

FastQC Report

Summary

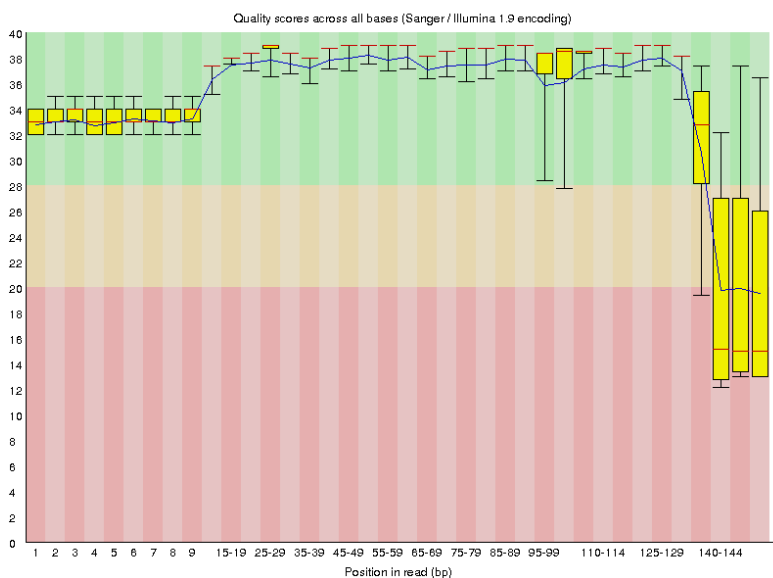
Sat 24 Mar 2018
GOOD_AMPLICON-2_S2_L001_R1_001_fastq

- 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

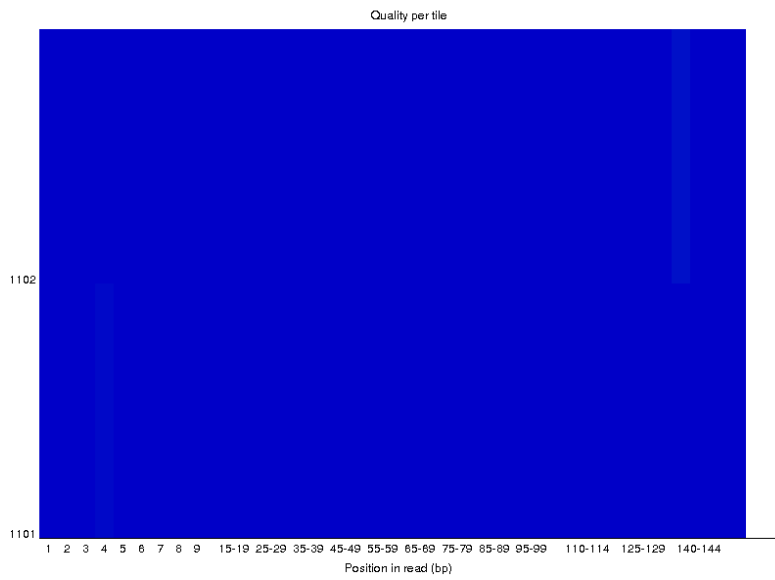
Basic Statistics

Measure	Value
Filename	GOOD_AMPLICON-2_S2_L001_R1_001_fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	51199
Sequences flagged as poor quality	0
Sequence length	151
%GC	42

