

Structural annotation in Apollo

Modifying a gene model

In this short tutorial we are showing you step-by-step how to modify an existing gene model in Apollo. Modifying a gene model can include adding additional exons, extending exons, deleting exons, splitting exons and adding UTRs.

1) Accessing Apollo

To access Apollo go to the gene record page of your gene of interest and click on the link **View and update community annotations in Apollo (1)**. You can also access Apollo from the gene models section by clicking on the button **Annotate in Apollo (2)**. Alternatively, go to the **Tools** menu and choose Apollo from the drop-down list (3).

The screenshot shows the ToxoDB gene record page for TGME49_305150. At the top, there's a navigation bar with links for 'My Strategies', 'Searcher', 'Tools' (circled in red), 'Gene', 'Data', 'About', 'Help', and 'Contact Us'. Below the navigation bar, there's a site search bar and a guest login link. The main content area displays gene details: Type: protein coding gene, Chromosome: IX, Location: TGME49_chrlX:5,245,620..5,257,794(+), Species: *Toxoplasma gondii*, Strain: ME49, Status: Reference Genome. There's a section for 'Add the first user comment' and a link to 'View and update community annotations in Apollo' (circled in red). Below this, there's a 'Shortcuts' section with links to Synteny, Alignments, Phenotype, SNPs, Transcriptomics, Protein Features, and Proteomics. A note says 'Also see TGME49_305150 in the Genome Browser or Protein Browser'. On the left, there's a sidebar with a tree view of gene models, annotations, and identifiers, and a 'Search section names...' input field. At the bottom, there's a 'Gene models' section with a count of 13 exons and 1 transcript, and a note saying 'This gene is available in Apollo for community annotation. To find out more about Apollo, please visit this help page.' A 'View in JBrowse genome browser' button and an 'Annotate in Apollo' button (circled in red) are also present. A red box highlights the 'Tools' menu item at the top.

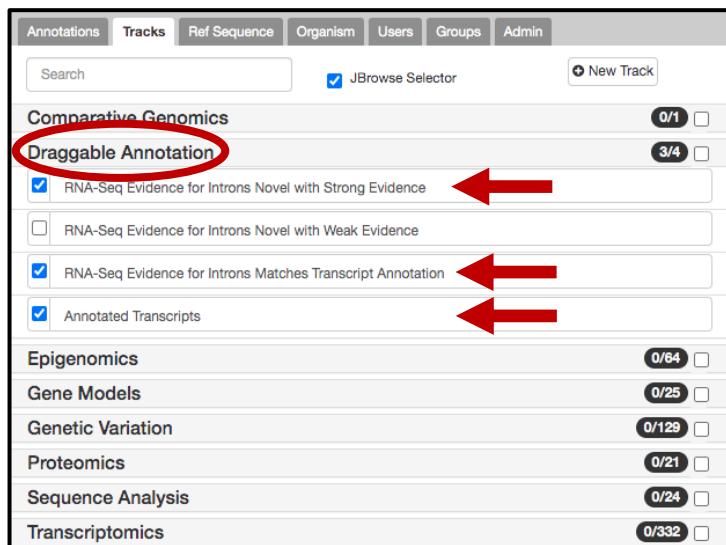
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

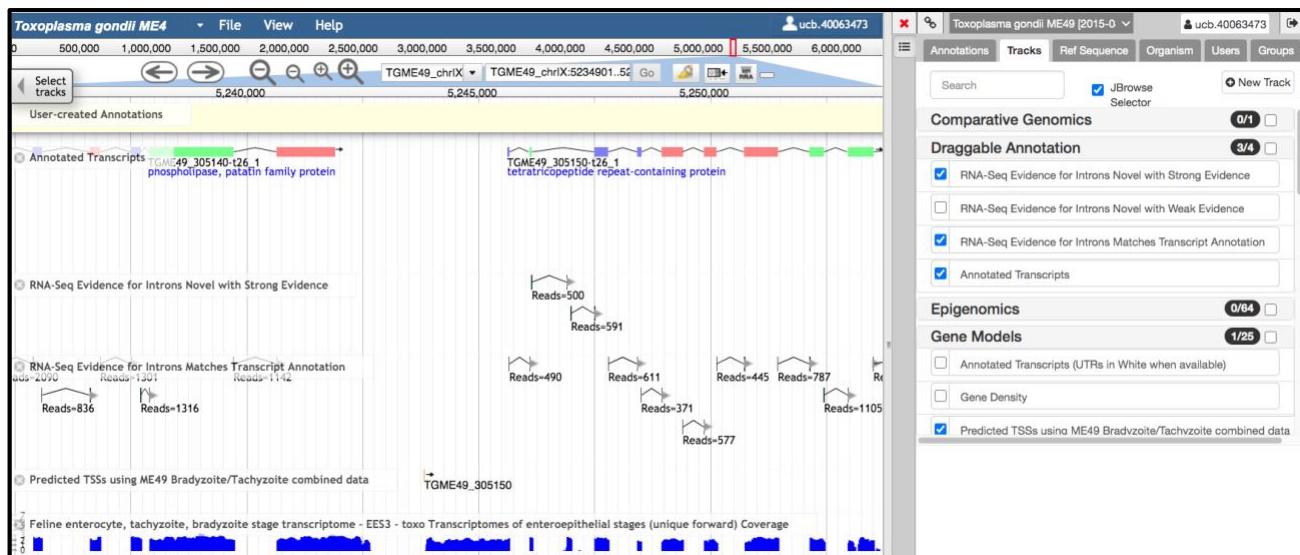
Select on the right-hand side the tab **Tracks**.

The screenshot shows the JBrowse interface for the Toxoplasma gondii ME4 genome. The top navigation bar includes 'File', 'View', 'Help', and a user account icon. The main area shows a genomic track for chromosome IX, with a scale from 0 to 6,000,000. A red box highlights the 'Tracks' tab in the top right corner of the interface. Other tabs include 'Annotations' and 'Ref Sequence'. Below the tracks, there are sections for 'Comparative Genomics' and 'Draggable Annotation'.

Click on the menu item **Draggable Annotation** select **Annotated Transcripts, RNA-Seq Evidence for Introns Novel with Strong Evidence and RNA-Seq Evidence for Introns Matches Transcript Annotation.**

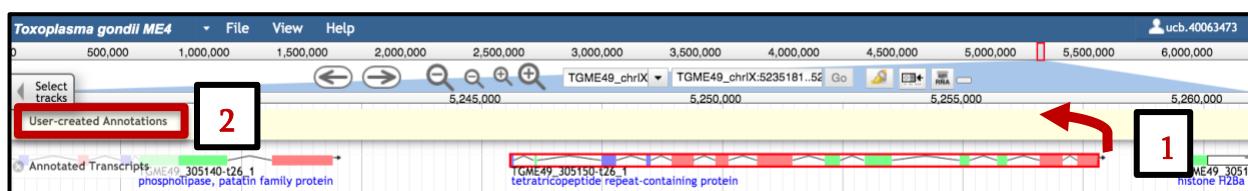


Select additional evidence, i.e. RNAseq plots or predicted TSS (transcription start sites).

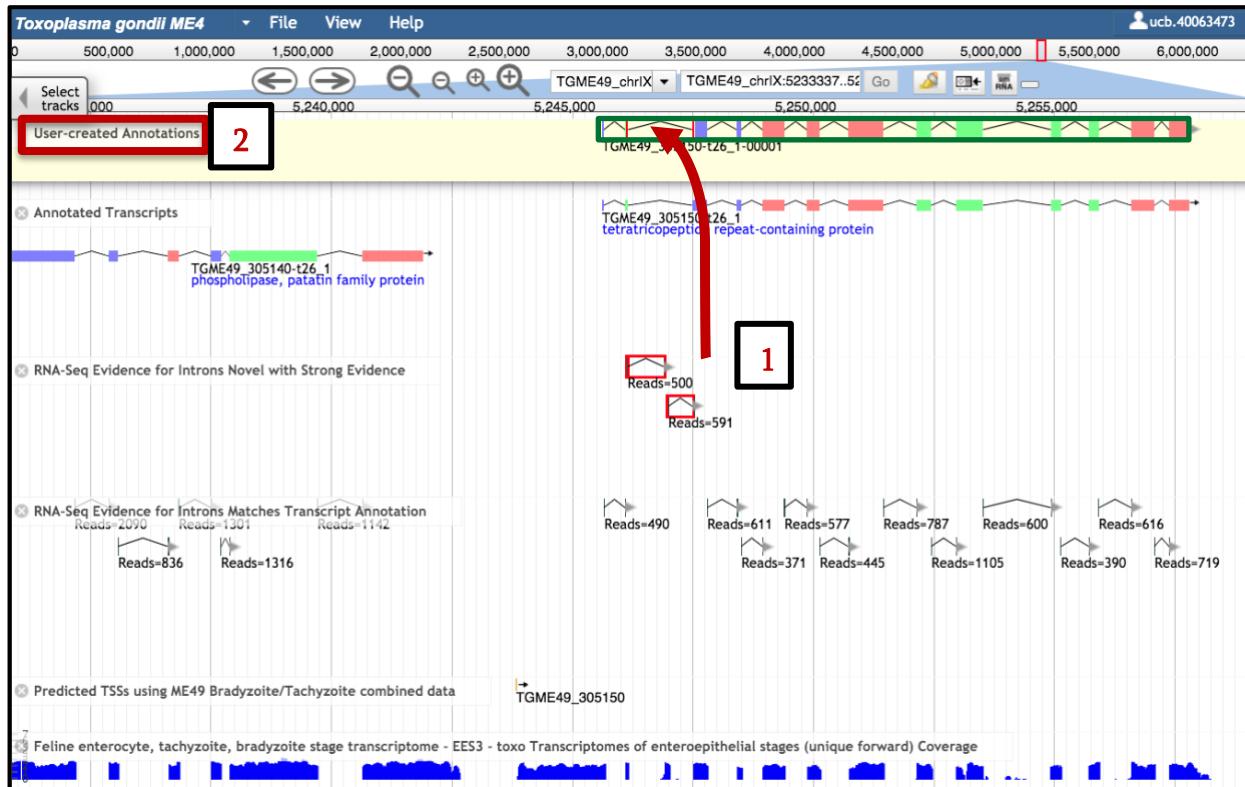


3) Modifying the gene

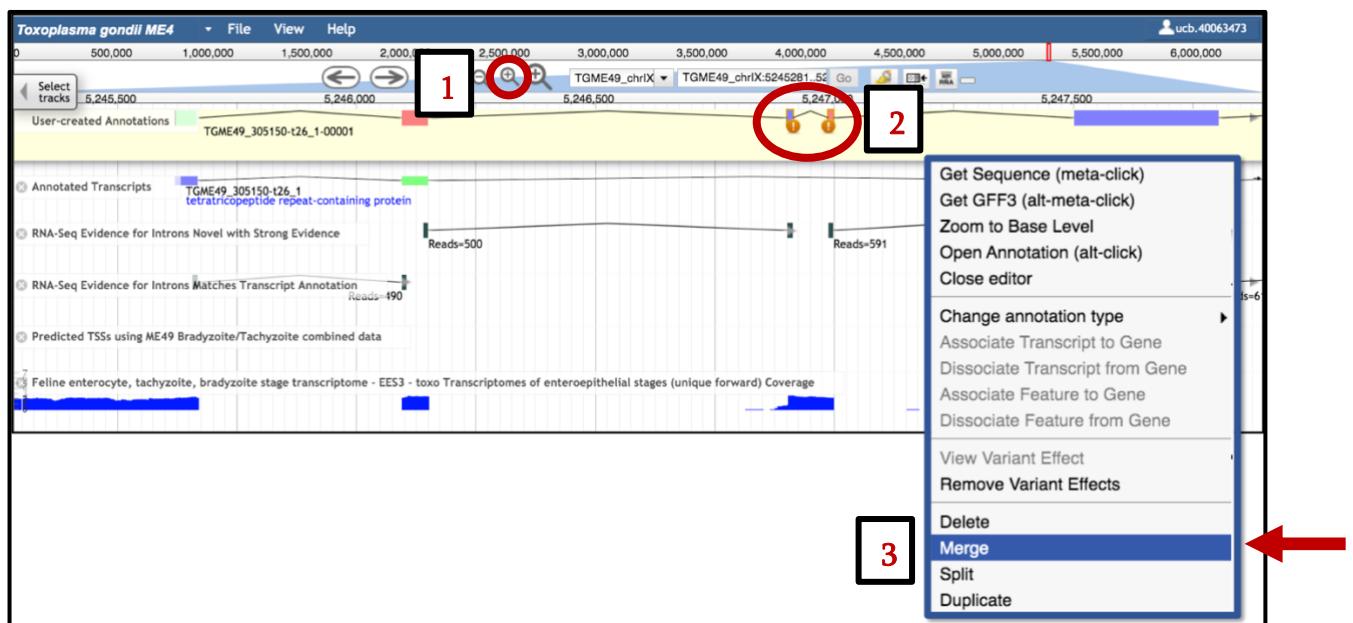
Select the gene model by clicking on one of the introns or by double clicking on the gene model (1). The gene model will show up with red boundaries. Drag and drop the gene into the User-created Annotations track (2). **Please note:** To add one-exon genes into the User-created Annotations area you need to **double-click** on the gene and then drag it into the user-created annotations area.



