

FastQC Report

Summary

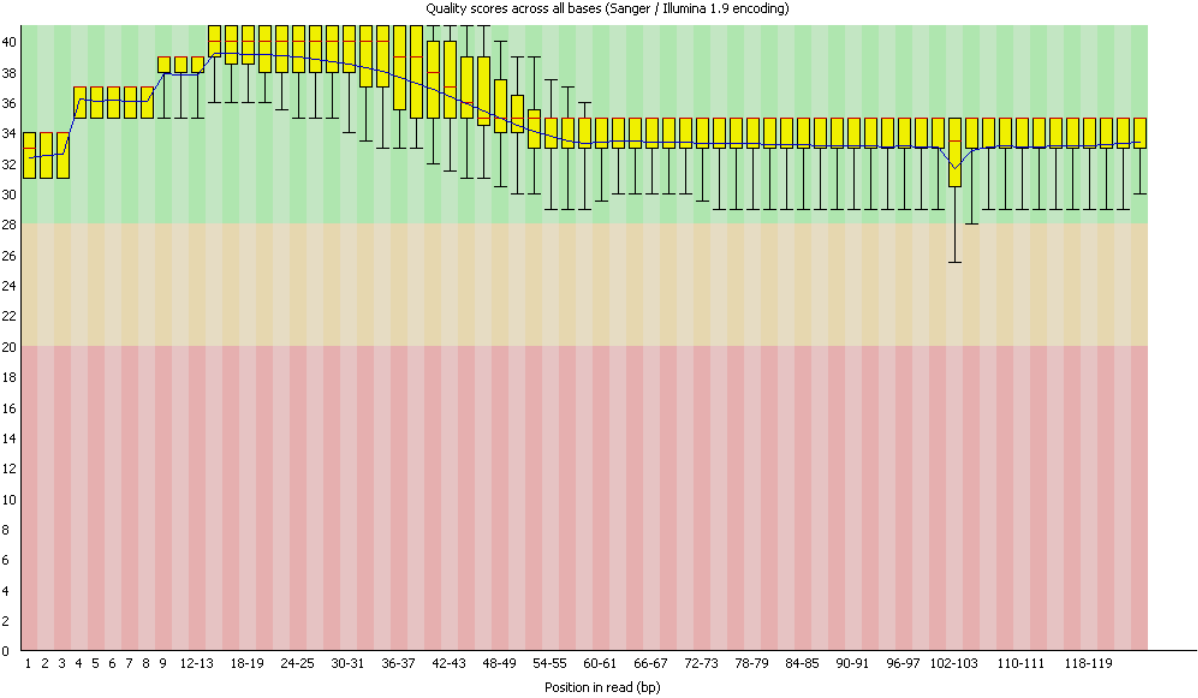
Thu 12 Feb 2015
H001_step04_clean_100_r1.fastq.gz

