

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

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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 to the search bar with the text "igv genome". The browser interface includes a title bar with icons, a navigation bar, and a user account section.

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 page is titled "Home" and features a large orange circle containing the word "Downloads". A blue arrow points from the top left towards the "Downloads" button on the left sidebar. The sidebar includes links for Home, Downloads (which is highlighted), Documents, IGV User Guide, Tutorial Videos, File Formats, Hosted Genomes, FAQ, Release Notes, Credits, and Contact. Below the sidebar is a search bar with a "search" button. At the bottom left, there is copyright information: "© 2013-2018 Broad Institute and the Regents of the University of California". The main content area has tabs for Overview, Downloads (selected), and Citing IGV. The Downloads tab contains a "Download" button with a blue arrow icon and the text "Download the IGV desktop application and igtools.". The Overview tab contains a brief description of IGV and its funding information. The Citing IGV tab provides citation details for publications.

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

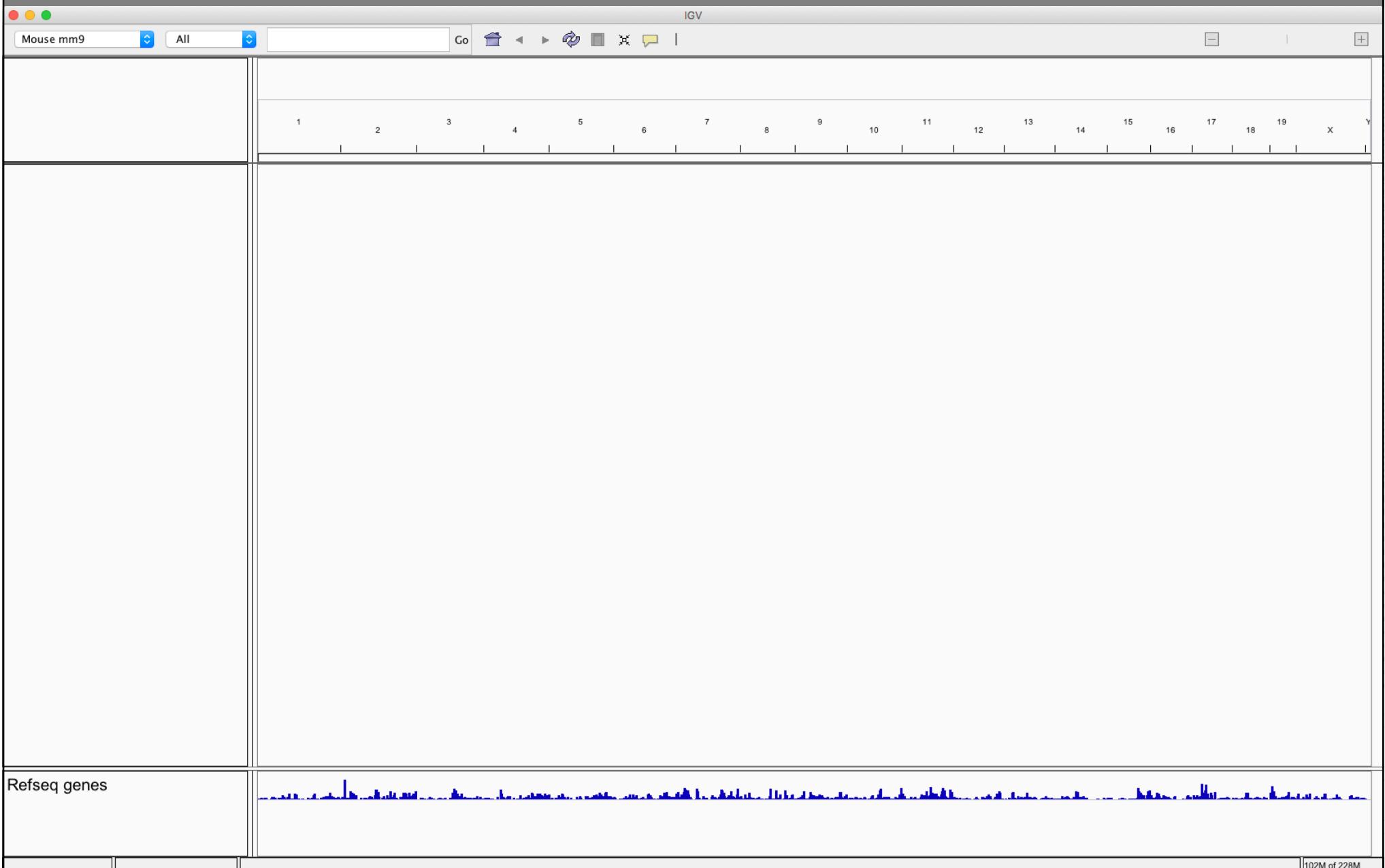
The screenshot shows the IGV Downloads page. On the left, there's a sidebar with links like Home, Downloads, Documents, and Contact. The main content area has a header "Downloads". Below it, there's a section titled "Install IGV 2.5.x" with four download options:

