

FastQC Report

Summary

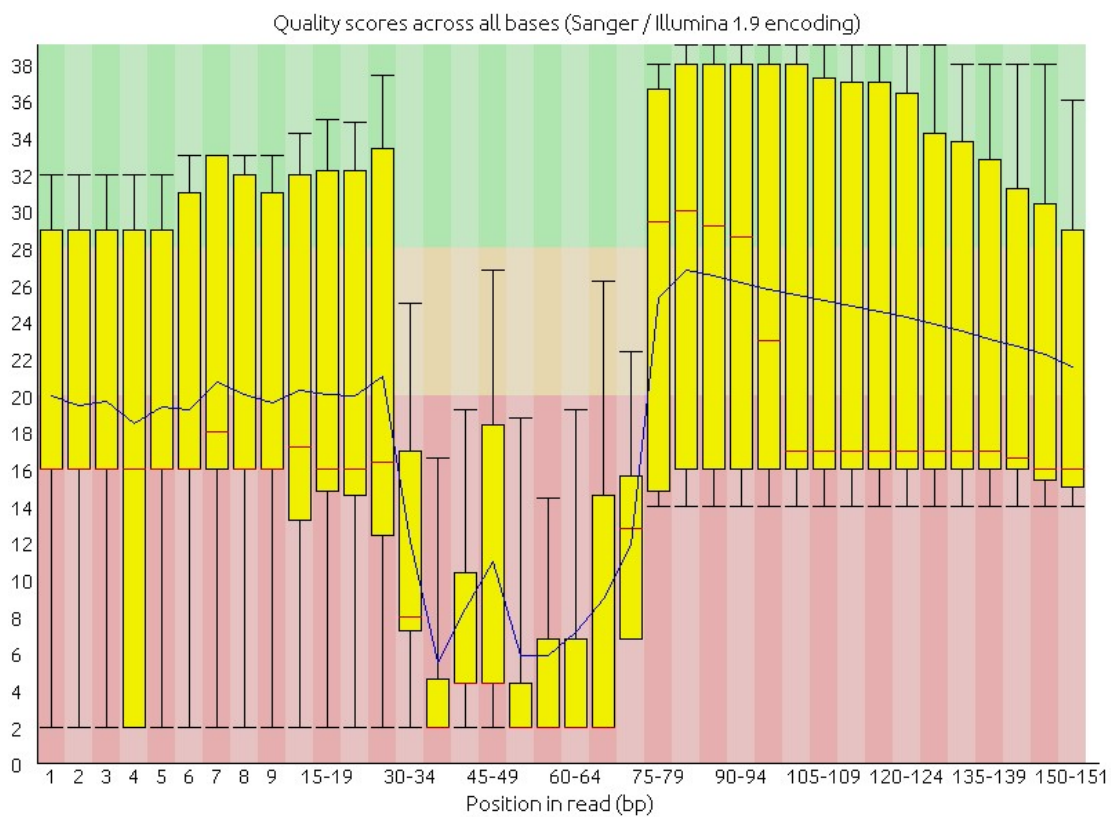
Tue 17 Jan 2017
Mix_S4_L001_R2_001.fastq.gz

