

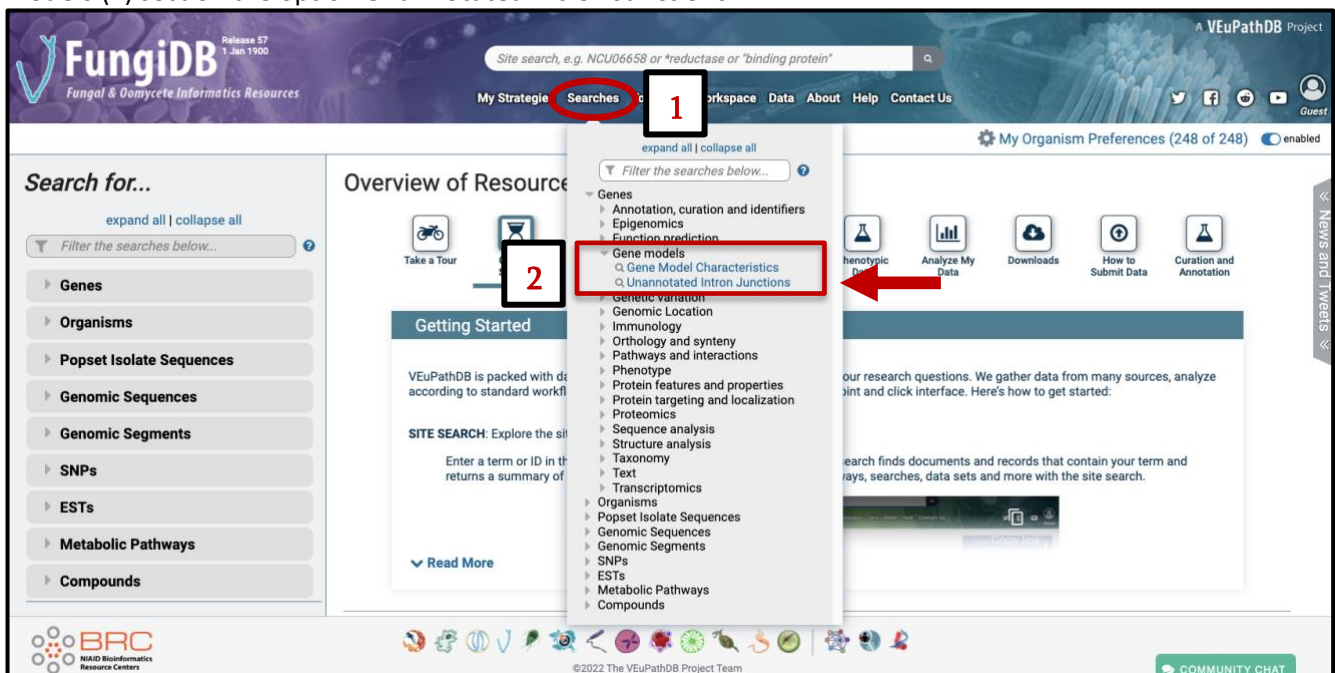
Unannotated Intron Junctions search

The **Unannotated Intron Junctions** search enables users to identify genes that contain, or are flanked by, unannotated high confidence intron junction-spanning reads from RNA-seq data. These genes may be incompletely or inaccurately annotated due to missing introns/exons and/or alternative splice variants. Once you've identified the genes with unannotated introns you can explore them in JBrowse and correct gene structures in Apollo, an open-source software enabling users to inspect, refine and add gene models to the current genome annotations. Apollo is available for reference genomes.

