



## Sample and Genotype Explorers

Answer key

*We recommend using a mouse with a track wheel rather than the inbuilt trackpad*

### 1) Compare variants for one *Anopheles funestus* exon between samples in different African countries, and export VCF files for each population

a) In the Tools menu select the Genotype Explorer. Add a species as a reference genome, e.g., *Anopheles funestus*, and a query, e.g., AFUN001649






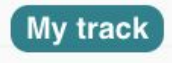







ADD NEW REFERENCE

*Click on this icon. A pop-out window will display.*

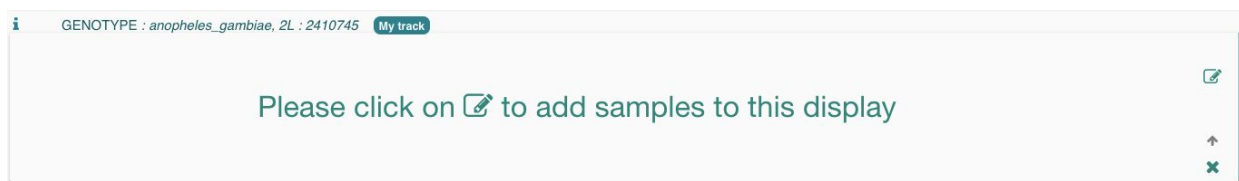
*Type a keyword and notice the autocomplete suggestions. Select the suggestion that matches your query. Selected terms are display below the query line in green. Click on 'ADD'.*

b) *Hover with your mouse* to discover the names/functions of all this tool icons. Complete this table with the information you learn. Come back again to this question once you finish all five exercises in this tutorial to complete or improve the information.

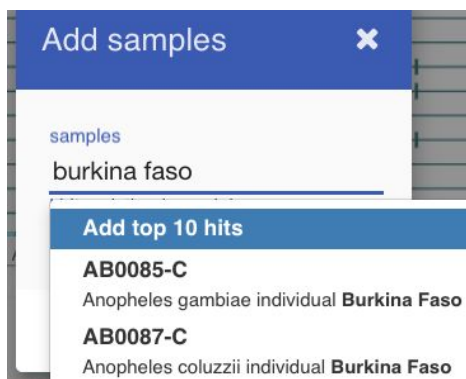
Icon	Name/Function
	Save session and load session. Save the current state of your work and load it later.
	Add a new reference, which is a system of coordinates (e.g, a Genome or proteins) to draw features on.

	Remove all data and go back to the front page/tutorial
	Undo the last action (returns to previous state of the application)
	Add track. Tracks are features (e.g., transcript, genotype and variations density) displayed in context of a specific reference. Tracks can be download (e.g., VCF file) or morphed (e.g., transcript ---> protein domains).
	Change location. Allows to move to a different gene.
	Remove a reference or track.
	Click on this box to give a name to your reference, track, job or query.
	Browse left, zoom out, zoom in and browse right.
	Optimize view. Displays a complete gene, transcript or protein.
	Show overview. Provides an overview of the reference and tracks in the form of a chart with a legend, the legend features can be hide/shown from the screen.
	Move track down and move track up. Allow to reorganize the tracks or reference order in the screen.
	Removes track or reference.
	Add samples to the tracks. You can not add more than 20 samples to a track
 AGAP004707-RA	The VectorBase gene/transcript ID, provides a link to the Genome Browser.

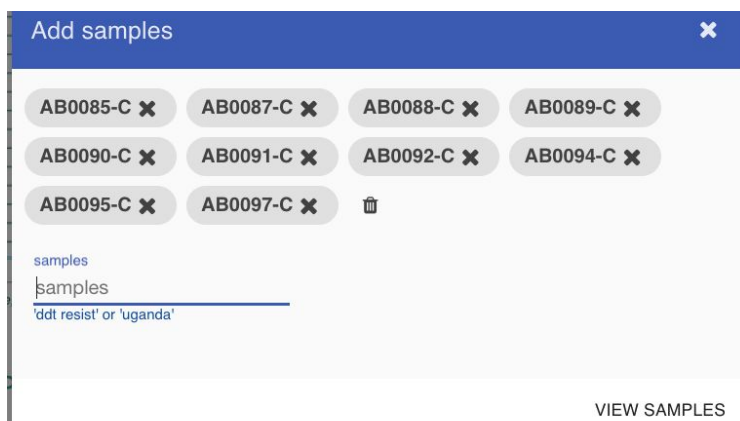
c) add samples - search for 'burkina faso'



Click on the pencil icon.

