

# Discovering novel genetic polymorphism using VIROME

Jaysheel Bhavsar, Shawn Polson, K. Eric Wommack

## Abstract

This tutorial explains how to use VIROME to discover novel genetic polymorphism from viral metagenome shotgun data.

Wommack, K. E., J. Bhavsar, S. W. Polson, J. Chen, M. Dumas, S. Srinivasiah, M. Furman, S. Jamindar, and D. J. Nasko. 2012. VIROME: a standard operating procedure for analysis of viral metagenome sequences. *Standards in Genomic Sciences* 6:427-439 [[PMC3558967](https://pubmed.ncbi.nlm.nih.gov/22811111/)]

[See site](#) for more information.

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[dx.doi.org/10.17504/protocols.io.d6p9dm](https://doi.org/10.17504/protocols.io.d6p9dm)

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## Guidelines

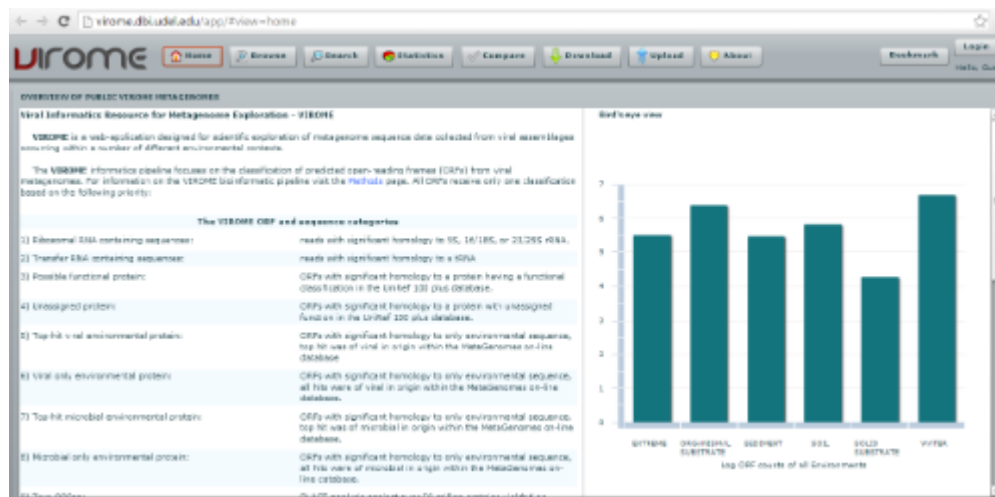
See full video below for more information.

YouTube link: <https://www.youtube.com/watch?v=Jj3KP5ri7mY>

## Protocol

### Step 1.

Go to [VIROME web application](#).



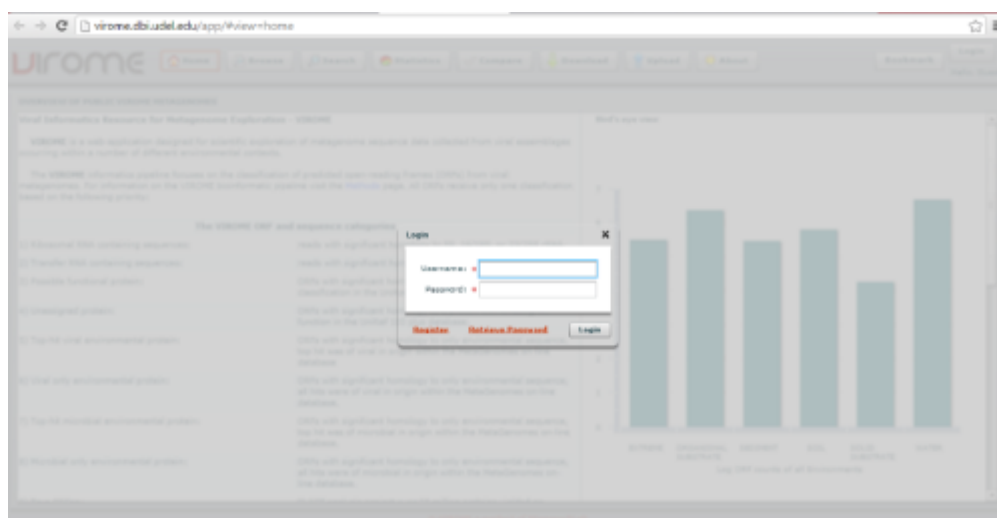
## Step 2.

Click the login button.



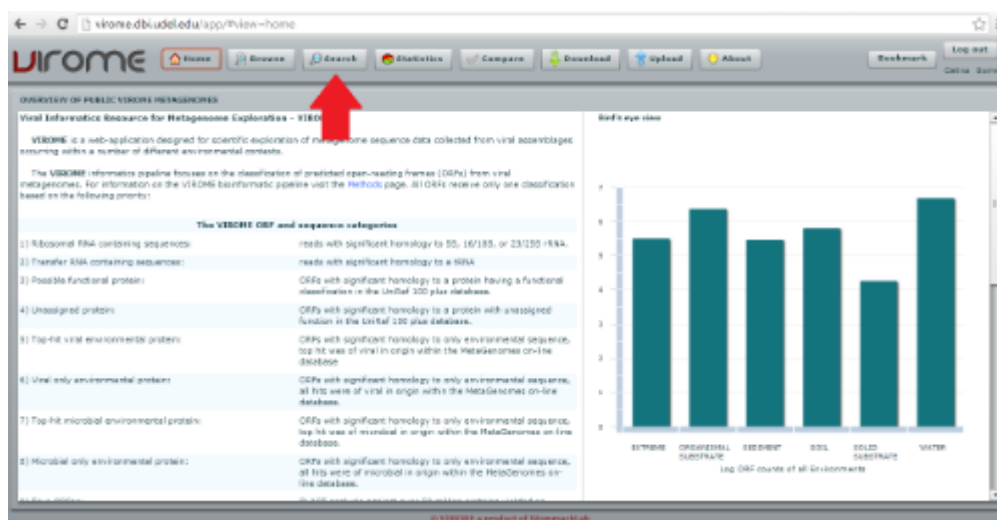
## Step 3.

