Report Summary

Wed 30 Aug 2017 Sample5_reverse_paired.fq.gz



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

Filename

moacaro	Value

Value

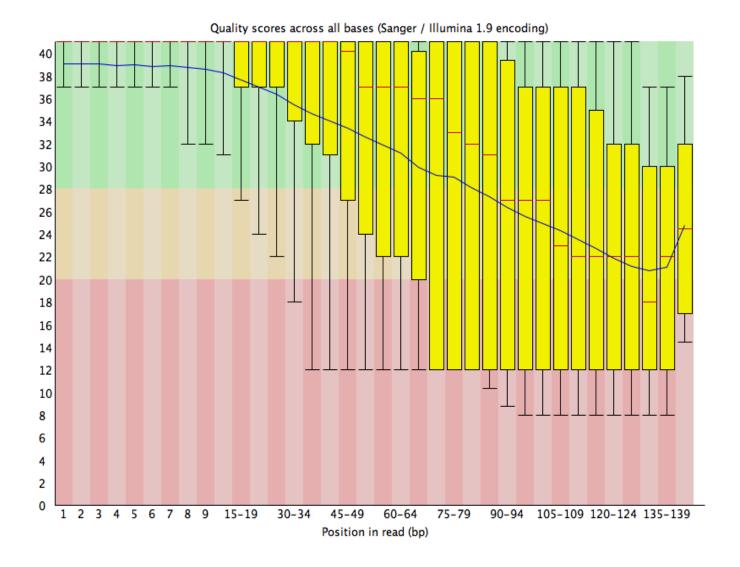
Sample5_reverse_paired.fq.gz File type Conventional base calls Encoding Sanger / Illumina 1.9

Total Sequences 36936739

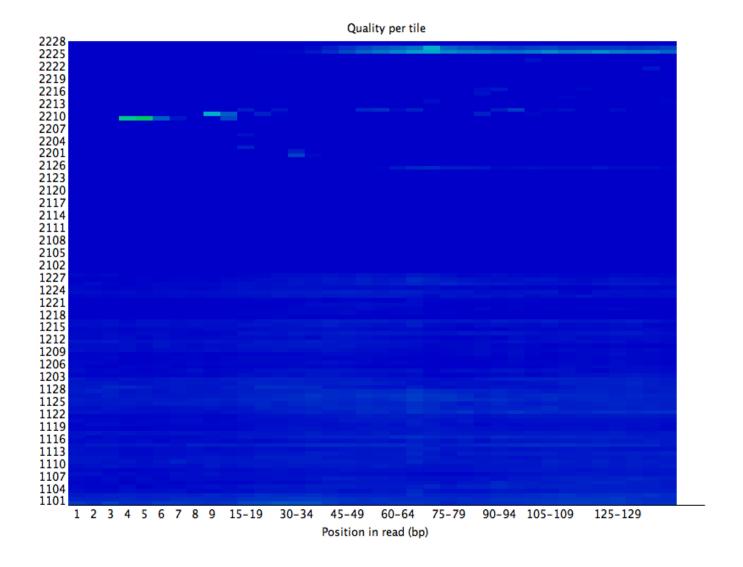
Sequences flagged as poor quality 0 Sequence length 6-143 %GC

