

FastQC Report

Summary

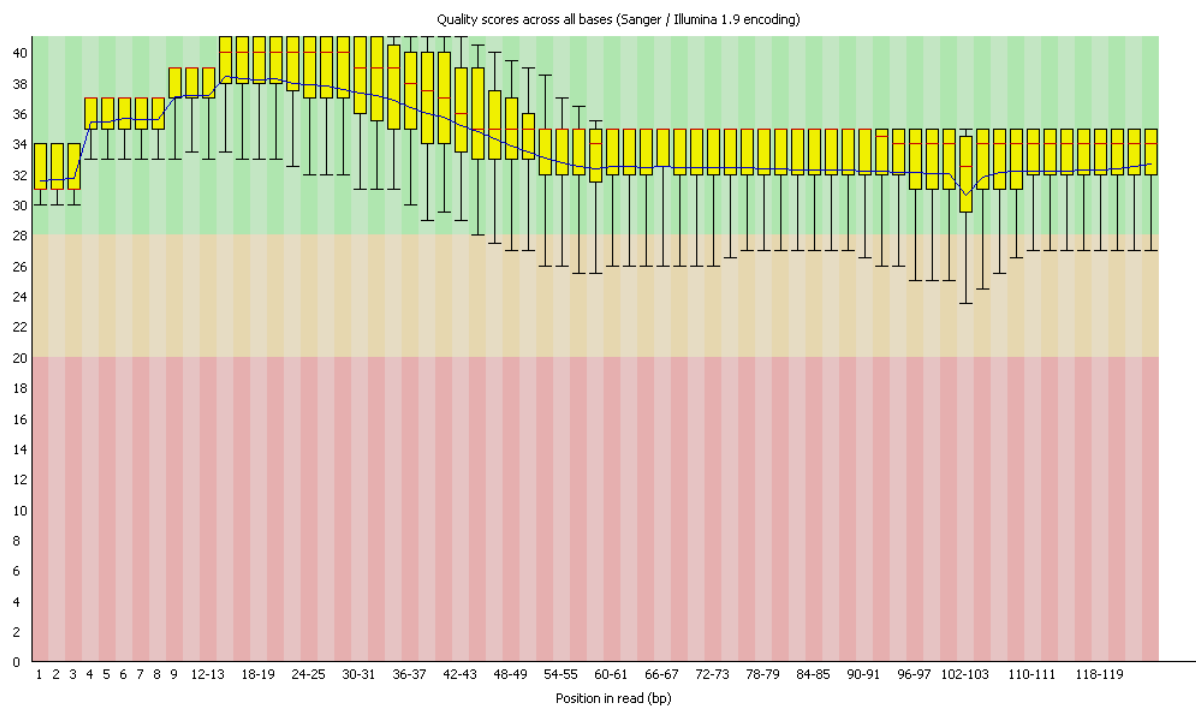
Thu 12 Feb 2015
H001_step04_clean_100_r2.fastq.gz

