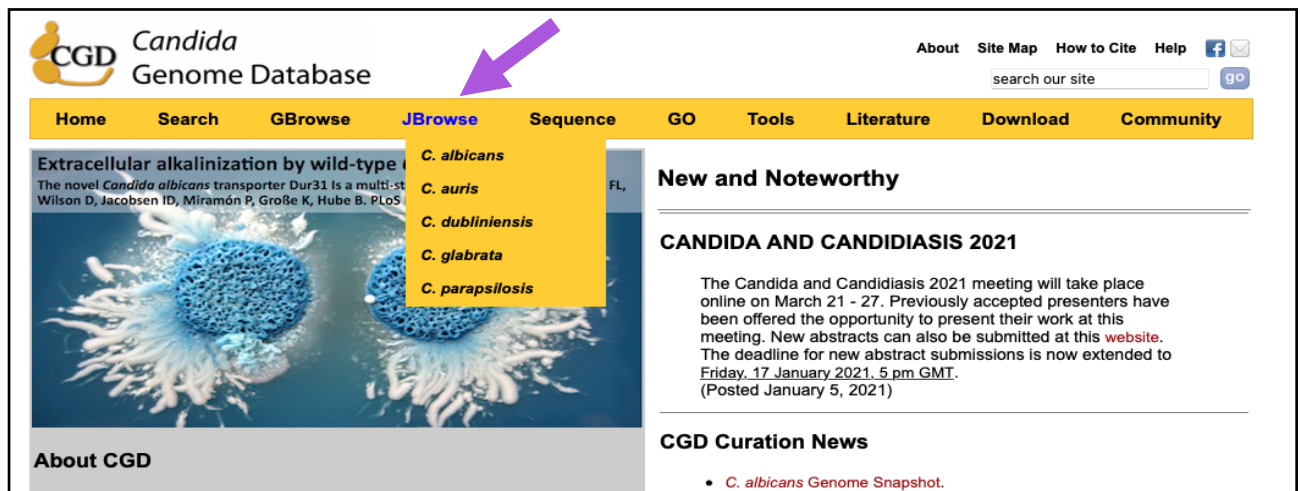


SGD/CGD JBrowse Genome Browser

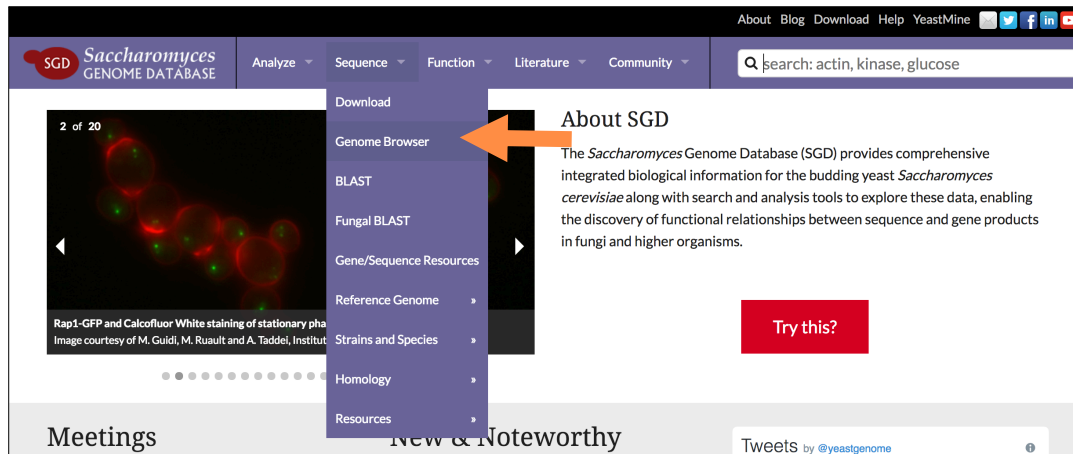
SGD and CGD both provide the genome browsing tool **JBrowse** to enable easy exploration of yeast genomes. JBrowse enables quick scrolling through genomic features and visualization of experimental information from large-scale studies in the form of **data tracks**. In this exercise, we will use JBrowse to visualize the location of genes related to galactose catabolism and use data tracks to visualize how these genes are transcriptionally regulated.

Accessing JBrowse

- You can access CGD's JBrowse genome browser in the following locations:
- From the home page (www.candidagenome.org) toolbar menu for **JBrowse**.



- From any Locus Summary page, by clicking on the JBrowse image link in the Basic Information section.
- CGD JBrowse provides *C. albicans*, *auris dubliniensis*, *glabrata*, and *parapsilosis*.
- You can access the SGD's JBrowse genome browser in the following locations:
 - From the home page (www.yeastgenome.org), by opening the Sequence menu in the top purple toolbar and selecting **Genome Browser**.
 - From any Locus Summary page, by selecting **View in JBrowse** under Sequence
 - Or by following this link: <https://browse.yeastgenome.org>



Analyzing transcriptional regulation of galactose catabolism

Using SGD's JBrowse genome browser, analyze the transcriptional regulation of **GAL10**.

