PastQC ReportSummary

Wed 30 Aug 2017 Sample12_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

Value

File type Sample12_reverse_paired.fq.gz

Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 22283987

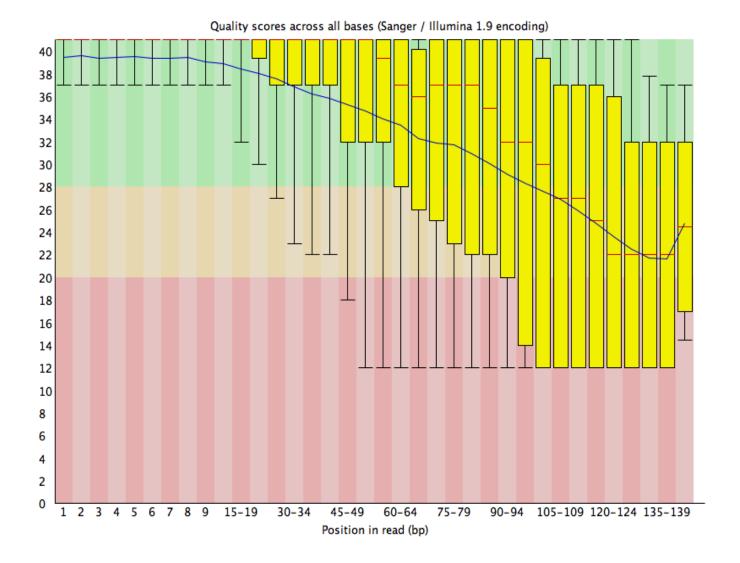
Sequences flagged as poor quality $\,\,0\,\,$

