

FastQC Report

Summary

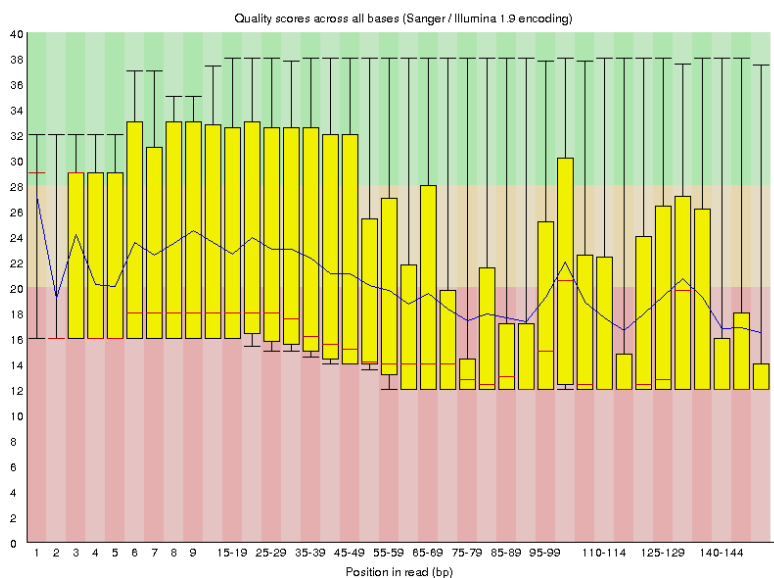
Sat 24 Mar 2018
BAD_AMPLICON-1_S10_L001_R2_001_fastq

- 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

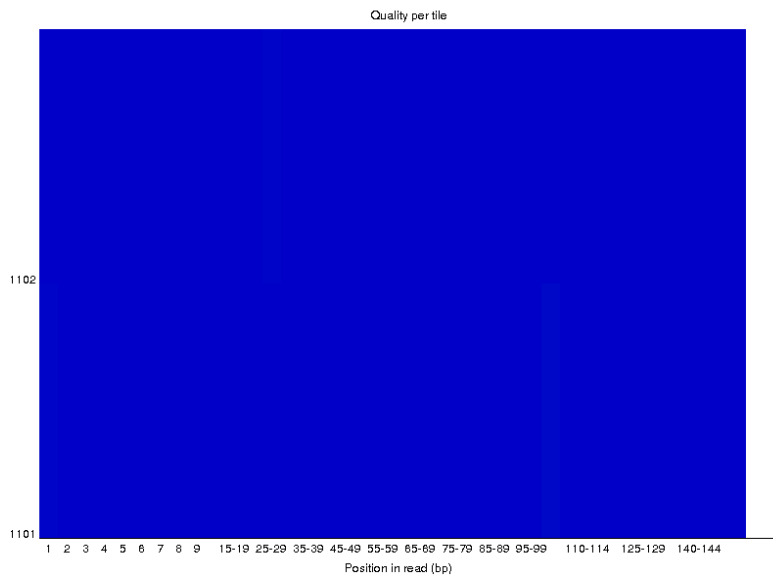
Basic Statistics

Measure	Value
Filename	BAD_AMPLICON-1_S10_L001_R2_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	64

