PastQC ReportSummary

Wed 30 Aug 2017 Sample7_reverse_paired.fq.gz





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
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File type

Conventional base calls

Encoding

Sample7_reverse_paired.fq.gz

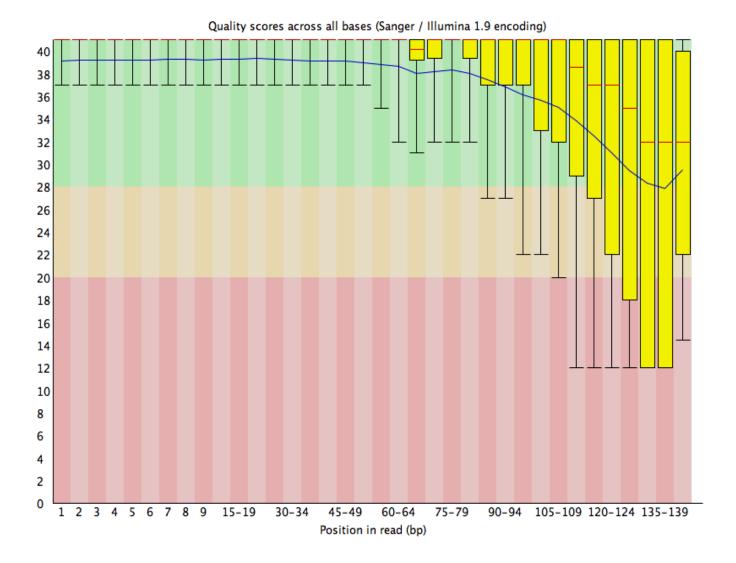
Conventional base calls

Sanger / Illumina 1.9

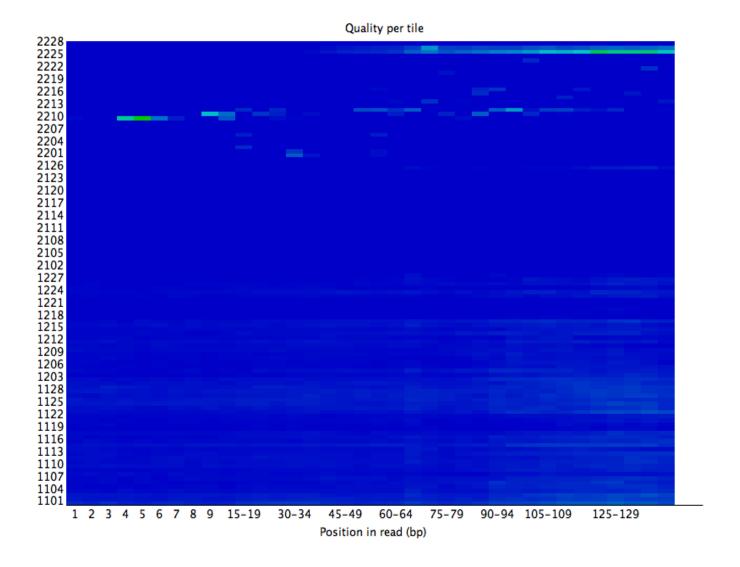
Total Sequences 22153627

Sequences flagged as poor quality 0Sequence length 9-143%GC 52

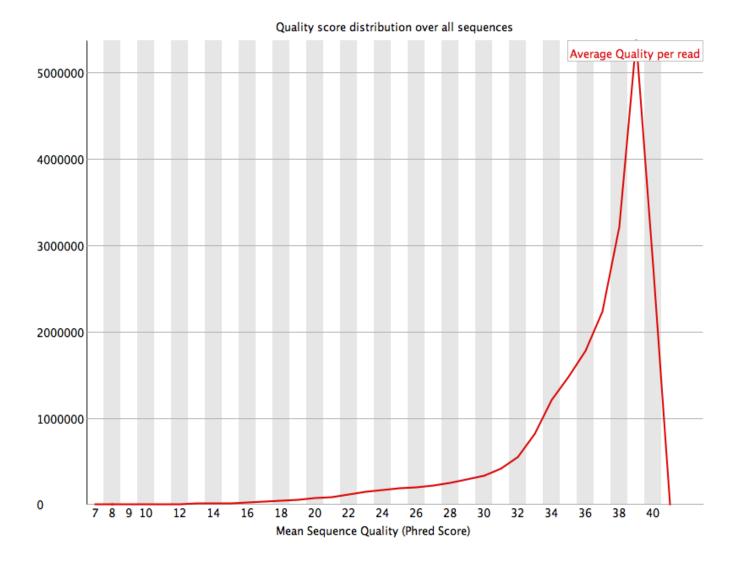
