

# Fastq quality data.

Your Name here

April 16, 2015

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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) '/private/tmp/RtmpbcYQyH/Rinst869252731c12/seqTools/extdata/g4_1.fastq'
[fastqq] File ( 2/2) '/private/tmp/RtmpbcYQyH/Rinst869252731c12/seqTools/extdata/g5_1.fastq'
```

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
```

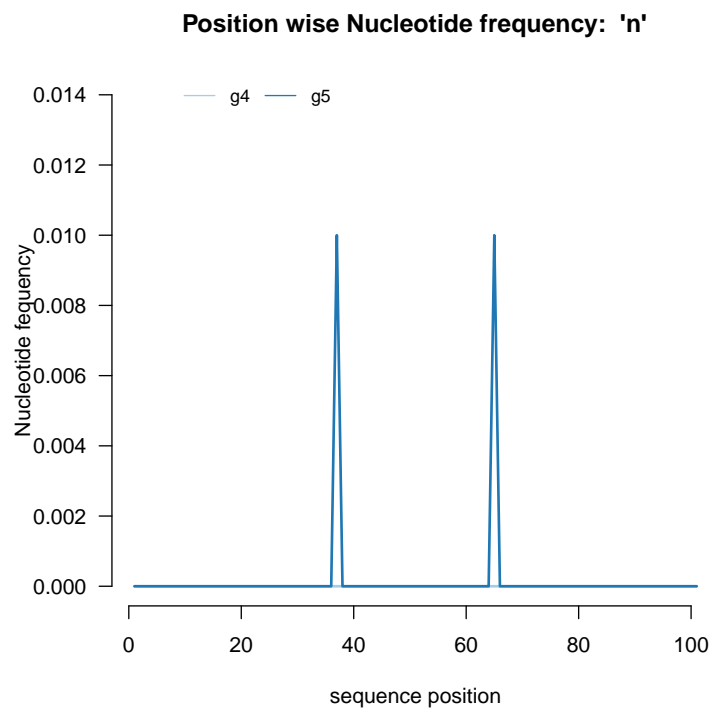
## 2.1 Project names and read numbers

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

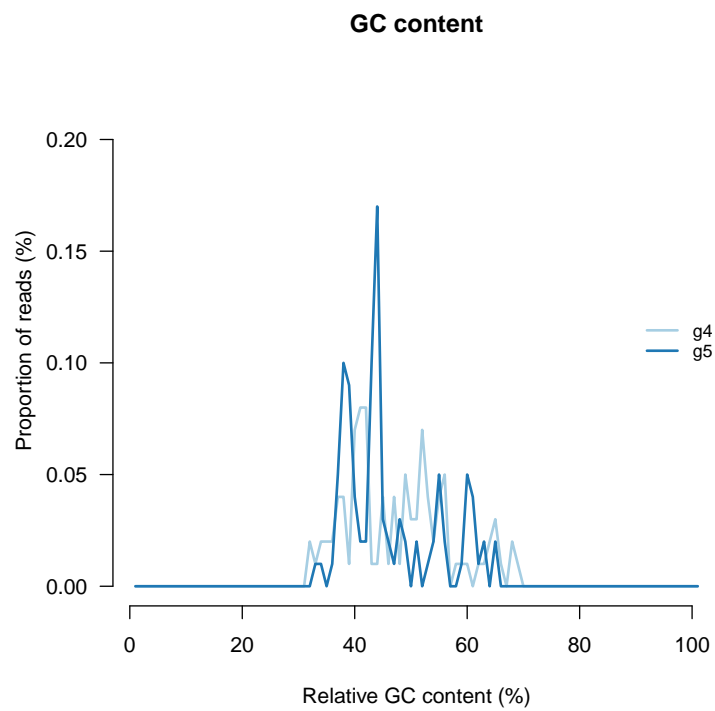
```
      file sample reads
1 g4_l101_n100.fq.gz    g4   100
2 g5_l101_n100.fq.gz    g5   100
```