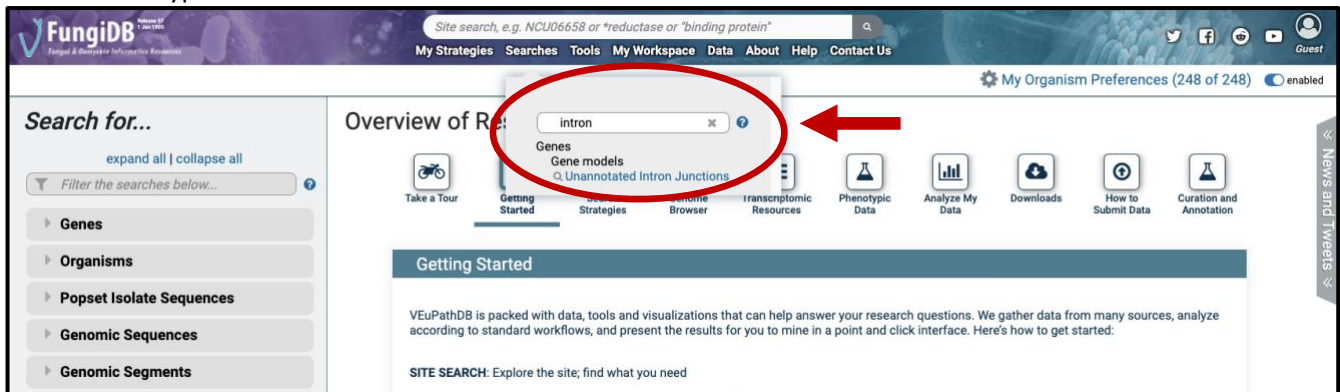
We will show you in this tutorial how to identify possible incorrect gene structures and correct them in Apollo.

1) Accessing the search Unannotated Intron Junctions

To access the search option in any VEuPathDB site go to the **Searches (1)** menu and choose from the **Gene models (2)** section the option **Unannotated Intron Junctions**.



You can also type into the search filter the word **intron** to find the search.



2) Select the search parameters

There are a number of parameters to manipulate in this search:

- Organism
- Minimum number of unique reads
- Percent of most abundant intron (MAI)
- 5' and 3' Flanking sequence (not available in VectorBase)

Using the default parameters on this search you will get a first impression on the number of genes with unannotated introns. If you think this number is too high to explore the data, change the search parameters, the minimum number of unique reads or percent of most abundant intron.

FungiDB Released 57 1 Jan 1990
Fungal & Oomycete Informatics Resources

Site search, e.g. NCU06658 or *reductase or *binding protein

My Strategies Searches Tools My Workspace Data About Help Contact Us

My Organism Preferences (248 of 248) enabled

Learn more about this search

Identify Genes based on Unannotated Intron Junctions

Reset values

Organism

This search is not available for organisms lacking RNA seq data since the query is based on the results of RNA seq analysis.

1 selected, out of 41

select all | clear all | expand all | collapse all

Filter list below...

- Fungi
 - Ascomycota
 - Eurotiomycetes
 - Saccharomycetes
 - Schizosaccharomycetes
 - Sordariomycetes
 - Hypocreales
 - Magnaporthales
 - Sordariales
 - ☒ Neurospora crassa OR74A [Reference]
 - ☐ Neurospora discreta FGSC 8579 [Reference]
 - ☐ Neurospora tetrasperma FGSC 2508 [Reference]
 - Basidiomycota
 - Mucoromycota
 - Oomycota

select all | clear all | expand all | collapse all

Minimum number of unique reads >=

20

Percent of Most Abundant Intron (MAI)

1 to 100

Consider 5' & 3' Flanking Sequence up to (bp)

0

Get Answer

Select organism(s) you wish to query against. Click the [+] to expand taxon groupings. You can also use the search bar to find your organism of interest. Please note, this search is only available for genomes to which RNA-seq data has been mapped.

Enter the minimum number of total unique reads required to consider an intron.

The most abundant intron (MAI; supported by the highest number of intron-spanning reads; ISRs) provides context for the expected observation frequency: introns mistakenly omitted from the gene model are likely to be as abundant as correctly annotated introns.

Enter the maximum number of nucleotides flanking the annotated gene model to explore when looking for unannotated introns. Search automatically includes the annotated gene model. Please note, this option is not available in VectorBase.

3) Explore the result table

You can order the search result by using the grey arrows on the top of the columns.