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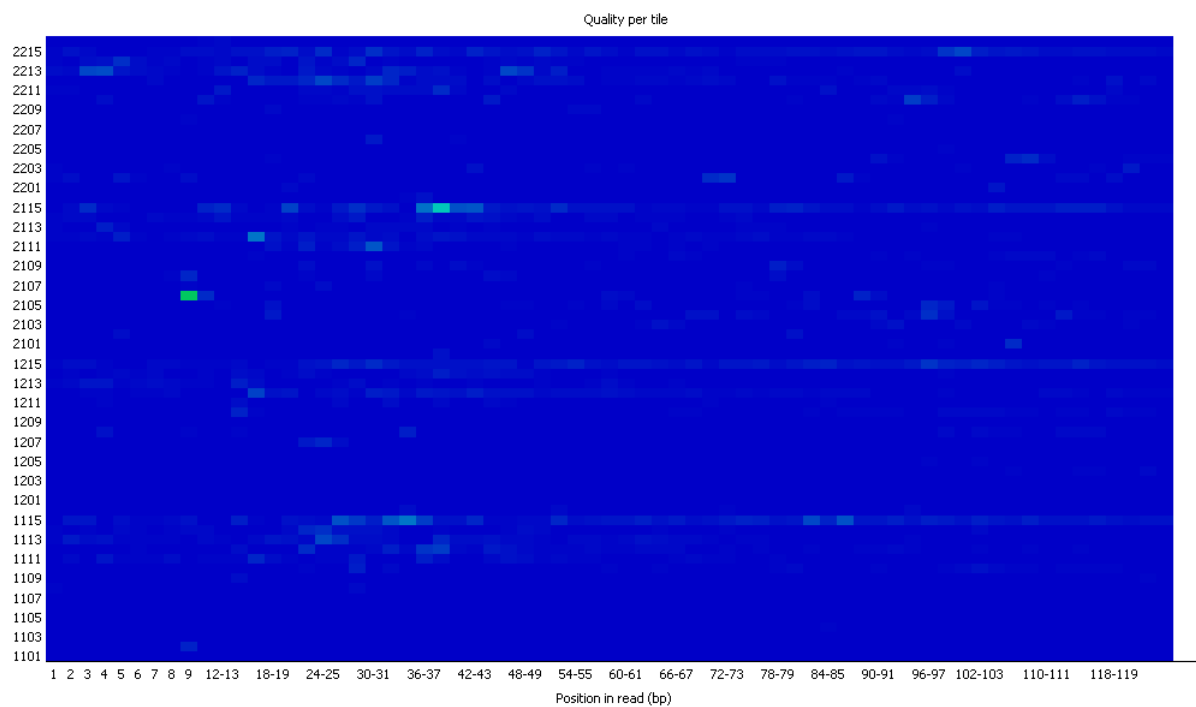
Basic Statistics

Measure	Value
Filename	H001_step04_clean_100_r2.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

