# **PastQC Report**Summary

Wed 30 Aug 2017 Sample4\_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 Sample4\_forward\_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9

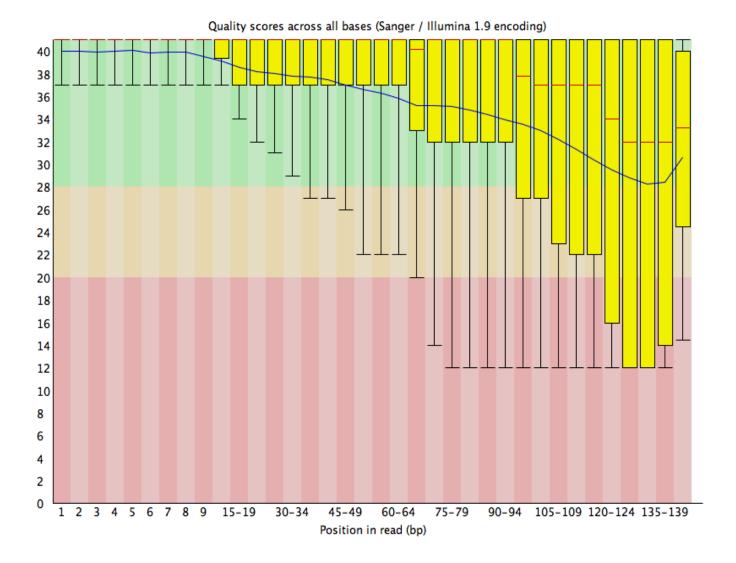
Total Sequences 41372891

Sequences flagged as poor quality 0

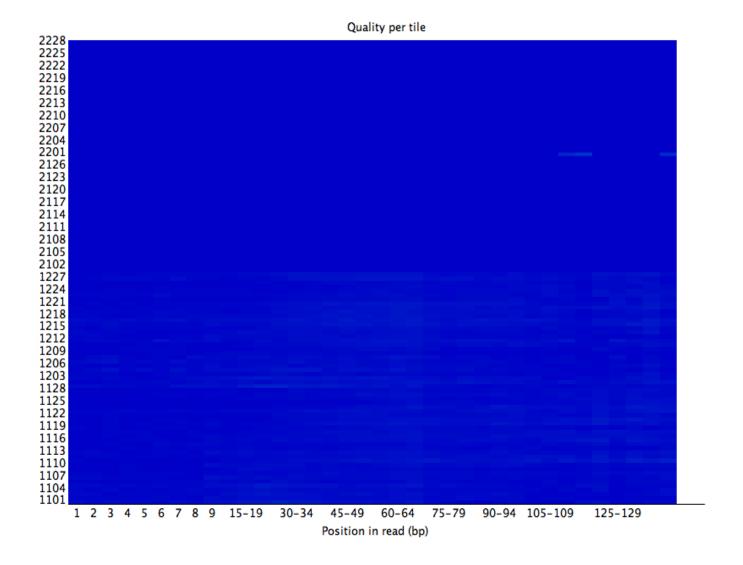
Sequence length 24-143

%GC 4

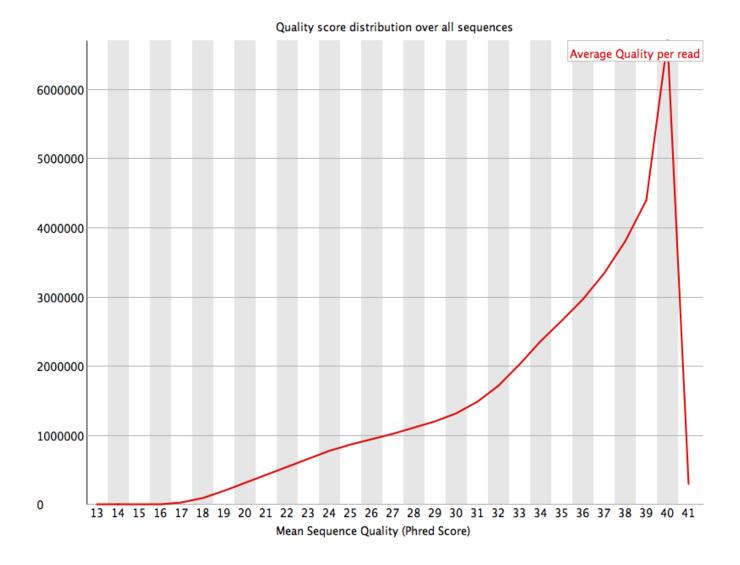
#### Per base sequence quality



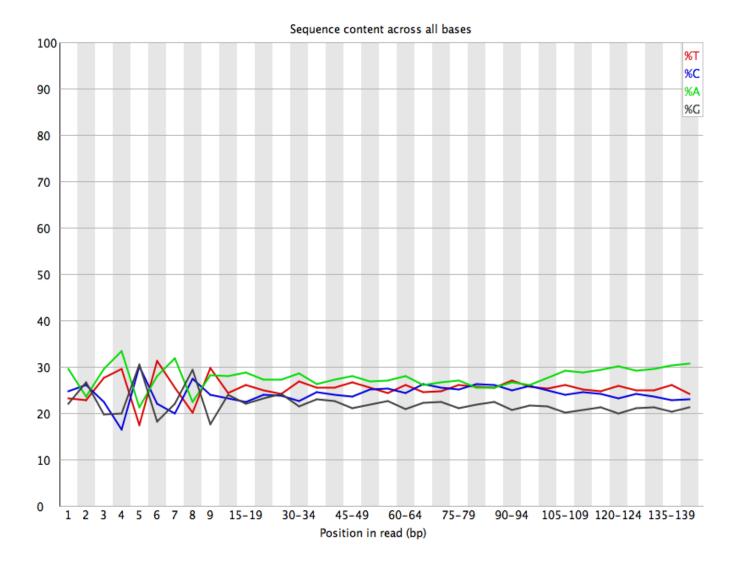
#### Per tile sequence quality



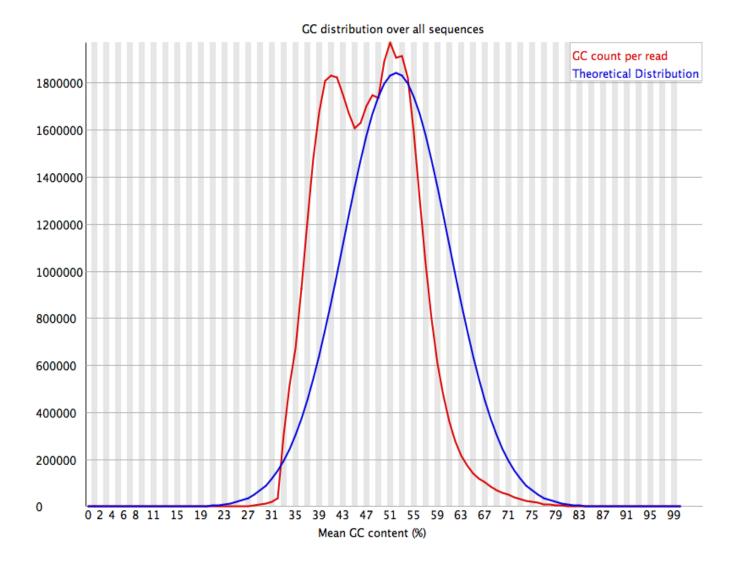
### Per sequence quality scores



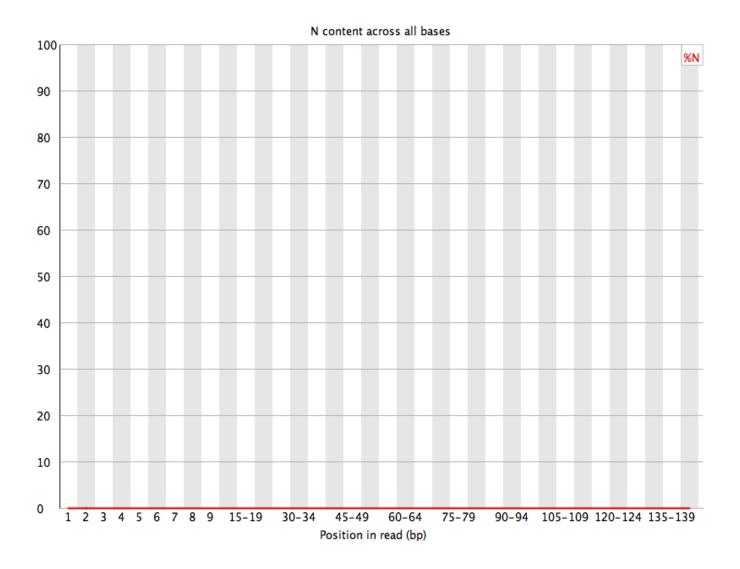
#### Per base sequence content



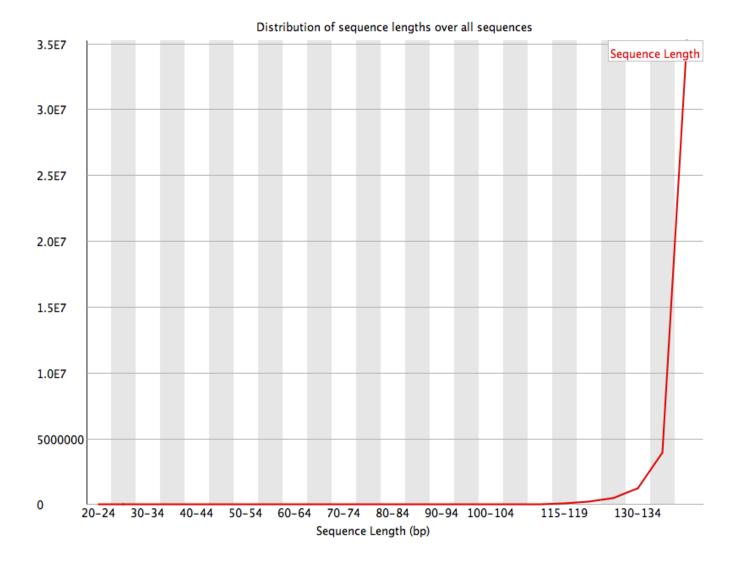