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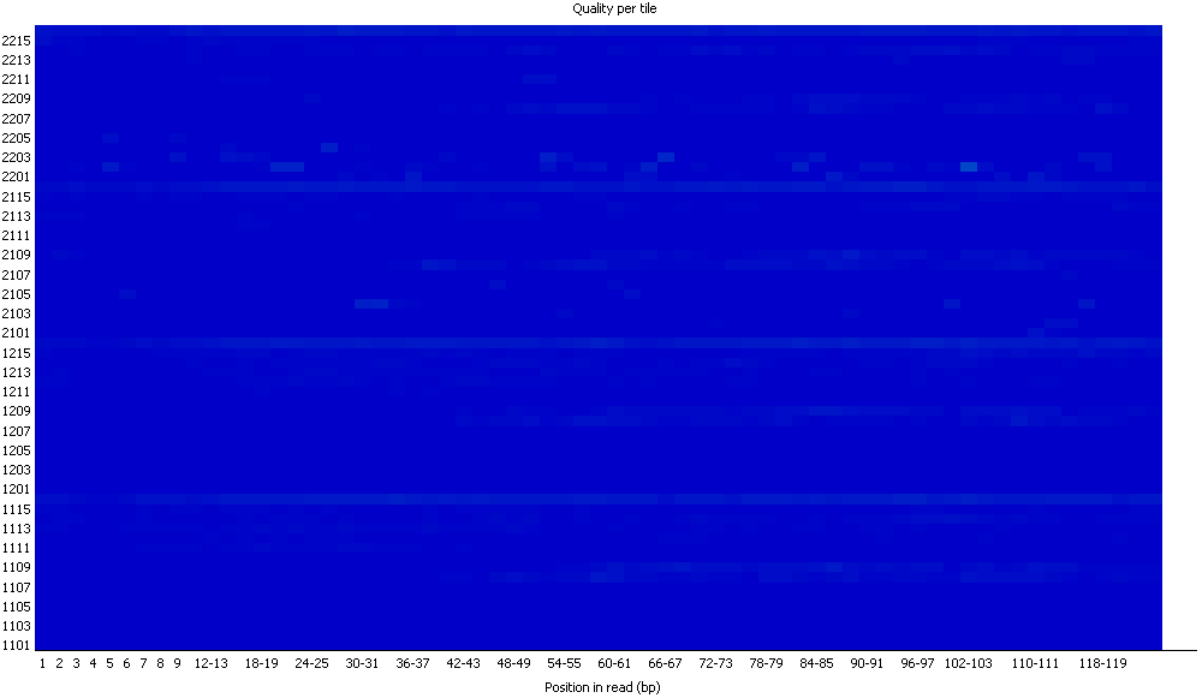
Basic Statistics

Measure	Value
Filename	H001_step04_clean_100_r1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2514650
Sequences flagged as poor quality	0
Sequence length	100-125
%GC	63

