

ChIP-Atlas の使い方とその応用

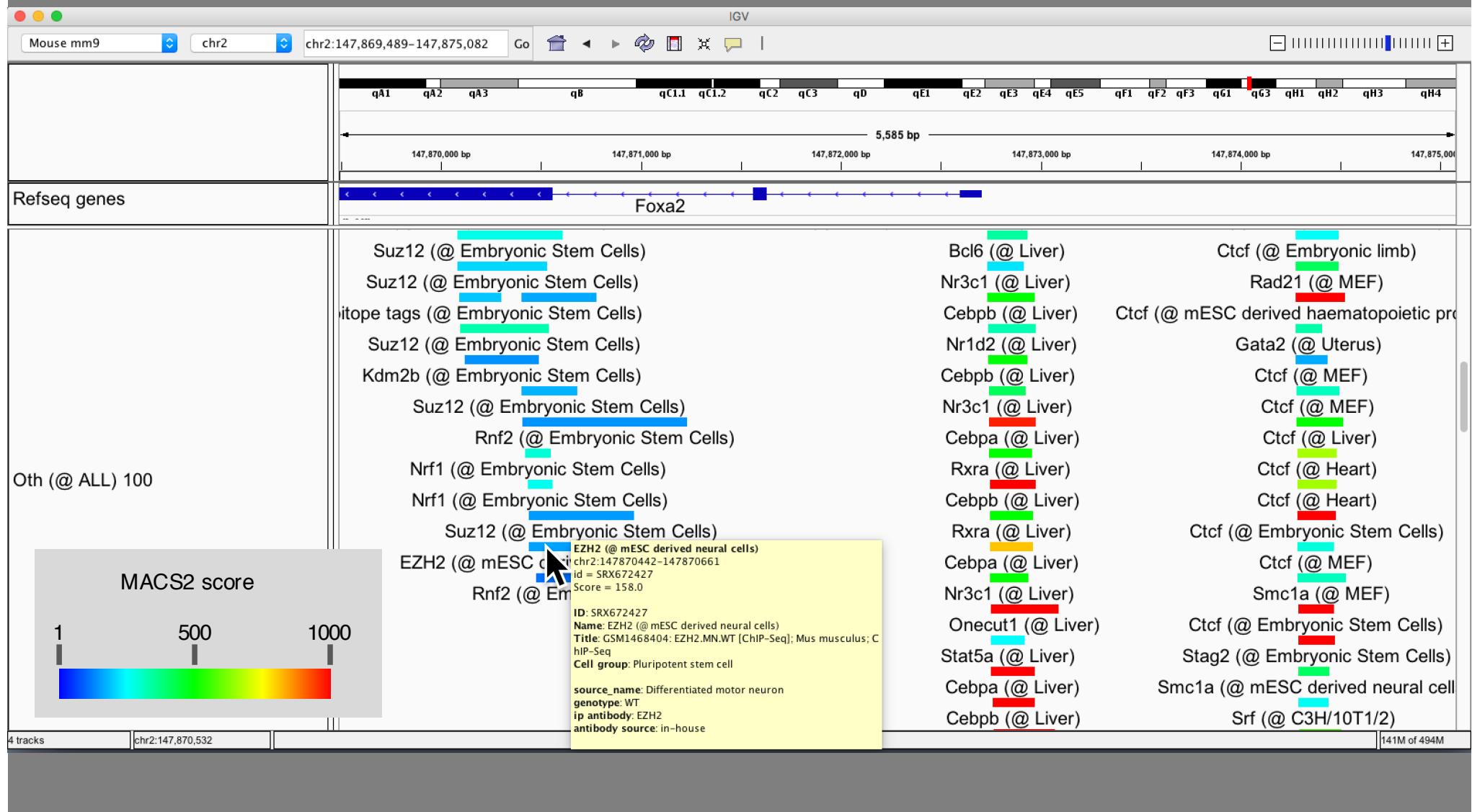


九州大学大学院・医学研究院
発生再生医学分野・助教

沖 真弥 (Oki, Shinya)

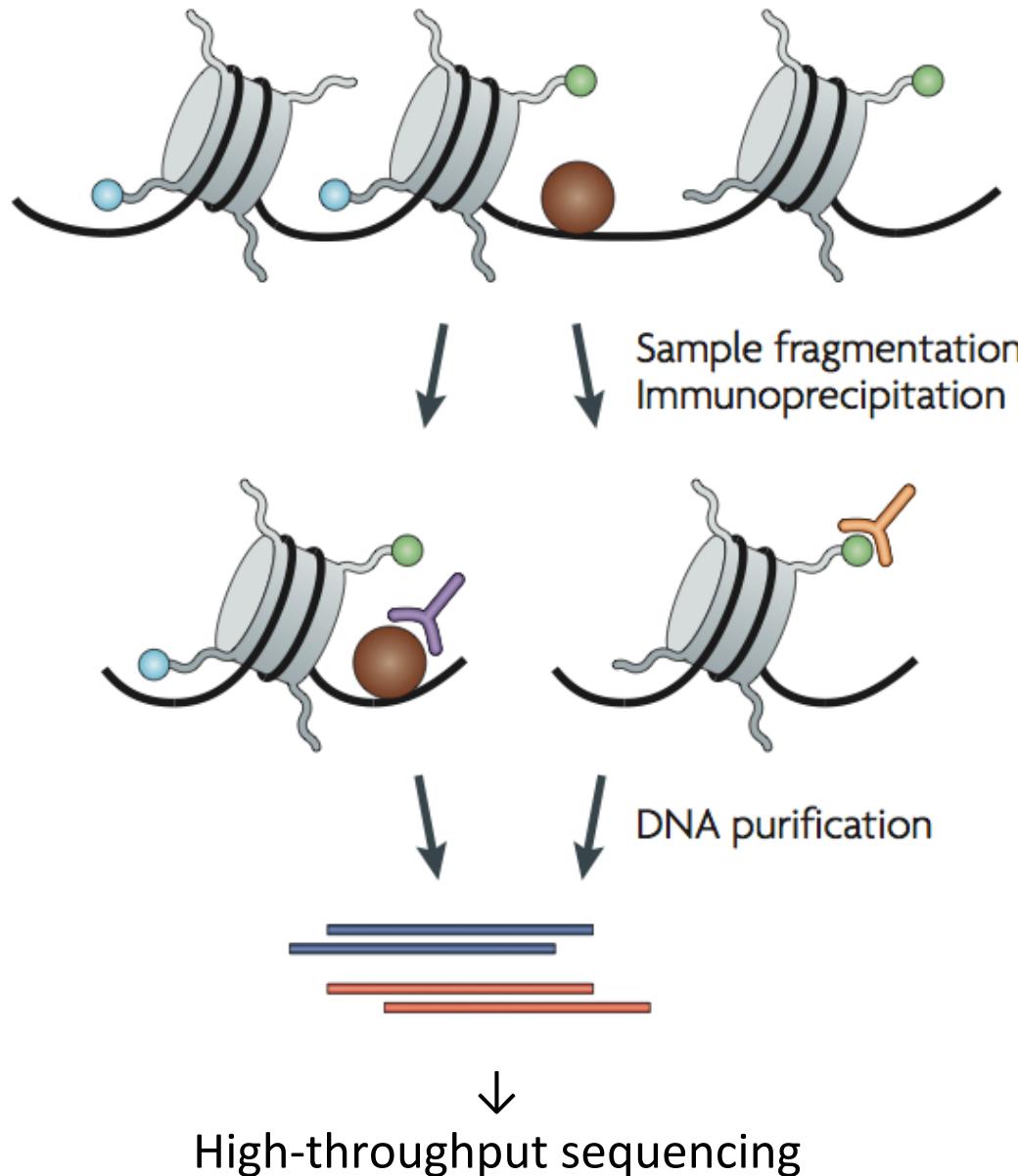
ChIP-Atlas

Genome-protein interaction が視覚的に理解できる



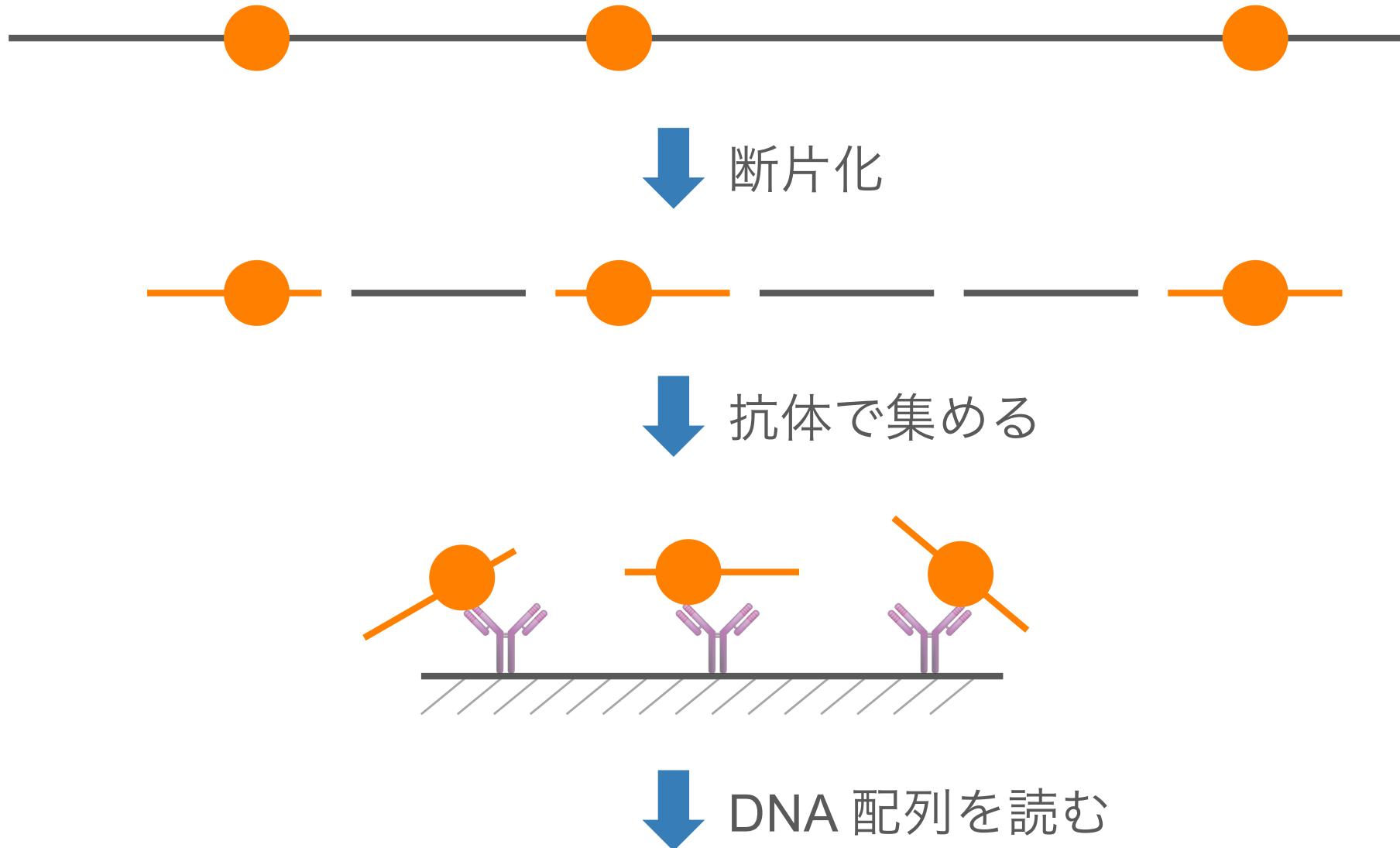
ChIP-seq: 転写因子の結合部位を同定できる

ChIP-seq = Chromatin Immunoprecipitation with Sequencing

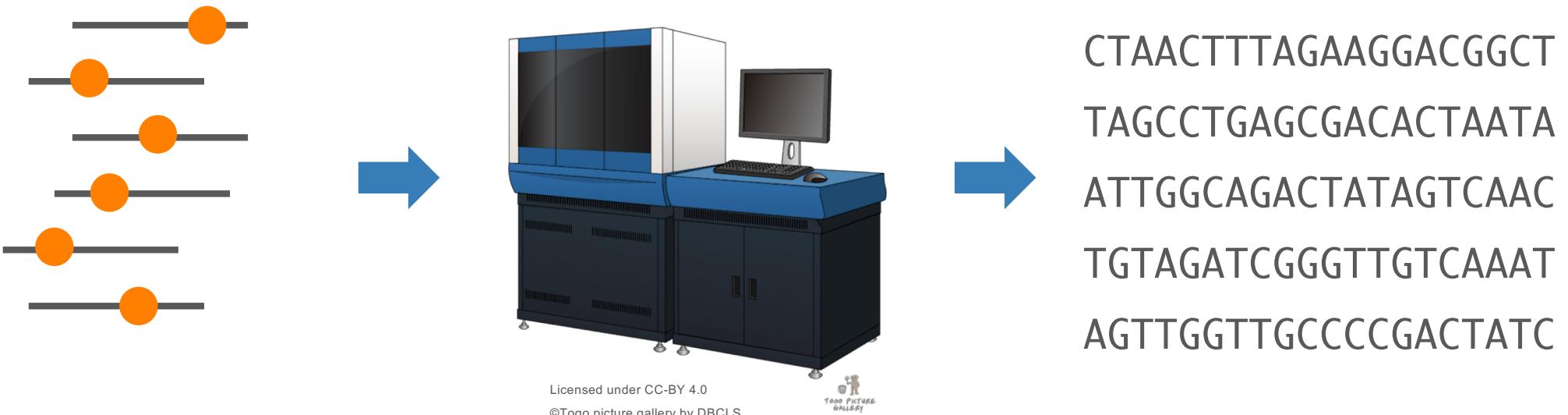


ChIP-seq: 転写因子の結合部位を同定できる

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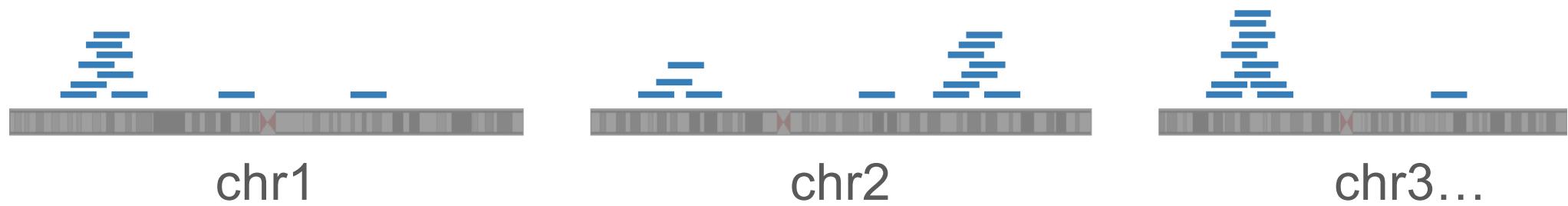


