

# Fastq quality data.

Your Name here

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## Contents

<b>1</b>	<b>Project characteristics</b>	<b>1</b>
<b>2</b>	<b>Global summaries</b>	<b>1</b>
2.1	Project names and read numbers . . . . .	2
<b>3</b>	<b>Nucleotide patterns</b>	<b>2</b>
3.1	N nucleotides . . . . .	3
3.2	GC content . . . . .	4
3.3	Nucleotide frequencies . . . . .	5
<b>4</b>	<b>Phred qualities</b>	<b>7</b>
<b>5</b>	<b>Hierarchical clustering</b>	<b>8</b>

## 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) '/private/var/folders/db/4tvngx8jx4z3fm1gzlnlzw9rc0000gq/T/RtmpD
```

```
[fastqq] File ( 2/2) '/private/var/folders/db/4tvngx8jx4z3fm1gzlnlzw9rc0000gq/T/RtmpD
```

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

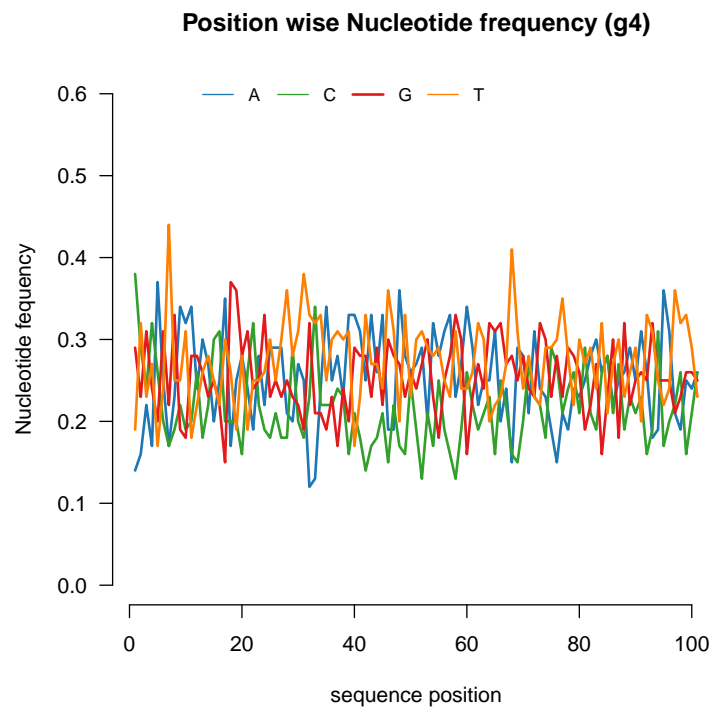
### 3.1 N nucleotides



## 3.2 GC content



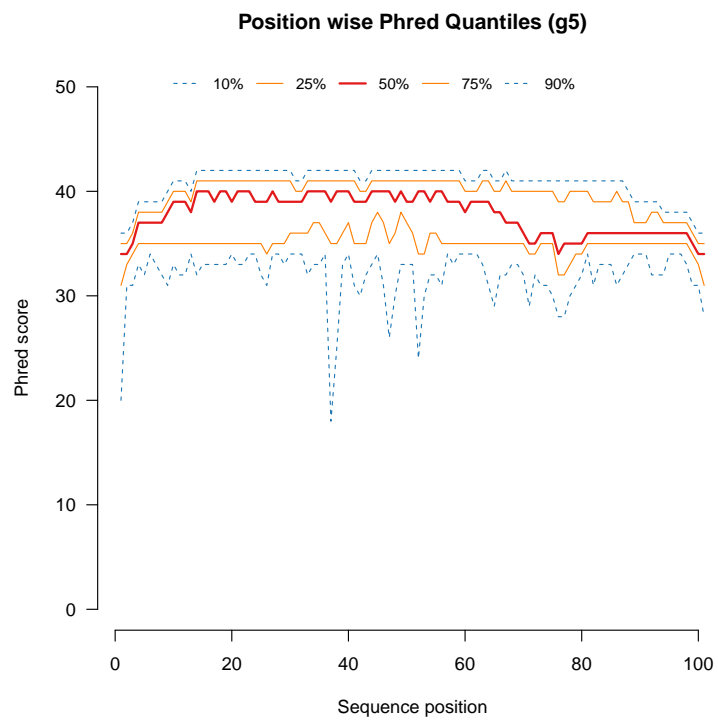
### 3.3 Nucleotide frequencies





## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



