

Tutorial for Tick Borne Pathogens Webinar: Bunyavirales and Ticks

Use Case 1: A recent paper has shown that "[A single mutation in Crimean-Congo hemorrhagic fever virus discovered in ticks impairs infectivity in human cells](#)". In this manuscript, the authors show that "R1116G", a point mutation in the glycoprotein precursor complex (GPC) protein determines host tropism of CCHFV (human versus tick). For this use case, we will compare CCHFV GPC proteins from human and tick hosts using the following methods:

Step 1a) Search and Assemble dataset (Documentation: [Genome/Protein Search](#))

- Navigate to <https://www.bv-brc.org> and click on "Viruses"

The screenshot shows the BV-BRC homepage. At the top, there is a navigation bar with links for ORGANISMS, SEARCHES, TOOLS & SERVICES, WORKSPACES, HELP, and ABOUT. Below the navigation bar is a search bar with the placeholder "Find a gene, genome, microarray, etc". Underneath the search bar are four blue buttons labeled BACTERIA, ARCHAEA, VIRUSES, and EUKARYOTIC HOSTS. The main content area features a heading "BACTERIAL AND VIRAL BIOINFORMATICS RESOURCE CENTER" and a welcome message about the website's purpose and beta status.

- This will take you to the Virus Overview Homepage. Now click on "[Bunyavirales](#)"

The screenshot shows the BV-BRC Virus Overview page for the Bunyavirales family. At the top, there is a navigation bar with links for ORGANISMS, SEARCHES, and TOOLS & SERVICES. Below the navigation bar is a section titled "Virus View" with a "Viruses (6399156 Genomes)" link. A horizontal menu bar includes tabs for Overview, Taxonomy, Genomes, Proteins, Protein Structures, Domains and Motifs, and Epitopes. The "Overview" tab is selected. The main content area is divided into two sections: "Virus Data Summary" and "Virus Families". The "Virus Data Summary" section contains a table with the following data:

Families	68
Genera	1639
Species	20666
Genomes / Segments	6386745
Protein Coding Genes (CDS)	107521840
Mature Peptides	109609101
3D Protein Structures (PDB)	11502

The "Virus Families" section displays five families under the "Single-Stranded Positive-Sense RNA" category: Caliciviridae, Bunyavirales, Coronaviridae, Filoviridae, Flaviviridae, and Paramyxoviridae. Each family is represented by a small image of its characteristic virus particles.

- Navigate to the genomes tab, use the “FILTER” button to select the following criteria and click “APPLY”:

Public = True

Genome Status = Complete

Segment = M

Host group =

Species = Crimean-Congo Hemorrhagic Fever Virus

Taxon View
Viruses » Negarnaviricota » Ellioviricetes » Bunyavirales (47788 Genomes)

[Overview](#) [Taxonomy](#) [Strains](#) [Genomes](#) [Proteins](#) [Protein Structures](#) [Domains and Motifs](#) [Epitopes](#) [Experiments](#)

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true M Complete Crimean-Congo hemorrhagic fever or Human or Tick

HOST_GROUP X

Public	Genome Status	Segment	Collection Year	Isolation Country	Host Group	Species
true (142)	Complete (142)	M (142)	1956 (2)	Afghanistan (1)	Tick (41)	filter species
	Partial (923)	L (137)	1958 (1)	Bulgaria (4)	Human (101)	Crimean-Congo hemorrhagic fever orthonalrovirus (14)
		S (156)	1965 (1)	China (7)	Nonhuman Mammal (4)	Alenquer phlebovirus (2)
			1967 (4)	Democratic Republic of the Congo (1)		Andes orthohantavirus (34)
			1968 (4)	Greece (1)		Bangui virus (1)

- After clicking “APPLY”, switch to the “Proteins” tab, select all GPC proteins, and select the “GROUP” option in the green action bar on the right, to create a “Protein Feature Group”.

Taxon View
Viruses » Negarnaviricota » Ellioviricetes » Bunyavirales PUBLIC IS "true" AND SEGMENT IS "M" AND GENOME STATUS IS "Complete" AND SPECIES IS "Crimean-Congo hemorrhagic fever or Human" OR HOST GROUP IS "Tick" (142 Genomes)

[Overview](#) [Taxonomy](#) [Strains](#) [Genomes](#) [Proteins](#) [Protein Structures](#) [Domains and Motifs](#) [Epitopes](#) [Experiments](#)

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CDS PATRIC

FEATURE_TYPE X ANNOTATION X

Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KU161584	CDS	fig 1980519.5996			93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KU161585	CDS	fig 1980519.5997			93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever MF287637	CDS	fig 1980519.6423			95	5149	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814856	CDS	fig 1980519.4255			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814857	CDS	fig 1980519.4256			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814858	CDS	fig 1980519.4257			90	5141	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814866	CDS	fig 1980519.4265			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814867	CDS	fig 1980519.4266			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814868	CDS	fig 1980519.4267			92	5140	+	5049	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814859	CDS	fig 1980519.4258			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814869	CDS	fig 1980519.4268			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814870	CDS	fig 1980519.4269			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814860	CDS	fig 1980519.4259			93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814871	CDS	fig 1980519.4270			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814861	CDS	fig 1980519.4260			93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814872	CDS	fig 1980519.4271			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814873	CDS	fig 1980519.4272			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814874	CDS	fig 1980519.4273			92	5143	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
<input checked="" type="checkbox"/> Crimean-Congo hemorrhagic fever KR814862	CDS	fig 1980519.4261			91	5142	+	5052	GPC	Pre-glycoprotein polyprotein GP complex

Add selection to a new or existing group

- You can also create a MSA directly from here using the MSA button in the green action bar on the right, making sure to select “Amino Acid”. Note: *not recommended for large data sets*.

Step 1b) Create MSA to verify and look for other genomes ([MSA and SNP/Variation Analysis](#), [Documentation](#))

- To perform a multi-sequence alignment, navigate to the “TOOLS & SERVICES” tab, and select “MSA and SNP Analysis”.

TOOLS & SERVICES ▾ WORKSPACES ▾ HELP ▾ All Da

Genomics **Protein Tools**
Assembly (B) MSA and SNP Analysis

- Select the appropriate “Feature Group” saved in the previous step.
- Select “Unaligned Sequences”, “Protein” and “Mafft” options.
- Specify appropriate “Output Folder” and “Output Name”, and click submit.

Services
Multiple Sequence Alignment and SNP/Variation Analysis  

The multiple sequence alignment service with variation and SNP analysis can be used with feature groups, fasta files, aligned fasta files, and user input fasta records. If a single alignment file is given, then only the variation analysis is run. For further explanation, please see the Multiple Sequence Alignment and SNP/Variation Analysis Service Quick Reference Guide and Tutorial.