- **Number of Novel Splice Junctions.** In case the number is 1, this means your gene has 1 possible unannotated intron. If this number is quite high, i.e. over 50 there is a possibility that your gene of interest is a rRNA, located in a repetitive region or it is part of a gene family. Therefore it is important to explore the results in JBrowse/Apollo with additional evidence.
- **Max % Mai:** Maximum percentage of intron with the maximum total unique reads in this gene for the novel introns that met search criteria
- **Max Unique Reads:** Maximum total unique reads for the novel introns that met search criteria
- **Max ISRPM:** Maximum total ISRPM (Intron Spanning Reads Per Million) for the novel introns

Note: Add an additional step to this search strategy if you would like to combine your search result with an additional search, i.e. a list of gene IDs or number of exons in a gene.

Opened (1) All (2) Public (52) Help

Unnamed Search Strategy *

Intron Junctions 3,959 Genes + Add a step Step 1

3,959 Genes (3,612 ortholog groups) Revise this search

Some Genes in your result have Transcripts that did not meet the search criteria. Explore

Gene Results Genome View Analyze Results

Genes: 3,959 Transcripts: 4,645 Show Only One Transcript Per Gene

Gene ID	Transcript ID	Product Description	# Novel Junctions	Max % MAI	Max Unique Reads	Max ISRPM
NCU17319	NCU17319-t26_1	rRNA	139	100	2002662	1691129.69
NCU15719	NCU15719-t26_1	rRNA	61	100	502137	355238.69
NCU06660	NCU06660-t26_1	plasma membrane proteolipid 3	1	100	405848	108695.59
NCU16992	NCU16992-t26_1	pheromone mfa-1	86	100	58486	9930.97
NCU06940	NCU06940-t26_1	hypothetical protein	2	100	49292	16973.98
NCU01957	NCU01957-t26_1	AR2	3	100	39488	18421.91
NCU14161	NCU14161-t26_1	unspecified product	1	100	26674	9968.07
NCU03163	NCU03163-t26_1	stress responsive A/B barrel domain-containing protein	3	100	15833	9268.5
NCU07487	NCU07487-t26_1	periplasmic beta-glucosidase	1	100	9091	4905.51

You can explore the results in JBrowse. For easy access use the option Add Columns to include a new column with links to JBrowse.

Gene Results Genome View Analyze Results

Genes: 3,981 Transcripts: 4,675 Show Only One Transcript Per Gene

Download Add to Basket Add Columns

Select Columns

Update Columns

select all | clear all | expand all | collapse all | reset to current | reset to default

Search Columns

- ☐ Search Specific
- ☒ Gene models
 - ☐ # Exons in Gene
 - ☐ # Exons in Transcript
 - ☐ # Transcripts
 - ☐ Annotated 3' UTR length
 - ☐ Annotated 5' UTR length
 - ☐ Gene Strand
 - ☐ Gene Type
 - ☐ Is Pseudo
 - ☒ JBrowse
 - ☐ Transcript Length
- ☐ Annotation, curation and identifiers

4) Explore the results in JBrowse/Apollo

Click on the JBrowse link in the table. Alternatively, go to the gene record page of your gene of interest by clicking on the Gene ID.

