

2019.08.05

統合データベース講習会
AJACS番町3

ChIP-Atlas

ハンズオンセミナー



九州大学大学院・医学研究院
発生再生医学分野・講師

沖 真弥 (Oki, Shinya)

IGV のインストール

IGV のインストール

A screenshot of a web browser window showing a Google search results page. The search query "igv genome" is entered in the search bar. A dropdown menu shows suggestions: "igv genome", "igv genome file", "igv genome 使い方", "igv genome file format", "igv genome format", "igv genome download", "igv genome server", and "igv genome could not be read". Below the suggestions are two buttons: "Google 検索" and "I'm Feeling Lucky". An orange speech bubble points from the left towards the search bar area.

日本

広告 ビジネス Googleについて プライバシー 規約 設定

IGV のインストール

The screenshot shows a web browser window with the URL software.broadinstitute.org. The main content is the IGV (Integrative Genomics Viewer) download page. On the left, there's a sidebar with links like Home, Downloads, and Documents. A large orange circle highlights the 'Downloads' link in the sidebar. The main area has tabs for Overview, Downloads, and Citing IGV. The Downloads tab is active, showing a download button with a blue arrow icon and the text 'Download the IGV desktop application and igtools.' Below the tabs, there's information about funding and citation.

Downloads

The Integrative Genomics Viewer (IGV) is a high-performance visualization tool for interactive exploration of large, integrated genomic datasets. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

Funding

Development of IGV has been supported by funding from the [National Cancer Institute \(NCI\)](#) of the [National Institutes of Health](#), the [Informatics Technology for Cancer Research \(ITCR\)](#) of the NCI, and the [Starr Cancer Consortium](#).

IGV participates in the [GenomeSpace](#) initiative, which is funded by the [National Human Genome Research Institute](#).

Downloads

Download the IGV desktop application and igtools.

Citing IGV

To cite your use of IGV in your publication:

James T. Robinson, Helga Thorvaldsdóttir, Wendy Winckler, Mitchell Guttman, Eric S. Lander, Gad Getz, Jill P. Mesirov. [Integrative Genomics Viewer](#). *Nature Biotechnology* 29, 24–26 (2011).

Helga Thorvaldsdóttir, James T. Robinson, Jill P. Mesirov. [Integrative Genomics Viewer \(IGV\): high-performance genomics data visualization and exploration](#). *Briefings in Bioinformatics* 14, 178–192 (2013).

IGV のインストール

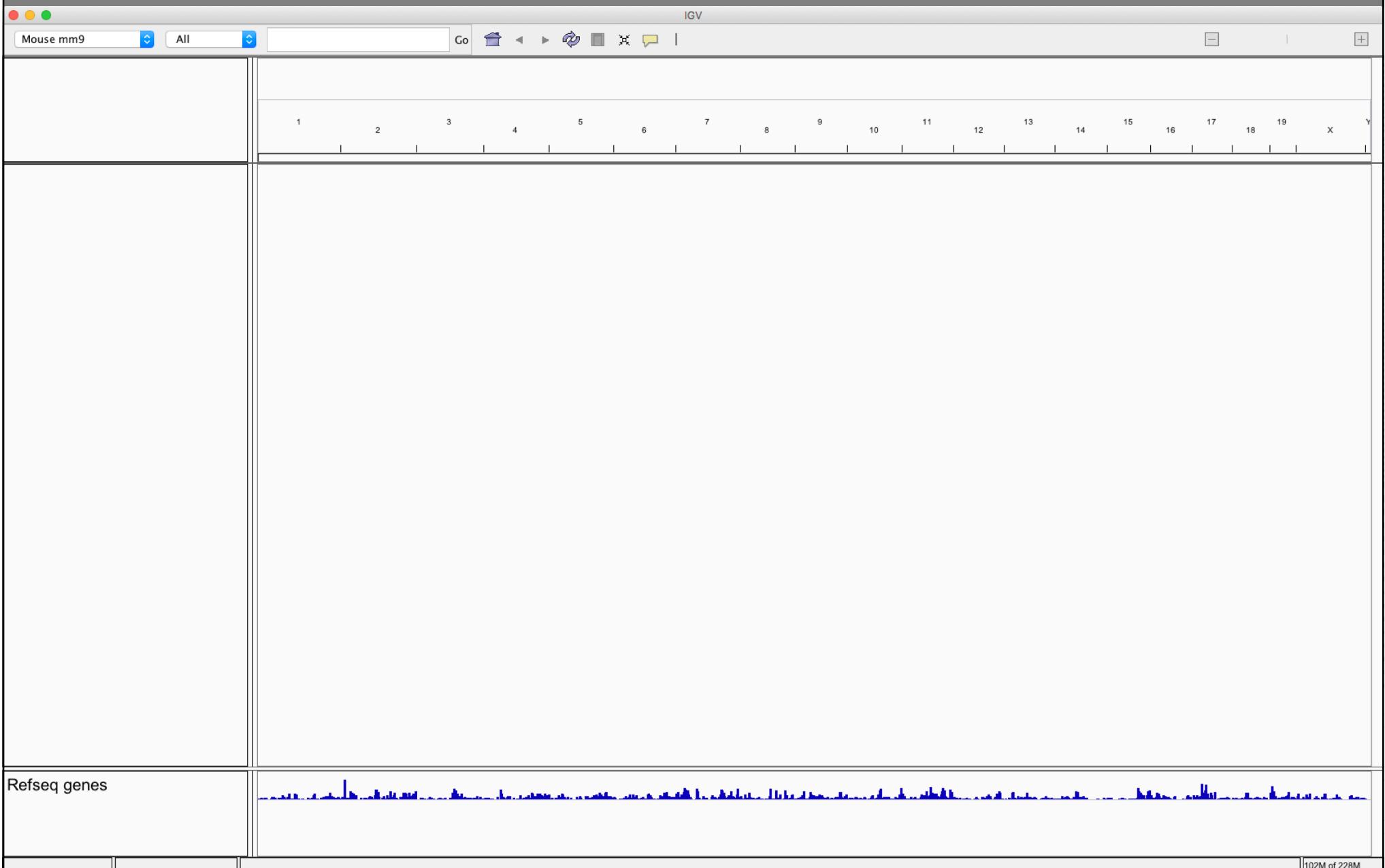
The screenshot shows the IGV Downloads page. On the left, there's a sidebar with links like Home, Downloads, Documents, and Contact. The main content area has a header "Downloads". Below it, there's a section titled "Install IGV 2.5.x" with four download options:

- IGV Mac App**: An orange callout bubble points to this section. It says: "Download and unzip the Mac App Archive, then double-click the IGV application to run it. You can move the app to the Applications folder, or anywhere else."
- IGV for Windows**: An orange callout bubble points to this section. It says: "Download and run the .exe file. An IGV shortcut will be created on your desktop. Double-click the icon to run the application."
- IGV for Linux**: It says: "Download and unzip the Archive. See the downloaded *readme.txt* for further instructions."
- IGV and igvtools to run on the command line (all platforms)**: It says: "Download and unzip the Archive. **Requires Java 11**. See the downloaded *readme.txt* and *igvtools_readme.txt* for further instructions."

Below these sections, there's a "Other IGV Versions" section with links to "Development Snapshot Build" and "Archived Versions". At the bottom, there's a "Source Code" section with a link to GitHub.

うまくいかない時：
- Java のバージョンを 8 以降にアップデート

IGV のインストール



ChIP-Atlas 利用前に起動しておく

ChIP-Atlasへのアクセス

chip-atlas

chip-atlas
chip-atlas 使い方
atlas chip heater
atlas blue chip gloves
atlas chip v2
vw atlas chip tuning
vw atlas chip
hazel atlas chip and dip

Google 検索 I'm Feeling Lucky

不適切な検索候補の報告

日本

広告 ビジネス Googleについて プライバシー 規約 設定

ChIP-Atlasへのアクセス

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

ChIP-Atlas

ChIP-Atlas is an integrative and comprehensive database for visualizing and making use of public ChIP-seq data. ChIP-Atlas covers almost all public ChIP-seq data submitted to the SRA (Sequence Read Archives) in NCBI, DDBJ, or ENA, and is based on over 78,000 experiments.

