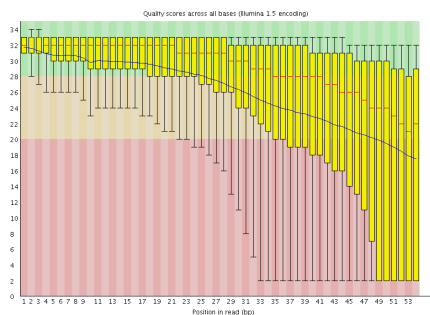
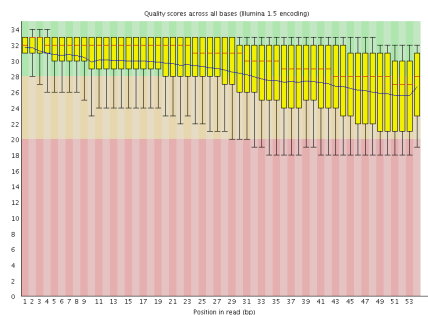


# 1 Base Quality Graph

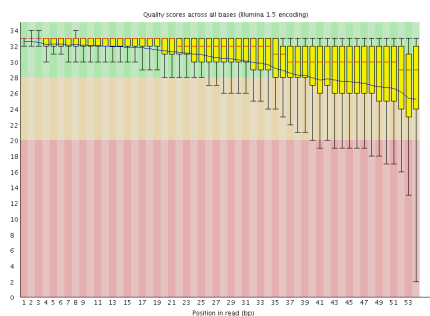
*This graph shows an overview of the range of quality values across all bases at each position in the FastQ file.*