シークエンス



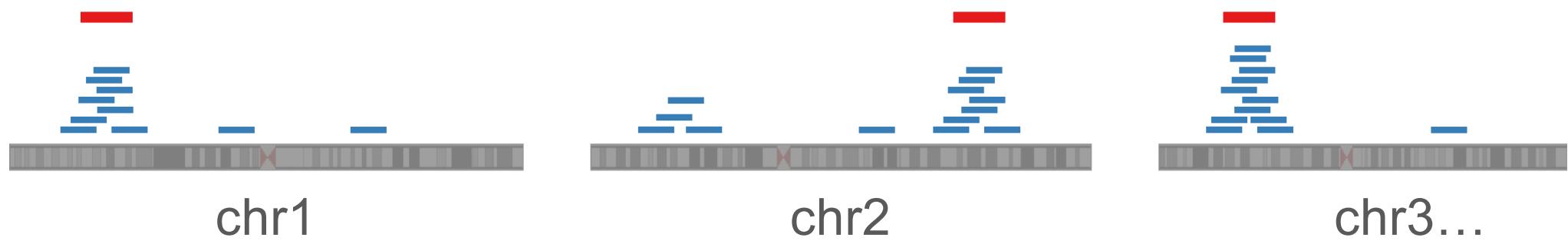
アライメント

DNA 配列をゲノム座標に変換

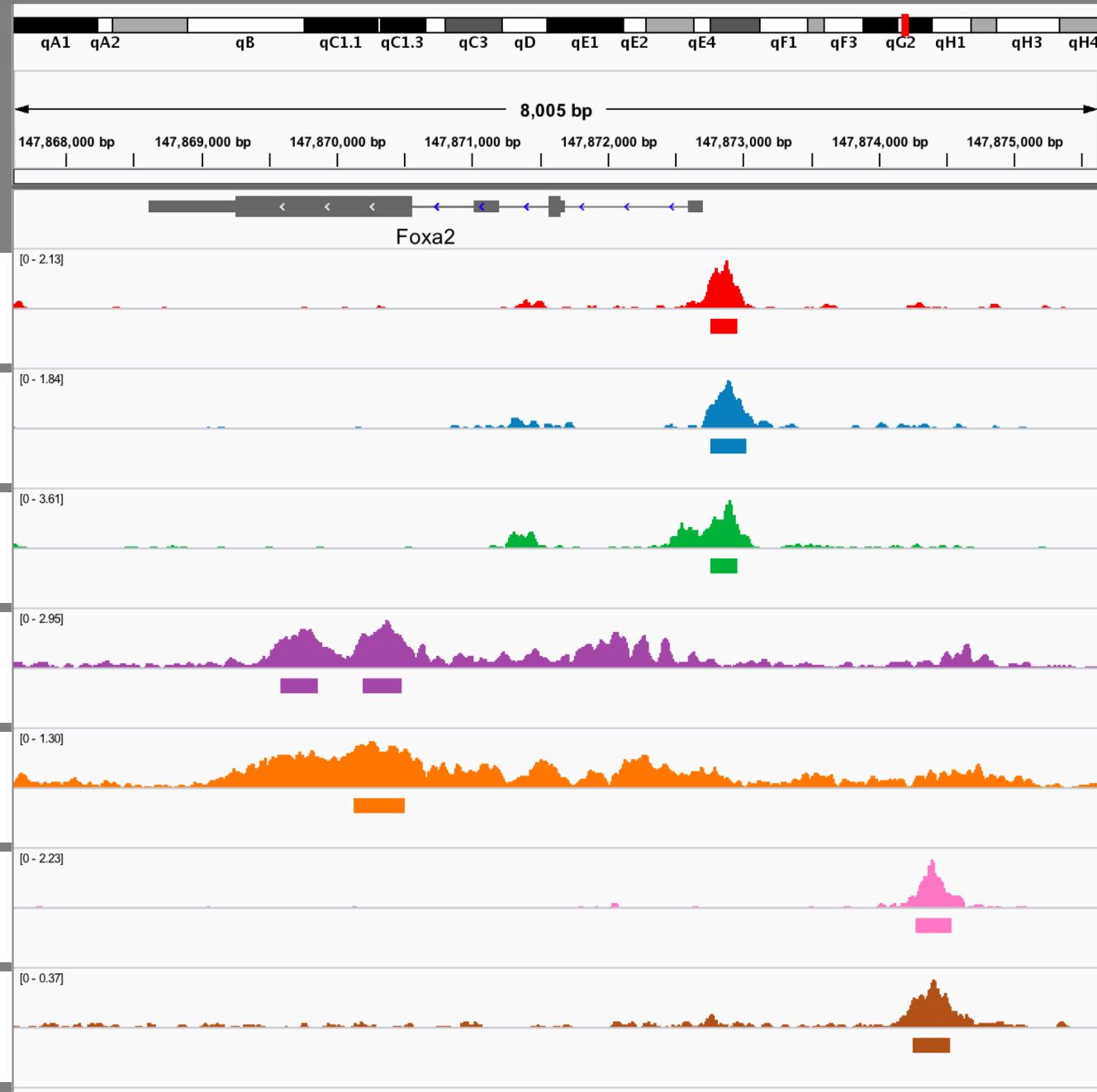


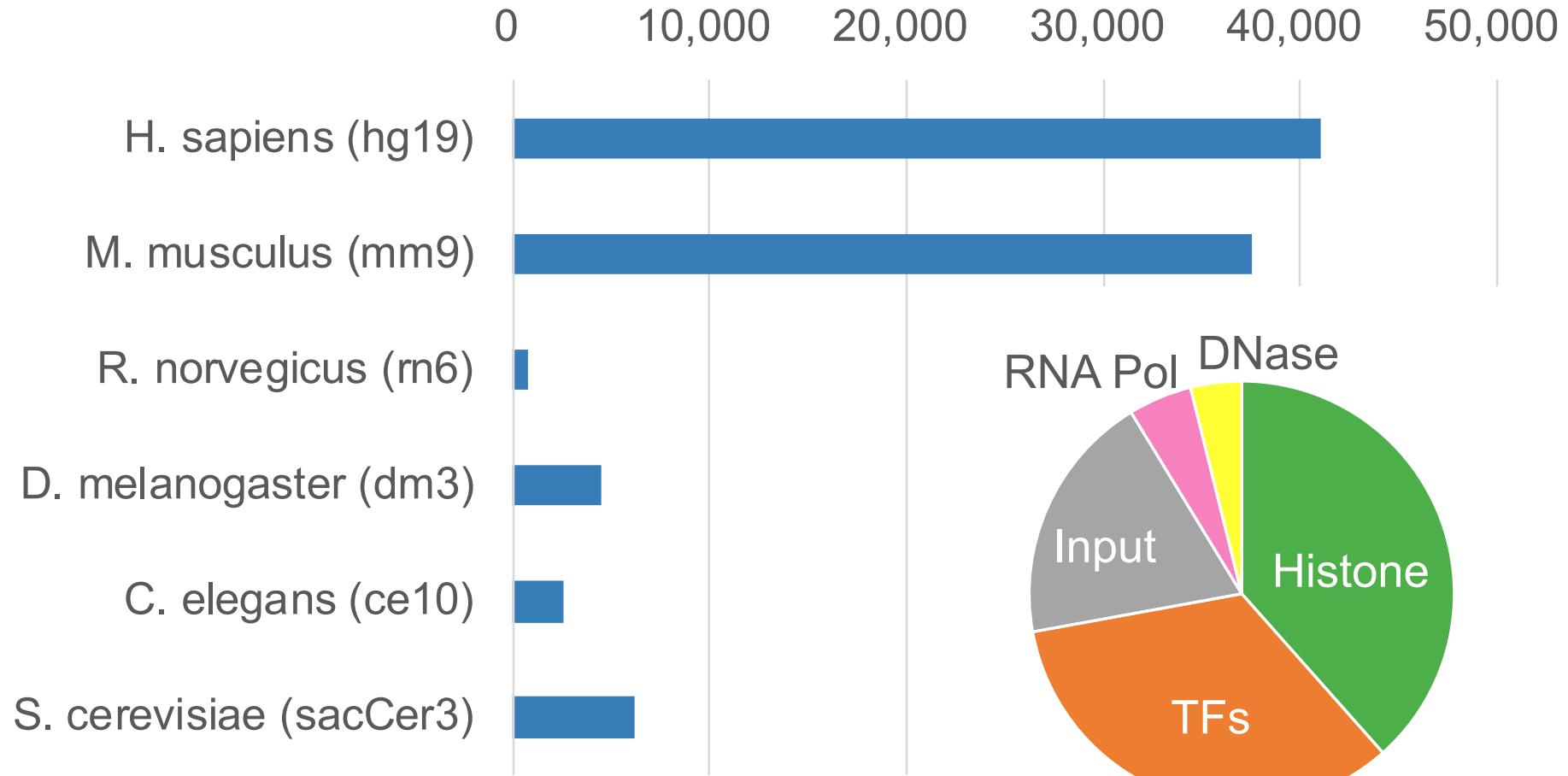
ピークコール

統計学的に有意な領域を特定。



ゲノムブラウザで閲覧





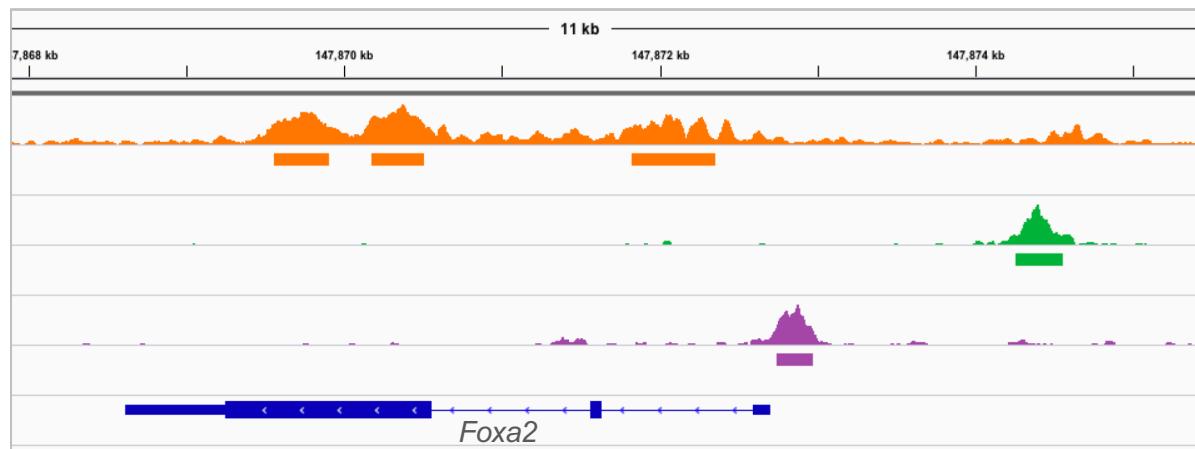
データ処理・公開しているデータ



SRA (配列生データ)



Alignment
Peak-call



Sample metadata



Curation

ID	抗原	細胞
SRX330668	Ezh2	ES cells
SRX310198	Ctcf	Mast cells
SRX1092953	Cebpa	Liver

メタ情報のキュレーション

属性	属性値
ID	ERX626807
Title	Illumina HiSeq 2500 sequencing
Sample Name	ERS420364
Sex	male
Species	Homo sapiens
cell type	U937
organism part	blood
phenotype	Cancer
Immunoprecipitate	Pu.1

細胞名 = U-937 (ハイフンあり)

抗原名 = SPI1 (Official gene symbol)

メタ情報のキュレーション

BEFORE

ID	Original sample metadata
ERX200492	ArrayExpress-Sex=male; ArrayExpress-CellType=B-Lymphocyte; ArrayExpress-Immunoprecipitate=CTCF; ArrayExpress-Species=Homosapiens; source_name=chronic myelogenous leukemia cell line; cell line=K562; antibody=AGO2
SRX1024932	source_name=CD4+CD25+CD45RA+ expanded naive regulatory T cells; donor=S030b; cell type=CD4+CD25+CD45RA+ expanded naive regulatory T cells; antibody=STAT5B (Invitrogen, cat#I50-101); source_name=Pre-activated CD8+ T cells; tissue=Peripheral blood; cell type=Pre-activated CD8+ T cells; chip antibody=STAT5B (Invitrogen, cat#I50-101)
SRX212431	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1
SRX831872	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1
SRX100477	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1
SRX530184	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1
SRX159094	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1
SRX644410	source_name=HepG2; biomaterial_provider=ATCC; datatype=ChIPSeq; datatype_description=Chromatin IP Sequencing; cell type=primary human hepatocytes; tissue=Liver; chip antibody=FXR (1:1 mixture of sc-1204x and sc-13063x, ChIP grade, cat#sc-13063); source_name=HuH7 cells, mitotic block and release; cell type=HuH7; cycling state=mitotic; antibody=FoxA1; vendor/catalog/lot=Abcam (cat#ab11200); source_name=PANC1 Pancreatic cancer cell line; antibody=ETS1 (Santa Cruz, sc-350, lot #F1312); cell line=PANC1

メタ情報のキュレーション

AFTER

ID	Antigen	Cell type Class	Cell type
ERX200492	CTCF	Blood	B-Lymphocytes
SRX1024932	AGO2	Blood	K-562
SRX212431	STAT5A	Blood	CD4-Positive T-Lymphocytes
SRX831872	STAT5B	Blood	CD8-Positive T-Lymphocytes
SRX100477	FOXA1	Liver	Hep G2
SRX530184	NR1H4	Liver	Hepatocytes
SRX159094	FOXA1	Liver	HuH-7
SRX644410	ETS1	Pancreas	PANC-1

毎月更新中（1,500件／月）

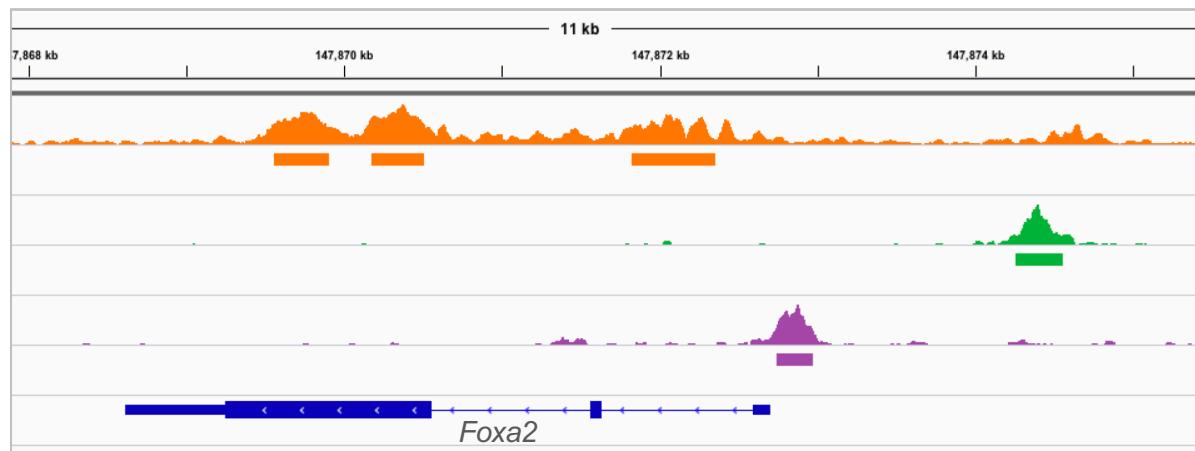
データ処理・公開しているデータ



SRA (配列生データ)



Alignment
Peak-call



Sample metadata



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データ統合・データマイニング

ChIP-Atlas の HP

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

ChIP-Atlas

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[Watch movie introduction](#)

The four main features of ChIP-Atlas are:

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[Watch Movie](#)

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predicts target genes bound by given transcription factors.

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

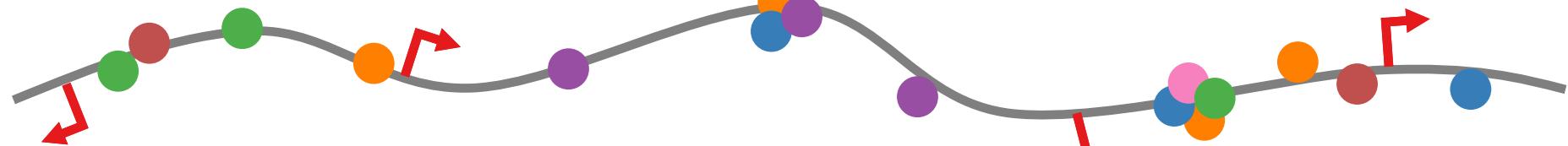
[Watch Movie](#)

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ChIP-Atlas でできること

Peak Browser



Target Genes

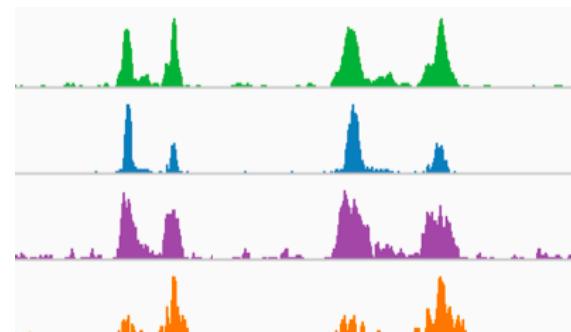
Enrichment Analysis



⋮



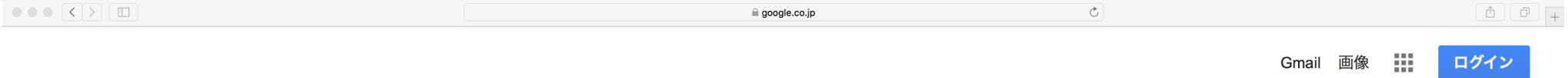
Colocalization



⋮

IGV のインストール

IGV のインストール



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 displaying the IGV (Integrative Genomics Viewer) software download page. The URL in the address bar is software.broadinstitute.org. The page 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.

Downloads

Overview

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 software download page from software.broadinstitute.org. The page includes a sidebar with links for Home, Downloads, Documents, User Guide, Tutorial Videos, File Formats, Hosted Genomes, FAQ, Release Notes, Credits, and Contact. A search bar is also present. The main content area displays four download options:

- Mac:** Download IGV Mac App. A large orange speech bubble labeled "Mac" points to this section.
- Win:** Download IGV on Windows. A large orange speech bubble labeled "Win" points to this section.
- Linux / MacOS command line:** Download IGV to run on Linux / MacOS command line. A small orange speech bubble labeled "うまくいかないとき" (not working) points to this section.
- Java Web Start:** Launch IGV using Java Web Start. Three launch buttons are shown: 1.2 GB (Max memory for Windows with 32-bit Java), 2 GB, and 10 GB (Only for large memory machines with 64-bit Java).

Note: IGV 2.4.x releases require Java 8. For Java 10 see the development snapshot build.

ほかに、Java 8 にするなどの対処法がある

ChIP-Atlasへのアクセス



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

The screenshot shows the ChIP-Atlas website's main page. At the top, there is a dark header bar with the ChIP-Atlas logo and several navigation links: ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a dropdown menu for 'Find an experiment'. Below the header, the main content area features a large, bold 'ChIP-Atlas' title. Underneath the title is a descriptive paragraph about the database. A blue link 'Watch movie introduction' is located below the paragraph.

The four main features of ChIP-Atlas are:

Peak Browser

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

[Watch Movie](#)

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predicts target genes bound by given transcription factors.

[Watch Movie](#)

Colocalization

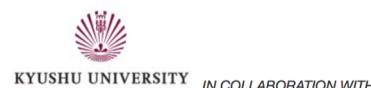
predicts partner proteins colocalizing with given transcription factors.

[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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4つの解析ツール

ChIP-Atlasへのアクセス

The screenshot shows the ChIP-Atlas homepage. At the top, there's a navigation bar with links for "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", and "Publications". On the right side of the navigation bar is a dropdown menu labeled "Find an experiment". Below the navigation bar, the main content area features a large title "ChIP-Atlas" in bold black font. Underneath the title, a descriptive paragraph explains what ChIP-Atlas is: "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." Below this text is a blue link "Watch movie introduction".

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動画マニュアル（英語）

個別データの閲覧

データの検索

The screenshot shows the ChIP-Atlas homepage. At the top right, there is a search bar with the placeholder text "Enter an SRA experimental ID beginning with SRX, DRX, or ERX. Keyword search". An orange callout bubble points to the input field containing "SRX512370". Below the search bar, there is a "Go" button.

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](#)

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データの検索

The screenshot shows a web browser window for the ChIP-Atlas website. The URL in the address bar is chip-atlas.org. The page title is "ChIP-Atlas - details for SRX512370". The top navigation bar includes links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar labeled "Find an experiment".

SRX512370

GSM1364026: SOX2 iPSC; Homo sapiens; ChIP-Seq

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

Curated Sample Data

Genome	hg19
Antigen Class	TFs and others
Antigen	SOX2
Cell type Class	Pluripotent stem cell
Cell type	iPS cells

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

データの検索

The screenshot shows the ChIP-Atlas homepage. At the top, there is a navigation bar with links to "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", and "Publications". A search bar is located at the top right with the placeholder "Find an experiment ▾". Below the navigation bar, the main title "ChIP-Atlas" is displayed in large, bold, dark font. A descriptive text block follows, stating: "ChIP-Atlas is an integrative and comprehensive database for visualizing public ChIP-seq data. ChIP-Atlas covers almost all public ChIP-seq data submitted to the SRA (Sequence Read Archive) in NCBI, DDBJ, or ENA, and is based on over 78,000 experiments." To the right of this text, there is a search input field containing "SRX512370" with a "Go" button below it. A tooltip for the search field says: "Enter an SRA experimental ID beginning with SRX, DRX, or ERX. Keyword search". An orange callout bubble points from the text "Keyword search" towards the search input field.

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[Watch Movie](#)

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データの検索

dbarchive.biosciencedbc.jp

ChIP-Atlas / Keyword search

Search for ChIP-seq data with keywords.

- Simple search
 Advanced search

Show entries

Showing 1 to 10 of 27 entries (filtered from 78,155 total entries)

iPS Sox2

Search:

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX1813586	SRA430376	GSM2183781	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX1813587	SRA430376	GSM2183782	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX512370	SRA156563	GSM1364026	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX968908	SRA248747	GSM1643794	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968909	SRA248747	GSM1643795	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968910	SRA248747	GSM1643796	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968911	SRA248747	GSM1643797	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968912	SRA248747	GSM1643798	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX1184107	SRA245567	GSM1867739	mm9	TFs and others	Sox2	Pluripotent stem cell	iPSC intermediates
SRX3038016	SRA592182	GSM2718352	mm9	TFs and others	Sox2	Pluripotent stem cell	iPS cells

Previous 2 3 Next

データの検索

dbarchive.biosciencedbc.jp

ChIP-Atlas / Keyword search

Search for ChIP-seq data with keywords.

- Simple search
 Advanced search

Show 10 entries

Showing 1 to 10 of 27 entries

Copy

TSV

Search: iPS Sox2

SRX ID	SRA ID	GSM ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX1813586	SRA423586	GSM1364026	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX1813587	SRA423587	GSM1364026	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX512370	SRA156563	GSM1364026	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS cells
SRX968908	SRA248747	GSM1643794	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968909	SRA248747	GSM1643795	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968910	SRA248747	GSM1643796	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968911	SRA248747	GSM1643797	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX968912	SRA248747	GSM1643798	hg19	TFs and others	SOX2	Pluripotent stem cell	iPS derived neural cells
SRX1184107	SRA245567	GSM1867739	mm9	TFs and others	Sox2	Pluripotent stem cell	iPSC intermediates
SRX3038016	SRA592182	GSM2718352	mm9	TFs and others	Sox2	Pluripotent stem cell	iPS cells

Previous 1 2 3 Next

SRX512370

サンプル情報の閲覧

The screenshot shows a web browser window for the ChIP-Atlas website. The URL in the address bar is chip-atlas.org. The page title is "ChIP-Atlas - details for SRX512370". The main content area displays sample information for "SRX512370" (GSM1364026: SOX2 iPSC; Homo sapiens; ChIP-Seq). Below the title are four blue buttons: "View on IGV ▾", "View Analysis ▾", "Download ▾", and "Link Out ▾". A large orange speech bubble with the Japanese text "キュレーション結果" (Curated results) points to the "View on IGV" button.

SRX512370

GSM1364026: SOX2 iPSC; Homo sapiens; ChIP-Seq



[View on IGV ▾](#)

[View Analysis ▾](#)

[Download ▾](#)

[Link Out ▾](#)

Curated Sample Data

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キュレーション
結果

Cell type information

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source_name	Induced pluripotent stem cells
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オリジナルの
メタ情報

サンプル情報の閲覧

chip-atlas.org

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

Metadata from Sequence Read Archive

Library Description

library_strategy ChIP-Seq
library_source GENOMIC
library_selection ChIP
library_construction_... Chromatins were fragmented by sonication and immunoprecipitated with an anti-FLAG M2 antibody or antibodies against protein-of-interest. Immunoprecipitated DNA fragments were purified by QIAGEN's PCR purification Kit. Ten ng of co-immunoprecipitated DNA fragments, except for Of-S-M and O-Sf-M, were subjected to preparation of Illumina's sequencing library using NEBNext ChIP-seq Library Prep Reagent (New England Biolabs), according manufacturer's instruction. After adapter ligation, DNA fragments were amplified by PCR with Illumina primers and library fragments of ~250 bp (insert plus adaptor and PCR primer sequences) were band isolated by Caliper XT (PerkinElmer). For Of-S-M and O-Sf-M, Illumina's sequencing libraries were generated by Ovation SP Ultralow Library System (NuGEN). The purified DNA was captured on an Illumina flow cell for cluster generation.

Platform Information

instrument_model Illumina Genome Analyzer IIx

External Database Query

Query antigen WikiGenes PosMed PDBj

Query cell-type ATCC MeSH RIKEN BRC

Logs in read processing pipeline

Number of total reads 31281692
Reads aligned (%) 66.5
Duplicates removed (%) 15.5
Number of peaks 20967 (qval < 1E-05)

サンプル情報の閲覧

chip-atlas.org

ChIP-Atlas - details for SRX512370

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

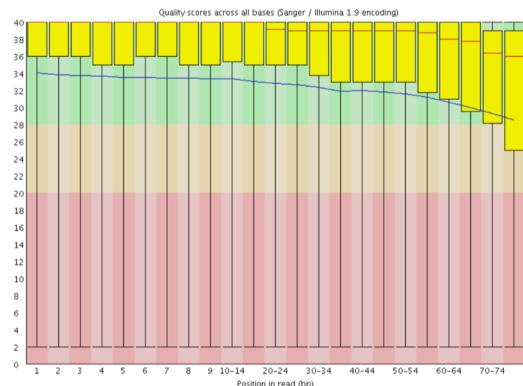
Logs in read processing pipeline

Number of total reads	31281692
Reads aligned (%)	66.5
Duplicates removed (%)	15.5
Number of peaks	20967 (qval < 1E-05)

