# **PastQC Report**Summary

Mon 28 Aug 2017 Sample3\_reverse\_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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File type

Conventional base calls

Encoding

Sample3\_reverse\_paired.fq.gz

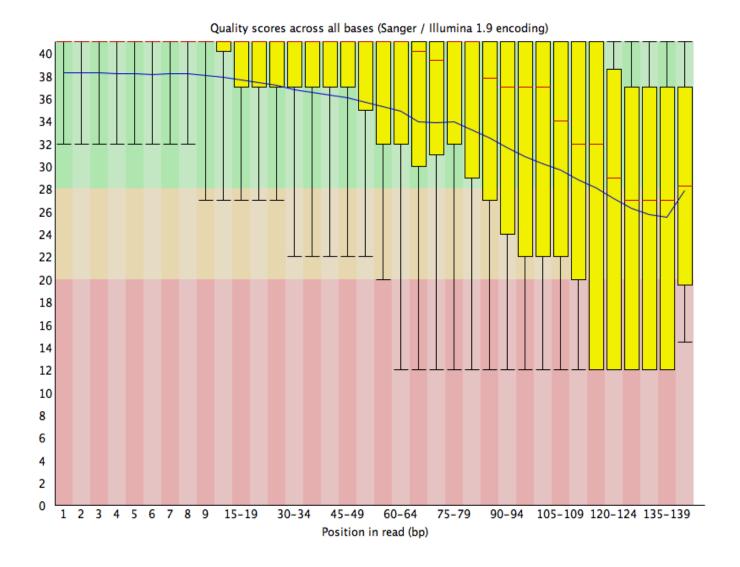
Conventional base calls

Sanger / Illumina 1.9

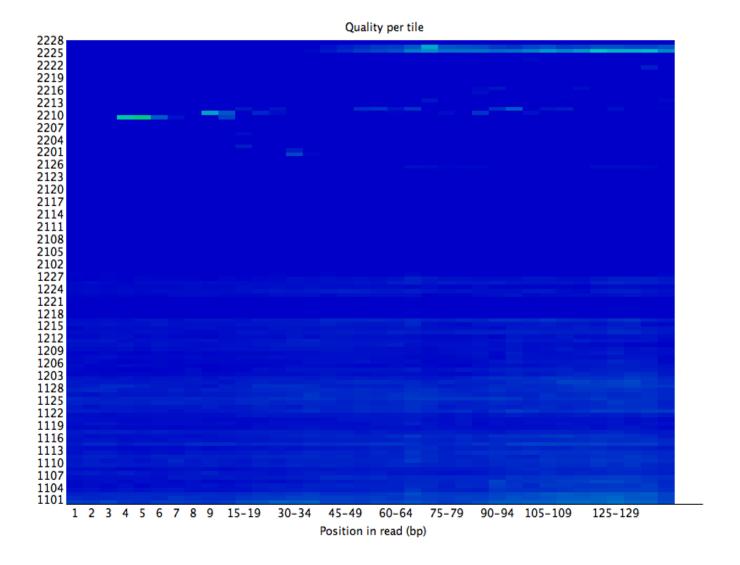
Total Sequences 20401753

Sequences flagged as poor quality 0
Sequence length 2-143
%GC 53

