

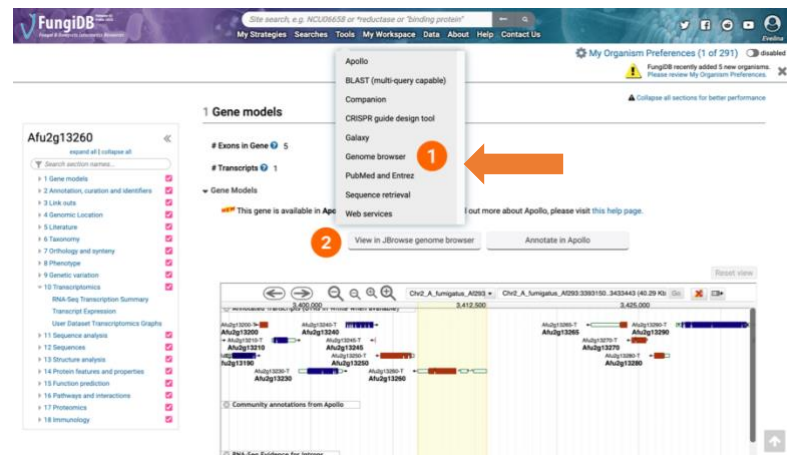
## Exploring records in JBrowse

Learning objectives

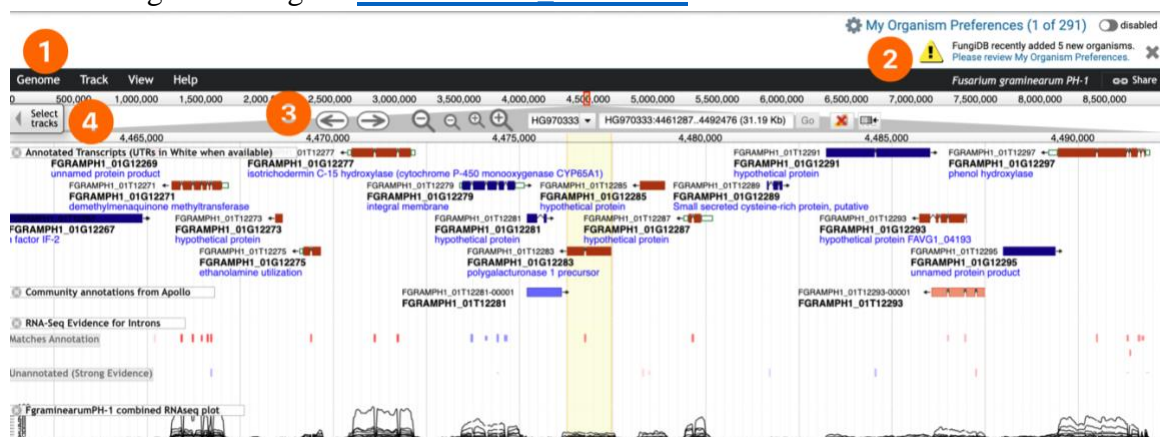
- Become familiar with JBrowse layout and navigation menus

JBrowse can be accessed from the main menu and also gene record pages.

Accessing JBrowse from gene record pages will pre-select the genome automatically. If navigating directly from the main page, the genome of choice can be chosen under the Genome tab.

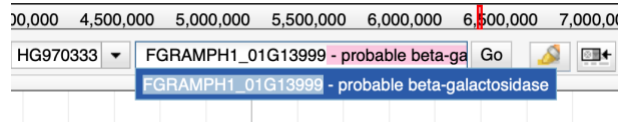


1. Navigate to the gene [FGRAMPH1\\_01T12283](#) in JBrowse.



1. The main menu provides options to select genomes, upload sequences or tracks, customize the JBrowse view, and access several help articles.
2. The current genome selection is indicated on the right. The Share link generates a custom URL specific to the JBrowse session & tracks loaded.
3. The navigation bar contains zooming (magnifying glass icons), panning (left/right arrows) and highlighting (yellow highlighter) buttons, a reference sequence selector (drop-down with sequences from the selected genome sorted by length), a text box to search for features such as gene ids, and overview bar showing the location of the region in view.
4. Select additional tracks (transcriptomics, SNPs, sequence, ploidy, etc.) to customise your JBrowse view.

If you navigated away from the gene, you could type **FGRAMPH1\_01T12283** directly in the location search box and select the highlighted match to return to your original position.



- **Displaying more information about a gene**

Left clicking on a gene of interest will display a pop-up window that provides additional information about gene classification, position, orthology, links to JBrowse and gene record pages, as, well CDS and protein sequences.

- **Highlighting gene for easy tracking**

Right-click (or control click) on the gene feature to display the context menu. The context menu offers gene highlighting and also options to display the gene record page and left-click details menu described above.