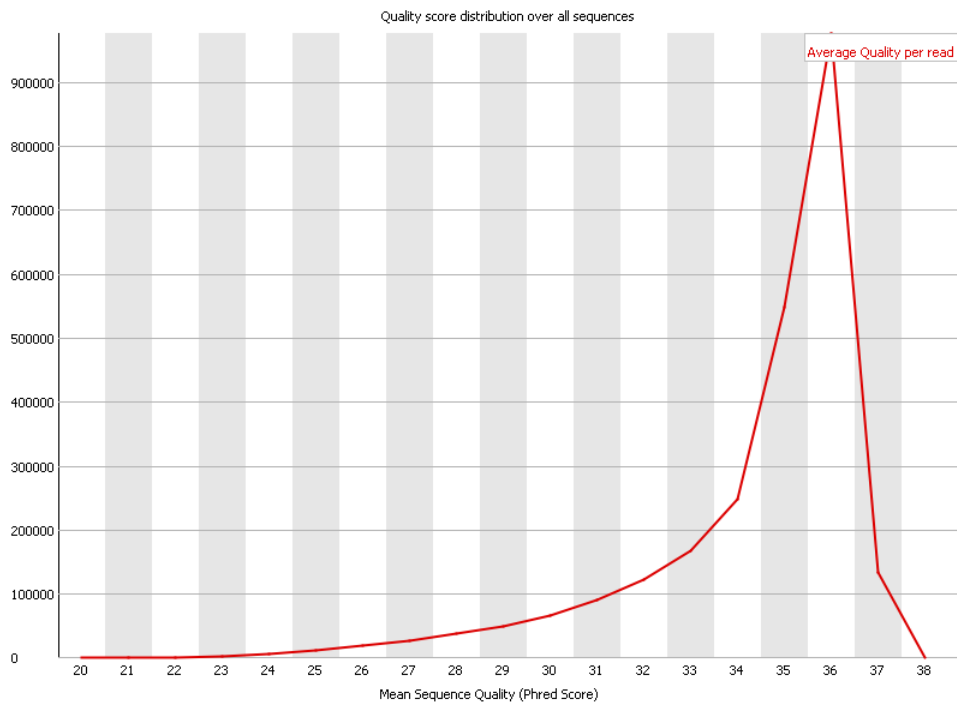
✔ **Per base sequence quality**



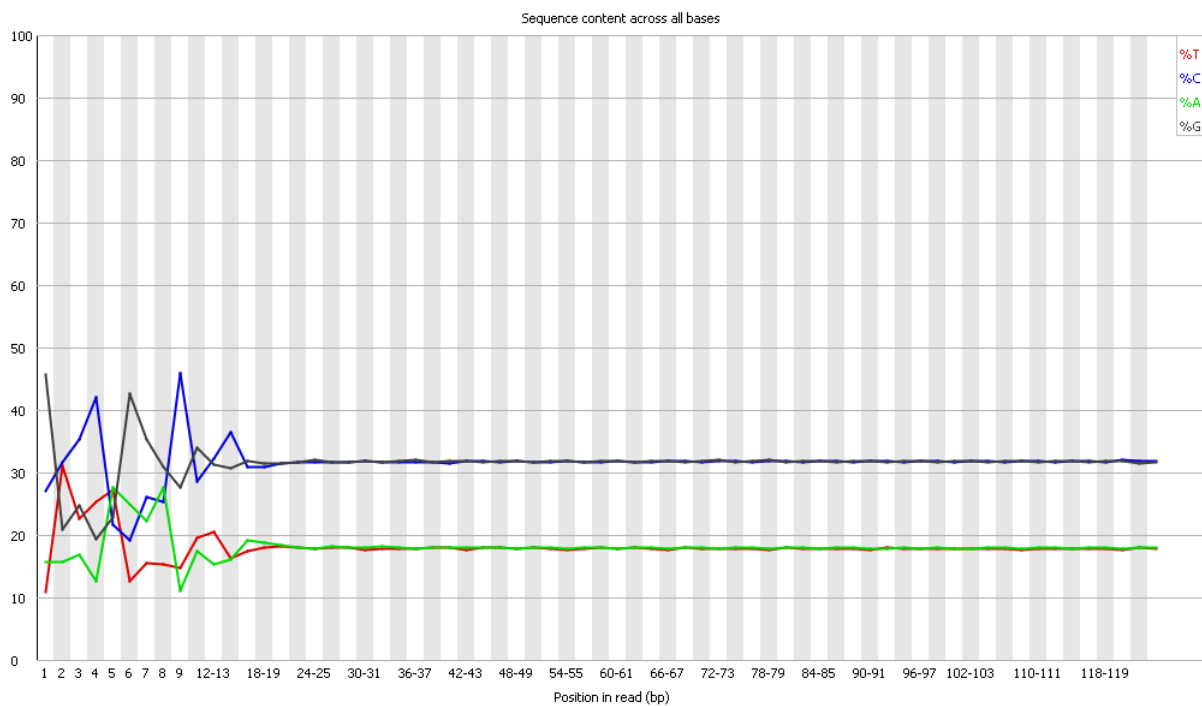
✔ **Per tile sequence quality**



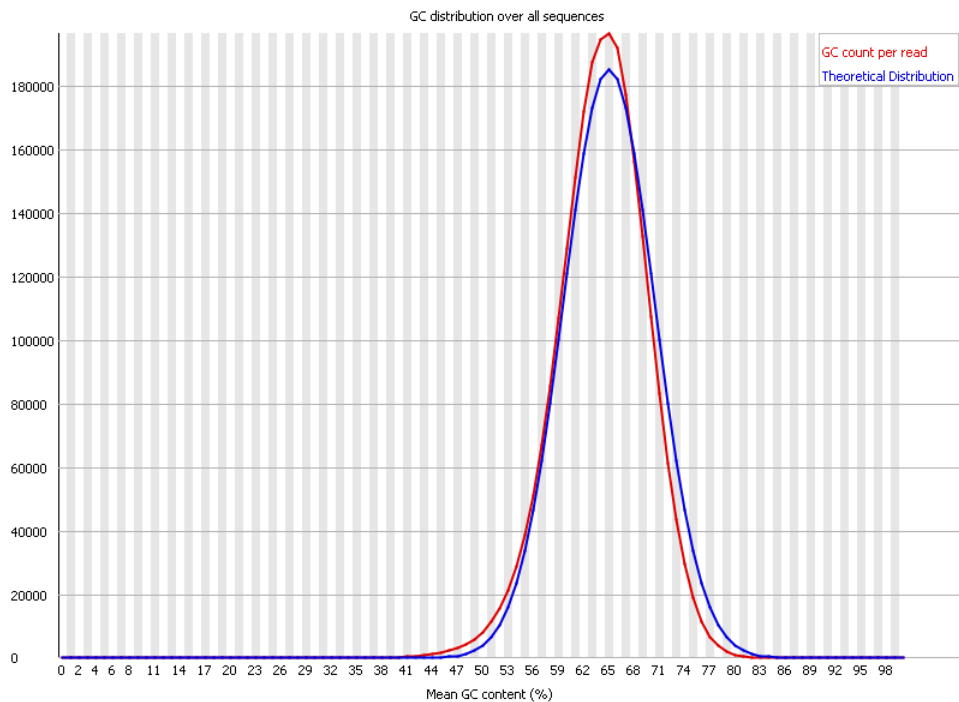
✔ **Per sequence quality scores**



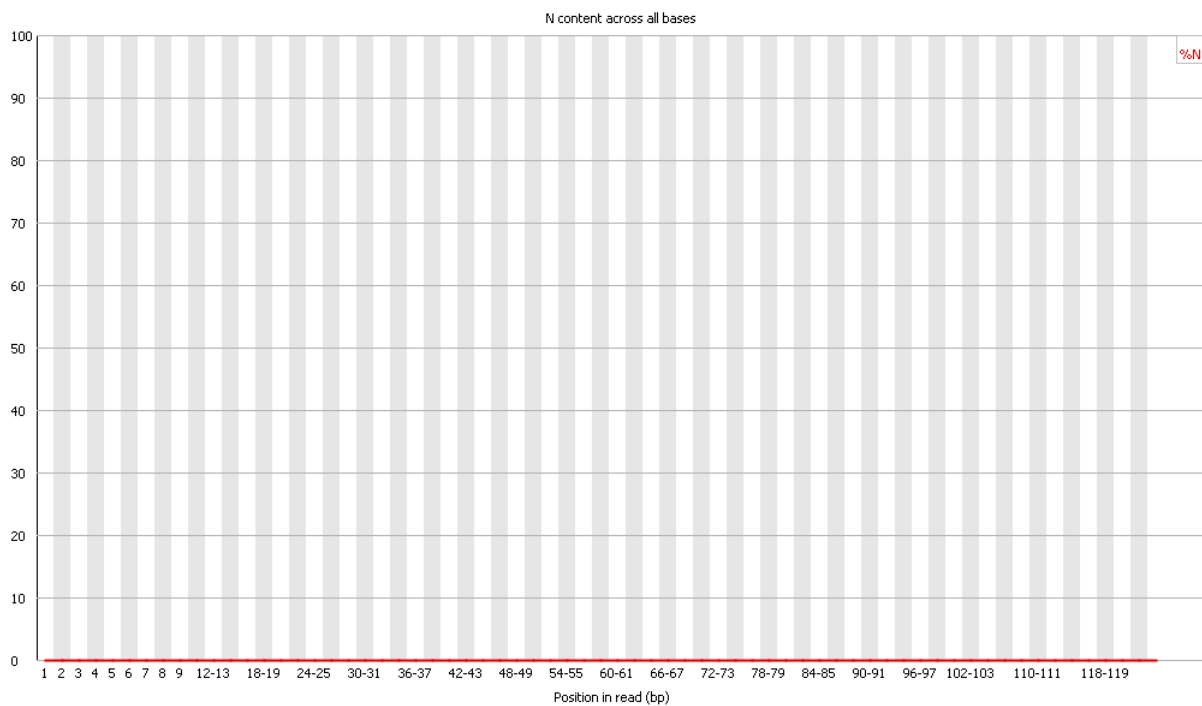
✖ Per base sequence content