リード数や
マップ率など

Sequence Quality Data from DBCLS SRA

SRR1220680_fastqc



リードの
クオリティ

個別データの閲覧

SRX512370
GSM1364026: SOX2 antibody ChIP-seq

View on IGV ▾

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

Genome: hg19

Antigen Class: TFs and others

Antigen: SOX2

Cell type Class: Pluripotent stem cell

Cell type: iPS cells

Cell type information

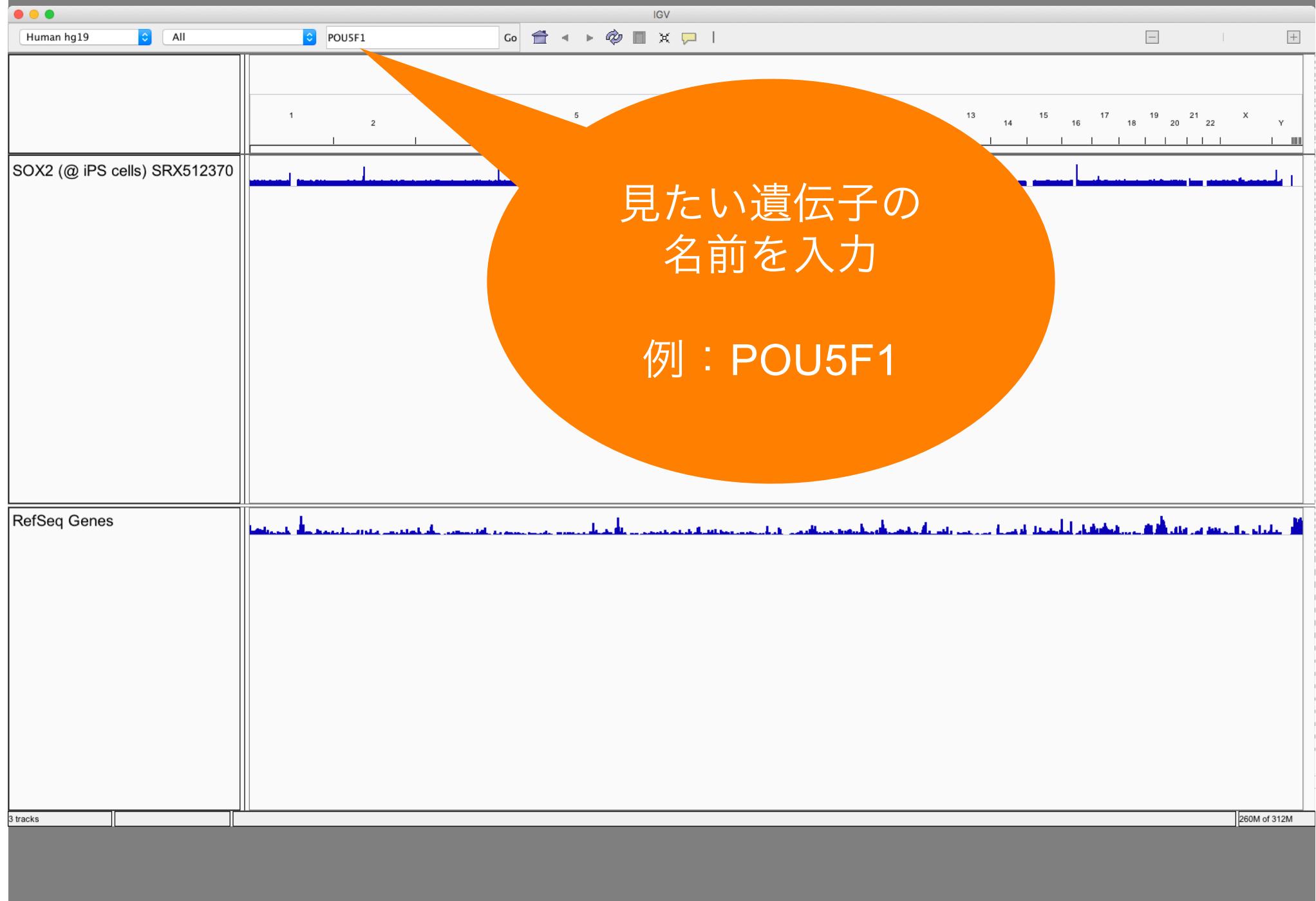
NA NA

Attributes by Original Data Submitter

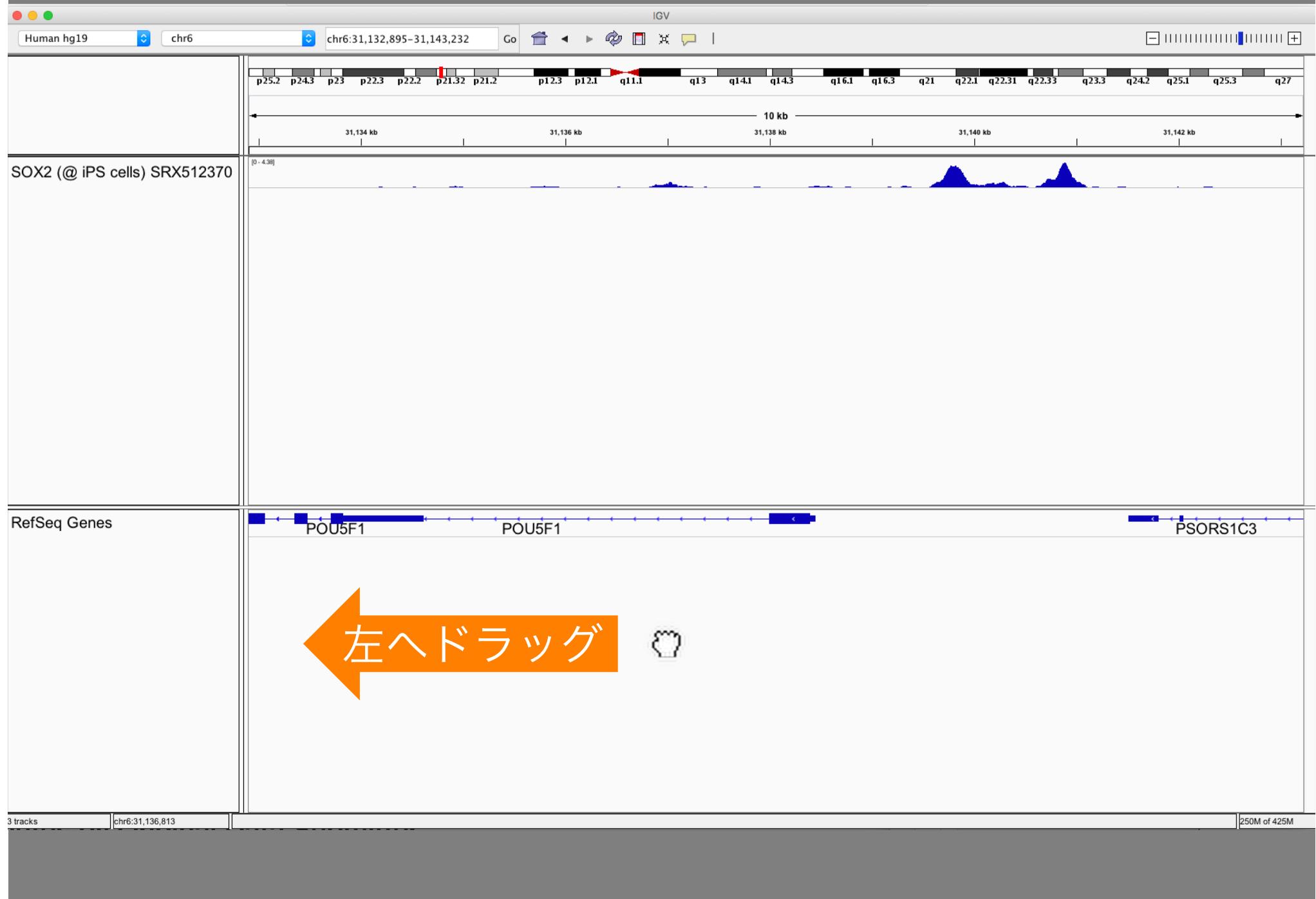
source_name	Induced pluripotent stem cells
cell type	Induced pluripotent stem cells
chip antibody	anti SOX2 antibody

BigWig = アライメントデータのこと

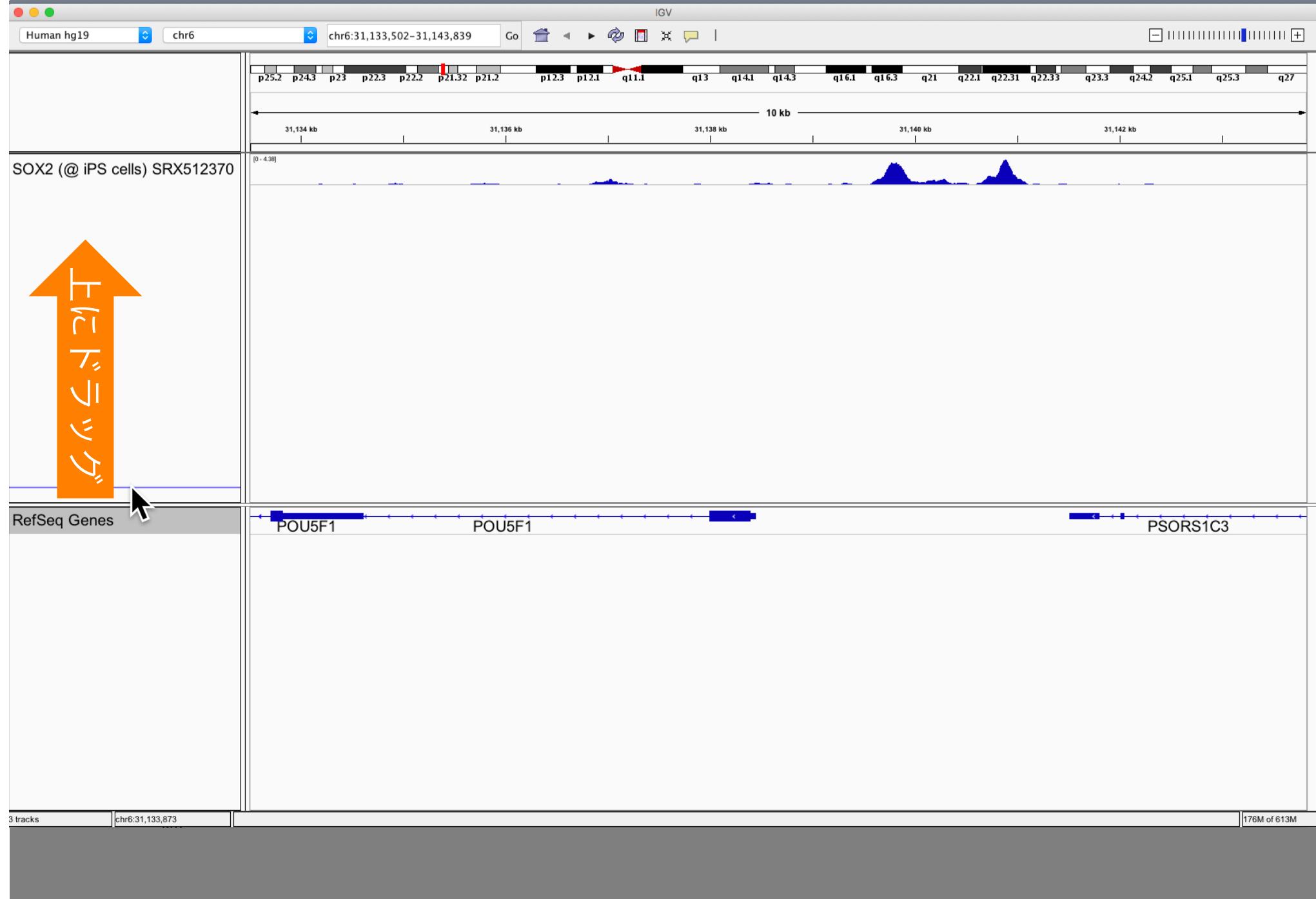
個別データの閲覧



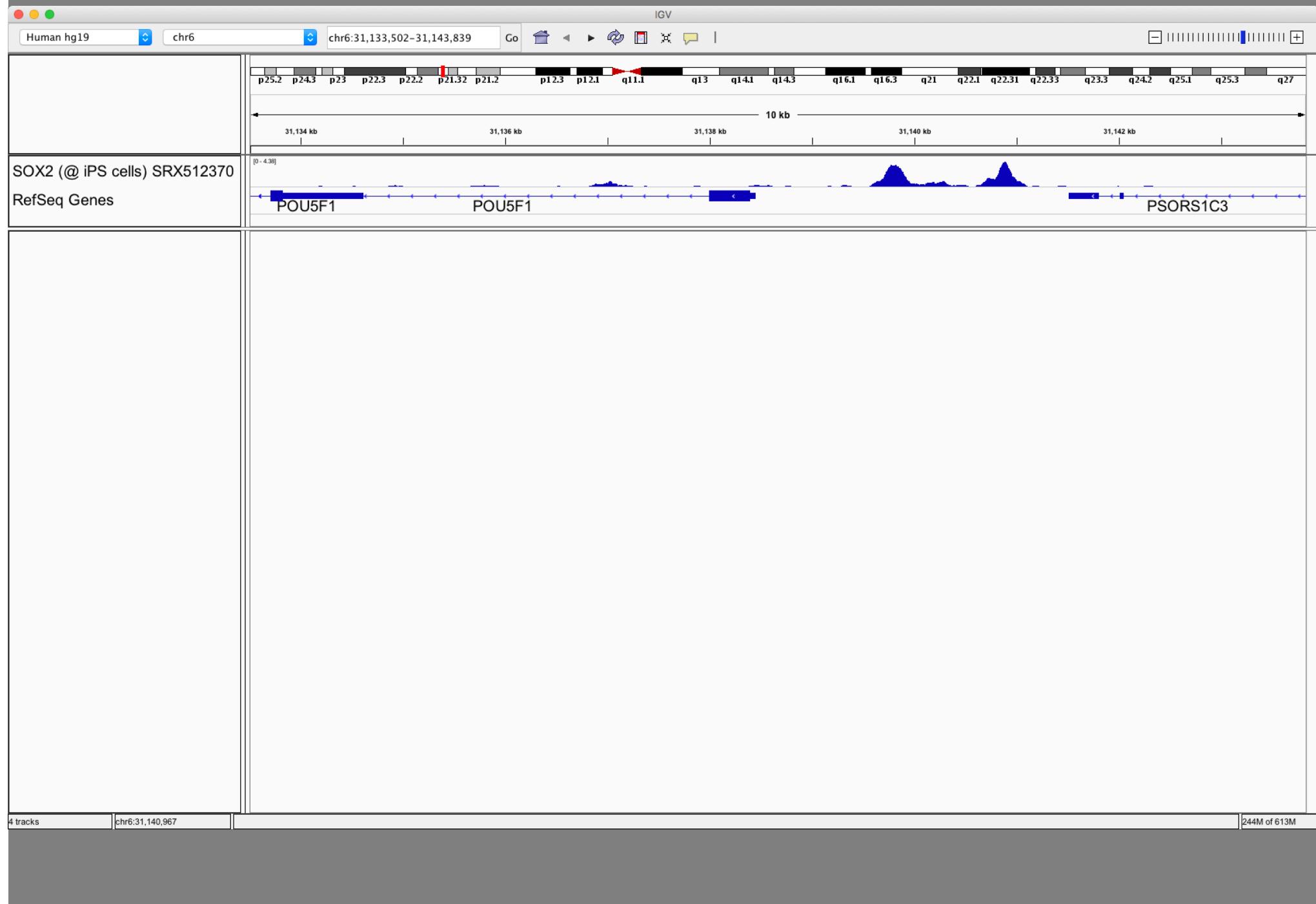
個別データの閲覧



個別データの閲覧



個別データの閲覧



個別データの閲覧

The screenshot shows a web browser window for the ChIP-Atlas website. The URL in the address bar is chip-atlas.org. The page title is "ChIP-Atlas - details for SRX512370". The top navigation bar includes links for "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", "Publications", and "Find an experiment". The main content area displays experiment details for "SRX512370" (GSM1364026: SOX2 iPSC; Homo Sapiens). A large orange speech bubble highlights the "Peak-call" option in the dropdown menu of the "View on IGV" button.

SRX512370

GSM1364026: SOX2 iPSC; Homo Sapiens

View on IGV ▾ View All ▾ Link Out ▾

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

Genome: hg19

Antigen Class	TFs and others
Antigen	SOX2
Cell type Class	Pluripotent stem cell
Cell type	iPS cells

Peak-call

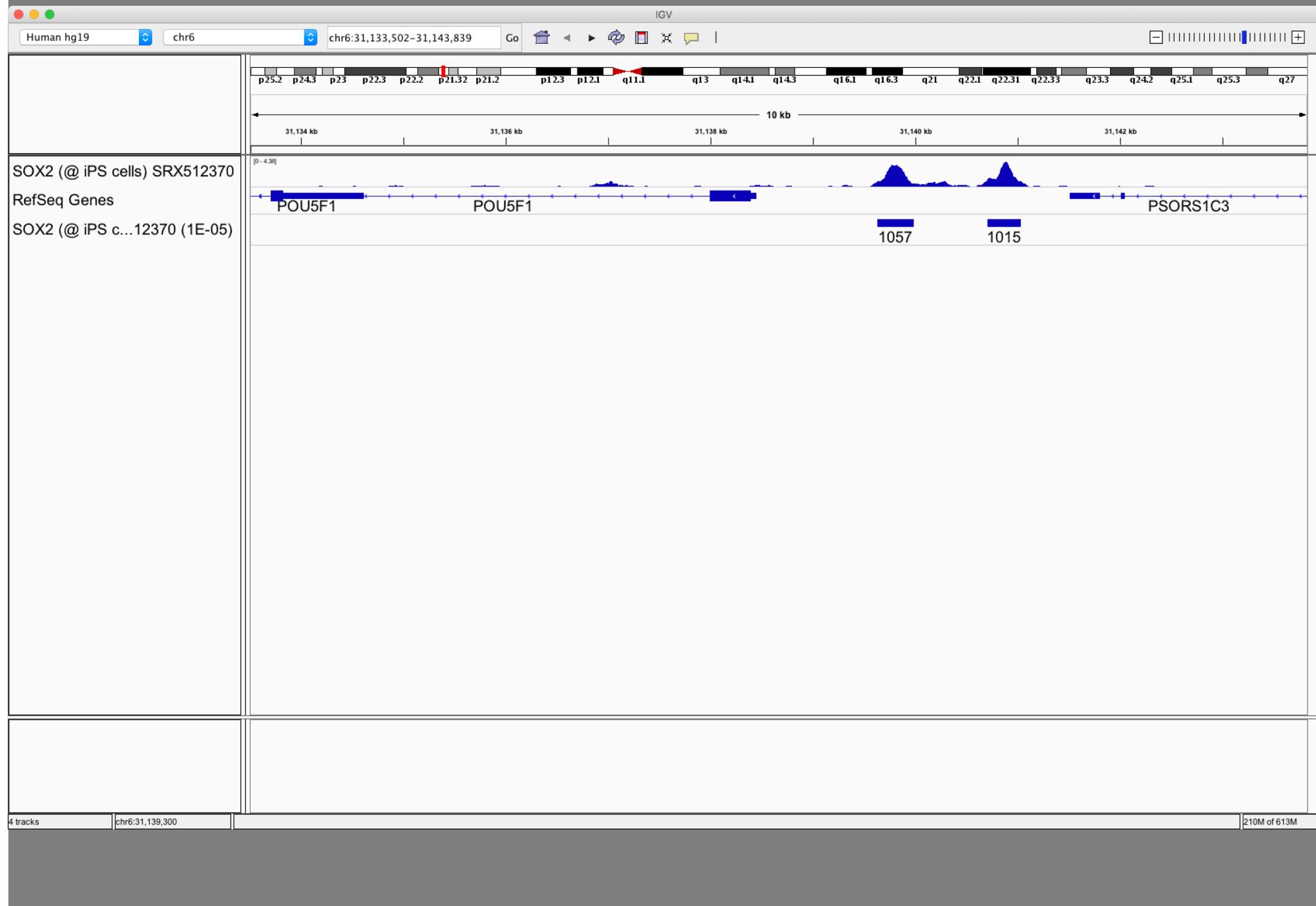
Cell type information

NA NA

Attributes by Original Data Submitter

source_name	Induced pluripotent stem cells
cell type	Induced pluripotent stem cells
chip antibody	anti SOX2 antibody

個別データの閲覧



複数データをまとめて見る

複数データをまとめて見る

The screenshot shows the ChIP-Atlas homepage. 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, dark font. A subtitle explains 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, based on over 78,000 experiments. There's also a link to "Watch movie introduction". On the left, a large orange speech bubble contains the Japanese word "クリック" (Click). Below the bubble, under the heading "The four main features of ChIP", 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

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

[Watch Movie](#)



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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

