

Learning objectives:

- Examine gene models in JBrowse
- Assess gene models based on RNA-Seq or other types of data (e.g. intron evidence).
- Determine if a gene model is accurate or if alternate models are possible
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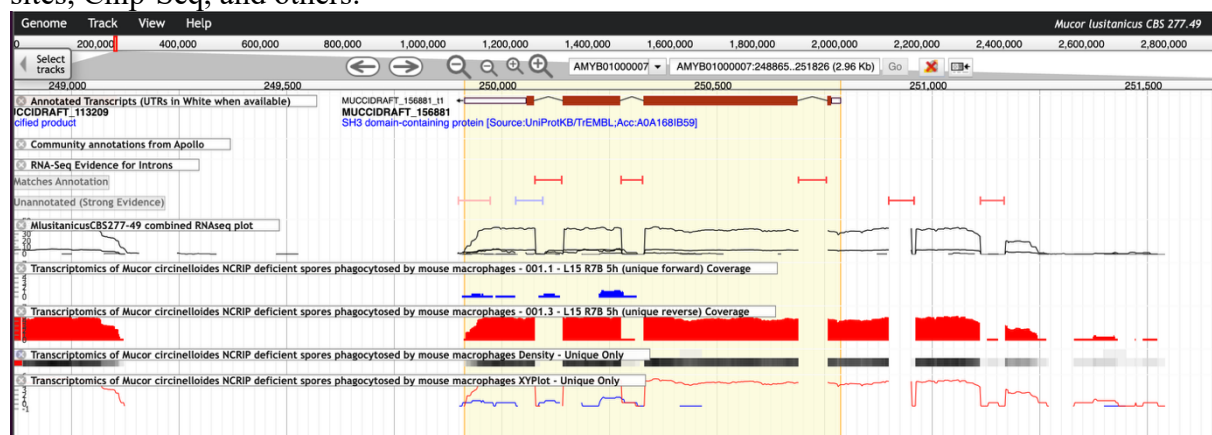
In previous exercises, you spent some time learning about gene pages and examining genes in the context of the JBrowse genome browser. It is important to recognize that gene models (structural annotation) are often open to interpretation, especially with respect to:

- transcript initiation and termination sites (5' and 3' untranslated regions, or UTRs)
- alternative processing events ... if you sequence deep enough, virtually *all* genes (in organisms that process transcripts) display alternative splicing, even for single exon genes.
- the potential significance of non-coding RNAs

Even actively curated genomes for well-established model organisms do not fully reflect all available knowledge about stage-specific splicing, as new information is constantly emerging! In addition, many gene models were computationally derived using methods that may not have relied on experimental evidence supporting intron/exon boundaries (e.g., RNA-Seq data).

In this exercise, we will explore several lines of evidence to interpret gene models and assess their accuracy and completeness. You will apply your newfound skills to examine a couple of genes and discuss your findings within the group.

The screenshot below shows a sample of data tracks that can be turned on in JBrowse. Stranded RNA-Seq data and RNA-Seq evidence for introns would be two useful tracks to begin with when evaluating gene models for the correct annotation of exons, introns, and UTRs. Depending on the species, other data types may be available as well - transcript start sites, Chip-Seq, and others.



- Take a look at several genes from the list below and activate several tracks in JBrowse that can help you evaluate gene models.
- Do you agree with the current annotated model? Would you have any modifications?

Examples of how users can modify genes in Apollo and make the corrected gene records available in FungiDB:

***Aspergillus nidulans* FGSC A4**

AN10121 –

https://fungidb.org/fungidb/jbrowse/index.html?loc=ChrVIII_A_nidulans_FGSC_A4%3A2525354..2526710&data=%2Ffungidb%2Fservice%2Fjbrowse%2Ftracks%2FanidFGSCA4&tracks=gene%2CCommunity%20annotations%20from%20Apollo%2CRNA-Seq%20Evidence%20for%20Introns%2CanidFGSCA4_Lind_SecondaryMetabolism_Anid_ebi_rnaSeq_RSRC%202_WT_TRV502_veA_matched_unique_forward%20Coverage%2CanidFGSCA4_Lind_SecondaryMetabolism_Anid_ebi_rnaSeq_RSRC%201_DeltamtFA_TRVp_unique_forward%20Coverage%2CanidFGSCA4_Lind_SecondaryMetabolism_Anid_ebi_rnaSeq_RSRC%202_WT_TRV502_veA_matched_unique_reverse%20Coverage%2CanidFGSCA4_Lind_SecondaryMetabolism_Anid_ebi_rnaSeq_RSRC%20XYPlot%20-%20Unique%20Only%2CanidulansFGSCA4%20combined%20RNAseq%20plot%2CanidFGSCA4_Lind_SecondaryMetabolism_Anid_ebi_rnaSeq_RSRC%20Density%20-%20Unique%20Only&highlight=ChrVIII_A_nidulans_FGSC_A4%3A2525354..2526710

***Aspergillus fumigatus* Af293**

Afu7g04610

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In class work

***Aspergillus nidulans* FGSC A4**

AN4483

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AN8437

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AN12338

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Aspergillus fumigatus Af293

Afu8g04420

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***Neurospora crassa* OR74A**

NCU05356

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NCU06817

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NCU06787

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NCU01605

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***Mucor lusitanicus* CBS 277.49**

MUCCIDRAFT_156881

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MUCCIDRAFT_127064

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MUCCIDRAFT_149865

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MUCCIDRAFT_149755

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MUCCIDRAFT_150170

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