Measure

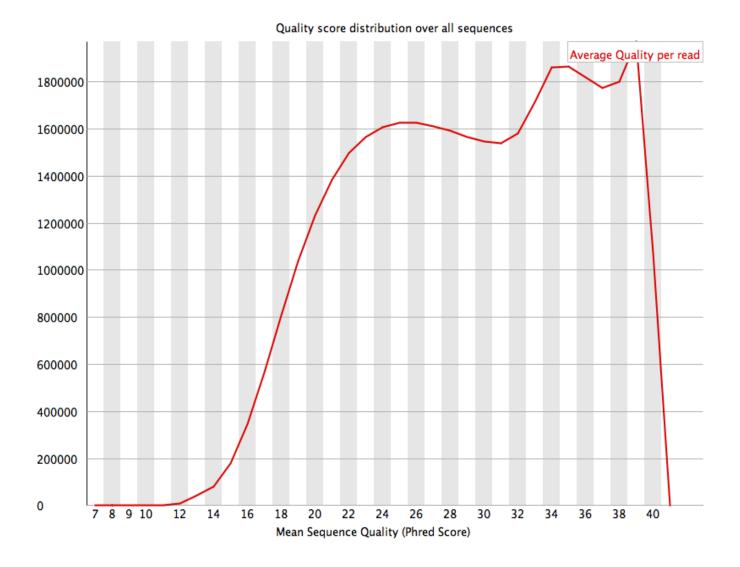
②Per base sequence quality



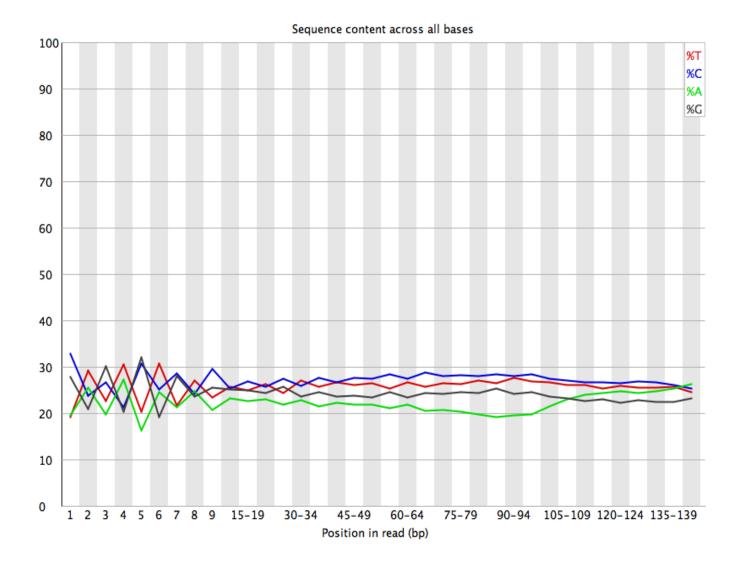
Per tile sequence quality



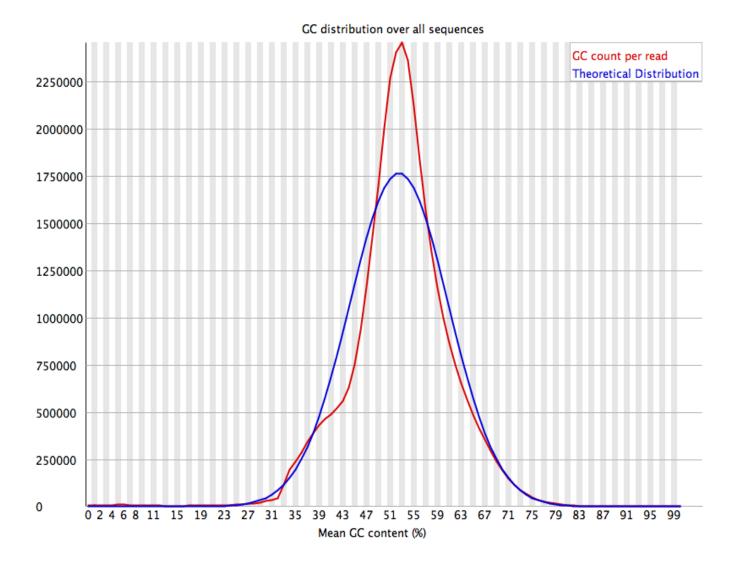
Per sequence quality scores



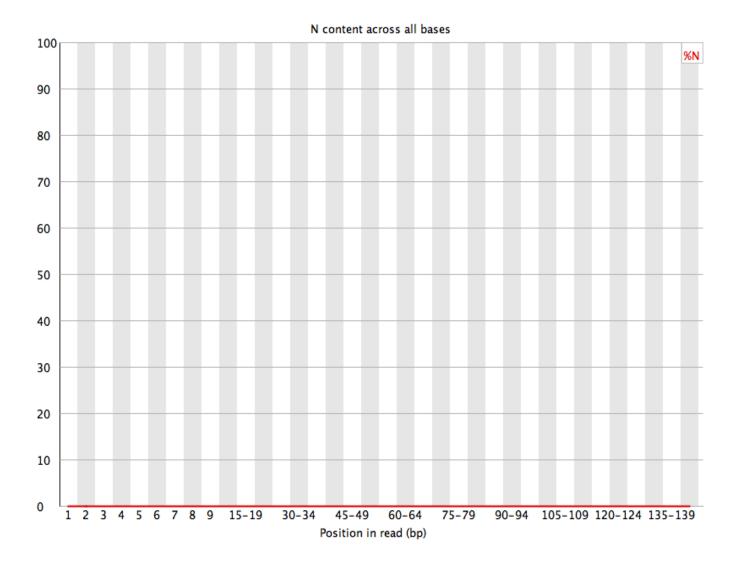
Per base sequence content



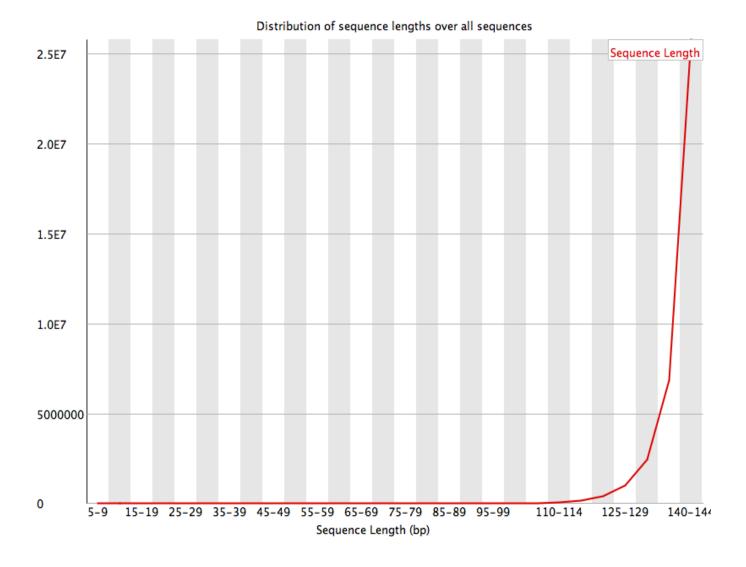
Per sequence GC content



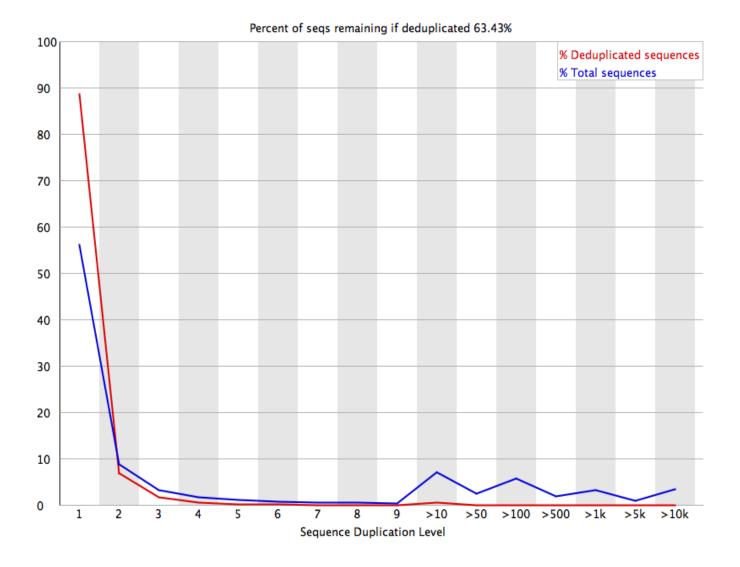




Sequence Length Distribution



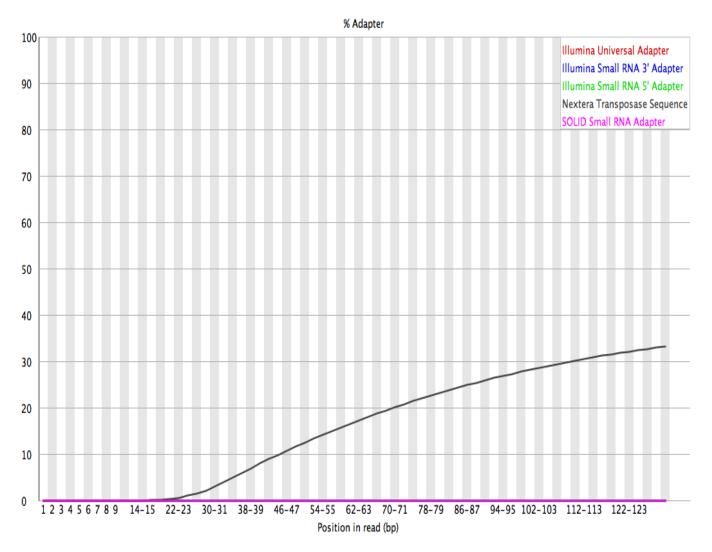
Sequence Duplication Levels



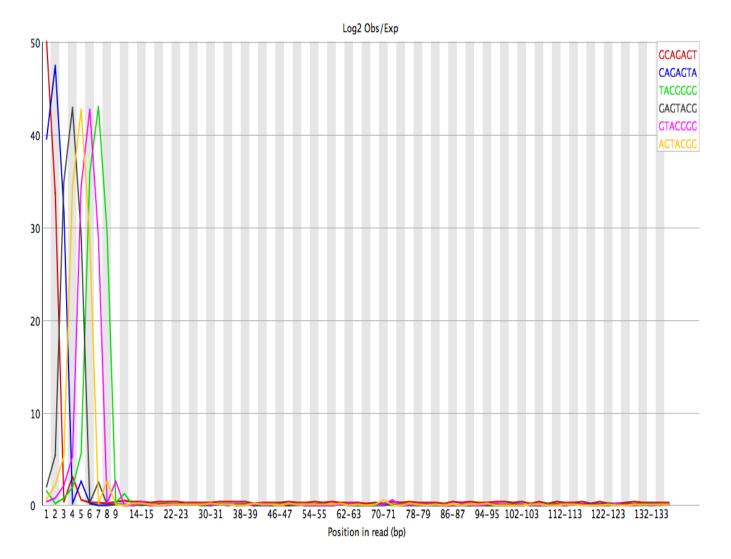
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt ACAACAACAACAACAACAACAACAACAACAACAACAACA$	201396	0.5452457511205848	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	190100	0.5146637335797294	No Hit