Enter username and password to authenticate into the application.



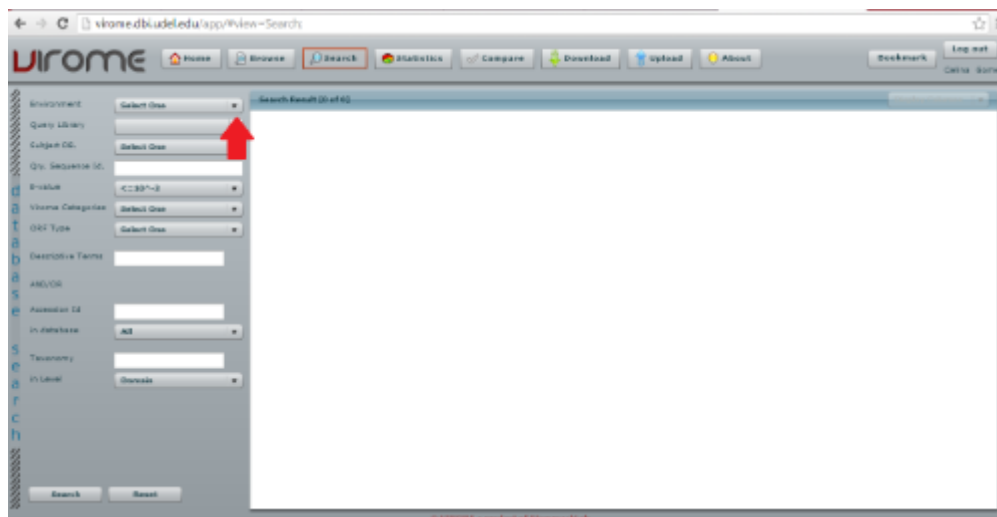
## Step 4.

Click the search button.



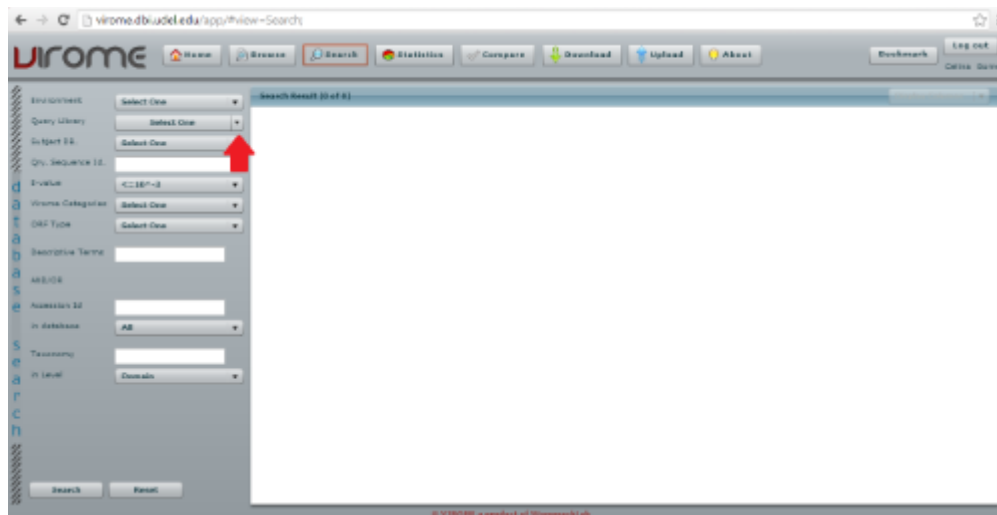
## Step 5.

Select an environment.



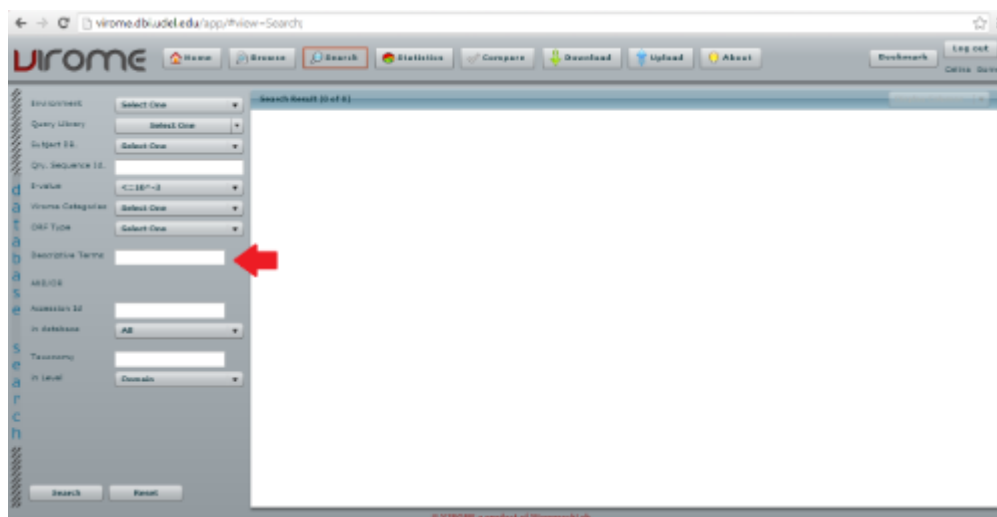
## Step 6.

Select a library.