Antigen

Cell type

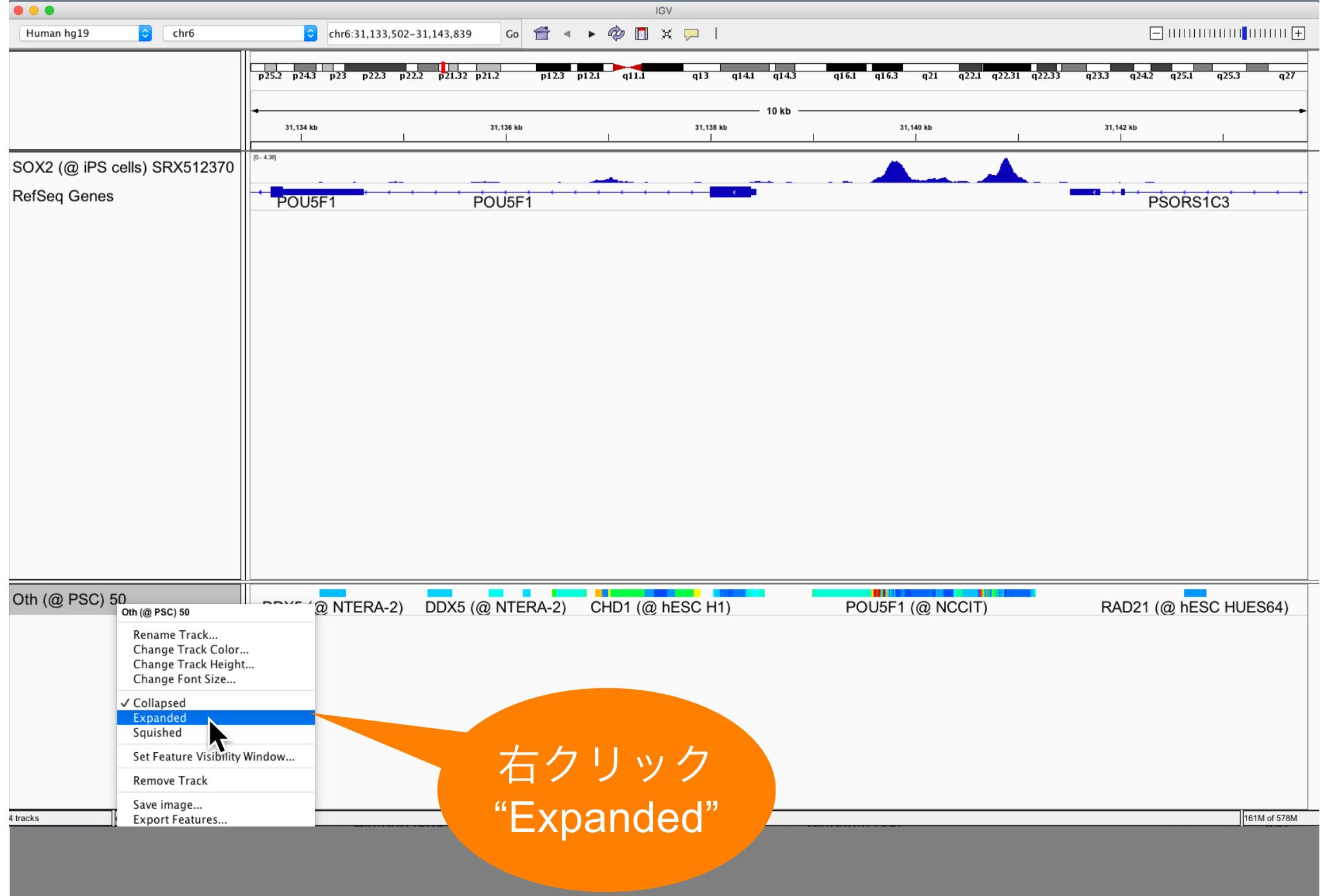
クリック

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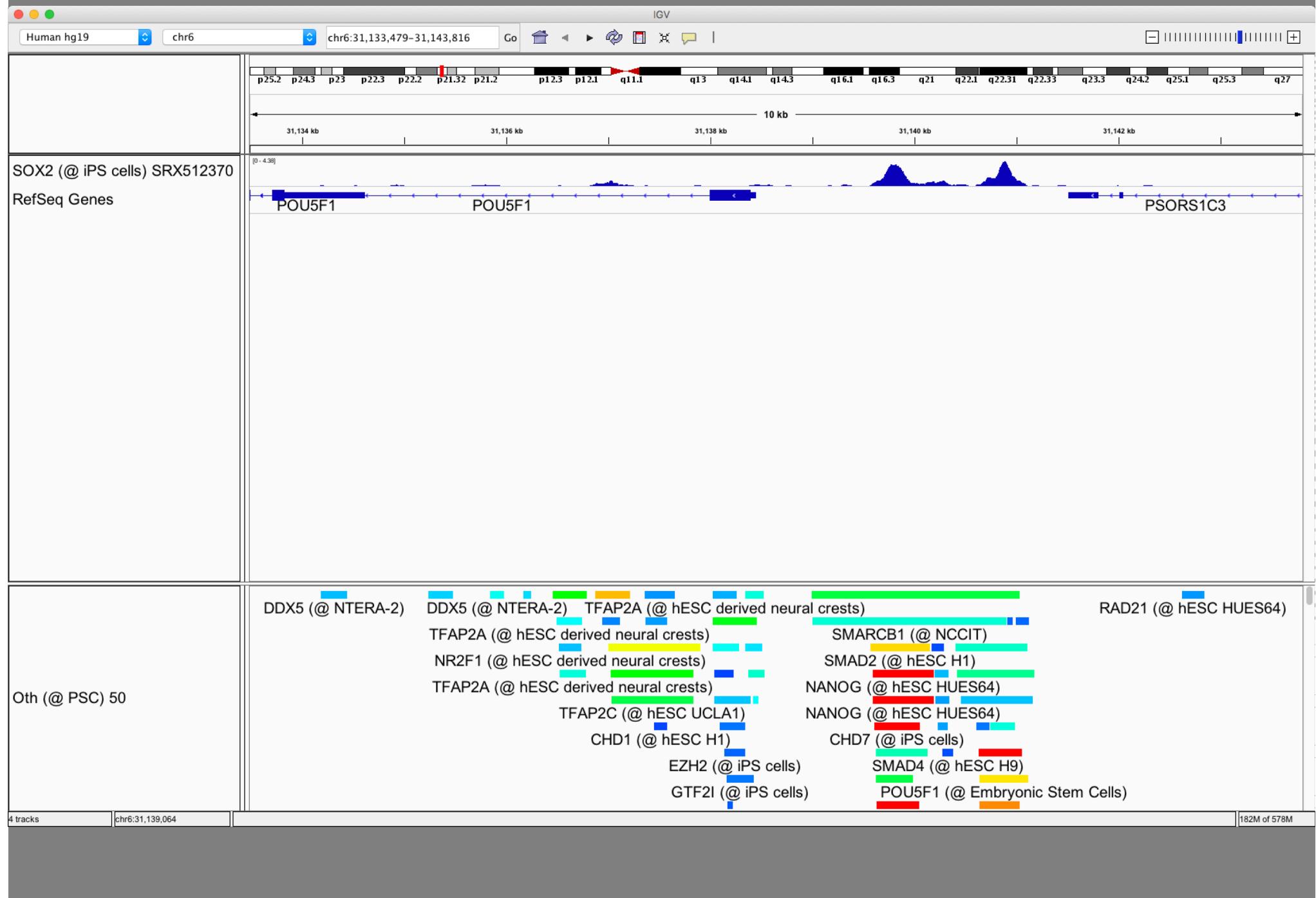
NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

KYUSHU UNIVERSITY IN COLLABORATION WITH DBCLS Database Center for Life Science

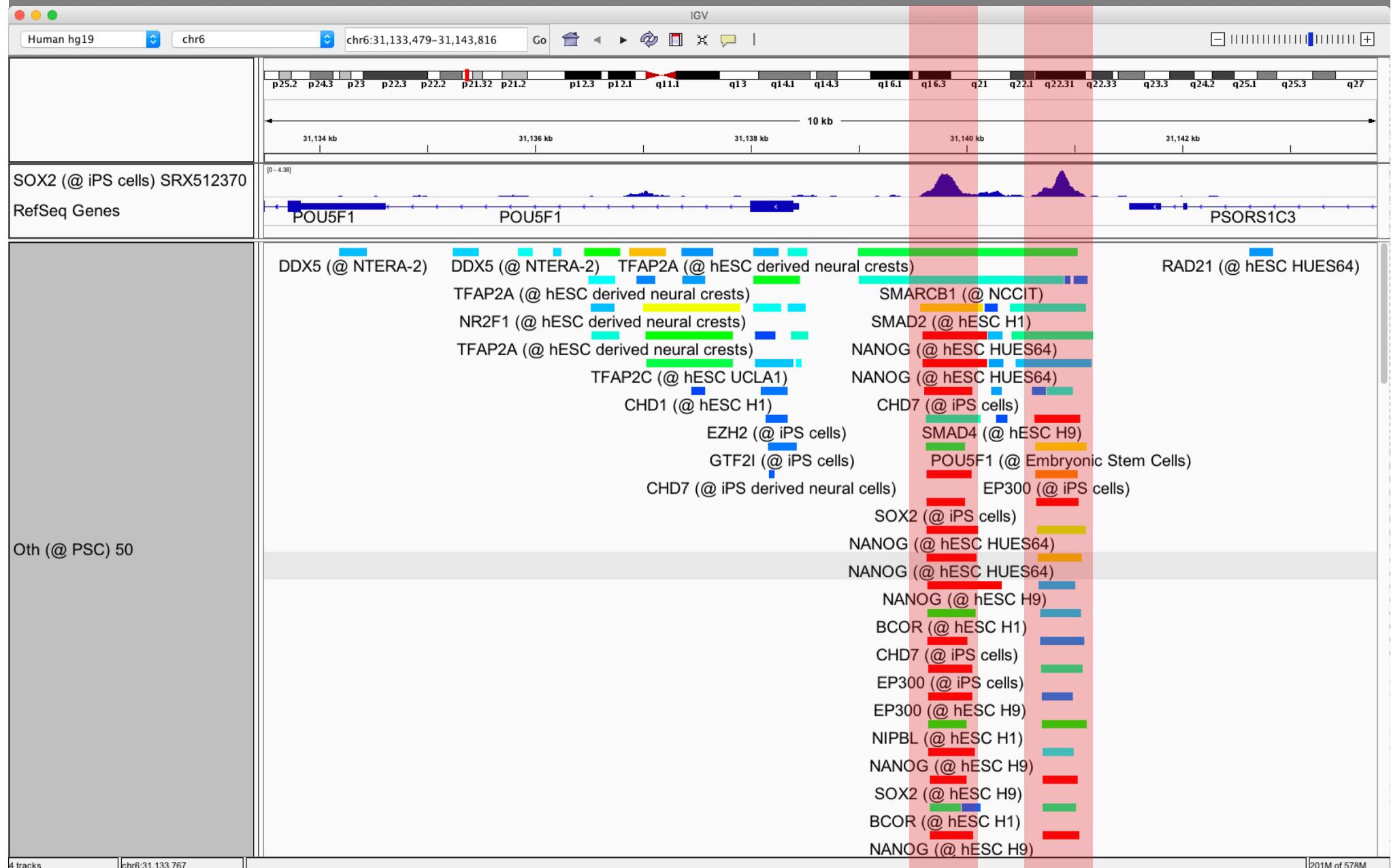
複数データをまとめて見る



複数データをまとめて見る

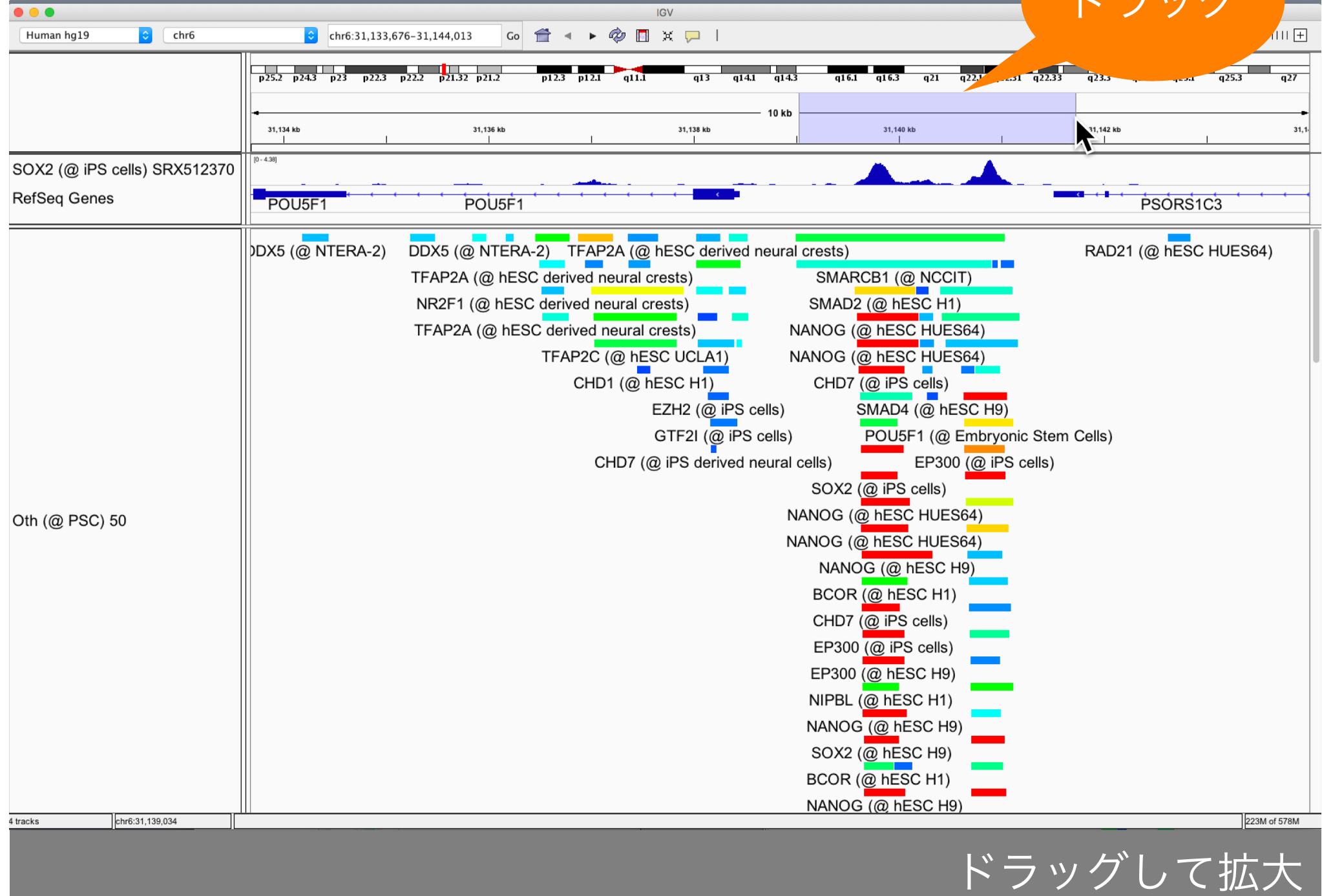


複数データをまとめて見る

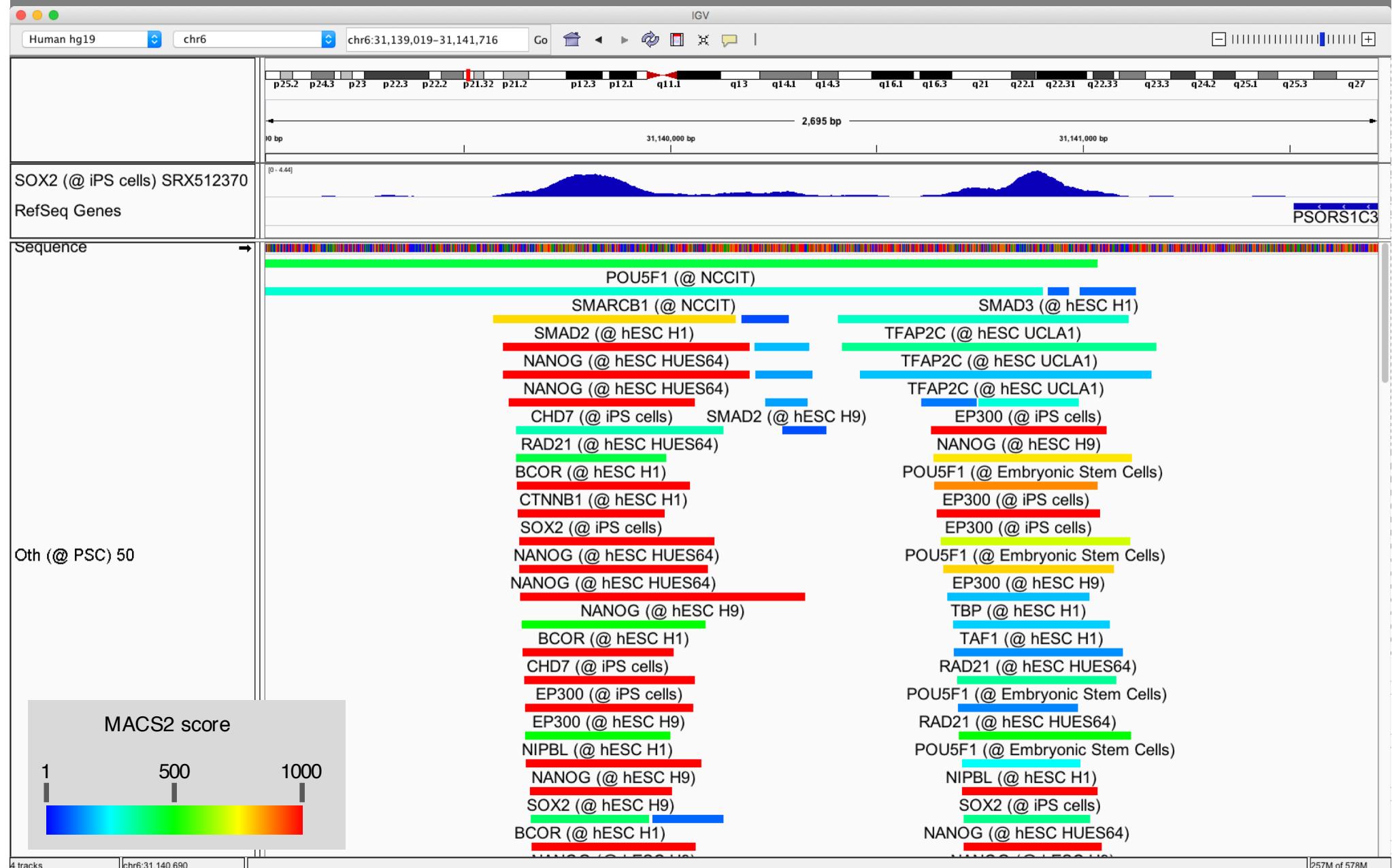


Stem cell 業界では、超有名なエンハンサー

複数データをまとめて見る



複数データをまとめて見る



結合の度合いをヒートカラー表示

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 ▾

ChIP-Atlas - Peak Browser

Visualize All Peaks from Published ChIP-Seq data.

H. sapiens M. musculus R. norvegicus D. melanogaster

しきい値の設定

MACS2 score

1 500 1000

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)

