

Fastq quality data.

Your Name here

October 17, 2016

Contents

1 Project characteristics	1
2 Global summaries	1
2.1 Project names and read numbers	2
3 Nucleotide patterns	2
3.1 N nucleotides	3
3.2 GC content	4
3.3 Nucleotide frequencies	5
4 Phred qualities	7
5 Hierarchical clustering	8

1 Project characteristics

Project characteristics
Contact
Phone
Institute
Mail
Start date

2 Global summaries

Input data: Summarized data on FASTQ files.

```
[fastqq] File ( 1/2) '/tmp/RtmpT3QhXv/Rinst5382772550a9/seqTools/extdata/g4_1101_n10
[fastqq] File ( 2/2) '/tmp/RtmpT3QhXv/Rinst5382772550a9/seqTools/extdata/g5_1101_n10
```

Printout of Fastqq object:

```

> fqq

Class      :          Fastqq
nFiles     :             2
maxSeqLen  :           101
k (Kmer len):           4

nReads     :           200
nr N nuc   :             2
Min seq len :           101
Max seq len :           101

```

2.1 Project names and read numbers

```

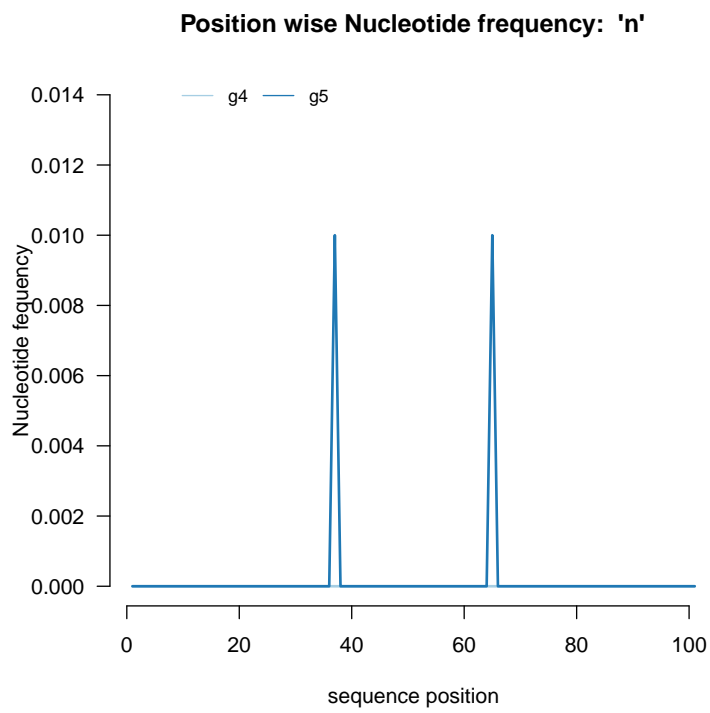
> dfr<-data.frame(file=basename(fileNames(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)

```

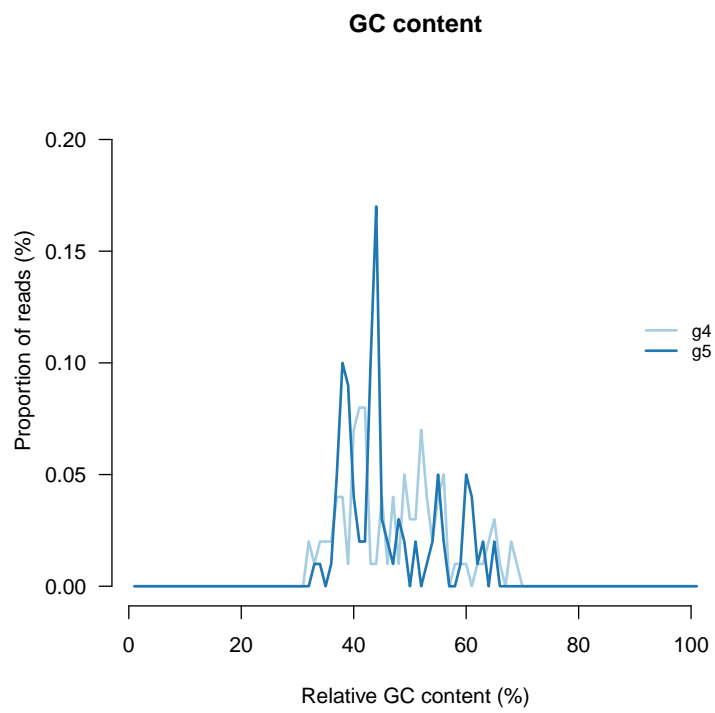
	file	sample	reads
1	g4_l101_n100.fq.gz	g4	100
2	g5_l101_n100.fq.gz	g5	100