- **Practice activating tracks in JBrowse** by clicking on the Select tracks tab and choosing to display the following tracks:

1. Intron Evidence (if not selected by default already)
2. RNA-Seq (mycelium and 6days post-infection of wheat with Fusarium (6dpi))
3. Chip-Seq tracks of chromatin marks in WT and kmt6 mutant (KMT6 is Histone H3 K27 Methyltransferase)
4. Syntenic Sequences and Genes (Shaded by Orthology)

- Select the **Transcriptomics** category, **RNA-seq** subcategory and choose tracks:
  1. Click on the “**Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1**” dataset
  2. Select **unique** in the RNA-Seq Alignment category
  3. Select two tracks: **infected 6dpi** and **mycelia** as shown below

<input checked="" type="checkbox"/>	Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1 - infected 6dpi (unique) Coverage	Transcriptomics	RNA-Seq	Transcriptomic analysis during vegetative and infectious growth of Fusarium graminearum PH-1	Coverage	unique	not strand specific
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<input checked="" type="checkbox"/>	Transcriptomic analysis during vegetative and infectious growth of <i>Fusarium graminearum</i> PH-1 - mycelia (unique) Coverage	Transcriptomics	RNA-Seq	Transcriptomic analysis during vegetative and infectious growth of <i>Fusarium graminearum</i> PH-1	Coverage	unique	not strand specific
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- Clear your search by clicking on the “Clear All Filters” button.
- Select the **Epigenomics** category, **ChIP-Seq** subcategory and select H3K27me3 and H3K4me3 methylation marks in kmt6 deletion mutant and WT in low nitrogen growth conditions (low). The exact track names are provided below. Use the “Contains text” filter window to search for the tracks (copy and paste names listed below (text only) into the filter window).

For kmt6 deletion mutant:

- H3K27me3\_DELkmt6\_neoR\_low-R2
- H3K4me2\_DELkmt6\_neoR\_low-R2

For WT:

- H3K27me3\_WT\_low
- H3K4me2\_WT\_low

- Activate the **Syntenic Sequences and Genes (Shaded by Orthology)** track, which is located under the **Comparative Genomics** category, **Orthology and Synteny** subcategory but can be also searched for in the “Contains text” filter box at the top.

- Click on the **Back to browser** button to return to JBrowse.
- Customize the JBrowse syntenic view to display *Fusarium* species only.

Tip: Click on the drop-down menu in the **Syntenic Sequences and Genes (Shaded by Orthology)** track, choose **Select Subtracks**, unselect current tracks, use the filter to identify “*Fusarium*” and then click on the “Save” button at the bottom.

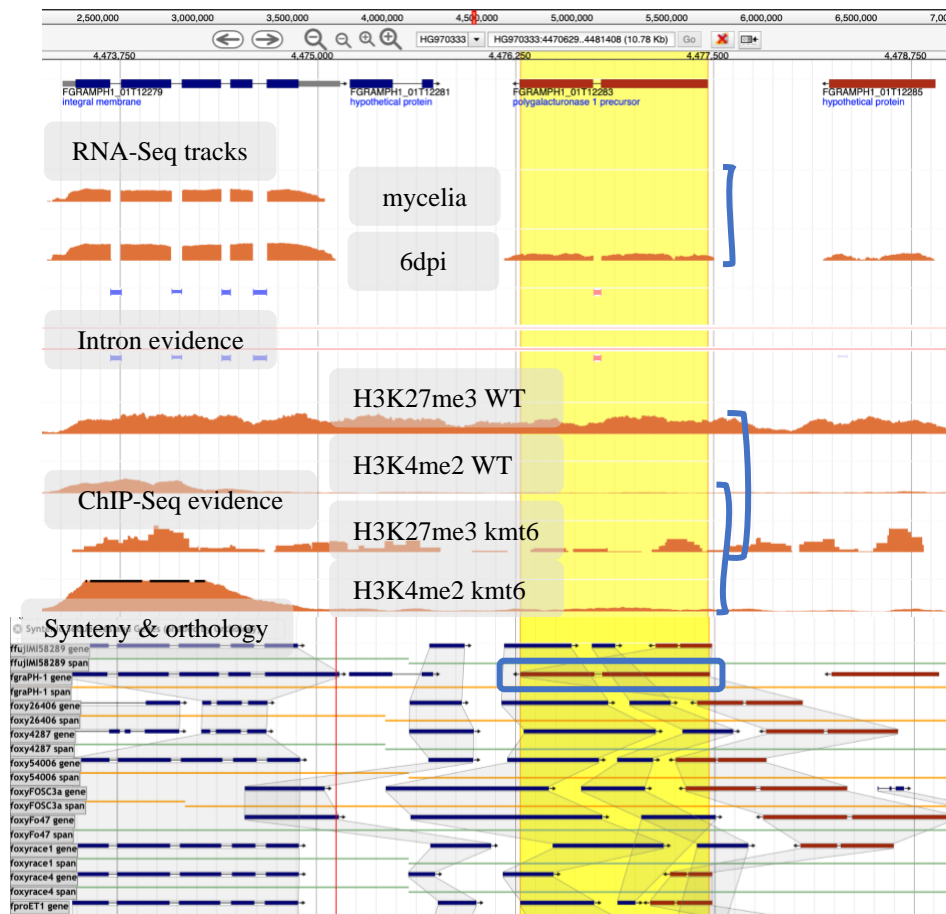
- Re-arrange tracks within JBrowse in the following order:
  - Pin the highlighted gene and gene model track to the top.