- 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
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THIS WORK IS SUPPORTED BY [NIG SUPERCOMPUTER SYSTEM](#) AND [NATIONAL BIOSCIENCE DATABASE CENTER](#).
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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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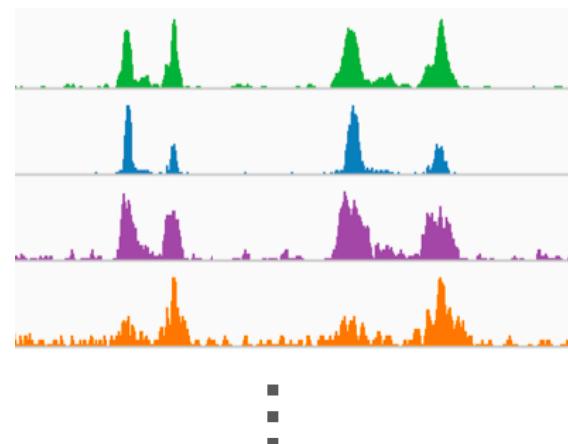
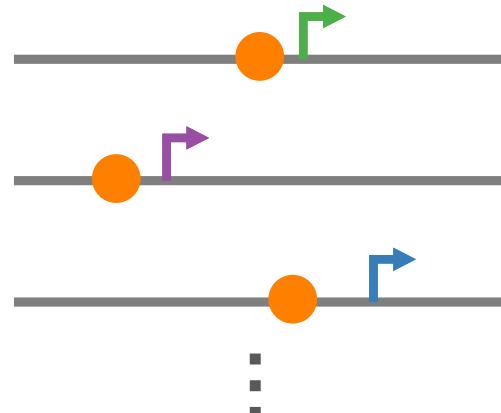
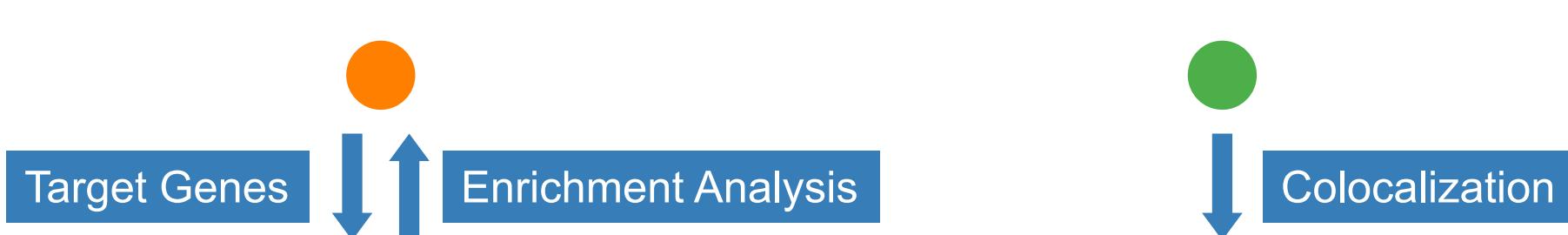
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4つの解析ツール

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 is a large orange speech bubble containing the Japanese word "クリック" (Click). To the left of the bubble, the text "The four main features of ChIP" is visible. On the right, there are four sections: "Peak Browser", "Target Genes", "Colocalization", and "Enrichment Analysis", each with a brief description and a "Watch Movie" link.

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](#)

Enrichment Analysis

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[Watch Movie](#)



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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

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for Life Science

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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

