













Summary

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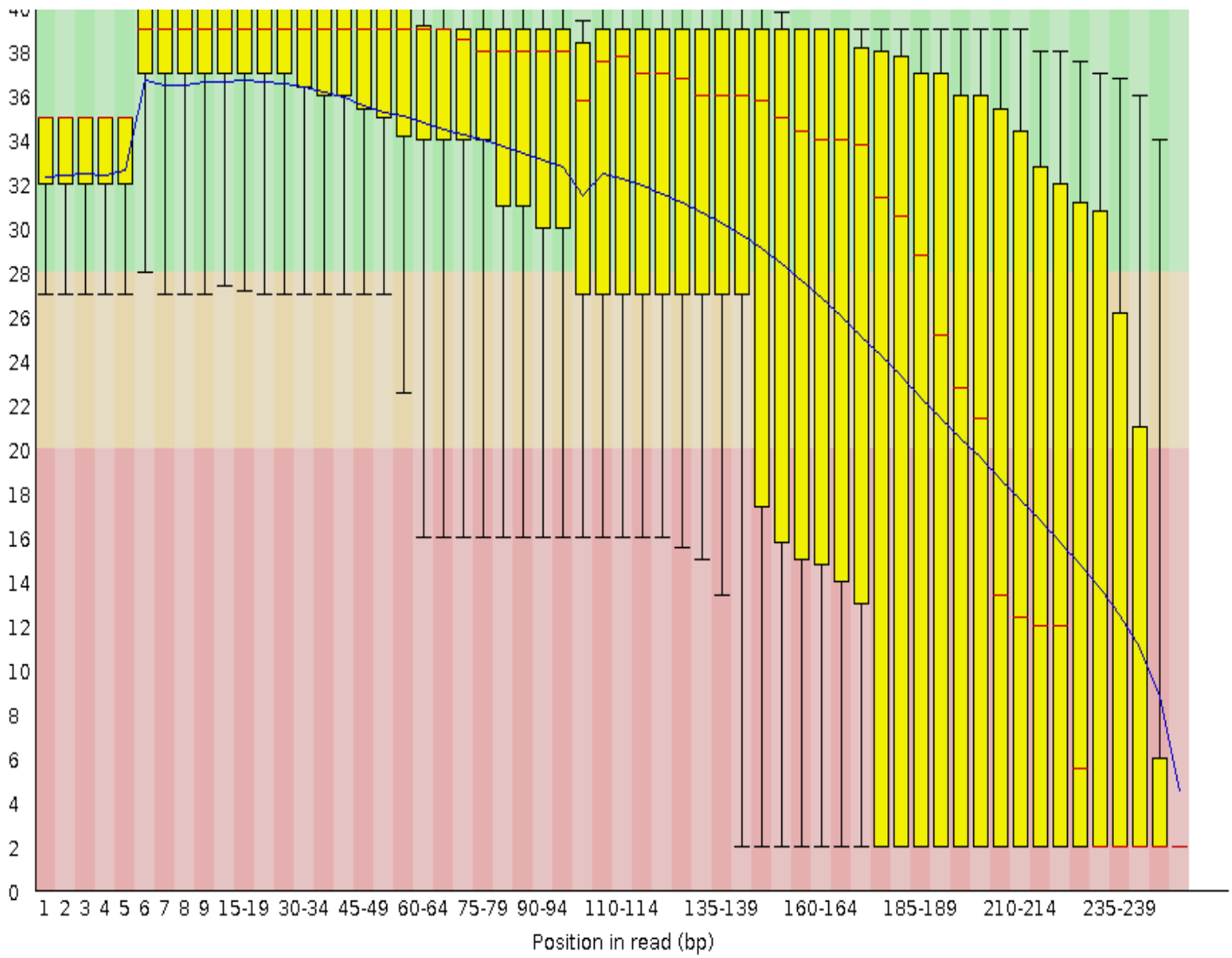
Basic Statistics

Measure	Value
Filename	BS_MK_noAdap_R2.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	42