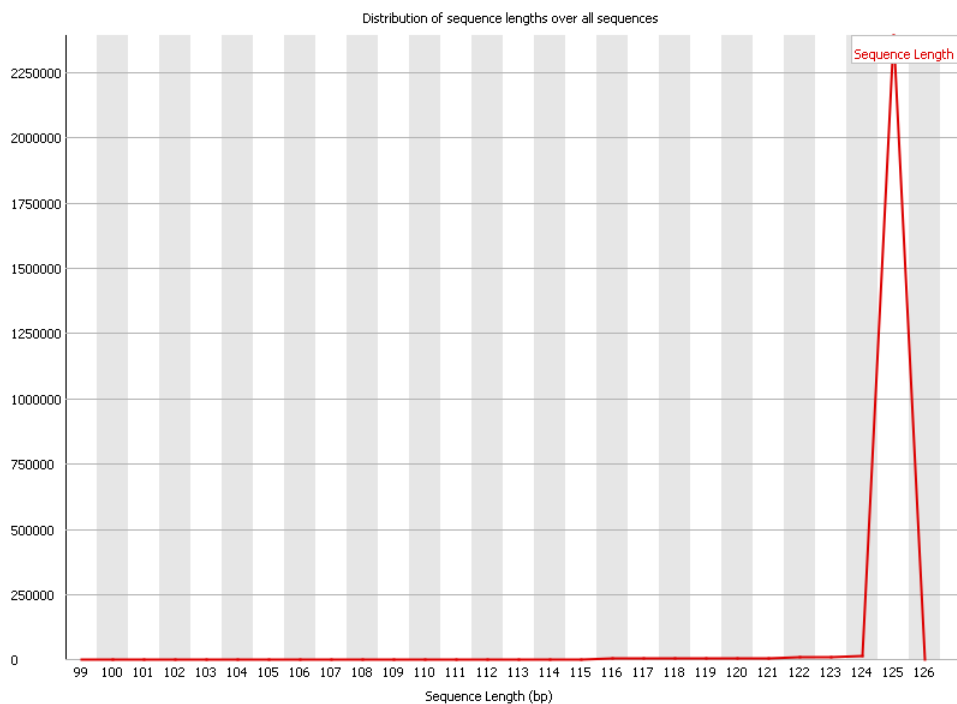
✔ Per sequence GC content



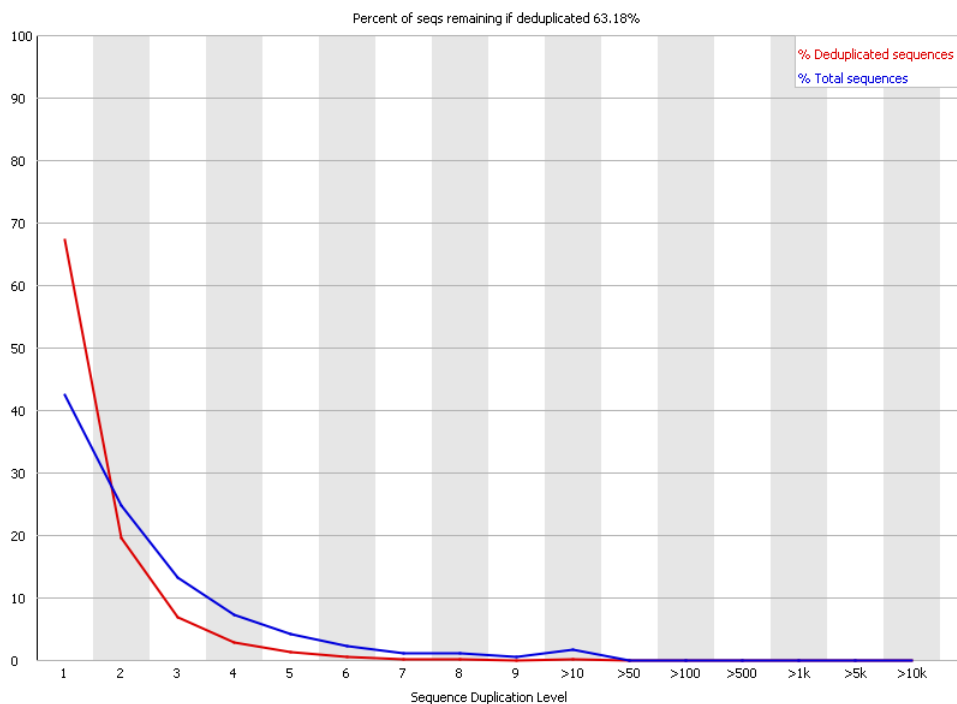
✔ Per base N content



⚠ Sequence Length Distribution



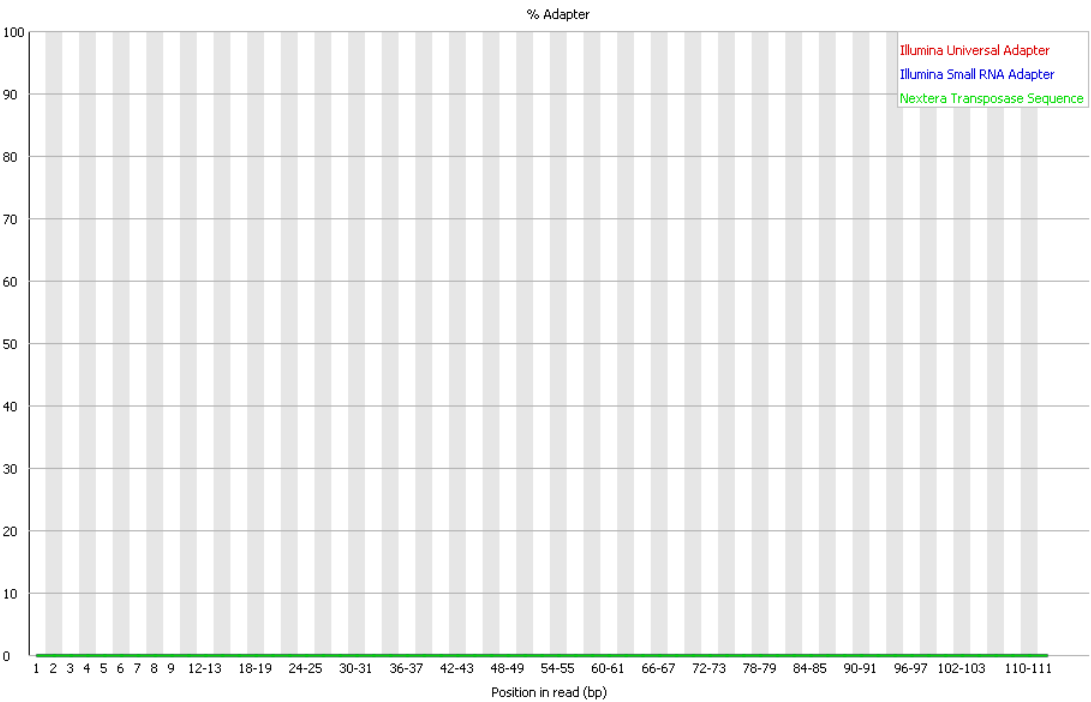
Sequence Duplication Levels



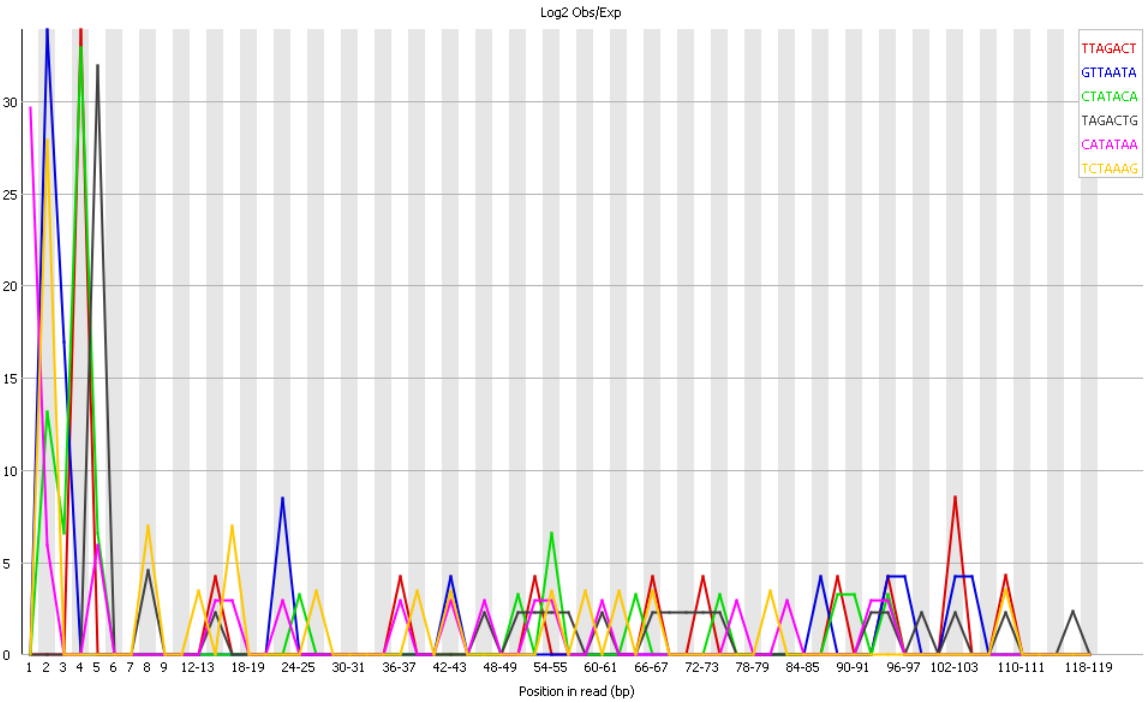
Overrepresented sequences