You can either select the intron junctions individually, or hold down the shift key and select both intron junctions with strong evidence (1), drag and drop them into the gene model (2). The gene will get a green box when dragging and dropping the intron evidence.



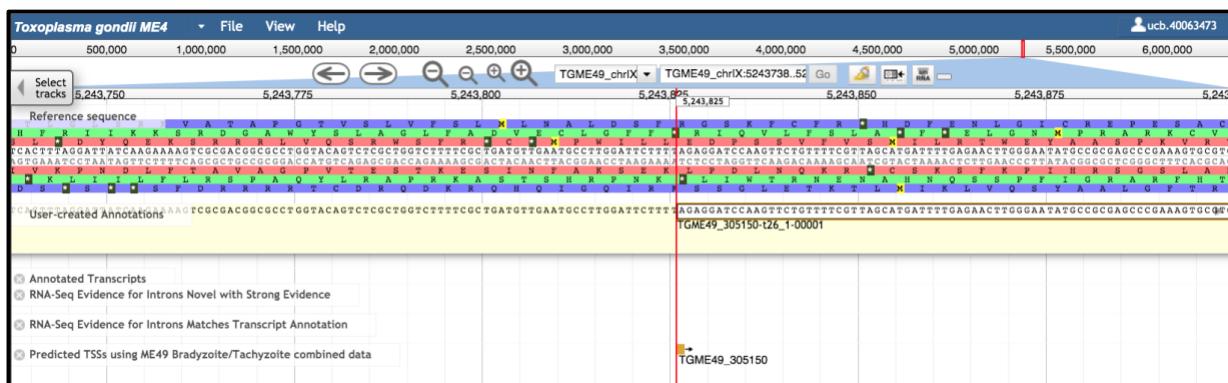
Zoom in by clicking on the + sign on the top (1). Press the Shift key and select the two small exons in the middle (2). With a right-click open the drop-down menu and choose **Merge** (3). Alternatively, select one of the exons you would like to merge, go to the edge of the feature until a little arrow appears and extend the exon until it overlaps with the second exon.



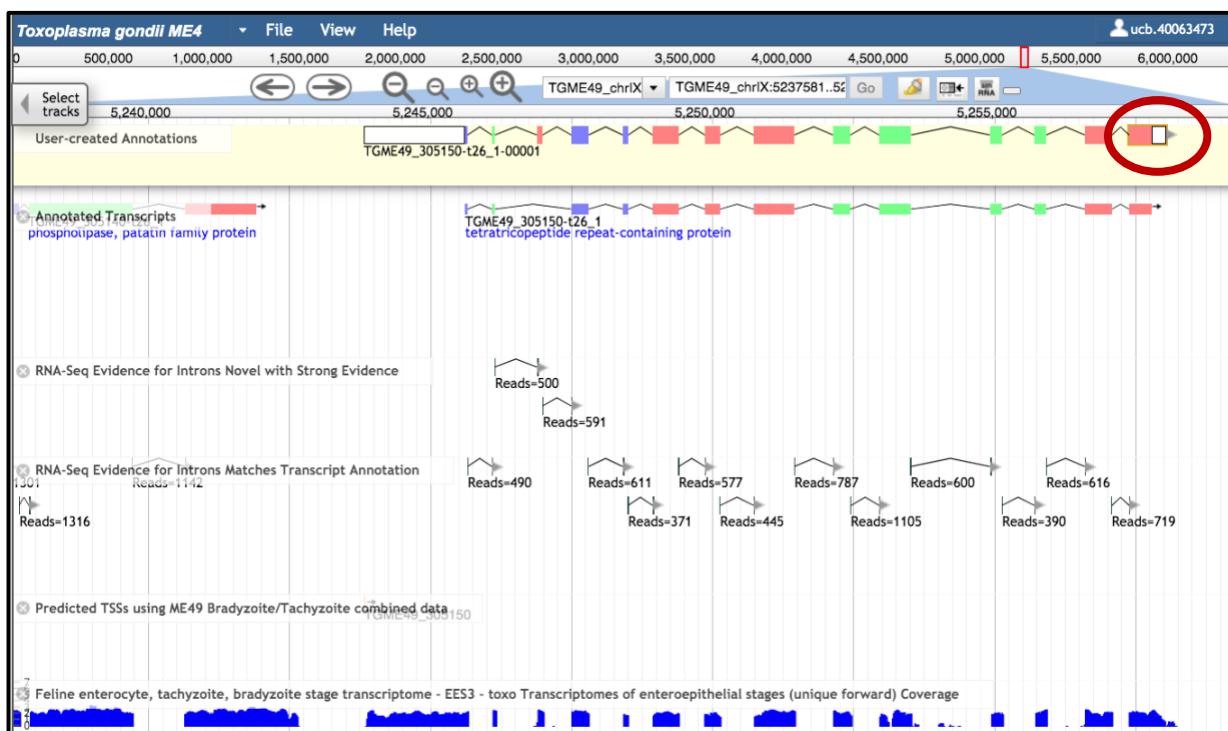
Select the first exon, point your mouse at the edge of the feature, a little arrow will appear, then extend the exon to the transcription start. Apollo will automatically create the 5'UTR!



You can zoom in to recheck the transcription start site.

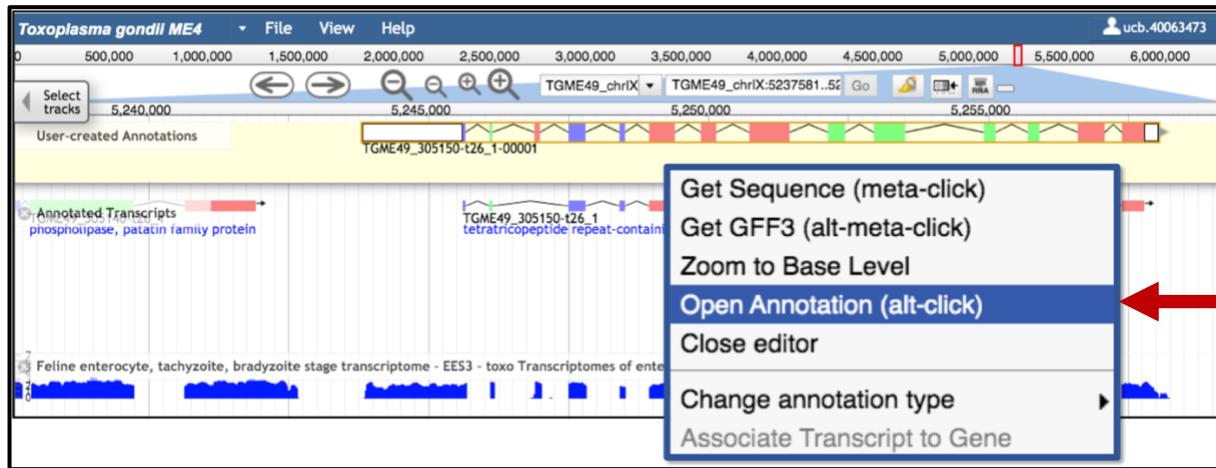


Select the last exon, point your mouse at the edge and extend the exon. Apollo will create the 3'UTR automatically!

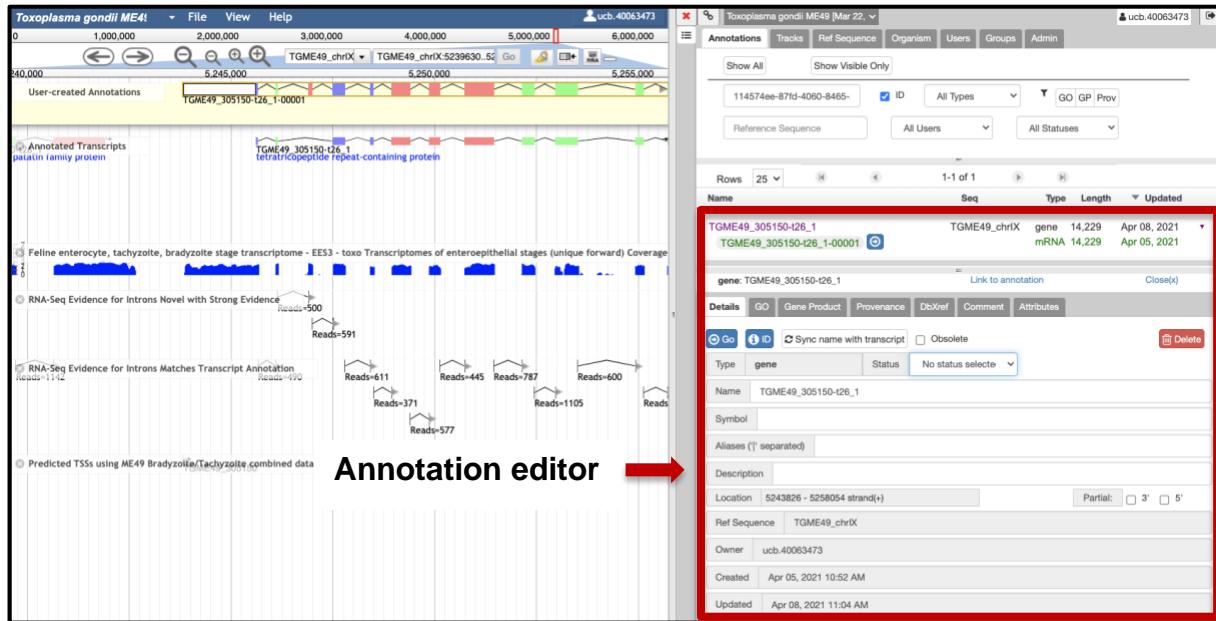


4) Opening of the Annotation editor window

Select the gene in the User-created Annotation track and with a right-click open the drop-down menu and choose **Open Annotation**. Alternatively, you can use the short-cut **alt-click**.

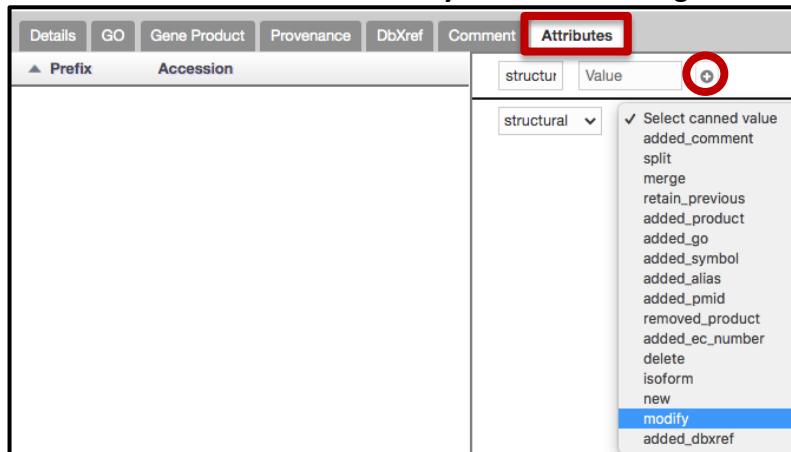


The annotation editor window is now shown on the right-hand side.



5) Finalizing the structural annotation

Once the annotations panel is open click on the Attributes tab, select from the canned tag **structural** and from the canned value **modify**. Click on the + sign.



If there is no change in the functional annotation choose from the canned tag - **annotation** and from the canned value in the Attributes section **retain previous**. Click on the + sign.

TGME49_305150-t26_1	TGME49_chrlX	gene	14,229	Apr 05, 2021
TGME49_305150-t26_1-00001	(+)	mRNA	14,229	Apr 05, 2021
gene: TGME49_305150-t26_1				
Details	GO	Gene Product	Provenance	DbXref
Comment	Attributes			
Prefix	Accession			
structural	new			
annotation	retain_previous			

Finally go the Details tab and select the status **Finished** on the gene.

TGME49_305150-t26_1 TGME49_chrlX gene 14,229 Apr 05, 2021

TGME49_305150-t26_1-00001 mRNA 14,229 Apr 05, 2021

gene: TGME49_305150-t26_1

Details	GO	Gene Product	Provenance	DbXref	Comment	Attributes	
+ Go	+ ID	Delete					
Type	gene	Status	<input checked="" type="checkbox"/> No status selected <input type="checkbox"/> Not Finished <input checked="" type="checkbox"/> Finished <input type="checkbox"/> Requires Curator				
Name	TGME49_305150-t26_1						
Symbol							
Aliases (' ' separated)							
Description							
Location	5243825 - 5258054 strand(+)						
Ref Sequence	TGME49_chrlX						
Owner	ucb.40063473						
Created	Apr 05, 2021 10:52 AM						
Updated	Apr 05, 2021 10:52 AM						

The following day, the corrected gene model is visible on the gene record page in the Community annotations from Apollo track.