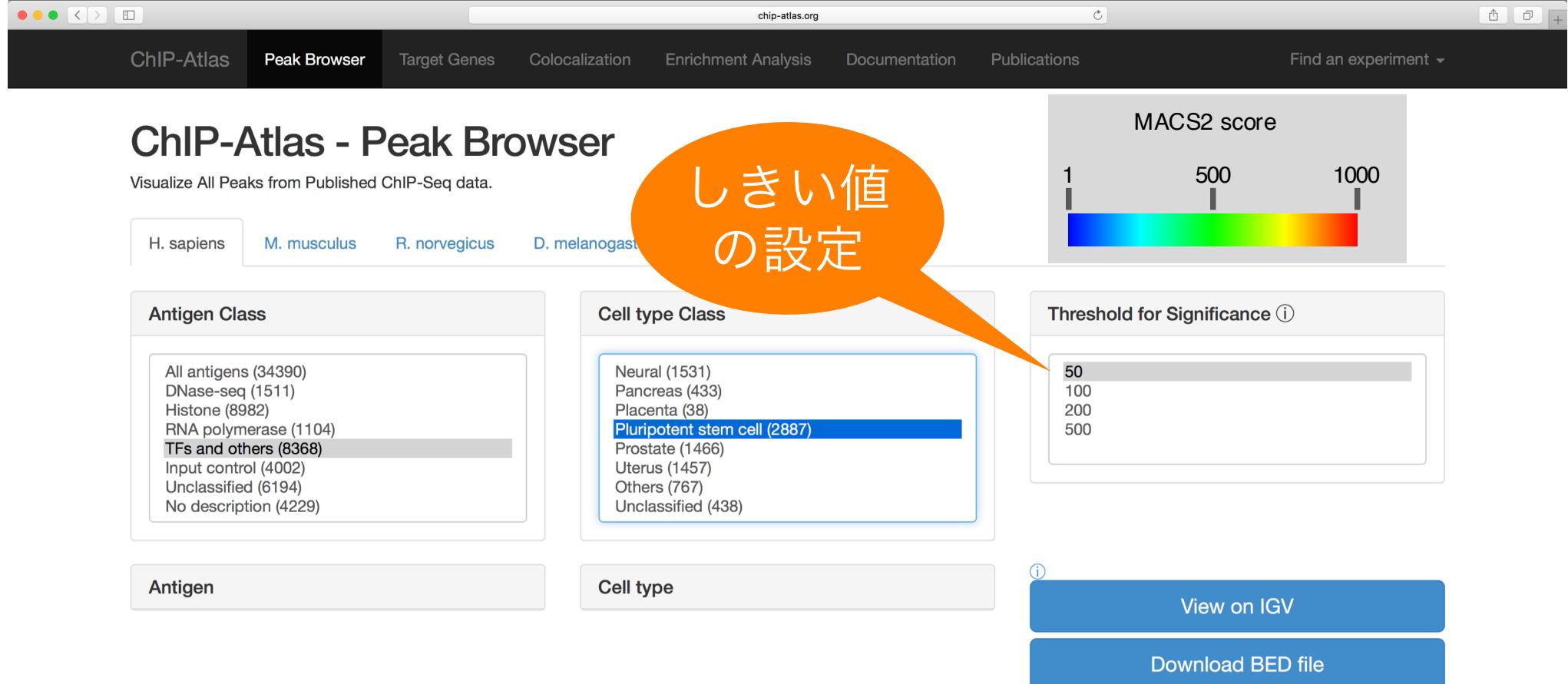
Threshold for Significance ⓘ

- 50
- 100
- 200
- 500

View on IGV

Download BED file

Antigen Cell type

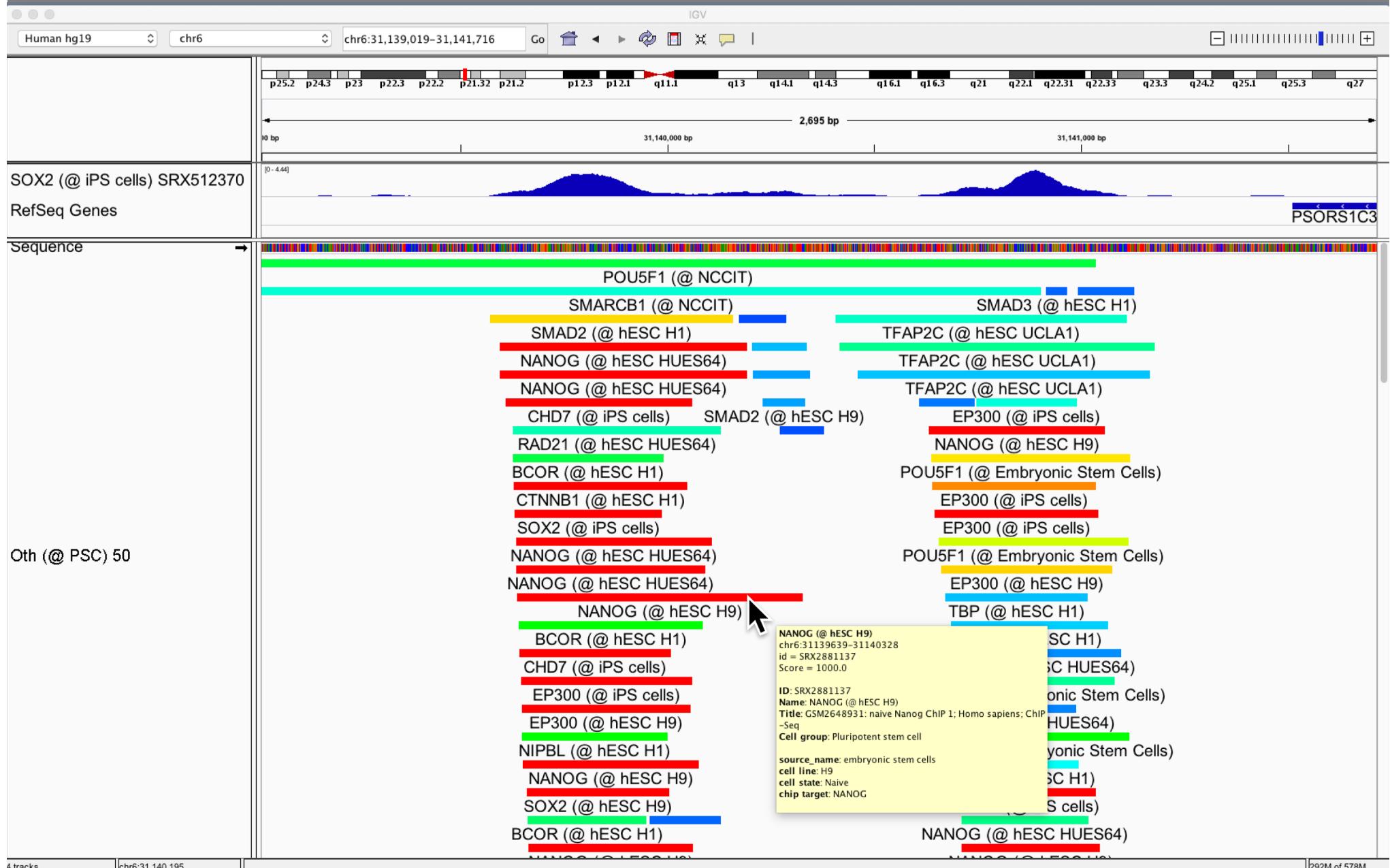


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NEED HELP? CREATE AN ISSUE ON [GITHUB](#) OR CONTACT US

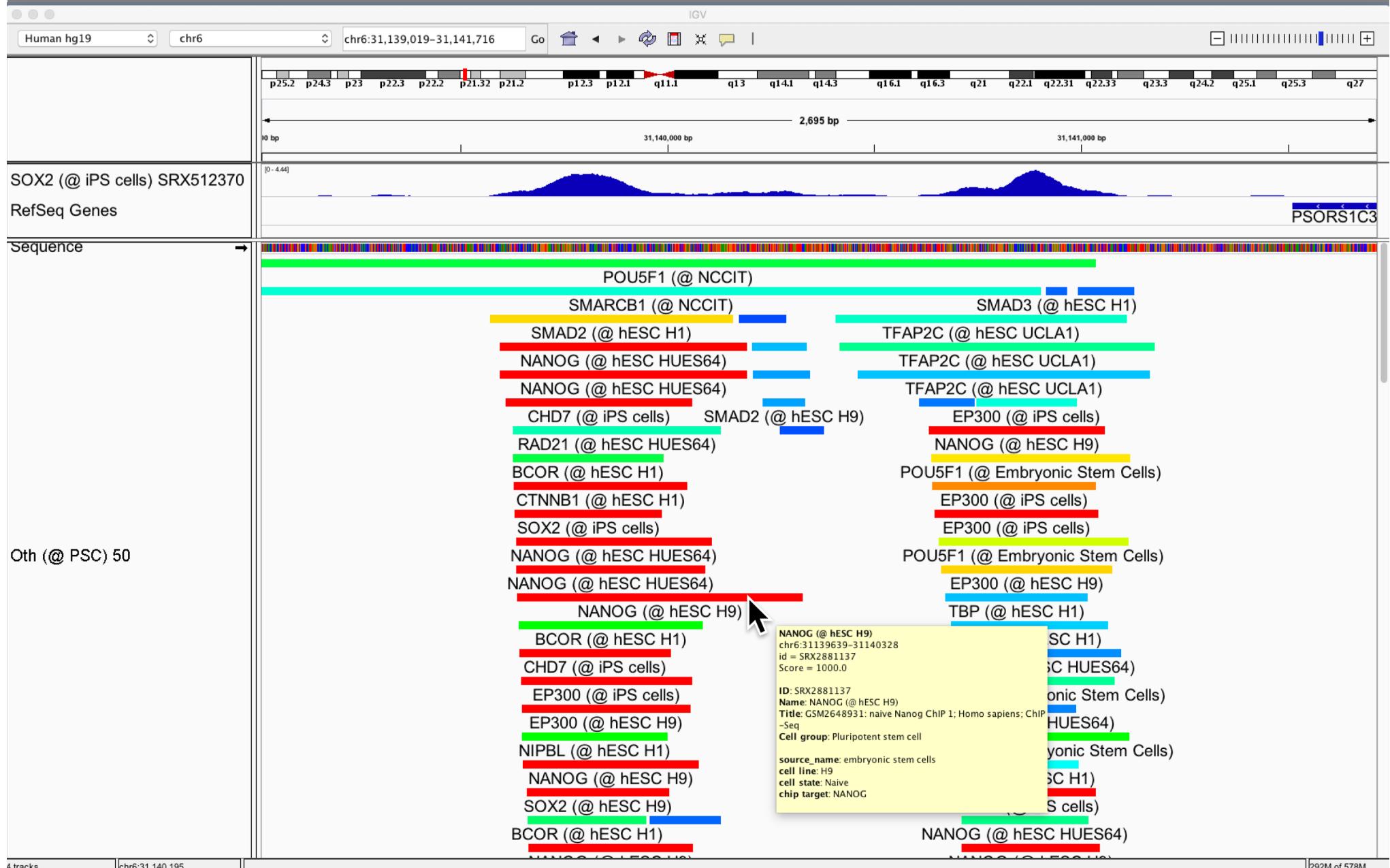
MACS2 score = $-10 \times \log_{10}[\text{Q-val}]$ (100 以上だとほぼ信頼できる)

複数データをまとめて見る



カーソルを当てる → 詳細な情報が表示される

複数データをまとめて見る



左クリック → 詳細な情報が Web で表示される

複数データをまとめて見る

The screenshot shows a web browser window for the ChIP-Atlas website (chip-atlas.org). The main header includes links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar for 'Find an experiment'. Below the header, the specific experiment details for 'SRX2881137' are displayed, including its GSE identifier 'GSM2648931: naive Nanog seq'. A large orange speech bubble with the Japanese text 'クリック' (Click) points to the 'View on IGV' button in the action bar below.

SRX2881137

GSM2648931: naive Nanog seq

View on IGV ▾

View Analysis ▾

Download ▾

Link Out ▾

Curated Sample Data

Genome	hg19
Antigen Class	TFs and others
Antigen	NANOG
Cell type Class	Pluripotent stem cell
Cell type	hESC H9

Cell type information

NA

NA

Attributes by Original Data Submitter

source_name	embryonic stem cells
cell line	H9
cell state	Naive
chip target	NANOG

複数データをまとめて見る

The screenshot shows a web browser window for the ChIP-Atlas website (chip-atlas.org). The main header includes links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis, Documentation, Publications, and a search bar for 'Find an experiment'. The specific experiment page for SRX2881137 is displayed, showing details like 'GSM2648931: naive; ChIP-Seq' and 'ChIP-Seq: ChIP-Seq'. A large orange speech bubble highlights the 'View on IGV' button, which has a dropdown menu open showing options: BigWig, Peak-call (q < 1E-05), Peak-call (q < 1E-10), and Peak-call (q < 1E-20). Below this, there's a table with columns for 'Genome', 'Antigen Class', 'Antigen', 'Cell type Class', and 'Cell type'. The table entries are: Genome (hg19), Antigen Class (TFs and others), Antigen (NANOG), Cell type Class (Pluripotent stem cell), and Cell type (hESC H9).

SRX2881137

GSM2648931: naive; ChIP-Seq; ChIP-Seq

BigWig

View on IGV ▾

Download ▾

Link Out ▾

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

Genome

hg19

Antigen Class

TFs and others

Antigen

NANOG

Cell type Class

Pluripotent stem cell

Cell type

hESC H9

Cell type information

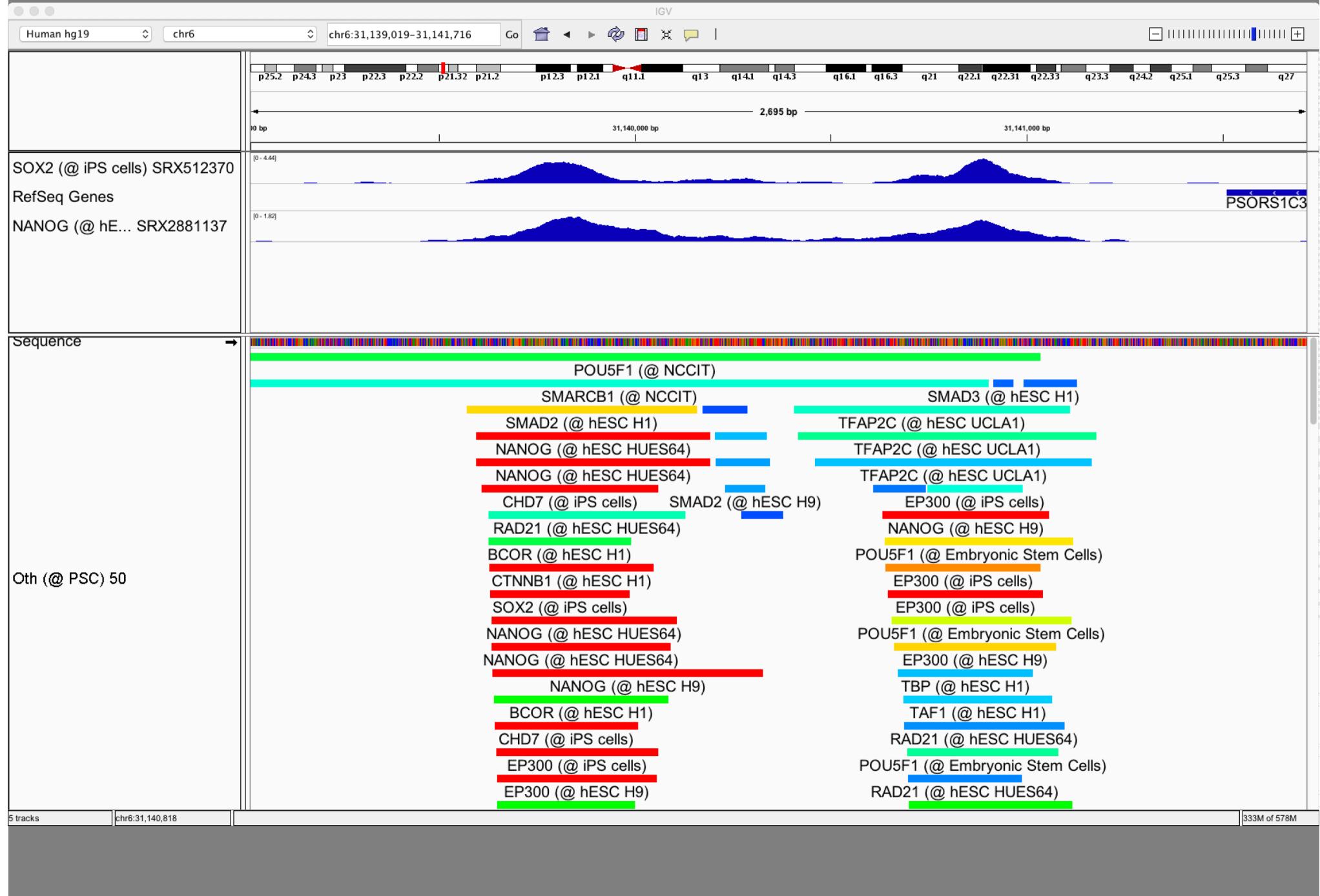
NA

NA

Attributes by Original Data Submitter

source_name	embryonic stem cells
cell line	H9
cell state	Naive
chip target	NANOG

複数データをまとめて見る



複数データをまとめて見る

ChIP-Atlas H. sapience

Visualize All Peaks from P... Tutorial movies ▾

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

- Liver (1167)
- Lung (2719)
- Muscle (293)
- Neural (1531)
- Pancreas (433)
- Placenta (38)
- Pluripotent stem cell (2887)**
- Prostate (1466)

Threshold for Significance ⓘ

- 50
- 100
- 200
- 500

クリック

View on IGV

Download BED file

Histone

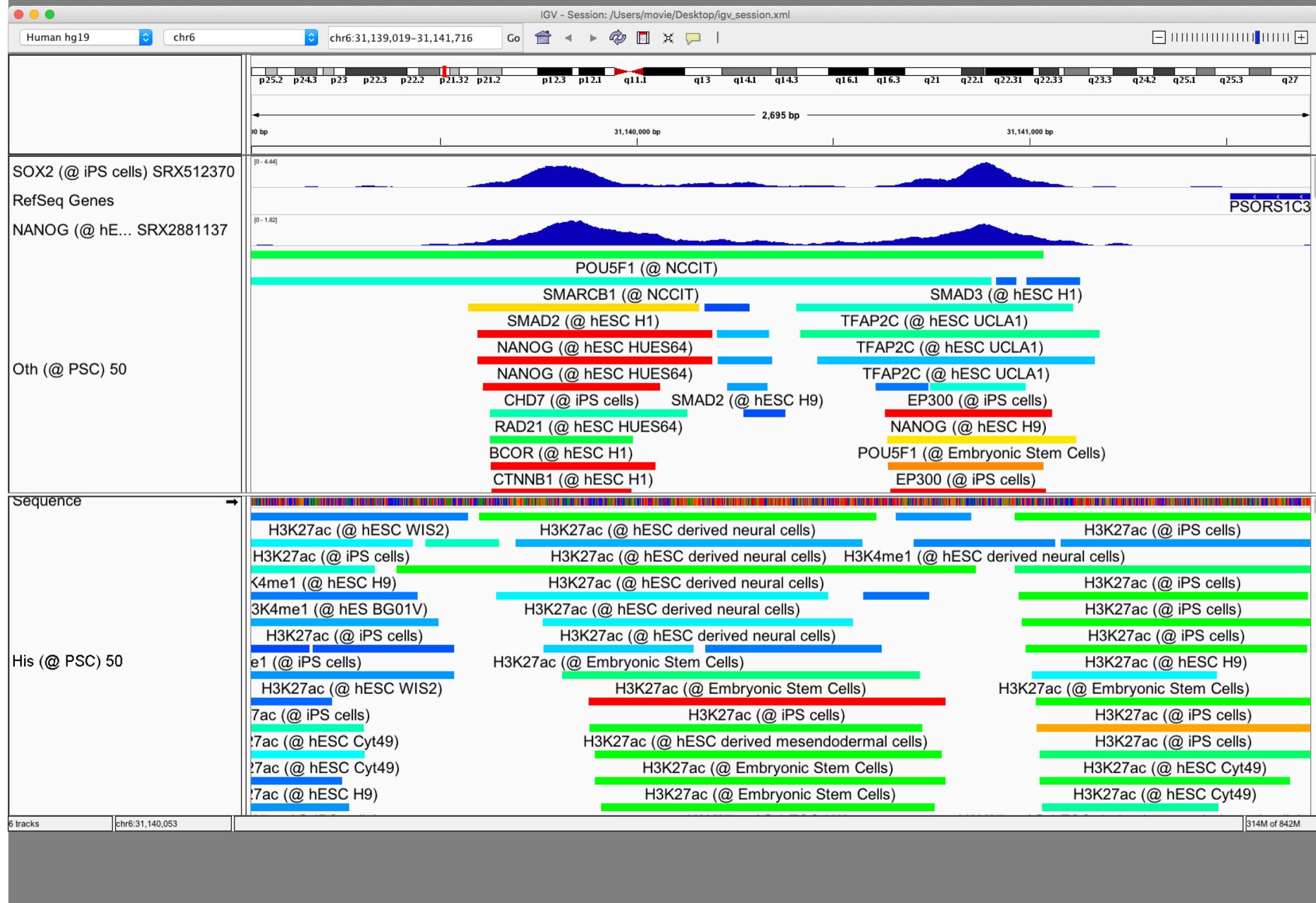
Pluripotent stem cell

KYUSHU UNIVERSITY IN COLLABORATION WITH

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複数データをまとめて見る



標的遺伝子を探す

標的遺伝子を探す

The screenshot shows the ChIP-Atlas website with a dark header bar. The header includes the URL 'chip-atlas.org' in the address bar, and navigation links for 'ChIP-Atlas', 'Peak Browser', 'Target Genes', 'Colocalization', 'Enrichment Analysis', 'Documentation', and 'Publications'. A search bar labeled 'Find an experiment ▾' is also present.

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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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標的遺伝子を探す

chip-atlas.org

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

ChIP-Atlas - Target Genes

Predict potential target genes of TFs.

Tutorial movie ▾

H. sapiens

M. musculus

R. norvegicus

D. melanogaster

C. elegans

S. cerevisiae

1. Choose Antigen

NANOG

MYBL2
MYC
MYCN
MYF6
MYH11
MYNN
MYOD1
NANOG

2. Choose Distance from TSS

- ±1k
- ±5k
- ±10k

± 5 K

NANOG

View Potential Target Genes

Download (TSV)

クリック



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標的遺伝子を探す

dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

Query protein: NANOG

Distance from TSS: ± 1 kb ± 5 kb ± 10 kb

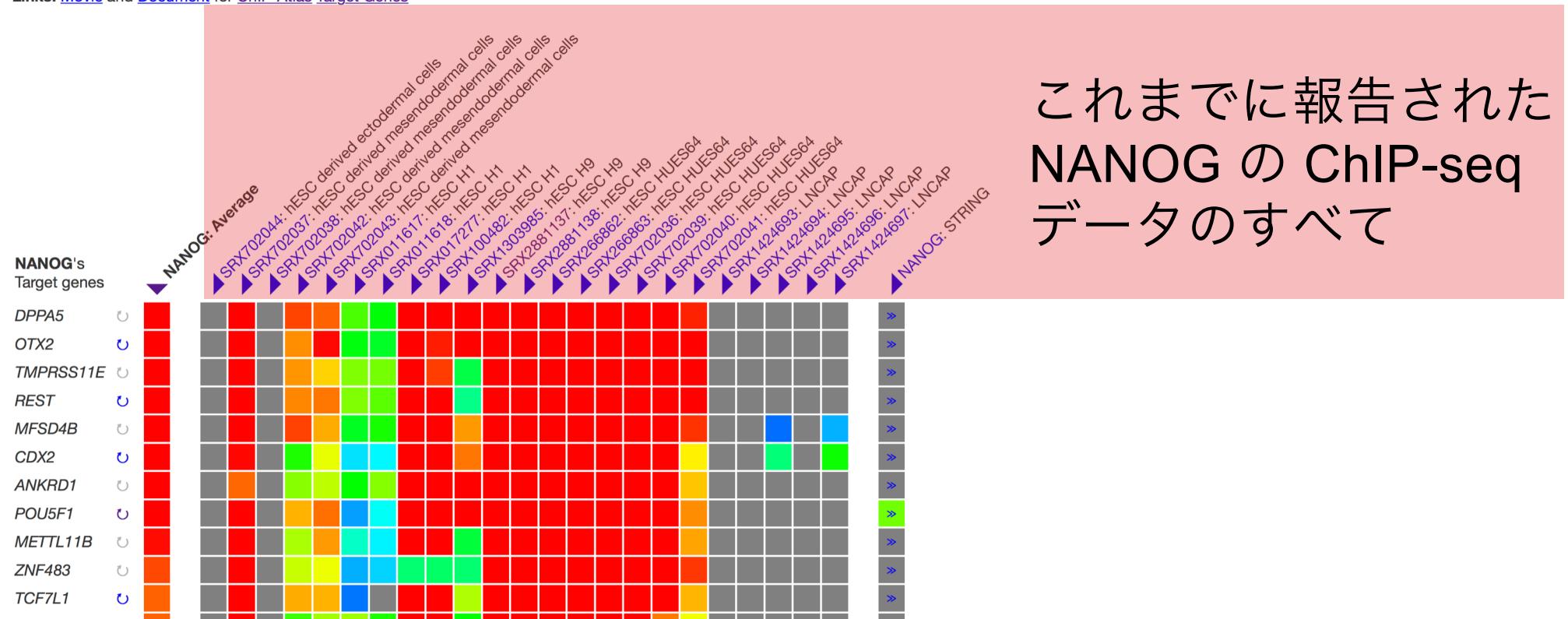
Sort key: NANOG | Average

Color legends

1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

Download: [TSV](#) (text)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Target Genes



これまでに報告された
NANOG の ChIP-seq
データのすべて

標的遺伝子を探す

dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

Query protein: NANOG

Distance from TSS: \pm 1 kb \pm 5 kb \pm 10 kb

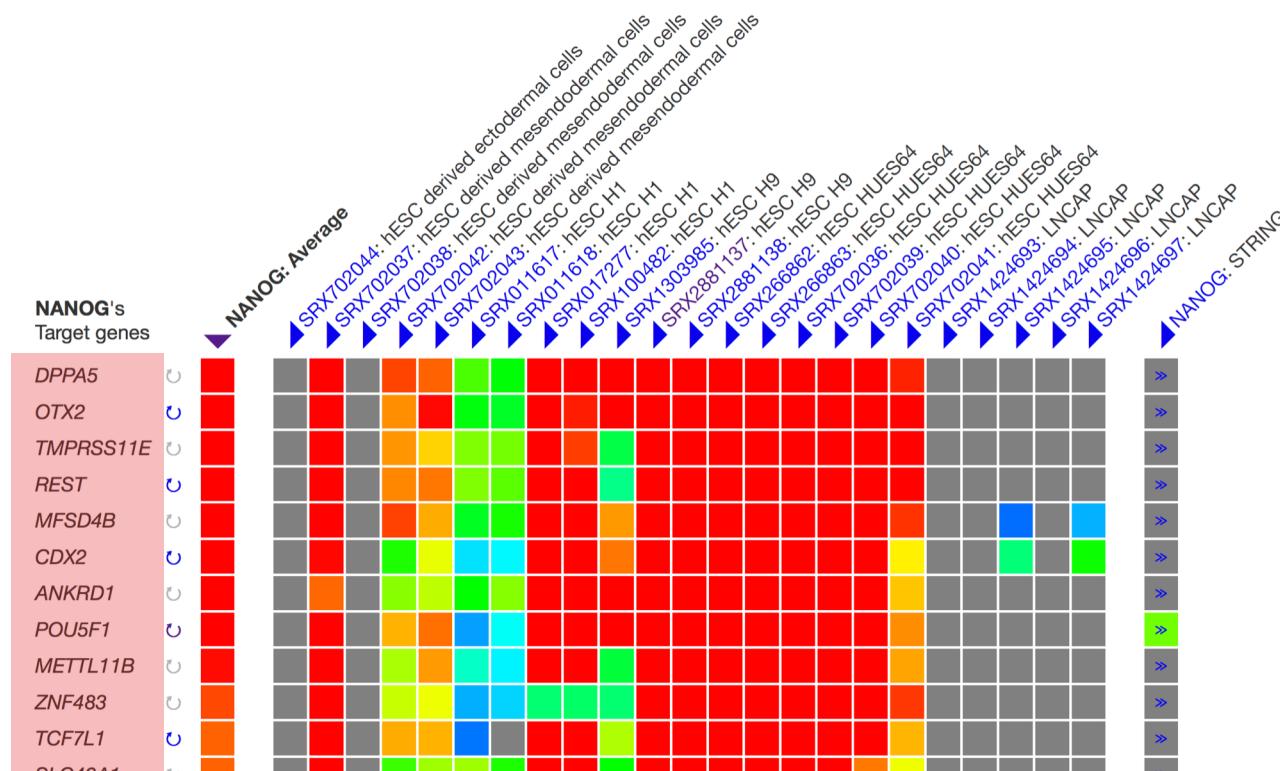
Sort key: NANOG | Average

Color legends



Download: [TSV](#) (text)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Target Genes



