













FastQC Report

Summary

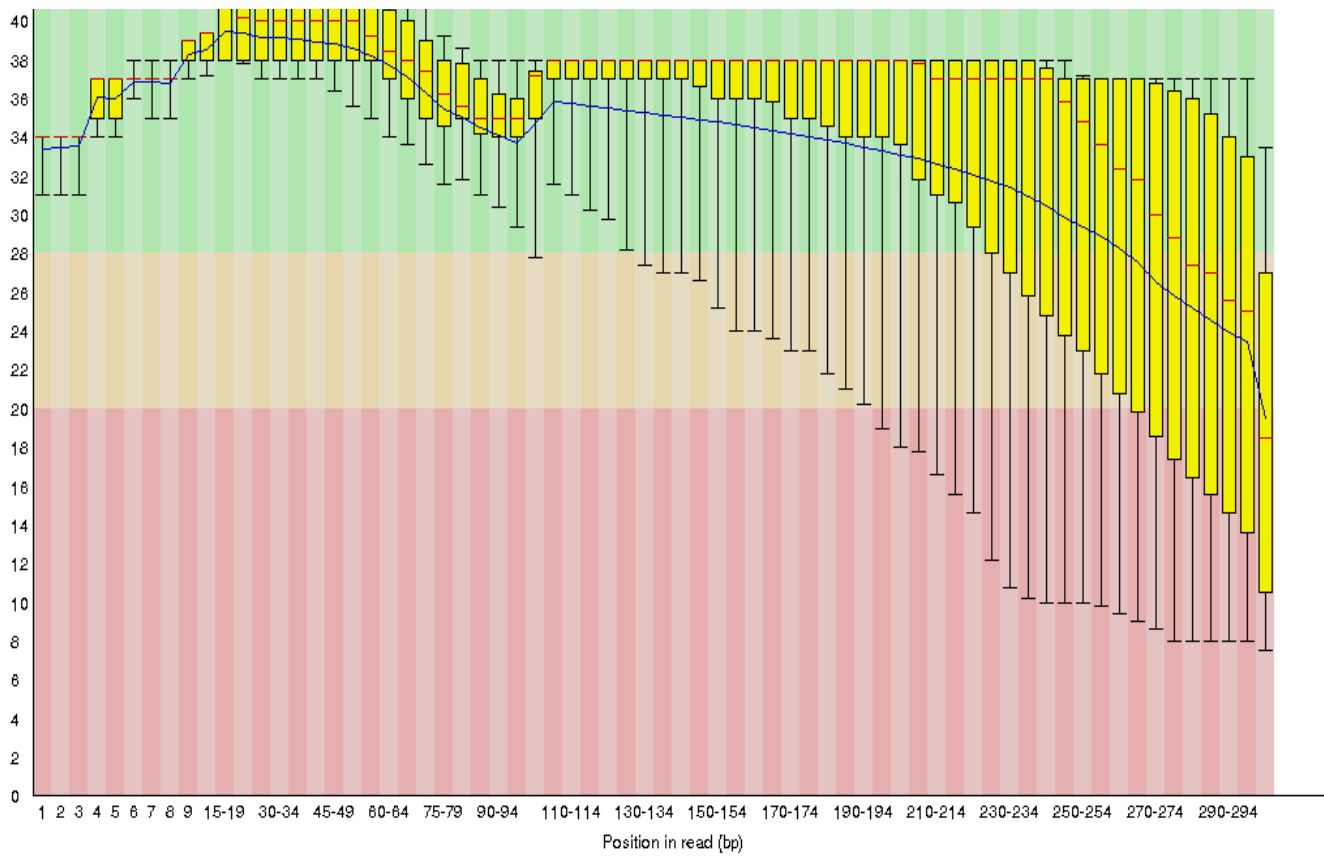
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per tile sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented sequences](#)
-  [Adapter Content](#)
-  [Kmer Content](#)

Basic Statistics

Measure	Value
Filename	SW019_adapterTrimmed_dupRemoved_150424_R1.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

