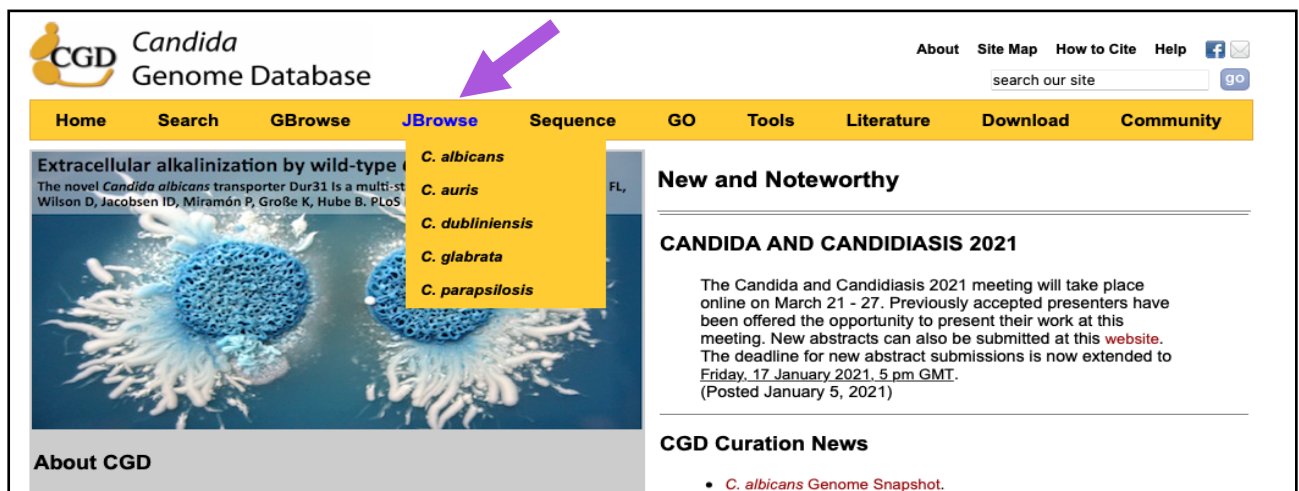


SGD/CGD JBrowse Genome Browser

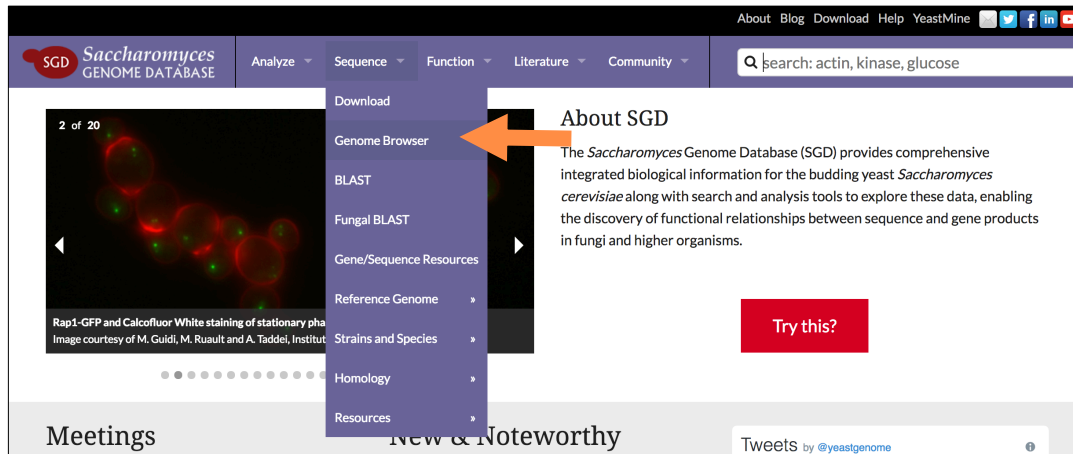
SGD and CGD both provide the genome browsing tool **JBrowse** to enable easy exploration of yeast genomes. JBrowse enables quick scrolling through genomic features and visualization of experimental information from large-scale studies in the form of **data tracks**. In this exercise, we will use JBrowse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