ToxoDB Toxoplasma gondii Database

Site search, e.g. TGME49_239250 or "reductase or "binding protein"

My Strategies Searches Tools My Workspace Data About Help Contact Us

My Organism Preferences (37 of 37) Manage, or select one for better performance

1 Gene models

Exons in Gene 13

Transcripts 1

Gene Models

INFO This gene is available in Apollo for community annotation. To find out more about Apollo, please visit this help page.

[View in JBrowse genome browser](#) [Annotate in Apollo](#)

Scroll and zoom

TGME49_305150

expand all | collapse all

Search reaction names...

- 1 Gene models
- 2 Annotation, curation and identifiers
- 3 Link outs
- 4 Genomic Location
- 5 Literature
- 6 Taxonomy
- 7 Orthology and synteny
- 8 Phenotype
- 9 Genetic variation
- 10 Transcriptomics
- 11 Sequence analysis
- 12 Sequences
- 13 Structure analysis
- 14 Protein features and properties
- 15 Protein targeting and localization
- 16 Function prediction
- 17 Pathways and interactions
- 18 Proteomics
- 19 Immunology

expand all | collapse all

Done! For additional questions, please get in touch with the VEuPathDB help desk.

Structural annotation in Apollo

Merging/Splitting gene models

In this short tutorial we are showing you step-by-step how to merge/split gene models in Apollo.

1) Accessing Apollo

To access Apollo go to the gene record page of your gene of interest and click on the link **View and update community annotations in Apollo (1)**. You can also access Apollo from the gene models section by clicking on the button **Annotate in Apollo (2)**. Alternatively, go to the **Tools** menu and choose Apollo from the drop-down list (3).

The screenshot shows the ToxoDB gene record page for *TGME49_319312*, a hypothetical protein. On the left, there's a sidebar with gene details: Type: protein coding gene, Chromosome: IV, Location: *TGME49_chrlV:1,041,310..1,050,287(+)*, Species: *Toxoplasma gondii*, Strain: ME49, and Status: Reference Strain. Below this is a section for user comments and a link to view and update community annotations in Apollo. In the center, there's a 'Gene models' section with a table showing 1 Gene model, 9 Exons, and 1 Transcript. At the bottom of this section is an 'Annotate in Apollo' button. On the right, there are various data visualization tools like Synteny, Alignments, Phenotype, SNPs, Transcriptomics, Protein Features, and Proteomics. A 'Tools' menu item is highlighted with a red square.

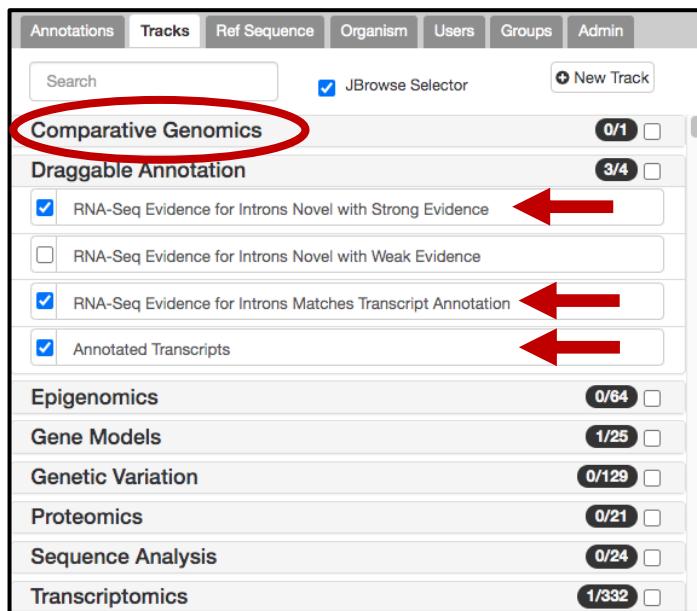
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

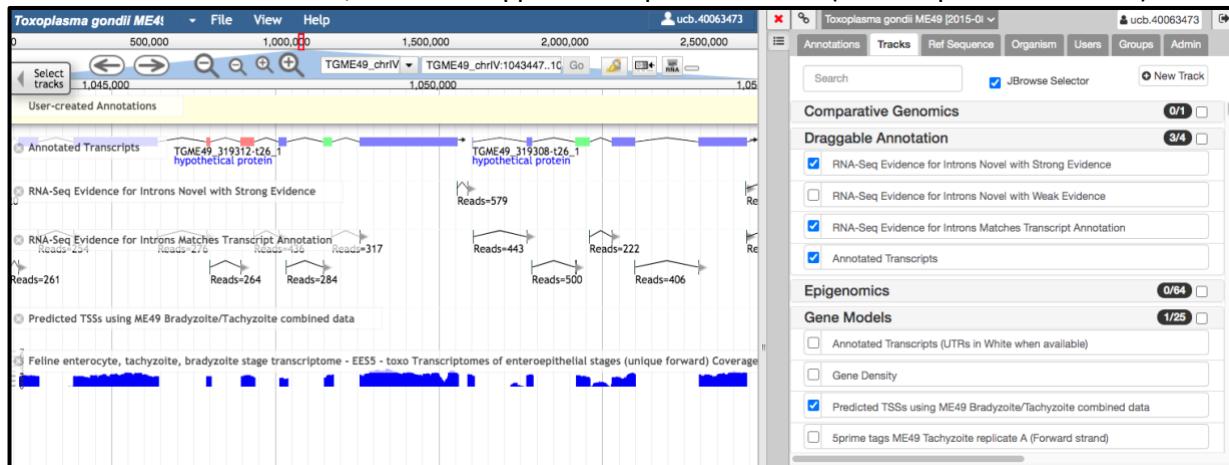
Select on the right-hand side the tab **Tracks**.

The screenshot shows the JBrowse genome browser interface for *Toxoplasma gondii* ME49. The genome browser displays a genomic track for chromosome IV, showing genes *TGME49_319308-28_1* and *TGME49_319308*, both labeled as hypothetical proteins. On the right, a panel titled 'Tracks' lists available data sources: Comparative Genomics (0/1), Draggable Annotation (0/4), Epigenomics (0/64), Gene Models (1/25), and Genetic Variation (0/129). The 'Tracks' tab is currently selected.

Click on the menu item **Draggable Annotation** select **Annotated Transcripts, RNA-Seq Evidence for Introns Novel with Strong Evidence and RNA-Seq Evidence for Introns Matches Transcript Annotation**.



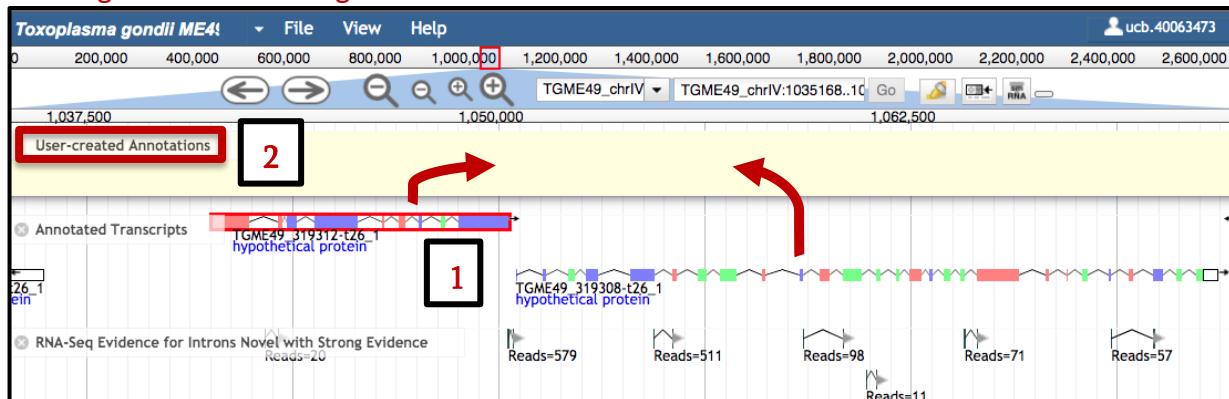
Select additional evidence, i.e. RNAseq plots and predicted TSS (transcription start sites).



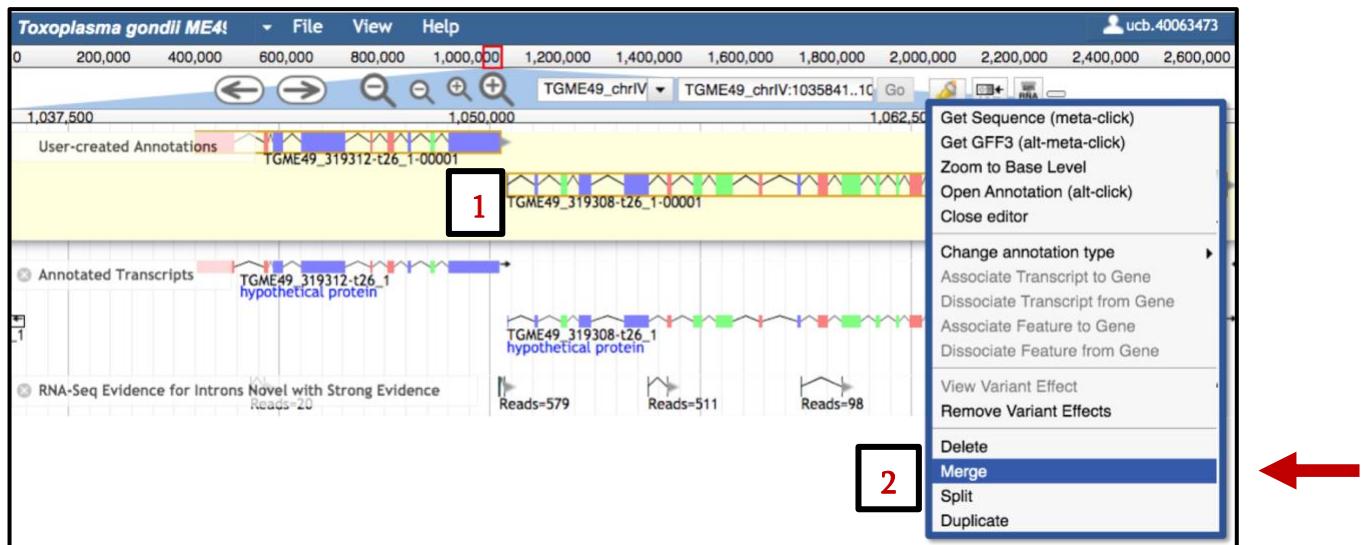
3) Merging genes

Select the gene models that you would like to merge by clicking on one of the introns or by double clicking on the gene model (1). Drag and drop the genes into the User-created Annotations track (2).

Please note: To add one-exon genes into the User-created Annotations area you need to **double-click** on the gene and then drag it into the user-created annotations area.

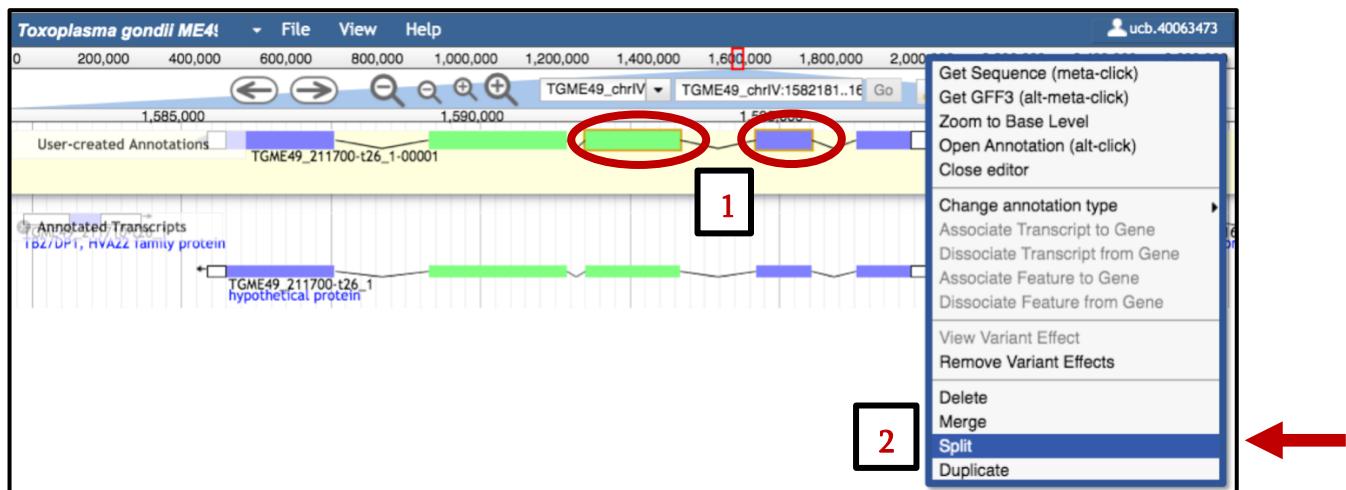


Hold down the shift key and select both gene models in the User-created Annotations track (1). With a right-click open the drop-down menu and choose **Merge** (2).