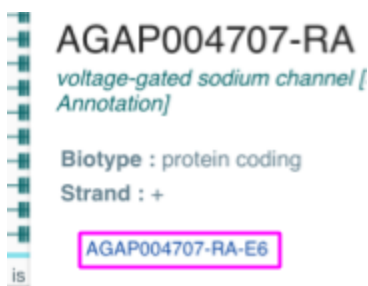


Type the query. From the autocomplete suggestions select 'Add top 10 hits'.



Click on 'VIEW SAMPLES'.

d) pick an exon or location, e.g., KB668221:2514743 and zoom in until you can view genotypes



Locate the exon and click on it. A pop-out window confirm you are in the right position



Use the plus/minus and arrowheads to zoom and browse in the right position.

e) add a new track (click on + icon on top left display bar and select genotype)

f) scroll down to the new track and add samples

g) export VCF for each population (click on the VCF icon in the right hand vertical bar item in each of the genotype tracks)



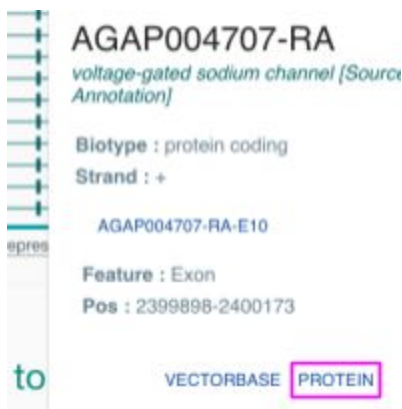
Keep this query results for the next exercise.

## 2) display protein altering variants

a) return to the transcript track and scroll out so that you can view the entire AFUN001649 gene (Click on the 'Optimise view' icon)



b) select one of the transcripts (click on any exon or intron) and on the pop up box select the 'Protein' (soon to be changed to "Protein domains") button. This will add a new track showing the protein domains and the variants in the context of the protein sequence for each of the previously selected populations.



c) Click on the 'Show overview' icon to show/hide features



The 'Show overview' icon turns orange when you have hide features from the display.

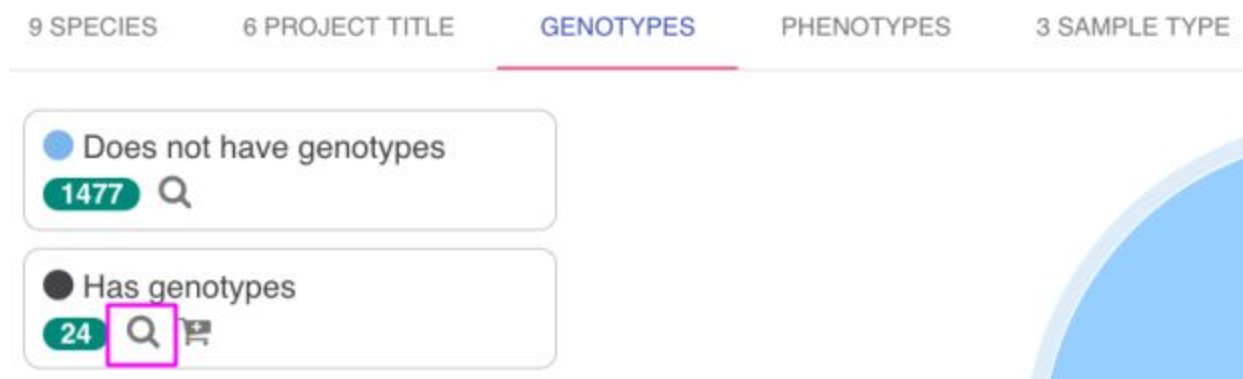
### 3) Sample Explorer<sup>1</sup>

a) In the Tools menu select the Sample Explorer. Type the term Senegal. How many species have data for this country?

9 species

b) Which of these species has genotype data?

*Aedes aegypti*



Select the 'Genotypes' tab. Click on the magnifying glass icon on the has genotypes box

<sup>1</sup> Sample Explorer tutorial, <https://www.vectorbase.org/tutorials/tools-and-resources-tutorials/sample-explorer>



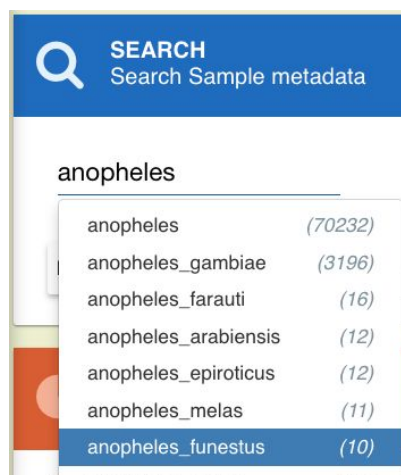
Click on the species tab

c) What sample types are these genotyping data from Senegal? Individuals or pools? (Click on the 'Sample type' tab)

*Individual*

**4) Use the Sample Explorer to find all the *Anopheles funestus* Burkina Faso samples collected in 2005 with genotypes for the AFUN001544-RA transcript, and display them in the Genotype Explorer**

a) in Sample Explorer query for “anopheles funestus” + has genotypes + “burkina” + “2005”



When typing queries, select the available options from the autocomplete suggestions.



