

MinION

Bioinformatic Analysis

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INMI «L. Spallanzani»





Basecalling and primary data analysis with Guppy

Guppy is a data processing toolkit that contains the Oxford Nanopore Technologies' basecalling algorithms, and several bioinformatic post-processing features. It is provided as binaries to run on Windows, OS X and Linux platforms, as well as being integrated with MinKNOW, the Oxford Nanopore device control software.

Early downstream analysis components such as barcoding/demultiplexing, adapter trimming and alignment are contained within Guppy. Furthermore, Guppy now performs modified basecalling (5mC, 6mA and CpG) from the raw signal data, producing an additional FAST5 file of modified base probabilities.

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**A quality control tool for high
throughput sequence data.**

Program: **FastQC**

FastQC **aims** to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing pipelines.

Basic Statistics

Per Base Sequence Quality

Per Sequence Quality Scores

Per Base Sequence Content Summary

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Duplicate Sequences

Overrepresented Sequences

Adapter Content

Kmer Content

Per Tile Sequence Quality

Supported files:

- FastQ (all quality encoding variants)
- Casava FastQ files*
- Colourspace FastQ
- GZip compressed FastQ
- SAM
- BAM
- SAM/BAM Mapped only (normally used for colourspace data)



File Help



FastQC High Throughput Sequence QC Report

Version: 0.11.7

www.bioinformatics.babraham.ac.uk/projects/

© Simon Andrews, Pierre Lindenbaum, Brian Howard, Phil Ewels 2011-17,

Picard BAM/SAM reader ©The Broad Institute, 2013

BZip decompression ©Matthew J. Francis, 2011

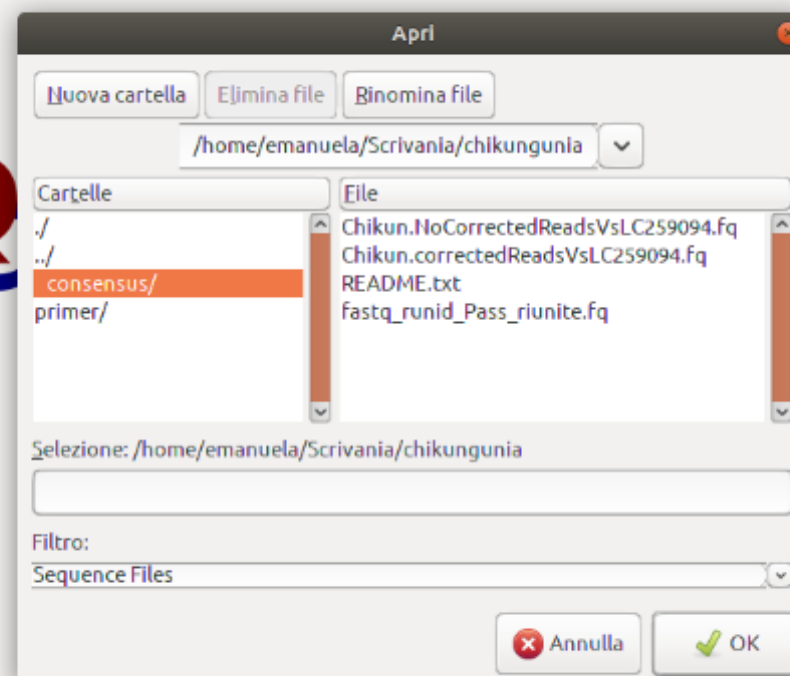
Base64 encoding ©Robert Harder, 2012

Java HDF5 reader ©ETH, CISD and SIS, 2007-14

Use File > Open to select the sequence file you want to check

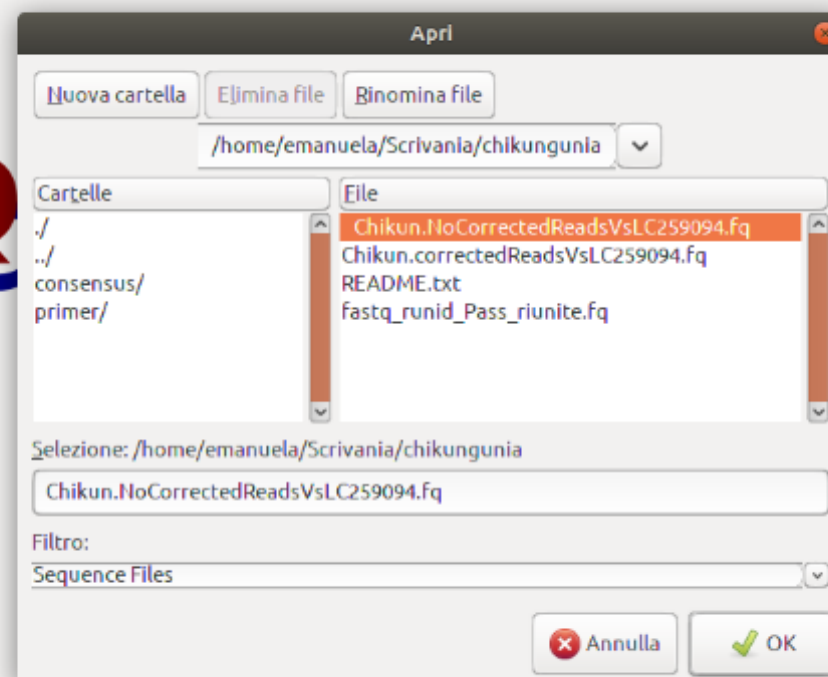


File Help





File Help





File Help



fastq_runid_Pass_runit.fq



- Basic Statistics
- Per base 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 sequence stats

Measure	Value
Filename	fastq_runid_Pass_runit.fq
File type	Conventional base calls
Encoding	Sanger / illumina 1.9
Total Sequences	485522
Sequences flagged as poor quality	0
Sequence length	93-16622
%GC	48



File Help

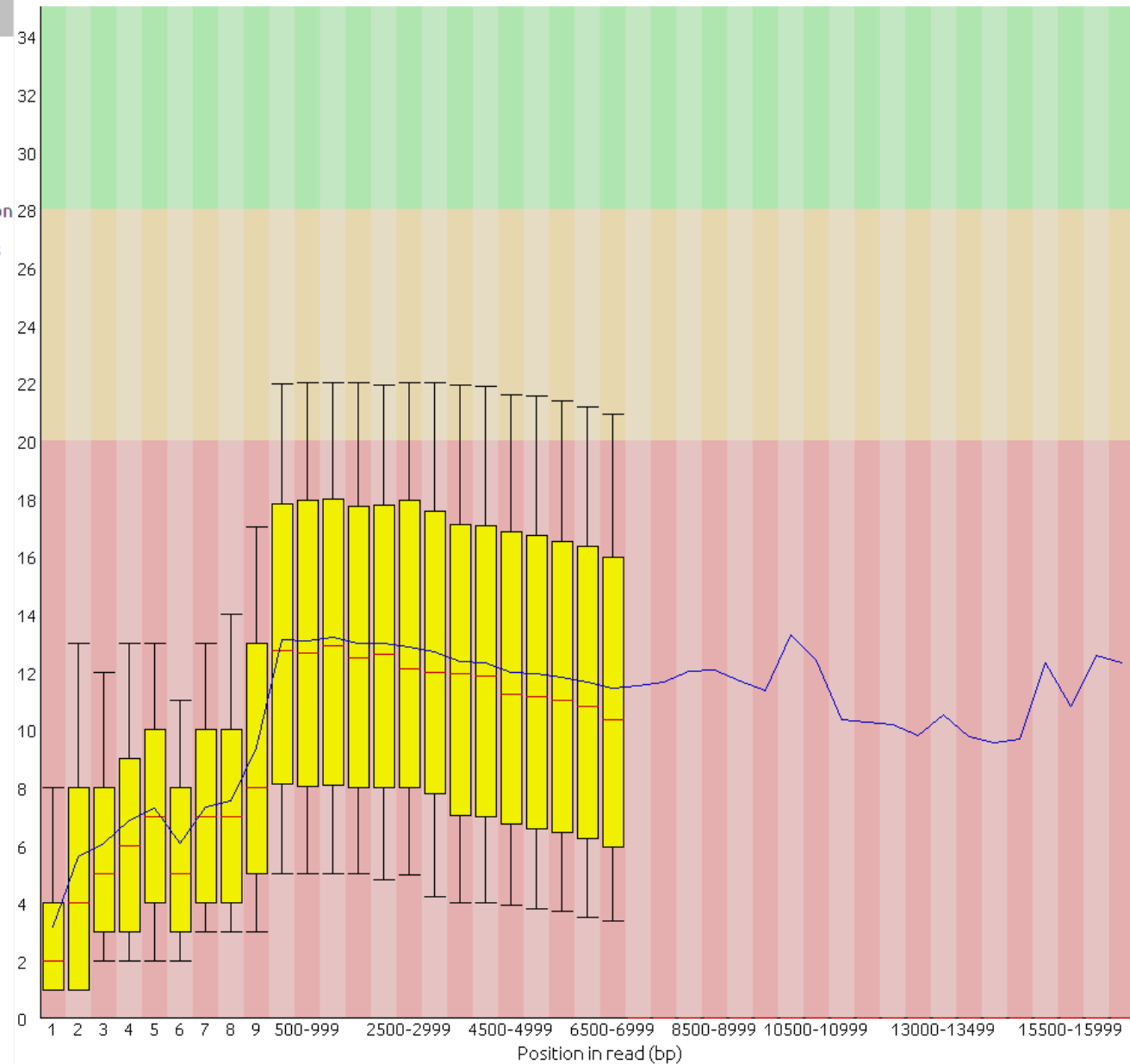


fastq_runid_Pass_riunite.fq

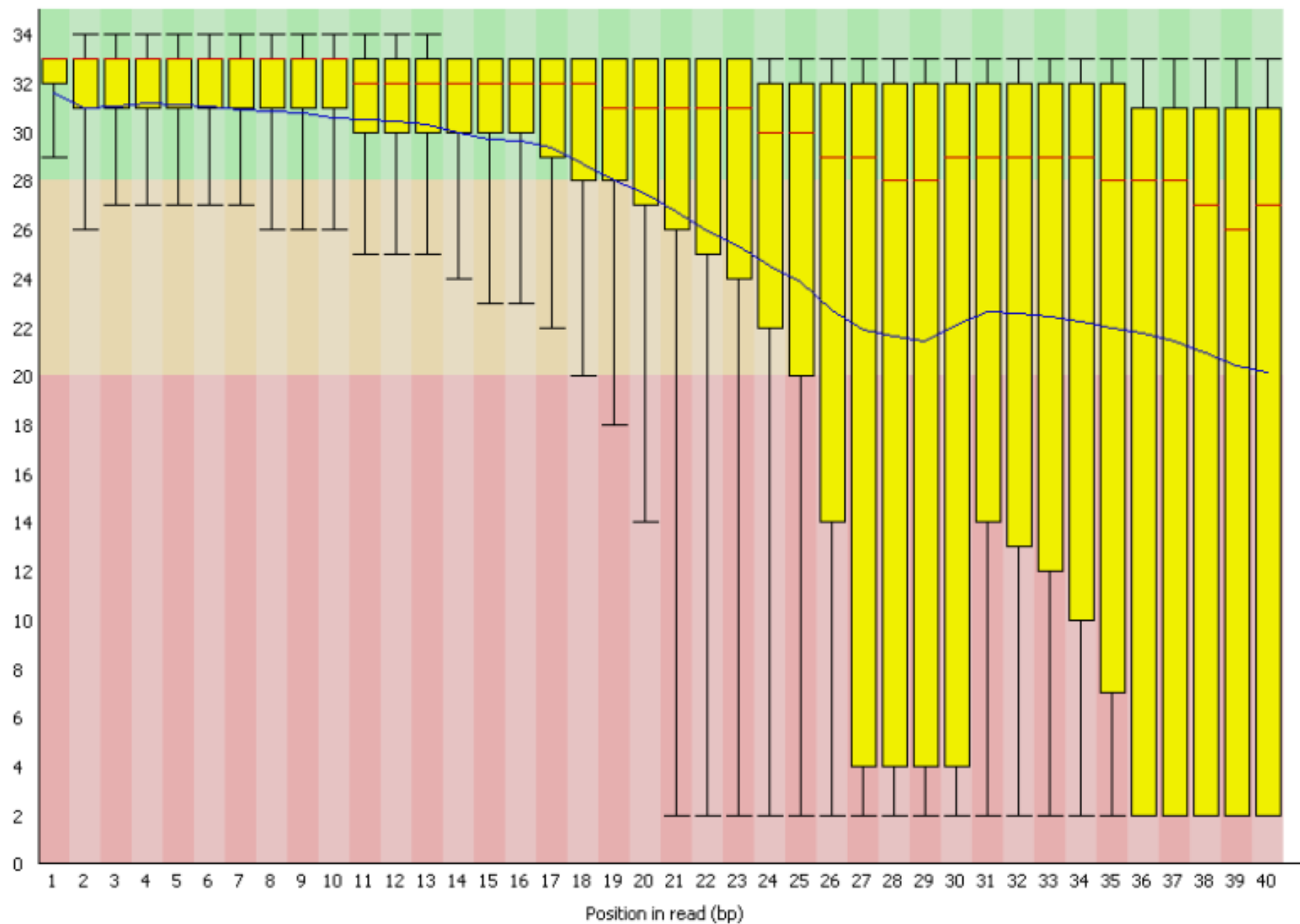
- ✓ Basic Statistics
- ✗ Per base sequence quality
- ✗ Per sequence quality scores
- ✗ Per base sequence content
- ✗ Per sequence GC content
- ✓ Per base N content
- ⚠ Sequence Length Distribution
- ✓ Sequence Duplication Levels
- ⚠ Overrepresented sequences
- ✓ Adapter Content



Quality scores across all bases (Sanger / Illumina 1.9 encoding)



Quality scores across all bases (Illumina >v1.3 encoding)





File Help

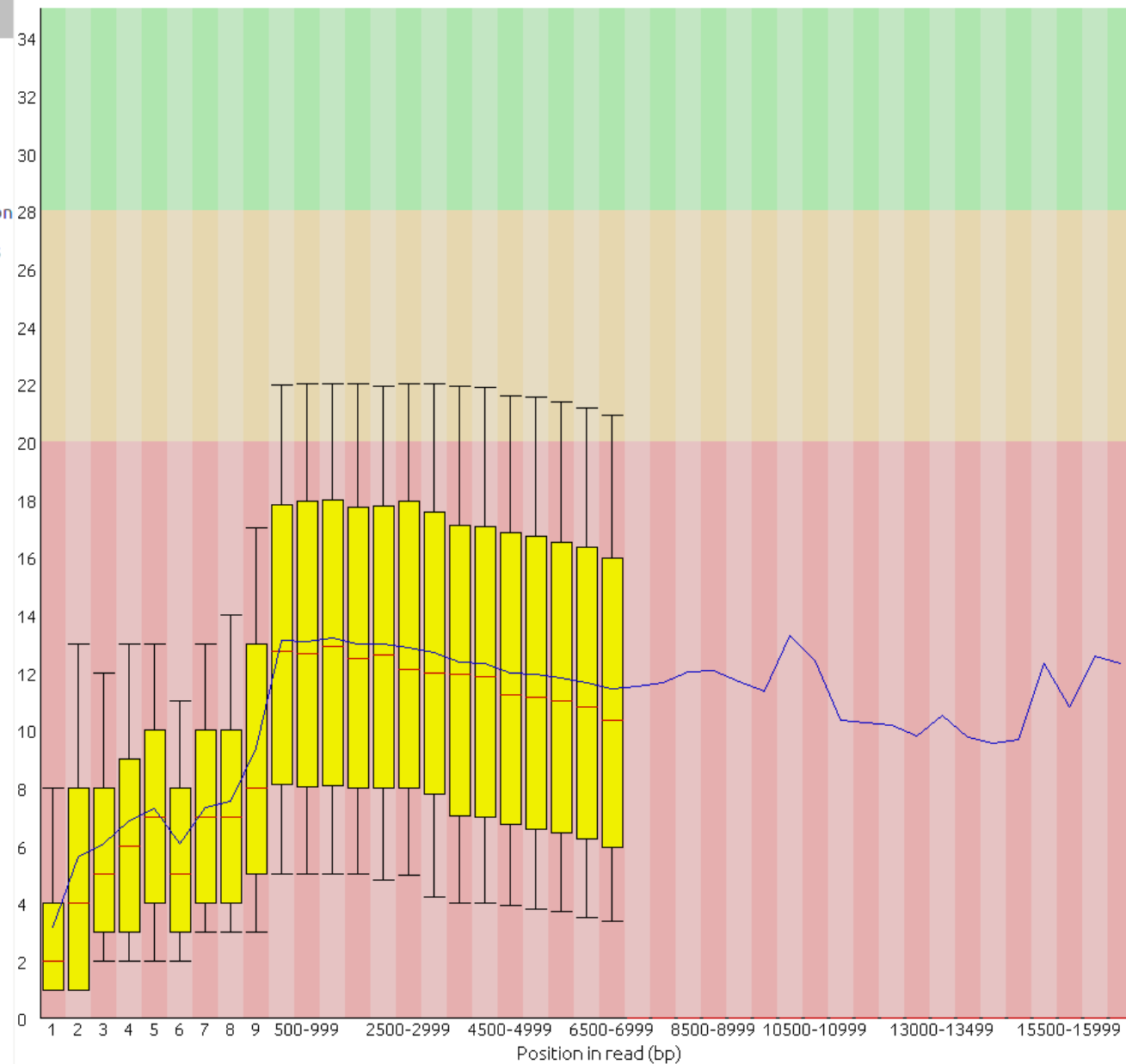


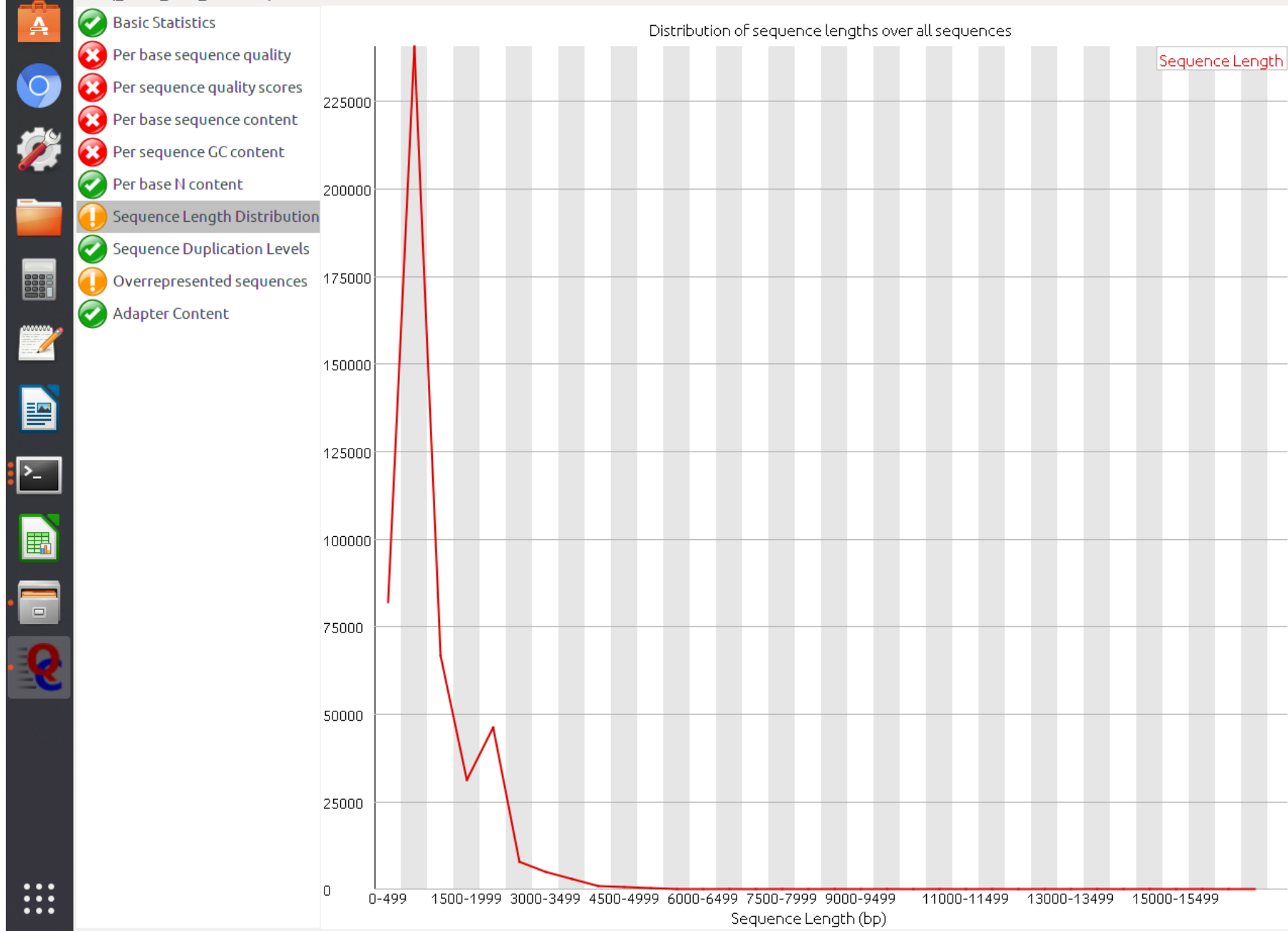
fastq_runid_Pass_riunite.fq

- ✓ Basic Statistics
- ✗ Per base 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



