

# 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) '/private/tmp/RtmpzdM0eD/Rinst25faeb6d0ce/seqTools/extdata/g4_11
```

```
[fastqq] File ( 2/2) '/private/tmp/RtmpzdM0eD/Rinst25faeb6d0ce/seqTools/extdata/g5_11
```

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

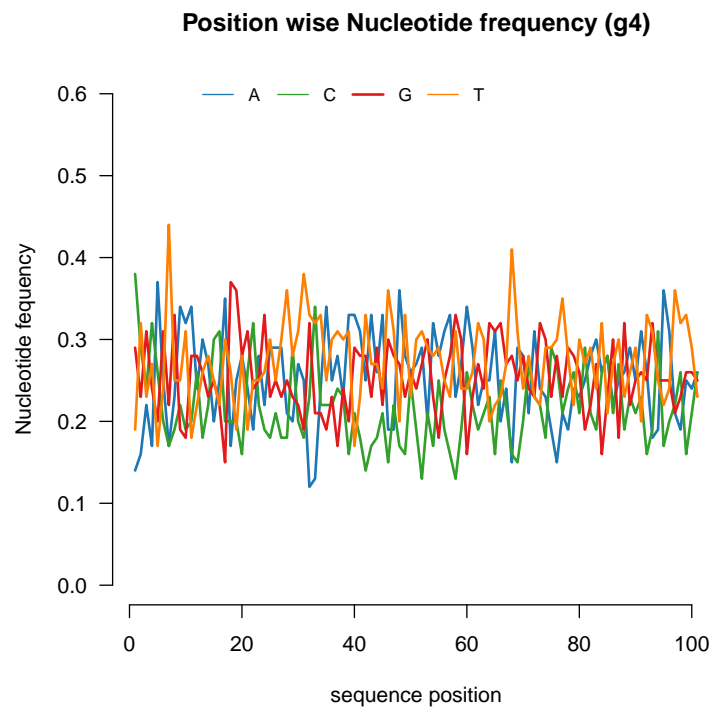
### 3.1 N nucleotides



### 3.2 GC content



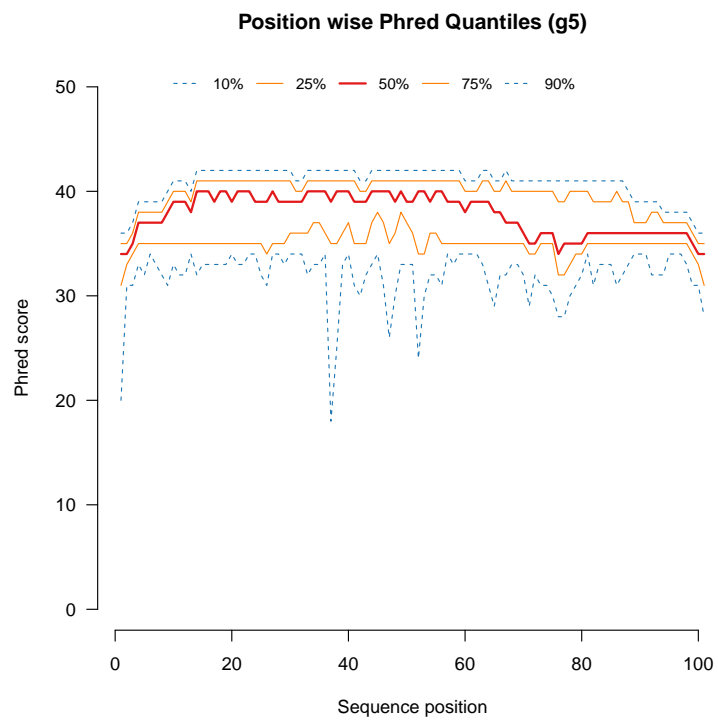
### 3.3 Nucleotide frequencies





## 4 Phred qualities





## 5 Hierarchical clustering

1_g4	1
2_g5	2



