

Fastq quality data.

Your Name here

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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) '/private/tmp/RtmpVSQPUM/Rinst177b9330a1d48/seqTools/extdata/g4  
[fastqq] File ( 2/2) '/private/tmp/RtmpVSQPUM/Rinst177b9330a1d48/seqTools/extdata/g5
```

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
```

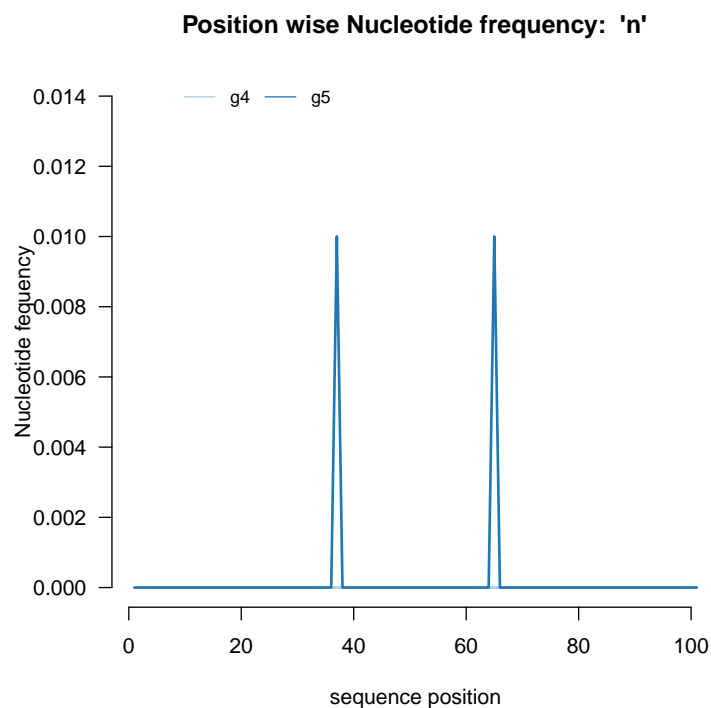
2.1 Project names and read numbers

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

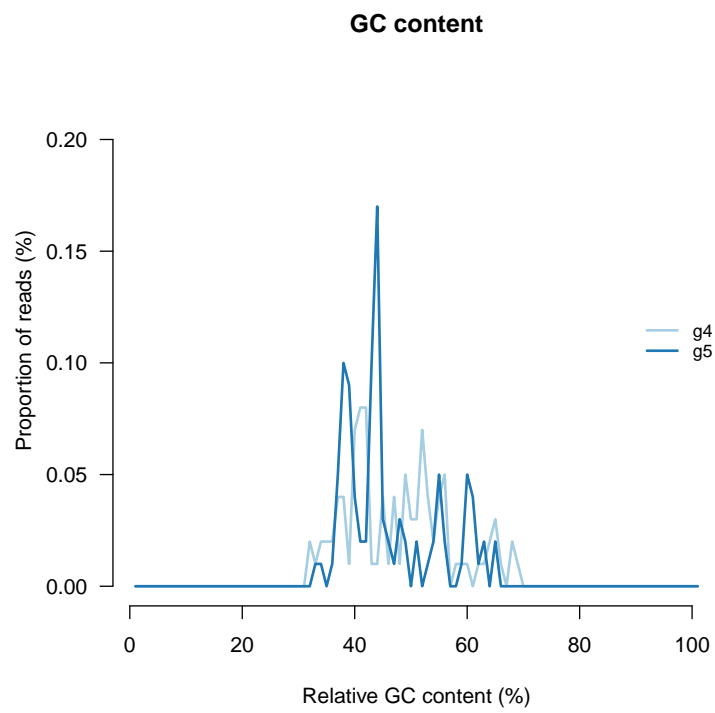
	file	sample	reads
1	g4_l101_n100.fq.gz	g4	100
2	g5_l101_n100.fq.gz	g5	100

