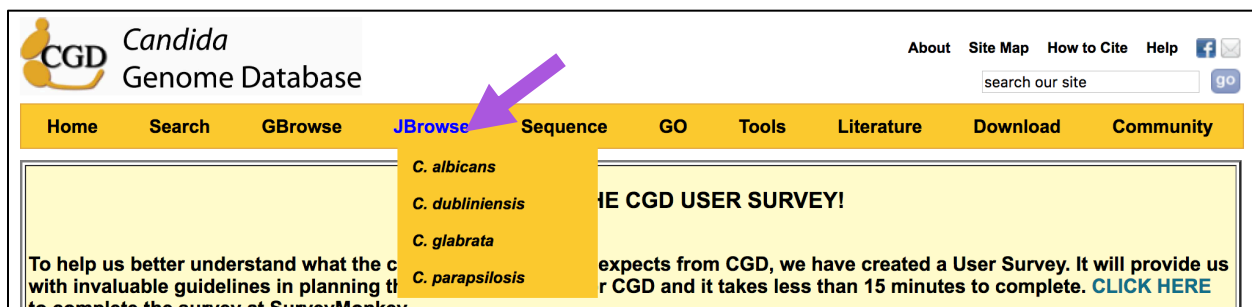


SGD/CGD JBrowse Genome Browser

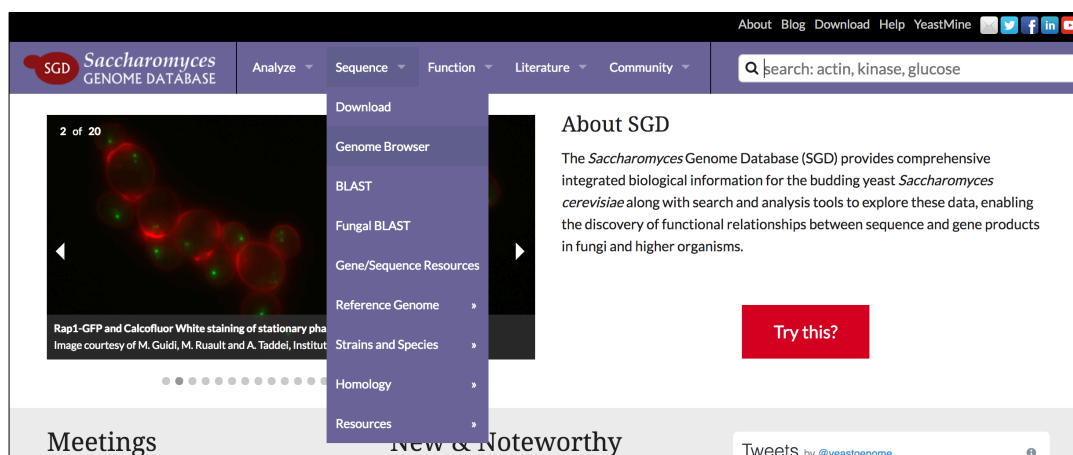
SGD and CGD both provide the genome browsing tool **JBrowse** to enable easy exploration of yeast genomes. JBrowse enables quick scrolling through genomic features and visualization of experimental information from large-scale studies in the form of **data tracks**. In this exercise, we will use JBrowse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