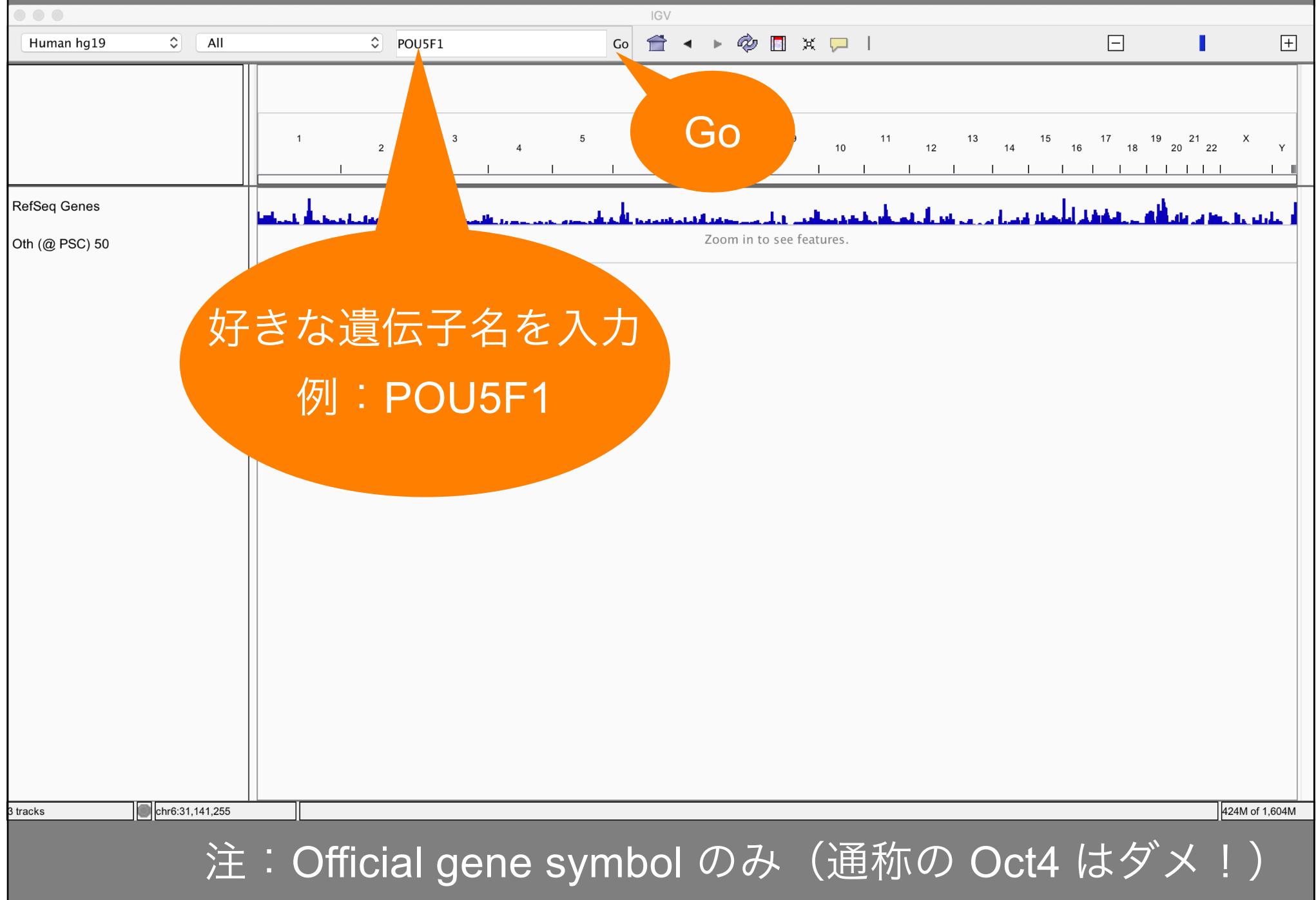
Pluripotent stem cell

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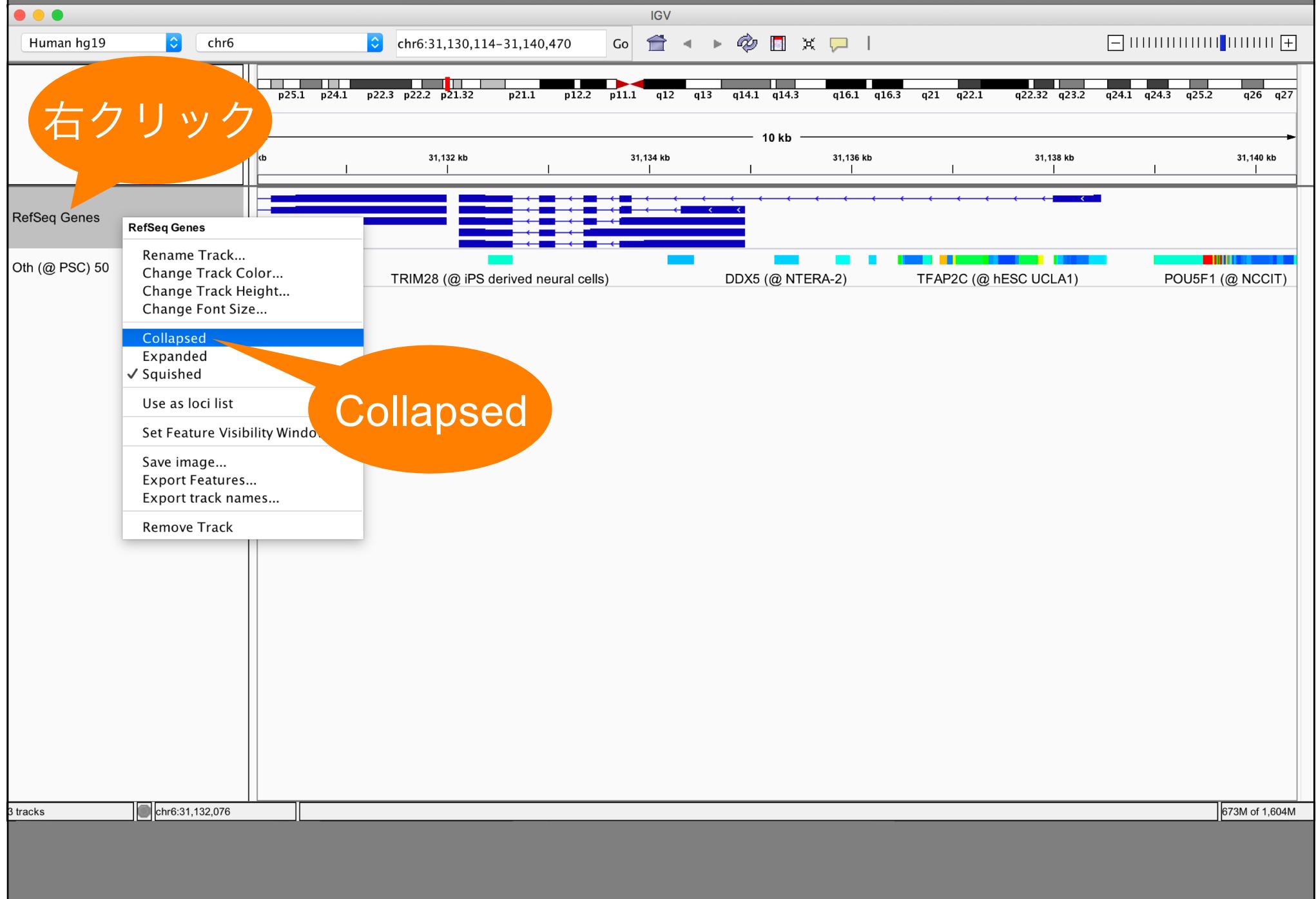
THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND NATIONAL BIOSCIENCE DATABASE CENTER.

