I5k Workspace updates: What's new with Apollo2

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Updates at the i5k Workspace

- Introduction
- Apollo2.1.1 vs Apollo2.6.5
  - New look
  - New interfaces
- Apollo1.0.4 Vs Apollo2.6.5
  - LOTS of changes
- An example annotation workflow

This has been a long time coming…

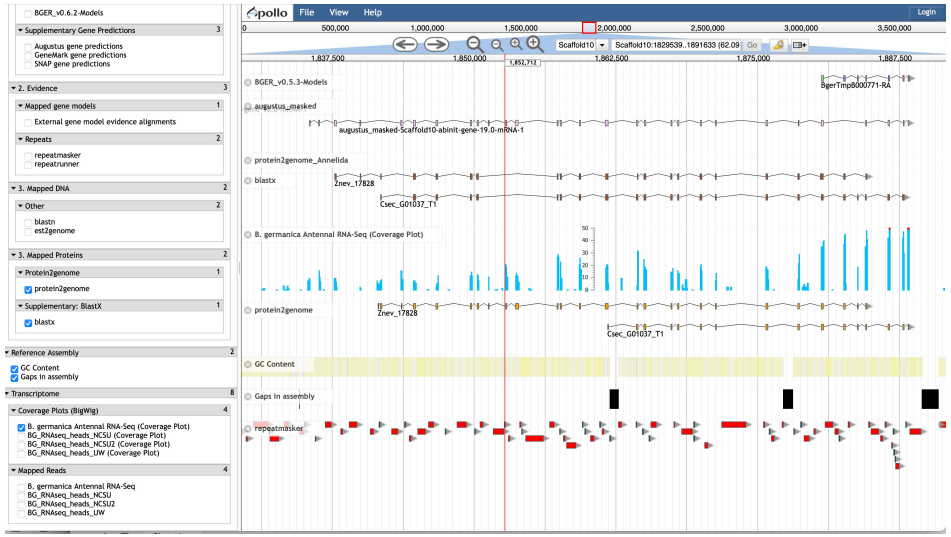
- Updating Apollo to this version has taken a lot longer than anticipated
- A large number of updates on the back-end
- Reworking the track styling system
- Manually checking each evidence track for issues
- Creating a new feature type for showing BLAST hits

- If you see any issues, please let us know
- i5k@usda.gov

What is Apollo?

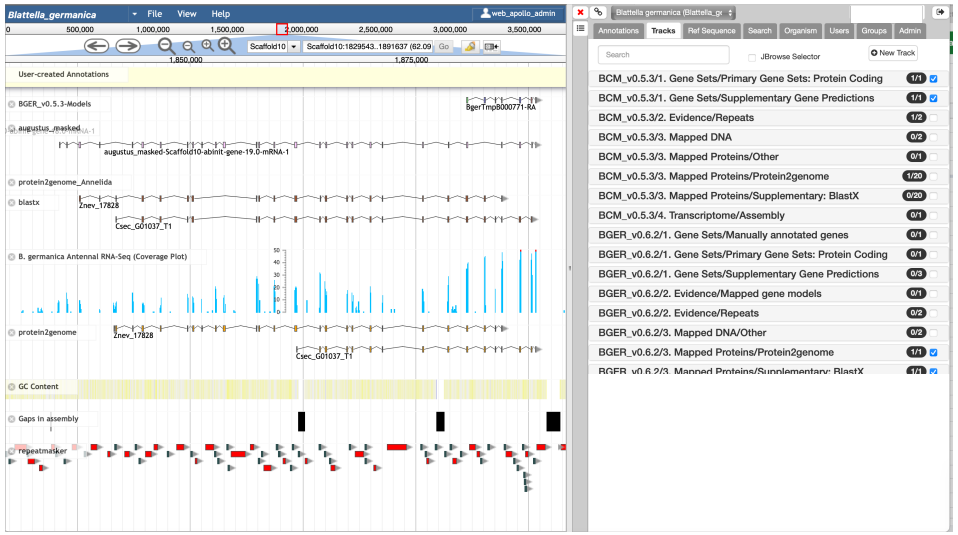
- Apollo is a web-based visual gene curation tool
- Apollo is an extension for the JBrowse genome browser