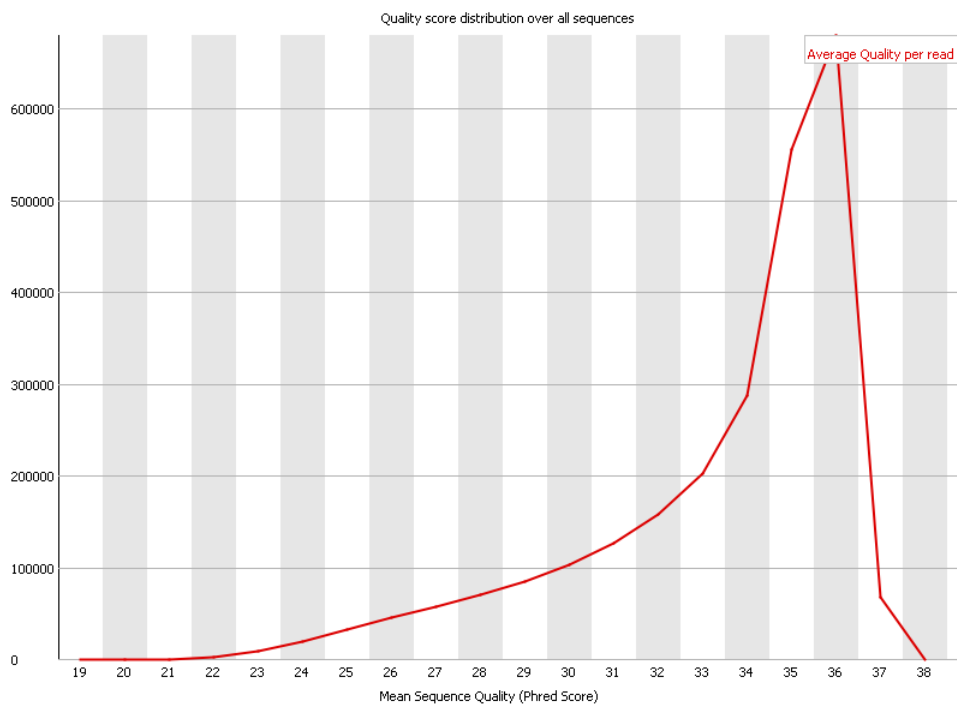
✓ Per base sequence quality



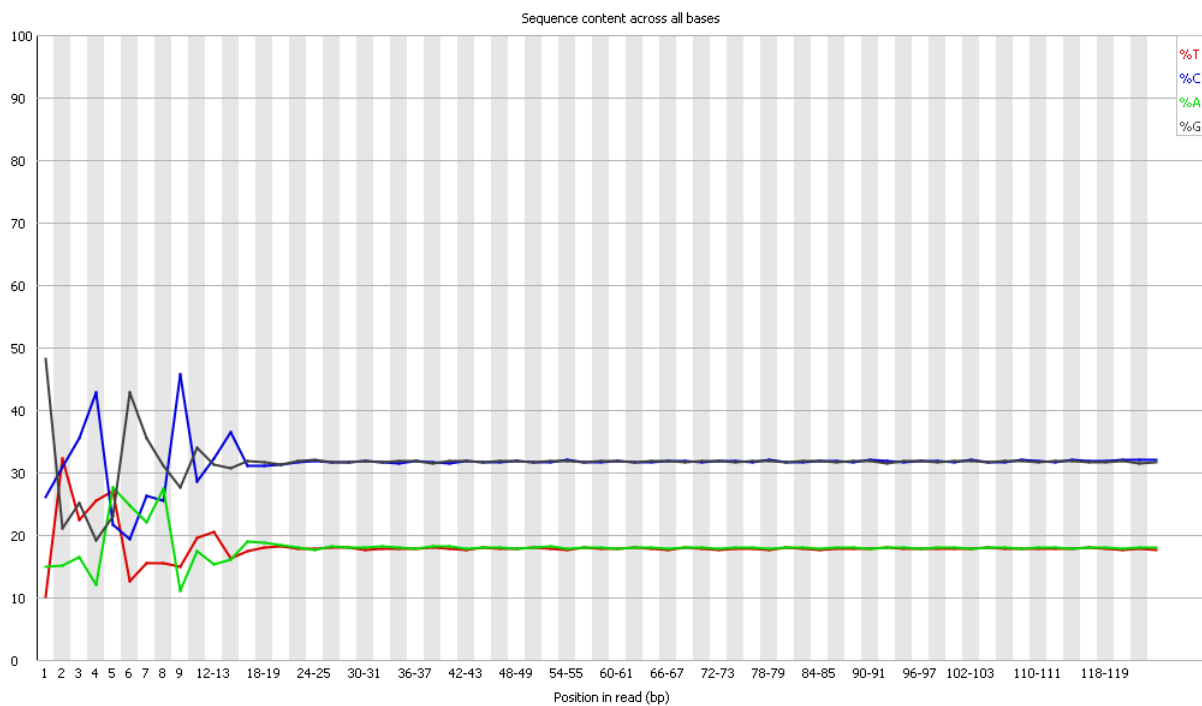
✓ Per tile sequence quality



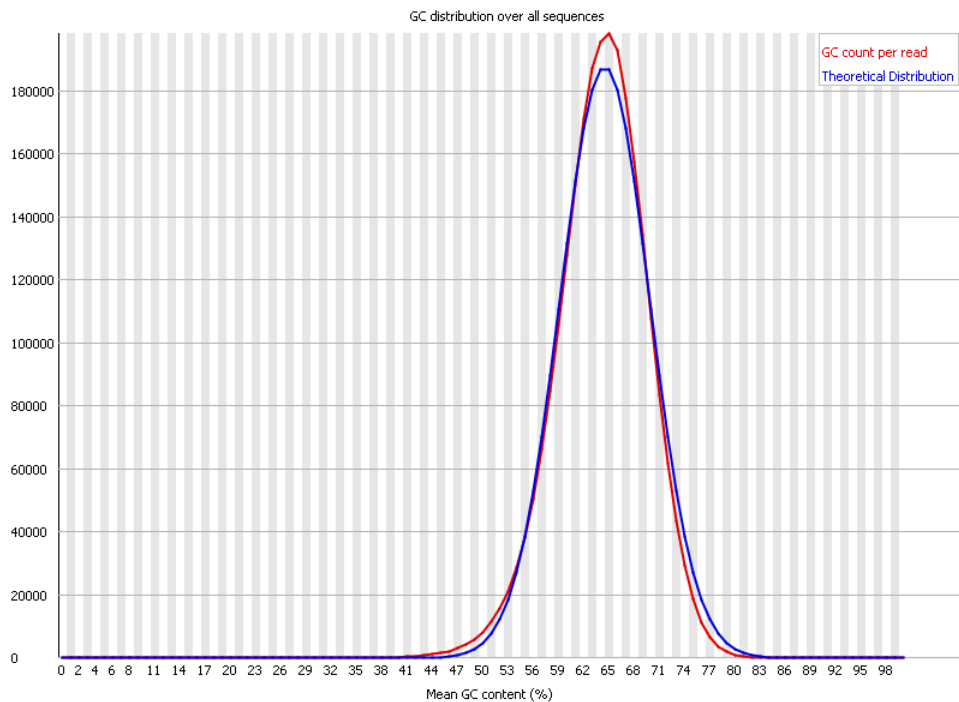
✓ Per sequence quality scores



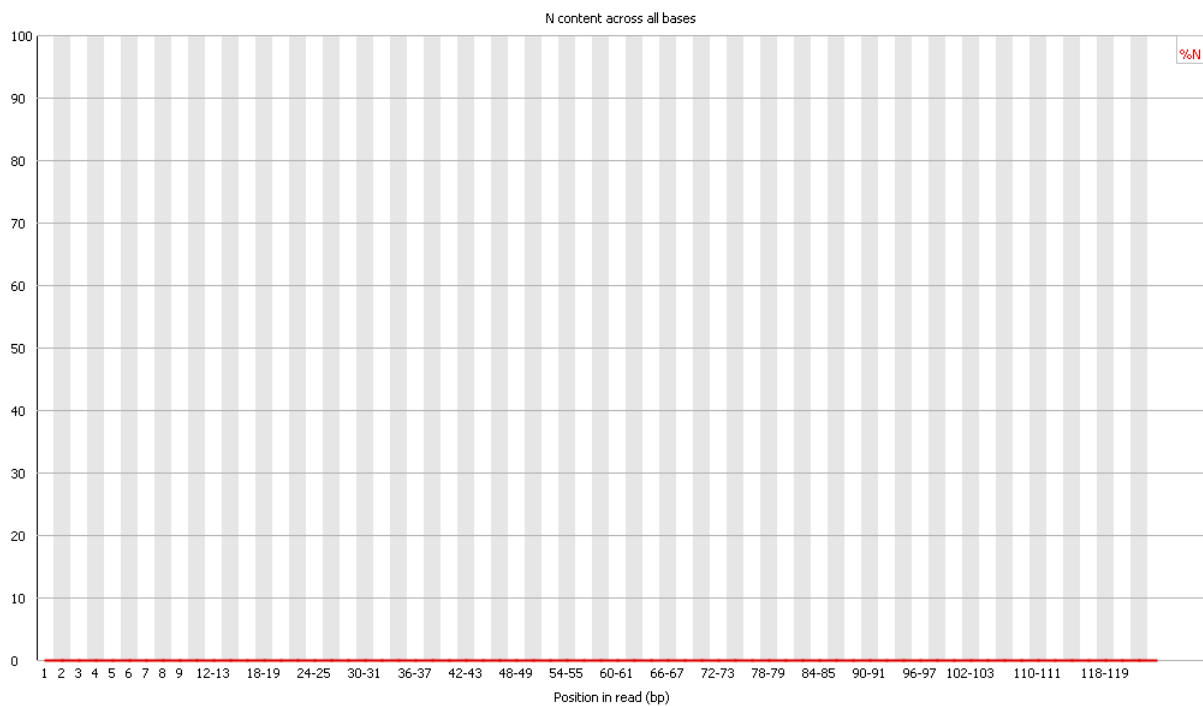
✖ Per base sequence content