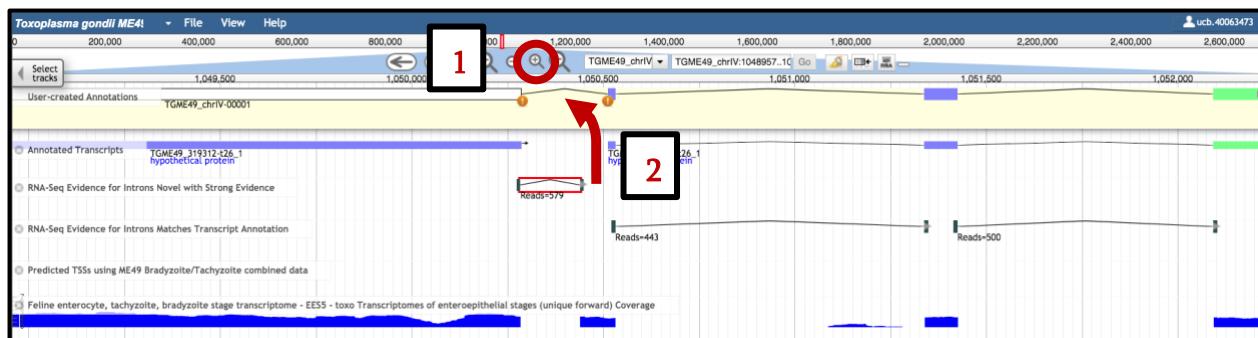
3.1) Splitting gene models

For splitting gene models, select the exons that border the intron that should be split. With a right-click open the annotation drop-down menu and choose split. Once you've split the gene model, recheck if the gene model has the correct start and stop.

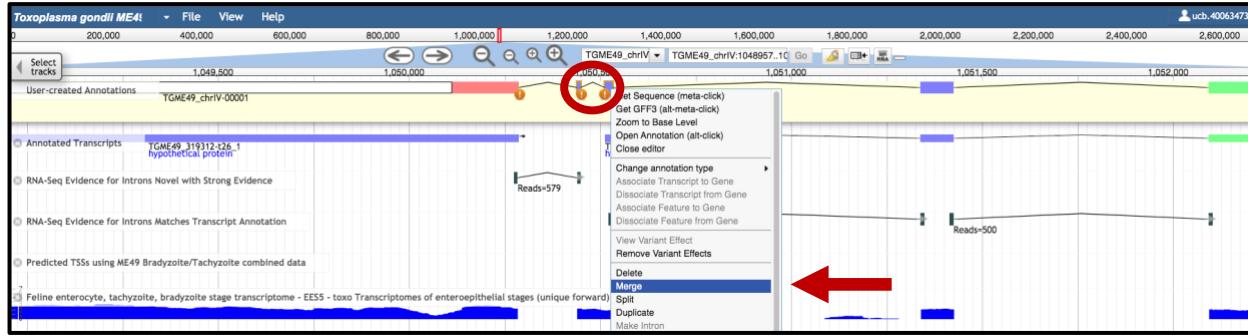


4) Correcting intron-exon boundaries

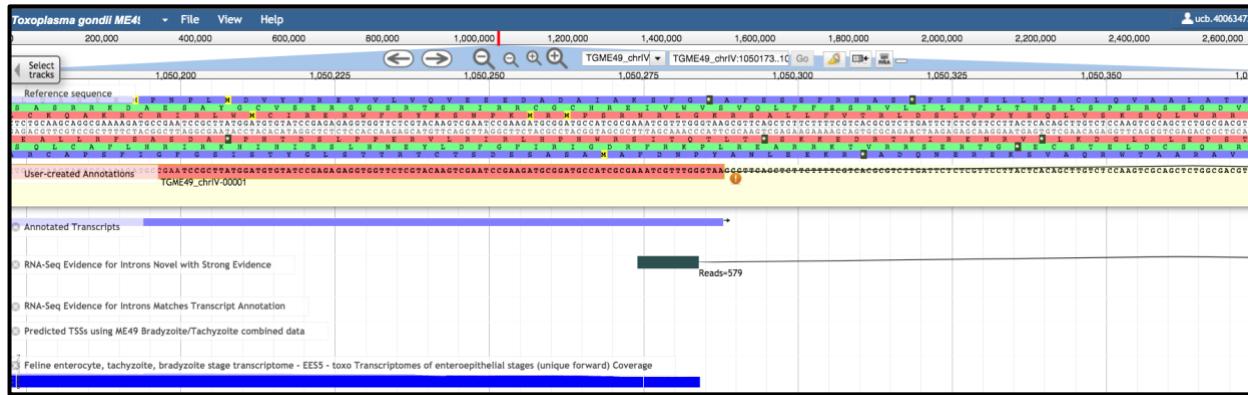
Once you've merged the gene zoom in by clicking on the + sign on the top (1). Select the new splice junction and drag it into the gene model (2).



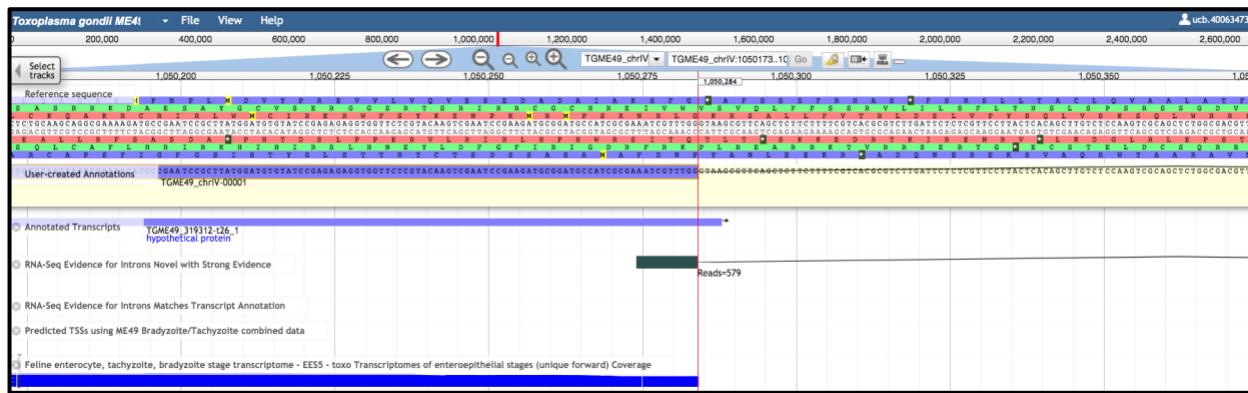
Hold down the shift key and select the two small exons. With a right-click open the drop-down menu and select merge. Hint: The exclamation mark tells you that there are non-canonical splice sites.



Zoom in, select the exon on the left side, point your mouse at the edge of the exon, a little arrow will appear.

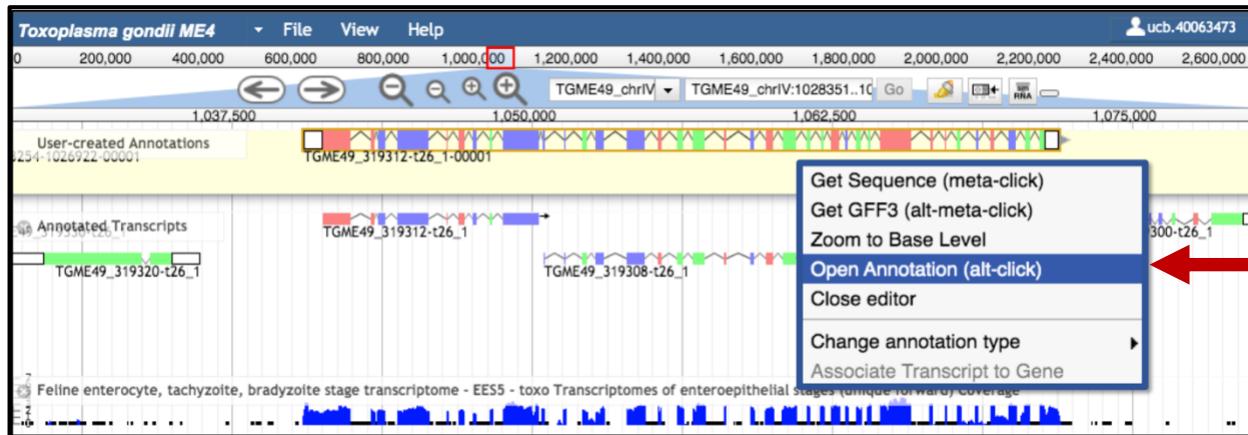


Shorten the exon to the correct splice site.

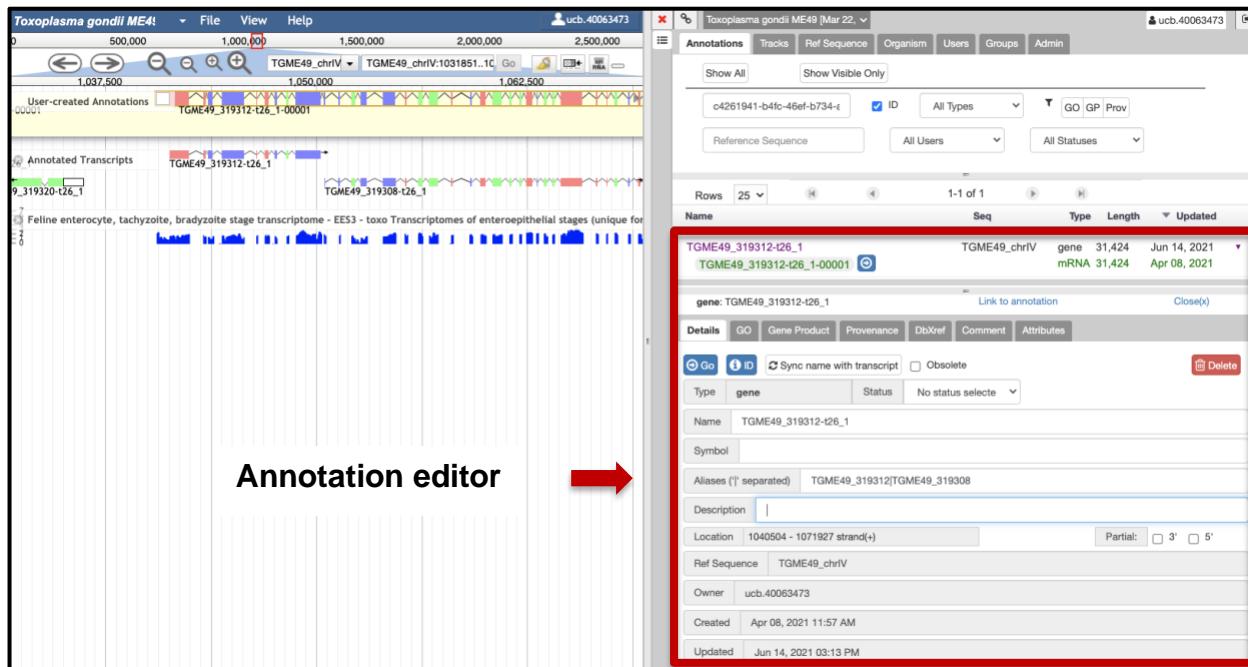


5) Opening of the Annotation editor window

Select the gene in the User-created Annotation track and with a right-click open the drop-down menu and choose **Open Annotation**. Alternatively, you can use the short-cut **alt-click**.



The annotation editor window is now shown on the right-hand side.



6) Finalizing the structural annotation

Once the annotations panel is open click on the Attributes tab, select from the canned tag **structural** and from the canned value **merge**. Click on the + sign.



Open the Details section and add the gene IDs that you've merged in the Aliases section. Ideally, also add a Description/Gene Product.

