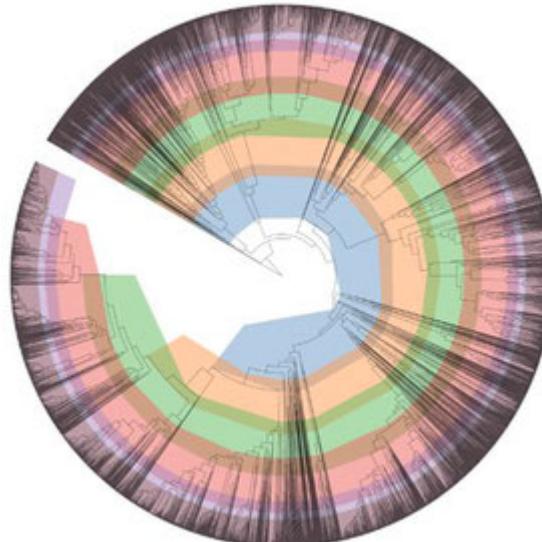


ENVIRONMENTAL METAGENOMICS

Physalia course, online, 11-15 November 2024

Data pre-processing: quality control and adapter removal

Nikolay Oskolkov, Lund University, NBIS SciLifeLab
Luis Pedro Coelho, Queensland University of Technology



NB: original course material courtesy:
Dr. Antti Karkman, University of Helsinki
Dr. Igor Pessi, Finnish Environment Institute (SYKE)

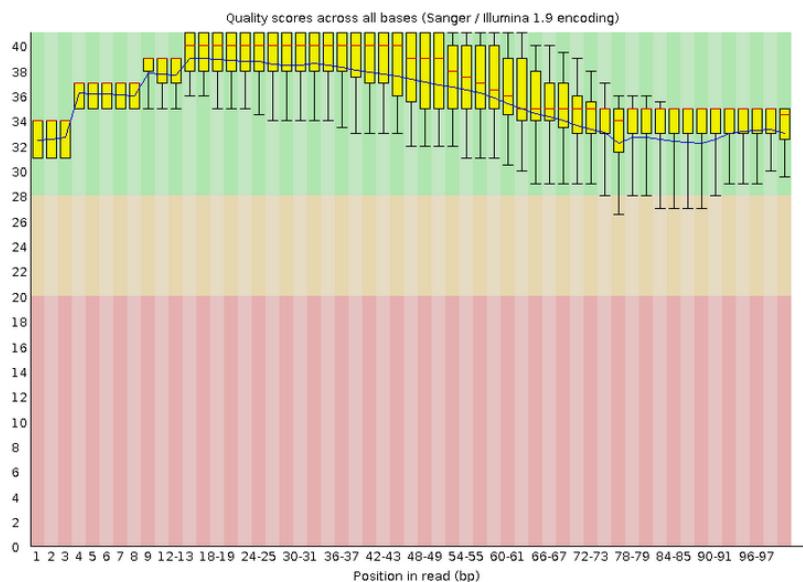
Summary

- ✓ Basic Statistics
- ✓ Per base sequence quality
- ✓ Per tile sequence quality
- ✓ Per sequence quality scores
- ! Per base sequence content
- ✓ Per sequence GC content
- ✓ Per base N content
- ! Sequence Length Distribution
- ✓ Sequence Duplication Levels
- ✓ Overrepresented sequences
- ✗ Adapter Content

Basic Statistics

Measure	Value
Filename	G69146_pe_1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	8997912
Sequences flagged as poor quality	0
Sequence length	77-101
%GC	49

Per base sequence quality



Quality Scores

A quality score (or Q-score) expresses an error probability. In particular, it serves as a convenient and compact way to communicate very small error probabilities.

Given an assertion, A, the quality score, Q(A), expresses the probability that A is not true, P(~A), according to the relationship:

$$Q(A) = -10 \log_{10}(P(\sim A))$$

where $P(\sim A)$ is the estimated probability of an assertion A being wrong.

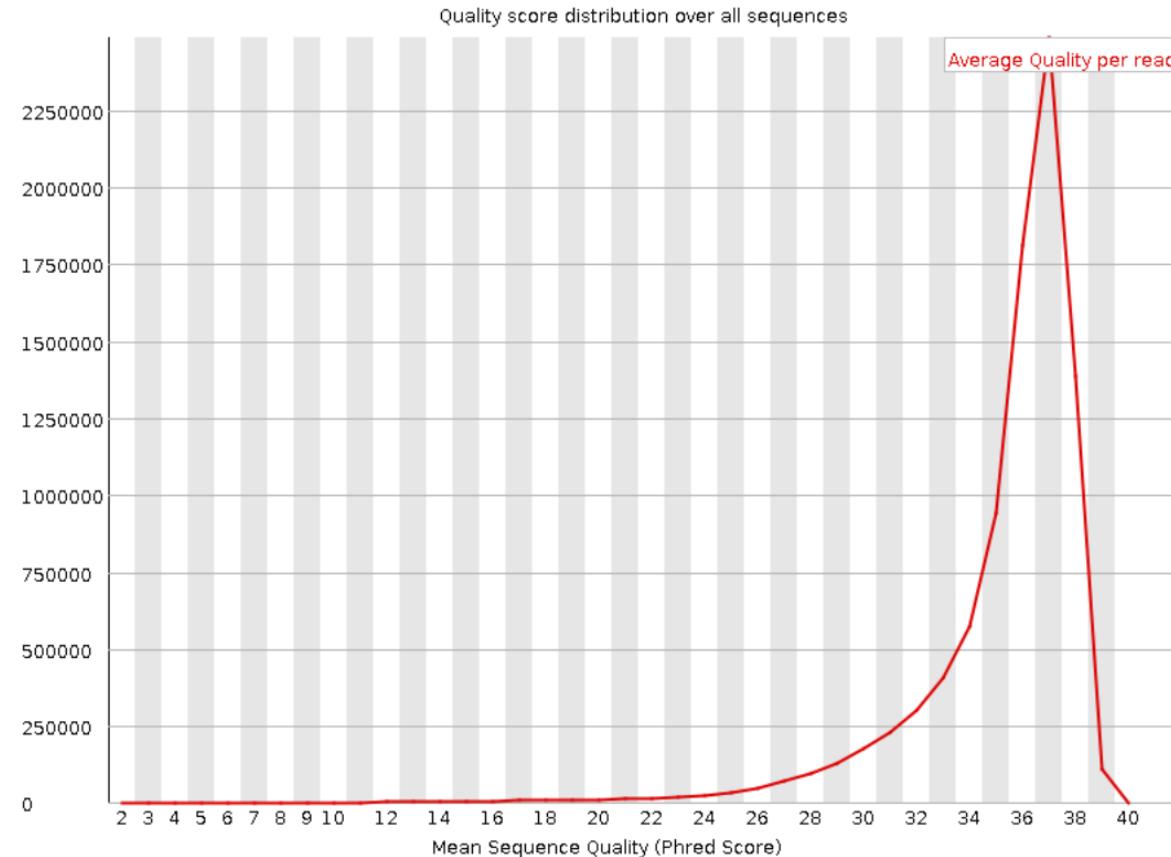
The relationship between the quality score and error probability is demonstrated with the following table:

