Fastq quality data.

Your Name here

October 29, 2024

Contents

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/Rtmp04ON7P/Rinst1b36b364118384/seqTools/extdata/g4_l101_n1
[fastqq] File ( 2/2) '/tmp/Rtmp04ON7P/Rinst1b36b364118384/seqTools/extdata/g5_l101_n1
```

Printout of `Fastqq` object:

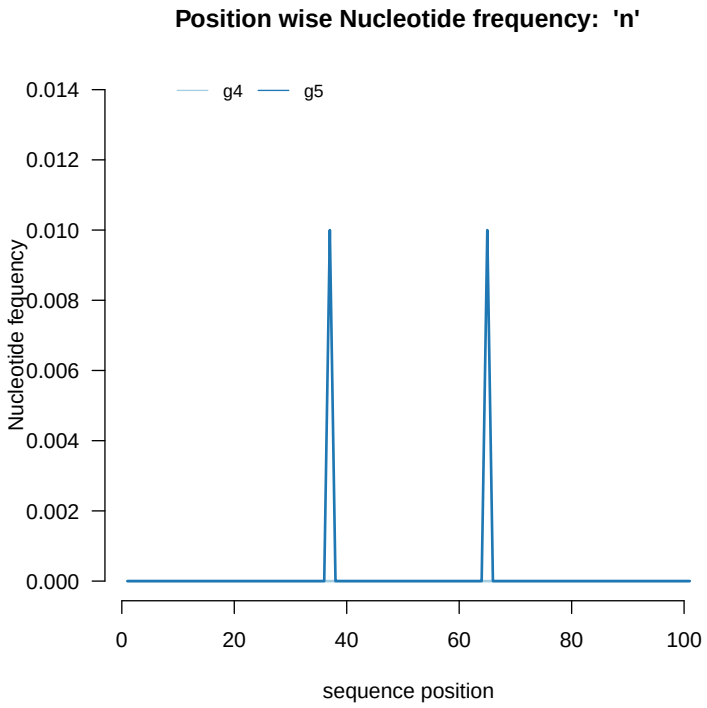
```
> fqq