NEED HELP? CREATE AN ISSUE ON GITHUB OR CONTACT US

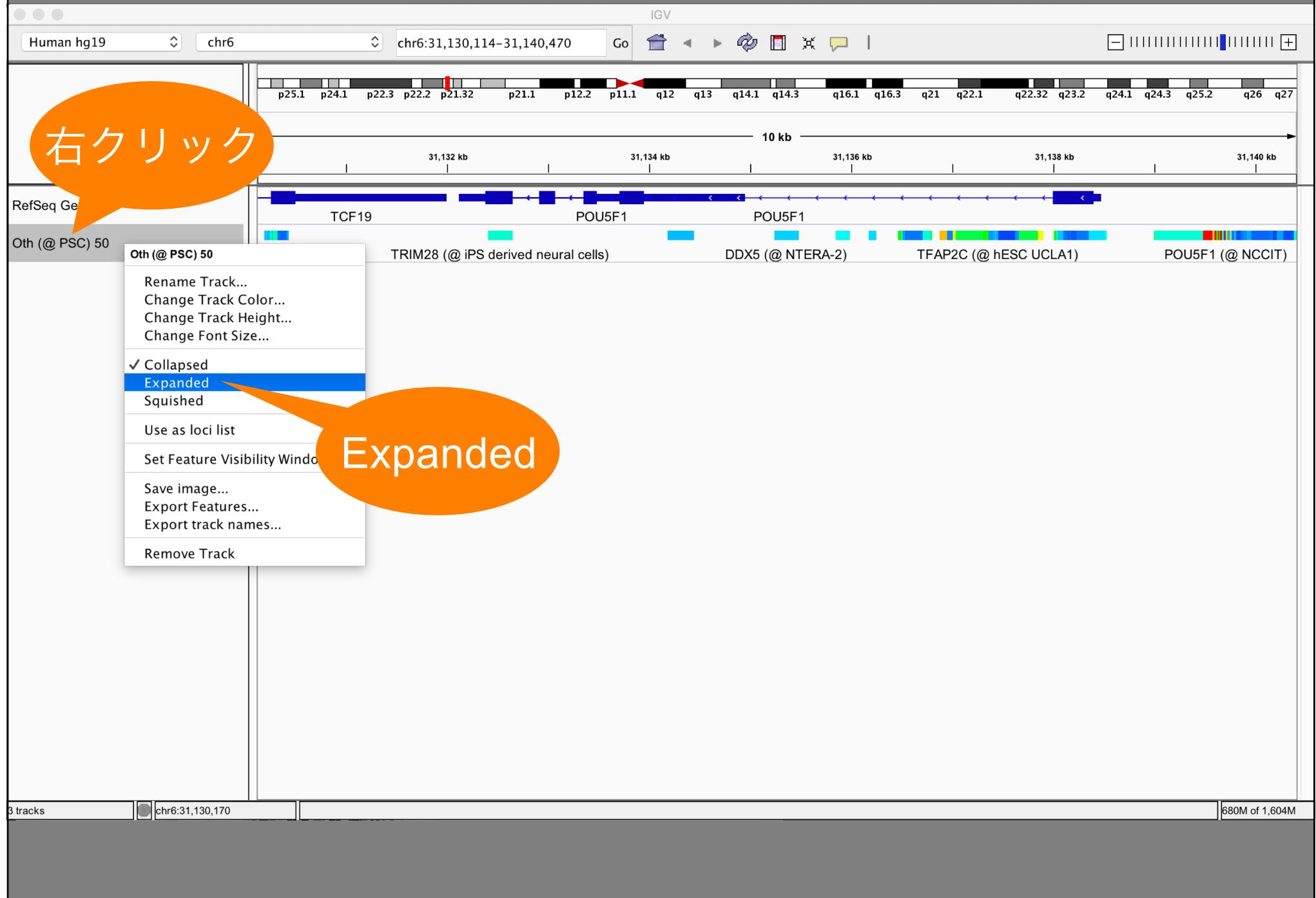
複数データをまとめて見る