[Watch movie introduction](#)

The four main features of ChIP-Atlas are:

Peak Browser graphically visualizes protein binding on given genomic loci with genome browser (IGV). Watch Movie	Target Genes predicts target genes bound by given transcription factors. Watch Movie	Colocalization predicts partner proteins colocalizing with given transcription factors. Watch Movie	Enrichment Analysis predicts proteins bound to given genomic loci and genes (formerly known as <i>in silico</i> ChIP). Watch Movie
---	---	--	---

THIS WORK IS SUPPORTED BY [NIG SUPERCOMPUTER SYSTEM](#) AND [NATIONAL BIOSCIENCE DATABASE CENTER](#).
NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

KYUSHU UNIVERSITY IN COLLABORATION WITH 

ChIP-Atlasへのアクセス

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

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[Watch movie introduction](#)

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Peak Browser
graphically visualizes protein binding on given genomic loci with genome browser (IGV).
[Watch Movie](#)

Target Genes
predicts target genes bound by given transcription factors.
[Watch Movie](#)

Colocalization
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[Watch Movie](#)

Enrichment Analysis
predicts proteins bound to given genomic loci and genes (formerly known as *in silico* ChIP).
[Watch Movie](#)

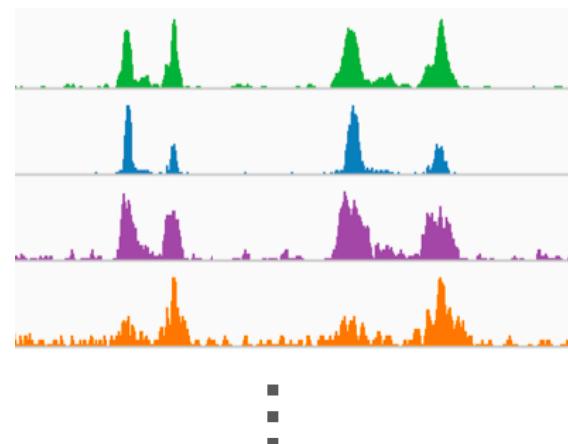
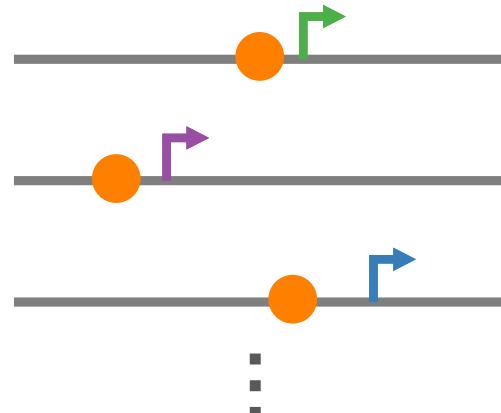
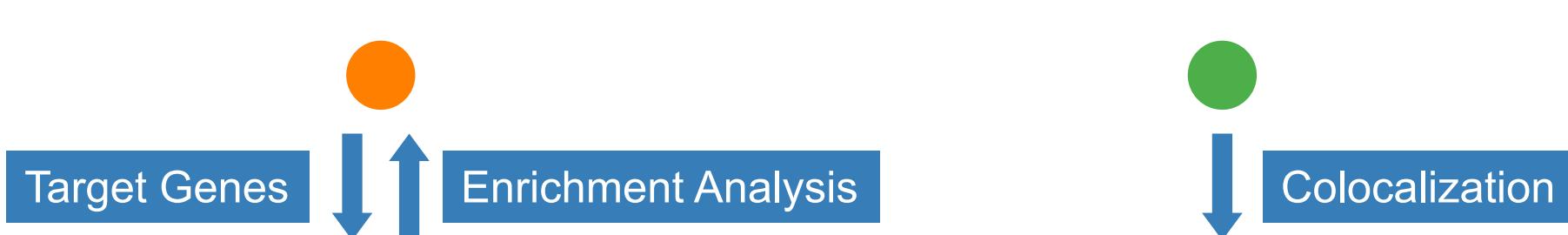
THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND NATIONAL BIOSCIENCE DATABASE CENTER.
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4つの解析ツール

複数データをまとめて見る Peak Browser の使い方

ChIP-Atlas でできること

Peak Browser



複数データをまとめて見る

The screenshot shows the ChIP-Atlas website. At the top, there's a navigation bar with links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar labeled "Find an experiment". Below the navigation bar, the main title "ChIP-Atlas" is displayed in a large, bold font. A descriptive text follows, stating that ChIP-Atlas is an integrative and comprehensive database for visualizing and making use of public ChIP-seq data, covering almost all public ChIP-seq data submitted to the SRA in NCBI, DDBJ, or ENA, and is based on over 78,000 experiments. There's also a link to "Watch movie introduction".

ChIP-Atlas

ChIP-Atlas is an integrative and comprehensive database for visualizing and making use of public ChIP-seq data. ChIP-Atlas covers almost all public ChIP-seq data submitted to the SRA (Sequence Read Archives) in NCBI, DDBJ, or ENA, and is based on over 78,000 experiments.

[Watch movie introduction](#)

クリック

The four main features of ChIP

Peak Browser

graphically visualizes protein binding on given genomic loci with genome browser (IGV).

[Watch Movie](#)

Target Genes

predicts target genes bound by given transcription factors.

[Watch Movie](#)

Colocalization

predicts partner proteins colocalizing with given transcription factors.

[Watch Movie](#)

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[Watch Movie](#)



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NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

複数データをまとめて見る

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾ Tutorial movies ▾

ChIP-Atlas - Peak Browser

Visualize All Peaks from Published ChIP-Seq data.

H. sapiens M. musculus R. norvegicus D. melanogaster C. elegans S. cerevisiae

Antigen Class

- All antigens (34390)
 - DNase-seq (1511)
 - Histone (8982)
 - RNA polymerase (1104)
 - TFs and others (8368)
 - Input control (4002)
 - Unclassified (6194)
 - No description (4229)

Cell type Class

- All cell types (34390)
 - Adipocyte (292)
 - Blood (9096)
 - Bone (655)
 - Breast (3699)
 - Cardiovascular (1080)
 - Digestive tract (2447)
 - Epidermis (1089)

Threshold for Significance ⓘ

- 50
- 100
- 200
- 500

Antigen

Cell type

View on IGV

Download BED file

KYUSHU UNIVERSITY IN COLLABORATION WITH

  DBCLS
Database Center
for Life Science

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NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

複数データをまとめて見る

ChIP-Atlas H. sapience

Visualize All Peaks from Public Experiments

H. sapiens M. musculus R. norvegicus D. melanogaster C. elegans S. cerevisiae

Antigen Class

- All antigens (34390)
- DNase-seq (1511)
- Histone (8982)
- RNA polymerase (1104)
- TFs and others (8368)**
- Input control (4002)
- Unclassified (6194)
- No description (4229)

Cell type Class

- Neural (1531)
- Pancreas (433)
- Placenta (38)
- Pluripotent stem cell (2887)**
- Prostate (1466)
- Uterus (1457)
- Others (767)
- Unclassified (438)

