# **PastQC Report**Summary

Tue 29 Aug 2017 Sample2\_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

moacaro	Value		

Value

Filename Sample2\_reverse\_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9

Total Sequences 24954266

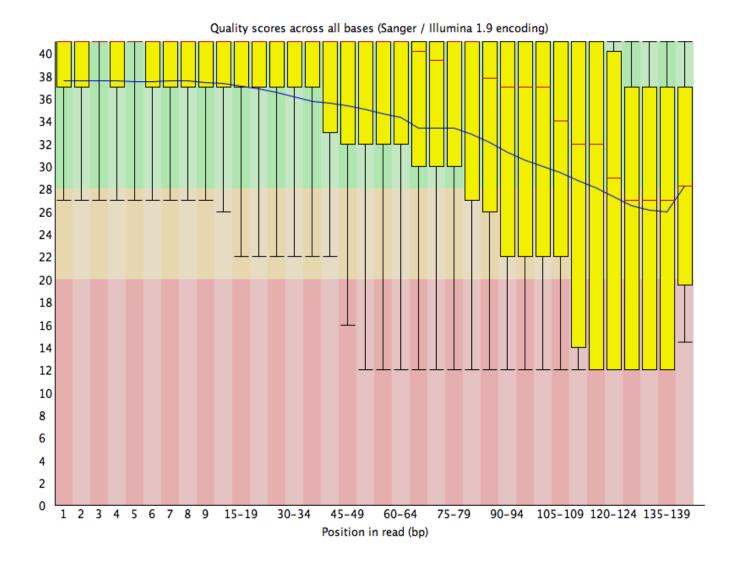
Sequences flagged as poor quality  $\,\,0\,\,$ 