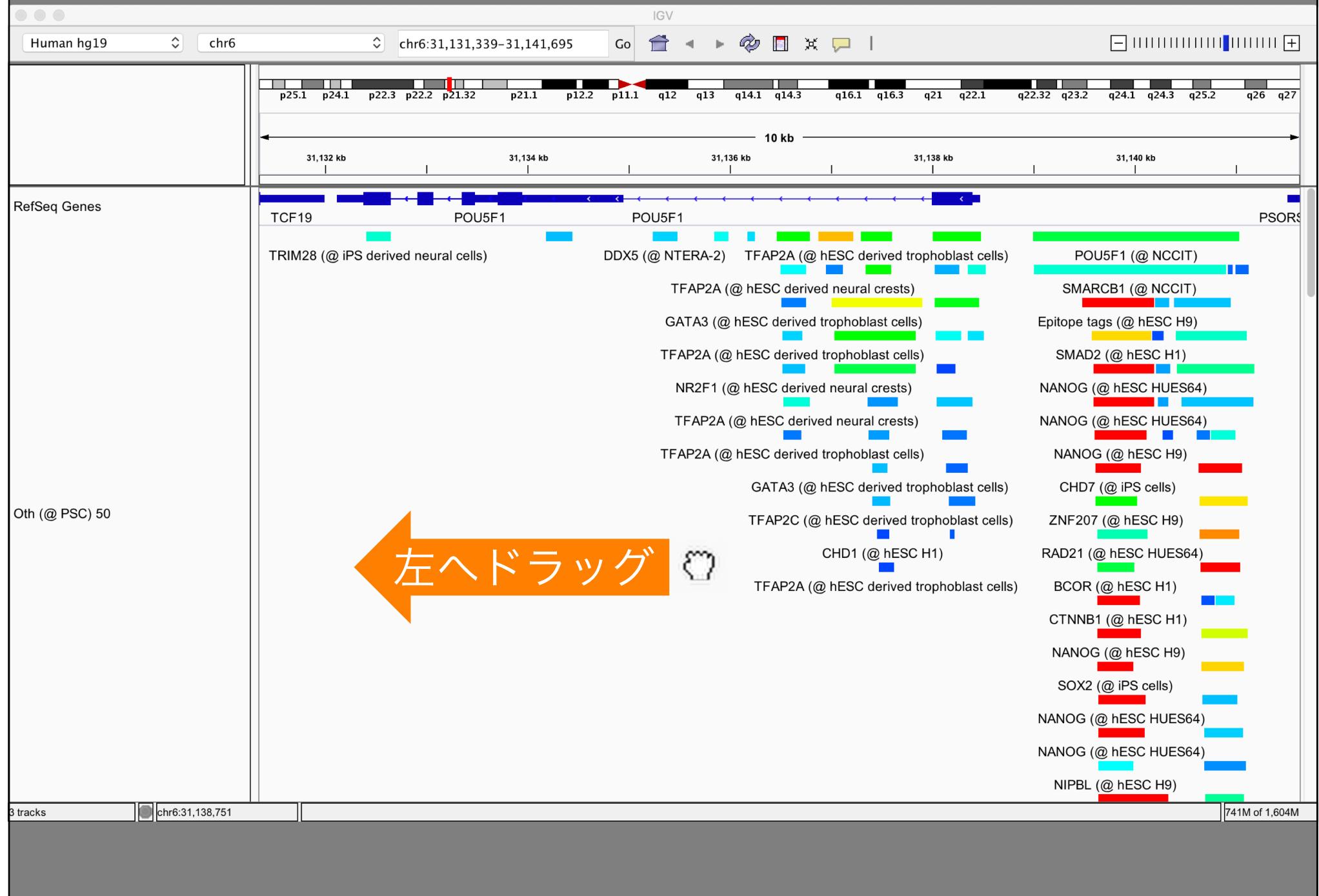
複数データをまとめて見る



複数データをまとめて見る



複数データをまとめて見る

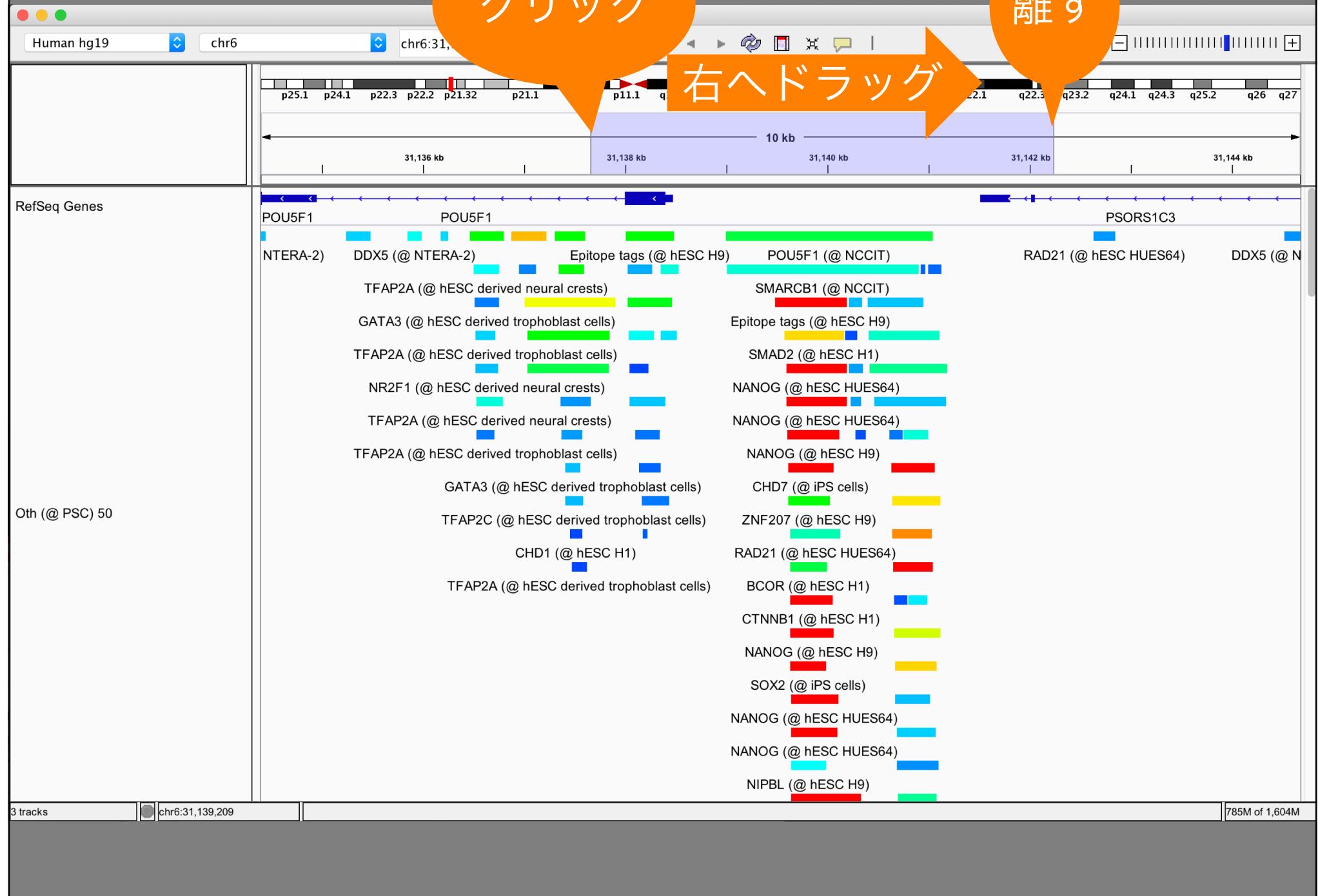


複数データをまとめて表示