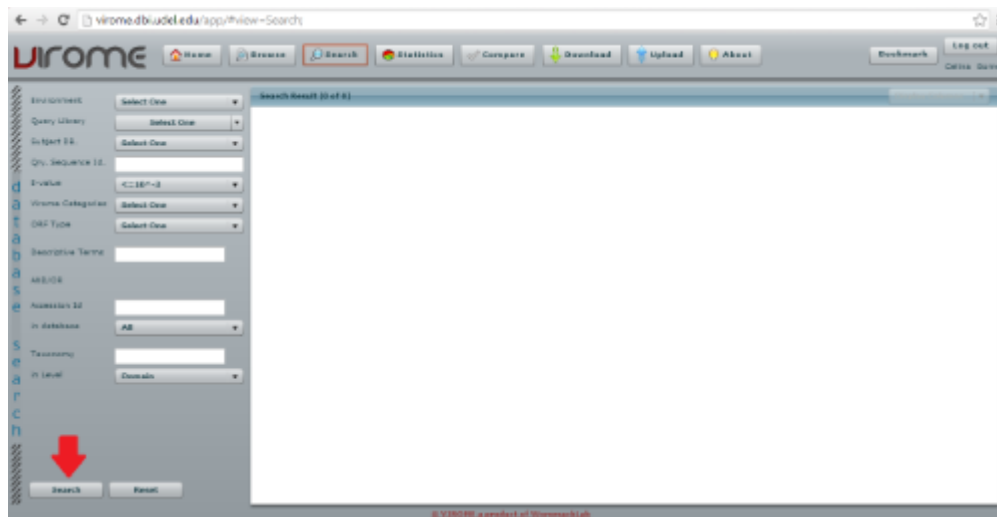
## Step 7.

Enter search term.



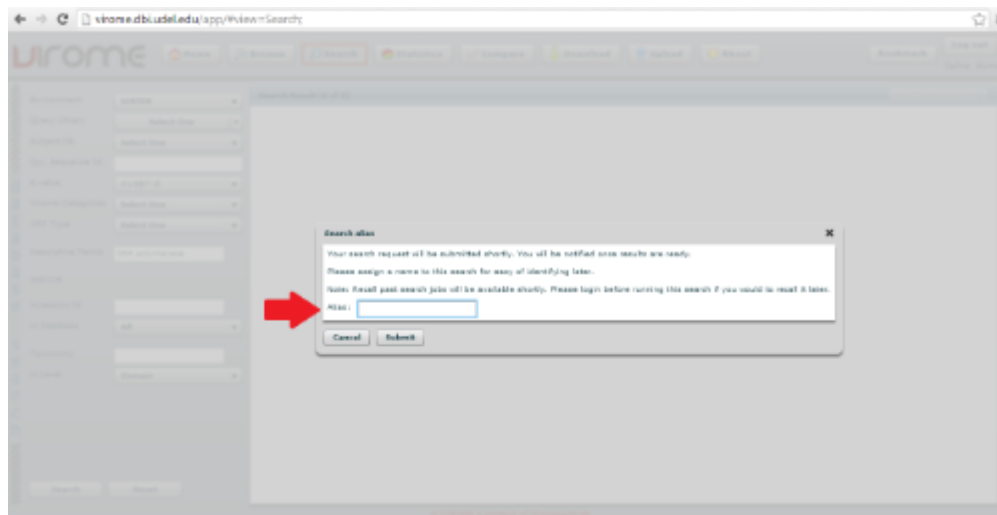
## Step 8.

Click "Search".



## Step 9.

Name the search.