Start with: 

UNALIGNED SEQUENCES ALIGNED SEQUENCES

SELECT FEATURE GROUP
 Step1a_CCHFV_GPC  

DNA PROTEIN

SELECT DNA OR PROTEIN FASTA FILE
 FASTA file  

INPUT FASTA SEQUENCE
Enter fasta records of sequences to align.

ALIGNER
Mafft 

OUTPUT FOLDER
 +TickTutorial  

OUTPUT NAME
Step2a_CCHFV_GPC_MSA

Reset **Submit**

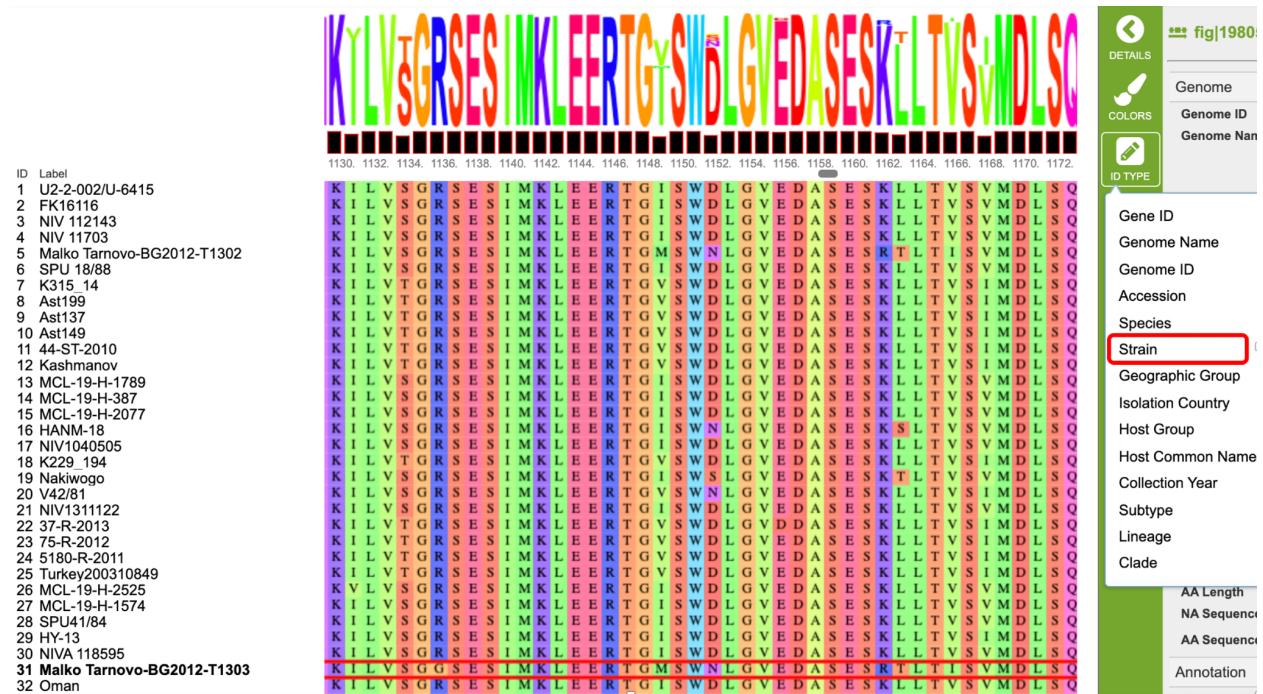
- Navigate to the job results and click on the appropriate job. Click the “eye” icon to view the aligned sequences.

MSA Job Result

Job ID	6987090
Start time	3/21/22, 9:52 PM
End time	3/21/22, 9:53 PM
Run time	22s
Parameters	

Name	Size	Owner	Members	Created
Parent folder	-	-	-	-
Step2a_CCHFV_GPC_MSA.afa	260.0 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.aln	442.7 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.consensus.fasta	1.8 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.entropy.svg	353.2 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.nexus	340.6 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.phy	401.1 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.pir	267.7 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.snp.tsv	63.4 kB	me	Only me	3/21/22, 9:53 PM
mafft.job.log	140.1 kB	me	Only me	3/21/22, 9:53 PM

- Scroll to the appropriate area “LVSGRSES” consensus region (~1134) to view the region of interest. Use the “ID TYPE” button shown below to select “Strain” name as the genome ID, and search for the “Malko Tarnovo-BG2012-T1303” name to find the genome reported in the publication referenced above.



- Explore “ID Type” and “Color” schemes as desired, or return to the file list to select and view the SNP variation report (snp.tsv file extension) for a detailed view of variation in the MSA.

Name	Size	Owner	Members	Created
Parent folder		-		
Step2a_CCHFV_GPC_MSA.afa	260.0 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.aln	442.7 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.consensus.fasta	1.8 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.entropy.svg	353.2 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.nexus	340.6 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.phy	401.1 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.pir	267.7 kB	me	Only me	3/21/22, 9:53 PM
Step2a_CCHFV_GPC_MSA.snp.tsv	63.4 kB	me	Only me	3/21/22, 9:53 PM
mafft.job.log	140.1 kB	me	Only me	3/21/22, 9:53 PM

Position	Score	Consensus	Detail	NumberOfSequence
10	130	Aaa	Leu=0,Pro=13,Ser=0	141
16	0	Leu	Leu=141	141
17	202	Xaa	Ala=2,Ile=23,Leu=8,Met=52,Thr=1	141
18	139	Xaa	Asn=12,Cys=66,Ser=1,Tyr=62	141
19	160	Xaa	Ala=70,Leu=3,Phe=52,Thr=4,Val=1	141
20	122	Val	Ala=3,Ile=63,Phe=2,Val=73	141
21	97	Leu	Ile=2,Leu=98,Phe=41	141
22	112	Cys	Cys=92,His=4,Leu=1,Tyr=44	141

Step 1c) Use MetaCATS to search for other tick specific sites ([MetaCATS, Documentation](#)).

While our MSA only identified one strain with the published mutation relevant to tick host tropism, users may wish to use our Meta-CATS tool to search for other sites that may occur at a higher frequency in CCHFV strains isolated from tick hosts rather than human hosts. (Note this tool can be used to look for positions that significantly differ between user-defined groups of sequences, or groups based on database metadata such as genotype, geography, or time of isolation).

- Returning to the “Proteins” tab, use the “Host Group” Filter to create separate “Tick” and “Human” feature groups for GPC.