Measure

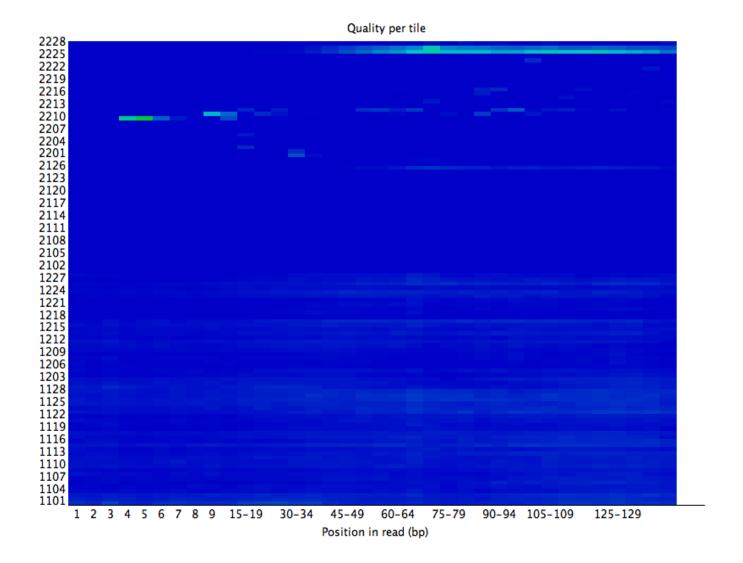
Sequence length 20-143

%GC 46

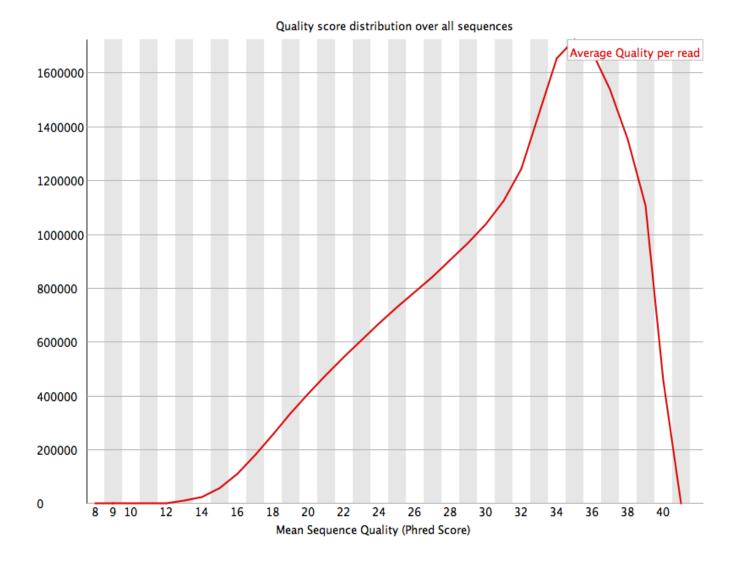
Per base sequence quality



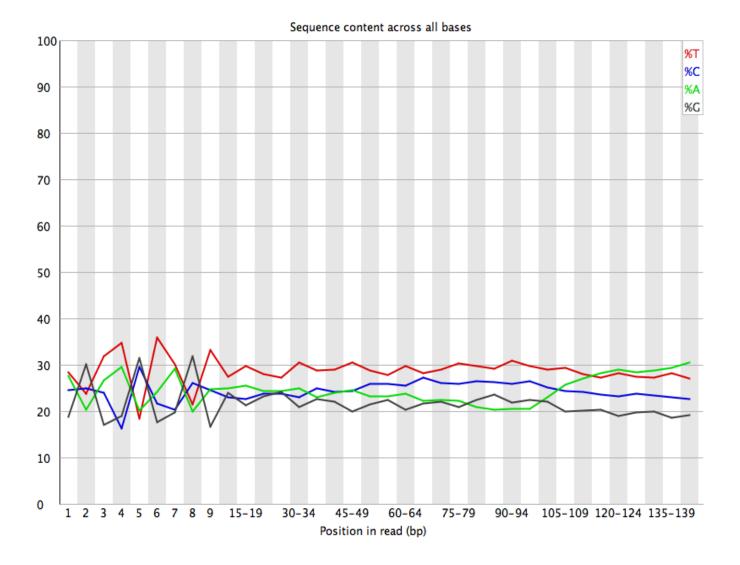
Per tile sequence quality



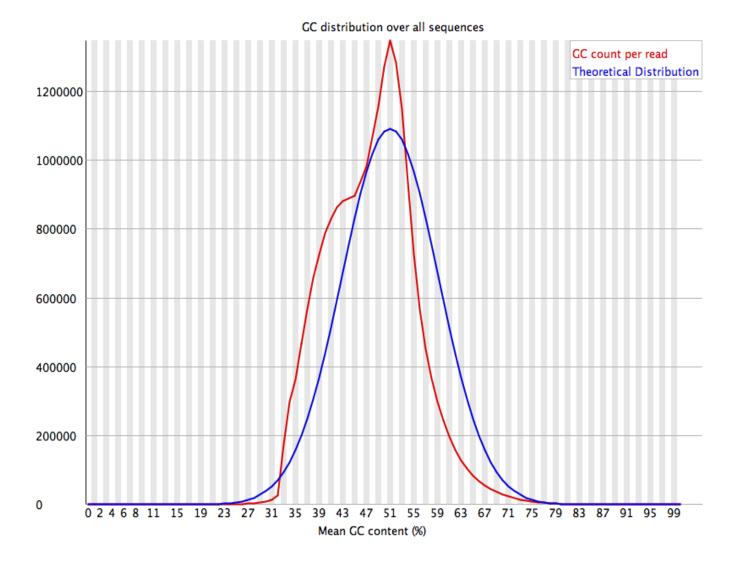
Per sequence quality scores



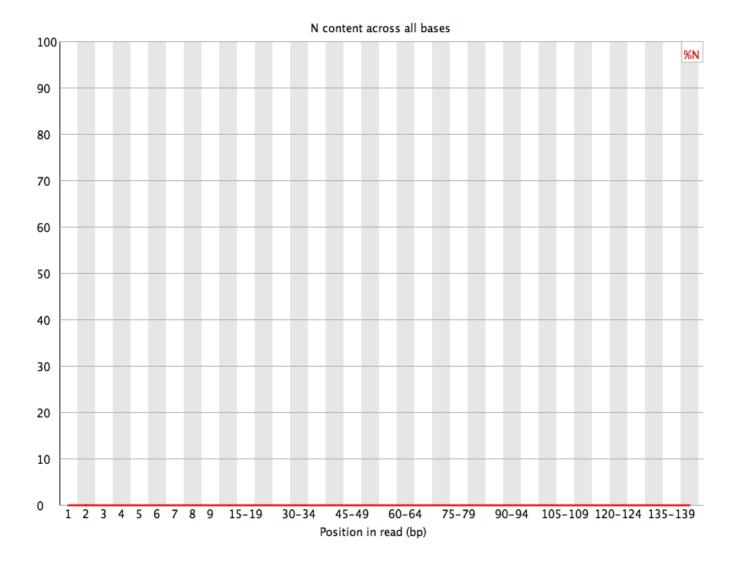
Per base sequence content



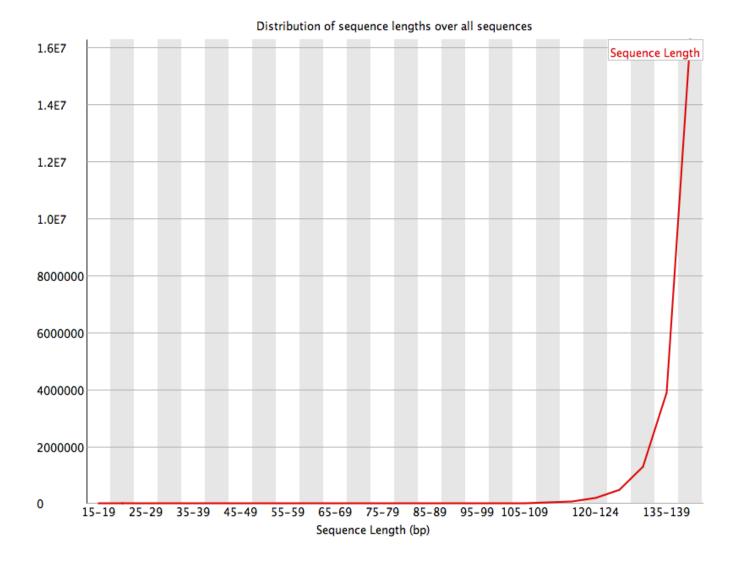
Per sequence GC content



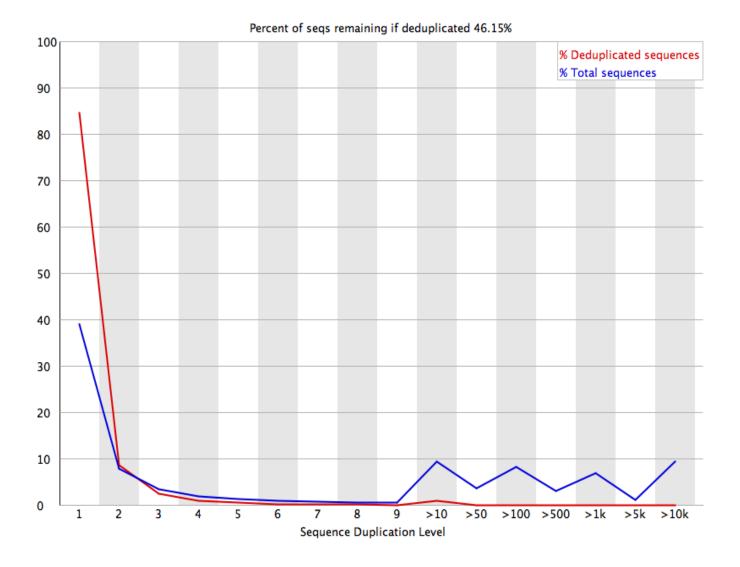




Sequence Length Distribution



Sequence Duplication Levels

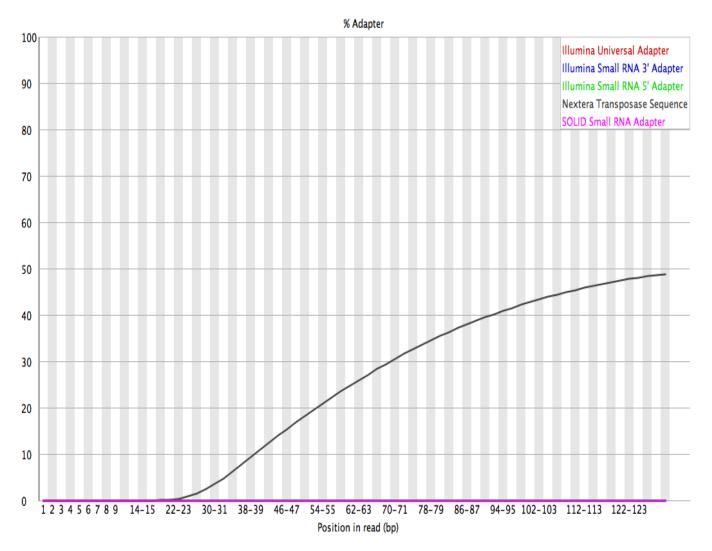


Overrepresented sequences

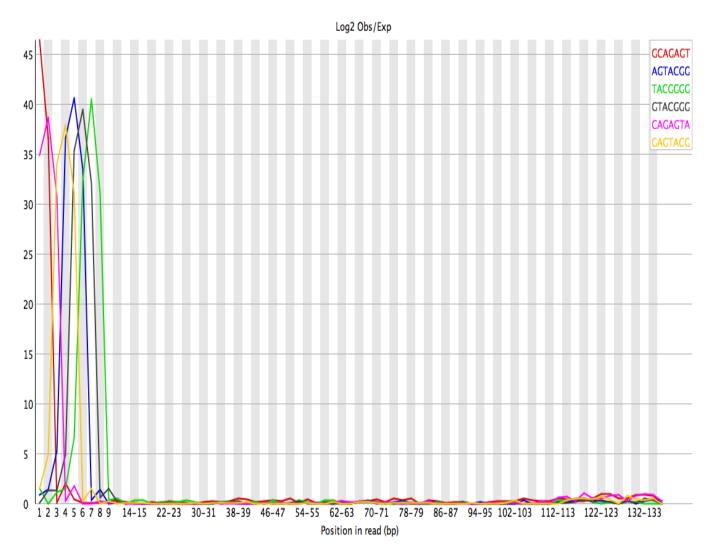
Sequence	Count	Percentage	Possible Source
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	518031	2.324678254389576	No Hit
${\tt ACAACAACAACAACAACAACAACAACAACAACAACAACA$	409096	1.83582946803909	No Hit
${\tt GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	127556	0.5724110321909629	No Hit
