

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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chip-atlas.org

ChIP-Atlas Peak Browser ChIP-seq Data Localization Enrichment Analysis Documentation Publications Find an experiment ▾ Tutorial movies ▾

ChIP-Atlas H. sapience

Visualize All Peaks from Public ChIP-seq 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

TFs and others

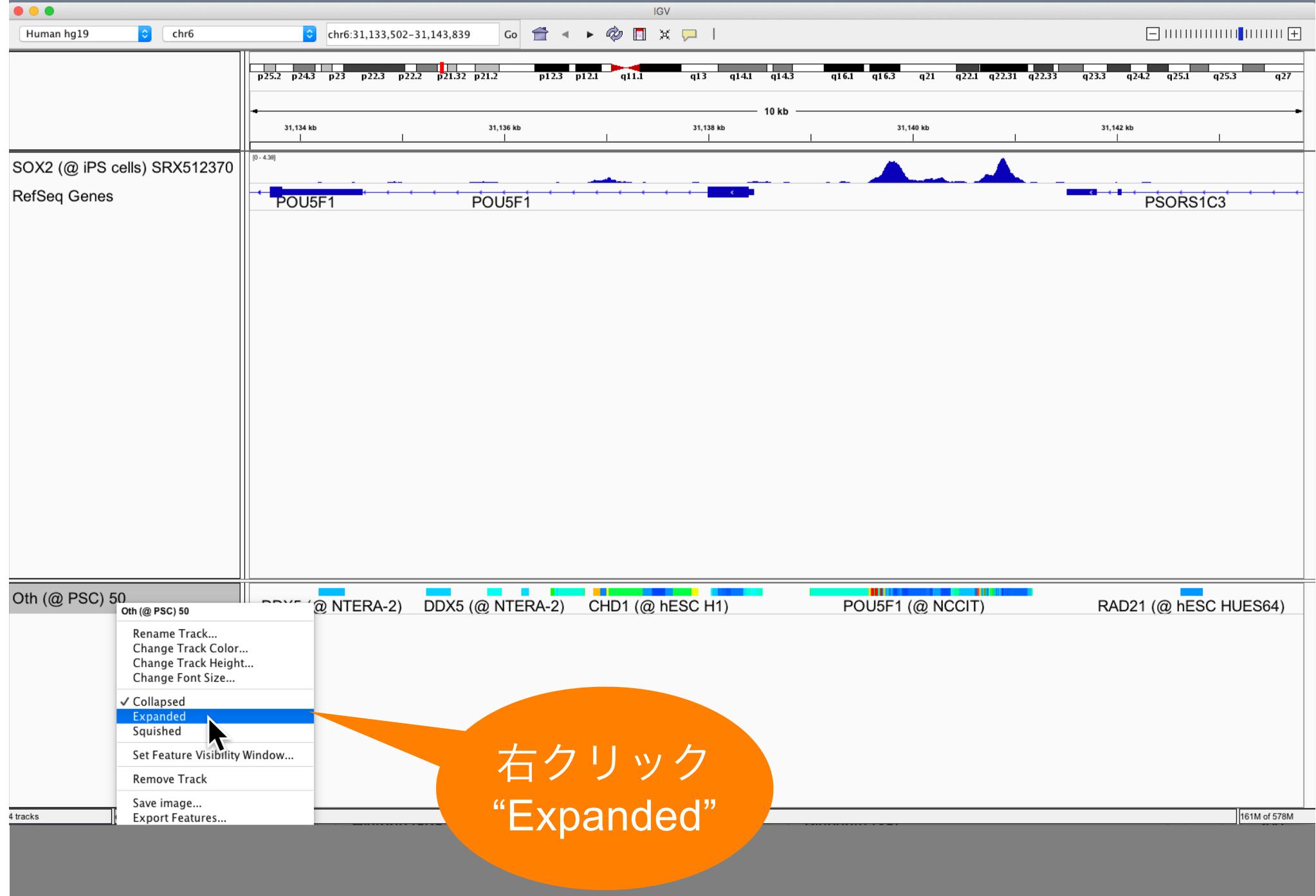
Pluripotent stem cell

