

# Fastq quality data.

Your Name here

April 16, 2015

## Contents

<b>1 Project characteristics</b>	<b>1</b>
<b>2 Global summaries</b>	<b>1</b>
2.1 Project names and read numbers . . . . .	2
<b>3 Nucleotide patterns</b>	<b>2</b>
3.1 N nucleotides . . . . .	3
3.2 GC content . . . . .	4
3.3 Nucleotide frequencies . . . . .	4
<b>4 Phred qualities</b>	<b>7</b>
<b>5 Hierarchical clustering</b>	<b>10</b>

## 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/Rtmp040jGJ/Rinst268d250ef438/seqTools/extdata/g4_1101_n10
[fastqq] File ( 2/2) '/tmp/Rtmp040jGJ/Rinst268d250ef438/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

```

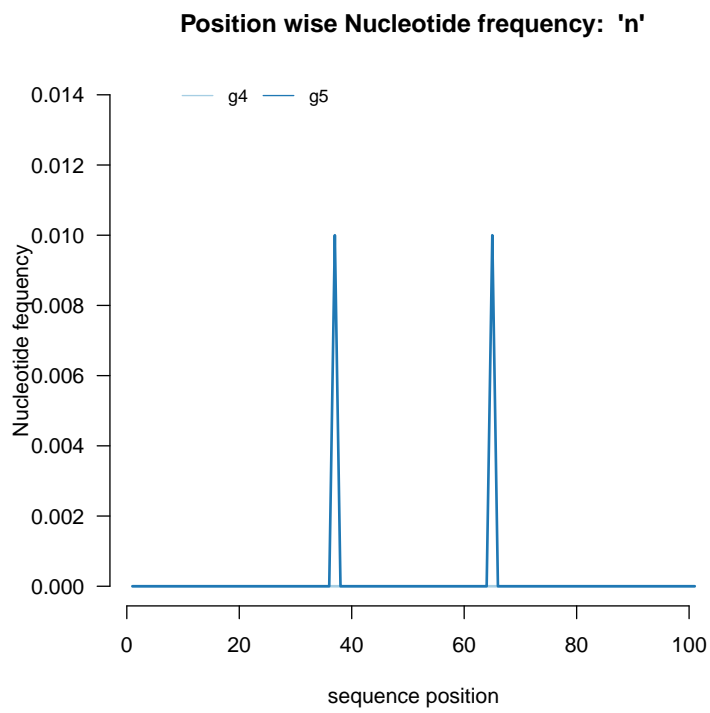
> dfr<-data.frame(file=basename(fileNames(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)

```

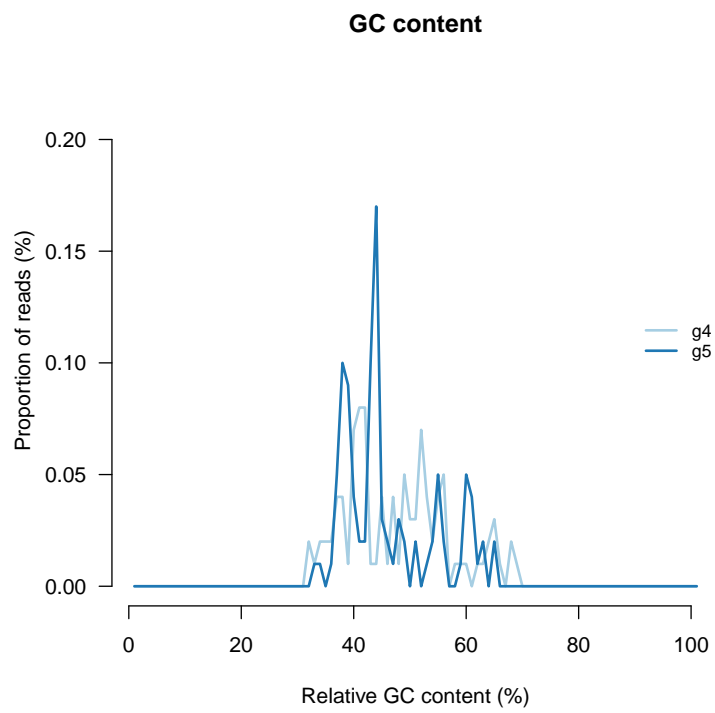
	file	sample	reads
1	g4_l101_n100.fq.gz	g4	100
2	g5_l101_n100.fq.gz	g5	100

