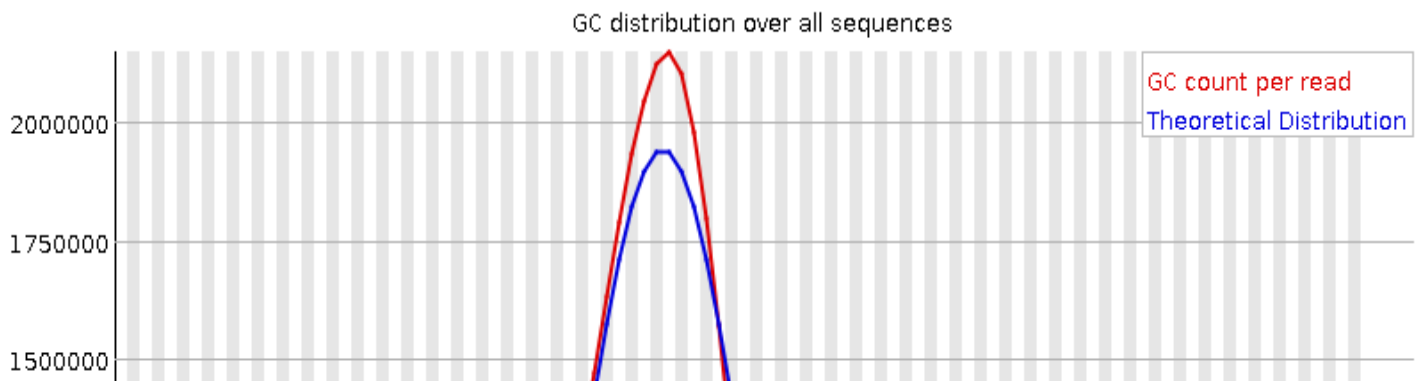


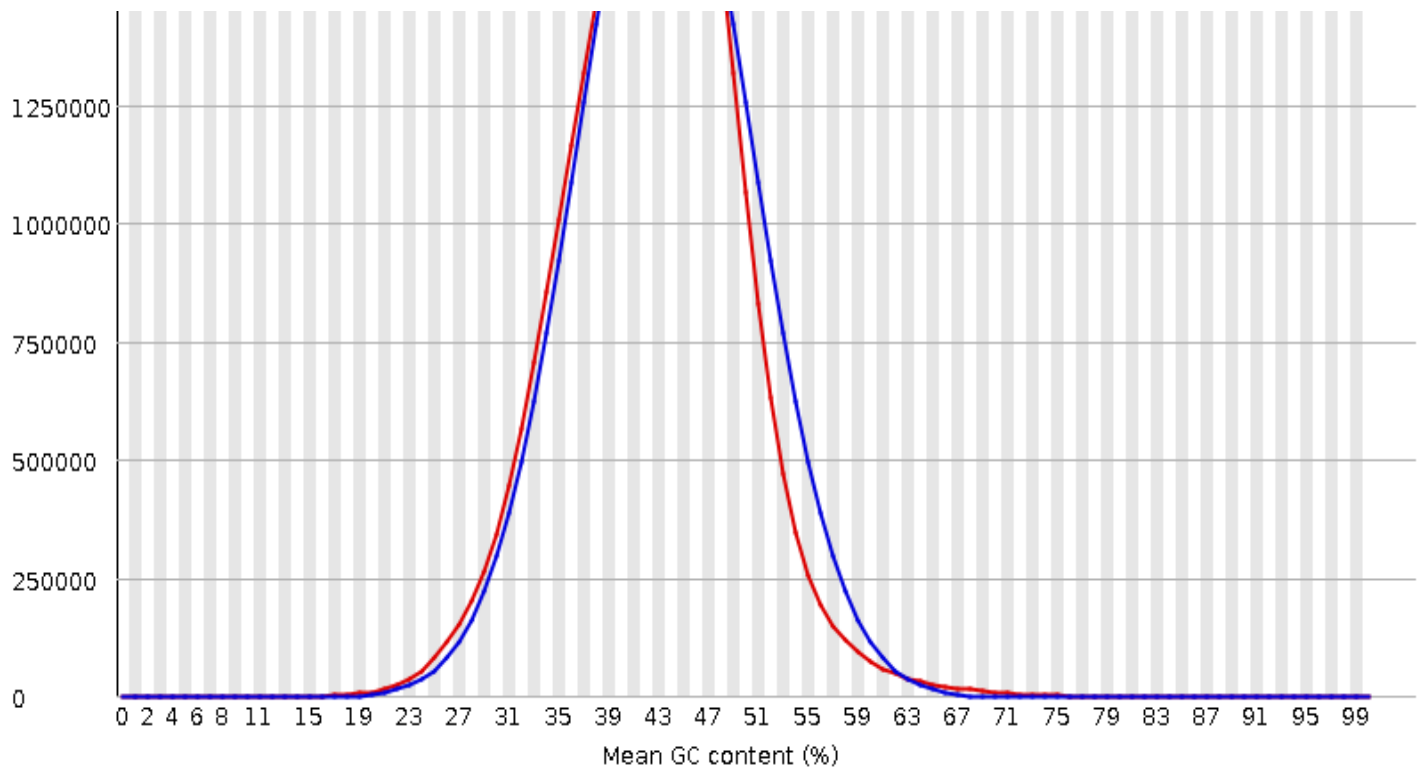
❌ Per base sequence content



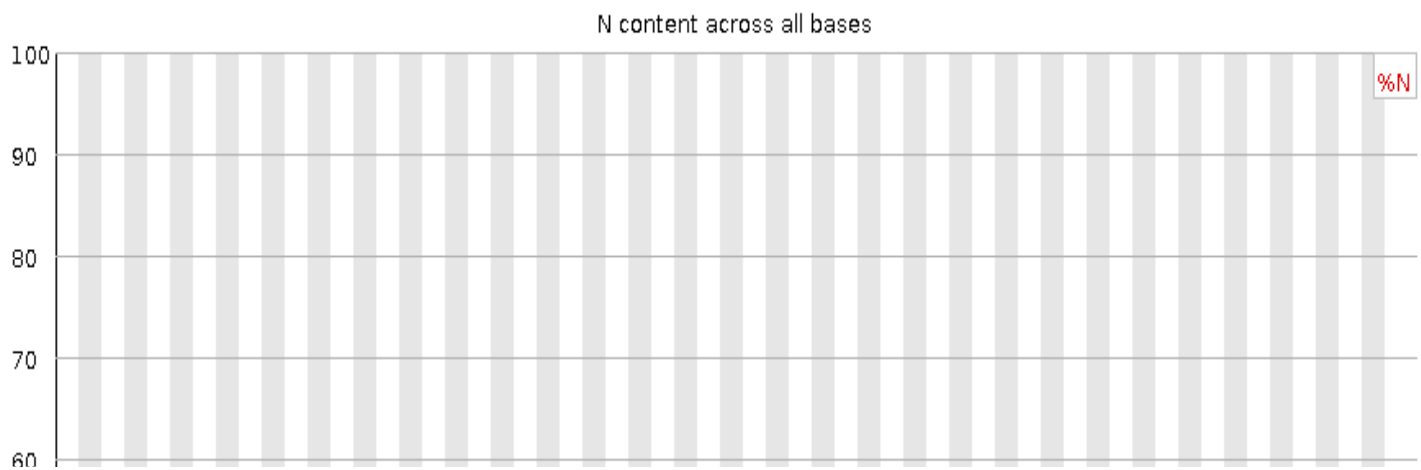


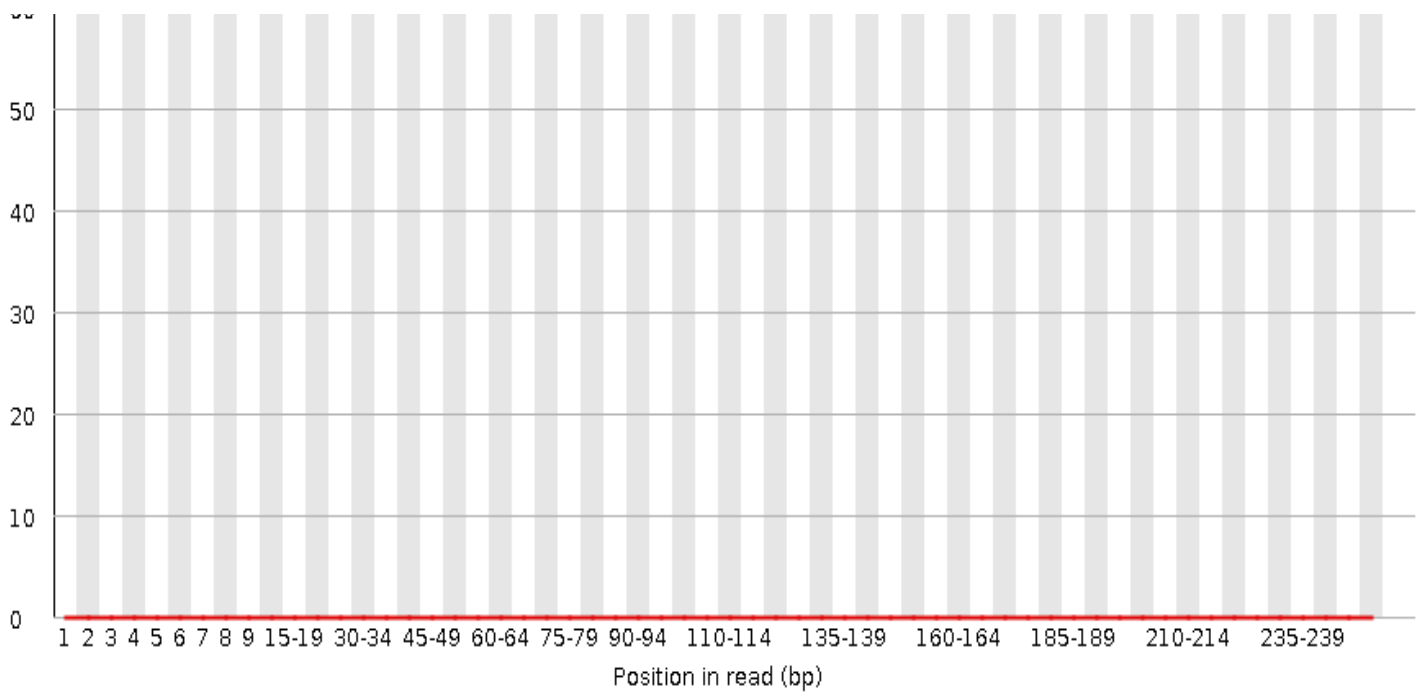