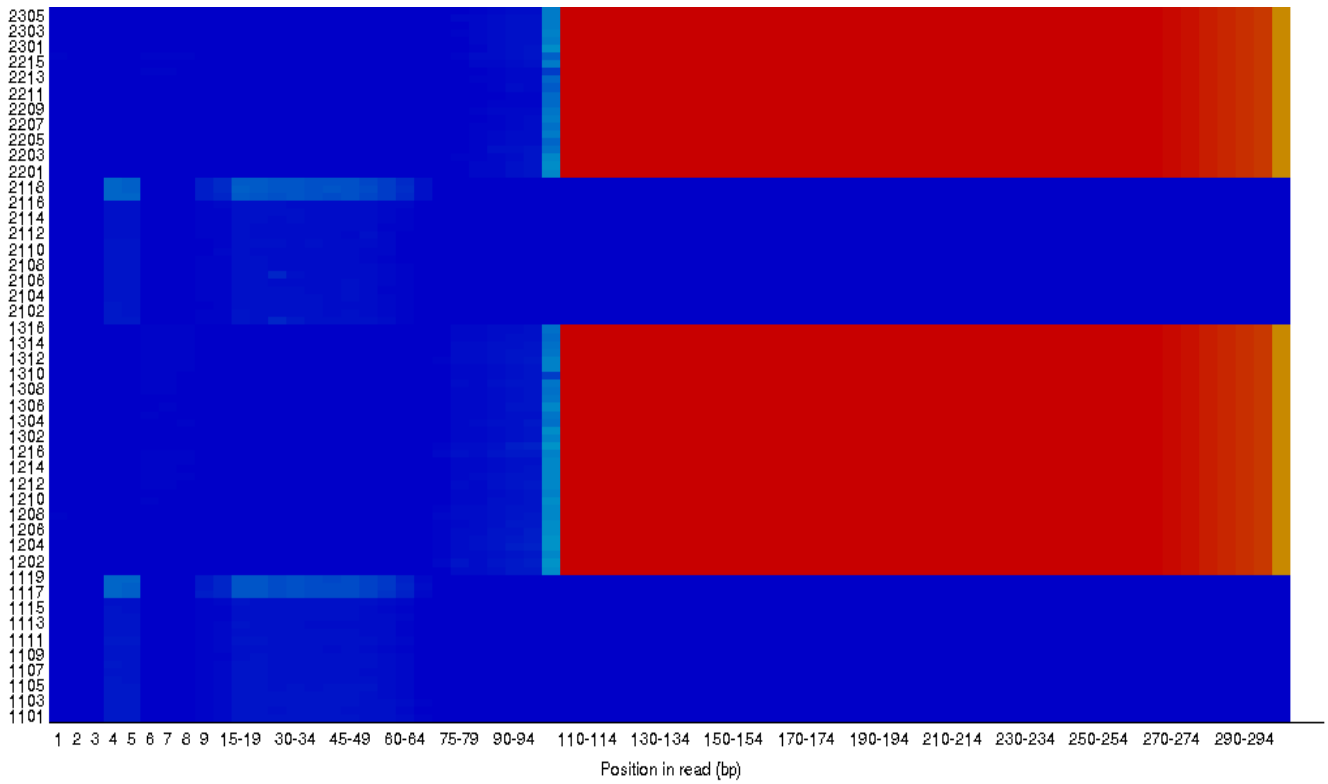
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