Quality scores across all bases (Sanger / Illumina 1.9 encoding)







File Help



fastq_runid_Pass_r1unit.fq

Basic Statistics

Per base 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

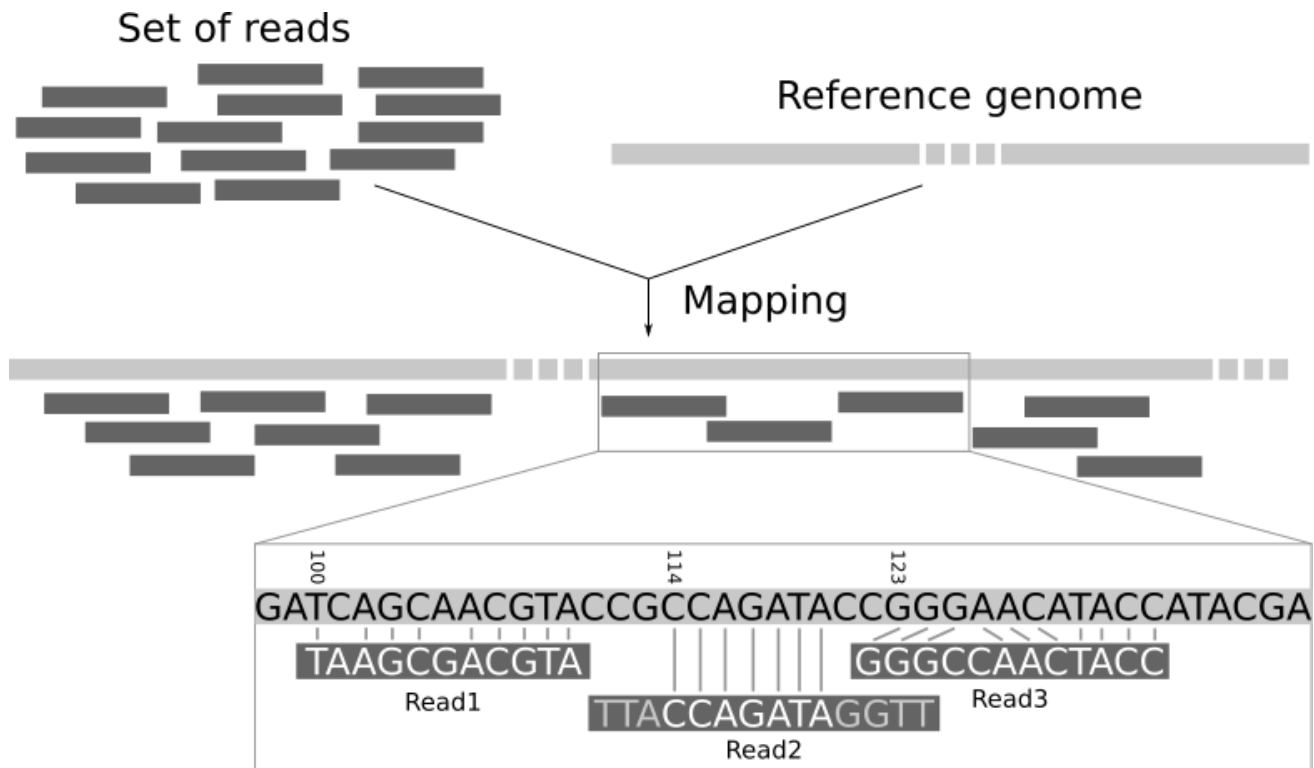
Adapter Content

Overrepresented sequences

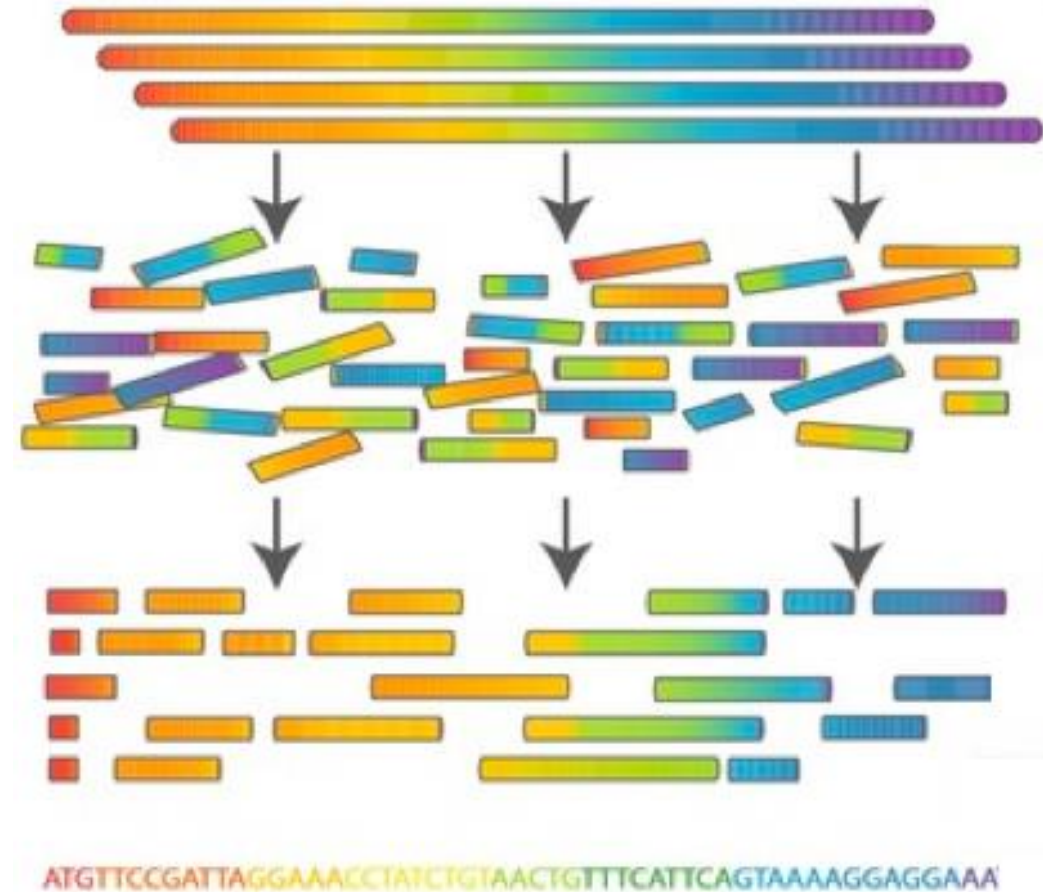
Sequence	Count	Percentage	Possible Source
TTGTTGACTTCGTTACGTA...	2498	0,514	No Hit
TTGTTGACTTCGTTACGTA...	1641	0,338	No Hit
TTGTTGACTTCGTTACGTA...	967	0,199	No Hit
TTGTTGACTTCGTTACGTA...	936	0,193	No Hit
TTGTTGACTTCGTTACGTA...	851	0,175	No Hit
TTGTTGACTTCGTTACGTA...	798	0,164	No Hit
TTATTGACTTCGTTACGTA...	617	0,127	No Hit
TCGGTATTACTTCGTTACGT...	567	0,117	No Hit
TTATTGACTTCGTTACGTA...	566	0,117	No Hit
TTGTTGACTTCGTTACGTA...	562	0,116	No Hit

Genome Reconstruction

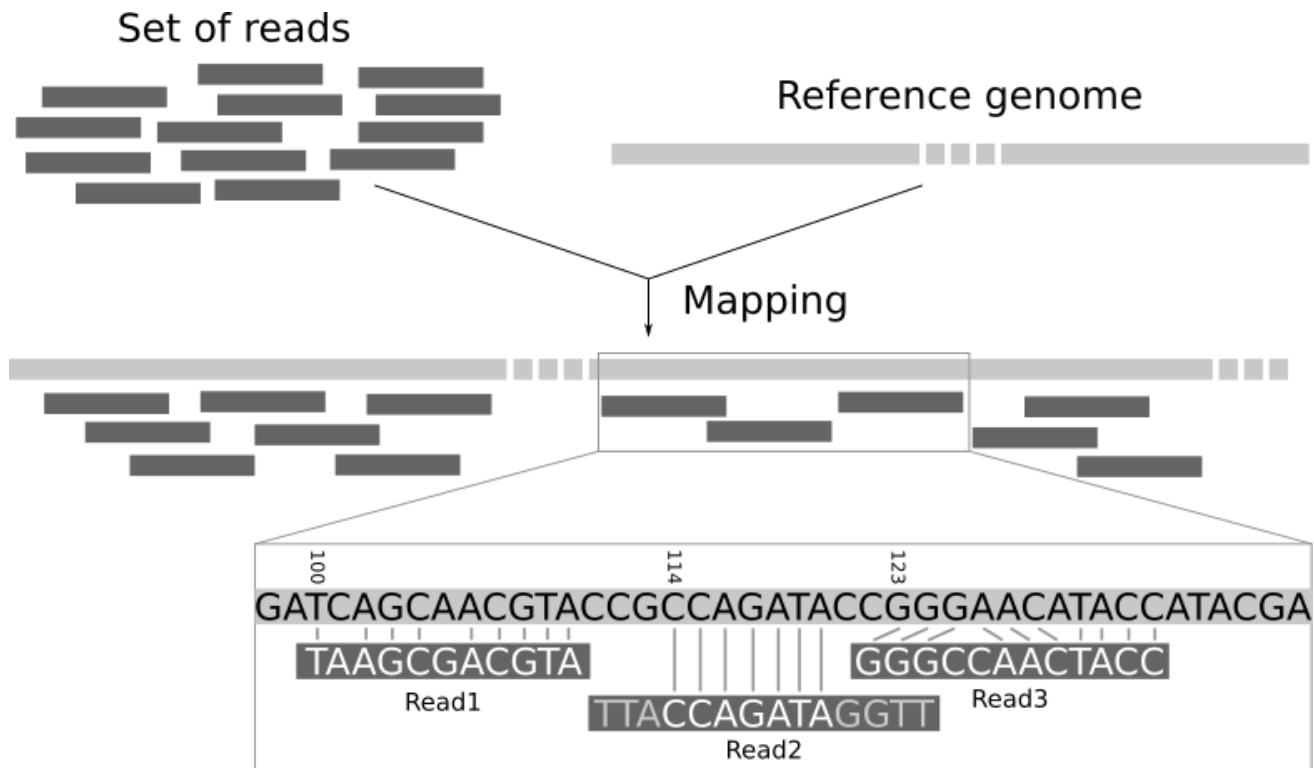
Mapping



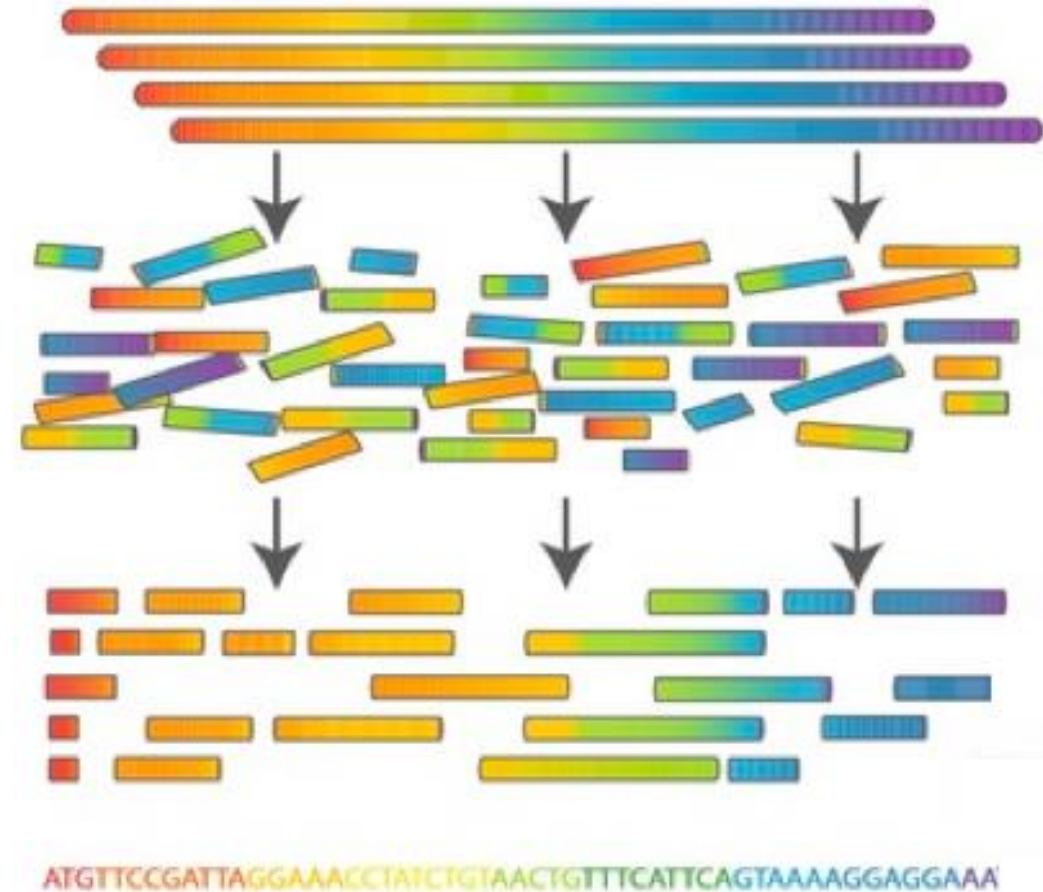
De Novo Assembly



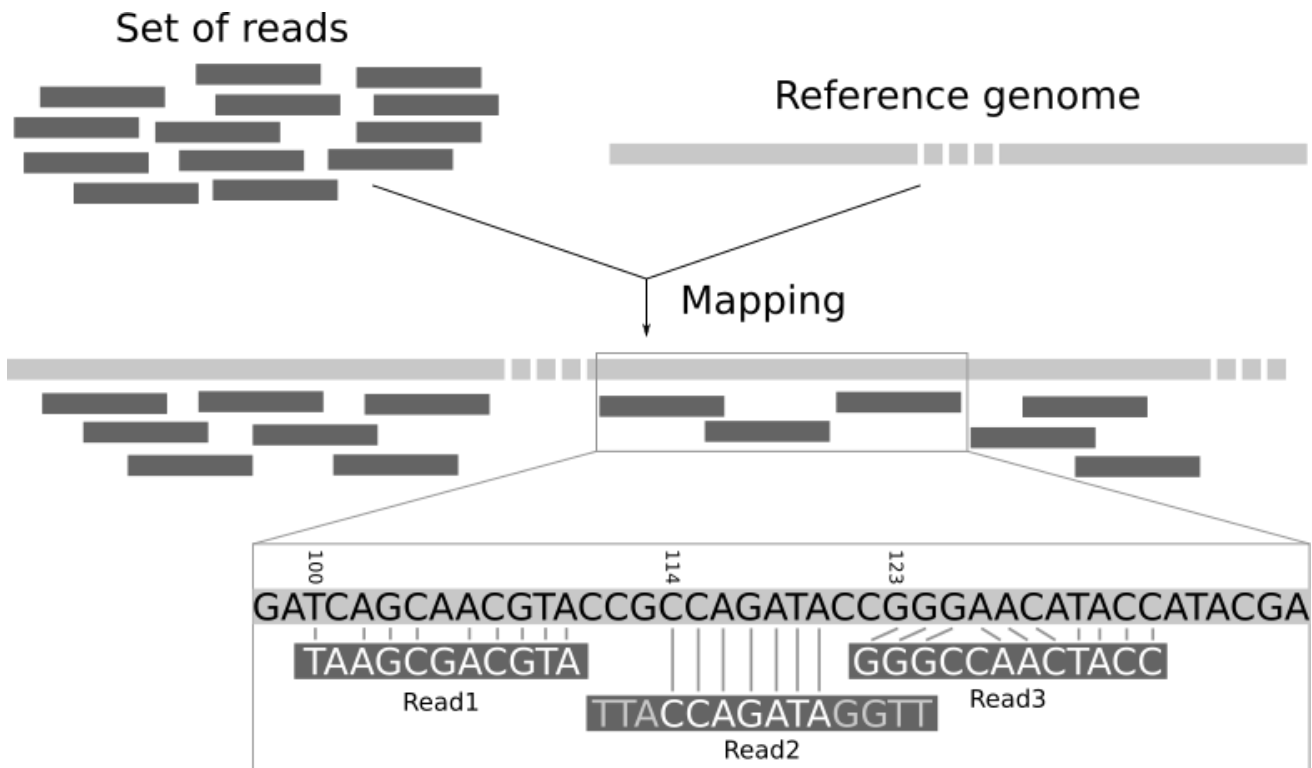
Mapping



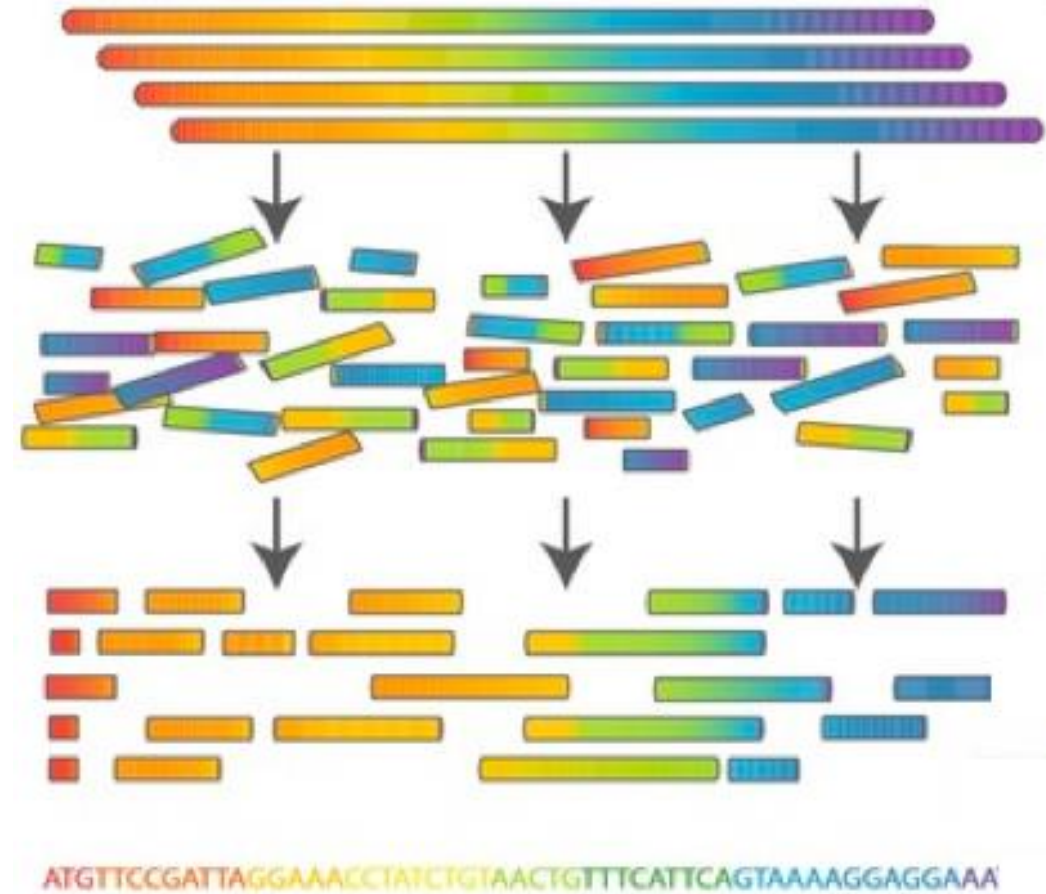
De Novo Assembly Pre-correction (Canu)



