# **PastQC Report**Summary

Wed 30 Aug 2017 Sample12\_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

Total Sequences

#### Measure Value

File type

Sample12\_forward\_paired.fq.gz

Conventional base calls

22283987

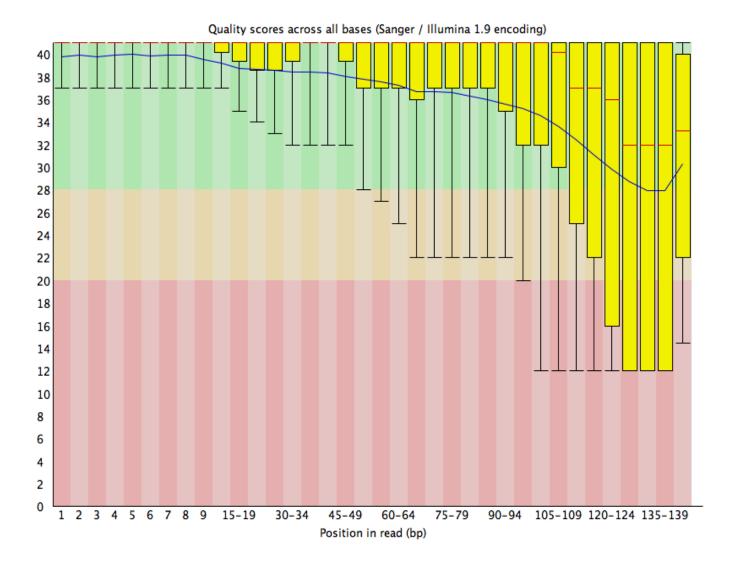
Encoding Sanger / Illumina 1.9

Sequences flagged as poor quality 0

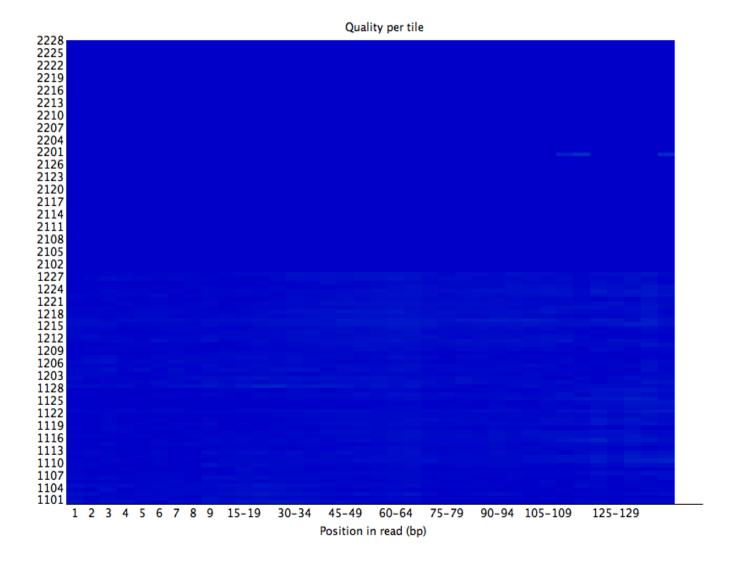
Sequence length 33-143

%GC 45

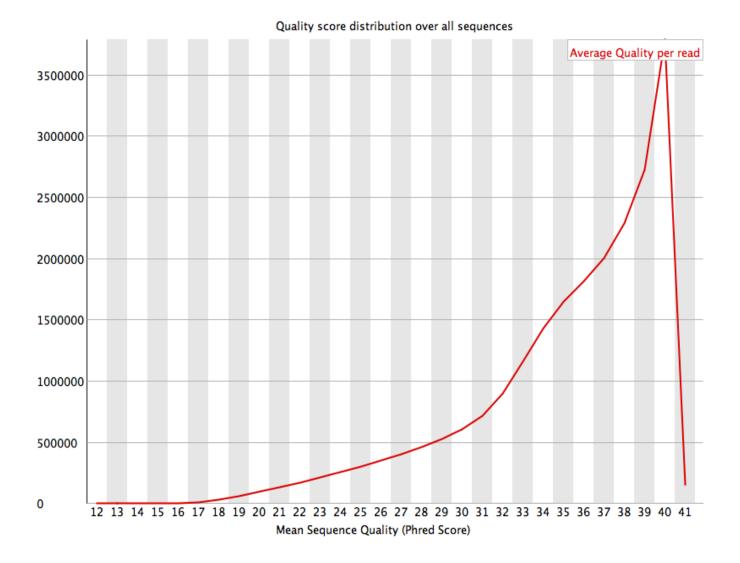
### Per base sequence quality



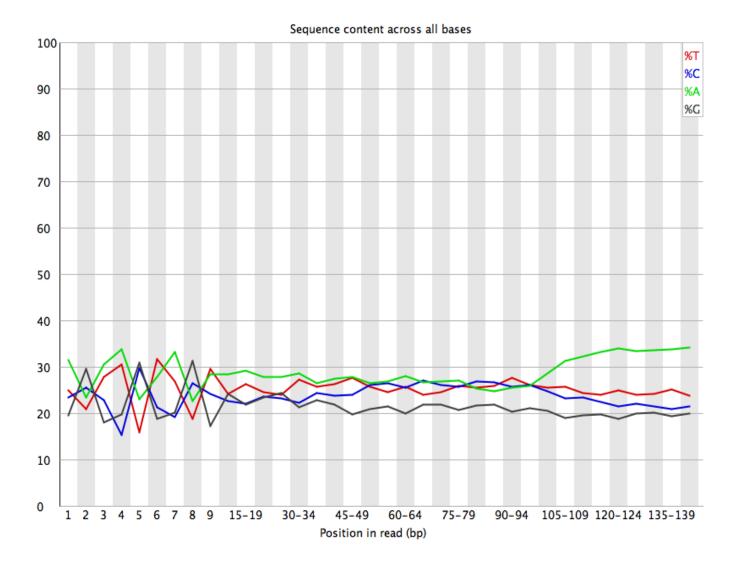
#### Per tile sequence quality



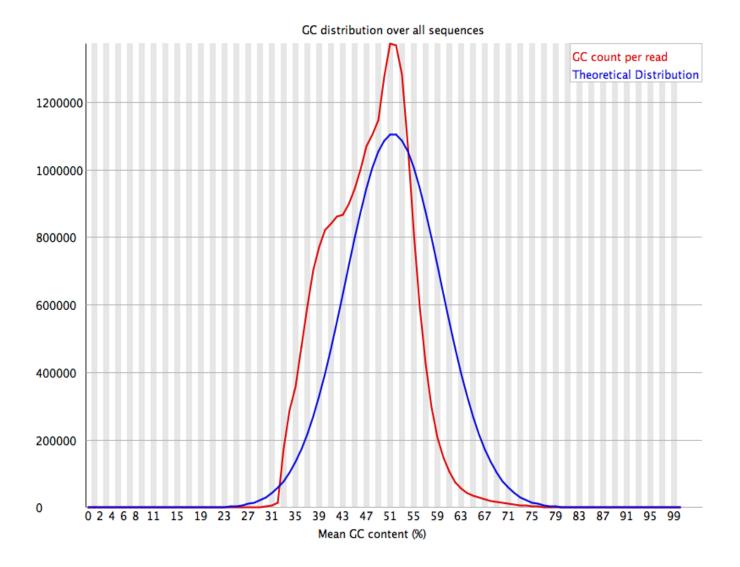
# Per sequence quality scores



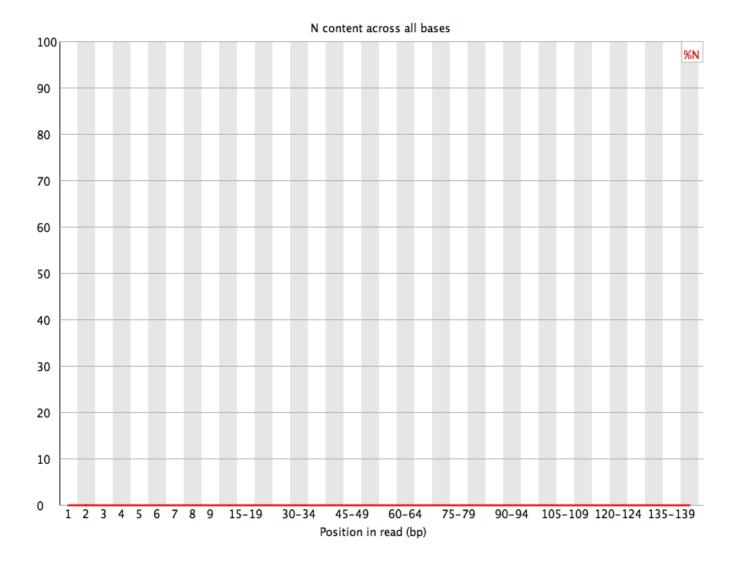
#### Per base sequence content



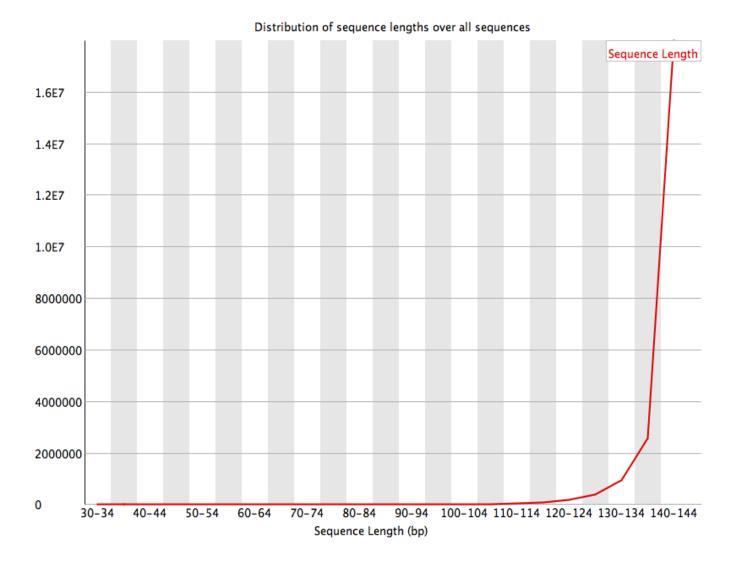
## Per sequence GC content



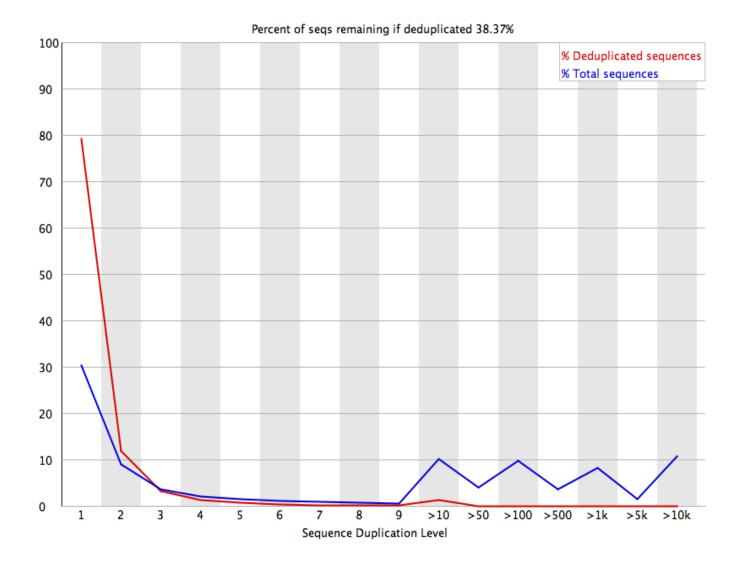




