













Mon 4 May 2015

SW019_adapterTrimmed_dupRemoved_150424_R2.fastq

FastQC Report

Summary

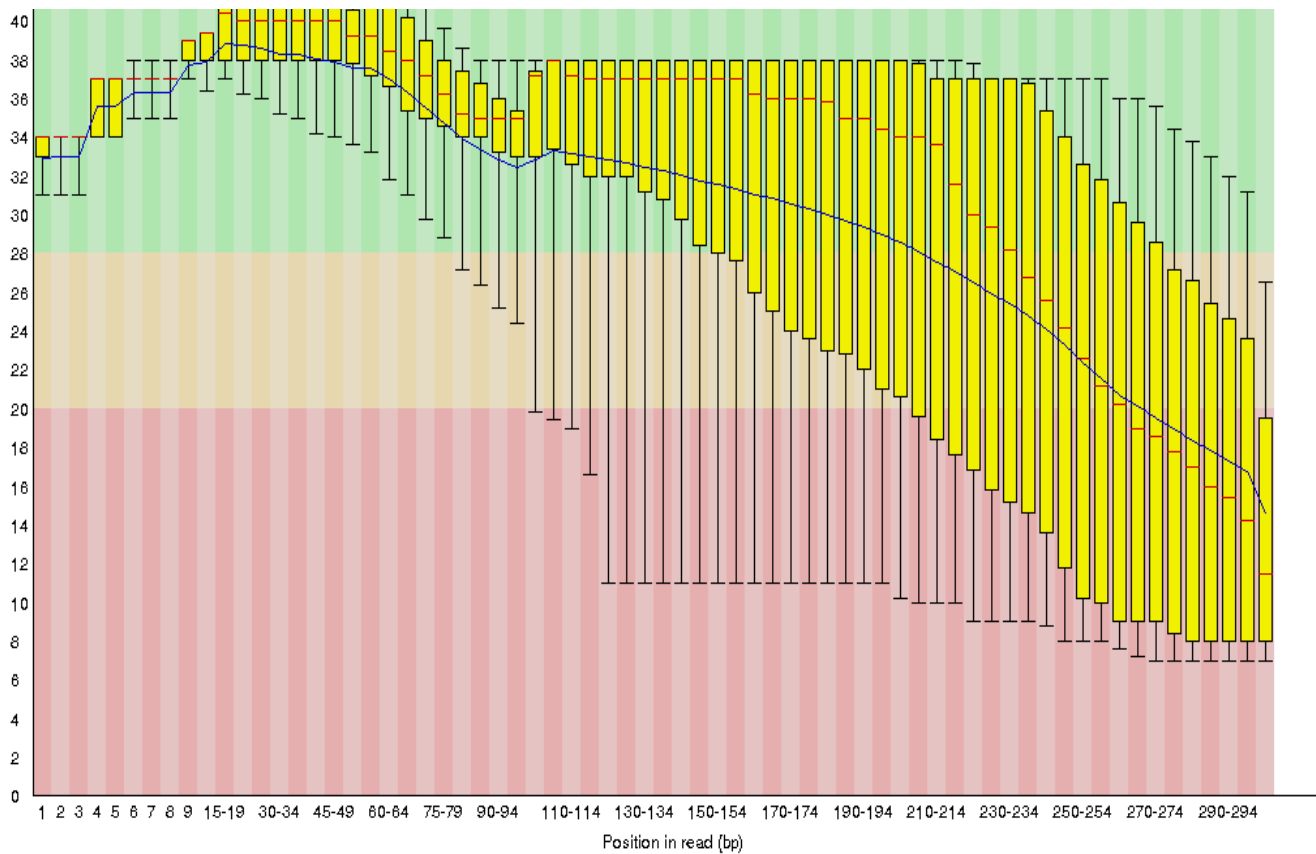
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
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-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per sequence GC content](#)
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Basic Statistics

Measure	Value
Filename	SW019_adapterTrimmed_dupRemoved_150424_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	124970747
Sequences flagged as poor quality	0
Sequence length	25-301
%GC	41

