

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 green header with the ToxoDB logo, release information (Release 51, 16 Mar 2021), and a search bar. Below the header, there are links for 'My Strategies', 'Searcher', 'Tools' (circled with a red box and labeled 3), 'Gene', 'Data', 'About', 'Help', and 'Contact Us'. On the far right, there are social media icons and a 'Guest' 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. Below this, there's a section for user comments ('Add the first user comment') and a link to 'View and update community annotations in Apollo' (circled with a red box and labeled 1). Further down, 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'. At the bottom, there's a 'Gene models' section (labeled 2) with a table showing 13 exons and 1 transcript. A note says 'This gene is available in Apollo for community annotation. To find out more about Apollo, please visit this help page.' There are buttons for 'View in JBrowse genome browser' and 'Annotate in Apollo' (circled with a red box and labeled 2). A collapse all button is at the bottom right.

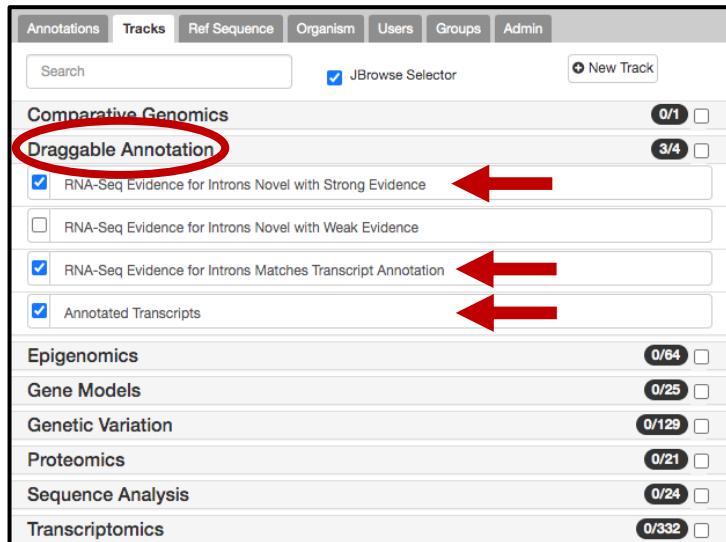
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

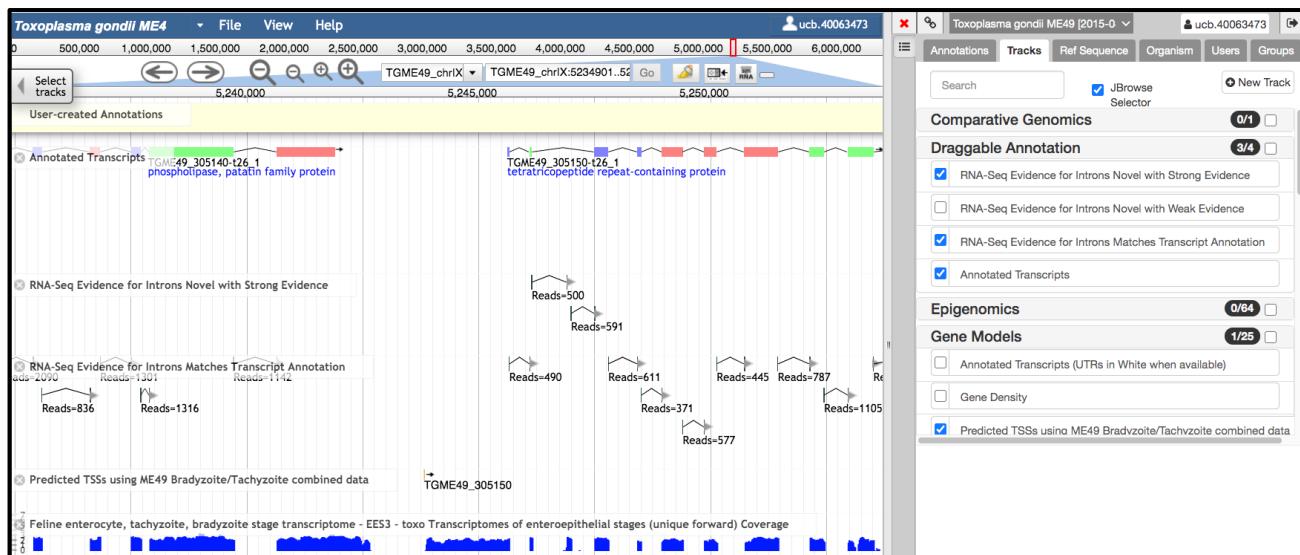
Select on the right-hand side the tab **Tracks**.

The screenshot shows the JBrowse interface for the Toxoplasma gondii ME49 genome. At the top, there's a navigation bar with 'File', 'View', 'Help', and a user ID 'ucb.40063473'. Below the navigation bar is a genomic track viewer showing chromosome chrlX with coordinates 0 to 6,000,000. A red box highlights the 'Tracks' tab (labeled 1). To the left of the tracks, there's a 'User-created Annotations' track. On the right, there's a panel with tabs for 'Annotations' (selected), 'Ref Sequence', 'Organism', 'Users', 'Groups', and 'Admin'. The 'Annotations' panel contains a 'Search' field, a 'JBrowse Selector' checkbox, and sections for 'Comparative Genomics' (0/1) and 'Draggable Annotation' (0/4). A 'New Track' button is also present.

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.**

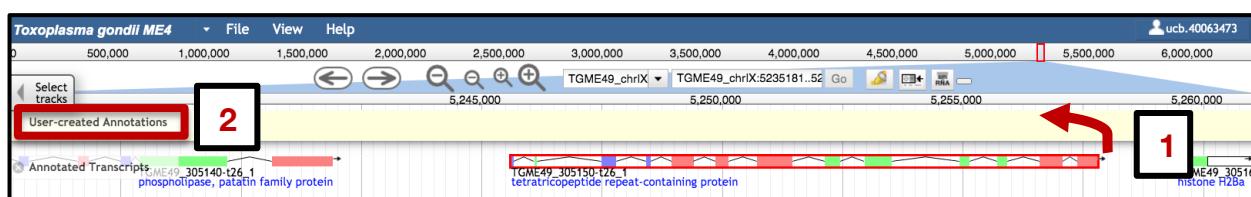


Select additional evidence, i.e. RNAseq plots or predicted TSS (transcription start sites).

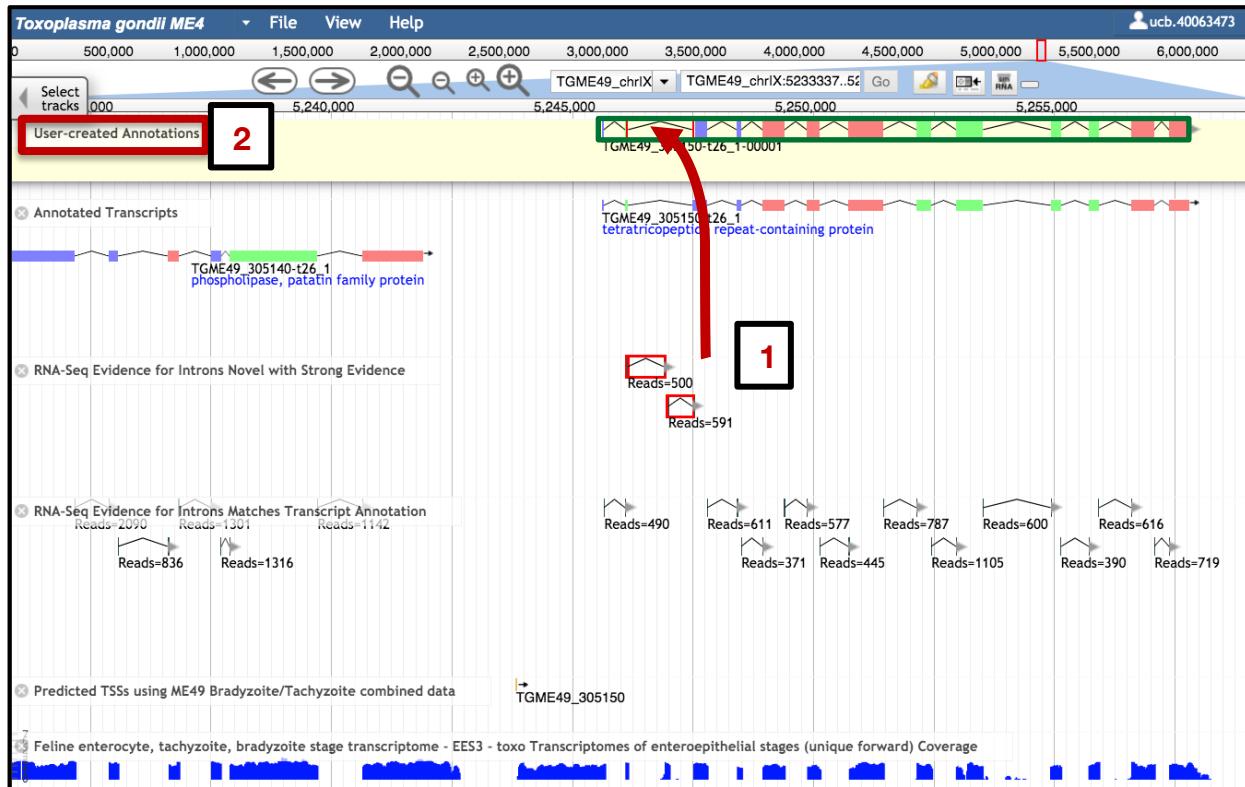


3) Modifying the gene

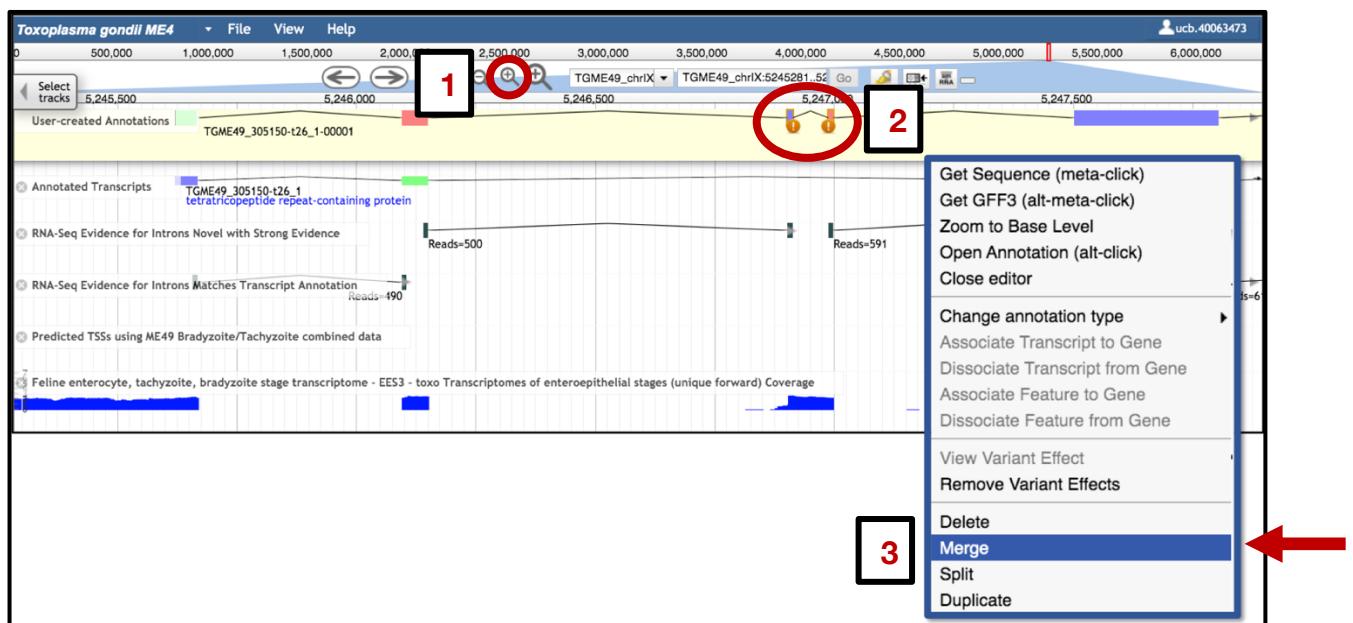
Select the gene model by clicking on one of the introns or by double clicking on the gene model (1). The gene model will show up with red boundaries. Drag and drop the gene into the User-created Annotations track (2).