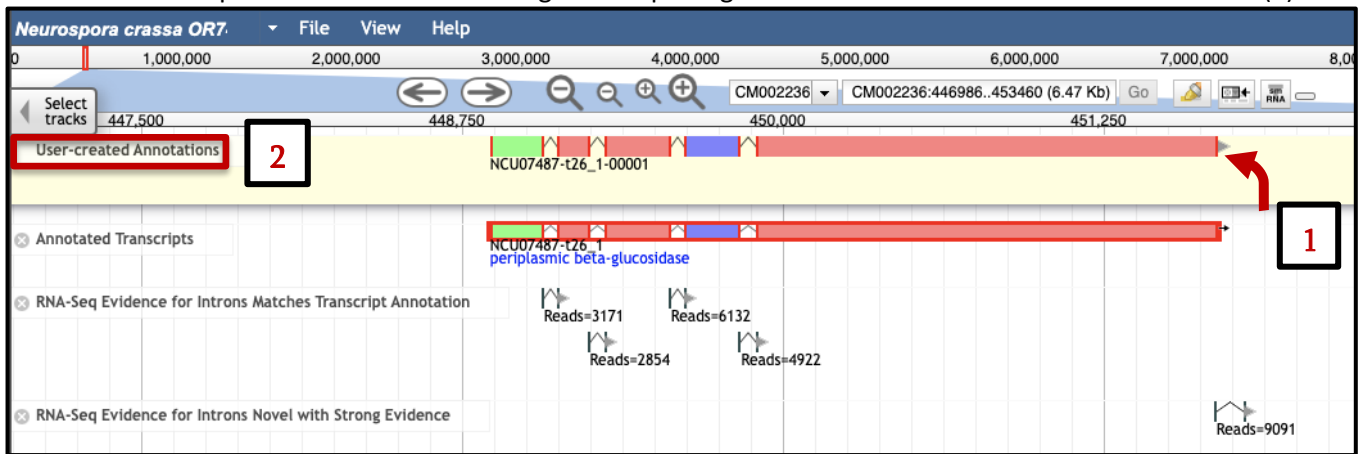
Gene ID	Transcript ID	Product Description	# Novel Junctions	Max % MAI	Max Unique Reads	Max ISRPM	JBrowse
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NCU15719	NCU15719-26_1	rRNA	61	100	502137	355238.69	JBrowse
NCU06660	NCU06660-26_1	plasma membrane proteolipid 3	1	100	405848	108695.59	JBrowse
NCU16992	NCU16992-26_1	pheromone mfa-1	86	100	58486	9930.97	JBrowse
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NCU03163	NCU03163-26_1	stress responsive A/B barrel domain-containing protein	3	100	15833	9268.5	JBrowse
NCU07487	NCU07487-26_1	periplasmic beta-glucosidase	1	100	9091	4905.51	JBrowse

Select **View in JBrowse genome browser (1)** to explore your search result. For reference genomes, you can view and correct the gene structure in Apollo. To open Apollo select **Annotate in Apollo (2)** on the gene record page. To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now in with your VEuPathDB user ID and password.