Per base sequence quality

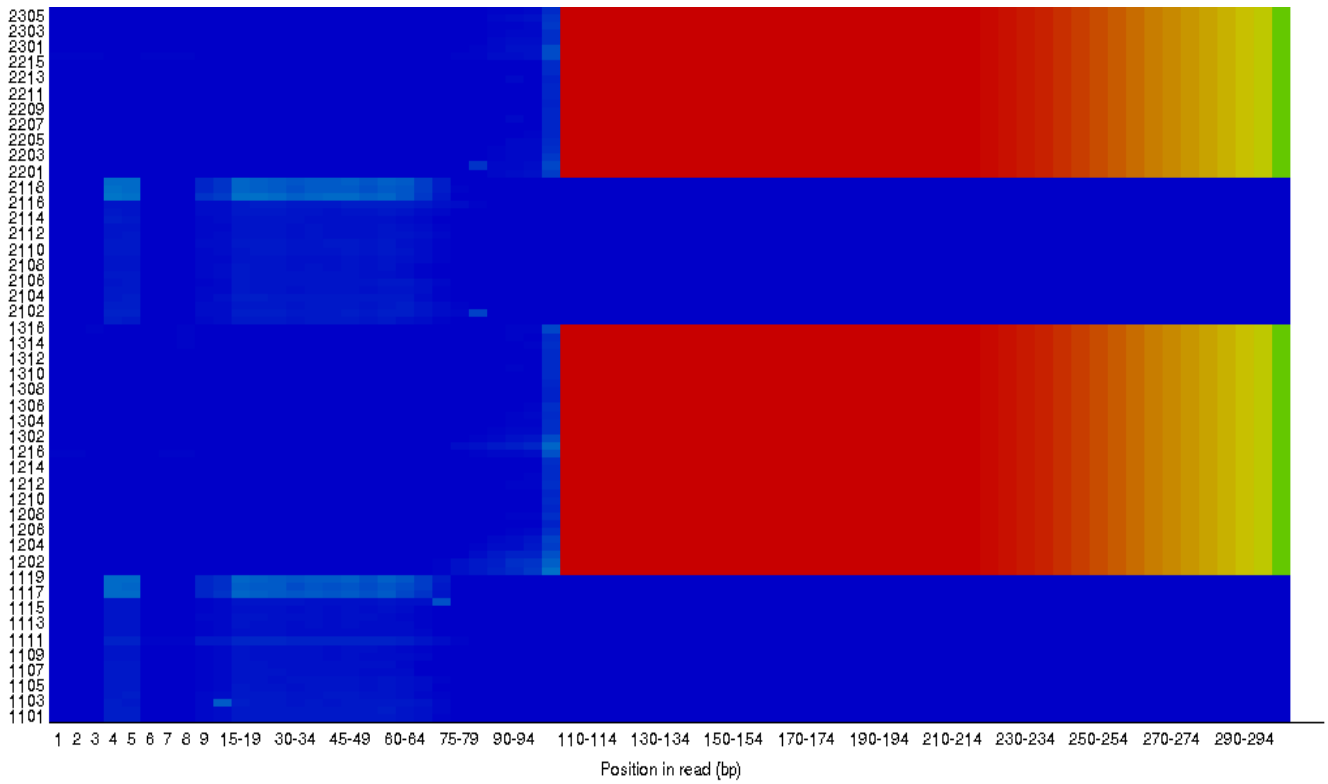
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



