PastQC ReportSummary

Wed 30 Aug 2017 Sample7_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
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File type

Sample7_forward_paired.fq.gz

File type

Conventional base calls

Encoding

Sanger / Illumina 1.9

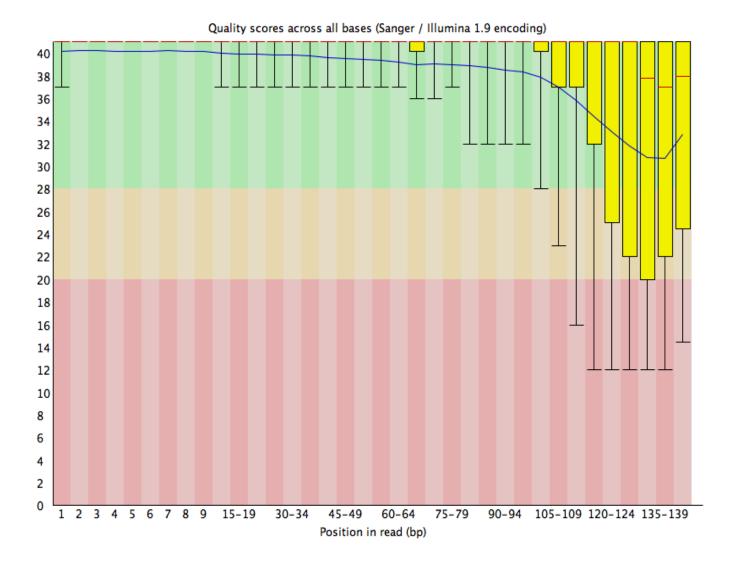
Total Sequences 22153627

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

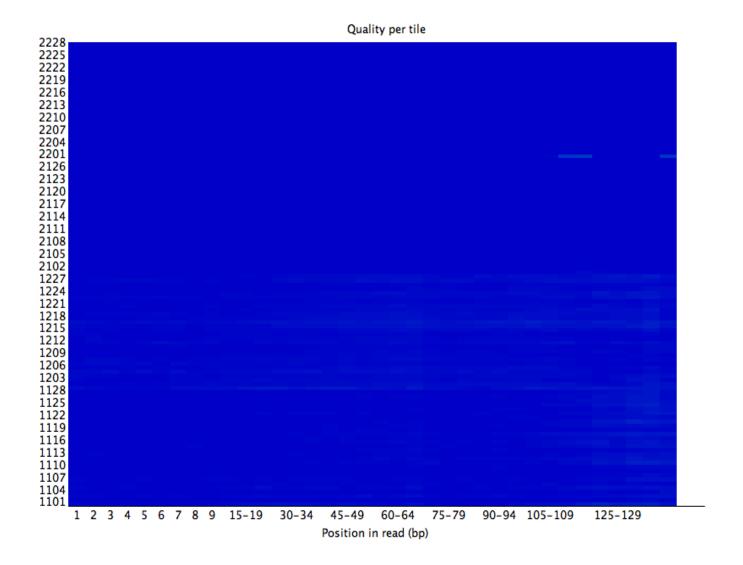
Sequence length 31-143

%GC 5

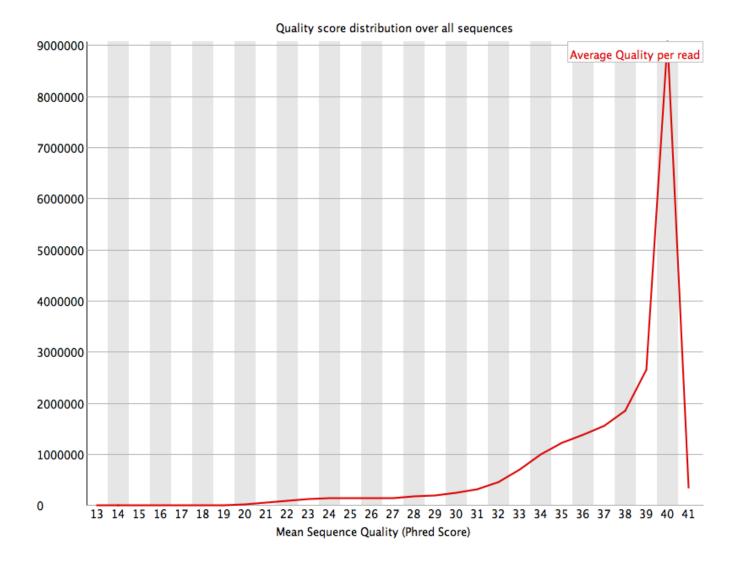
Per base sequence quality