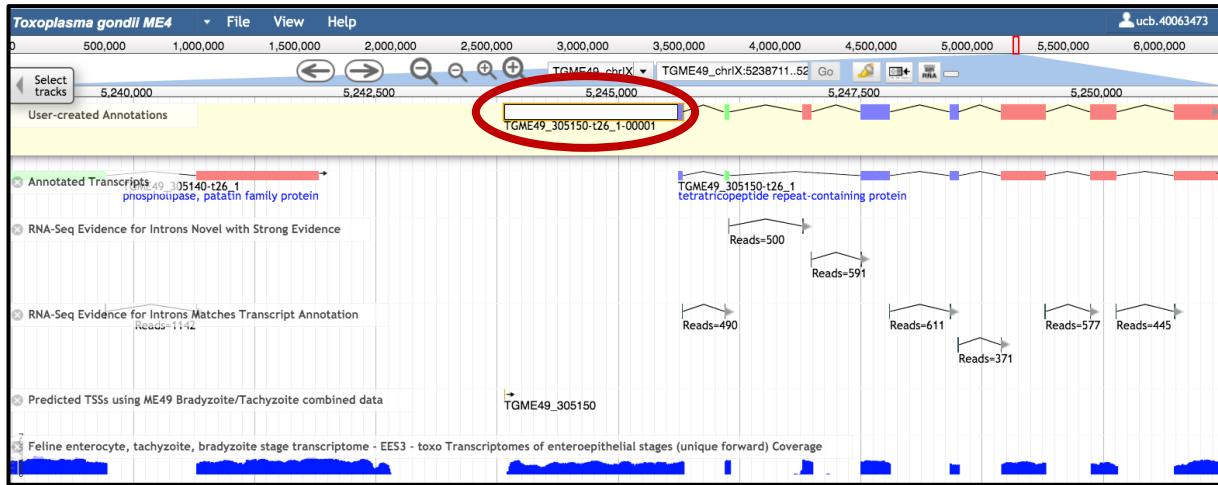
You can either select the intron junctions individually, or hold down the shift key and select both intron junctions with strong evidence (1), drag and drop them into the gene model (2). The gene will get a green box when dragging and dropping the intron evidence.



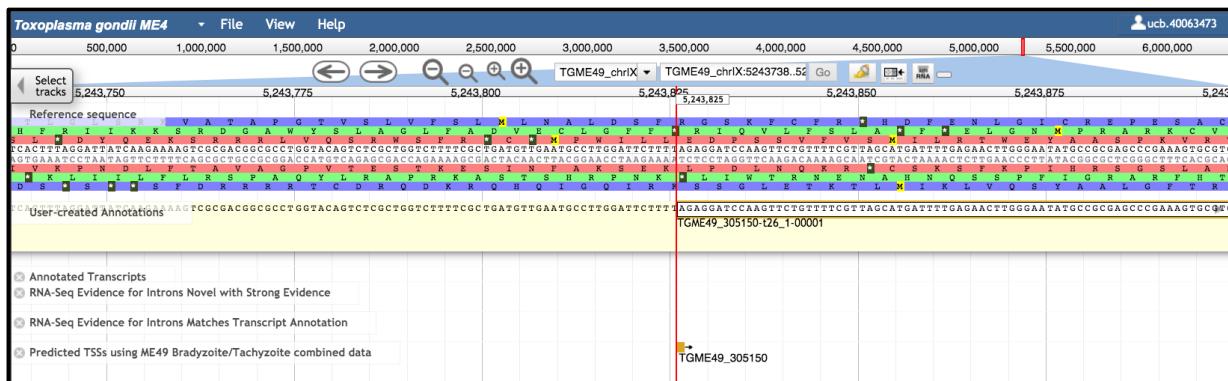
Zoom in by clicking on the + sign on the top (1). Press the Shift key and select the two small exons in the middle (2). With a right-click open the drop-down menu and choose **Merge** (3). Alternatively, select one of the exons you would like to merge, go to the edge of the feature until a little arrow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



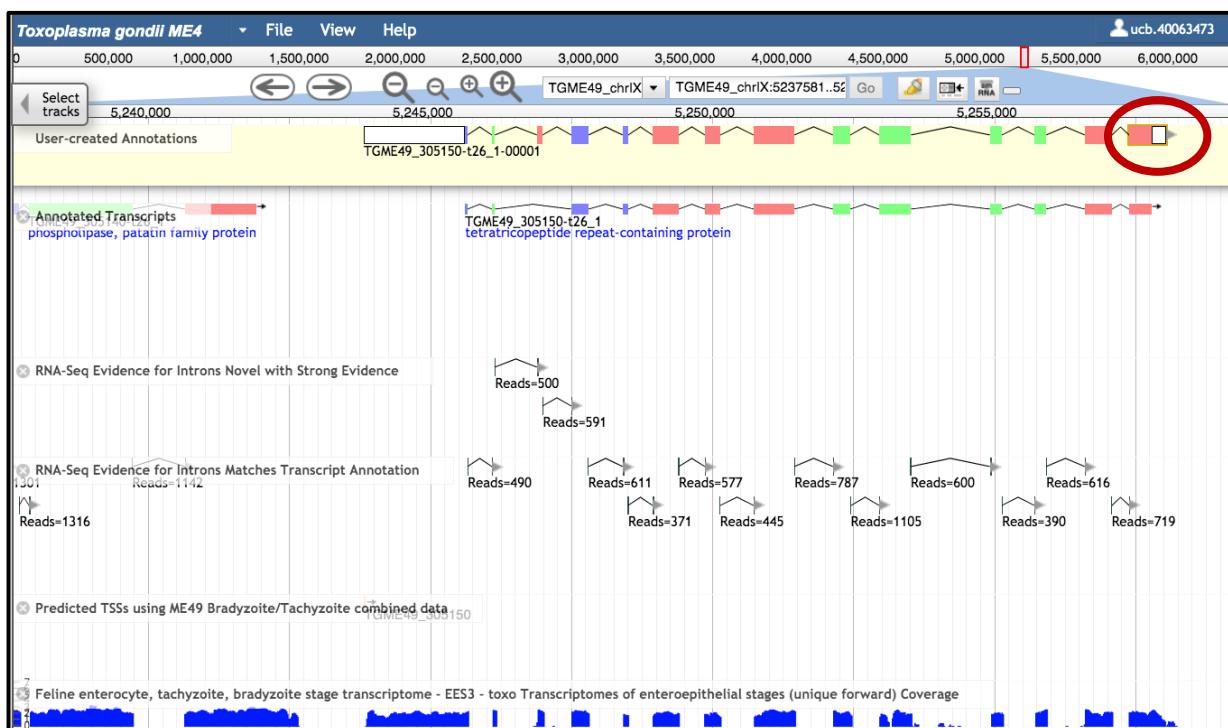
Select the first exon, point your mouse at the edge of the feature, a little arrow will appear, then extend the exon to the transcription start. Apollo will automatically create the 5'UTR!



You can zoom in to recheck the transcription start site.

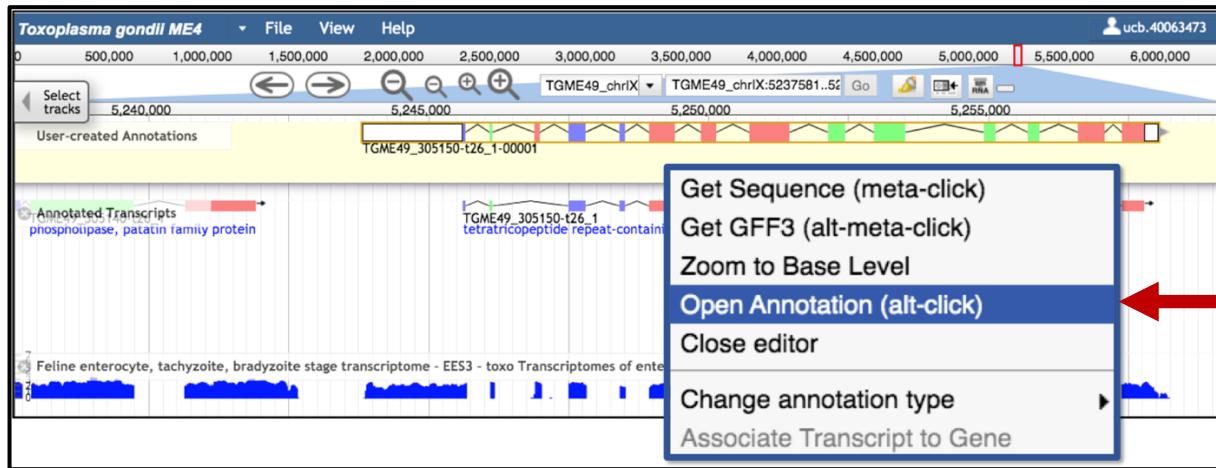


Select the last exon, point your mouse at the edge and extend the exon. Apollo will create the 3'UTR automatically!

