

# Fastq quality data.

Your Name here

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## 1 Project characteristics

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Project characteristics

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Contact  
Phone  
Institute  
Mail  
Start date

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## 2 Global summaries

Input data: Summarized data on FASTQ files.

```
[fastqq] File ( 1/2) '/tmp/Rtmp0J5dDp/Rinst2f6a45cbaa25/seqTools/extdata/g4_1101_n10  
[fastqq] File ( 2/2) '/tmp/Rtmp0J5dDp/Rinst2f6a45cbaa25/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

```

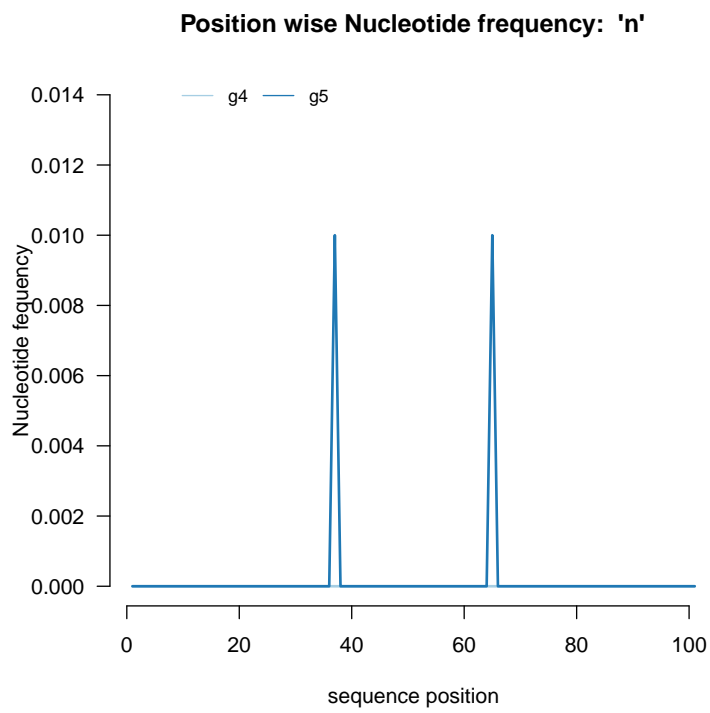
