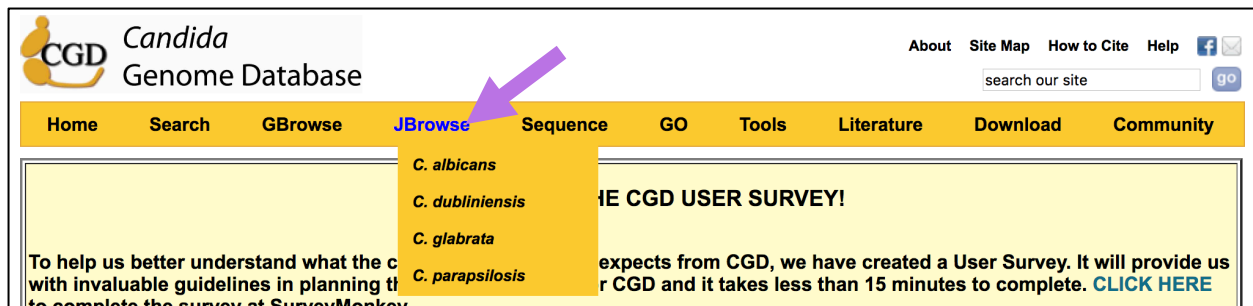


SGD/CGD JBrowse Genome Browser

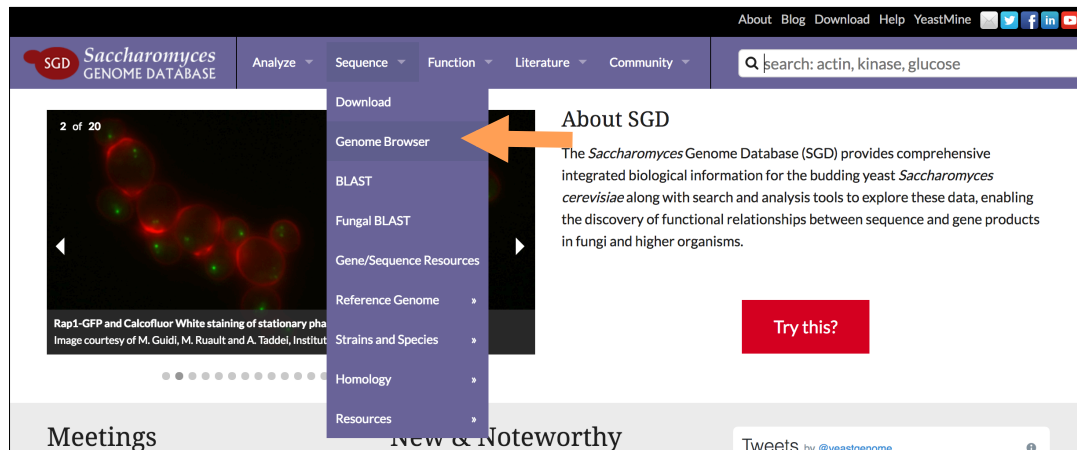
SGD and CGD both provide the genome browsing tool **JBrowse** to enable easy exploration of yeast genomes. JBrowse enables quick scrolling through genomic features and visualization of experimental information from large-scale studies in the form of **data tracks**. In this exercise, we will use JBrowse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



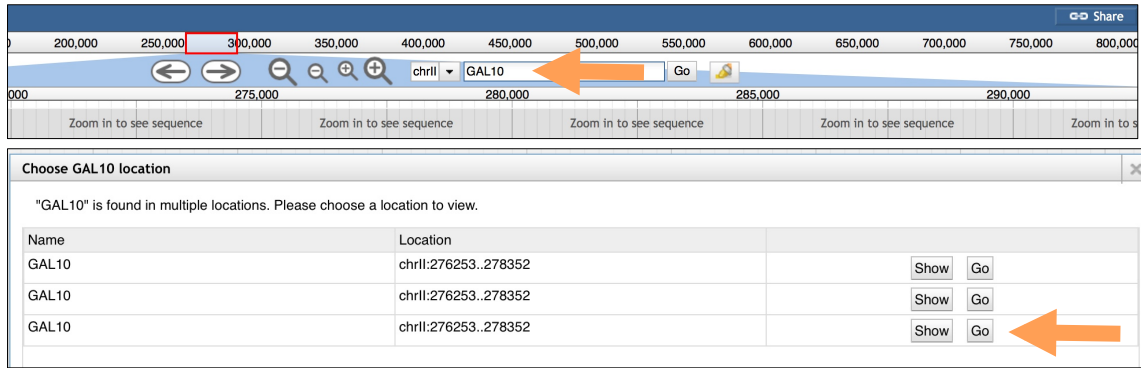
- From any Locus Summary page, by clicking on the JBrowse image link in the Basic Information section.
 - CGD JBrowse provides *C. albicans*, *dubliniensis*, *glabrata*, and *parapsilosis*.
- You can access the SGD's JBrowse genome browser in the following locations:
 - From the home page (www.yeastgenome.org),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

