

Session 2.2 – Quality assessment and read preprocessing

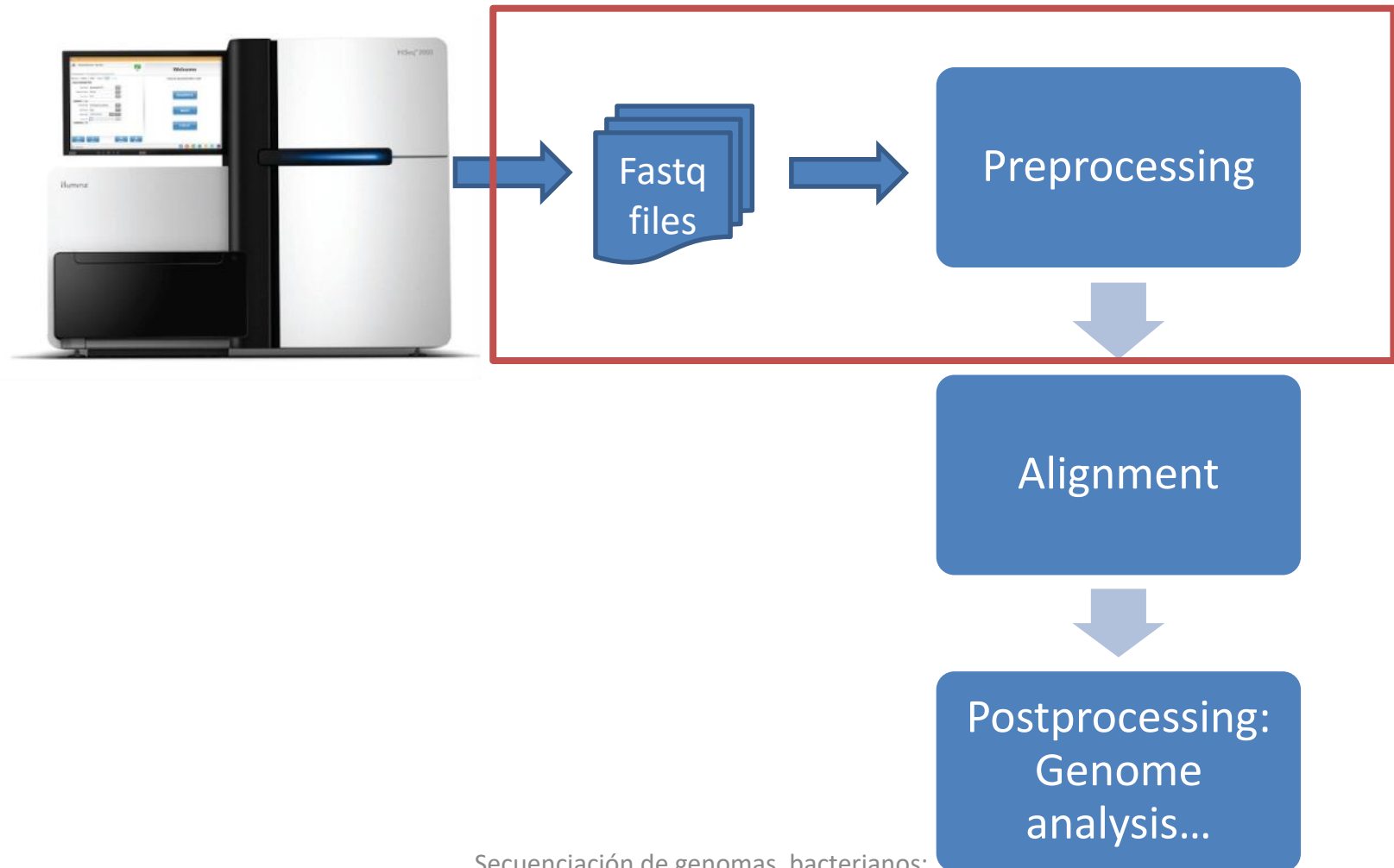
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Programa Formación Continua, ISCIII

Step in the process



Raw output files format

Illumina



.fastq



454 .sff



SOLiD

.fasta
.qual



Nanopore
FAST5



PacBio RSII
Bax.h5
fasta

FASTQ format

- Is a FASTA file with quality information
- Within HTS, FASTA contain genomes y FASTQ reads

>SEQ_ID|

```
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGC
TTCTGAACTGGTTACCTGCCGTGAGTAAATTTAAATTTTATTGACTTAGGTCACTAAATACTTTAACCBA
TATAGGCATAGCGCACAGACAGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACC
ATTACCACCACCATTACCATTACCACAGGTAACGGTGCAGGCTGACGCGTACAGGAAACACAGAAAAAAG
```

Sequence

@SEQ_ID

```
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
```

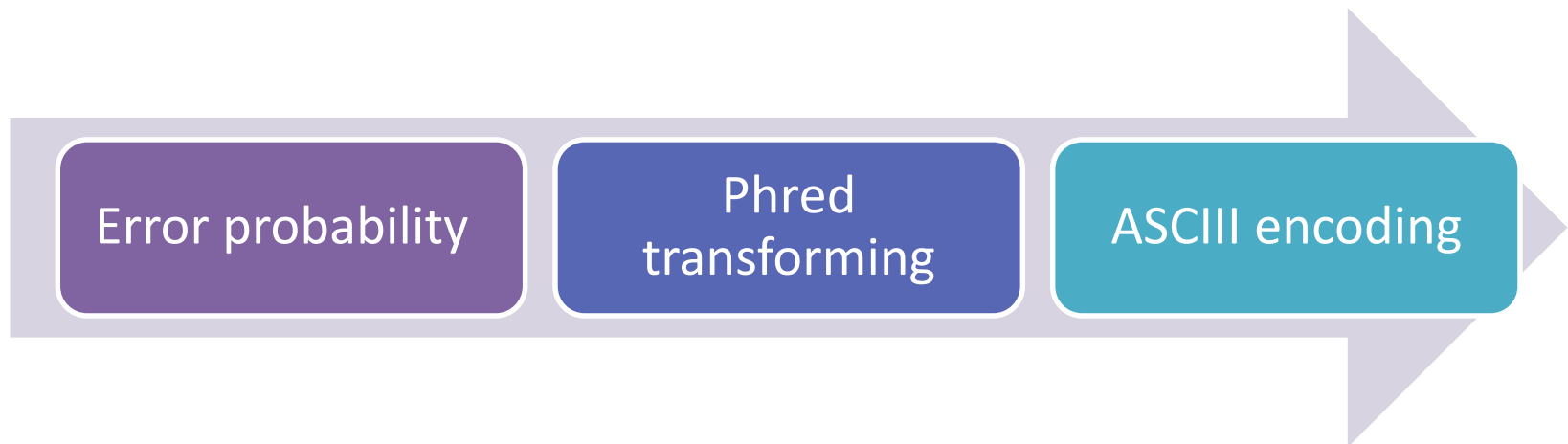
+

```
!''*(((((***+))%%%+))(%%%).1***-+*''))**55CCF>>>>>CCCCCCC65
```

Quality: must be 1 bit

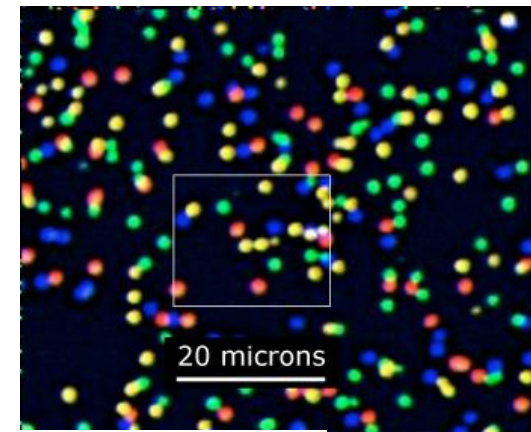
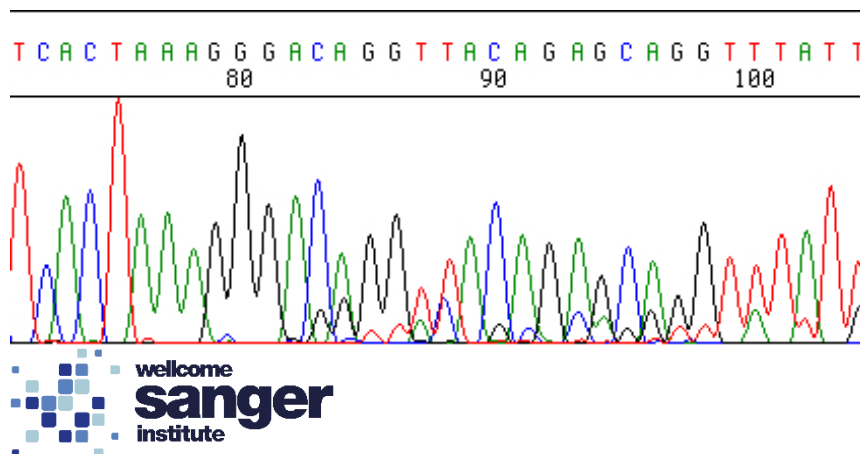
FASTQ format

- Each base has an assigned quality score
 - Sequencing quality scores measure the probability that a base is called incorrectly
- How is it calculated?