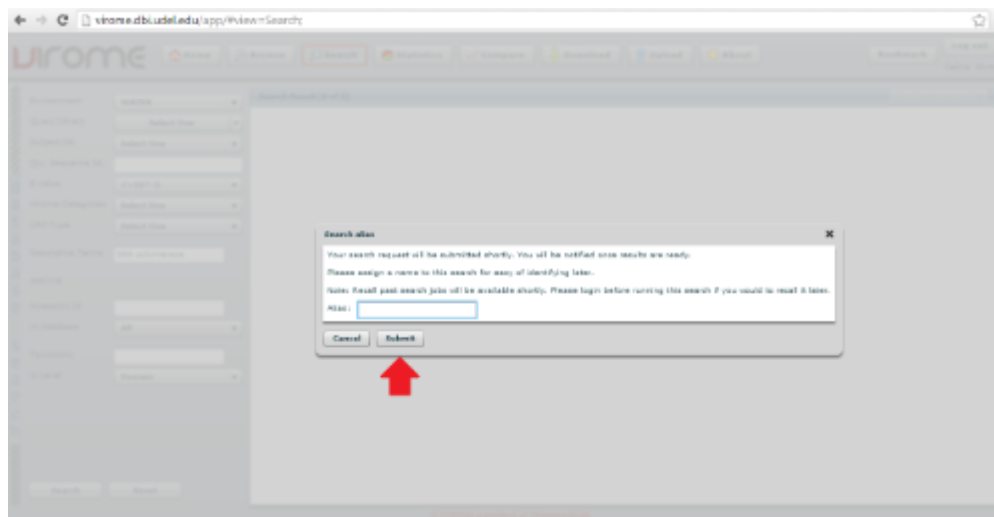
## ⊕ NOTES

**Bonnie Hurwitz** 09 Nov 2015

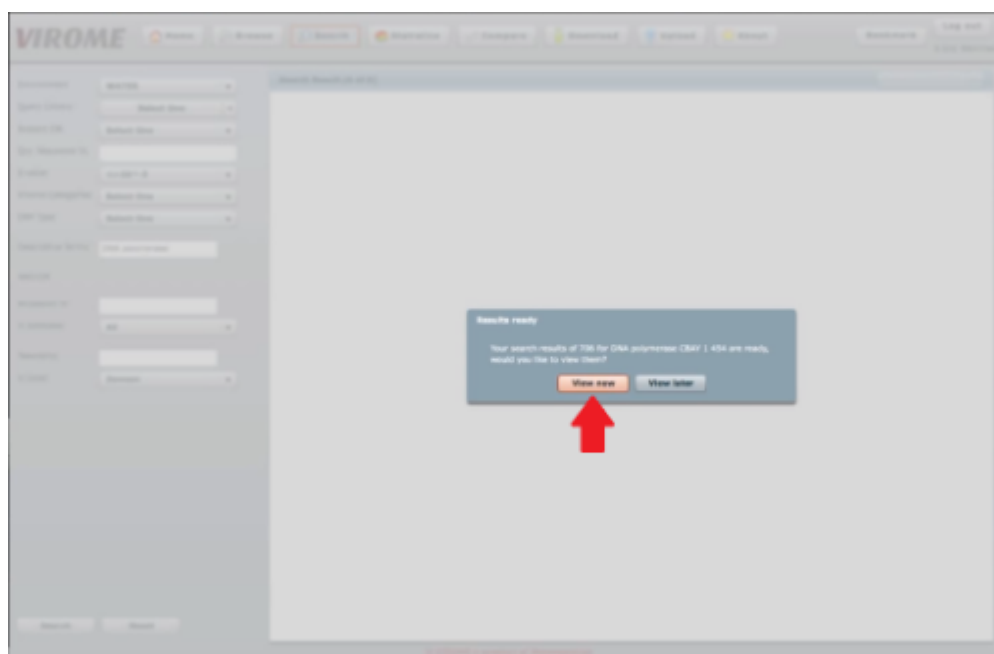
Adding a name will help for bookmarking to go back and see it at a later time.

## Step 10.

Click "Submit".



**Step 11.**  
Click "View now".



**Step 12.**  
Results columns are sortable.

**VIROME** Home Browse Search Statistics Compare Download Upload About Bookmark Log out

Environment: WATER

Query Library: Select One

Subject DB: Select One

Qry Sequence ID:

E-value: <1E-2

Virome Categories: Select One

Qry Type: Select One

Descriptive Terms: DNA polymerase

Accession ID:

In database: All

Secondary:

In label: Domain

Search Results (706 of 706)

Sequence Name	Hit Name/Accession	Description	E-value	% QRY Cov	% Similarity	% Identity	Organism
CYE_GPHFSDGSGZPU_485_1_1	DB2J5	DNA polymerase I	3.0E-5	77.64 %	50.0	32.0	Acetivibrio
CYE_GPHFSDGSGZPU_1_394_1	DBH50	DNA polymerase I	2.0E-6	96.13 %	53.8	31.1	Acetivibrio
CYE_GPHFSDGSGZPU_1_395_1	CDW428	DNA-directed DNA polymerase	3.0E-12	77.33 %	49.5	39.8	Acetivibrio
CYE_GPHFSDGSGZPU_1_396_1	CDW428	DNA-directed DNA polymerase	3.0E-6	90.32 %	49.8	34.4	Acetivibrio
CYE_GPHFSDGSGZPU_1_397_1	CDW428	DNA-directed DNA polymerase	6.0E-8	90.71 %	66.6	47.2	Acetivibrio
CYE_GPHFSDGSGZPU_1_398_1	CDW428	DNA-directed DNA polymerase	1.0E-12	90.60 %	64.7	33.3	Acetivibrio
CYE_GPHFSDGSGZPU_1_399_1	CDW428	DNA-directed DNA polymerase	1.0E-22	90.91 %	56.0	40.4	Acetivibrio
CYE_GPHFSDGSGZPU_1_400_1	Q2U85	DNA polymerase I	9.0E-5	90.70 %	63.4	35.2	Acetivibrio
CYE_GPHFSDGSGZPU_1_401_1	Q2U85	DNA polymerase I	3.0E-29	93.59 %	66.5	44.1	Acetivibrio
CYE_GPHFSDGSGZPU_1_402_1	A6TV73	DNA-directed DNA polymerase	2.0E-13	77.78 %	65.1	43.0	Alkaliphilus
CYE_GPHFSDGSGZPU_1_403_1	B4R5C7	Phage-related DNA polymerase	2.0E-14	71.93 %	64.7	49.4	Alkaliphilus
CYE_GPHFSDGSGZPU_1_404_1	B4R5C7	Phage-related DNA polymerase	2.0E-14	73.33 %	64.4	46.7	Alkaliphilus
CYE_GPHFSDGSGZPU_1_405_1	B4R5C7	DNA-directed DNA polymerase I	4.0E-6	90.13 %	53.2	31.0	Alkaliphilus
CYE_GPHFSDGSGZPU_1_406_1	B4R5C7	DNA-directed DNA polymerase I	2.0E-6	94.55 %	56.0	31.8	Alkaliphilus

Download Search Sequences

### Step 13.

Click on "Download Search Sequences".

**VIROME** Home Browse Search Statistics Compare Download Upload About Bookmark Log out

Environment: WATER

Query Library: Select One

Subject DB: Select One

Qry Sequence ID:

E-value: <1E-2

Virome Categories: Select One

Qry Type: Select One

Descriptive Terms: DNA polymerase

Accession ID:

In database: All

Secondary:

In label: Domain

Search Results (706 of 706)