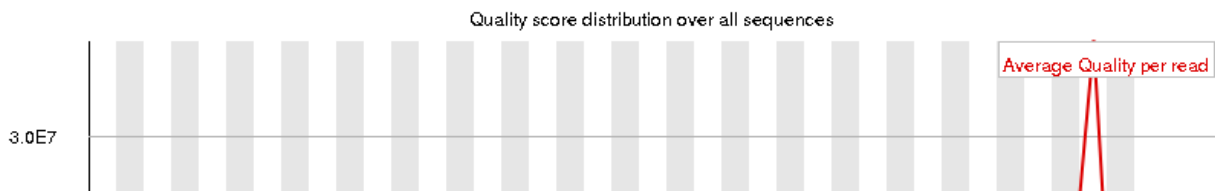
Per tile sequence quality

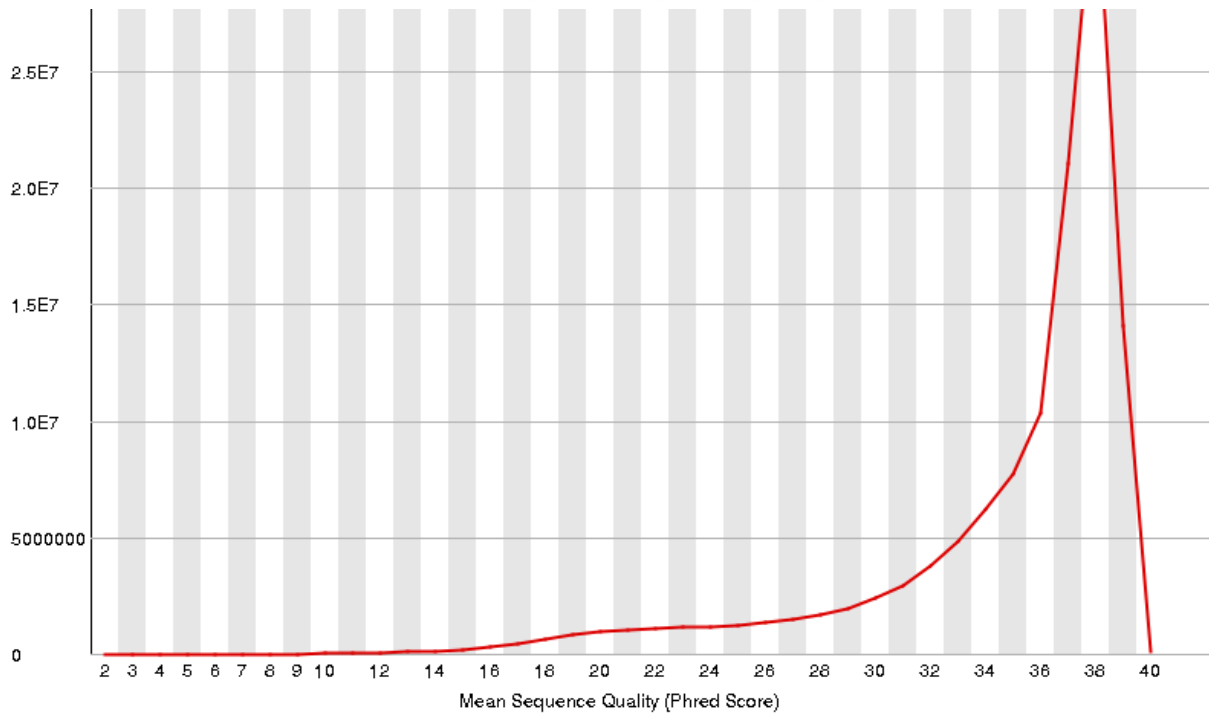
Quality per tile

2315
2313
2311
2309
2307

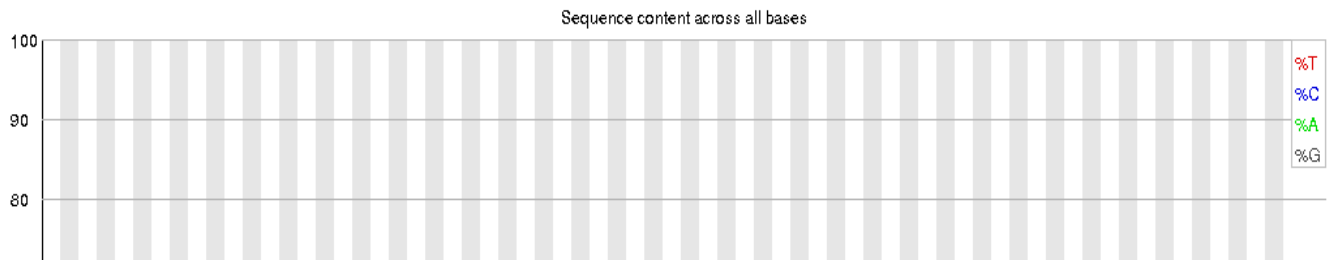


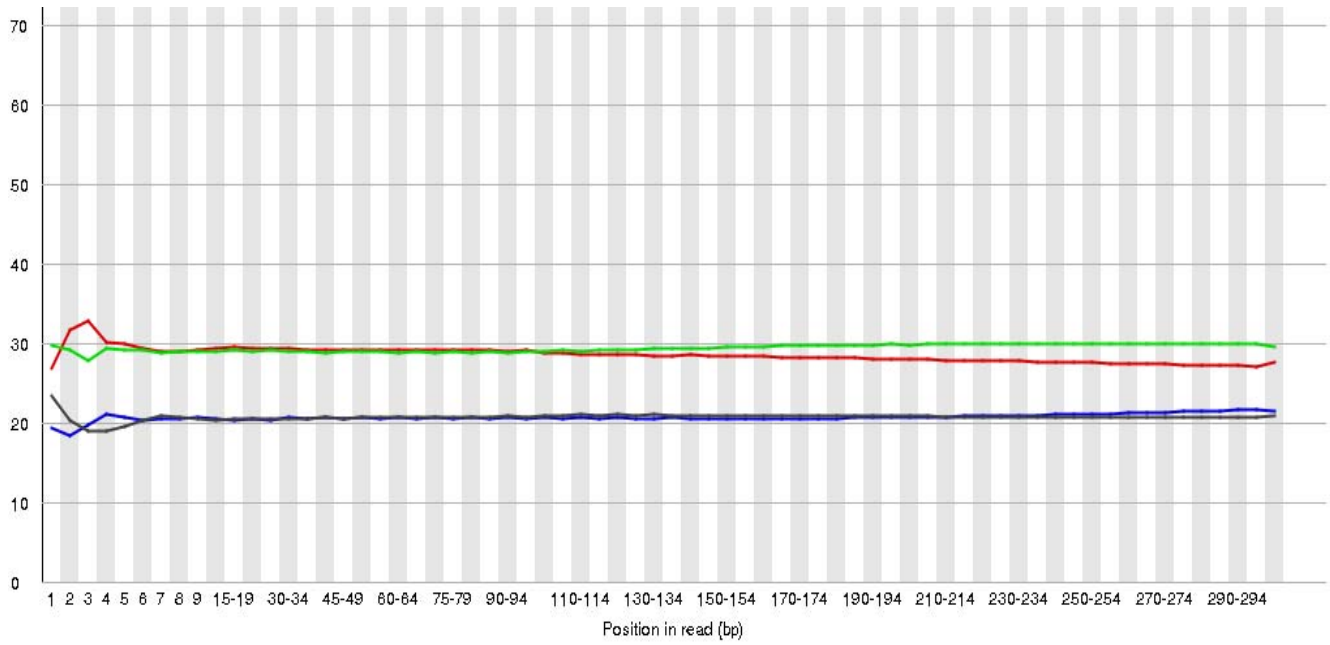
 **Per sequence quality scores**



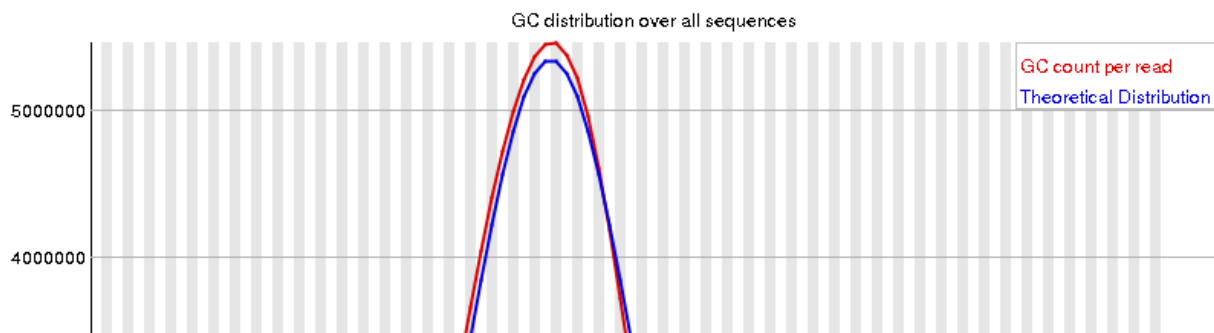