Per base sequence quality

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

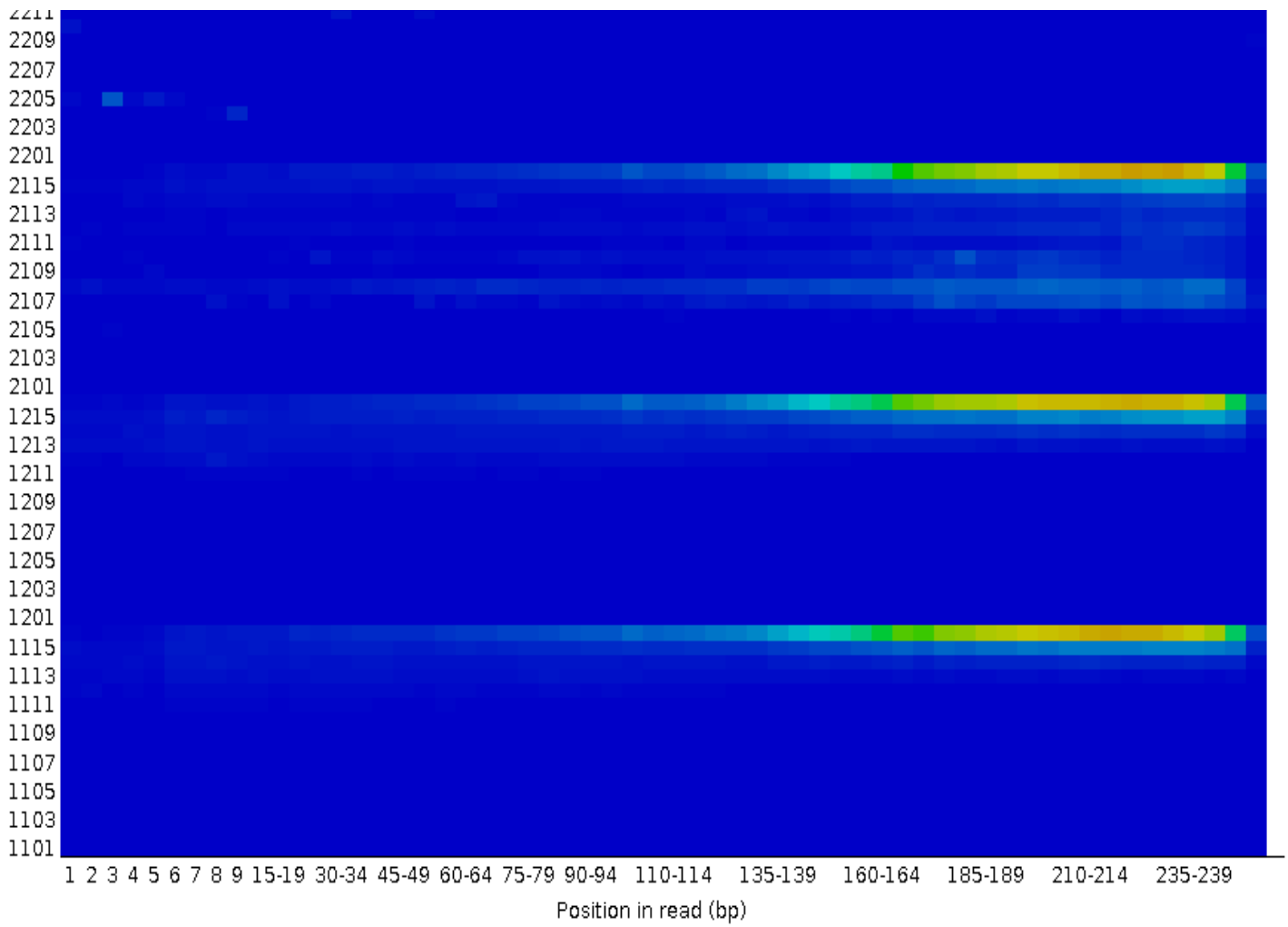




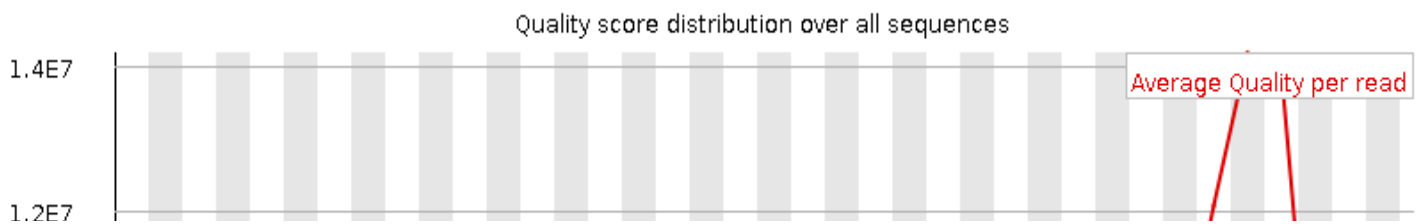
! Per tile sequence quality

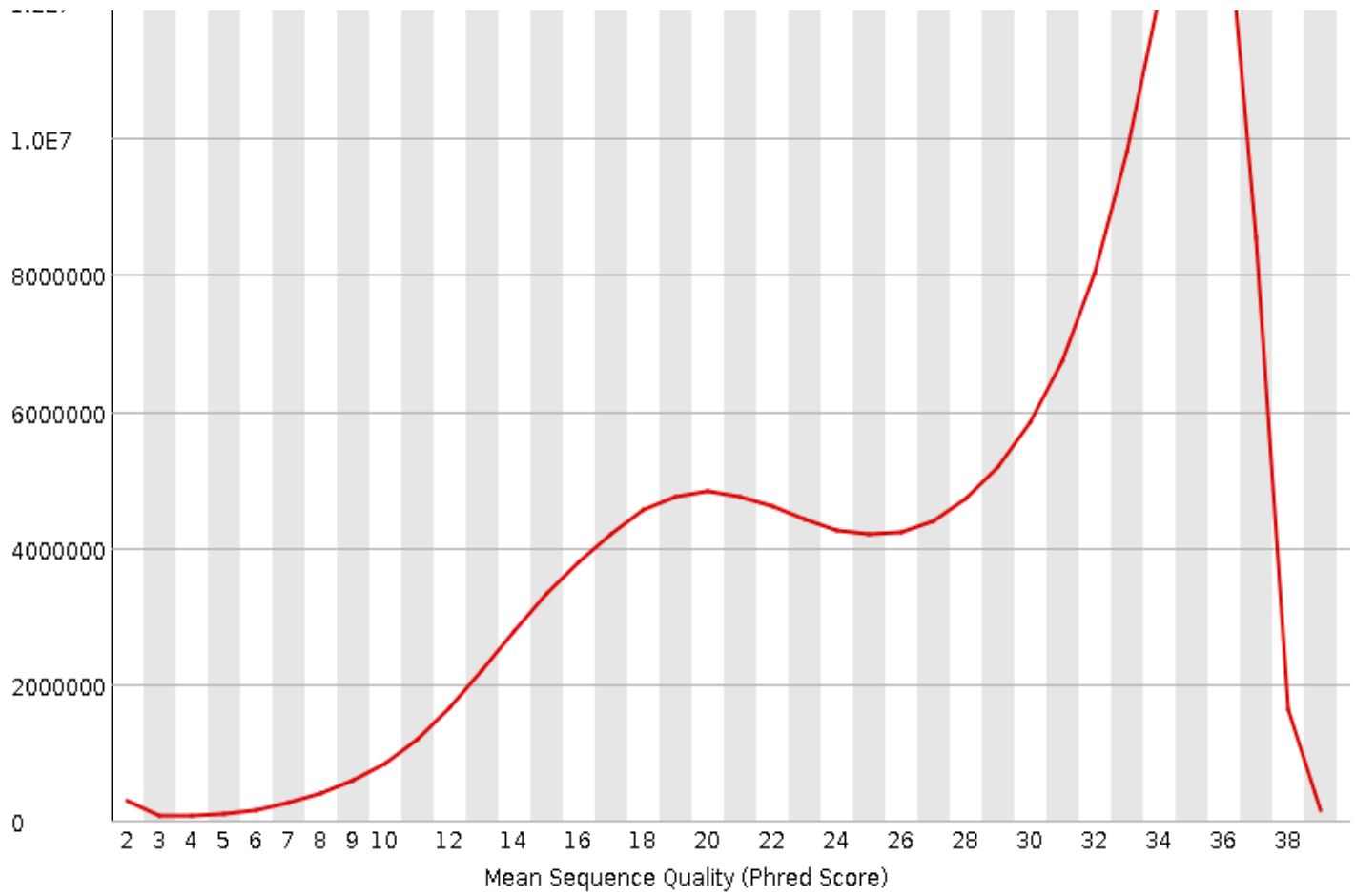
Quality per tile