 **Per sequence GC content**



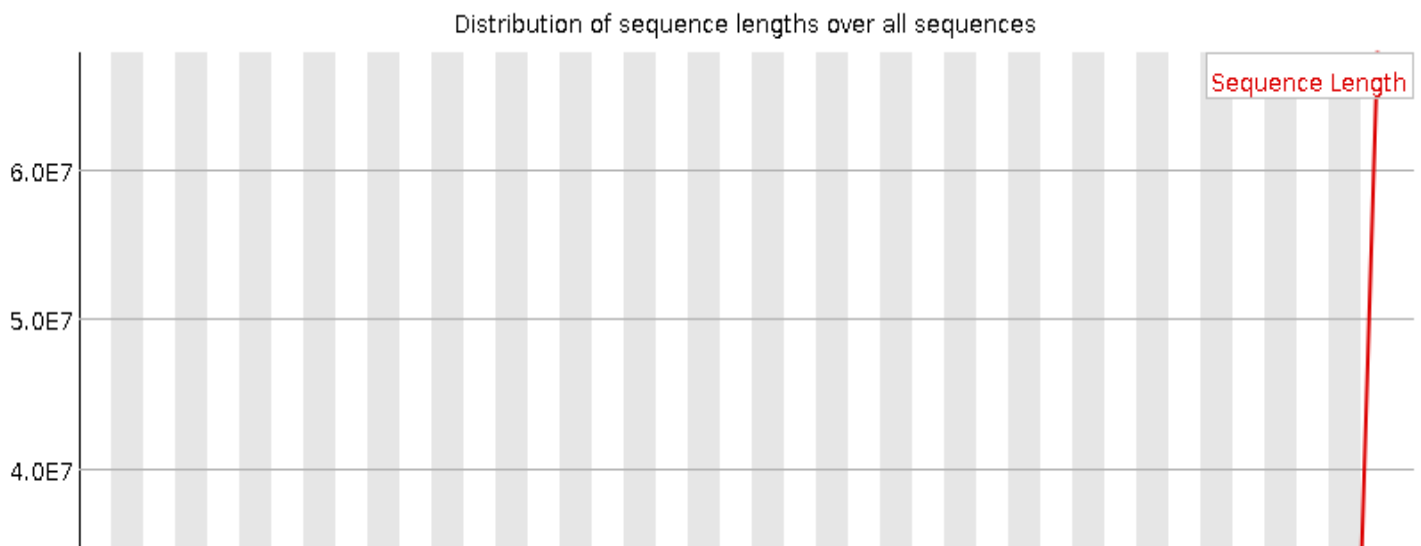


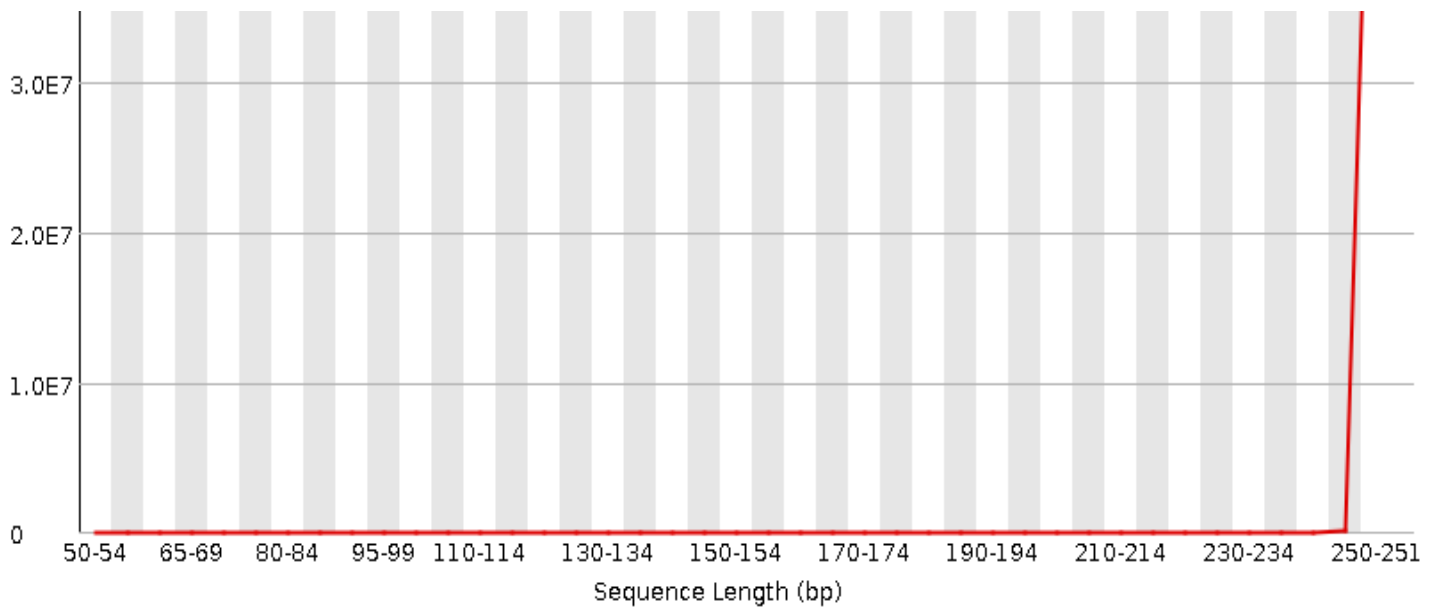
Per base N content



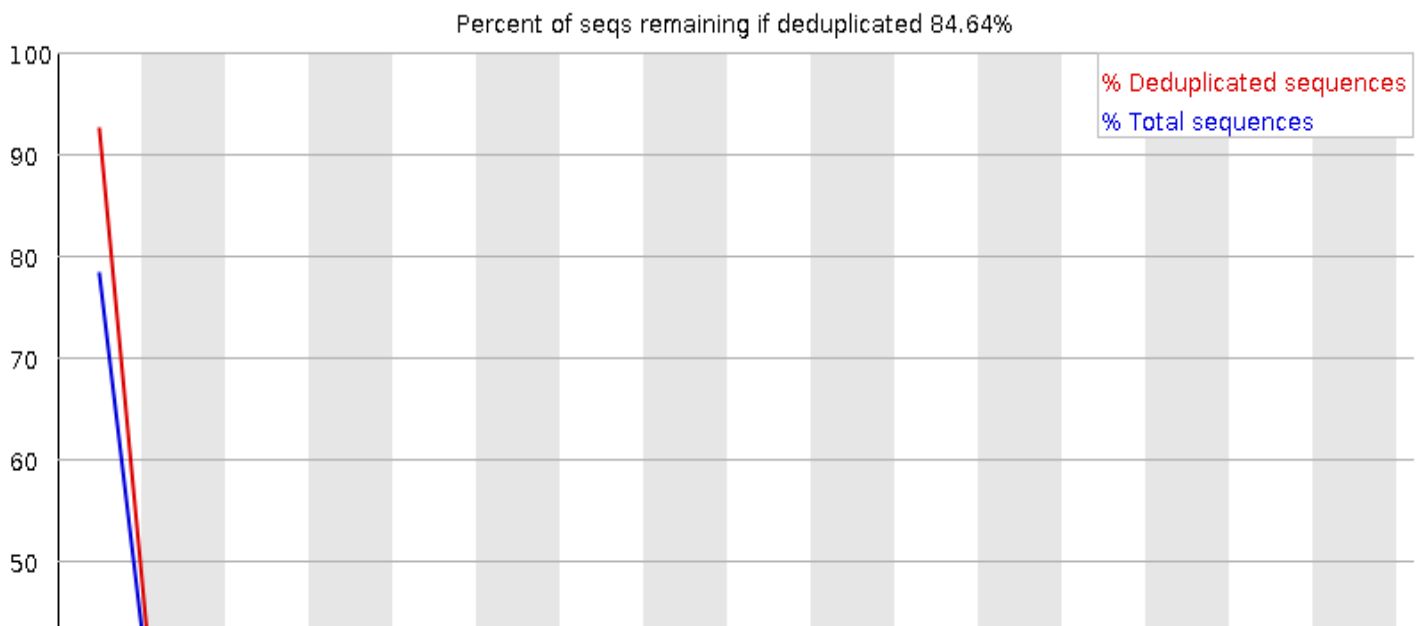


