

Fastq quality data.

Your Name here

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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) '/home/biocbuild/bbs-3.20-bioc/tmpdir/Rtmp4b0YLr/Rinstdabdd63abc
```

```
[fastqq] File ( 2/2) '/home/biocbuild/bbs-3.20-bioc/tmpdir/Rtmp4b0YLr/Rinstdabdd63abc
```

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)

```

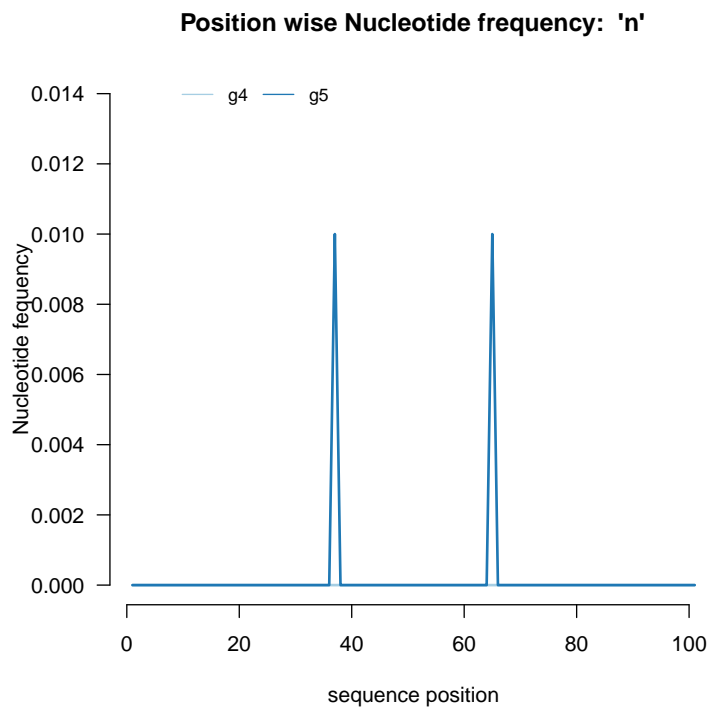
```

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

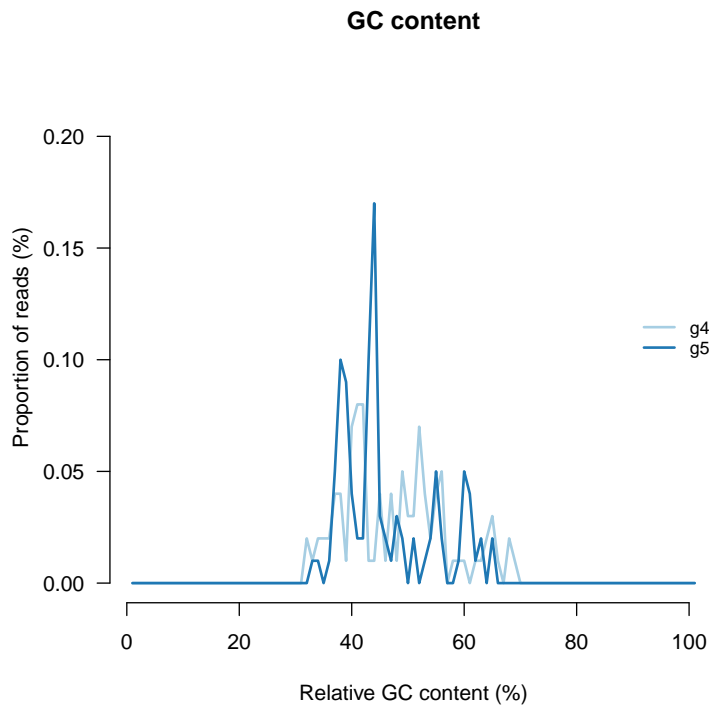
```