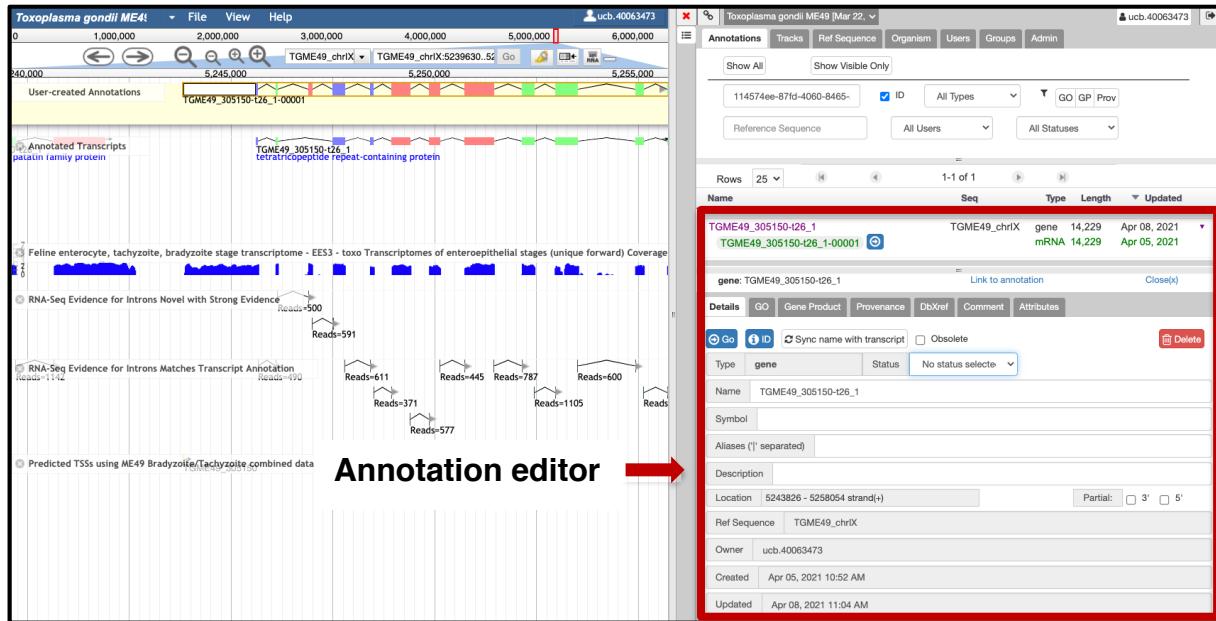


4) Opening of the Annotation editor window

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) Finalising 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.

The screenshot shows the VEuPathDB gene editor interface. The top navigation bar includes tabs for Details, GO, Gene Product, Provenance, DbXref, Comment, and Attributes. The Attributes tab is highlighted with a red box. Below the tabs is a table with two rows: Prefix (Accession) and Value. The Value row has a 'structural' dropdown and a '+' sign button. To the right is a dropdown menu listing various actions like 'Select canned value', 'added_comment', etc., with 'modify' highlighted by a red arrow.

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.

This screenshot shows the VEuPathDB gene editor with the Attributes tab selected. The table structure is identical to the previous one, with 'structural' and 'annotation' in the Prefix row and 'new' and 'retain_previous' in the Value row. The 'annotation' dropdown is highlighted with a red box, and a red arrow points to the 'retain_prev' dropdown.

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

This screenshot shows the VEuPathDB gene editor with the Details tab selected. The 'Status' field is open, showing a dropdown menu with options: 'No status selected', 'Not Finished', 'Finished' (which is highlighted with a red box and a red arrow), and 'Requires Curator'.

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. The top navigation bar includes links for My Strategies, Searcher, Tools (circled in red), My Works, Data, About, Help, and Contact Us. A guest user is logged in. Below the navigation is a search bar and a green banner for VEuPathDB. The main content area displays 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. A red circle highlights the "View and update community annotations in Apollo" link. A red box highlights the "Annotate in Apollo" button in the gene models section. A white box highlights the "Tools" menu item in the top navigation bar. The gene models section shows 1 Gene models, 9 Exons in Gene, 1 Transcript, and a note about Apollo community annotation. The right side features a "Shortcuts" panel with links to Synteny, Alignments, Phenotype, SNPs, Transcriptomics, Protein Features, and Proteomics.

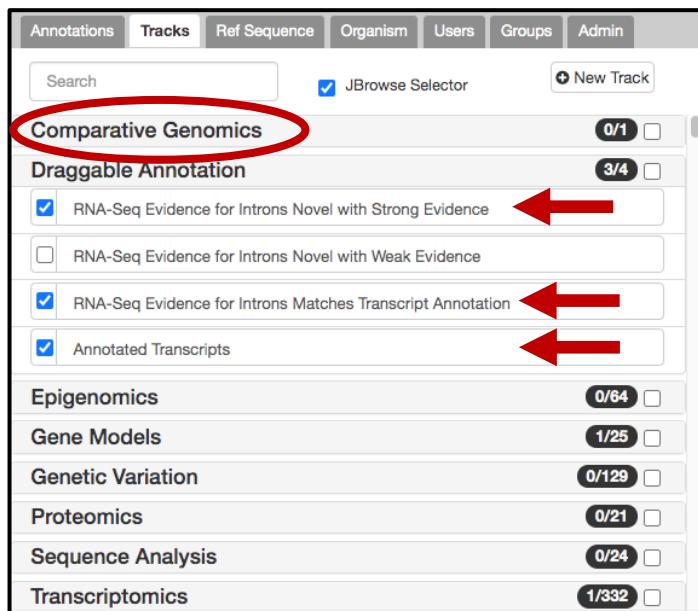
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

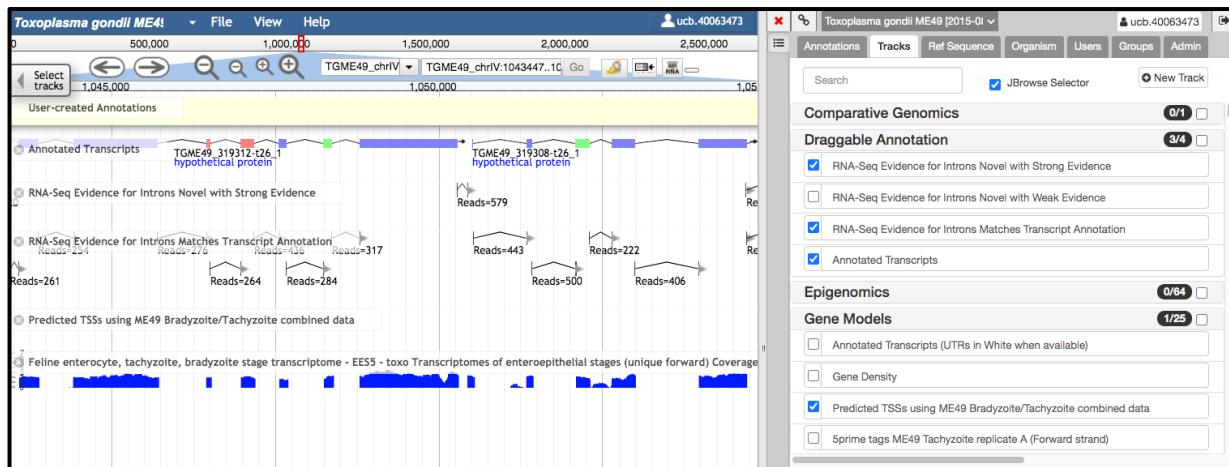
Select on the right-hand side the tab **Tracks**.



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**.

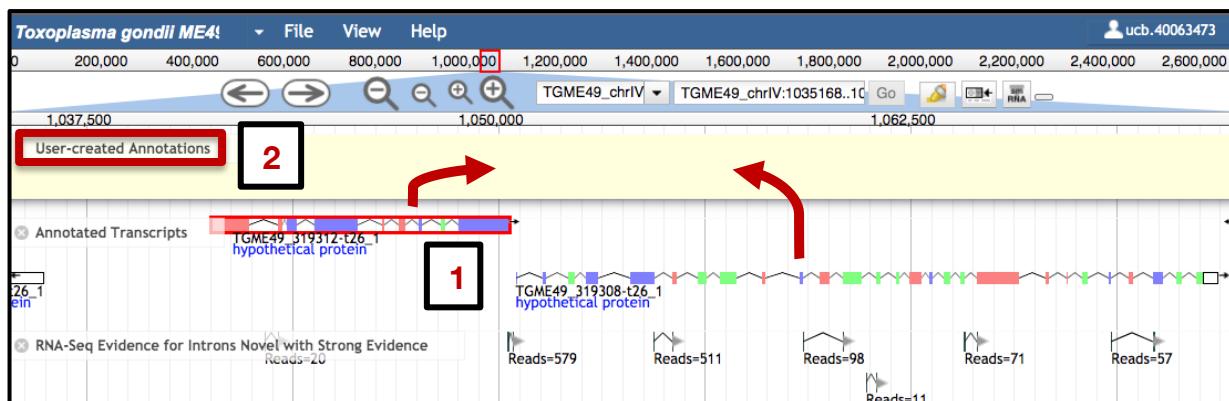


Select additional evidence, i.e. RNAseq plots and predicted TSS (transcription start sites).

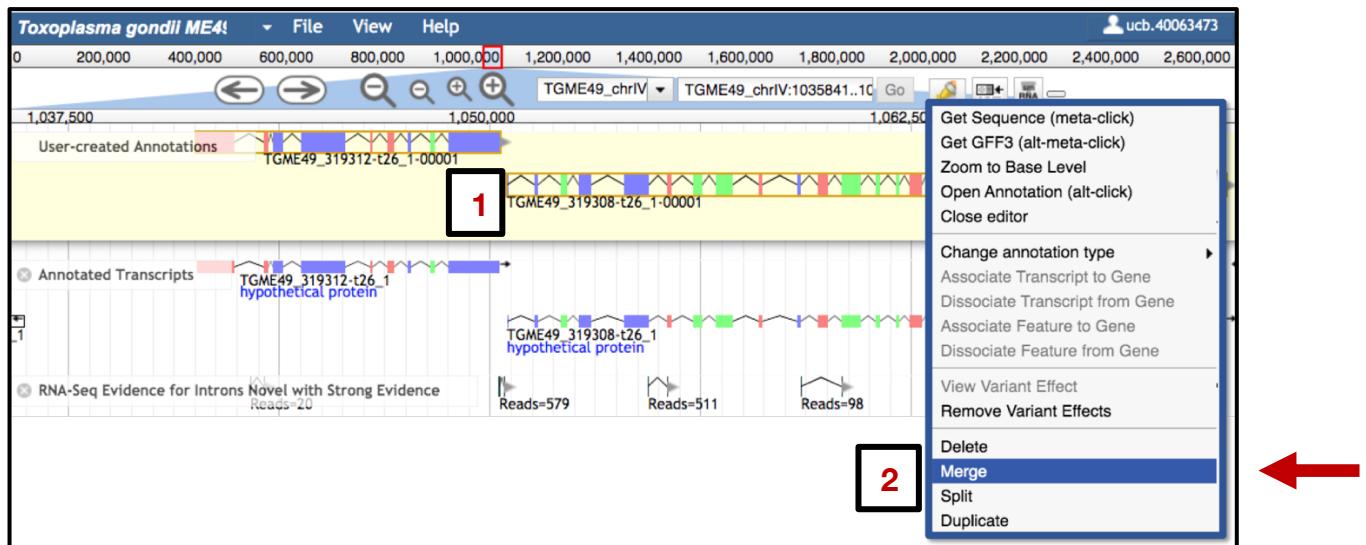


3) Merging genes

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).