KYUSHU UNIVERSITY IN COLLABORATION WITH DBCLS Database Center for Life Science

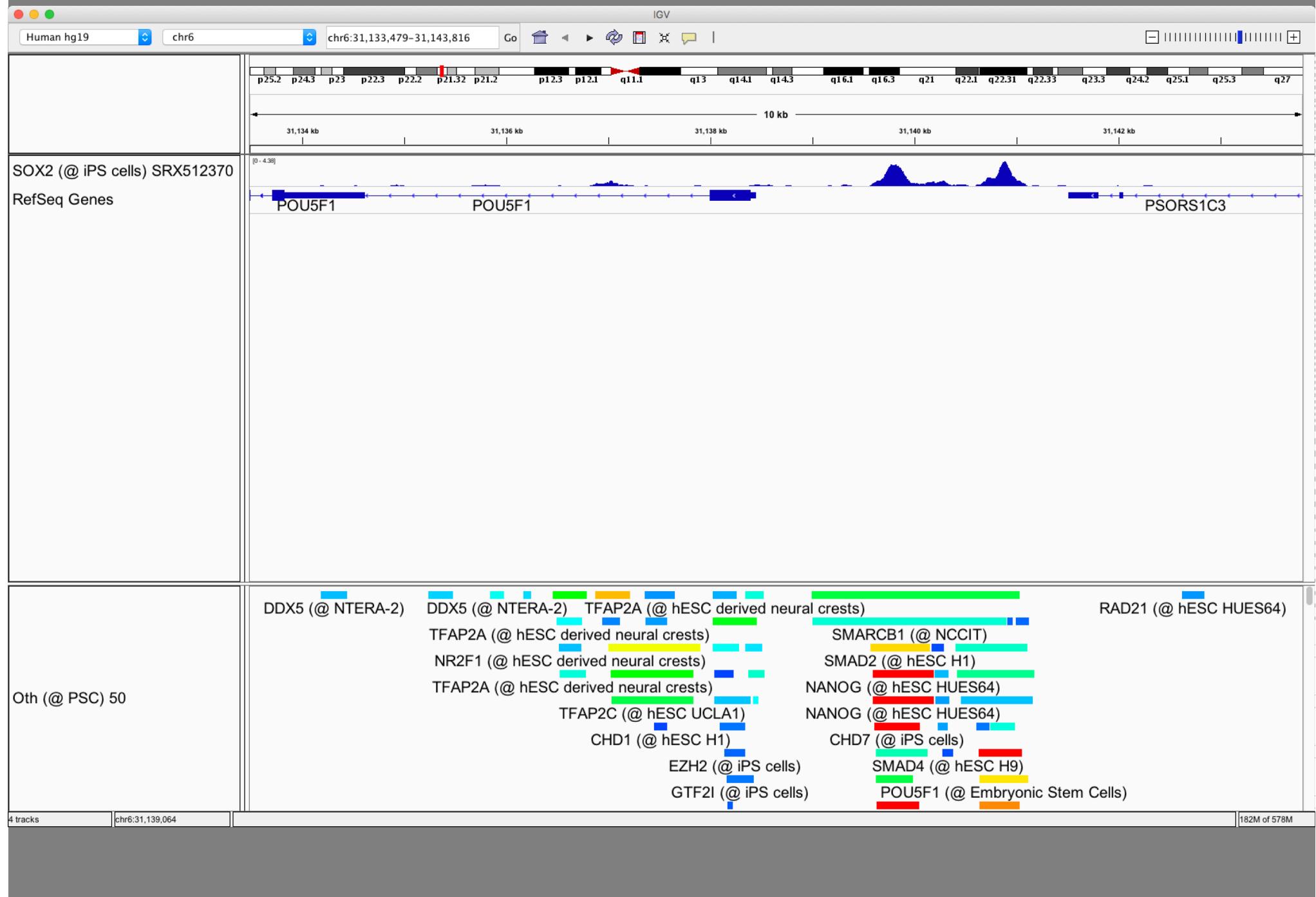
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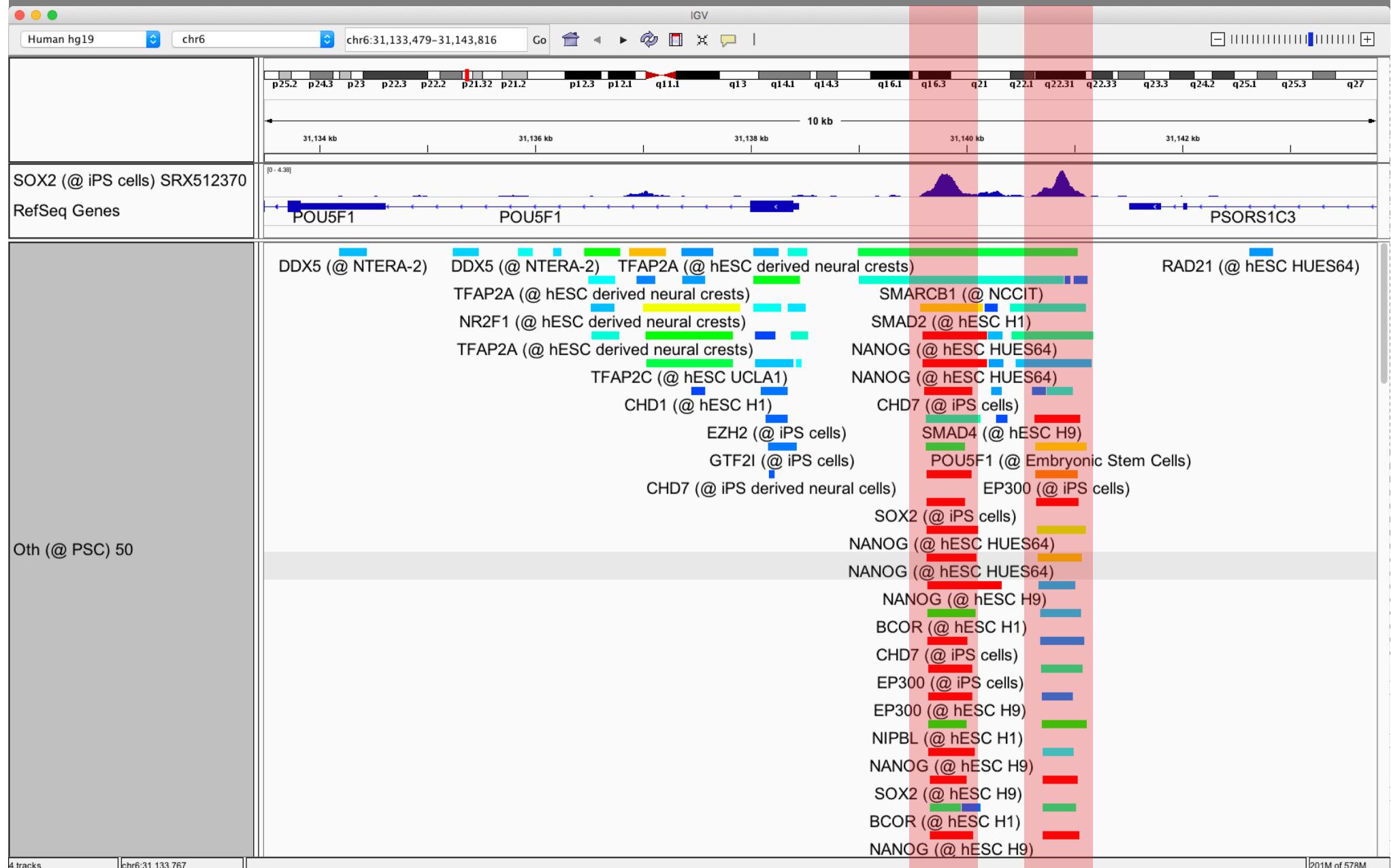
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複数データをまとめて見る