Quality score, Q(A)	Error probability, P(~A)
10	0.1
20	0.01
30	0.001

Summary

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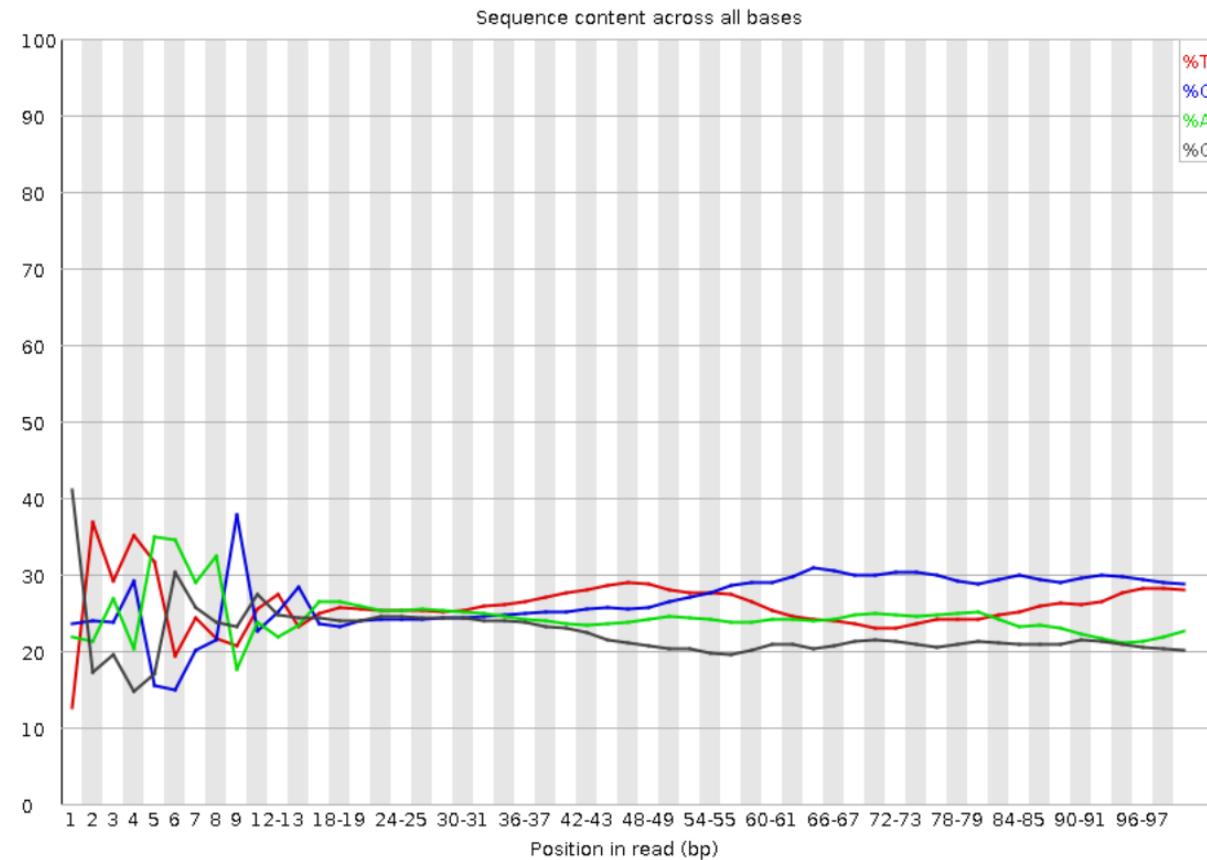
Per sequence quality scores