JBrowse



Login

Apollo



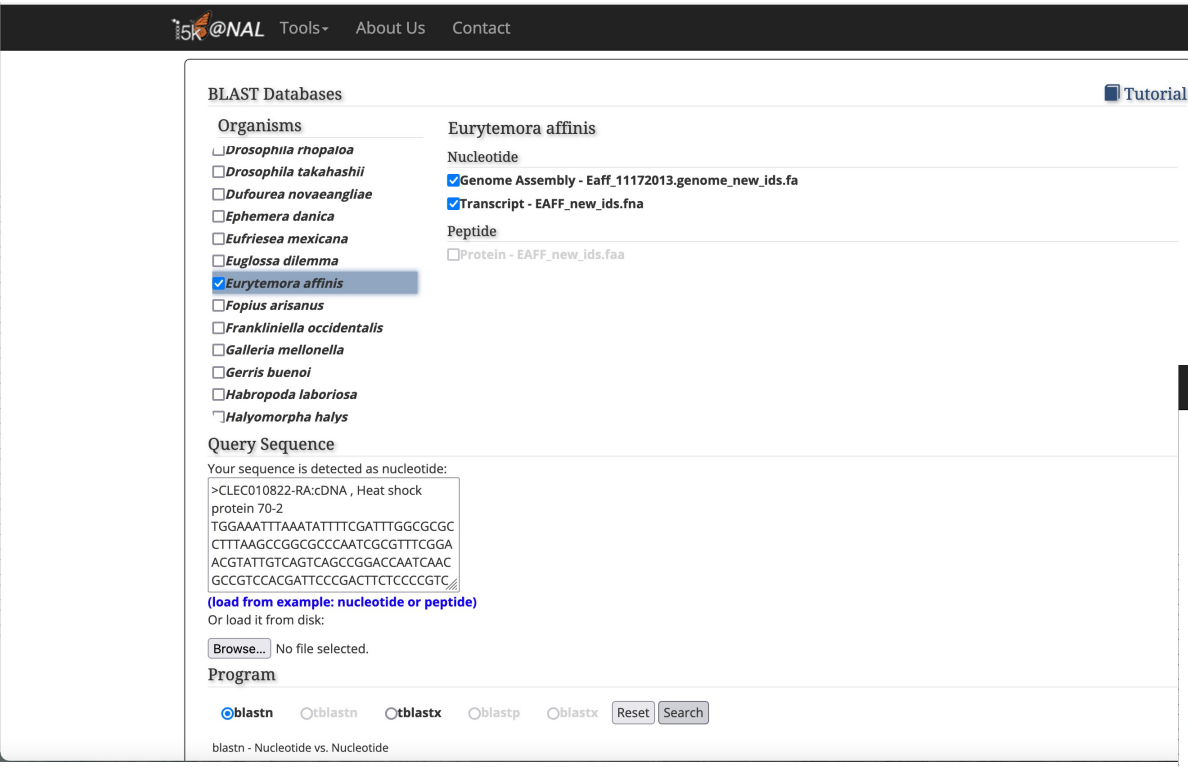
Apollo Basics

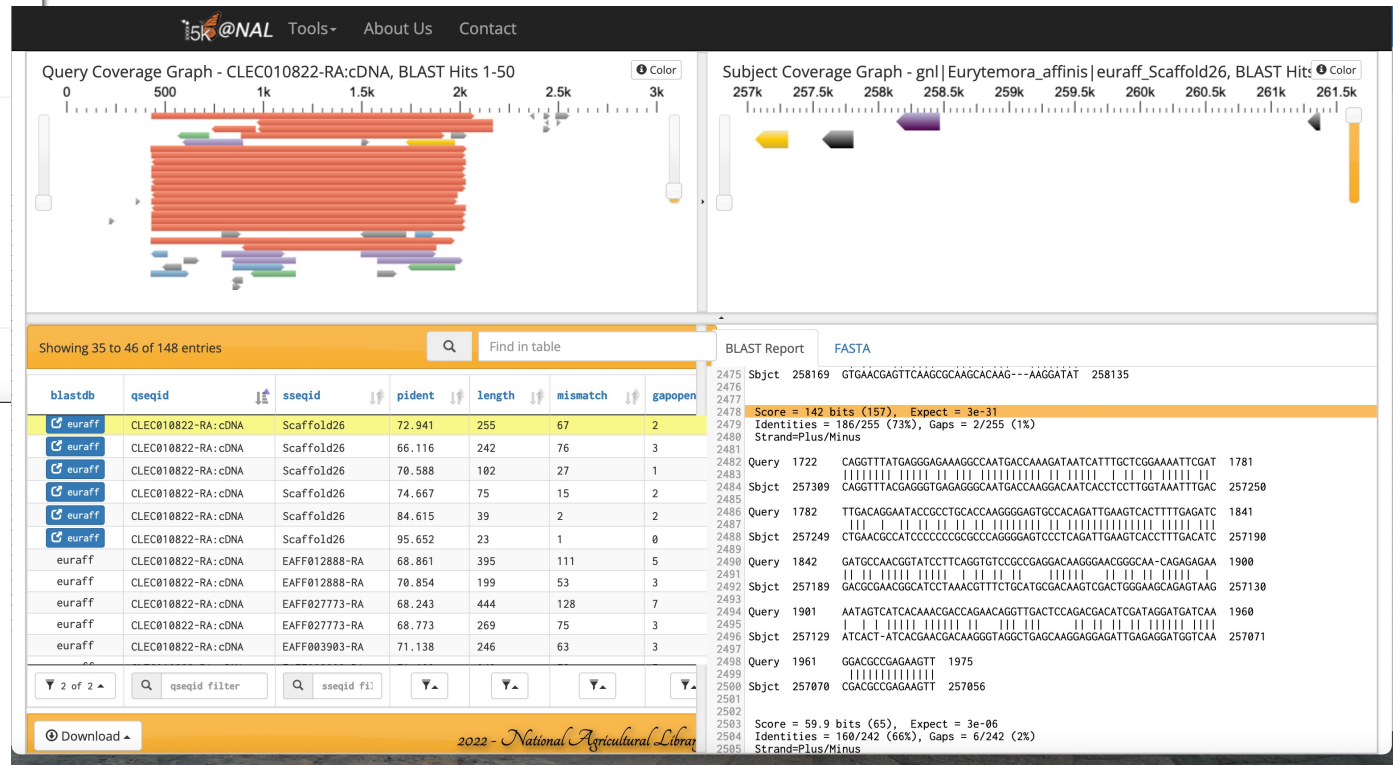
- Many of the functions are located in the panel on the right
- Your account can have access to multiple organisms
- Tabs allow quick access to the tools
- Annotations – show annotations created by users
- Tracks – shows the groups of tracks, can be turned on/off by group
- Ref Sequences – view and navigate to any scaffold
- Search – BLAT sequence search

