# **PastQC Report**Summary

Wed 30 Aug 2017 Sample5\_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

Sample5\_forward\_paired.fq.gz

File type

Conventional base calls

Encoding

Sanger / Illumina 1.9

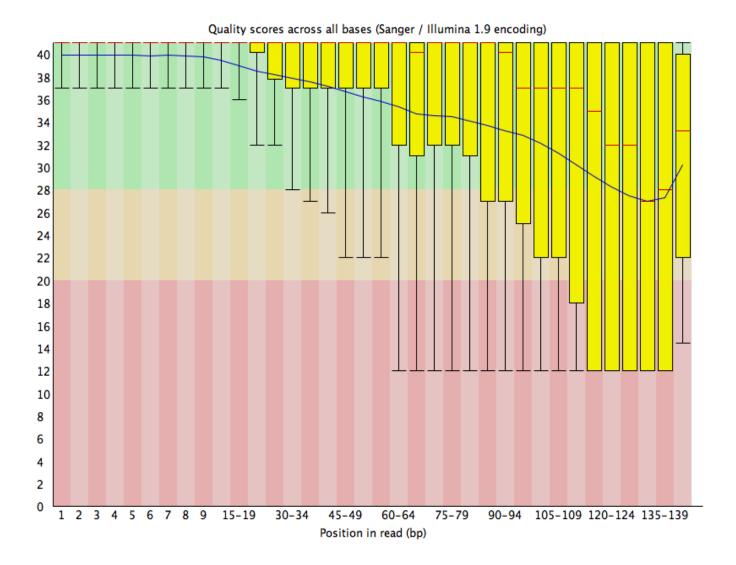
Total Sequences 36936739

Sequences flagged as poor quality 0

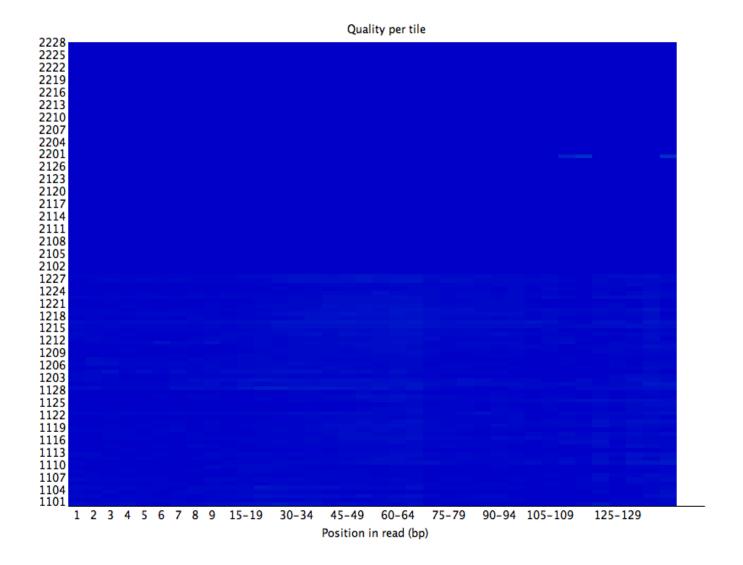
Sequence length 26-143

%GC 50

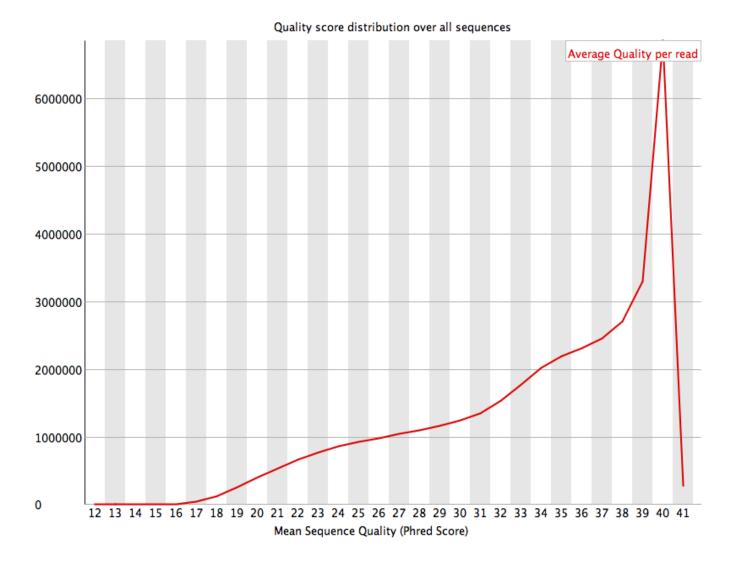
#### Per base sequence quality



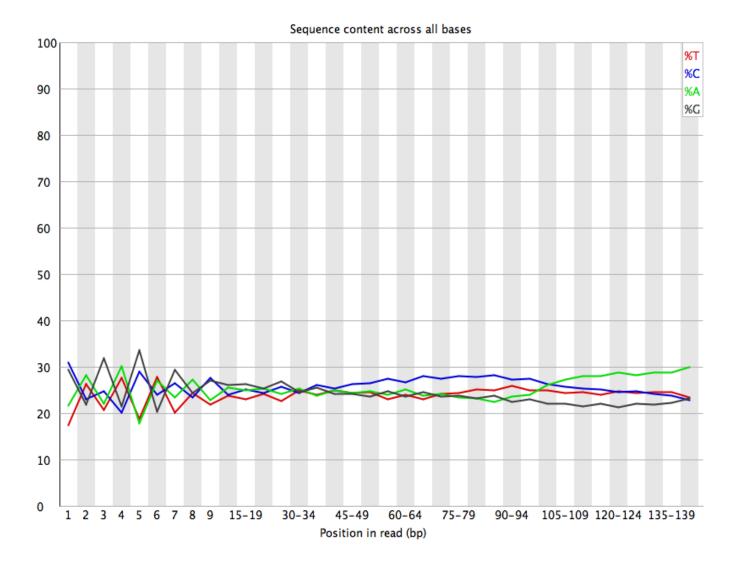
#### Per tile sequence quality



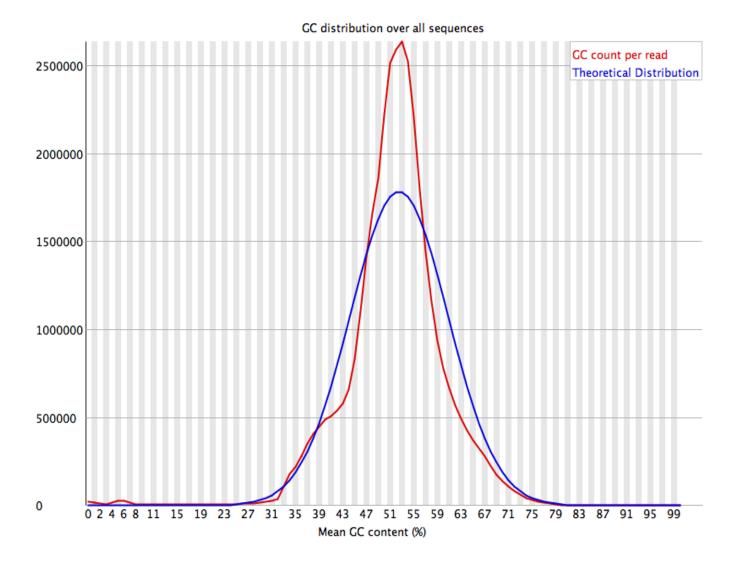
# Per sequence quality scores



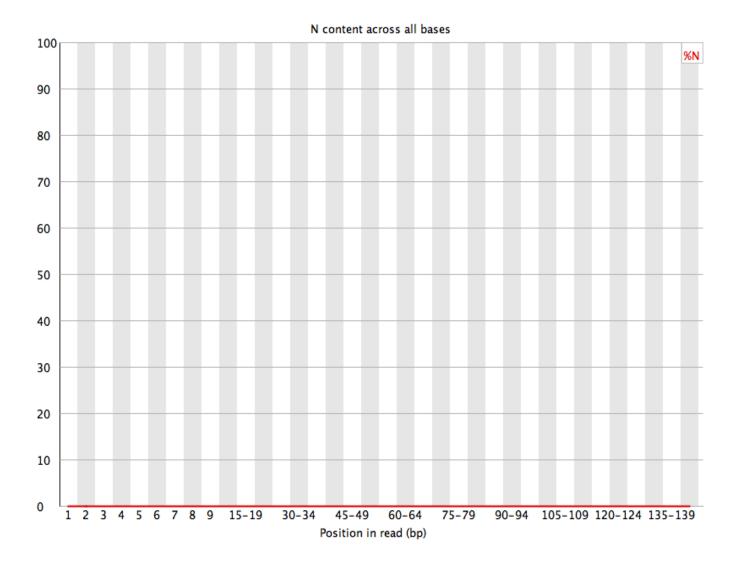
#### Per base sequence content



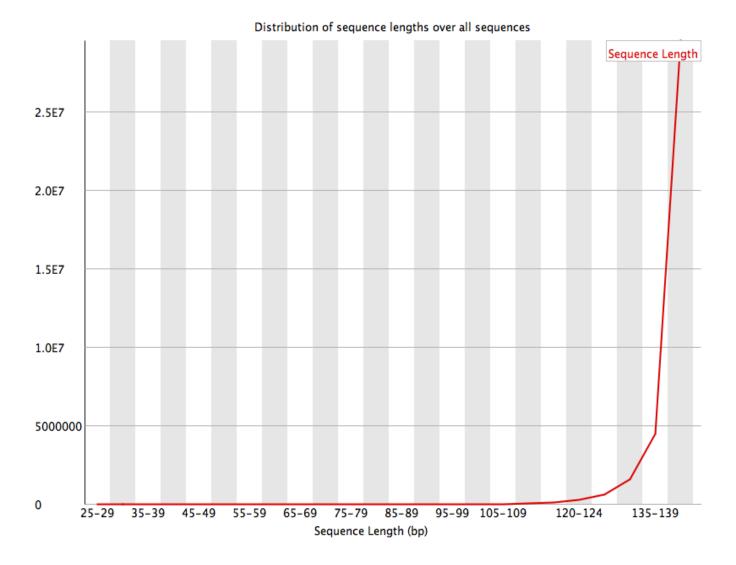
