

Project Chocokoffie

SRR1106138_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR1106138.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 5627599
Sequences flagged as poor quality 0
Sequence length 25-57
%GC 30
PASS Basic Statistics SRR1106138.fastq
FAIL Per base sequence quality SRR1106138.fastq
FAIL Per sequence quality scores SRR1106138.fastq
FAIL Per base sequence content SRR1106138.fastq
PASS Per sequence GC content SRR1106138.fastq
PASS Per base N content SRR1106138.fastq
WARN Sequence Length Distribution SRR1106138.fastq
PASS Sequence Duplication Levels SRR1106138.fastq
PASS Overrepresented sequences SRR1106138.fastq
PASS Adapter Content SRR1106138.fastq
=== Summary ===
```

```
Total reads processed:      5,627,599
Reads with adapters:        0 (0.0%)
Reads written (passing filters):  5,627,599 (100.0%)
```

```
Total basepairs processed: 179,811,193 bp
Quality-trimmed:           179,811,193 bp (100.0%)
Total written (filtered):   0 bp (0.0%)
```

Project Chocokoffie

SRR1106139_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR1106139.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 6810659
Sequences flagged as poor quality 0
Sequence length 25-57
%GC 30
PASS Basic Statistics SRR1106139.fastq
FAIL Per base sequence quality SRR1106139.fastq
FAIL Per sequence quality scores SRR1106139.fastq
FAIL Per base sequence content SRR1106139.fastq
PASS Per sequence GC content SRR1106139.fastq
PASS Per base N content SRR1106139.fastq
WARN Sequence Length Distribution SRR1106139.fastq
PASS Sequence Duplication Levels SRR1106139.fastq
PASS Overrepresented sequences SRR1106139.fastq
PASS Adapter Content SRR1106139.fastq
=== Summary ===
```

```
Total reads processed:      6,810,659
Reads with adapters:        0 (0.0%)
Reads written (passing filters): 6,810,659 (100.0%)
```

```
Total basepairs processed: 217,266,386 bp
Quality-trimmed:           217,266,386 bp (100.0%)
Total written (filtered):   0 bp (0.0%)
```

Project Chocokoffie

SRR1106140_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR1106140.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 4183530
Sequences flagged as poor quality 0
Sequence length 25-57
%GC 30
PASS Basic Statistics SRR1106140.fastq
FAIL Per base sequence quality SRR1106140.fastq
FAIL Per sequence quality scores SRR1106140.fastq
FAIL Per base sequence content SRR1106140.fastq
PASS Per sequence GC content SRR1106140.fastq
PASS Per base N content SRR1106140.fastq
WARN Sequence Length Distribution SRR1106140.fastq
PASS Sequence Duplication Levels SRR1106140.fastq
PASS Overrepresented sequences SRR1106140.fastq
PASS Adapter Content SRR1106140.fastq
=== Summary ===
```

```
Total reads processed:      4,183,530
Reads with adapters:        0 (0.0%)
Reads written (passing filters): 4,183,530 (100.0%)
```

```
Total basepairs processed: 134,754,043 bp
Quality-trimmed:           134,754,043 bp (100.0%)
Total written (filtered):   0 bp (0.0%)
```

Project Chocokoffie

SRR1106118_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR1106118.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 6827156
Sequences flagged as poor quality 0
Sequence length 25-57
%GC 31
PASS Basic Statistics SRR1106118.fastq
FAIL Per base sequence quality SRR1106118.fastq
FAIL Per sequence quality scores SRR1106118.fastq
FAIL Per base sequence content SRR1106118.fastq
PASS Per sequence GC content SRR1106118.fastq
PASS Per base N content SRR1106118.fastq
WARN Sequence Length Distribution SRR1106118.fastq
PASS Sequence Duplication Levels SRR1106118.fastq
WARN Overrepresented sequences SRR1106118.fastq
PASS Adapter Content SRR1106118.fastq
=== Summary ===
```

Total reads processed:	6,827,156
Reads with adapters:	0 (0.0%)
Reads written (passing filters):	6,827,156 (100.0%)

Total basepairs processed:	217,846,819 bp
Quality-trimmed:	217,846,819 bp (100.0%)
Total written (filtered):	0 bp (0.0%)

Project Chocokoffie

SRR1106122_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR1106122.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 11078113
Sequences flagged as poor quality 0
Sequence length 25-57
%GC 31
PASS Basic Statistics SRR1106122.fastq
FAIL Per base sequence quality SRR1106122.fastq
FAIL Per sequence quality scores SRR1106122.fastq
FAIL Per base sequence content SRR1106122.fastq
PASS Per sequence GC content SRR1106122.fastq
PASS Per base N content SRR1106122.fastq
WARN Sequence Length Distribution SRR1106122.fastq
PASS Sequence Duplication Levels SRR1106122.fastq
WARN Overrepresented sequences SRR1106122.fastq
PASS Adapter Content SRR1106122.fastq
=== Summary ===
```

```
Total reads processed:      11,078,113
Reads with adapters:        0 (0.0%)
Reads written (passing filters): 11,078,113 (100.0%)
```