Phred quality and error probability

- **Light intensity** is used to calculate the error probabilities
- Convert error probability into Phred score quality - Ewing B, Green P. (1998)
- Phred originated as an algorithmic approach that considered Sanger sequencing metrics, such as **peak resolution and shape**



illumina®

Phred quality and error probability

- Convert error probability into Phred score quality - in real time on Illumina platforms
- Q scores are defined as a property that is logarithmically related to the base calling error probabilities (P)
- Phred quality range between 0-40 for Sanger and Illumina 1.8+

$$Q = -10 \log_{10} P$$

Phred Quality Score	Probability of Incorrect Base Call	Base Call Accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%

Phred quality and error probability

- Convert Phred quality score into ASCII, a compact form, which uses only 1 byte per quality value

ASCII_BASE=33 Illumina, Ion Torrent, PacBio and Sanger

Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII
0	1.00000	33 !	11	0.07943	44 ,	22	0.00631	55 7	33	0.00050	66 B
1	0.79433	34 "	12	0.06310	45 -	23	0.00501	56 8	34	0.00040	67 C
2	0.63096	35 #	13	0.05012	46 .	24	0.00398	57 9	35	0.00032	68 D
3	0.50119	36 \$	14	0.03981	47 /	25	0.00316	58 :	36	0.00025	69 E
4	0.39811	37 %	15	0.03162	48 0	26	0.00251	59 ;	37	0.00020	70 F
5	0.31623	38 &	16	0.02512	49 1	27	0.00200	60 <	38	0.00016	71 G
6	0.25119	39 '	17	0.01995	50 2	28	0.00158	61 =	39	0.00013	72 H
7	0.19953	40 (18	0.01585	51 3	29	0.00126	62 >	40	0.00010	73 I
8	0.15849	41)	19	0.01259	52 4	30	0.00100	63 ?	41	0.00008	74 J
9	0.12589	42 *	20	0.01000	53 5	31	0.00079	64 @	42	0.00006	75 K
10	0.10000	43 +	21	0.00794	54 6	32	0.00063	65 A			

- Phred+33 (Sanger and current Illumina). 0 Phred quality correspond to decimal 33, which is the symbol !

ASCII_BASE=64 Old Illumina

Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII	Q	P_error	ASCII
0	1.00000	64 @	11	0.07943	75 K	22	0.00631	86 V	33	0.00050	97 a
1	0.79433	65 A	12	0.06310	76 L	23	0.00501	87 W	34	0.00040	98 b
2	0.63096	66 B	13	0.05012	77 M	24	0.00398	88 X	35	0.00032	99 c
3	0.50119	67 C	14	0.03981	78 N	25	0.00316	89 Y	36	0.00025	100 d
4	0.39811	68 D	15	0.03162	79 O	26	0.00251	90 Z	37	0.00020	101 e
5	0.31623	69 E	16	0.02512	80 P	27	0.00200	91 [38	0.00016	102 f
6	0.25119	70 F	17	0.01995	81 Q	28	0.00158	92 \	39	0.00013	103 g
7	0.19953	71 G	18	0.01585	82 R	29	0.00126	93]	40	0.00010	104 h
8	0.15849	72 H	19	0.01259	83 S	30	0.00100	94 ^	41	0.00008	105 i
9	0.12589	73 I	20	0.01000	84 T	31	0.00079	95 _	42	0.00006	106 j
10	0.10000	74 J	21	0.00794	85 U	32	0.00063	96 `			

- Phred+64 (Solexa and Illumina 1.3-1.5)

Phred quality and error probability

- Phred 33 example

```
@HWI-ST731_6:1:1101:1322:1938#1@0/1
NTGACAAAGGGCTAATATCCAGAATCTACAAAGAACTTAAACAAATGTATAAGAATAAAAGTATAGTGCTAACAAT
+
#1:BDDADFDFFDD@F>BGFIIIB@CFHIIHICAGBC9CBCBGGIGCFF??>GGHFHIGGEGI<FECGDE=FHCHEG=
```

$P=0.001 \rightarrow Q=-10*\log_{10}(0.001)=30 \rightarrow \text{ASCII } 33+30=63 \rightarrow ?$

$P=0.0001 \rightarrow Q=-10*\log_{10}(0.0001)=40 \rightarrow \text{ASCII } 33+40=73 \rightarrow I$

Quality encoding: !"#\$%&'()*+,-./0123456789:;<=>?@ABCDEFGHI

Quality score: 0.....10.....20.....30.....40

FASTQ format

Illumina read header

@HWUSI-EAS100R:6:73:941:1973#0/1

HWUSI-EAS100R	the unique instrument name
6	flowcell lane
73	tile number within the flowcell lane
941	'x'-coordinate of the cluster within the tile
1973	'y'-coordinate of the cluster within the tile
#0	index number for a multiplexed sample (0 for no indexing)
/1	the member of a pair, /1 or /2 (<i>paired-end or mate-pair reads only</i>)

```
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:2458:1027 1:N:0:ACAGTG
AGAAAAAACCTTGGANGGAAAAAATCAGACATTTTCTAGAGGTGGAAGGCAAACTGAACAAAGAAATAATTACA
+
DGGGEDHHHHGGGFE#CBACBCA<?HHHHBHHHHHHHHDHHHEHEFEFGGGGGG/GGDDDGHFHGFCHFHEHEH8
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:3082:1029 1:N:0:ACAGTG
GGTAATACAGACTGANATGATCAAAGGCATGCTGGAACAAACCTATTAAGATAAGCTTGGATCAAGCTTTCATT
+
B:B?BB/:=55177#55877<775EDD>E=B?BBBBGGGDDAG@G>GGGGGG@)EEEEBEG>GGGGGGGAAA?<D
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:3185:1033 1:N:0:ACAGTG
TCTGGGACATTGCTCNTGGCTGGGAGTCACCTGTCTGGGACATTGCTCAGGCTGGGAGACACGTGTTGGAGGGAC
+
BC??A66; )74781<#7??;452.27'64(8,851DDG8GB?#####
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:3268:1033 1:N:0:ACAGTG
ATTCAAATTAGAAGANAGTTGATCGTTCTTCATGATGCCCAAAATTTCACTGAGAAAACCTTTTTTAAAGCCAC
+
IIIIIIIIIIFFFFE#ABACFEFFFIIGIIIFIHE@BIIIIIIIIHHIIFIIF>HHIHFIDIIIIIGFHIIEGH
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:3400:1035 1:N:0:ACAGTG
TCCTGCTTTAGGAGANTCCTCATGCTCTGACAGGATGCTCTCTATGTGAGTTGAGCTGGTCTTCTCACTTTTATAG
+
IIIIHHIHIIGGEGG#AACA@=?>BHIIIIIIHHIHHIHHIHHIHHGHIHHGHIHHGEGGGHG@EFGGCEFAB
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:3962:1033 1:N:0:ACAGTG
CCACCAACACAGTCTNCACCTTCTGTTGCTGGTGATAGATTTTGCACCTTCCATCTCCAGGTTTCAAATAGC
+
HHFHHDHDDH>C?CA#EEEE>?A?>HHDGHEGBGBCEEEEGHHF8HEHEEHECH,=>==EAE>BEBBAEACAB
@HWUSI-EAS1752R:21:FC64JUKAAXX:3:1:4491:1028 1:N:0:ACAGTG
AGAGAGAGAGAGAGANAGAGGACTCTGGAGATGCCGAAGCACAAGCCTGCAAGAGTCCAGCAAAGAAAATAAAAA
+
GADGGEGGEGBBB?B#@=@@72:64GGGFG>GGGBDG<DBG<DA??/?#####
```

ASCII-coded (0-40):

- “!\"#\$%” lowest quality
- “FGHI” highest quality

Sequencing quality assessment

- To assess quality, software uses **Phred per-base quality** score is used
- Is the **first quality control step** after sequencing. There should be one after every step of the analysis
- After quality assessment user can know how **reliable** are their datasets
- QC will determine the next **filtering** step
- Filtering decisions will **impact** directly in **further analysis**
- Many other steps also use this quality as variable in their **algorithms**

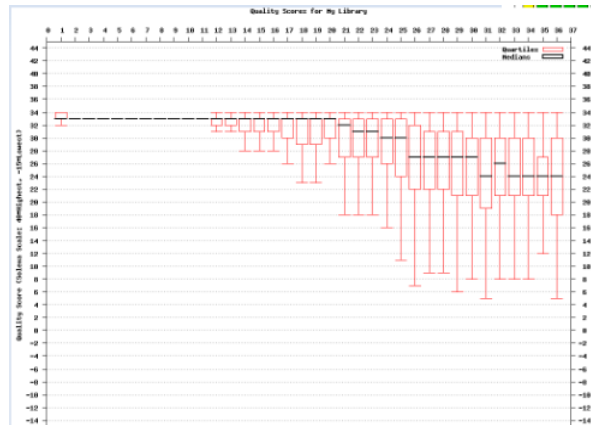
Sequencing quality assessment: Artifacts