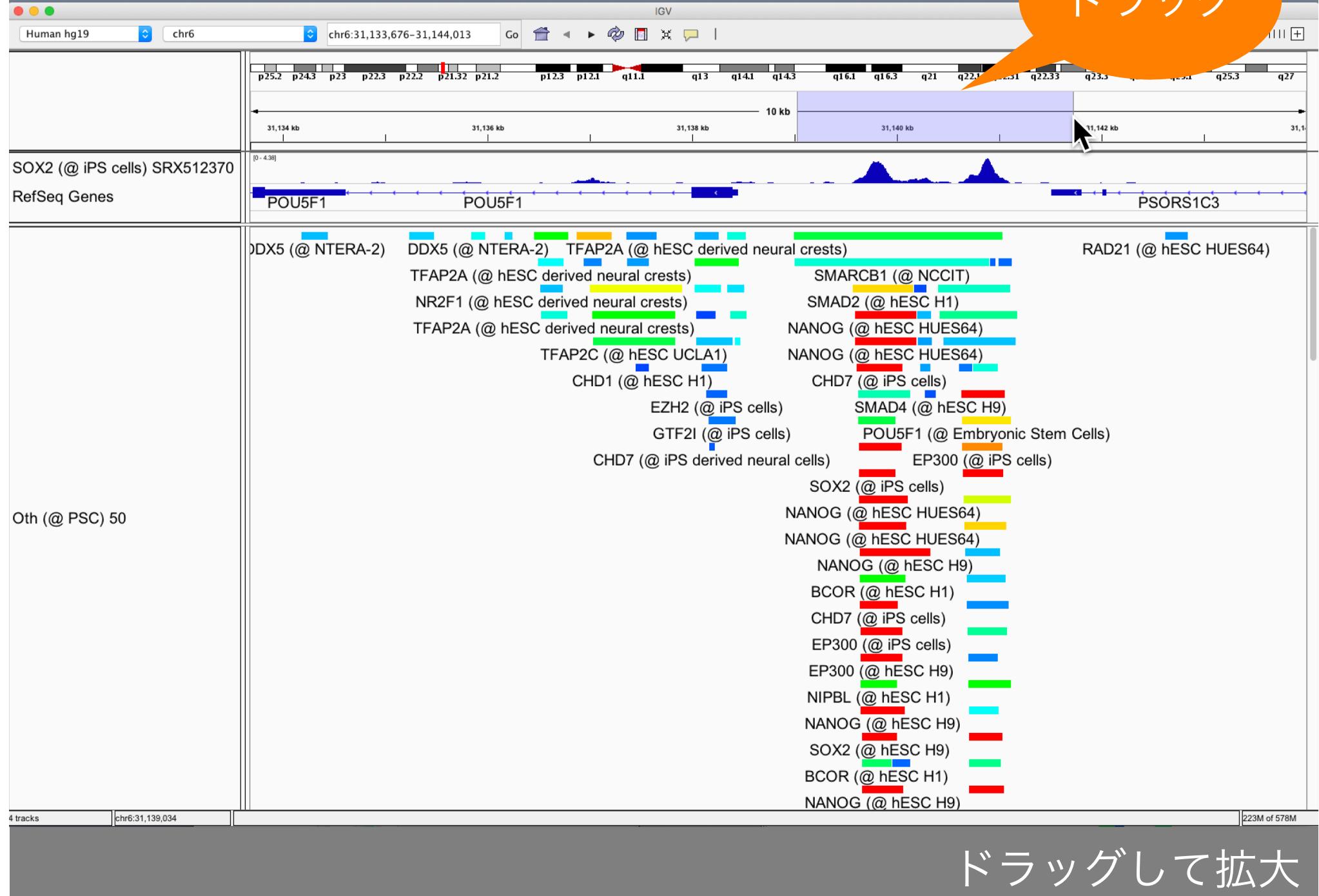


複数データをまとめて見る

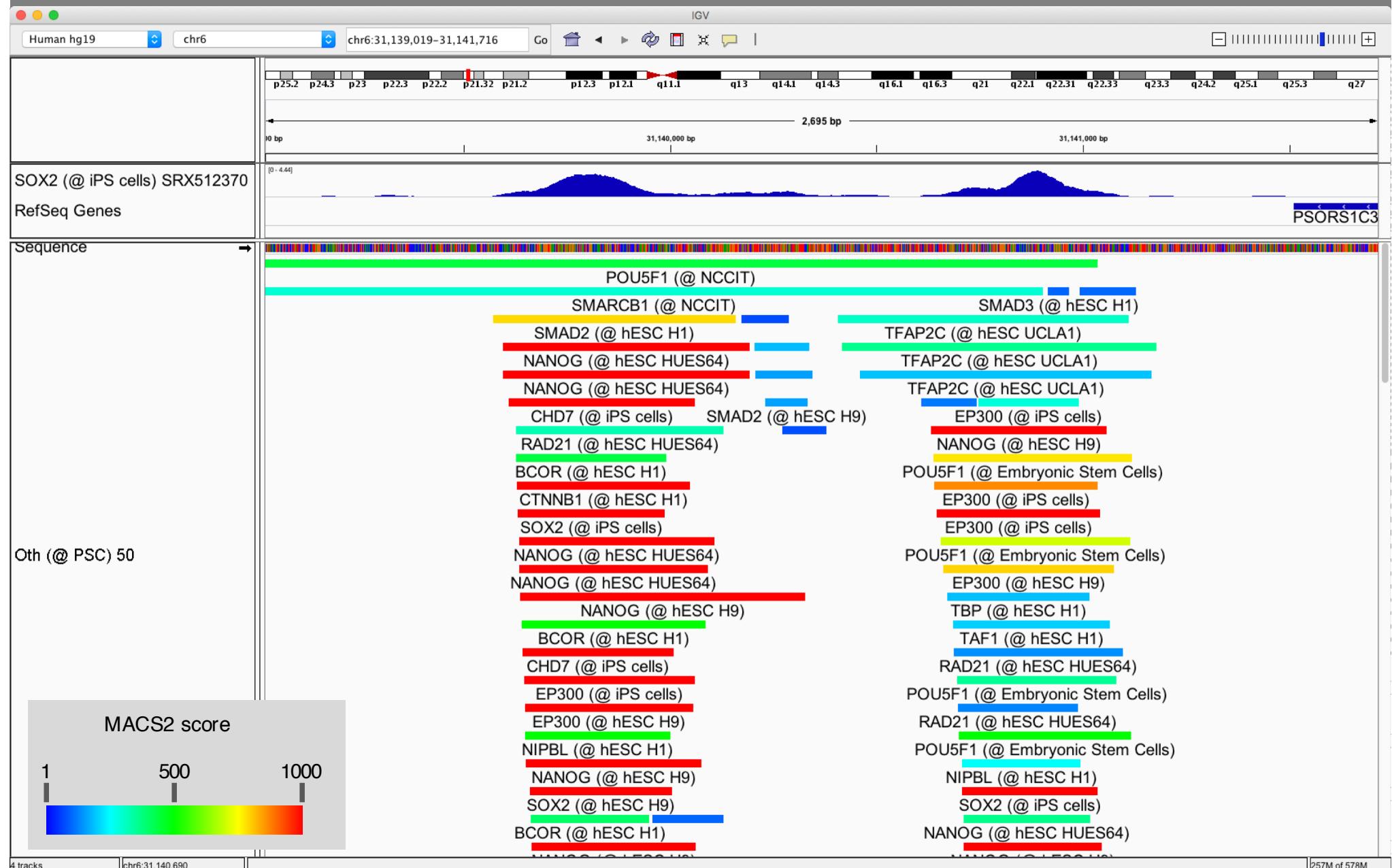


Stem cell 業界では、超有名なエンハンサー

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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)
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- Unclassified (438)