#### Per sequence GC content



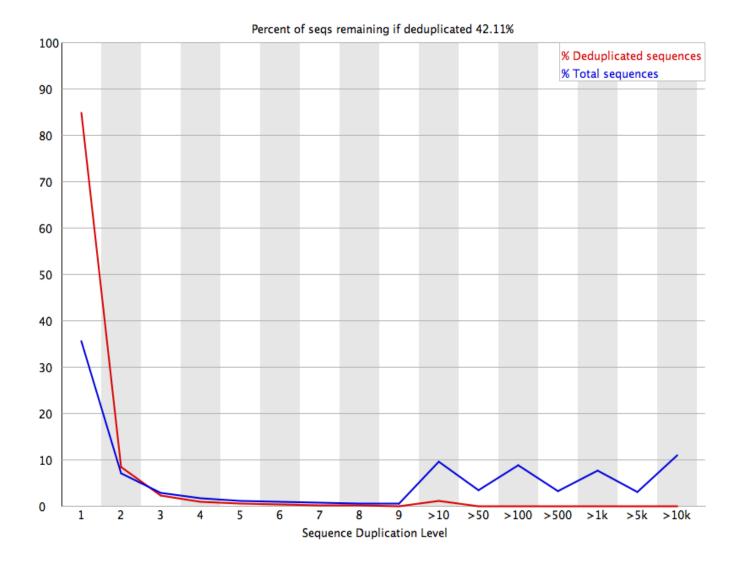




#### Sequence Length Distribution



## Sequence Duplication Levels

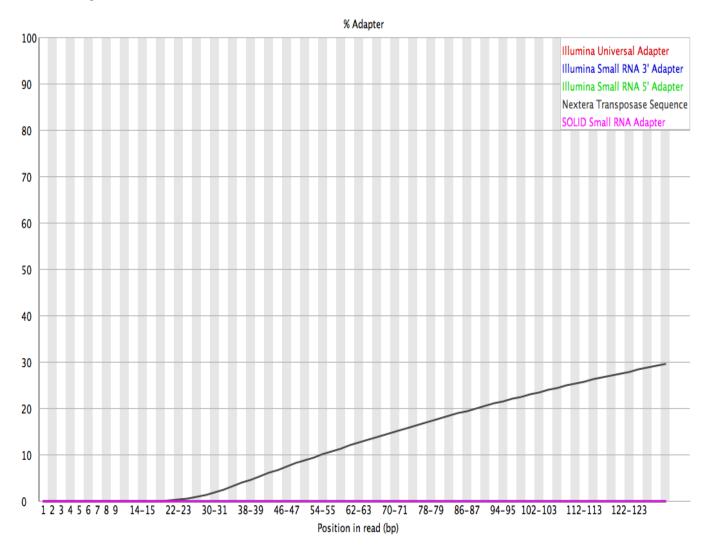


#### **Overrepresented sequences**

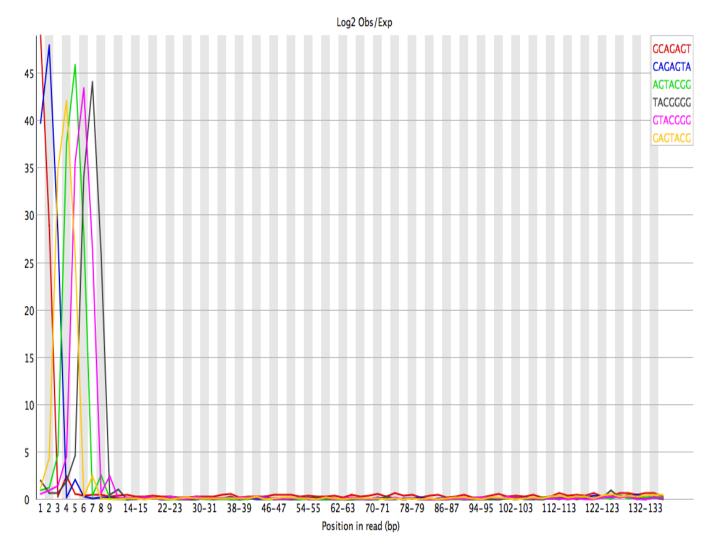
Sequence	Count	Percentage	Possible Source
${\tt ACAACAACAACAACAACAACAACAACAACAACAACAACA$	807476	1.9517031091687551	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	696148	1.6826186983162479	No Hit
${\tt GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	278144	0.6722856278039647	No Hit
${\tt AACAACAACAACAACAACAACAACAACAACAACAACAAC$	198864	0.4806625671868084	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	148900	0.3598974990652696	No Hit
