PastQC ReportSummary

Tue 29 Aug 2017 Sample2_forward_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

Measure Value

Filename Sample2_forward_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9

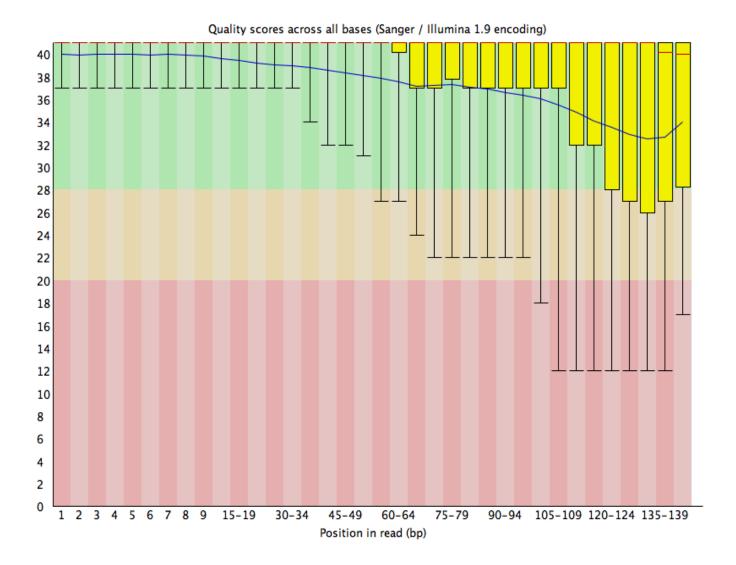
Total Sequences 24954266

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

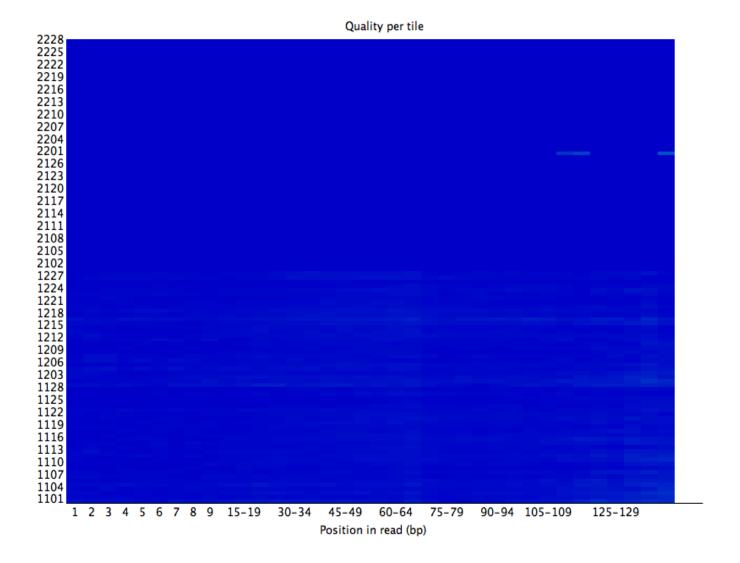
Sequence length 31-143

%GC 5-

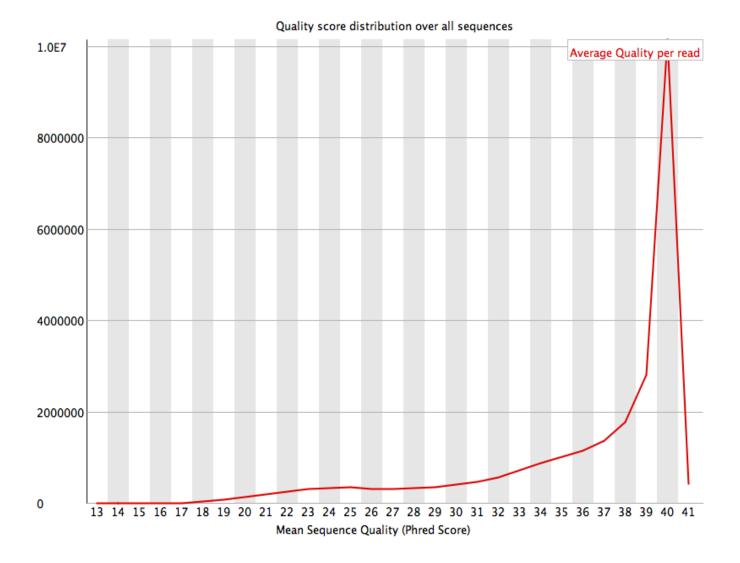
Per base sequence quality



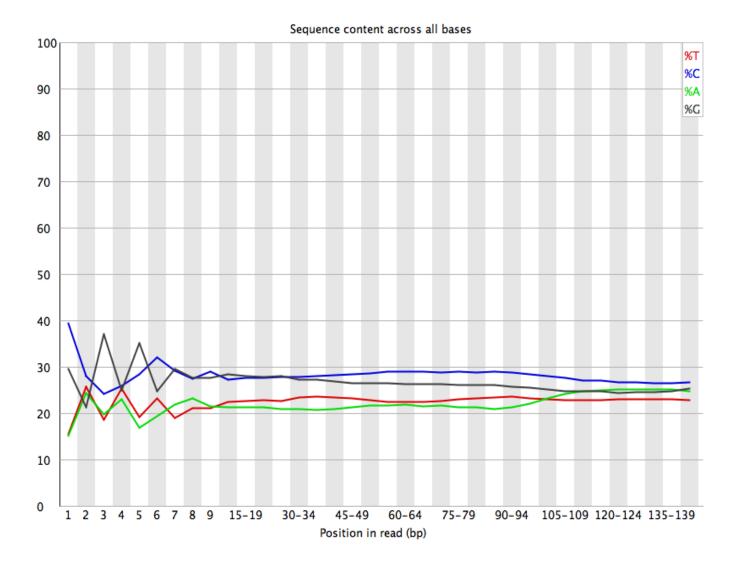
Per tile sequence quality



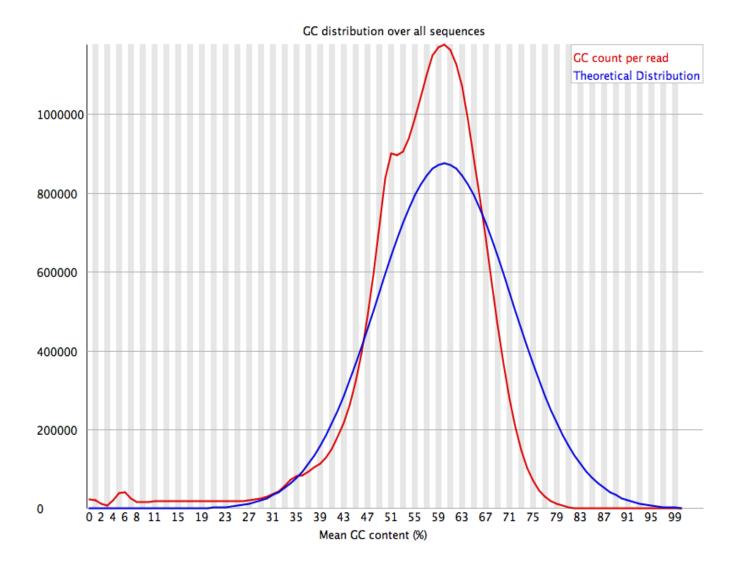
Per sequence quality scores



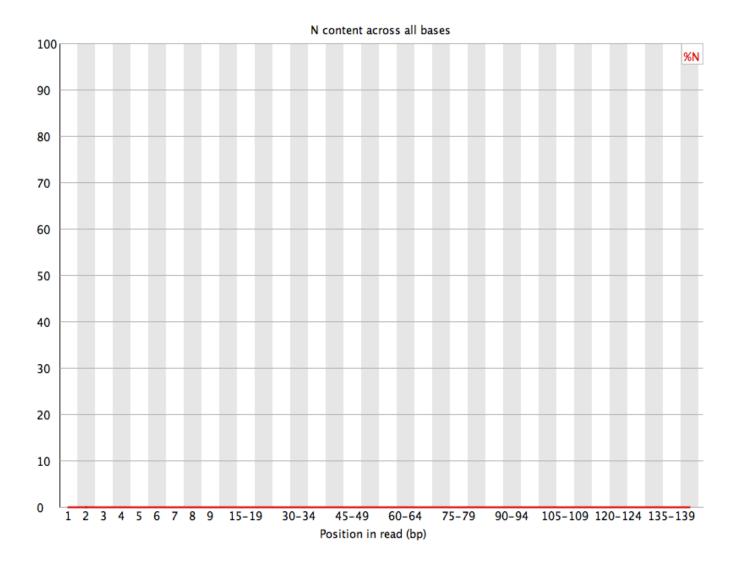