Threshold for Significance ⓘ

- 50
- 100
- 200
- 500

View on IGV

Download BED file

Tutorial movies ⓘ

Antigen

Cell type

クリック

TFs and others

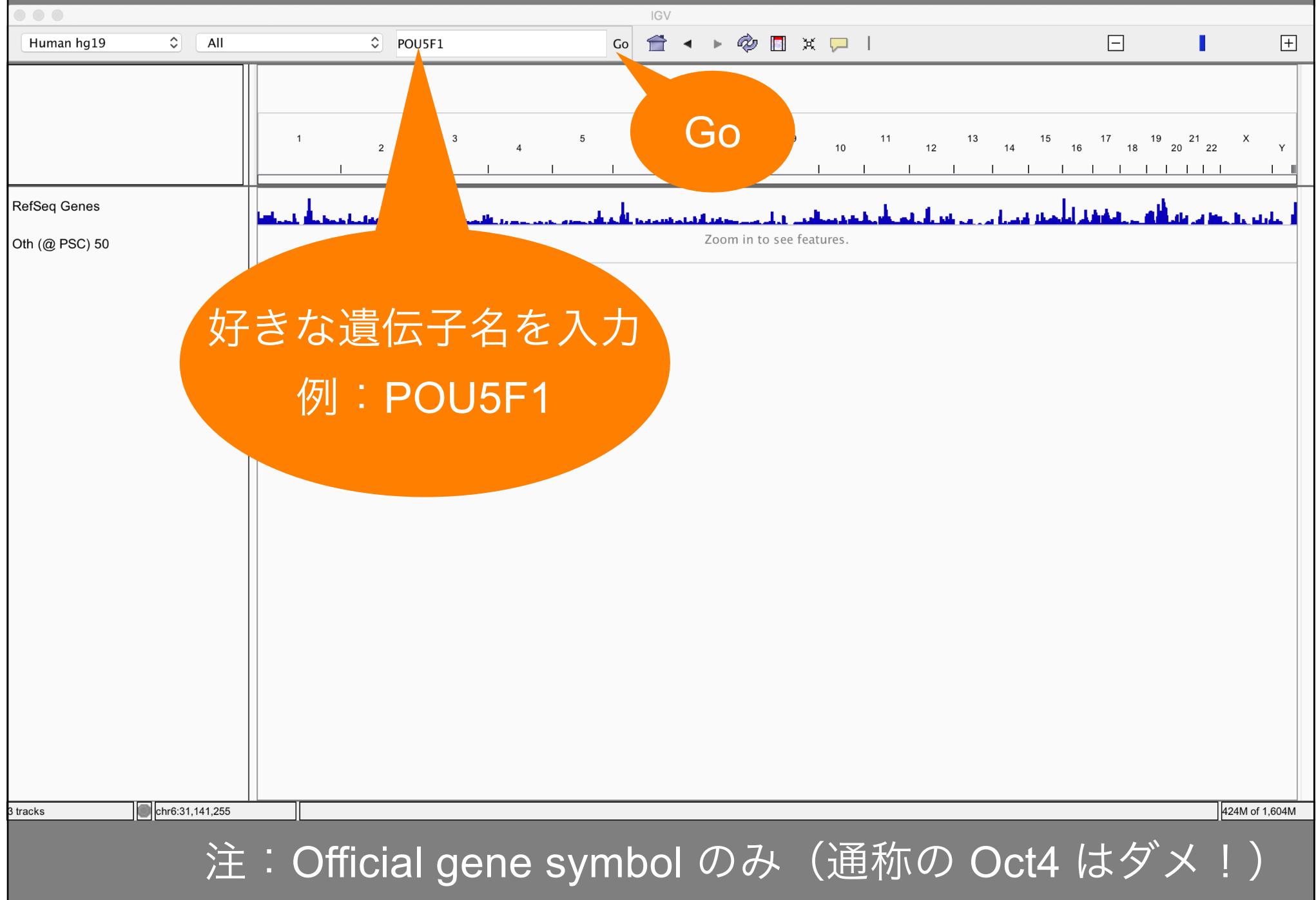
Pluripotent stem cell

KYUSHU UNIVERSITY IN COLLABORATION WITH DBCLS Database Center for Life Science

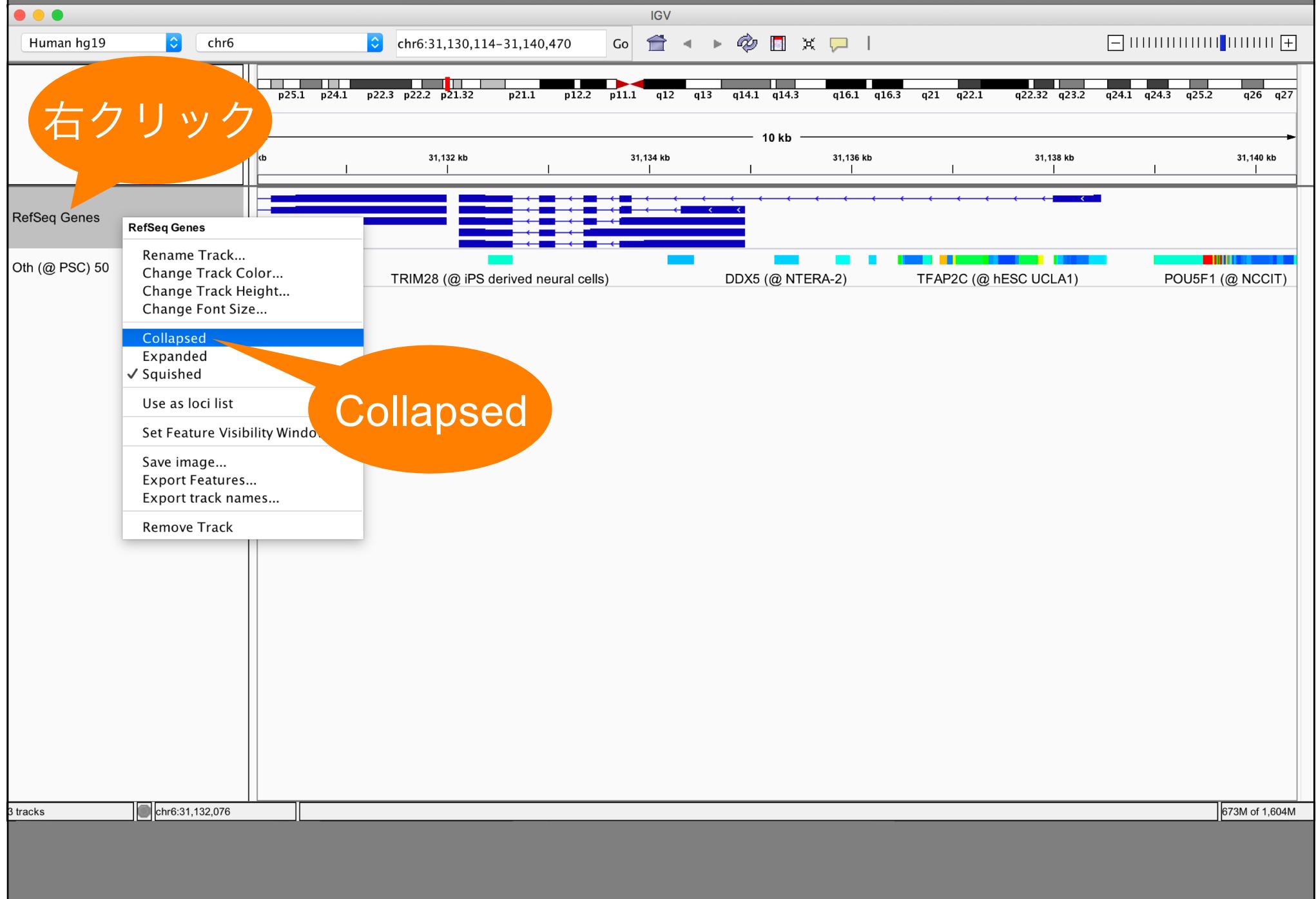
THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND NATIONAL BIOSCIENCE DATABASE CENTER.