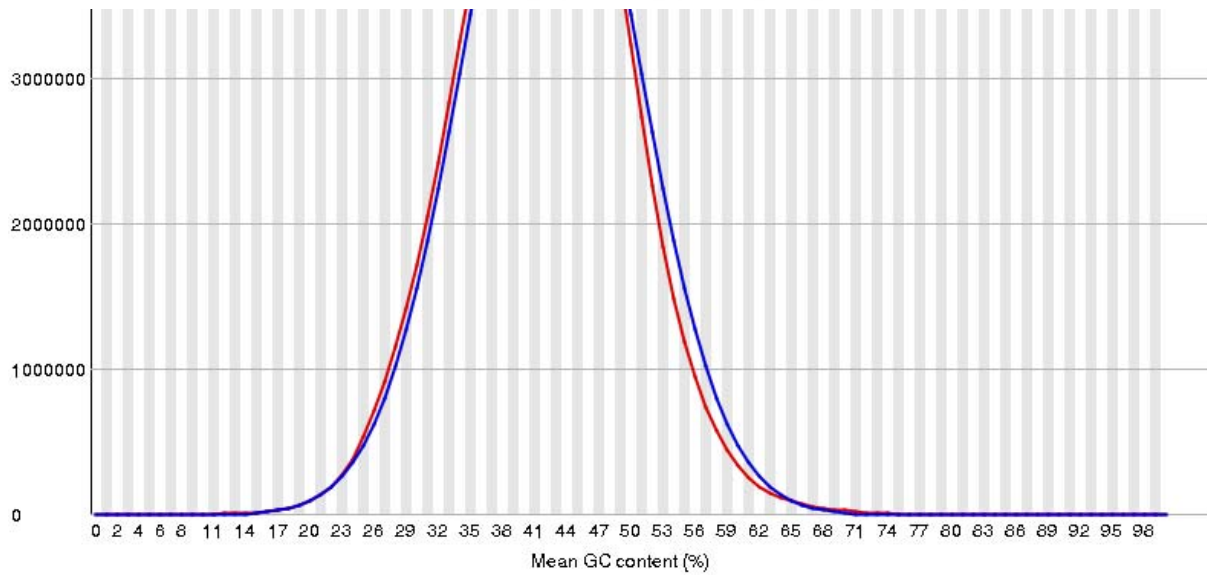
🚨 Per base sequence content



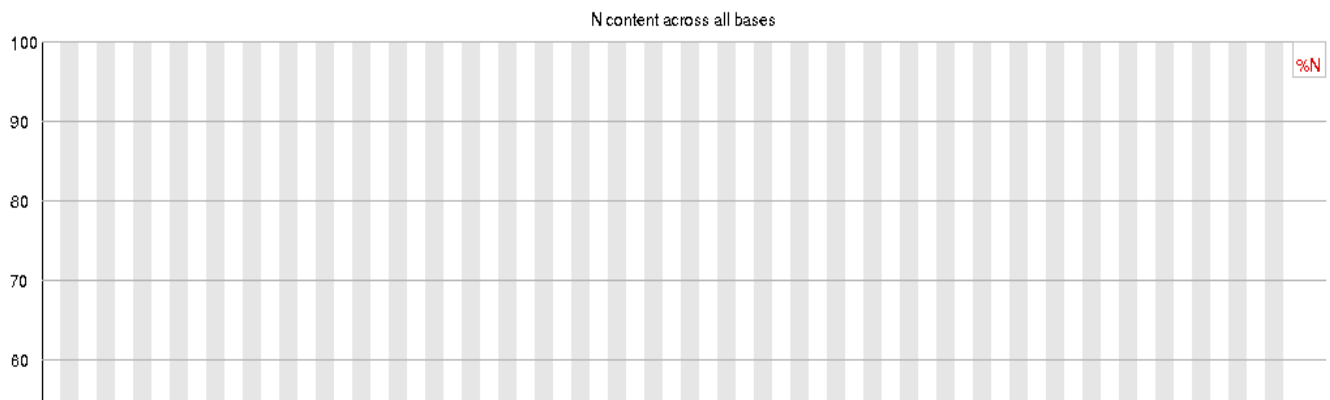


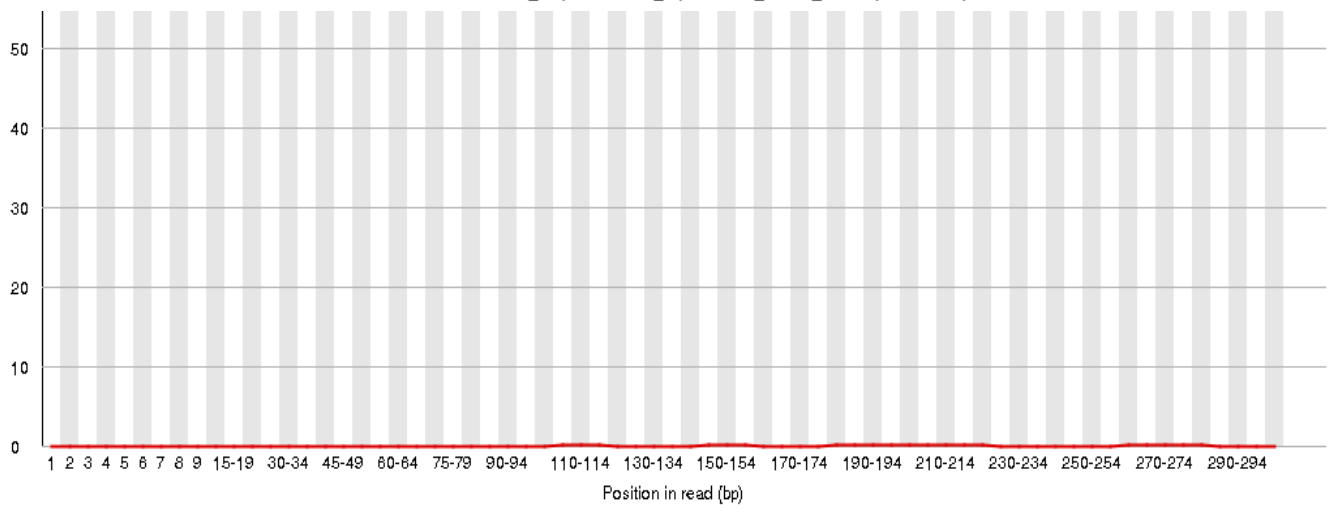
✔ Per sequence GC content



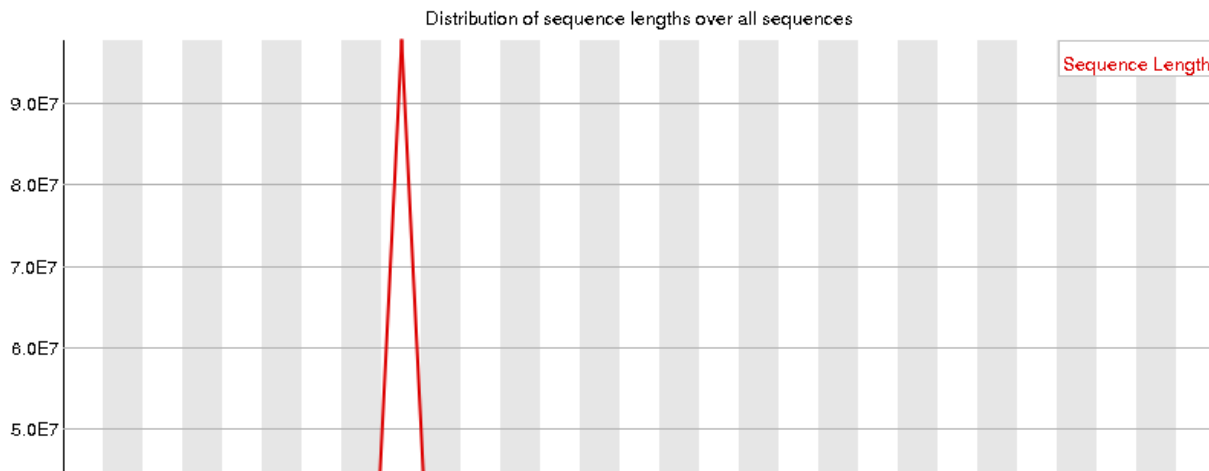