Measure

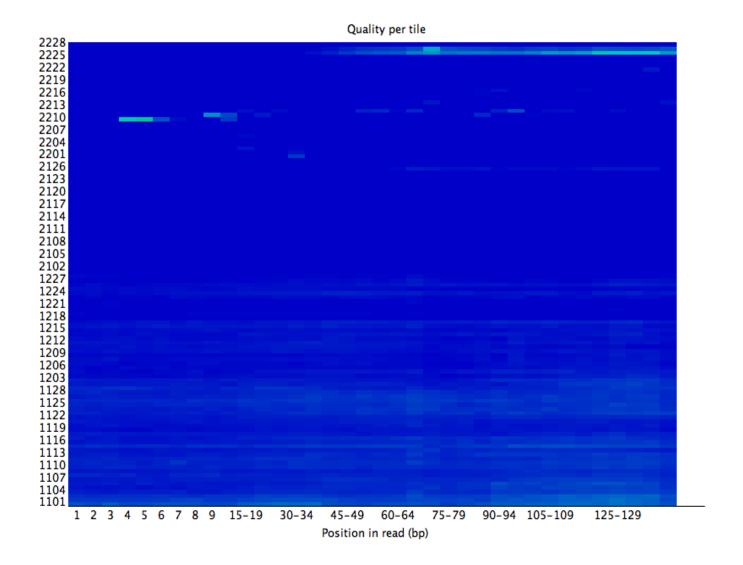
Sequence length 13-143

%GC 55

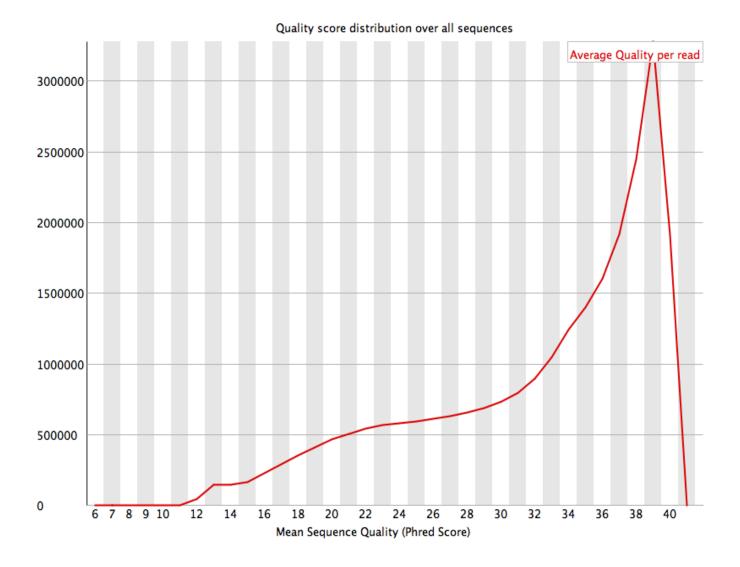
#### Per base sequence quality



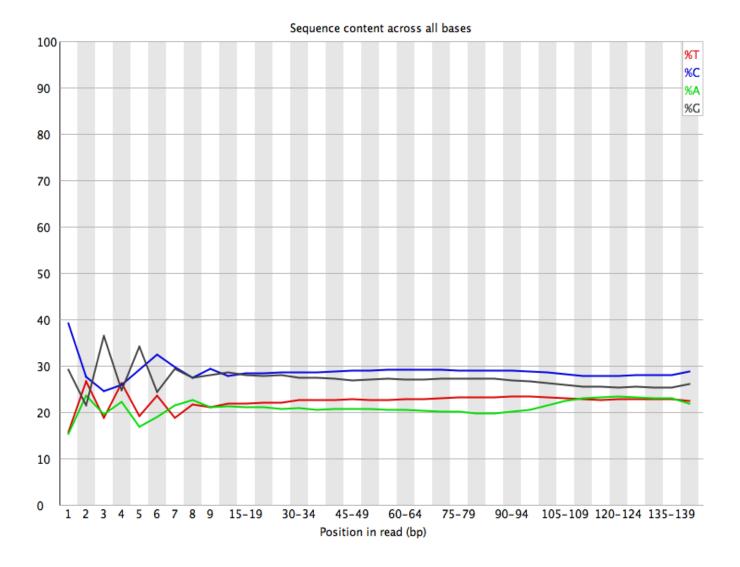
#### Per tile sequence quality



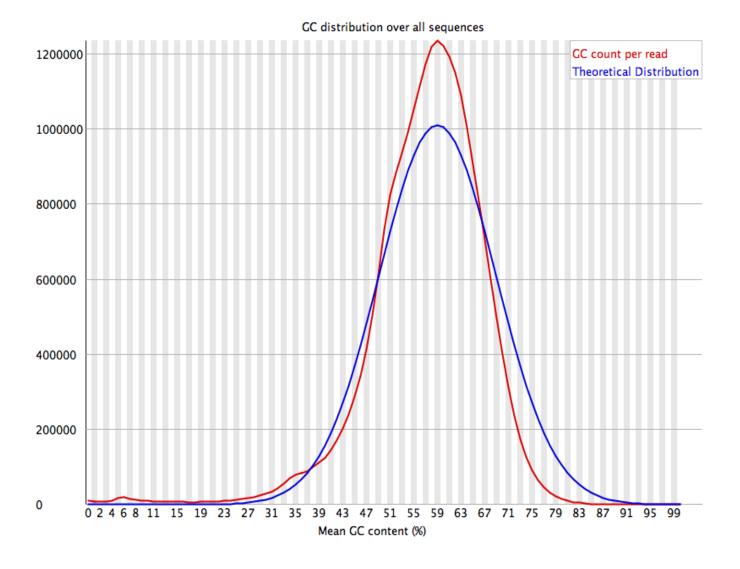
# Per sequence quality scores



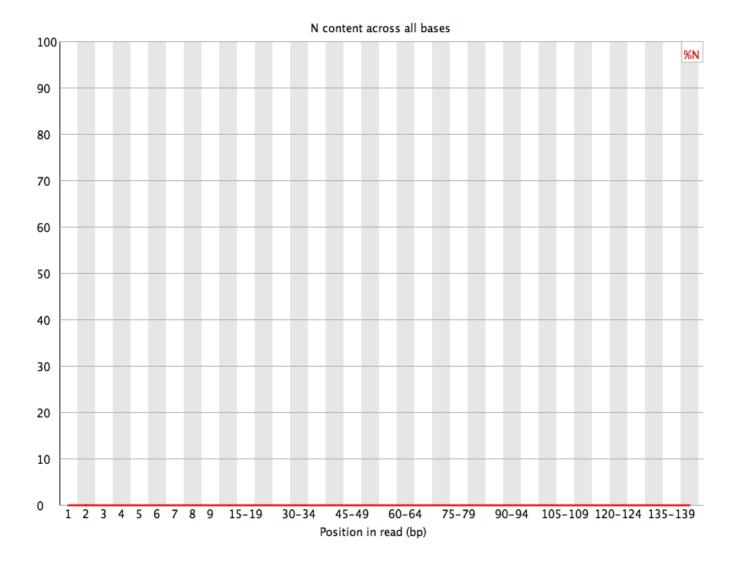
#### Per base sequence content



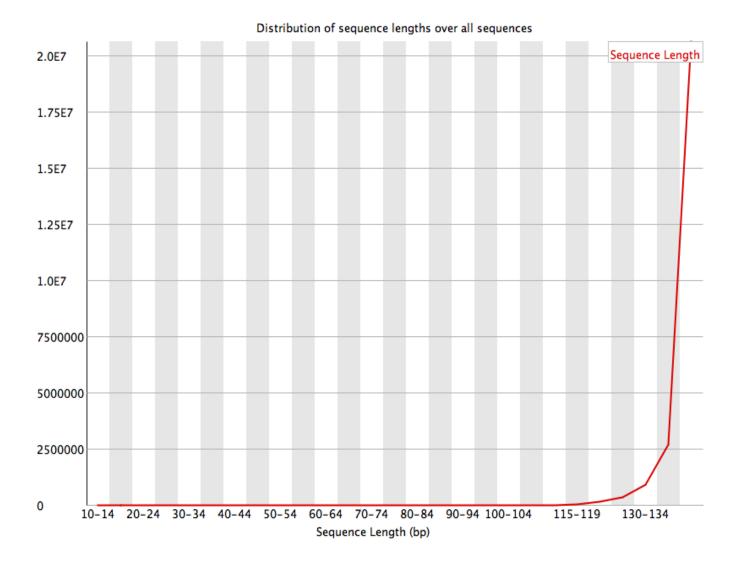
### Per sequence GC content



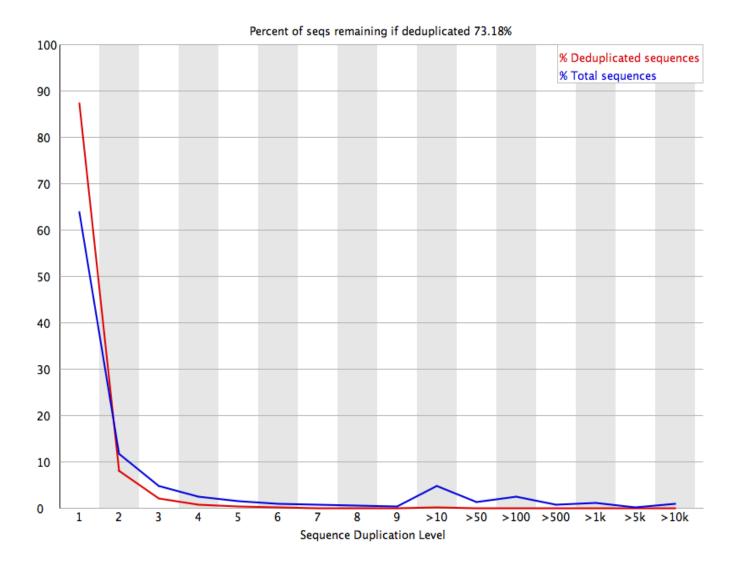