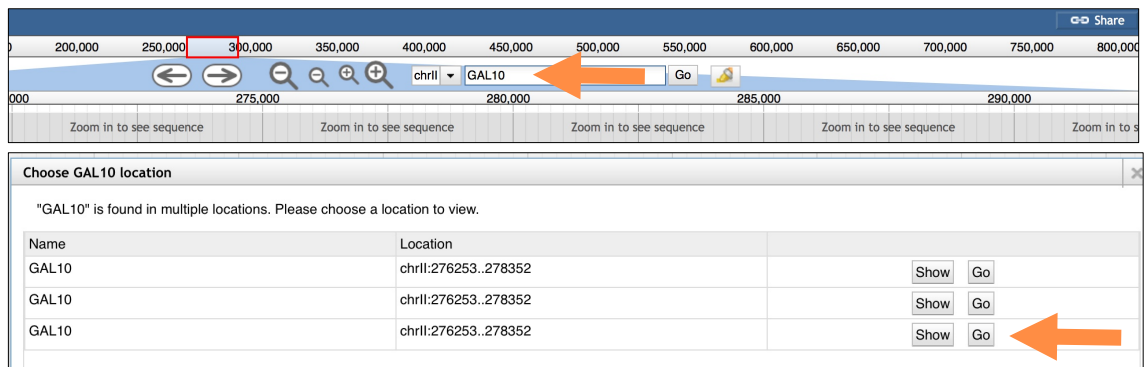
- From any Locus Summary page, by clicking on the JBrowse image link in the Basic Information section.
- CGD JBrowse provides *C. albicans*, *auris dubliniensis*, *glabrata*, and *parapsilosis*.
- You can access the SGD's JBrowse genome browser in the following locations:
 - From the home page (www.yeastgenome.org),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

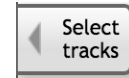
- In the JBrowse window, enter **GAL10** into the search box in the navigation bar on top and press **Go**. Multiple results will be listed, but all refer to the same gene.



- 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>Assay Term Name</div> <div>Category</div> <div>First author</div>		<div>Back to browser</div> <div>Clear All Filters</div> <div>Contains text</div> <div>67 matching tracks</div>								
<input type="checkbox"/>	PMID	First author	Lab PI	Lab	Assay Term Name	Biosample Term Name	Strain background	Category	GBrowse Category	Track
<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
<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_ARIS_identified
<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_Predicted_ARs
<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	Known_Predicted_ARs
<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	MCM2_ChIP_chip_binding
<input type="checkbox"/>	17067396	Xu	Simon Tavare	Cancer Research UK Cambridge Institute	ChIP-chip assay	DNA extract	W303	transcription	RNA expression profiling	ORC_ChIP_chip_binding
<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	transcription regulation	PollI_occupancy_WT
<input type="checkbox"/>	17157256	Steinmetz	David A. Brow	University of Wisconsin	ChIP-chip assay	DNA extract	Other	transcription	transcription regulation	PollI_occupancy_sen1
<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	Dst1_RNA_PollIII_SC_L16C_ChIP_chip
<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	Dst1_RNA_PollIII_SC_L16C_ChIP_chip
<input type="checkbox"/>	18628399	Ghavi-Helm	Julie Soutourina	CEA	ChIP-chip assay	DNA extract	S288C	transcription	transcription regulation	WT_RNA_PollIII_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.

Genome Track View Help

50,000 100,000 150,000 200,000 250,000 300,000 350,000 400,000 450,000 500,000

chrII:275001..282010 (7.01 Kb)

276,250 277,500 278,750 280,000

Reference sequence sequence Zoom in to see sequence Zoom in to see sequence Zoom in to see sequence Zoom in to see sequence

All Annotated Sequence Features

MacIsaac_2006_ChIP_chip_TFBSS_V64

GAL4 binding site

NRG1 binding site

NRG1 binding site

YpGal_nucleosome_occupancy

GAL1 Galactokinase; phosphorylates alpha-D-galactose to alpha-D-galactose-1-phosphate

GAL10 UDP-glucose-4-epimerase; catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; a...