Note: you can use the drag and drop function in JBrowse to rearrange tracks in the order that helps you to evaluate the data.

In *Fusarium* and other fungi, H3K4me2 and H3K27me3 are found in large, mutually exclusive, gene-rich blocks of the genome. About one-third of the *F. graminearum* genome is associated with H3K27me3 when the fungus is grown in a minimal medium with low nitrogen. Kmt6 encodes a DNA methylase that deposits repressive chromatin mark H3K27me3. kmt6 mutants in *Fusarium* and other species demonstrate reorganization of chromatin marks (e.g., absence of the repressive chromatin mark H3K27me3) and upregulation of genes that are normally suppressed.

Having this information in hand and using JBrowse track view, answer the following questions:

- What can you tell about FGRAMPH1\_01T12283 expression mycelia and 6 days post-infection?
- Does this gene show de-regulation of repressive chromatin marks (H3K27me3) in the kmt6 mutant? Would you expect the expression of this gene to be up-regulated or down-regulated in the kmt6 mutant?
- Is this gene conserved in *Fusarium* species?
- How would you generate a unique URL to this JBrowse view?



URL: [https://fungidb.org/fungidb/browse/index.html?loc=HG970333%3A4474707..4479028&data=%2Ffungidb%2Fservice%2Fbrowse%2Ftracks%2FgrampH-1&tracks=gene%2CCommunity%20annotations%20from%20Apollo%2CRNA-Seq%20Evidence%20for%20Introns%2CFgraminearumPH-1%20combined%20RNAseq%20plot%2CFgrPH-1%20Wang\\_VegetativeAndInfectiousGrowth\\_ebi\\_rnaSeq\\_RSRC%201\\_infected\\_6dpi\\_unique%20Coverage%2CFgrPH-1%20Wang\\_VegetativeAndInfectiousGrowth\\_ebi\\_rnaSeq\\_RSRC%201\\_mycelia\\_unique%20Coverage%2CFgrPH-1\\_Freitag\\_histonemod\\_nitrogenLevel\\_chipSeq\\_RSRC%20H3K27me3\\_DELkmt6\\_neoR\\_low-R2%20Coverage%2CFgrPH-1\\_Freitag\\_histonemod\\_nitrogenLevel\\_chipSeq\\_RSRC%20H3K4me2\\_DELkmt6\\_neoR\\_low-R2%20Coverage%2CFgrPH-1\\_Freitag\\_histonemod\\_nitrogenLevel\\_chipSeq\\_RSRC%20H3K27me3\\_WT\\_low%20Coverage%2CFgrPH-1\\_Freitag\\_histonemod\\_nitrogenLevel\\_chipSeq\\_RSRC%20H3K4me2\\_WT\\_low%20Coverage%2CSyntenic%20Sequences%20and%20Genes%20Shaded%20by%20Orthology%20highlight-HG970333%3A4474707..4479028](https://fungidb.org/fungidb/browse/index.html?loc=HG970333%3A4474707..4479028&data=%2Ffungidb%2Fservice%2Fbrowse%2Ftracks%2FgrampH-1&tracks=gene%2CCommunity%20annotations%20from%20Apollo%2CRNA-Seq%20Evidence%20for%20Introns%2CFgraminearumPH-1%20combined%20RNAseq%20plot%2CFgrPH-1%20Wang_VegetativeAndInfectiousGrowth_ebi_rnaSeq_RSRC%201_infected_6dpi_unique%20Coverage%2CFgrPH-1%20Wang_VegetativeAndInfectiousGrowth_ebi_rnaSeq_RSRC%201_mycelia_unique%20Coverage%2CFgrPH-1_Freitag_histonemod_nitrogenLevel_chipSeq_RSRC%20H3K27me3_DELkmt6_neoR_low-R2%20Coverage%2CFgrPH-1_Freitag_histonemod_nitrogenLevel_chipSeq_RSRC%20H3K4me2_DELkmt6_neoR_low-R2%20Coverage%2CFgrPH-1_Freitag_histonemod_nitrogenLevel_chipSeq_RSRC%20H3K27me3_WT_low%20Coverage%2CFgrPH-1_Freitag_histonemod_nitrogenLevel_chipSeq_RSRC%20H3K4me2_WT_low%20Coverage%2CSyntenic%20Sequences%20and%20Genes%20Shaded%20by%20Orthology%20highlight-HG970333%3A4474707..4479028)