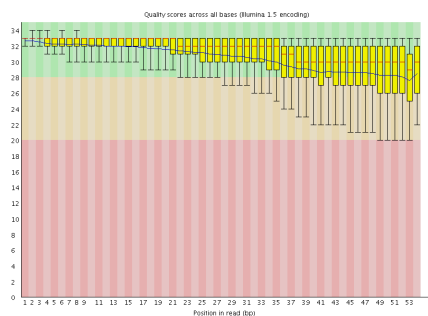
(a) Pre F0002



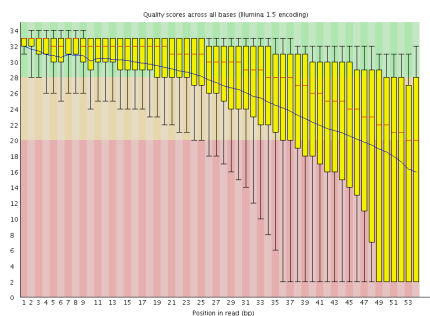
(b) Post F0002



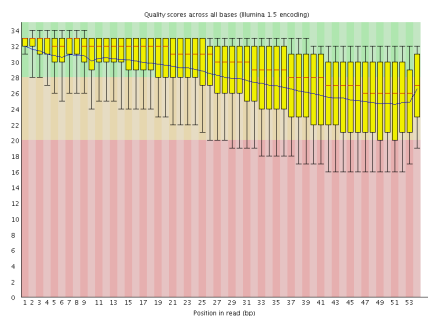
(a) Pre F135



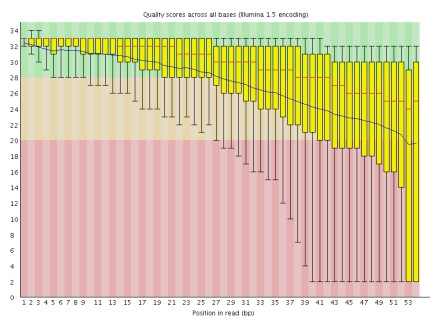
(b) Post F135



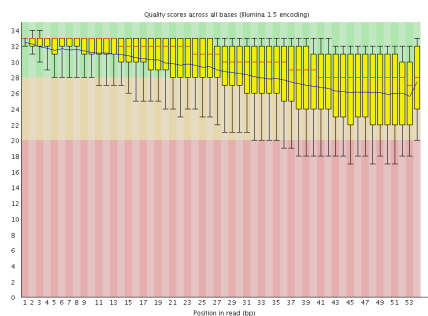
(a) Pre F195



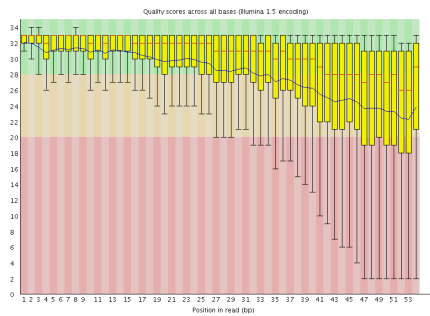
(b) Post F195



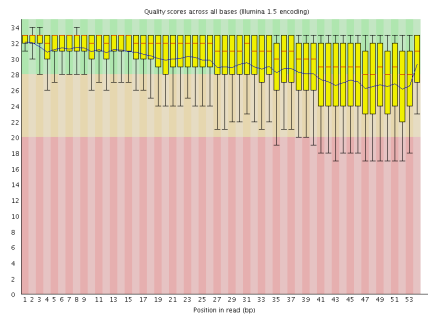
(a) Pre F210



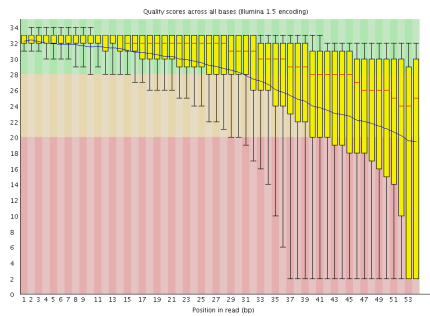
(b) Post F210



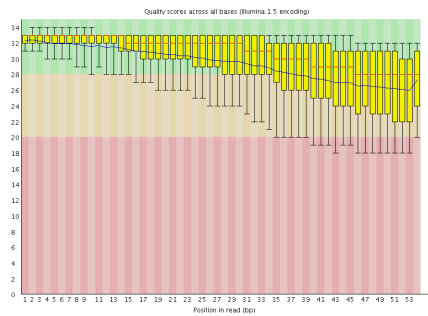
(a) Pre F280



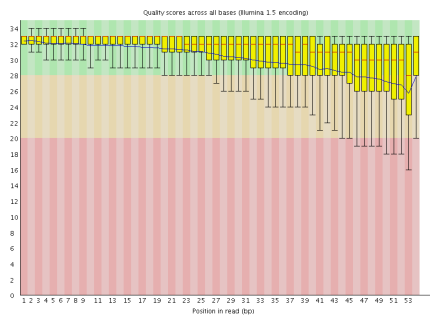
(b) Post F280



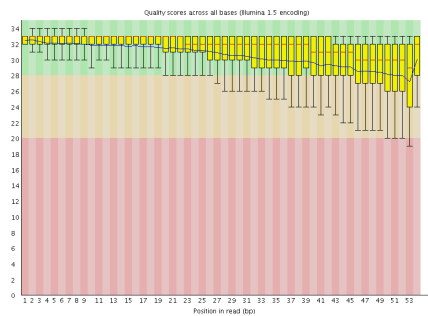
(a) Pre F419



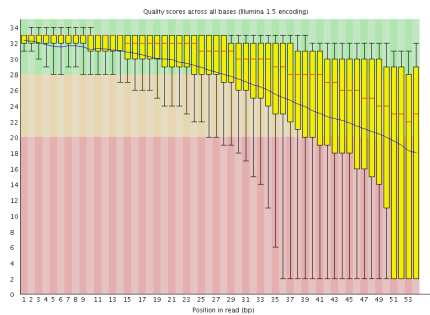
(b) Post F419



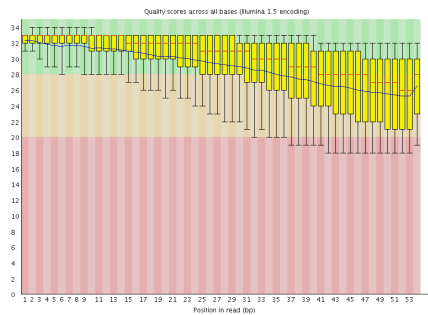
(a) Pre F468



(b) Post F468



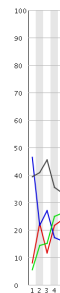
(a) Pre F506

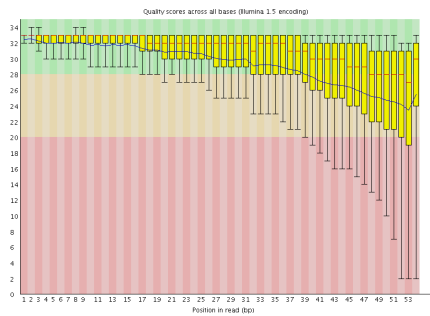


(b) Post F506

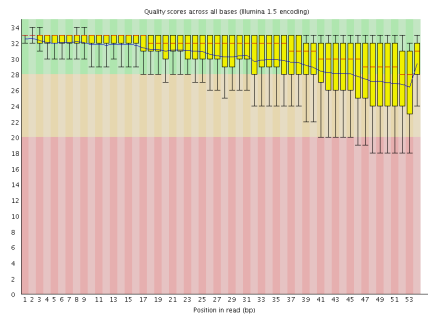
## 2 Per Base Sequence Content Graph

*This graph plots out the proportion of each base position in a file for which each of the four normal DNA bases has been called.*