Summary

- [Basic Statistics](#)
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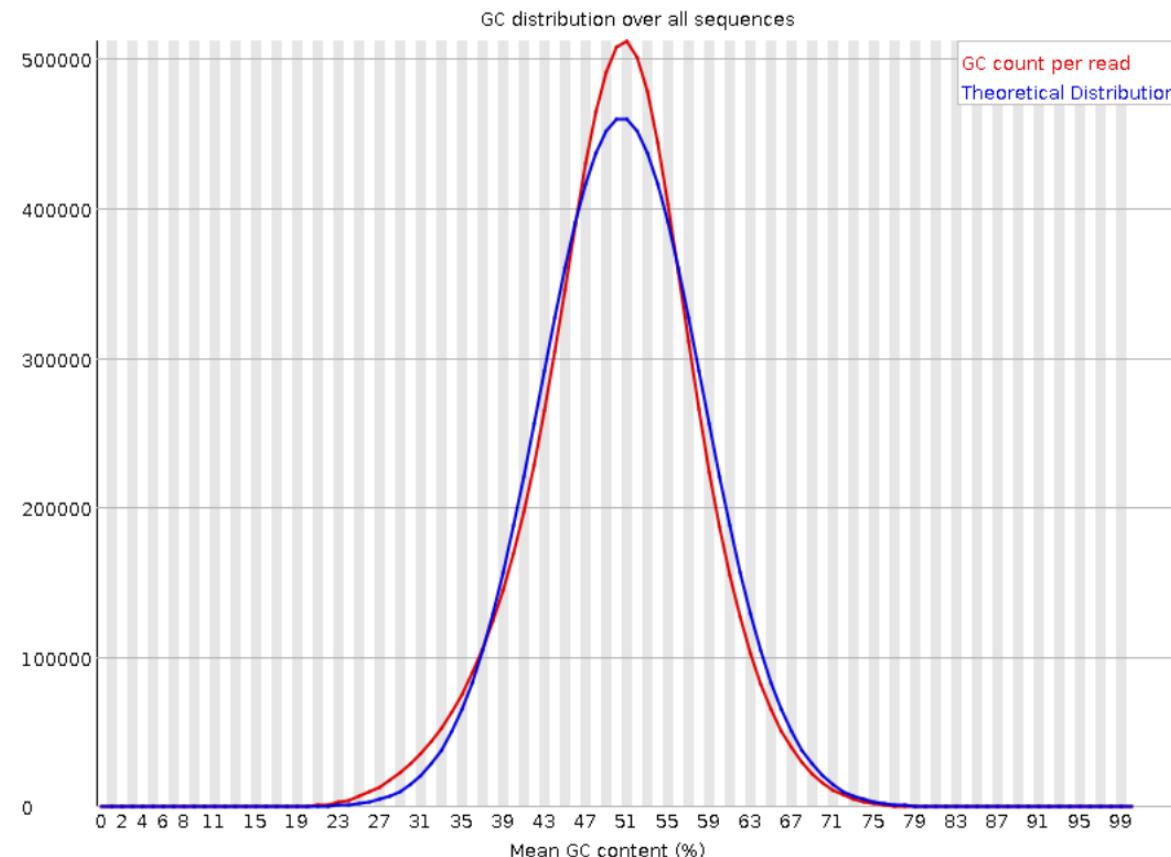
⚠ Per base sequence content



Summary

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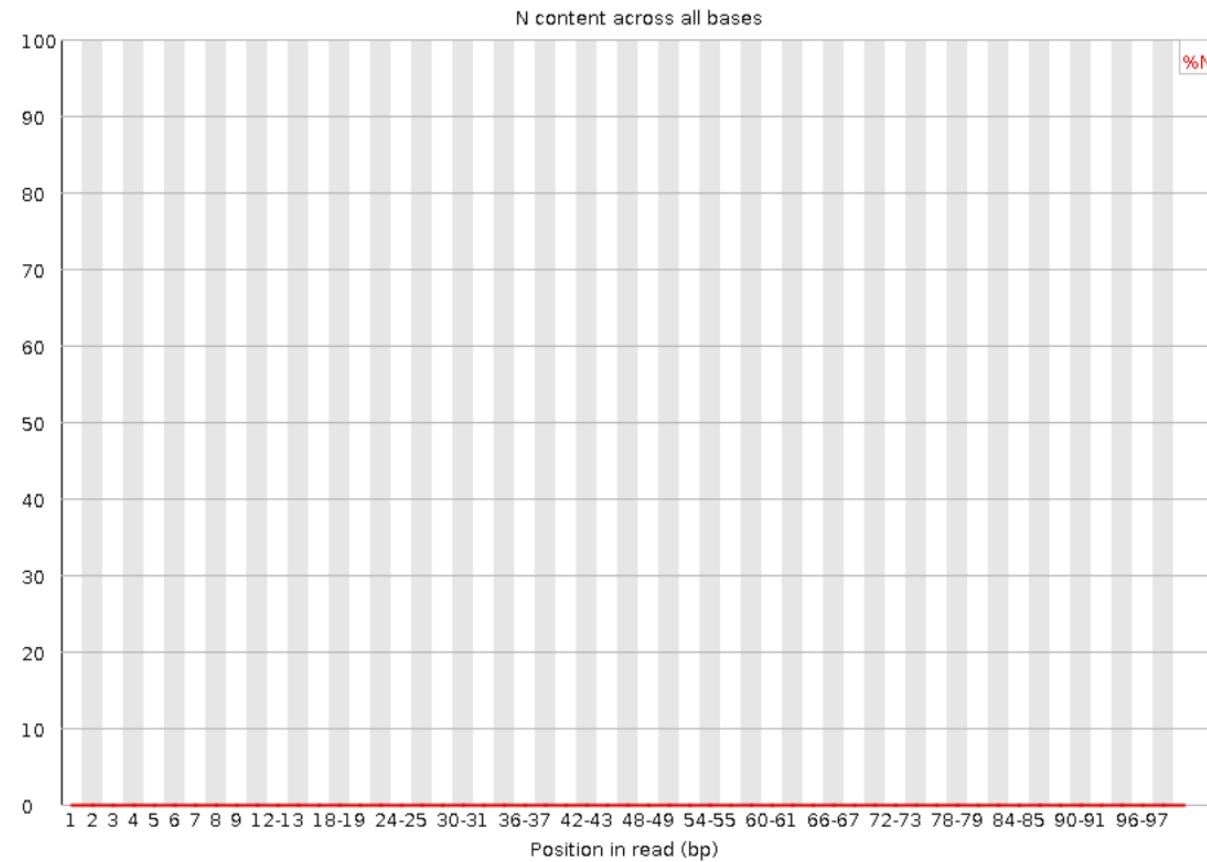
✓ Per sequence GC content



Summary

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- ✓ [Sequence Duplication Levels](#)
- ✓ [Overrepresented sequences](#)
- ✗ [Adapter Content](#)