Per base sequence quality



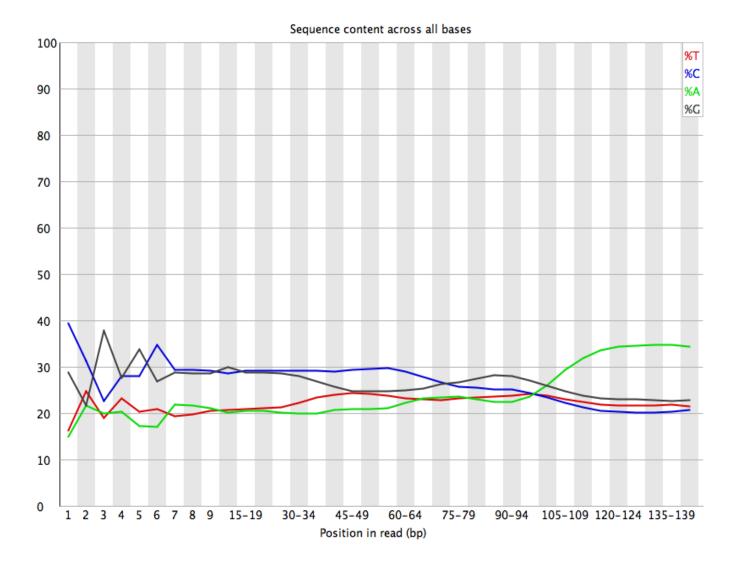
Per tile sequence quality



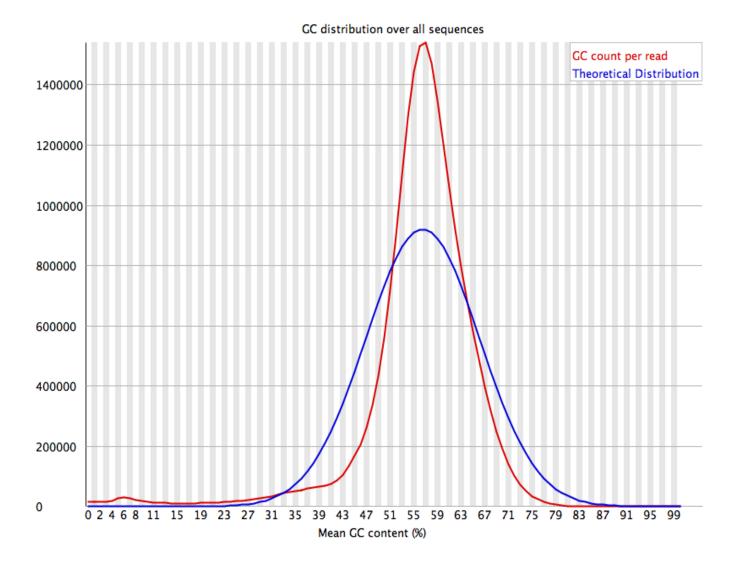
Per sequence quality scores



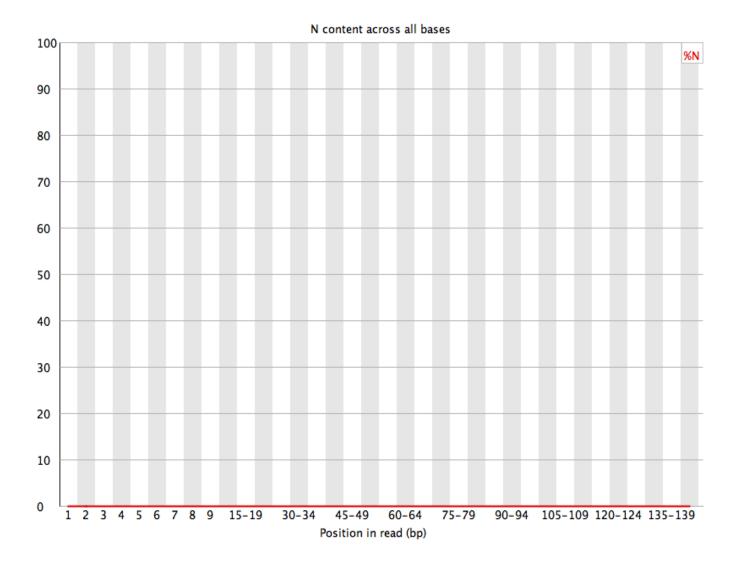
Per base sequence content



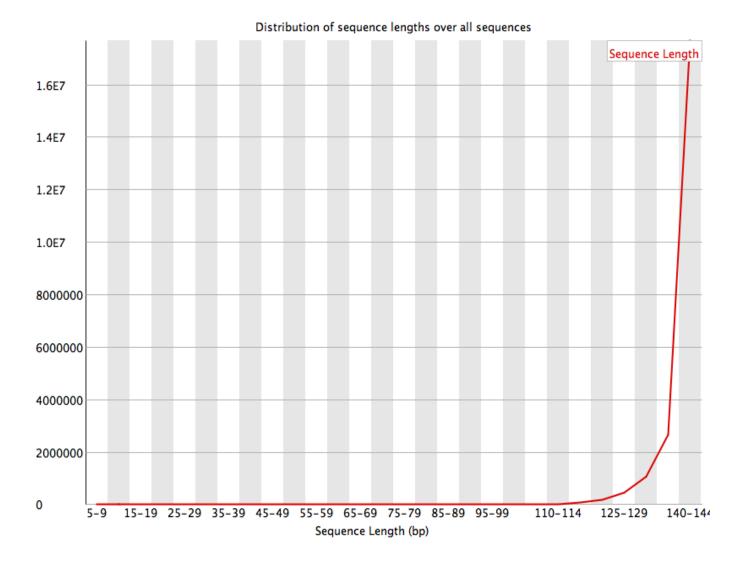
Per sequence GC content



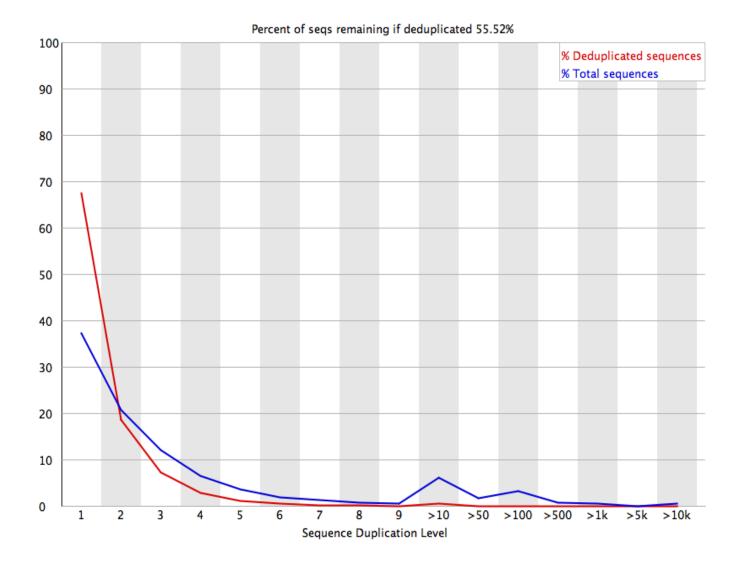




Sequence Length Distribution



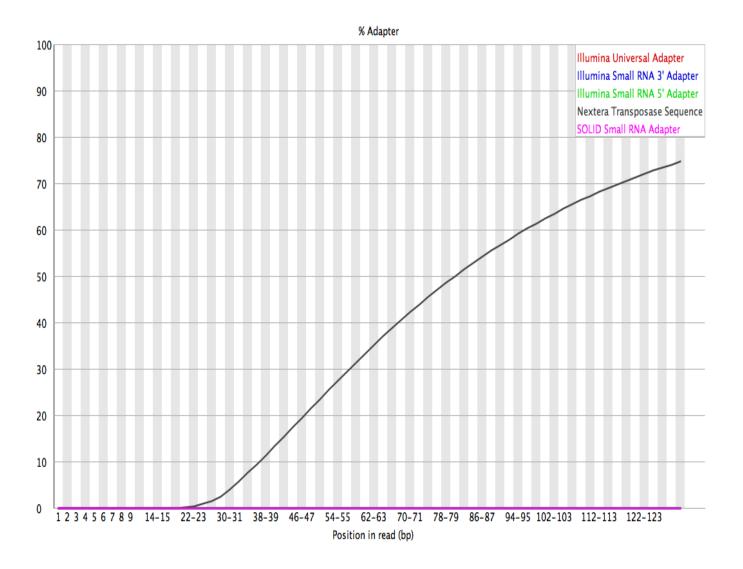
Sequence Duplication Levels



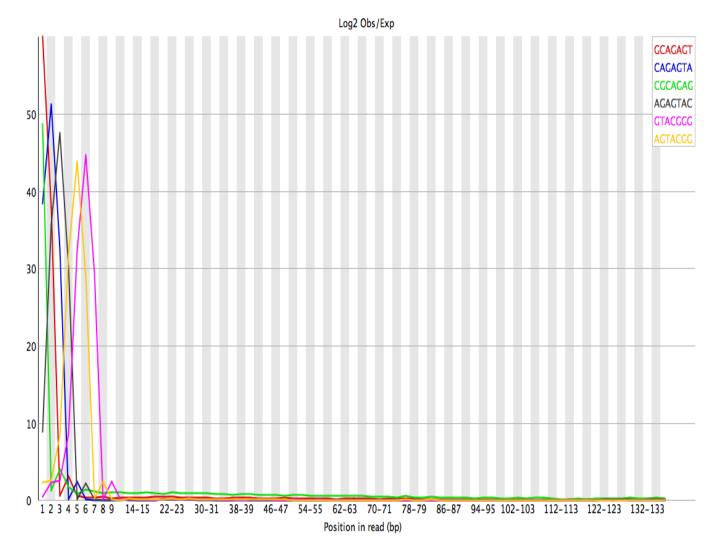