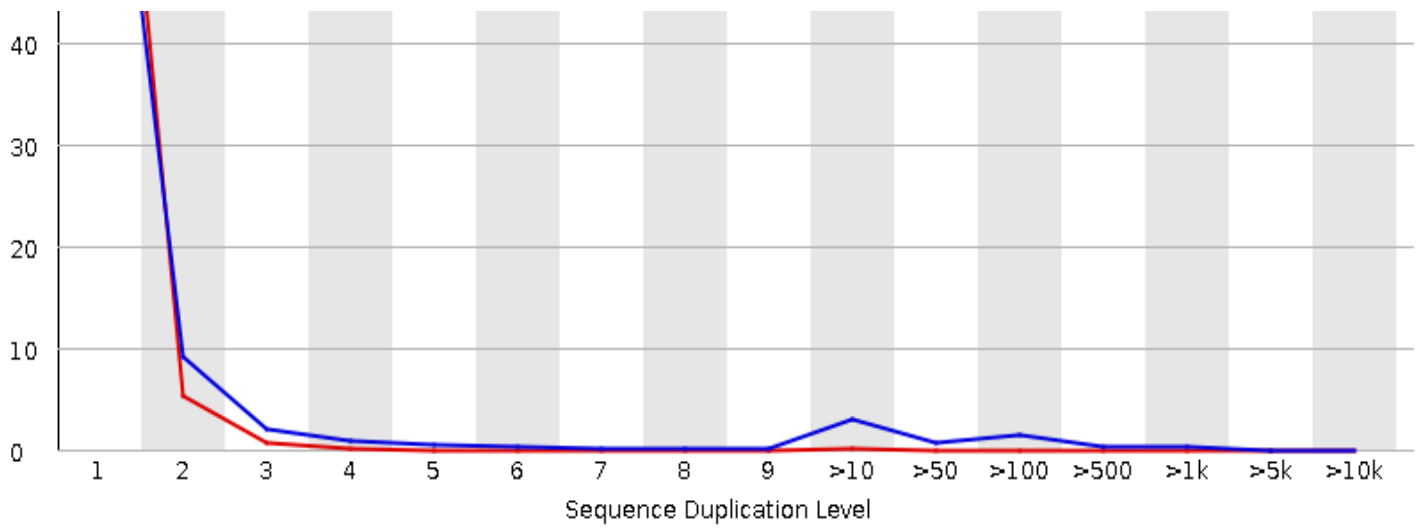
! Sequence Length Distribution





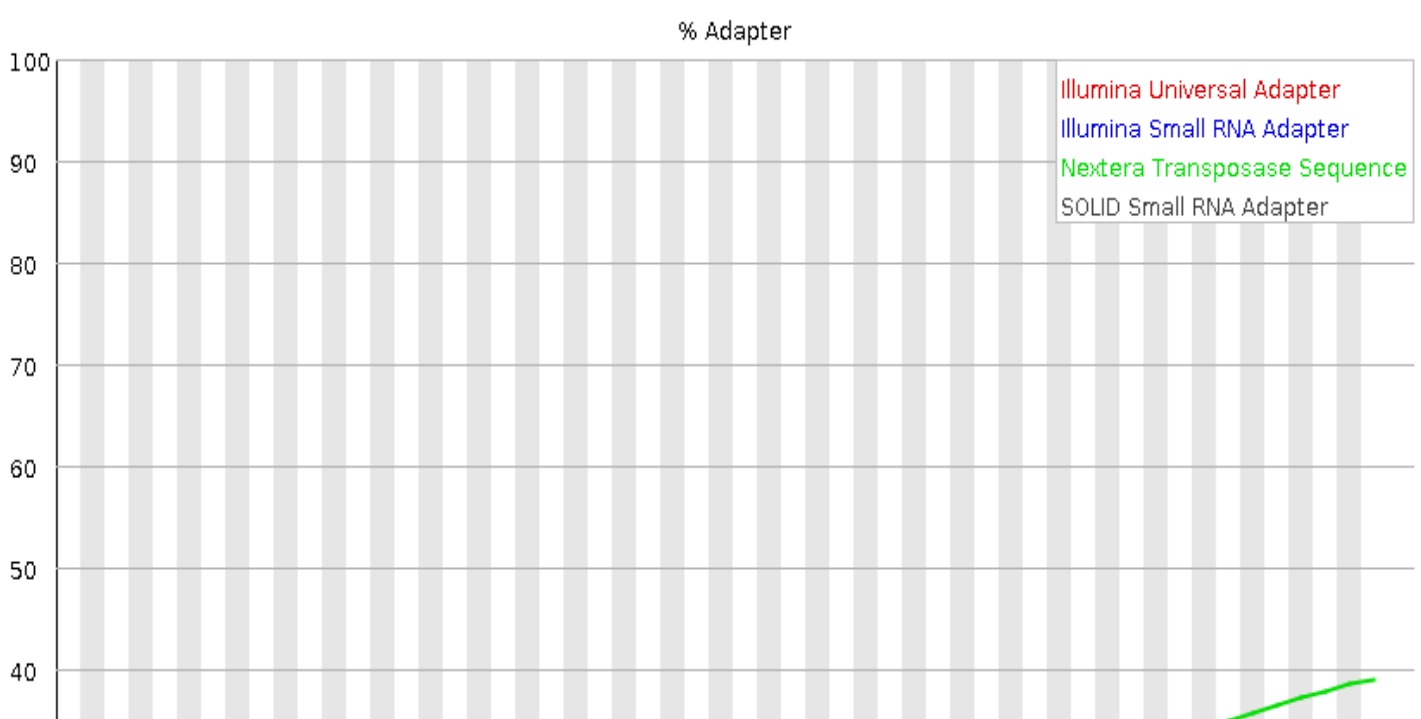
✔ Sequence Duplication Levels