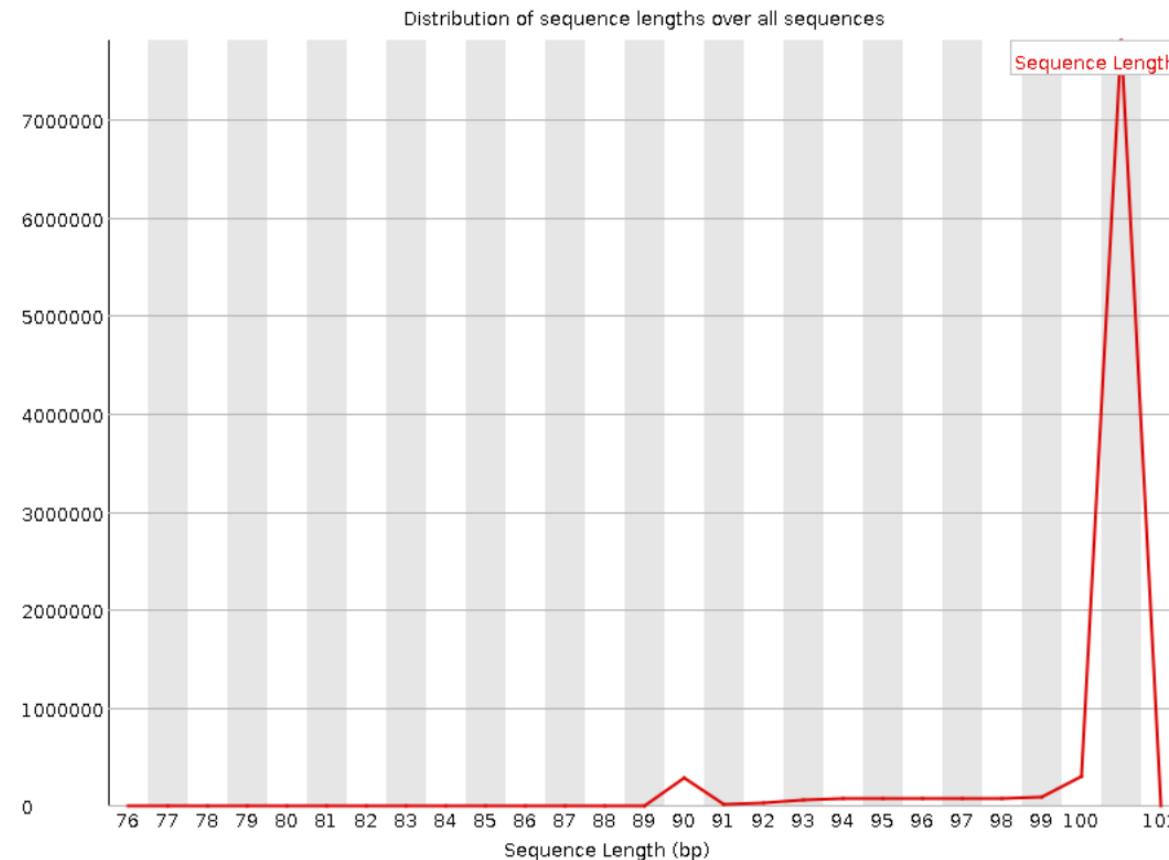
✓ Per base N content



Summary

- [Basic Statistics](#)
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- [Per sequence quality scores](#)
- [Per base sequence content](#)
- [Per sequence GC content](#)
- [Per base N content](#)
- [Sequence Length Distribution](#)
- [Sequence Duplication Levels](#)
- [Overrepresented sequences](#)
- [Adapter Content](#)

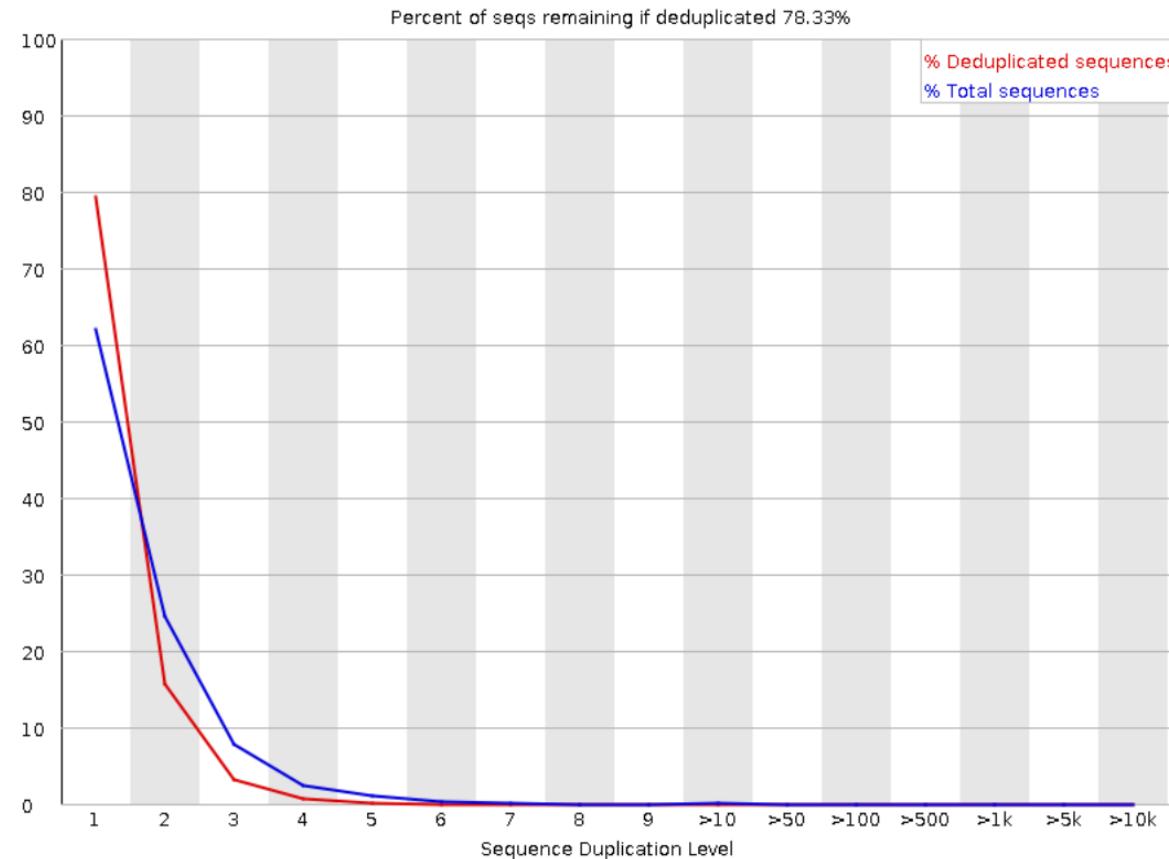
⚠ Sequence Length Distribution



Summary

- ✓ [Basic Statistics](#)
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- ! [Sequence Length Distribution](#)
- ✓ [Sequence Duplication Levels](#)
- ✓ [Overrepresented sequences](#)
- ✗ [Adapter Content](#)