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	44126	0.199181831489715	No Hit
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	34566	0.15602862682485355	No Hit
${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	26158	0.11807547360077877	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	22860	0.10318852077811007	No Hit





WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	61560	0.0	59.98186	1
CAGAGTA	71880	0.0	51.258667	2
CGCAGAG	48415	0.0	48.68542	1
AGAGTAC	77215	0.0	47.56898	3
GTACGGG	65170	0.0	44.71016	6
AGTACGG	66505	0.0	43.89792	5
GAGTACG	67635	0.0	43.32081	4
TACGGGG	39505	0.0	43.25884	7
GTACTTT	19245	0.0	38.445583	6
TACGGGA	11740	0.0	36.6495	7
TACGGGT	9355	0.0	36.492153	7
TACTTTT	20750	0.0	35.69521	7
AGTACTT	22690	0.0	32.900757	5

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GAGTACT	22675	0.0	32.68281	4
TACGGGC	13690	0.0	32.511227	7
ACGGGGG	25725	0.0	31.60094	8
ACTTTTT	24245	0.0	31.057589	8
ACGGGGT	11585	0.0	26.161621	8
ACGGGGA	15710	0.0	25.89458	8
ACTAGGT	2005	0.0	24.171162	4

Produced by FastQC (version 0.11.5)