## 3 Nucleotide patterns

### 3.1 N nucleotides

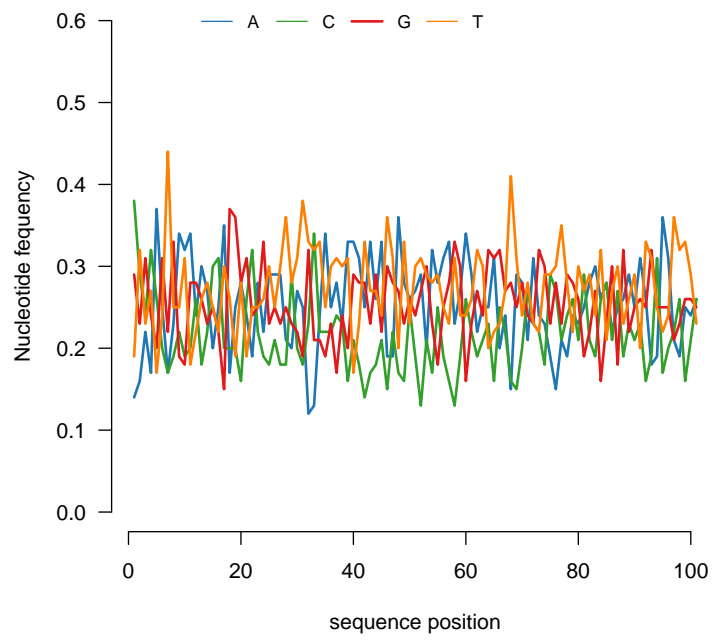


### 3.2 GC content

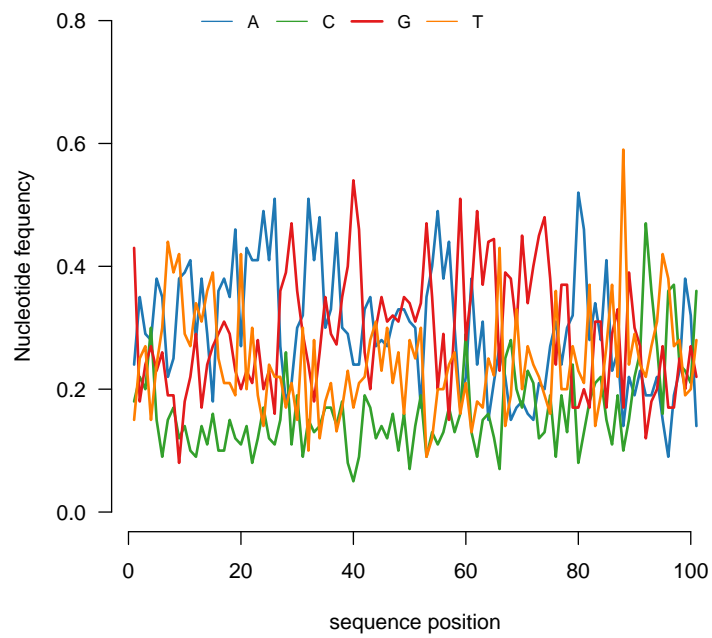


### 3.3 Nucleotide frequencies

**Position wise Nucleotide frequency (g4)**

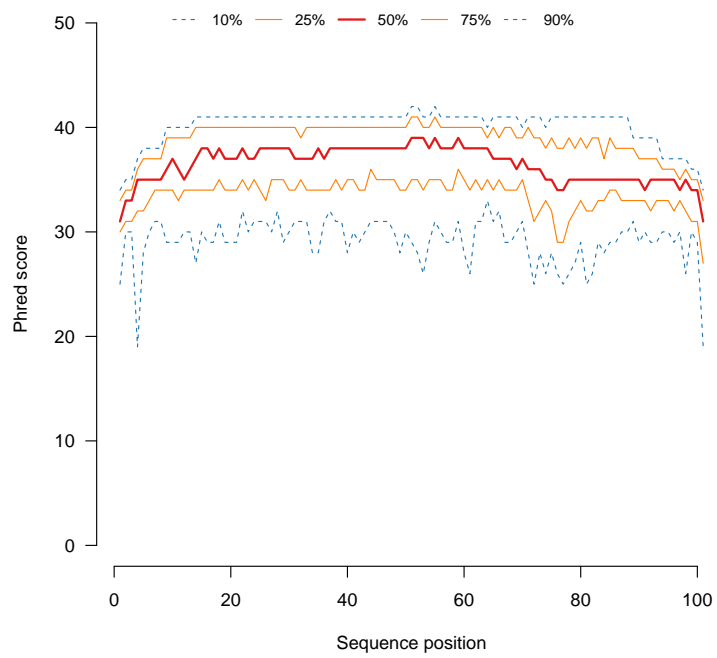


**Position wise Nucleotide frequency (g5)**

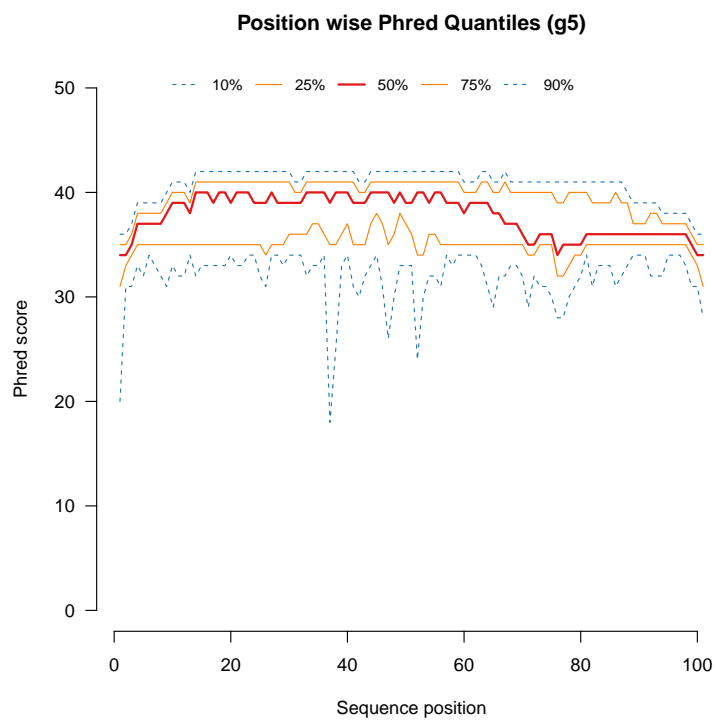


## 4 Phred qualities

**Position wise Phred Quantiles (g4)**







## 5 Hierarchical clustering

1_g4	1
2_g5	2

