

Fastq quality data.

Your Name here

April 27, 2020

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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/Rtmp1bEzGs/Rinst51c5485fb887/seqTools/extdata/g4_1101_n10
```

```
[fastqq] File ( 2/2) '/tmp/Rtmp1bEzGs/Rinst51c5485fb887/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

```

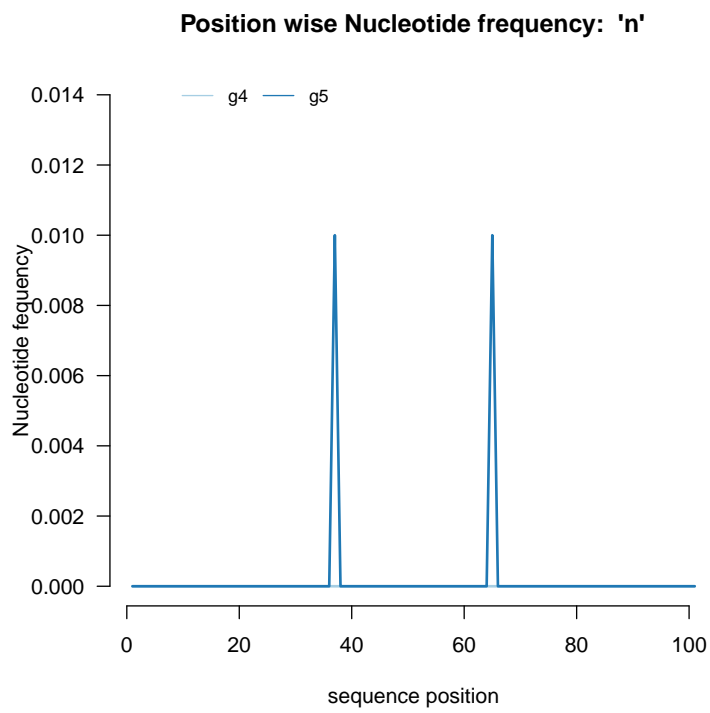
> dfr<-data.frame(file=basename(fileNames(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)

```

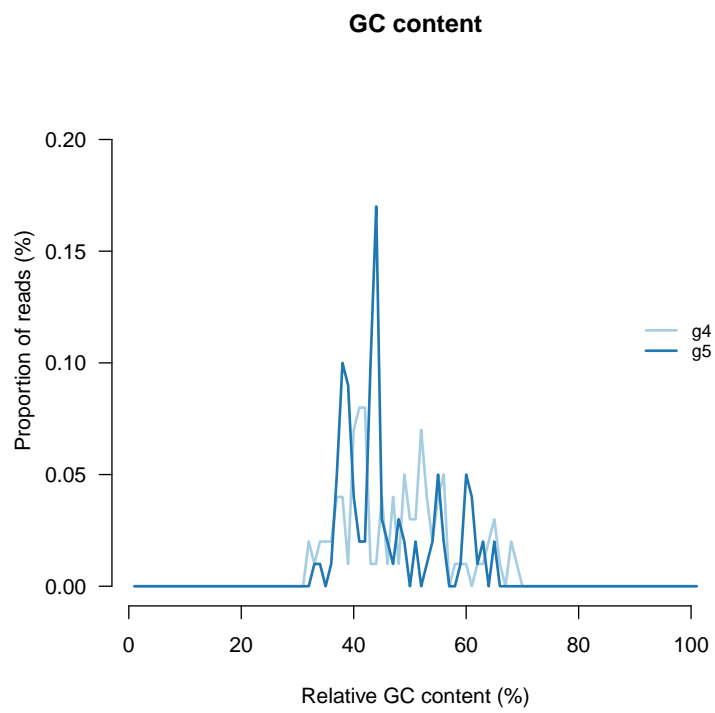
	file	sample	reads
1	g4_l101_n100.fq.gz	g4	100
2	g5_l101_n100.fq.gz	g5	100

