PastQC ReportSummary

Mon 28 Aug 2017 Sample8_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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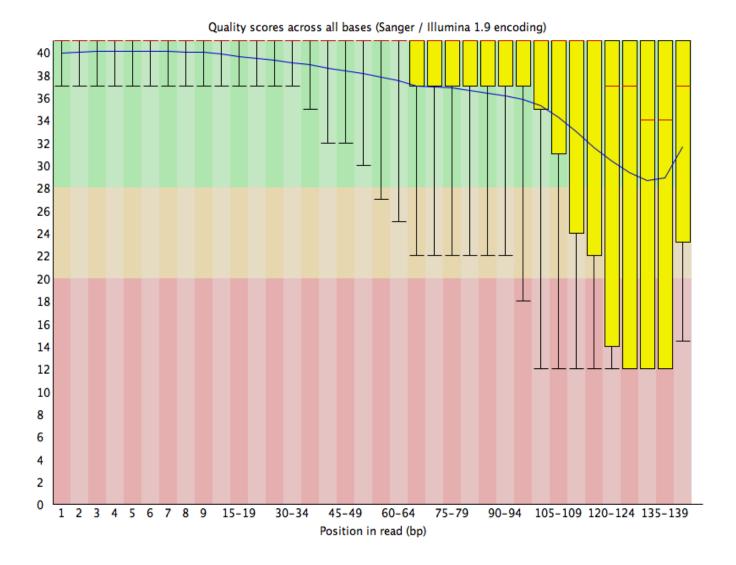
Filename Sample8_forward_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 19702055