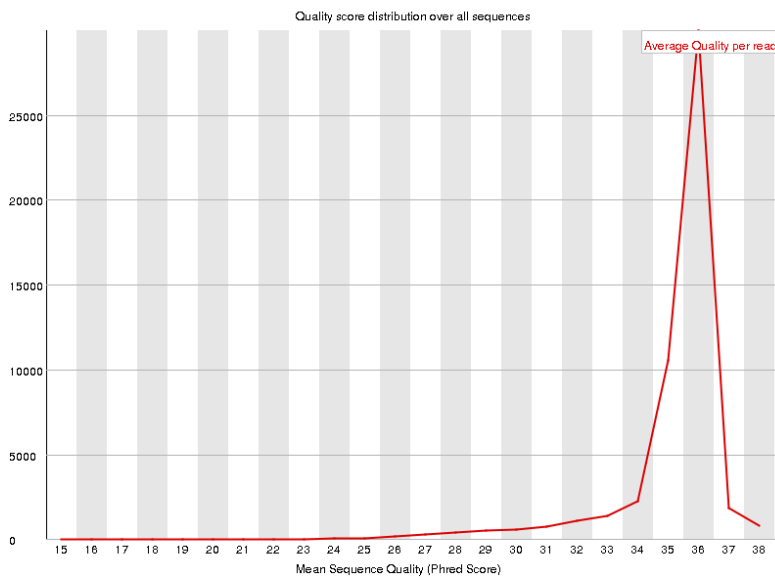
Per base sequence quality



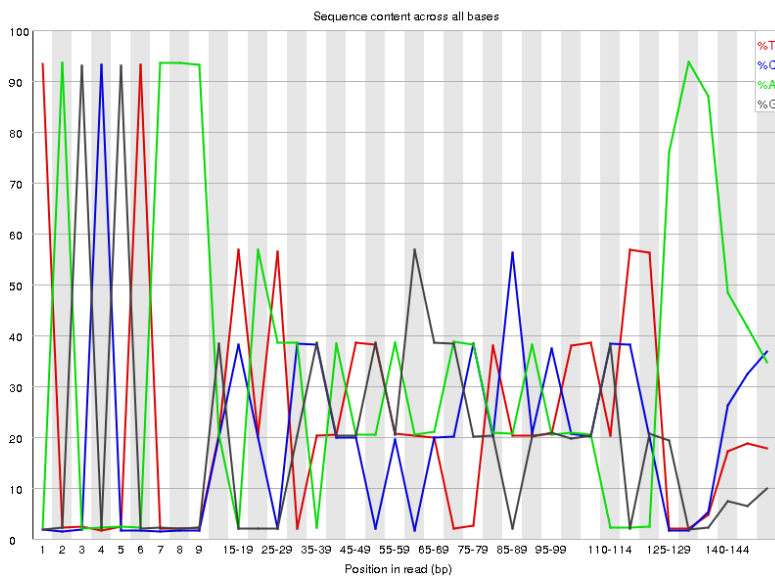
Per tile sequence quality



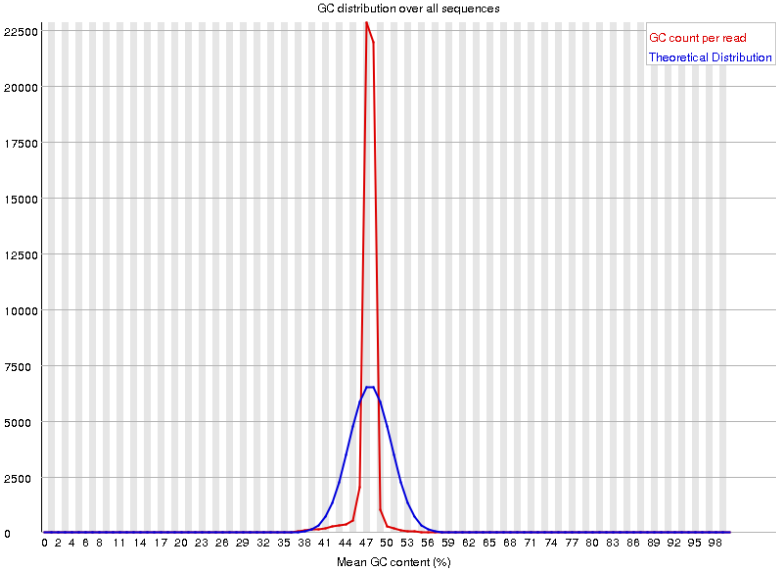
✔ Per sequence quality scores



