

FastQC Report

Summary

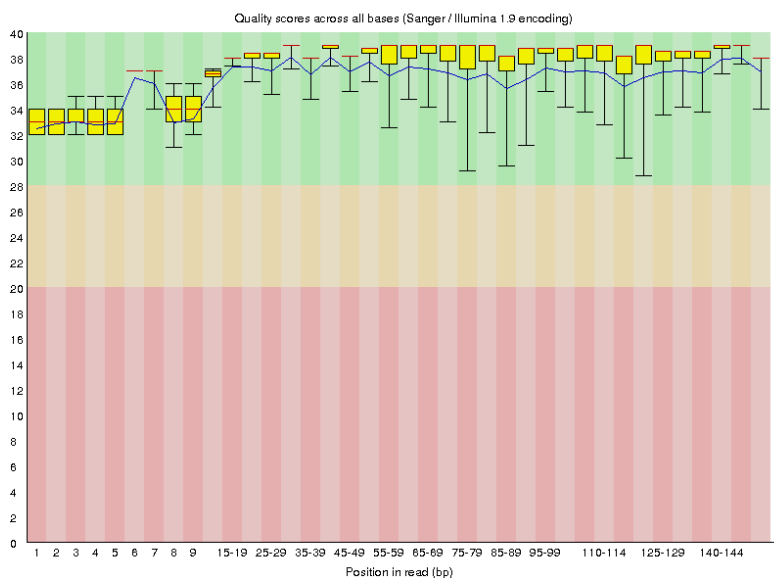
Sat 24 Mar 2018
BAD_AMPLICON-1_S10_L001_R1_001_fastq

- 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

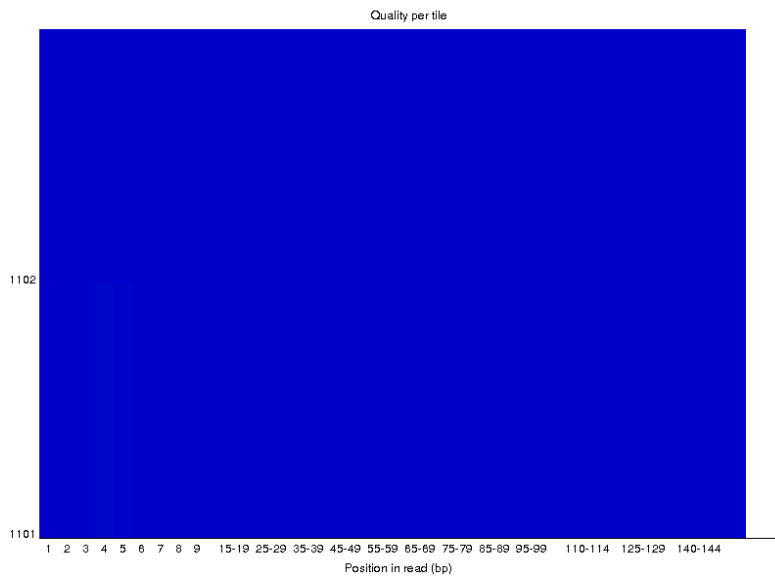
Basic Statistics

Measure	Value
Filename	BAD_AMPLICON-1_S10_L001_R1_001_fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	65349
Sequences flagged as poor quality	0
Sequence length	151
%GC	51