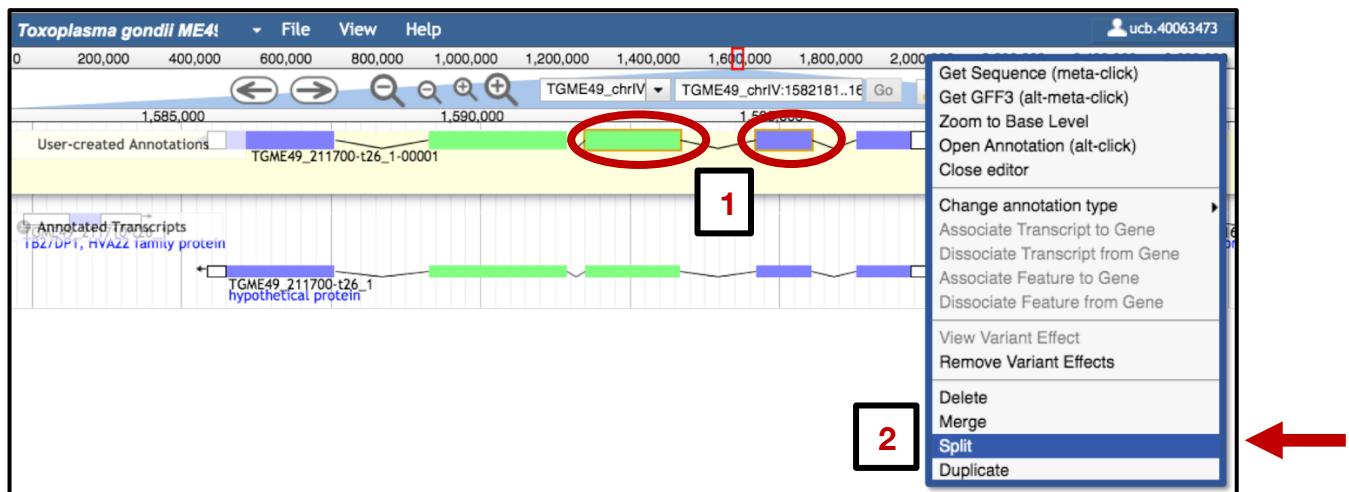


Hold down the shift key and select both gene models in the User-created Annotations track (1). With a right-click open the drop-down menu and choose **Merge** (2).



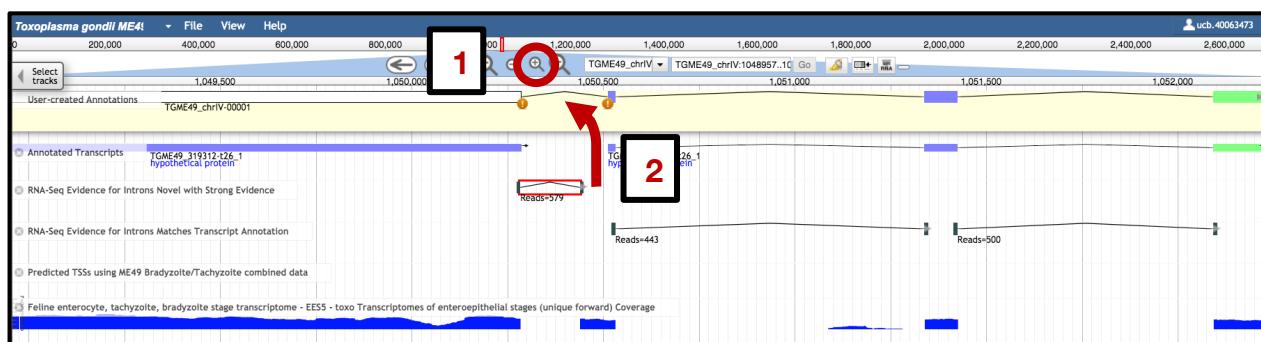
3.1) Splitting gene models

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.

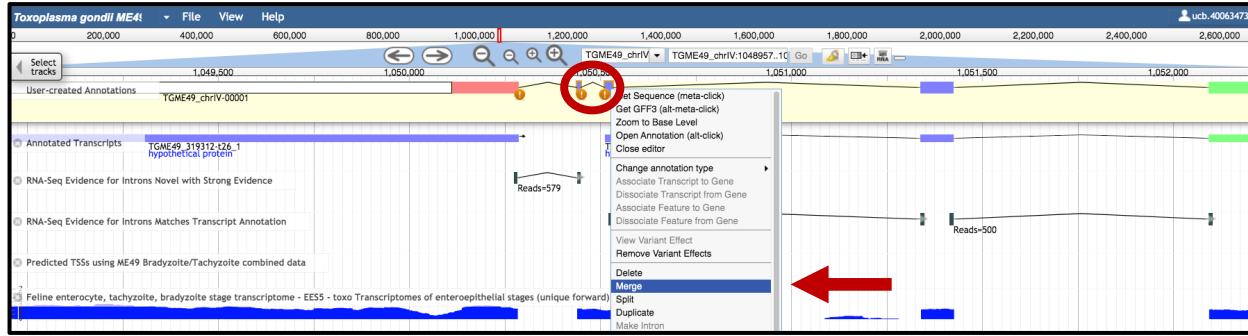


4) Correcting intron-exon boundaries

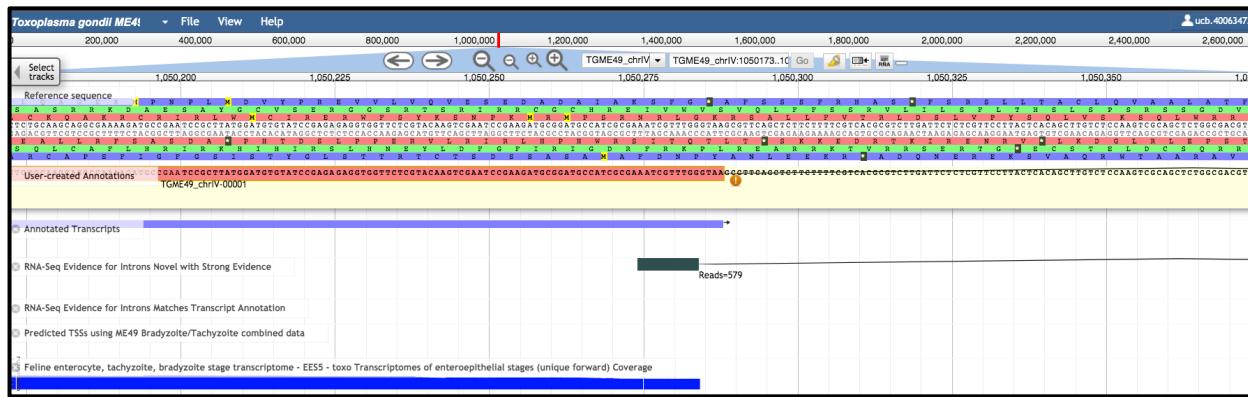
Once you've merged the gene zoom in by clicking on the + sign on the top (1). Select the new splice junction and drag it into the gene model (2).



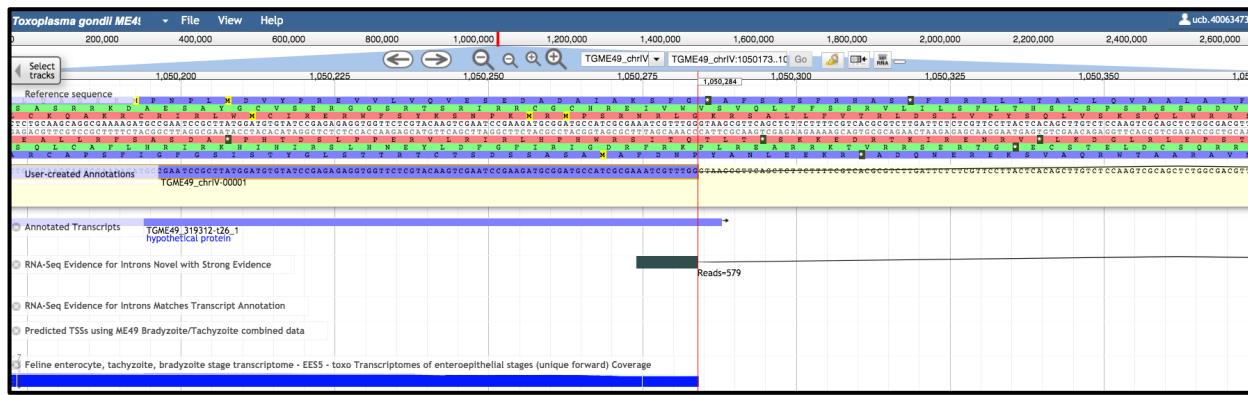
Hold down the shift key and select the two small exons. With a right-click open the drop-down menu and select merge. Hint: The exclamation mark tells you that there are non-canonical splice sites.



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

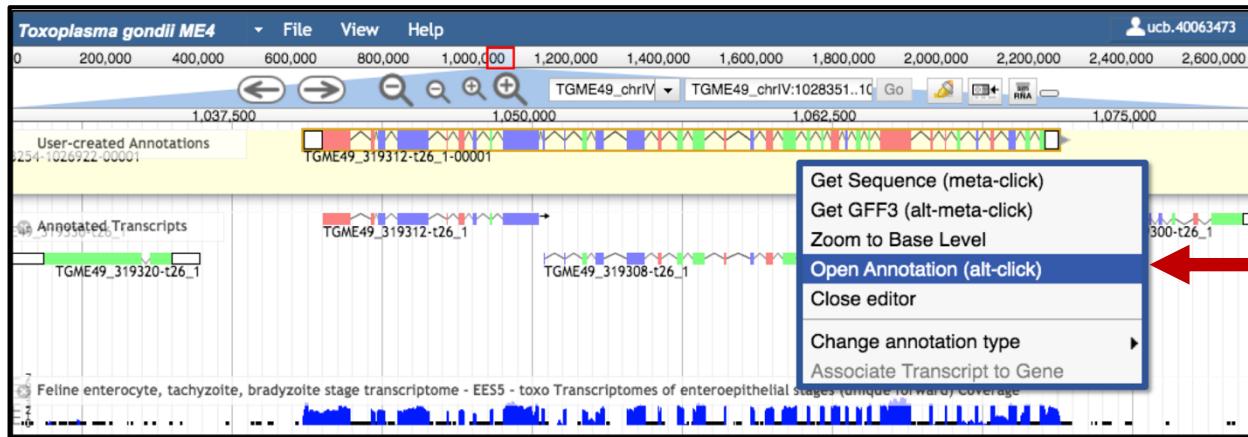


Shorten the exon to the correct splice site.

