PastQC ReportSummary

Wed 30 Aug 2017 Sample6_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

Measure Value

Filename Sample6_reverse_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9

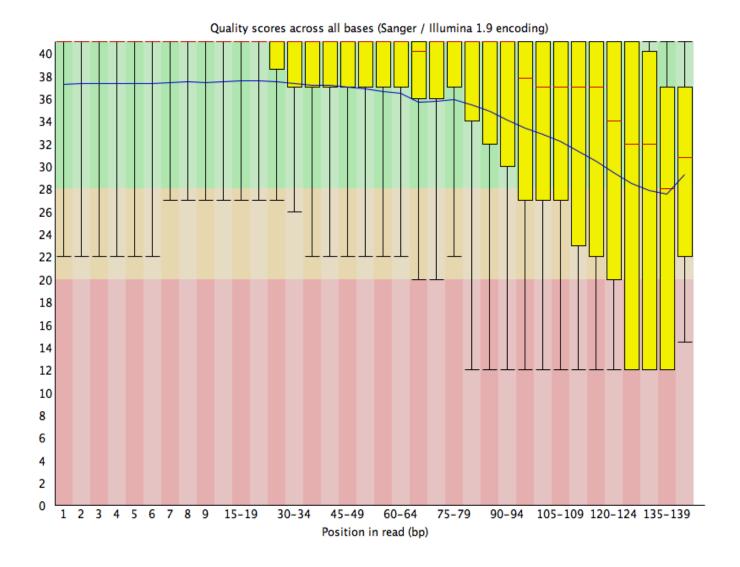
Total Sequences 44863497

Sequences flagged as poor quality $\ 0$

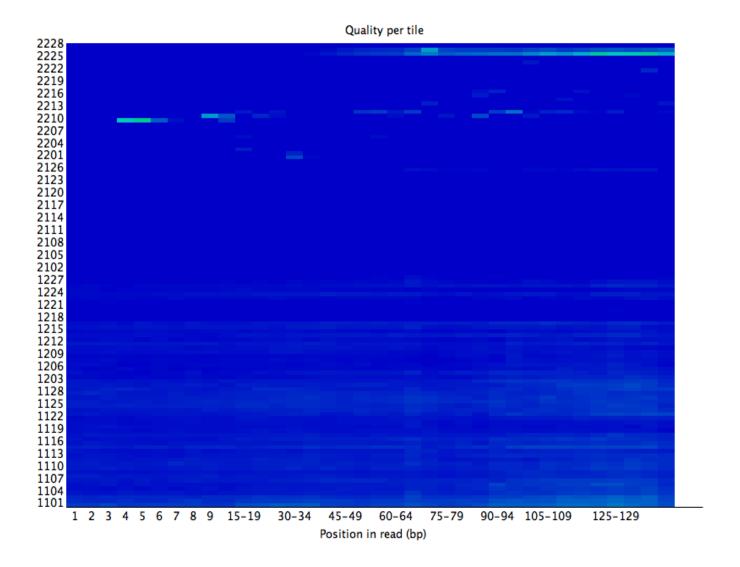
Sequence length 25-143

%GC 5

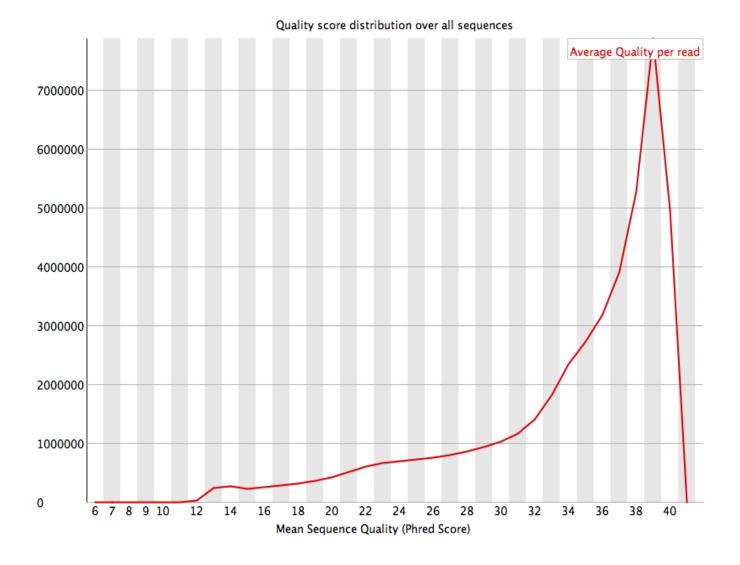
Per base sequence quality



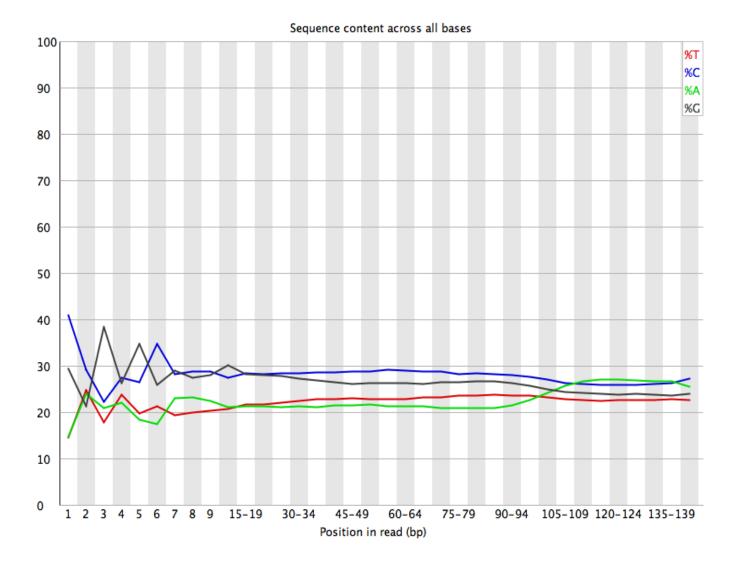