Sequences flagged as poor quality 0

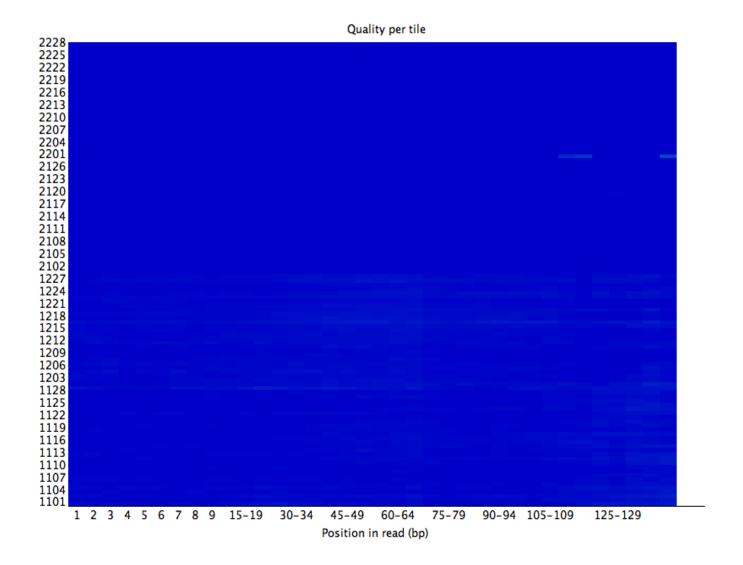
Sequence length 31-143

%GC 51

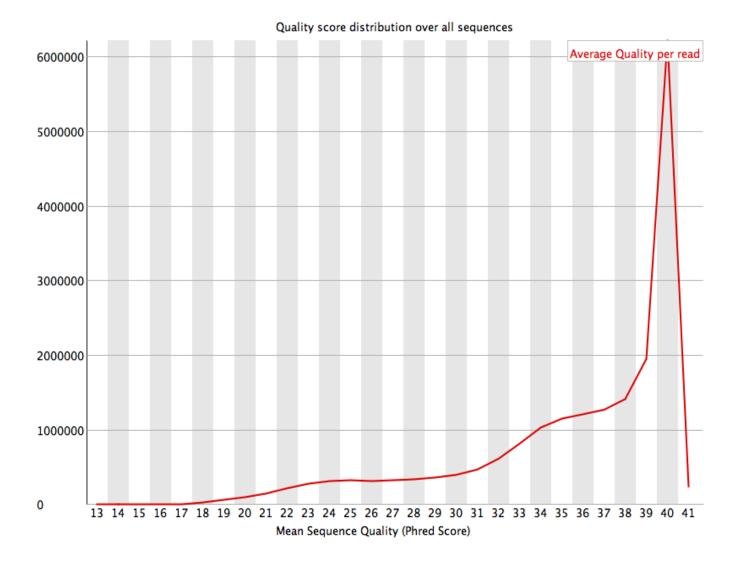
Per base sequence quality



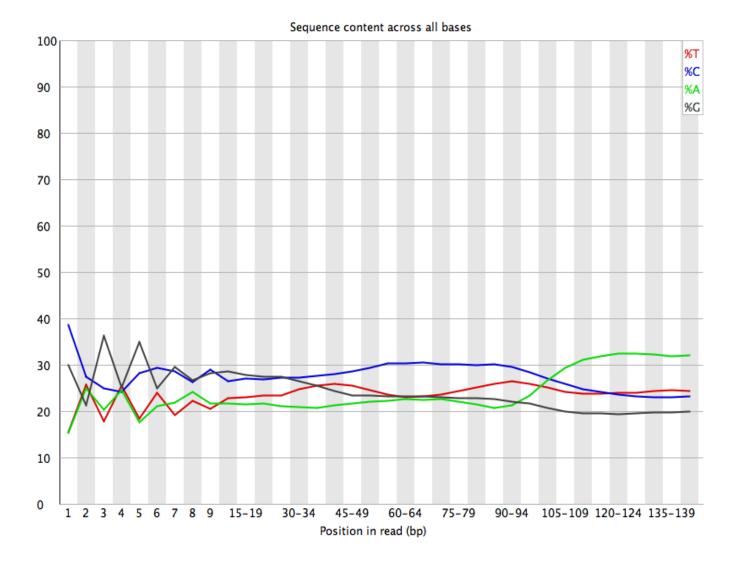
Per tile sequence quality



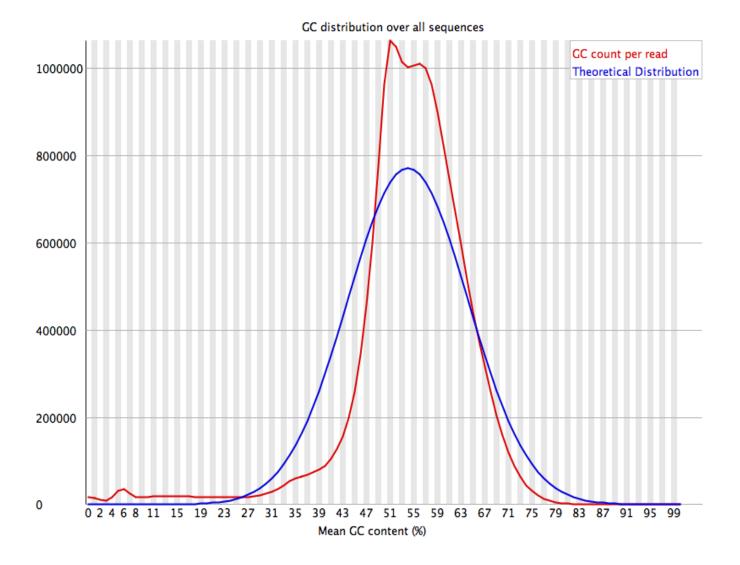
Per sequence quality scores



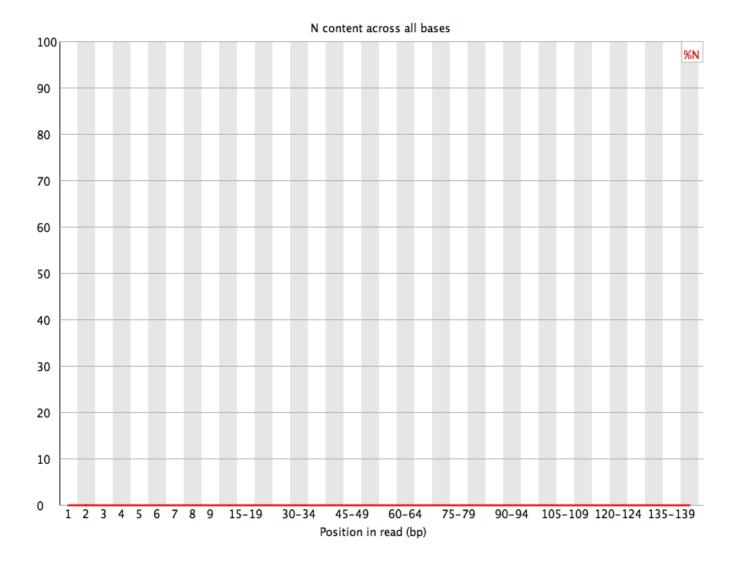
Per base sequence content



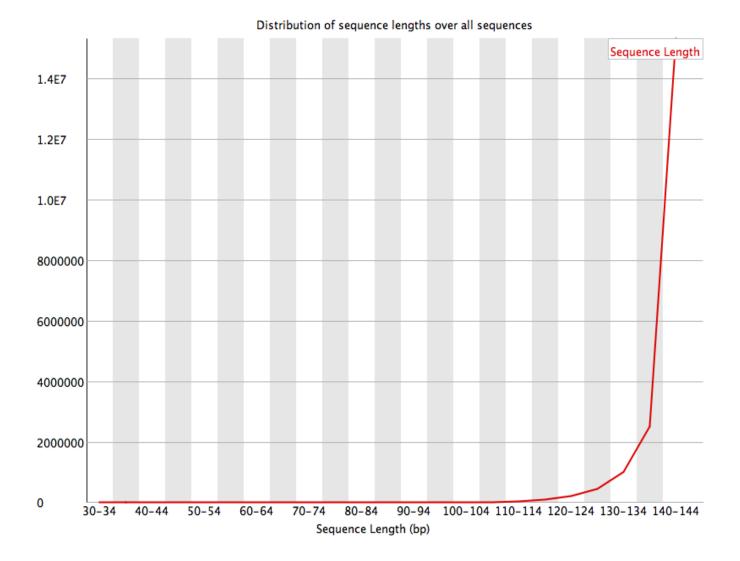
Per sequence GC content



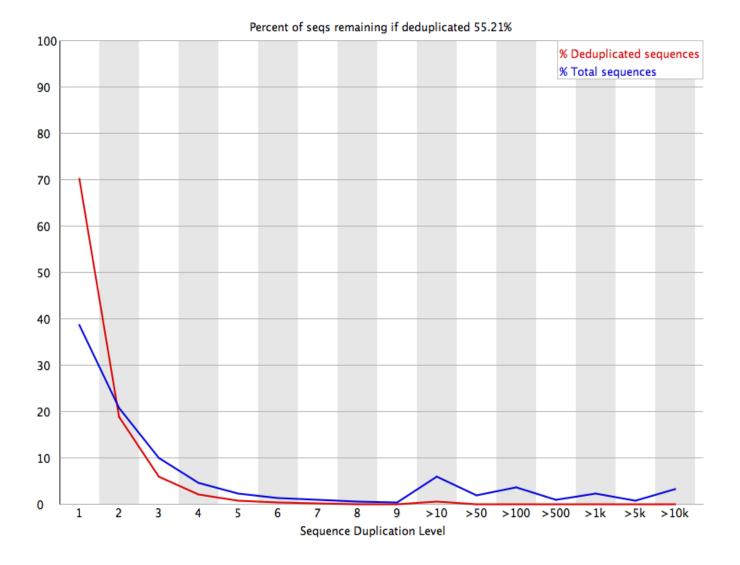




Sequence Length Distribution



Sequence Duplication Levels

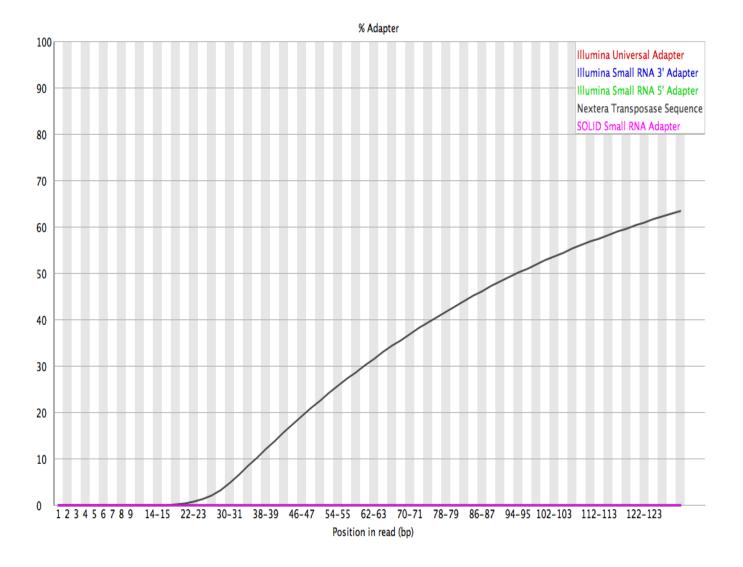


Overrepresented sequences

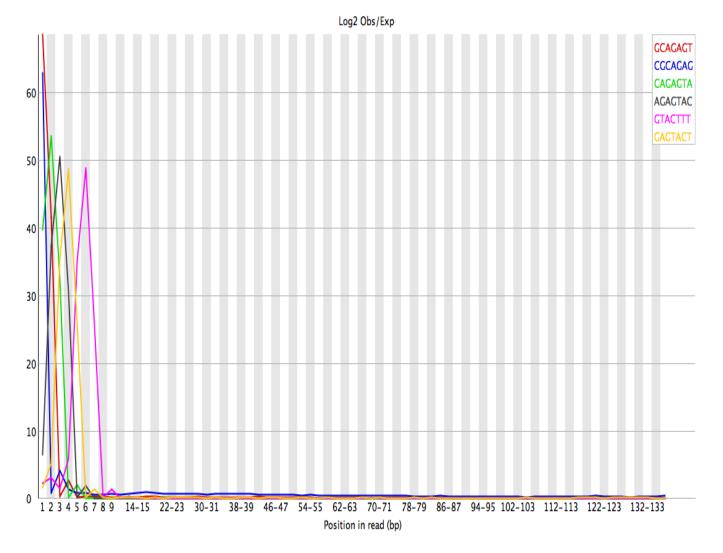
Sequence	Count	Percentage	Possible Source
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	89380	0.45365826052155467	No Hit
${\tt GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA$	80864	0.4104343430165026	No Hit
${\bf CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	62202	0.3157132593528949	No Hit