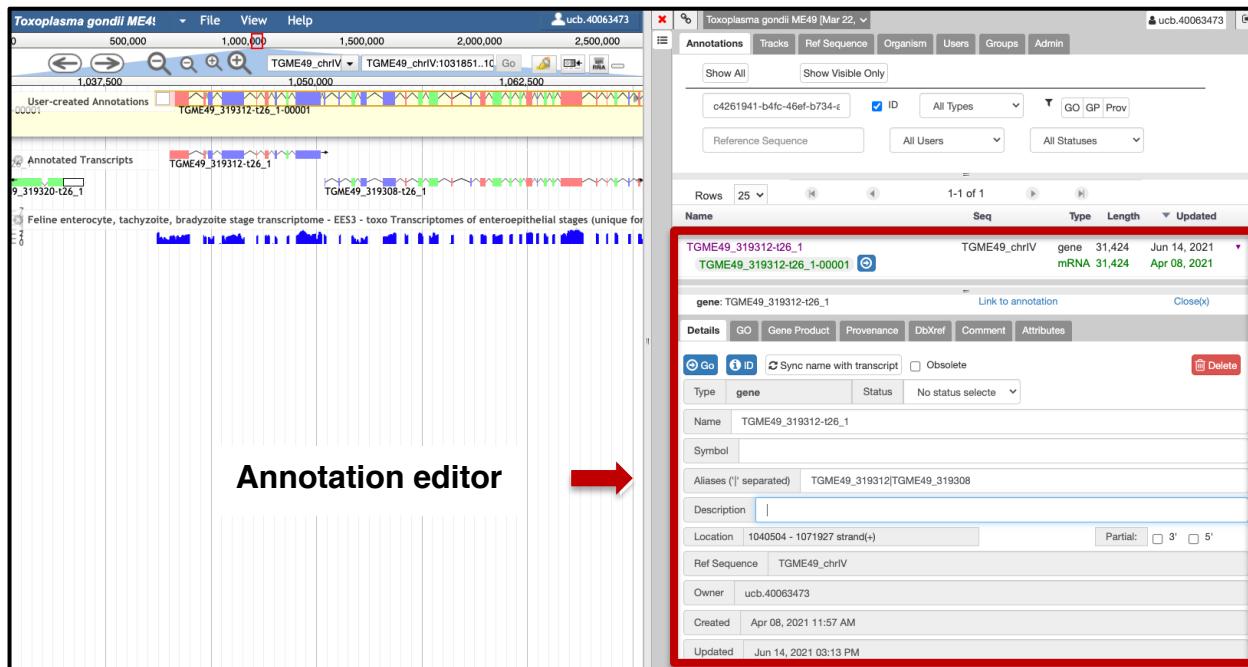


5) Opening of the Annotation editor window

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**.

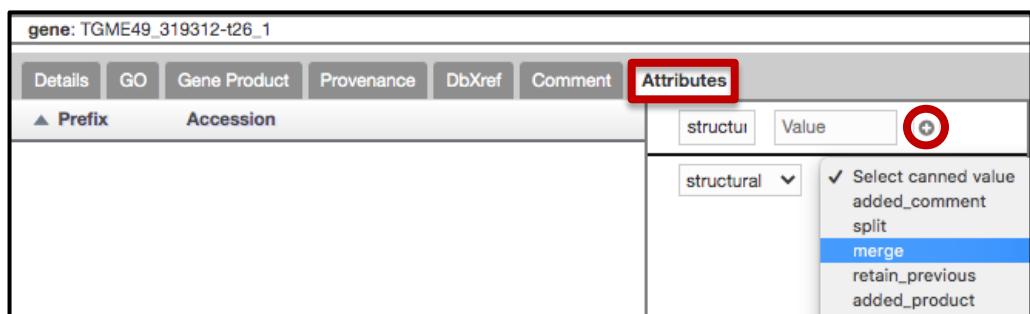


The annotation editor window is now shown on the right-hand side.



6) Finalising 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.

The screenshot shows the 'Details' tab selected in the top navigation bar. The 'Aliases ('|' separated)' field contains 'TGME49_319308|TGME49_319312'. A red arrow points to this field.

TGME49_319312-t26_1		TGME49_chrlV	gene	30,508	Apr 08, 2021
TGME49_319312-t26_1-00001		mRNA	30,508	Apr 08, 2021	▼
gene: TGME49_319312-t26_1					
Details GO Gene Product Provenance DbXref Comment Attributes					
+ Go ID Delete					
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_chrlV				
Owner	ucb.40063473				
Created	Apr 08, 2021 11:57 AM				
Updated	Apr 08, 2021 11:57 AM				

To finalise the annotation select the status **Finished** on the gene.

The screenshot shows the 'Details' tab selected. The 'Status' dropdown menu is open, showing 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.

TGME49_319312-t26_1		TGME49_chrlV	gene	30,508	Apr 08, 2021
TGME49_319312-t26_1-00001		mRNA	30,508	Apr 08, 2021	▼
gene: TGME49_319312-t26_1					
Details GO Gene Product Provenance DbXref Comment Attributes					
+ Go ID Delete					
Type	gene	Status	✓ No status selected		
Name	TGME49_319312-t26_1				
Symbol					
Aliases (' ' separated)	TGME49_319312 TGME49_319308				
Description	Hypothetical protein, conserved				
Location	1041309 - 1071817 strand(+)				
Ref Sequence	TGME49_chrlV				
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.

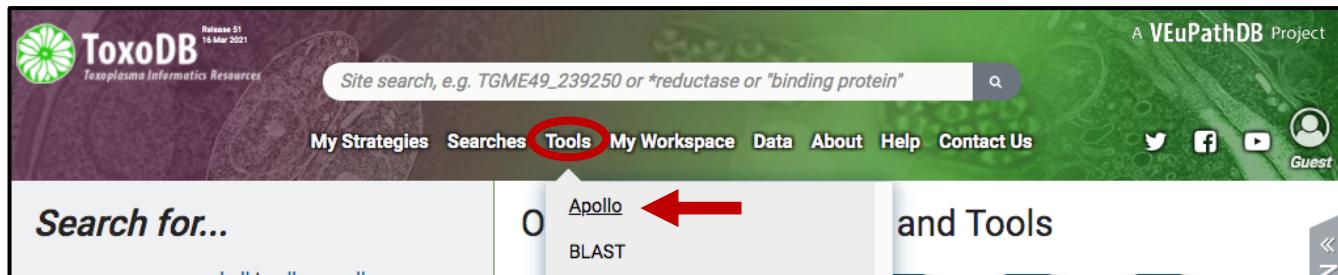
Structural annotation in Apollo

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**.

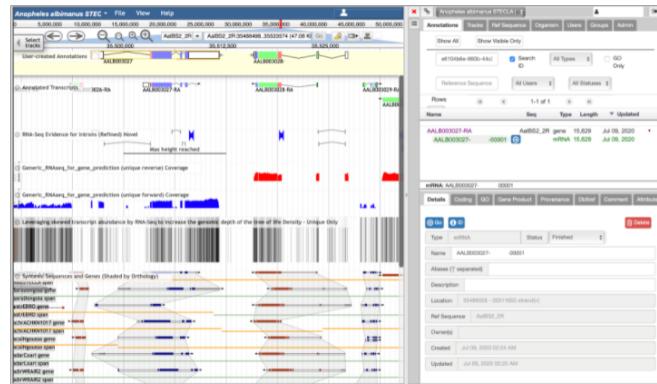
Structural and functional community curation in Apollo

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).

The screenshot shows the JBrowse interface for *Toxoplasma gondii* ME4. On the left, a dropdown menu is open under 'Annotations' with various tracks listed. A red box labeled '2' highlights the track 'TGME49_chrVII'. On the right, another dropdown menu is open under 'Annotations' with the genome 'Toxoplasma gondii ME49 [2015-0]' selected. A red box labeled '1' highlights this selection. The main genome browser window shows a genomic track for chromosome VII.

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).

The screenshot shows the JBrowse interface for *Toxoplasma gondii* ME4. A red box labeled '1' highlights the search bar at the top where 'TGME49_chrVII' is typed. A red box labeled '2' highlights the coordinate range '6,925,000' to '6,950,000' in the main genome browser window. The right panel shows the genome selection dropdown again.

3) Adding draggable annotation and supporting evidence

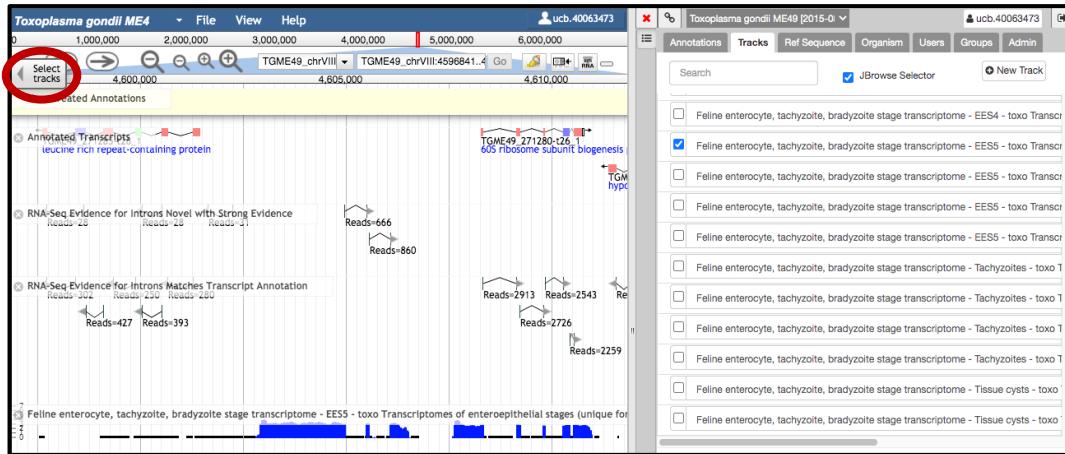
Select on the right-hand side the tab **Tracks**.

The screenshot shows the JBrowse interface for *Toxoplasma gondii* ME4. The 'Tracks' tab is highlighted with a red box. The right panel lists several annotation categories: Comparative Genomics (0/1), Draggable Annotation (0/4), Epigenomics (0/64), and Gene Models (0/25). The 'Draggable Annotation' section is circled in red.

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**.

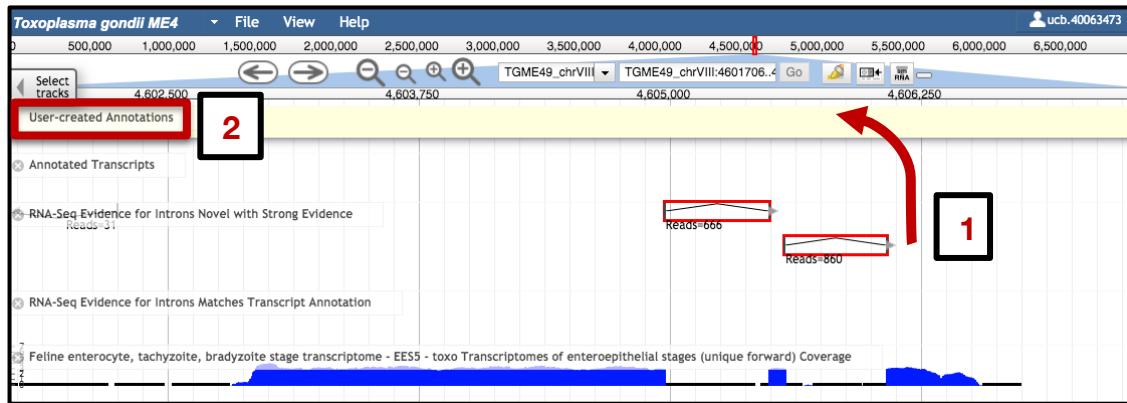
The screenshot shows the JBrowse 'Tracks' tab with the 'Draggable Annotation' section circled in red. Three checkboxes are selected with red arrows pointing to them: 'RNA-Seq Evidence for Introns Novel with Strong Evidence', 'RNA-Seq Evidence for Introns Matches Transcript Annotation', and 'Annotated Transcripts'. Other sections like 'Comparative Genomics', 'Epigenomics', 'Gene Models', etc., are also visible.