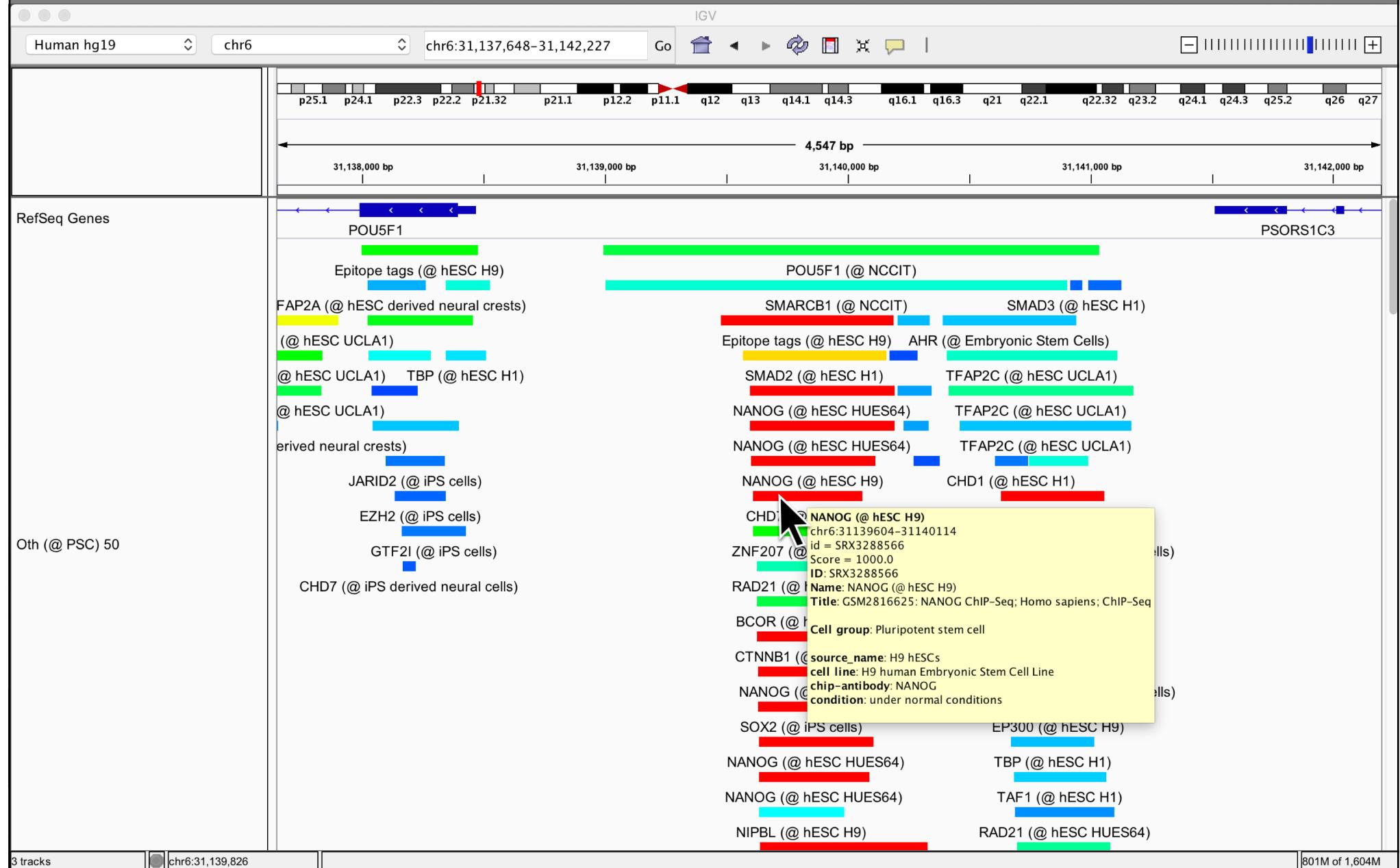
クリック

離す

右へドラッグ

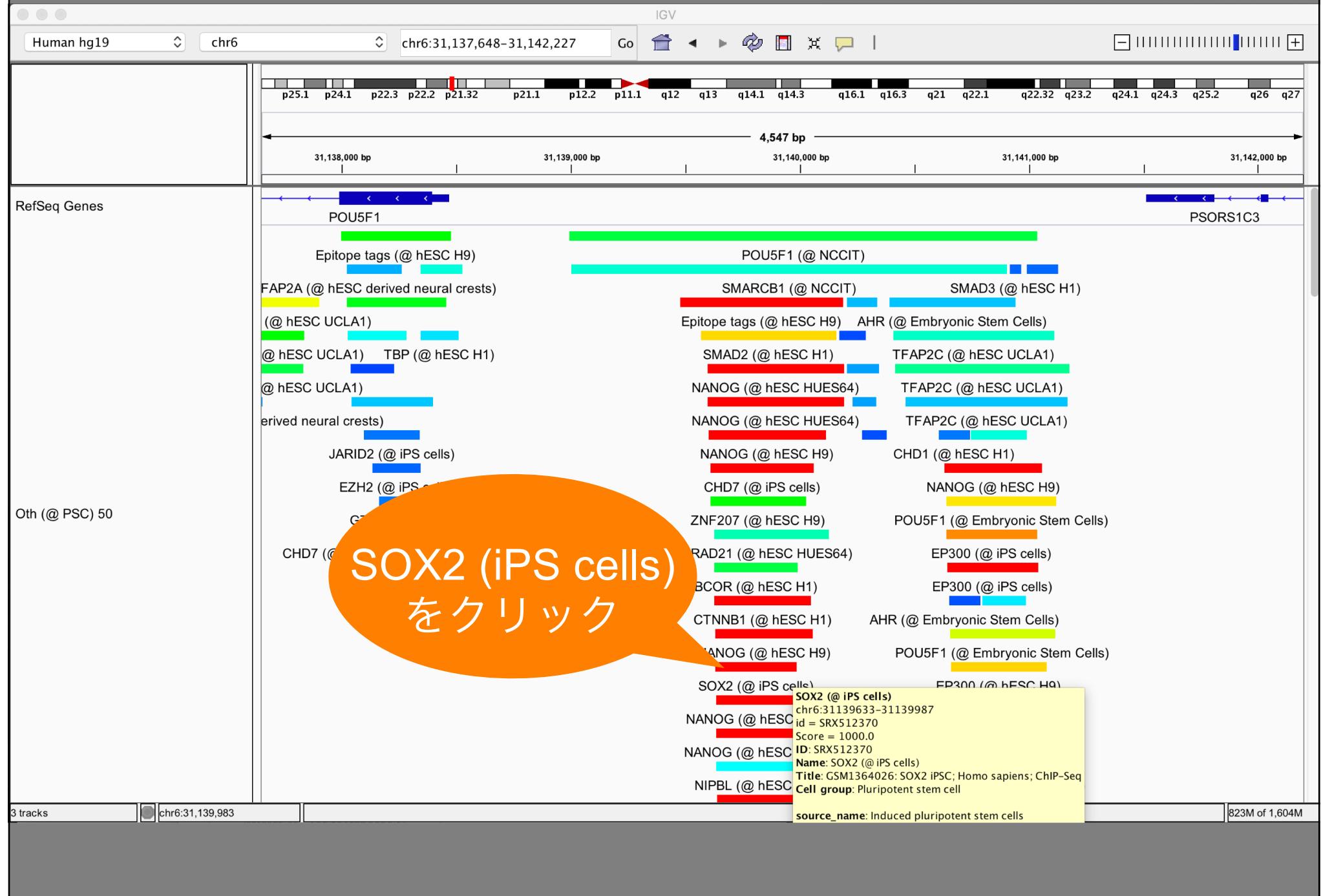


複数データをまとめて見る