Per tile sequence quality



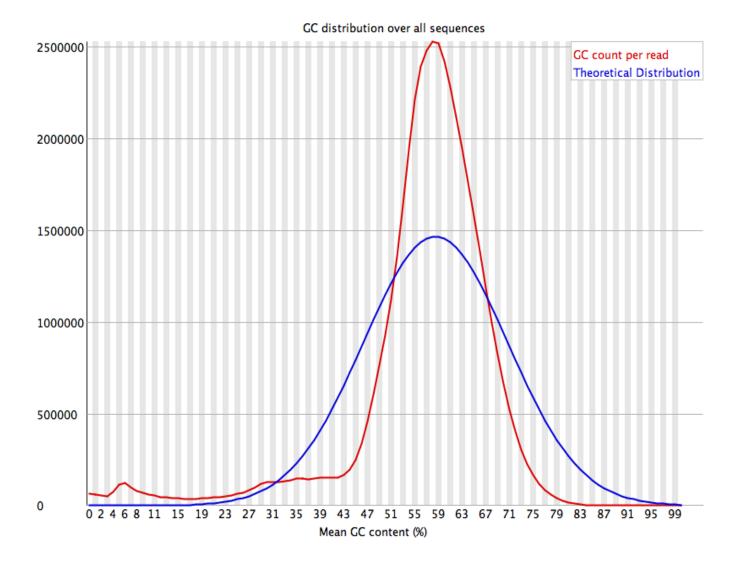
Per sequence quality scores



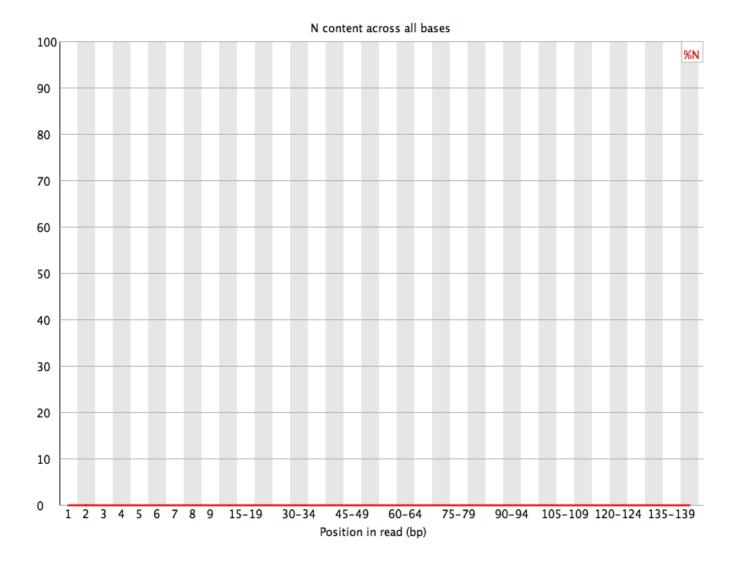
Per base sequence content



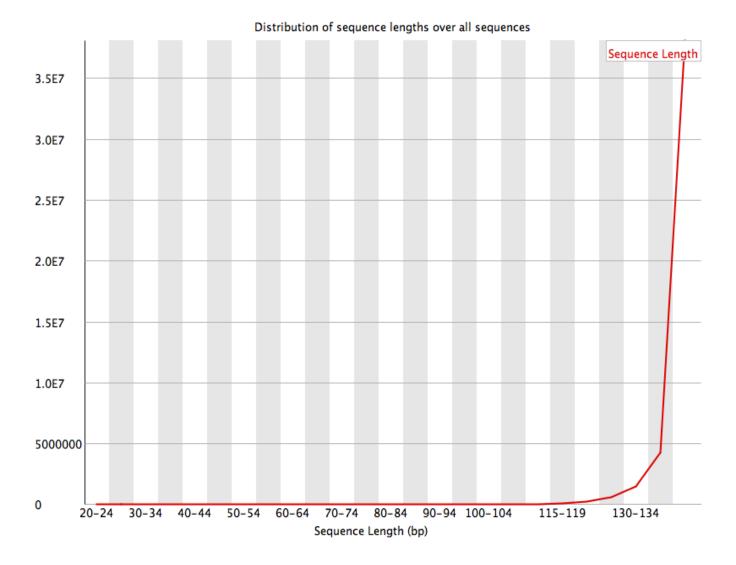
Per sequence GC content



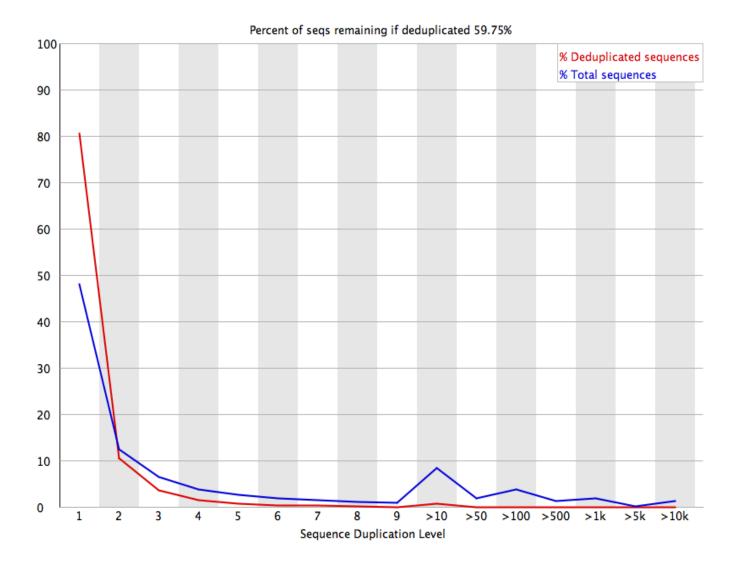




Sequence Length Distribution



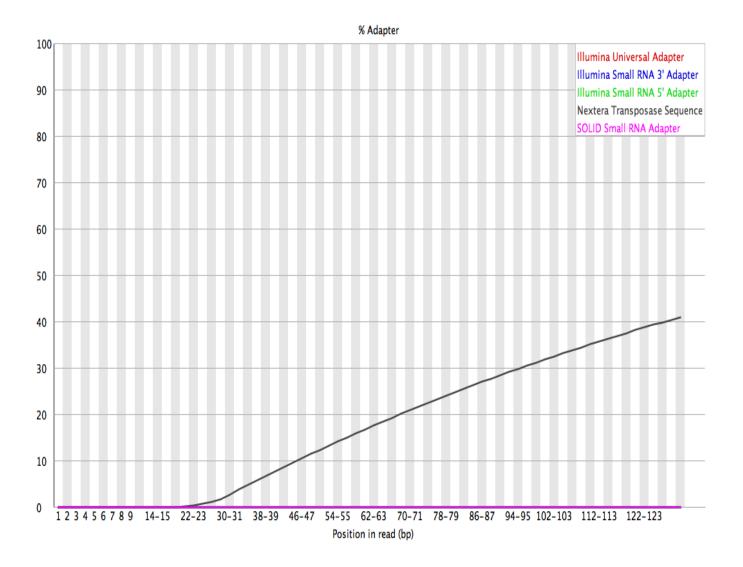
Sequence Duplication Levels



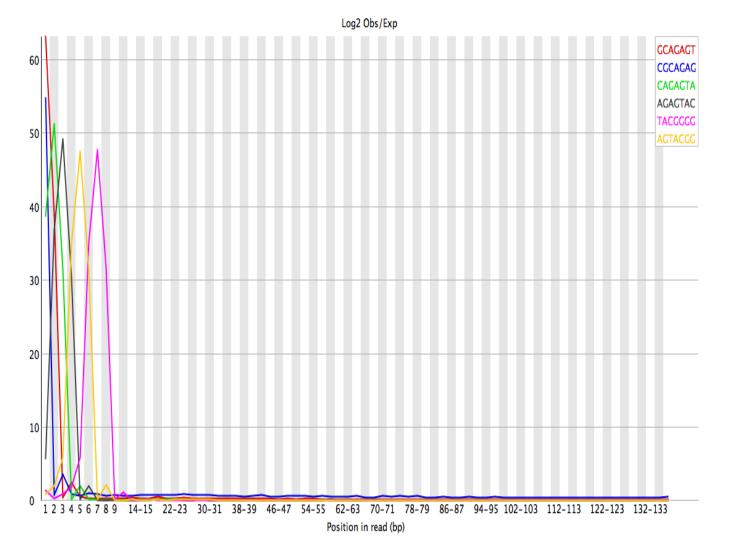
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	172049	0.3834944030332722	No Hit
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	129675	0.2890434510711459	No Hit
${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	83393	0.18588163111760994	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	82956	0.18490756527517238	No Hit





WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	190210	0.0	63.080566	1
CGCAGAG	136440	0.0	54.776955	1
CAGAGTA	235315	0.0	51.21425	2
AGAGTAC	244300	0.0	49.24517	3
TACGGGG	138100	0.0	47.715298	7
AGTACGG	188605	0.0	47.47864	5
GTACGGG	188345	0.0	47.40242	6
GAGTACG	200550	0.0	44.718304	4
GTACTTT	72035	0.0	41.932285	6
GAGTACT	73000	0.0	41.740532	4
TACTTTT	73310	0.0	41.080627	7
ACTTTTT	77070	0.0	39.16333	8
AGTACTT	80185	0.0	37.758762	5

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGGGGG	77335	0.0	36.11899	8
ACGGGGT	45545	0.0	35.55432	8
TACGGGT	27710	0.0	35.358116	7
TACGGGA	26970	0.0	35.175785	7
ACGGGGA	50605	0.0	32.05266	8
TAATCCG	3660	0.0	24.186958	9
ACGGGTA	12260	0.0	23.979773	8

Produced by FastQC (version 0.11.5)