Example Gene annotation workflow

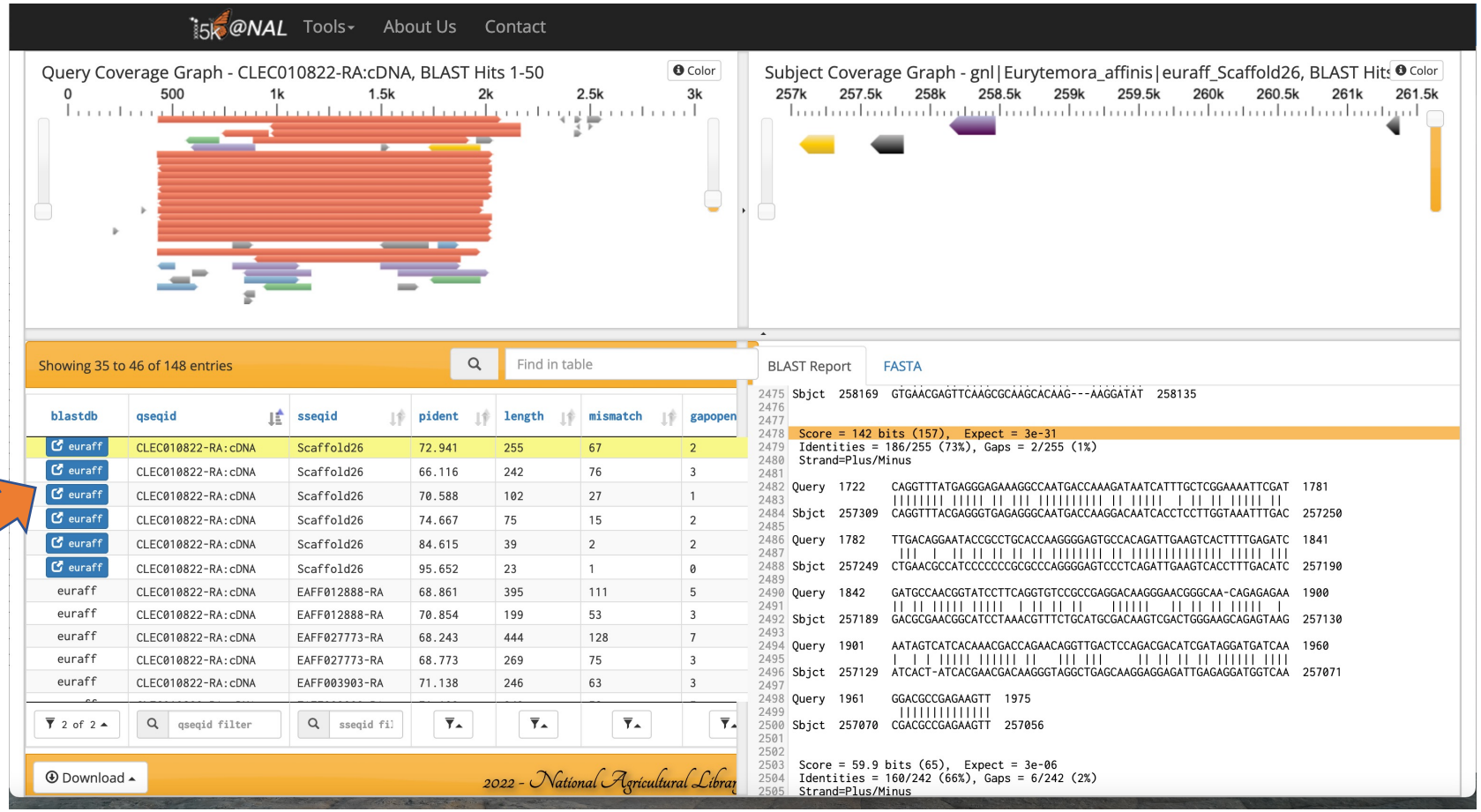
- Obtain sequence of interest / map to assembly using BLAST
- Use link in BLAST results to see the matches in JBRowse
- Turn on other evidence tracks (gene predictions, Transcriptome, etc)
- Login to Apollo -> create and refine the gene model