NANOG の標的遺伝子候補

標的遺伝子を探す

dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

Query protein: NANOG

Distance from TSS: ± 1 kb ± 5 kb ± 10 kb

Sort key: NANOG | Average

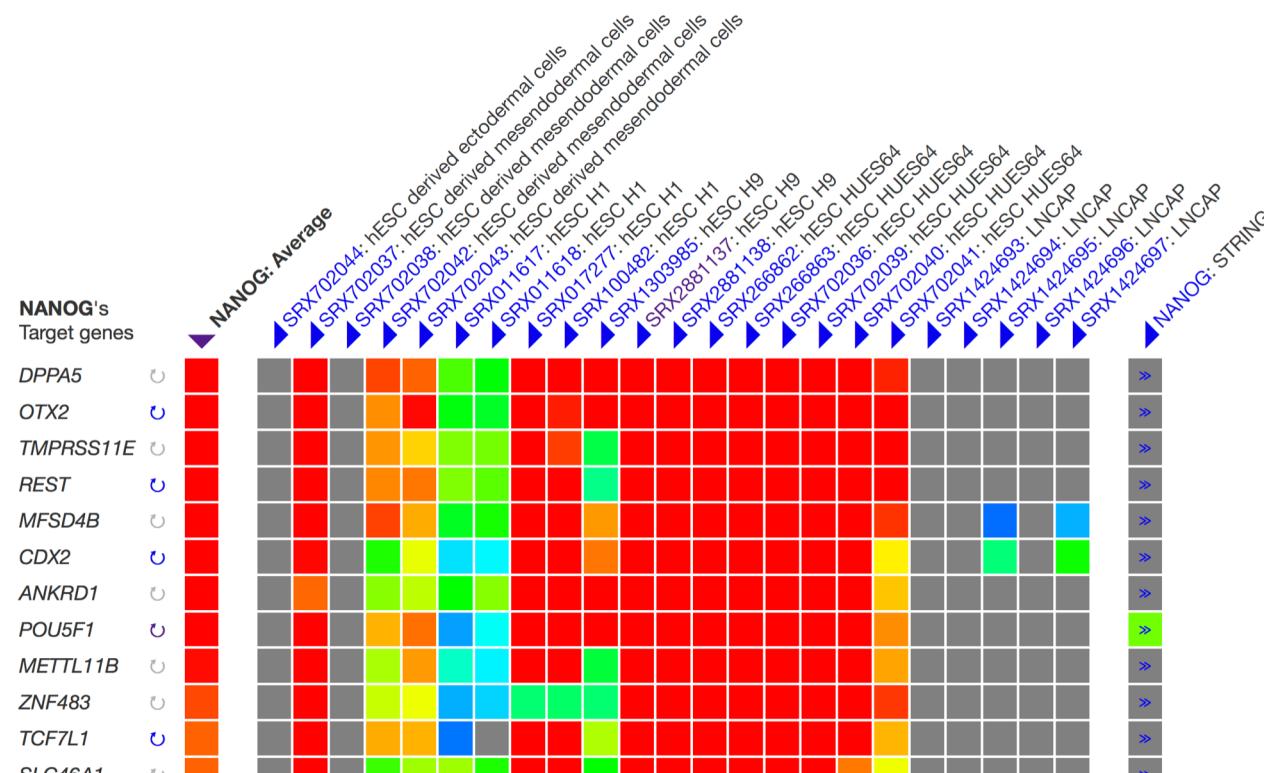
Color legends

1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

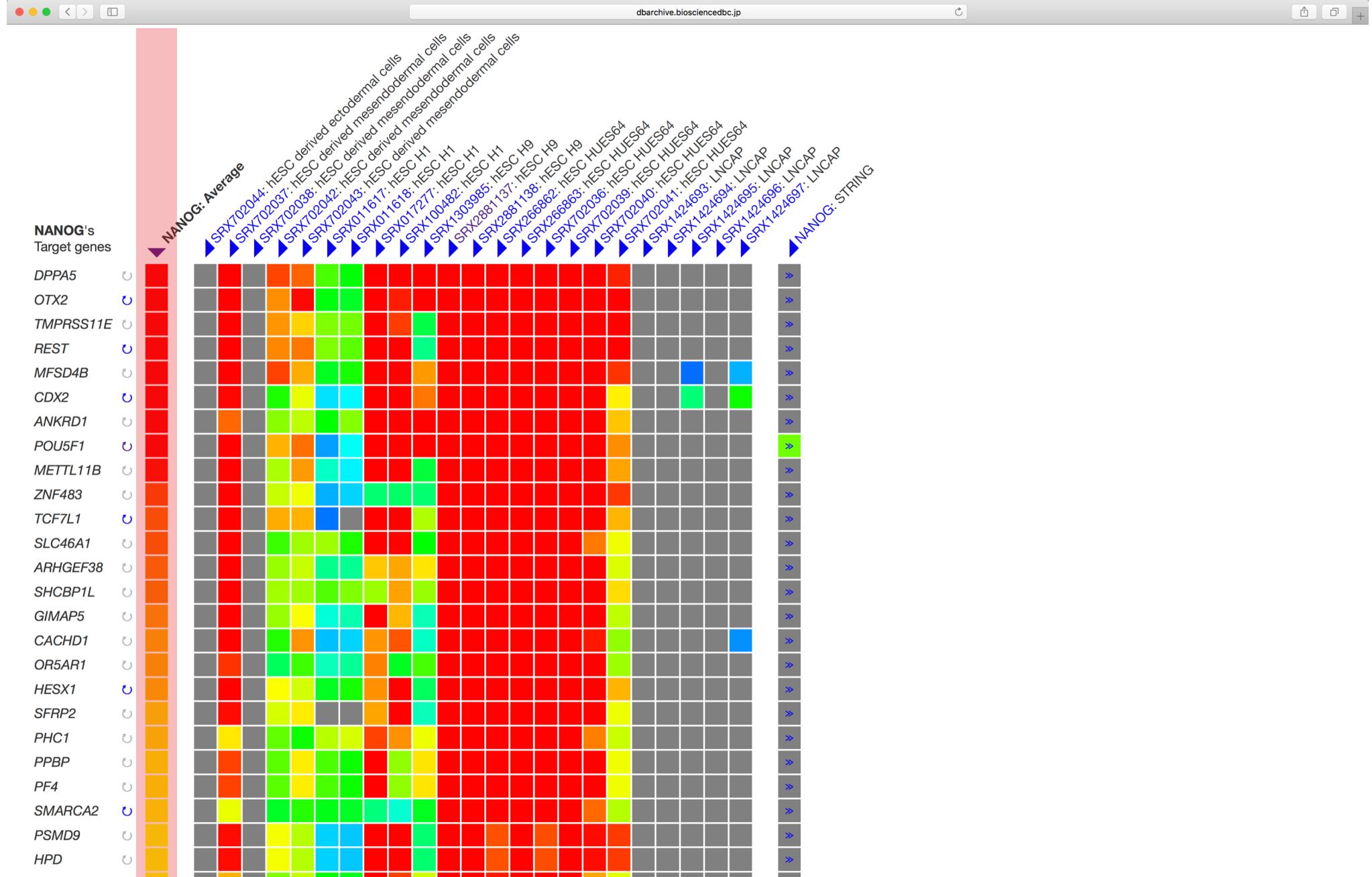
MACS2 score

Download: [TSV](#) (text)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Target Genes