TGME49_319312-t26_1 TGME49_chrIV gene 30,508 Apr 08, 2021
TGME49_319312-t26_1-00001

gene: TGME49_319312-t26_1

Details GO Gene Product Provenance DbXref Comment Attributes

Type gene Status No status selected

Name TGME49_319312-t26_1

Symbol

Aliases ('|' separated) TGME49_319308|TGME49_319312

Description

Location 1041309 - 1071817 strand(+)

Ref Sequence TGME49_chrIV

Owner ucb.40063473

Created Apr 08, 2021 11:57 AM

Updated Apr 08, 2021 11:57 AM

To finalize the annotation select the status **Finished** on the gene. The following day, the corrected gene model will be visible on the gene record page in the Community annotations from Apollo track.

TGME49_319312-t26_1 TGME49_chrIV gene 30,508 Apr 08, 2021
TGME49_319312-t26_1-00001

gene: TGME49_319312-t26_1

Details GO Gene Product Provenance DbXref Comment Attributes

Type gene Status ✓ No status selected
Not Finished
Finished
Requires Curator

Name TGME49_319312-t26_1

Symbol

Aliases ('|' separated) TGME49_319312|TGME49_319308

Description Hypothetical protein, conserved

Location 1041309 - 1071817 strand(+)

Ref Sequence TGME49_chrIV

Owner ucb.40063473

Created Apr 08, 2021 11:57 AM

Updated Apr 08, 2021 02:00 PM

Done! For additional questions, please get in touch with the VEuPathDB help desk.

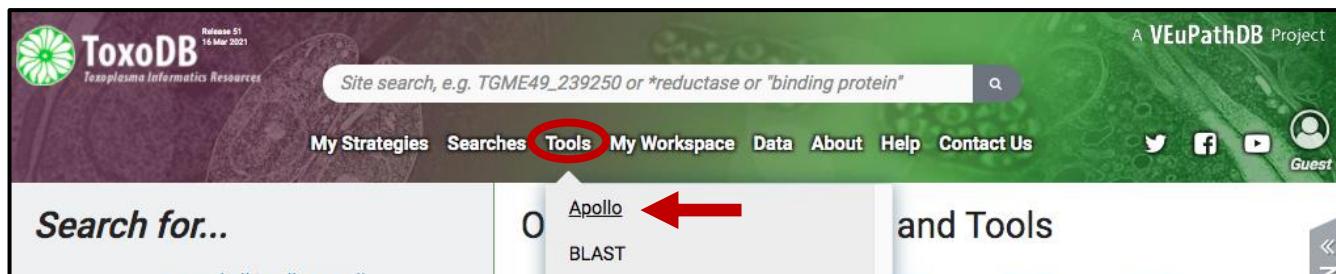
Structural annotation in Apollo

Adding a new gene

In this short tutorial we are showing you step-by-step how to add a new gene in Apollo.

1) Accessing Apollo

To access Apollo select **Tools** from the top menu and choose **Apollo** from the drop-down menu.



Click on the button **Go to Apollo**.

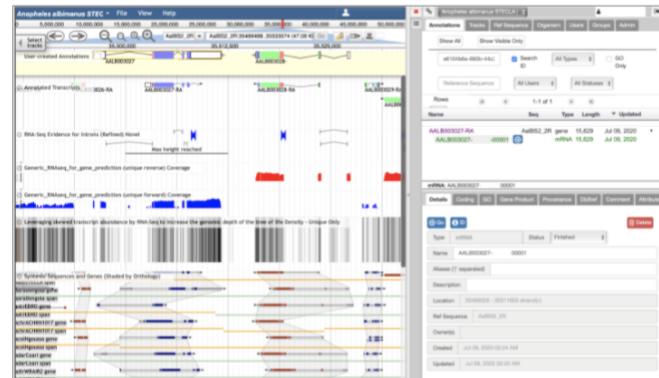
Structural and functional community curation in Apollo

Welcome to the VEuPathDB Apollo service (Dunn et al. 2019), a real time collaborative genome annotation and curation platform.

Use Apollo to integrate new or update current structural and functional data, for gene models in the organisms available in VEuPathDB. Organisms in AmoebaDB, CryptoDB, FungiDB, GiardiaDB, MicrosporidiaDB, PiroplasmaDB, PlasmoDB, ToxoDB, TrichDB, TriTrypDB & VectorBase are available for community curation.

Apollo help and documentation:

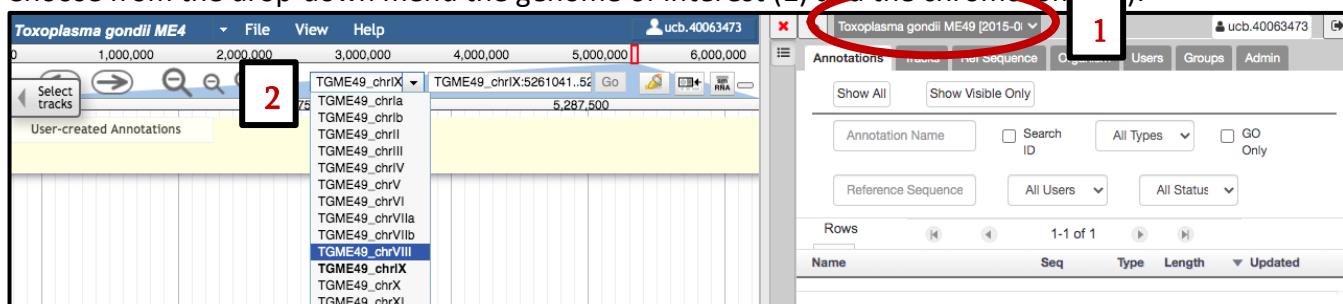
- A **sandbox** is available for you to get familiar with all Apollo menus, tools, and tracks before you decide to use it for your real gene manual annotations. These changes will not affect any of the organism's official gene set, neither will be preserved.
- Comprehensive webinar to learn [how to use Apollo](#) (57:40 min)
- [Quick commands](#)
- Functional annotation tutorial
- About Apollo (Login required)
- User Guide
- Request feature/Report a bug
- Powered by JBrowse
- [Web Service API](#) (Login required)



To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Navigate to the genome and chromosome coordinates

Choose from the drop-down menu the genome of interest (1) and the chromosome (2).

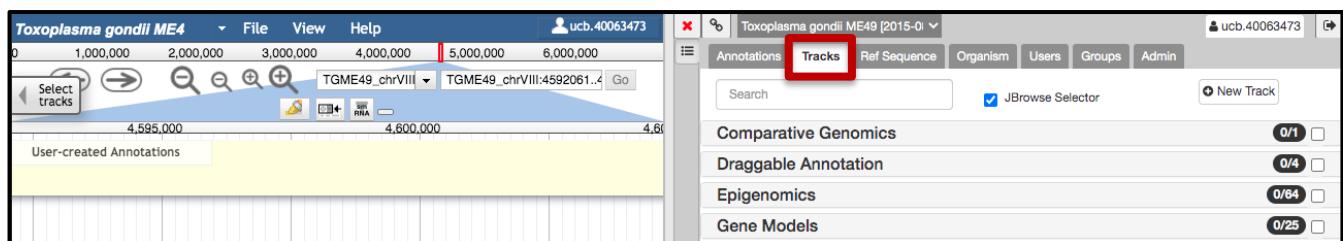


Go to the coordinates with the missing gene. Use the arrows to navigate to the coordinates (1), or type the coordinates in the search box (2).

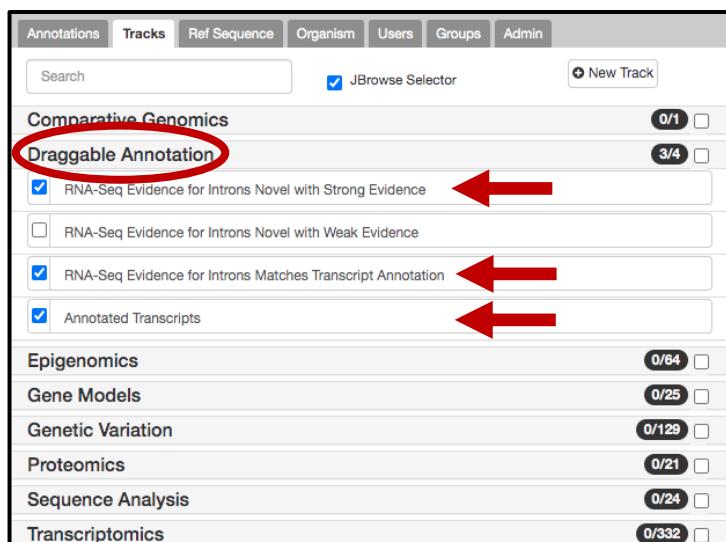


3) Adding draggable annotation and supporting evidence

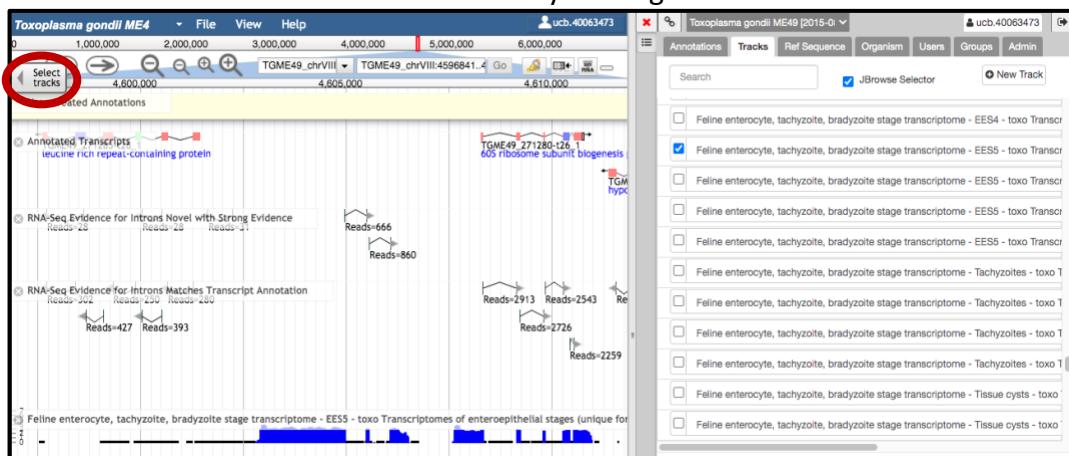
Select on the right-hand side the tab **Tracks**.



Click on the menu item **Draggable Annotation** select **Annotated Transcripts, RNA-Seq Evidence for Introns Novel with Strong Evidence and RNA-Seq Evidence for Introns Matches Transcript Annotation**.

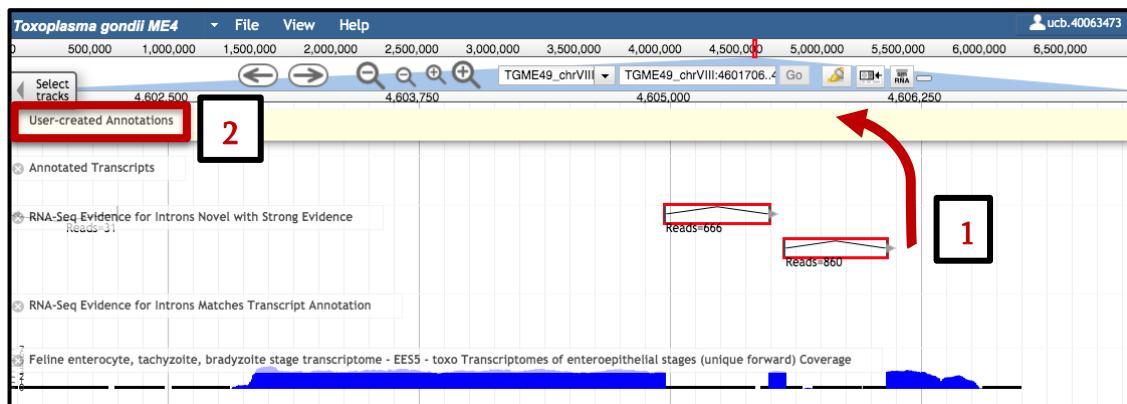


Select additional evidence, i.e. RNAseq plots from the Transcriptomics section. Alternatively, you can select evidence from the JBrowse menu by clicking on **Select tracks**.