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**.

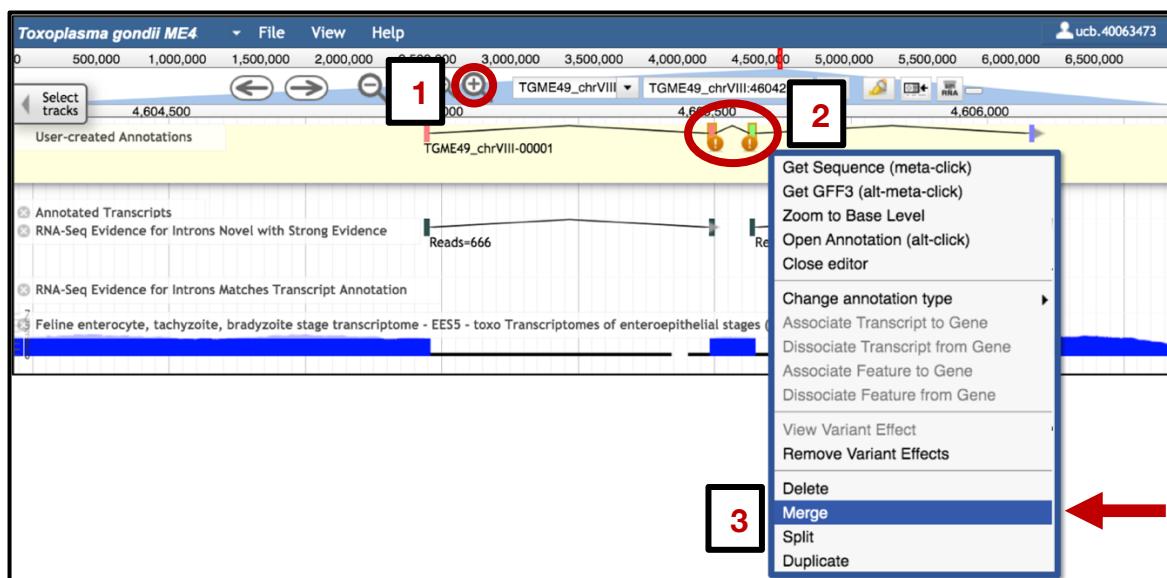


4) Building the new gene

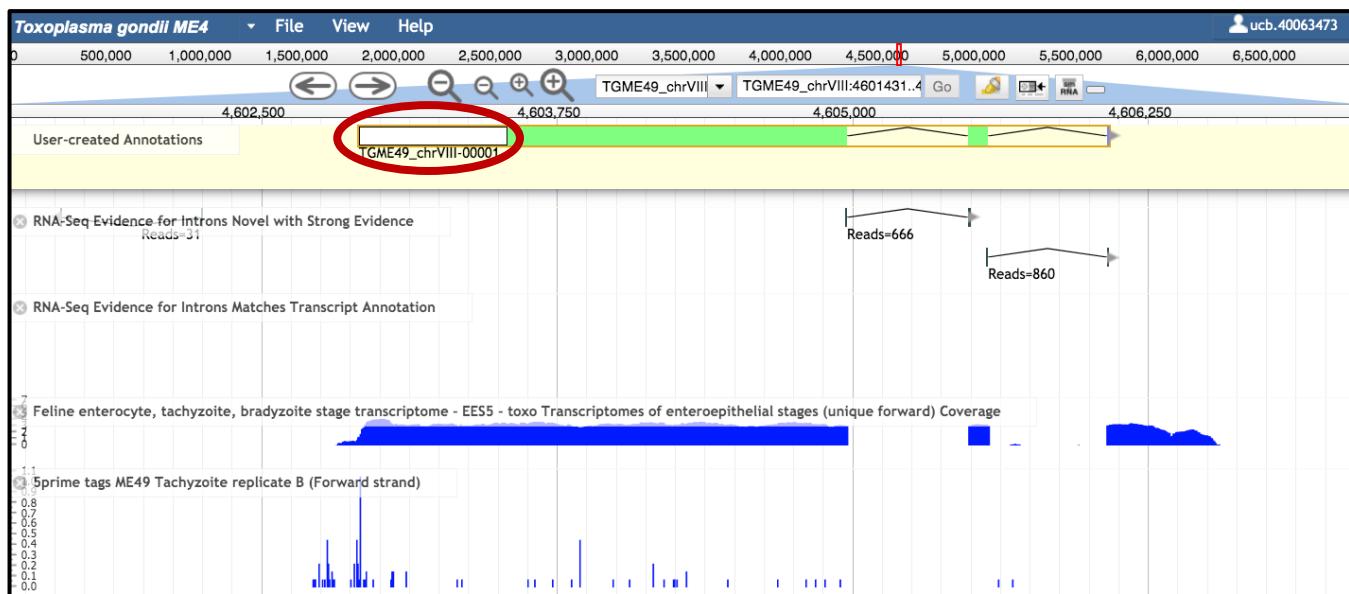
Hold down the shift key and select the introns with strong evidence (1), drag and drop them into the User-created Annotations track (2).



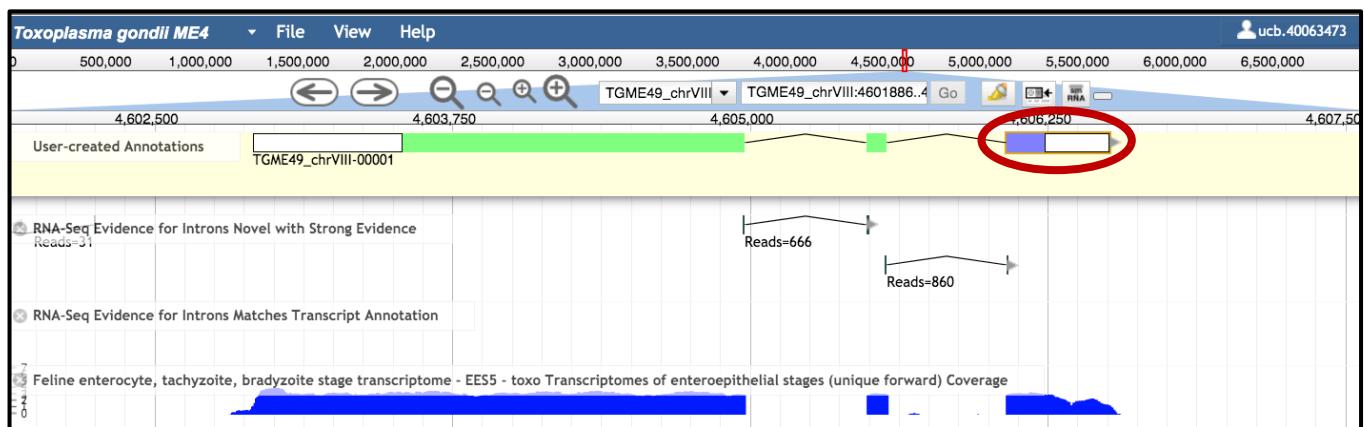
Zoom in by clicking on the + sign on the top (1). Press the Shift key and select the two small exons in the middle (2). With a right-click open the drop-down menu and choose **Merge** (3). Alternatively, select one of the exons you would like to merge, go to the edge of the feature until a little arrow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



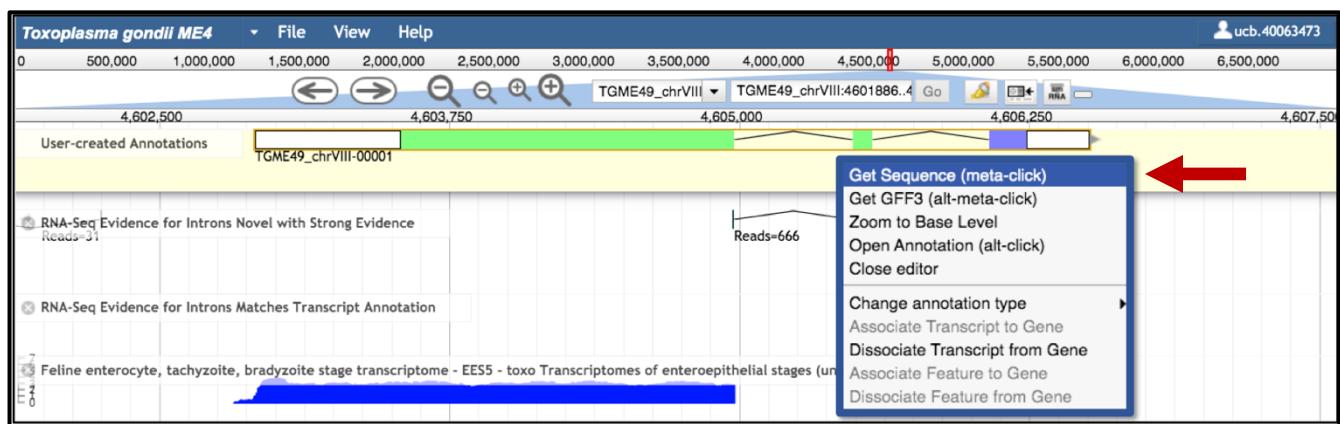
Select the first exon, point your mouse at the edge of the feature until a little arrow appears, then extend the exon to the transcription start. Apollo will automatically create the 5'UTR!



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!