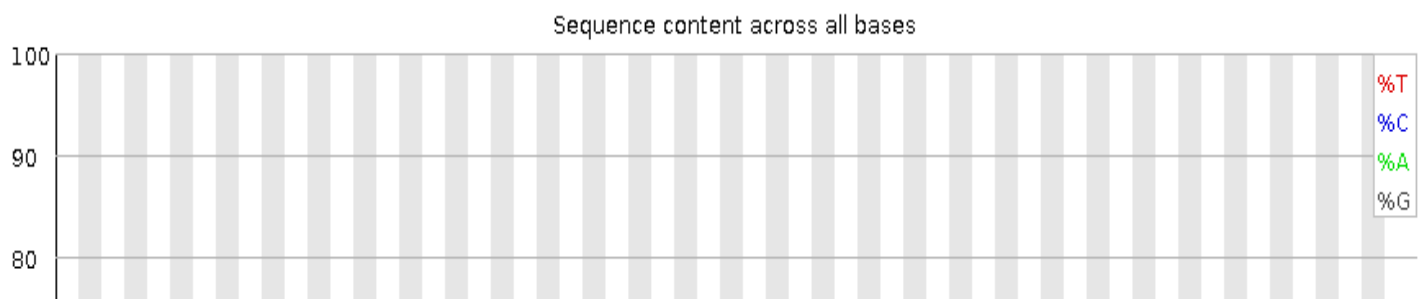


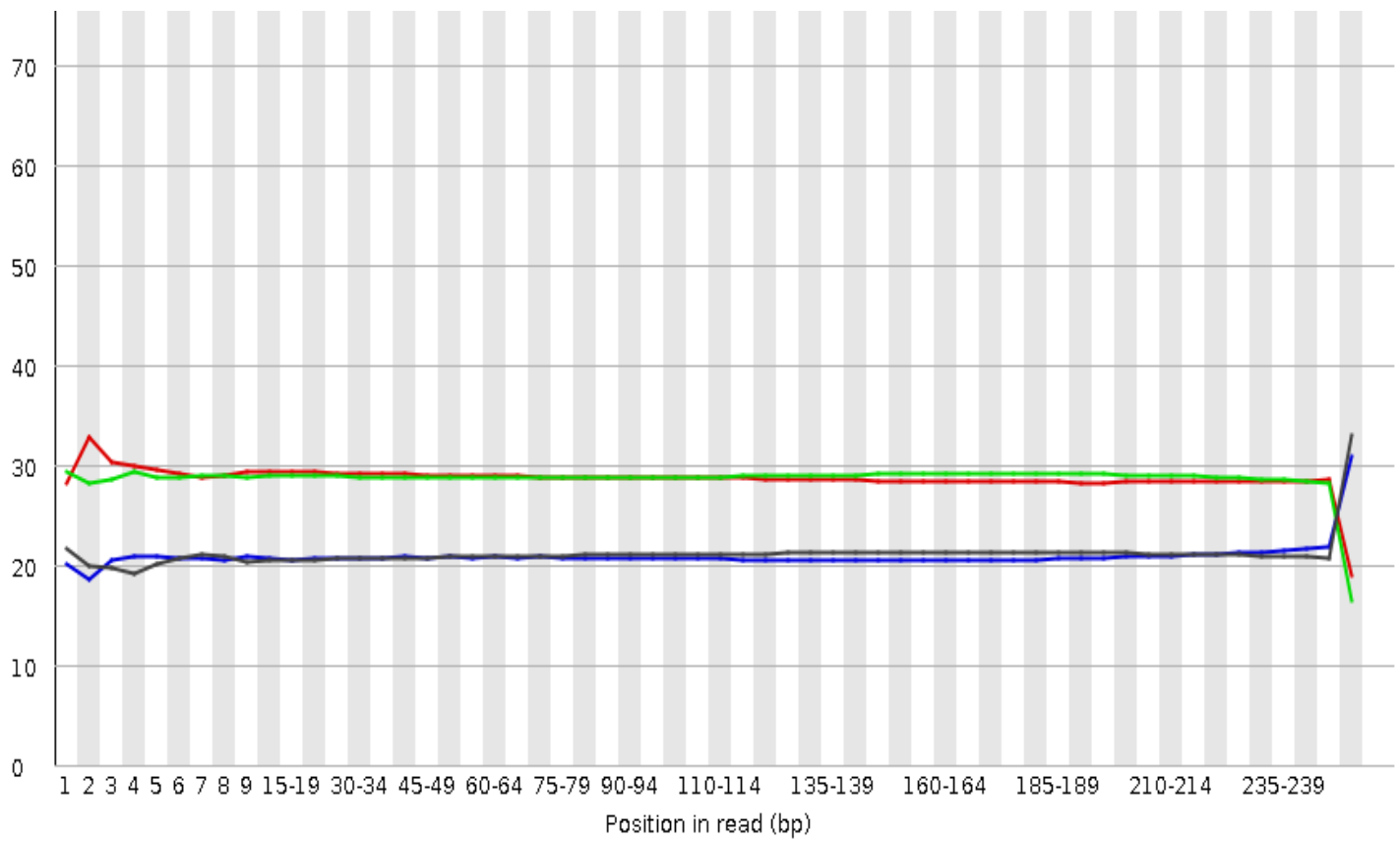
 **Per sequence quality scores**



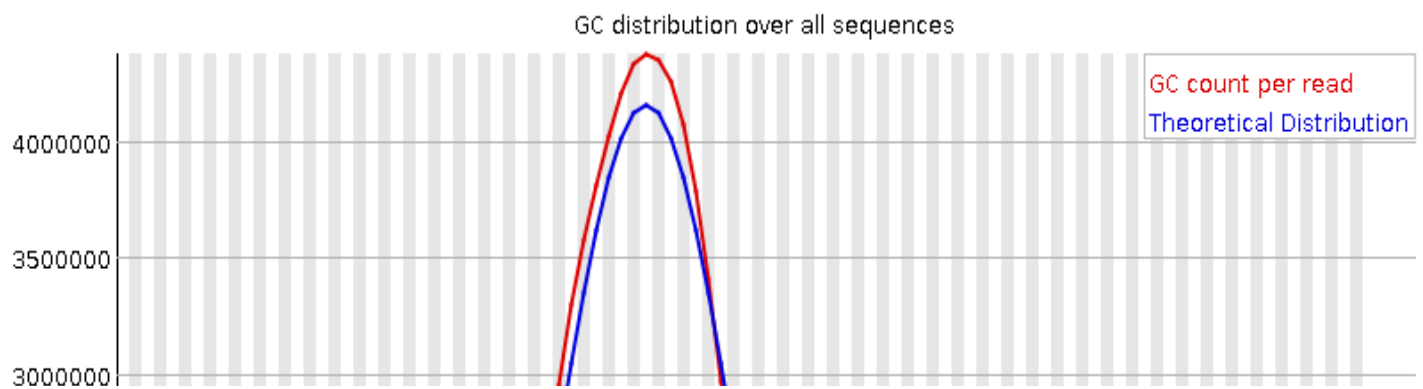


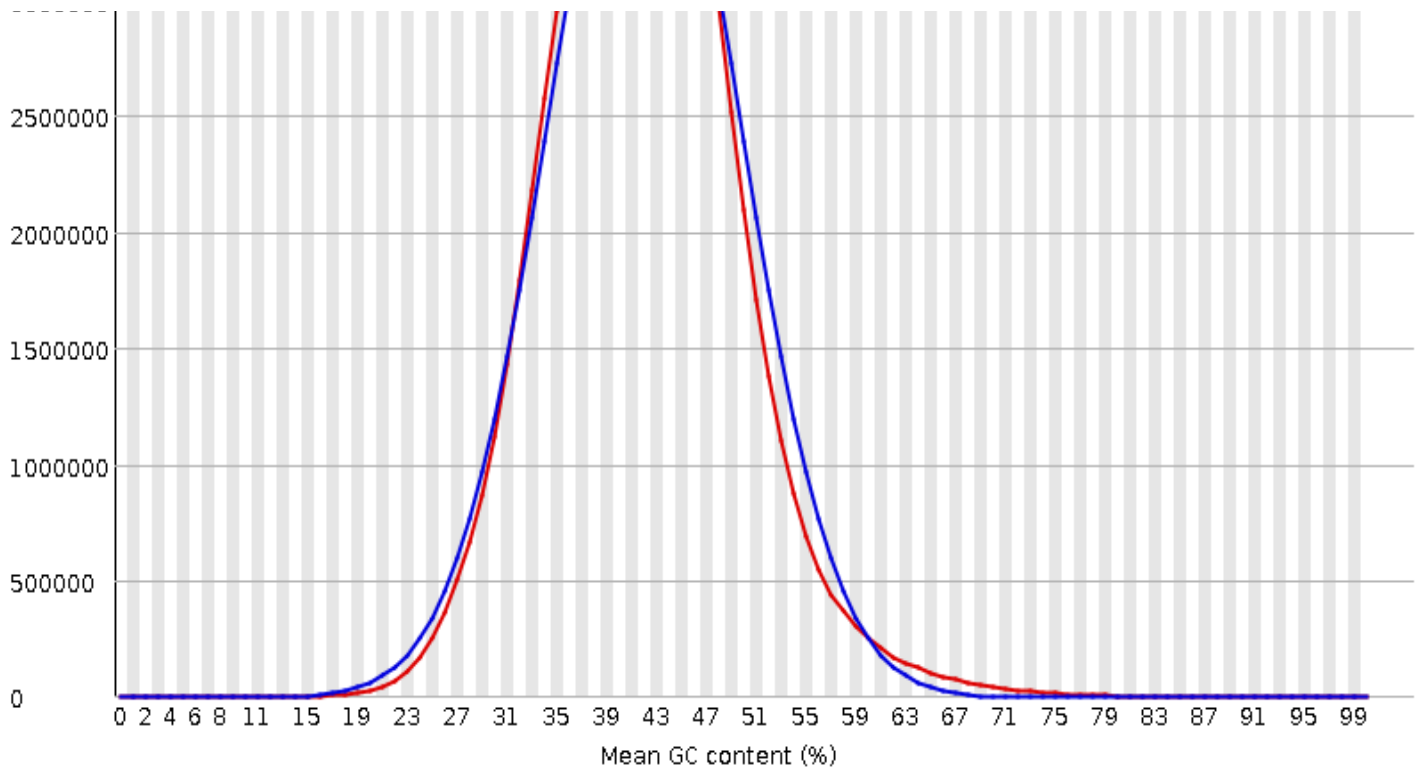
! Per base sequence content