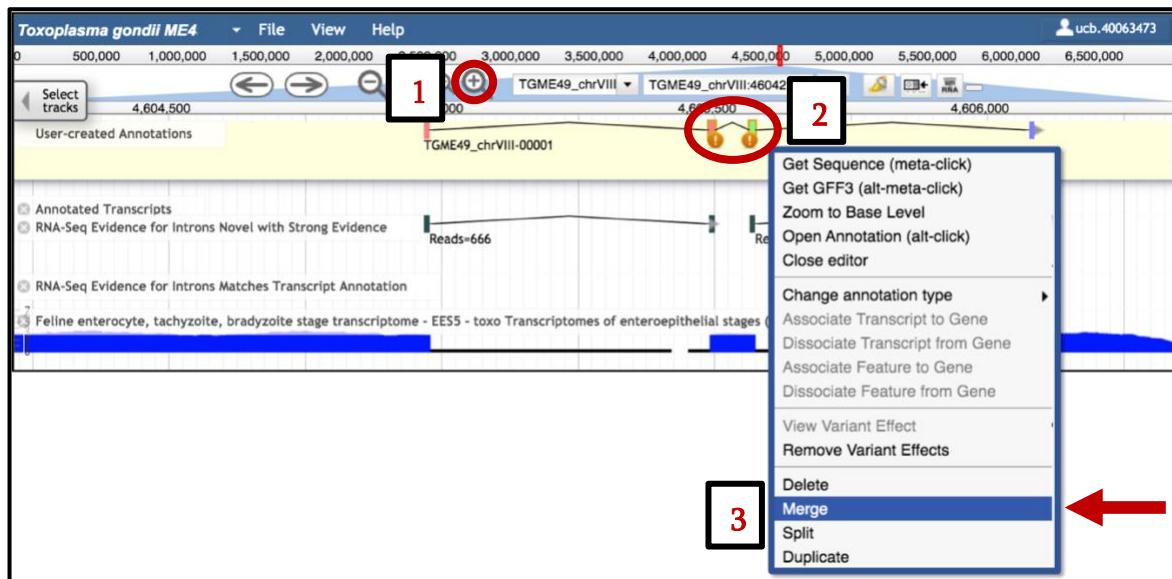


4) Building the new gene

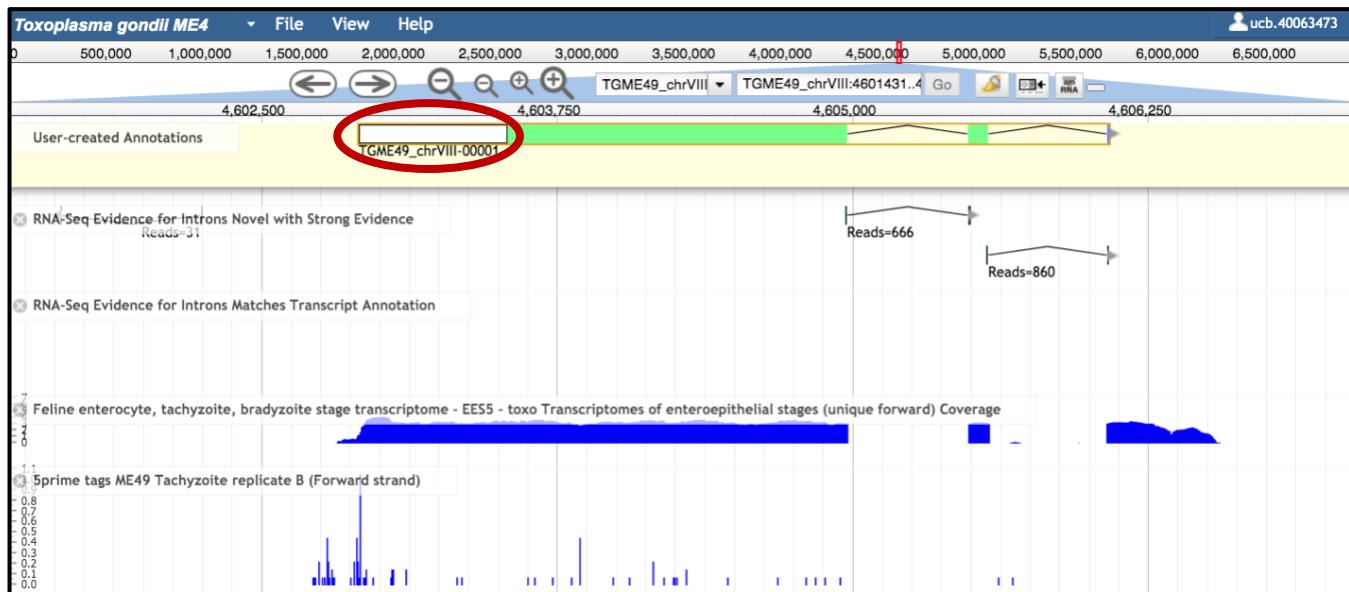
Hold down the shift key and select the introns with strong evidence (1), drag and drop them into the User-created Annotations track (2).



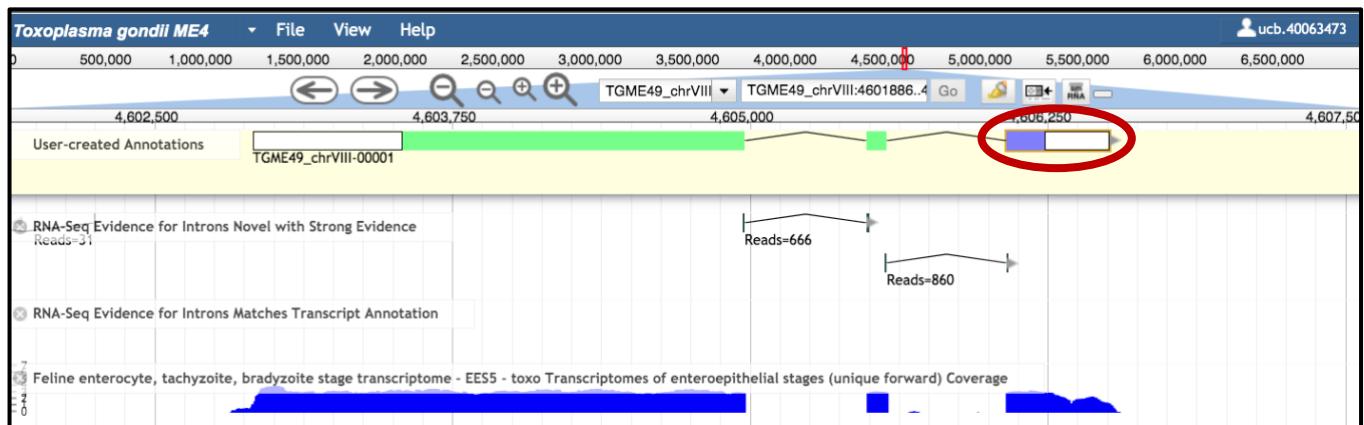
Zoom in by clicking on the + sign on the top (1). Press the Shift key and select the two small exons in the middle (2). With a right-click open the drop-down menu and choose **Merge** (3). Alternatively, select one of the exons you would like to merge, go to the edge of the feature until a little arrow appears and extend the exon until it overlaps with the second exon.



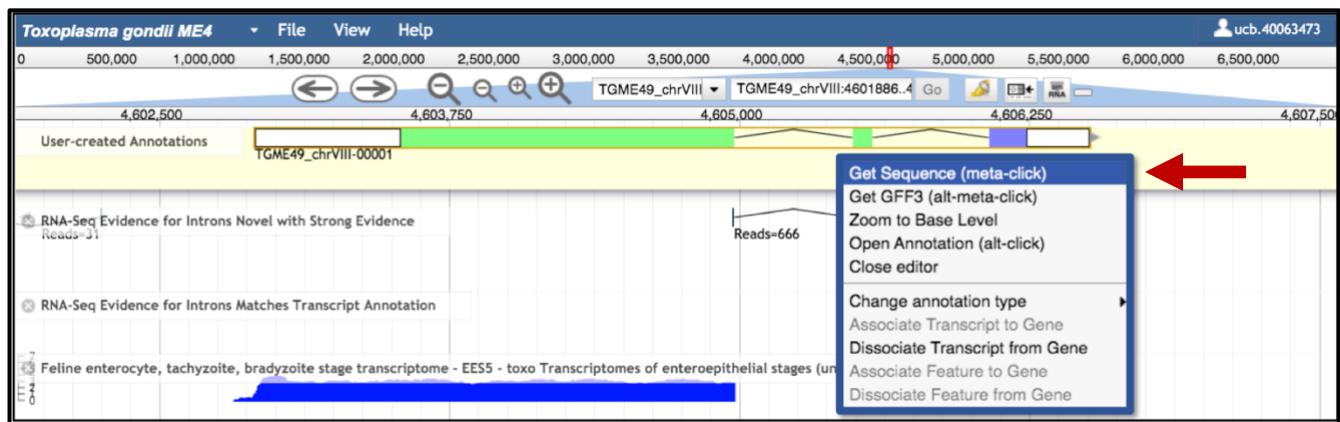
Select the first exon, point your mouse at the edge of the feature until a little arrow appears, then extend the exon to the transcription start. Apollo will automatically create the 5'UTR!



Select the last exon, point your mouse at the edge and extend the exon to the end of the gene model. Apollo will create the 3'UTR automatically!

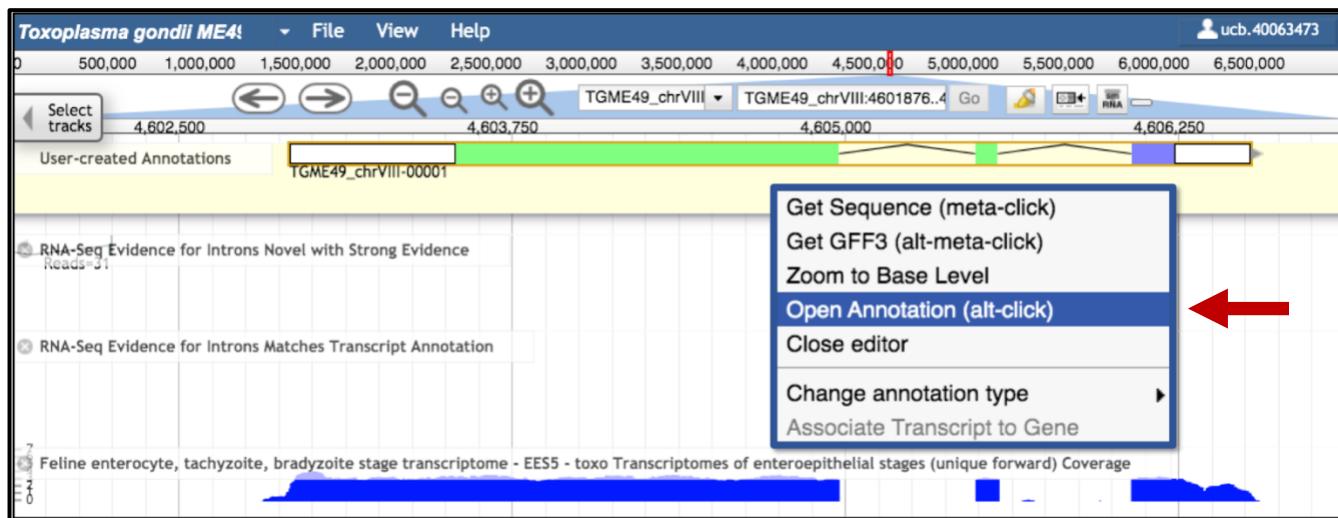


Select the new gene, with a right-click open the annotation drop-down menu and choose **Get Sequence**. Copy the sequence and run blast (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) and InterPro (<https://www.ebi.ac.uk/interpro>) to get additional information about the new gene.

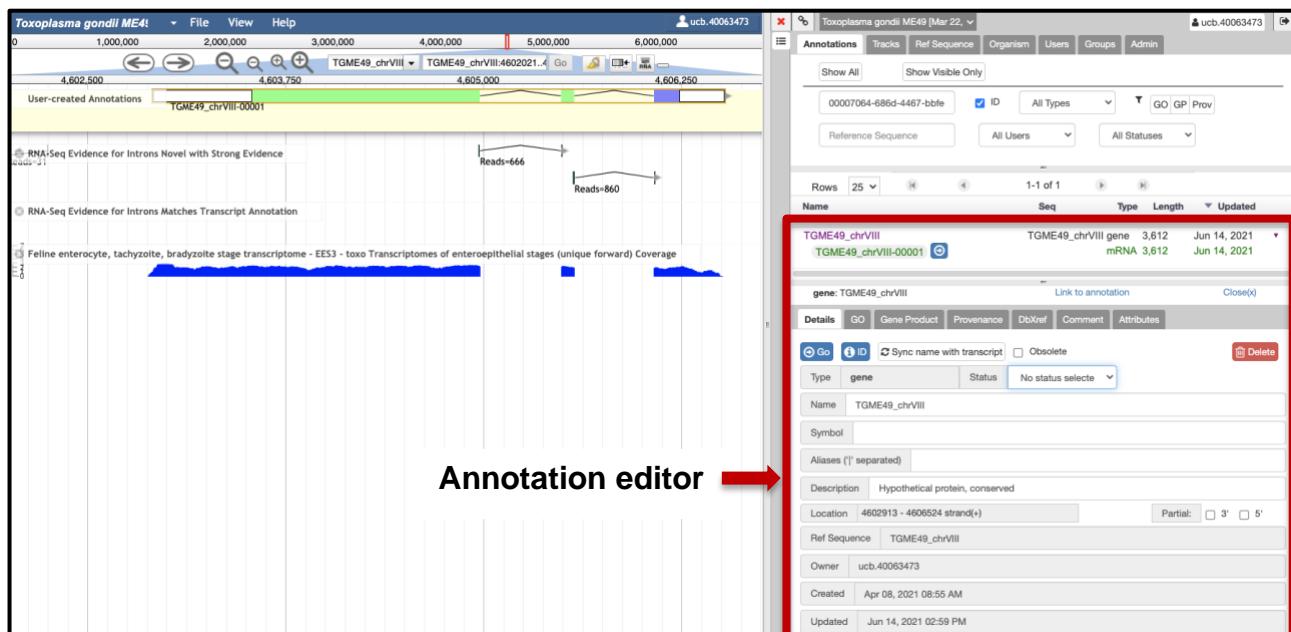


5) Opening of the Annotation editor window

Select the gene in the User-created Annotation track and with a right-click open the drop-down menu and choose **Open Annotation**. Alternatively, you can use the short-cut **alt-click**.



