PastQC ReportSummary

Wed 30 Aug 2017 Sample4_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

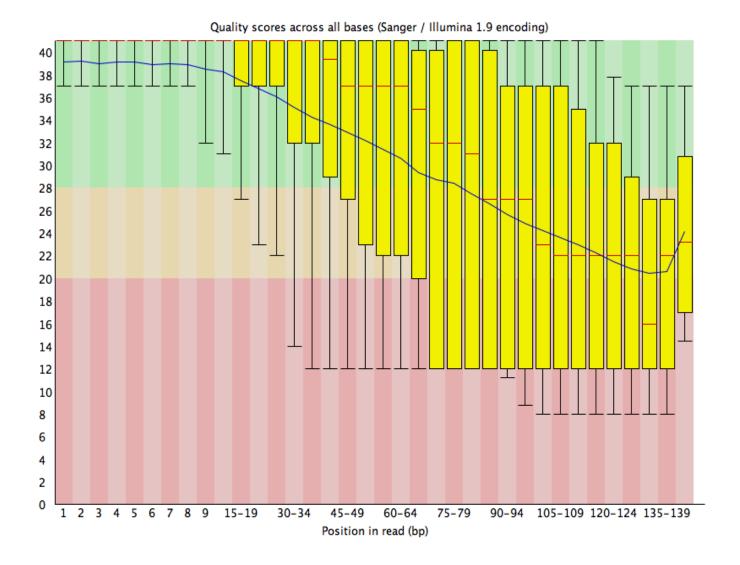
Basic Statistics

Measure	Value
Measure	value

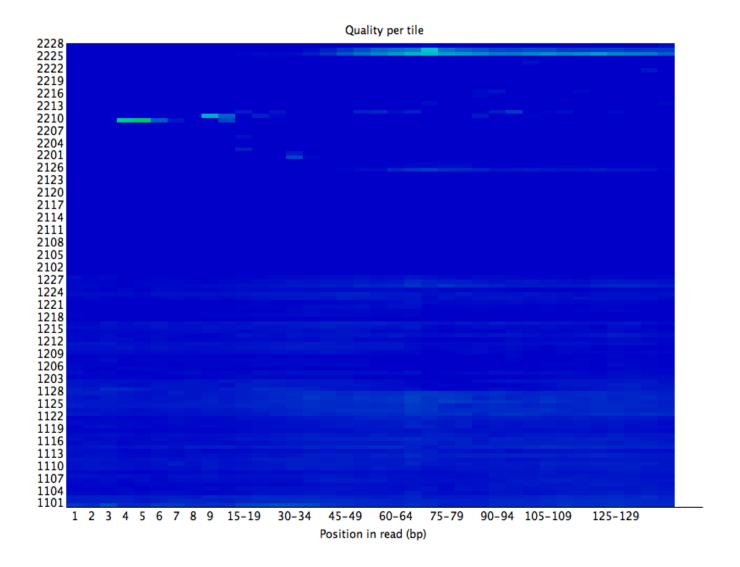
File type
Conventional base calls
Encoding
Sanger / Illumina 1.9
Total Sequences
41372891
Sequences flagged as poor quality 0