Mapping



De Novo Assembly



Identification of sequence reference

Literature

Standard reference

Bioinformatic analysis

Mapping Sequence nearest sequence our data

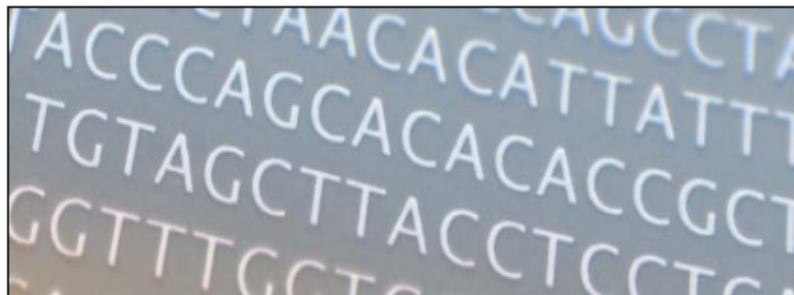
Nucleotide

Nucleotide ▾

Search

[Advanced](#)

[Help](#)



Nucleotide

The Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

Using Nucleotide

[Quick Start Guide](#)

[FAQ](#)

[Help](#)

[GenBank FTP](#)

[RefSeq FTP](#)

Nucleotide Tools

[Submit to GenBank](#)

[LinkOut](#)

[E-Utilities](#)

[BLAST](#)

[Batch Entrez](#)

Other Resources

[GenBank Home](#)

[RefSeq Home](#)

[Gene Home](#)

[SRA Home](#)

[INSDC](#)

Nucleotide

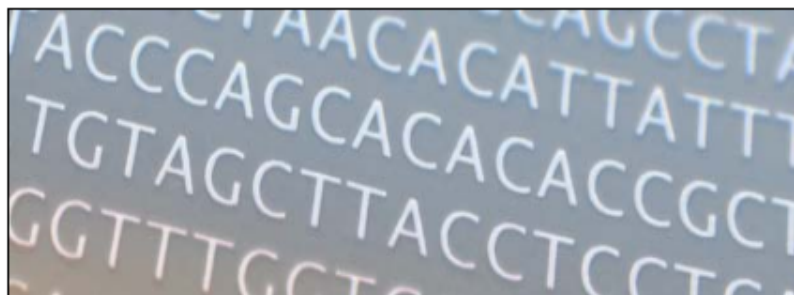
Nucleotide ▼

LC259094.1

Search

[Advanced](#)

[Help](#)



Nucleotide

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[GenBank Home](#)

[RefSeq Home](#)

[Gene Home](#)

[SRA Home](#)

[INSDC](#)

FASTA Format

NCBI Resources ▾ How To ▾

emanuelagiombini My NCBI Sign Out

Nucleotide

Nucleotide ▾

Search

Advanced

Help

GenBank ▾

Send to: ▾

1 item shown ▾

Chikungunya virus genomic RNA, nearly complete genome, isolate: CHIKV/Hu/Angola/NIID54/2016

GenBank: LC259094.1

[FASTA](#) [Graphics](#)

Go to: ▾

LOCUS LC259094 11825 bp RNA linear VRL 22-DEC-2017

DEFINITION Chikungunya virus genomic RNA, nearly complete genome, isolate: CHIKV/Hu/Angola/NIID54/2016.

ACCESSION LC259094

VERSION LC259094.1

KEYWORDS .

SOURCE Chikungunya virus

ORGANISM [Chikungunya virus](#)

Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus; SFV complex.

REFERENCE 1

AUTHORS Nakayama,E., Tajima,S., Kotaki,A. and Tomohiko,T.

TITLE A summary of the imported cases of Chikungunya fever in Japan from 2006 to June 2016

JOURNAL J Travel Med 25, tax072 (2018)

REMARK DOI:10.1093/jtm/tax072

REFERENCE 2 (bases 1 to 11825)

☒ Complete Record

☐ Coding Sequences

Choose Destination

☒ File

☐ Clipboard

☐ Collections

☐ Analysis Tool

Download 1 item.

Format

GenBank ▾

Summary

GenBank

GenBank (full)

FASTA

ASN.1

XML

INSDSeq XML

TinySeq XML

Feature Table

Accession List

GI List

GFF3

Protein

Taxonomy

Functional Class

Genomic Neighbours

RefSeq Genome for Species

RefSeq Genome Sequences

Alignment of reads on the reference



<https://www.geneious.com/resources/getting-started/>

<https://www.geneious.com/tutorials/>



Sources

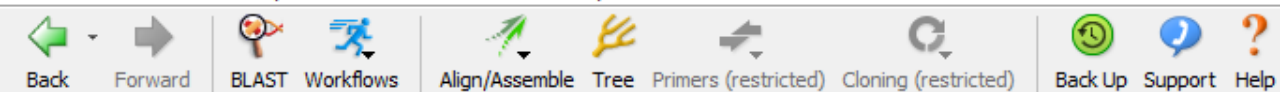
- Local (770, 1 unread)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Enter search text

Hide

No document selected

Select documents in the table above to view

 Search

Sources

- Local (1)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (0)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Using 98 / 13836 MB memory

Features Restricted

0 of 0 selected

Hide

No document selected

Select documents in the table above to view

- New >
- Rename Folder...
- Set Folder Color... (restricted)
- Move Folder...
- Delete Folder Elimina
- Delete Folder Permanently... Maiusc+Elimina
- Restore from Deleted Items
- Erase All Deleted Items...
- Save Ctrl+S
- Save As... Ctrl+Maiusc+S
- Download Documents Ctrl+W
- Cancel Downloads Ctrl+Maiusc+W
- Back Up Data...
- Restore Backup...
- Import >
- Export >
- Print... Ctrl+P
- Save As Image File... Ctrl+Alt+S
- Exit

File Tree Primers (restricted) Cloning (restricted) Back Up Support Help

Filter Search

0 of 0 selected

Hide

No document selected

Select documents in the table above to view

- New
 - Folder... Ctrl+Maiusc+N
 - Sequence... Ctrl+N
 - Enzyme Set... (restricted)
 - Text Document... (restricted)
- Rename Folder...
- Set Folder Color... (restricted)
- Move Folder...

- Delete Folder Elimina
- Delete Folder Permanently... Maiusc+Elimina
- Restore from Deleted Items
- Erase All Deleted Items...

- Save Ctrl+S
- Save As... Ctrl+Maiusc+S
- Download Documents Ctrl+W
- Cancel Downloads Ctrl+Maiusc+W

- Back Up Data...
- Restore Backup...

- Import >
- Export >

- Print... Ctrl+P
- Save As Image File... Ctrl+Alt+S

- Exit

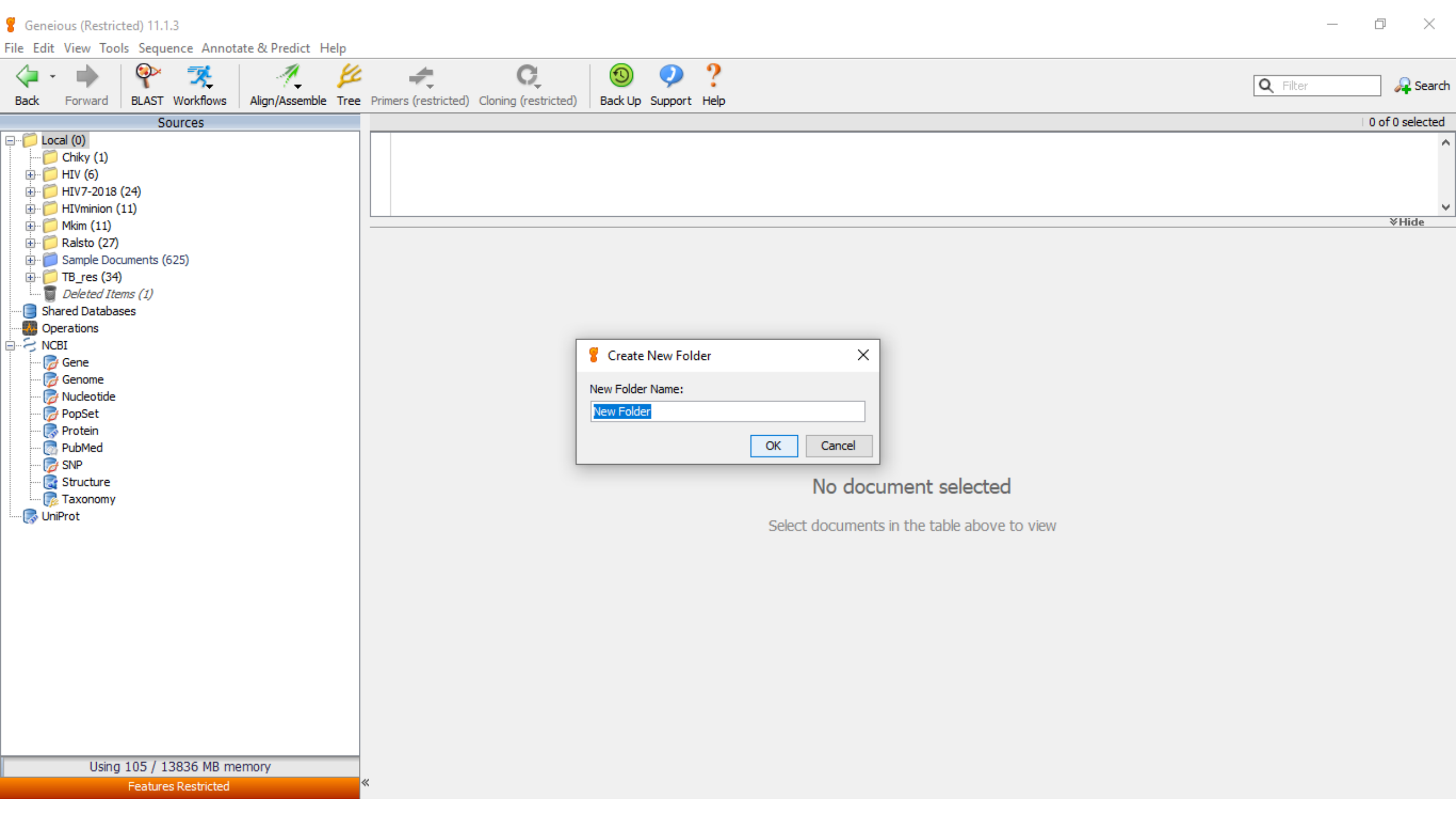
 Search

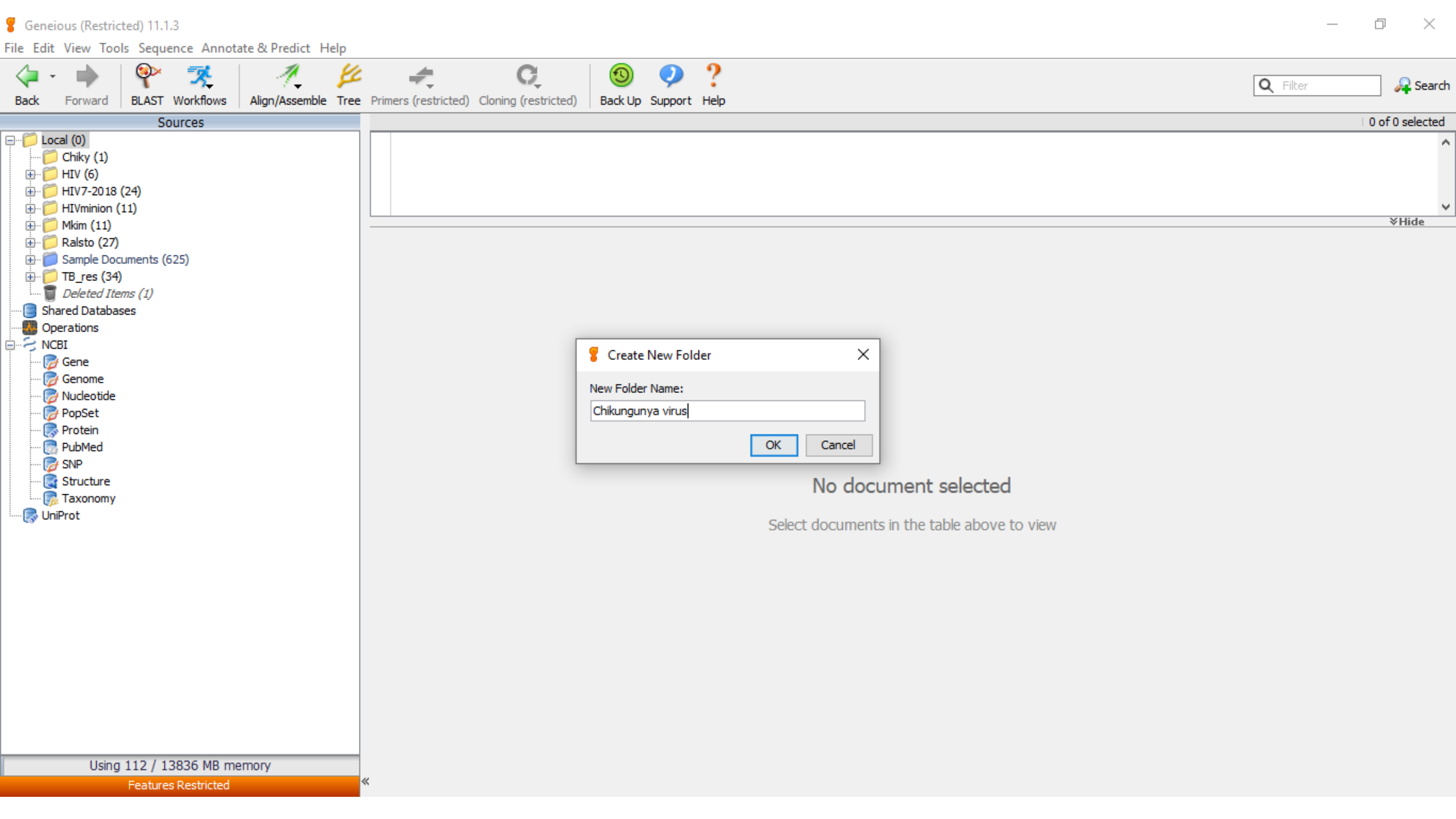
0 of 0 selected

Hide

No document selected

Select documents in the table above to view





- New >
- Rename Folder...
- Set Folder Color... (restricted)
- Move Folder...
- Delete Folder Elimina
- Delete Folder Permanently... Maiusc+Elimina
- Restore from Deleted Items
- Erase All Deleted Items...
- Save Ctrl+S
- Save As... Ctrl+Maiusc+S
- Download Documents Ctrl+W
- Cancel Downloads Ctrl+Maiusc+W
- Back Up Data...
- Restore Backup...
- Import >
- Export >
- Print... Ctrl+P
- Save As Image File... Ctrl+Alt+S
- Exit

Drop files here to import

- New
- Rename Folder...
- Set Folder Color... (restricted)
- Move Folder...
- Delete Folder Elimina
- Delete Folder Permanently... Maiusc+Elimina
- Restore from Deleted Items
- Erase All Deleted Items...
- Save Ctrl+S
- Save As... Ctrl+Maiusc+S
- Download Documents Ctrl+W
- Cancel Downloads Ctrl+Maiusc+W
- Back Up Data...
- Restore Backup...
- Import
- Export
- Print... Ctrl+P
- Save As Image File... Ctrl+Alt+S
- Exit