Sequence Name	Hit Name/Accession	Description	E-value	% QRY Cov	% Similarity	% Identity	Organism
CYE_GPHFSDGSGZPU_1_136_1	Q6L776	DNA polymerase	3.0E-4	75.00 %	74.3	62.9	Vibrio phage Vp1
CYE_GPHFSDGSGZPU_1_137_1	B4X549	DNA polymerase	1.0E-26	97.80 %	77.4	54.8	Cyanophage S-C
CYE_GPHFSDGSGZPU_1_138_1	F1R522	DNA polymerase	2.0E-12	89.29 %	62.3	51.9	Enterococcus
CYE_GPHFSDGSGZPU_1_139_1	B4X549	DNA polymerase	9.0E-09	97.62 %	87.2	77.6	Cyanophage S-C
CYE_GPHFSDGSGZPU_1_140_1	A47588	DNA polymerase	4.0E-18	95.87 %	94.1	39.8	Synchromobium
CYE_GPHFSDGSGZPU_1_141_1	Q5D877	DNA polymerase	9.0E-9	92.00 %	94.8	43.2	Phage phiC001
CYE_GPHFSDGSGZPU_1_142_1	B4X549	DNA polymerase	7.0E-19	96.27 %	94.1	39.4	Cyanophage S-C
CYE_GPHFSDGSGZPU_1_143_1	Q6L776	DNA polymerase	4.0E-20	91.86 %	94.5	40.0	Vibrio phage Vp1
CYE_GPHFSDGSGZPU_1_144_1	B4X549	DNA polymerase	4.0E-49	96.08 %	88.2	78.9	Cyanophage S-C
CYE_GPHFSDGSGZPU_1_145_1	Q5D877	DNA polymerase	2.0E-22	96.51 %	94.9	42.7	Phage phiC001
CYE_GPHFSDGSGZPU_1_146_1	Q6L776	DNA polymerase	2.0E-14	89.96 %	94.5	38.3	Vibrio phage Vp1
CYE_GPHFSDGSGZPU_1_147_1	Q5D877	DNA polymerase	1.0E-09	96.81 %	90.3	77.4	Prochlorococcus
CYE_GPHFSDGSGZPU_1_148_1	B4X549	DNA polymerase	1.0E-14	96.36 %	94.2	34.8	Cyanophage S-C
CYE_GPHFSDGSGZPU_1_149_1	Q5D877	DNA polymerase	1.0E-9	91.18 %	94.8	43.2	Phage phiC001

Download Search Sequences

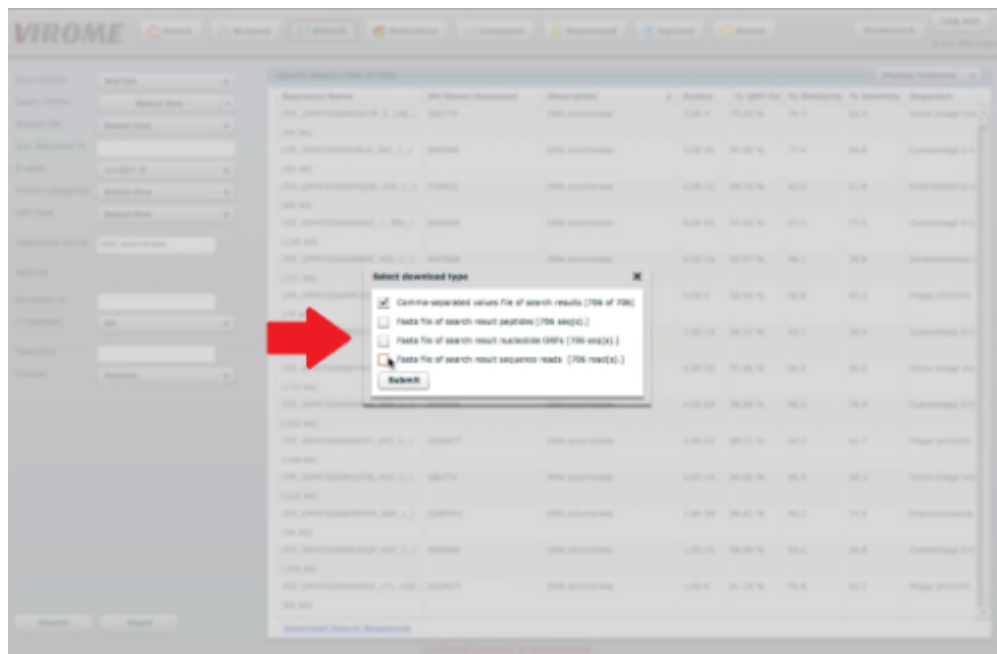
### NOTES

**Bonnie Hurwitz** 09 Nov 2015

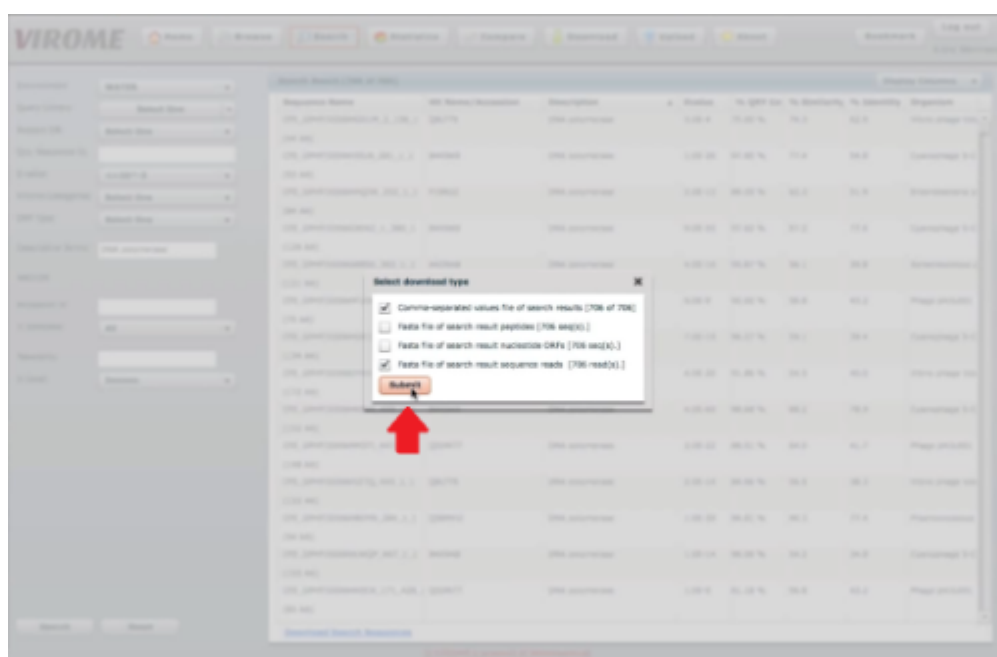
Can be found in the bottom left hand corner of the page.

