



Automated bioinformatics for microbiology labs.

Analysis Name	SISPA_Pilot_flowcell_1
Run ID	4844acd9-2617-4e70-a1e2-3bca358adc1d
BugSeq Pipeline Version	Latest
Contact E-mail	support@bugseq.com

Report generated on 2022-03-28, 18:28

General Statistics

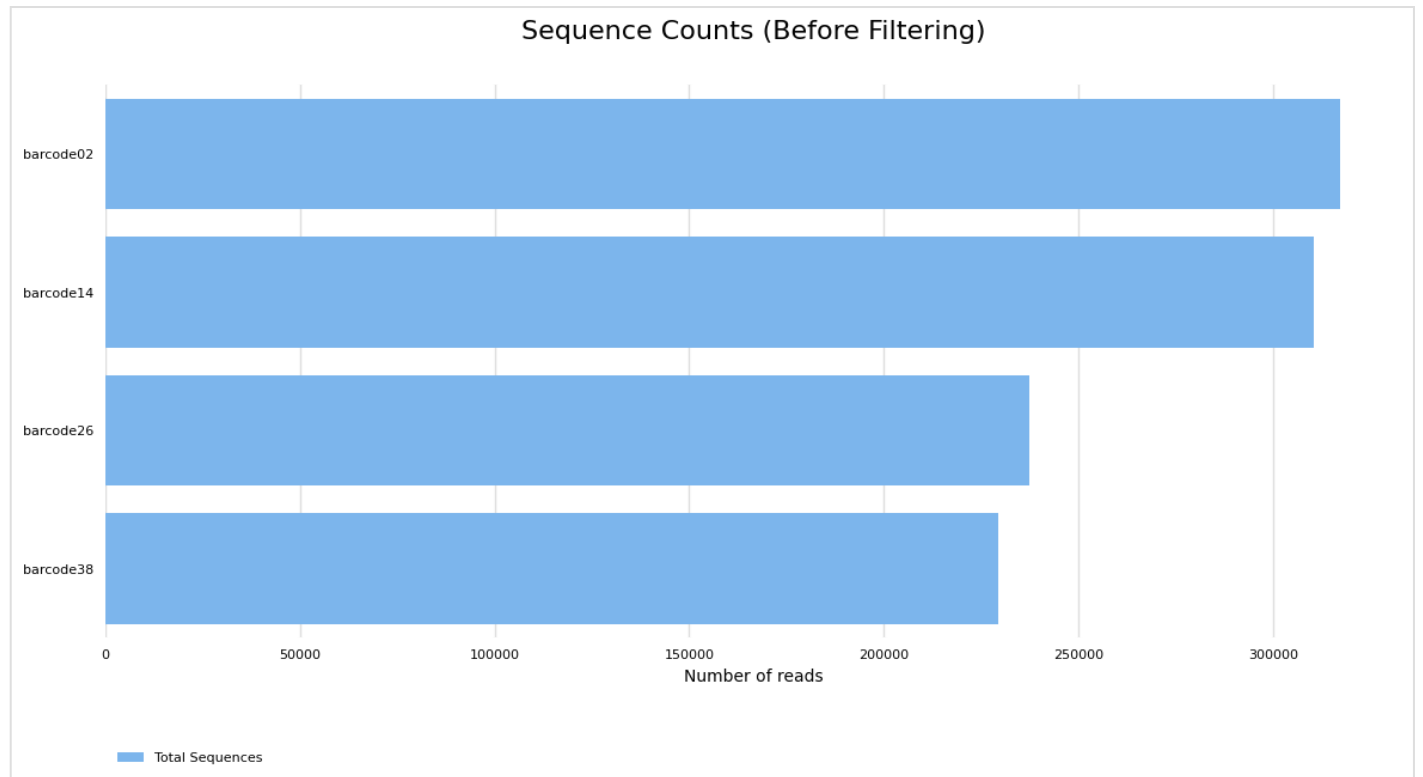
Sample Name	Read Length	K Seqs	% PF
barcode02	212 bp	317.3	100.0%
barcode14	202 bp	310.3	100.0%
barcode26	202 bp	237.5	100.0%
barcode38	199 bp	229.3	100.0%

Read Quality Control

Read Quality Control assesses the quality of input reads before any processing. BugSeq automatically trims and filters reads before downstream analysis.