(101 results for CCHFV M segments isolated from humans with the below criteria)

Taxon View
Viruses » Negarnaviricota » Ellioviricetes » Bunyavirales » Nairoviridae » Orthonairovirus » Crimean-Congo hemorrhagic fever orthonairovirus (4063 Genomes)

Genomes

Overview Taxonomy Strains Genomes Proteins Protein Structures Domains and Motifs Epitopes Experiments

KEYWORDS: Human

ADV Search PUBLIC X GENOME_STATUS X SEGMENT X HOST_GROUP X

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Public	Genome Status	Segment	Collection Year	Isolation Country	Geographic Group	Host Common Name
true (101)	Complete (101) Partial (773)	M (101) L (99) S (116)	1956 (2) 1958 (1) 1967 (4) 1968 (3) 1969 (1) 1981 (1)	Afghanistan (1) Bulgaria (1) Democratic Republic of the Congo (1) India (35) Iran (1) Namibia (1)	Africa (19) Asia (45) Europe (35)	Human (101)

(41 results for CCHFV M segments isolated from ticks with the below criteria)

Taxon View
Viruses » Negarnaviricota » Ellioviricetes » Bunyavirales » Nairoviridae » Orthonairovirus » Crimean-Congo hemorrhagic fever orthonairovirus (4063 Genomes)

Genomes

Overview Taxonomy Strains Genomes Proteins Protein Structures Domains and Motifs Epitopes Experiments

KEYWORDS: Human or Tick

ADV Search PUBLIC X GENOME_STATUS X SEGMENT X

DOWNLOAD HIDE APPLY

Public	Genome Status	Segment	Reference Genome	Collection Year	Isolation Country	Geographic Group	Host Group
true (41)	Complete (41) Partial (150)	M (41) L (38) S (40)	Reference (1)	1965 (1) 1968 (1) 1969 (2) 1971 (1) 1973 (2) 1981 (1)	Bulgaria (3) China (7) Greece (1) India (12) Kazakhstan (1) Nigeria (2)	Africa (6) Asia (24) Europe (11)	Tick (41) Human (101)

- Click apply, switch to the proteins tab and save the tick and human GPC protein datasets as feature groups named “CCHFV_M_tickAA” and “CCHFV_M_humanAA” respectively.

Taxon View
 Viruses » Negarnaviricota » Ellioviretes » Bunyavirales » Nairoviridae » Orthonairovirus » Crimean-Congo hemorrhagic fever orthonairovirus » PUBLIC IS "true" AND GENOME STATUS IS "Complete" AND SEGMENT IS "M" AND HOST GROUP IS "Tick" (41 Genomes)

Overview Taxonomy Strains Genomes Proteins Protein Structures Domains and Motifs Epitopes Experiments

DOWNLOAD KEYWORDS ADV Search CDS PATRIC FEATURE_TYPE X ANNOTATION X FILTERS

Genome Name	Accession	Feature Type	BCR ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
Crimean-Congo hemorrhagic fever c KU161585		CDS	fig 1980519.5997.		93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c GU477493		CDS	fig 1980519.6536		99	5171	+	5073	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c DQ211626		CDS	fig 1980519.5922.		36	5180	+	5103	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c MF547416		CDS	fig 1980519.6483.		93	5147	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KY484026		CDS	fig 1980519.6186.		36	5180	+	5103	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c MG659726		CDS	fig 1980519.6546.		92	5146	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c MN832722		CDS	fig 1980519.7906.		93	5147	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KY484032		CDS	fig 1980519.6192.		93	5147	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c AY900145		CDS	fig 1980519.5776.		16	5070	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KY484035		CDS	fig 1980519.6195.		93	5147	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c NC_005300		CDS	fig 1980519.4147.		93	5147	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KY484038		CDS	fig 1980519.6198.		53	5162	+	5097	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013454		CDS	fig 1980519.6056.		81	5135	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013460		CDS	fig 1980519.6062.		77	5131	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013457		CDS	fig 1980519.6059.		76	5130	+	5055	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013463		CDS	fig 1980519.6065.		91	5142	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013466		CDS	fig 1980519.6068.		85	5136	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013469		CDS	fig 1980519.6071.		93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013472		CDS	fig 1980519.6074.		93	5144	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c KX013475		CDS	fig 1980519.6077.		83	5134	+	5052	GPC	Pre-glycoprotein polyprotein GP complex
Crimean-Congo hemorrhagic fever c MN866193		CDS	fig 1980519.7993.		19	5160	+	5103	GPC	Pre-glycoprotein polyprotein GP complex

Add selection to a new or existing group GROUP

Add selected items to group

Group Type

Feature

New/Existing

New Group

Group Folder (defaults to your groups folder)

Feature Groups

Group Name

CCHFV_M_tickAA

Cancel Add

- Navigate to the MetaCATS tool underneath the “Genomics” header in the “TOOLS & SERVICES” tab.

The screenshot shows a vertical navigation bar on the left with several icons. The 'Genomics' section is expanded, displaying the following options:

- Assembly (B)
- Annotation
- Comprehensive Genome
- Analysis (B)
- BLAST
- SARS-CoV-2 Genome
- Assembly and Annotation (V)
- Similar Genome Finder (B)
- Meta-CATS

- Specify the desired Output folders and names.

Services

Metadata-driven Comparative Analysis Tool (meta-CATS)

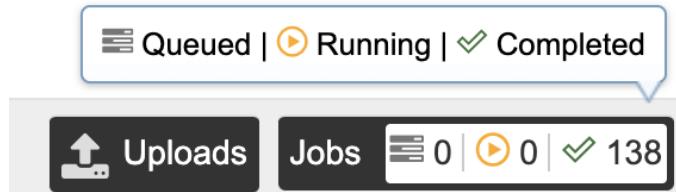
The meta-CATS tool looks for positions that significantly differ between user-defined groups of sequences. However, biological biases due to covariation, codon biases, and differences in genotype, geography, time of isolation, or others may affect the robustness of the underlying statistical assumptions. For further explanation, please see [Metadata-driven Comparative Analysis Tool \(meta-CATS\) Service Quick Reference Guide](#) and [Tutorial](#).

The form contains the following fields:

- P-VALUE: A text input field containing "0.05".
- OUTPUT FOLDER: A dropdown menu currently set to "+TickTutorial".
- OUTPUT NAME: A text input field containing "Step1c".

- Select “feature groups”: “CCHFV_M_tickAA” and “CCHFV_M_humanAA”, and click the “+” button to add them to the “selected groups table” (see below).
- Confirm “Protein” is selected, and click submit to launch the job.

- To view results, click on the job status box in the bottom right corner of the webpage..



- Navigate to your job, and click on “View” to view results.

