

# 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) '/tmp/RtmpcQNbMB/Rinst43bb1b11ca81/seqTools/extdata/g4_1101_n10
```

```
[fastqq] File ( 2/2) '/tmp/RtmpcQNbMB/Rinst43bb1b11ca81/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
```

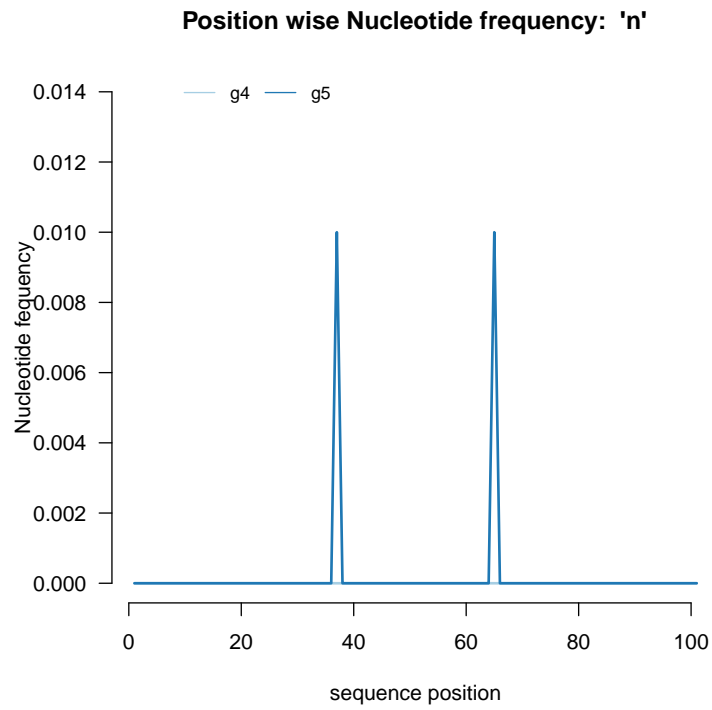
## 2.1 Project names and read numbers

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

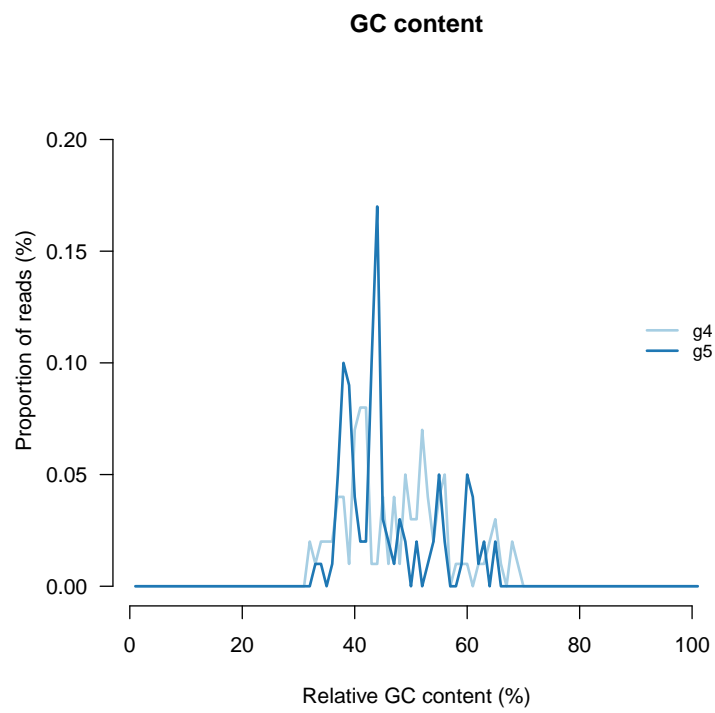
```