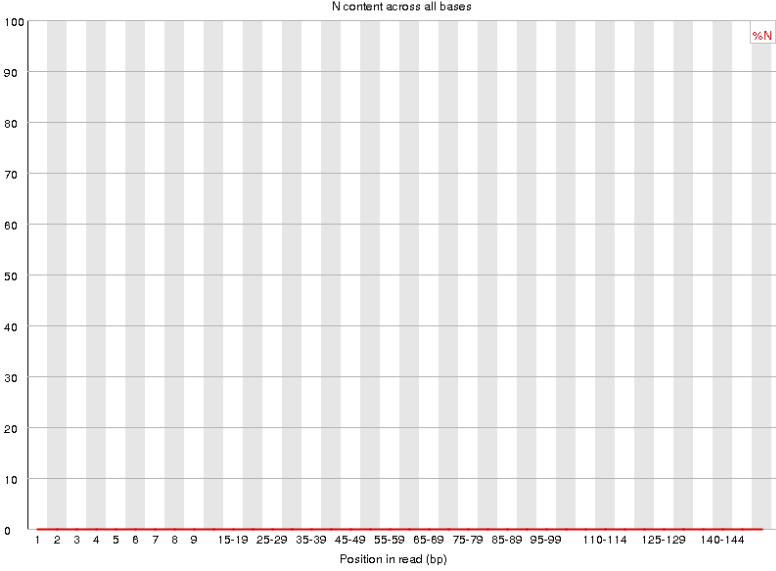
✖ Per base sequence content



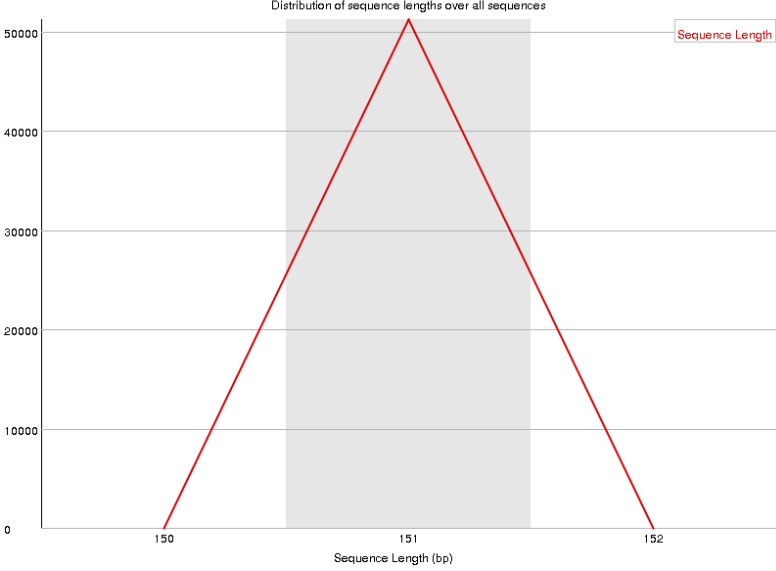
 Per sequence GC content

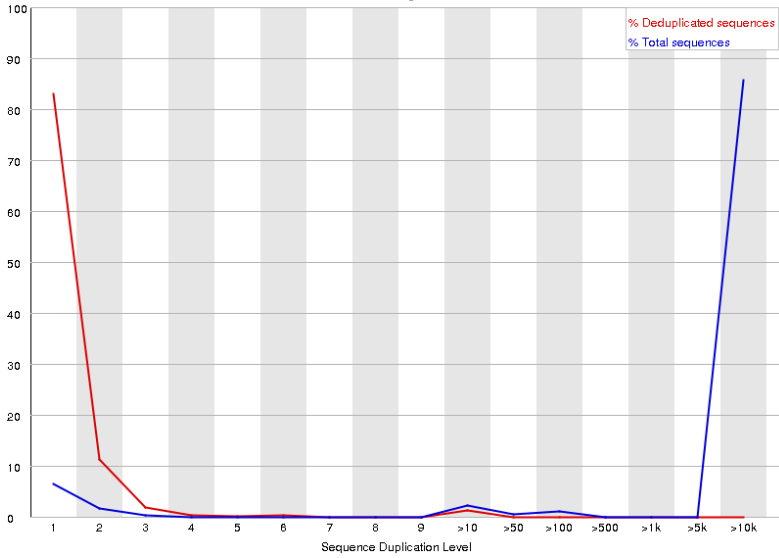
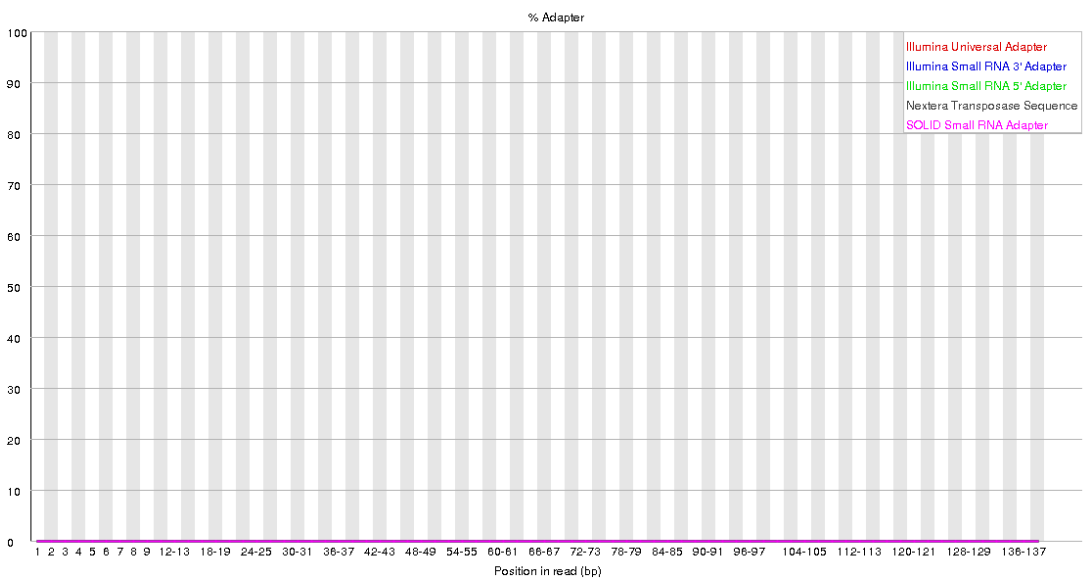