 **Per tile sequence quality**

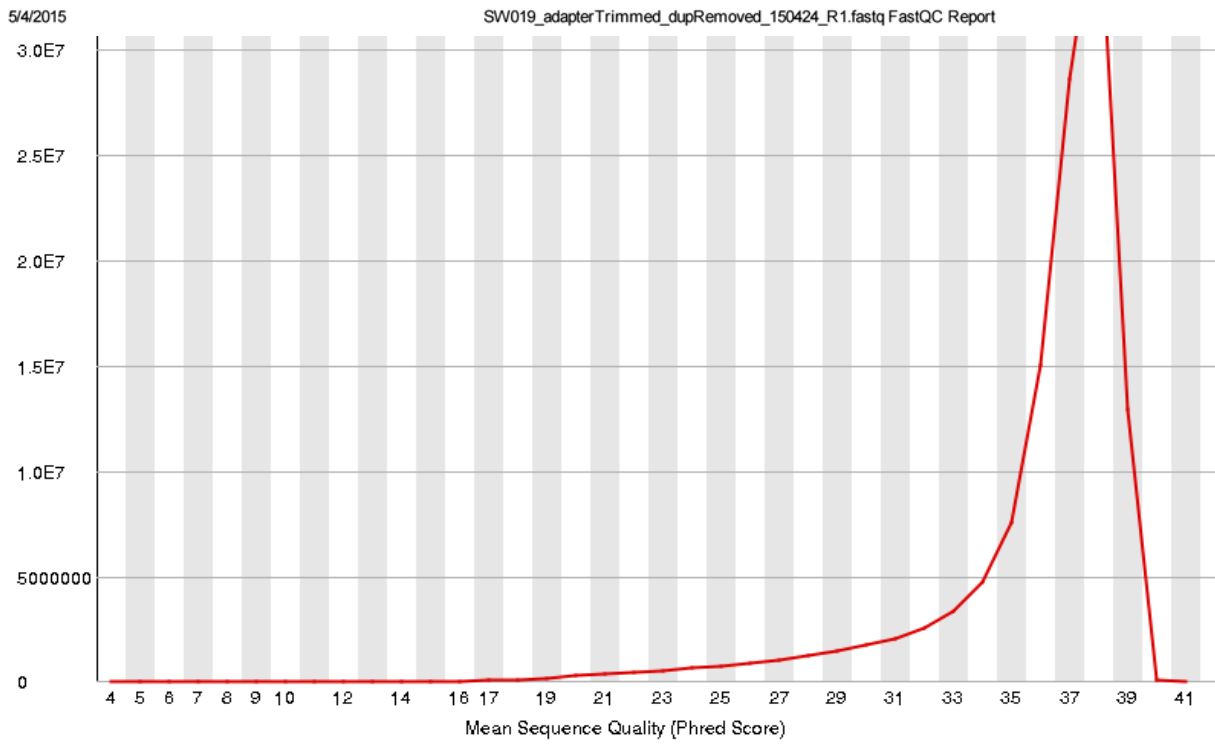
Quality per tile

2315
2313
2311
2309
2307

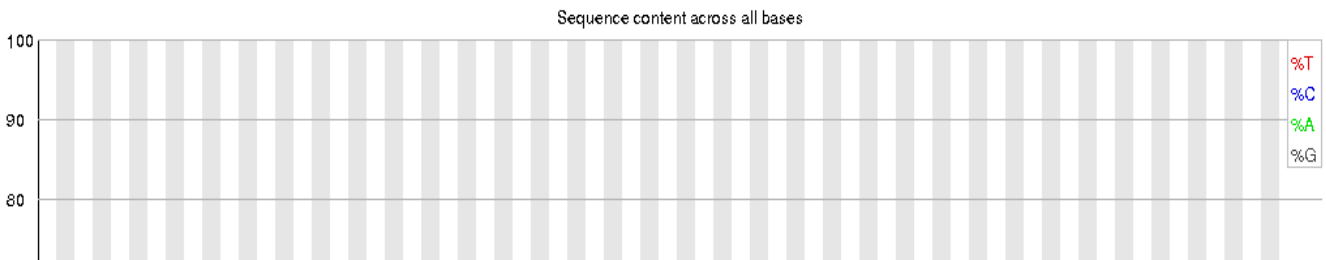


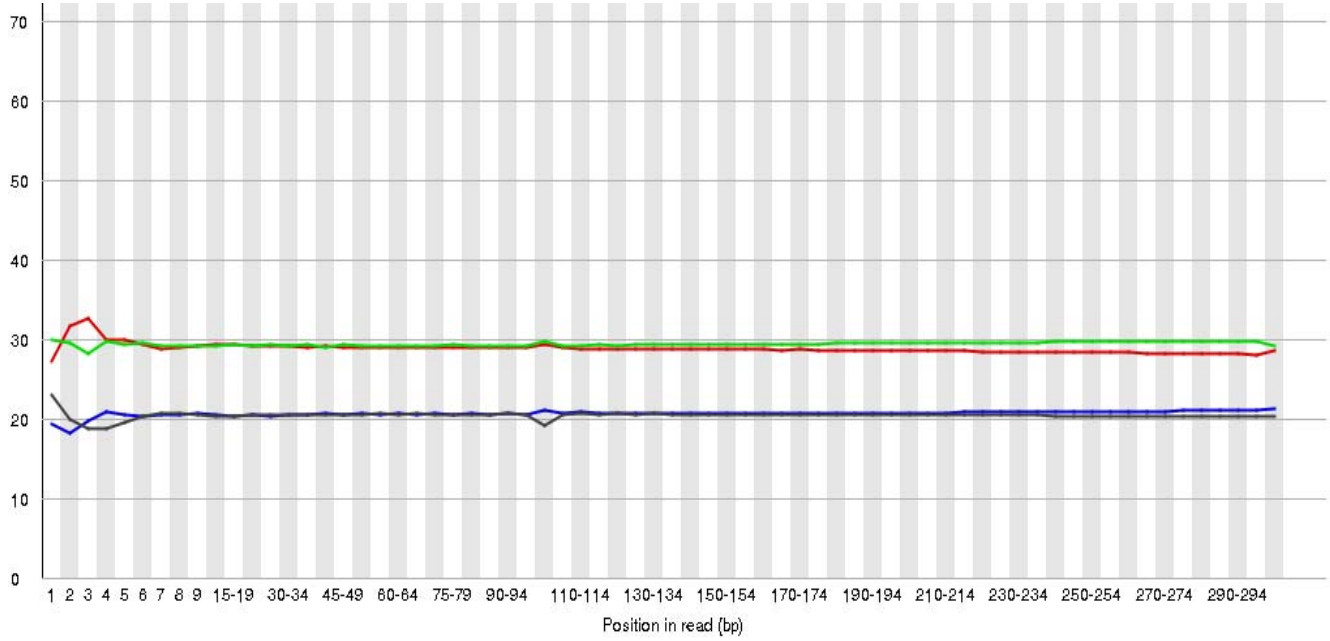
 **Per sequence quality scores**



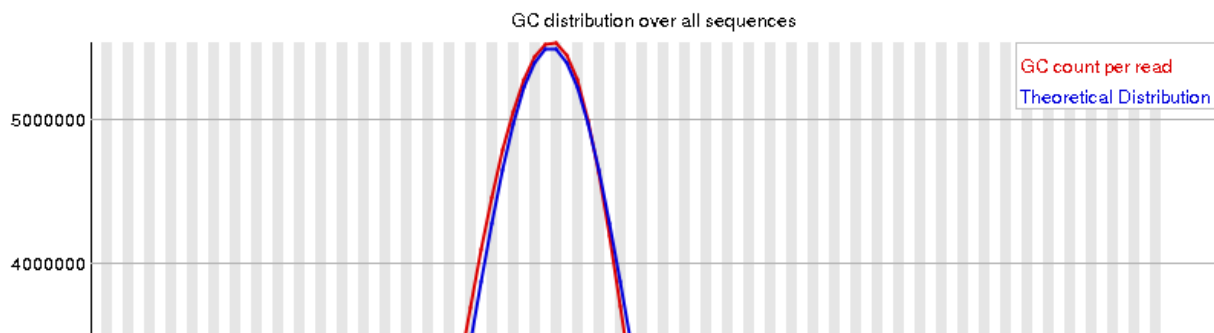