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

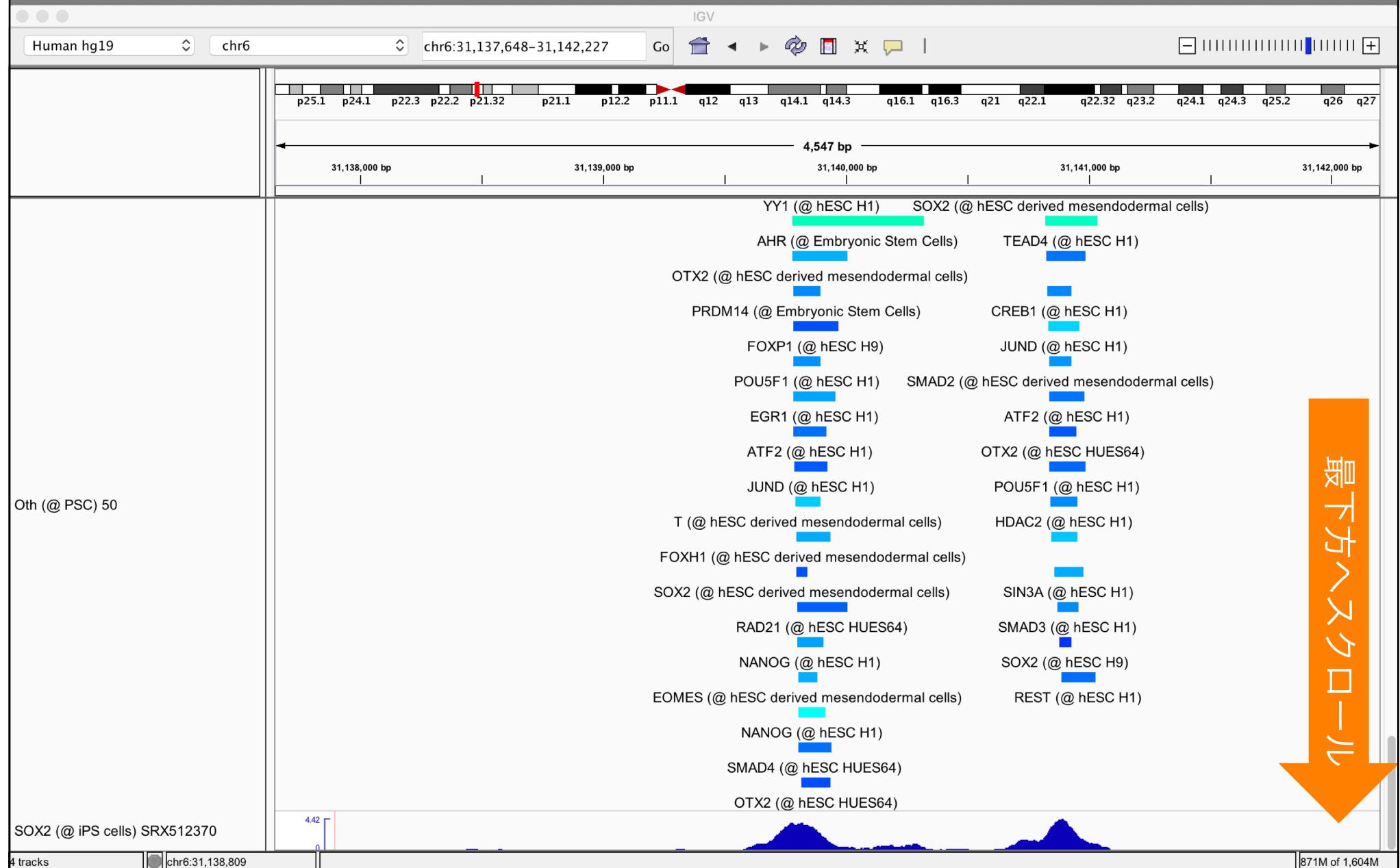
Induced pluripotent stem cells

chip antibody