1. Find sequence/search the assembly

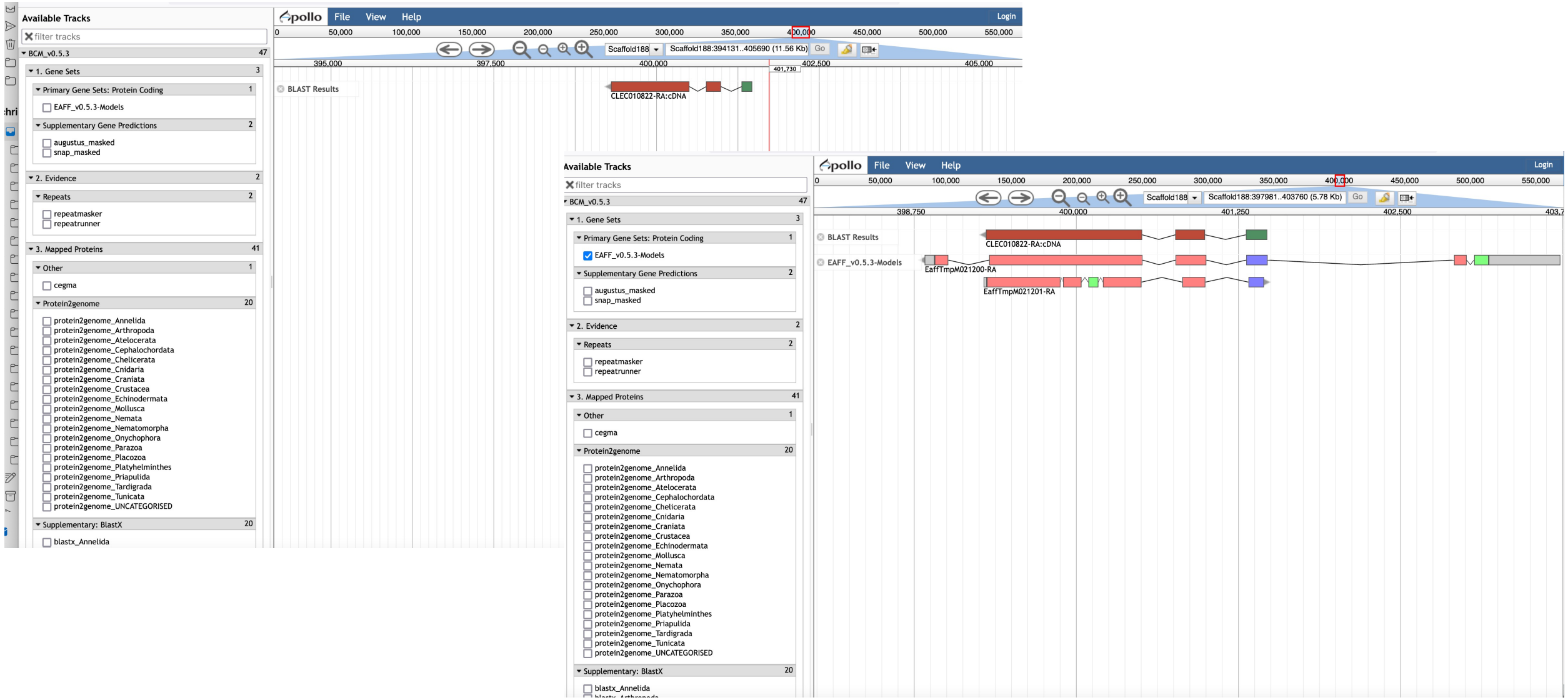




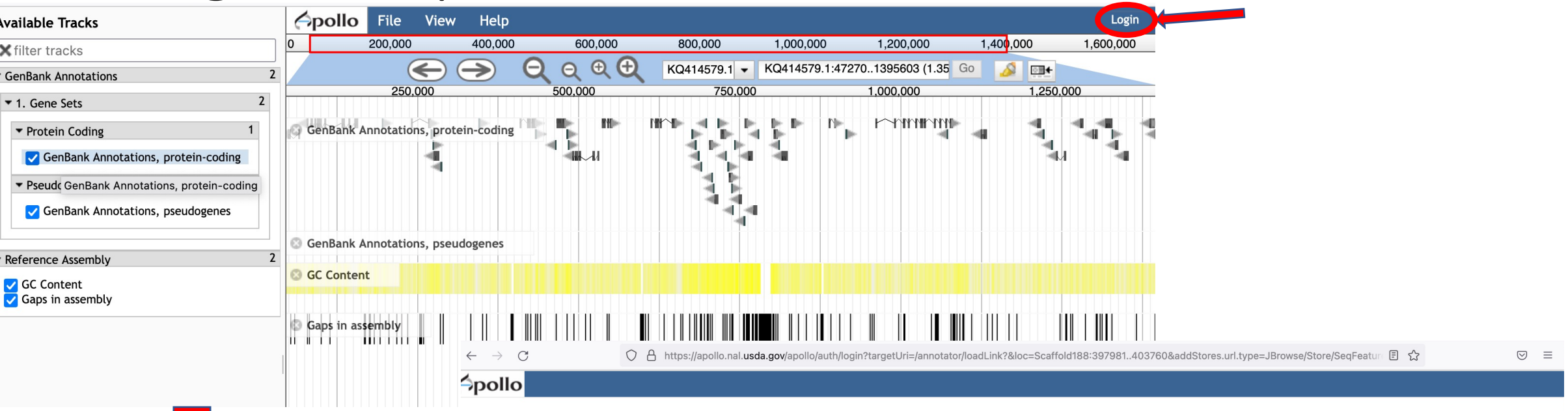
3. Use BLAST linkouts to see hits in the assembly