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

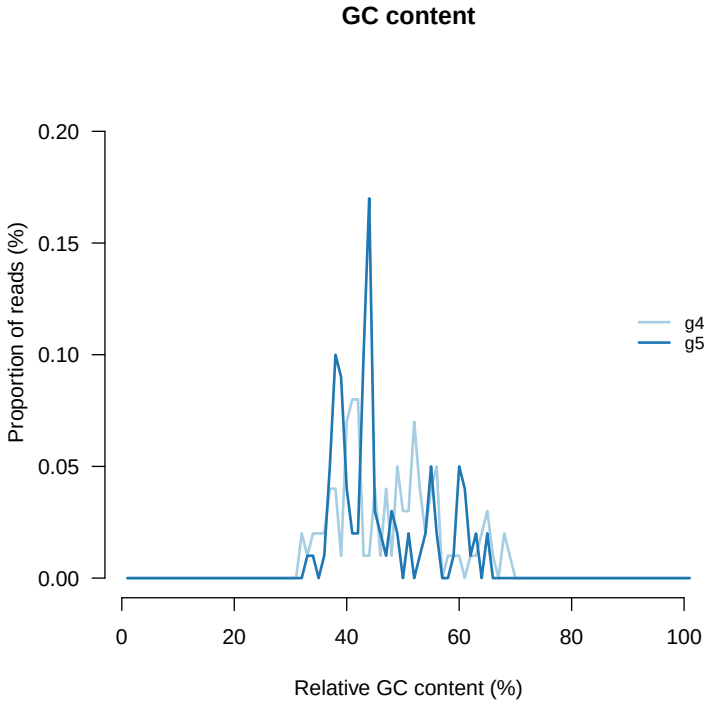
```
> dfr<-data.frame(file=basename(fileNames(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)

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

3 Nucleotide patterns

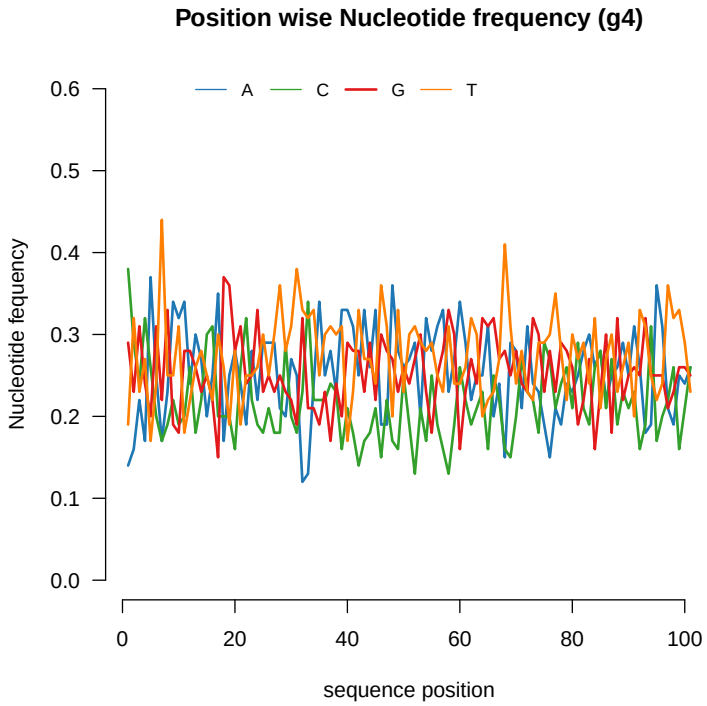
3.1 N nucleotides

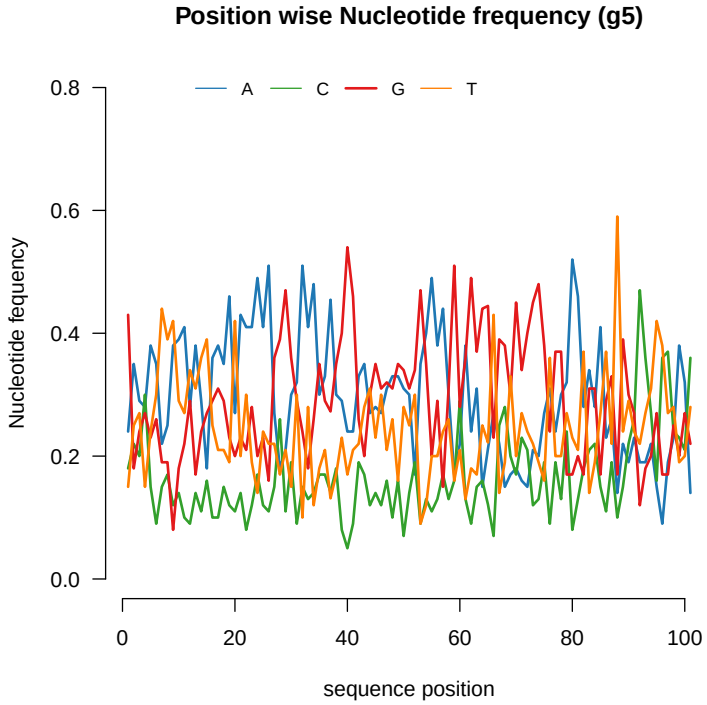