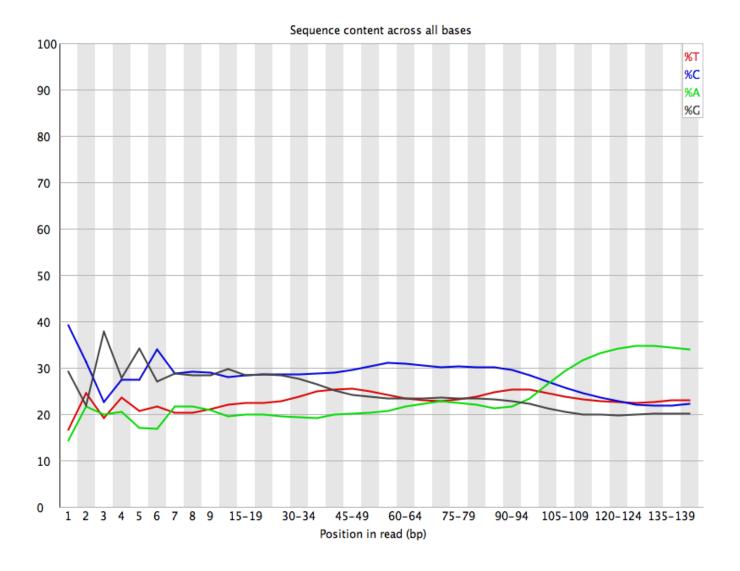
Per tile sequence quality



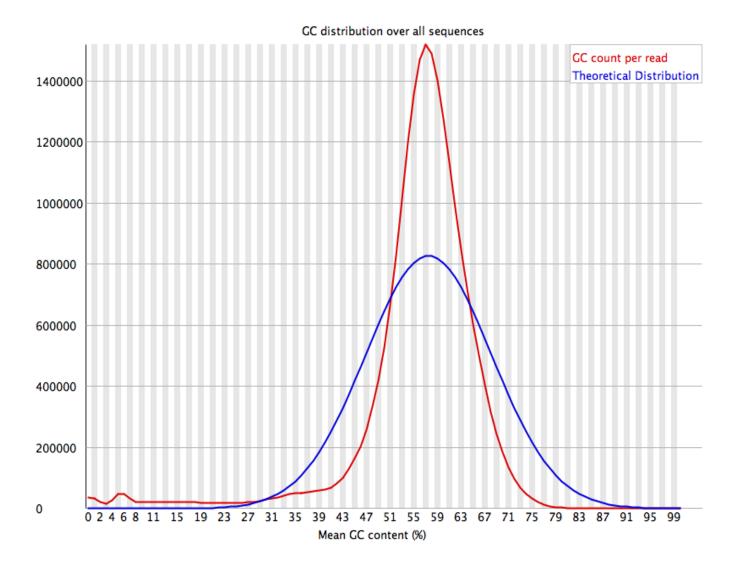
Per sequence quality scores



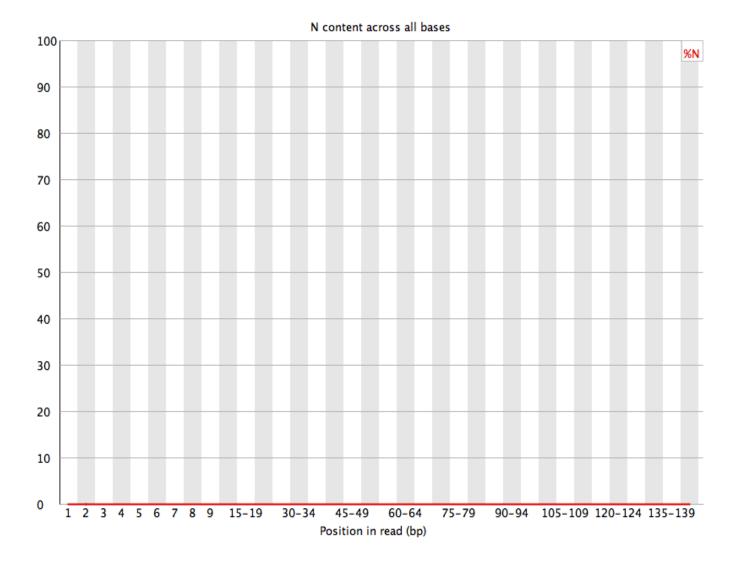
Per base sequence content



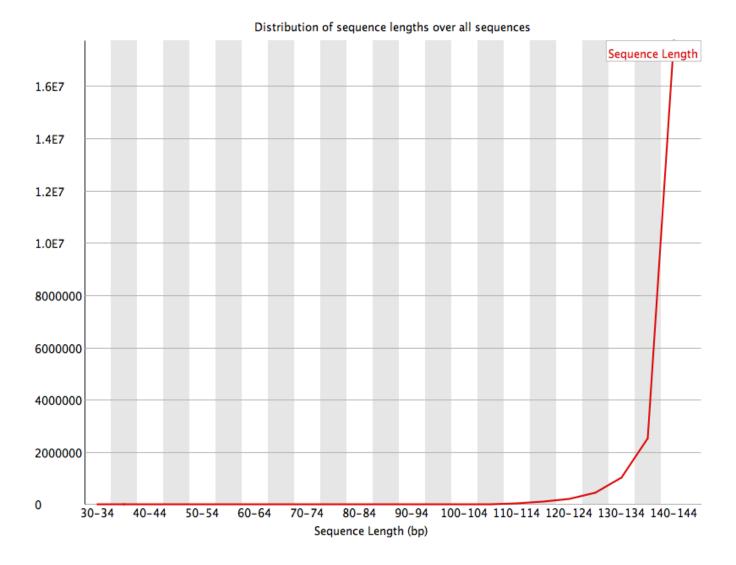
Per sequence GC content



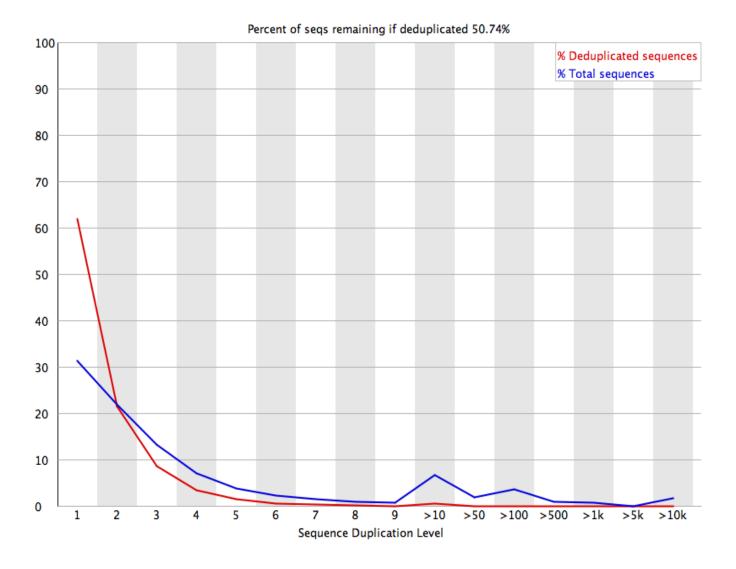




Sequence Length Distribution



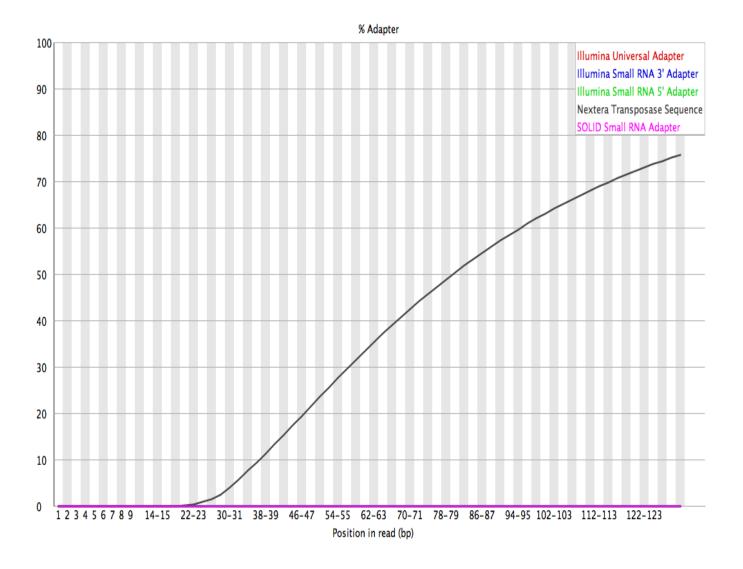
Sequence Duplication Levels



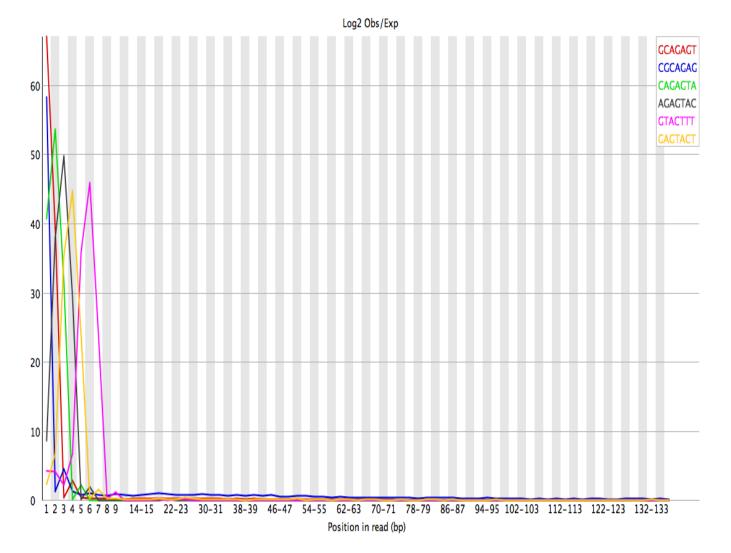
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	105303	0.47533074381003165	No Hit