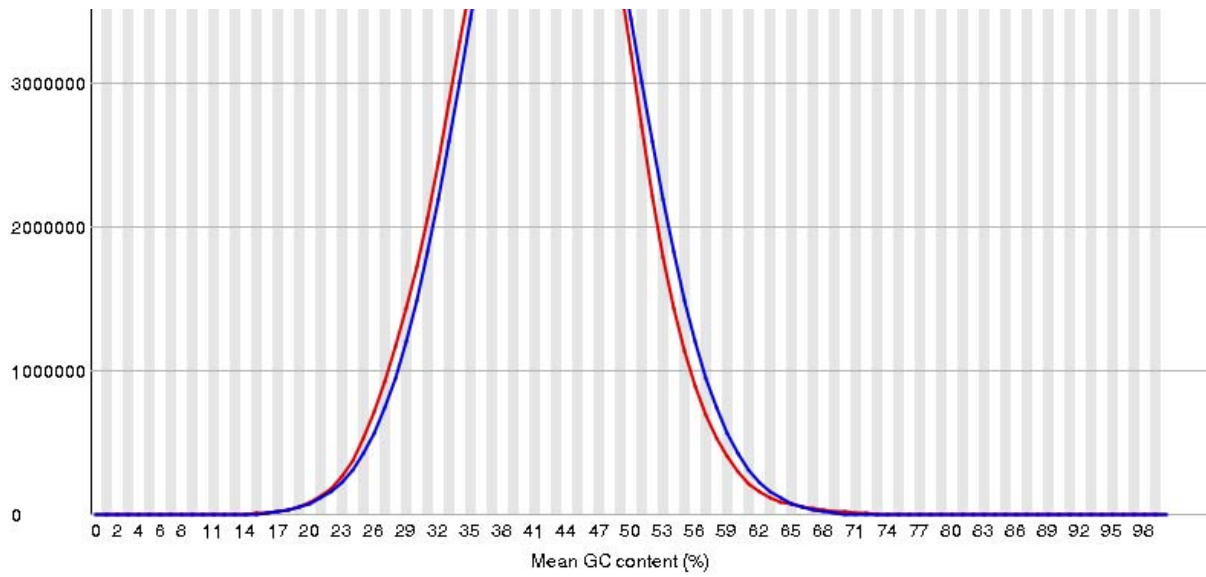
 **Per base sequence content**



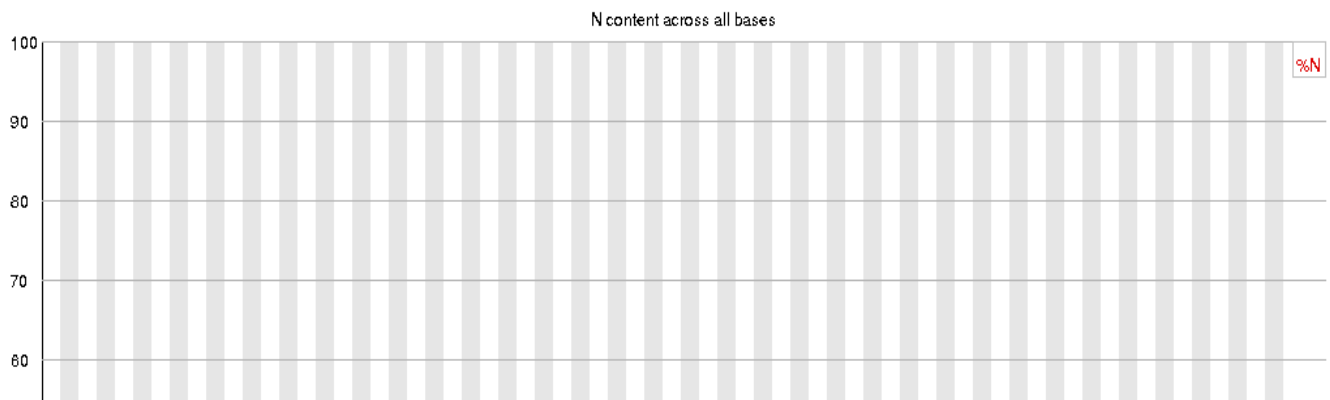


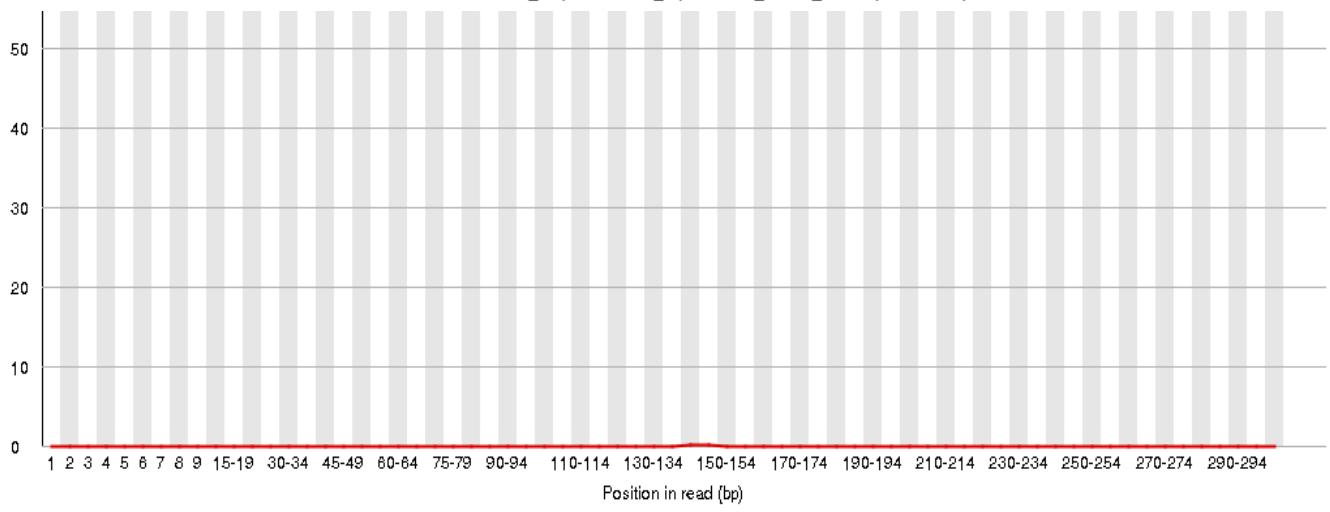
✔ Per sequence GC content



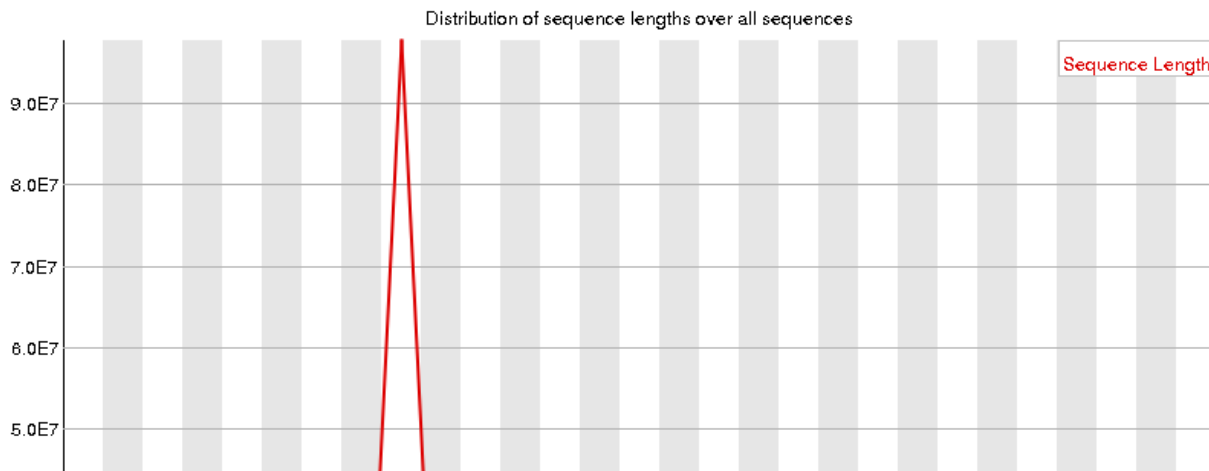


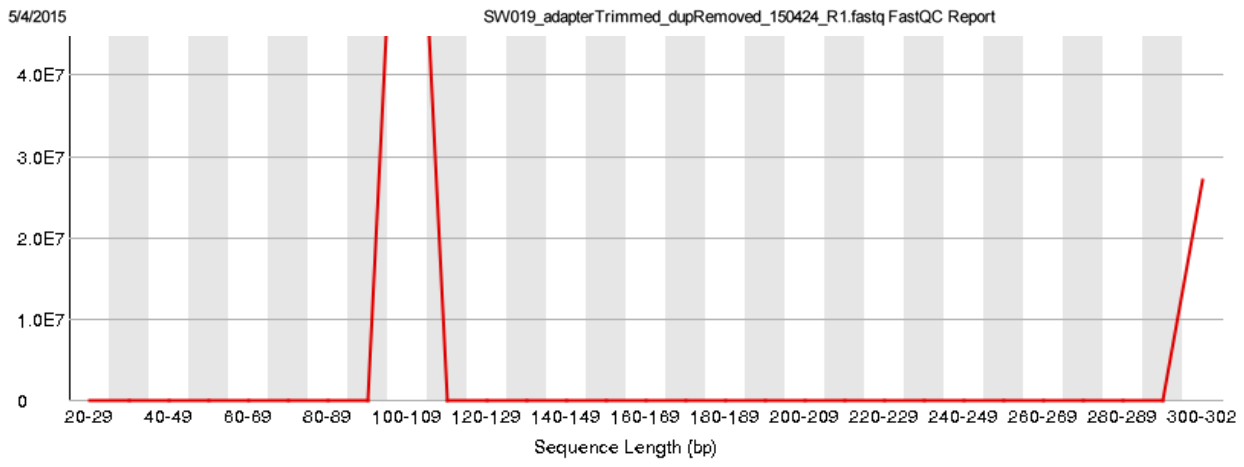
