PastQC ReportSummary

Mon 28 Aug 2017 Sample3_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

File type Sample3_forward_paired.fq.gz

Conventional base calls

Encoding Sanger / Illumina 1.9

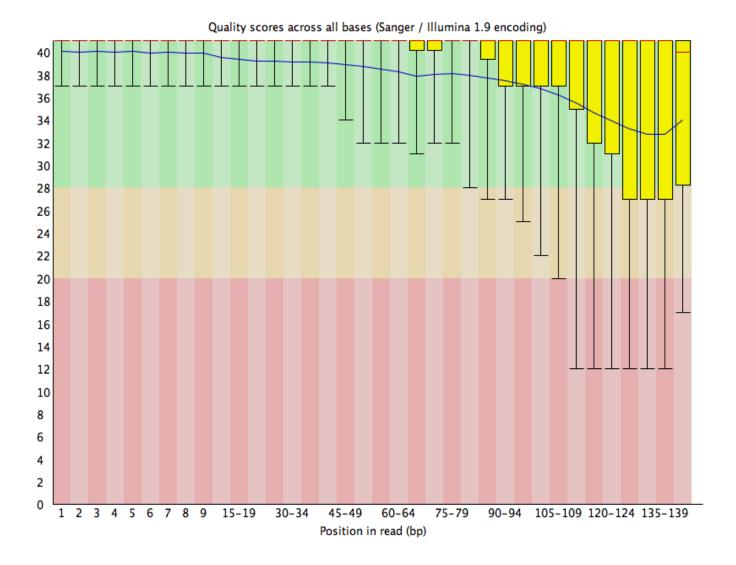
Total Sequences 20401753

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

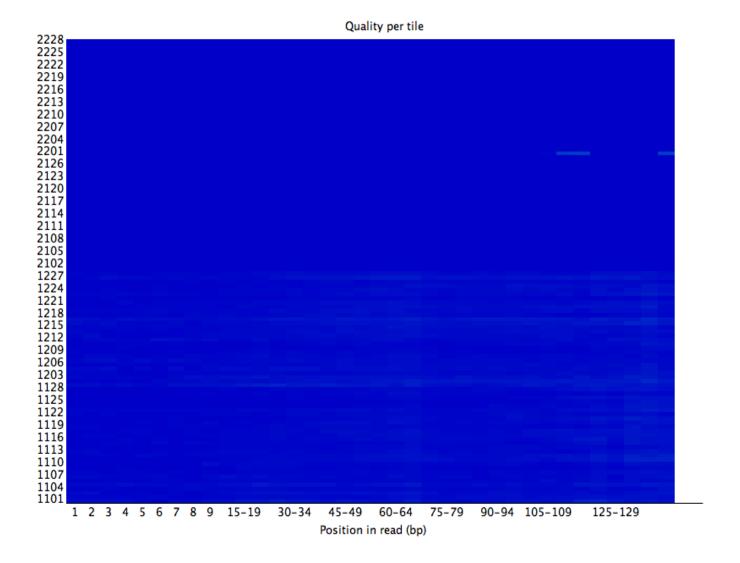
Sequence length 32-143

%GC 5

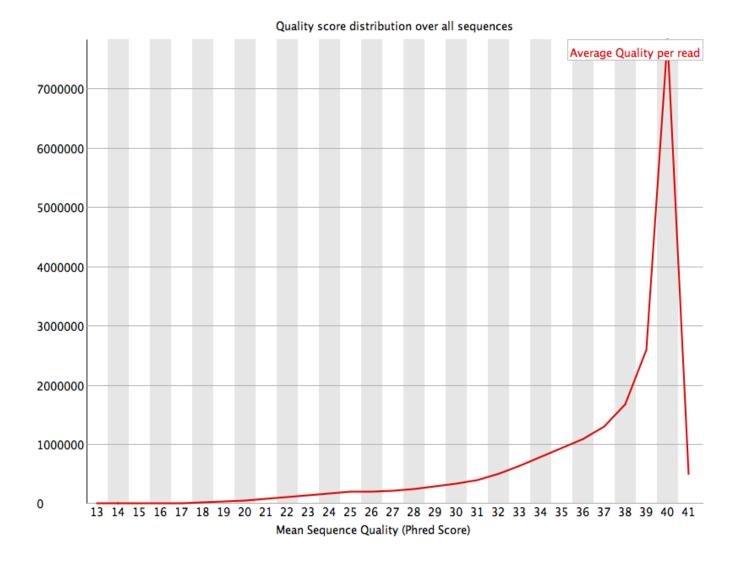
Per base sequence quality



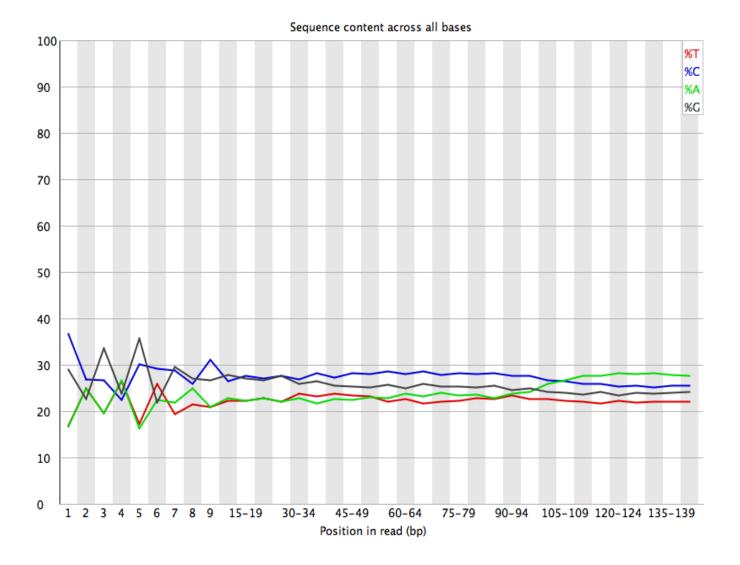
Per tile sequence quality



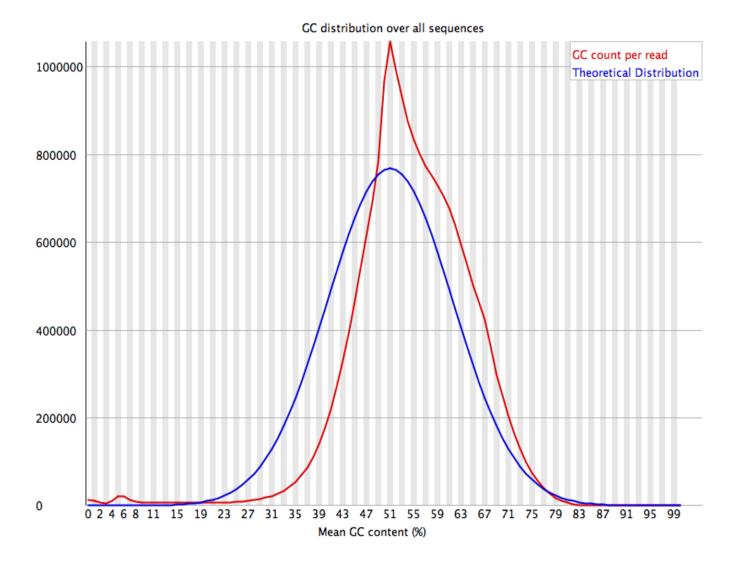
Per sequence quality scores