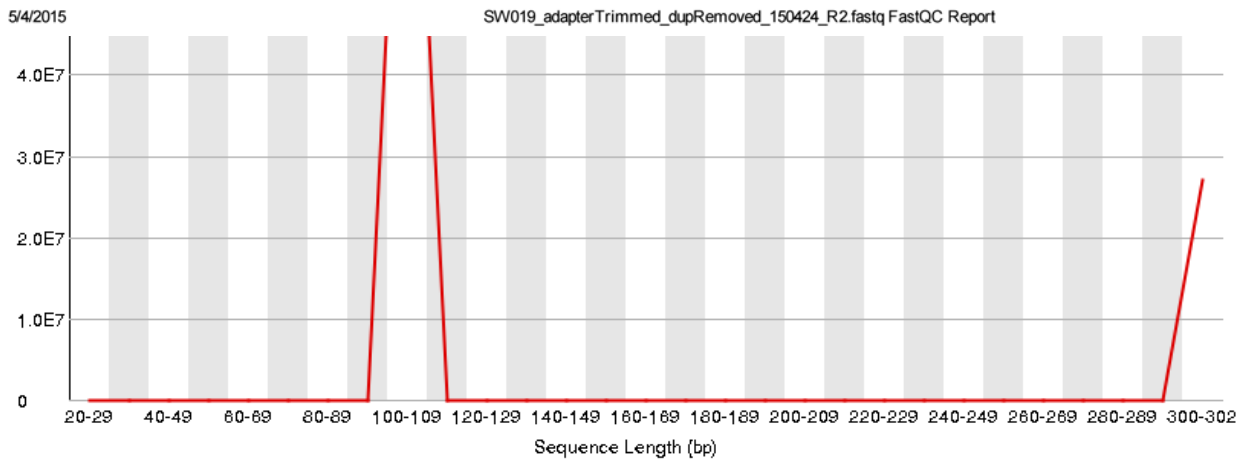
Per base N content



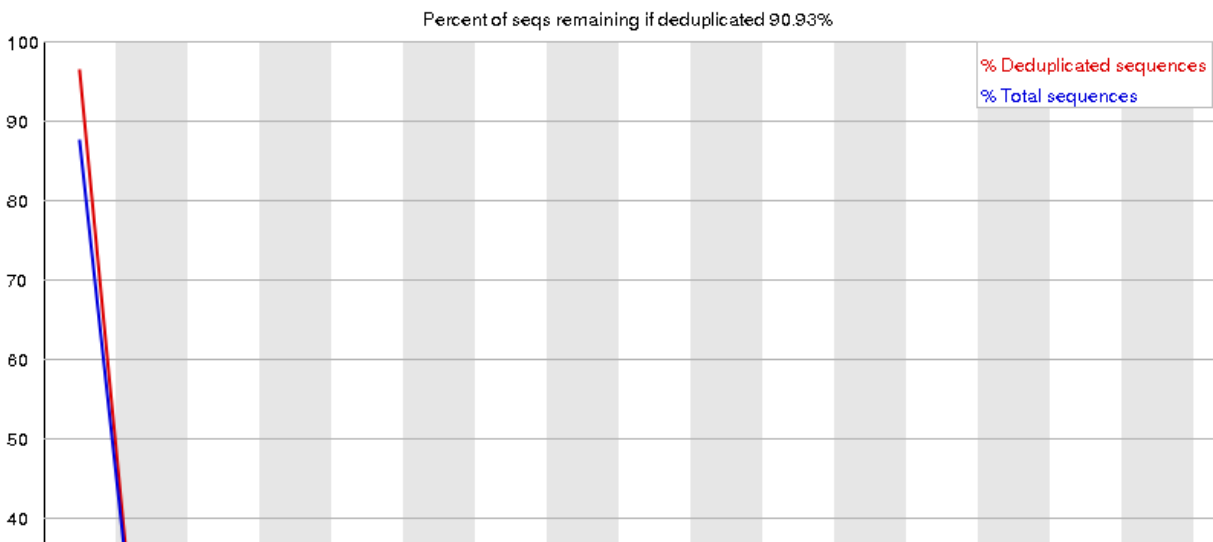


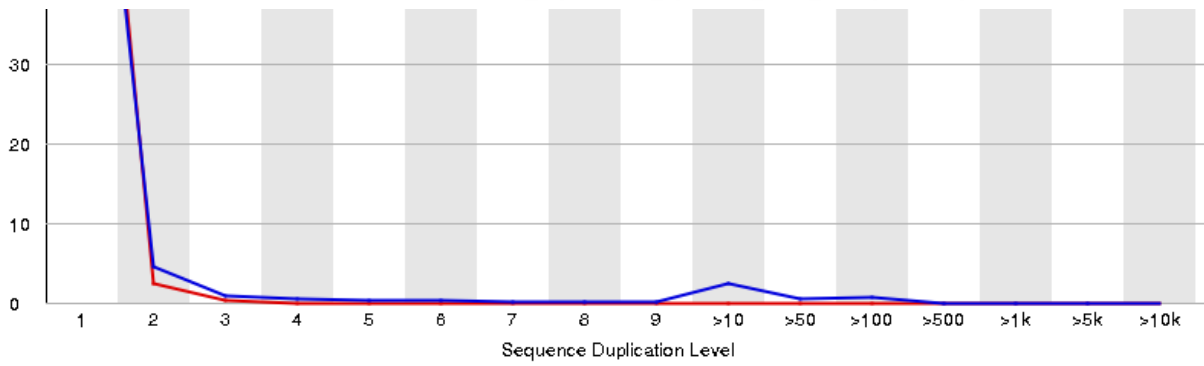
! Sequence Length Distribution





 **Sequence Duplication Levels**

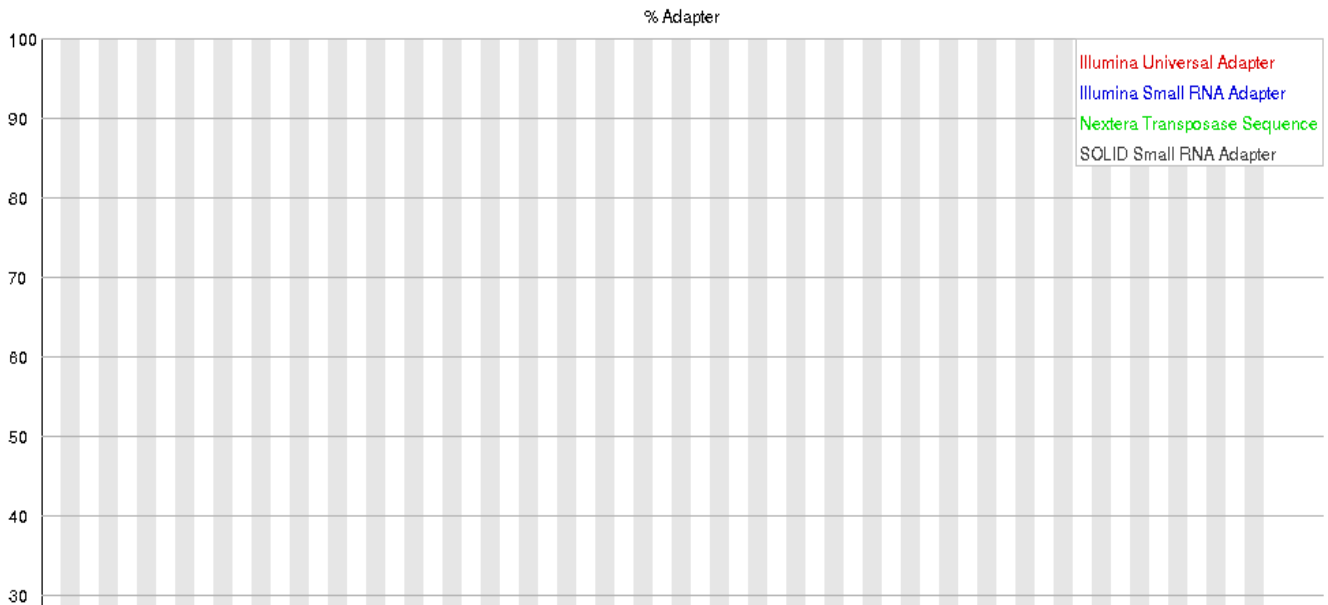


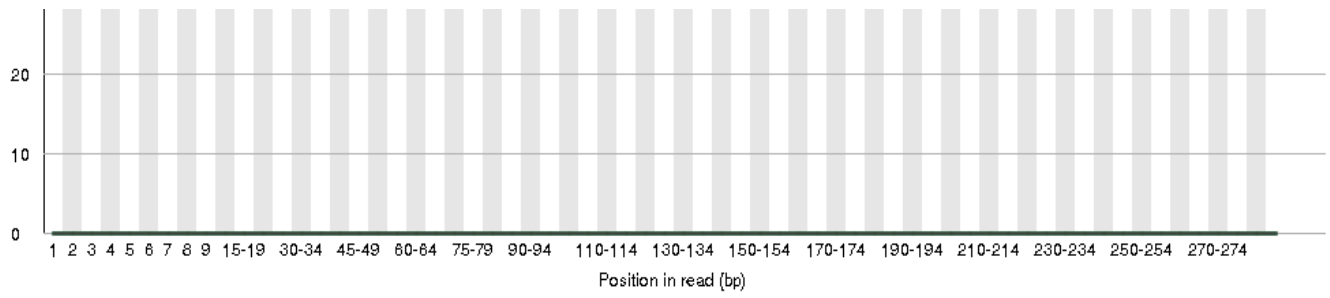