NEED HELP? CREATE AN ISSUE ON GITHUB OR CONTACT US

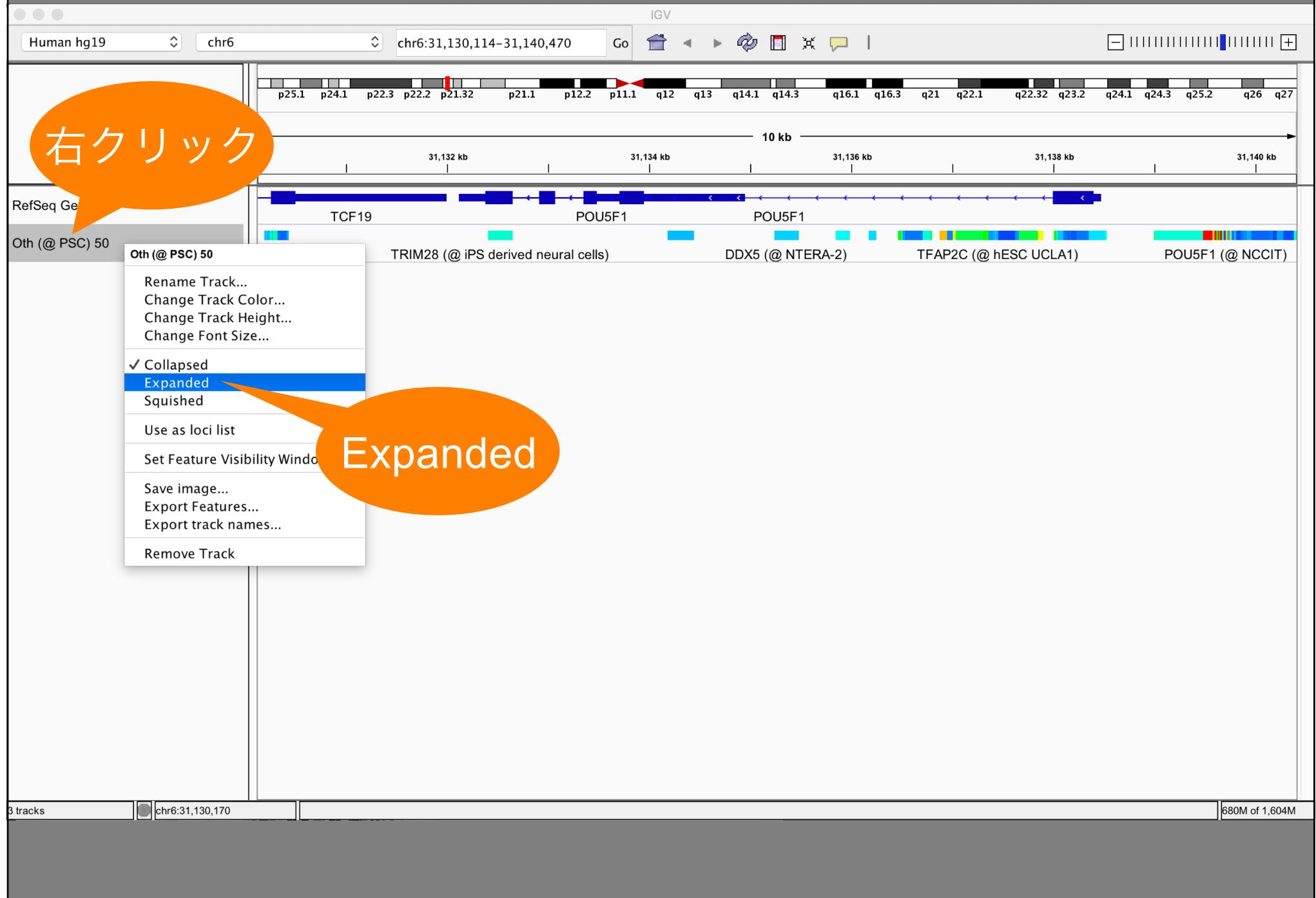
複数データをまとめて見る



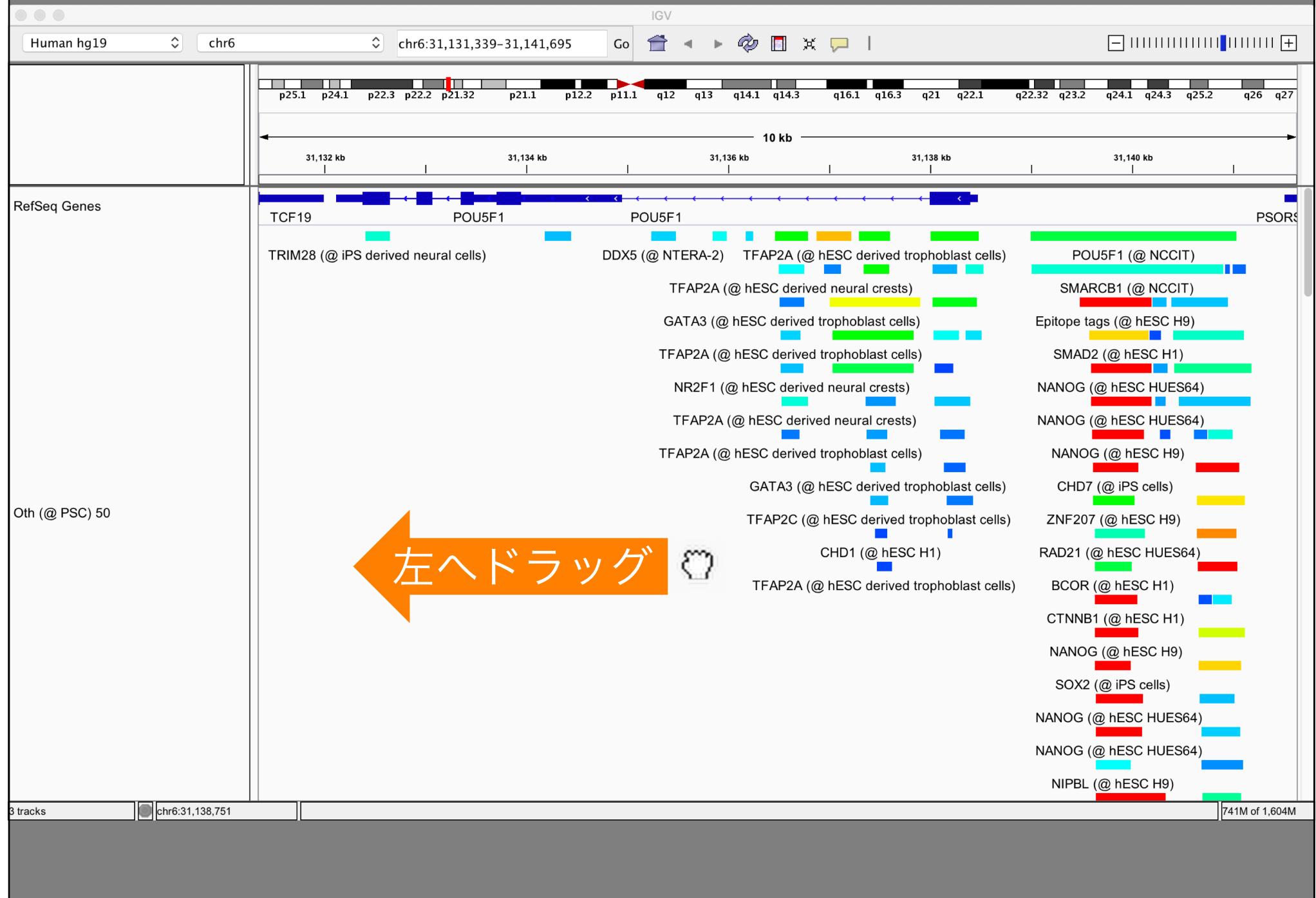
複数データをまとめて見る



複数データをまとめて見る



複数データをまとめて見る

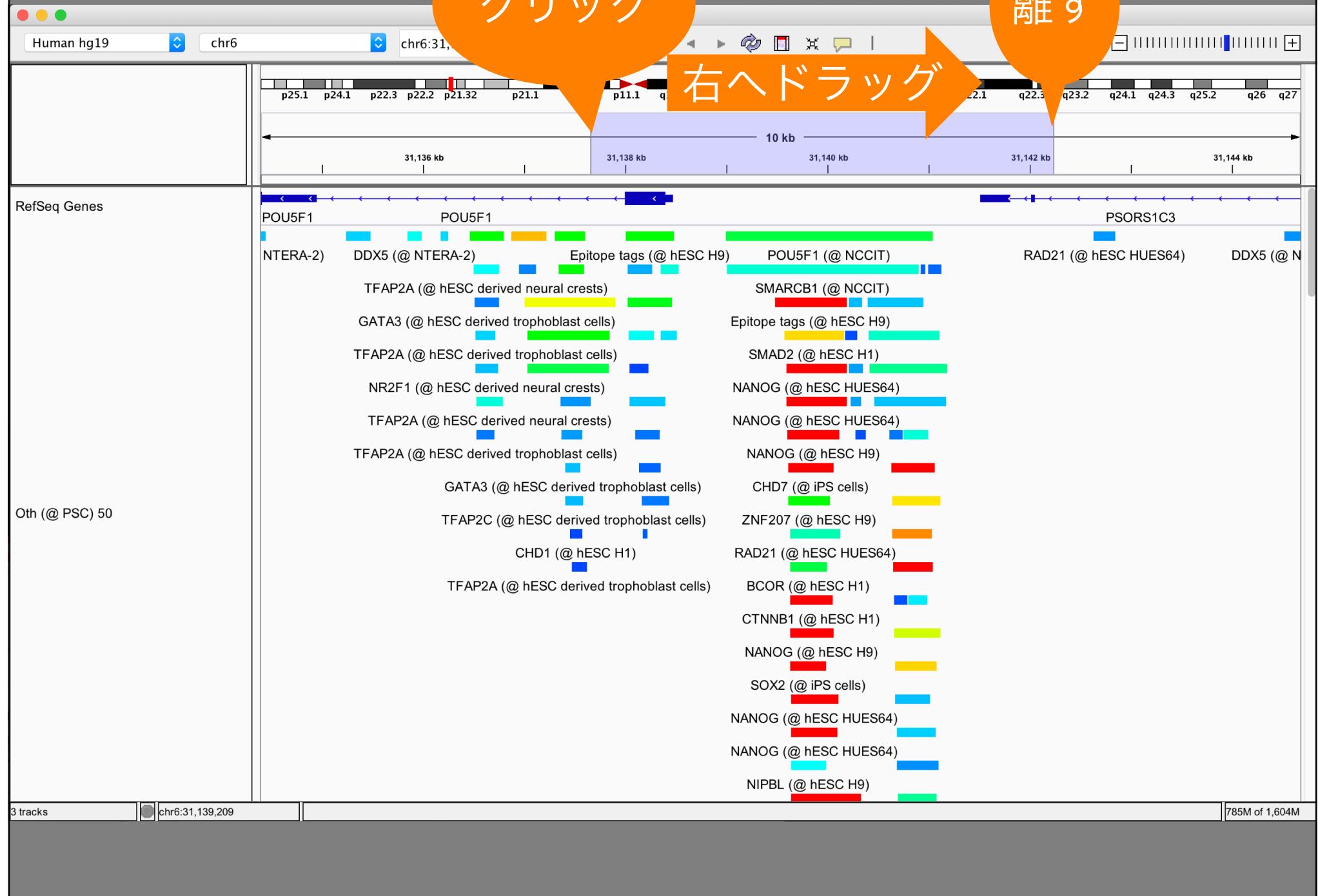


複数データをまとめて表示

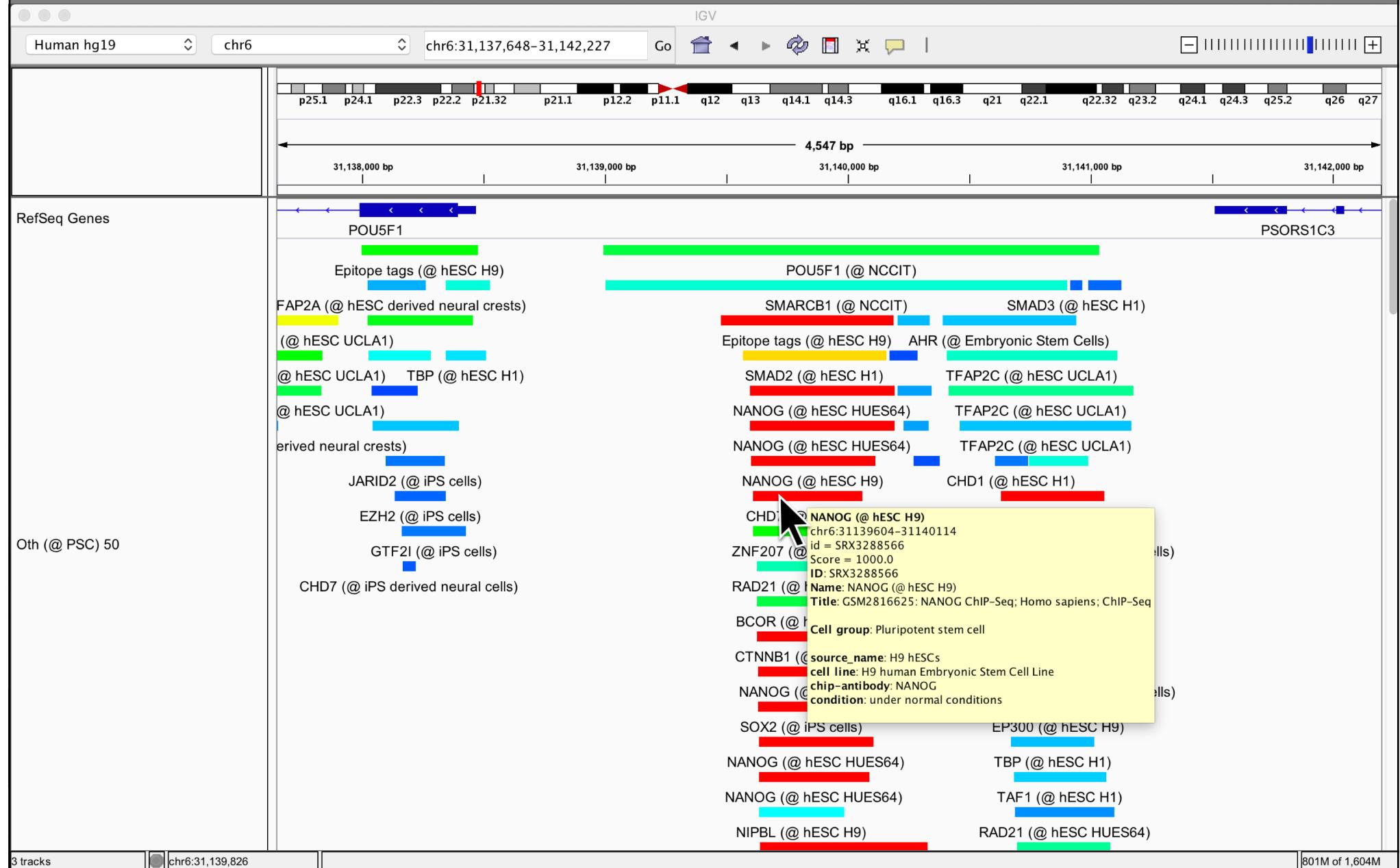
クリック

離す

右へドラッグ

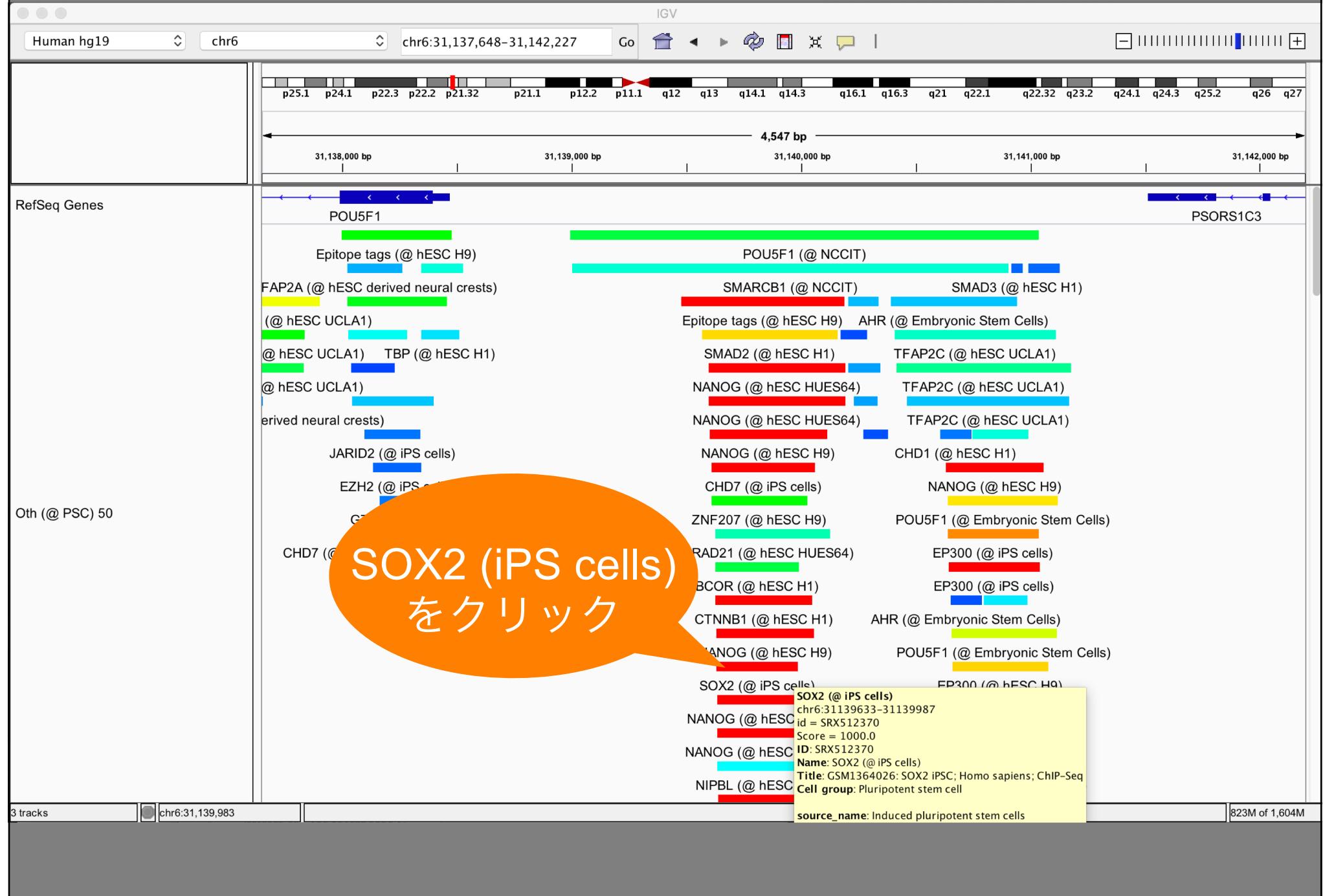


複数データをまとめて見る



カーソルを当てる → メタ情報が表示される

個別のデータ見る



個別のデータ見る

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)

SRX512370

GSM1364026: SOX2 iPSC; Homo sapiens; ChIP-Seq

[View on IGV ▾](#)[View Analysis ▾](#)[Download ▾](#)[Link Out ▾](#)

BigWig

Peak-call ($q < 1E-05$)Peak-call ($q < 1E-10$)Peak-call ($q < 1E-20$)

Genome

Antigen Class

Antigen

Cell type Class

Cell type

BigWig
(アライメントデータ)