Job Status		All Services		0 queued	0 running	139 completed	35 failed
Status	ID	Service	Output Name	Submit	Start	Completed	View Job Results
completed	6987114	TaxonomicClassification	Step2a_SRR107694	3/21/22, 10:10 PM	3/21/22, 10:14 PM		
completed	6987113	MetaCATS	Step1c_tickVhuman	3/21/22, 10:08 PM	3/21/22, 10:08 PM	3/21/22, 10:10 PM	
completed	6987090	MSA	Step2a_CCHEV_GB	3/21/22, 9:52 PM	3/21/22, 9:52 PM	3/21/22, 9:53 PM	

- A list output files is provided for the user (see explanations in the documentation). You may explore these individually, or use the eye-shaped “View” icon (red circle below) to navigate to view a list of sites that differ significantly between proteins isolated from tick versus human hosts.

aniewiad1 / home / +TickTutorial / MetaCats (3 items)

MetaCats Job Result

Job ID	6987714
Start time	3/22/22, 8:40 AM
End time	3/22/22, 8:41 AM
Run time	1m10s

▶ Parameters

File List:

Name	Size	Owner	Members	Created
Parent folder	-	-	-	-
MetaCats-chisqTable.tsv	318.4 kB	me	Only me	3/22/22, 8:41 AM
MetaCats-mcTable.tsv	543.6 kB	me	Only me	3/22/22, 8:41 AM
MetaCats.mafft.log	515.6 kB	me	Only me	3/22/22, 8:41 AM

- Results can further be filtered to only display statistically significant results, using "Keywords" filters as shown below.

aniewiad1 / home / +TickTutorial / .MetaCats / MetaCats-chisqTable.tsv

KEYWORDS Significant

First Row Contains Column Headers

<input type="checkbox"/>	Position	Chi-square_value	P-value	Significant	Degrees_of_free	Fewer_5	/aniewiad1@bvb	/aniewiad1@bvb
<input type="checkbox"/>	28	11.9792495039919	0.00745458201374	Y	3	Y	2 C	8 M, 1 V, 1 Y
<input type="checkbox"/>	30	11.974067264756	0.01754515318067	Y	4	Y	2 Q	2 A, 5 E, 2 G, 1 P
<input type="checkbox"/>	31	15.9643795091847	0.00306733536348	Y	4	Y	2 H	3 C, 1 I, 6 S, 4 T
<input type="checkbox"/>	33	20.5874404798575	0.00832797116773	Y	8	Y	3 F, 2 L, 2 P, 2 T	1 I, 9 L, 3 M, 3 Q,
<input type="checkbox"/>	35	14.2603010270892	0.04674065714289	Y	7	Y	3 L, 2 M, 4 N	7 G, 1 H, 1 L, 6 M
<input type="checkbox"/>	53	16.7409170260938	0.01914538886145	Y	7	Y	2 I, 3 R, 2 S, 2 T	2 -, 2 F, 3 G, 1 I, 7

Use Case 2: Isolation and characterization of an “unknown” Nairovirus.

Often, researchers or clinicians encounter patients with symptoms of hemorrhagic fever but with unknown etiology. In this case, diagnostic measures may include whole genome sequencing of a patient sample, to try to detect the causative infectious disease agent.

For the purposes of this exercise, we will pretend that the following raw reads deposited in the Sequence Read Archive (SRA) database, are from just such a sample. Run number:

[SRR10769498](#)

Step 2a) SRA file analysis ([Taxonomic classifier, Documentation](#))

In order to assess read content in this sample, we will use taxonomic classification.

- Navigate to the “Taxonomic Classification” tool underneath the “Metagenomics” header in the “TOOLS & SERVICES” tab.

The screenshot shows the CBV-BRC BETA website interface. At the top, there is a navigation bar with links for ORGANISMS, SEARCHES, TOOLS & SERVICES, WORKSPACES, HELP, and ABOUT. The TOOLS & SERVICES menu is expanded, revealing several categories: Genomics, Protein Tools, and Metagenomics. Under Genomics, options like Assembly (B), Annotation, and Comprehensive Genome Analysis (B) are listed. Under Protein Tools, MSA and SNP Analysis, Gene Tree, and Proteome Comparison (B) are listed. Under Metagenomics, Metagenomic Read Mapping (B), Taxonomic Classification, and Metagenomic Binning are listed. Below the menu, a main content area titled "BACTERIAL AND VIRAL BIOINFO" displays a welcome message and information about the beta version of the website.

- Input the above SRA run number (SRR10769498) into the appropriate box (red rectangle below), then click the indicated arrow (red circle below) to move the dataset to the “Selected Libraries” box.

Services

Taxonomic Classification

The Taxonomic Classification Service computes taxonomic classification for read data. For further explanation, please see the Taxonomic Classification Service Quick Reference Guide and Tutorial.

The screenshot shows the Taxonomic Classification service interface. On the left, under "Input File", there are three sections: PAIRED READ LIBRARY (with dropdowns for READ FILE 1 and READ FILE 2), SINGLE READ LIBRARY (with a dropdown for READ FILE), and SRA RUN ACCESSION (with a text input field containing "SRR10769498" and a red box around it). To the right, under "Selected libraries", there is a list box containing "SRR10769498" with an "i" and an "x" icon. A red circle highlights the "i" icon, indicating where to click to move the dataset to the Selected Libraries box.

- Select the appropriate parameters as shown below, specifying your desired “output folder” and “output name”. Once selected, the “submit” button can be clicked to launch the job.

Parameters [i](#)

ALGORITHM
Kraken2

DATABASE
All genomes

SAVE CLASSIFIED SEQUENCES
 NO YES

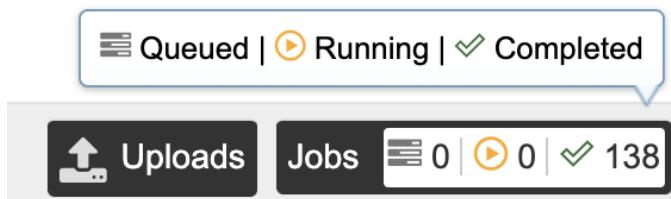
SAVE UNCLASSIFIED SEQUENCES
 NO YES

OUTPUT FOLDER
↓

OUTPUT NAME

[Reset](#) [Submit](#)

- To view results, click on the job status box in the bottom right corner of the webpage.



- Navigate to your job, and click on “View” to view results.

Job Status
Last updated: 11:46:09

		All Services		0 queued	0 running	138 completed	35 failed
Status	ID	Service	Output Name	Submit	Start	Completed	+
completed	6987745	Annotation	Nairoviridae Annotation	3/22/22, 8:57 AM	3/22/22, 8:57 AM	3/22/22, 9:01 AM	+ View
completed	6987740	Homology	Test2	3/22/22, 8:55 AM	3/22/22, 8:55 AM	3/22/22, 8:55 AM	+ View
completed	6987734	GenomeAssembly2	Assembly_CCHFV	3/22/22, 8:51 AM	3/22/22, 8:52 AM	3/22/22, 8:52 AM	+ View
completed	6987727	FastqUtils	CCHFV_Align	3/22/22, 8:48 AM	3/22/22, 8:48 AM	3/22/22, 8:55 AM	+ View
completed	6987720	TaxonomicClassification	SRR10769498_Tax	3/22/22, 8:45 AM	3/22/22, 8:45 AM	3/22/22, 8:52 AM	+ View

[HIDE](#) [VIEW](#) [REPORT ISSUE...](#) [RERUN](#)

- A list output files is provided for the user (see explanations in the documentation). You may explore these individually, or use the eye-shaped “View” icon (red circle below) to navigate to the “Taxonomic Report”.