HTS methods are bounded by their technical and theoretical limitations and sequencing errors cannot be completely eliminated (Hadigol M, Khiabani H. 2018)

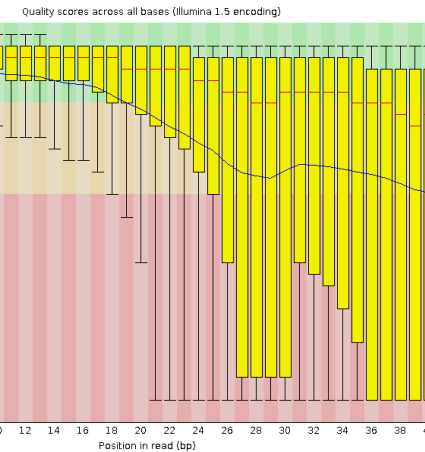
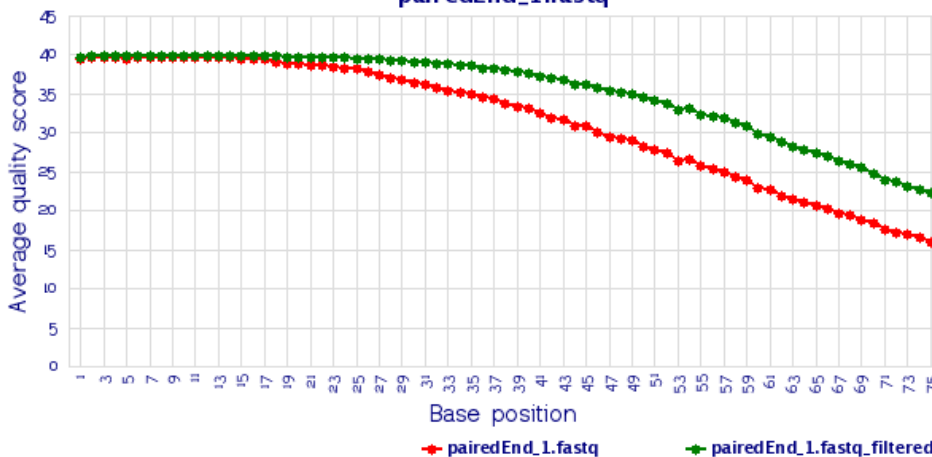
- **Artifacts in library preparation**
 - Remaining adapters
 - High rate of duplicates
 - GC regions bias
 - Polymerase error rate
 - DNA damage during breakdown
- **Artifacts during sequencing**
 - Low quality in sequence ends(Phasing: cluster loose sync)
 - Complication in certain regions:
 - Repetitions
 - Homopolymers
 - High CG content

Sequencing quality assessment

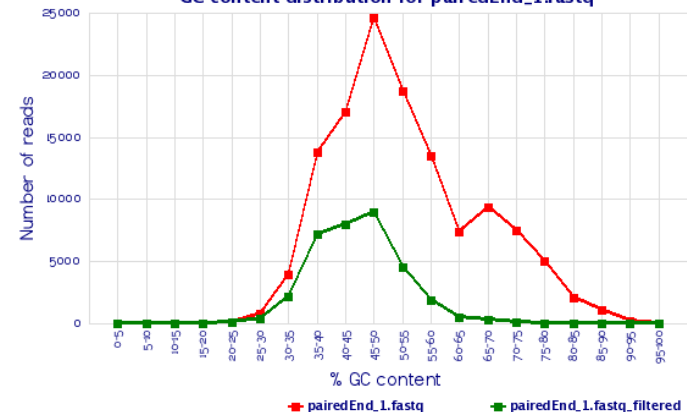
- FastQC, fastx-toolkit, sfftools, NGSQCToolkit, etc...



pairedEnd_1.fastq

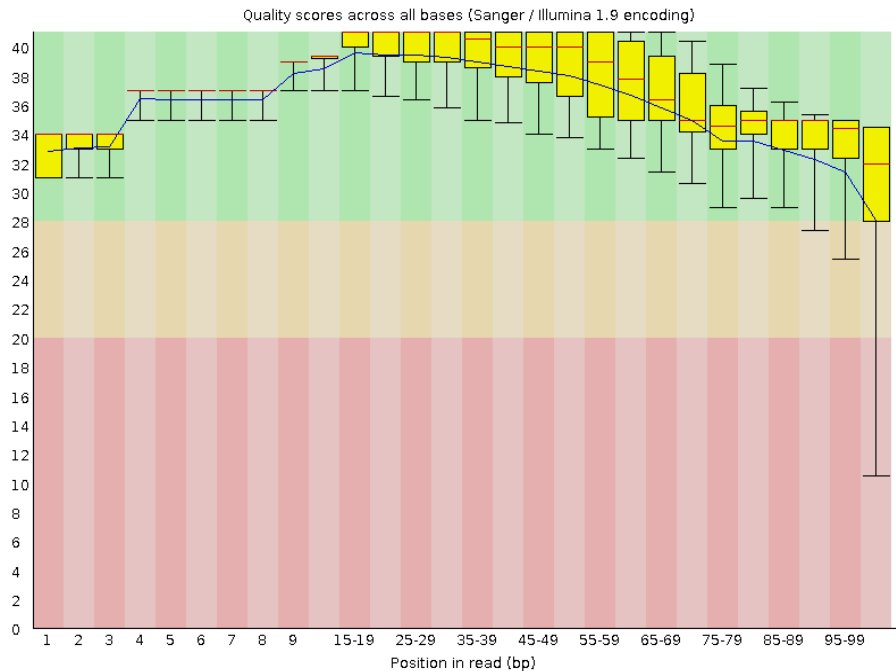


GC content distribution for pairedEnd_1.fastq

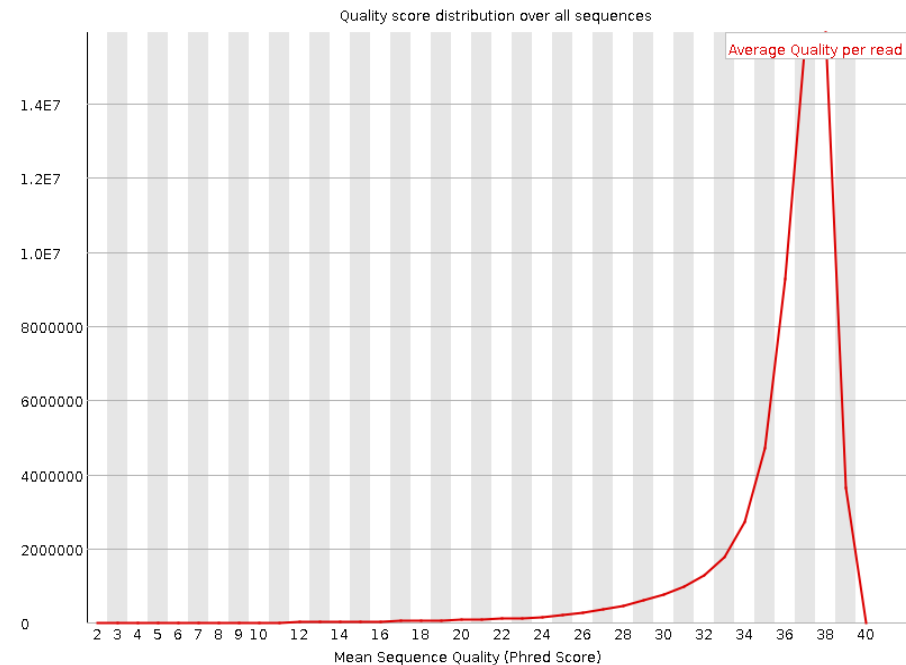


Sequencing quality assessment: FastQC

Per base sequence quality



Per sequence quality scores



<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

FastQC: Basic Statistics

- Self defined overall stats
 - Encoding: Phred33 or Phred64



Basic Statistics

Measure	Value
Filename	bad_sequence.txt
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	395288
Sequences flagged as poor quality	0
Sequence length	40
%GC	47



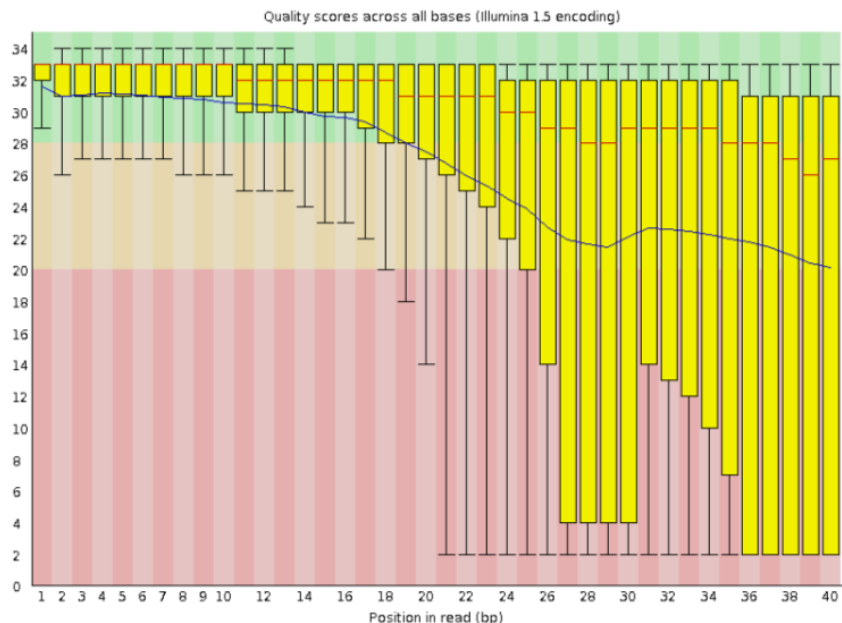
Basic Statistics

Measure	Value
Filename	good_sequence_short.txt
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	250000
Sequences flagged as poor quality	0
Sequence length	40
%GC	45