## 3 Nucleotide patterns

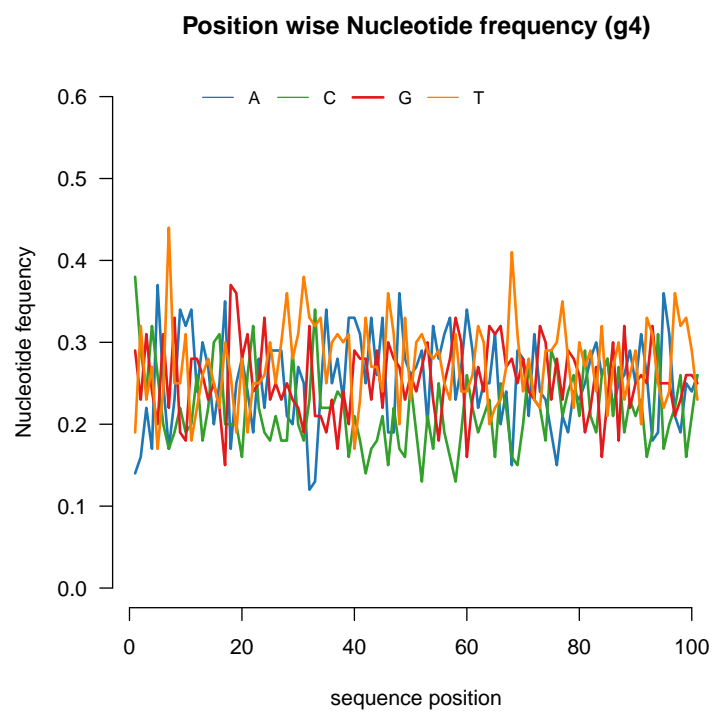
### 3.1 N nucleotides

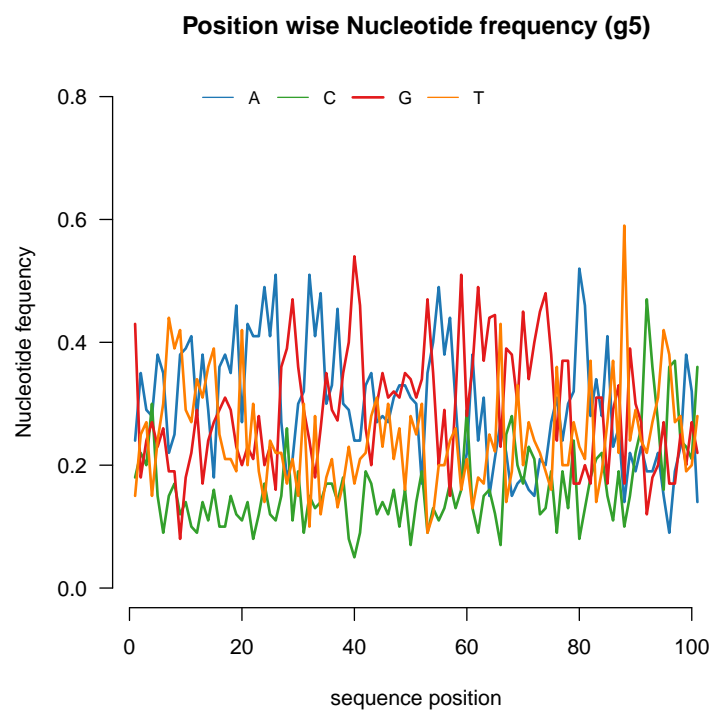


### 3.2 GC content

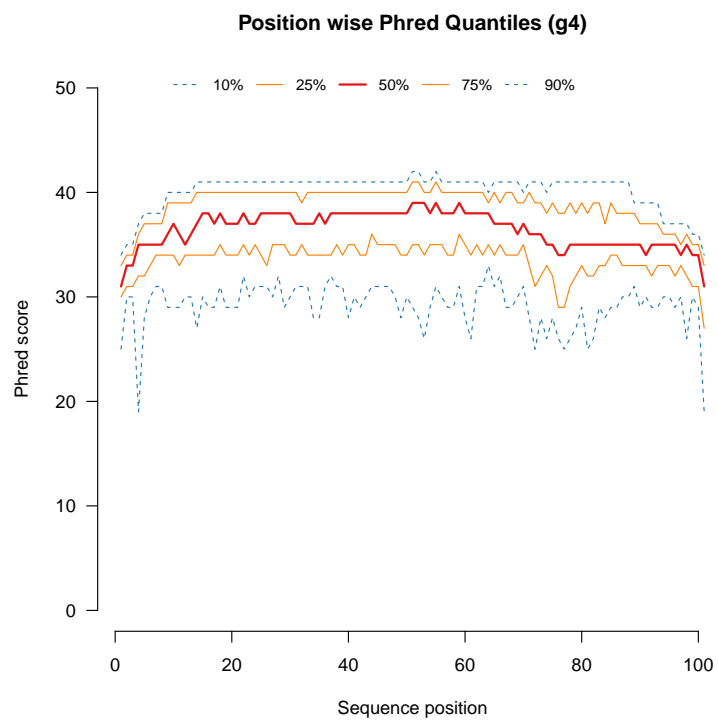


### 3.3 Nucleotide frequencies

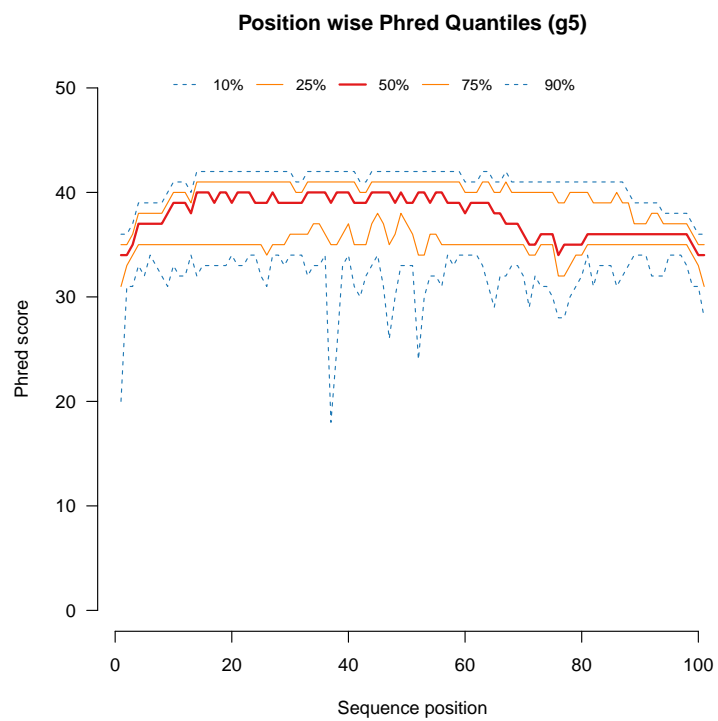




## 4 Phred qualities







## 5 Hierarchical clustering

1_g4	1
2_g5	2