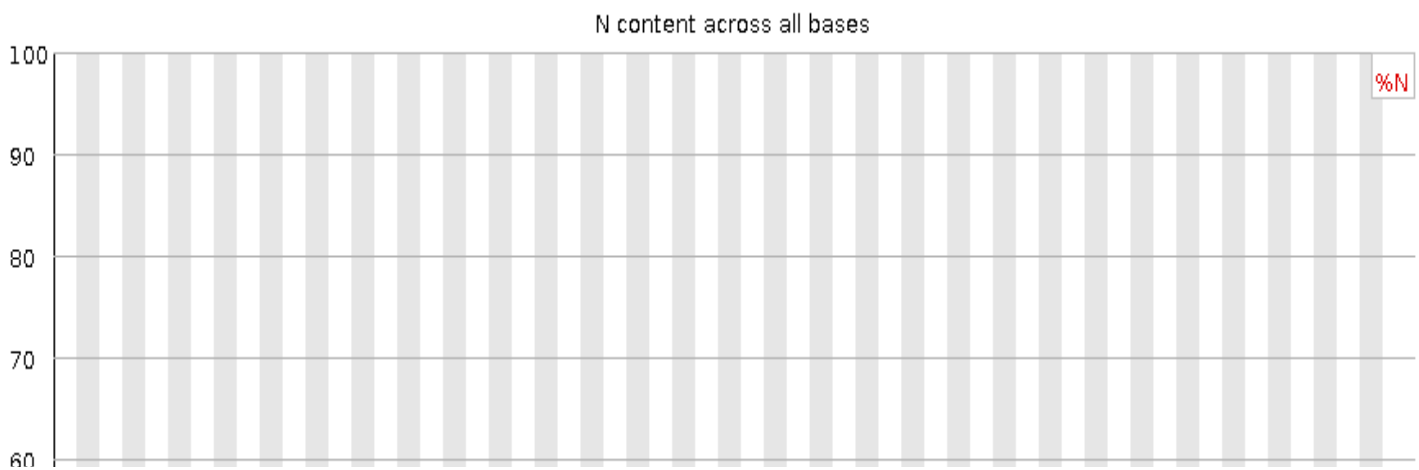


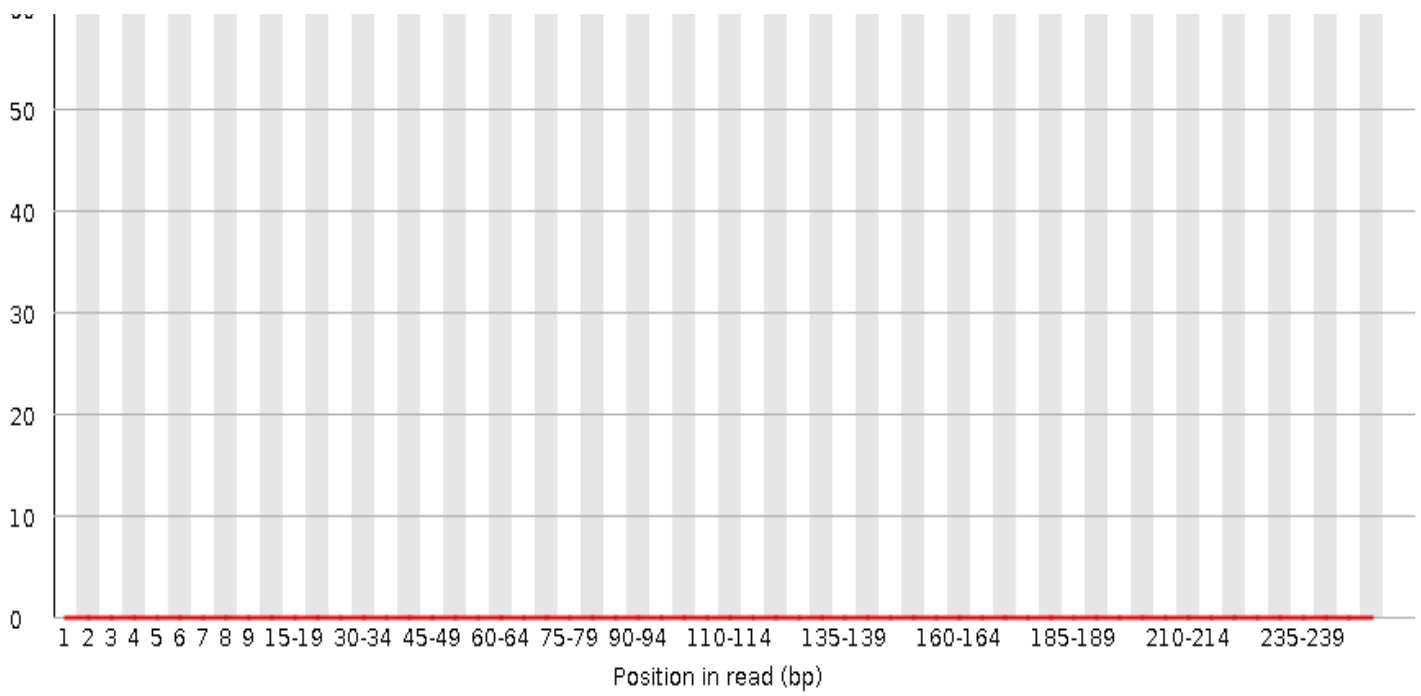
 **Per sequence GC content**



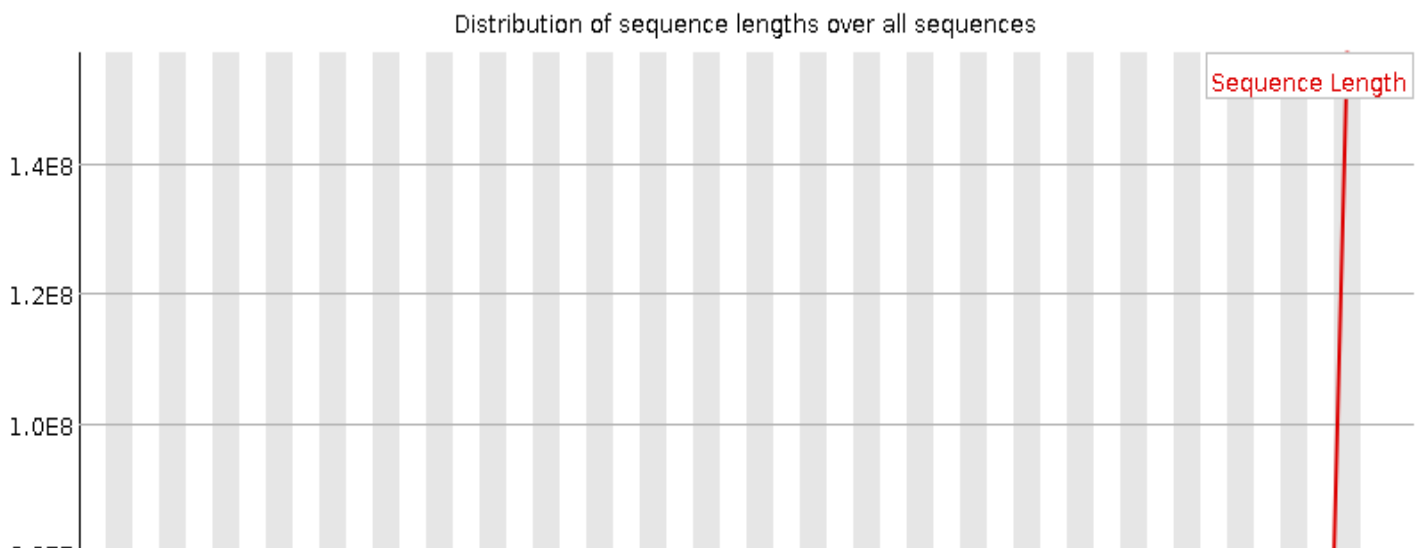


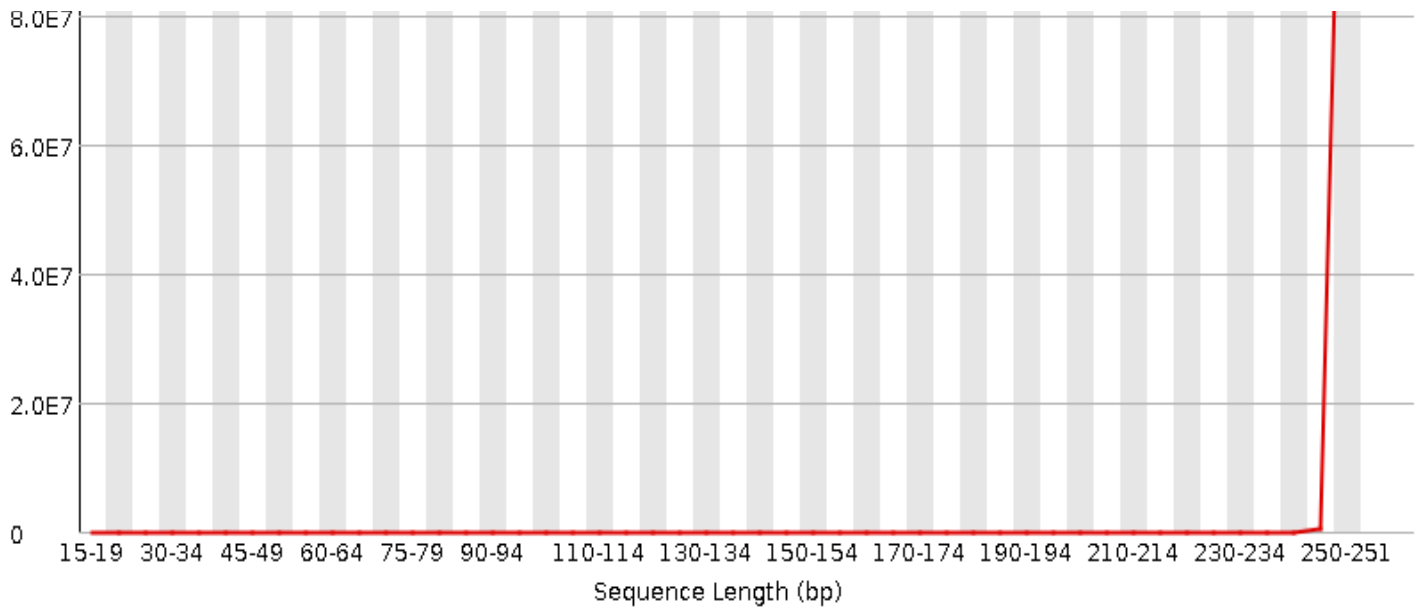
 **Per base N content**



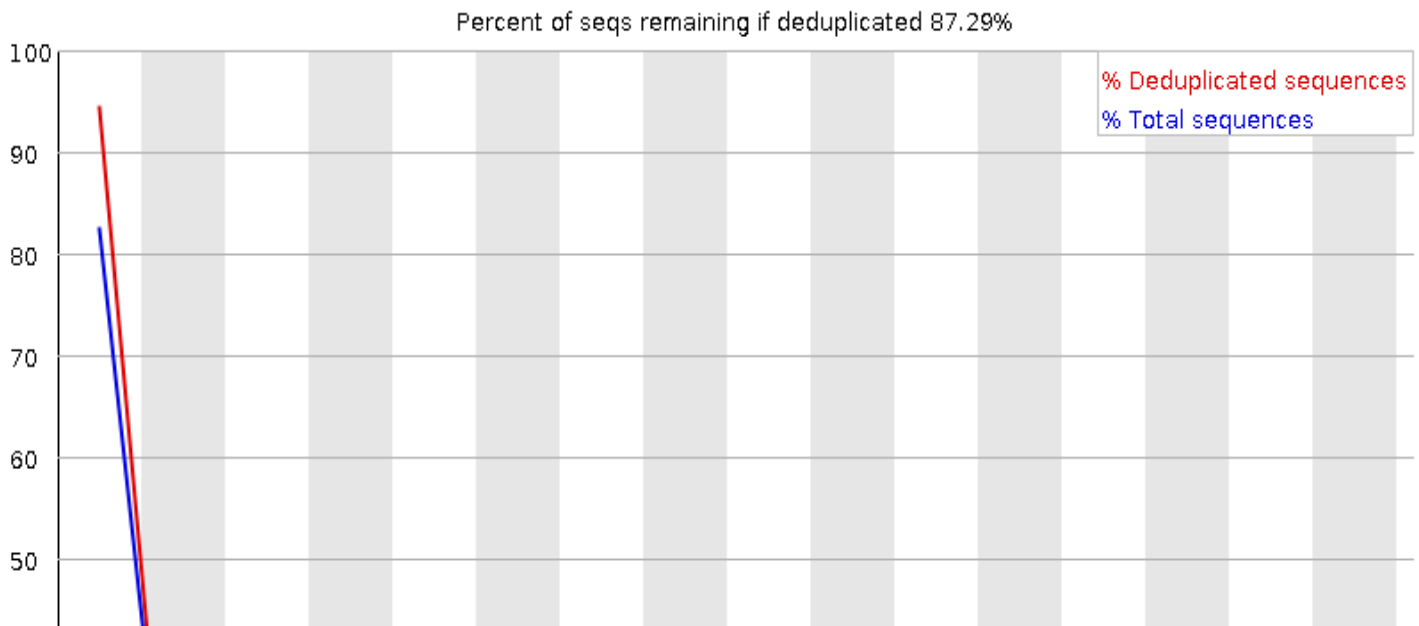