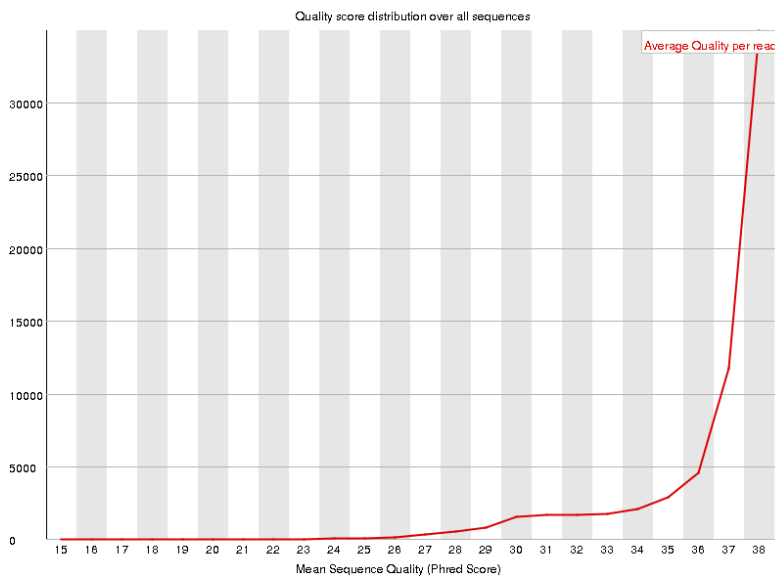
Per base sequence quality



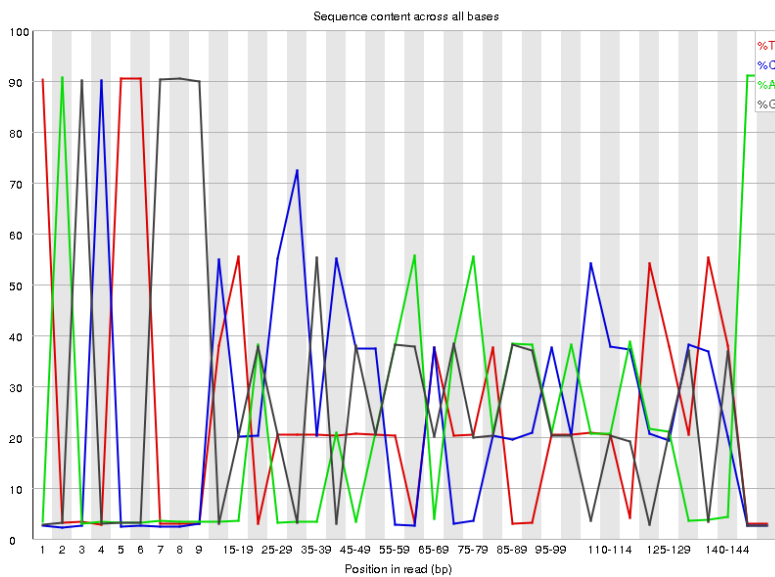
Per tile sequence quality



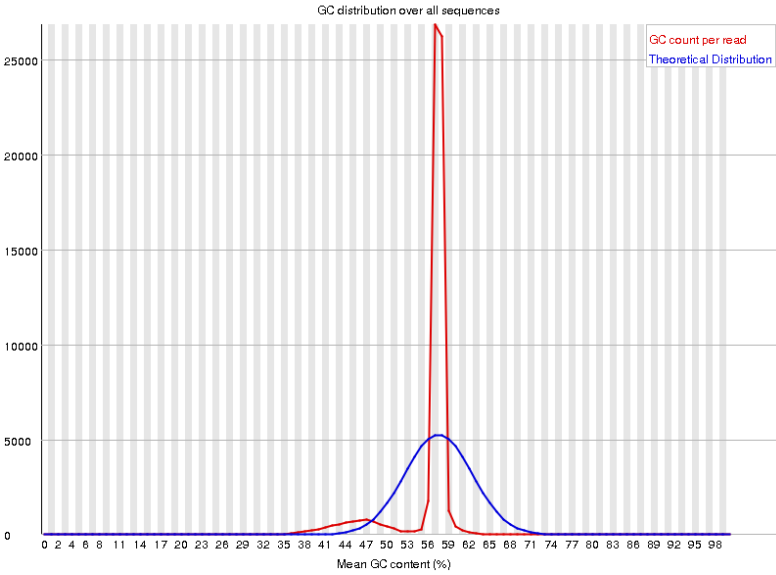
✔ Per sequence quality scores