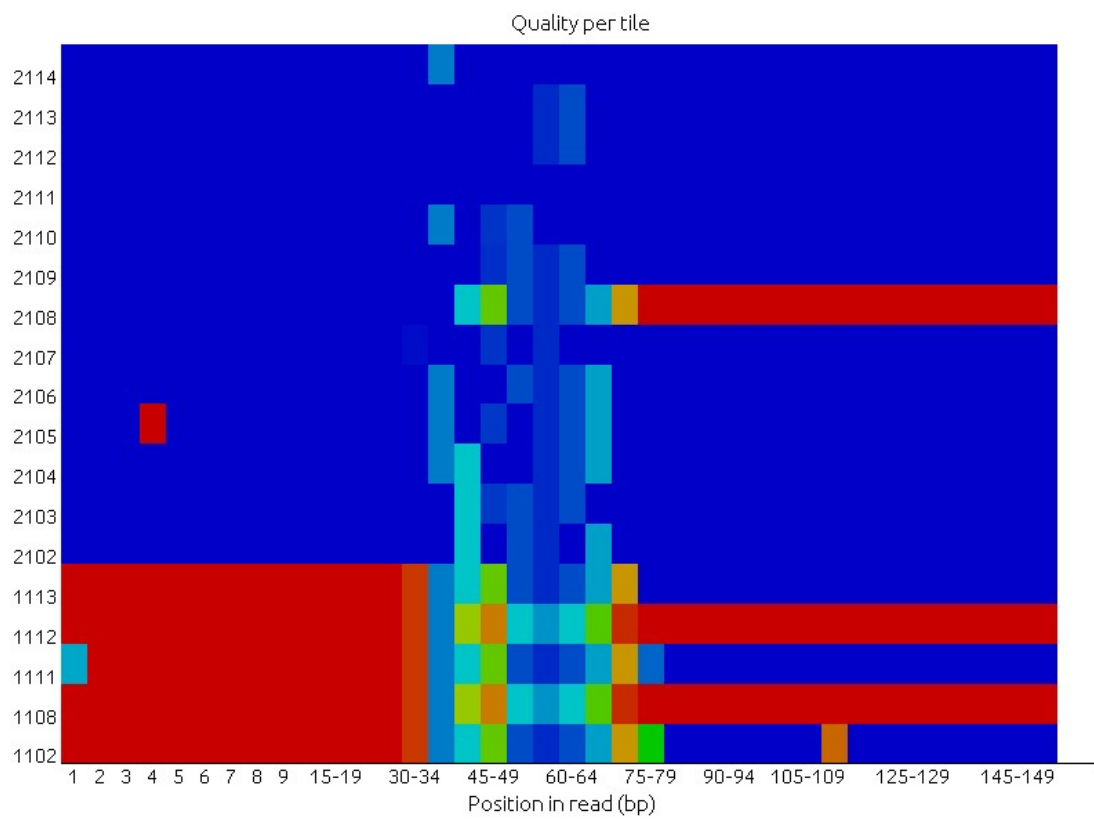
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Basic Statistics

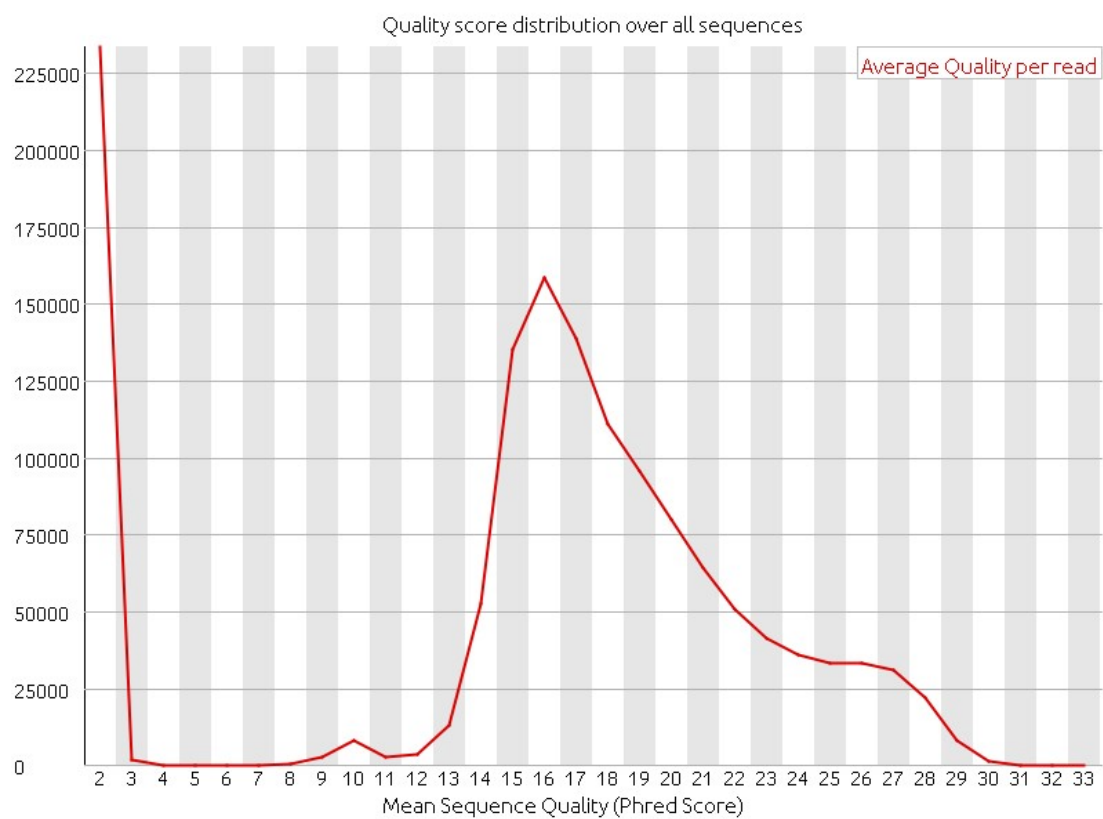
Measure	Value
Filename	Mix_S4_L001_R2_001.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1364964
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	48