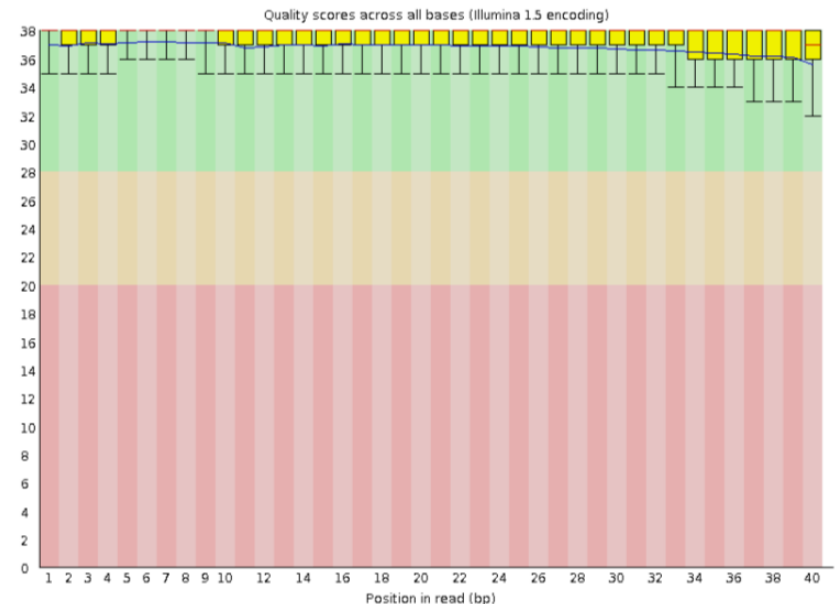
FastQC: Per base sequence quality

- Overview of the range of quality values across all bases at each position in the FastQ file
- **Median**, **inter-quartile range (25-75%)**, **10-90% points**, **mean quality**

✗ Per base sequence quality

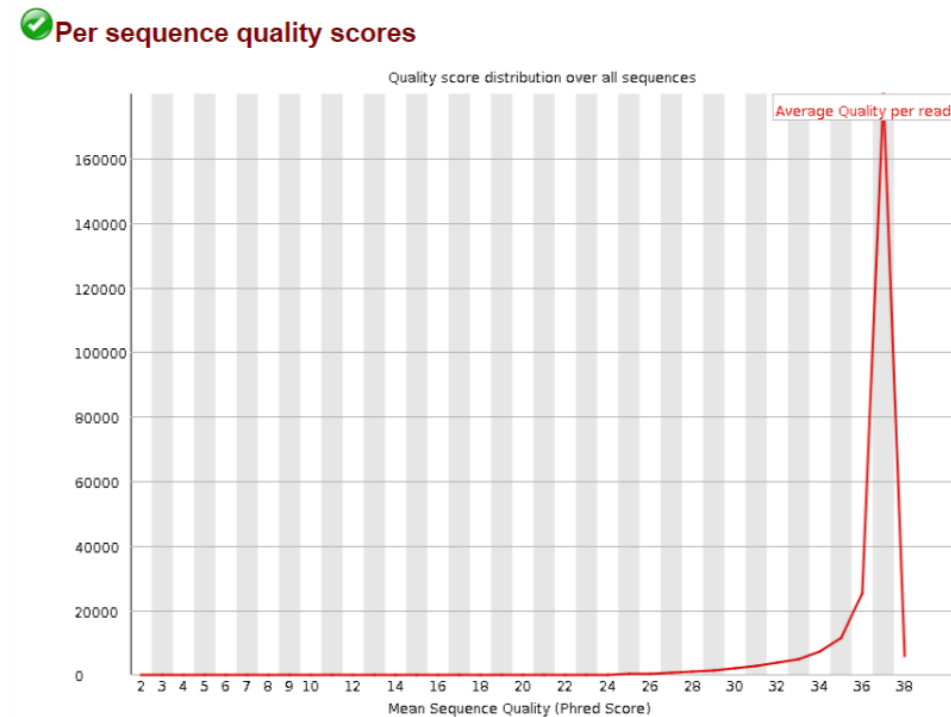
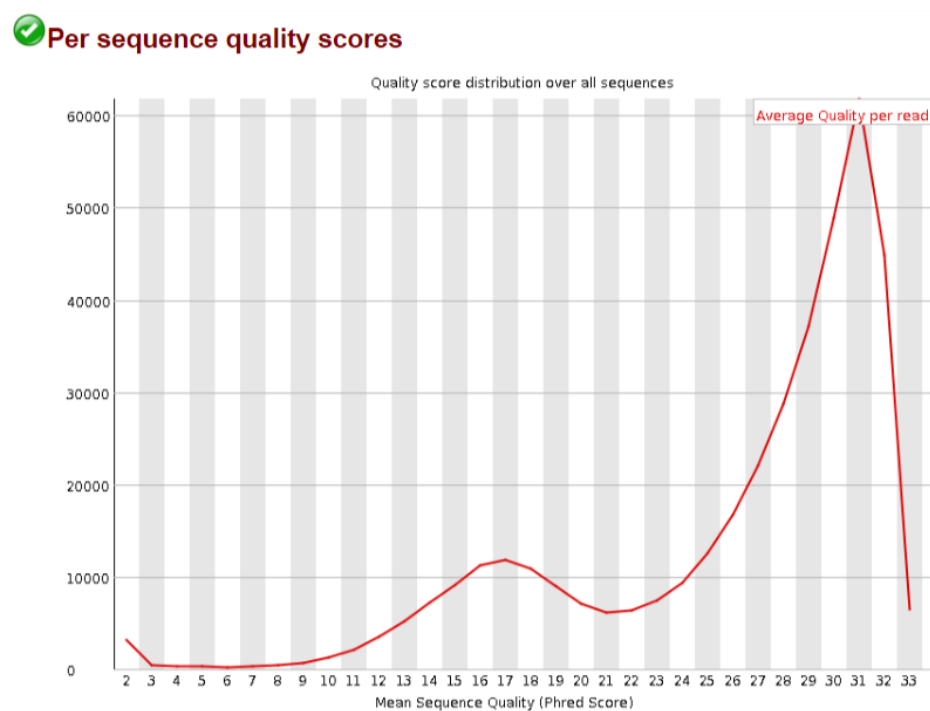


✓ Per base sequence quality



FastQC: Per sequence quality score

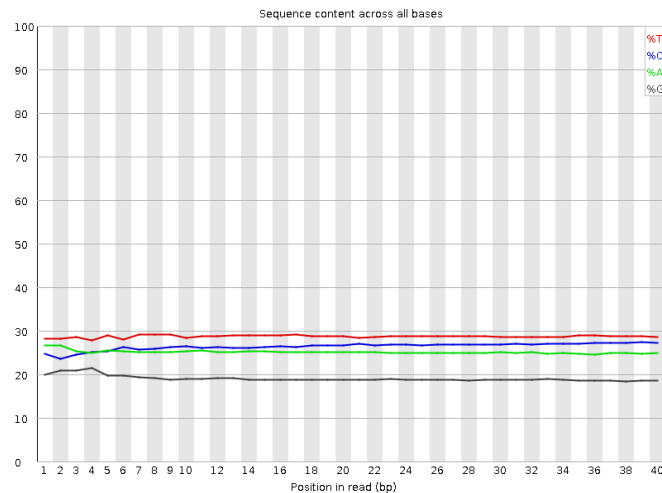
- Number of sequences with the same mean quality



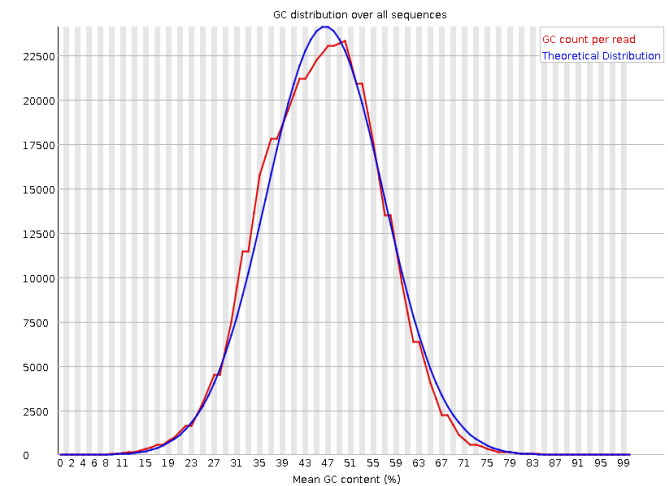
FastQC: Nucleotide related errors

- How expected nucleotide distribution deviates from expected
 - Per base sequence content
 - Per base GC content
 - Per sequence GC content
 - Per base N content