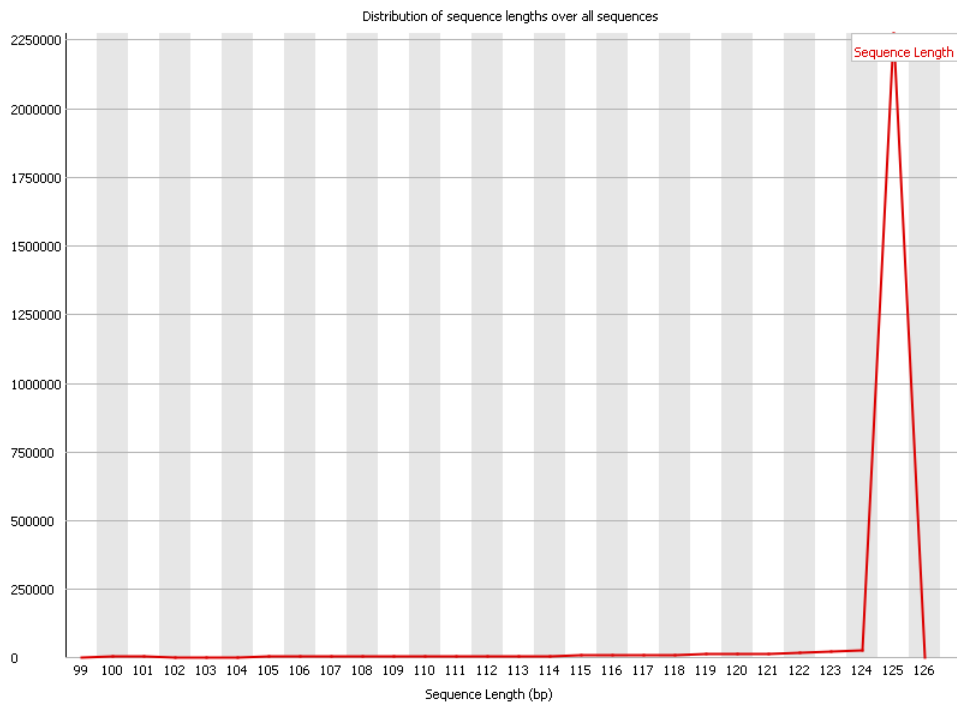
✔ Per sequence GC content



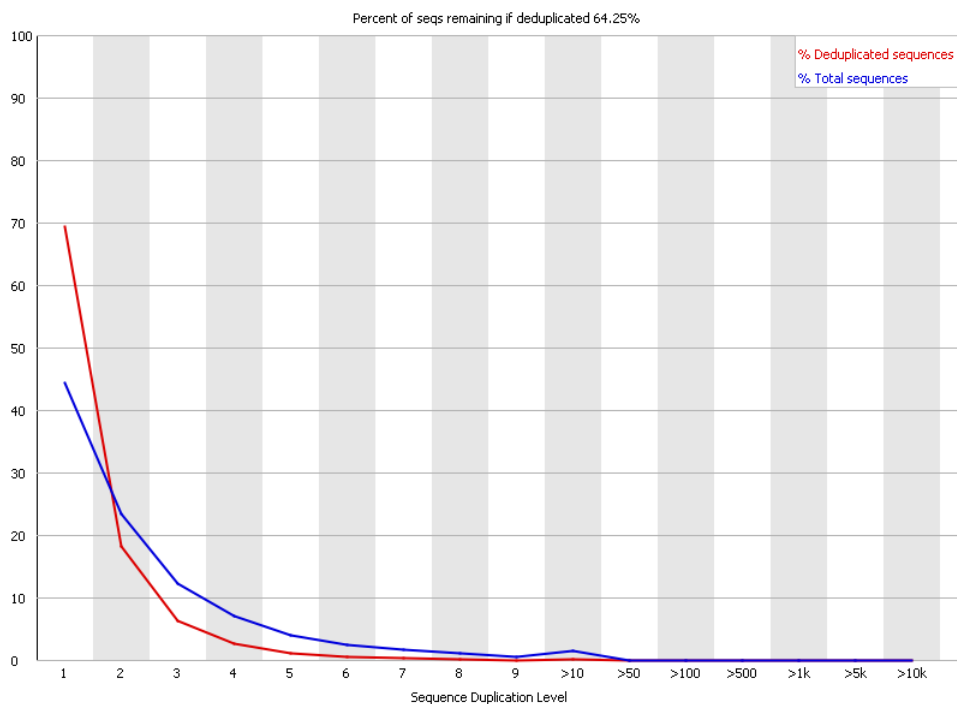
✓ Per base N content



⚠ Sequence Length Distribution



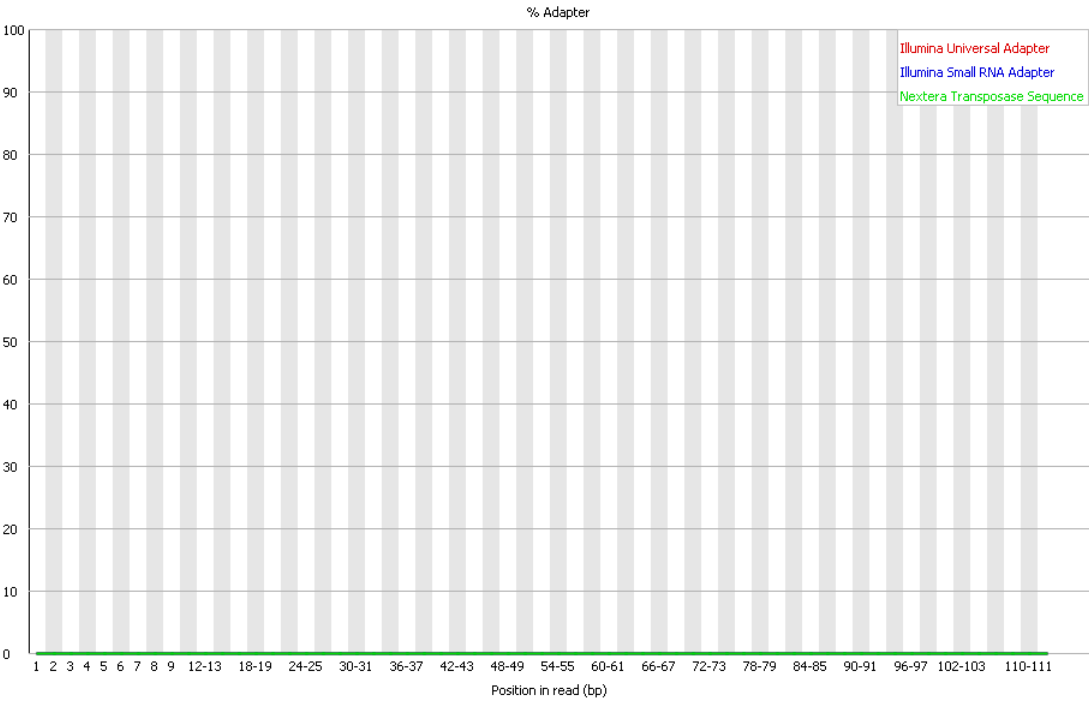
Sequence Duplication Levels



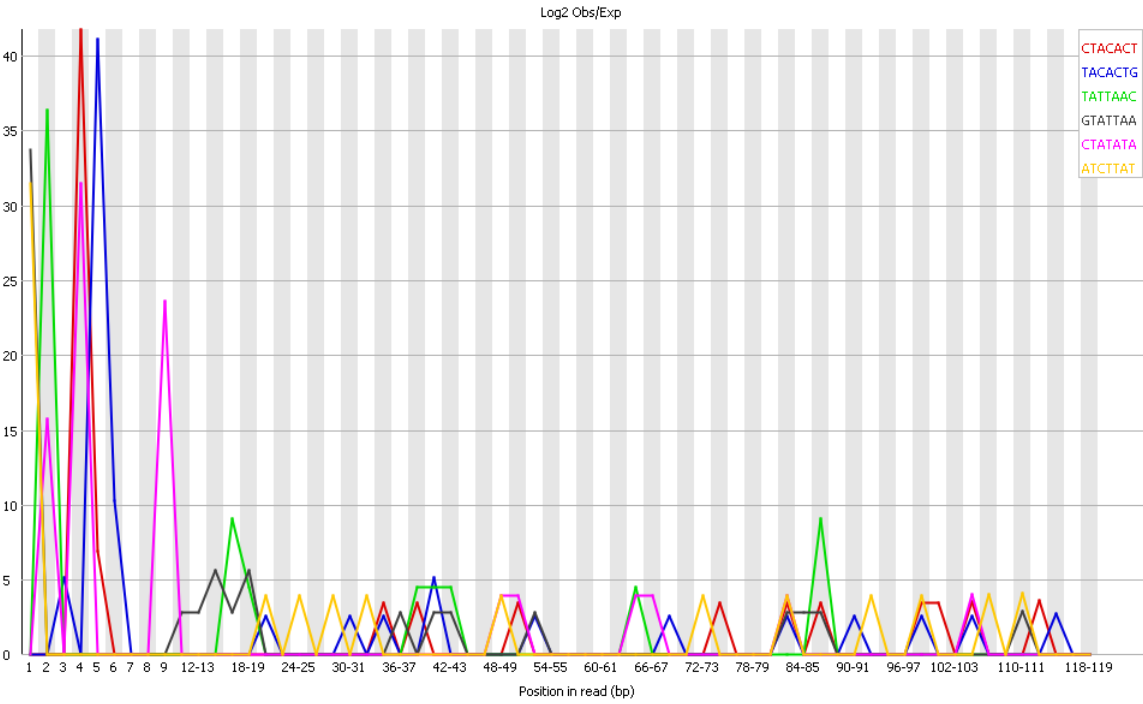
Overrepresented sequences

No overrepresented sequences

Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTACACT	85	3.648347E-6	41.71681	4
TACACTG	115	1.5150363E-8	41.112217	5
TATTAAC	65	0.0020101178	36.348976	2
GTATTAA	105	1.5604724E-5	33.75262	1
CTATATA	75	0.0040430613	31.51937	4
ATCTTAT	75	0.0040537026	31.502445	1
TTAGACT	105	6.146066E-4	28.142292	4
TCTAAAT	105	6.165399E-4	28.127182	2

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTTATAC	85	0.0074541015	27.811207	3
ATACACT	110	8.0663833E-4	26.863098	4
TTCTATA	110	8.091725E-4	26.848675	2
TAGAGAG	245	6.002665E-10	26.534163	5
TCTTAGA	120	0.0013442904	24.611288	2
TAGACTT	130	0.0021351734	22.730312	5
TCTATAT	160	2.7348023E-4	22.162056	3
TAAATCT	165	3.3672218E-4	21.490477	4
ATATAGA	230	6.544693E-6	20.545073	1
TATAGAT	145	0.00403575	20.367962	2
TATTGAA	210	7.563047E-5	19.689028	2
CCTATAA	150	0.0049105203	19.689028	1

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