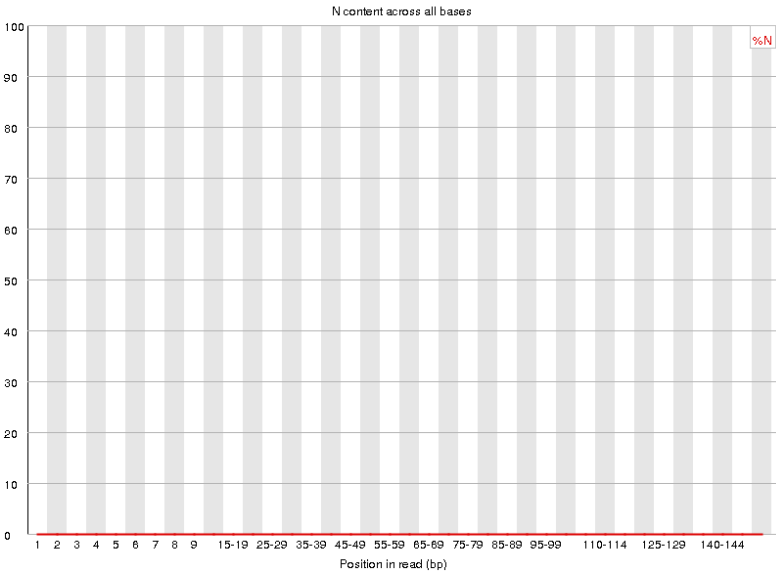
✖ Per base sequence content



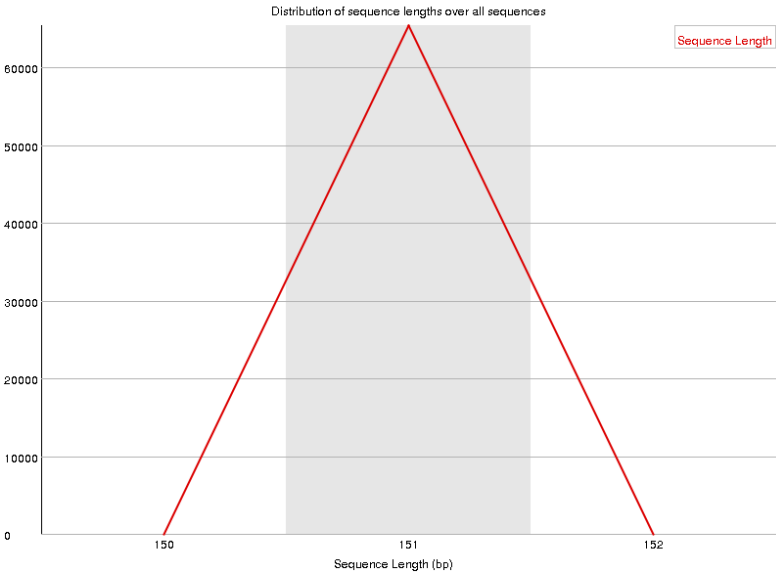
✖ Per sequence GC content

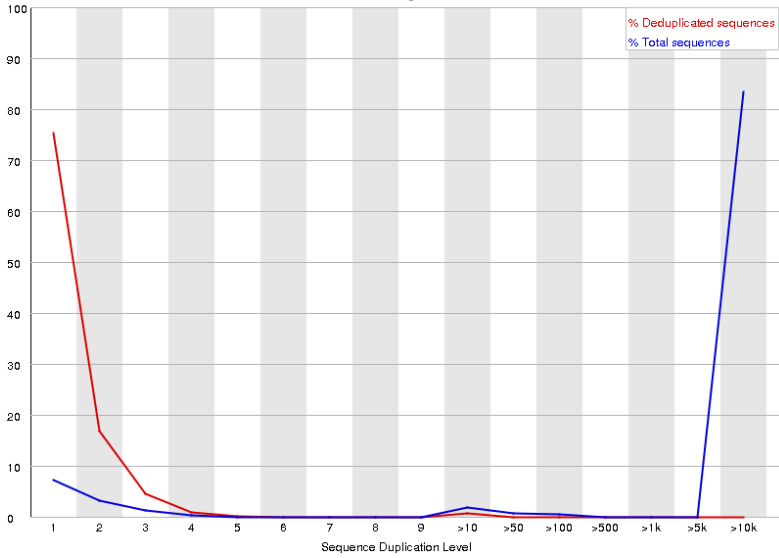
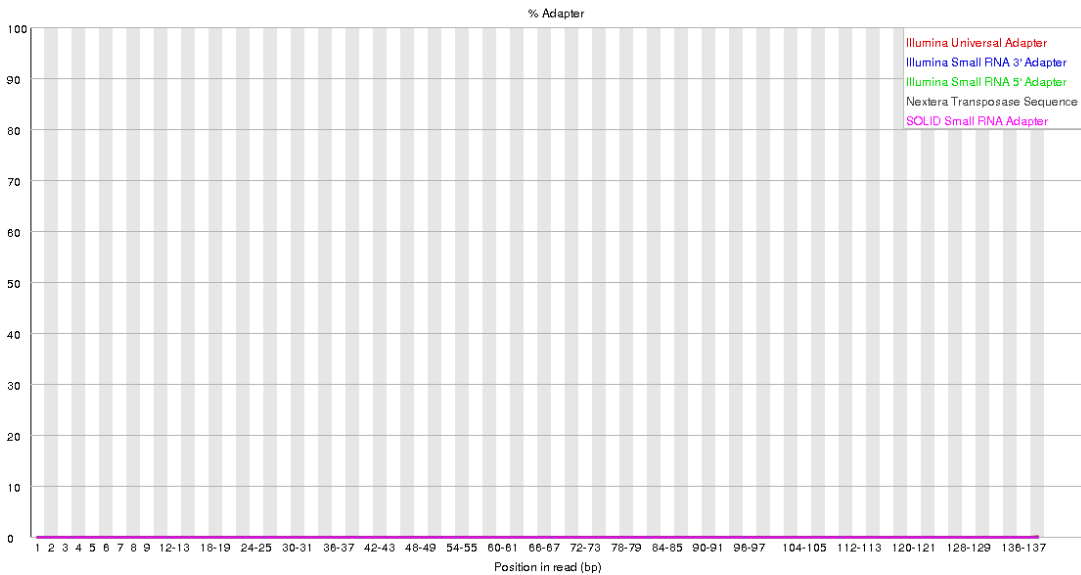