anti SOX2 antibody

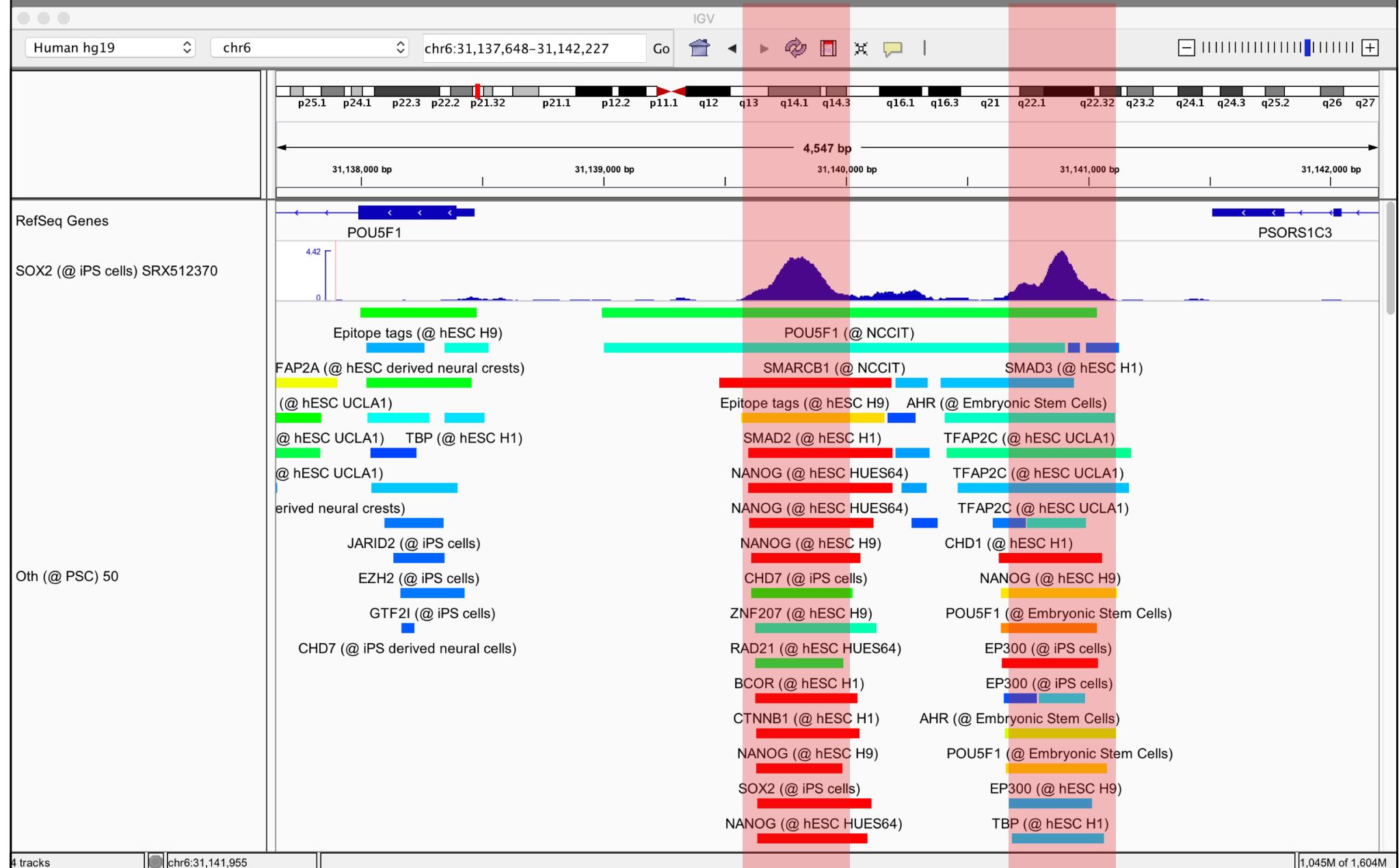
アライメント情報も閲覧できる

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