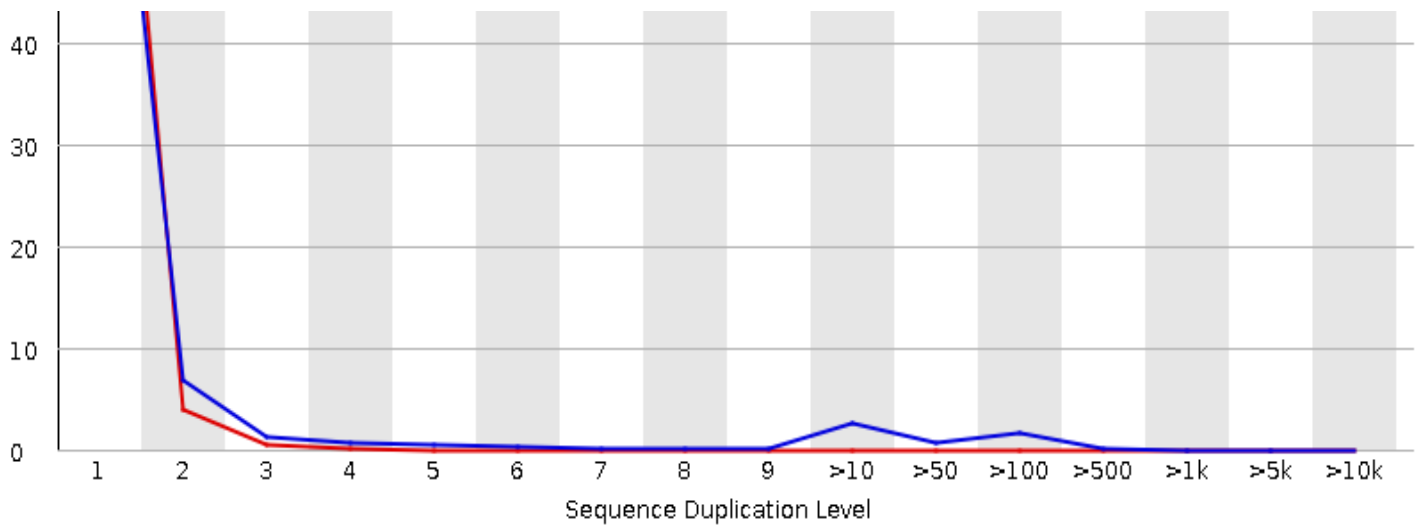
! Sequence Length Distribution





Sequence Duplication Levels

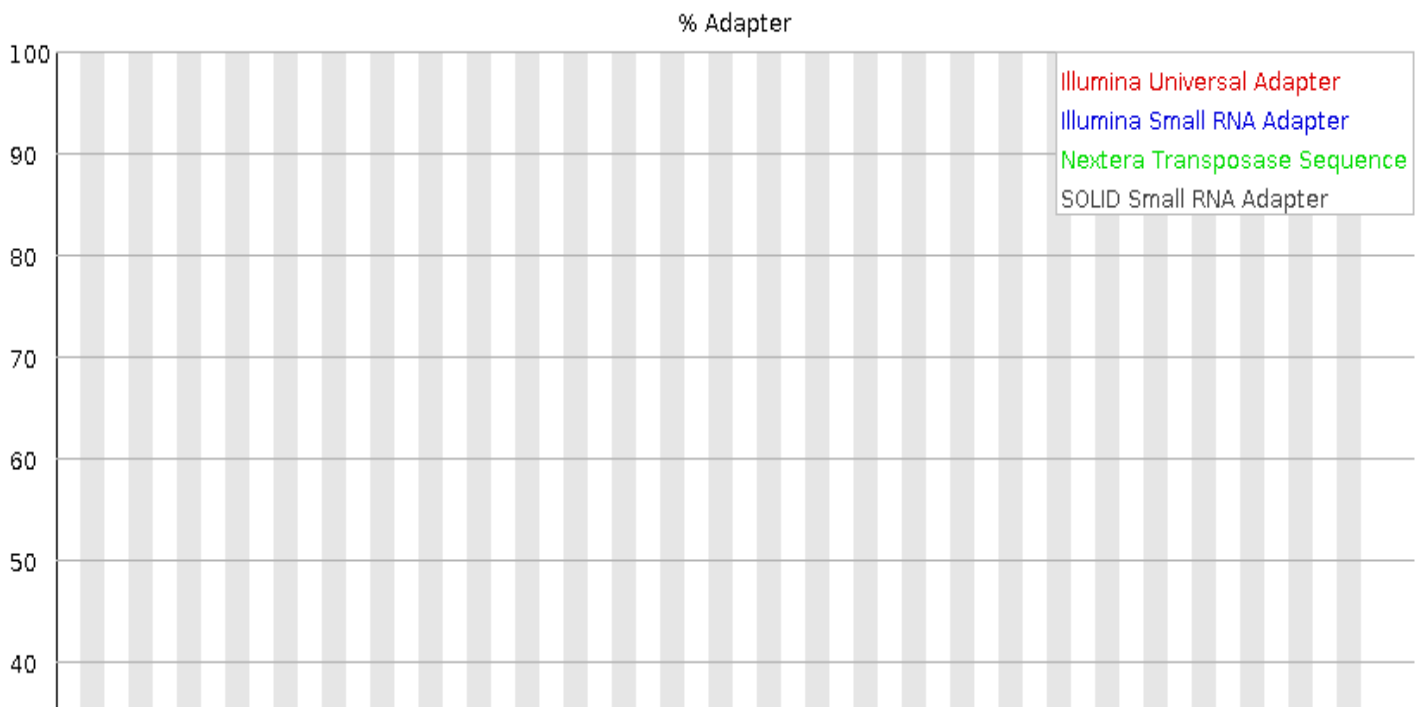




 **Overrepresented sequences**

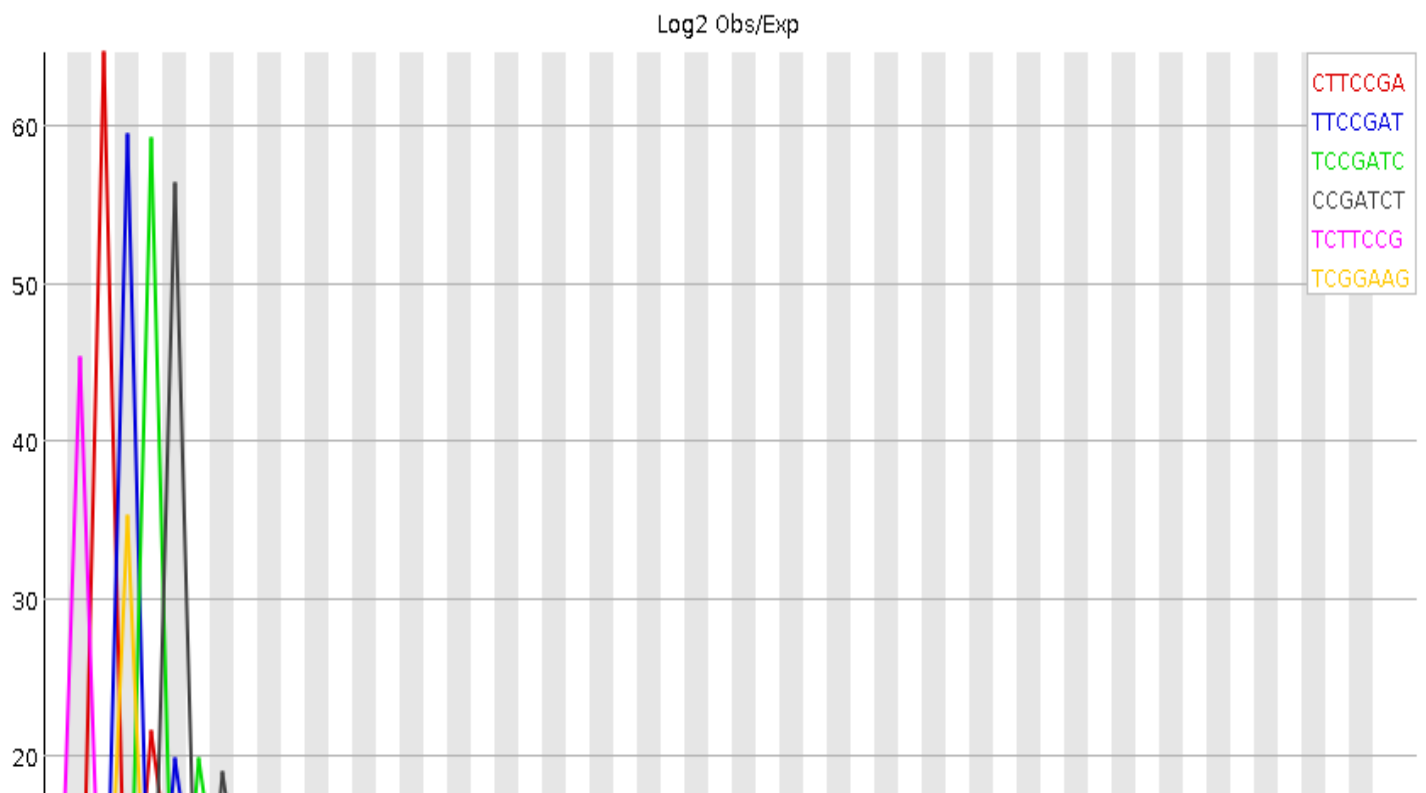
No overrepresented sequences

