

# Fastq quality data.

Your Name here

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## 1 Project characteristics

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Project characteristics
Contact
Phone
Institute
Mail
Start date

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## 2 Global summaries

Input data: Summarized data on FASTQ files.

```
[fastqq] File ( 1/2) 'F:/biocbuild/bbs-3.20-bioc/tmpdir/Rtmpm2joJx/Rinstd0a4594e12e3/'
[fastqq] File ( 2/2) 'F:/biocbuild/bbs-3.20-bioc/tmpdir/Rtmpm2joJx/Rinstd0a4594e12e3/'
```

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

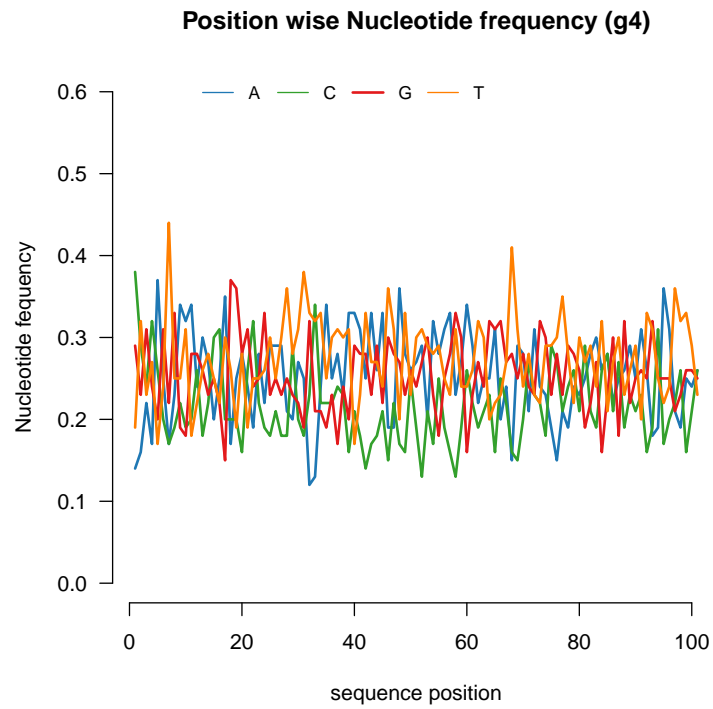
### 3.1 N nucleotides



### 3.2 GC content



### 3.3 Nucleotide frequencies





## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