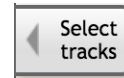
- In the JBrowse window, enter **GAL10** into the search box in the navigation bar on top and press **Go**. Multiple results will be listed, but all refer to the same gene.

Name	Location	Show	Go
GAL10	chrII:276253..278352	Show	Go
GAL10	chrII:276253..278352	Show	Go
GAL10	chrII:276253..278352	Show	Go

- Click on the GAL10 red feature bar to see an overview of GAL10 sequence data. What is the chromosomal location, strand, and sequence of this gene?
- What genes are upstream and downstream of GAL10? Zoom in/out using the magnifying glass icons in the navigation bar, or double-click on an empty spot in the browser. Move the viewing window left/right by using the arrow buttons on the navigation bar, the arrow keys on your keyboard, or by clicking the screen and dragging with your mouse.
- Notice that GAL10 shares its promoter region with the neighboring gene, GAL1, which is located on the opposite strand and transcribed in the opposite direction. Zoom in on the shared promoter by holding down the shift button on your keyboard and dragging over the region with your mouse.

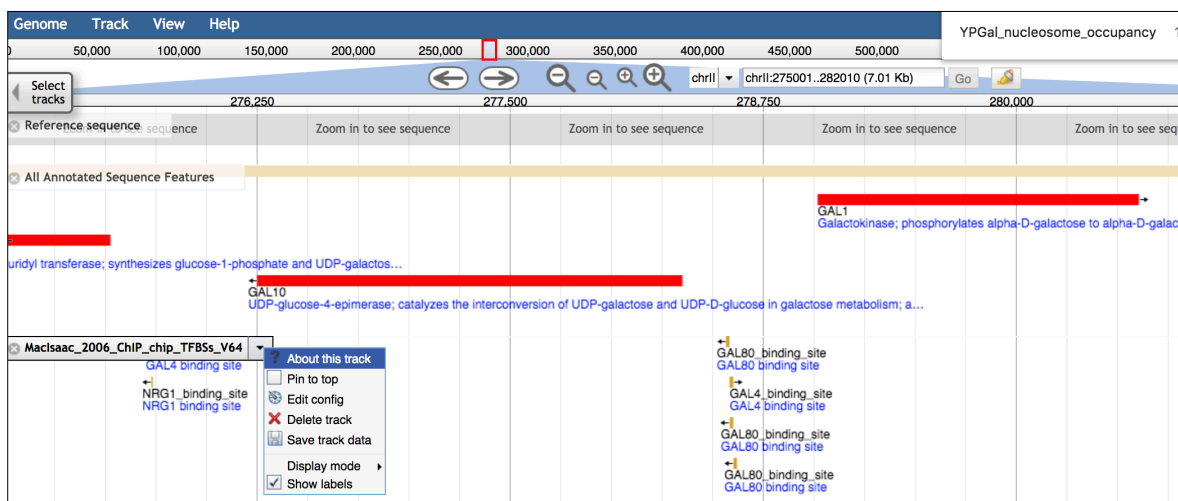
- What transcription factors bind to the GAL1-10 promoter? Add a track with transcription factor binding data to the browser window:

- Press the **Select tracks** button in the upper left corner.
- On the left side of the menu, click on **transcription** (under **Category**).
- In the list of tracks, check the box next to the track that has **MacIsaac** in the “First author” column and **TF_ChIP_ChIP** in Track column (you can sort each column by clicking on its header). Click on “**Back to browser**” in the upper left corner.



Select Tracks										
<div>My Tracks</div> <div>Currently Active</div> <div>Recently Used</div>		<div>Back to browser</div> <div>Clear All Filters</div>		<div>Contains text</div> <div>67 matching tracks</div>						
Assay Term Name	PMID	First author	Lab PI	Lab	Assay Term Name	Biosample Term Name	Strain background	Category	GBrowse Category	Track
42 ChIP-chip assay										
1 ChIP-seq assay	15905473	Zhang	Fred S. Dietrich	Duke University	Serial Analysis of Gene Expression (SAGE)	polyA RNA extract	W303	transcription	...	Transcription_start...
5 Chromatin immunoprecipitation with exonuclease sequencing assay (ChIP-exo)	<input checked="" type="checkbox"/> 16522208	MacIsaac	Ernest Fraenkel	MIT	ChIP-chip assay	DNA extract	W303	transcription	transcription recombination	TF_ChIP_ChIP
4 RNA-seq assay	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	polyA RNA extract	S288C	transcription	RNA expression profiling	Transcribed_regions_polyA_RNA
8 Serial Analysis of Gene Expression (SAGE)	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	RNA extract	S288C	transcription	RNA expression profiling	Transcribed_regions_total_RNA
7 transcription profiling by tiling array assay										
Category										
10 (no data)										
1 DNA replication recombination and repair										
11 DNA replication recombination and repair										
16 RNA structure										
1 Reference sequence										
1 carbon utilization										
44 chromatin organization										
1 chromatin organization transcription										
49 histone modification										
14 mRNA processing										
1 mitotic cell cycle										
17 stress heat shock carbon utilization nutrient utilization osmotic stress oxidative stress phosphorus utilization										
67 transcription										
2 translation regulation										
First author										
2 David										
15 Chedoke										