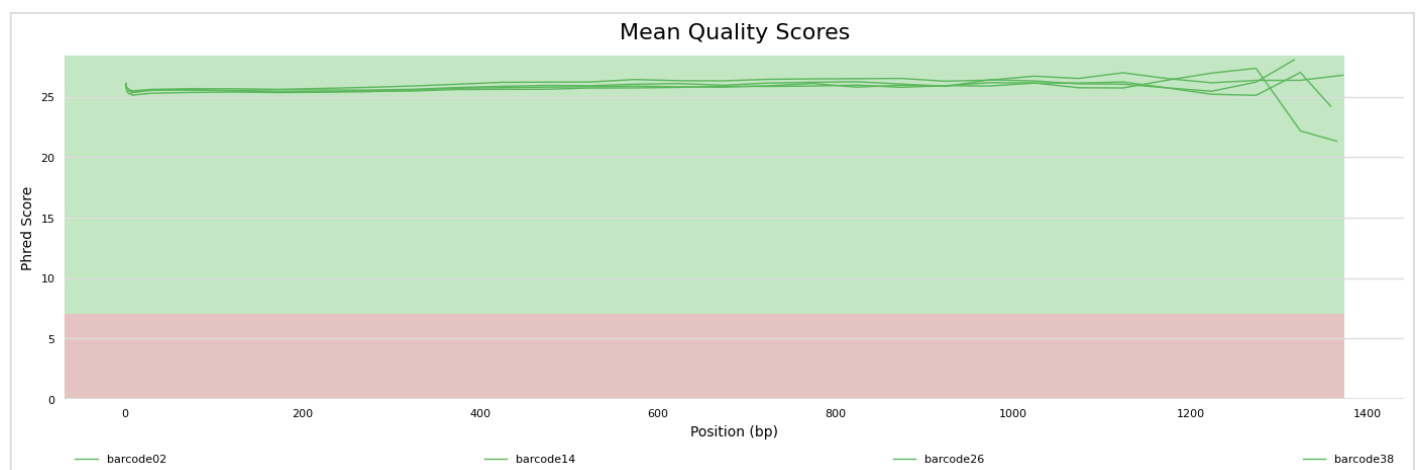
Sequence Counts

Sequence counts for each sample.



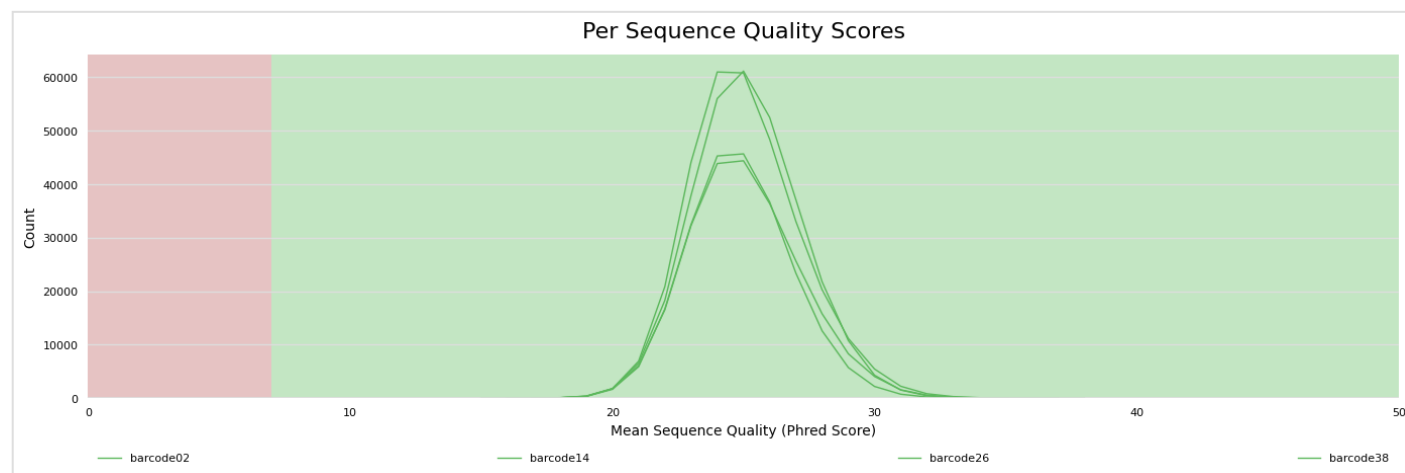
Sequence Quality Histograms

The mean quality value across each base position in the read.