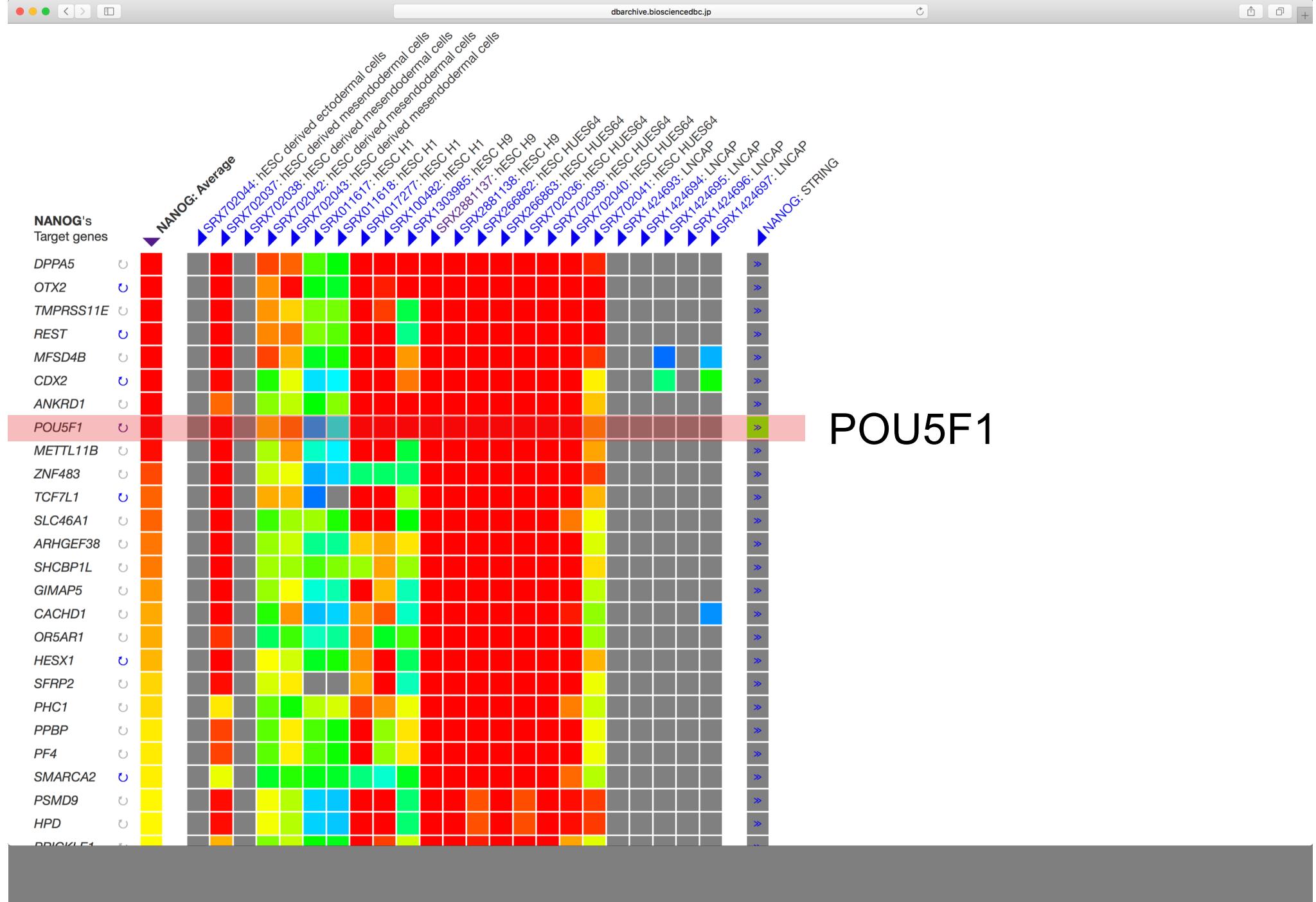


標的遺伝子を探す

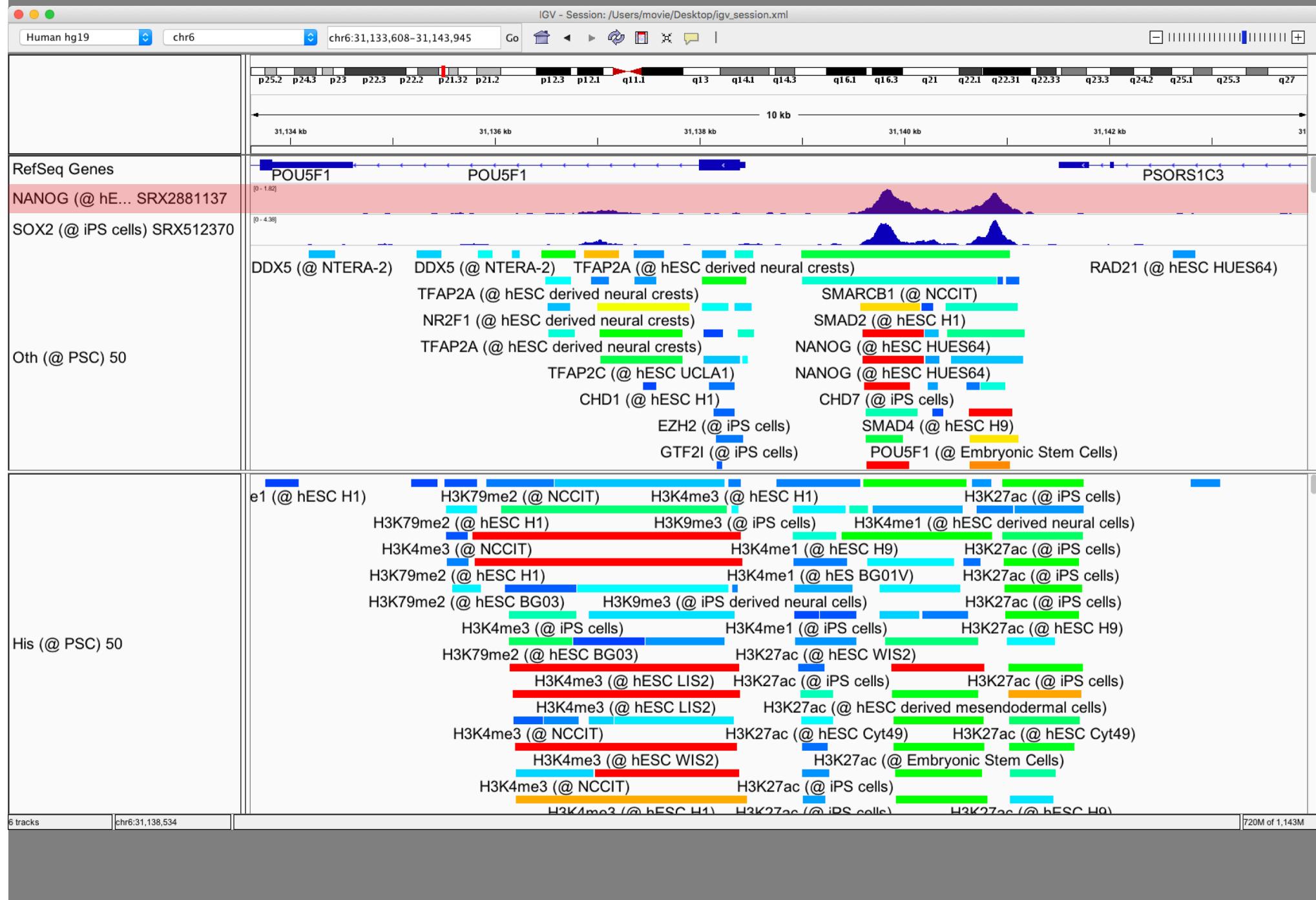


各行の平均値でソート

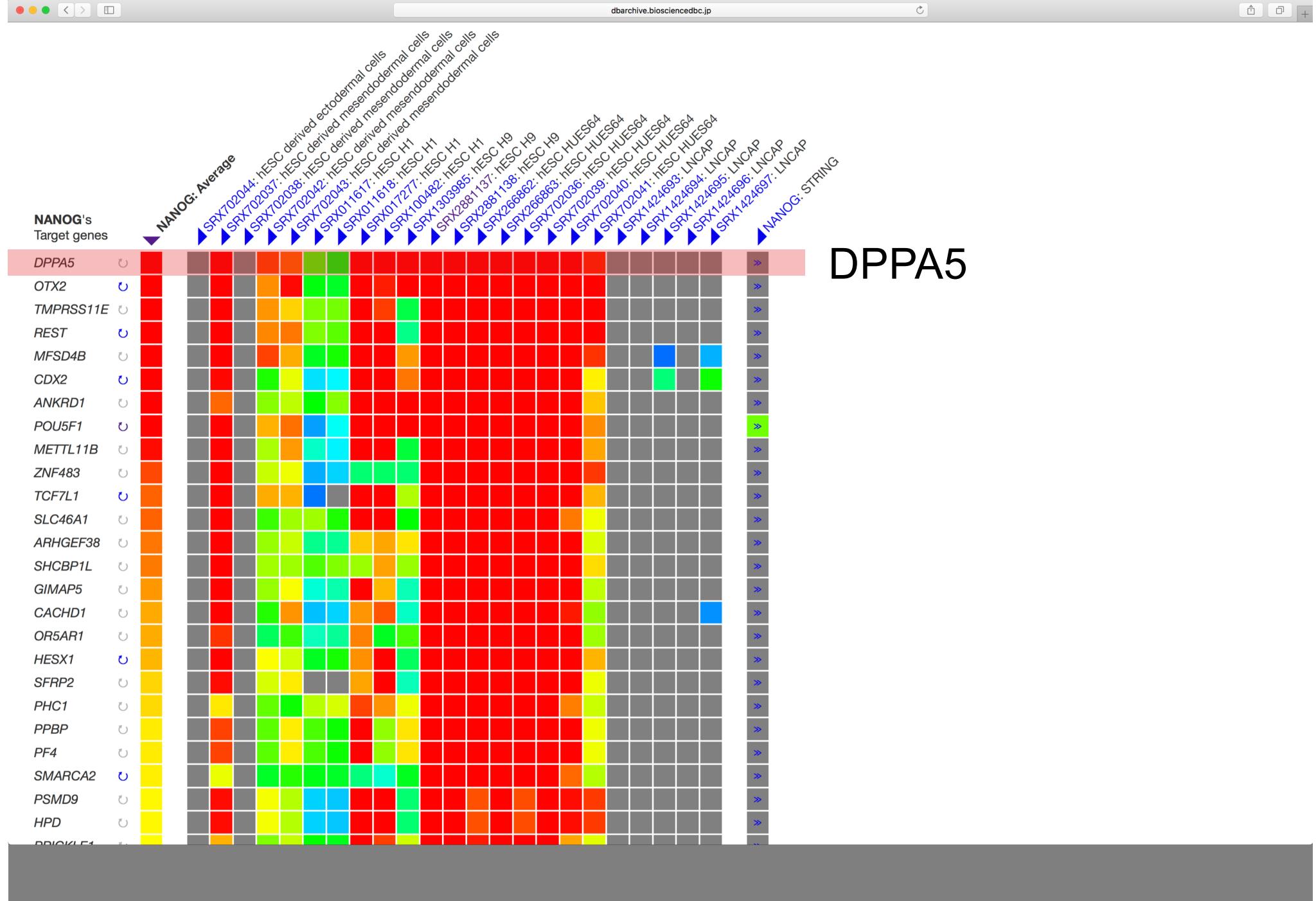
標的遺伝子を探す



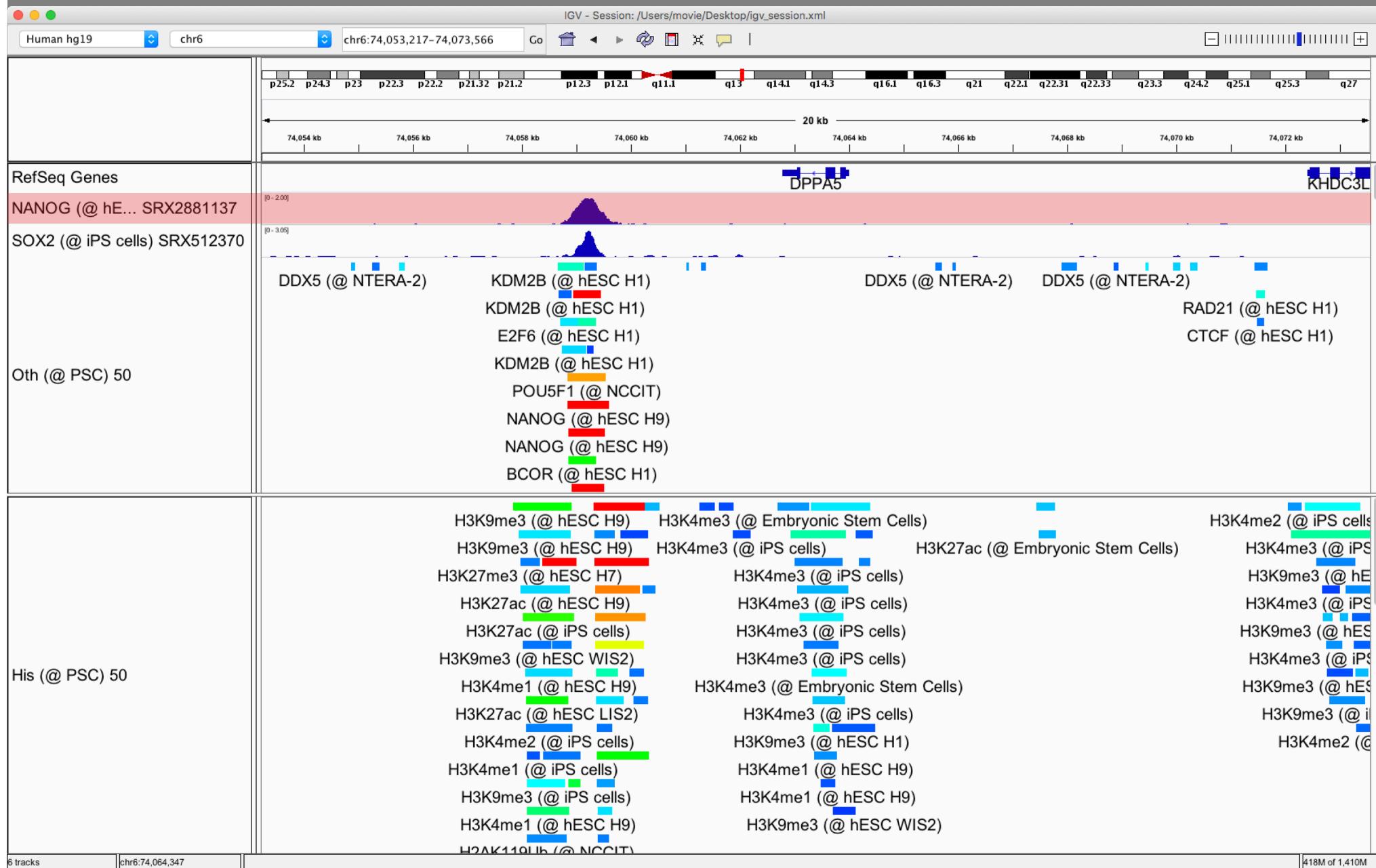
標的遺伝子を探す



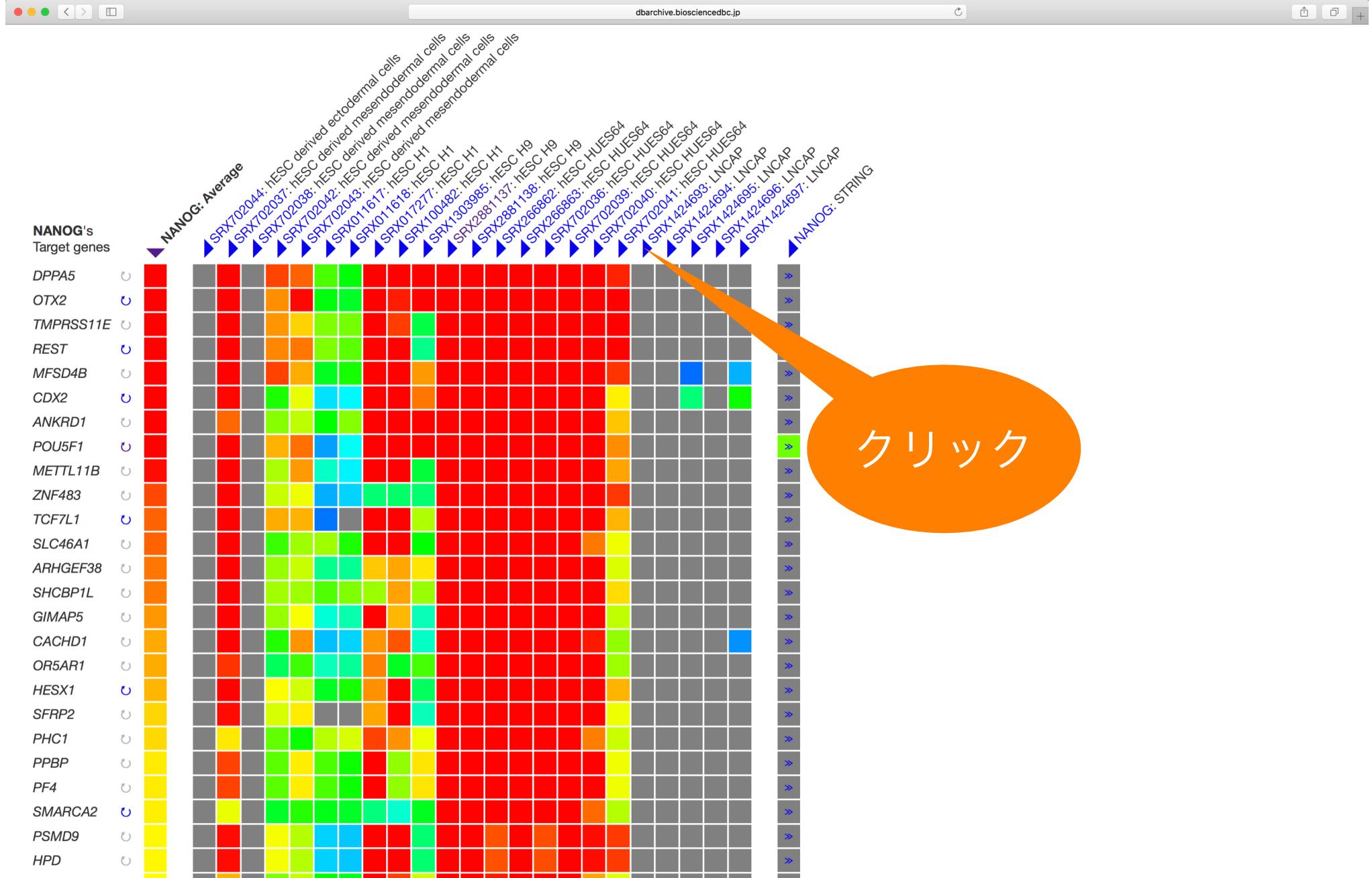
標的遺伝子を探す



標的遺伝子を探す



標的遺伝子を探す



LNCAP 細胞の NANOG ChIP-seq データでソートする

標的遺伝子を探す

dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

Query protein: NANOG

Distance from TSS: ± 1 kb ± 5 kb ± 10 kb

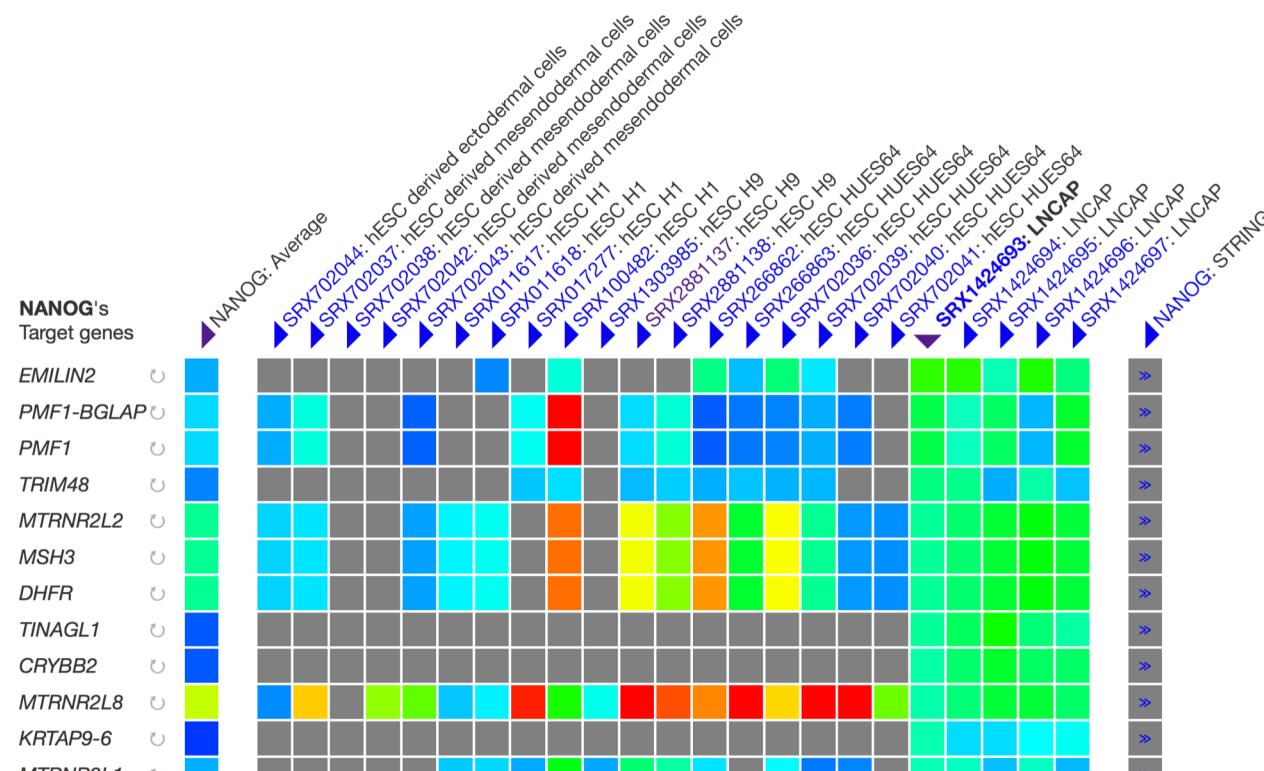
Sort key: SRX1424693 | LNCAP

Color legends

1000 750 500 250 1 0 (Values = Binding scores of MACS2 and STRING)

Download: [TSV](#) (text)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Target Genes



LNCAP 細胞の NANOG ChIP-seq データでソートする

共局在因子を探す

全局在因子を探す

The screenshot shows the ChIP-Atlas website with a dark header bar. The header includes the URL 'chip-atlas.org' in the address bar, and navigation links for 'ChIP-Atlas', 'Peak Browser', 'Target Genes', 'Colocalization', 'Enrichment Analysis', 'Documentation', and 'Publications'. A search bar labeled 'Find an experiment ▾' is also present.

ChIP-Atlas

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[Watch movie introduction](#)

クリック

The four main features of ChIP-Atlas are:

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[Watch Movie](#)

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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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共局在因子を探す

ChIP-Atlas | Target genes chip-atlas.org ChIP-Atlas

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

ChIP-Atlas - Colocalization

Predict colocalization partners of TFs.

H. sapiens

M. musculus

R. norvegicus

D. melanogaster

C. elegans

S. cerevisiae

1. Search mode

- Antigens → Cell Type
 Cell Type → Antigen

2. Choose Antigen

NANOG

MYOD1
NANOG
NCAPG
NCAPG2
NCAPH2
NCOA1
NCOA2
NCOA3

3. Choose Cell Type Class

type to search

Pluripotent stem cell
Prostate

NANOG

Pluripotent
stem cell

クリック

View Colocalization Data

Download (TSV)

Download (GML)



DBCLS
Database Center
for Life Sciences

共局在因子を探す



ChIP-Atlas: Colocalization analysis

Colocalization analysis for NANOG

Query protein: NANOG

Cell class: Pluripotent stem cell

Sort key: NANOG | Average

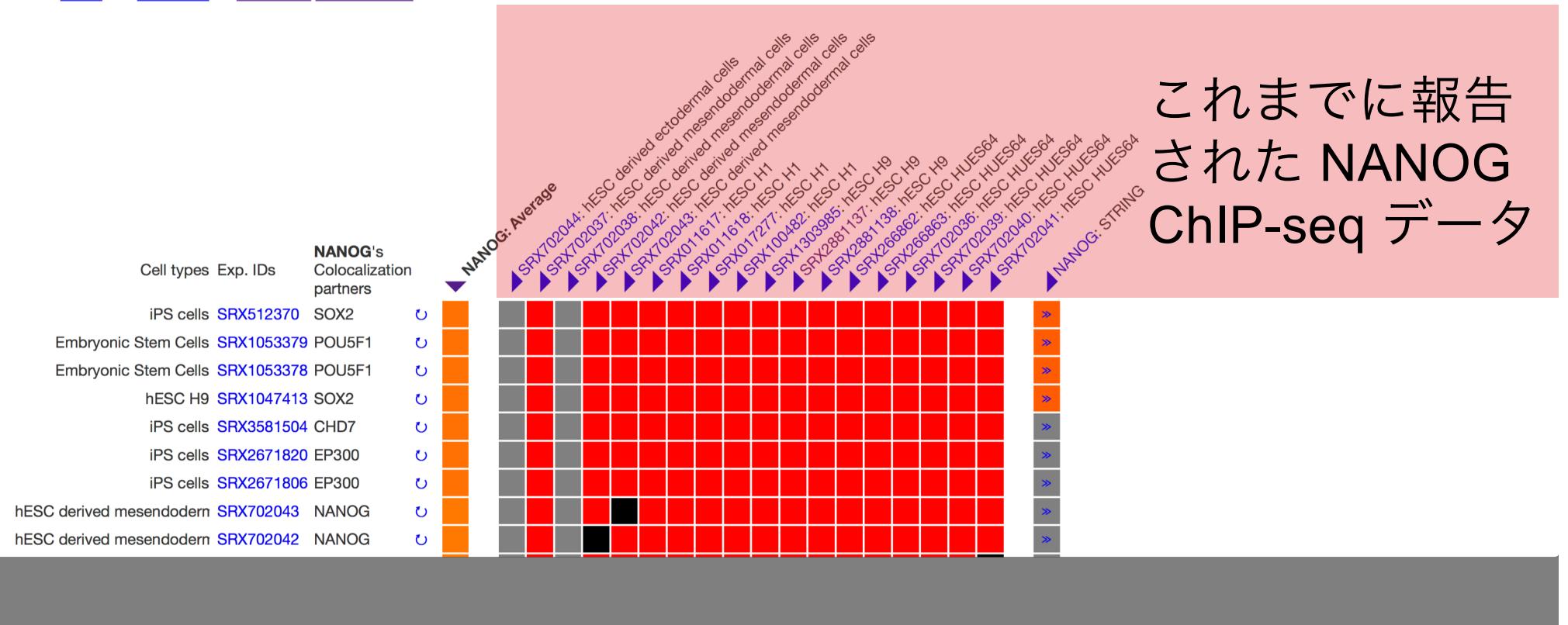
Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are High, Middle or Low)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Colocalization



共局在因子を探す



ChIP-Atlas: Colocalization analysis

Colocalization analysis for NANOG

Query protein: NANOG

Cell class: Pluripotent stem cell

Sort key: NANOG | Average

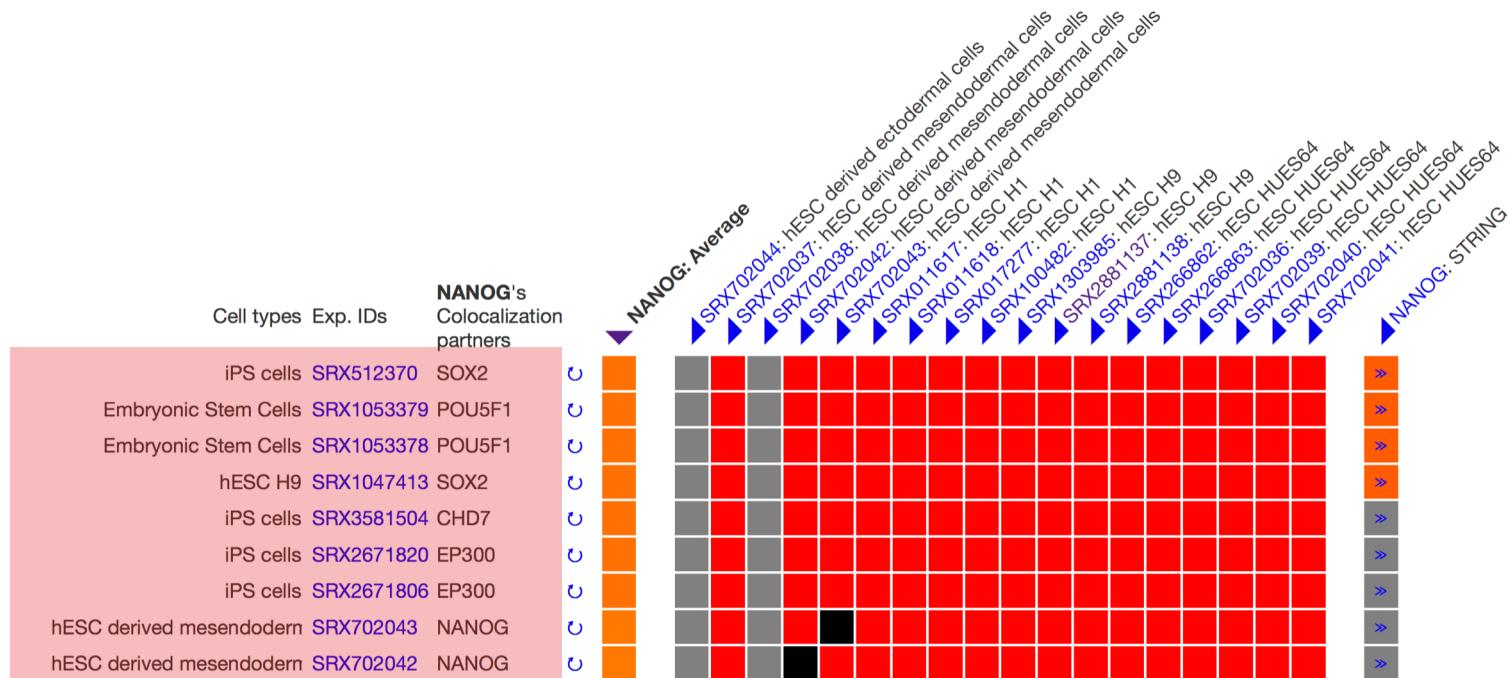
Color legends

ChIP-seq data: H-H H-M M-M H-L M-L L-L N.D. Same (Peak intensities are High, Middle or Low)

STRING data: 1000 750 500 250 0 N.D. (Values = STRING's binding scores)

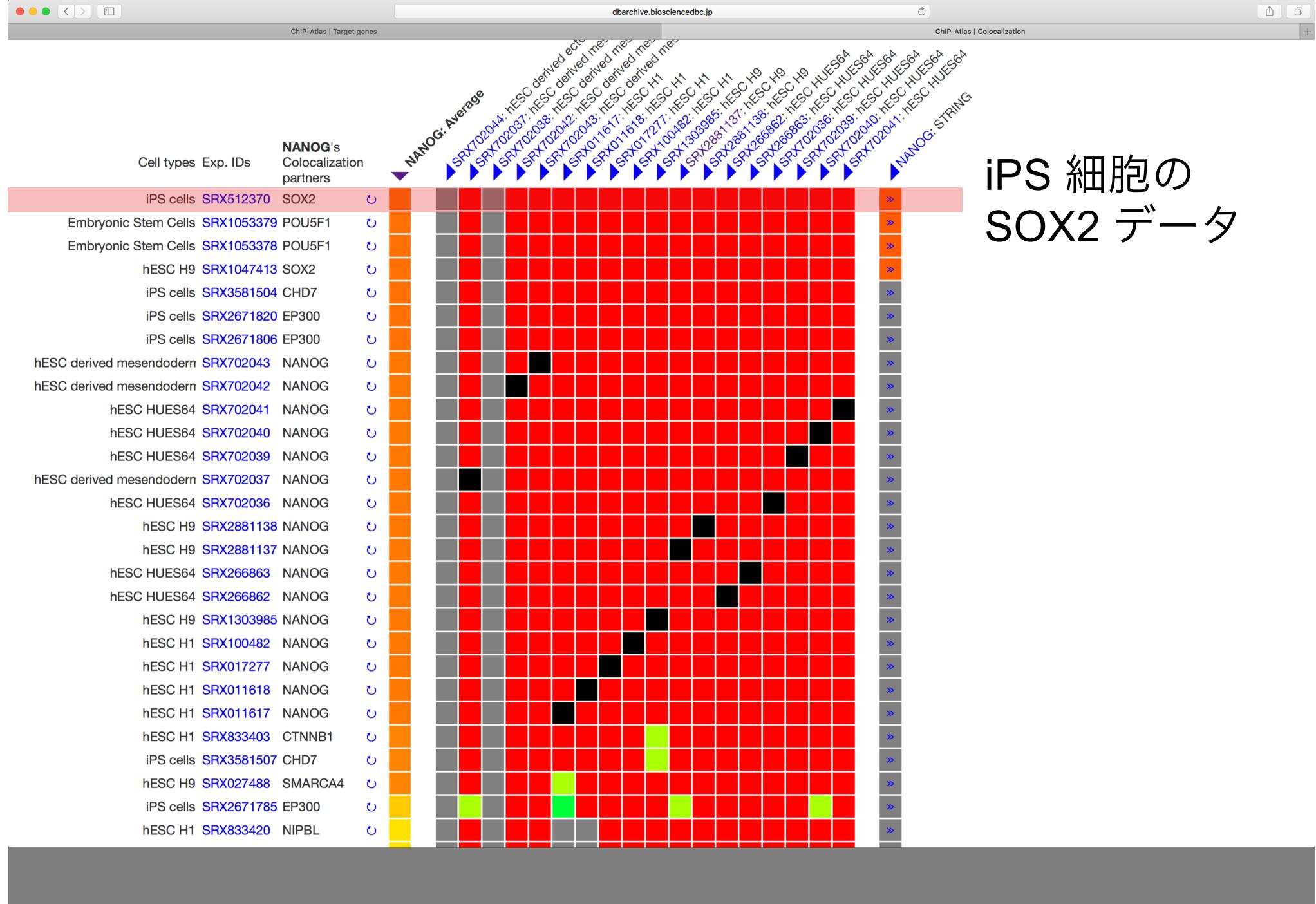
Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