File Tree Primers (restricted) Cloning (restricted) Back Up Support Help

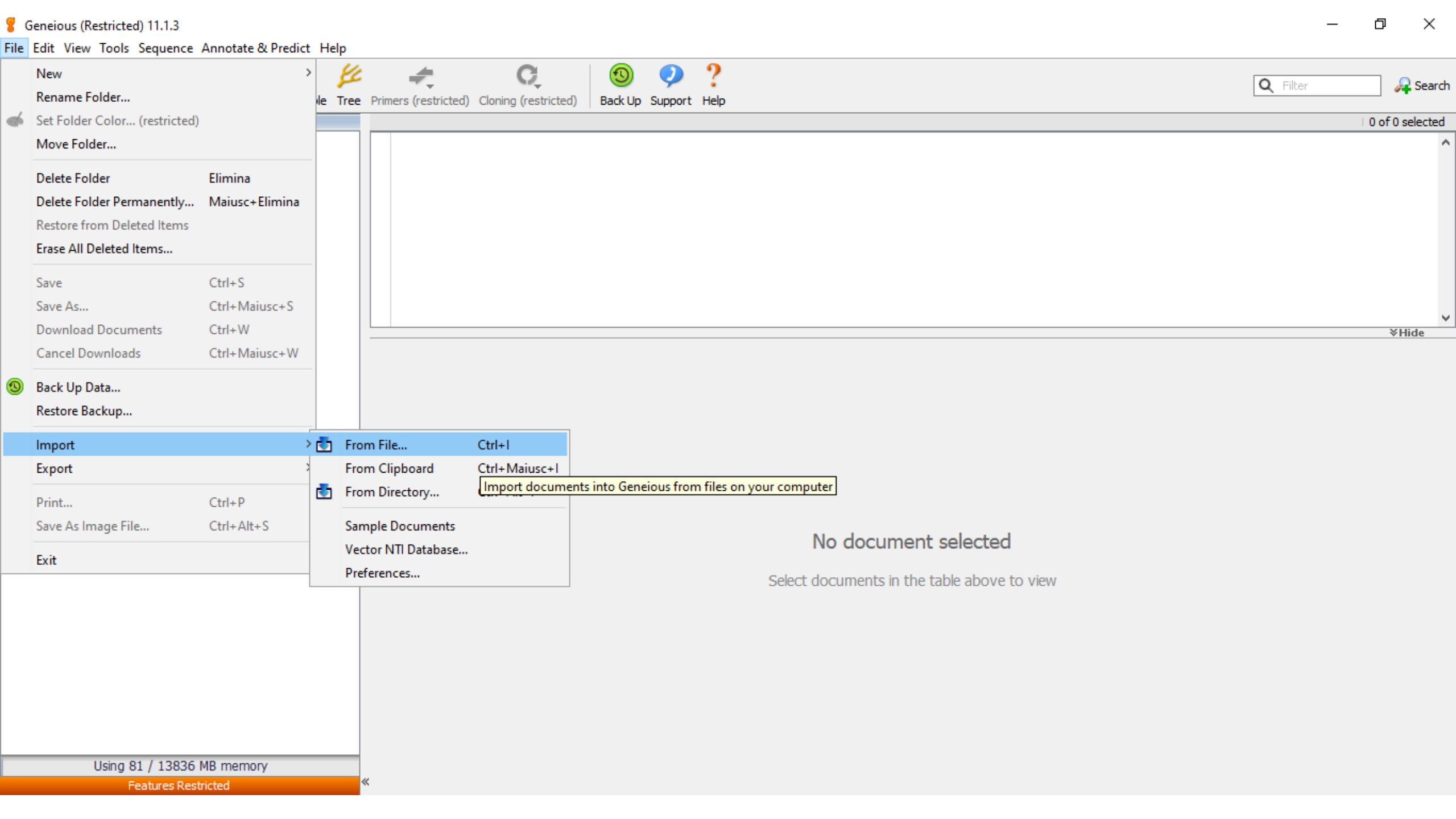
Filter Search

0 of 0 selected

Drop files here to import

Hide

- From File... Ctrl+I
- From Clipboard Ctrl+Maiusc+I
- From Directory... Ctrl+Alt+I
- Sample Documents
- Vector NTI Database...
- Preferences...

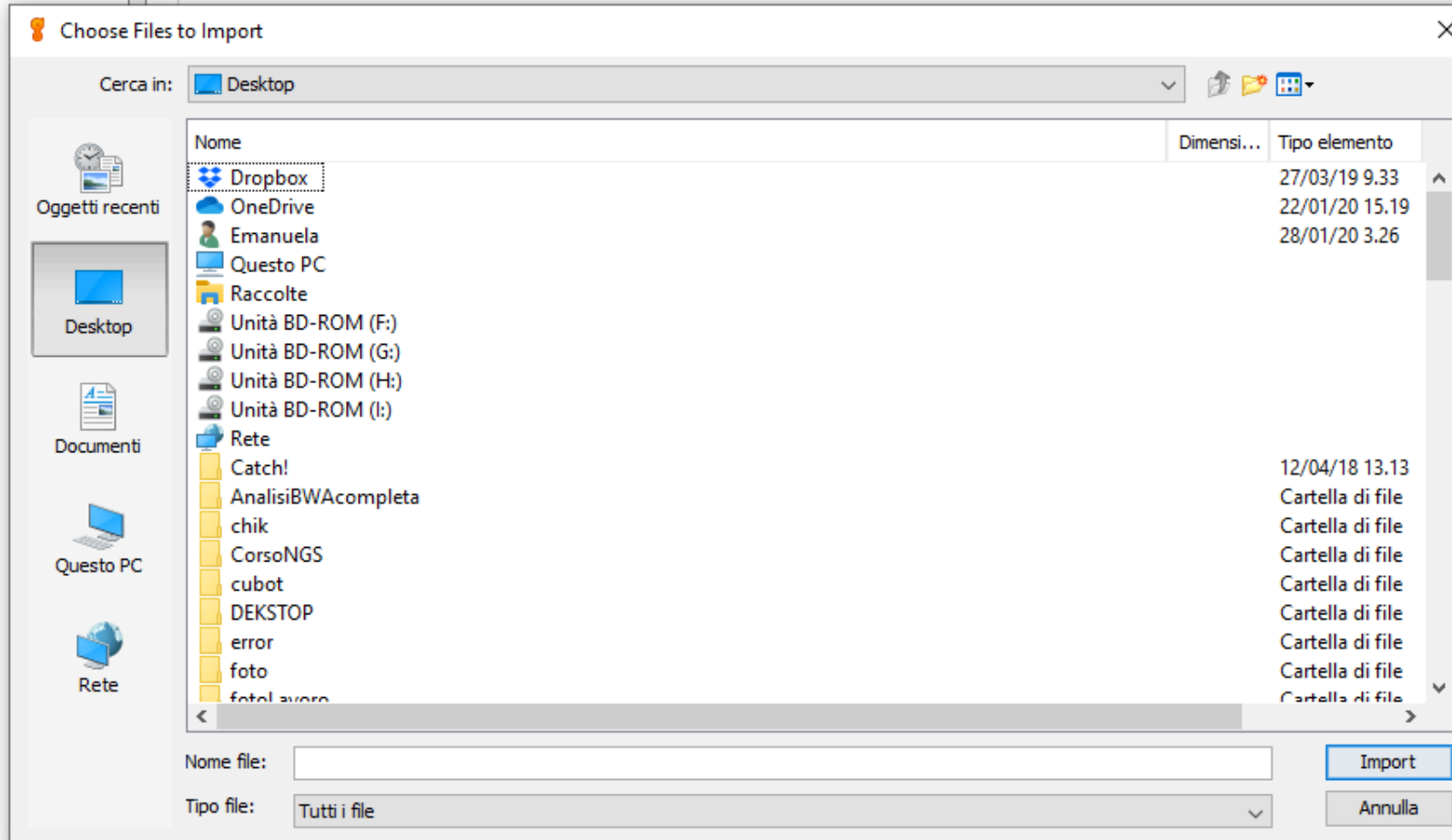


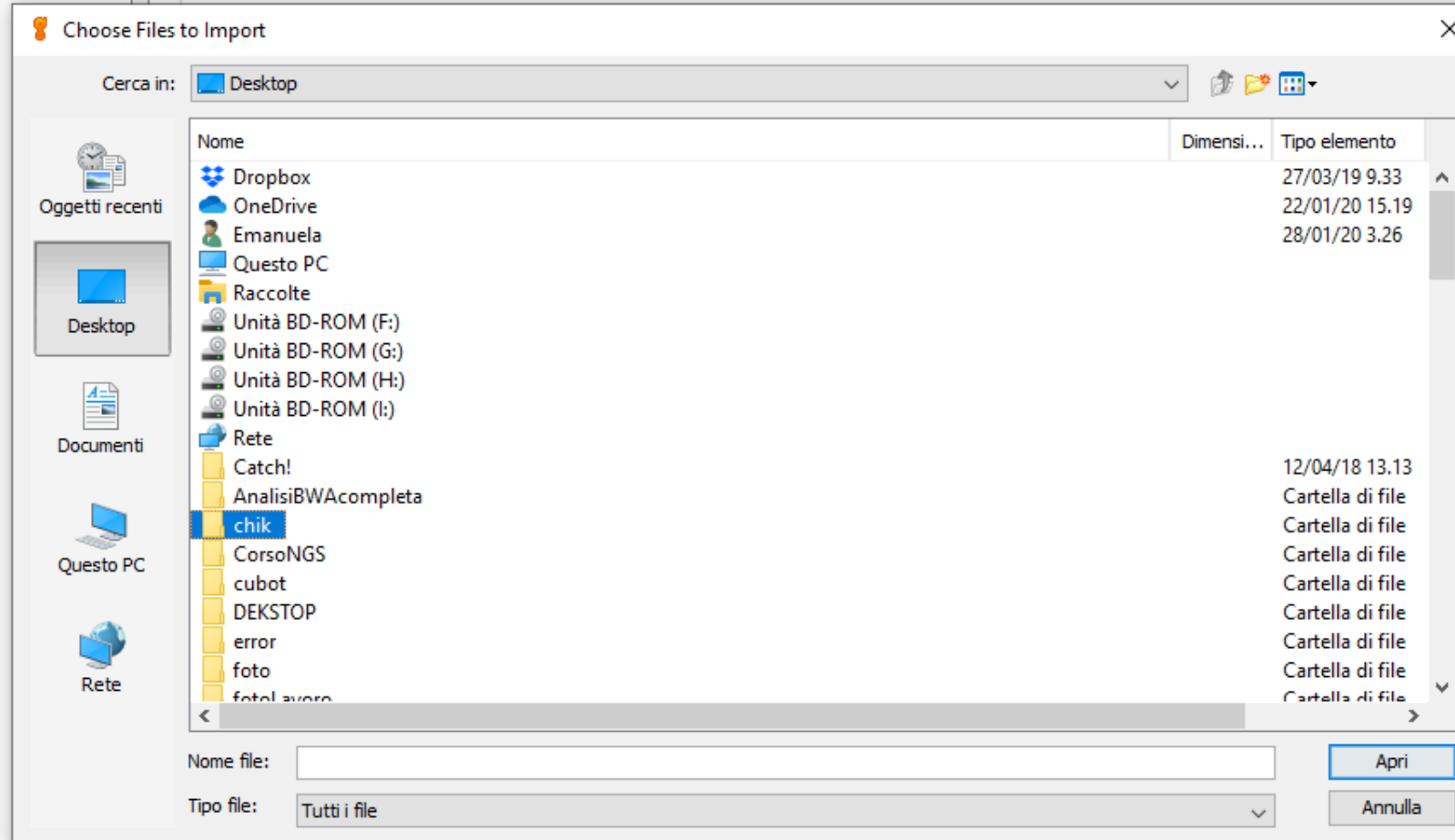
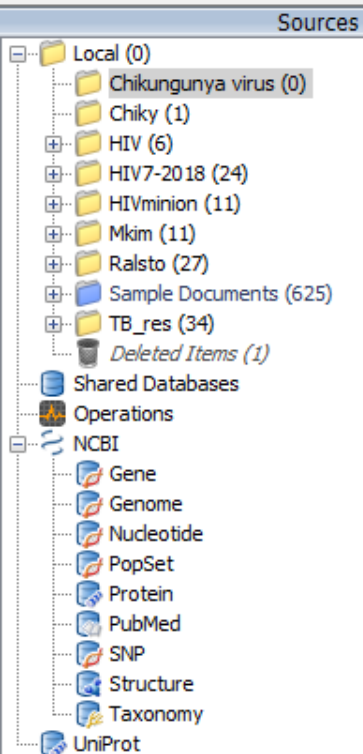


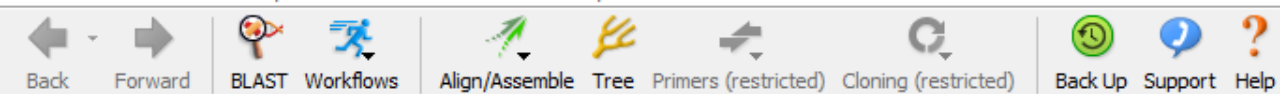
Sources

- Local (0)
- Chikungunya virus (0)
- Chiky (1)
- HIV (6)
- HIV7-2018 (24)
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- Mkim (11)
- Ralsto (27)
- Sample Documents (625)
- TB_res (34)
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- UniProt

0 of 0 selected



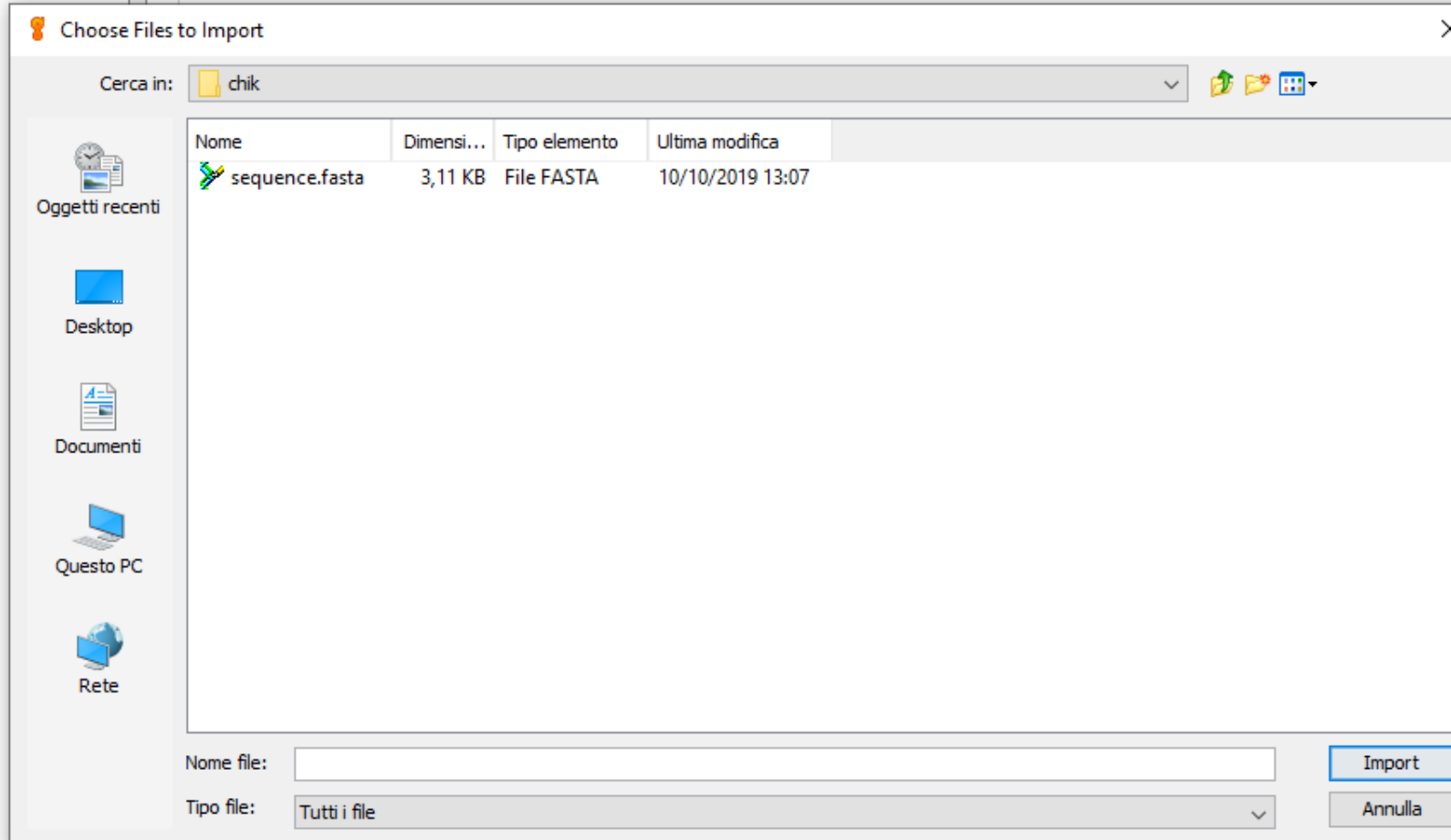




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0 of 0 selected

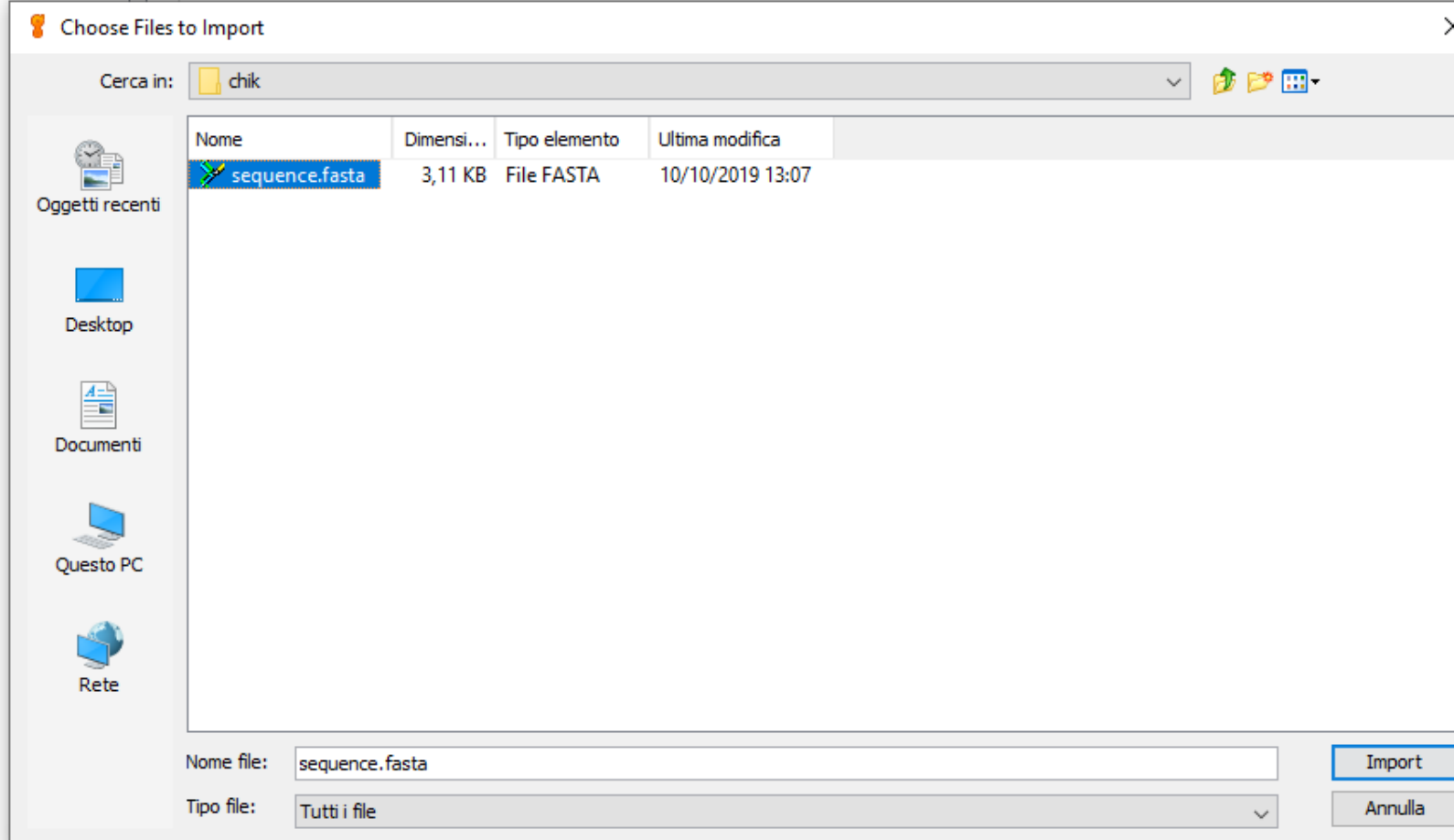




Sources

- Local (0)
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- Mkim (11)
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- Sample Documents (625)
- TB_res (34)
- Deleted Items (1)
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- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

0 of 0 selected



Geneious (Restricted) 11.1.3

File Edit View Tools Sequence Annotate & Predict Help

Back

Forward

BLAST

Workflows

Align/Assemble

Tree

Primers (restricted)

Cloning (restricted)

Back Up

Support

Help

Filter

Search

Sources

Local (0)

Chikungunya virus (1)

Chiky (1)

HIV (6)

HIV7-2018 (24)

HIVminion (11)

Mkim (11)

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Sample Documents (625)

TB_res (34)

Deleted Items (5)

Shared Databases

Operations

NCBI

Gene

Genome

Nucleotide

PopSet

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

1 of 1 selected

<input checked="" type="checkbox"/>	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...03 Feb 2020 1:21 AM	11,825	50.3%	linear	

Sequence View

Fragments

Dotplot (Self)

DNA Fold

RNA Fold

Text View

Lineage

Info

Extract

R.C.