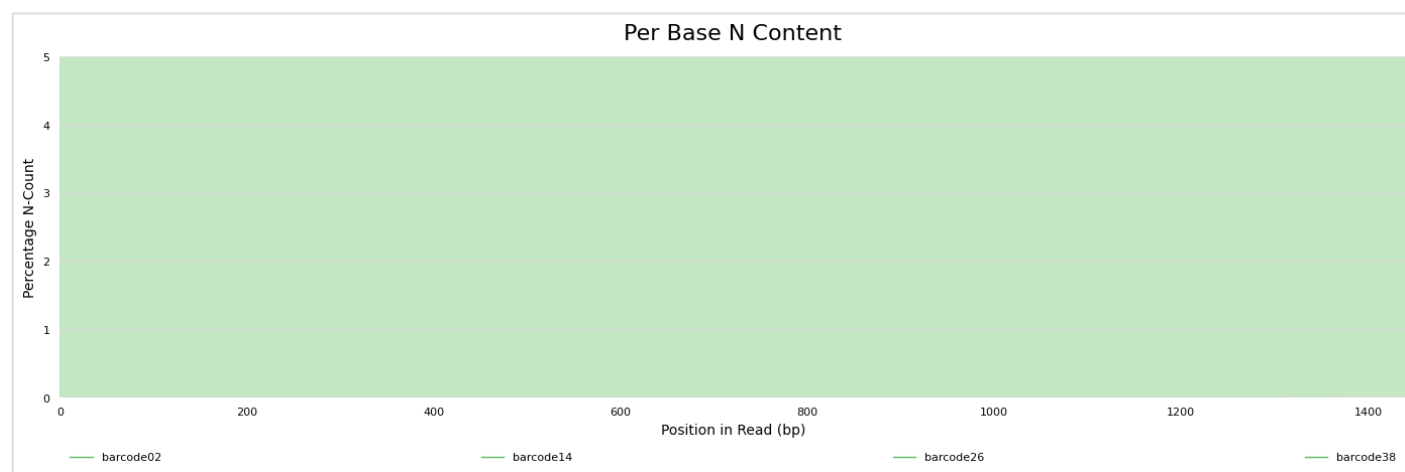
Per Sequence Quality Scores

The number of reads with average quality scores. Shows if a subset of reads has poor quality.