TaxonomicClassification Job Result

Job ID	6987720
Start time	3/22/22, 8:45 AM
End time	3/22/22, 8:52 AM
Run time	7m15s
▶ Parameters	

Name	Size	Owner	Members	Created	C
↑ Parent folder	-	-	-	-	
TaxonomicReport.html	19.1 kB	me	Only me	3/22/22, 8:52 AM	
chart.html	2.5 MB	me	Only me	3/22/22, 8:52 AM	
classified.fastq.gz	55.1 MB	me	Only me	3/22/22, 8:52 AM	
full_report.txt	2.0 MB	me	Only me	3/22/22, 8:52 AM	
output.txt.gz	14.9 MB	me	Only me	3/22/22, 8:52 AM	
report.txt	427.8 kB	me	Only me	3/22/22, 8:52 AM	

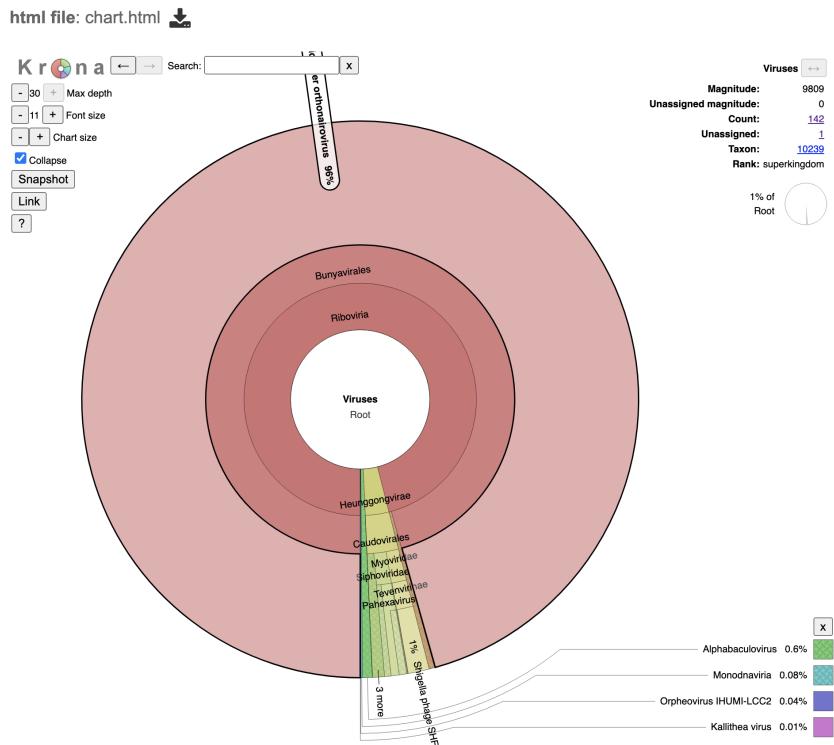
- Results can be viewed either in a “Table format” or as an “Interactive chart” (see below).

html file: TaxonomicReport.html

...there were zero hits.

In addition, the output file [output.txt.gz](#) contains information about each input sequence. Documentation on this format is available [here](#).

Pct Coverage	Frags in Clade	Frags in Taxon	Rank	NCBI Taxon ID	Scientific Name
1.29	9809	0	D	10239	Viruses
1.24	9418	0	D1	2559587	Riboviria
1.24	9386	0	K	2732396	Orthornavirae
1.24	9386	0	P	2497569	Negarnaviricota
1.24	9386	0	P1	2497571	Polyploviricotina
1.24	9386	0	C	2497576	Ellioviricetes
1.24	9386	0	O	1980410	Bunyavirales
1.24	9378	0	F	1980415	Nairoviridae
1.24	9378	0	G	1980517	Orthonaïrovirus
1.24	9378	9378	S	1980519	Crimean-Congo hemorrhagic fever orthonaïrovirus



- Results for this SRA run number indicate the presence of Crimean-Congo Hemorrhagic Fever Virus reads.

Step 2b) Read QC and mapping ([Fastq Utilities](#), [Documentation](#))

After detection of a virus of interest in a sample, users may want to assemble their reads into viral contigs for further analysis. While reference based sequencing is not yet available for viral sequences (*pipeline coming soon!*), users can utilize a combination of our “Fastq Utilities” and *de novo* sequence “Assembly” services to extract and assemble their viral reads (see below).

- Navigate to the “Fastq Utilities” tool underneath the “Utilities” header in the “TOOLS & SERVICES” tab.

Primer Design

Variation Analysis (B)

Tn-Seq Analysis (B)

Utilities

ID Mapper

Fastq Utilities

- Enter the SRA run accession number from the previous step (don't forget to press the arrow to transfer the data to the “Selected libraries” box as in the previous step!).
- Specify your desired “output folder” and “output name”.
- Select the appropriate analysis pipelines, “FastQC” and “Align”, as shown below, and click the “+” button to add these services.
- Select the appropriate “Target Genome”, in this case, CCHFV.
- Once selected, the “submit” button can be clicked to launch the job.

Services

Fastq Utilities

The Fastq Utilities Service provides capability for aligning, measuring base call quality, and trimming fastq read files. For further explanation, please see the [Fastq Utilities Service Quick Reference Guide and Tutorial](#).

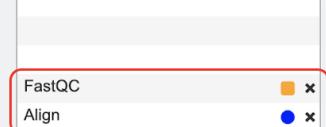
Parameters 

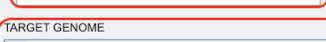
OUTPUT FOLDER
 

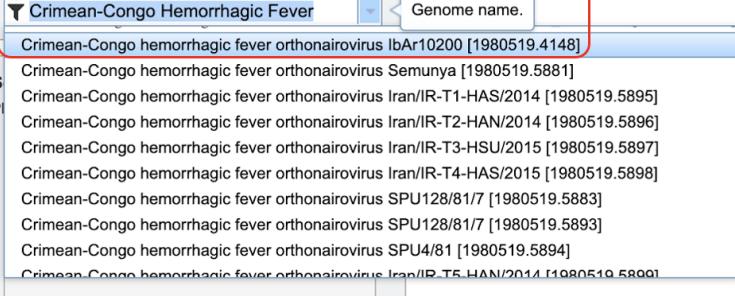
OUTPUT NAME

Pipeline 

Align 





TARGET GENOME


Crimean-Congo Hemorrhagic Fever   
 Crimean-Congo hemorrhagic fever orthonaïrovirus lbAr10200 [1980519.4148]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Semunya [1980519.5881]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Iran/IR-T1-HAS/2014 [1980519.5895]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Iran/IR-T2-HAN/2014 [1980519.5896]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Iran/IR-T3-HSU/2015 [1980519.5897]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Iran/IR-T4-HAS/2015 [1980519.5898]
 Crimean-Congo hemorrhagic fever orthonaïrovirus SPU128/81/7 [1980519.5883]
 Crimean-Congo hemorrhagic fever orthonaïrovirus SPU128/81/7 [1980519.5893]
 Crimean-Congo hemorrhagic fever orthonaïrovirus SPU4/81 [1980519.5894]
 Crimean-Congo hemorrhagic fever orthonaïrovirus Iran/IR-T5-HAN/2014 [1980519.5899]