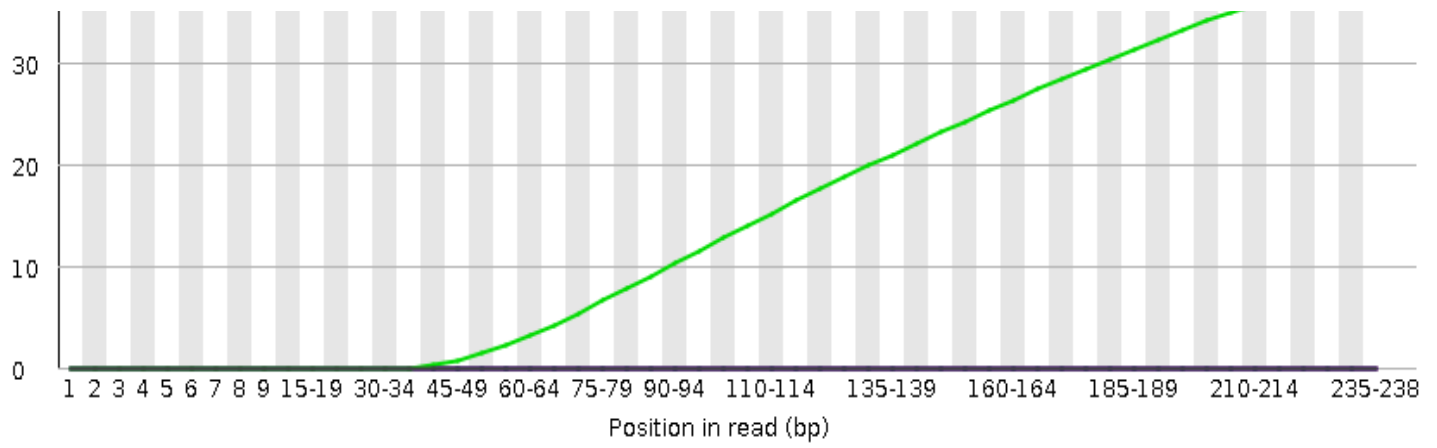




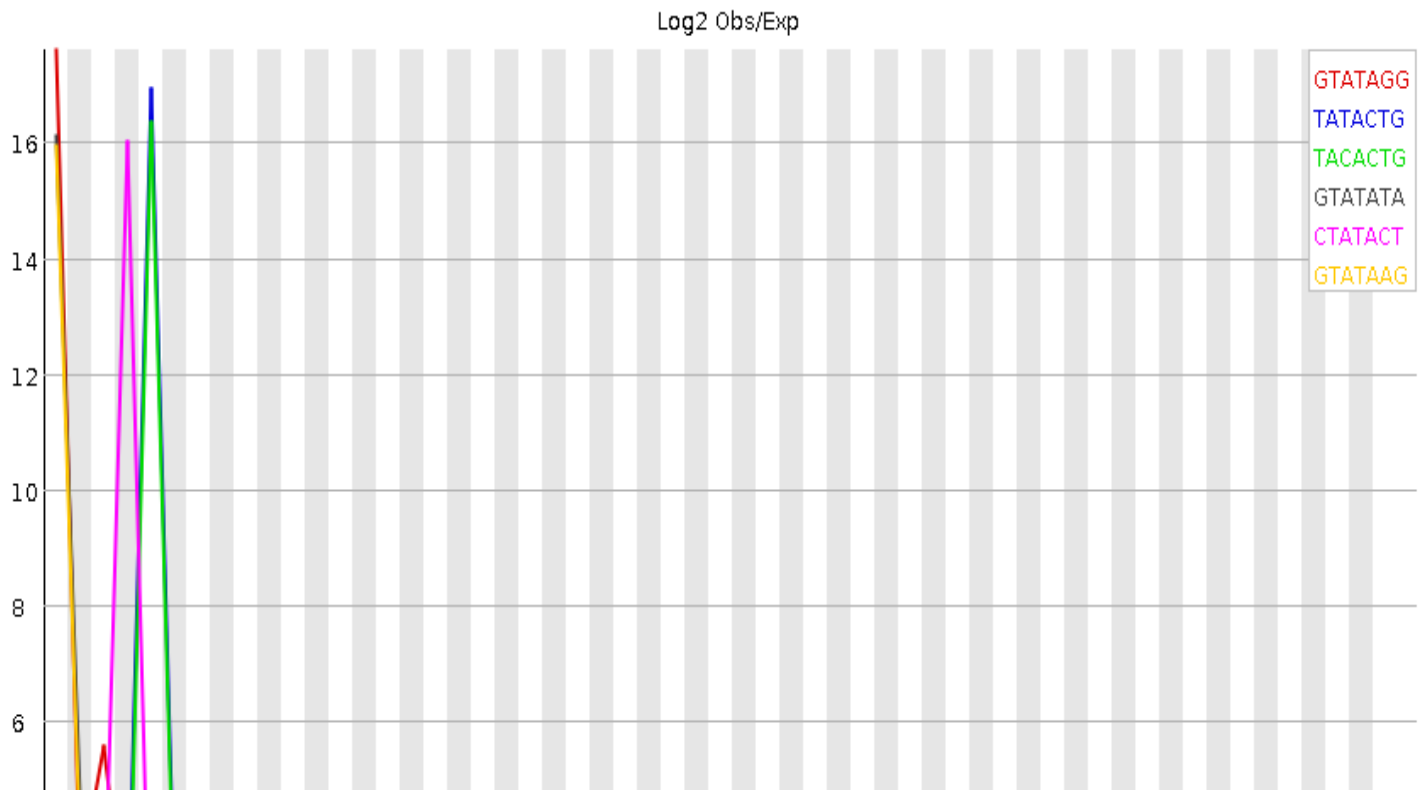
 **Overrepresented sequences**
No overrepresented sequences

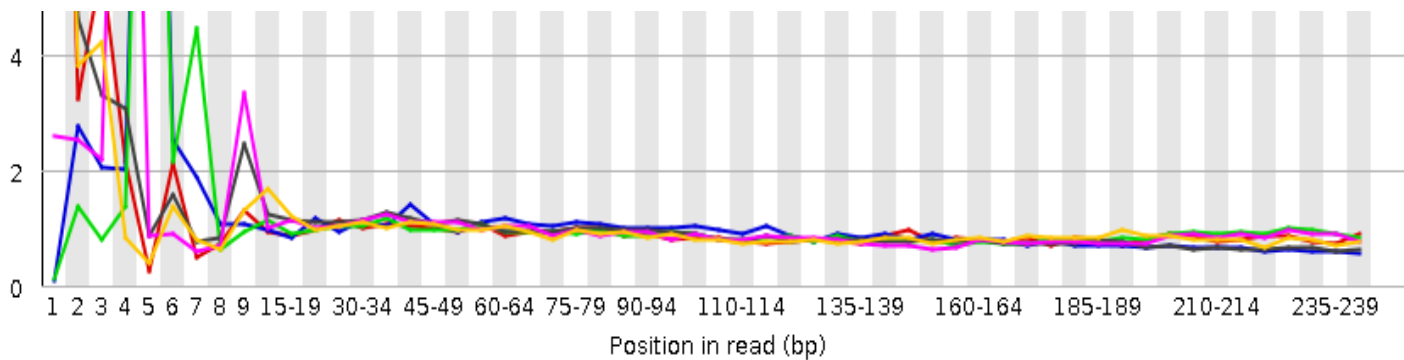
 **Adapter Content**





❌ Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTATAGG	52855	0.0	17.58862	1
TATACTG	169915	0.0	16.938044	5
TACTACTG	125020	0.0	16.365173	5
GTATATA	156455	0.0	16.1259	1
CTATACT	83180	0.0	16.016615	4
GTATAAG	66360	0.0	15.939532	1
TATACAG	146515	0.0	15.904436	5
GTATAGA	90290	0.0	15.471368	1
TATACCG	32655	0.0	15.467413	5
GTCCTAG	52115	0.0	15.403734	1
TCTATAC	90075	0.0	14.966312	3
TTATACT	126755	0.0	14.84179	4
GTATAAA	140675	0.0	14.51782	1
GTCTTAG	79470	0.0	14.415351	1
GTCCTAT	67825	0.0	14.390074	1
GTATTAG	89240	0.0	14.081228	1
TAGACAG	142730	0.0	14.001213	5
GTCCTAA	52840	0.0	13.853238	1
GTCTAGG	56945	0.0	13.604451	1
GTATATG	120560	0.0	13.529789	1

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