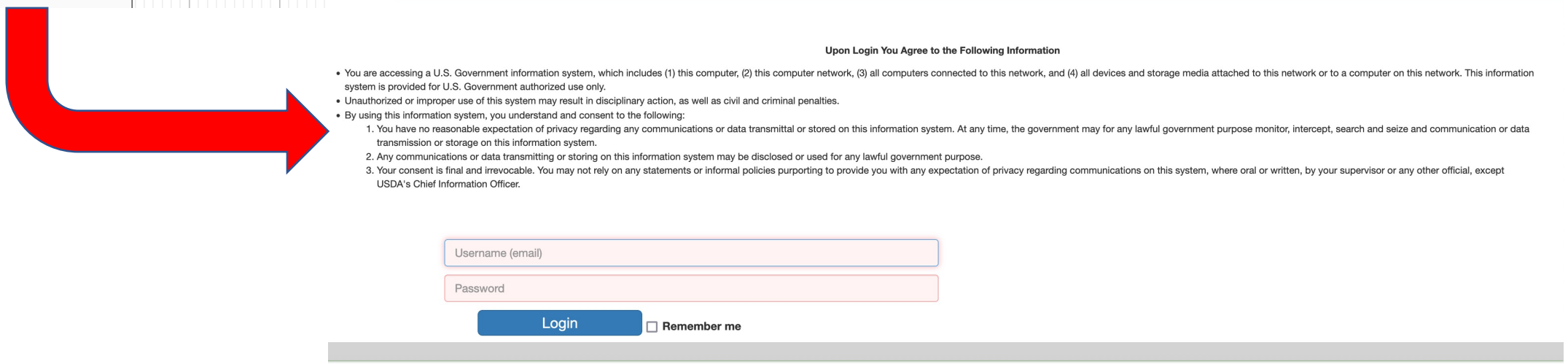


View in Jbrowse, turn on evidence tracks

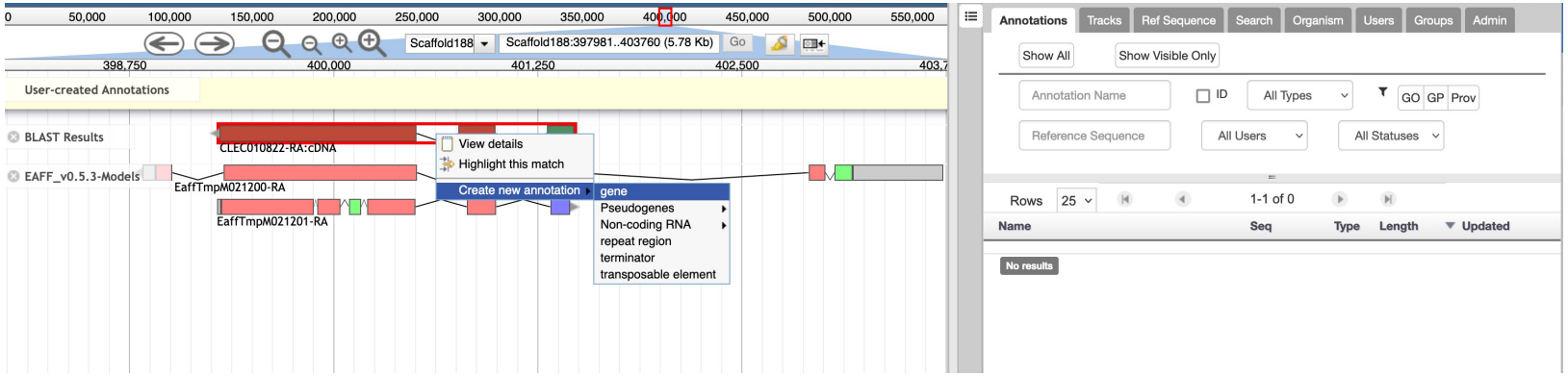


Login to Apollo



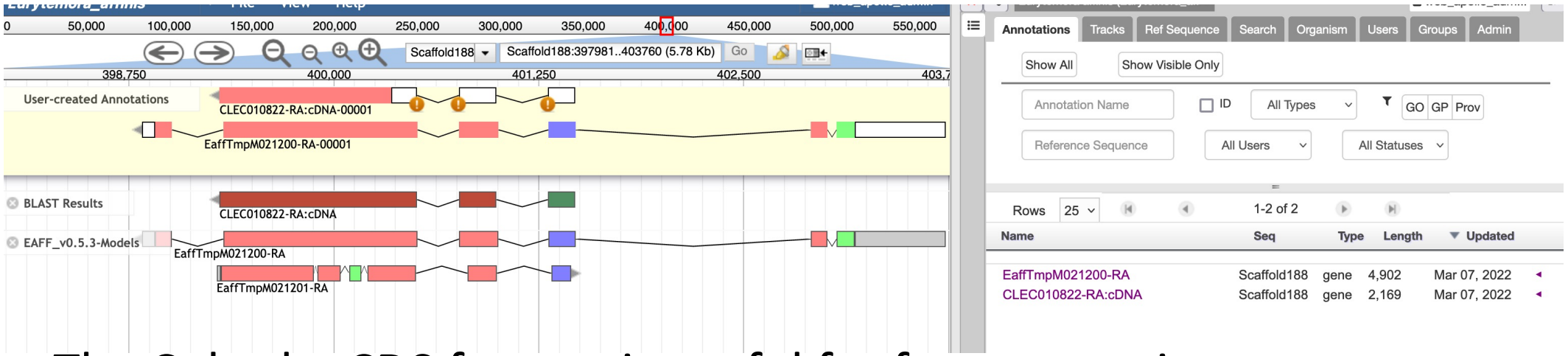


Start curating



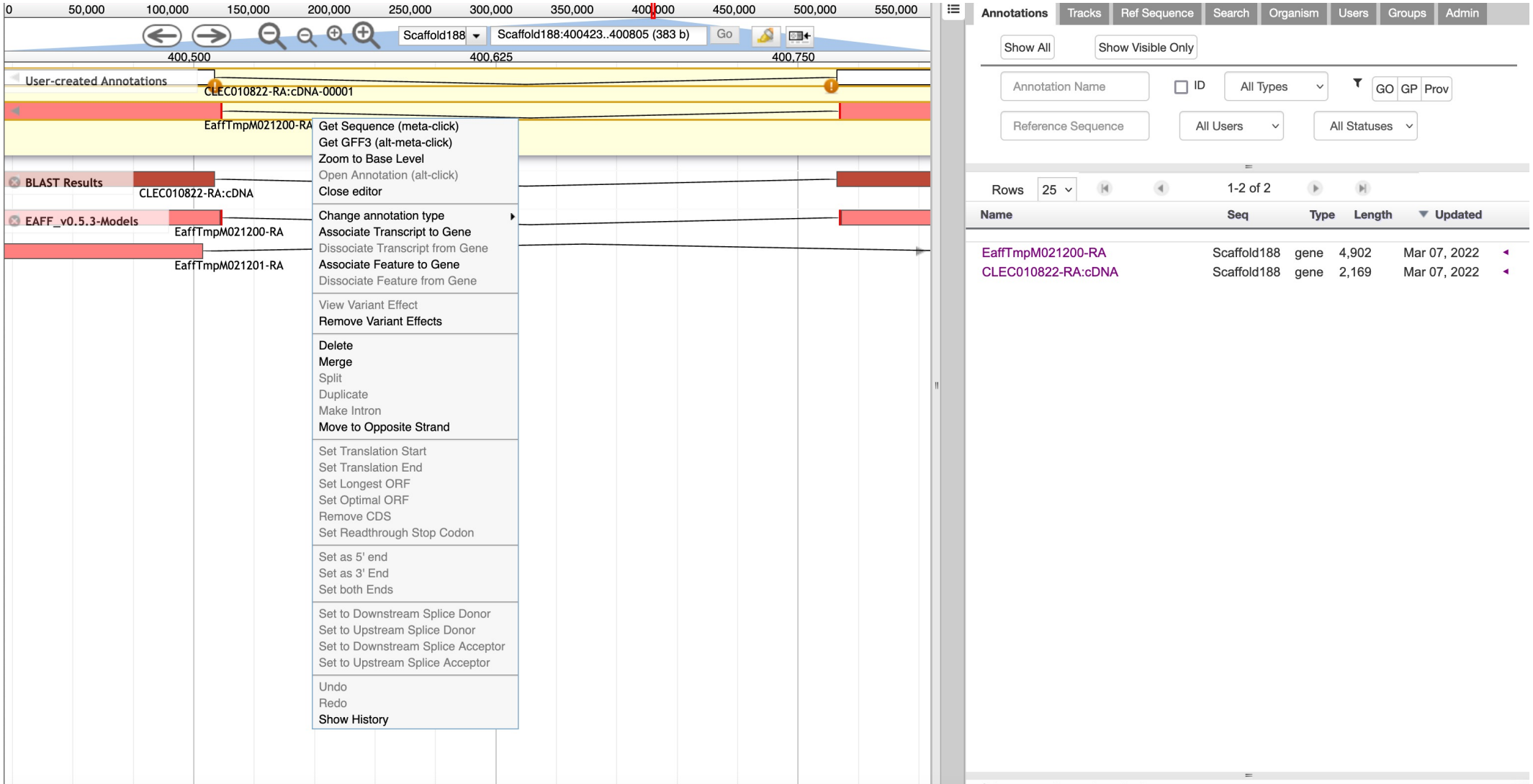
- Annotations may be created by
- Click-dragging a model to the User created Annotations panel
- Right-clicking a model then clicking through the “Create new annotation” menu

A few Apollo tips



- The Color by CDS feature is useful for fast comparisons
- The CDS is auto-calculated whenever a change is made
- Special symbols show if exons don’t end with canonical splice sites
- Edge matching – select a model and other models that have the same splice sites become highlighted in red (next slide)