${\tt AACAACAACAACAACAACAACAACAACAACAACAACAAC$	124302	0.5578086183590036	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	74067	0.3323776844780963	No Hit
${\tt TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG$	48353	0.21698540750360334	No Hit
${\tt CACAACAACAACAACAACAACAACAACAACAACAACAAC$	40430	0.18143072871115928	No Hit
${\tt TGTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	30355	0.13621889117059707	No Hit
TGTTGTTGTGGGGTTGTTGTTGTTGTTGTTGTTGTTGTT	28284	0.1269252221337232	No Hit

Sequence	Count	Percentage	Possible Source
${\tt TGTTGTGGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	26415	0.11853803361131021	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	26152	0.11735781393159132	No Hit
${\tt ACAACCCACAACAACAACAACAACAACAACAACAACAAC$	24823	0.11139389015080649	No Hit
${\tt TGTTGTTGTTGTGGGTTGTTGTTGTTGTTGTTGTTGTTG$	23926	0.10736857816332418	No Hit
${\tt ACAACAACCACAACAACAACAACAACAACAACAACAACA$	23252	0.1043439847635883	No Hit
${\tt ACAACAACCACCACAACAACAACAACAACAACAACAACA$	23020	0.10330287843014806	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTGGG}$	22416	0.10059241194136398	No Hit
TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	22363	0.10035457299450048	No Hit

Adapter Content



WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	3855	0.0	46.381577	1
AGTACGG	3640	0.0	40.66335	5
TACGGGG	1720	0.0	40.509197	7
GTACGGG	3785	0.0	39.465755	6
CAGAGTA	4505	0.0	38.649773	2
GAGTACG	3900	0.0	37.94965	4
TACGGGC	1095	0.0	35.493946	8
TACGGGA	655	0.0	33.753696	7
ACGGGGT	1025	0.0	32.034107	8
AGAGTAC	5575	0.0	31.231861	3

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGT	935	0.0	30.810986	7
ACGGGCT	1100	0.0	25.582867	9
CAGTTAC	250	0.001224393	25.009926	136-137
GAGTACT	1115	0.0	24.625727	4
ACGGGTC	550	0.0	24.367317	8
ACGGGAC	630	0.0	23.400358	8
AGTACTT	1090	0.0	23.347328	4
TAGTCAC	455	3.6389683E-6	21.986748	136-137
GTACTTT	1195	0.0	21.30086	6
GGCTAAC	110	3.9747127E-4	20.970236	130-131

Produced by FastQC (version 0.11.5)