

# Fastq quality data.

Your Name here

April 15, 2025

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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) '/tmp/RtmpXCn2jI/Rinst27af394cf55710/seqTools/extdata/g4_1101_n1
```

```
[fastqq] File ( 2/2) '/tmp/RtmpXCn2jI/Rinst27af394cf55710/seqTools/extdata/g5_1101_n1
```

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
```

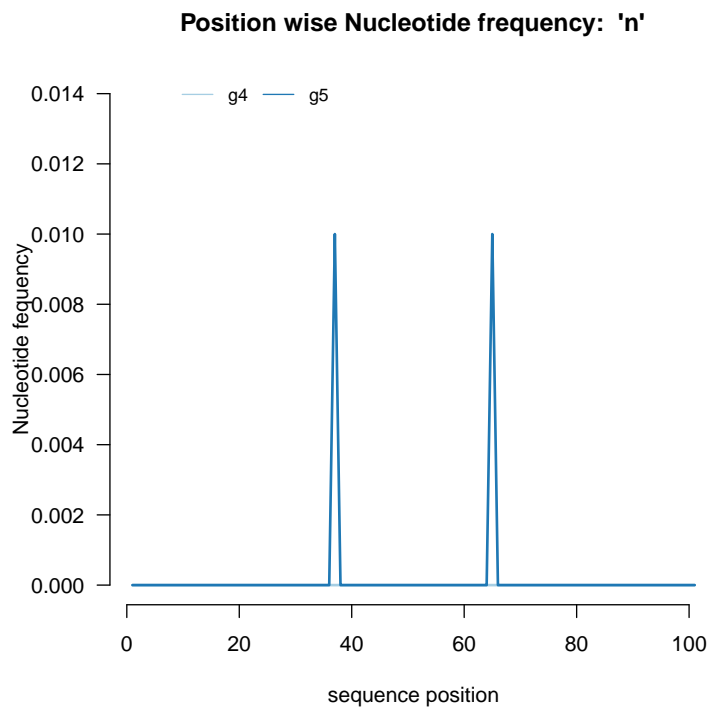
## 2.1 Project names and read numbers

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

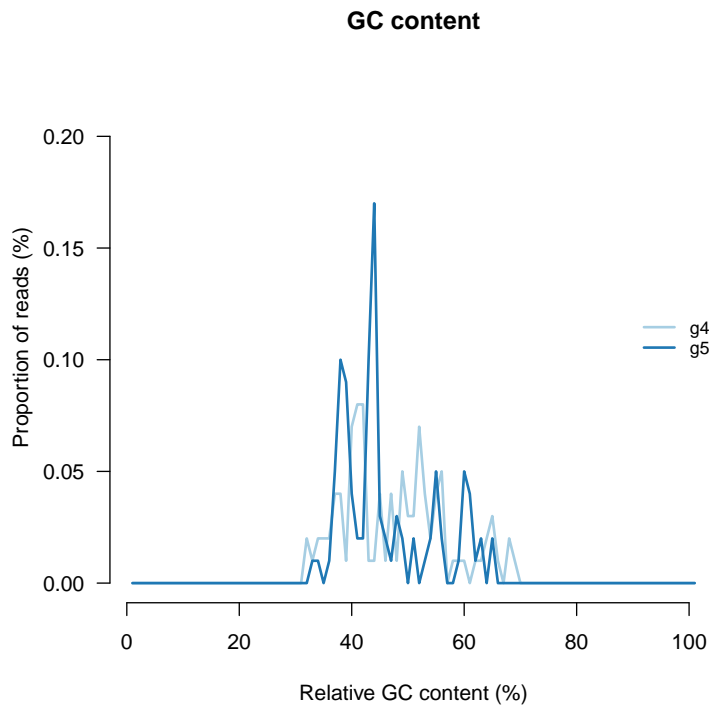
```
      file sample reads
1 g4_l101_n100.fq.gz   g4  100
2 g5_l101_n100.fq.gz   g5  100
```