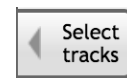
Using SGD's JBrowse genome browser, analyze the transcriptional regulation of **GAL10**.

- 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						
Currently Active Recently Used		<input type="checkbox"/>	PMID	▲ First author	Lab PI	Lab	Assay Term Name	Biosample Term Name	Strain background	Category	GBrowse Category	Track		
▼ Assay Term Name		<input type="checkbox"/>	42 ChIP-chip assay 1 ChIP-seq assay 5 Chromatin immunoprecipitation with exonuclease sequencing assay (ChIP-exo) 4 RNA-seq assay 8 Serial Analysis of Gene Expression (SAGE) 7 transcription profiling by tiling array 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
		<input checked="" type="checkbox"/>	16522208	MacIsaac	Ernest Fraenkel	MIT	ChIP-chip assay	DNA extract	W303	transcription	transcription recombination	TF_Chip_Chip		
		<input type="checkbox"/>	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	polyA RNA extract	S288C	transcription	RNA expression profiling	Transcribed_regions_polyA_RNA		
		<input type="checkbox"/>	16569694	David	Lars M. Steinmetz	EMBL	transcription profiling by tiling array assay	RNA extract	S288C	transcription	RNA expression profiling	Transcribed_regions_total_RNA		
▼ Category		<input checked="" type="checkbox"/>	(no data)											
10 (no data)		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_ARS_identified		
11 DNA replication, recombination and repair		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_Predicted_ACSs		
16 RNA structure		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_Predicted_ARSs		
1 Reference sequence		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	MCM2_Chip_chip_binding		
1 carbon utilization		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	ORC_Chip_chip_binding		
44 chromatin organization		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	ORC_Chip_chip_binding		
1 chromatin organization transcription		<input type="checkbox"/>	17067396	Xu	Simon Tavaré	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	ORC_Chip_chip_binding		
49 histone modification		<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	transcription regulation	Poili_occupancy_WT		
14 mRNA processing		<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	transcription regulation	Poili_occupancy_sen1		
1 mitotic cell cycle		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	Dst1_RNA_Poili_SC_L16C_Chip_chip		
17 stress heat shock carbon utilization nutrient utilization osmotic stress oxidative stress phosphorus utilization		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	Dst1_RNA_Poili_SC_L16C_Chip_chip		
67 transcription		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	Dst1_RNA_Poili_SC_L16C_Chip_chip		
2 translation regulation		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	WT_RNA_Poili_YPD		
▼ First author		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	WT_RNA_Poili_YPD		
2 David		<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	WT_RNA_Poili_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.