3 Nucleotide patterns

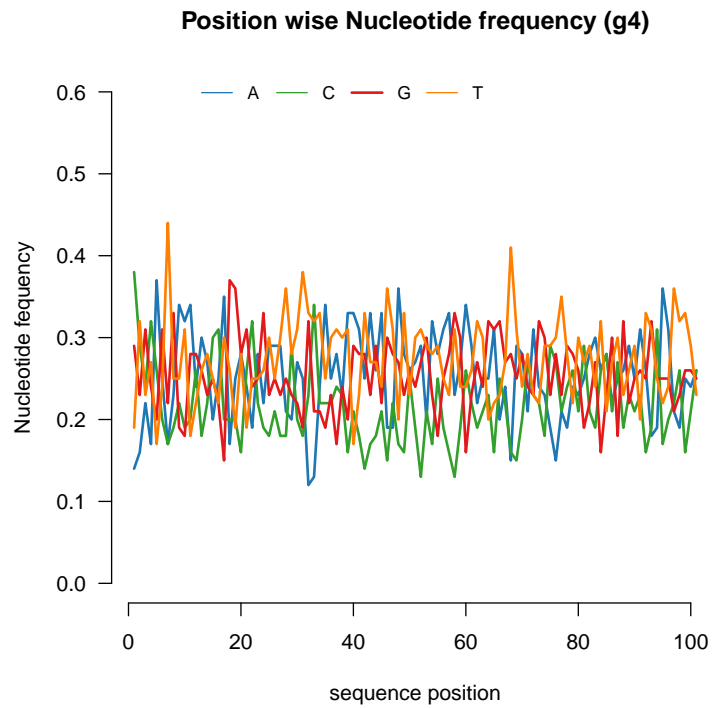
3.1 N nucleotides



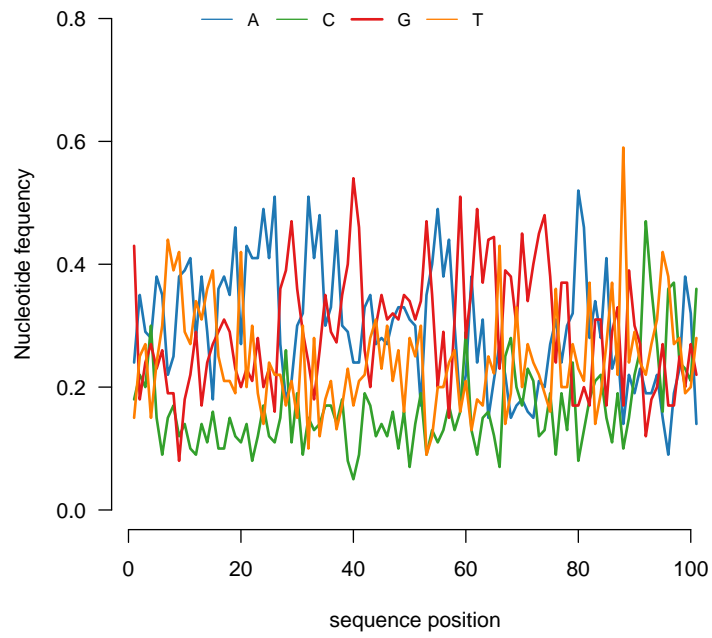
3.2 GC content



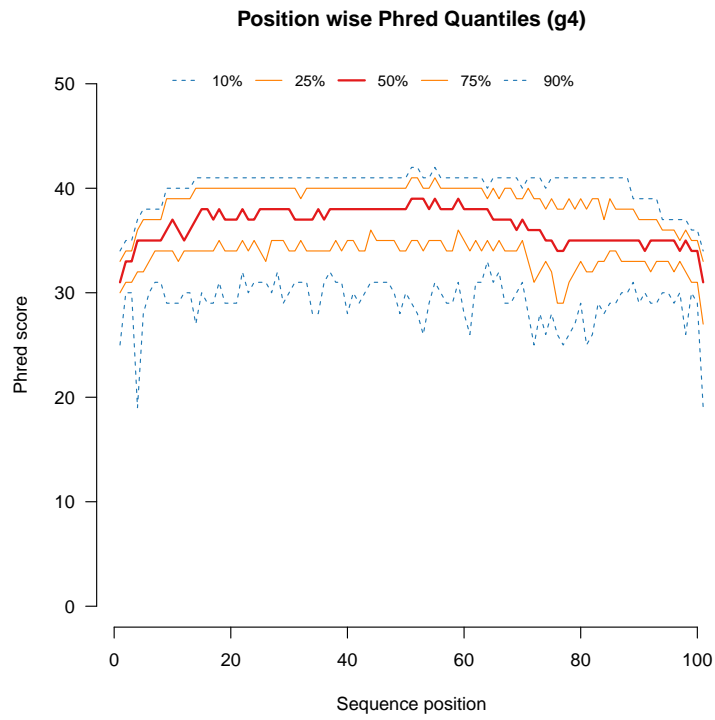
3.3 Nucleotide frequencies

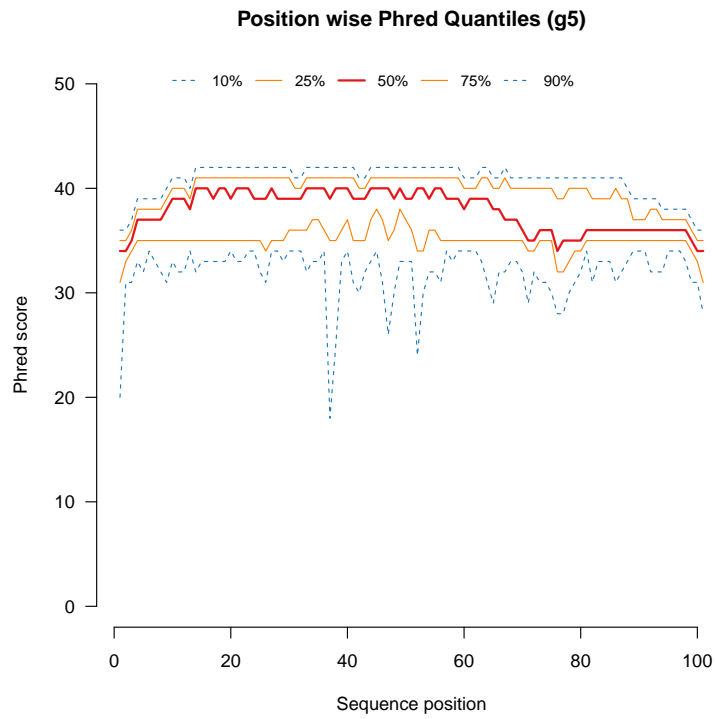


Position wise Nucleotide frequency (g5)



4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2