### Step 14.

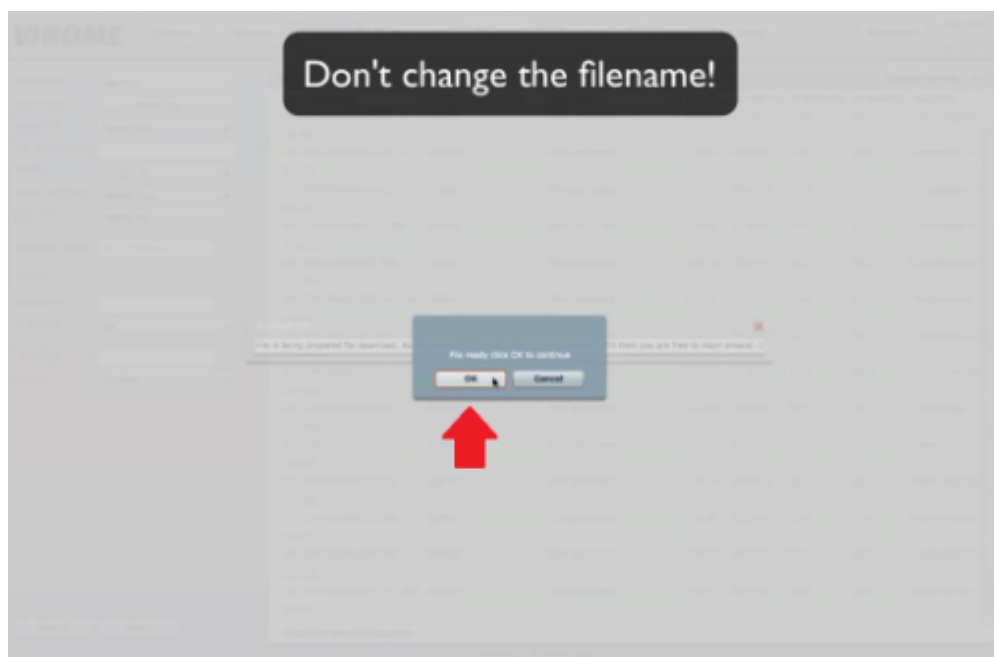
Select data types for download.



**Step 15.**  
Click "Submit".



**Step 16.**  
Click "OK".



### Step 17.

Once prompted to save the file, do not change the file name!

### Step 18.

Navigate to the Finder.



### Step 19.

Double click the file to unzip it.

Excel example

### Step 20.

Open csv file in Excel.

Excel example

### Step 21.

Use Excel pivot table to summarize data.





## Geneious example

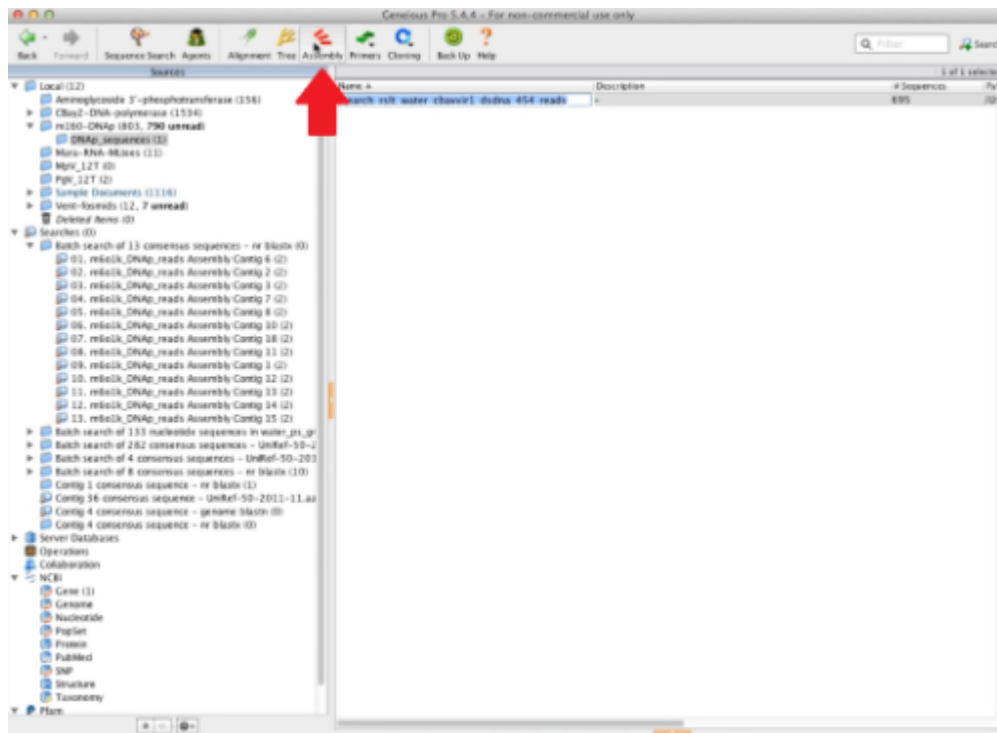
**Step 24.**

Click on the file.