No overrepresented sequences

Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TTAGACT	70	0.0028405439	33.874744	4
GTTAATA	70	0.0028405439	33.874744	2
CTATACA	90	2.4462282E-4	32.93378	4
TAGACTG	130	1.7879374E-6	31.920435	5
CATATAA	100	4.537132E-4	29.640402	1
TCTAAAG	85	0.007343076	27.89685	2
CTAGGAC	215	4.2018655E-9	27.572466	3
TTTAGAC	110	7.922805E-4	26.94582	3

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AACTATA	45	0.0097049875	26.347025	58-59
TACACTG	90	0.009704083	26.347025	5
GTATAGA	305	1.0913936E-11	25.26723	1
CTAGTGT	120	0.0013162963	24.700335	4
TATAAGG	150	1.730127E-4	23.71232	3
TTATTGT	130	0.0020973529	22.80031	4
TAATGTG	130	0.0020973529	22.80031	5
TATAGAA	240	3.6955498E-7	22.2303	2
TTCTATA	190	3.4032026E-5	21.840296	2
GIGTTAG	260	7.980434E-7	20.520279	1
ATTTAGA	145	0.0039522196	20.441656	2
CCTAGGA	145	0.0039522196	20.441656	2

Produced by [FastQC](#) (version 0.11.2)