Per base sequence content



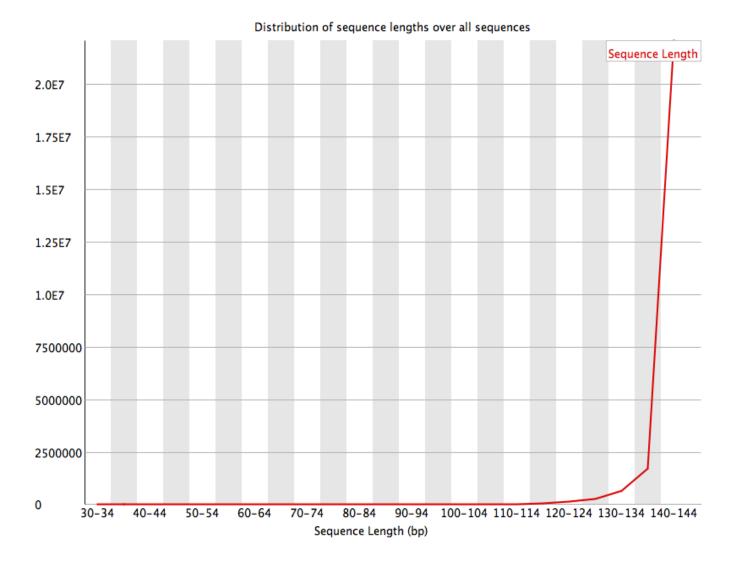
Per sequence GC content



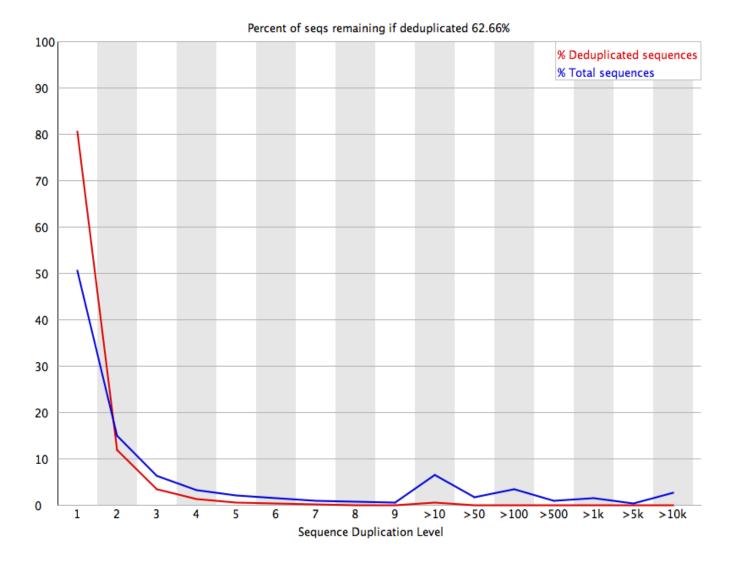




Sequence Length Distribution



Sequence Duplication Levels

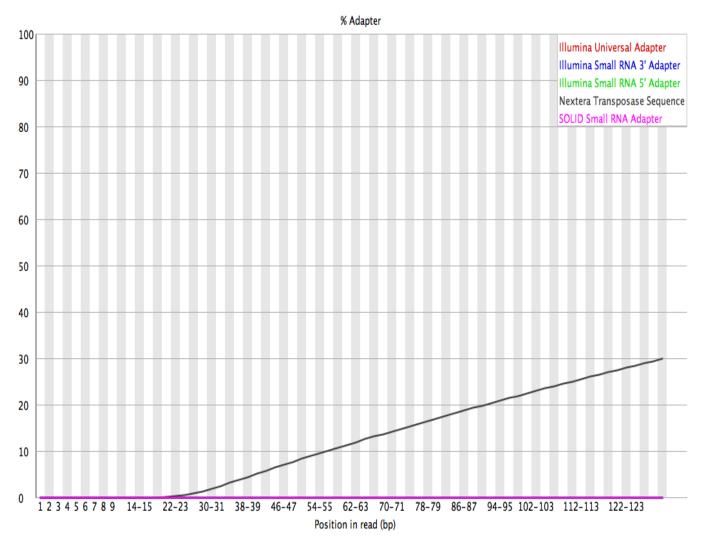


Overrepresented sequences

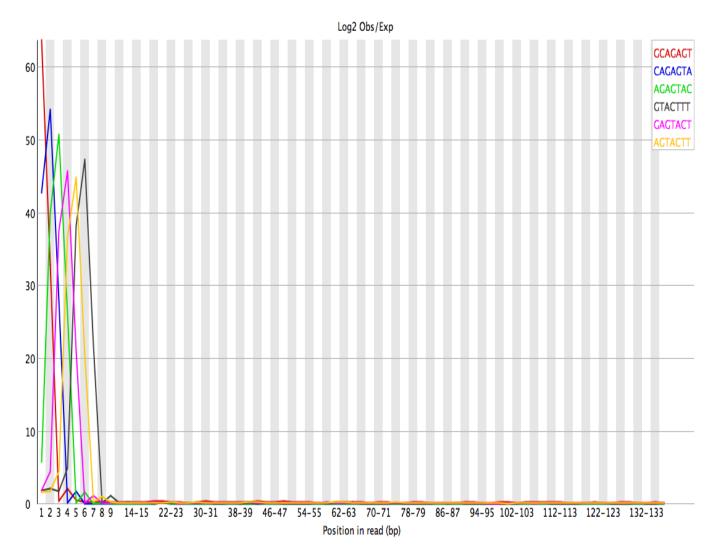
Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	101784	0.4078821633142806	No Hit
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	73862	0.29598947129921593	No Hit
${\tt GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA$	60313	0.24169414560219885	No Hit
CATCTCCGAGCCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCT	50398	0.2019614602168623	TruSeq Adapter, Index 11 (96% over 26bp)