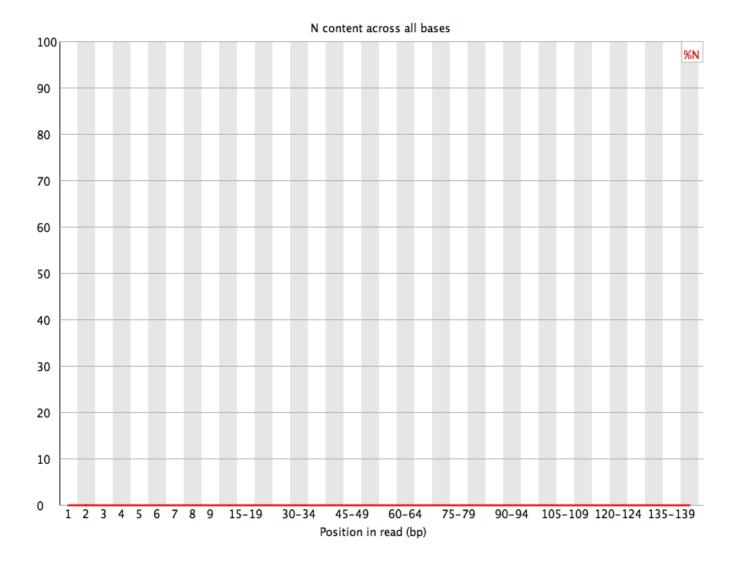
Per base sequence content



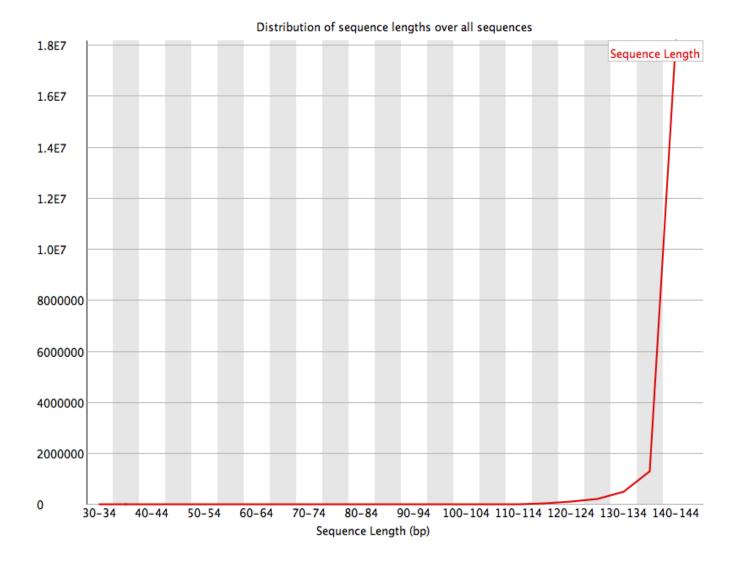
Per sequence GC content



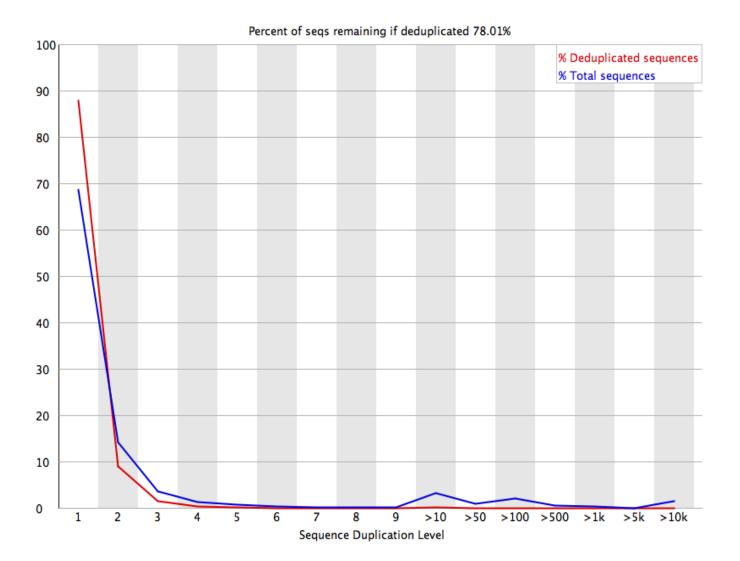




Sequence Length Distribution



Sequence Duplication Levels

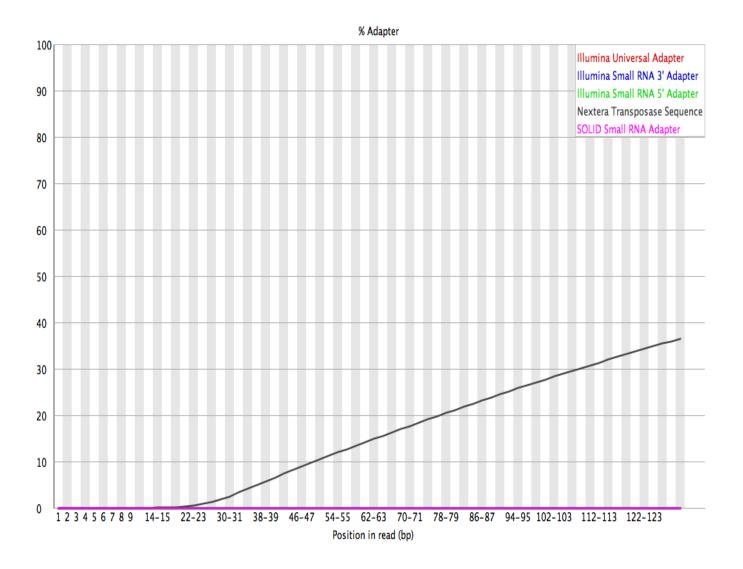


 $file: ///Volumes/Le\ Drobo/XBOTT.20170727.ILLUMINA_DATA...$

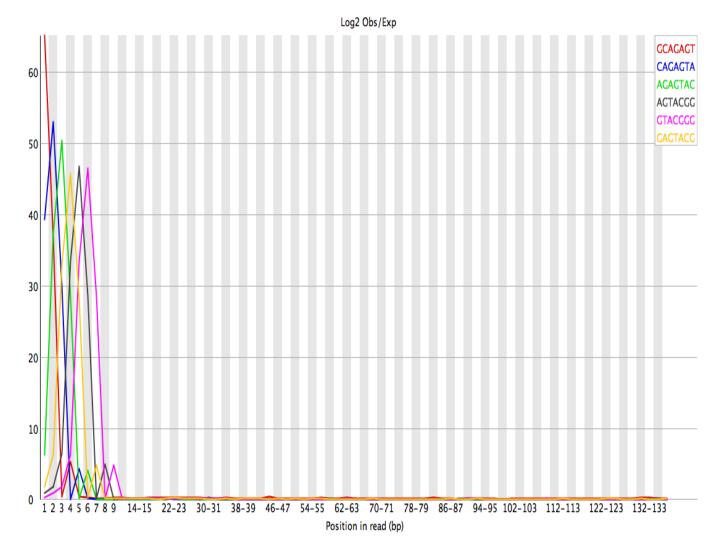
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	48244	0.23646987589742902	No Hit
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	35590	0.1744457939472162	No Hit