Paired read library 

READ FILE 1
 

READ FILE 2
 

Single read library 

READ FILE
 

SRA run accession 

SRR ACCESSION

Reset
Submit

- Once your job has completed, and you have selected the appropriate job from the list, you can view the results of either the “FastQC” or “Align” pipelines (See eye view icon below).

aniewiad1 / home / +TickTutorial / CCHFV_Align (8 items)

FastqUtils Job Result

Job ID	6987727
Start time	3/22/22, 8:48 AM
End time	3/22/22, 8:55 AM
Run time	6m9s
▶ Parameters	

- The FastQC results summarize several quality control metrics for the sequence reads as shown below (for more information on each of these, see linked service documentation above).

html file: SRR10769498_fastqc.html [Download](#)

FastQC Report

Tue 22 Mar 2022
SRR10769498.fastq

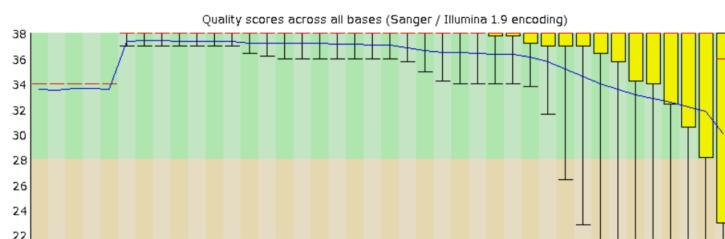
Summary

- [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	SRR10769498.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	757773
Sequences flagged as poor quality	0
Sequence length	160
%GC	49

Per base sequence quality



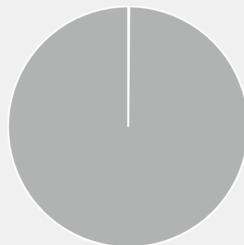
- For the results of the “Align” pipeline, a summary of reads, read length, and base quality is displayed (note: only 0.1% of reads are mapped to the target CCHFV genome previously specified).

html file: SRR10769498.all.bam.samstat.html [Download](#)

SRR10769498.all.bam

757773 reads, size:63437778 bytes, created 2022-03-22 15:50:26

Mapping stats:



- MAPQ >= 30
- MAPQ < 30
- MAPQ < 20
- MAPQ < 10
- MAPQ < 3
- Unmapped

Number of alignments in various mapping quality (MAPQ) intervals and number of unmapped sequences.

	Number	Percentage
MAPQ >= 30	761.0	0.1
MAPQ < 30	108.0	0.0
MAPQ < 20	0.0	0.0
MAPQ < 10	82.0	0.0
MAPQ < 3	0.0	0.0
Unmapped	756822.0	99.9
Total	757773.0	100.0

Number of alignments in various mapping quality (MAPQ) intervals and number of unmapped sequences.

- At this point, you may download the aligned reads or use them for further analysis, as shown in “**step 2c**”.

anieviad1 / home / +TickTutorial / CCHFV_Align (8 items)

FastqUtils Job Result

Job ID	6987727
Start time	3/22/22, 8:48 AM
End time	3/22/22, 8:55 AM
Run time	6m9s
Parameters	

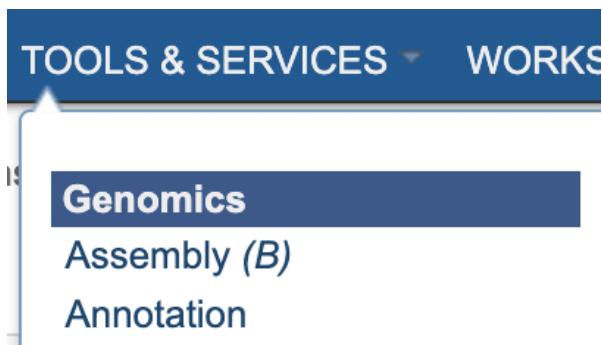
VIEW SHOW GUIDE DOWNLOAD DELETE RENAME COPY MOVE EDIT TYPE

Name

	Name	Size	Owner	Members	Created
Parent folder		-	-	-	-
SRR10769498.aligned.bam	52.7 kB	me	Only me	3/22/22, 8:54 AM	
SRR10769498.aligned.bam.bai	96 B	me	Only me	3/22/22, 8:54 AM	
SRR10769498.aligned.fq.gz	107.7 kB	me	Only me	3/22/22, 8:54 AM	
SRR10769498.all.bam.samstat.html	232.2 kB	me	Only me	3/22/22, 8:55 AM	
SRR10769498.unmapped.fq.gz	74.5 MB	me	Only me	3/22/22, 8:55 AM	

Step 2c) de novo sequence assembly ([Genome Assembly Service, Documentation](#))

- To assemble the aligned reads from the previous step, navigate to the “Assembly” tool beneath the “Genomics” header underneath the “Tools & Services” tab.