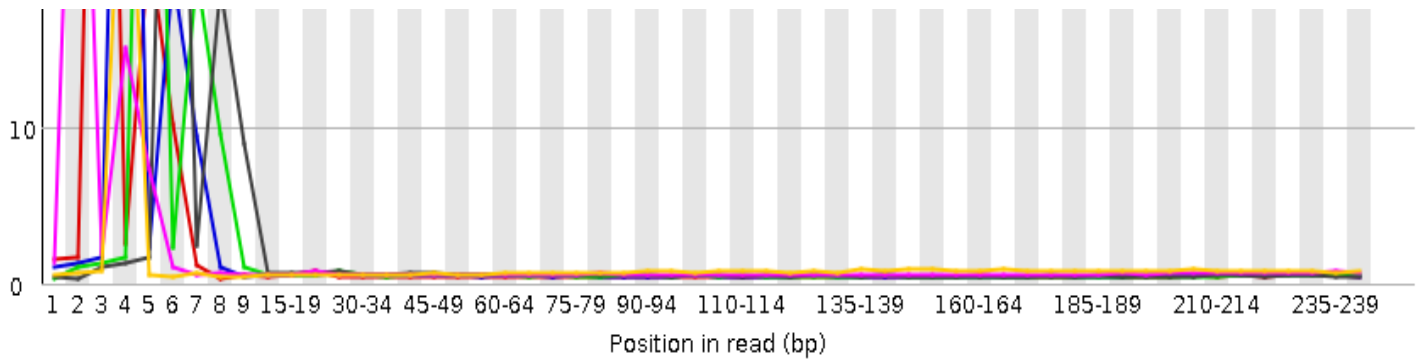
 **Adapter Content**





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	144050	0.0	64.53496	3
TTCCGAT	156190	0.0	59.34881	4
TCCGATC	156625	0.0	59.129513	5
CCGATCT	164180	0.0	56.319508	6
TCTTCCG	208640	0.0	45.193775	2
TCGGAAG	116960	0.0	35.173603	4
ATCGGAA	127025	0.0	32.500862	3
GATCGGA	127690	0.0	32.30884	2
AGATCGG	140985	0.0	29.369858	1
CGATCTA	103490	0.0	27.461481	7
CGGAAGA	185340	0.0	22.57787	5
CGATCTT	135045	0.0	20.475975	7
CTCTTCC	481790	0.0	20.125328	1
GAAGAGC	275855	0.0	15.495697	7
ACGCTCT	99880	0.0	14.64044	1
CAAGTCG	113605	0.0	14.362661	5
CGATCTC	148735	0.0	13.64838	7
GCTCTTC	252370	0.0	12.72138	2
AAGTCGT	139590	0.0	11.985828	6
CGATCTG	171170	0.0	11.980596	7

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