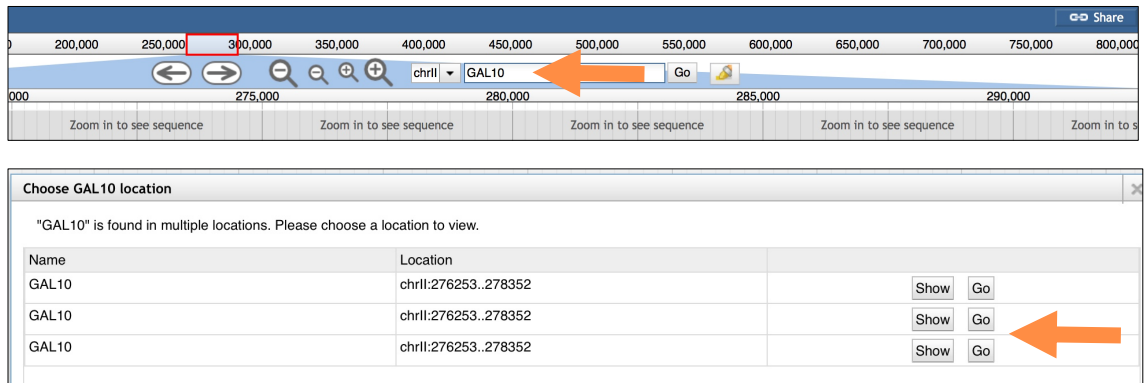
- From any Locus Summary page, by clicking on the JBrowse image link in the Basic Information section.
- CGD JBrowse provides *C. albicans*, *dubliniensis*, *glabrata*, *auris*, and *parapsilosis*.
- You can access the SGD's JBrowse genome browser in the following locations:
 - From the home page (www.yeastgenome.org), 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>



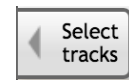
Analyzing transcriptional regulation of galactose catabolism

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.



- 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 **MacIssac** 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 Help										
▼ My Tracks	Back to browser Clear All Filters Contains text 67 matching tracks									
▼ Assay Term Name	<input type="checkbox"/>	PMD	First author	Lab PI	Lab	Assay Term Name	Biosample Term Name	Strain background	Category	Track
42 ChIP-chip assay	<input type="checkbox"/>	15905473	Zhang	Fred S. Dietrich	Duke University	Serial Analysis of Gene Expression (SAGE)	polyA RNA extract	W303	transcription	Transcription_start_sites
1 ChIP-seq assay	<input checked="" type="checkbox"/>	16522208	MacIsaac	Ernest Fraenkel	MIT	ChIP-chip assay	DNA extract	W303	transcription	TF_ChIP_ChIP
5 Chromatin immunoprecipitation with exonuclease sequencing assay (ChIP-exo)	<input type="checkbox"/>	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	polyA RNA extract	S288C	transcription	Transcribed_regions_polyA_RNA
4 RNA-seq assay	<input type="checkbox"/>	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	RNA extract	S288C	transcription	Transcribed_regions_total_RNA
8 Serial Analysis of Gene Expression (SAGE)	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_AR_S_identified
7 transcription profiling by tiling array assay	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
▼ Category	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Rs
10 (no data)	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
1 DNA replication, recombination and repair	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
11 DNA replication, recombination and repair	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
16 RNA structure	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
1 Reference sequence	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
1 carbon utilization	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
44 chromatin organization	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
1 chromatin organization transcription	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
49 histone modification	<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	Known_Predicted_A_Cs
14 mRNA processing	<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	PolII_occupancy_WT
1 mitotic cell cycle stress heat shock carbon utilization nutrient utilization osmotic stress oxidative stress phosphorus utilization	<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	PolII_occupancy_sen1
67 transcription	<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	Dst1_RNA_PolIII_SC_L16C_ChIP_chip
2 transcription regulation	<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	Dst1_RNA_PolIII_SC_L16C_ChIP_chip
▼ First author	<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	Dst1_RNA_PolIII_SC_L16C_ChIP_chip
2 David	<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	Dst1_RNA_PolIII_SC_L16C_ChIP_chip
15 Ghavi-Helm	<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	WT_RNA_PolIII_YPD

- 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.