❗ Per base sequence content



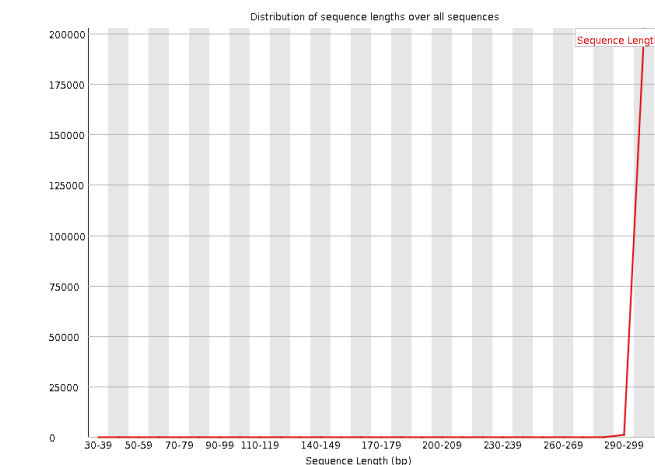
✅ Per sequence GC content



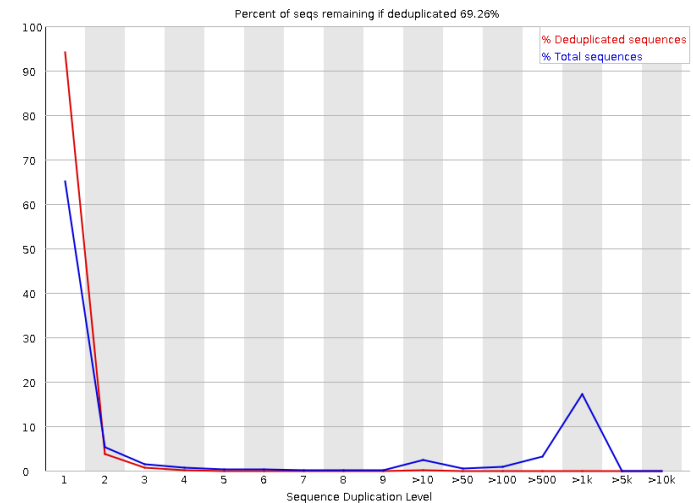
FastQC: Sequence related errors

- How expected nucleotide distribution deviates from expected
 - Sequence Length Distribution - Fragments
 - Sequence Duplication Levels
 - Overrepresented sequences
 - Adapter Content