## 3 Nucleotide patterns

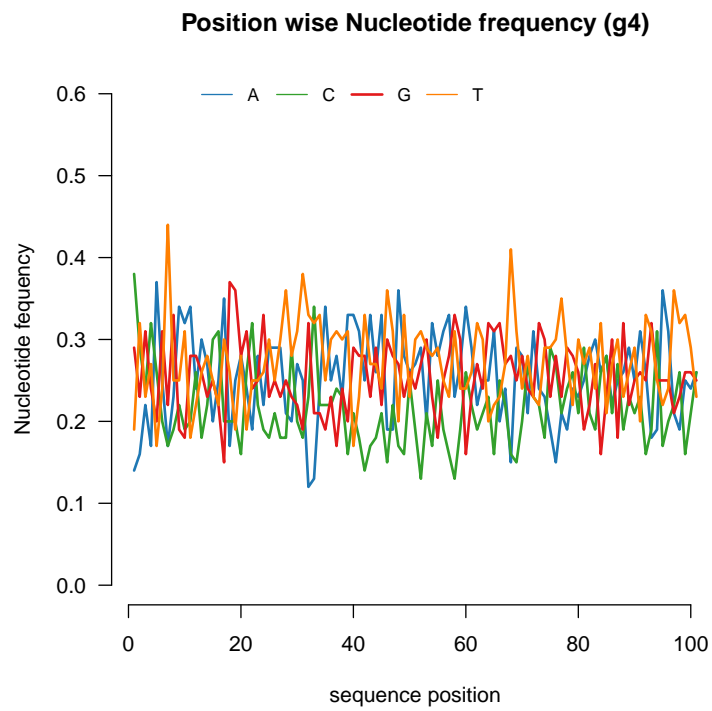
### 3.1 N nucleotides



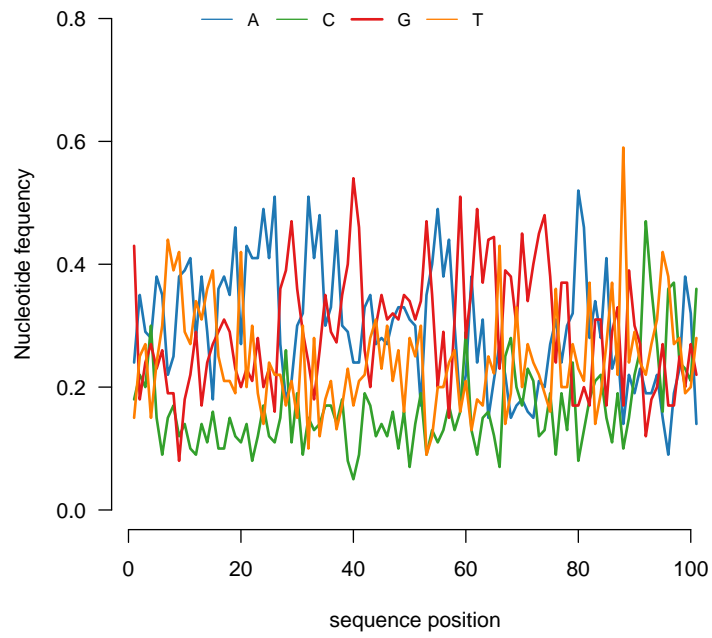
### 3.2 GC content



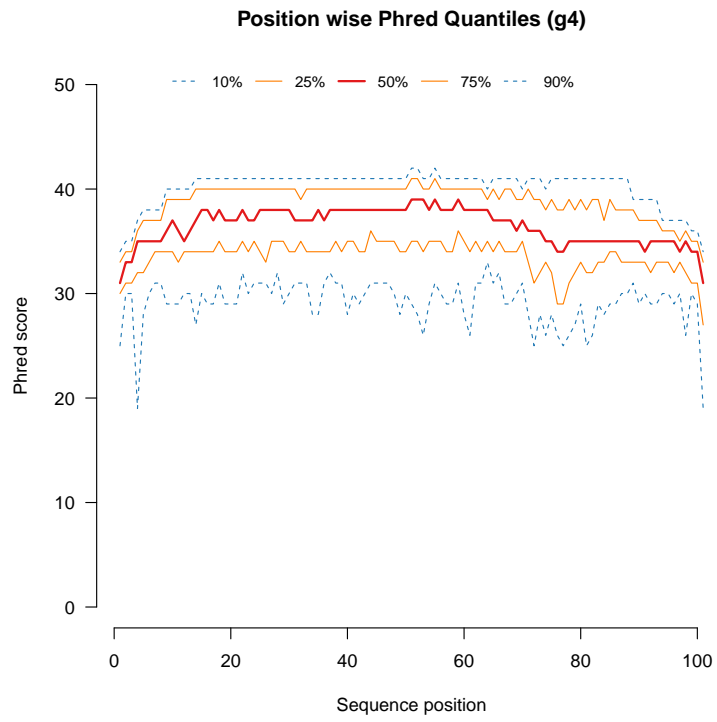
### 3.3 Nucleotide frequencies

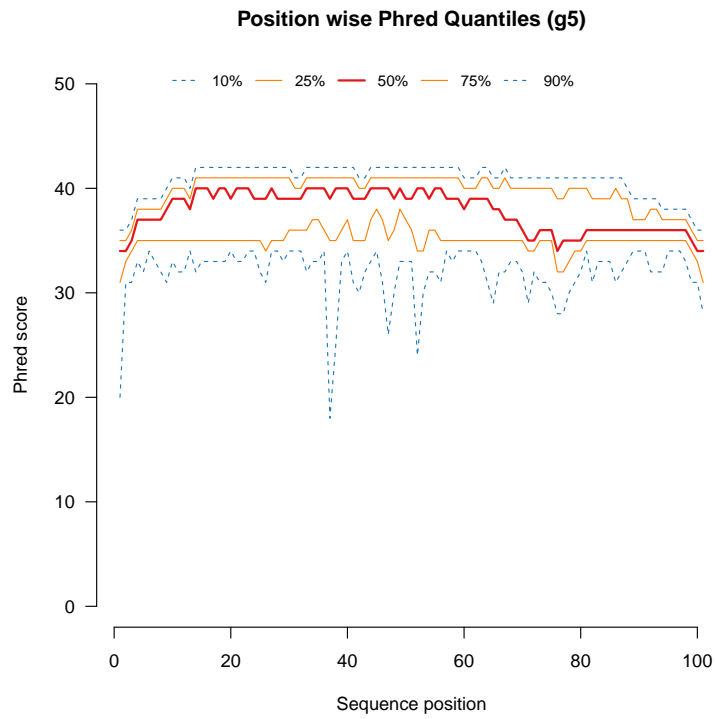


### Position wise Nucleotide frequency (g5)



## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