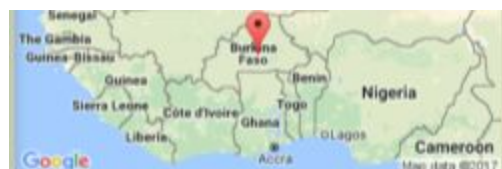
Select the 'Genotypes' tab. In the has genotypes box select magnifying glass.

anopheles\_funestus ✕ true (has genotypes) ✕ burkina ✕ 200

2005 (5)

Notice how the query is constructed (gray bubbles) to obtain the data of interest.

b) scroll to the sample cards and click on the 2005 next to the calendar icon. This extra step helps you filter for data collected on year 2005 (and discard the data published on 2005).



Click for detailed view

Name folonzo\_05-00553

Project(s) VBP0000119

Koubri Department

Reference genome Anopheles funestus

2005

Description Anopheles funestus Burkina Faso field isolate, Folonzo chromosomal form, Koubri 2005 individual insect

b) scroll up again, to the overview panel. add the samples (5) to the shopping cart

Has genotypes

5

Q

🛒

c) go to the shopping cart at the top of the page and add the transcript you wish to view (AFUN001544-RA)

### SAMPLES CART

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To send samples to the genome transcript id must be provided.

transcript

AFUN001544-RA

AFUN001544-RA

AFUN001544-RA



d) click on the '[BETA] view in LERA' menu icon (3rd along from left, the compass)

The screenshot shows the VectorBase interface. On the left, a 'SAMPLES CART' sidebar is open, displaying a list of samples. The first sample is 'transcript AFUN001544-RA', which is selected. Below it, 'Query 1' is shown with the query: 'anopheles\_funestus & true (has\_genotypes) & burkina & 2005'. The main panel on the right shows a header with navigation links (About, Organisms, Downloads, Tools, Data, Help, Community, Contact) and a status bar indicating 'Displaying 5 of 5 samples'. Below this, a search bar and filters for 'types', 'burkina', and '2005' are visible. The main content area is a large orange rectangle, likely representing a list of samples or a map view.



Keep this query results for the next exercise.

5) compare the *Anopheles funestus* AFUN001544 gene to its ortholog in *Anopheles epiroticus* (note this is an example of cross species genome browsing rather than looking variation data)

a) using the display from from 4(d) click on the AFUN001544-RA transcript object and select “Orthologs”

AFUN001544-RA

Biotype : protein coding  
Strand : -

AFUN001544-RA-E2

Feature : Exon  
Pos : 1073173-1073355

VECTORBASE PROTEIN **ORTHOLOGS** ZOOM

folonzo\_05-00553  
folonzo\_05-00570  
folonzo\_05-00602  
folonzo\_08-00031

b) type “epiroticus” into the search box and select the supplied transcript

c) zoom out (or click on ‘Optimise view’) in the transcript tracks of each species and compare the genomic organisation (optional: close the ‘genotype’ tracks)

TRANSCRIPT Anopheles funestus, KB668221 : 1073177 My track

AFUN001544-RA

Interval size is 664 bp. A tick represents 66 bp

GENOTYPE : Anopheles funestus, KB668221 : 1073177 My track

Interval size is 664 bp. A tick represents 66 bp

Legend: Homozygous ref allele (green), Heterozygous ref/alt allele (yellow), Homozygous alt allele (red), Heterozygous alt allele (blue)

TRANSCRIPT Anopheles epiroticus, KB670169 My track

AEPI002806-RA

Optimise view

c) does the AFUN016088-RA gene (*Anopheles funestus*) have an ortholog in *Anopheles epiroticus*?  
(If in any doubt, confirm with a gene tree or other displays from VectorBase comparative genomics <sup>2</sup>)

d) the AEPI002805-RA gene has an exon that overlaps the AEPI002806-RA gene - does it have an *An. funestus* homolog, and how does this relate to the genomic structure shown in *An. funestus*.

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<sup>2</sup> Comparative Genomics tutorial,  
<https://www.vectorbase.org/tutorials/tools-and-resources-tutorials/comparative-genomics>