${\tt TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG$	75803	0.18321900686128026	No Hit
${\tt CACAACAACAACAACAACAACAACAACAACAACAACAAC$	64921	0.156916759817437	No Hit
${\tt ACAACCCACAACAACAACAACAACAACAACAACAACAAC$	56262	0.13598759632243249	No Hit
TGTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	49496	0.11963389263757275	No Hit

Sequence	Count	Percentage	Possible Source
${\tt ACAACAACCACCACAACAACAACAACAACAACAACAACA$	44730	0.10811427221752523	No Hit
${\tt ACAACAACCACAACAACAACAACAACAACAACAACAACA$	44567	0.10772029443144304	No Hit
TGTTGTTGTGGGGTTGTTGTTGTTGTTGTTGTTGTTGTT	44061	0.10649727136544555	No Hit

#### **Adapter Content**







Sequence	Count	<b>PValue</b>	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	10065	0.0	48.89756	1
CAGAGTA	10230	0.0	47.910873	2
AGTACGG	7760	0.0	45.824345	5
TACGGGG	3925	0.0	44.093025	7
GTACGGG	8195	0.0	43.391937	6
GAGTACG	8445	0.0	42.10734	4
AGTACTT	3580	0.0	37.012234	5
TACGGGC	2365	0.0	36.58882	7
GAGTACT	3625	0.0	36.552727	4
AGAGTAC	14095	0.0	34.7732	3
GTACTTT	3955	0.0	33.502857	6
TACGGGA	1640	0.0	29.679613	7
ACGGGGT	2310	0.0	28.680302	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACTTTT	4955	0.0	26.74127	7
TACGGGT	1870	0.0	25.66782	6
ACTTTTT	5655	0.0	23.550667	8
ACGGGCT	2360	0.0	22.916464	8
ACGGGTC	1405	0.0	16.840748	8
ACGGGGA	3610	0.0	14.9814005	8
CGCAGAG	20320	0.0	14.738377	1

Produced by FastQC (version 0.11.5)