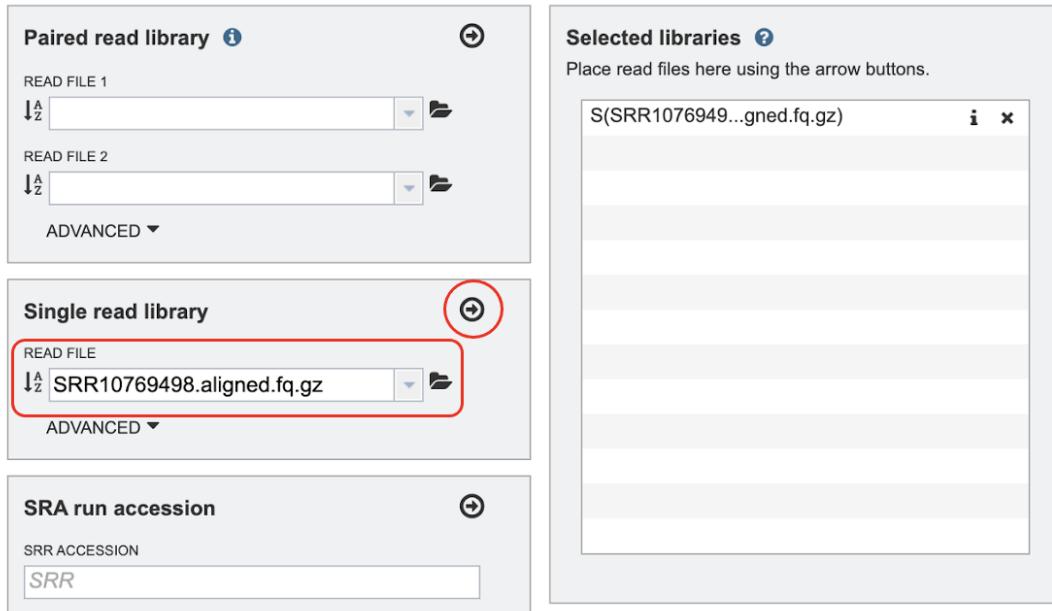


- Select or upload as appropriate the “SRR10769498.aligned.fq.gz” from the previous step, under Single Read Library and click the arrow to move it to the “Selected Libraries” box.

Services

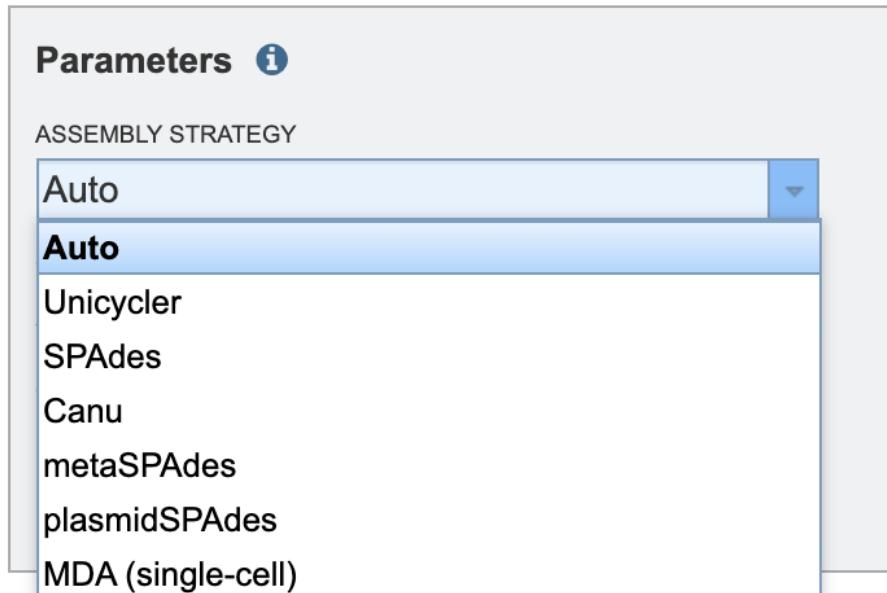
Genome Assembly

The Genome Assembly Service allows single or multiple assemblers to be invoked to compare results. The service attempts to select the best assembly. For further explanation, please see the Genome Assembly Service Quick Reference Guide and Tutorial..



The screenshot shows the "Genome Assembly" service interface. It includes sections for "Paired read library", "Single read library", and "SRA run accession". The "Selected libraries" section on the right lists a selected file: "S(SRR1076949...gned.fq.gz)". A red box highlights the "Single read library" input field, which contains the value "SRR10769498.aligned.fq.gz".

- Specify your desired “output folder” and “output name”.
- You may select your desired assembly strategy, or for the purposes of this exercise leave the “Auto” option selected.



The screenshot shows the "Parameters" section with a dropdown menu for "ASSEMBLY STRATEGY". The "Auto" option is selected and highlighted in blue. Other options listed include Unicycler, SPAdes, Canu, metaSPAdes, plasmidSPAdes, and MDA (single-cell).

- Once all of the appropriate criteria have been specified, the “submit” button can be clicked to launch the job.
- After completion, users can view an assembly report as shown below.

arieviad1 / home / +TickTutorial / Assembly_CCHFV (3 items)

GenomeAssembly2 Job Result

Job ID	6987734
Start time	3/22/22, 8:52 AM
End time	3/22/22, 8:52 AM
Run time	23s
▶ Parameters	

Name Size Owner Members Created

- Parent folder
- Assembly_CCHFV_assembly_report.html 17.5 kB me Only me 3/22/22, 8:52 AM
- Assembly_CCHFV_contigs.fasta 4.7 kB me Only me 3/22/22, 8:52 AM
- details me Only me 3/22/22, 8:52 AM

- Alternatively, users can download assembled contigs for further downstream analysis as shown below.

GenomeAssembly2 Job Result

Job ID	6987734
Start time	3/22/22, 8:52 AM
End time	3/22/22, 8:52 AM
Run time	23s
▶ Parameters	

Name Size Owner Members Created

- Parent folder
- Assembly_CCHFV_assembly_report.html 17.5 kB me Only me 3/22/22, 8:52 AM
- Assembly_CCHFV_contigs.fasta 4.7 kB me Only me 3/22/22, 8:52 AM
- details me Only me 3/22/22, 8:52 AM

Step 2d) Blast against viral database ([BLAST, Documentation](#))

Next we will utilize the BLAST service to search the BV-BRC databases for the genomes most similar to our assembled contigs.

- Navigate to the “BLAST” tool underneath the “Genomics” header in the “TOOLS & SERVICES” tab.

GenomicsAssembly (*B*)

Annotation

Comprehensive Genome

Analysis (*B*)[BLAST](#)

- Select the “BLASTN” program (given that our contigs are nucleotide sequences).
- Next we can input our query either by copying and pasting contigs downloaded from the previous step (as shown below), or by directly selecting the fasta file from your workspace.

Services

BLAST  

The BLAST service integrates the BLAST (Basic Local Alignment Search Tool) algorithms to perform searches against public or private genomes or other reference databases using DNA or protein sequence(s). For further explanation, please see [BLAST Service Quick Reference Guide and Tutorial](#).