3 Nucleotide patterns

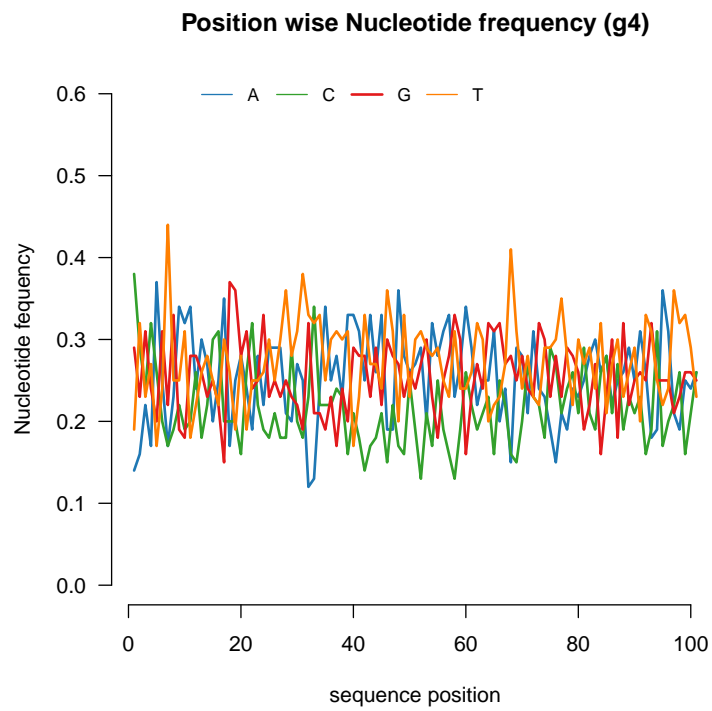
3.1 N nucleotides



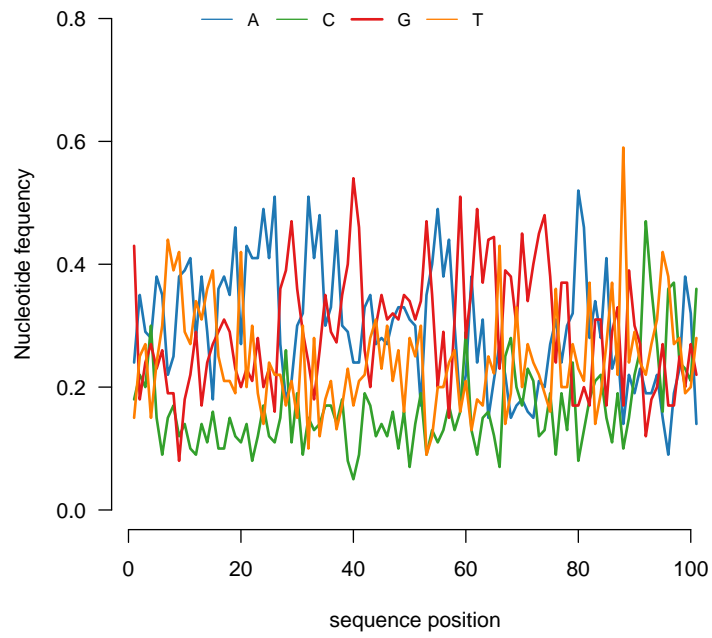
3.2 GC content



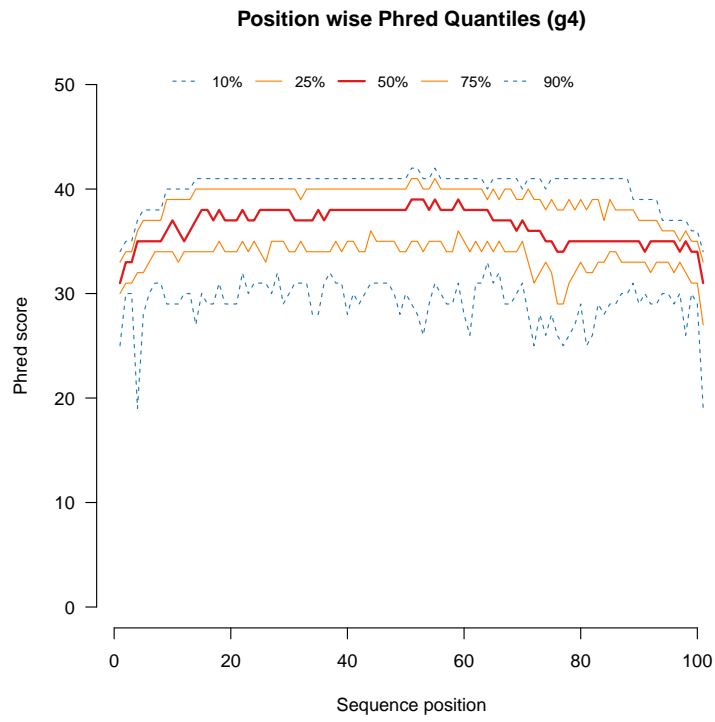
3.3 Nucleotide frequencies

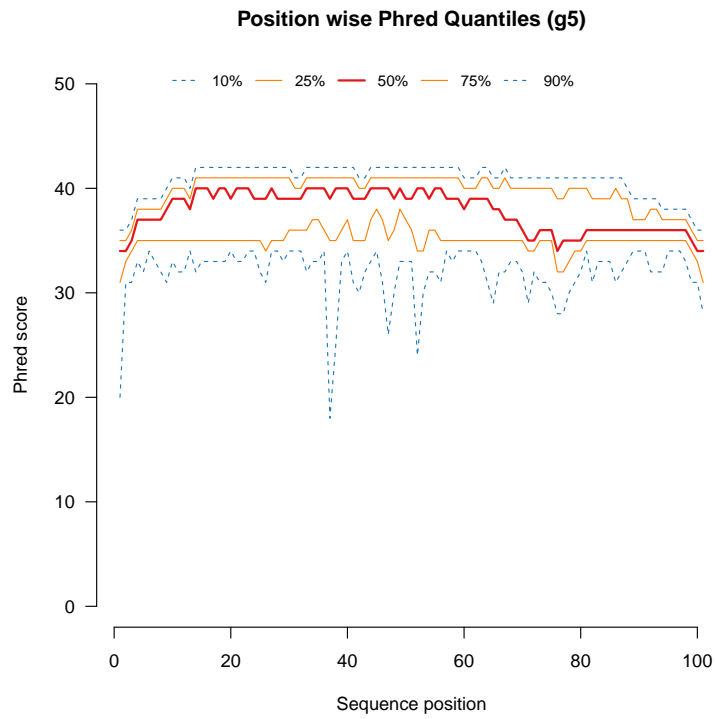


Position wise Nucleotide frequency (g5)



4 Phred qualities





5 Hierarchical clustering

1_g4	1
2_g5	2