${\tt CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	48876	0.19586230266199775	No Hit
${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	45625	0.18283447006616022	No Hit
AG	32521	0.13032240659773364	No Hit

Sequence	Count	Percentage	Possible Source
CCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCTTGAAAAAAA	32193	0.12900800207868265	RNA PCR Primer, Index 17 (96% over 27bp)
CTCCGAGCCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCTTGA	30465	0.12208333436856046	RNA PCR Primer, Index 11 (96% over 28bp)

Adapter Content



WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	67565	0.0	63.650246	1
CAGAGTA	79160	0.0	54.207375	2
AGAGTAC	84605	0.0	50.68665	3
GTACTTT	50690	0.0	47.30131	6
GAGTACT	52320	0.0	45.711056	4
AGTACTT	53380	0.0	44.816048	5
GTACGGG	42705	0.0	44.430847	6
TACGGGG	30255	0.0	43.982784	7
TACTTTT	56685	0.0	42.262768	7
AGTACGG	46475	0.0	40.914185	5

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GAGTACG	48590	0.0	39.119343	4
CGCAGAG	57645	0.0	38.98348	1
ACTTTTT	62870	0.0	38.342274	8
TACGGGA	7420	0.0	32.341408	7
ACGGGGG	24145	0.0	28.946165	8
TACGGGT	5625	0.0	25.669455	7
TACGGGC	9650	0.0	20.090849	7
ACGGGGT	11835	0.0	19.016449	8
ACGGGGA	16950	0.0	18.756971	8
CTTTTTT	160410	0.0	15.01511	9

Produced by FastQC (version 0.11.5)