${\tt CACACACACACACACACACACACACACACACACACACA$	31008	0.15198693955367462	No Hit
CATCTCCGAGCCCACGAGACAGGCAGAAATCTCGTATGCCGTCTTCTGCT	31004	0.15196733339532148	RNA PCR Primer, Index 17 (96% over 26bp)
${\tt GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT$	24963	0.1223571327424658	No Hit
${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	24305	0.11913191969337145	No Hit
CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	23177	0.11360298303778112	No Hit





WKmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	50520	0.0	65.05974	1
CAGAGTA	61780	0.0	53.015602	2
AGAGTAC	65015	0.0	50.30451	3
AGTACGG	49190	0.0	46.71538	5
GTACGGG	49245	0.0	46.53925	6
GAGTACG	50175	0.0	45.784782	4
TACGGGG	21380	0.0	45.20668	7
GTACTTT	21485	0.0	45.111805	6
CGCAGAG	42365	0.0	44.363068	1
GAGTACT	22615	0.0	43.15762	4
AGTACTT	23360	0.0	41.57799	5
TACGGGC	13955	0.0	40.632343	7
TACTTTT	23995	0.0	40.477875	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACTTTTT	24425	0.0	39.765266	8
TACGGGT	12645	0.0	37.43967	7
TACGGGA	8590	0.0	33.873463	7
ACGGGGG	11935	0.0	30.972017	8
ACGGGGT	8725	0.0	25.653341	8
ACGGGTG	11875	0.0	23.246428	8
ACGGGGA	11065	0.0	20.534723	8

Produced by FastQC (version 0.11.5)