Sequence Length Distribution



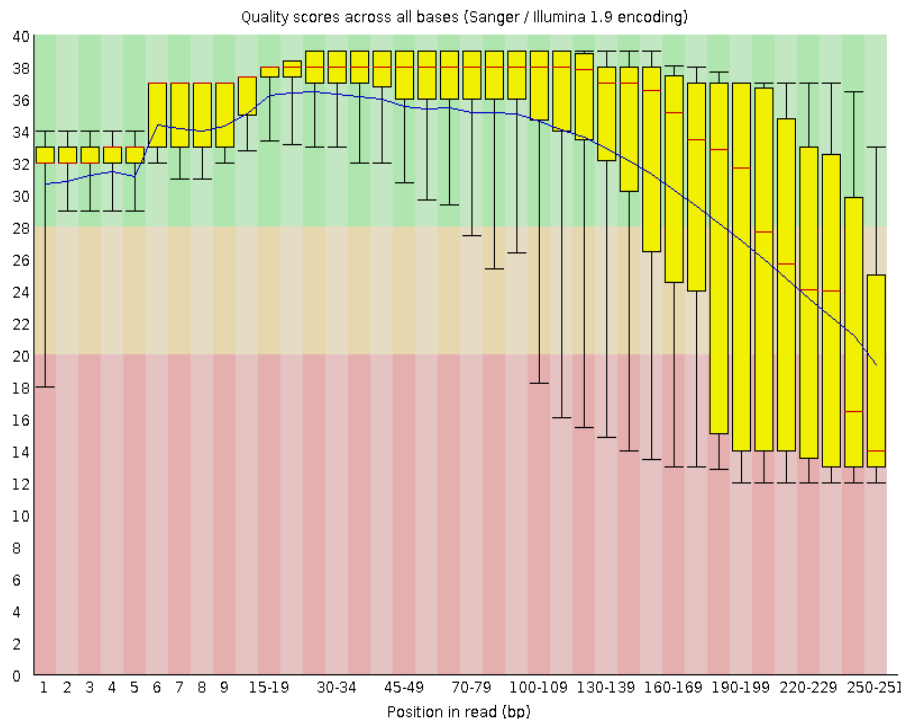
Sequence Duplication Levels



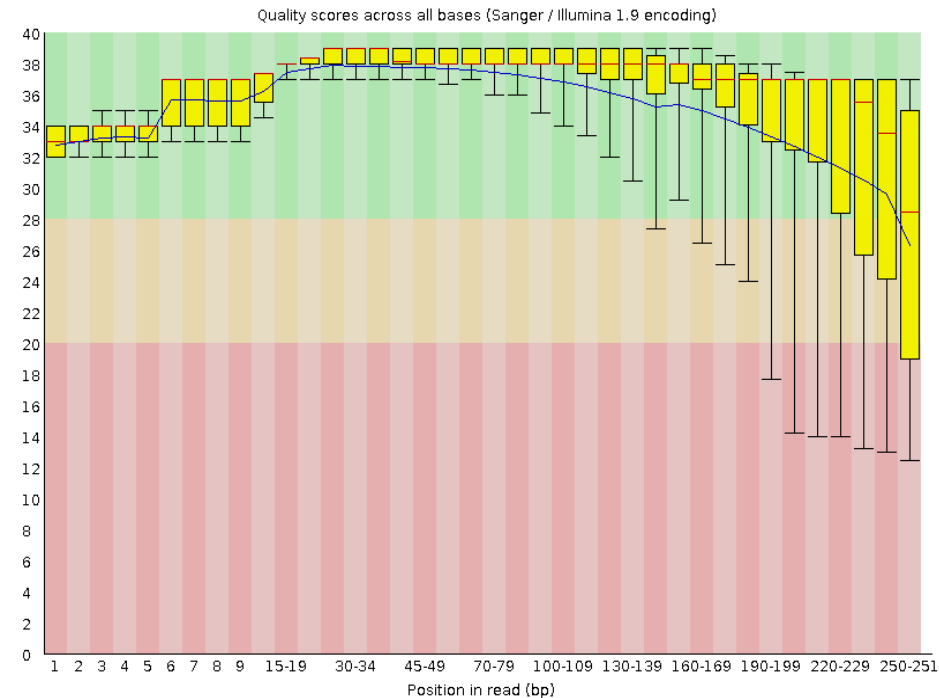
FastQC: Per base sequence quality

- Miseq assymetry

✗ Per base sequence quality

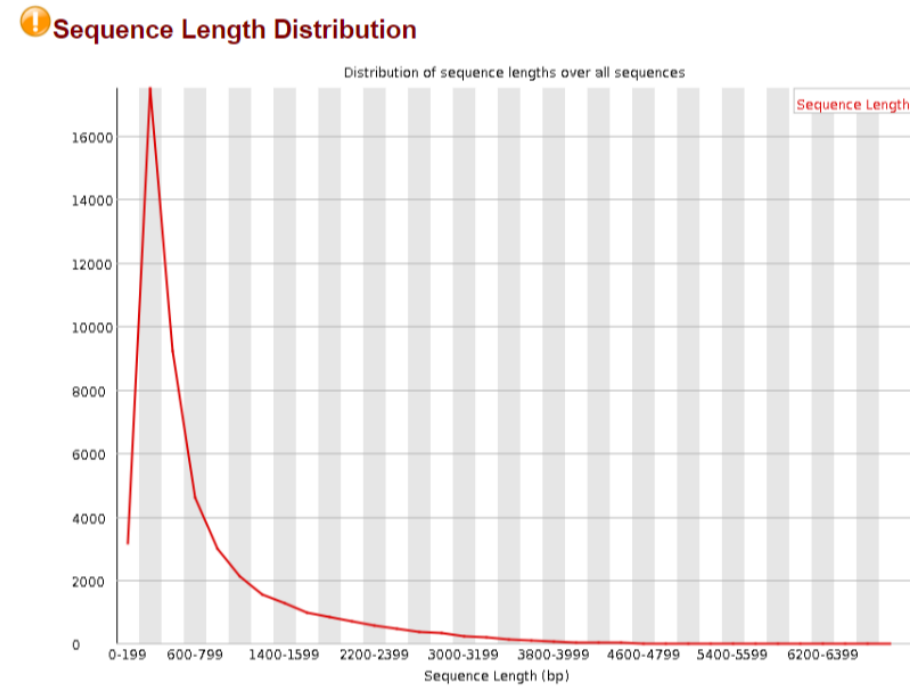
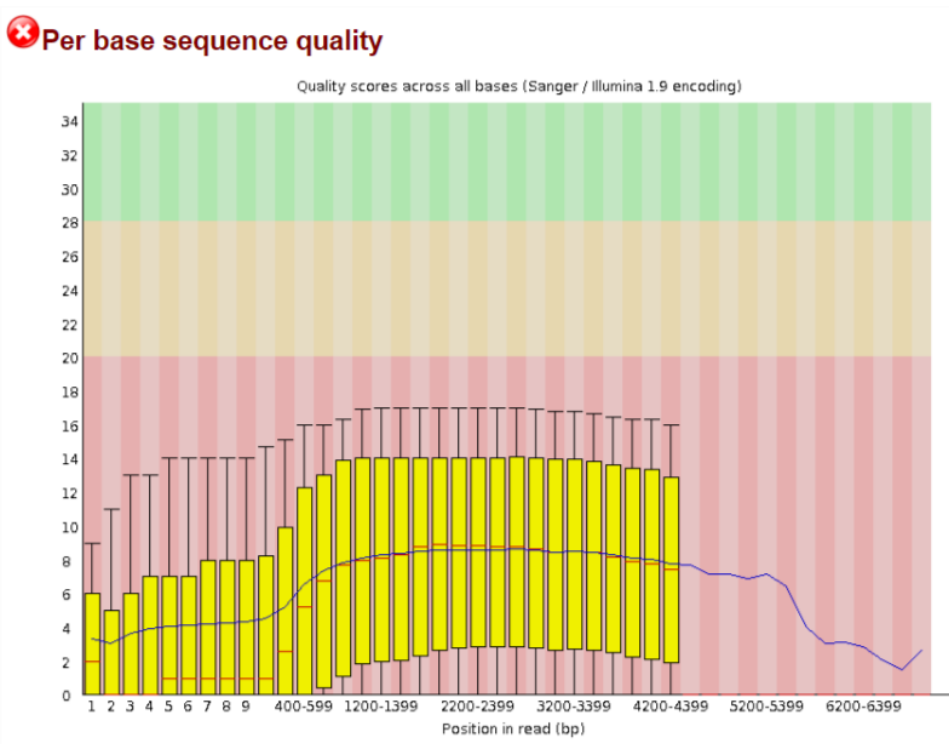


✓ Per base sequence quality



FastQC: Per base sequence quality

- SMRT PacBio



Sequence filtering

- Remove residual adapters
 - Depending on used library
- Filtering parameters
 - Quality filtering
 - Overall mean quality
 - Local mean quality
 - Sequence end
 - Sliding window
 - Size filtering
 - Overall sequence size
 - Remaining sequence size after filtering

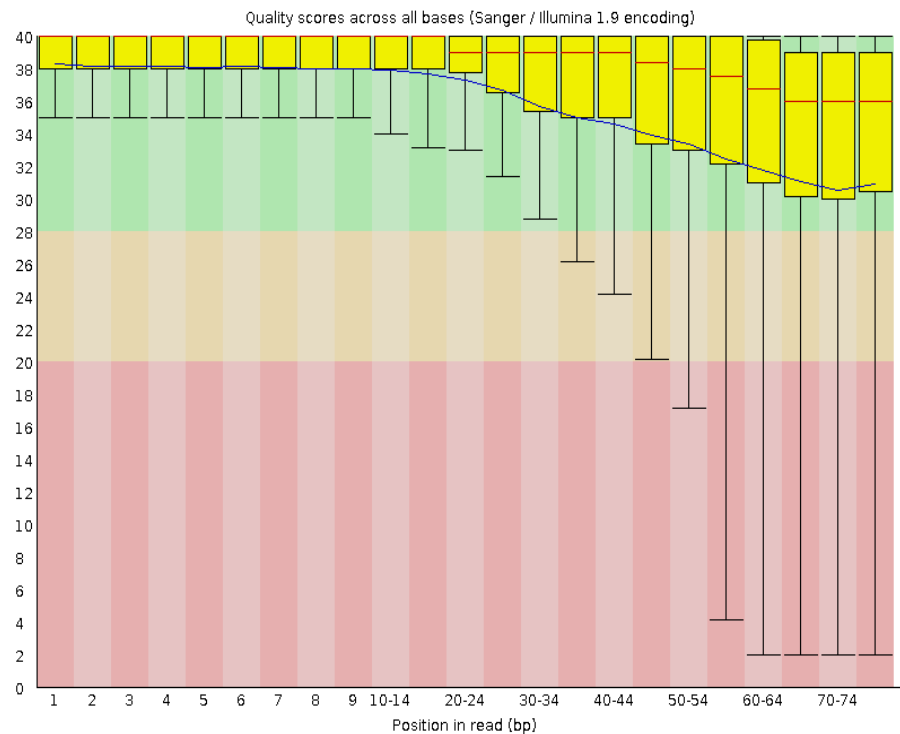


Sequence filtering

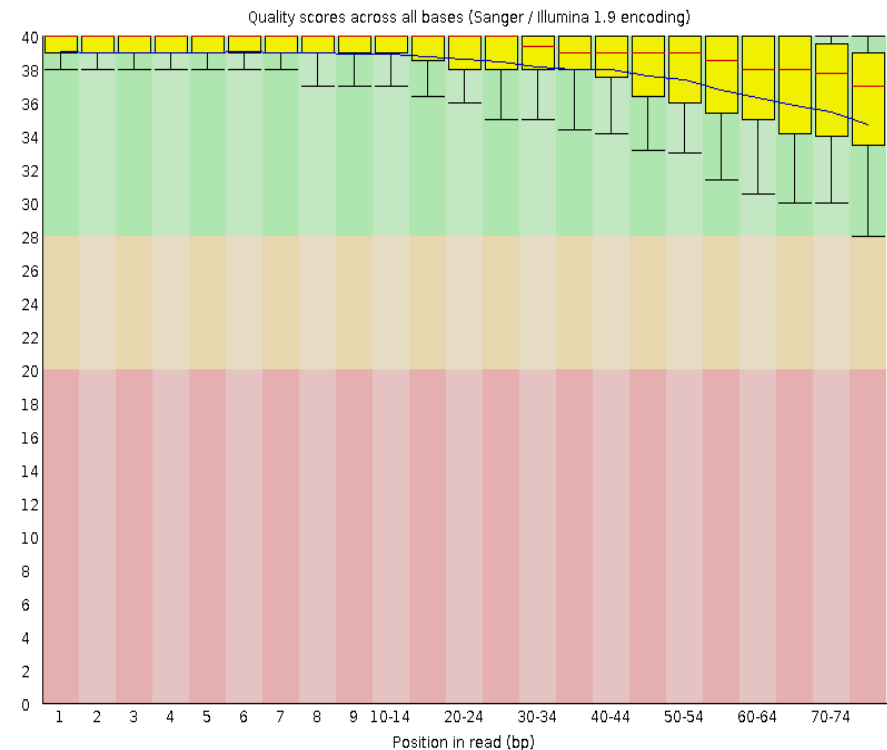
- Example of quality filtering



Per base sequence quality



Per base sequence quality



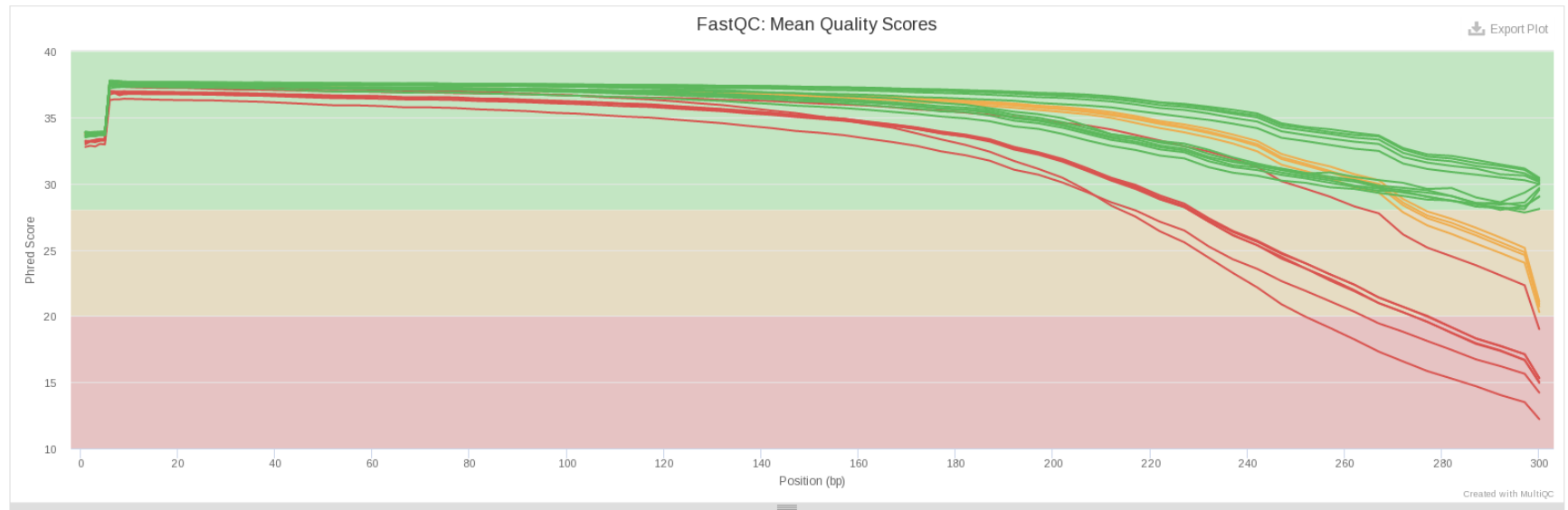
Sequence filtering: stats with MultiQC

Sequence Quality Histograms

11 4 7

The mean quality value across each base position in the read. See the [FastQC help](#).