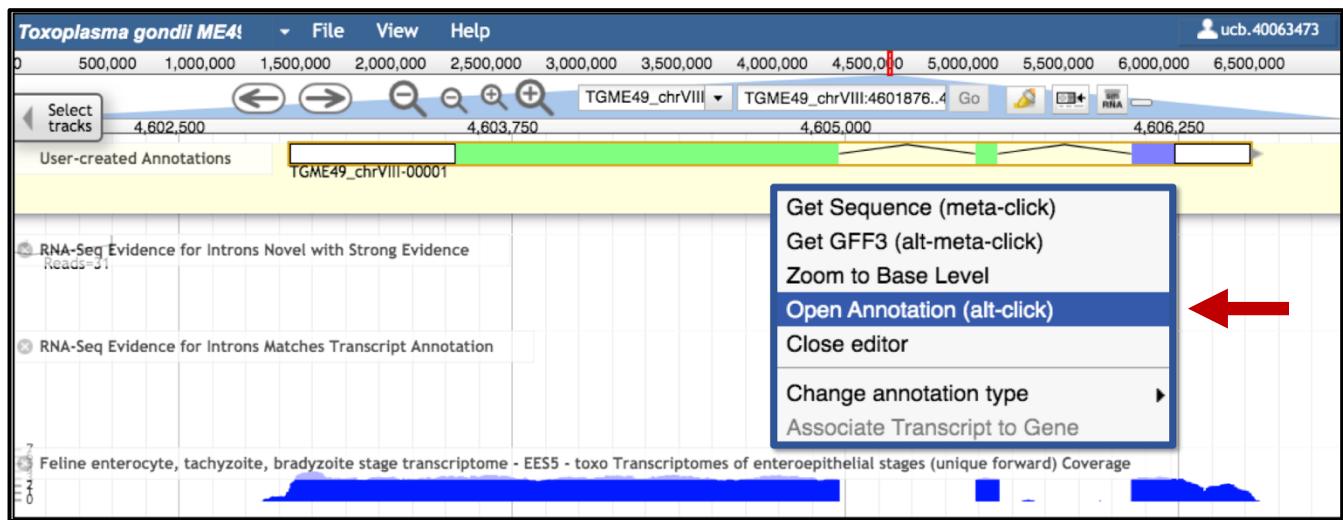


Select the new gene, with a right-click open the annotation drop-down menu and choose **Get Sequence**. Copy the sequence and run blast (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) and InterPro (<https://www.ebi.ac.uk/interpro>) to get additional information about the new gene.

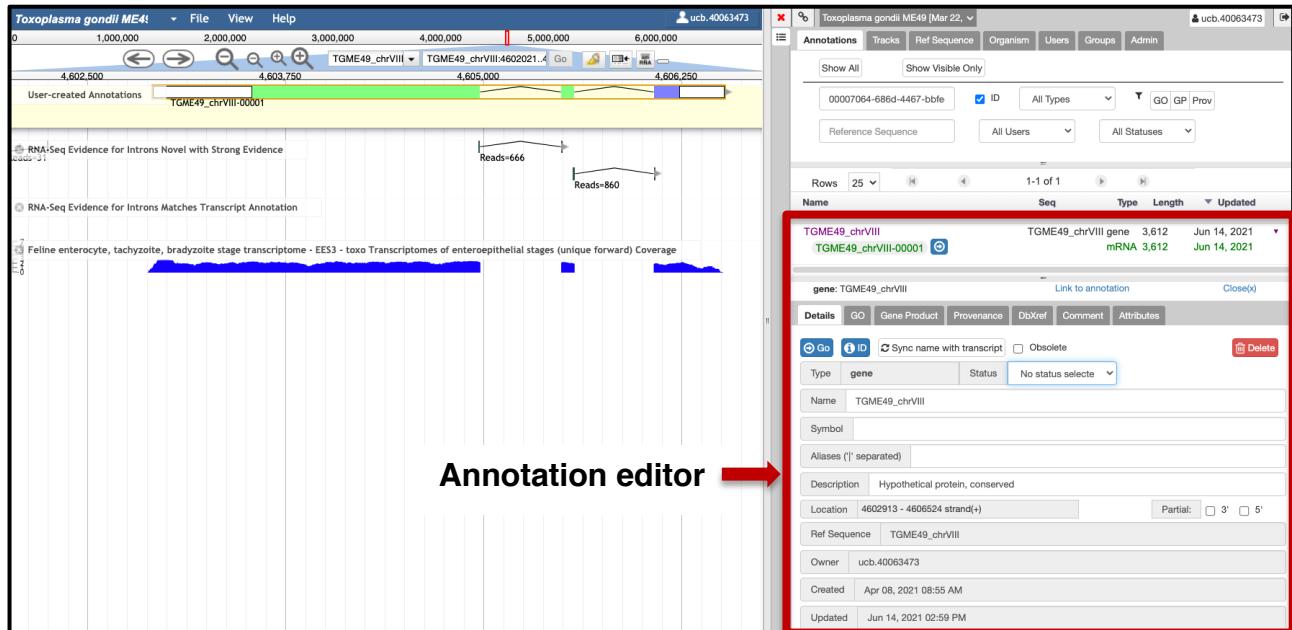


5) Opening of the Annotation editor window

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) Finalising 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 VEuPathDB annotations interface for a gene named TGME49_chrVIII. The top navigation bar shows the gene ID, version (3,603), date (Apr 04, 2021), and mRNA count (3,603). The 'Attributes' tab is selected. A dropdown menu is open under the 'Value' field, with 'structural' selected. The 'new' option in the list is highlighted with a blue background and has a red arrow pointing to it. Other options include added_comment, split, merge, retain_previous, added_product, added_go, added_symbol, added_alias, added_pmid, removed_product, added_ec_number, delete, isoform, modify, and added_dbxref.

Go to the Details tab, add a description/gene product to your new gene and select the status **Finished** on the gene.

The screenshot shows the VEuPathDB details interface for the same gene. The 'Details' tab is selected. A dropdown menu is open under the 'Status' field, with 'No status selected' checked. The 'Finished' option is highlighted with a blue background and has a red arrow pointing to it. Other options include Not Finished, Requires Curator, and a placeholder 'Symbol'.

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 like 'My Strategies', 'Searcher', 'Tools' (circled in red), 'My', 'Data', 'About', 'Help', and 'Contact Us'. Below the navigation, there's a search bar and several data visualization links: Synteny, Alignments, Phenotype, SNPs, Transcriptomics, Protein Features, and Proteomics. The main content area displays gene details: 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 'View 4 user comments, or add a comment' and a link to 'View and update community annotations in Apollo' (circled in red). In the 'Gene models' section, there's a summary of # Exons in Gene (9), # Transcripts (1), and Gene Models. A note says 'This gene is available in Apollo for community annotation.' A 'View in JBrowse genome browser' button and an 'Annotate in Apollo' button (circled in red) are present. A red box highlights the 'Tools' menu item in the top navigation bar.

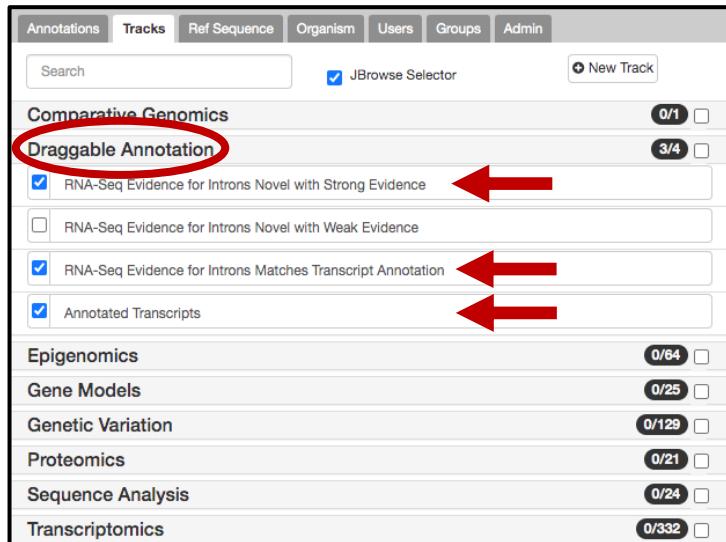
To use Apollo you need to be logged into VEuPathDB. If you have not done so yet log now into Apollo with your VEuPathDB user ID and password.

2) Adding draggable annotation and supporting evidence

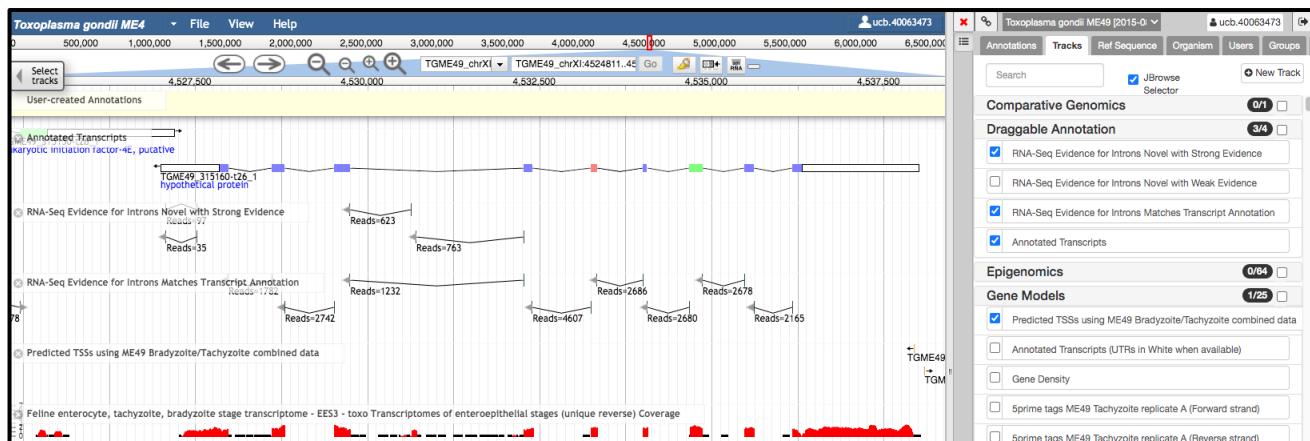
Select on the right-hand side the tab **Tracks**.

The screenshot shows the Apollo interface. On the left, there's a genome browser view for *Toxoplasma gondii* ME49, showing a chromosome X with coordinates from 0 to 6,000,000. A red box highlights the 'Tracks' tab in the top navigation bar. To the right of the genome browser, there are several tabs: Annotations, Tracks (highlighted in red), Ref Sequence, Organism, Users, Groups, and Admin. Below these tabs, there are sections for Comparative Genomics (0/1) and Draggable Annotation (0/4). There are also buttons for 'Search', 'JBrowse Selector', and 'New Track'.

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**.

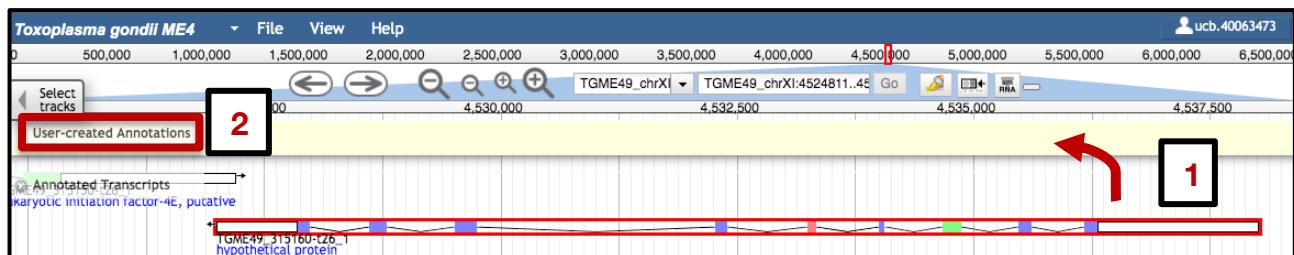


Select additional evidence, i.e. RNAseq plots and predicted TSS (transcription start sites).