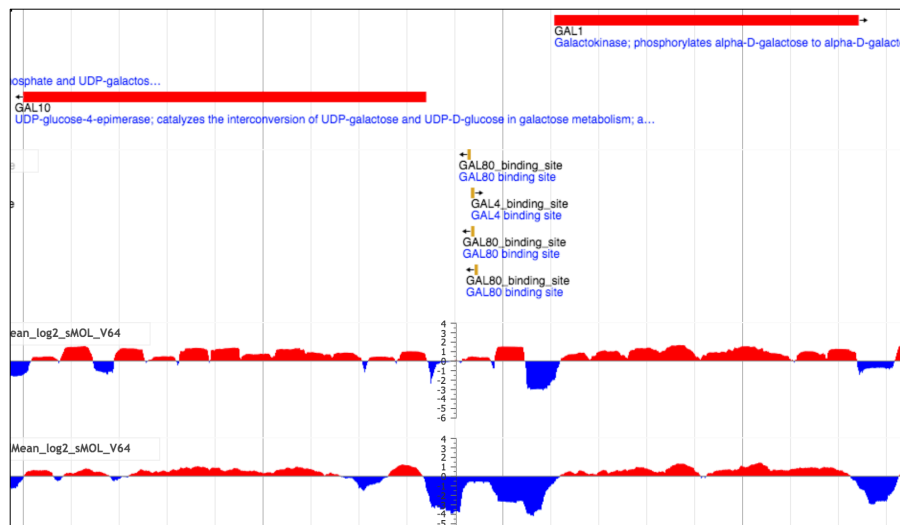
The screenshot shows the Genomes browser interface. The top navigation bar includes 'Genome', 'Track', 'View', and 'Help'. Below the navigation bar, a genomic track is displayed with a scale from 50,000 to 500,000. The 'MacIsaac_2006_Chip_chip_TFB5s_V64' track is highlighted, and a context menu is open over it. The menu options are: 'About this track', 'Pin to top', 'Edit config', 'Delete track', 'Save track data', 'Display mode', and 'Show labels'. The 'About this track' option is selected, and an orange arrow points to it. The track itself shows binding sites for GAL4 and GAL80, with labels like 'GAL4 binding site' and 'GAL80 binding site'.

- 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		<div>Back to browser</div> <div>Clear All Filters</div>		Contains text		nucleosome					13 matching tracks	
		<div>PMID</div>	<div>First author</div>	<div>Lab PI</div>	<div>Lab</div>	<div>Assay Term Name</div>	<div>Biosample Term Name</div>	<div>Strain background</div>	<div>Category</div>	<div>GBrowse Category</div>	<div>Track</div>	
* Assay Term Name		<div>17392789</div>	<div>Albert</div>	<div>Frank Pugh</div>	<div>Penn State</div>	<div>ChIP-seq assay</div>	<div>DNA extract</div>	<div>S288C</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>H2AZ_Nucleosome_positions</div>	
1 ChIP-seq assay												
3 DNA sequencing												
8 micrococcal nuclease digestion followed by high throughput sequencing assay		<div>17873876</div>	<div>Lee</div>	<div>Corey Nislow</div>	<div>UBC</div>	<div>micrococcal nuclease digestion followed by tiling array assay</div>	<div>DNA extract</div>	<div>S288C</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>Predicted_nucleosome_occupancy_model</div>	
1 micrococcal nuclease digestion followed by tiling array assay												
* Category		<div>18550805</div>	<div>Mavrich</div>	<div>Frank Pugh</div>	<div>Penn State</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>S288C</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>H3H4_Nucleosome_positions</div>	
13 chromatin organization												
* First author		<div>18989395</div>	<div>Field</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>DNA sequencing</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>predicted_average_nucleosome_occupancy</div>	
1 Albert												
3 Field												
7 Kaplan												
1 Lee												
1 Mavrich		<div>18989395</div>	<div>Field</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>DNA sequencing</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>predicted_nucleosome_positioning_model_score</div>	
* GBrowse Category		<div>18989395</div>	<div>Field</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>DNA sequencing</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>summarized_nucleosome_occupancy</div>	
13 chromatin structure												
* Lab PI		<div>19092803</div>	<div>Kaplan</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>InVivo_nucleosome_occupancy_map_dMean_log2_sMOL</div>	
1 Corey Nislow												
10 Eran Segal												
2 Frank Pugh												
* PMID		<div>17392789</div>										
1 17392789												
1 17873876												
1 18550805		<div>19092803</div>	<div>Kaplan</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>YPD_nucleosome_occupancy_map_dMean_log2_sMOL</div>	
3 18989395												
7 19092803												
* Strain background		<div>19092803</div>	<div>Kaplan</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>YPETOH_nucleosome_occupancy_map_dMean_log2_sMOL</div>	
10 Other												
3 S288C												
		<div>19092803</div>	<div>Kaplan</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>YPGal_nucleosome_occupancy_map_dMean_log2_sMOL</div>	
		<div>19092803</div>	<div>Kaplan</div>	<div>Eran Segal</div>	<div>Weizmann Institute of Science</div>	<div>micrococcal nuclease digestion followed by high throughput sequencing assay</div>	<div>DNA extract</div>	<div>Other</div>	<div>chromatin organization</div>	<div>chromatin structure</div>	<div>YPGal_nucleosome_occupancy_map_dMean_log2_sMOL</div>	

- 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.