      file sample reads
1 g4_l101_n100.fq.gz    g4   100
2 g5_l101_n100.fq.gz    g5   100
```

## 3 Nucleotide patterns

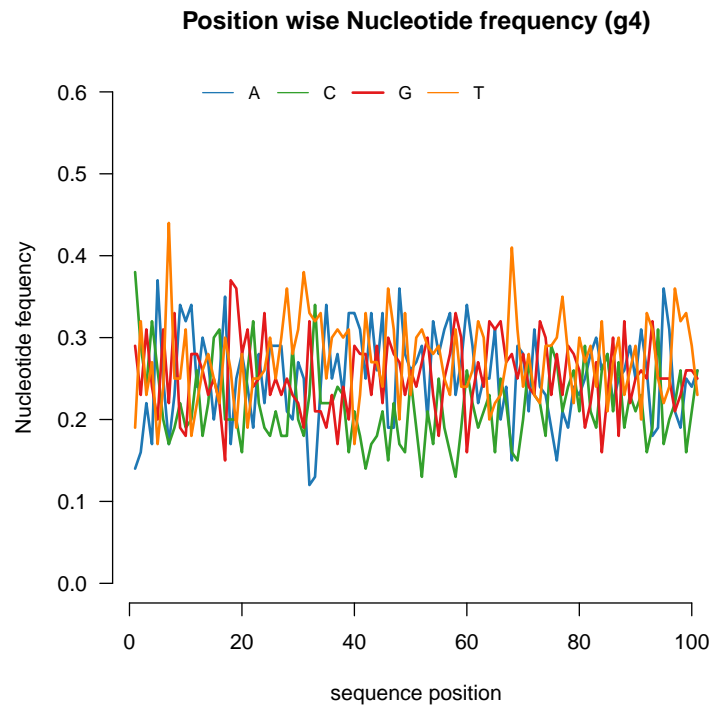
### 3.1 N nucleotides

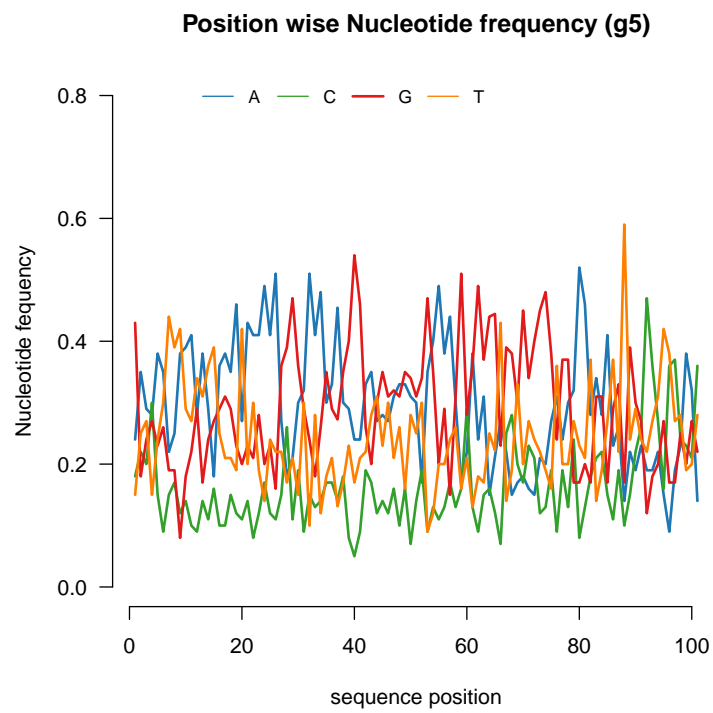


## 3.2 GC content

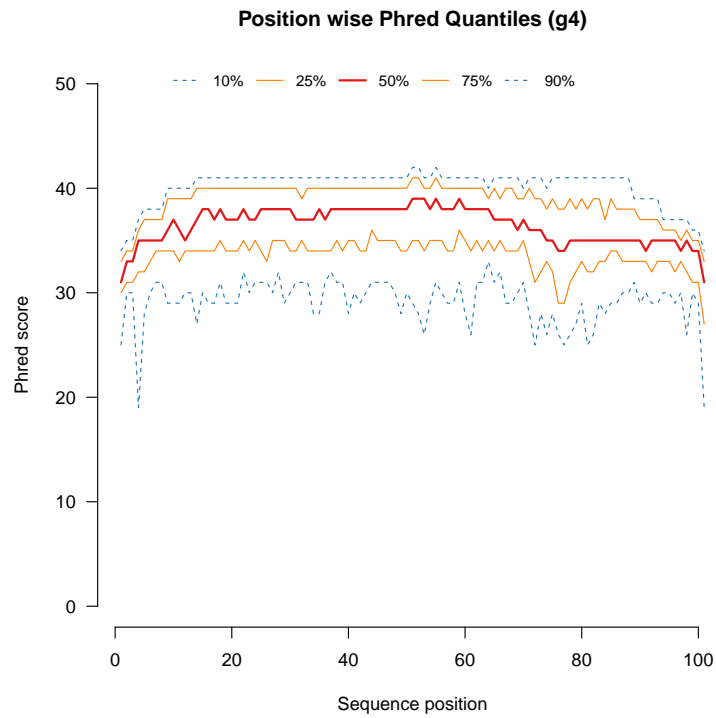


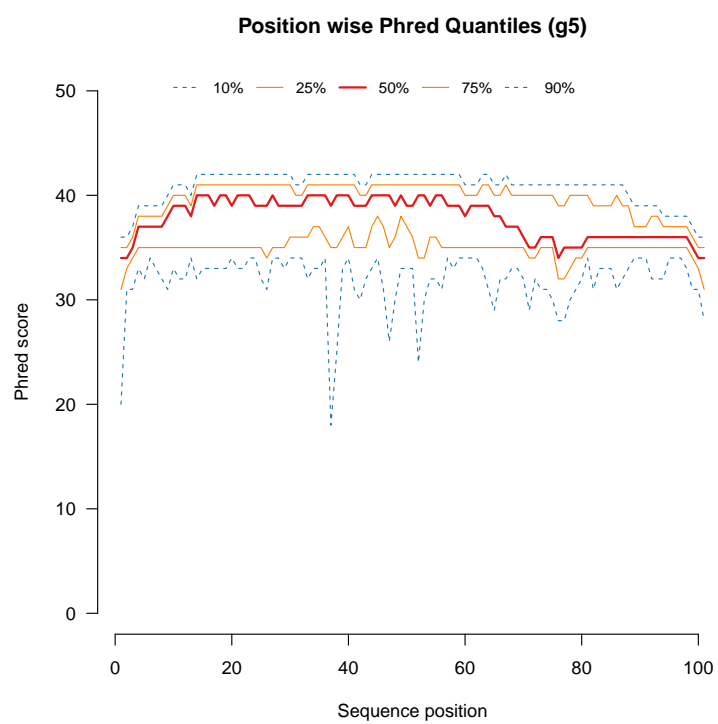
### 3.3 Nucleotide frequencies





## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