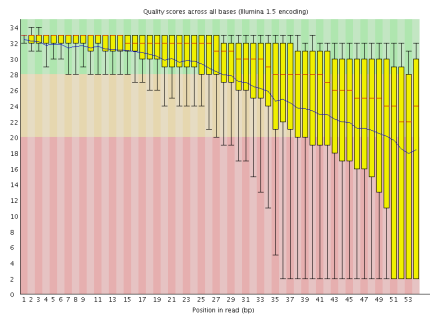




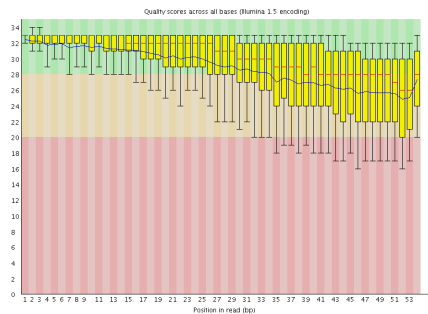
(a) Pre F520



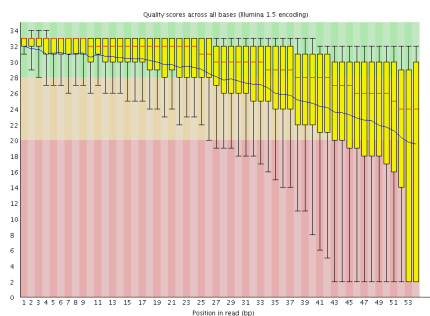
(b) Post F520



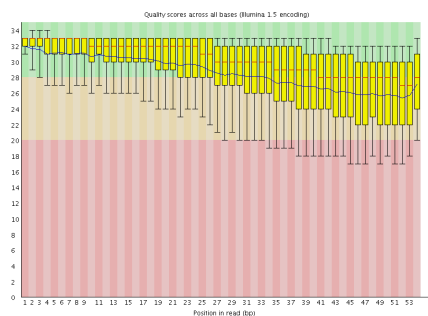
(a) Pre F528



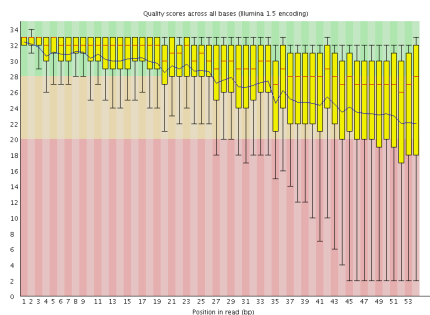
(b) Post F528



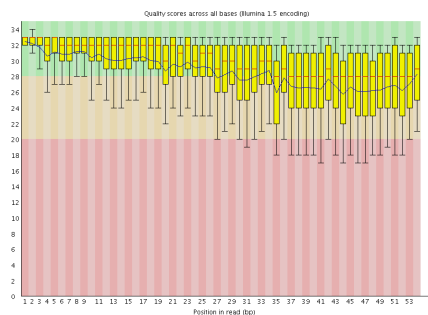
(a) Pre F550



(b) Post F550



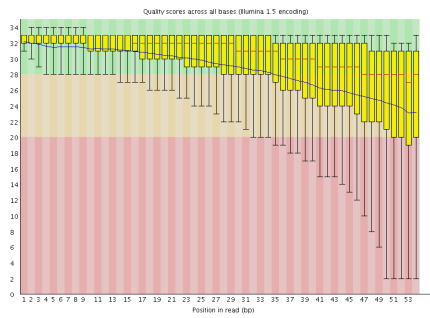
(a) Pre F577



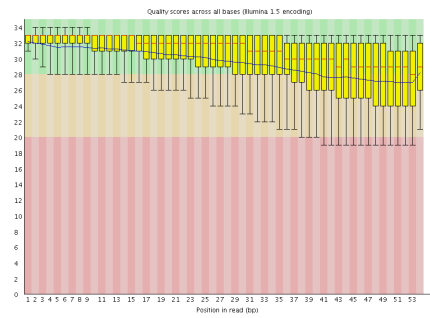
(b) Post F577

### 3 Data Summary

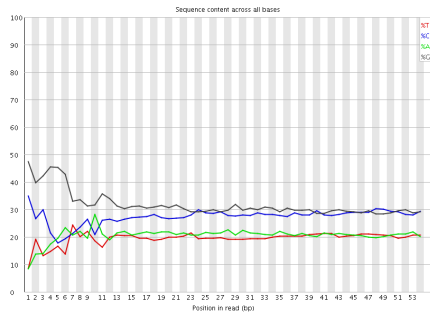
*This section contains post trimming FastQC summary results.*