GAL80 binding site

GAL80 binding site

GAL4 binding site

GAL4 binding site

GAL80 binding site

GAL80 binding site

GAL80 binding site

GAL80 binding site

About this track

Pin to top

Edit config

Delete track

Save track data

Display mode

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

My Tracks

Currently Active

Recently Used

Back to browser

Clear All Filters

Contains text

nucleosome

13 matching tracks

Assay Term Name

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

Category

13 chromatin organization

First author

1 Albert

3 Field

7 Kaplan

1 Lee

1 Mavrich

Browse Category

13 chromatin structure

Lab PI

1 Corey Nislow

10 Eran Segal

2 Frank Pugh

PMID

1 17392789

1 17873876

1 18550805

3 18989395

7 19092803

Strain background

10 Other

3 S288C

PMID

17392789

First author

Albert

Lab PI

Frank Pugh

Lab

Penn State

Assay Term Name

ChIP-seq assay

Biosample Term Name

DNA extract

Strain background

S288C

Category

chromatin organization

Browse Category

chromatin structure

Track

H2A2_Nucleosome_positions

PMID

17873876

First author

Lee

Lab PI

Corey Nislow

Lab

UBC

Assay Term Name

micrococcal nuclease digestion followed by tiling array assay

Biosample Term Name

DNA extract

Strain background

S288C

Category

chromatin organization

Browse Category

chromatin structure

Track

Predicted_nucleosome_occupancy_map_dMean_log2_sMOL

Category

13 chromatin organization

PMID

18550805

First author

Mavrich

Lab PI

Frank Pugh

Lab

Penn State

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

S288C

Category

chromatin organization

Browse Category

chromatin structure

Track

H3H4_Nucleosome_positions

PMID

18989395

First author

Field

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

DNA sequencing

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

predicted_average_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

18989395

First author

Field

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

DNA sequencing

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

predicted_nucleosome_positioning_model_score

PMID

18989395

First author

Field

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

DNA sequencing

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

summarized_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

19092803

First author

Kaplan

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

InVivo_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

19092803

First author

Kaplan

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

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Track

YPD_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

19092803

First author

Kaplan

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

YPEiCHL_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

19092803

First author

Kaplan

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

Browse Category

chromatin structure

Track

YPGal_nucleosome_occupancy_map_dMean_log2_sMOL

PMID

19092803

First author

Kaplan

Lab PI

Eran Segal

Lab

Weizmann Institute of Science

Assay Term Name

micrococcal nuclease digestion followed by high throughput sequencing assay

Biosample Term Name

DNA extract

Strain background

Other

Category

chromatin organization

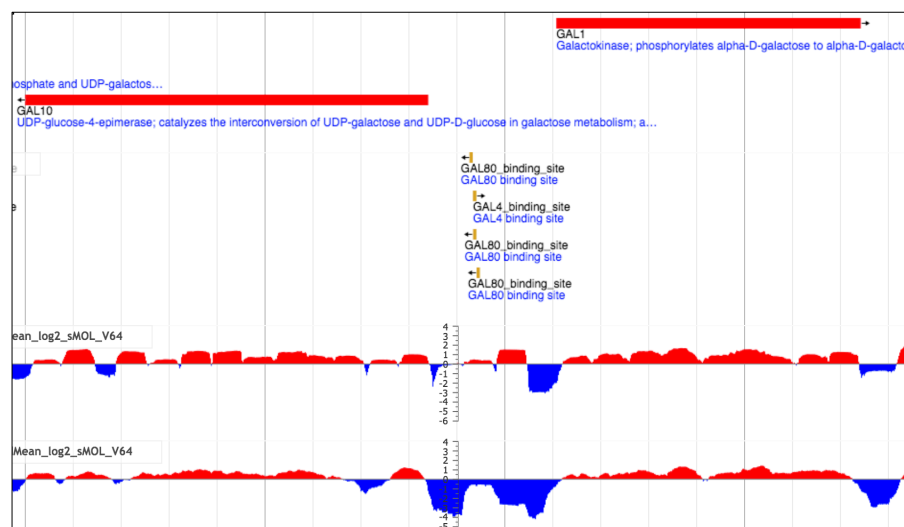
Browse Category

chromatin structure

Track

predicted_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?



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