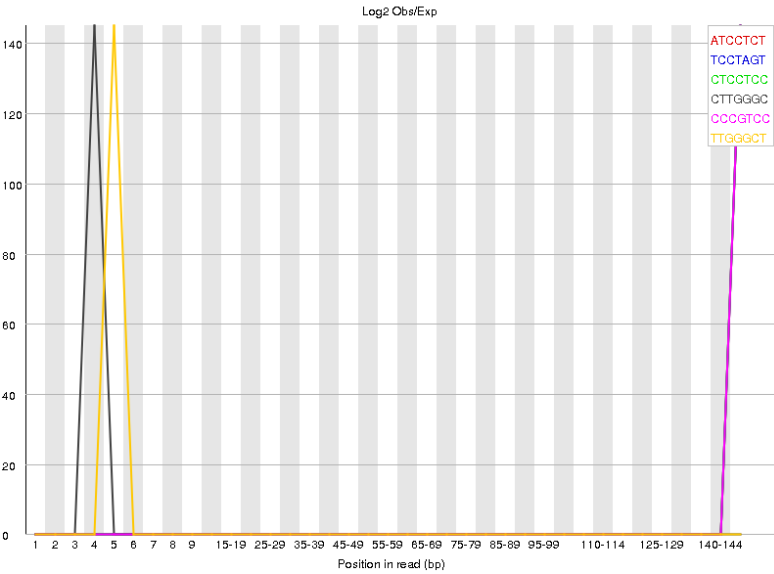
 Per base N content



 Sequence Length Distribution



[illegible]



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCTCT	10	0.0070713446	145.0	145
TCCTAGT	10	0.0070713446	145.0	145
CTCCTCC	10	0.0070713446	145.0	145
CTTGGGC	20	2.1111318E-6	145.0	4
CCCGTCC	10	0.0070713446	145.0	145
TTGGGCT	20	2.1111318E-6	145.0	5
ATAAATG	10	0.0070713446	145.0	5
GGCTCCT	20	2.1111318E-6	145.0	8
CTTATCC	10	0.0070713446	145.0	145
CAGCGTA	10	0.0070713446	145.0	1
ATCAACC	10	0.0070713446	145.0	145
GGGCTCC	20	2.1111318E-6	145.0	7
TAGCGTA	4605	0.0	145.0	1
AGCGTAA	4625	0.0	144.6865	2
GCGTAAA	4625	0.0	144.52974	3
CGTAAAT	4620	0.0	144.52922	4
TAAATGG	4630	0.0	144.37366	6
ATGGACT	4630	0.0	144.37366	9
AATGGAC	4630	0.0	144.37366	8
AAATGGA	4625	0.0	144.37297	7