Translate

Add/Edit Annotation (restricted)

Allow Editing (restricted)

Annotate & Predict

Save

1

50

100

150

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11,750

11,825

General

Colors: A C G T - Edit

☒ Graphs

Options >

☒ Annotations

Options >

☐ Complement

Options >

☐ Translation

Options >

☐ Circular Overview

☒ Linear View

☒ Wrap

☐ Show Name

☐ Show Description

Using 70 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

File Edit View Tools Sequence Annotate & Predict Help

Back Forward BLAST Workflows Align/Assemble Tree Primers (restricted) Cloning (restricted) Back Up Support Help

Filter Search

Sources

Local (0)

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Genome

Nucleotide

PopSet

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

1 of 1 selected

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

Sequence View Fragments Dotplot (Self) DNA Fold RNA Fold Text View Lineage Info

Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

1 10 20 30 40 50 60

ATGGCTGCGTGAGACACACGTAGCCTACCAGTTTCTTACTGCTCTACTCTGCAAAGCAAG

70 80 90 100 110 120

AGATTAAAGAACCCATCATGGATCCTGTGTACGTGGACATAGACGCTGACAGCGCCTTTT

130 140 150 160 170 180

GAAAGGCCCTGCAACGTGCGTACCCCATGTTTGAGGTGGAATCTAGGCAGGTCACACCGAA

190 200 210 220 230 240

TGACCATGCTAATGCTAGAGCGTTCTCGCATCTAGCTATAAACTAATAGAGCAGGAAAT

250 260 270 280 290 300

TGATCCCCGACTCAACCATCCTGGATATCGGGCAGTGCGCCAGCAAGGAGGATGATGTCGGA

310 320 330 340 350 360

CAGGAAGTACCACTGCGTCTGCCCGATGCGCAGCGCAGAAGATCCCCGAGAGACTCGCCAA

370 380 390 400 410 420

TTATGCGAGAAAGCTAGCATCTGCCGCAAGAAAAGTCCTGGACAGAAACATCTCTGGA

430 440 450 460 470 480

GATCGGGGACTTACAAGCAGTAATGGCCGTGCCAGACACGGAGACGCCGACATTCTGCTT

490 500 510 520 530 540

ACACACAGATGTCTCATGTAGACAGAGAGCAGACGTCGCGATATACCAAGACGTCTATGC

550 560 570 580 590 600

TGTACACGGACCCACGTCGCTATACCACAGGCGATTAAAGGGGTCCGAGTGGCGTACTG

610 620 630 640 650 660

GGTAGGGTTGACACAACCCTTCATGTACAATGCCATGGCGGGTGCCTACCCCTCATA

670 680 690 700 710 720

CTCGACAAACTGGGCGAGATGAGCAGGTACTGAAGGCTAAGAACATAGGATTATGTTCAAC

730 740 750 760 770 780

Using 70 / 13836 MB memory

Features Restricted

General

Colors: A C G T - Edit

☒ Graphs Options >

☒ Annotations Options >

☐ Complement Options >

☐ Translation

☐ Circular Overview

☒ Linear View

☒ Wrap

☐ Show Name

☐ Show Description

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

File

Edit

View

Tools

Sequence

Annotate & Predict

Help

New

Rename Folder...

Set Folder Color... (restricted)

Move Folder...

Delete Document/Folder

Elimina

Erase Document/Folder Permanently...

Maiusc+Elimina

Restore from Deleted Items

Erase All Deleted Items...

Save

Ctrl+S

Save As...

Ctrl+Maiusc+S

Download Documents

Ctrl+W

Cancel Downloads

Ctrl+Maiusc+W

Back Up Data...

Restore Backup...

Import

Export

Print...

Ctrl+P

Save As Image File...

Ctrl+Alt+S

Exit

Primers (restricted)

Cloning (restricted)

Back Up

Support

Help

1 of 1 selected

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

Sequence View

Fragments

Dotplot (Self)

DNA Fold

RNA Fold

Text View

Lineage

Info

Extract

R.C.

Translate

Add/Edit Annotation (restricted)

Allow Editing (restricted)

Annotate & Predict

Save

1

10

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100

110

120

130

140

150

160

170

180

190

200

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470

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580

590

600

610

620

630

640

650

660

670

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720

730

740

750

760

770

780

ATGGCTGCGTGAGACACACGTAGCCTACCAGTTTCTTACTGCTCTACTCTGCAAAGCAAG

GATCCTGTGTACGTGGACATAGACGCTGACAGCGCCTTTTT

ACCCCATGTTTGAGGTGGAATCTAGGCAGGTCACACCGAA

CGTTCTCGCATCTAGCTATAAACTAATAGAGCAGGAAAT

TGGATATCGGCAGTGGCCAGCAAGGAGGATGATGTCGGA

GCCCCGATGCGCAGCGCAGAAAGATCCCCGAGAGACTCGCCAA

TTATGCGAGAAAGCTAGCATCTGCCGAGGAAAAGTCCTGGACAGAAACATCTCTGGAAA

GATCGGGGACTTACAAGCAGTAATGGCCGTGCCAGACACGGAGACGCCGACATTCTGCTT

ACACACAGATGTCTCATGTAGACAGAGAGCAGACGTTCGCATATACCAAGACGTCTATGC

TGTACACGCACCCACGTCGTATACCACAGGCGATTAAAGGGTCCGAGTGGCGTACTG

GGTAGGGTTTGACACAACCCCGTTTCATGTACAATGCCATGGCGGGTGCCTACCCCTCATA

CTCGACAAACTGGGCAGATGAGCAGGTACTGAAGGCTAAGAACATAGGATTATGTTCAAC

General

Colors: A C G T -

☒ Graphs

Options >

☒ Annotations

Options >

☐ Complement

Options >

☐ Translation

Options >

☐ Circular Overview

☒ Linear View

☒ Wrap

☐ Show Name

☐ Show Description

Using 107 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

File

Edit

View

Tools

Sequence

Annotate & Predict

Help

New

Rename Folder...

Set Folder Color... (restricted)

Move Folder...

Delete Document/Folder

Elimina

Erase Document/Folder Permanently...

Maiusc+Elimina

Restore from Deleted Items

Erase All Deleted Items...

Save

Ctrl+S

Save As...

Ctrl+Maiusc+S

Download Documents

Ctrl+W

Cancel Downloads

Ctrl+Maiusc+W

Back Up Data...

Restore Backup...

Import

Export

Print...

Ctrl+P

Save As Image File...

Ctrl+Alt+S

Exit

Primers (restricted)

Cloning (restricted)

Back Up

Support

Help

1 of 1 selected

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

Sequence View

Fragments

Dotplot (Self)

DNA Fold

RNA Fold

Text View

Lineage

Info

Extract

R.C.

Translate

Add/Edit Annotation (restricted)

Allow Editing (restricted)

Annotate & Predict

Save

1

10

20

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40

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100

110

120

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170

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200

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670

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690

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710

720

730

740

750

760

770

780

ATGGCTGCGTGAGACACACGTAGCCTACCAGTTTCTTACTGCTCTACTCTGCAAAGCAAG

GATCCTGTGTACGTGGACATAGACGCTGACAGCGCCTTTTT

GTGGAACTCTAGGCGAGGTCACACCGAA

CGTTCTCGCATCTAGCTATAAACTAATAGAGCAGGAAAT

TGGATATCGGCAGTGGCCAGCAAGGAGGATGATGTCGGA

GCCCCGATGCGCAGCGCAGAAAGATCCCCGAGAGACTCGCCAA

TTATGCGAGAAAGCTAGCATCTGCCGAGGAAAAGTCCTGGACAGAAACATCTCTGGAAA

GATCGGGGACTTACAAGCAGTAATGGCCGTGCCAGACACGGAGACGCCGACATTCTGCTT

ACACACAGATGTCTCATGTAGACAGAGAGCAGACGTTCGGATATACCAAGACGTCTATGC

TGTACACGCACCCACGTGCTATACCACAGGCGATTAAAGGGTCCGAGTGGCGTACTG

GGTAGGGTTGACACAACCCCGTTTCATGTACAATGCCATGGCGGGTGCTTACCCCTCATA

CTCGACAAACTGGGCGAGATGAGCAGGTACTGAAGGCTAAGAACATAGGATTATGTTCAAC

General

Colors: A C G T -

☒ Graphs

Options >

☒ Annotations

Options >

☐ Complement

Options >

☐ Translation

Options >

☐ Circular Overview

☒ Linear View

☒ Wrap

☐ Show Name

☐ Show

Description

Using 119 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

10:28

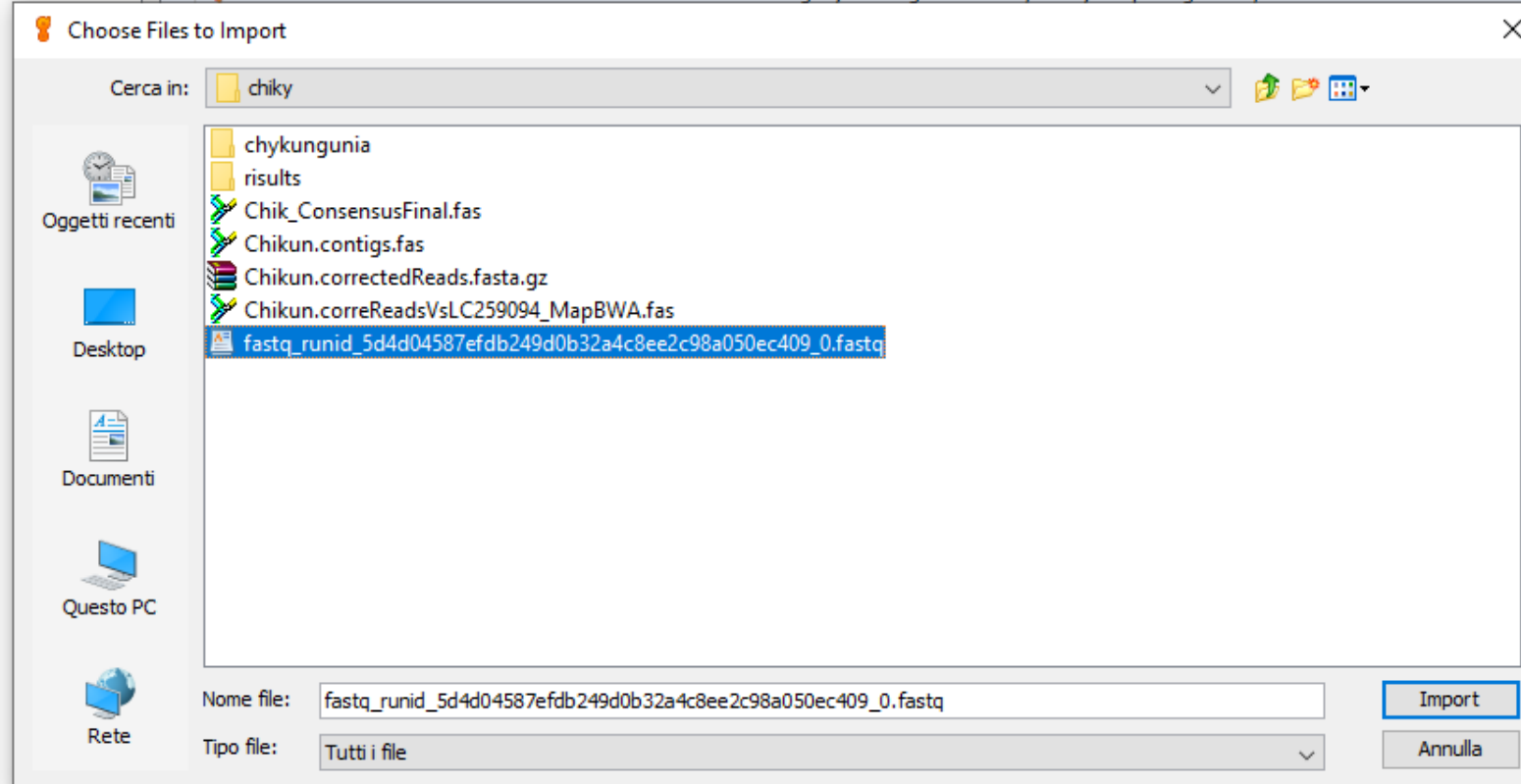


Sources

- Local (0)
 - Chikungunya virus (1)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (8)
- Shared Databases
 - Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

0 of 1 selected



 Search

Sources

- Local (0)
 - Chikungunya virus (1)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (5)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

0 of 1 selected						
<input type="checkbox"/>	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

FASTQ Sequences Import

Read Technology: ILLUMINA

☒ Don't pair (Sequences are unpaired or require a separate file)

☐ Paired End (inward pointing) interlaced sequences

Import via *Sequence->Set Paired Reads*

with insert size

500

Reset to Defaults

?

OK

Cancel

ILLUMINA

Ion Torrent

PacBio CLR

PacBio CCS

Oxford Nanopore

Sanger

454

Solid

Unknown

No document selected

Select documents in the table above to view

Using 94 / 13836 MB memory

Features Restricted

Geneious (Restricted) 11.1.3

FileEditViewToolsSequenceAnnotate & PredictHelp

BackForward

BLASTWorkflows

Align/AssembleTree

Primers (restricted)Cloning (restricted)

Back UpSupportHelp

Filter

Search

Sources

Local (0)

Chikungunya virus (1)

Chiky (1)

HIV (6)

HIV7-2018 (24)

HIVminion (11)

Mkim (11)

Ralsto (27)

Sample Documents (625)

TB_res (34)

Deleted Items (5)

Shared Databases

Operations

NCBI

Gene

Genome

Nucleotide

PopSet

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
<input type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

FASTQ Sequences Import

Read Technology: Oxford Nanopore

☒ Don't pair

(Sequences are unpaired or require advanced pairing after import via *Sequence->Set Paired Reads*)

☐ Paired End (inward pointing)

interlaced sequences within each file

with insert size 500

Reset to Defaults

?

OK

Cancel

No document selected

Select documents in the table above to view

Using 98 / 13836 MB memory

Features Restricted



Sources

- Local (0)
 - Chikungunya virus (1)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (8)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Using 213 / 13836 MB memory

Features Restricted

0 of 1 selected

	Name ▲	Description	Modified	Sequence Le...	%GC	Topology
	LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	linear

Hide

Grouping Sequences

How do you want to store the sequences from **fastq_runid_5d4d04587efdb249d0b32a4c8ee2c98a050ec409_0.fastq** in Geneious?

This file contains a large number of sequences so creating a list is highly recommended. Large numbers of separately stored sequences may cause Geneious to run slowly and use more memory.

Sequences can be grouped into or extracted from lists at any time using the Sequence menu.



☐ Remember my preference












Keep sequences separate Create sequence list

No document selected

Select documents in the table above to view

1 of 2 selected

<input checked="" type="checkbox"/>	Name ▲	Description	Modified	Sequence Le...	%GC	# Sequenc
<input checked="" type="checkbox"/>	 fastq_runid_5d4d04587efdb249d0b32a4c8ee2c98a... -		04 Feb 2020 11:09 PM	-	48.9%	4,000
	 LC259094.1	Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	-


 Extract
 
 R.C.
 
 Translate
 
 Add/Edit Annotation (restricted)
 
 Allow Editing (restricted)
 
 Annotate & Predict
 
 Save
 




Statistics

Length: 4,289
Sequences: 4,000

Read Lengths (restricted):
Mean: - Std Dev: -
Minimum: - Maximum: -

Confidence Mean: (restricted)
Expected Errors: (restricted)
At least Q20: (restricted)
At least Q30: (restricted)
At least Q40: (restricted)

	Freq	%
A:	910,799	25.1%
C:	877,120	24.2%
G:	894,225	24.7%
T:	943,452	26.0%
GC:	1,771,345	48.9%
All:	3,625,596	100.0%

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

File Edit View Tools Sequence Annotate & Predict Help

Back Forward

Align/Assemble

Tree...

Primers

Cloning

BLAST...

Add/Remove Databases

16S Biodiversity... (restricted)

Extract Annotations... (restricted)

Mask Alignment... (restricted)

Concatenate Sequences or Alignments... (restricted)

Generate Consensus Sequence...

Workflows

Plugins...

Preferences...

Local (0)

Chikun

Chiky

HIV (6)

HIV7-2

HIVmir

Mkim (

Ralsto

Sample

TB_res

Delete

Shared Da

Operations

NCBI

Gene

Genom

Nucleo

PopSe

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

Back Up Support Help

Filter

Search

1 of 2 selected

Description	Modified	Sequence Le...	%GC	# Sequen...
587efdb249d0b32a4c8ee2c98a...	06 Feb 2020 10:34 AM	-	48.9%	4,000
Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	-

Text View Lineage Info

Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

1 500 1,000 1,500 2,000 2,500 3,000 3,500 4,289

Ctrl+Maiusc+P

1-ff8365d7a42a...

d-95c87f92ee00...

3. 8918a7a6-7f77-4170-958d-ecdea74a250...

4. 2913e195-ca09-4abd-a8f2-057a382db62...

5. afe3e0f7-8e88-4ce4-81bb-79ef9a6a1a5a...

6. 30dab17c-dc42-4087-9008-b996232c43f...

7. 8361447f-2ab7-466c-81bd-13f3d59e5509...

8. 218582b7-d12f-4d00-80b9-392a560d198...

9. f9ab0d08-1e1b-472a-896e-66e01ae6944...

10. 420c3b9a-2d75-4746-a5c9-ef5ac9152d...

11. 76053865-9bd5-4171-b684-31f79fff224...

12. 0348daaa-a36c-4c6f-a23d-33b20a8021...

13. eeb84d51-cdda-4965-ab1f-6dc39b7ccaf...

14. 41baa98f-9c2f-4602-8e9d-05d5fc9ece9...