✖ Per base sequence quality

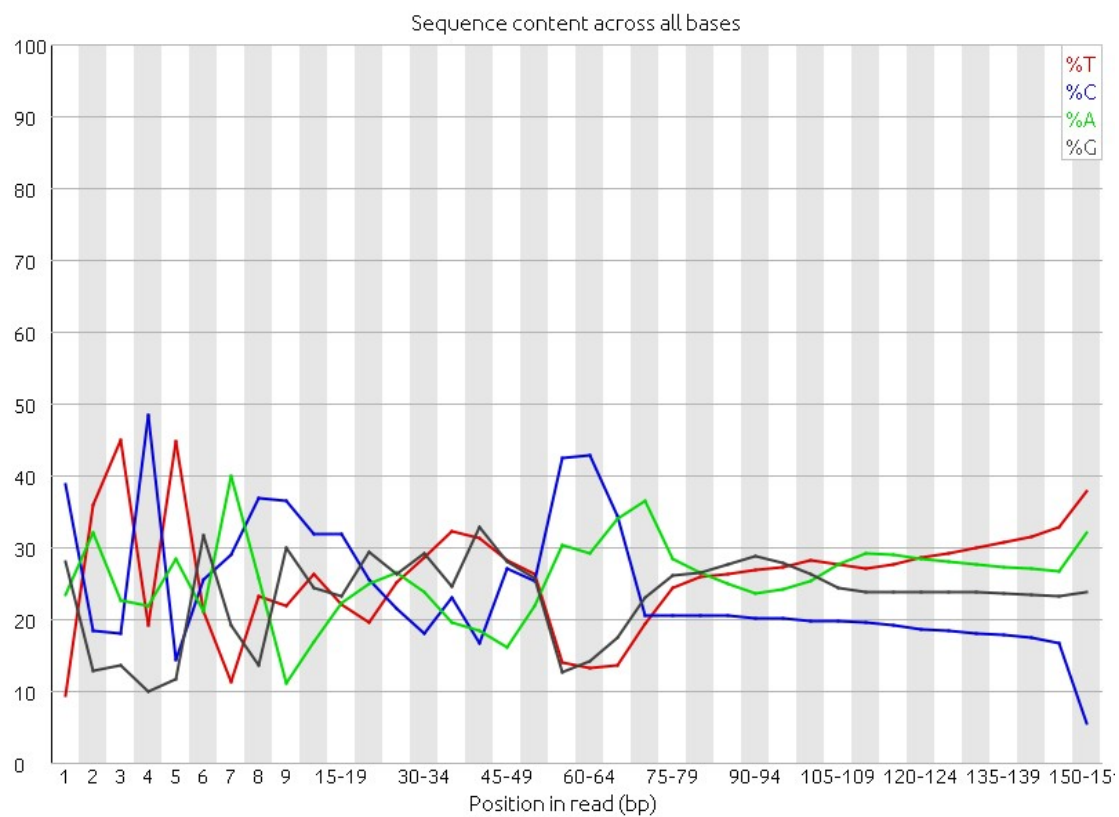




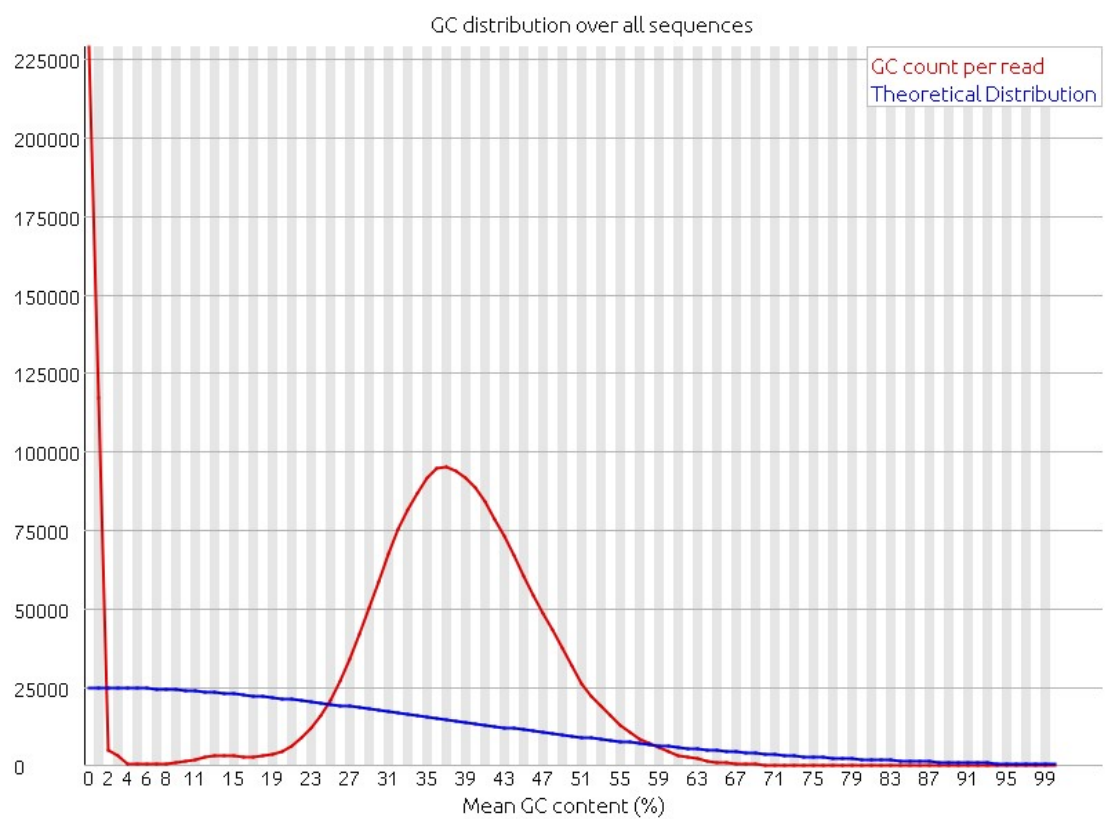
✖ Per sequence quality scores



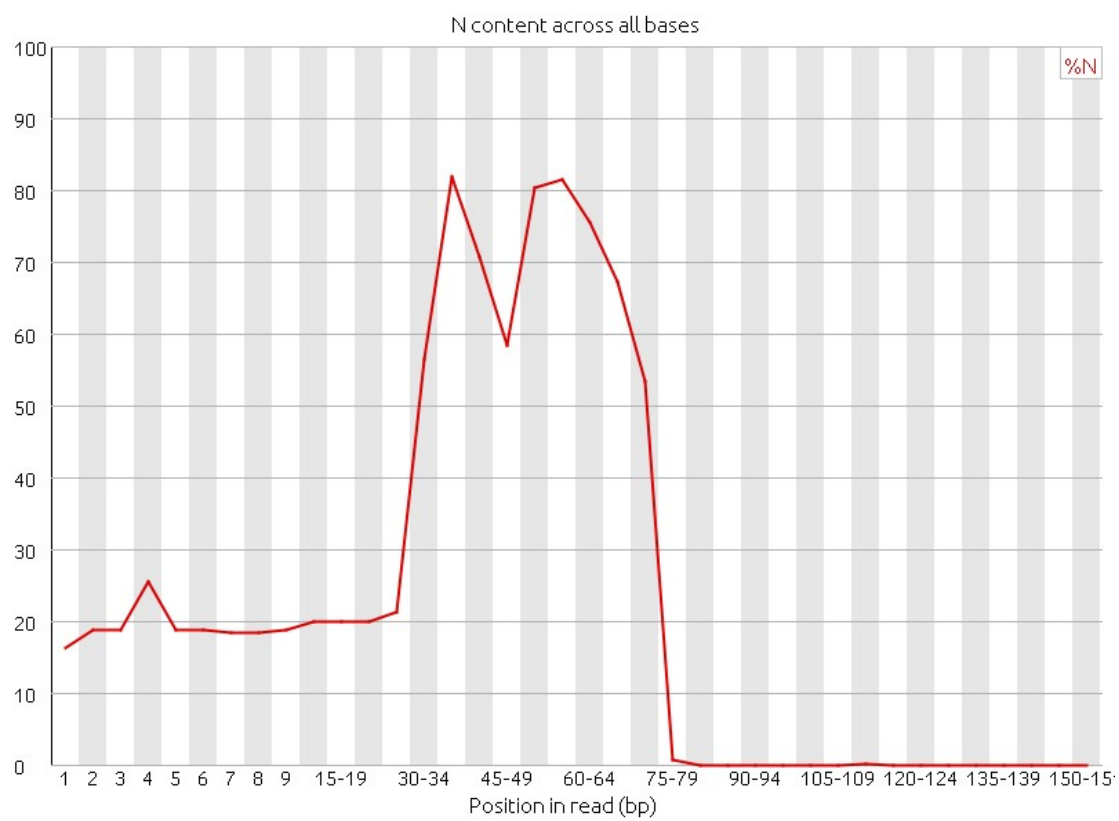
❌ Per base sequence content