Sequence Duplication Levels



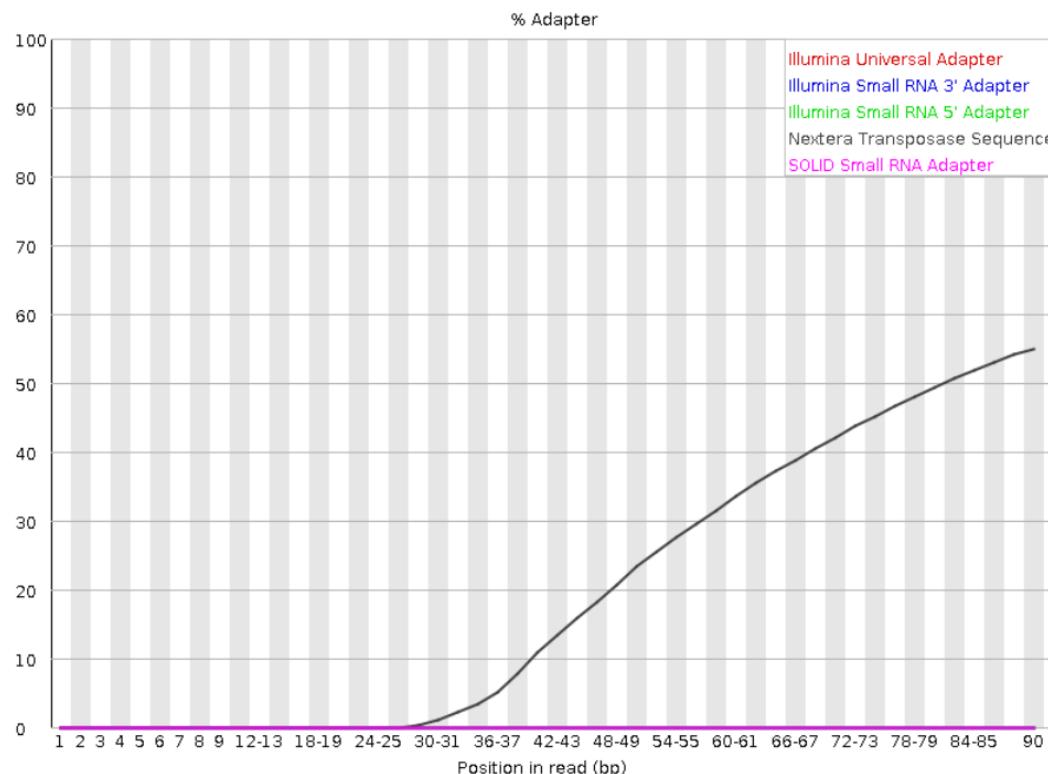
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- ✗ [Adapter Content](#)

✓ Overrepresented sequences

No overrepresented sequences

✗ Adapter Content



General Stats
FastQC
Sequence Quality Histograms
Per Sequence Quality Scores
Per Base Sequence Content
Per Sequence GC Content
Per Base N Content
Sequence Length Distribution
Sequence Duplication Levels
Overrepresented sequences
Adapter Content

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2017-09-01, 09:26 based on data in: /pica/v11/b2017206_nobackup/private/wabi/RNAseq/multiQC_raw_vs_trimmed

ⓘ Welcome! Not sure where to start?

[Watch a tutorial video \(6:06\)](#)

don't show again

General Statistics

Copy table

Configure Columns

Plot

Showing 18/18 rows and 4/5 columns.

Sample Name	% Dups	% GC	Length	M Seqs
P8205_101_S1_L001_R1_001	75.7%	46%	126 bp	81.2
P8205_101_S1_L001_R1_001.trimmomatic	75.7%	46%	126 bp	80.5
P8205_101_S1_L001_R1_001.trimmomatic_unpaired	38.7%	47%	106 bp	0.7
P8205_101_S1_L001_R2_001	71.9%	47%	126 bp	81.2
P8205_101_S1_L001_R2_001.trimmomatic	72.0%	46%	126 bp	80.5
P8205_101_S1_L001_R2_001.trimmomatic_unpaired	7.7%	47%	126 bp	0.0
P8205_102_S2_L001_R1_001	83.5%	46%	126 bp	86.2
P8205_102_S2_L001_R1_001.trimmomatic	83.5%	46%	126 bp	85.5
P8205_102_S2_L001_R1_001.trimmomatic_unpaired	50.3%	47%	108 bp	0.7
P8205_102_S2_L001_R2_001	80.0%	47%	126 bp	86.2
P8205_102_S2_L001_R2_001.trimmomatic	80.1%	47%	126 bp	85.5
P8205_102_S2_L001_R2_001.trimmomatic_unpaired	4.0%	41%	126 bp	0.0

FastQC

[FastQC](#) is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Quality Histograms

10 2 6

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

on

Mean Quality Scores

Export Plot

FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

General Stats

FastQC

Sequence Quality Histograms

10 2 6

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

Y-Limits:

on

Toolbox



Per Sequence Quality Scores

15 3

The number of reads with average quality scores. Shows if a subset of reads has poor quality. See the [FastQC help](#).