15. bf730e9e-23c0-4fa1-9be1-2f6fc4979f4c...

16. 30585870-b2b1-4851-a706-c8a5a1ba4e...

17. 07adc4fd-e30e-4d6a-94f9-95abb583537...

18. 841c3aca-accc-4431-8df4-fe71f6e11bf2...

19. fee26486-f332-4b91-81f6-9a0f12203cac...

20. 3a901440-2729-4793-b3cf-3ae8a1c4eb...

21. aa193085-d5ff-488e-92ad-16458c21180...

22. 1eb02afb-b8e7-46b6-a424-7a1839454f...

23. 62bcfe8a-9ffb-437c-9933-bdd267e2e47...

24. 29757172-628a-4dcb-99c7-c25f347ab2...

25. ebf8b08f-1c46-4170-b139-9f5a10c0176...

26. 91079d69-ecb5-461a-9aa2-60819220e7...

27. 013463d9-389c-4d38-942a-84cf4d86e1...

Statistics

Length: 4,289

Sequences: 4,000

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

Freq %

A: 910,799 25.1%

C: 877,120 24.2%

G: 894,225 24.7%

T: 943,452 26.0%

GC: 1,771,345 48.9%

All: 3,625,596 100.0%

Using 149 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

FileEditViewToolsSequenceAnnotate & PredictHelp

BackForward

Align/Assemble

Align or assemble sequences

Primers

Cloning

BLAST...

Add/Remove Databases

16S Biodiversity... (restricted)

Extract Annotations... (restricted)

Mask Alignment... (restricted)

Concatenate Sequences or Alignments... (restricted)

Generate Consensus Sequence...

Workflows

Plugins...

Preferences...

Multiple Align...

Map to Reference...

De Novo Assemble...

Align Whole Genomes...

Map Primers... (restricted)

Local (0)

Chikun

Chiky

HIV (6)

HIV7-2

HIVmir

Mkim (

Ralsto

Sample

TB_res

Delete

Shared Da

Operations

NCBI

Gene

Genom

Nucleo

PopSe

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

1 of 2 selected

Description	Modified	Sequence Le...	%GC	# Sequen...
Chikungunya virus genomic RNA, nearly complete genome, isolate: ...	03 Feb 2020 1:21 AM	11,825	50.3%	-

Text ViewLineageInfo

TranslateAdd/Edit Annotation (restricted)Allow Editing (restricted)Annotate & PredictSave

15002,0002,5003,0003,5004,289

Ctrl+Maiusc+P

1

500

1,000

1,500

2,000

2,500

3,000

3,500

4,289

3. 8918a7a6-7f77-4170-958d-ecdea74a250...

4. 2913e195-ca09-4abd-a8f2-057a382db62...

5. afe3e0f7-8e88-4ce4-81bb-79ef9a6a1a5a...

6. 30dab17c-dc42-4087-9008-b996232c43f...

7. 8361447f-2ab7-466c-81bd-13f3d59e5509...

8. 218582b7-d12f-4d00-80b9-392a560d198...

9. f9ab0d08-1e1b-472a-896e-66e01ae6944...

10. 420c3b9a-2d75-4746-a5c9-ef5ac9152d...

11. 76053865-9bd5-4171-b684-31f79fff224...

12. 0348daaa-a36c-4c6f-a23d-33b20a8021...

13. eeb84d51-cdda-4965-ab1f-6dc39b7ccaf...

14. 41baa98f-9c2f-4602-8e9d-05d5fc9ece9...

15. bf730e9e-23c0-4fa1-9be1-2f6fc4979f4c...

16. 30585870-b2b1-4851-a706-c8a5a1ba4e...

17. 07adc4fd-e30e-4d6a-94f9-95abb583537...

18. 841c3aca-accc-4431-8df4-fe71f6e11bf2...

19. fee26486-f332-4b91-81f6-9a0f12203cac...

20. 3a901440-2729-4793-b3cf-3ae8a1c4eb...

21. aa193085-d5ff-488e-92ad-16458c21180...

22. 1eb02afb-b8e7-46b6-a424-7a1839454f...

23. 62bcfe8a-9ffb-437c-9933-bdd267e2e47...

24. 29757172-628a-4dcb-99c7-c25f347ab2...

25. ebf8b08f-1c46-4170-b139-9f5a10c0176...

26. 91079d69-ecb5-461a-9aa2-60819220e7...

27. 013463d9-389c-4d38-942a-84cf4d86e1...

Statistics

Length: 4,289

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Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

	Freq	%
A:	910,799	25.1%
C:	877,120	24.2%
G:	894,225	24.7%
T:	943,452	26.0%
GC:	1,771,345	48.9%
All:	3,625,596	100.0%

Using 163 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Geneious (Restricted) 11.1.3

FileEditViewToolsSequenceAnnotate & PredictHelp

BackForward

Align/Assemble

Tree...

Primers

Cloning

BLAST...

Add/Remove Databases

16S Biodiversity... (restricted)

Extract Annotations... (restricted)

Mask Alignment... (restricted)

Concatenate Sequences or Alignments... (restricted)

Generate Consensus Sequence...

Workflows

Plugins...

Preferences...

Multiple Align...

Map to Reference...

De Novo Assemble

Align Whole Genomes...

Map Primers... (restricted)

Chikungunya virus genomic RNA, nearly complete genome, isolate: ...

04 Feb 2020 11:09 PM

-

48.9%

4,000

03 Feb 2020 1:21 AM

11,825

50.3%

-

Local (0)

Chikun

Chiky

HIV (6

HIV7-2

HIVmir

Mkim (

Ralsto

Sample

TB_res

Delete

Shared Da

Operations

NCBI

Gene

Genom

Nucleo

PopSe

Protein

PubMed

SNP

Structure

Taxonomy

UniProt

Ctrl+Maiusc+P

1

500

1,000

1,500

2,000

2,500

3,000

3,500

4,289

3. 8918a7a6-7f77-4170-958d-ecdea74a250...

4. 2913e195-ca09-4abd-a8f2-057a382db62...

5. afe3e0f7-8e88-4ce4-81bb-79ef9a6a1a5a...

6. 30dab17c-dc42-4087-9008-b996232c43f...

7. 8361447f-2ab7-466c-81bd-13f3d59e5509...

8. 218582b7-d12f-4d00-80b9-392a560d198...

9. f9ab0d08-1e1b-472a-896e-66e01ae6944...

10. 420c3b9a-2d75-4746-a5c9-ef5ac9152d...

11. 76053865-9bd5-4171-b684-31f79fff224...

12. 0348daaa-a36c-4c6f-a23d-33b20a8021...

13. eeb84d51-cdda-4965-ab1f-6dc39b7ccaf...

14. 41baa98f-9c2f-4602-8e9d-05d5fc9ece9...

15. bf730e9e-23c0-4fa1-9be1-2f6fc4979f4c...

16. 30585870-b2b1-4851-a706-c8a5a1ba4e...

17. 07adc4fd-e30e-4d6a-94f9-95abb583537...

18. 841c3aca-accc-4431-8df4-fe71f6e11bf2...

19. fee26486-f332-4b91-81f6-9a0f12203cac...

20. 3a901440-2729-4793-b3cf-3ae8a1c4eb...

21. aa193085-d5ff-488e-92ad-16458c21180...

22. 1eb02afb-b8e7-46b6-a424-7a1839454f...

23. 62bcfe8a-9ffb-437c-9933-bdd267e2e47...

24. 29757172-628a-4dcb-99c7-c25f347ab2...

25. ebf8b08f-1c46-4170-b139-9f5a10c0176...

26. 91079d69-ecb5-461a-9aa2-60819220e7...

27. 013463d9-389c-4d38-942a-84cf4d86e1...

Translate

Add/Edit Annotation (restricted)

Allow Editing (restricted)

Annotate & Predict

Save

Statistics

Length: 4,289

Sequences: 4,000

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

Freq

%

A: 910,799 25.1%

C: 877,120 24.2%

G: 894,225 24.7%

T: 943,452 26.0%

GC: 1,771,345 48.9%

All: 3,625,596 100.0%

Using 195 / 13836 MB memory

Features Restricted

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.



Sources

- Local (0)
 - Chikungunya virus (2)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (5)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Map to Reference

Data

Reference Sequence: Choose... ?

IsolatoTNScaffsConsensuCorr_-consensus will be mapped to LC259094

☐ Assemble by: part of name, separated by

☐ Assemble each sequence list separately

Method

Mapper: ?

Sensitivity: ?

☐ Find structural variants, short insertions, and deletions of any size ?

☐ Find short insertions and large deletions up to bp

Fine Tuning: ?

Memory Required: 24 MB of 122 GB

*Note: Paired reads can be set up or changed using **Sequence > Set Paired Reads***

Trim Before Mapping

☐ Use existing trim regions

☐ Remove existing trim regions from sequences

☐ Trim sequences

☒ Do not trim

Results

Assembly Name ...

☒ Save assembly report

☐ Save list of unused reads

☐ Save list of used reads ☐ Include mates

☐ Save in sub-folder

☒ Save contigs

☒ Save consensus sequences

Using 131 / 13836 MB memory

Features Restricted

25. 12049099-8434-43e8-bc00-b120c300d9...

26. e34d26bf-ed7c-49db-9092-ee049ab8fae...

27. 663ee3c1-ad7e-41f3-95fc-7bb8d074609...

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

- Local (0)
 - Chikungunya virus (2)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (5)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Select Nucleotide Sequences

- Local
 - Chikungunya virus
 - Chiky
 - HIV
 - HIV7-2018
 - HIVminion
 - Mkim
 - Ralsto
 - Sample Documents
 - TB_res

Subfolders not included.

Name	Sequence Length	# Sequences	Organism	Description
Chikun.Reads	-	214	-	-
LC259094.1	11825	-	-	Chikungunya viru...

Select

Use Folder

Cancel

Using 146 / 13836 MB memory

Features Restricted

25. 12d49699-8434-43e8-bc00-b120c306d9...
26. e34d26bf-ed7c-49db-9092-ee049ab8fae...
27. 663ee3c1-ad7e-41f3-95fc-7bb8d074609...

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Filter Search

1 of 2 selected

Sequence Le...	%GC	# Sequences
-	49.7%	214
11,825	50.3%	-

Hide

0 %

General

ACGT - Edit

Options >

Options >

Options >

Circular Overview

Trap

Show Names

Show Description

Show sequence numbers



Sources

- Local (0)
 - Chikungunya virus (2)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (5)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Map to Reference

Data

Reference Sequence: LC259094.1 - Chikungunya virus Choose... ?

IsolateTNScaffsConsensuCorr_-consensus will be mapped to LC259094

☐ Assemble by: 1st part of name, separated by -(Hyphen)☐ Assemble each sequence list separately

Method

Mapper: Geneious ?

Sensitivity: Highest Sensitivity / Slow ?

☐ Find structural variants, short insertions, and deletions of any size ?☐ Find short insertions and large deletions up to 1,000 bp

Fine Tuning: None (fast / read mapping) ?

Memory Required: 24 MB of 122 GB

Note: Paired reads can be set up or changed using Sequence > Set Paired Reads

Trim Before Mapping

- ☐ Use existing trim regions
- ☐ Remove existing trim regions from sequences
- ☐ Trim sequences Options
- ☒ Do not trim

Results

Assembly Name {Reads Name} assembled to {Reference Name} ...

- ☒ Save assembly report
- ☐ Save list of unused reads
- ☐ Save list of used reads ☐ Include mates
- ☐ Save in sub-folder
- ☒ Save contigs
- ☒ Save consensus sequences Options



More Options

OK

Cancel

Using 141 / 13836 MB memory

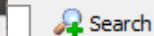
Features Restricted

25. 12049093-8434-43e8-bc00-b120c300d9...

26. e34d26bf-ed7c-49db-9092-ee049ab8fae...

27. 663ee3c1-ad7e-41f3-95fc-7bb8d074609...

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.



1 of 2 selected

Sequences

214

-

v

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v



Sources

- Local (0)
 - Chikungunya virus (2)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (5)
- Shared Databases
 - Operations
 - NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
 - UniProt

Map to Reference

Data

Reference Sequence: LC259094.1 - Chikungunya virus Choose... ?

IsolatoTNScaffsConsensusCorr_-consensus will be mapped to LC259094

☐ Assemble by: 1st part of name, separated by -(Hyphen)☐ Assemble each sequence list separately

Method

Mapper: Geneious ?

Sensitivity: Fast Sensitivity / Slow ?

☐ Find structural variants, short insertions, and deletions of any size ?

Find short insertion and short deletions up to 1,000 bp

Fine Tuning: None (fast / read mapping) ?

Memory: 128 MB of 122 GB

Mapped reads can be changed using Sequence > Set Paired Reads

Trim Before Mapping

☐ Use existing trim regions☐ Remove existing trim regions from sequences☐ Trim sequences Options☒ Do not trim

Results

Assembly Name {Reads Name} assembled to {Reference Name} ...

☒ Save assembly report☐ Save list of unused reads☐ Save list of used reads ☐ Include mates☐ Save in sub-folder☒ Save contigs☒ Save consensus sequences Options

More Options

OK

Cancel

Using 141 / 13836 MB memory

Features Restricted

25. 12049093-8434-43e8-bc00-b120c300d9...

26. e34d26bf-ed7c-49db-9092-ee049ab8fae...

27. 663ee3c1-ad7e-41f3-95fc-7bb8d074609...

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

Running velocity depend to multi factors such as:

- Type of computer (laptop, workstation, server...)
- Number of the reads
- Length of the reads
- Number and type of the CPU
- Type of computer processor

At the end....

 Search

Sources

- Local (0)
 - Chikungunya virus (4)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (11)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
- UniProt

Using 189 / 13836 MB memory

Features Restricted




0 of 4 selected

	Name ▲	Description	Modified	Sequence Le...	%GC	# Sequences	Topology
	Chikun.NoCorrectedReadsVsLC259094_sorted - LC259094.1	256,334 reads assembled to LC259094.1	06 Feb 2020 1:18 AM	98,817	49.9%	256,335	linear
	Chikun.NoCorrectedReadsVsLC259094_sorted - Unmapped sequences	-	06 Feb 2020 1:18 AM	-	47.4%	246,533	-
	fastq_runid_5d4d04587efdb249d0b32a4c8ee2c98a050ec409_0	-	04 Feb 2020 11:09 PM	-	48.9%	4,000	-
	LC259094.1	Chikungunya virus genomic RNA, nearly ...	03 Feb 2020 1:21 AM	11,825	50.3%	-	linear

No document selected

Select documents in the table above to view

1 of 4 selected

<input checked="" type="checkbox"/>	Name ▲	Description	Modified	Sequence Le...	%GC	# Sequences	Topology
	Chikun.NoCorrectedReadsVsLC259094_sorted - LC259094.1	256,334 reads assembled to LC259094.1	06 Feb 2020 1:18 AM	98,817	49.9%	256,335	linear
<input checked="" type="checkbox"/>	Chikun.NoCorrectedReadsVsLC259094_sorted - Unmapped sequences	-	06 Feb 2020 1:18 AM	-	47.4%	246,533	-
	fastq_runid_5d4d04587efdb249d0b32a4c8ee2c98a050ec409_0	-	04 Feb 2020 11:09 PM	-	48.9%	4,000	-
	LC259094.1	Chikungunya virus genomic RNA, nearly ...	03 Feb 2020 1:21 AM	11,825	50.3%	-	linear

Hide





Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.



Filter Search

Sources

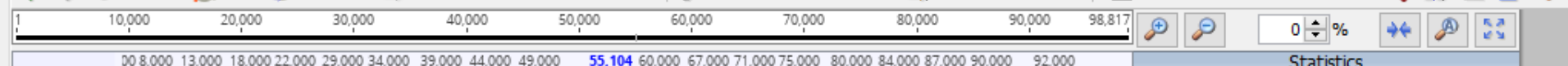
- Local (0)
 - Chikungunya virus (4)
 - Chiky (1)
 - HIV (6)
 - HIV7-2018 (24)
 - HIVminion (11)
 - Mkim (11)
 - Ralsto (27)
 - Sample Documents (625)
 - TB_res (34)
 - Deleted Items (11)
- Shared Databases
- Operations
- NCBI
 - Gene
 - Genome
 - Nucleotide
 - PopSet
 - Protein
 - PubMed
 - SNP
 - Structure
 - Taxonomy
 - UniProt

1 of 4 selected

<input checked="" type="checkbox"/>	Name ▲	Description	Modified	Sequence Le...	%GC	# Sequences	Topology
<input checked="" type="checkbox"/>	Chikun.NoCorrectedReadsVsLC259094_sorted - LC259094.1	256,334 reads assembled to LC259094.1	06 Feb 2020 1:18 AM	98,817	49.9%	256,335	linear
<input checked="" type="checkbox"/>	Chikun.NoCorrectedReadsVsLC259094_sorted - Unmapped sequences	-	06 Feb 2020 1:18 AM	-	47.4%	246,533	-
<input checked="" type="checkbox"/>	fastq_runid_5d4d04587efdb249d0b32a4c8ee2c98a050ec409_0	-	04 Feb 2020 11:09 PM	-	48.9%	4,000	-
<input checked="" type="checkbox"/>	LC259094.1	Chikungunya virus genomic RNA, nearly ...	03 Feb 2020 1:21 AM	11,825	50.3%	-	linear

Contig View Annotations Lengths Graph Text View Lineage Info

Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save



Consensus (calculating ...)

85,523

C...