Per base N content



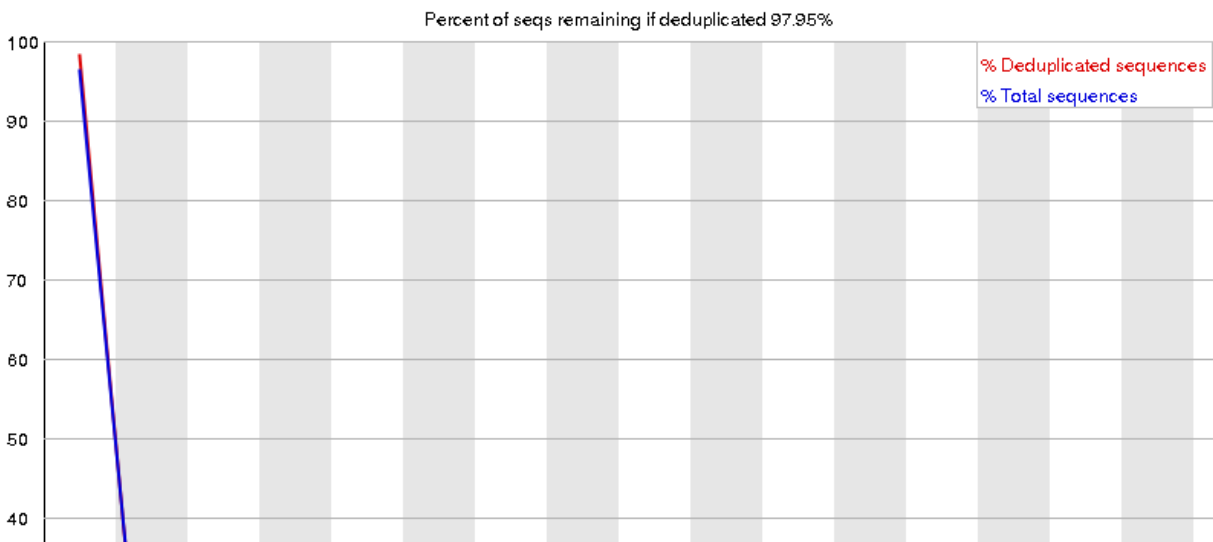


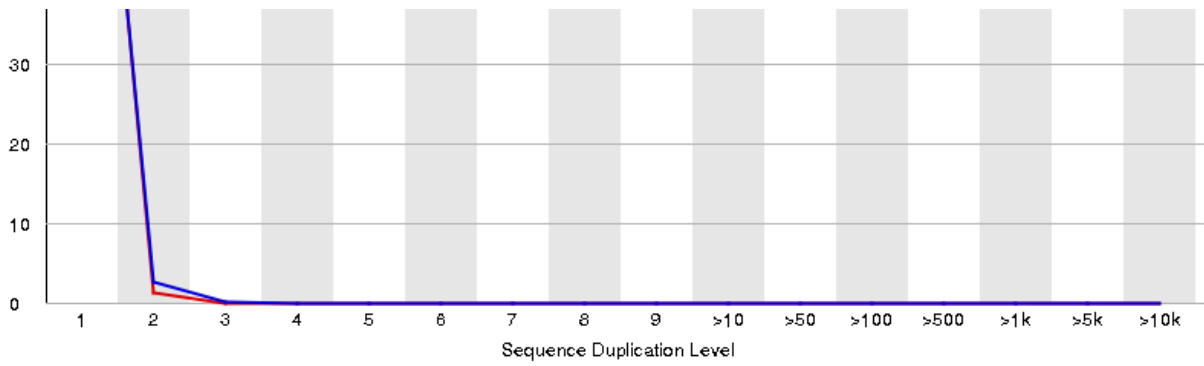
! Sequence Length Distribution





 **Sequence Duplication Levels**

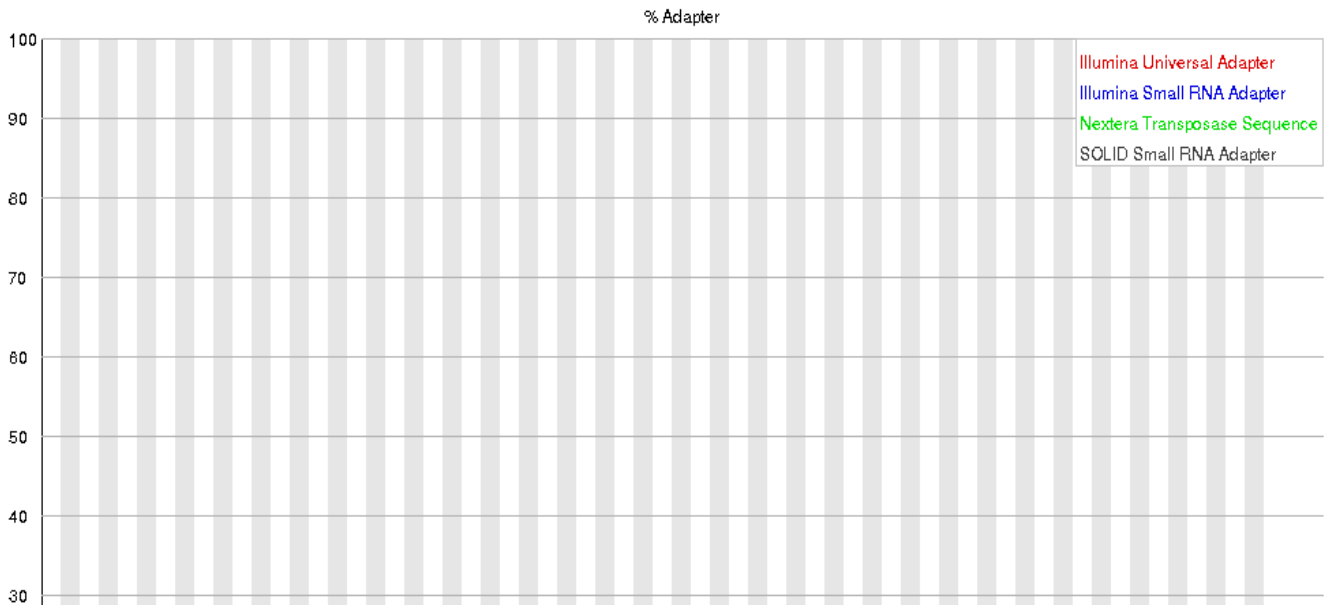


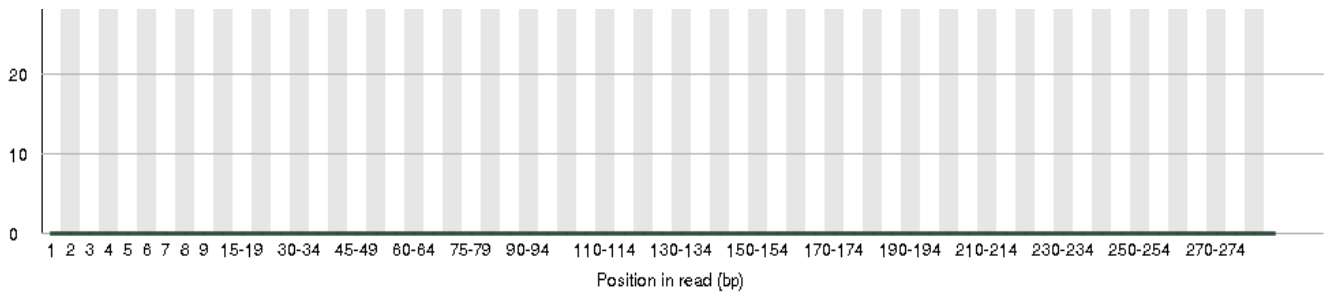


Overrepresented sequences