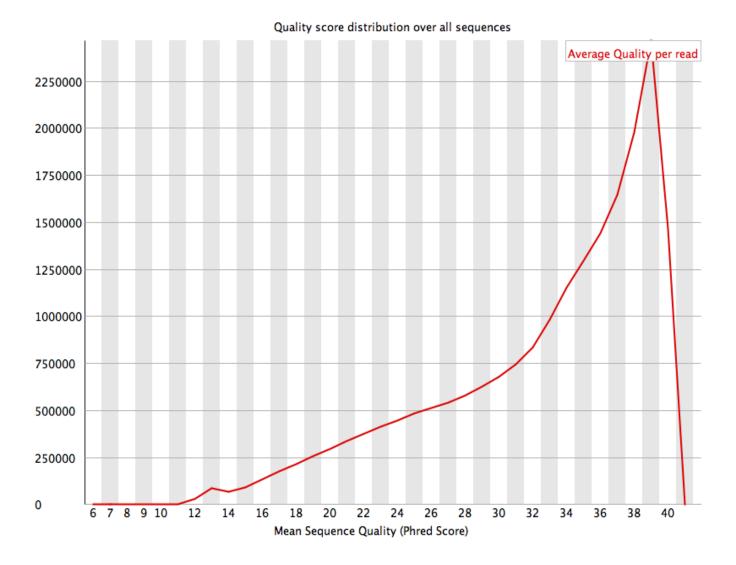
Per base sequence quality



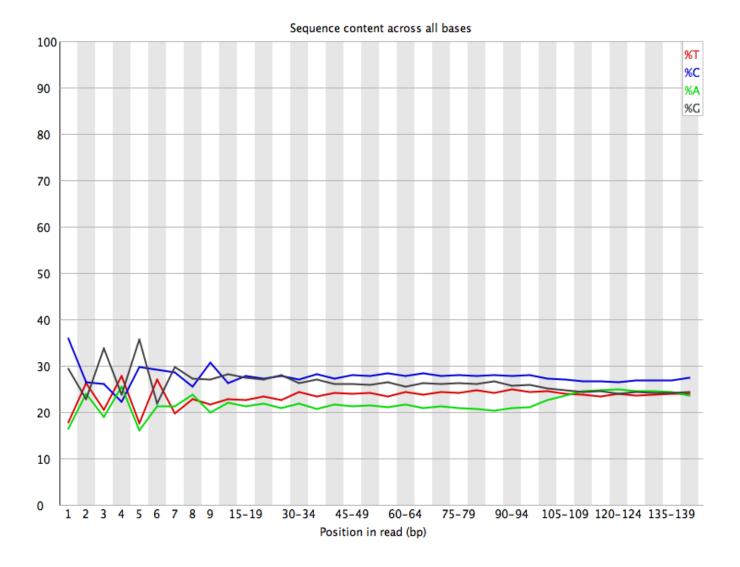
#### Per tile sequence quality



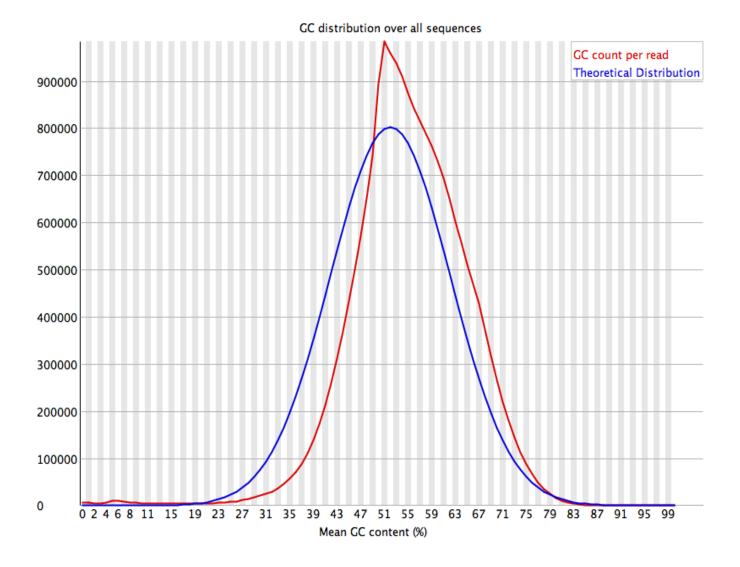
# Per sequence quality scores



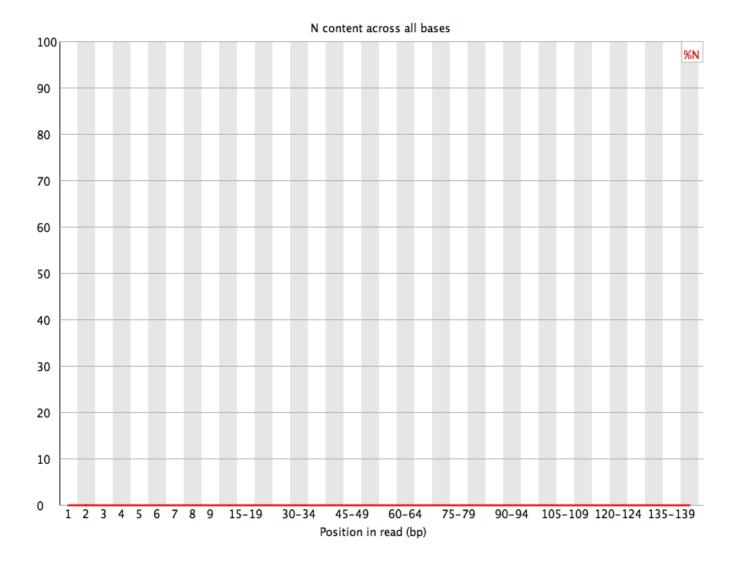
#### Per base sequence content



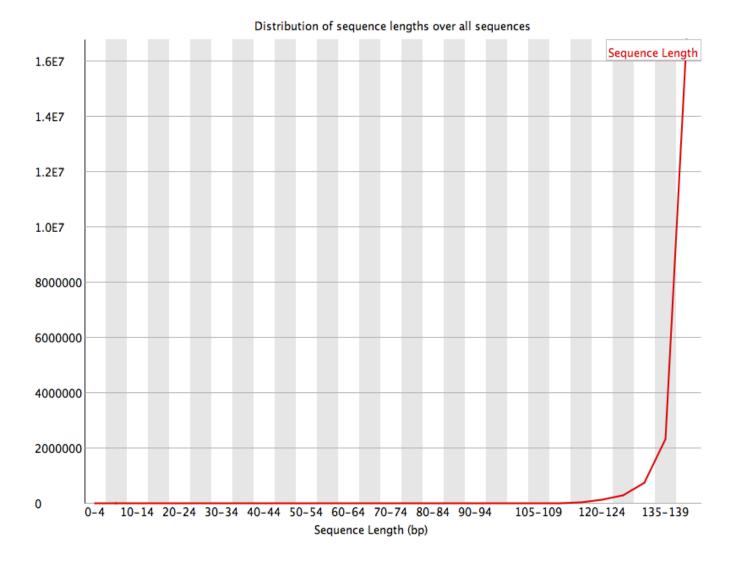
## Per sequence GC content



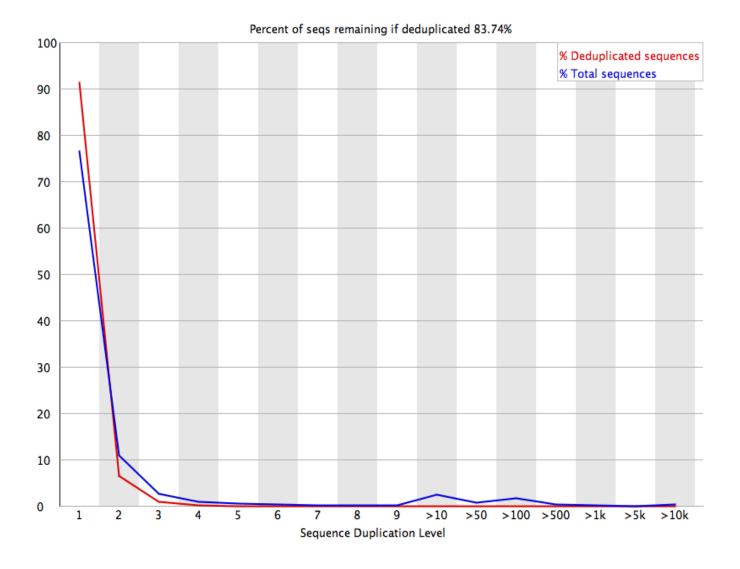




#### Sequence Length Distribution



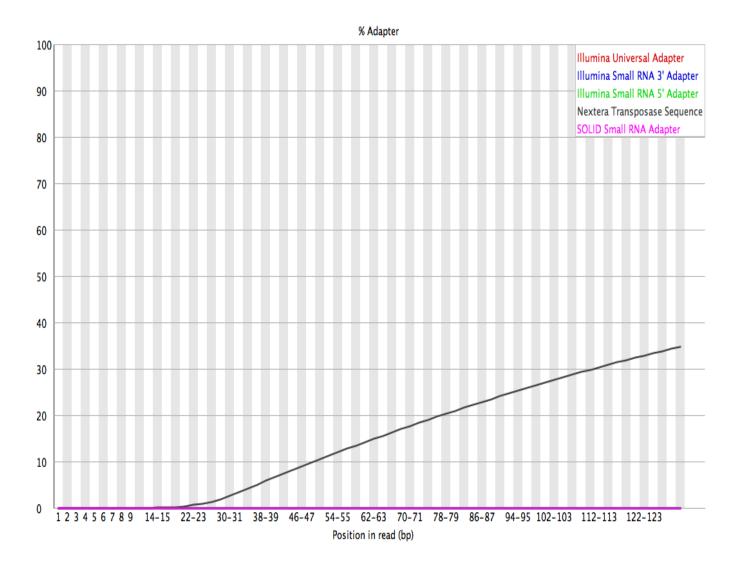