## Geneious example

**Step 25.**

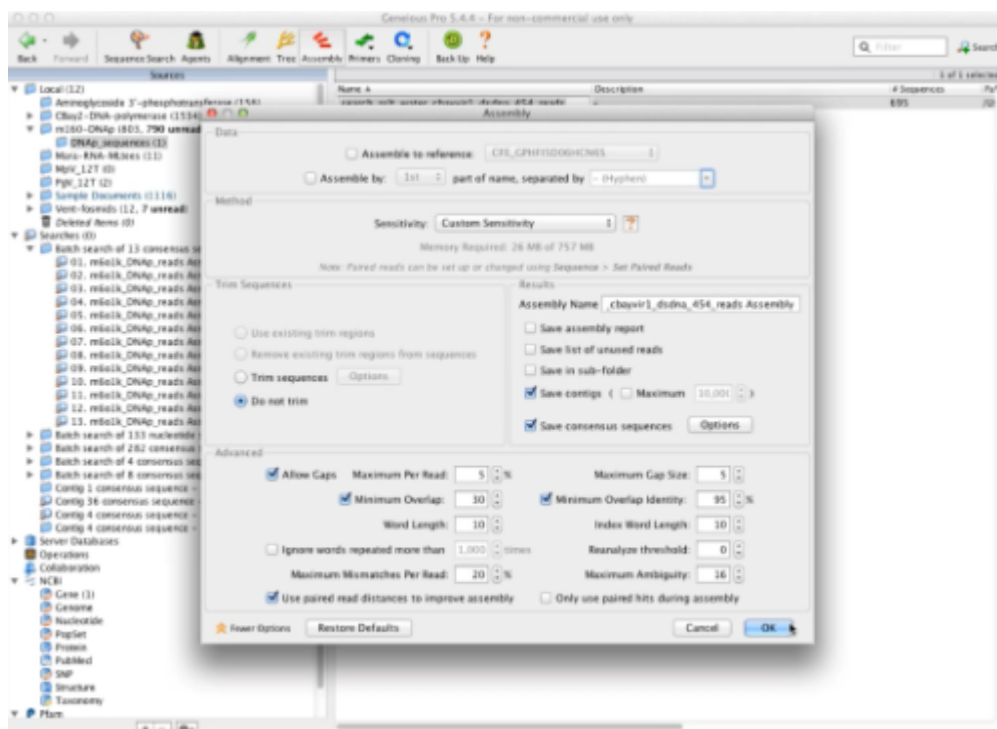
Click on "Assembly".



## Geneious example

**Step 26.**

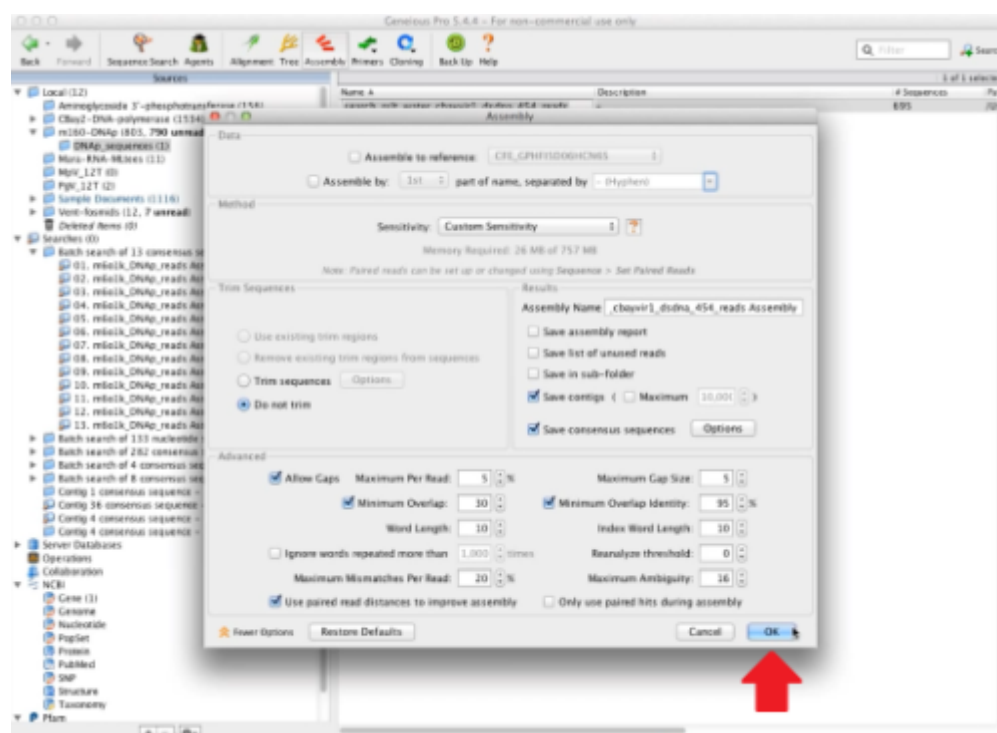
Pre-set parameters.



## Geneious example

### Step 27.

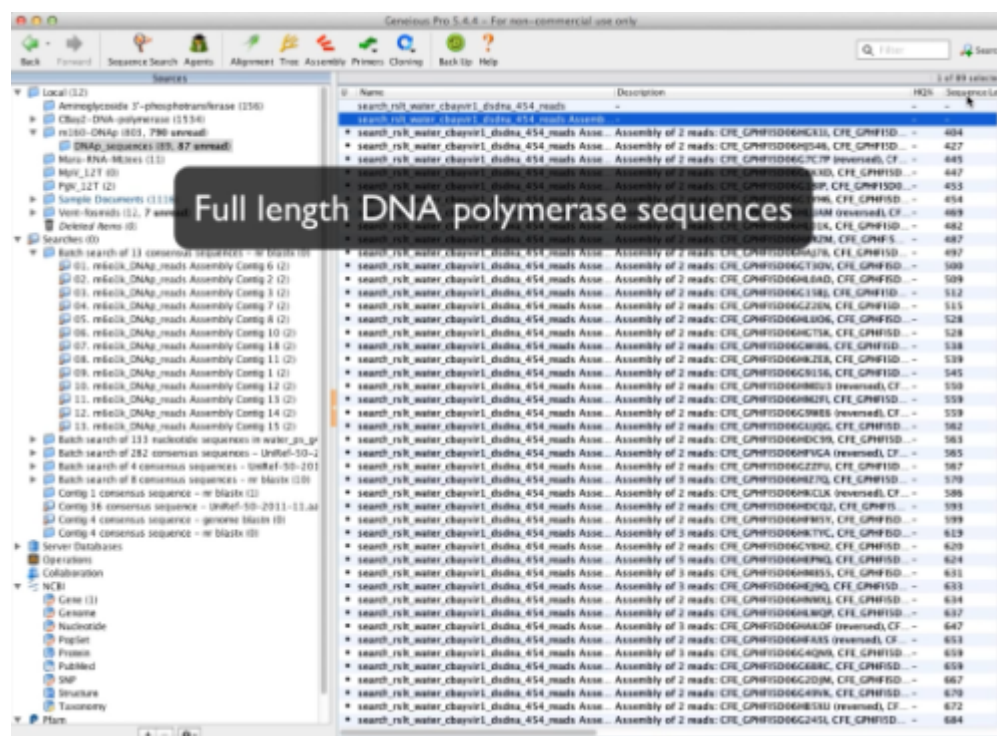
Click "OK".