The annotation editor window is now shown on the right-hand side.



6) Finalizing the structural annotation

Once the annotations panel is open click on the Attributes tab, select from the canned tag **structural** and from the canned value **new**. Click on the + sign.

The screenshot shows the Apollo annotations interface. At the top, the gene record is displayed: TGME49_chrVIII gene 3,603 mRNA 3,603 Apr 04, 2021. Below this, the 'Attributes' tab is selected. In the 'Value' input field, a dropdown menu is open, showing a list of canned values under the 'structural' tag. The 'new' option is highlighted with a blue background and a red arrow points to it from the right side of the screen.

Go to the Details tab, add a description/gene product to your new gene and select the status **Finished** on the gene. The following day, the new gene model will be visible on the gene record page in the Community annotations from Apollo track.

The screenshot shows the Apollo Details tab. The 'Status' field is currently set to 'No status selected'. A dropdown menu is open, showing four options: 'No status selected', 'Not Finished', 'Finished', and 'Requires Curator'. The 'Finished' option is highlighted with a blue background and a red arrow points to it from the right side of the screen.

Done! For additional questions, please get in touch with the VEuPathDB help desk.

Structural annotation in Apollo

Alternative transcripts

In this short tutorial we are showing you step-by-step how to create alternative transcripts in Apollo.

1) Accessing Apollo

To access Apollo go to the gene record page of your gene of interest and click on the link **View and update community annotations in Apollo (1)**. You can also access Apollo from the gene models section by clicking on the button **Annotate in Apollo (2)**. Alternatively, go to the **Tools** menu and choose Apollo from the drop-down list (3).

The screenshot shows the ToxoDB gene record page for TGME49_315160. At the top, there's a navigation bar with links for 'My Strategies', 'Searcher', 'Tools' (circled in red), 'My...', 'Data', 'About', 'Help', and 'Contact Us'. Below the navigation is a search bar and a 'Site search' input field. The main content area displays gene information: Type: protein coding gene; Chromosome: XI; Location: TGME49_chrXI:4,526,997..4,538,020(-); Species: *Toxoplasma gondii*; Strain: ME49; Status: Reference strain. It also shows 'Shortcuts' for Synteny, Alignments, Phenotype, SNPs, Transcriptomics, Protein Features, and Proteomics. A message says 'Also see TGME49_315160 in the Genome Browser or Protein Browser'. On the left, a sidebar lists sections like Gene models, Annotation, curation and identifiers, Link outs, Genomic Location, Literature, and Taxonomy. At the bottom right, there's a 'Collapse all sections for better performance' button. A red circle highlights the 'View and update community annotations in Apollo' link. A red box highlights the 'Tools' menu item. A red box highlights the 'Annotate in Apollo' button.

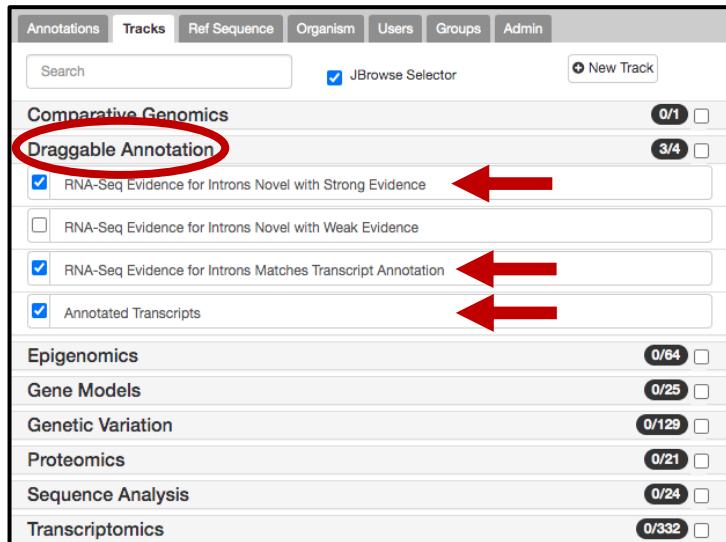
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

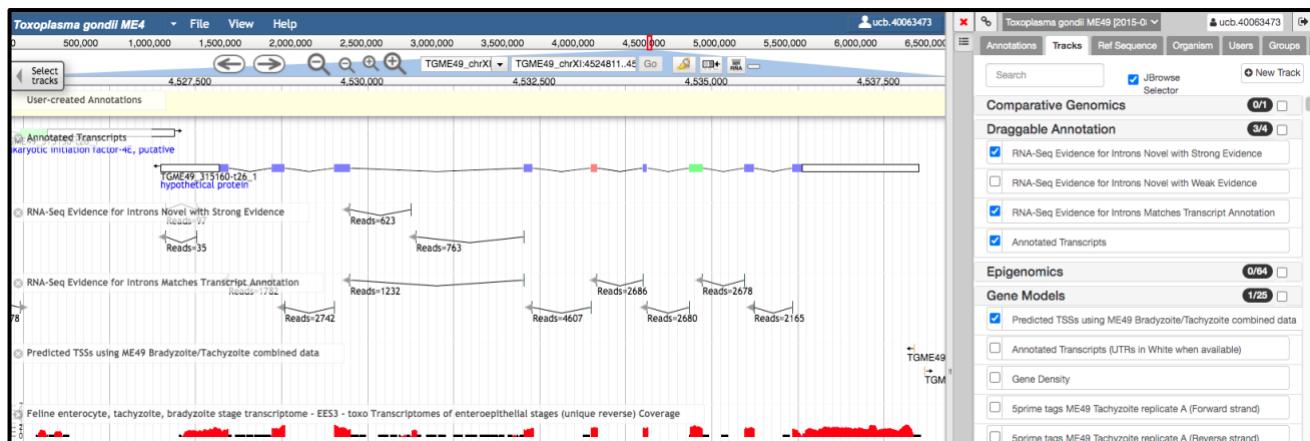
Select on the right-hand side the tab **Tracks**.

The screenshot shows the JBrowse genome browser interface for *Toxoplasma gondii* ME49. The top navigation bar includes 'File', 'View', 'Help', and a user account icon. The main area shows a genomic track for chromosome X, with coordinates 0 to 6,000,000. A red box highlights the 'Tracks' tab in the top right corner of the interface. The 'Tracks' tab panel contains a search bar, a 'JBrowse Selector' checkbox, and two sections: 'Comparative Genomics' (0/1) and 'Draggable Annotation' (0/4).

Click on the menu item **Draggable Annotation** select **Annotated Transcripts, RNA-Seq Evidence for Introns Novel with Strong Evidence and RNA-Seq Evidence for Introns Matches Transcript Annotation**.

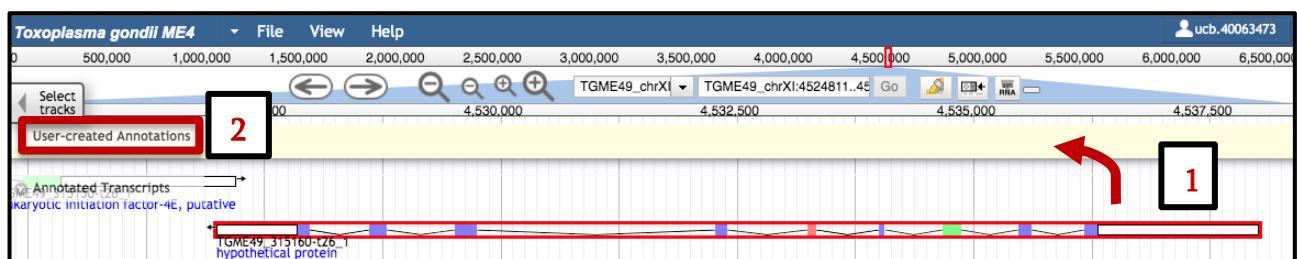


Select additional evidence, i.e. RNAseq plots and predicted TSS (transcription start sites).

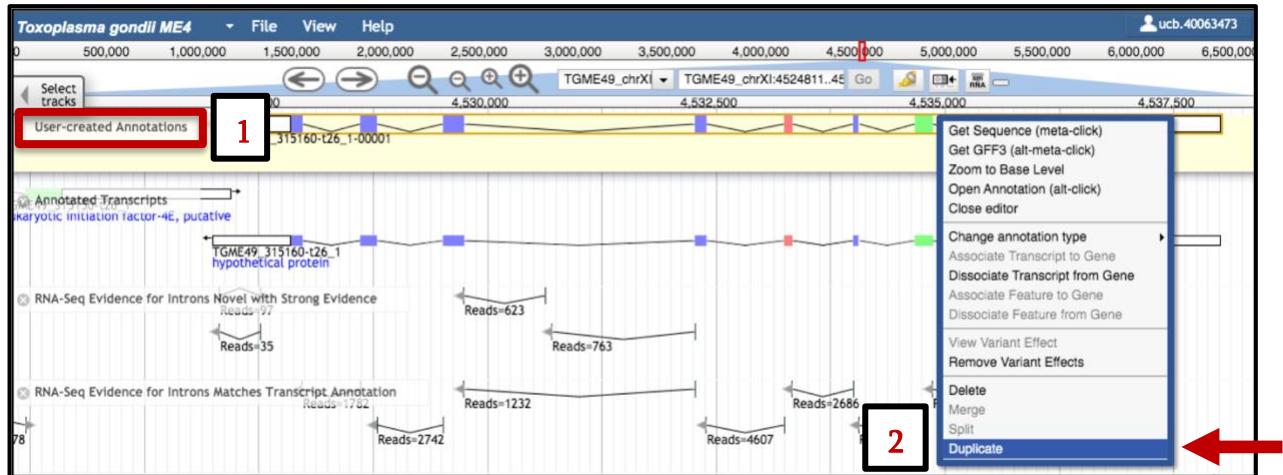


3) Adding alternative transcripts

Select the gene model by clicking on one of the introns or by double clicking on the gene model (1). The gene will show up with red boundaries. Drag and drop the gene into the User-created Annotations track (2). **Please note:** To add one-exon genes into the User-created Annotations area you need to **double-click** on the gene and then drag it into the user-created annotations area.

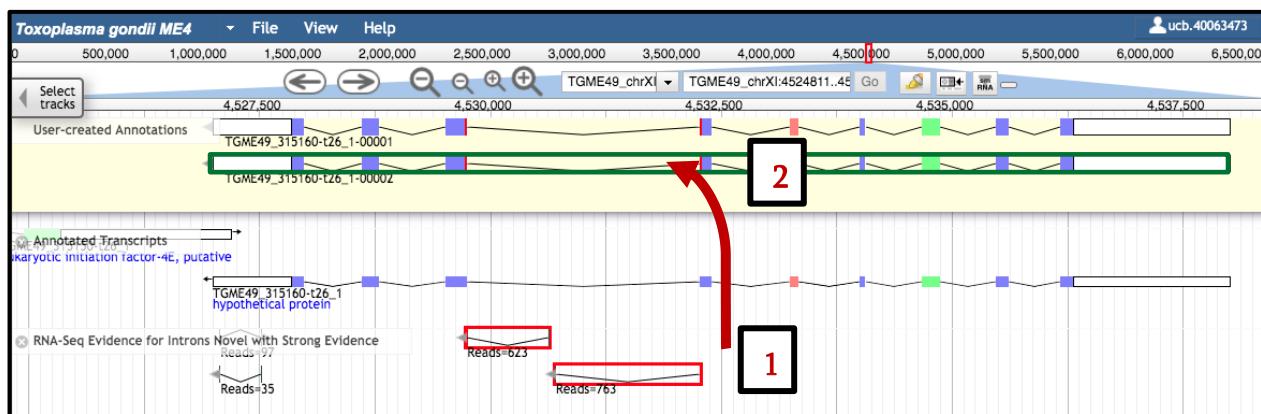


Select the gene in the User-created Annotations area (1). With a right-click open the annotation drop-down menu and choose duplicate (2).