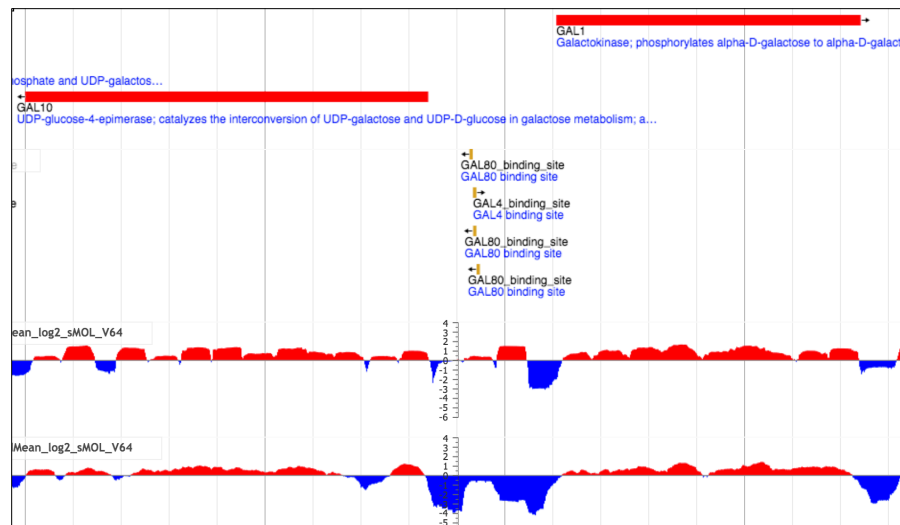
The screenshot shows a genome browser window with a track named 'MacIsaac_2006_ChIP_chip_TFB5s_V64'. The track displays binding sites for GAL4 and GAL80. A red arrow points to the 'About this track' option in the pull-down menu for the MacIsaac track. The menu also includes options like 'Pin to top', 'Edit config', 'Delete track', 'Save track data', 'Display mode', and 'Show labels'.

- 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										
<ul style="list-style-type: none"> My Tracks Currently Active Recently Used 	Back to browser Clear All Filters	Contains text: nucleosome		13 matching tracks						
Assay Term Name	PMID	First author	Lab PI	Lab	Assay Term Name	Biosample Term Name	Strain background	Category	GBrowse Category	Track
1 ChIP-seq assay	17392789	Albert	Frank Pugh	Penn State	ChIP-seq assay	DNA extract	S288C	chromatin organization	chromatin structure	H2AZ_Nucleosome_positions
3 DNA sequencing	17873876	Lee	Corey Nislow	UBC	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	S288C	chromatin organization	chromatin structure	Predicted_nucleosome_occupancy_map_dMean_log2_sMOL
6 micrococcal nuclease digestion followed by high throughput sequencing assay	18550805	Mavrich	Frank Pugh	Penn State	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	S288C	chromatin organization	chromatin structure	H3H4_Nucleosome_positions
1 micrococcal nuclease digestion followed by tiling array assay	18989395	Field	Eran Segal	Weizmann Institute of Science	DNA sequencing	DNA extract	Other	chromatin organization	chromatin structure	predicted_average_nucleosome_occupancy_map_dMean_log2_sMOL
Category	13 chromatin organization									
First author										
GBrowse Category	13 chromatin structure									
Lab PI										
PMID										
Strain background										
	17392789	Kaplan	Eran Segal	Weizmann Institute of Science	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	Other	chromatin organization	chromatin structure	YPD_nucleosome_occupancy_map_dMean_log2_sMOL
	17873876	Kaplan	Eran Segal	Weizmann Institute of Science	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	Other	chromatin organization	chromatin structure	YPGal_nucleosome_occupancy_map_dMean_log2_sMOL
	18550805	Kaplan	Eran Segal	Weizmann Institute of Science	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	Other	chromatin organization	chromatin structure	predicted_average_nucleosome_occupancy_map_dMean_log2_sMOL
	18989395	Kaplan	Eran Segal	Weizmann Institute of Science	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	Other	chromatin organization	chromatin structure	predicted_average_nucleosome_occupancy_map_dMean_log2_sMOL
	19092803	Kaplan	Eran Segal	Weizmann Institute of Science	micrococcal nuclease digestion followed by high throughput sequencing assay	DNA extract	Other	chromatin organization	chromatin structure	predicted_average_nucleosome_occupancy_map_dMean_log2_sMOL

- 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.