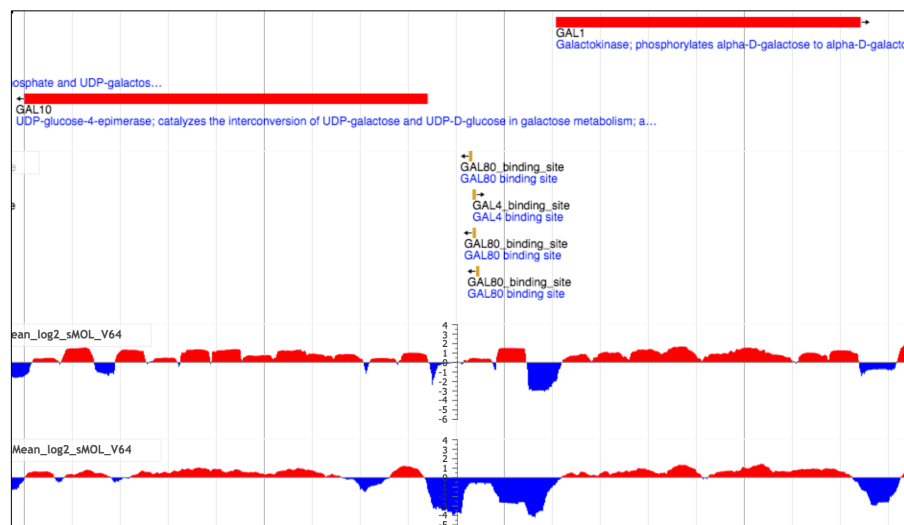
- In the main browser window, a new data track for the MacIsaac dataset will be shown. Click on the binding sites for **GAL4** or **GAL80** for more information about the sites. To learn more about the track itself (techniques, experimental design, reference), hover your mouse cursor over the track name and select **About this track** from the pull-down menu.



- What is the nucleosome occupancy around the GAL1-10 promoter and how does it change during growth on galactose? Add tracks with nucleosome occupancy data:
 - Click on **Select tracks** button again and then **Clear All Filters**
 - Under Category, select **chromatin organization** and filter tracks by typing **nucleosome** in “Contains text” search box
 - Check the boxes next to **First author: Kaplan**, Track: **YPD_nucleosome_occupancy_map_dMean_log2_sMOL** and **YPGal_nucleosome_occupancy_map_dMean_log2_sMOL**. Exit the tracks tab.

Select Tracks										Help
My Tracks Currently Active Recently Used 1 ChIP-seq assay 3 DNA sequencing 8 micrococcal nuclease digestion followed by high throughput sequencing assay 1 micrococcal nuclease digestion followed by tiling array assay	<input type="checkbox"/> PMD <input type="checkbox"/> 17392789 <input type="checkbox"/> 17873876 <input type="checkbox"/> 18550805 <input type="checkbox"/> 18989395 <input type="checkbox"/> 18989395 <input type="checkbox"/> 18989395 <input type="checkbox"/> 19092803 <input checked="" type="checkbox"/> 19092803 <input type="checkbox"/> 19092803 <input checked="" type="checkbox"/> 19092803	First author Albert Lee Mavrich Field Field Field Kaplan Kaplan Kaplan Kaplan	Lab PI Frank Pugh Corey Nislow Frank Pugh Eran Segal Eran Segal Eran Segal Eran Segal Eran Segal Eran Segal	Lab Penn State UBC Penn State Weizmann Institute of Science Weizmann Institute of Science Weizmann Institute of Science Weizmann Institute of Science Weizmann Institute of Science Weizmann Institute of Science	Assay Term Name ChIP-seq assay micrococcal nuclease digestion followed by high throughput sequencing assay micrococcal nuclease digestion followed by high throughput sequencing assay DNA sequencing DNA sequencing DNA sequencing micrococcal nuclease digestion followed by high throughput sequencing assay micrococcal nuclease digestion followed by high throughput sequencing assay micrococcal nuclease digestion followed by high throughput sequencing assay	Biosample Term Name DNA extract DNA extract DNA extract DNA extract DNA extract DNA extract DNA extract DNA extract DNA extract	Strain background S288C S288C S288C Other Other Other Other Other Other	Category chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization chromatin organization	GBrowse Category chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure chromatin structure	Track H2AZ_Nucleosome_positions Predicted_nucleosome_occupancy_model H3H4_Nucleosome_positions predicted_average_nucleosome_occupancy predicted_nucleosome_positioning_model_score summarized_nucleosome_occupancy InVivo_nucleosome_occupancy_map_dMean_log2_sMOL YPD_nucleosome_occupancy_map_dMean_log2_sMOL YPEtOH_nucleosome_occupancy_map_dMean_log2_sMOL YPGal_nucleosome_occupancy_map_dMean_log2_sMOL predicted_average...

- Look for differences in nucleosome occupancy between the galactose condition and the YPD condition. Given that GAL1 and GAL10 function in galactose catabolism, do the nucleosome occupancy tracks suggest something about the regulation of GAL1 and GAL10?



To save the current display, or to share it with colleagues, simply copy and save the browser URL.