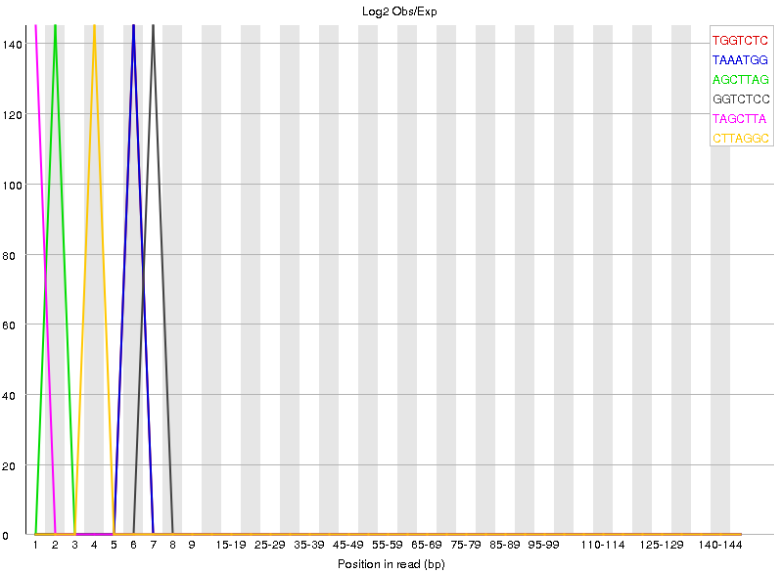
✔ Per base N content



✔ Sequence Length Distribution



[illegible]



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TGGTCTC	10	0.007075801	144.99998	6
TAAATGG	10	0.007075801	144.99998	6
AGCTTAG	20	2.1155683E-6	144.99998	2
GGTCTCC	10	0.007075801	144.99998	7
TAGCTTA	20	2.1155683E-6	144.99998	1
CTTAGGC	20	2.1155683E-6	144.99998	4
ATGGACT	10	0.007075801	144.99998	9
TTGGGCC	10	0.007075801	144.99998	5
GTCTCCT	10	0.007075801	144.99998	8
AGGCTCC	20	2.1155683E-6	144.99998	7
AATGGAC	10	0.007075801	144.99998	8
TTAGGCT	20	2.1155683E-6	144.99998	5
TGGGCCC	10	0.007075801	144.99998	6
AAATGGA	10	0.007075801	144.99998	7
GTAAATG	10	0.007075801	144.99998	5
TGGCTCC	10	0.007075801	144.99998	6
TAGGCTC	20	2.1155683E-6	144.99998	6
GGGCCCC	10	0.007075801	144.99998	7
TAGCGTA	10	0.007075801	144.99998	1
TAGCTTG	5745	0.0	144.7476	1