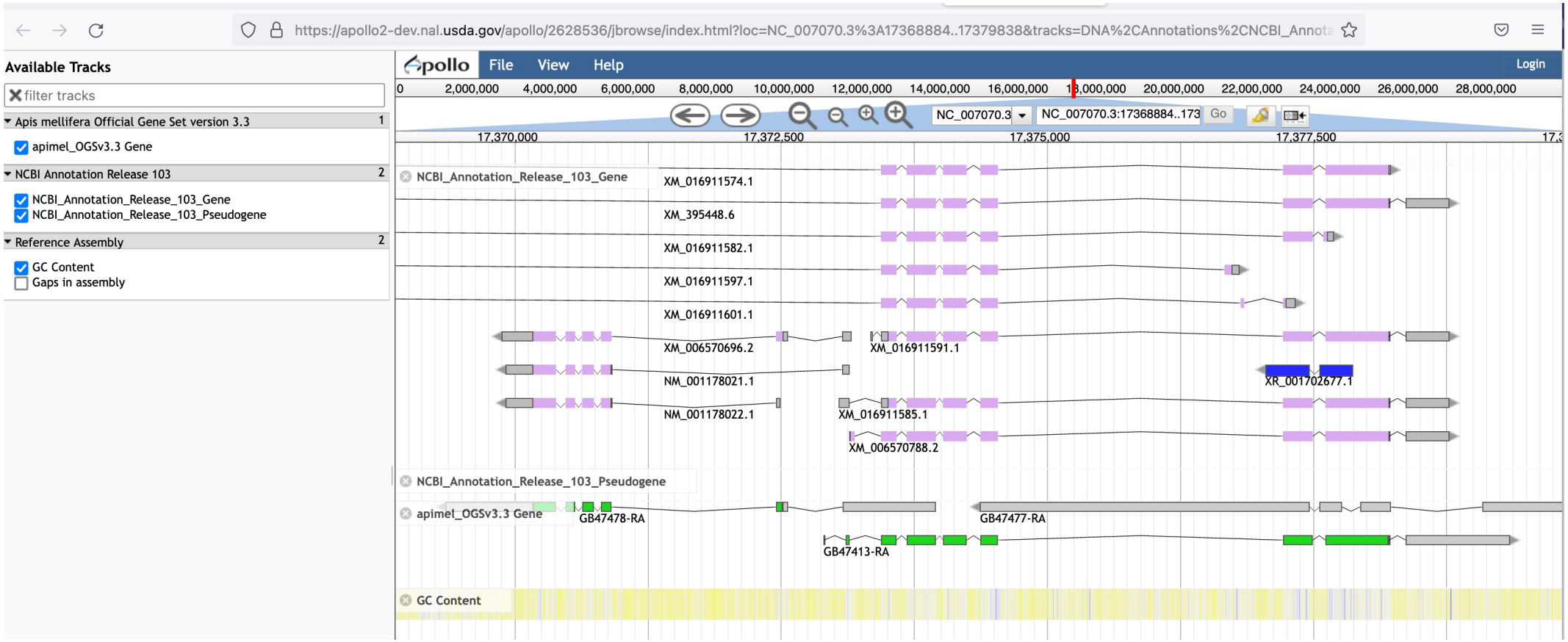
Right-click menu for many options



Updates in Apollo 2.6.5

- Many under-the-hood updates
  - Bug fixes, improved responsiveness
  - Supports newer versions of Jbrowse
- User interface changes
  - Better
  - Faster
  - More stable
  - Updated styles

Updated styles



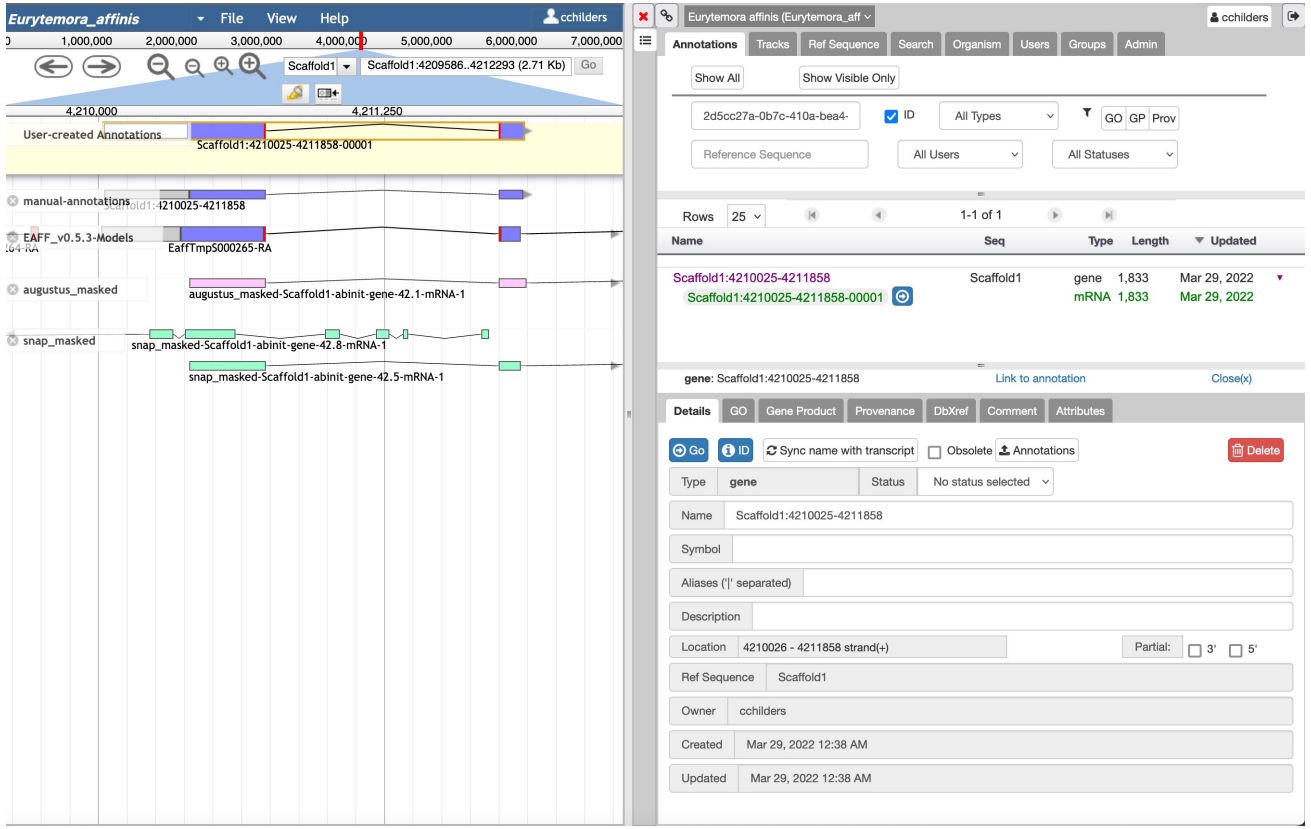
“NeatFeatures” – draw introns to show the direction a model goes
New built-in support for color by feature type (previously was a plugin)