3 Nucleotide patterns

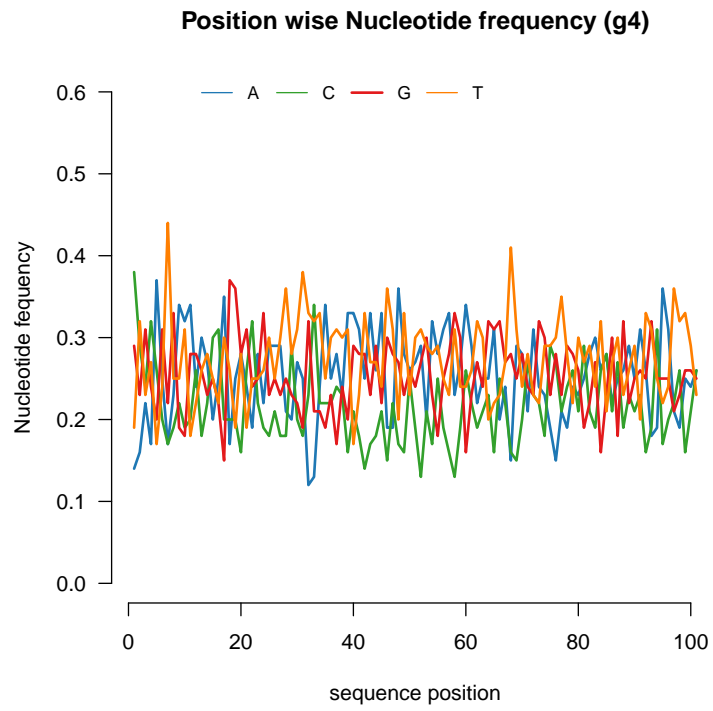
3.1 N nucleotides



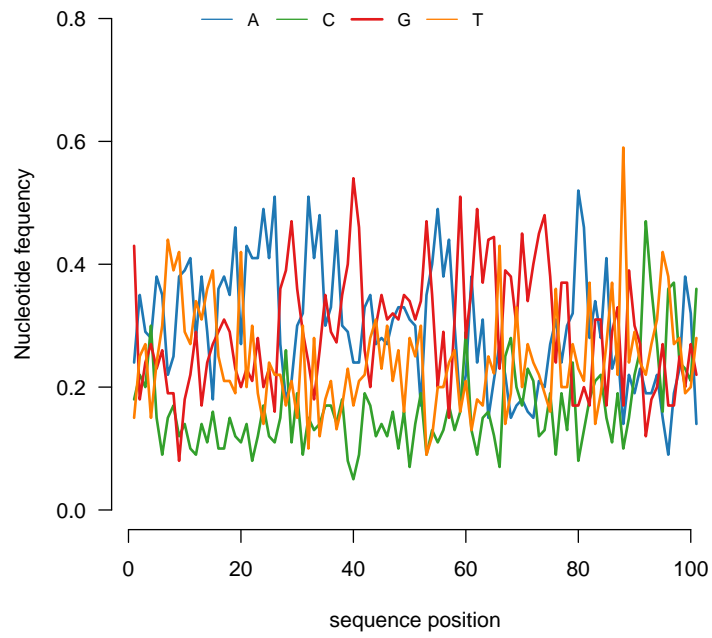
3.2 GC content



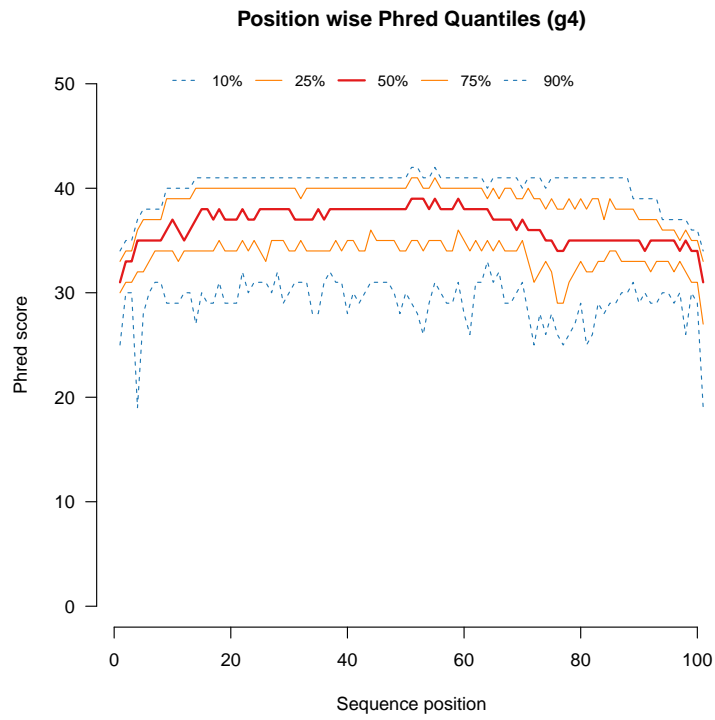
3.3 Nucleotide frequencies

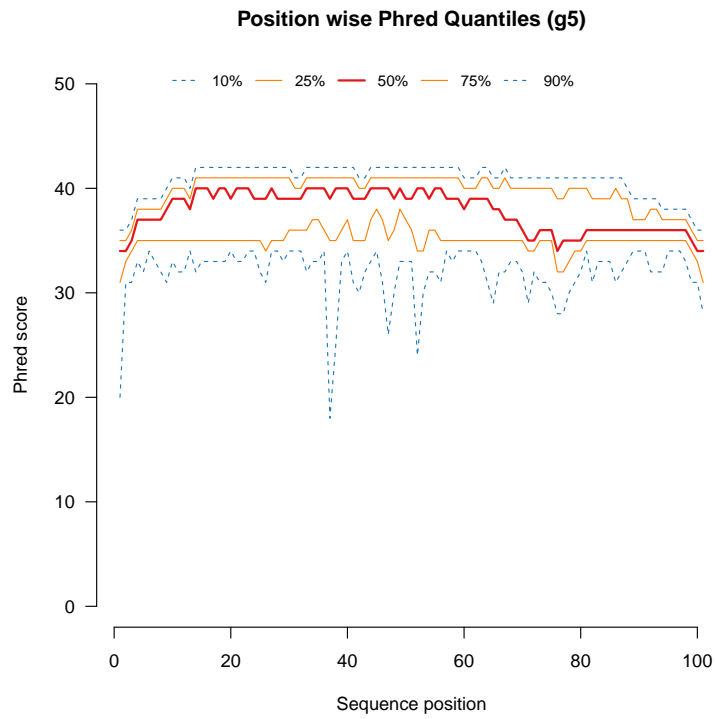


Position wise Nucleotide frequency (g5)



4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2