Cell type information

NA

NA

Attributes by Original Data Submitter

source_name

Induced pluripotent stem cells

cell type

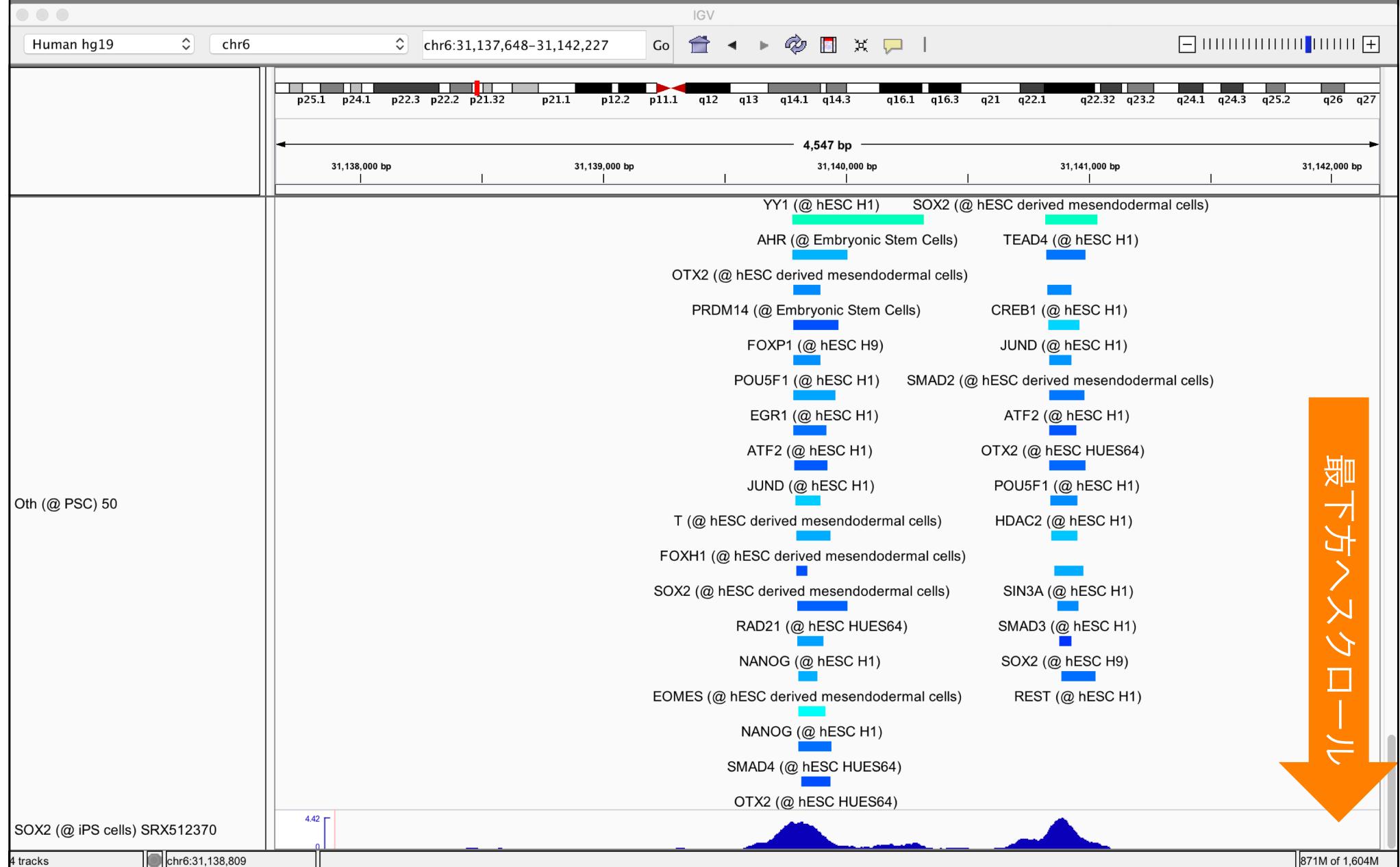
Induced pluripotent stem cells

chip antibody

anti SOX2 antibody

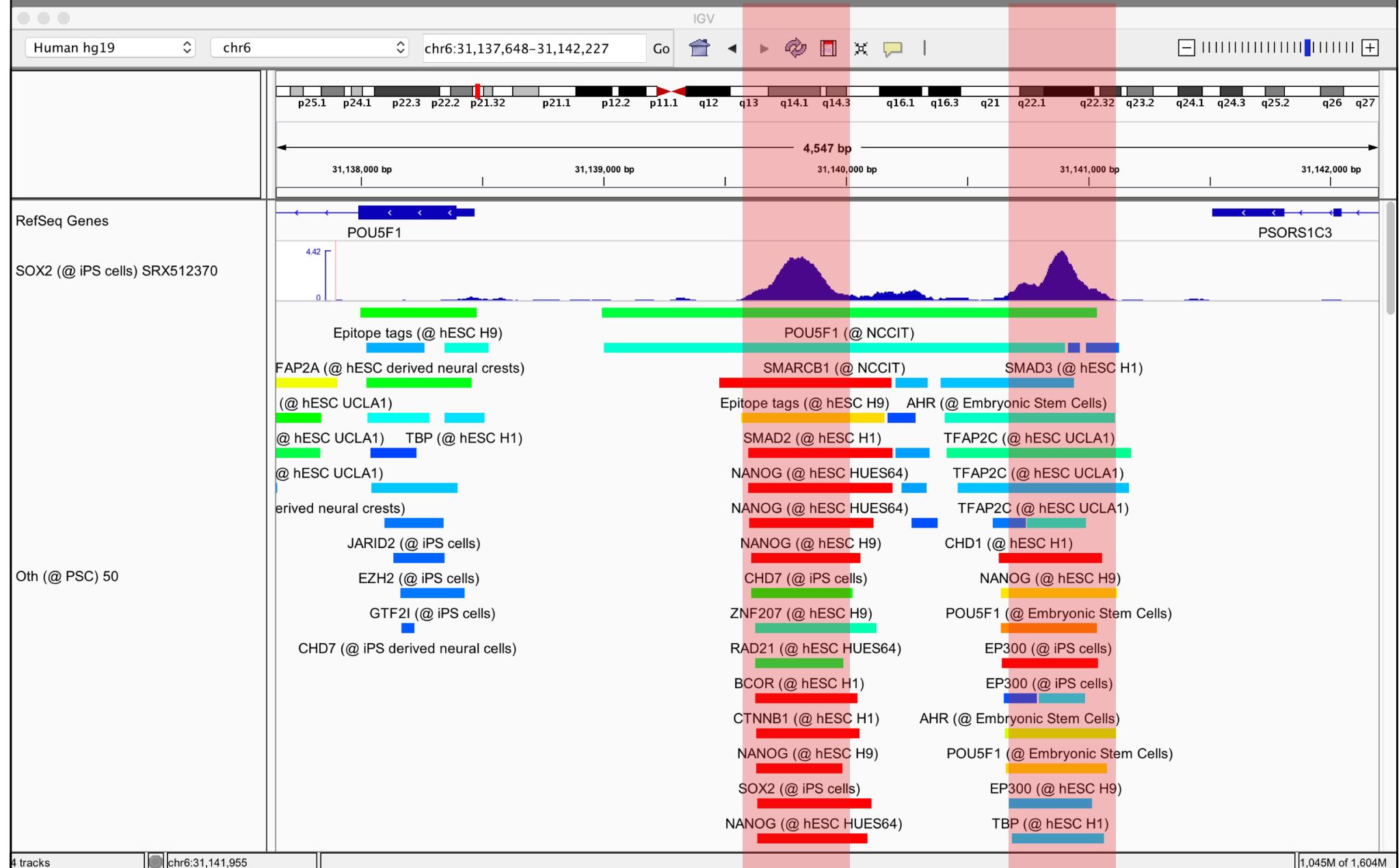
アライメント情報も閲覧できる

個別のデータ見る



アライメント情報も閲覧できる

エンハンサーと転写因子結合が理解できる

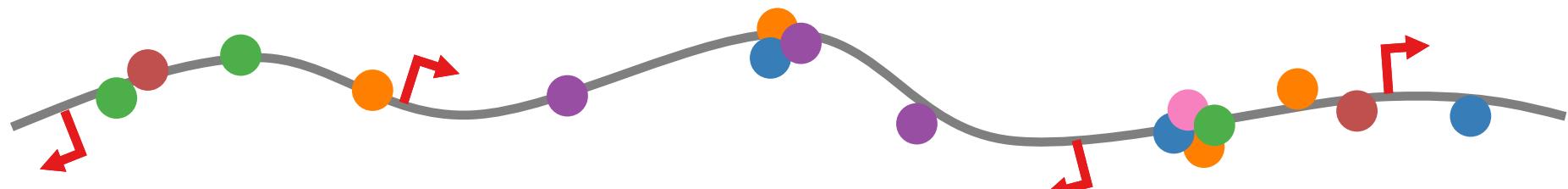


ES 業界では超有名なエンハンサー

エンリッチメント解析

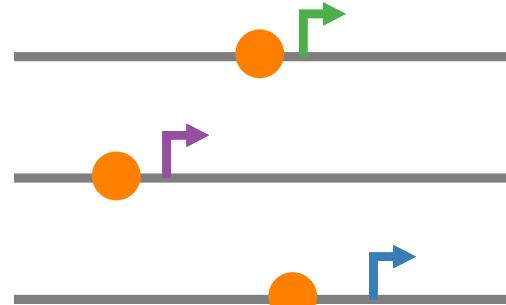
Enrichment Analysis でできること

Peak Browser

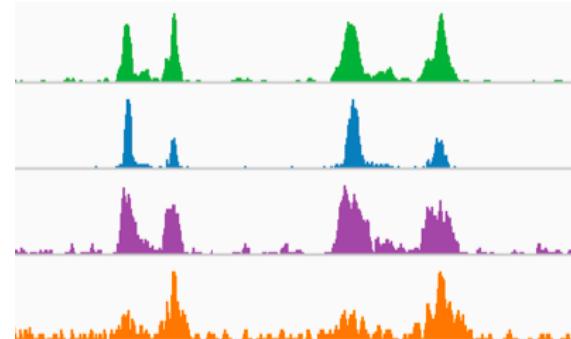


Target Genes

Enrichment Analysis



Colocalization



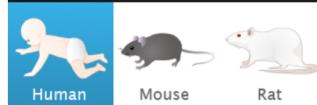
課題：肝臓特異的遺伝子群の上流因子の探索

RefEx より肝臓特異的遺伝子群を取得

Reference
Expression
Dataset
[English](#) | [日本語](#)



RefExの論文が出版されました。あなたの研究に役立ったらぜひ引用を!!
▼もっと詳しく



キーワードで検索

検索

ex) troponin, ALB

肝臓

組織特異的に発現する
遺伝子を見る

遺伝子オントロジー
Gene Ontology

- [cellular process](#)
- [biological regulation](#)
- [metabolic process](#)

- [multicellular organismal process](#)
- [response to stimulus](#)
- [developmental process](#)

他のオントロジーを選ぶ

遺伝子ファミリー

[refex.dbcls.jp/genelist.php?lang=ja&db=human&roku_valid=1&r\[31\]=31&order_key=score](http://refex.dbcls.jp/genelist.php?lang=ja&db=human&roku_valid=1&r[31]=31&order_key=score)

- [RNA recognition motif, RNP-1](#)
- [Pleckstrin homology](#)
- [Kruppel-associated box](#)

- [Protein kinase-like domain](#)
- [Zinc finger,C2H2-like](#)
- [GPCR,rhodopsin-like superfamily](#)

他のファミリーを選ぶ

Google

RefEx



RefEx より肝臓特異的遺伝子群を取得

Reference
Expression
Dataset
[English](#) | [日本語](#)


RefEx

[検索](#)

[RefExの論文が出版され](#)

[ました](#)

[ダウンロード](#)

 Human Mouse Rat

結果一覧 470 件中 1 - 10 件を表示

10 [最初](#) < > [最後](#)

ソート: Tissue Specificity, high

[リストをクリア](#)

[リストを見る 0](#)

[ダウンロード](#)



[エクセルで開く](#)

検索条件

遺伝子名

条件なし

組織

• 肝臓

オントロジー

条件なし

ファミリー

条件なし

遺伝子名

3Dマップ

相対発現量

[mannose-binding lectin \(protein C\) 2, soluble \(opsonic defect\)](#)

[リストに追加する](#) [リストから削除する](#)

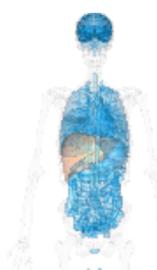
同義遺伝子名 Mannan-binding protein, MBL, MGC116833, MBL2, MBP-C, Mannose-binding protein C precursor, MGC116832, Mannose-binding lectin, COLEC1, HSMBPC, MBP1

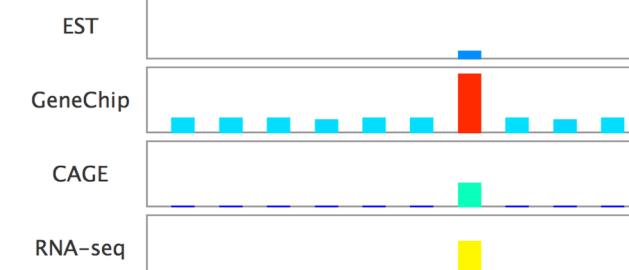
Refseq ID NM_000242

GenelID 4153

Unigene ID Hs.499674

Probe set ID 207256_at





[fibrinogen alpha chain](#)

refex.dbcls.jp/genelist_dl.php?lang=ja&db=human&roku_valid=1&rk[]=%20&order_key=score



RefEx



RefEx より肝臓特異的遺伝子群を取得

db=human&roku_valid=1&rk()=31&order_key=score								
#	RefseqID	GeneID	UnigeneID	ProbesetID	Description	Interpro_top	Chromosome	est10_max
1	NM_000242	4153	Hs.499674	207256_at	mannose-bin	C-type lectin	10q21.1(-)	52.799999
2	NM_000508	2243	Hs.351593	205649_s_at	fibrinogen alp	NULL	4q31.3(-)	724
3	NM_005989	6718	Hs.201667	207102_at	aldo-keto red	Aldo/keto red	7q33(+)	105.59999
4	NM_001737	725		206707_at	complement	Thrombopos	Fn12_1(+)	-
5	NM_001638							84.400001
6	NM_019844							232.19999