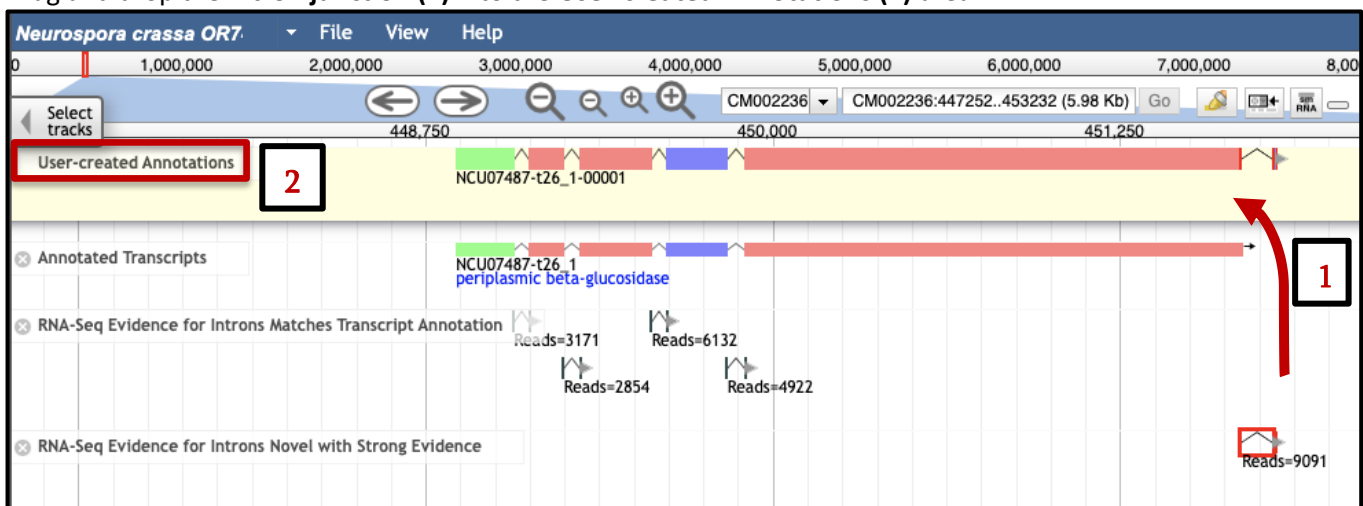
5) Correct the gene structure in Apollo

Select on the right-hand side the tab **Tracks**. Click on the menu item **Draggable Annotation** select **RNA-Seq Evidence for Introns Novel with Strong Evidence** and **RNA-Seq Evidence for Introns Matches Transcript Annotation**. Select additional evidence, i.e. Transcriptomics evidence.

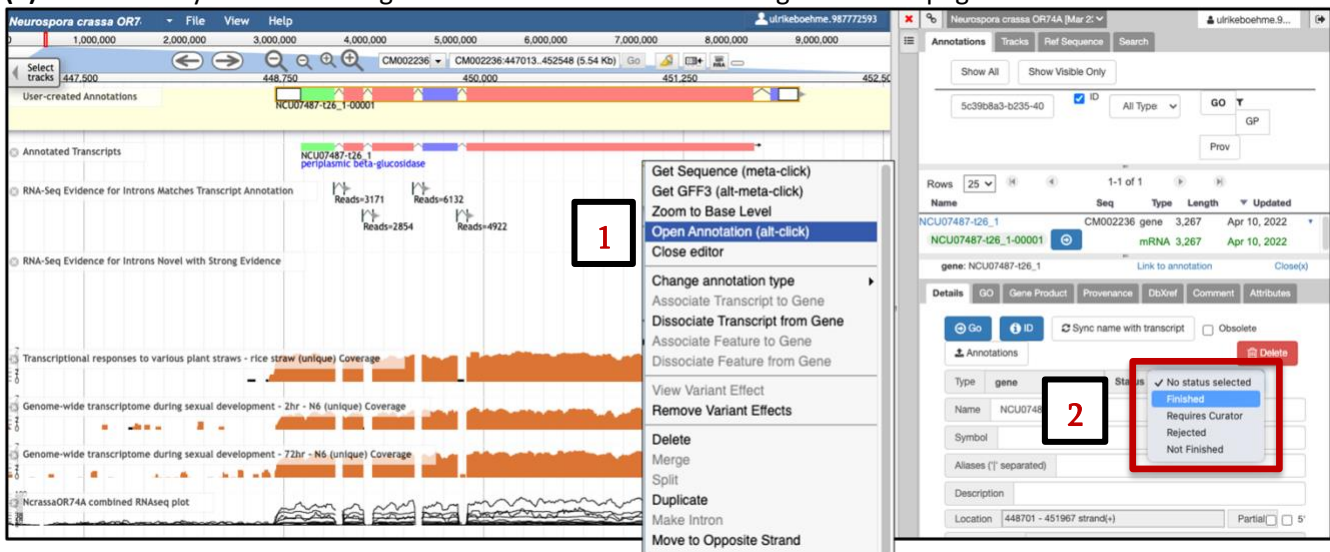
Select the gene model by clicking on one of the introns or by double clicking on the gene model (1). The gene model will show up with red boundaries. Drag and drop the gene into the **User-created Annotation** track (2).



Drag and drop the **intron junction** (1) into the **User-created Annotations** (2) area.



With a right-click on the gene in the **User-created annotations** area you can access the menu. Once you are happy with the corrected gene model choose **Open Annotation** (1) and select from the status menu **Finished** (2). The next day the corrected gene model will be visible on the gene record page.



Additional information and tutorials on Apollo can be found in the Help section on VEuPathDB!