Statistics

Stats include 74,170 hidden columns

Length: 98,817

Sequences: 256,335

Identical Sites: 376 (0.4%)

Pairwise % Identity: 81.1%

Coverage (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Forward: - Reverse: -

Ref-Seq: 99.7% (11,787 of 11,825)

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

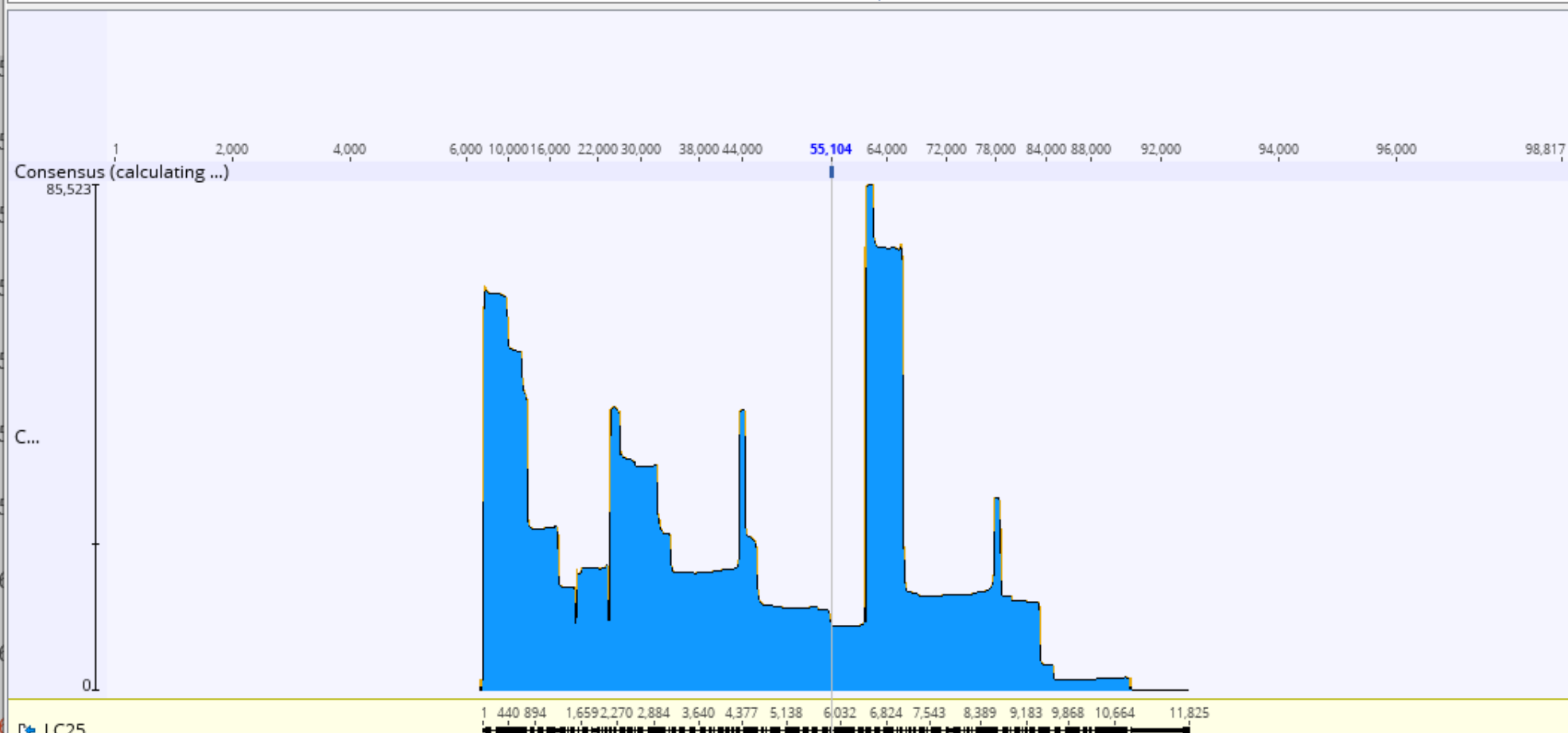
At least Q30: (restricted)

At least Q40: (restricted)

Using 432 / 13836 MB memory

Features Restricted

Cursor before column 55,104.



Zoom in to see 256,334 reads

Statistics

Stats include 74,170 hidden columns
Length: 98,817
Sequences: 256,335
Identical Sites: 376 (0.4%)
Pairwise % Identity: 81.1%

Coverage (restricted):

Mean: - Std Dev: -
Minimum: - Maximum: -
Forward: - Reverse: -
Ref-Seq: 99.7% (11,787 of 11,825)

Read Lengths (restricted):

Mean: - Std Dev: -
Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

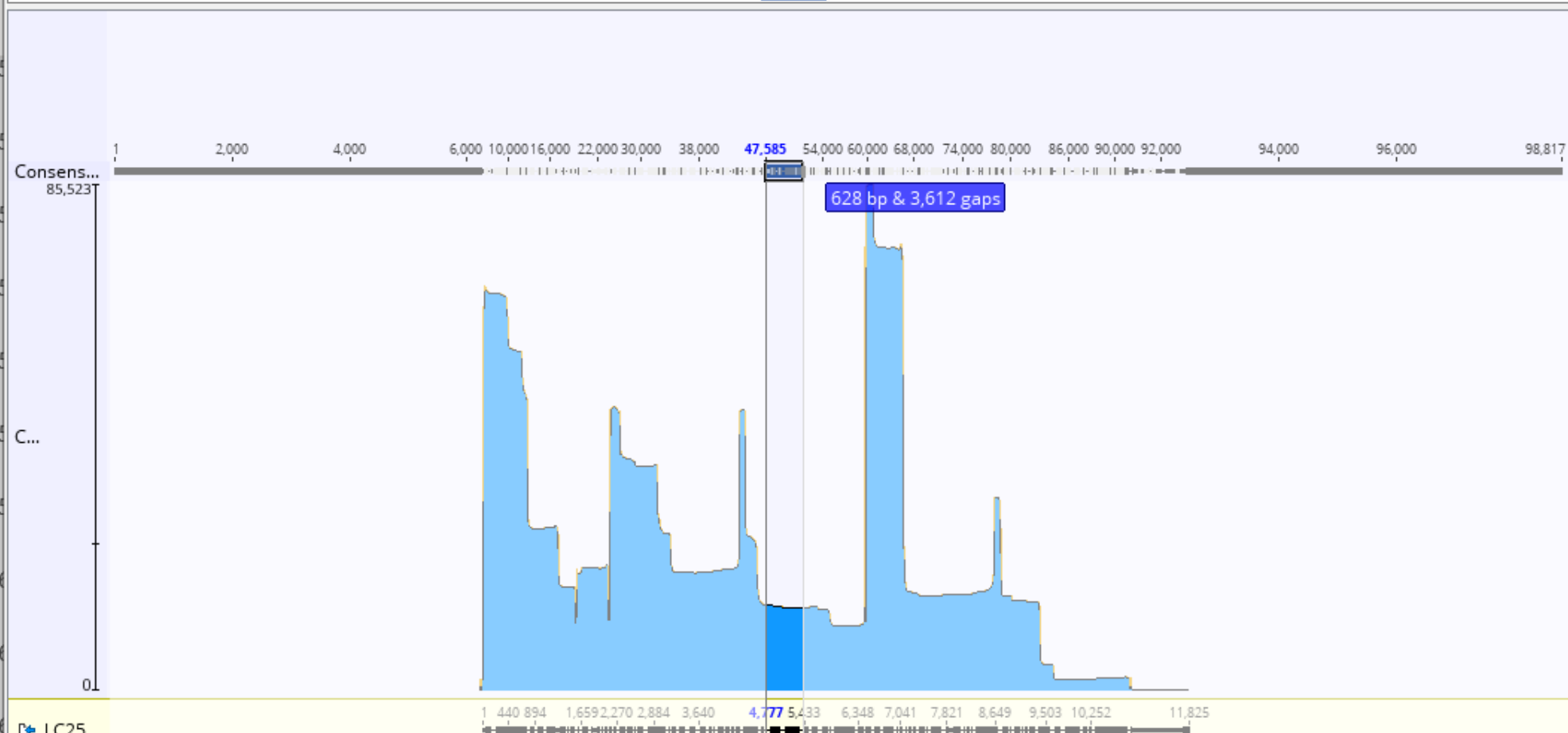
	Freq	% of non-gaps
A:	88,286,111	28.5%
C:	76,280,864	24.6%
G:	78,207,550	25.3%
T:	66,755,253	21.6%

GC: 154,588,414 49.9%

All: 309,729,778 100.0%

-: 2,516,511,870 89.0% (of any)

Rough Tm: (restricted)



Statistics

Stats include 74,170 hidden columns
Length: 98,817
Sequences: 256,335
Identical Sites: 376 (0.4%)
Pairwise % Identity: 81.1%

Coverage (restricted):

Mean: - Std Dev: -
Minimum: - Maximum: -
Forward: - Reverse: -
Ref-Seq: 99.7% (11,787 of 11,825)

Read Lengths (restricted):

Mean: - Std Dev: -
Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

	Freq	% of non-gaps
A:	88,286,111	28.5%
C:	76,280,864	24.6%
G:	78,207,550	25.3%
T:	66,755,253	21.6%

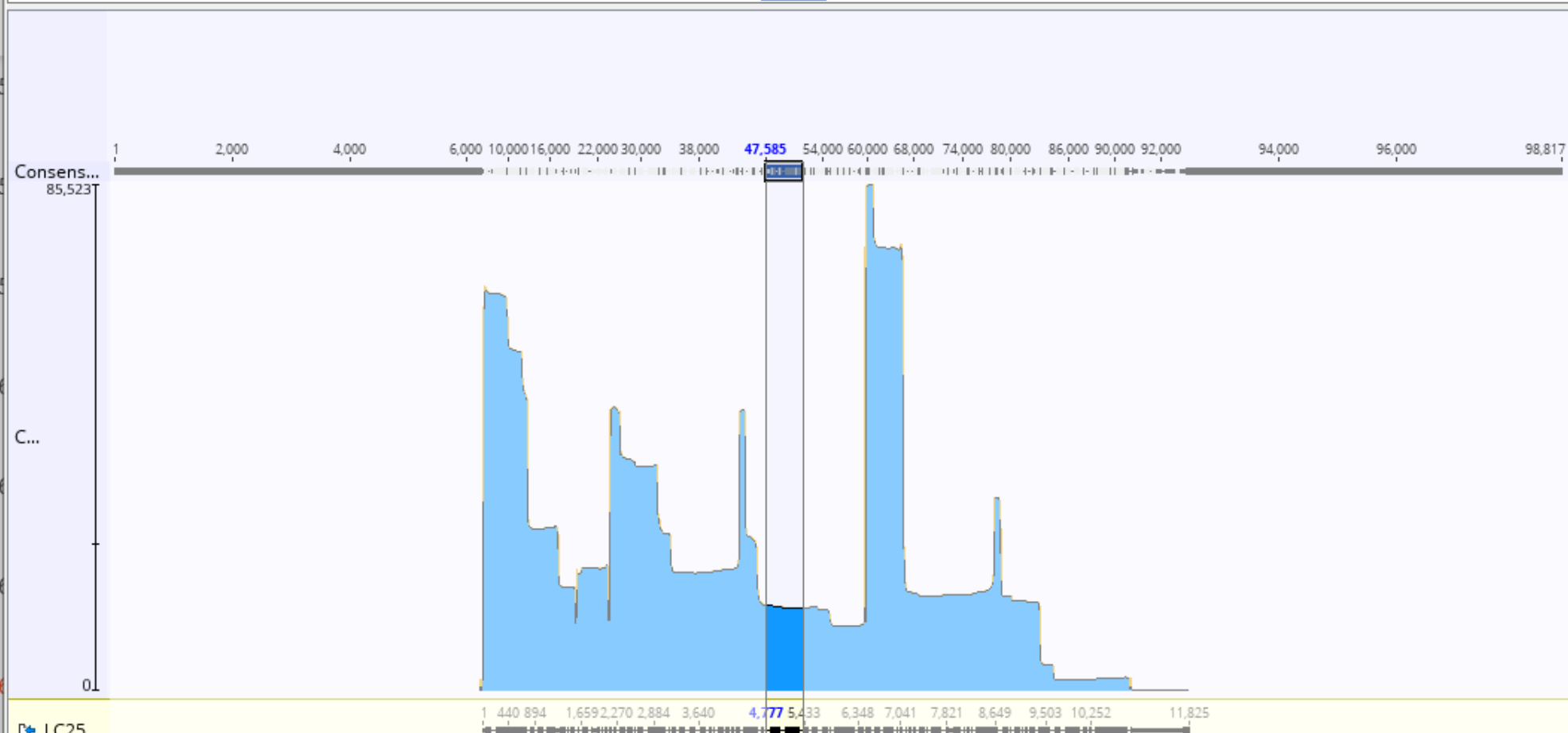
GC: 154,588,414 49.9%

All: 309,729,778 100.0%

-: 2,516,511,870 89.0% (of any)

Rough Tm: (restricted)

Calculating...



Zoom in to see 256,334 reads

Statistics

Zoom to selection

Stats may include hidden columns

Length: 4,240

Sequences: 1

Identical Sites: 0 (0.0%)

Pairwise % Identity: 80.8%

Coverage (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Forward: - Reverse: -

Ref-Seq: 100% of 631 bp

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

	Freq	% of non-gaps
A:	170	27.1%
C:	176	28.0%
G:	162	25.8%
T:	120	19.1%

GC: 338 53.8%

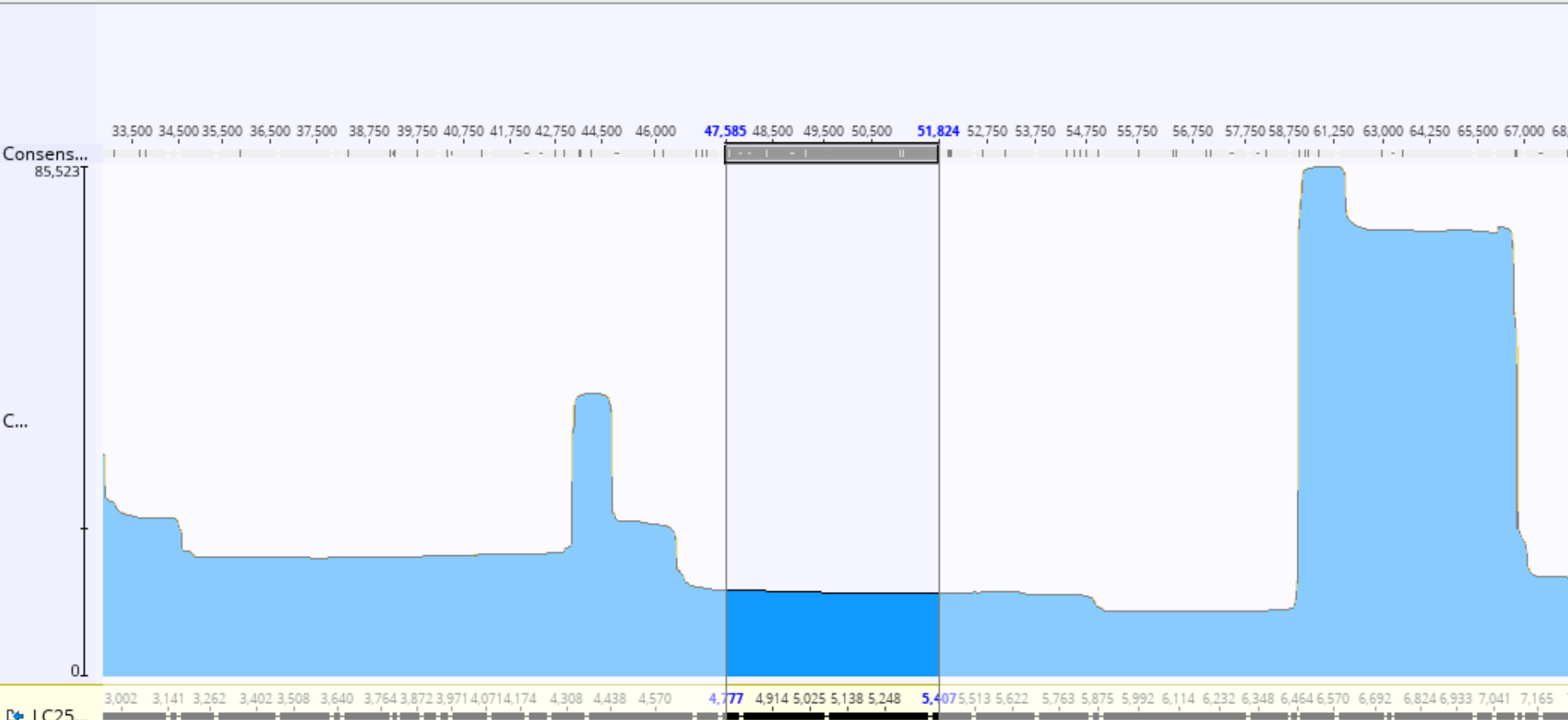
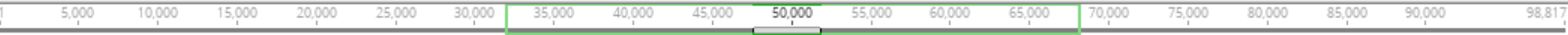
All: 628 100.0%

-: 3,612 85.2% (of any)

Rough Tm: (restricted)

Molecular weight:

ssDNA: 193.977 kDa



Zoom in to see reads

Statistics

Stats may include hidden columns
 Length: 4,240
 Sequences: 1
 Identical Sites: 0 (0.0%)
 Pairwise % Identity: 80.8%

Coverage (restricted):
 Mean: - Std Dev: -
 Minimum: - Maximum: -
 Forward: - Reverse: -
 Ref-Seq: 100% of 631 bp

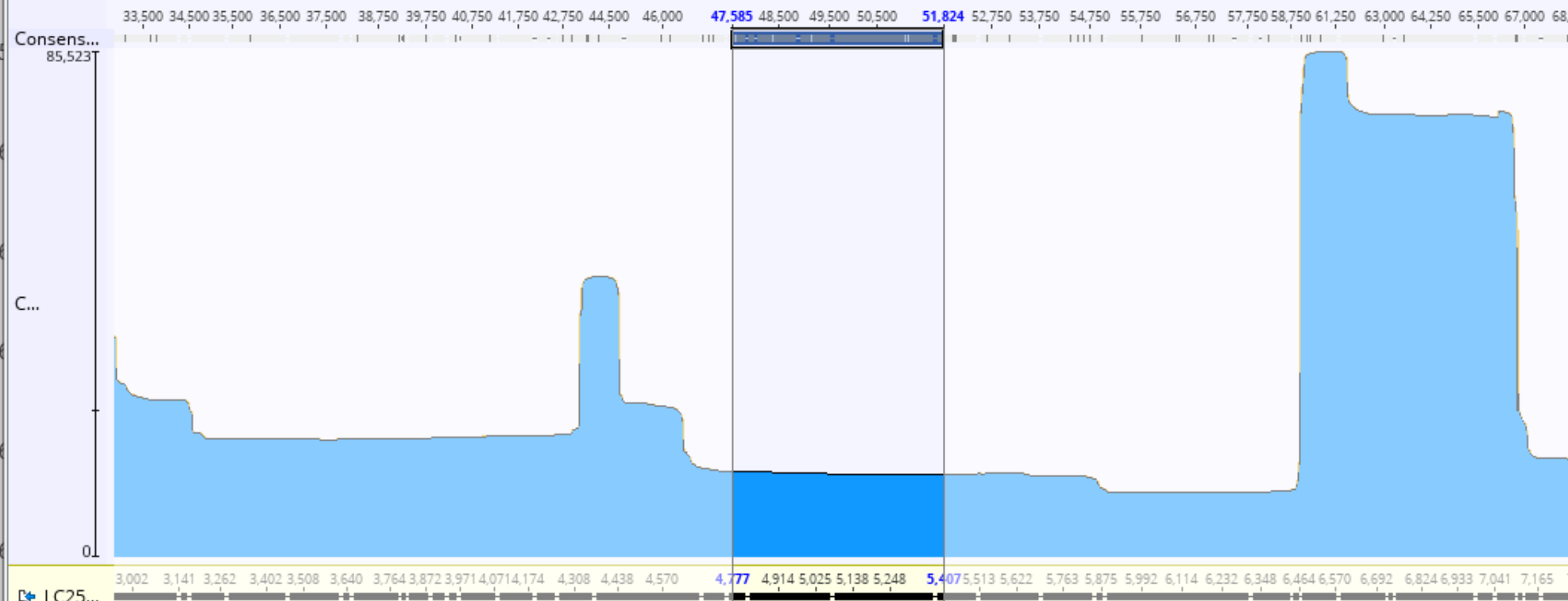
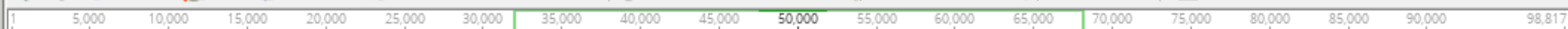
Read Lengths (restricted):
 Mean: - Std Dev: -
 Minimum: - Maximum: -

Confidence Mean: (restricted)
 Expected Errors: (restricted)
 At least Q20: (restricted)
 At least Q30: (restricted)
 At least Q40: (restricted)

	Freq	% of non-gaps
A:	170	27.1%
C:	176	28.0%
G:	162	25.8%
T:	120	19.1%

GC:	338	53.8%
All:	628	100.0%
-:	3,612	85.2% (of any)

Rough Tm: (restricted)
 Molecular weight:
 ssDNA: 193.977 kDa



Stats may include hidden columns

Length: 4,240

Sequences: 1

Identical Sites: 0 (0.0%)

Pairwise % Identity: 80.8%

Coverage (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Forward: - Reverse: -

Ref-Seq: 100% of 631 bp

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

	Freq	% of non-gaps
A:	170	27.1%
C:	176	28.0%
G:	162	25.8%
T:	120	19.1%

GC: 338

All: 628

-: 3,612 85.2% (of any)

Rough Tm: (restricted)

Molecular weight:

ssDNA: 193.977 kDa

File Edit View Tools Sequence Annotate & Predict Help

Contig View Annotations Lengths Graph Text View Lineage Info

Extract R.C. Translate Add Annotation (restricted) Allow Editing (restricted) Annotate & Predict Primer Design Save

5,000 10,000 15,000 20,000 25,000 30,000 35,000 40,000 45,000 50,000 55,000 60,000 65,000 70,000 75,000 80,000 85,000 90,000 95,000 98,817

141 %

Consens... 85,523
19,490 49,510 49,530 49,550 49,570 49,590 49,610 49,630 49,650 49,670 49,680 49,690 49,700 49,720 49,730 49,750 49,760 49,780 49,800 49,820 49,840 49,870 49,880
- T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

C...