#### Per sequence GC content



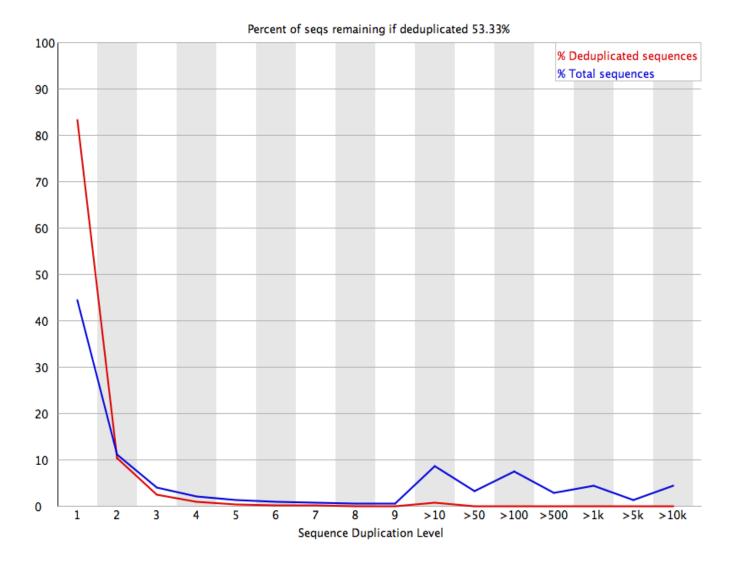




## Sequence Length Distribution



#### Sequence Duplication Levels

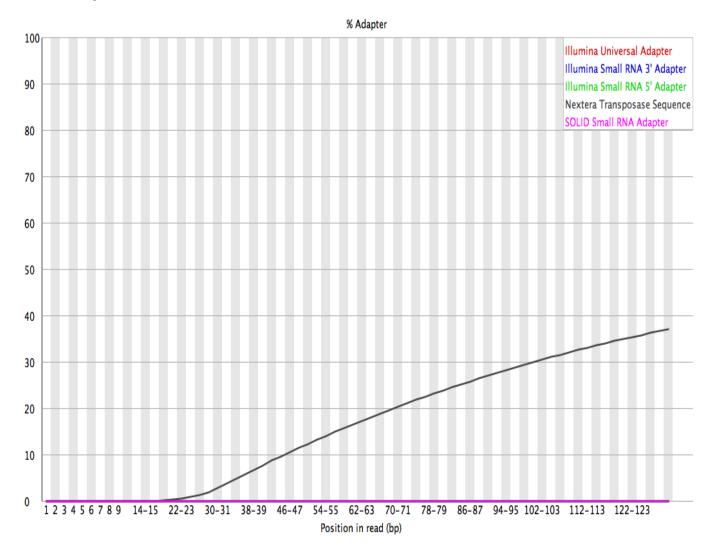


#### Overrepresented sequences

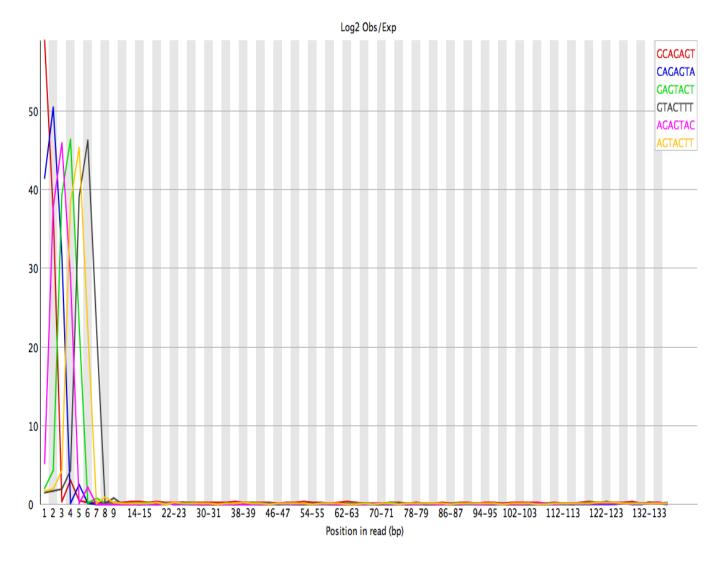
Sequence	Count	Percentage	Possible Source
${\tt ACAACAACAACAACAACAACAACAACAACAACAACAACA$	234357	0.6344821073674101	No Hit
${\tt GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA$	211175	0.5717207466528109	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	188302	0.5097959513967922	No Hit
$\tt CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT$	101945	0.27599891804200694	No Hit