## Geneious example

### Step 28.

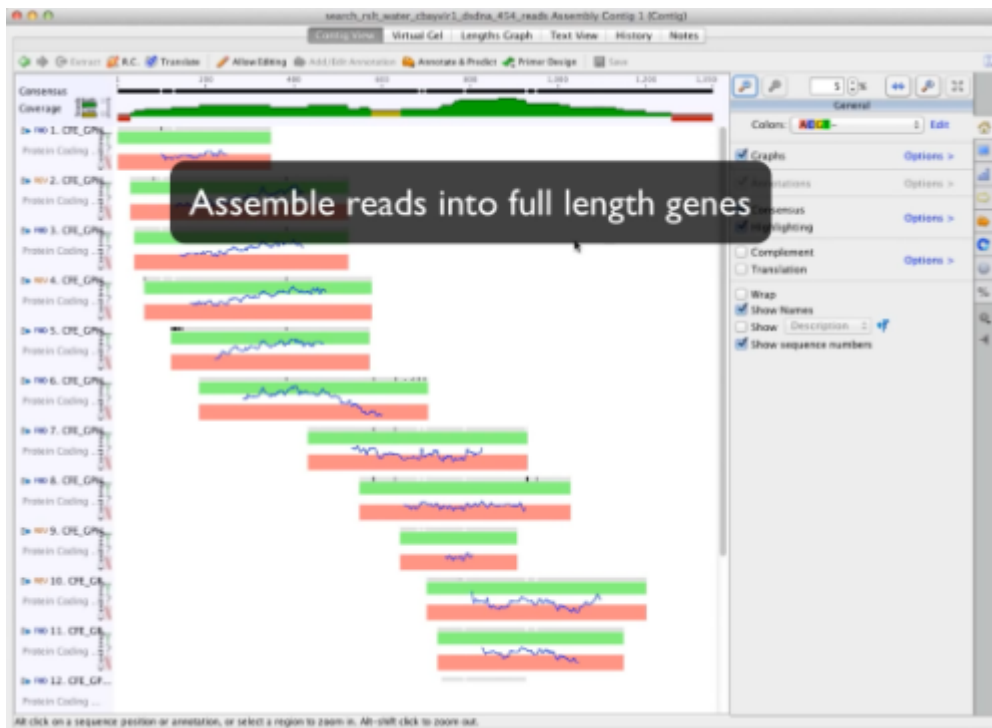
Full length sequences generated.



## Geneious example

### Step 29.

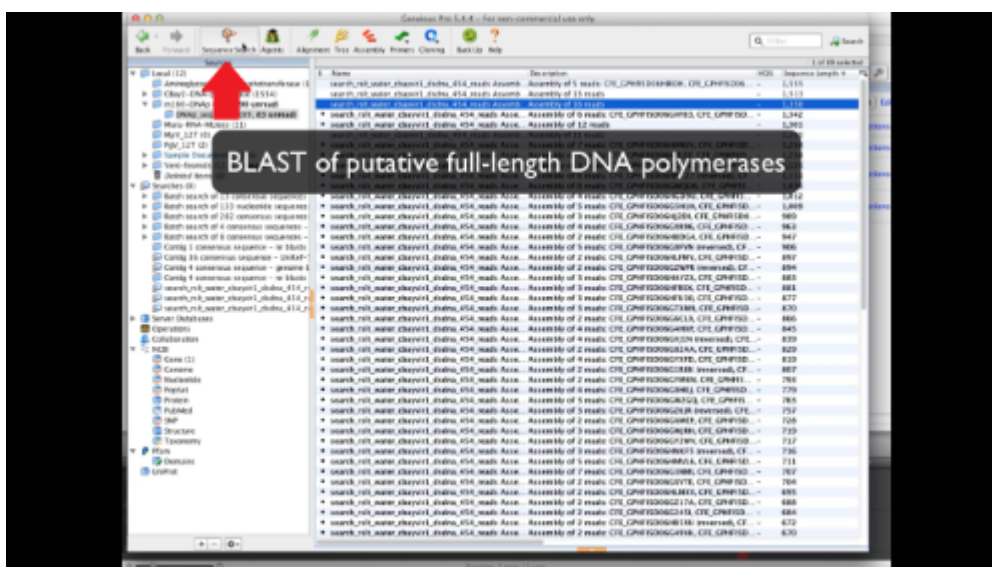
Assemble reads into full length genes.



Geneious example

### Step 30.

BLAST putative full length comparative sequences.



Geneious example

### Step 31.

Inspect results.

Geneious example

### Step 32.

See [video](#) for detailed example.

### Step 33.

For full video tutorial see guidelines.

LINK:

<https://www.youtube.com/watch?v=Jj3KP5ri7mY>