Apollo updates in the latest release

- More functions are moved into the right side panel
- Updated Search features
  - New results
  - Hits can be used to create annotations

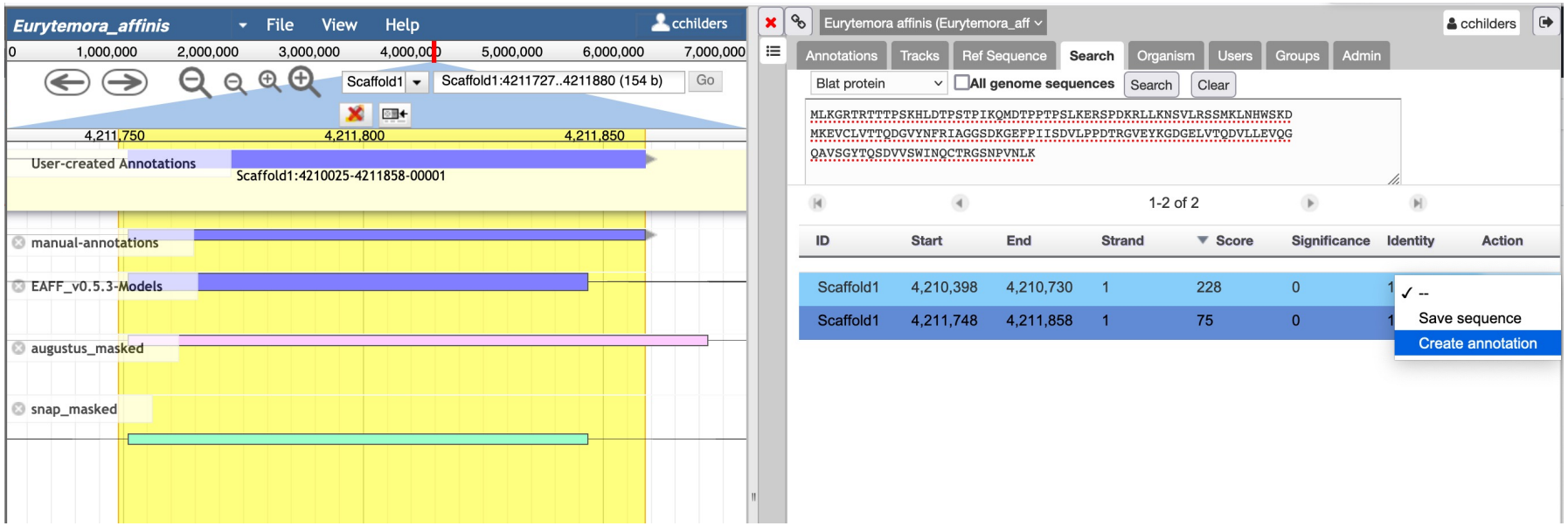
Annotation Editor updates

- More functions moved to the right side panel
- Gene is the default level
- GO Annotations, name, etc
- Many more validation steps



Built in BLAT search

- Moved to the right-side panel
- Updated Search features
  - New results
  - Hits can be used to create annotations



Special instructions for *E. affinis*

- This is a community that transitioned from Apollo1 to the newest Apollo during their annotation window.
  - Special considerations
  - The previously created annotations were migrated as a new data track
    - Only visible to logged in users
    - Will have to be harmonized with newly created annotations for generation of the new OGS/submission to NCBI
  - Annotation editor window now defaults to Gene level.
  - Annotation information may still need to be entered into the transcript section

Training session for *E. affinis*

- https://i5k.nal.usda.gov/training/webapp/blast

Thanks!

If you have questions or comments reach out to us at

i5k@usda.gov