7	NM_005141							7473.200
8	NM_000780							15.
9	NM_000133							9
10	NM_000488							812.79998
11	NM_001872							390.60000
12	NM_016413							390.60000
13	NM_001643							1372.1999
14	NM_005577							10.600000
15	NM_001643							1372.1999
16	NM_006446	10599	Hs.449750	210500_at	solute carrier	major facilitat	12p12.2(+)	316.70001
17	NM_031479	83729	Hs.632713	210587_at	inhibin, beta	I Transforming	12q13.3(+)	42.200000
18	NM_006684	10877	-	207874_s_at	complement	Sushi/SCR/C	1q31.3(+)	-

エル エル
<http://bit.ly/2KhMLTu>

liver_genes.txt をダウンロード

Refseq ID を全てコピー

エンリッチメント解析

The screenshot shows the ChIP-Atlas website. At the top, there's a dark header bar with the title "エンリッチメント解析" in Japanese. Below it is a standard browser navigation bar with icons for back, forward, and search. The main menu includes "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", "Publications", and a "Find an experiment" dropdown. The main content area features a large orange speech bubble containing the Japanese word "クリック" (Click). To the left of the bubble, there's a section titled "ChIP-Atlas" with a brief description and a "Watch movie introduction" link.

ChIP-Atlas

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[Watch movie introduction](#)

クリック

The four main features of ChIP-Atlas are:

Peak Browser

graphically visualizes protein binding on given genomic loci with genome browser (IGV).

[Watch Movie](#)

Target Genes

predicts target genes bound by given transcription factors.

[Watch Movie](#)

Colocalization

predicts partner proteins colocalizing with given transcription factors.

[Watch Movie](#)

Enrichment Analysis

predicts proteins bound to given genomic loci and genes (formerly known as *in silico* ChIP).

[Watch Movie](#)



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エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[Tutorial movie ▾](#)[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

All antigens (43086)
DNase-seq (1632)
Histone (10578)
RNA polymerase (1532)
TFs and others (9868)
Input control (5080)
Unclassified (10053)
No description (4343)

2. Cell type Class

All cell types (43086)
Adipocyte (324)
Blood (10674)
Bone (819)
Breast (5050)
Cardiovascular (1136)
Digestive tract (2970)
Epidermis (1244)

3. Threshold for Significance ⓘ

50
100
200
500

4. Select your data

- Genomic regions (BED) or sequence motif ⓘ
 Gene list (Gene symbols) ⓘ

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ファイルを選択 ファイル未選択

Choose local file

Try with example

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ
 Gene list (Gene symbols) ⓘ

6. Describe datasets

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

Estimated run time: 5 mins

エンリッチメント解析

H. sapiens

Target Genes

Colocalization

Enrichment Analysis

Documentation

Publications

Find an experiment ▾

ChIP-seq - Enrichment Analysis

Analyze your data with public ChIP-seq data.