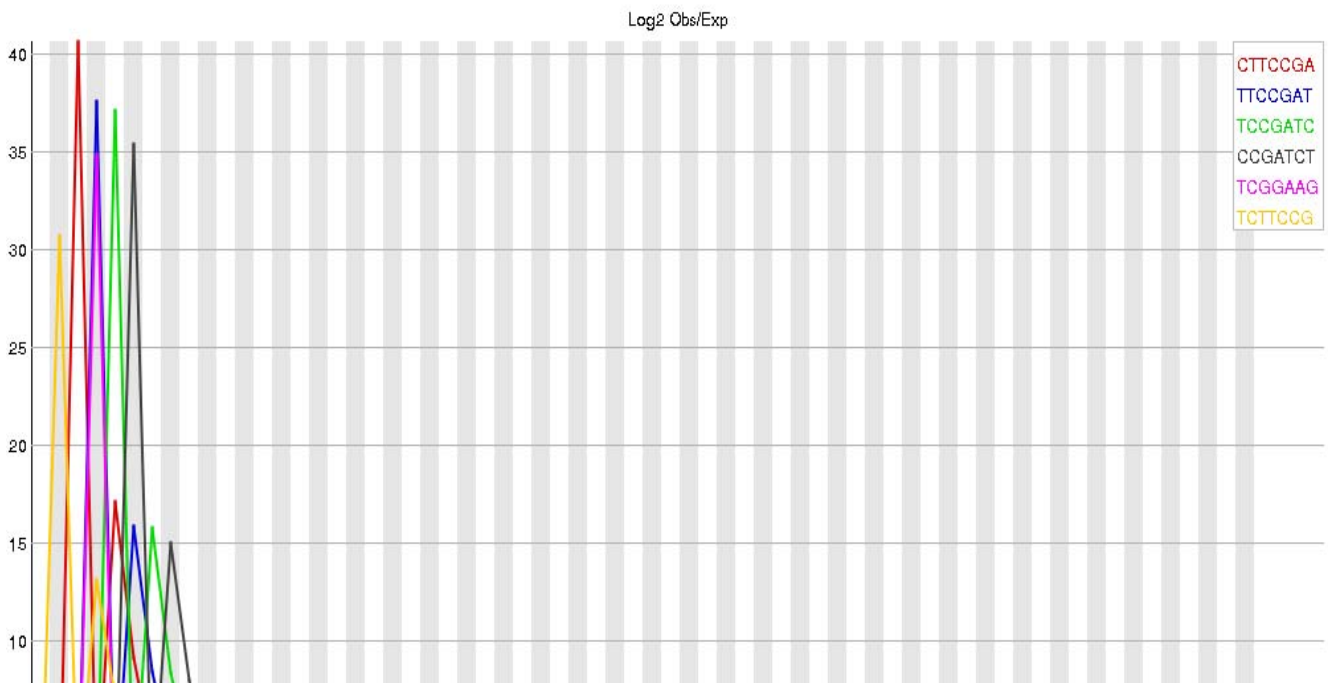
No overrepresented sequences

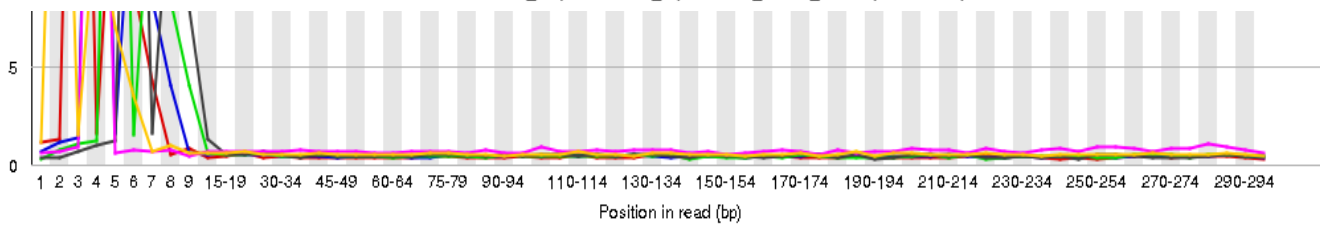
Adapter Content





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTTCCGA	77500	0.0	40.589767	3
TTCCGAT	83985	0.0	37.56877	4
TCCGATC	84675	0.0	37.147182	5
CCGATCT	88880	0.0	35.420135	6
TCGGAAG	48790	0.0	34.816486	4
TCTTCCG	103615	0.0	30.712257	2
ATCGGAA	55350	0.0	30.703745	3
GATCGGA	56645	0.0	30.014687	2
AGATCGG	60495	0.0	28.209106	1
CGGAAGA	75580	0.0	22.692913	5
CGATCTA	49935	0.0	19.563553	7
CTCTTCC	217335	0.0	15.213012	1
GAAGAGC	116290	0.0	15.014597	7
ACGCTCT	46670	0.0	14.868084	1
CGATCTT	62715	0.0	13.843705	7
CGCTCTT	60030	0.0	11.702538	2
GCTCTTC	119070	0.0	11.620703	2
CGATCTG	78395	0.0	10.0392685	7
CGATCTC	72020	0.0	9.743422	7
GGAAGAG	191315	0.0	9.51141	6

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