${\tt GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT$	101346	0.27437722642488827	No Hit
${\tt AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG$	59388	0.16078300794230915	No Hit
${\tt AACAACAACAACAACAACAACAACAACAACAACAACAAC$	54718	0.14813976945826215	No Hit
${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	50994	0.13805766664999852	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	50127	0.13571041016912727	No Hit

Sequence	Count	Percentage	Possible Source
${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$	41243	0.11165847640204514	No Hit
AGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	37297	0.10097534598276257	No Hit

## **Adapter Content**



**W**Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	52545	0.0	58.846935	1
CAGAGTA	61060	0.0	50.44212	2
GAGTACT	22205	0.0	46.3975	4
GTACTTT	22230	0.0	46.28468	6
AGAGTAC	66995	0.0	45.91321	3
AGTACTT	22740	0.0	45.276306	5
TACGGGG	22000	0.0	44.503353	7
GAGTACG	46450	0.0	44.084373	4
GTACGGG	46825	0.0	43.65936	6
AGTACGG	47040	0.0	43.560074	5
TACGGGC	10780	0.0	39.539936	7
TACGGGA	5965	0.0	39.39726	7
TACTTTT	26765	0.0	38.416943	7

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACTTTTT	28360	0.0	36.232586	8
TACGGGT	12070	0.0	33.69618	7
ACGGGTC	7645	0.0	30.827732	8
ACGGGGA	14975	0.0	30.39701	8
ACGGGGG	9855	0.0	28.219183	8
ТАААСТА	3755	0.0	26.898947	2
ACGGGGT	6275	0.0	25.539608	8

Produced by FastQC (version 0.11.5)