#### Sequence Length Distribution



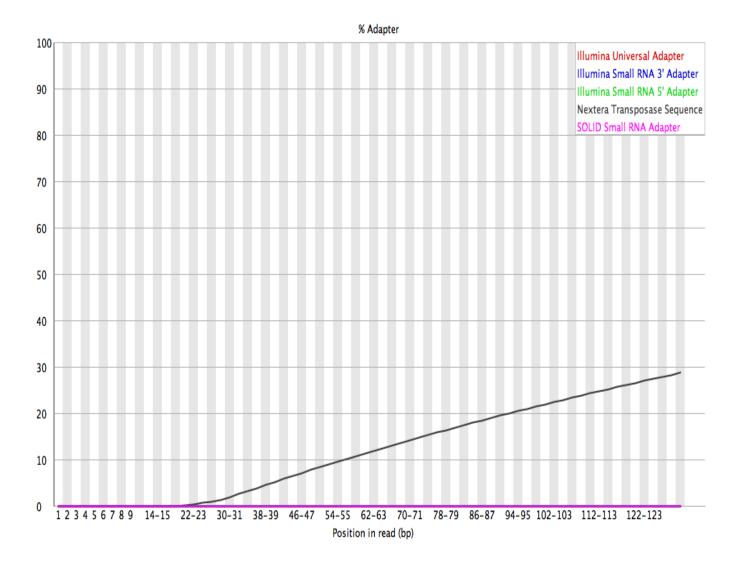
# Sequence Duplication Levels



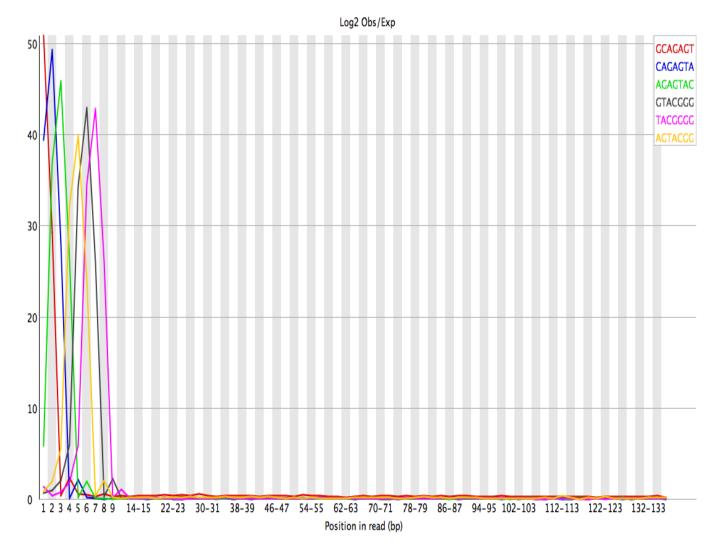
#### Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GA	44478	0.1782380615803326	No Hit
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	30439	0.12197914376644058	No Hit
AG	25030	0.10030349119465184	No Hit





#### **W**Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	46395	0.0	50.79644	1
CAGAGTA	47840	0.0	49.23426	2
AGAGTAC	51115	0.0	45.881992	3
GTACGGG	40925	0.0	42.907757	6
TACGGGG	29275	0.0	42.834587	7
AGTACGG	44040	0.0	39.94305	5
GAGTACG	46585	0.0	38.090992	4
GTACTTT	16665	0.0	34.30104	6
TACTTTT	17410	0.0	32.52813	7
TACGGGA	7030	0.0	31.839138	7
GAGTACT	19160	0.0	30.214483	4
AGTACTT	19420	0.0	29.39559	5
CGCAGAG	51145	0.0	26.933111	1

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGGGGG	25120	0.0	26.46795	8
ACTTTTT	22110	0.0	26.075966	8
TACGGGT	6220	0.0	21.24439	7
ACGGGGA	17210	0.0	18.14108	8
TACGGGC	9640	0.0	16.295116	7
ACTAGGT	1545	0.0	16.139524	4
ACGGGGT	12480	0.0	15.831282	8

Produced by FastQC (version 0.11.5)