> dfr<-data.frame(file=basename(fileNames(fqq)),
+                 sample=probeLabel(fqq),
+                 reads=format(nReads(fqq), big.mark=Sys.localeconv()[7]))
> print(dfr)

```

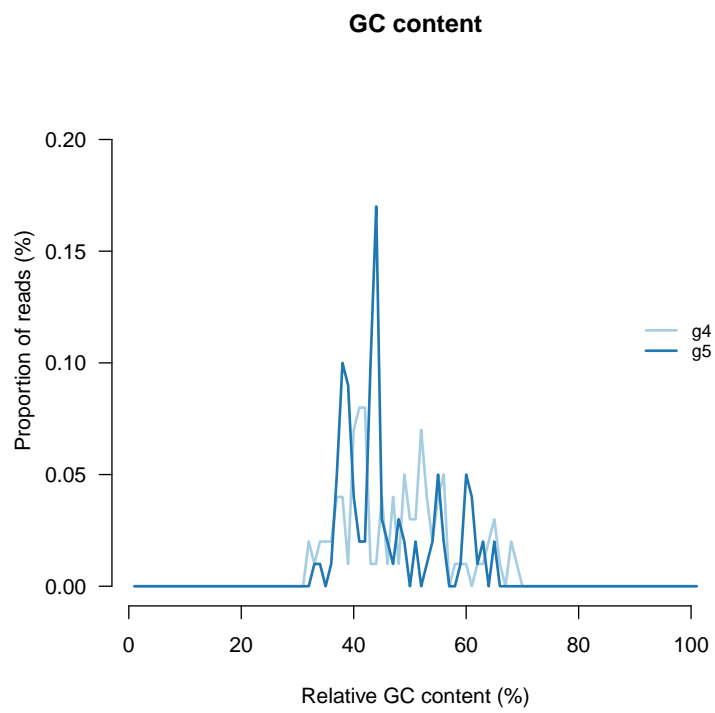
	file	sample	reads
1	g4_l101_n100.fq.gz	g4	100
2	g5_l101_n100.fq.gz	g5	100

## 3 Nucleotide patterns

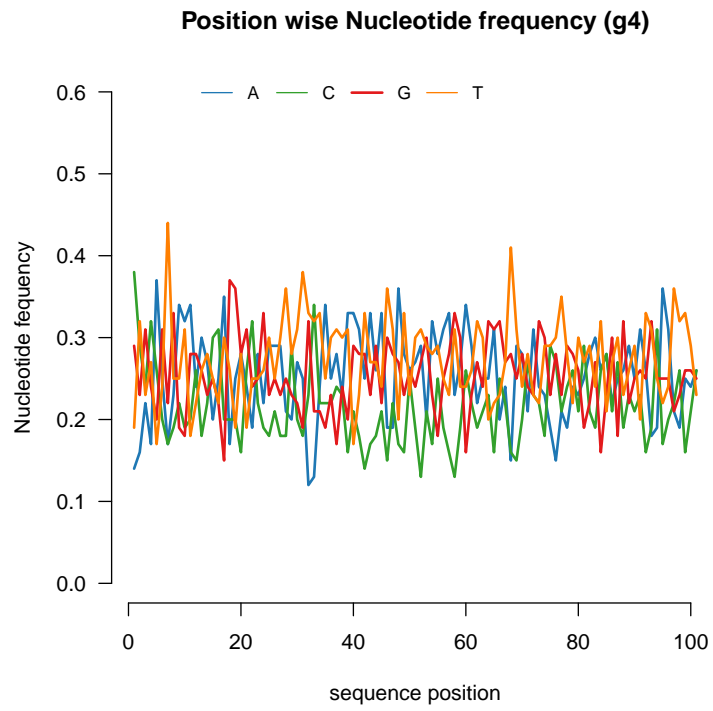
### 3.1 N nucleotides



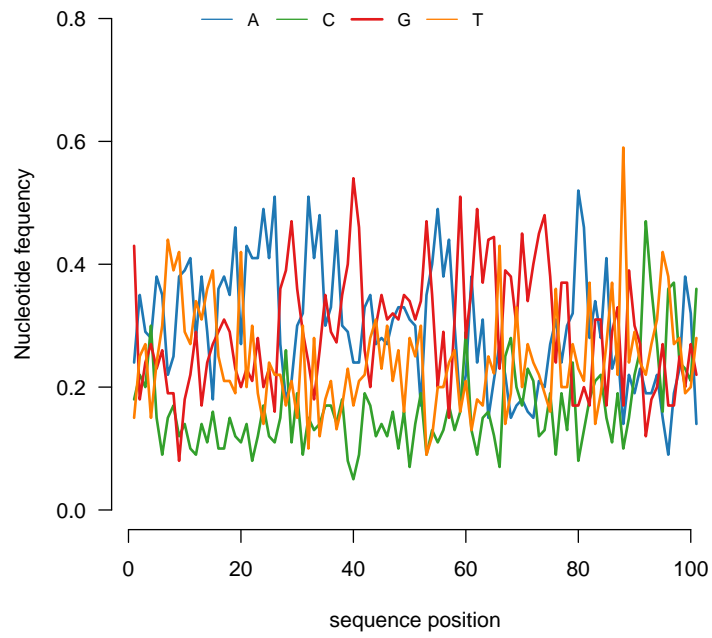
### 3.2 GC content



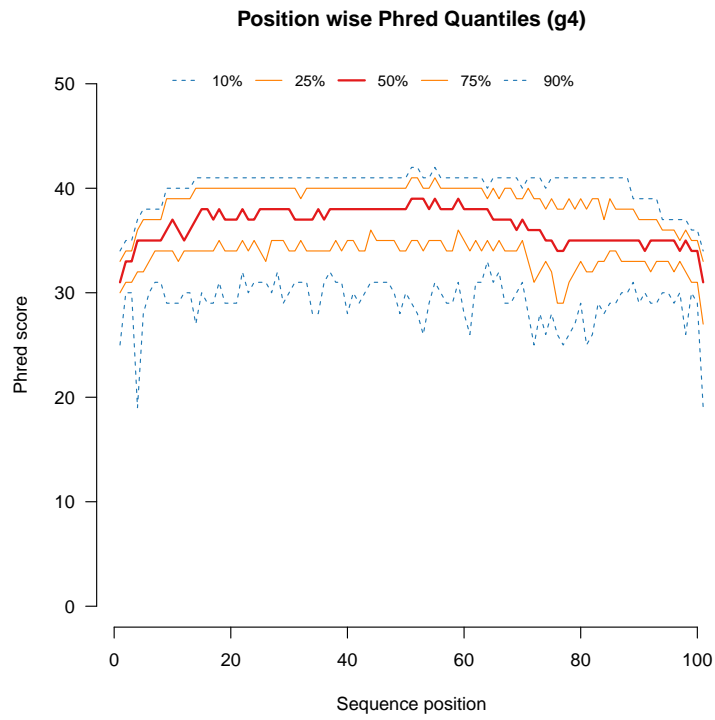
### 3.3 Nucleotide frequencies

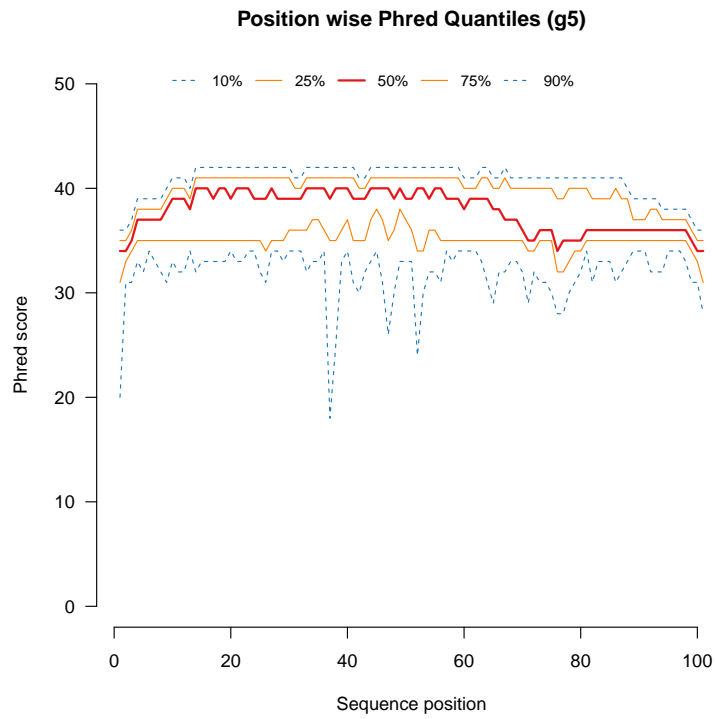


### Position wise Nucleotide frequency (g5)



## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