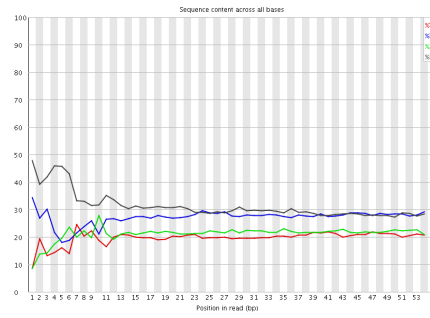
(a) Pre F\_2129



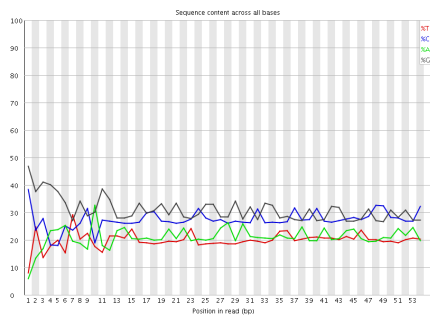
(b) Post F\_2129



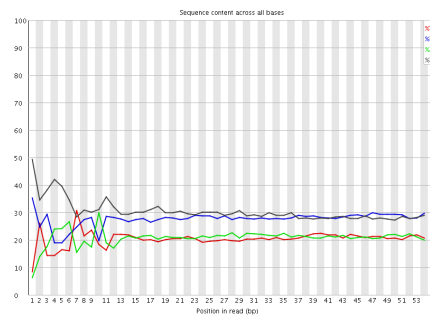
(a) Pre F0002



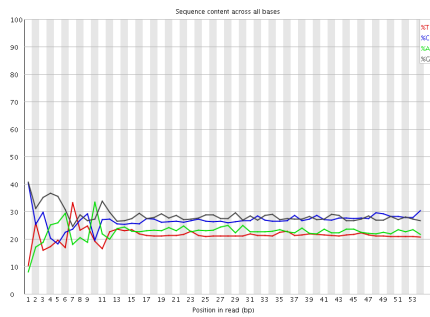
(b) Post F0002



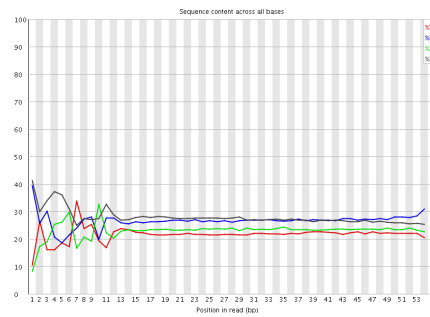
(a) Pre F135



(b) Post F135



(a) Pre F195



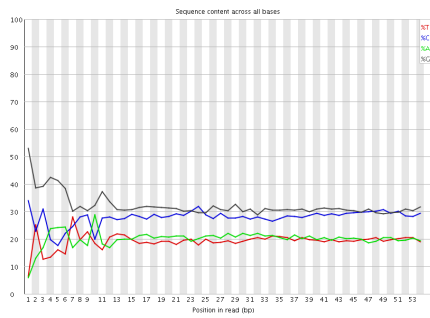
(b) Post F195

### 3.1 F0002.fastq.gz

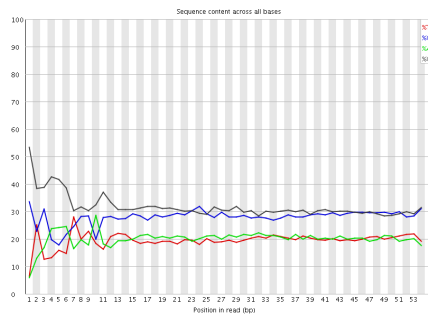
Basic Statistics:

-----

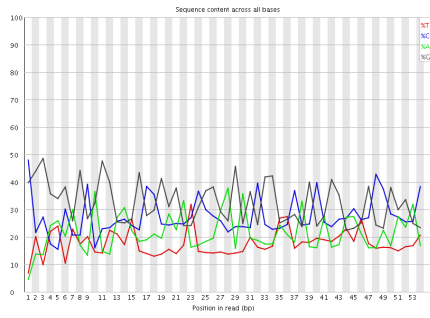
Total Sequences 16995797



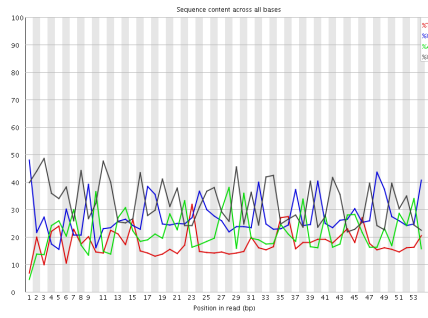
(a) Pre F210



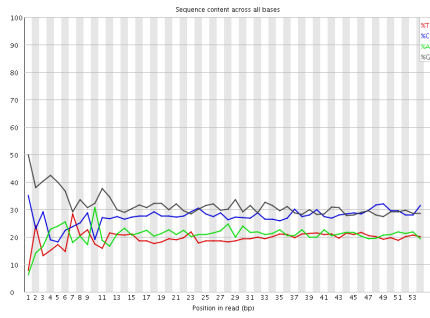
(b) Post F210



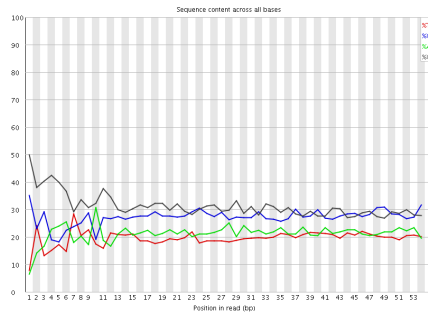
(a) Pre F280



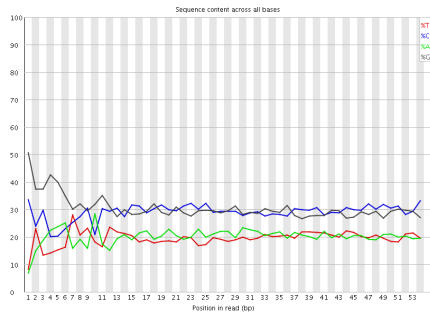
(b) Post F280



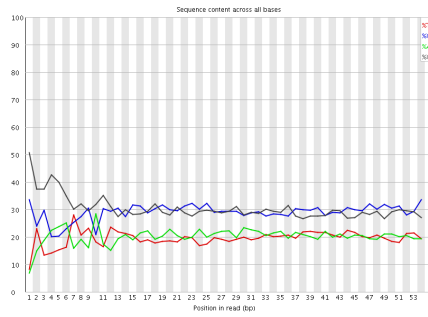
(a) Pre F419



(b) Post F419



(a) Pre F468

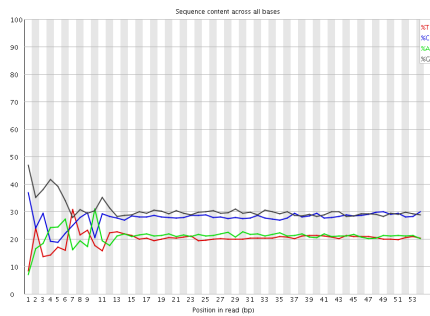


(b) Post F468

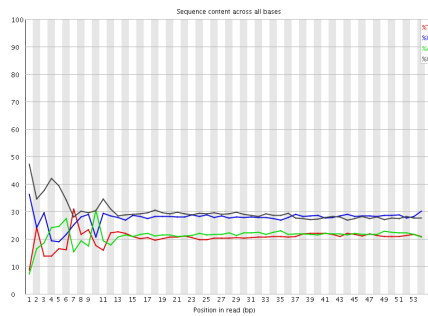
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 58