${\tt GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA$	170750	0.46227686748415986	No Hit
$\tt CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT$	113908	0.3083867257475003	No Hit
${\tt GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	106764	0.28904554893164774	No Hit
${\tt AACAACAACAACAACAACAACAACAACAACAACAACAAC$	47738	0.12924259502172078	No Hit
${\tt AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG$	47085	0.12747470749921913	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	43327	0.11730055541719588	No Hit

Adapter Content



WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	42395	0.0	50.029953	1
CAGAGTA	44690	0.0	47.46149	2
TACGGGG	20635	0.0	43.079304	7
GAGTACG	44515	0.0	42.92487	4
GTACGGG	44695	0.0	42.744987	6
AGTACGG	44755	0.0	42.741978	5
AGAGTAC	50490	0.0	41.890553	3
TACGGGC	10050	0.0	39.07566	7
TACGGGA	5850	0.0	38.816654	7
ACGGGTC	7615	0.0	32.37009	8
TACGGGT	13460	0.0	30.565445	7
GAGTACT	7215	0.0	28.315928	4
AGTACTT	7360	0.0	27.939499	4

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTACTTT	7375	0.0	27.612734	5
ACGGGGA	14575	0.0	27.591505	8
ТАААСТА	4070	0.0	24.27738	2
ACGGGGT	6585	0.0	24.143967	8
TAGAACC	4330	0.0	23.290785	7
CTAGAAC	4355	0.0	23.153416	6
CGGGTCT	9090	0.0	23.073143	9

Produced by FastQC (version 0.11.5)