Overrepresented sequences

No overrepresented sequences

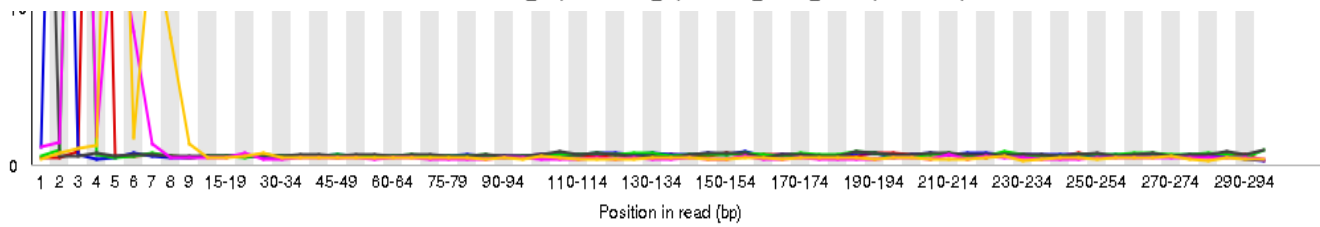
Adapter Content





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGAAG	60015	0.0	50.283707	4
GATCGGA	66025	0.0	45.981297	2
ATCGGAA	65915	0.0	45.940586	3
AGATCGG	70985	0.0	42.86412	1
CTCCGA	77575	0.0	42.530083	3
TCCGATC	82640	0.0	39.94522	5
TTCCGAT	82725	0.0	39.864758	4
CCGATCT	85785	0.0	38.46924	6
CGGAAGA	89525	0.0	33.744705	5
TCTTCCG	104660	0.0	31.939705	2
GAAGAGC	129885	0.0	23.40561	7
CGATCTA	49025	0.0	20.632553	7
CTCTTCC	213890	0.0	16.175085	1
GGAAGAG	214990	0.0	14.559399	6
CGATCTT	64380	0.0	14.257983	7
ACGCTCT	46700	0.0	13.9385	1
AAGAGCG	68530	0.0	13.193829	8
CGCTCTT	60975	0.0	11.025464	2
GCTCTTC	117740	0.0	10.852805	2
CGATCTG	78360	0.0	10.792217	7

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