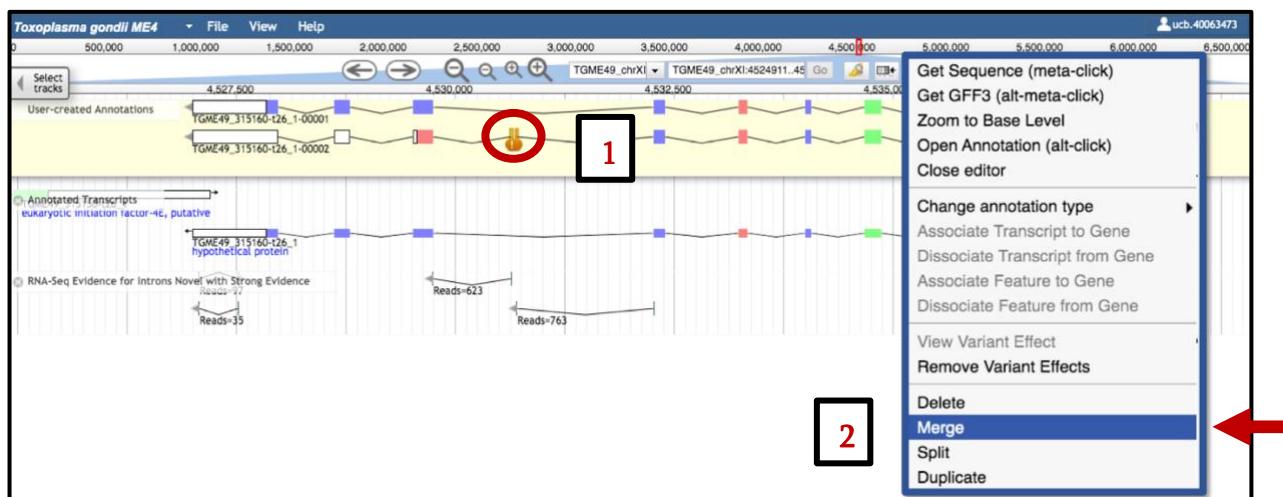


4) Modifying the alternative transcript

Select the intron junctions individually, or hold down the shift key and select both intron junctions with strong evidence (1), drag and drop them into the gene model (2). The gene will get a green box when dragging and dropping the intron evidence.

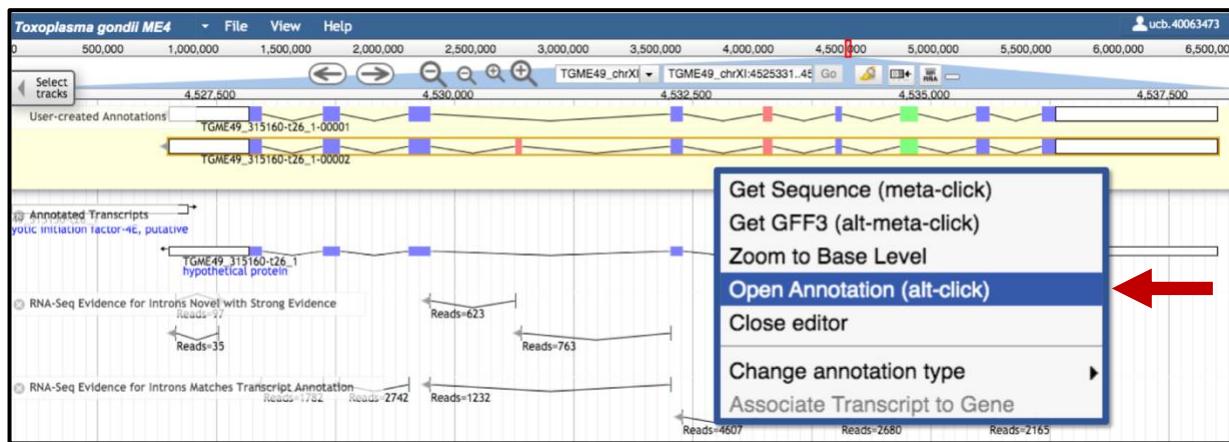


Hold down the shift key and select the two small exons. With a right-click open the drop-down menu and select merge.

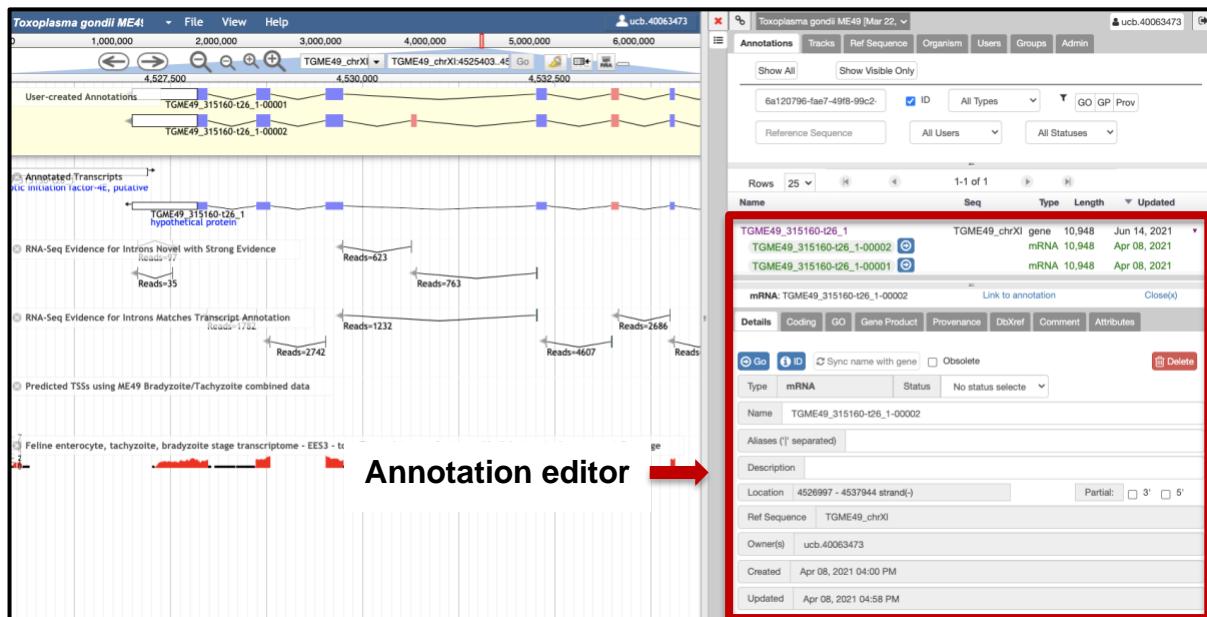


5) Opening of the Annotation editor window

Select one of the transcripts in the User-created Annotation track, with a right-click open the drop-down menu and choose **Open Annotation**. Alternatively, you can use the short-cut **alt-click**.

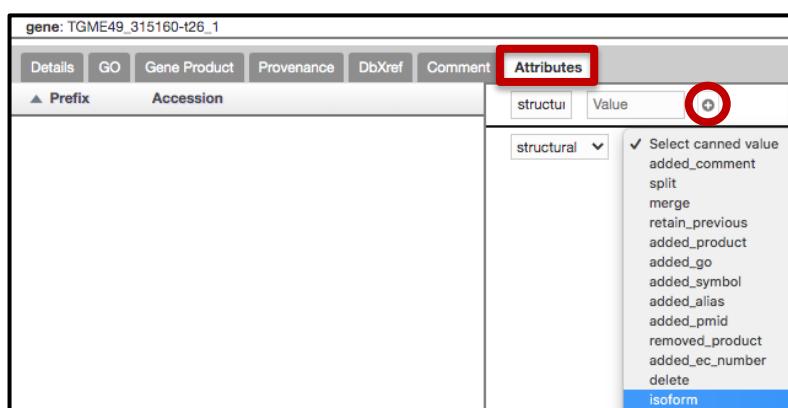


The annotation editor window is now shown on the right-hand side.



6) Finalizing the structural annotation

Once the annotations panel is open click on the Attributes tab, select from the canned tag **structural** and from the canned value **isoform**. Click on the + sign.



Go to the Details tab and select the status **Finished**. The following day, the alternative transcript will be visible on the gene record page in the Community annotations from Apollo track.

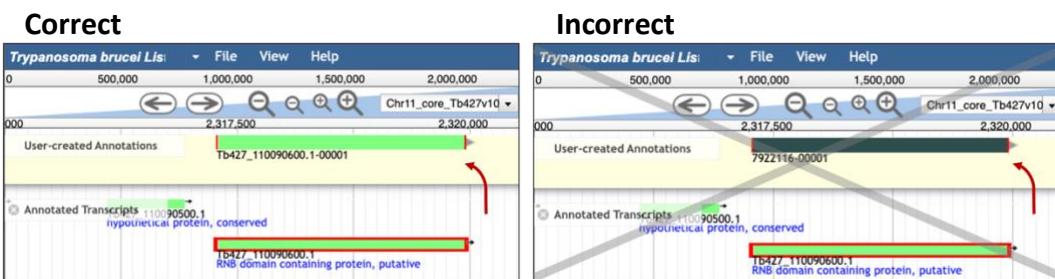
The screenshot shows the 'Details' tab selected in the gene record interface. A dropdown menu is open under the 'Status' field, listing four options: 'No status selected' (unchecked), 'Not Finished' (unchecked), 'Finished' (selected and highlighted in blue), and 'Requires Curator' (unchecked). A red arrow points to the 'Finished' option. The gene record includes fields for Type (gene), Name (TGME49_315160-t26_1), Symbol, Aliases, Description, Location (4526996 - 4538020 strand(-)), Ref Sequence (TGME49_chrXI), Owner (ucb.40063473), Created (Apr 08, 2021 03:51 PM), and Updated (Apr 08, 2021 04:00 PM).

Done! For additional questions, please get in touch with the VEuPathDB help desk.

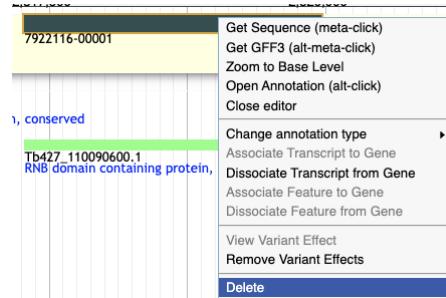
Possible problems

1) Problem with single exon genes

If your gene is a single exon gene, you need to double-click on the gene. Once you see the red border drag the gene into the pale-yellow User-created Annotations track. The gene model should have a red, green or blue colour indicating the different frames. Pseudogenes are shown with the colour blue, ncRNAs with the colour green. The gene in the User-created Annotation track should not be shown as a grey box.

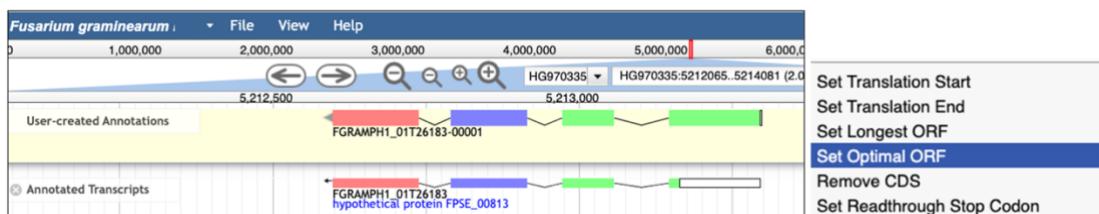


If you see a grey box when you are trying to drag a single exon gene, you need to delete it and try again. Select the grey box. With a right-click open the menu and choose Delete.

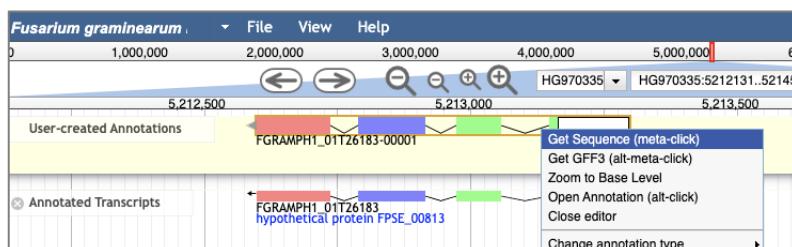


2) Missing start codon

When adding the gene model into the user-created annotations area, Apollo sometimes modifies the gene so that the start codon is lost. To correct this, use the option **Set Optimal ORF** from the right-click menu. This option will automatically create the longest ORF.



Open the menu with a right-click and select the option **Get Sequence** to recheck if your gene starts with the correct start codon.



A new window will open with the sequence. You can copy the sequence to the clipboard for further analysis.