Other Statistics Summary:

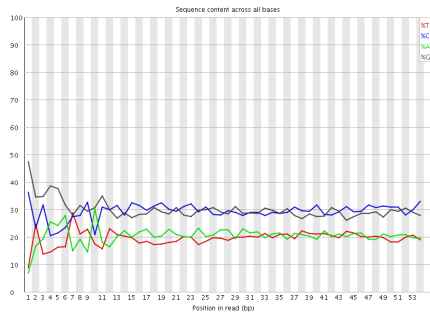
-----



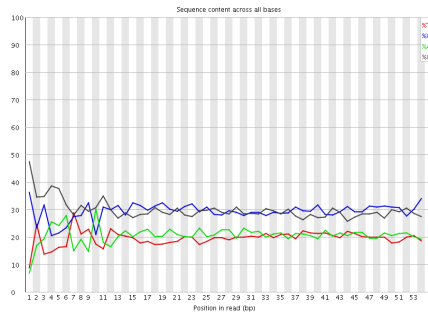
(a) Pre F506



(b) Post F506



(a) Pre F520



(b) Post F520

Metrics ResultBasic Statistics PASS

Per base sequence quality PASS

Per tile sequence quality FAIL

Per sequence quality scores PASS

Per base sequence content FAIL

This could've failed due to fragmentation bias in the first 13bp. Checking...

Only fragment bias in the first 13bp found.Per sequence GC content PASS

Per base N content PASS

Sequence Length Distribution WARN

Sequence Duplication Levels WARN

Overrepresented sequences WARN

Adapter Content PASS

Kmer Content FAIL

## 3.2 F135.fastq.gz

Basic Statistics:

Total Sequences 7877229

Sequences flagged as poor quality 0

Sequence length 2-54

%GC 58

Other Statistics Summary:

Metrics ResultBasic Statistics PASS

Per base sequence quality PASS

Per tile sequence quality PASS

Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content PASS  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences WARN  
Adapter Content PASS  
Kmer Content FAIL

### 3.3 F195.fastq.gz

Basic Statistics:

-----  
Total Sequences 11278843  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 55

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality PASS  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content PASS  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels PASS  
Overrepresented sequences WARN  
Adapter Content PASS  
Kmer Content FAIL

### 3.4 F210.fastq.gz

Basic Statistics:

-----  
Total Sequences 9924625  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 60

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality PASS  
Per sequence quality scores PASS  
Per base sequence content FAIL

This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content WARN  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels WARN  
Overrepresented sequences WARN  
Adapter Content PASS  
Kmer Content FAIL

### 3.5 F280.fastq.gz

Basic Statistics:

-----  
Total Sequences 12461046  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 60

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
The error isn't just due to fragment bias. Please check the reads to remove possible adapter contamination  
Per sequence GC content FAIL  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content FAIL  
Kmer Content FAIL

### 3.6 F419.fastq.gz

Basic Statistics:

-----  
Total Sequences 10936459  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 58

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...



Only fragment bias in the first 13bp found.Per sequence GC content WARN  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content PASS  
Kmer Content FAIL

### 3.7 F468.fastq.gz

Basic Statistics:

-----  
Total Sequences 12369854  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 59

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality PASS  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content FAIL  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content PASS  
Kmer Content FAIL

### 3.8 F506.fastq.gz

Basic Statistics:

-----  
Total Sequences 12663958  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 58

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content PASS  
Per base N content PASS

Sequence Length Distribution WARN  
Sequence Duplication Levels WARN  
Overrepresented sequences WARN  
Adapter Content PASS  
Kmer Content FAIL

### 3.9 F520.fastq.gz

Basic Statistics:

-----  
Total Sequences 8590866  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 59

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality WARN  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content FAIL  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content PASS  
Kmer Content FAIL

### 3.10 F528.fastq.gz

Basic Statistics:

-----  
Total Sequences 17323169  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 62

Other Statistics Summary:

-----  
Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
The error isn't just due to fragment bias. Please check the reads to remove possible adapter contamination  
Per sequence GC content FAIL  
Per base N content PASS  
Sequence Length Distribution WARN

Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content FAIL  
Kmer Content FAIL

### 3.11 F550.fastq.gz

Basic Statistics:

-----

Total Sequences 11367271  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 58

Other Statistics Summary:

-----

Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality PASS  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
The error isn't just due to fragment bias. Please check the reads to remove possible adapter contamination  
Per sequence GC content WARN  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content FAIL  
Kmer Content FAIL

### 3.12 F577.fastq.gz

Basic Statistics:

-----

Total Sequences 15228352  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 59

Other Statistics Summary:

-----

Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
The error isn't just due to fragment bias. Please check the reads to remove possible adapter contamination  
Per sequence GC content FAIL  
Per base N content PASS  
Sequence Length Distribution WARN

Sequence Duplication Levels FAIL  
Overrepresented sequences FAIL  
Adapter Content FAIL  
Kmer Content FAIL

### 3.13 F\_\_2129.fastq.gz

Basic Statistics:

-----

Total Sequences 11206374  
Sequences flagged as poor quality 0  
Sequence length 2-54  
%GC 57

Other Statistics Summary:

-----

Metrics ResultBasic Statistics PASS  
Per base sequence quality PASS  
Per tile sequence quality FAIL  
Per sequence quality scores PASS  
Per base sequence content FAIL  
This could've failed due to fragmentation bias in the first 13bp. Checking...  
Only fragment bias in the first 13bp found.Per sequence GC content WARN  
Per base N content PASS  
Sequence Length Distribution WARN  
Sequence Duplication Levels FAIL  
Overrepresented sequences WARN  
Adapter Content PASS  
Kmer Content FAIL

## 4 Post Mapping Data

### 4.1 F0002.fastq.gz

Post Mapping Metrics

### 4.2 F135.fastq.gz

Post Mapping Metrics

### 4.3 F195.fastq.gz

Post Mapping Metrics

### 4.4 F210.fastq.gz

Post Mapping Metrics

## 4.5 F280.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 12462040

QC failed: 0  
Optical/PCR duplicate: 0  
Non primary hits 0  
Unmapped reads: 3411636  
mapq < mapq\_cut (non-unique): 8704839

mapq >= mapq\_cut (unique): 345565  
Read-1: 0  
Read-2: 0  
Reads map to '+': 175027  
Reads map to '-': 170538  
Non-splice reads: 345565  
Splice reads: 0  
Reads mapped in proper pairs: 0  
Proper-paired reads map to different chrom:0

## 4.6 F419.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 10939668

QC failed: 0  
Optical/PCR duplicate: 0  
Non primary hits 0  
Unmapped reads: 2716427  
mapq < mapq\_cut (non-unique): 7511502

mapq >= mapq\_cut (unique): 711739  
Read-1: 0  
Read-2: 0  
Reads map to '+': 334514  
Reads map to '-': 377225  
Non-splice reads: 711739  
Splice reads: 0  
Reads mapped in proper pairs: 0  
Proper-paired reads map to different chrom:0

## 4.7 F468.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 12371766

QC failed: 0

Optical/PCR duplicate: 0

Non primary hits 0

Unmapped reads: 1355496

mapq < mapq\_cut (non-unique): 10361834

mapq >= mapq\_cut (unique): 654436

Read-1: 0

Read-2: 0

Reads map to '+' : 325237

Reads map to '-' : 329199

Non-splice reads: 654436

Splice reads: 0

Reads mapped in proper pairs: 0

Proper-paired reads map to different chrom:0

## 4.8 F506.fastq.gz

Post Mapping Metrics

## 4.9 F520.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 8592246

QC failed: 0

Optical/PCR duplicate: 0

Non primary hits 0

Unmapped reads: 1746473

mapq < mapq\_cut (non-unique): 6290950

mapq >= mapq\_cut (unique): 554823

Read-1: 0

Read-2: 0

Reads map to '+' : 263588

Reads map to '-' : 291235

Non-splice reads: 554823

Splice reads: 0

Reads mapped in proper pairs: 0

Proper-paired reads map to different chrom:0

## 4.10 F528.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 17324676

QC failed: 0

Optical/PCR duplicate: 0

Non primary hits 0

Unmapped reads: 4465909

mapq < mapq\_cut (non-unique): 12673017

mapq >= mapq\_cut (unique): 185750

Read-1: 0

Read-2: 0

Reads map to '+': 89052

Reads map to '-': 96698

Non-splice reads: 185750

Splice reads: 0

Reads mapped in proper pairs: 0

Proper-paired reads map to different chrom:0

## 4.11 F550.fastq.gz

Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 11368382

QC failed: 0

Optical/PCR duplicate: 0

Non primary hits 0

Unmapped reads: 3642734

mapq < mapq\_cut (non-unique): 7160646

mapq >= mapq\_cut (unique): 565002

Read-1: 0

Read-2: 0

Reads map to '+': 279923

Reads map to '-': 285079

Non-splice reads: 565002

Splice reads: 0

Reads mapped in proper pairs: 0

Proper-paired reads map to different chrom:0

## 4.12 F577.fastq.gz

### Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

Total records: 15229162

QC failed: 0  
Optical/PCR duplicate: 0  
Non primary hits 0  
Unmapped reads: 8717524  
mapq < mapq\_cut (non-unique): 5899753

mapq >= mapq\_cut (unique): 611885  
Read-1: 0  
Read-2: 0  
Reads map to '+': 294881  
Reads map to '-': 317004  
Non-splice reads: 611885  
Splice reads: 0  
Reads mapped in proper pairs: 0  
Proper-paired reads map to different chrom:0