#### Sequence Length Distribution



# Sequence Duplication Levels

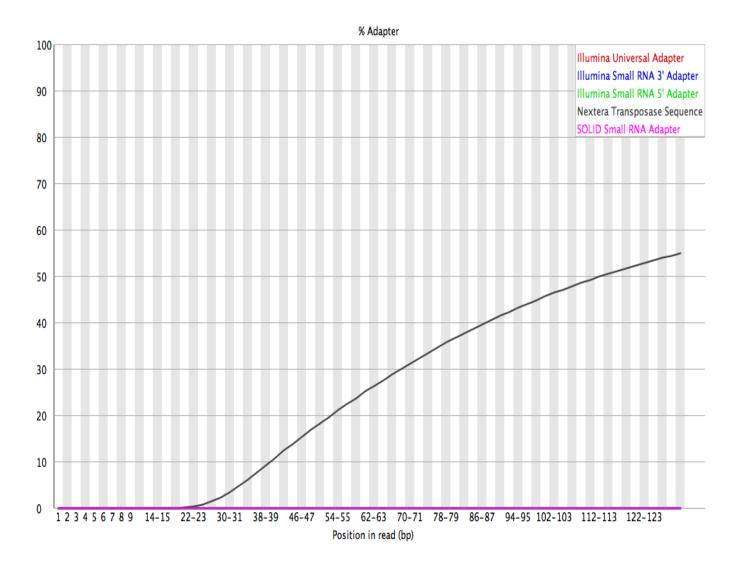


### **Overrepresented sequences**

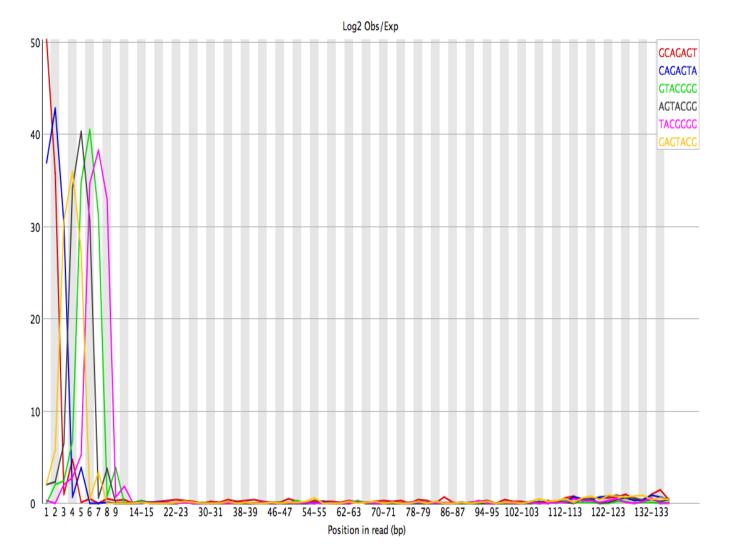
Sequence	Count	Percentage	Possible Source
TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	TTGTTGTTG 498654	2.237723437910819	No Hit
ACAACAACAACAACAACAACAACAACAACAACAACAACA	AACAACAAC 482294	2.164307491294085	No Hit
AACAACAACAACAACAACAACAACAACAACAACAACAAC	CAACAACAA 143612	0.6444627705087066	No Hit
GTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	TGTTGTTGT 118988	0.533961898290463	No Hit
CAACAACAACAACAACAACAACAACAACAACAACAACAA	ACAACAACA 85858	0.3852901188642769	No Hit
CACAACAACAACAACAACAACAACAACAACAACAACAAC	CAACAACAA 48468	0.21750147314302418	No Hit
TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	GTTGTTGTT 45964	0.20626470478554848	No Hit
ACAACCCACACAACAACAACAACAACAACAACAACAACA	AACAACAAC 31151	0.13979096290084894	No Hit
TGTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	TTGTTGTTG 29862	0.13400654021203656	No Hit

Sequence	Count	Percentage	Possible Source
${\tt ACAACAACCACAACAACAACAACAACAACAACAACAACA$	28501	0.12789901555767377	No Hit
${\tt ACAACAACCACCACAACAACAACAACAACAACAACAACA$	28417	0.1275220632645316	No Hit
${\tt TGTTGTTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTG$	28245	0.12675020856905006	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	27335	0.1226665587266767	No Hit
${\tt TGTTGTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	26351	0.11825083186415429	No Hit
${\tt ACAACAACAACCACCACCACAACAACAACAACAACAACA$	24314	0.10910973875545701	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	23963	0.10753461667339871	No Hit
${\tt TGTTGTTGTTGTGGGGTTGTTGTTGTTGTTGTTGTTGTT$	23934	0.10740447838171868	No Hit
${\tt TGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT$	23876	0.10714420179835861	No Hit
GA	22871	0.10263423686255069	No Hit





#### **W**Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCAGAGT	4105	0.0	50.22436	1
CAGAGTA	4815	0.0	42.81858	2
GTACGGG	4140	0.0	40.523422	6
AGTACGG	4215	0.0	40.281914	5
TACGGGG	1920	0.0	38.249653	7
GAGTACG	4725	0.0	35.934025	4
TACGGGC	1375	0.0	33.810272	7
AGAGTAC	6305	0.0	32.699677	3
AGTACTT	1165	0.0	31.230215	5
TACGGGT	920	0.0	30.758396	7
GAGTACT	1205	0.0	30.752665	4
ACGGGCT	1030	0.0	28.781784	7
GTACTTT	1265	0.0	28.76142	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TACGGGA	685	0.0	28.523949	7
ACGGGGT	900	0.0	26.950212	8
ACGGGTC	605	0.0	26.727486	8
TACTTTT	1725	0.0	21.091475	7
CTTAGTA	130	5.69965E-4	19.878824	134-135
GTTTAAC	140	7.530787E-5	19.701197	132-133
CGCAGAG	7665	0.0	19.68983	1

Produced by FastQC (version 0.11.5)