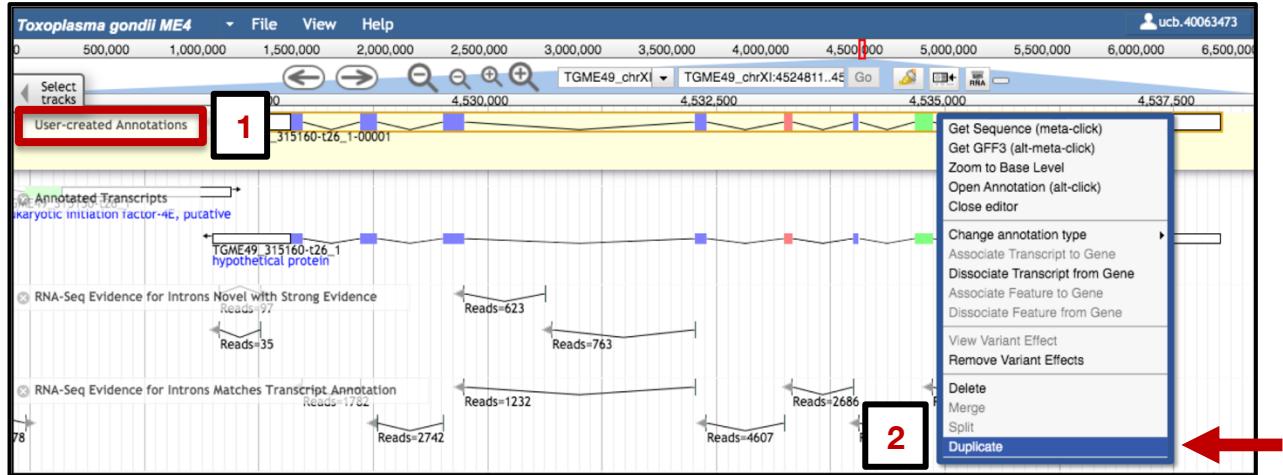


3) Adding alternative transcripts

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).

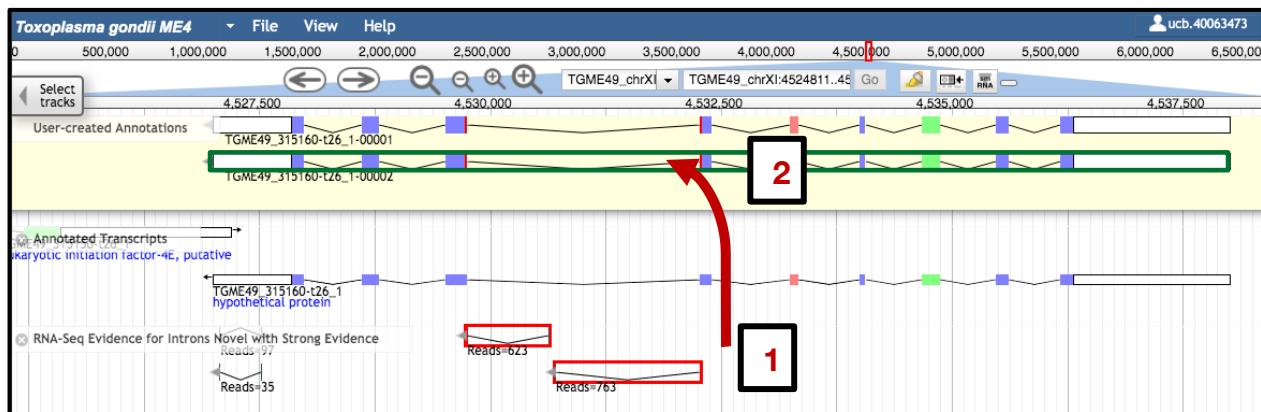


Select the gene in the User-created Annotations area (1). With a right-click open the annotation drop-down menu and choose duplicate (2).

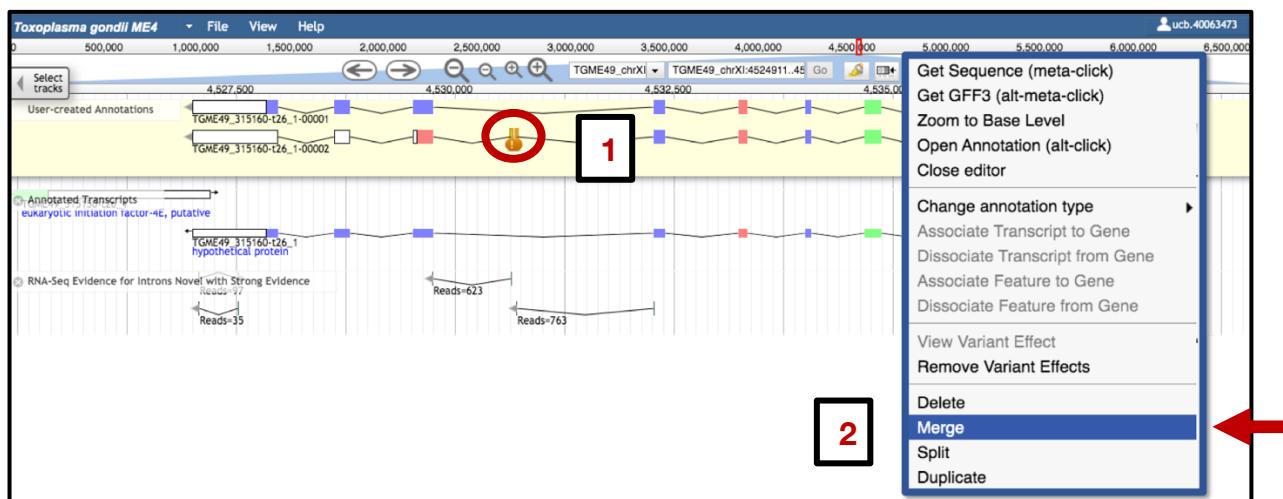


4) Modifying the alternative transcript

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.

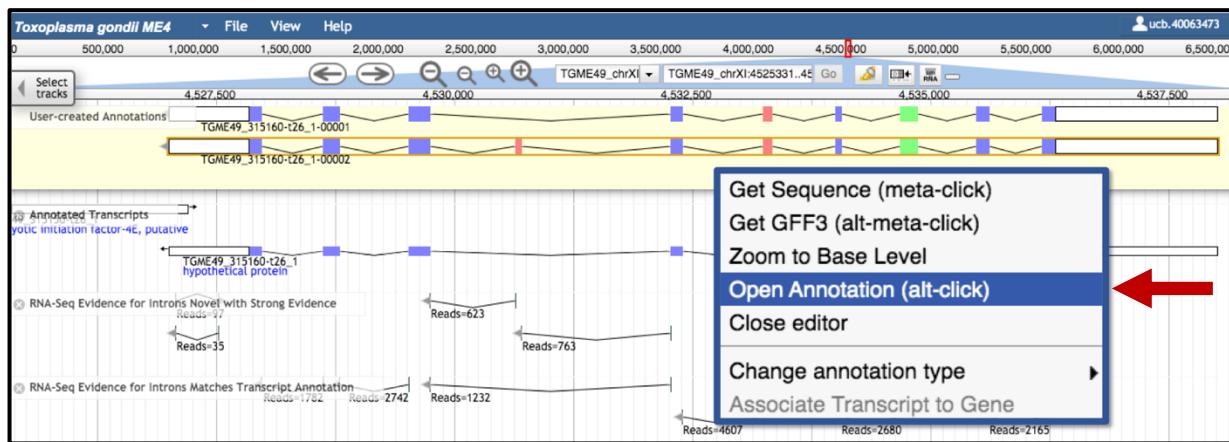


Hold down the shift key and select the two small exons. With a right-click open the drop-down menu and select merge.

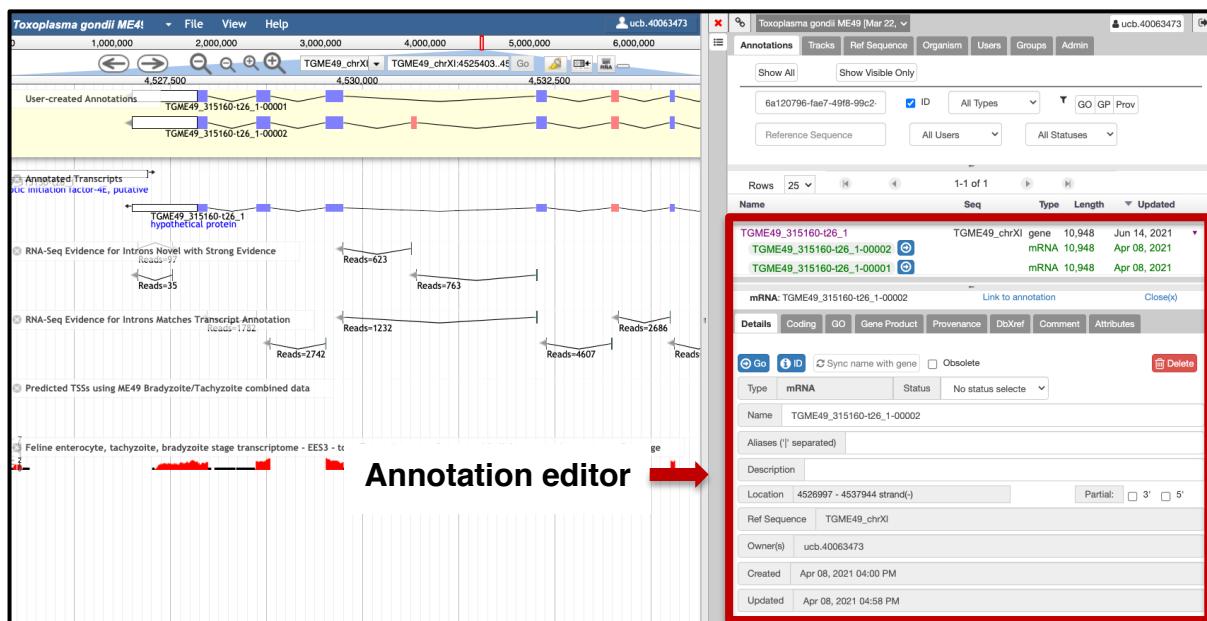


5) Opening of the Annotation editor window

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) Finalising 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.



Add a Description/Gene Product. Finally go the Details tab and select the status **Finished** on the gene.

The screenshot shows a gene details page for 'TGME49_315160-t26_1'. The 'Details' tab is selected. A dropdown menu is open under the 'Status' field, listing four options: 'No status selected' (unchecked), 'Not Finished' (unchecked), 'Finished' (checked and highlighted with a blue background), and 'Requires Curator' (unchecked). A red arrow points to the 'Finished' option. The rest of the page displays various gene information fields like Name, Description, Location, Ref Sequence, Owner, Created, and Updated.

Type	gene	Status
Name	TGME49_315160-t26_1	✓ No status selected Not Finished Finished (selected) Requires Curator
Symbol		
Aliases (' ' separated)		
Description		
Location	4526996 - 4538020 strand(-)	
Ref Sequence	TGME49_chrXI	
Owner	ucb.40063473	
Created	Apr 08, 2021 03:51 PM	
Updated	Apr 08, 2021 04:00 PM	

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