3.2 GC content

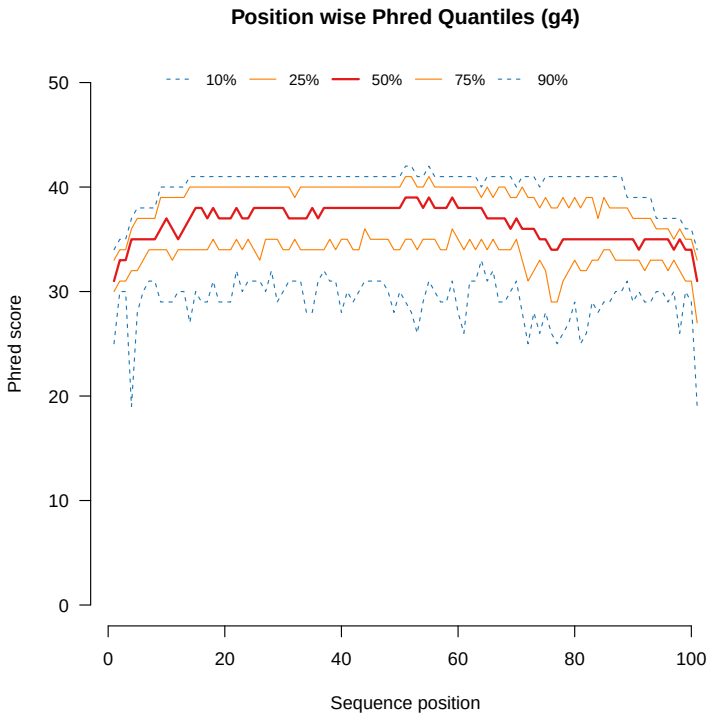


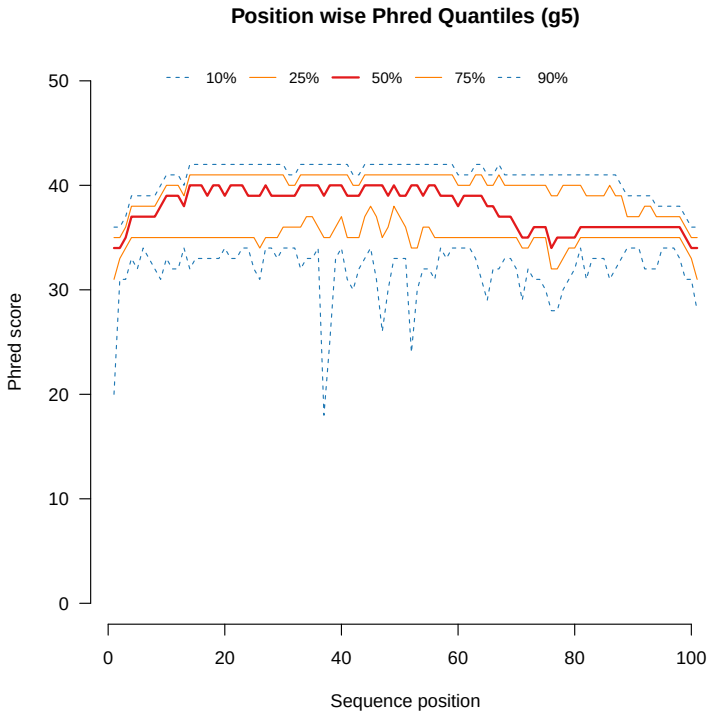
3.3 Nucleotide frequencies




Position wise Nucleotide frequency (g5)
A
C
G
T
0.8
0.6
0.4
0.2
0.0
Nucleotide fequency
0
20
40
60
80
100
sequence position

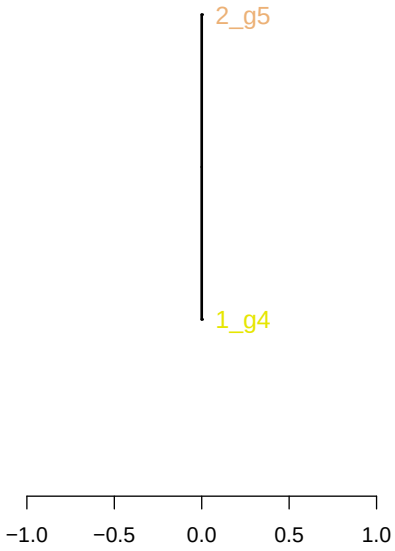
4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2


2_g5
1_g4
−1.0
−0.5
0.0
0.5
1.0