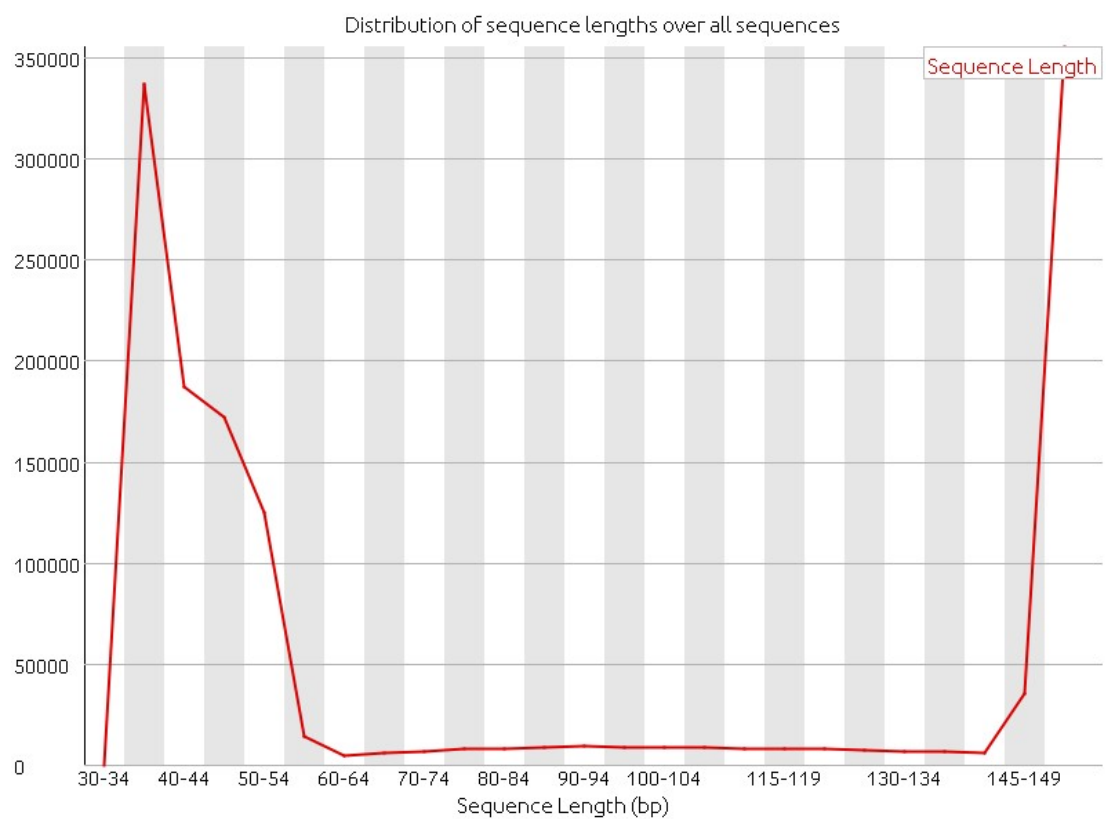
✖ Per sequence GC content



Per base N content

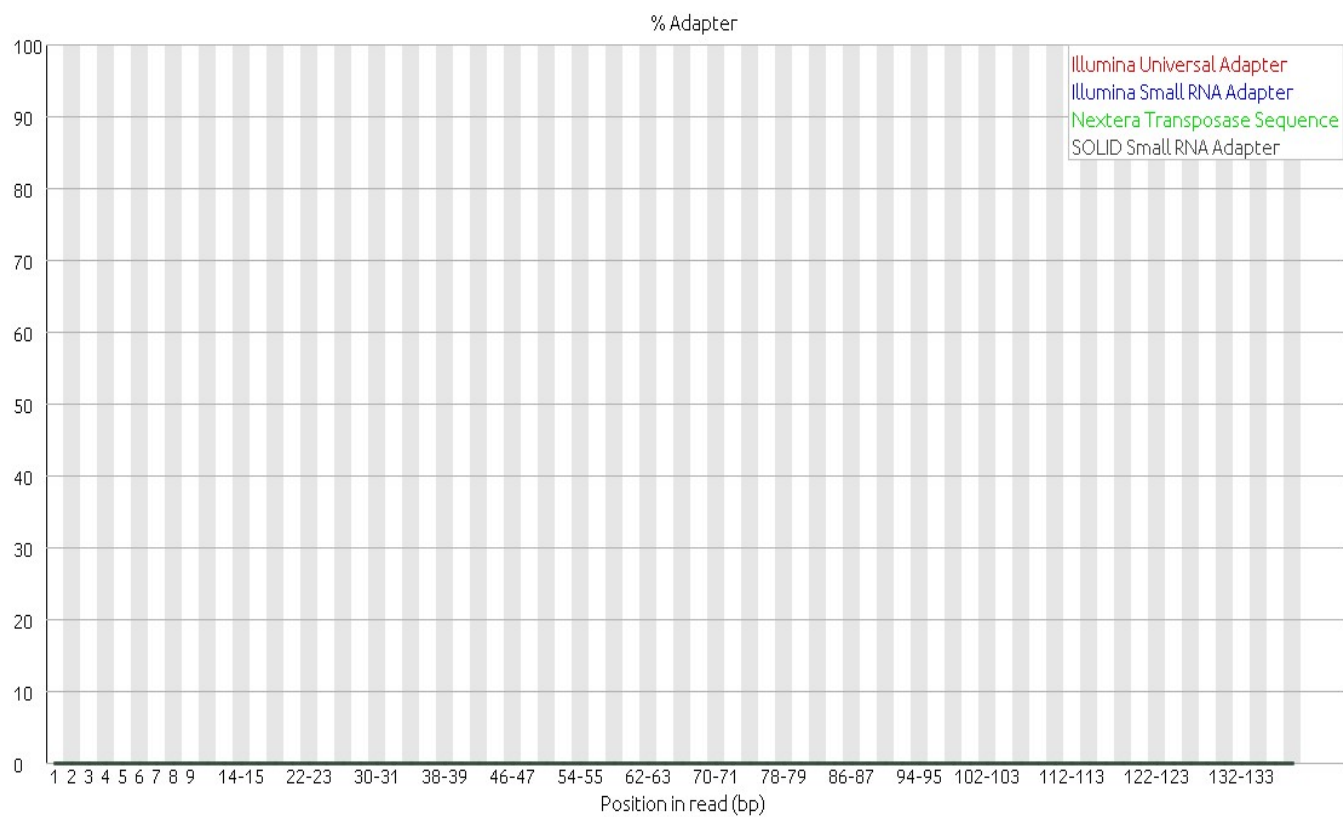


! Sequence Length Distribution

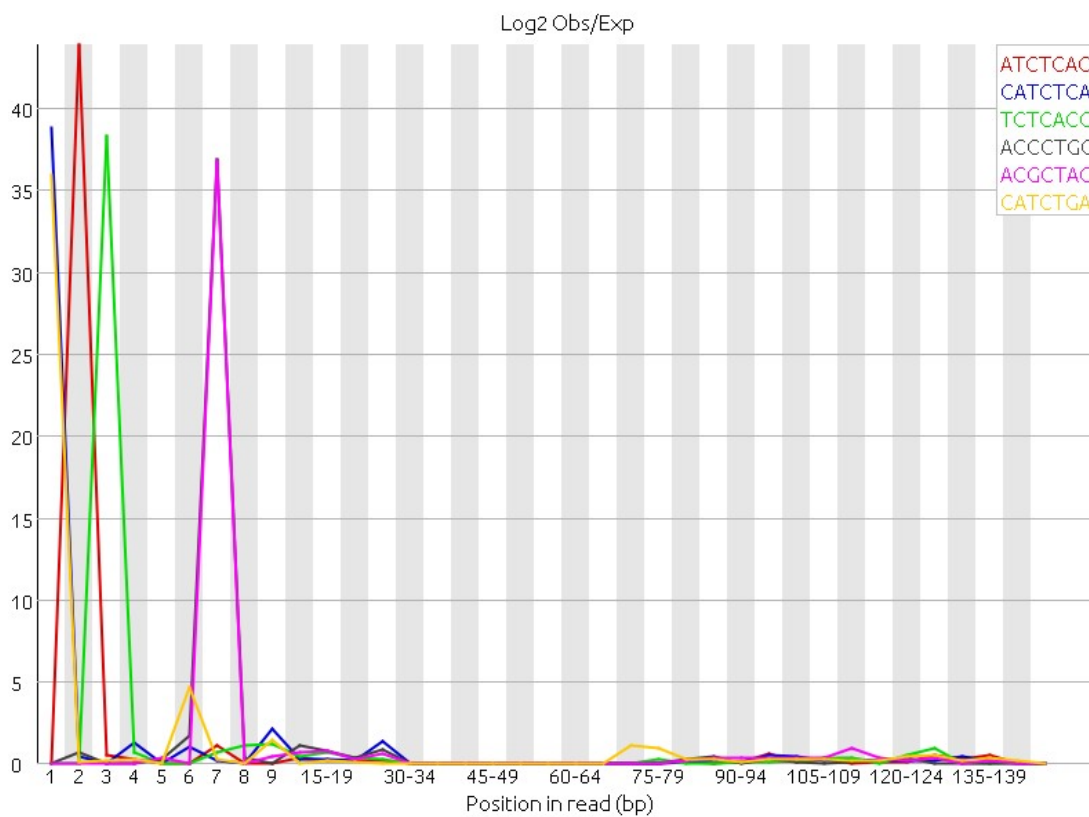


[illegible]

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCTCAC	965	0.0	43.85497	2
CATCTCA	1285	0.0	38.861988	1
TCTCACC	750	0.0	38.370174	3
ACCCTGC	800	0.0	36.933517	7
ACGCTAC	695	0.0	36.844948	7
CATCTGA	3245	0.0	35.99486	1
CGCTACC	755	0.0	35.407722	8
ATCTGAC	3125	0.0	33.76575	2
CTAGTGT	840	0.0	33.568913	25-29
GCTACCC	320	0.0	33.42811	9
ACGCTCC	500	0.0	33.20499	7
TCTTACG	1080	0.0	33.176823	3
TTCTCAC	665	0.0	32.668102	2
ATCTTAC	1265	0.0	32.339424	2
CTTCTCA	625	0.0	32.05038	1
CATACGC	335	0.0	32.003216	4
CATCTTA	1440	0.0	31.93596	1
TCACACC	380	0.0	31.183191	3

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TGACCCT	675	0.0	31.02858	5
CTCACGC	730	0.0	30.918753	4

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