Y-Limits:

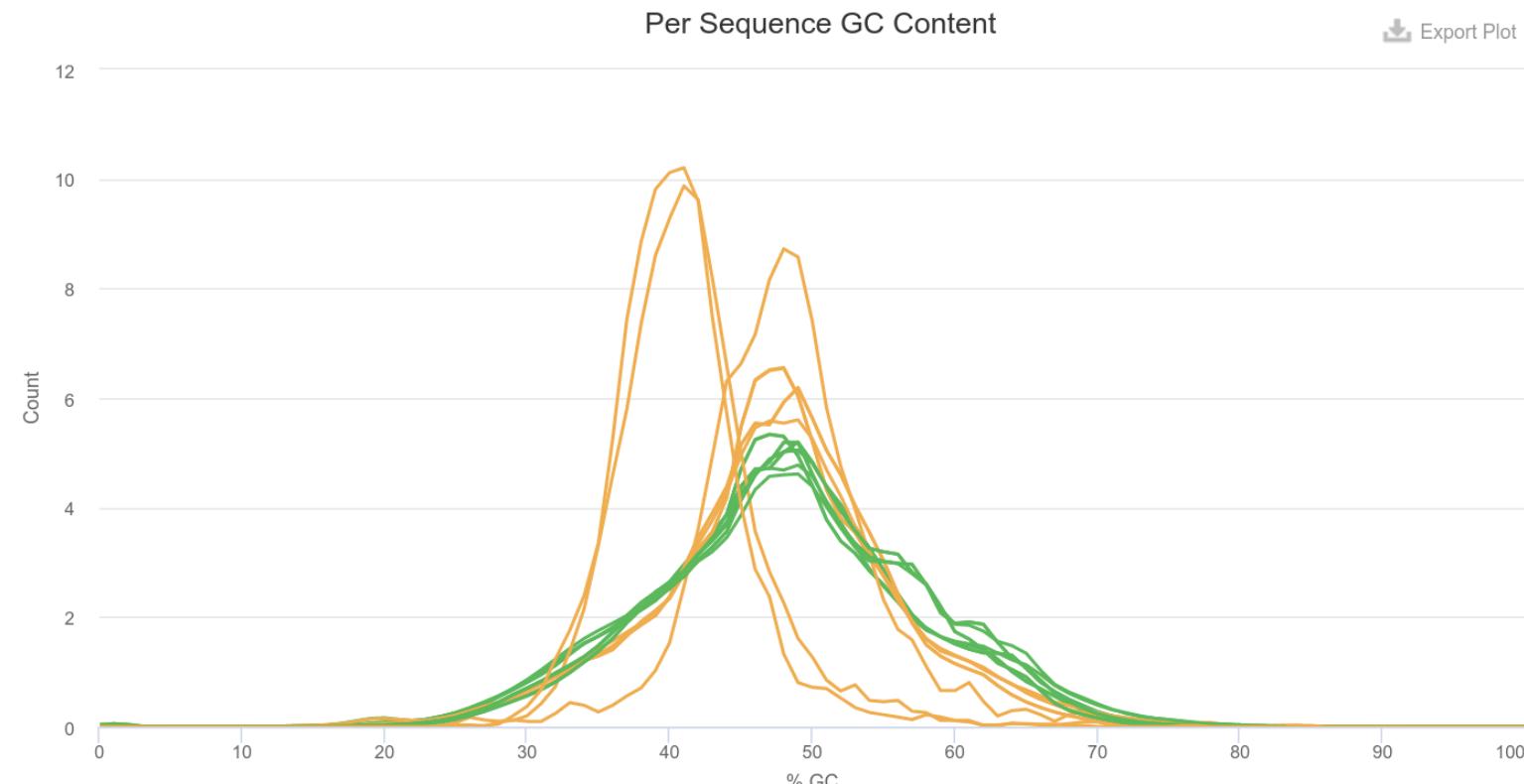
on



Per Sequence GC Content

10 8

The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content. See the [FastQC help](#). Y-Limits: on

 Percentages Counts

General Stats

FastQC

Sequence Quality Histograms

Per Sequence Quality Scores

Per Base Sequence Content

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Sequence Duplication Levels

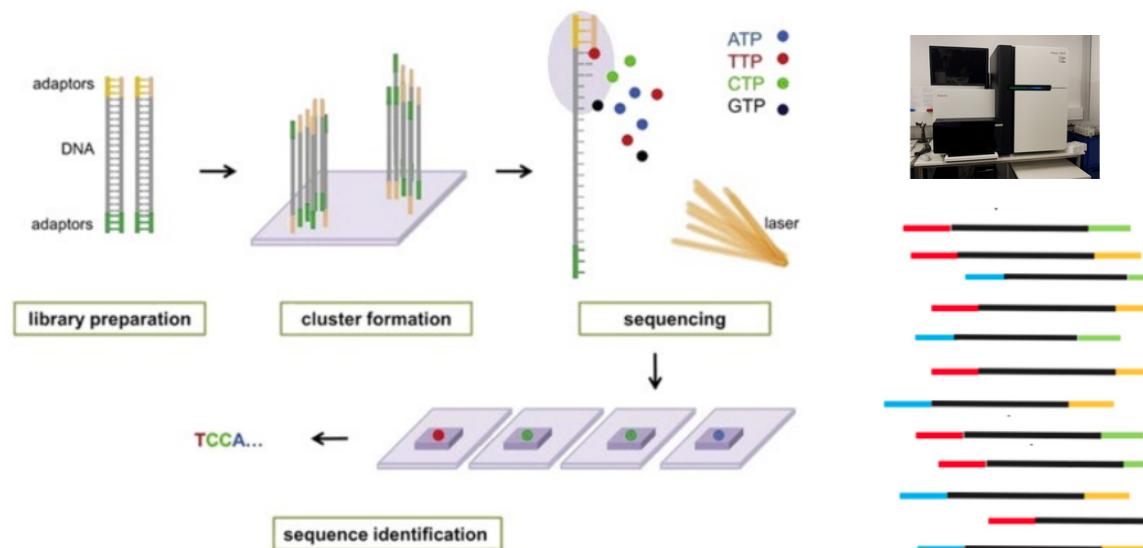
Overrepresented sequences

Adapter Content

Toolbox



Illumina DNA construct: indexes and adapters



Zhou et al. 2015. Atlas Oral Microbiol. <https://doi.org/10.1016/B978-0-12-802234-4.00002-1>