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	80806	0.3647529138230954	No Hit
${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	67314	0.3038509224697157	No Hit
${\tt CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	57443	0.2592938844731836	No Hit
${\tt TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	39977	0.18045352122250682	No Hit





WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	79965	0.0	66.97702	1
CGCAGAG	54400	0.0	58.305996	1
CAGAGTA	99475	0.0	53.624065	2
AGAGTAC	106855	0.0	49.819584	3
GTACTTT	49770	0.0	45.979996	6
GAGTACT	50850	0.0	44.804546	4
GTACGGG	67740	0.0	44.794594	6
AGTACGG	69115	0.0	44.06918	5
GAGTACG	69260	0.0	44.064384	4
AGTACTT	52050	0.0	43.952938	5
TACGGGG	41460	0.0	42.307053	7
TACTTTT	58730	0.0	38.85034	7
TACGGGA	11240	0.0	38.66885	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGT	9755	0.0	37.78574	7
ACTTTTT	63450	0.0	36.24704	8
TACGGGC	14425	0.0	33.727898	7
ACGGGGG	26950	0.0	32.6802	8
ACGGGGT	11670	0.0	25.406784	8
ACGGGGA	15915	0.0	24.134377	8
TGCGTTA	3140	0.0	18.026796	5

Produced by FastQC (version 0.11.5)