```
Total basepairs processed: 350,514,483 bp
Quality-trimmed:           350,514,483 bp (100.0%)
Total written (filtered):   0 bp (0.0%)
```

Project Chocokoffie

SRR057598_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR057598.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 14988768
Sequences flagged as poor quality 0
Sequence length 40
%GC 56
PASS Basic Statistics SRR057598.fastq
PASS Per base sequence quality SRR057598.fastq
PASS Per tile sequence quality SRR057598.fastq
PASS Per sequence quality scores SRR057598.fastq
FAIL Per base sequence content SRR057598.fastq
PASS Per sequence GC content SRR057598.fastq
PASS Per base N content SRR057598.fastq
PASS Sequence Length Distribution SRR057598.fastq
WARN Sequence Duplication Levels SRR057598.fastq
PASS Overrepresented sequences SRR057598.fastq
PASS Adapter Content SRR057598.fastq
=== Summary ===
```

Total reads processed:	14,988,768
Reads with adapters:	4,112,069 (27.4%)
Reads written (passing filters):	14,988,768 (100.0%)

Total basepairs processed:	599,550,720 bp
Quality-trimmed:	14,010,167 bp (2.3%)
Total written (filtered):	579,303,115 bp (96.6%)

Project Chocokoffie

SRR057599_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR057599.fastq
File type Conventional base calls
Encoding Sanger / Illumina 1.9
Total Sequences 15795216
Sequences flagged as poor quality 0
Sequence length 40
%GC 54
PASS Basic Statistics SRR057599.fastq
PASS Per base sequence quality SRR057599.fastq
FAIL Per tile sequence quality SRR057599.fastq
PASS Per sequence quality scores SRR057599.fastq
FAIL Per base sequence content SRR057599.fastq
PASS Per sequence GC content SRR057599.fastq
PASS Per base N content SRR057599.fastq
PASS Sequence Length Distribution SRR057599.fastq
WARN Sequence Duplication Levels SRR057599.fastq
PASS Overrepresented sequences SRR057599.fastq
PASS Adapter Content SRR057599.fastq
=== Summary ===
```

Total reads processed:	15,795,216
Reads with adapters:	4,620,578 (29.3%)
Reads written (passing filters):	15,795,216 (100.0%)

Total basepairs processed:	631,808,640 bp
Quality-trimmed:	14,833,027 bp (2.3%)
Total written (filtered):	610,282,895 bp (96.6%)

Project Chocokoffie

SRR018013_2_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR018013_2.fastq
File type Colourspace converted to bases
Encoding Sanger / Illumina 1.9
Total Sequences 67504183
Sequences flagged as poor quality 0
Sequence length 35
%GC 54
PASS Basic Statistics SRR018013_2.fastq
FAIL Per base sequence quality SRR018013_2.fastq
FAIL Per sequence quality scores SRR018013_2.fastq
FAIL Per base sequence content SRR018013_2.fastq
PASS Per sequence GC content SRR018013_2.fastq
PASS Per base N content SRR018013_2.fastq
PASS Sequence Length Distribution SRR018013_2.fastq
WARN Sequence Duplication Levels SRR018013_2.fastq
FAIL Overrepresented sequences SRR018013_2.fastq
FAIL Adapter Content SRR018013_2.fastq
```


Project Chocokoffie

SRR018013_1_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR018013_1.fastq
File type Colourspace converted to bases
Encoding Sanger / Illumina 1.9
Total Sequences 72729635
Sequences flagged as poor quality 0
Sequence length 35
%GC 53
PASS Basic Statistics SRR018013_1.fastq
FAIL Per base sequence quality SRR018013_1.fastq
FAIL Per sequence quality scores SRR018013_1.fastq
FAIL Per base sequence content SRR018013_1.fastq
PASS Per sequence GC content SRR018013_1.fastq
PASS Per base N content SRR018013_1.fastq
PASS Sequence Length Distribution SRR018013_1.fastq
WARN Sequence Duplication Levels SRR018013_1.fastq
FAIL Overrepresented sequences SRR018013_1.fastq
FAIL Adapter Content SRR018013_1.fastq
```

Project Chocokoffie

SRR018015_sum

```
##FastQC 0.11.9
>>Basic Statistics pass
#Measure Value
Filename SRR018015.fastq
File type Colospace converted to bases
Encoding Sanger / Illumina 1.9
Total Sequences 92914107
Sequences flagged as poor quality 0
Sequence length 35
%GC 50
PASS Basic Statistics SRR018015.fastq
FAIL Per base sequence quality SRR018015.fastq
FAIL Per sequence quality scores SRR018015.fastq
FAIL Per base sequence content SRR018015.fastq
PASS Per sequence GC content SRR018015.fastq
PASS Per base N content SRR018015.fastq
PASS Sequence Length Distribution SRR018015.fastq
PASS Sequence Duplication Levels SRR018015.fastq
PASS Overrepresented sequences SRR018015.fastq
WARN Adapter Content SRR018015.fastq
```