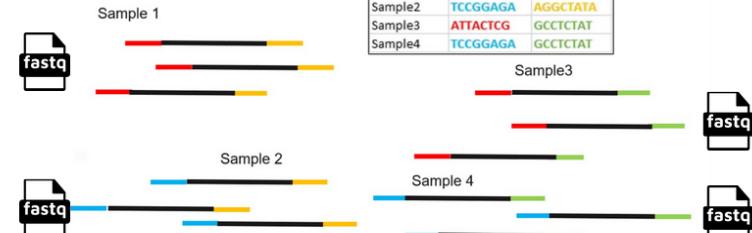
For Research Use Only. Not for use in diagnostic procedures.

illumina

Demultiplexing

- Assigns clusters to a sample, based on the cluster's index sequence which is provided in the sample sheet

[Data]		
Sample_ID	index	index2
Sample1	ATTACTCG	AGGGCTATA
Sample2	TCCGGAGA	AGGGCTATA
Sample3	ATTACTCG	GCTCTAT
Sample4	TCCGGAGA	GCTCTAT



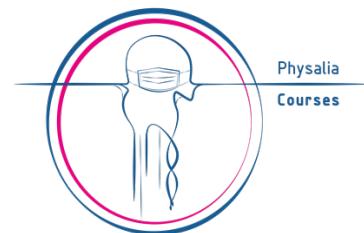
GGTGTATACGGCGACCACCAcaccgacGGCCCTACACGACGCTCTTCCGATCTXXXXXXXXAGCACACGTCGGGCTCCAGTCACgacactaCCGTCTTCTGTTG

TTTACTATGCCGCTGGTGGTGTggctatttGGGATGTGCTGCAGGGGGCTAGAxxxxxxxxTCGTTGTGCAGACTTGAGGTCACTGtcgttgtatGGCAGGGGACGGGCG

[Adapter/Index Primer] [Index] [Target primer] [Target] [Target primer] [Index] [Adapter/Index Primer]

K00233:37:HGHLYBBXX:3:1101:2646:1121 1:N:0:NACGCATC+NGCTGGTGG

NCGCATGAGCCGCTGTATCAGGCGCTGATCGGGCCGGCATTCAGTTGGGATAGATCGGGGGAGCACACGTCTG



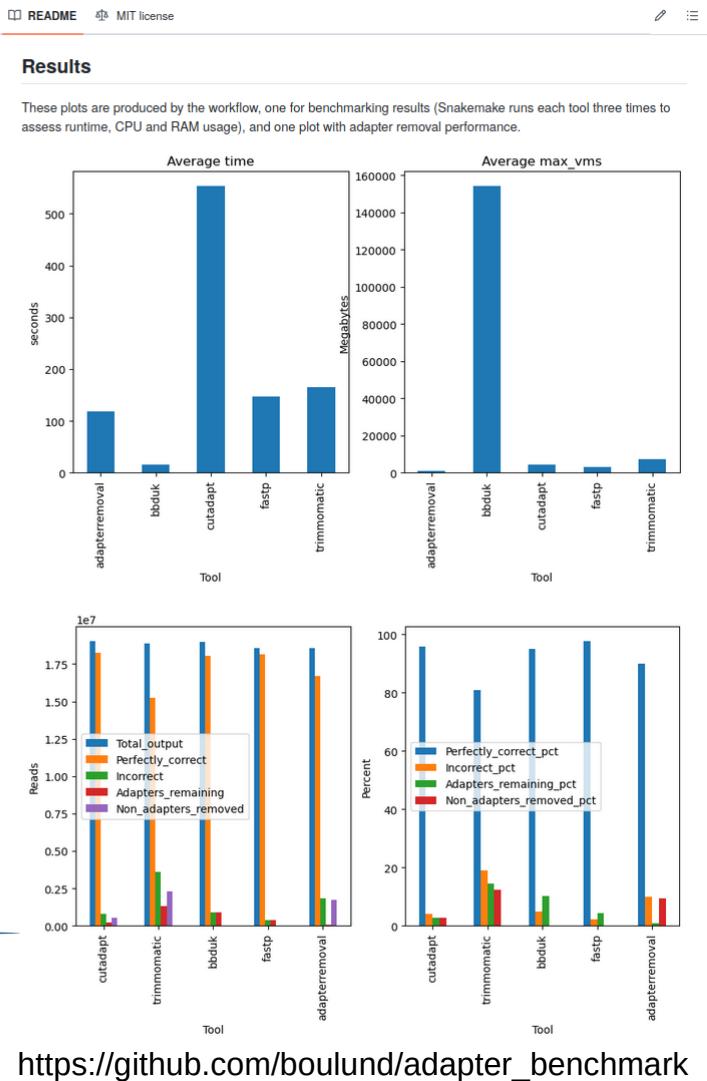
Popular adapter removal tools and benchmark results

Cutadapt

fastp

Trimmomatic

TrimGalore



https://github.com/boulund/adapter_benchmark

Benchmarking software tools for trimming adapters and merging next-generation sequencing data for ancient DNA

Annette Lien¹, Leonardo Pestana Legori², Louis Kraft¹, Peter Wad Sackett¹ and Gabriel Renaud^{1*}

¹Department of Health Technology, Section for Bioinformatics, Technical University of Denmark, Kongens Lyngby, Denmark, ²University of Debrecen, Debrecen, Hungary

Check for updates

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EDITED BY
Richard Allen White III,
University of North Carolina at Charlotte,
United States

REVIEWED BY
Emma Fay Harding,
University of New South Wales, Australia
Sydney Birch,
University of North Carolina at Charlotte,
United States