Tutorial movie ▾

H. sapiens

M. musculus

R. norvegicus

C. elegans

S. cerevisiae

1. Antigen Class

All antigens (43086)
DNase-seq (1632)
Histone (10578)
RNA polymerase (1532)
TFs and others (9868)
Input control (5080)
Unclassified (10053)
No description (4343)

TFs and
others

Gene list

4. Select your data

Genome regions (BED) or sequence motif ⓘ
 Gene list (Gene symbols) ⓘ

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ペースト
Refseq ID
Official gene symbol
UniProt ID

ファイルを選択 ファイル未選択
Choose local file Try web search

3. Threshold for Significance ⓘ

Background は
その他の RefSeq
遺伝子

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

Estimated run time: 5 mins

エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)[Tutorial movie ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

- All antigens (43086)
- DNase-seq (1632)
- Histone (10578)
- RNA polymerase (1532)
- TFs and others (9868)**
- Input control (5080)
- Unclassified (10053)
- No description (4343)

2. Cell type Class

- All cell types
- Adipocyte
- Blood
- Bone
- Breast
- Cardio
- Digestive
- Epidermis

3. Threshold for Significance ⓘ

- 50
- 100**
- 200
- 500

4. Select your data

- Genomic regions (BED) or sequence motif ⓘ
- Gene list (Gene symbols) ⓘ

- NM_000242
- NM_000508
- NM_005989
- NM_001737
- NM_001638
- NM_019844
- NM_005141
- NM_000780

[ファイルを選択](#)[ファイル未選択](#)[Try with example](#)

Choose local file

4. の名前
(任意)

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ
- Gene list (Gene symbols) ⓘ

6. Describe datasets

[User data title ⓘ](#)

Liver genes

[Compared data title ⓘ](#)

Other genes

[Project title ⓘ](#)

Test

[Distance range from TSS ⓘ](#)

- 5000 bp ≤ TSS ≤ + 5000 bp

[submit](#)

プロジェクト名
(任意)

Estimated run time: 5 mins

エンリッチメント解析

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[Enrichment Analysis](#)[Documentation](#)[Publications](#)[Find an experiment ▾](#)

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

[Tutorial movie ▾](#)[H. sapiens](#)[M. musculus](#)[R. norvegicus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Antigen Class

All antigens (43086)
DNase-seq (1632)
Histone (10578)
RNA polymerase (1532)
TFs and others (9868)
Input control (5080)
Unclassified (10053)
No description (4343)

2. Cell type Class

All cell types (43086)
Adipocyte (324)
Blood (10674)
Bone (819)
Breast (5050)
Cardiovascular (1136)
Digestive tract (2970)
Epidermis (1244)

3. Threshold for Significance ⓘ

50
100
200
500

4. Select your data

- Genomic regions (BED) or sequence motif ⓘ
 Gene list (Gene symbols) ⓘ

NM_000242
NM_000508
NM_005989
NM_001737
NM_001638
NM_019844
NM_005141
NM_000780

ファイルを選択 ファイル未選択
Choose local file Try with example

転写開始点 (TSS)
からの距離幅
例：± 5 kb

5. Select dataset to be compared

- Refseq coding genes (excluding user data) ⓘ

6. Describe datasets

User data title ⓘ

Liver genes

Compared data title ⓘ

Other genes

Project title ⓘ

Test

Distance range from TSS ⓘ

5000 bp ≤ TSS ≤ + 5000 bp

submit

submit

Estimated run time: 5 mins

エンリッチメント解析

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

Result page URL will be available for a week from the time when 'status' is 'finished'.

Project title	My project
Request ID	wabi_chipatlas_2018-1207-1735-03-394-748830
Submitted at:	17:35:04 (Dec-07-2018)
Estimated finishing time:	17:37:04 (Dec-07-2018)
Current time:	17:35:09 (Dec-07-2018)
Status	Requesting
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=tsv



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NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

計算終了まで数分間かかる

エンリッチメント解析

The screenshot shows the ChIP-Atlas website interface. At the top, there's a navigation bar with links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar labeled "Find an experiment". Below the navigation, the main title "ChIP-Atlas - Enrichment Analysis" is displayed, followed by the subtitle "Analyze your data with public ChIP-seq data.". A note says "Result page URL will be available for a week from the time when 'status' is 'finished'." To the right of this note, there's a large orange speech bubble containing the Japanese word "クリック" (Click). Below the note, there's a table of project details:

Project title	My project
Request ID	wabi_chipatlas_2018-1207-1735-03-394-748830
Submitted at:	17:35:04 (Dec-07-2018)
Estimated finishing time:	17:37:04 (Dec-07-2018)
Current time:	17:40:23 (Dec-07-2018)
Status	finished
Result URL:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=html
Download TSV:	http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&format=tsv

クリック

エル いちエル
http://bit.ly/2GLzA1l



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URL を控えておくと、後日また閲覧できる

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24336	123/219	4003/18220	-26.9	-23.1	2.56	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	93/219	2350/18220	-26.2	-22.6	3.29	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15922	105/219	3100/18220	-24.9	-21.5	2.82	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45142	134/219	5318/18220	-21.6	-18.4	2.10	TRUE
SRX190234	TFs and others	CEPB	Liver	Hep G2	12489	85/219	2290/18220	-21.6	-18.4	3.09	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50949	140/219	6058/18220	-19.4	-16.2	1.92	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19079	131/219	5588/18220	-17.9	-14.8	1.95	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	126/219	5229/18220	-17.8	-14.7	2.00	TRUE
SRX150698	TFs and others	HNF4A	Liver	Hep G2	10069	79/219	2321/18220	-17.6	-14.6	2.83	TRUE
SRX150701	TFs and others	CEPB	Liver	Hep G2	18637	106/219	4145/18220	-15.6	-12.6	2.13	TRUE
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE

Showing 1 to 100 of 10,585 entries

Previous 1 2 3 4 5 ... 106 Next

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test											
ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE

Liver 由来の Hep G2 細胞における HNF4A ChIP-seq データ

- ヒトゲノムの 21,265 箇所に結合。
 - ・ 肝臓特異的遺伝子 (219 個) のうち、120 個に結合
 - ・ その他の遺伝子 (18,220 個) のうち、3428 個に結合
- 両者の比 = $(120/219) / (3428/18220) = 2.91$
- Fisher の正確確率検定: $P = 1E-31.2$

エンリッチメント解析

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries Search:

Test

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver genes	Overlaps / Other genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21265	120/219	3428/18220	-31.2	-27.2	2.91	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24336	123/219	4003/18220	-26.9	-23.1	2.56	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	93/219	2350/18220	-26.2	-22.6	3.29	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15922	105/219	3100/18220	-24.9	-21.5	2.82	TRUE
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SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	126/219	5229/18220	-17.8	-14.7	2.00	TRUE
SRX150698	TFs and others	HNF4A	Liver	Hep G2	10069	79/219	2321/18220	-17.6	-14.6	2.83	TRUE
SRX150701	TFs and others	CEPB	Liver	Hep G2	18637	106/219	4145/18220	-15.6	-12.6	2.13	TRUE
SRX100625	TFs and others	HNF4A	Liver	Hep G2	2654	24/219	512/18220	-14.7	-11.7	5.52	TRUE

Showing 1 to 100 of 10,585 entries

Previous 1 2 3 4 5 ... 106 Next

エンリッチメント解析

chip-atlas.org

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Documentation Publications Find an experiment ▾

ChIP-Atlas - Enrichment Analysis

Analyze your data with public ChIP-seq data.

H. sapiens M. musculus R. norvegicus D. melanogaster C. elegans S. cerevisiae

1. Antigen Class
All antigens (34390)
DNA (1000)

2. Cell type Class
All cell types (34390)
Adipocyte (292)
Blood (9096)
Bone (655)
Breast (3699)
Cardiovascular (1080)
Digestive tract (2447)
Epidermis (1089)

3. Threshold for Significance ⓘ
50
100
200
500

4. Select your data
 Genomic regions (BED) or sequence motif ⓘ
 Gene list (Gene symbols) ⓘ

chr8 134339107 134339325
chr15 41548749 41548861
chr15 25207262 25207383
chr1 190561786 190561937
chr3 142208484 142208615
chr9 115544616 115544762
chr15 59846350 59846560
chr15 81109164 81109289

Choose File no file selected
Choose local file Try with example

5. Select dataset to be compared
 Random permutation of user data ⓘ
 BED or sequence motif ⓘ

chr15 32568482 32568742
chr16 17650550 17650705
chr6 134138703 134138846
chr17 43176564 43176809
chr14 100850102 100850298
chr20 48158343 48158558
chr18 43728802 43728955
chr15 88993498 88993718

Choose File no file selected
Choose local file Try with example

6. Describe datasets

User data title ⓘ
My data

Compared data title ⓘ
Control

Project title ⓘ
My project

submit

Estimated run time: 5 mins

Tutorial movie ▾



ゲノム座標を入れることもできる。