Search program 

- | | |
|--|--|
| <input checked="" type="radio"/> BLASTN (nucleotide > nucleotide database) | <input type="radio"/> BLASTP (protein > protein database) |
| <input checked="" type="radio"/> BLASTX (translated nucleotide > protein database) | <input type="radio"/> tBLASTN (protein > translated nucleotide database) |

Query source

- Enter sequence Select FASTA file Select feature group

```
>SRR10769498_aligned_assembly_contig_1 length 3405 coverage 59.1 normalized_cov 0.96
AGTAGTCTAGGTACAACCATCCAGGACATCCAGGAGGTGTTGAAGTGTGGCTCAATT
TATGAATTAGATGTCCATTACCTTACCCCTTTAATAAAATTCCGATGTGGTAGACCT
CTAGGCTCTCGGCACACCATGTGTCACACTGCAACTTACACACTGTGCTTGCCGATA
ACACCTTTGCACATGCATCAGGTCAAAAAAACCTTCTCGATCTAGGATGCAGTGTGA
TTATTCAGGAGGGAGTTTGTGGATGTTCTGGTTCTGACAGTGTGATGGTCACAG
GACCTAAATTGAACCTGTGCCCGCTTCATCAAGCTACACTGCCCTCTGACTAGTAA
GTTCTACACACACTATGGCCTCTGCTTGTGATGTTCAACTTCCACTTGACAAACATAT
AATCTGAAAAAGGTCTTCACATCTAATCCACAAACAGGTGCAGCCAGTCCCTACACCCC
```

- Next, select your desired query database. Appropriate options for this query include:
“Reference and representative genomes (virus)”
“Search within a genome group (*searches within a user-compiled dataset of viral genomes*)”
“Search within a taxon”
“Search within a selected fasta file”

Database Source

- Reference and representative genomes (virus)
- Reference and representative genomes (bacteria, archaea)
- Reference and representative genomes (virus)**
- Search within selected genome list
- Search within selected genome group
- Search within selected feature group
- Search within a taxon
- Search within selected fasta file

Database Type

- Contigs (NT)

- In the example below, I have selected a saved “Genome group” that I previously compiled, containing all the complete Nairovirus M segments that are in the BV-BRC. Results are displayed as shown below.

	Query ID	Genome	Subject ID	Product	Identit (%)	Query cover (%)	Subje cover (%)	Query Length	Subject Length	Score	E value
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho NC_005300		segment	100	100.00	63.27	3405	5366	6219	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KY484035		segment	100	100.00	63.27	3405	5366	6202	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KX013451		segment	98	100.00	63.62	3405	5336	5864	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho MF287637		segment	97	100.00	63.25	3405	5368	5781	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho MF547416		segment	97	99.94	63.23	3405	5366	5633	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KY484045		segment	96	100.00	63.28	3405	5365	5521	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KY484042		segment	96	100.00	63.28	3405	5365	5499	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KJ682814		segment	96	100.00	63.29	3405	5364	5493	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho AY900141		segment	96	100.00	67.16	3405	5055	5486	0
<input type="checkbox"/>	▶ SRR10769498_aligned_aser	Crimean-Congo hemorrhagic fever ortho KJ682813		segment	96	100.00	63.29	3405	5364	5454	0

Step 2e) Annotate my genome ([Genome Annotation Service, Documentation](#))

Now that we have our assembled contigs, we can further characterize our viral genomes by annotating the proteins they code for. For this, we will utilize the “Genome annotation service”.

- Navigate to the “Annotation” tool underneath the “Genomics” header in the “TOOLS & SERVICES” tab.

The screenshot shows the Biotools interface with the 'TOOLS & SERVICES' tab selected. Under the 'Genomics' section, the 'Assembly (B)' and 'Annotation' sections are visible. The 'Annotation' section is currently active.

- Upload or select your fasta formatted contig file as appropriate
- Select the desired annotation recipe; in this case “Viruses”
- Enter the appropriate Taxon name for annotation; in this case I have selected the entire *Nairoviridae* family, however users can also select CCHFV.
- Specify the appropriate output folders and names, and click “Annotate” to launch the job.

Services

Genome Annotation

The Genome Annotation Service provides annotation of genomic features using the RAST tool kit (RASTtk) for bacteria and VIGOR4 for viruses. The service accepts a FASTA formatted contig file and an annotation recipe based on taxonomy to provide an annotated genome. For further explanation, please see the Genome Annotation Service [Quick Reference Guide](#) and [Tutorial](#).

Parameters 

CONTIGS
 SRR10769498_aligned_assembly_contigs.fasta 

ANNOTATION RECIPE
Viruses

TAXONOMY NAME  Nairoviridae

TAXONOMY ID 1980415

MY LABEL Step2e_annotation

OUTPUT NAME Nairoviridae Step2e_annotation

OUTPUT FOLDER
 +TickTutorial 

Reset **Annotate**

- Results can be viewed in a variety of ways, including “Genome View”, “CDS view”, as well as in the “Genome Browser”..

aniewiad1 / home / +TickTutorial / Nairoviridae Annotation (24 items)

GenomeAnnotation Job Result



- Examples of the genome view and the protein list are shown below. Given that our sample only contained fragments of the genome, viewing it in the Genome Browser is not appropriate.

Genome View
Viruses » Negamaviricota » Ellioviricetes » Bunyavirales » Nairoviridae » Nairoviridae Annotation

Overview Genome Browser Proteins Protein Structures Domains and Motifs Experiments Interactions

Nairoviridae Annotation  Genomic Features

	PATRIC	RefSeq
CDS	2	0

Length: 4492bp, Contigs: 2

General Info

Genome ID	1980415.25
Genome Name	Nairoviridae Annotation

Taxonomy Info

Taxon ID	1980415
Superkingdom	Viruses
Kingdom	Orthornavirae
Phylum	Negamaviricota
Class	Ellioviricetes
Order	Bunyavirales
Family	Nairoviridae

Services Add To Group Share GUIDE

External Tools BEI Resources

Recent PubMed Articles  No recent articles found.

Genome View
Viruses » Negarnaviricota » Ellioviricetes » Bunyavirales » Nairoviridae » Nairoviridae Annotation

Overview Genome Browser Proteins Protein Structures Domains and Motifs Experiments Interactions

DOWNLOAD KEYWORDS ADV Search CDS PATRIC The "Interactions" tab shows a list of protein-protein interactions, inferred using computational and laboratory methods.

	Genome Name	Accession	Feature Type	BRCA ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
<input type="checkbox"/>	Nairoviridae Annotation	1980415.25.cor	CDS	fig 1980415.25.		1	3405	-	3401	GPC	putative Pre-glycoprotein polyprotein G
<input type="checkbox"/>	Nairoviridae Annotation	1980415.25.cor	CDS	fig 1980415.25.		1	951	+	951	GPC	putative Pre-glycoprotein polyprotein G

THANKS FOR FOLLOWING ALONG, AND PLEASE CONTACT US WITH YOUR QUESTIONS
AT BV-BRC.ORG!

BV-BRC BETA

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BACTERIAL AND VIRAL BIOINFORMATICS RESOURCE CENTER

Welcome to the Bacterial and Viral Bioinformatics Resource Center (BV-BRC), an information system for bacterial and viral infectious diseases. [Learn more about BV-BRC](#). Introductory material for training is provided in the sections at the bottom of this page.

This is the **Beta Version** of the website, designed to allow users to explore, try out features, and provide feedback.

- Quick Start
- Quick References
- Tutorials
- Common Tasks
- CLI Tutorial
- Webinars
- Instructional Videos
- Workshops
- Contact Us