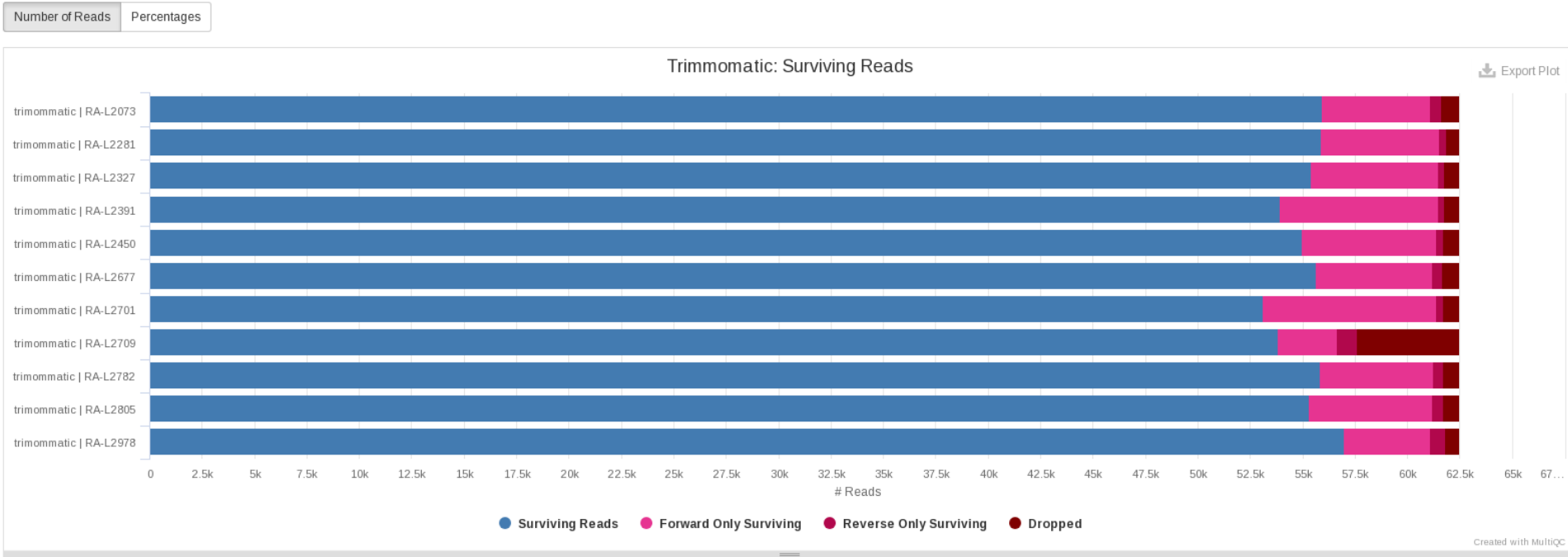
Y-Limits: ☐ off



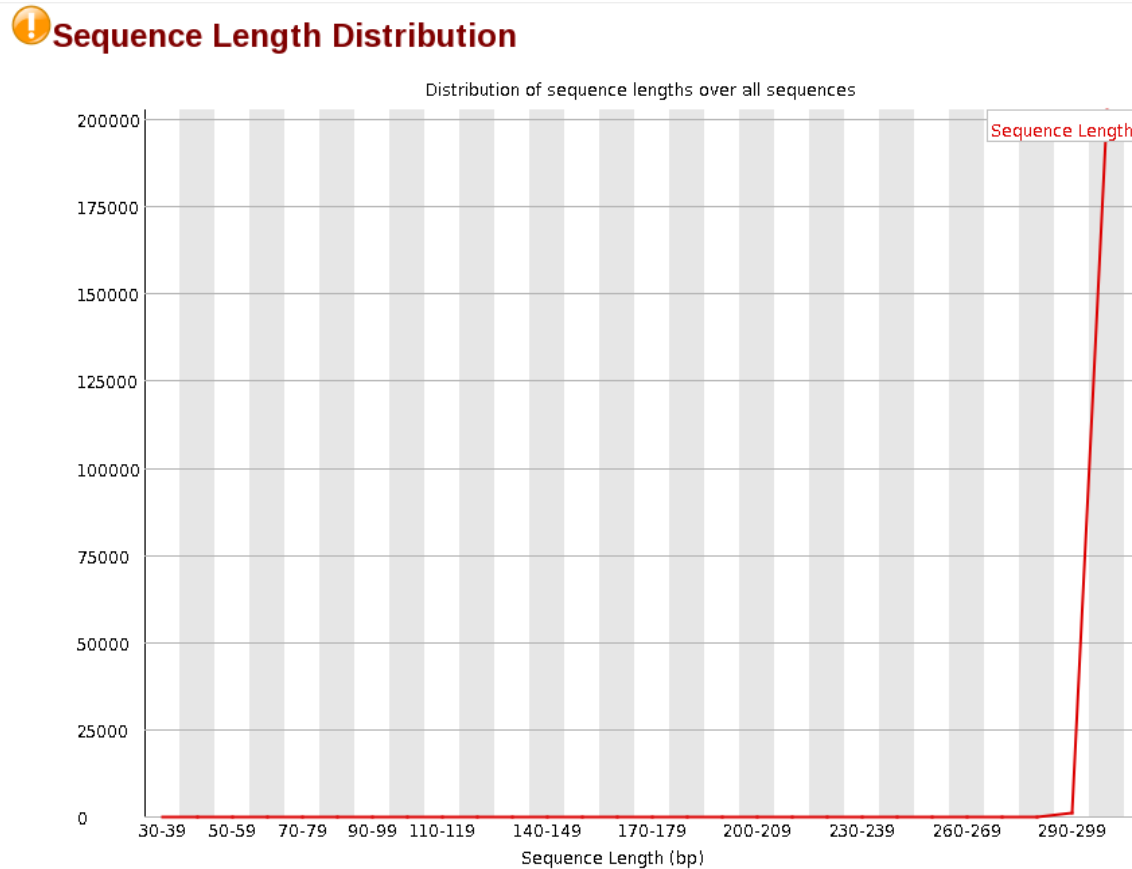
Sequence filtering: stats with MultiQC

Trimmomatic

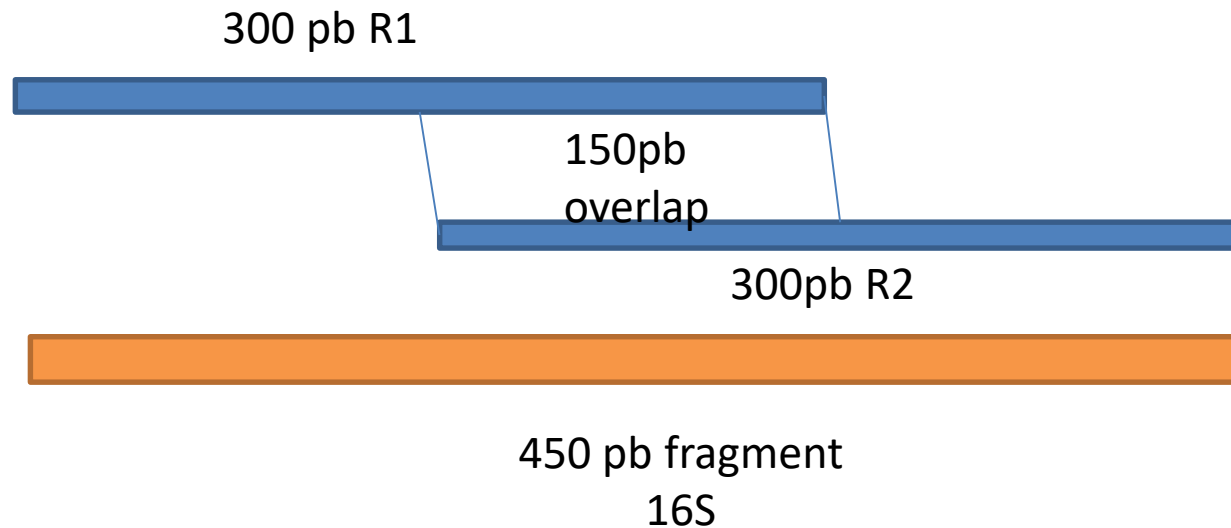
Trimmomatic is a flexible read trimming tool for Illumina NGS data.