Sequences riagged as poor quality 0
Sequence length 4-143
%GC 47

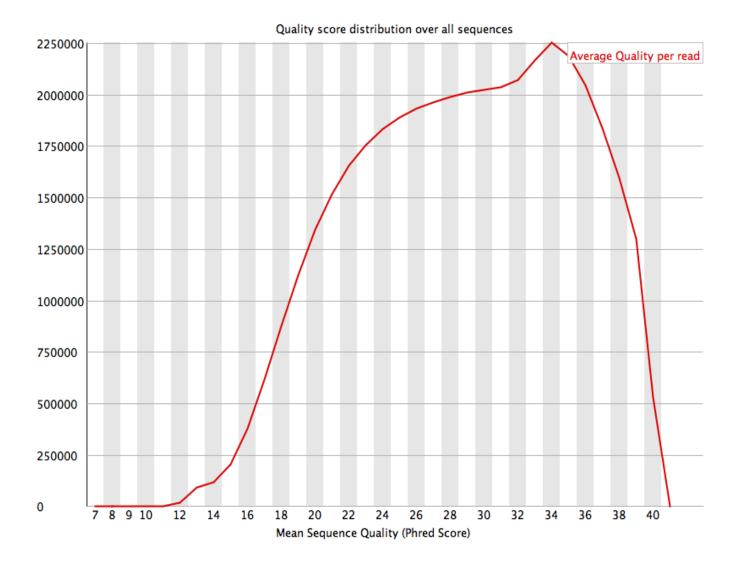
Per base sequence quality



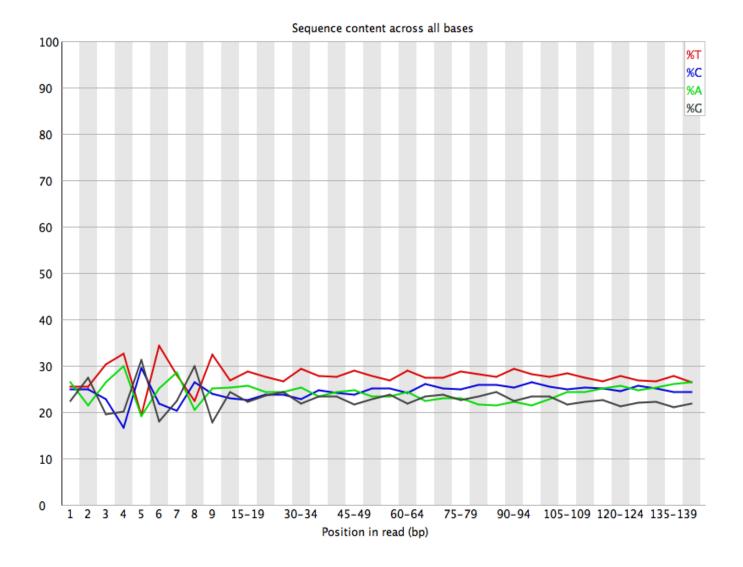
Per tile sequence quality



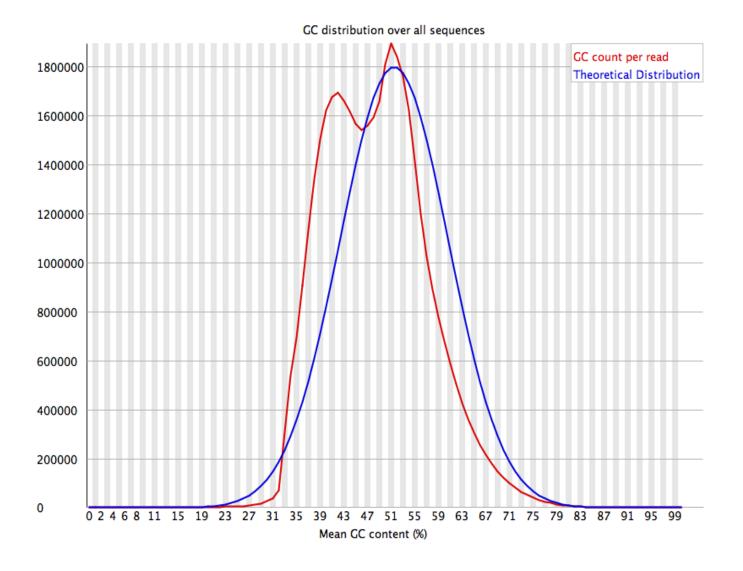
Per sequence quality scores



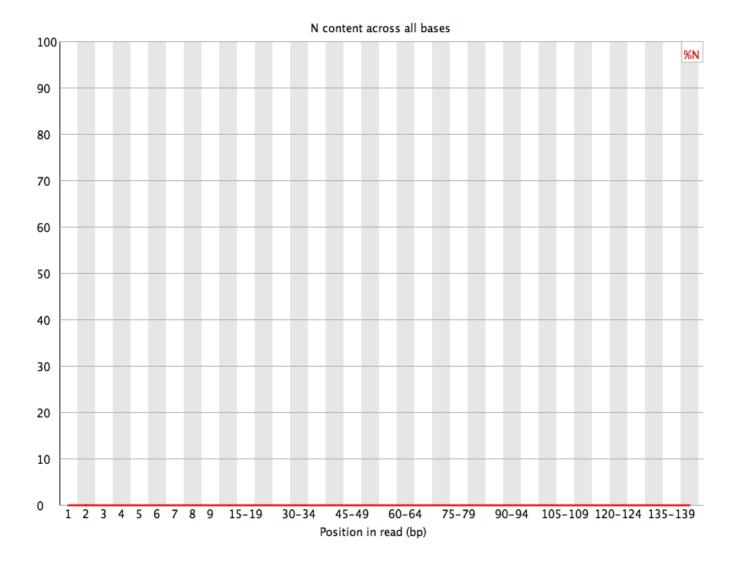
Per base sequence content



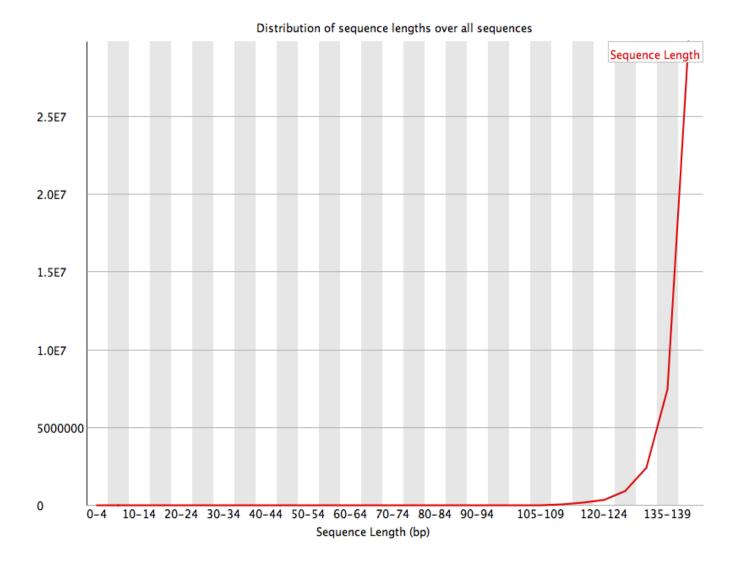
Per sequence GC content



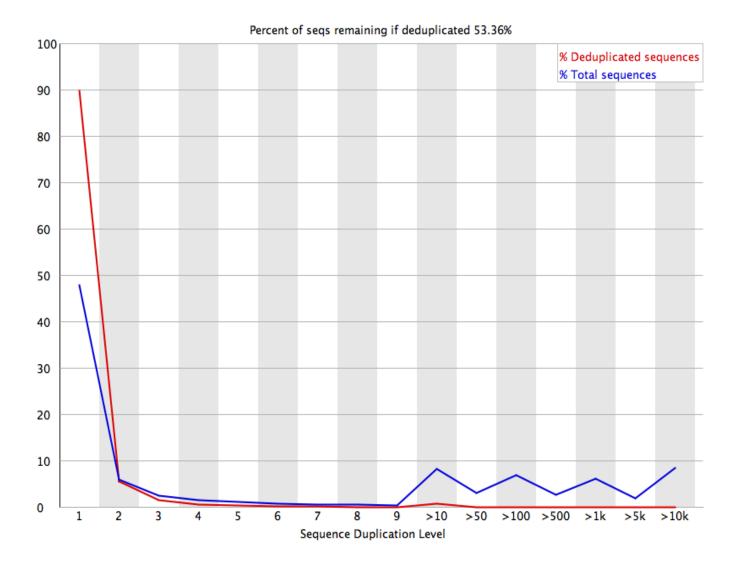




Sequence Length Distribution



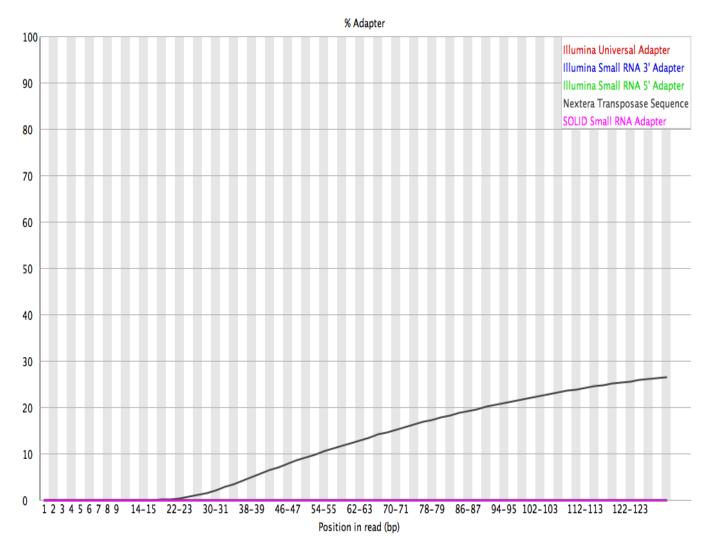
Sequence Duplication Levels



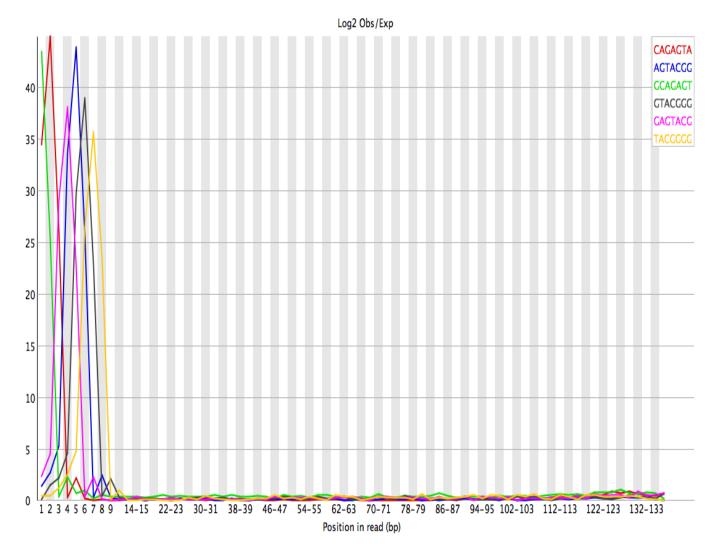
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt ACAACAACAACAACAACAACAACAACAACAACAACAACA$	680837	1.6456113738824778	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	675354	1.632358734611995	No Hit