${\tt AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG$	49380	0.2506337536871154	No Hit
${\tt CGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	48137	0.24432476713723517	No Hit
CATCTCCGAGCCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCT	40326	0.20467915656514005	TruSeq Adapter, Index 11 (96% over 26bp)
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	34764	0.17644859888981124	No Hit

Sequence	Count	Percentage	Possible Source
${\tt CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT$	34704	0.17614406212955958	No Hit
CCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCTTGAAAAAAAA	28721	0.1457766715197983	RNA PCR Primer, Index 17 (96% over 27bp)
CCGAGCCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCTTGAAA	24987	0.12682433380680339	RNA PCR Primer, Index 11 (96% over 28bp)
CTCCGAGCCCACGAGACCGTACTAGATCTCGTATGCCGTCTTCTGCTTGA	24801	0.12588026985002326	RNA PCR Primer, Index 11 (96% over 28bp)
${\tt CACACACACACACACACACACACACACACACACACACA$	24435	0.12402259561248814	No Hit
${\tt TACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	24241	0.1230379267543411	No Hit
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	23015	0.11681522561986554	No Hit









Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	63720	0.0	68.54475	1
CGCAGAG	42220	0.0	62.904655	1
CAGAGTA	81360	0.0	53.576252	2
AGAGTAC	86260	0.0	50.50167	3
GTACTTT	43275	0.0	48.895275	6
GAGTACT	43295	0.0	48.732918	4
AGTACTT	43510	0.0	48.53847	5
GTACGGG	48870	0.0	45.78764	6
TACGGGG	35285	0.0	44.627537	7
AGTACGG	50545	0.0	44.3235	5
GAGTACG	51150	0.0	43.864964	4
TACTTTT	51355	0.0	41.215267	7
ACGGGGG	22195	0.0	37.685246	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGA	7020	0.0	37.545258	7
ACTTTTT	56960	0.0	37.407475	8
TACGGGT	5590	0.0	33.558193	7
TACGGGC	7560	0.0	28.726774	7
ACGGGGT	9360	0.0	27.296936	8
ACGGGGA	13420	0.0	26.954788	8
CGGGGGA	9715	0.0	22.908627	9

Produced by FastQC (version 0.11.5)