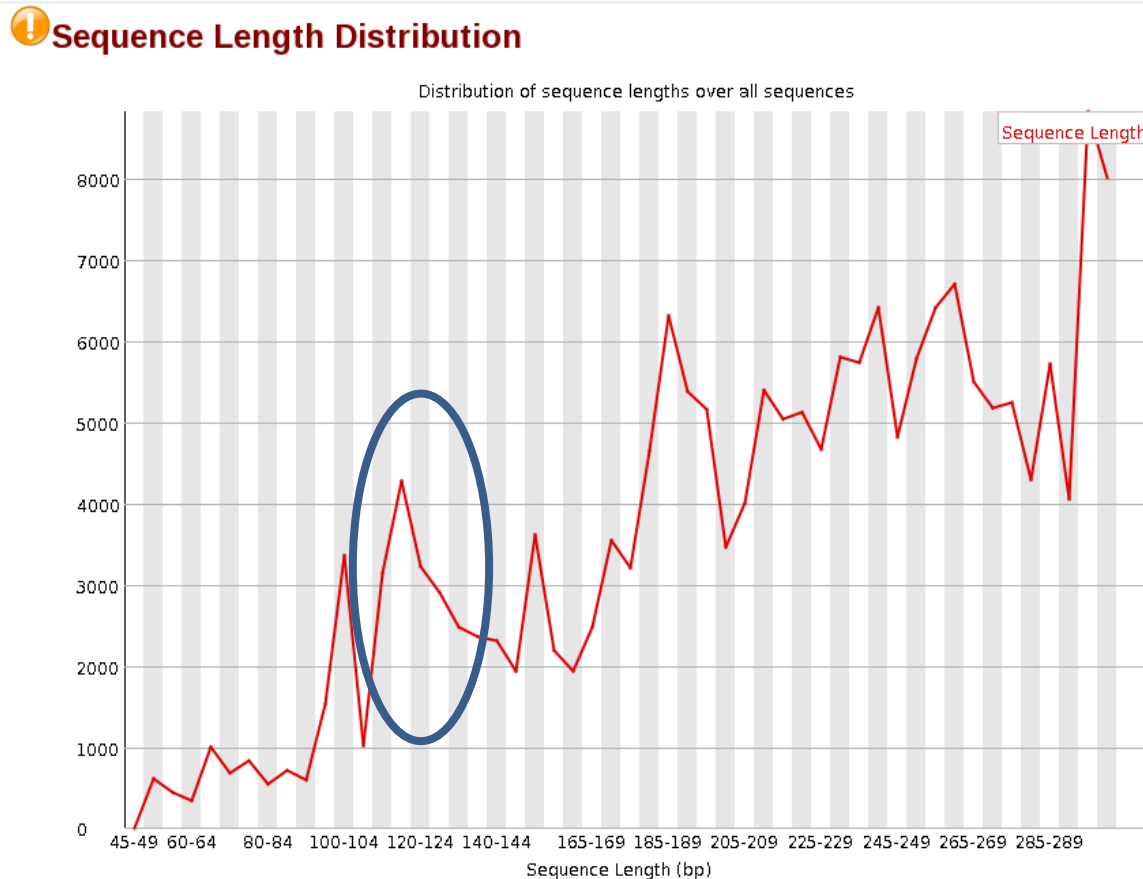
Quality filtering in metagenomic samples



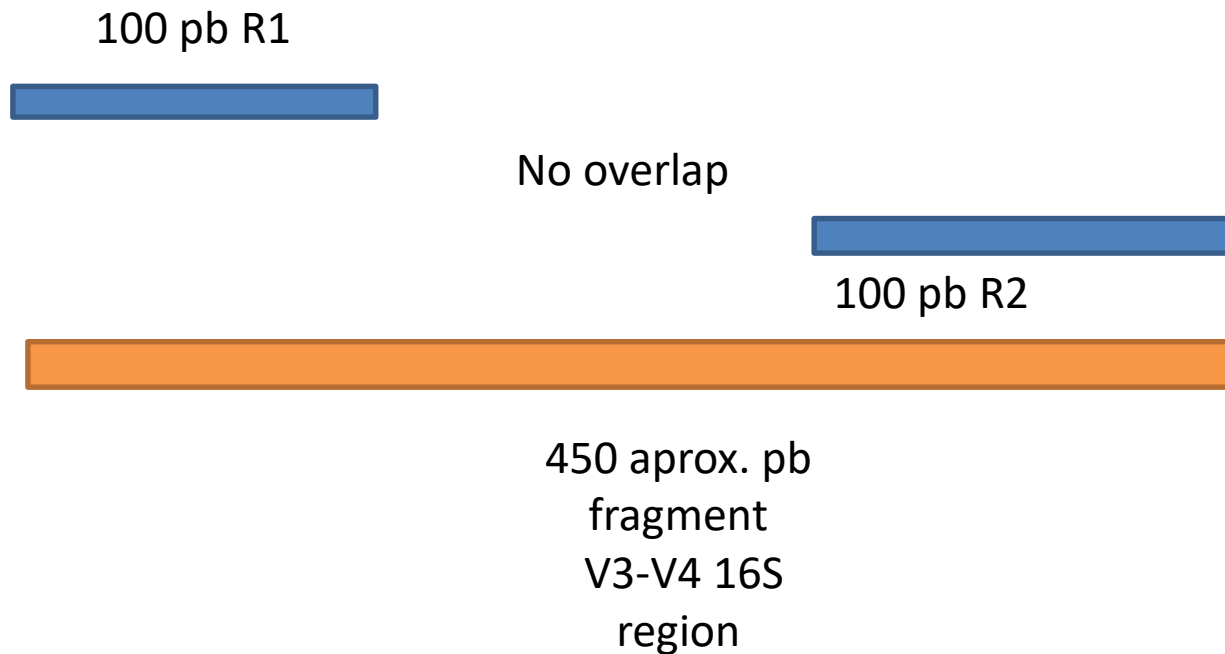
Quality filtering in metagenomic samples



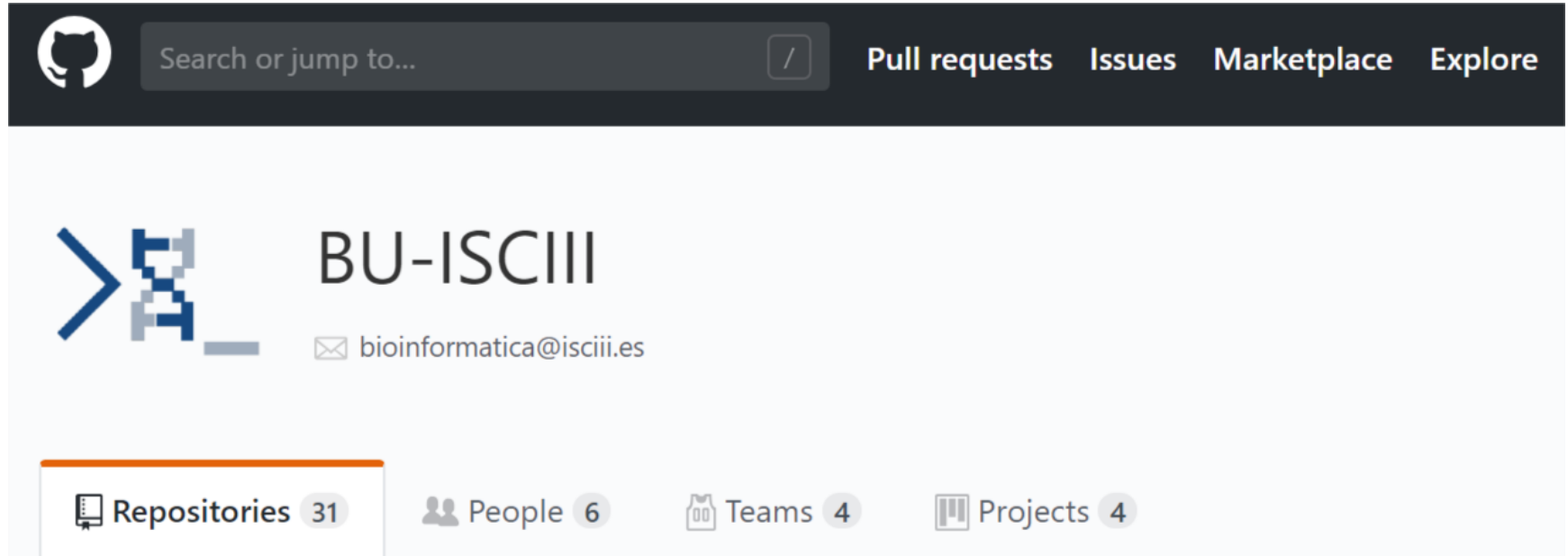
Quality filtering in metagenomic samples



Quality filtering in metagenomic samples



Hands on Quality Assessment



https://github.com/BU-ISCIII/bacterial_wgs_training/blob/master/exercises/02_QualityAndAssembly.md#exercise