# Sequence Duplication Levels



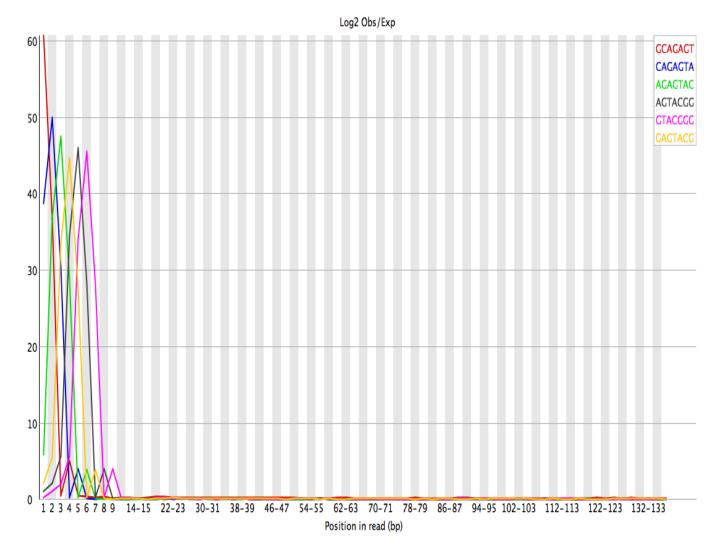
### Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT$	27931	0.13690490224050844	No Hit
CA	23652	0.11593121434221854	No Hit









Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	39215	0.0	60.63673	1
CAGAGTA	47265	0.0	49.981785	2
AGAGTAC	49660	0.0	47.544247	3
AGTACGG	46140	0.0	46.034374	5
GTACGGG	46445	0.0	45.520683	6
GAGTACG	47725	0.0	44.686775	4
TACGGGG	20330	0.0	42.771427	7
TACGGGC	13545	0.0	40.259735	7
CGCAGAG	36905	0.0	39.875282	1
TACGGGT	13460	0.0	35.9067	7
TACGGGA	7245	0.0	32.098305	7
ACGGGGG	12000	0.0	28.035892	8
GTACTTT	8370	0.0	27.699137	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACTTTTT	9075	0.0	25.482533	8
TACTTTT	9490	0.0	24.362917	7
AGTACTT	10360	0.0	22.504408	4
GAGTACT	10470	0.0	22.396688	4
ACGGGTG	12820	0.0	22.088	8
ACGGGGA	10020	0.0	21.397081	8
ACGGGGT	8985	0.0	21.23555	8

Produced by FastQC (version 0.11.5)