## 4.13 F\_2129.fastq.gz

### Post Mapping Metrics

```
#=====
#All numbers are READ count
#=====
```

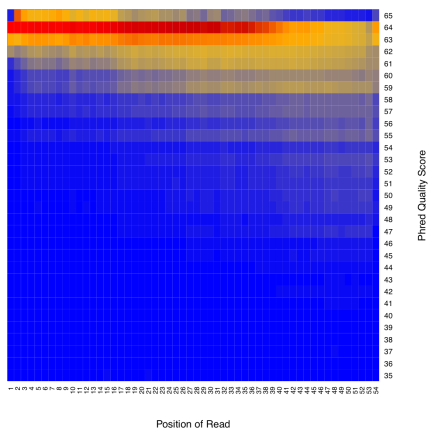
Total records: 11207762

QC failed: 0  
Optical/PCR duplicate: 0  
Non primary hits 0  
Unmapped reads: 2867241  
mapq < mapq\_cut (non-unique): 7313329

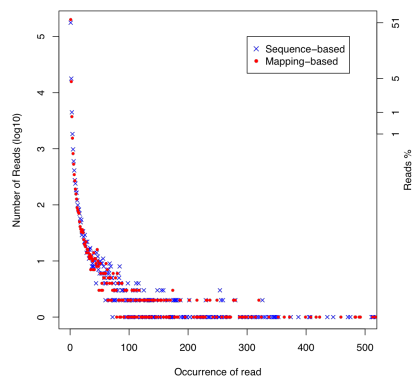
mapq >= mapq\_cut (unique): 1027192  
Read-1: 0  
Read-2: 0  
Reads map to '+': 521179  
Reads map to '-': 506013  
Non-splice reads: 1027192  
Splice reads: 0  
Reads mapped in proper pairs: 0  
Proper-paired reads map to different chrom:0