Links: [Movie](#) and [Document](#) for ChIP-Atlas Colocalization

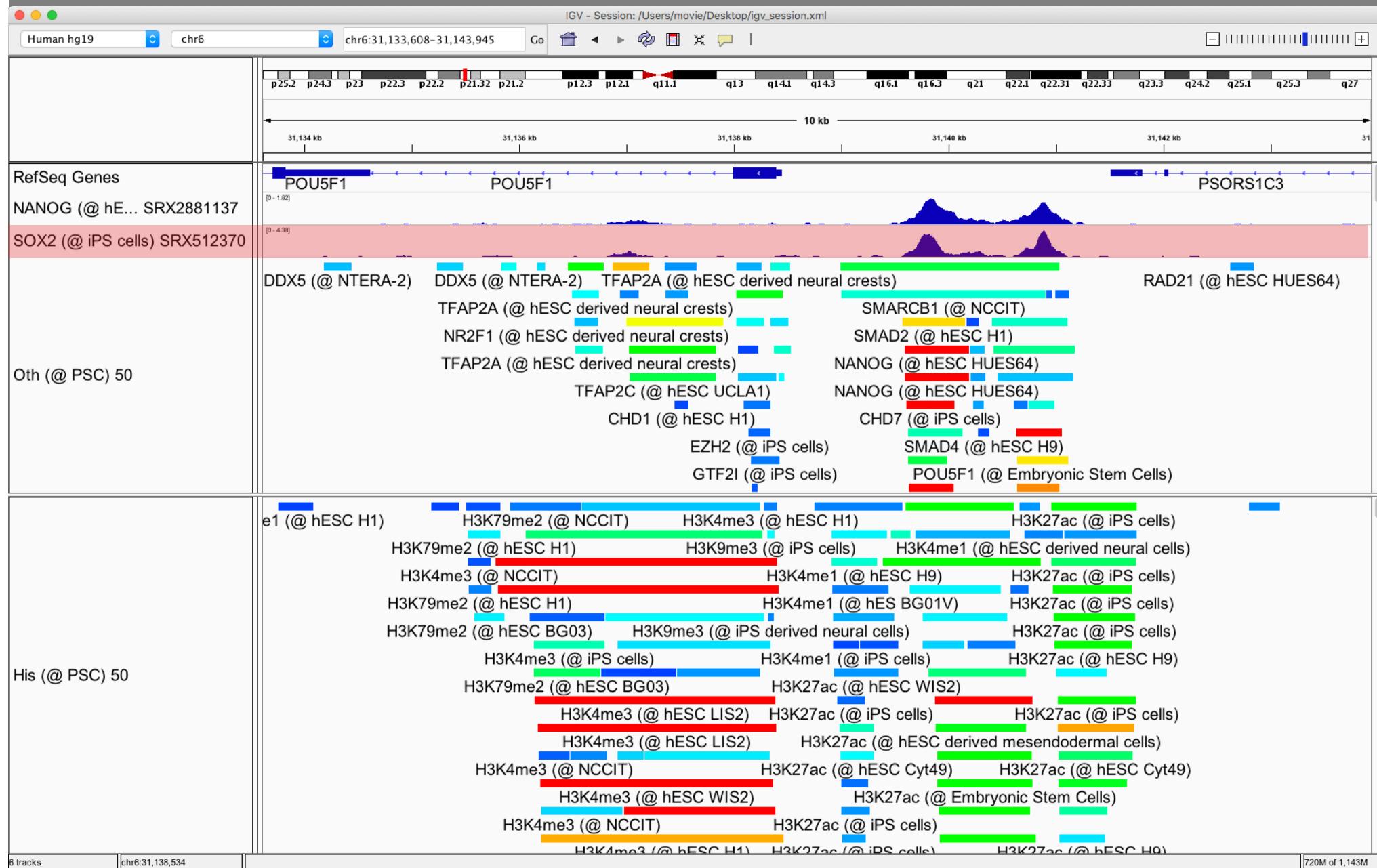


NANOG と同じゲノム領域に結合する ChIP-seq データ

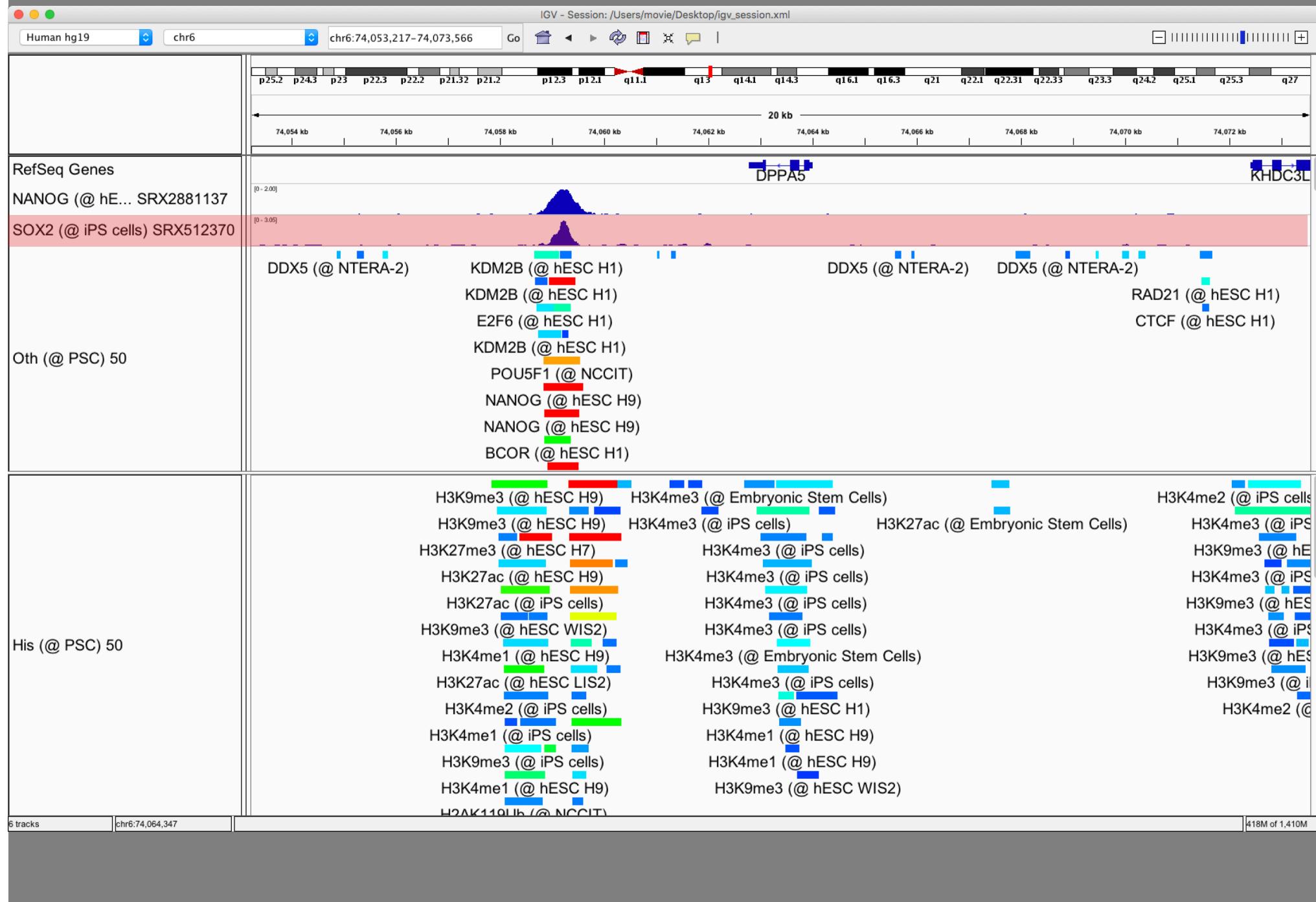
共局在因子を探す



共局在因子を探す



共局在因子を探す



エンリッチメント解析

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 URL "chip-atlas.org" in the center. Below the header is a navigation bar with links: "ChIP-Atlas", "Peak Browser", "Target Genes", "Colocalization", "Enrichment Analysis", "Documentation", "Publications", and "Find an experiment". 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

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

エンリッチメント解析

chip-atlas.org

ChIP-Atlas | Colocalization

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

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) ⓘ

Click info buttons above to show the description format.

Choose File no file selected
Choose local file Try with example

5. Select dataset to be compared

Random permutation of user data ⓘ
Permutation times x1 x10 x100
 BED or sequence motif ⓘ

6. Describe datasets

User data title ⓘ
My data

Compared data title ⓘ
Control

Project title ⓘ
My project

Estimated run time: 7 mins

submit

Dynamic and Coordinated Epigenetic Regulation of Developmental Transitions in the Cardiac Lineage

Joseph A. Wamstad,^{1,10} Jeffrey M. Alexander,^{2,3,10} Rebecca M. Truty,² Avanti Shrikumar,¹ Fugen Li,¹ Kirsten E. Eilertson,² Huiming Ding,¹ John N. Wylie,² Alexander R. Pico,² John A. Capra,² Genevieve Erwin,^{2,4} Steven J. Kattman,⁵ Gordon M. Keller,⁵ Deepak Srivastava,^{2,3,6,7} Stuart S. Levine,¹ Katherine S. Pollard,^{2,8} Alisha K. Holloway,² Laurie A. Boyer,^{1,*} and Benoit G. Bruneau^{2,3,7,9,*}

¹Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

²Gladstone Institute of Cardiovascular Disease, San Francisco, CA 94158, USA

³Program in Biomedical Sciences

⁴Integrative Program in Quantitative Biology

University of California, San Francisco, CA 94158, USA

⁵McEwen Center for Regenerative Medicine, University Health Network, Toronto M5G 1L7, Canada

⁶Department of Biochemistry and Biophysics

⁷Department of Pediatrics

⁸Department of Epidemiology & Biostatistics and Institute for Human Genetics

⁹Cardiovascular Research Institute

University of California, San Francisco, CA 94158, USA

¹⁰These authors contributed equally to this work

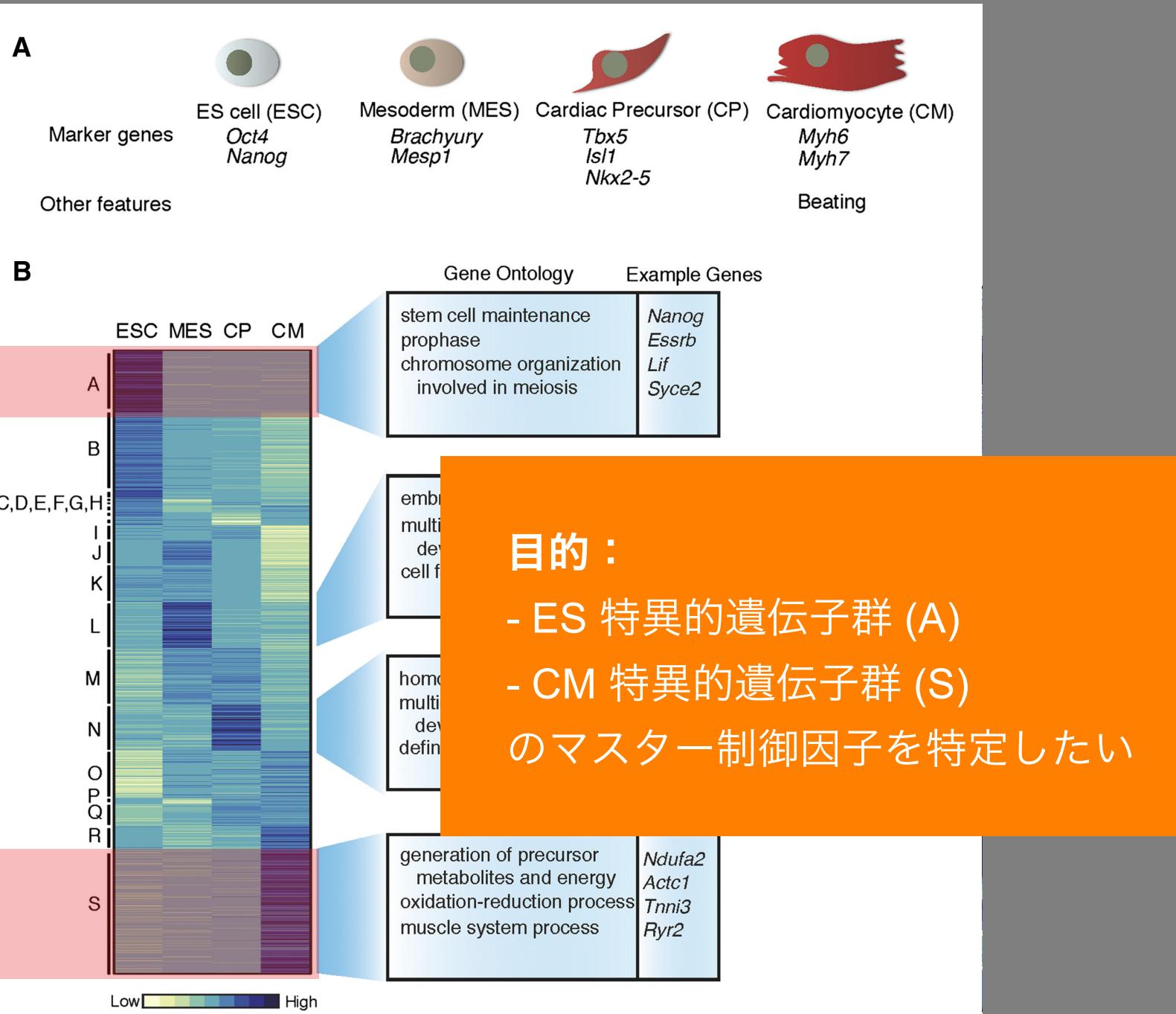
*Correspondence: lboyer@mit.edu (L.A.B.), bbruneau@gladstone.ucsf.edu (B.G.B.)

<http://dx.doi.org/10.1016/j.cell.2012.07.035>

エンリッチメント解析

ES で高発現する遺伝子

CM で高発現する遺伝子



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 ▾ 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 (31775)
- DNase-seq (700)
- Histone (10011)
- RNA polymerase (953)
- TFs and others (7879)**
- Input control (4345)
- Unclassified (5876)
- No description (2011)

2. Cell type Class

- All cell types (31775)**
- Adipocyte (424)
- Blood (7357)
- Bone (144)
- Breast (529)
- Cardiovascular (448)
- Digestive tract (473)
- Embryo (2821)

3. Threshold for Significance ①

- 50
- 100
- 200
- 500

4. Select your data

Genomic regions (BED) or sequence motif ①

Gene list (Gene symbols) ①

ES 特異的
遺伝子群

- Myh13
- Gm12569
- Ceacam20
- Rhox1
- Ighv3-3
- Gm13893
- CN725425
- Gm10323

Choose File no file selected

Choose local file Try with example

5. Select dataset to be compared

Refseq coding genes (excluding user data) ①

Gene list (Gene symbols) ①

CM 特異的
遺伝子群

- Rpl9-ps4
- 3425401B19Rik
- Fat3
- Mir208b
- Gm11096
- Tsnax
- Cdkn2d
- Rshp3a

Choose File no file selected

Choose local file Try with example

6. Describe datasets

User data title ①

ES

Compared data title ①

CM

Project title ①

My project

Distance range from TSS ①

- 5000 bp ≤ TSS ≤ + 5000 bp

submit

両者を比較し、どちらかに結合が enrich する ChIP-seq データを探査できる。

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 bar, the main content area has a title "ChIP-Atlas - Enrichment Analysis" and a subtitle "Analyze your data with public ChIP-seq data.". A message states "Result page URL will be available for a week from the time when 'status' is 'finished'." To the right of this message is a large orange speech bubble containing the Japanese word "クリック" (Click). Below the message is 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



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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 entries

Search:

My project

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / ES	Overlaps / CM	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX4017943	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	13721	240/1051	129/2326	-45.5	-41.6	4.12	TRUE
SRX213808	TFs and others	Nanog	Pluripotent stem cell	Embryonic Stem Cells	12869	254/1051	159/2326	-41.7	-38.2	3.54	TRUE
SRX3206545	TFs and others	Brd4	Muscle	Muscle, Skeletal	9561	412/1051	1486/2326	-40.2	-36.8	0.61	FALSE
SRX214083	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	7238	206/1051	109/2326	-39.0	-35.7	4.18	TRUE
SRX3342572	TFs and others	Nelfa	Embryonic fibroblast	MEF	17468	555/1051	1761/2326	-38.4	-35.3	0.70	FALSE
SRX194542	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	7535	189/1051	92/2326	-38.2	-35.1	4.55	TRUE
SRX2548308	TFs and others	Esr1	Uterus	Uterus	22995	469/1051	1589/2326	-37.9	-34.9	0.65	FALSE
SRX1585633	TFs and others	Foxf1	Lung	Lung	53555	457/1051	1556/2326	-36.8	-33.8	0.65	FALSE
SRX194541	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	5817	144/1051	51/2326	-35.9	-33.0	6.25	TRUE
SRX202800	TFs and others	Tbp	Embryonic fibroblast	C3H/10T1/2	16360	500/1051	1630/2326	-34.9	-32.0	0.68	FALSE
SRX2324494	TFs and others	Zfp384	Gonad	Spermatogonia	15595	635/1051	1877/2326	-33.8	-30.9	0.75	FALSE
SRX1585634	TFs and others	Foxf1	Lung	Lung	33831	413/1051	1439/2326	-33.6	-30.8	0.64	FALSE
	TFs and others		Pluripotent stem cell								

Showing 1 to 100 of 7,383 entries

Previous ... 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:

My project

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / ES	Overlaps / CM	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX4017943	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	13721	240/1051	129/2326	-45.5	-41.6	4.12	TRUE

ES 細胞における Pou5f1 ChIP-seq データ

- マウスゲノムの 13,721 箇所に結合。
 - ・ ES 遺伝子 (1,051 個) のうち、240 個に結合
 - ・ CM 遺伝子 (2,326 個) のうち、129 個に結合
- 両者の比 = $(240/1051) / (129/2326) = 4.12$
- Fold enrichment は 1 以上なので “TRUE”
(1 以下は “FALSE”)
- Fisher の正確確率検定: $P = 1E-45.5$

エンリッチメント解析

ddbj.nig.ac.jp

true

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries

Search: true

My project

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / ES	Overlaps / CM	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX4017943	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	13721	240/1051	129/2326	-45.5	-41.6	4.12	TRUE
SRX213808	TFs and others	Nanog	Pluripotent stem cell	Embryonic Stem Cells	12869	254/1051	159/2326	-41.7	-38.2	3.54	TRUE
SRX214083	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	7238	206/1051	109/2326	-39.0	-35.7	4.18	TRUE
SRX194542	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	7535	189/1051	92/2326	-38.2	-35.1	4.55	TRUE
SRX194541	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	5817	144/1051	51/2326	-35.9	-33.0	6.25	TRUE
SRX2437564	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	11070	254/1051	192/2326	-33.4	-30.6	2.93	TRUE
SRX499113	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	8672	179/1051	99/2326	-32.2	-29.5	4.00	TRUE
SRX499125	TFs and others	Ep300	Pluripotent stem cell	EpiLC	10224	193/1051	116/2326	-32.2	-29.5	3.68	TRUE
SRX236476	TFs and others	Pou5f1	Pluripotent stem cell	Embryonic Stem Cells	13644	247/1051	189/2326	-31.8	-29.2	2.89	TRUE
SRX499127	TFs and others	Pou5f1	Pluripotent stem cell	EpiLC	16182	251/1051	195/2326	-31.8	-29.1	2.85	TRUE
SRX194533	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	4724	121/1051	39/2326	-31.7	-29.1	6.87	TRUE
SRX027354	TFs and others	Ep300	Pluripotent stem cell	Embryonic Stem Cells	8069	205/1051	134/2326	-31.4	-28.8	3.39	TRUE
	TFs and others	Pluripotent stem cell									

Showing 1 to 100 of 3,061 entries (filtered from 7,383 total entries)

Previous 1 2 3 4 5 ... 31 Next

ES 特異的遺伝子群には Pou5f1, Nanog, Ep300 が結合

エンリッチメント解析

ddbj.nig.ac.jp

false

ChIP-Atlas / Enrichment Analysis

Search for proteins significantly bound to your data.

Show 100 entries

Search: false

My project

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / ES	Overlaps / CM	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX3206545	TFs and others	Brd4	Muscle	Muscle, Skeletal	9561	412/1051	1486/2326	-40.2	-36.8	0.61	FALSE
SRX3342572	TFs and others	Nelfa	Embryonic fibroblast	MEF	17468	555/1051	1761/2326	-38.4	-35.3	0.70	FALSE
SRX2548308	TFs and others	Esr1	Uterus	Uterus	22995	469/1051	1589/2326	-37.9	-34.9	0.65	FALSE
SRX1585633	TFs and others	Foxf1	Lung	Lung	53555	457/1051	1556/2326	-36.8	-33.8	0.65	FALSE
SRX202800	TFs and others	Tbp	Embryonic fibroblast	C3H/10T1/2	16360	500/1051	1630/2326	-34.9	-32.0	0.68	FALSE
SRX2324494	TFs and others	Zfp384	Gonad	Spermatogonia	15595	635/1051	1877/2326	-33.8	-30.9	0.75	FALSE
SRX1585634	TFs and others	Foxf1	Lung	Lung	33831	413/1051	1439/2326	-33.6	-30.8	0.64	FALSE
SRX2918122	TFs and others	Esr1	Uterus	Uterus	33816	451/1051	1509/2326	-32.2	-29.5	0.66	FALSE
SRX1568882	TFs and others	Sap130	Embryo	Embryonic heart	12549	567/1051	1728/2326	-30.3	-27.9	0.73	FALSE
SRX517512	TFs and others	Gtf2b	Cardiovascular	Heart	7653	341/1051	1248/2326	-29.8	-27.4	0.60	FALSE
SRX551542	TFs and others	Rbfox2	Cardiovascular	Heart	12753	487/1051	1557/2326	-28.9	-26.5	0.69	FALSE
SRX202801	TFs and others	Tbp	Embryonic fibroblast	C3H/10T1/2	10975	363/1051	1287/2326	-28.6	-26.2	0.62	FALSE
TFs and others											

Showing 1 to 100 of 4,322 entries (filtered from 7,383 total entries)

Previous 1 2 3 4 5 ... 44 Next

CM 特異的遺伝子群には Brd4 や Nelfa が結合

エンリッチメント解析

The screenshot shows the ChIP-Atlas Enrichment Analysis page. At the top, there's a navigation bar with links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis (which is the active tab), Documentation, Publications, and a search bar for 'Find an experiment'. Below the navigation is a section titled 'ChIP-Atlas - Enrichment Analysis' with the sub-instruction 'Analyze your data with public ChIP-seq data.' A 'Tutorial movie' button is also present. The main content area has tabs for different organisms: H. sapiens (selected), M. musculus, R. norvegicus, D. melanogaster, C. elegans, and S. cerevisiae. The interface is divided into six numbered sections: 1. Antigen Class, 2. Cell type Class, 3. Threshold for Significance, 4. Select your data, 5. Select dataset to be compared, and 6. Describe datasets. An orange speech bubble with the Japanese character 'クリック' (Click) points to the 'Genomic regions (BED) or sequence motif' radio button in section 4. The 'Genomic regions (BED) or sequence motif' radio button is selected (indicated by a blue outline). The 'Gene list (Gene symbols)' radio button is unselected (indicated by a grey outline). In section 4, there is a table of genomic coordinates:

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

Below the table are buttons for 'Choose File' (no file selected), 'Choose local file', and 'Try with example'. In section 5, the 'BED or sequence motif' radio button is selected. In section 6, the 'User data title' field contains 'My data', the 'Compared data title' field contains 'Control', and the 'Project title' field contains 'My project'. A large blue 'submit' button is at the bottom of section 6. An estimated run time of '5 mins' is shown below the submit button.

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 (34390)

DNA

クリック

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

ゲノム座標を入れることもできる。