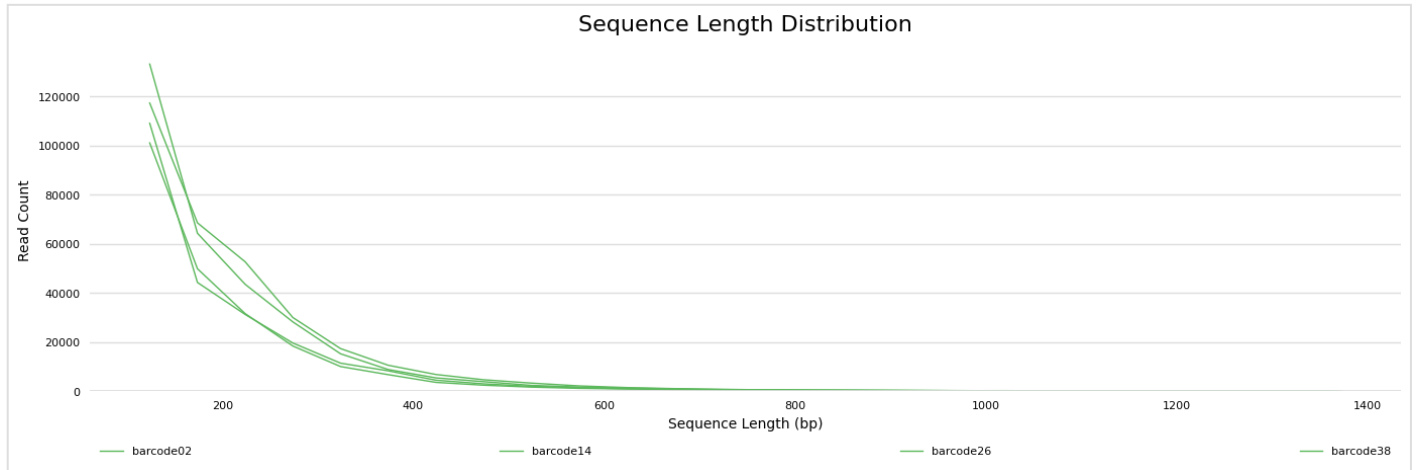
Per Base N Content

The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

The distribution of fragment sizes (read lengths) found. See the FastQC help



Adapter Content

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

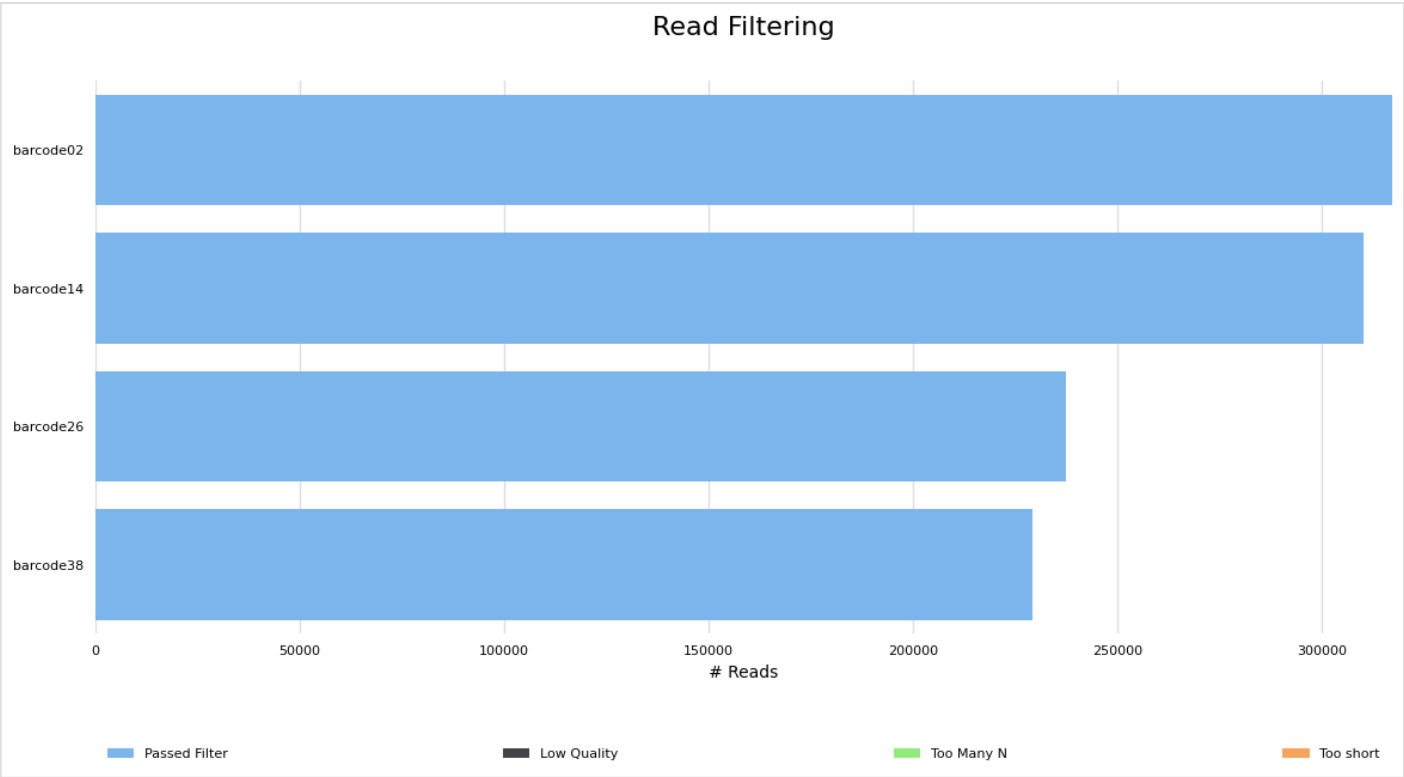
No samples found with any adapter contamination > 0.1%

Read Preprocessing

Read Preprocessing trims, filters and corrects reads before further processing. Thresholds for trimming and filtering are based on sequencing platform and experiment type. *DOI: 10.1093/bioinformatics/bty560.*

Filtered Reads

Filtering statistics of sampled reads.



Flowcell Quality Control

Flowcell Quality Control assesses the performance of the flowcell for a specific sequencing run. Reads from all barcodes on the sequencing run are aggregated if possible. DOI: [10.1093/bioinformatics/bty149](https://doi.org/10.1093/bioinformatics/bty149).

Seq summary stats

NanoStat statistics from albacore or guppy summary files.

Sample Name	Active channels	Median length	Read N50	Median Qual	# Reads (K)	Total Bases (Mb)
barcode02	496	293 bp	328 bp	16.3	540.8	171.2
barcode14	495	276 bp	311 bp	16.4	585.3	175.6
barcode26	494	267 bp	300 bp	16.2	461.5	138.4
barcode38	495	269 bp	300 bp	16.3	450.6	134.0

Reads by quality

Read counts categorised by read quality (phred score).