*CORRESPONDENCE
Gabriel Renaud,
✉ gabriel.renaud@gmail.com

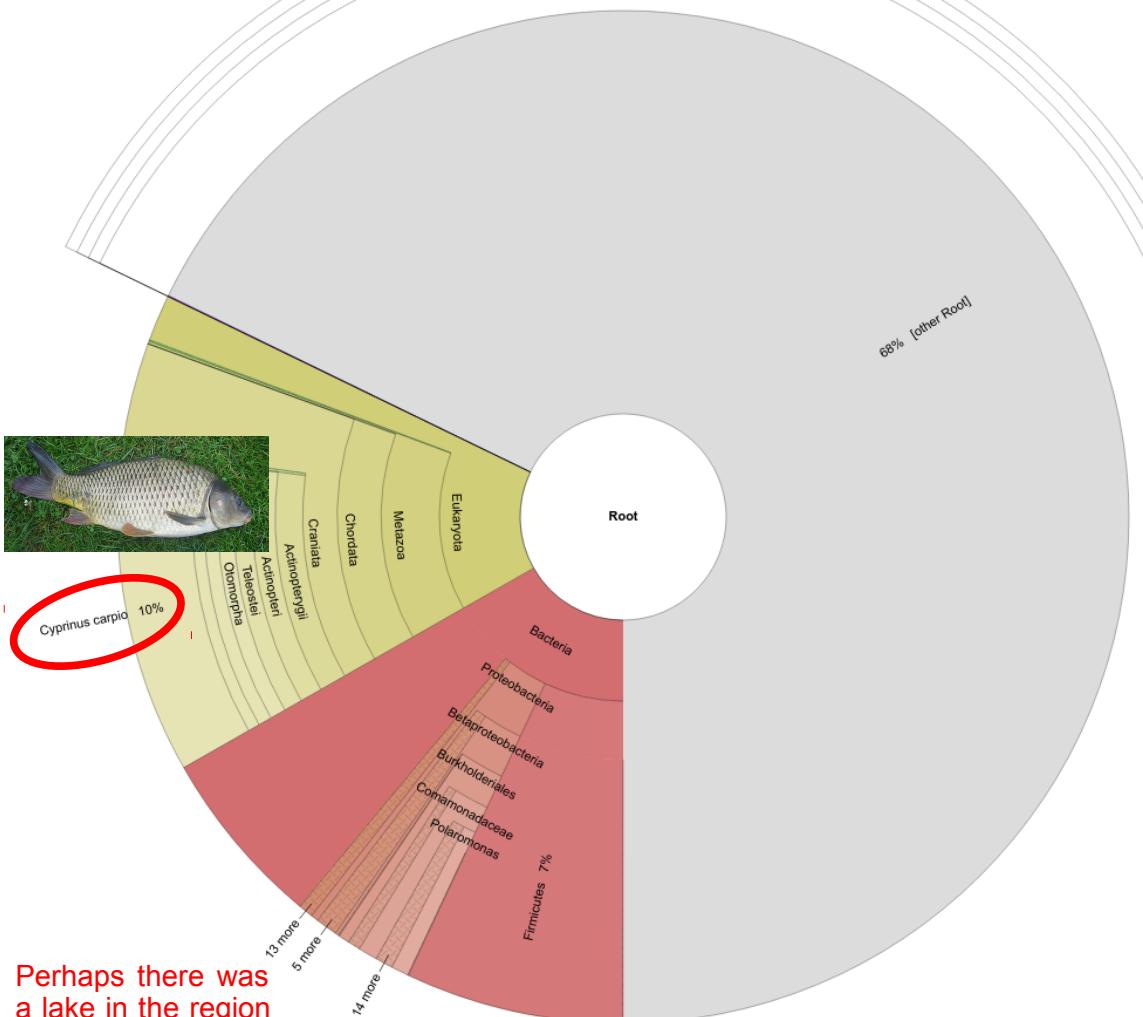
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Ancient DNA is highly degraded, resulting in very short sequences. Reads generated with modern high-throughput sequencing machines are generally longer than ancient DNA molecules, therefore the reads often contain some portion of the sequencing adaptors. It is crucial to remove those adaptors, as they can interfere with downstream analysis. Furthermore, overlapping portions when DNA has been read forward and backward (paired-end) can be merged to correct sequencing errors and improve read quality. Several tools have been developed for adapter trimming and read merging, however, no one has attempted to evaluate their accuracy and evaluate their potential impact on downstream analyses. Through the simulation of sequencing data, seven commonly used tools were analyzed in their ability to reconstruct ancient DNA sequences through read merging. The analyzed tools exhibit notable differences in their abilities to correct sequence errors and identify the correct read overlap, but the most substantial difference is observed in their ability to calculate quality scores for merged bases. Selecting the most appropriate tool for a given project depends on several factors, although some tools such as fastp have some shortcomings, whereas others like leeHom outperform the other tools in most aspects. While the choice of tool did not result in a measurable difference when analyzing population genetics using principal component analysis, it is important to note that downstream analyses that are sensitive to wrongly merged reads or that rely on quality scores can be significantly impacted by the choice of tool.

What if you forget to trim the adapters: soil sample



It turns out the Carp genome is full of Illumina adapters.

One of the first things we teach people in our [NGS courses](#) is how to remove adapters. It's not hard – we use [CutAdapt](#), but many other tools exist. It's simple, but really important – with De Bruijn graphs you will get paths through the graphs converging on kmers from adapters; and with OLC assemblers you will get spurious overlaps. With gap-filters, it's possible to fill the gaps with sequences ending in adapters, and this may be what happened in the Carp genome.

Why then are we finding such elementary mistakes in such important papers?

Why aren't reviewers picking up on this? It's frustrating.

This is a separate, but related issue, to genomic contamination – the [Wheat genome has PhiX in it; tons of bacterial genomes do too; and lots of bacterial genes were problematically included in the Tardigrade genome](#) and declared as horizontal gene transfer.

Bioinformatics Bits and Bobs

Rare and random blog posts about bioinformatics, genomics and evolution.

Monday, 29 September 2014

Why you should QC your reads AND your assembly

The genome sequence of the Common Carp *Cyprinus carpio* was [published in Nature last week](#). By coincidence, I was doing some QC on some domesticated Ferret (*Mustela putorius furo*) reads, which had thrown some kmer warnings in the [FastQC tool](#). I blasted the kmers in NCBI and was quite perplexed by the number of hits that I found in the carp genome. Nearly all of the first 150 hits were all from the carp genome. Anyway, I looked a bit further into my odd kmers and it turns out that they were the ends of some Illumina adapter sequences that had presumably been incorporated into the paired-reads on the shorter ends of the insert size. This then took me back to the Carp Genome - what had crept into that?