3 Nucleotide patterns

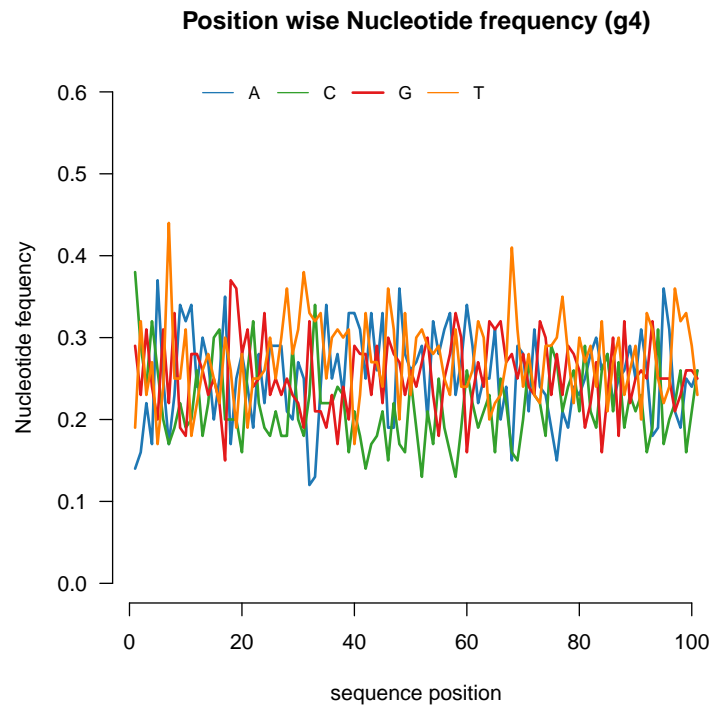
3.1 N nucleotides

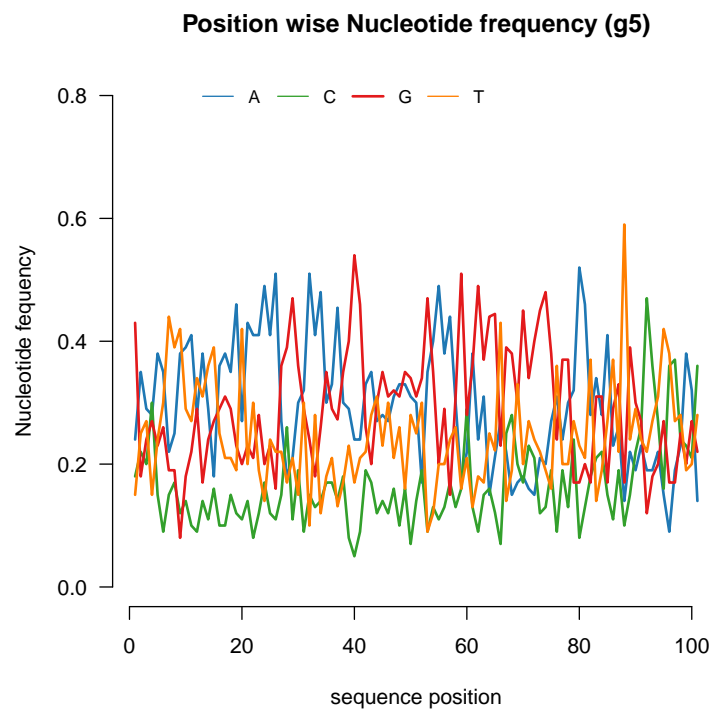


3.2 GC content

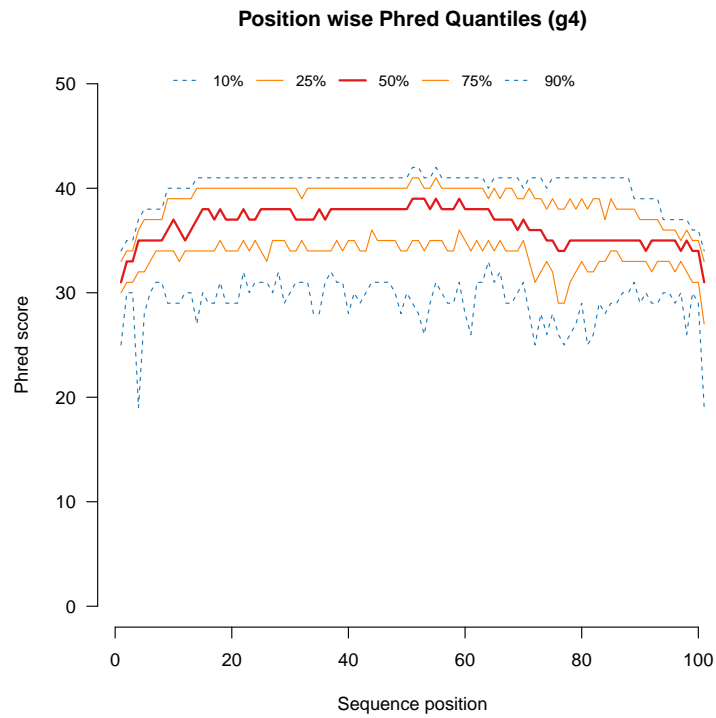


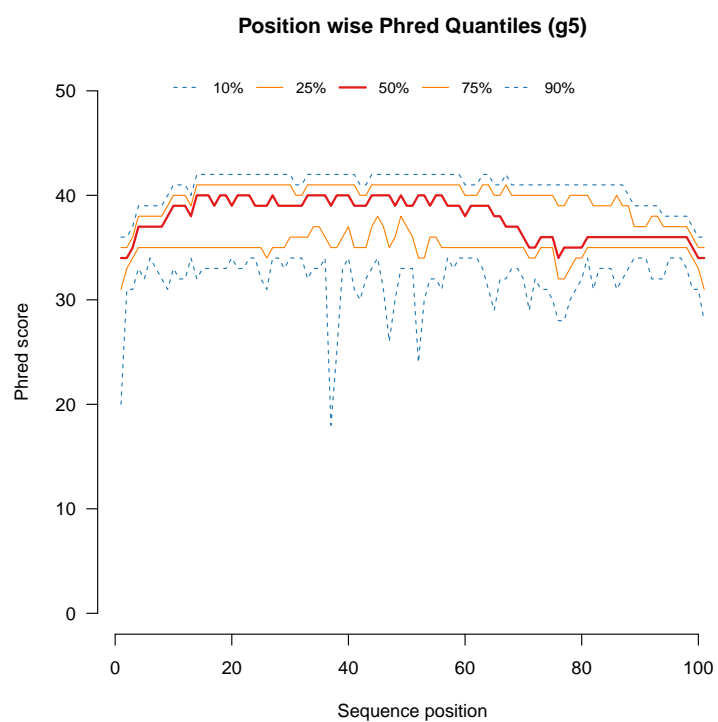
3.3 Nucleotide frequencies





4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2