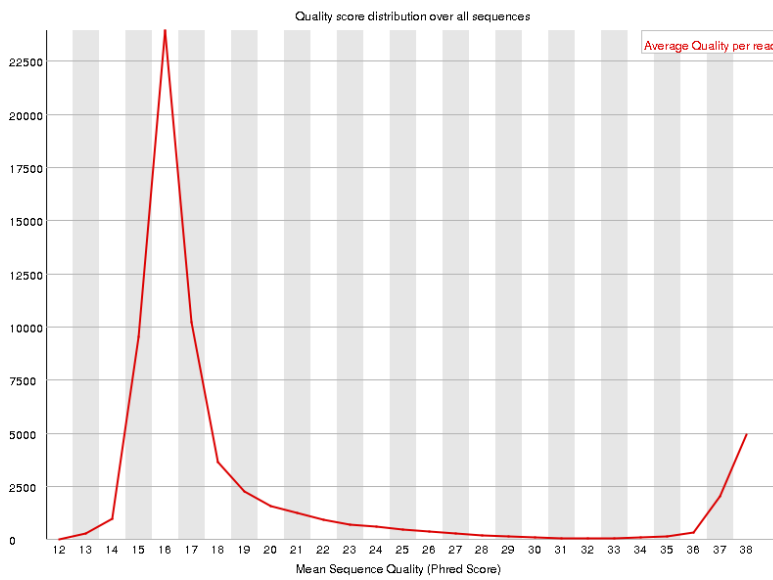
Per base sequence quality



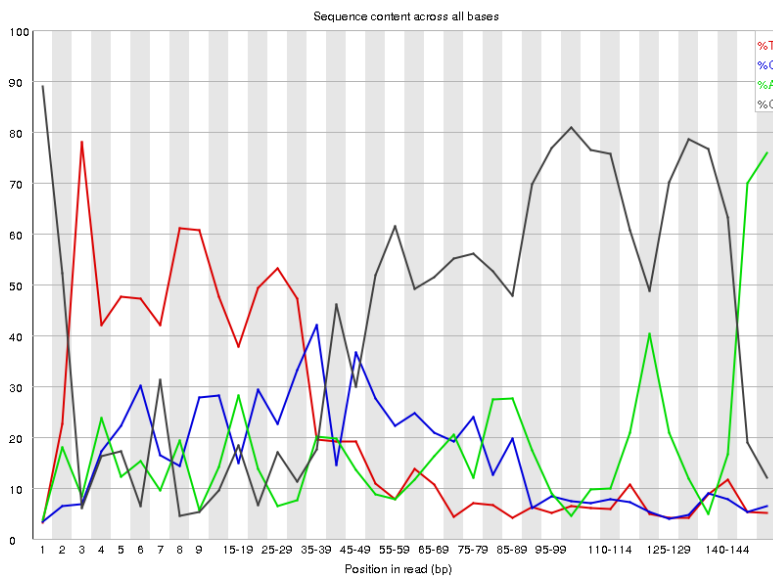
Per tile sequence quality



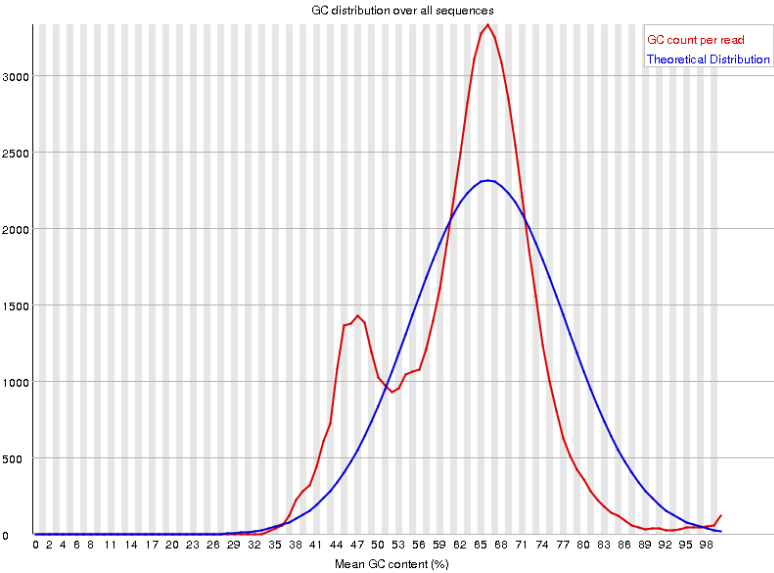
✖ Per sequence quality scores



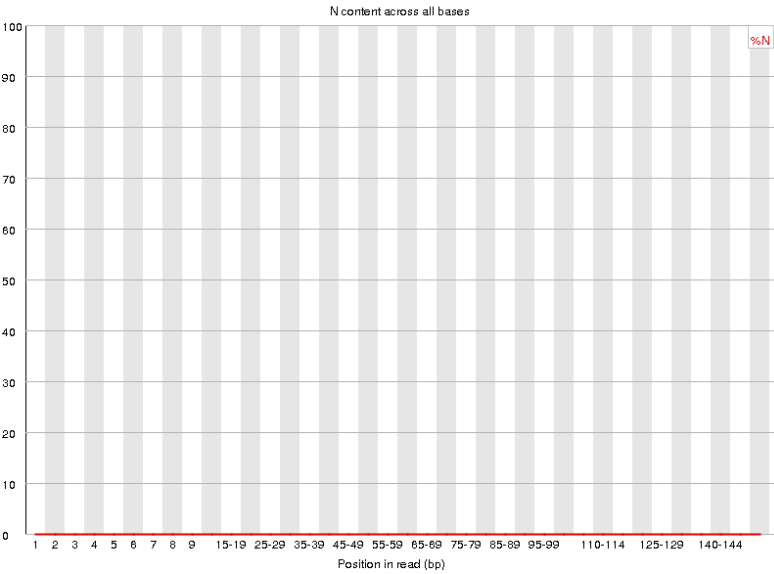
✖ Per base sequence content



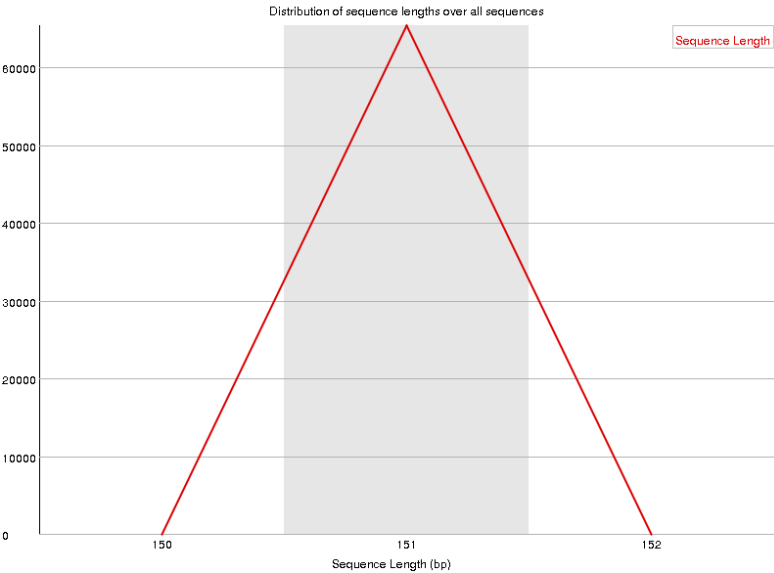
✖ Per sequence GC content

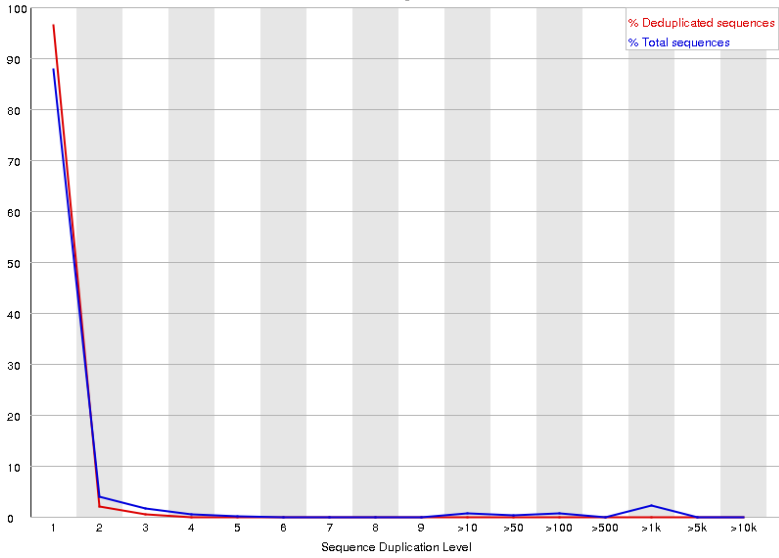


✔ Per base N content

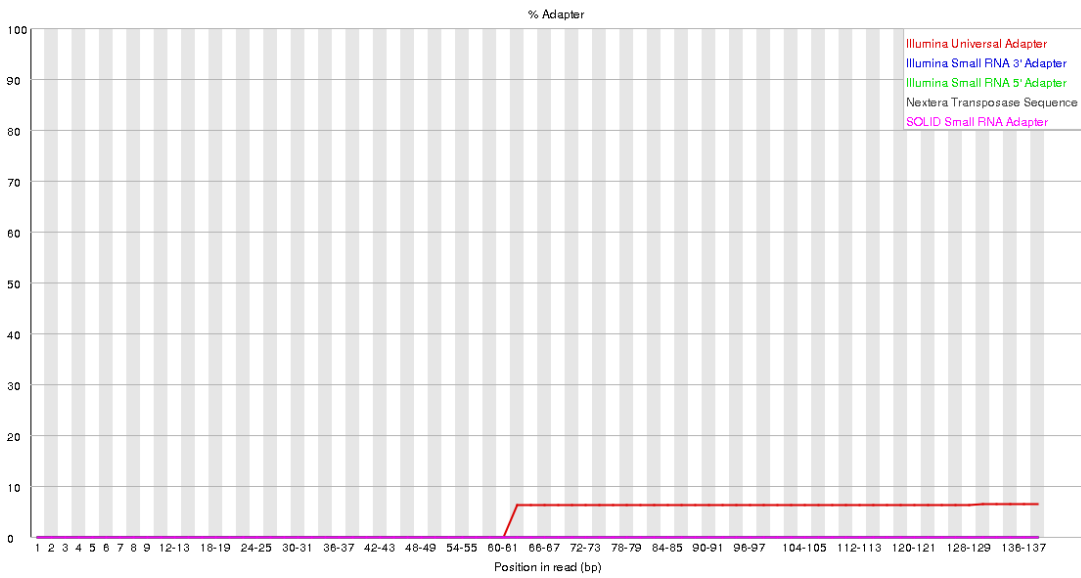


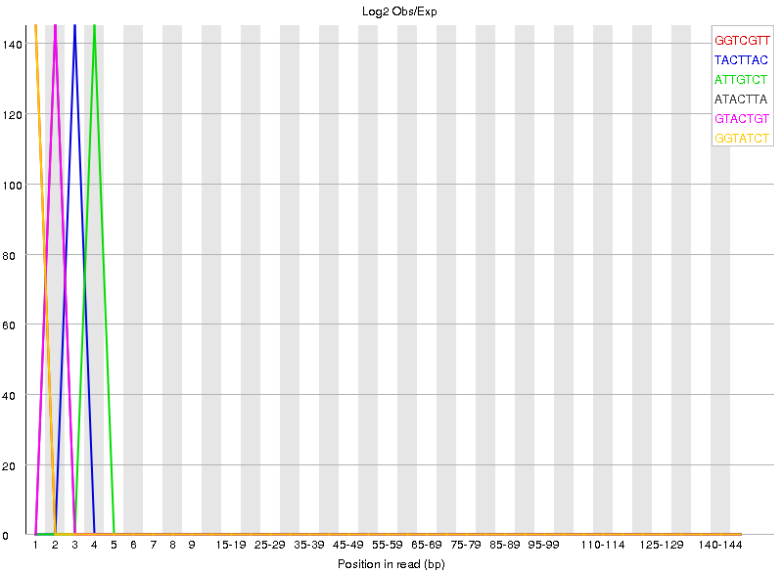
✔ Sequence Length Distribution





Sequence	Count	Percentage	Possible Source
GATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAAGGAAGTC	1593	2.4376807602258643	No Hit
CC	160	0.24483924773141133	No Hit
GATACTGACTCATCAGAAGTCTCATCTGCGTTAAAGTTTAAAGGAAGTC	149	0.22800654944987683	No Hit
CATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAAGGAAGTC	143	0.218825076765994888	No Hit
GATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAAGGACGTC	104	0.15914551102541738	No Hit
GATACTGACTCATCAGAAGTCTCAGCGTTCGGTTCAAGTTTAAAGGAAGTC	97	0.14843379393716813	No Hit
CC	74	0.11323815207577774	No Hit





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGTCGTT	15	1.2247877E-4	145.0	1
TACTTAC	45	0.0	145.0	3
ATTGTCT	55	0.0	145.0	4
ATACTTA	35	1.0913936E-11	145.0	2
GTACTGT	30	6.4028427E-10	145.0	2
GGTATCT	15	1.2247877E-4	145.0	1
GACTCTT	35	1.0913936E-11	145.0	7
ATATTGA	35	1.0913936E-11	145.0	2
TGACTCC	50	0.0	145.0	6
TTCTATA	10	0.007075801	144.99998	9
GTCGATT	10	0.007075801	144.99998	2
GGTGAT	40	0.0	144.99998	1
GGTCGAT	10	0.007075801	144.99998	1
ACTGATT	20	2.1155683E-6	144.99998	4
CCCTACT	10	0.007075801	144.99998	6
GTCCTGA	20	2.1155683E-6	144.99998	2
ATTACTG	10	0.007075801	144.99998	7
GAATAAT	10	0.007075801	144.99998	7
TATTGGG	10	0.007075801	144.99998	9
GAAACCT	10	0.007075801	144.99998	8