## 5 Post Mapping Visual Data



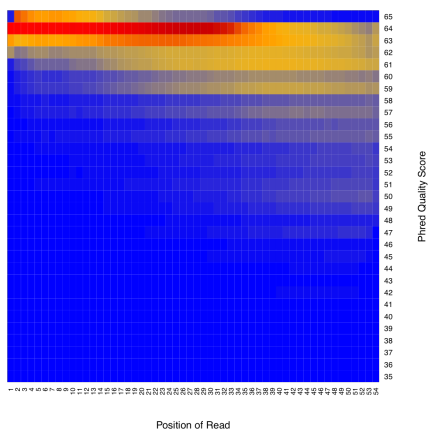


(a) Alignment Quality

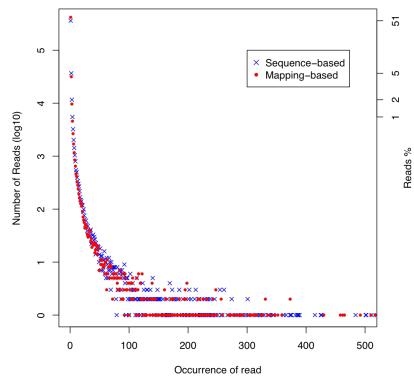


(b) Duplication Rate

Figure 27: F280.fastq.gz

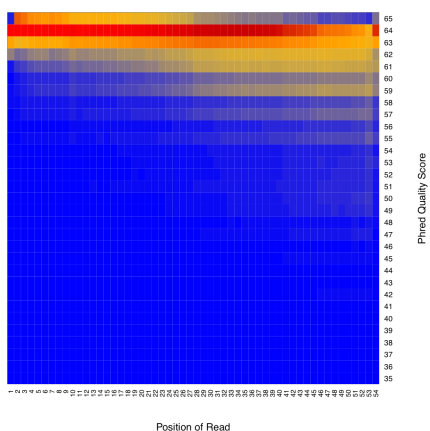


(a) Alignment Quality

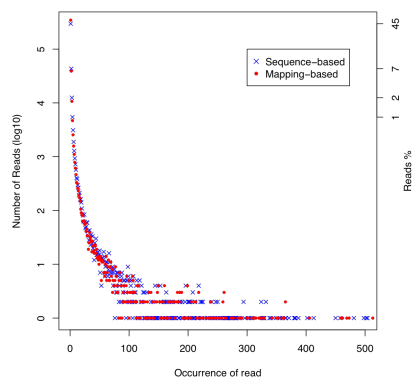


(b) Duplication Rate

Figure 28: F419.fastq.gz

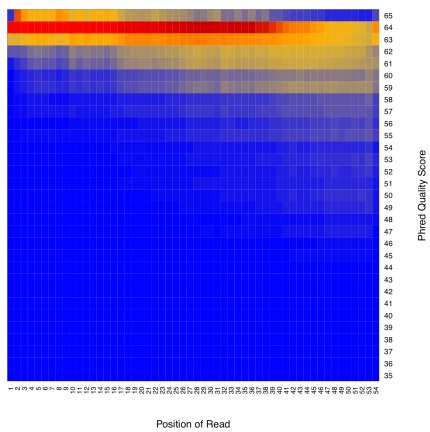


(a) Alignment Quality

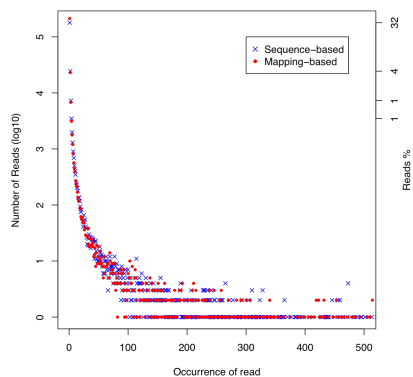


(b) Duplication Rate

Figure 29: F468.fastq.gz

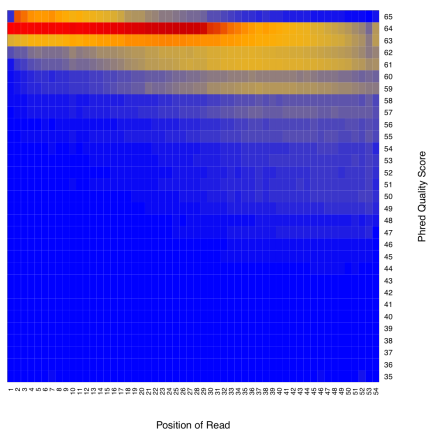


(a) Alignment Quality

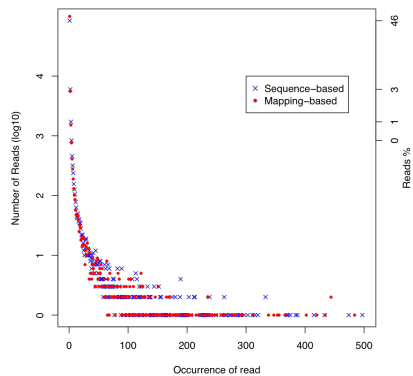


(b) Duplication Rate

Figure 30: F520.fastq.gz

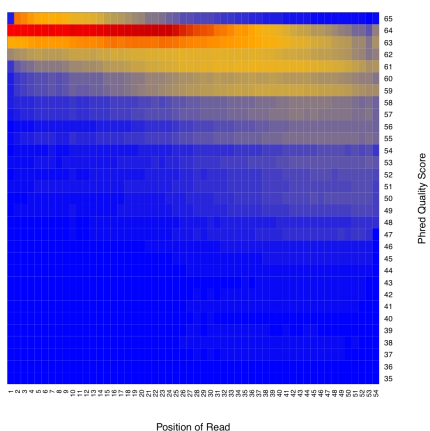


(a) Alignment Quality

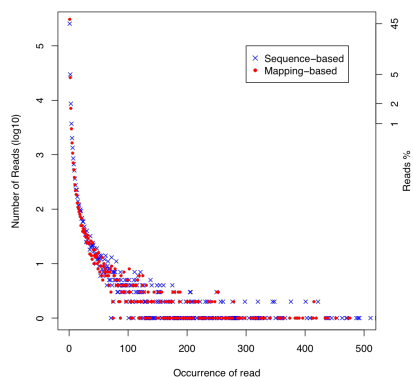


(b) Duplication Rate

Figure 31: F528.fastq.gz

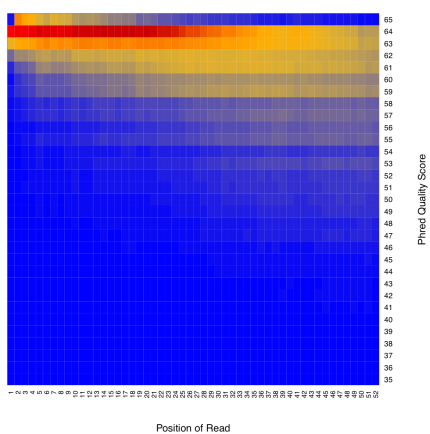


(a) Alignment Quality

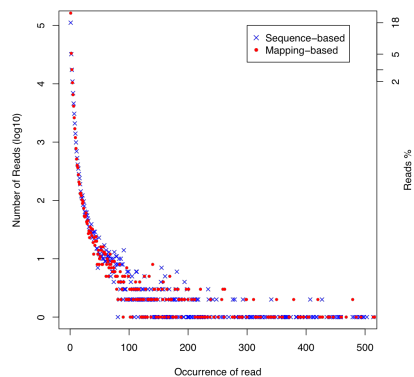


(b) Duplication Rate

Figure 32: F550.fastq.gz

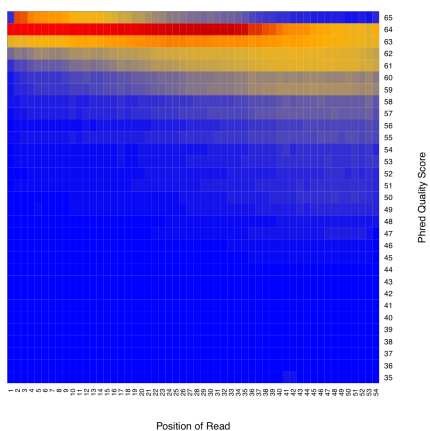


(a) Alignment Quality

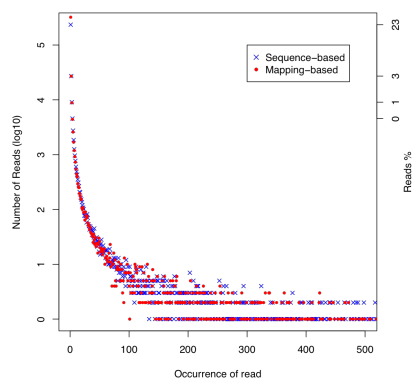


(b) Duplication Rate

Figure 33: F577.fastq.gz



(a) Alignment Quality



(b) Duplication Rate

Figure 34: F\_2129.fastq.gz