${\tt GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	285591	0.690285336840493	No Hit
${\tt AACAACAACAACAACAACAACAACAACAACAACAACAAC$	172759	0.41756569537284693	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	128638	0.31092340150945696	No Hit
${\tt TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG$	77394	0.18706452009843835	No Hit
${\tt CACAACAACAACAACAACAACAACAACAACAACAACAAC$	53135	0.12842950713789858	No Hit
${\tt TGTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	46409	0.1121724851183351	No Hit
ACAACCCACACAACAACAACAACAACAACAACAACAACA	44463	0.10746892210167282	No Hit

Adapter Content



WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CAGAGTA	8590	0.0	44.921562	2
AGTACGG	7230	0.0	43.94026	5
GCAGAGT	8930	0.0	43.510357	1
GTACGGG	8180	0.0	39.00622	6
GAGTACG	8375	0.0	38.170086	4
TACGGGG	4200	0.0	35.6809	7
TACGGGC	2365	0.0	35.077415	7
AGAGTAC	11765	0.0	33.02603	3
GAGTACT	2285	0.0	29.560734	4
TACGGGA	1270	0.0	29.499954	7
AGTACTT	2430	0.0	26.697638	5
GTACTTT	2795	0.0	24.889736	6
ACGGGGT	2695	0.0	20.857191	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACGGGTC	1445	0.0	20.376055	8
ACGGGAC	1570	0.0	18.753756	8
ACGGGCT	2875	0.0	17.689314	8
ACTTTTT	4500	0.0	17.398373	8
TACTTTT	4420	0.0	16.044294	7
TACGGGT	3695	0.0	14.122684	7
TAATTAC	620	1.2699475E-5	12.690177	136-137

Produced by FastQC (version 0.11.5)