0 5,065 5,067 5,070 5,073 5,076 5,077 5,079 5,082 5,084 5,086 5,088 5,091 5,093 5,095 5,097 5,100 5,102 5,104 5,107 5,110 5,113 5,115 5,118

LC25... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

FWD 8ddf... C A G G C G C G C C T G T G A C C T C A C C T C A T G T C T T C C A C C G C T G A A T A C A A G T T T C T A G

FWD 6d8a... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C G A A T T C G A C C T A A G C

REV 6086... T T C T G C C T T T T G G C C T A T G C C A C C G C C A T G T G G T C C A A T G T C C T C T C C

REV 6a4c... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

REV e6bb... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

FWD 3f22... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

FWD 6327... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

FWD 8ceb... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

FWD 5702... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

REV 1c7a... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

REV 6da7... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

REV 30a7... C T G C A C A G G A A G C - G A G T A C A A C C A C G T C A C T G A C G C A T A G C C A A T T C G A C C T A A G C

Statistics

Stats may include hidden columns

Length: 4,240

Sequences: 1

Identical Sites: 0 (0.0%)

Pairwise % Identity: 80.8%

Coverage (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Forward: - Reverse: -

Ref-Seq: 100% of 631 bp

Read Lengths (restricted):

Mean: - Std Dev: -

Minimum: - Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

At least Q20: (restricted)

At least Q30: (restricted)

At least Q40: (restricted)

	Freq	% of non-gaps
A:	170	27.1%
C:	176	28.0%
G:	162	25.8%
T:	120	19.1%

GC: 338

All: 628

--: 3,612

85.2% (of any)

Rough Tm: (restricted)

Molecular weight:

ssDNA: 193.977 kDa

Selected 4,240 columns from 47,585 to 51,824 (628 ungapped bases from 11,031 to 11,658).

Thanks to
INMI Bioinformatic Group

Emanuela Giombini

Francesco Messina

Cesare Gruber





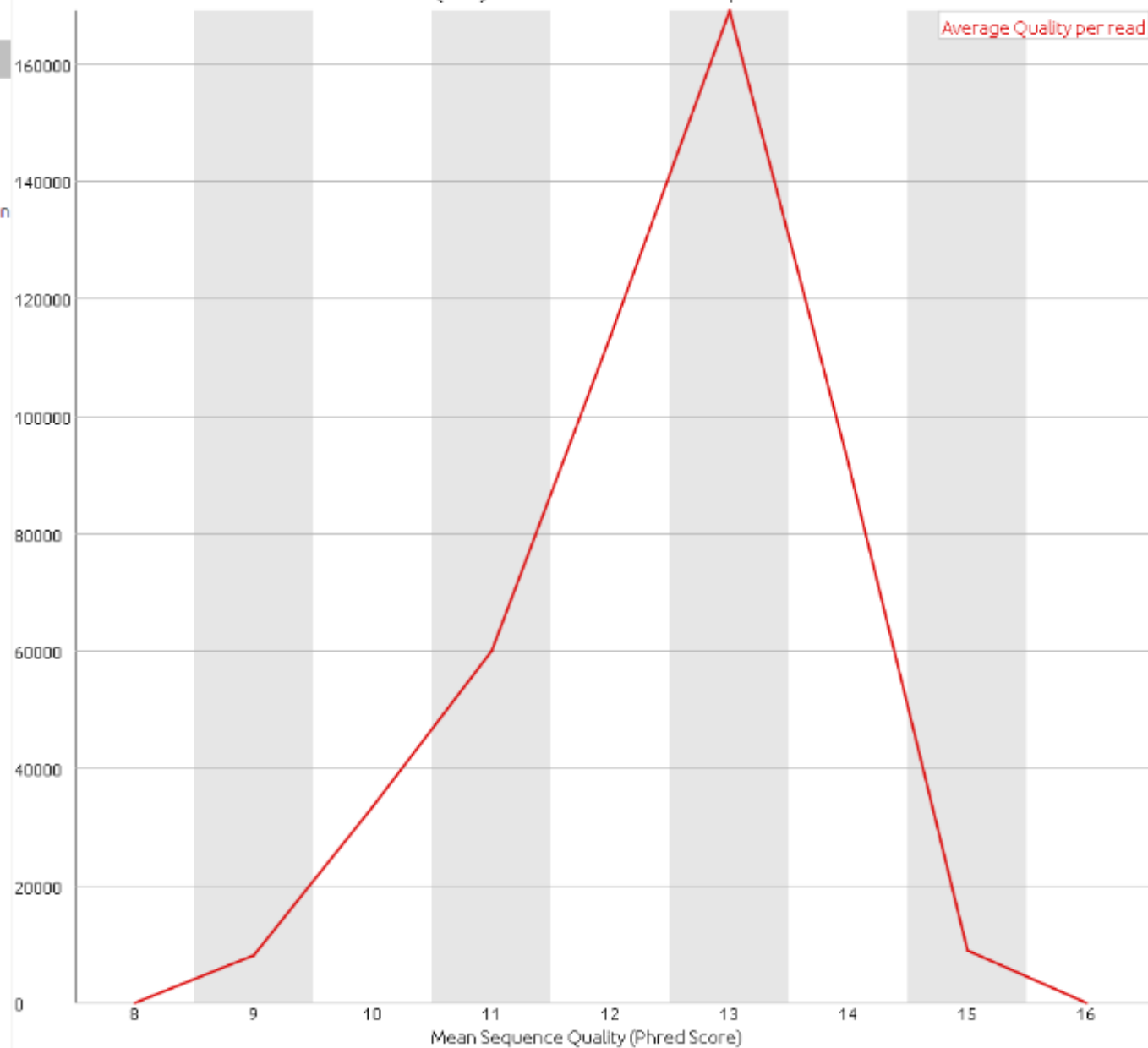
File Help



fastq_runid_Pass_runite.fq

- ✓ Basic Statistics
- ✗ Per base 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

Quality score distribution over all sequences



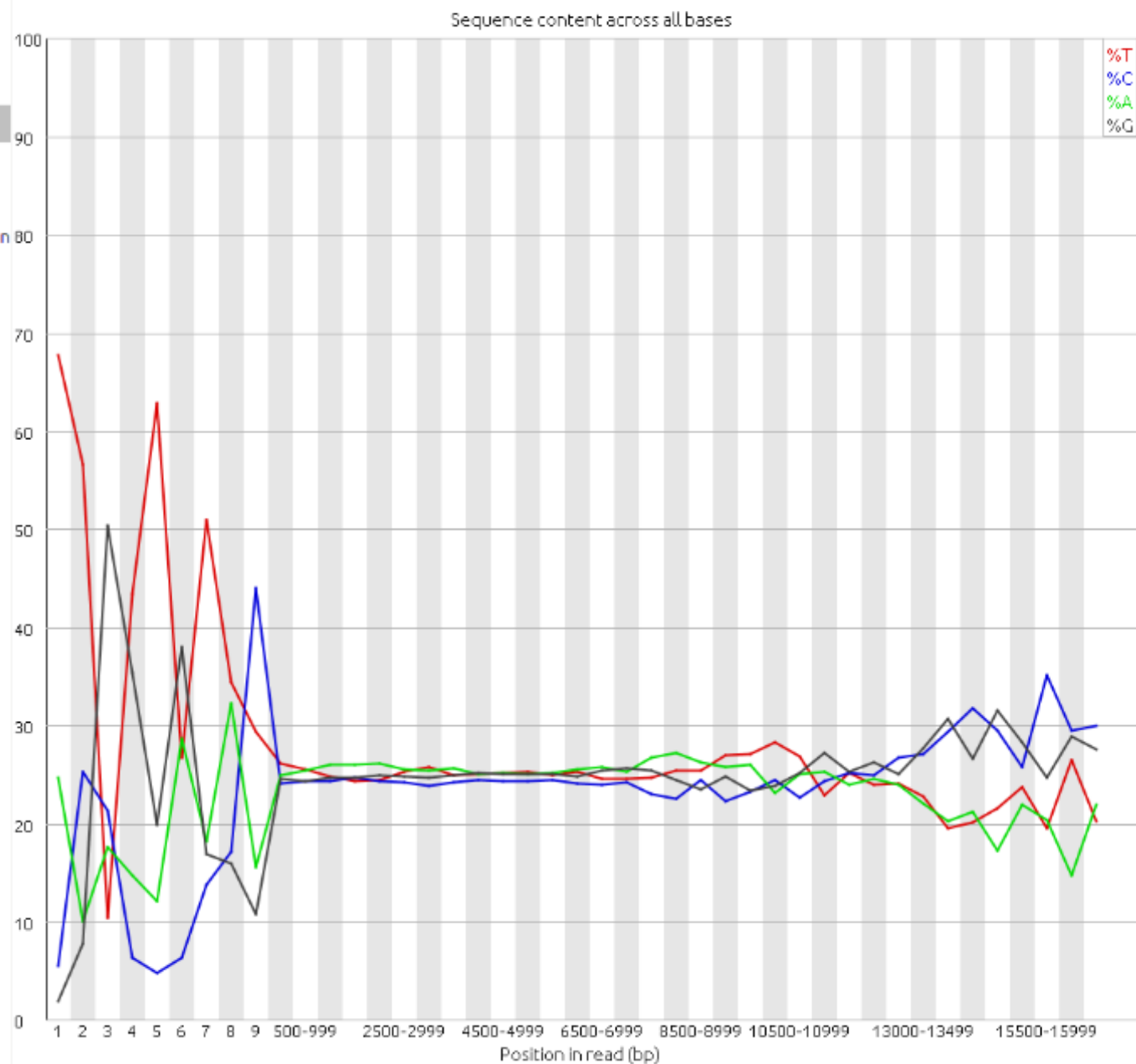


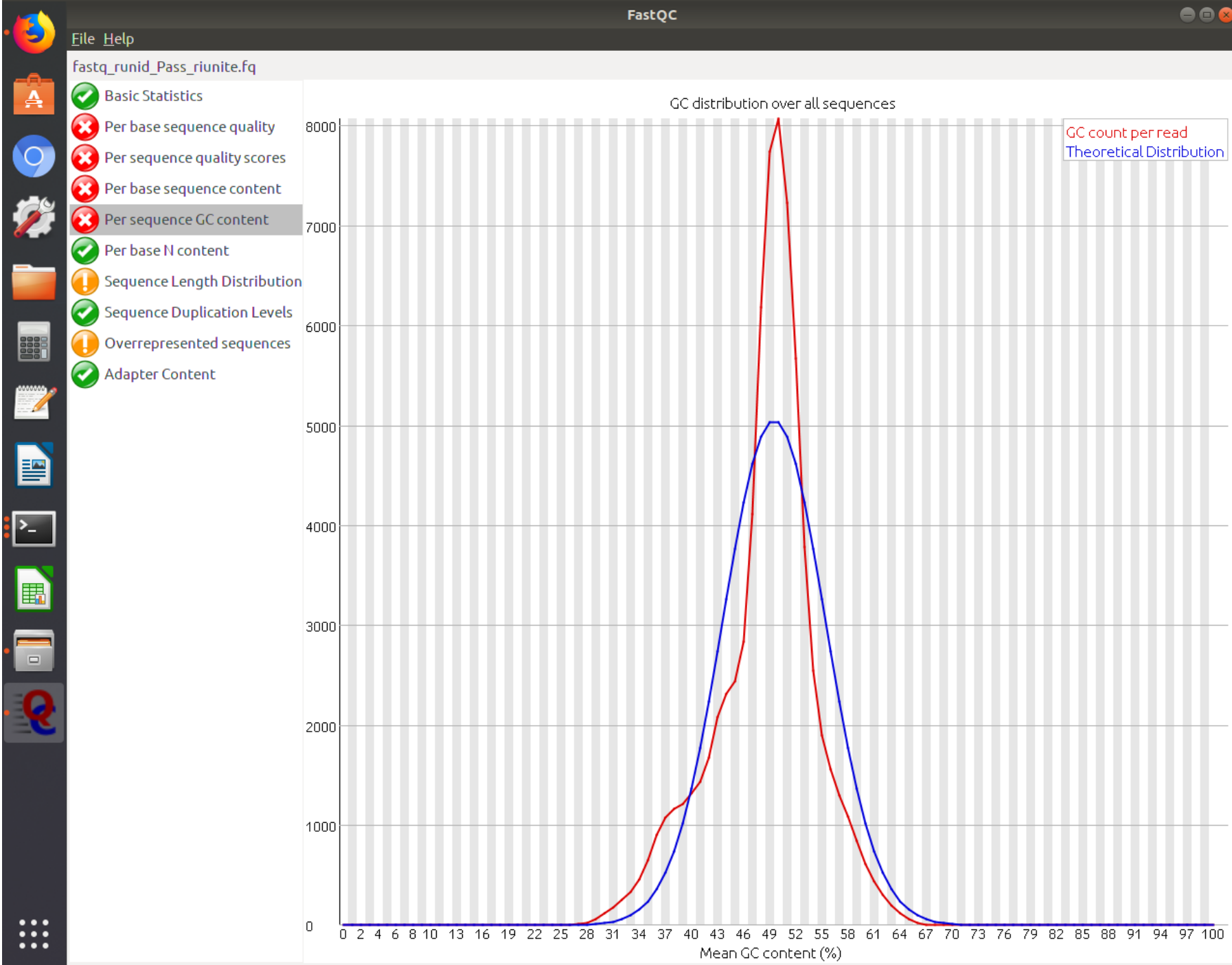
File Help

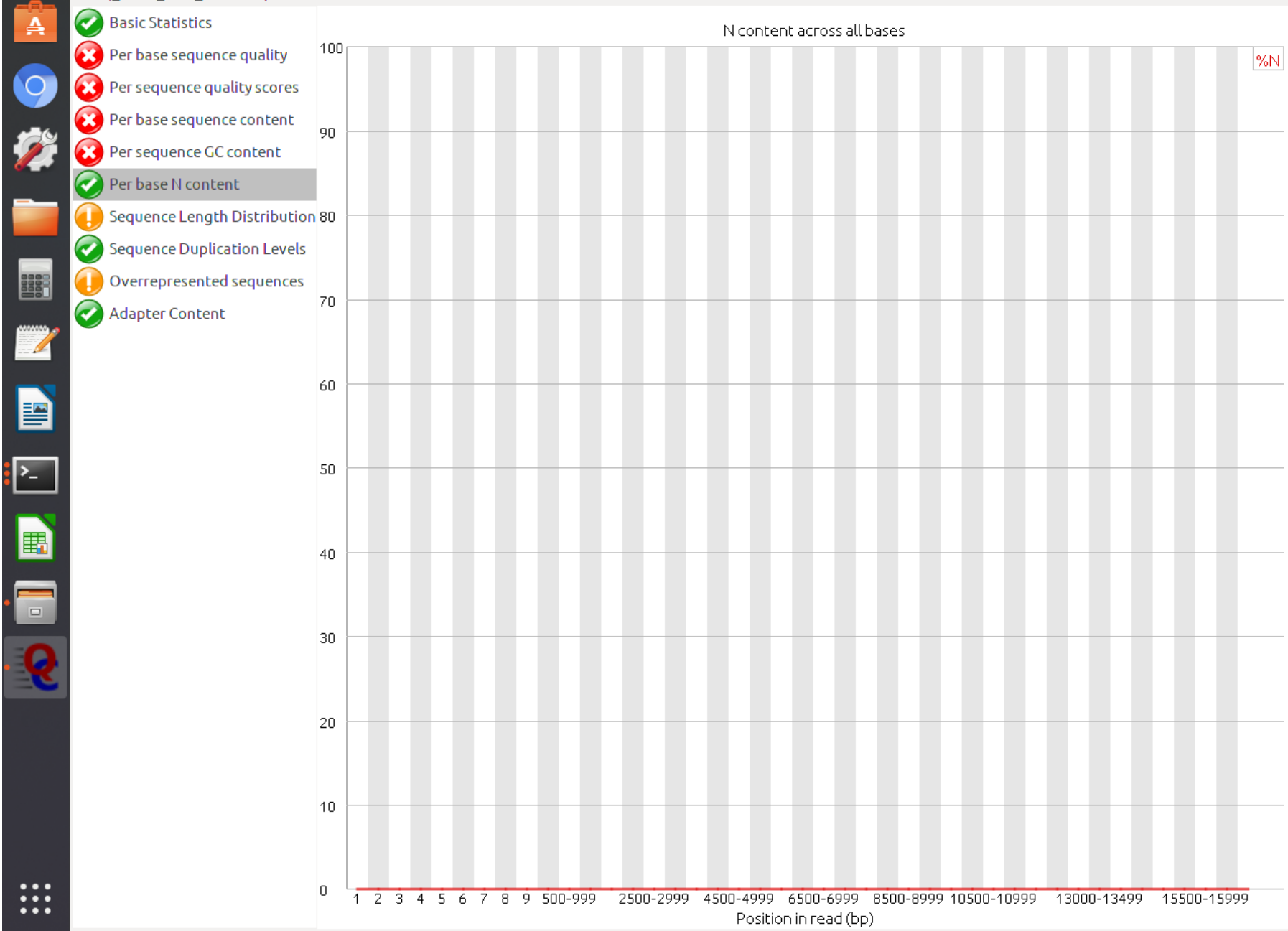


fastq_runid_Pass_r1unit.fq

- ✓ Basic Statistics
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- ✗ Per sequence quality scores
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- ✓ Per base N content
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- Basic Statistics
- Per base 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