Threshold for Significance ⓘ

50 100 200 500

View on IGV

Download BED file

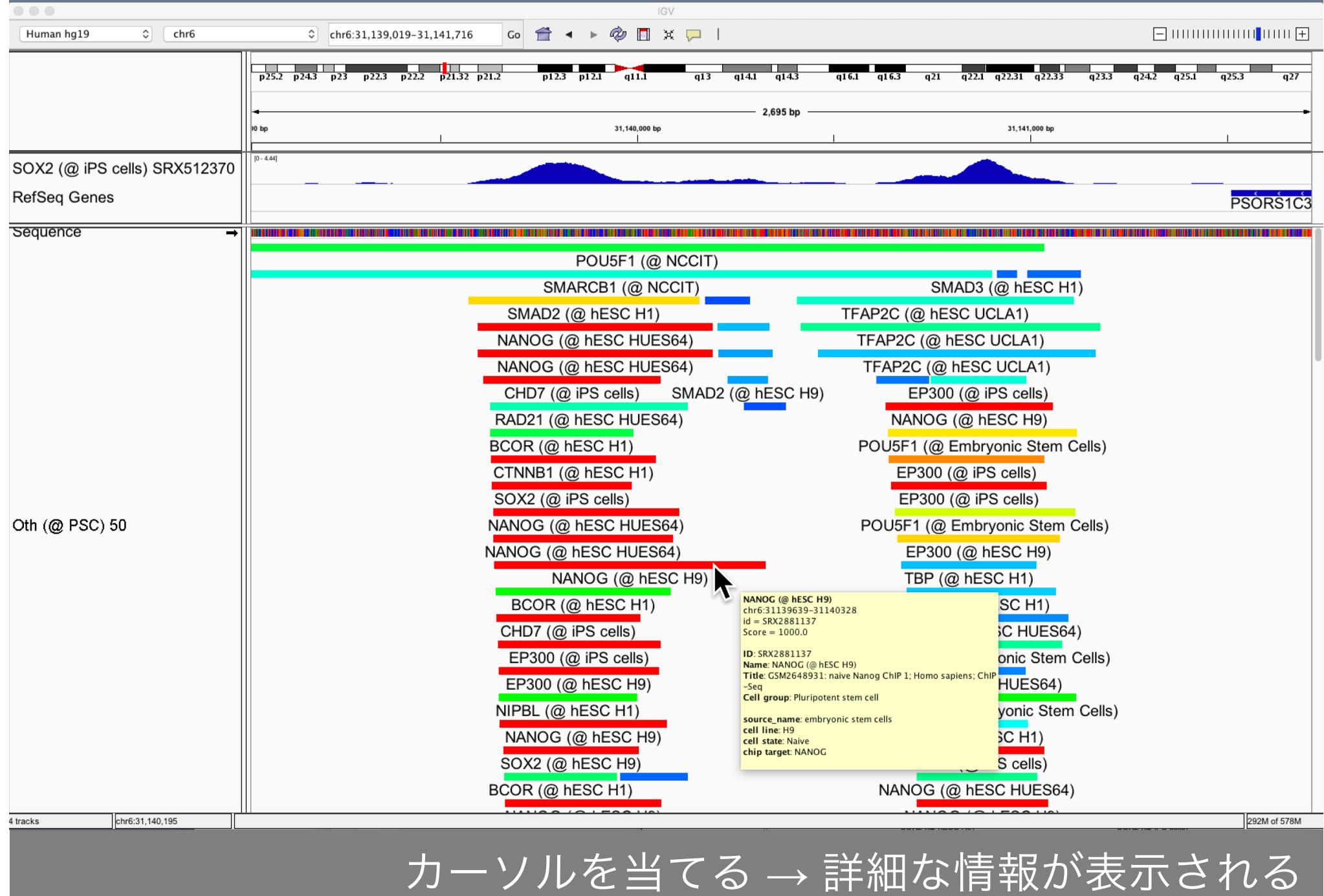


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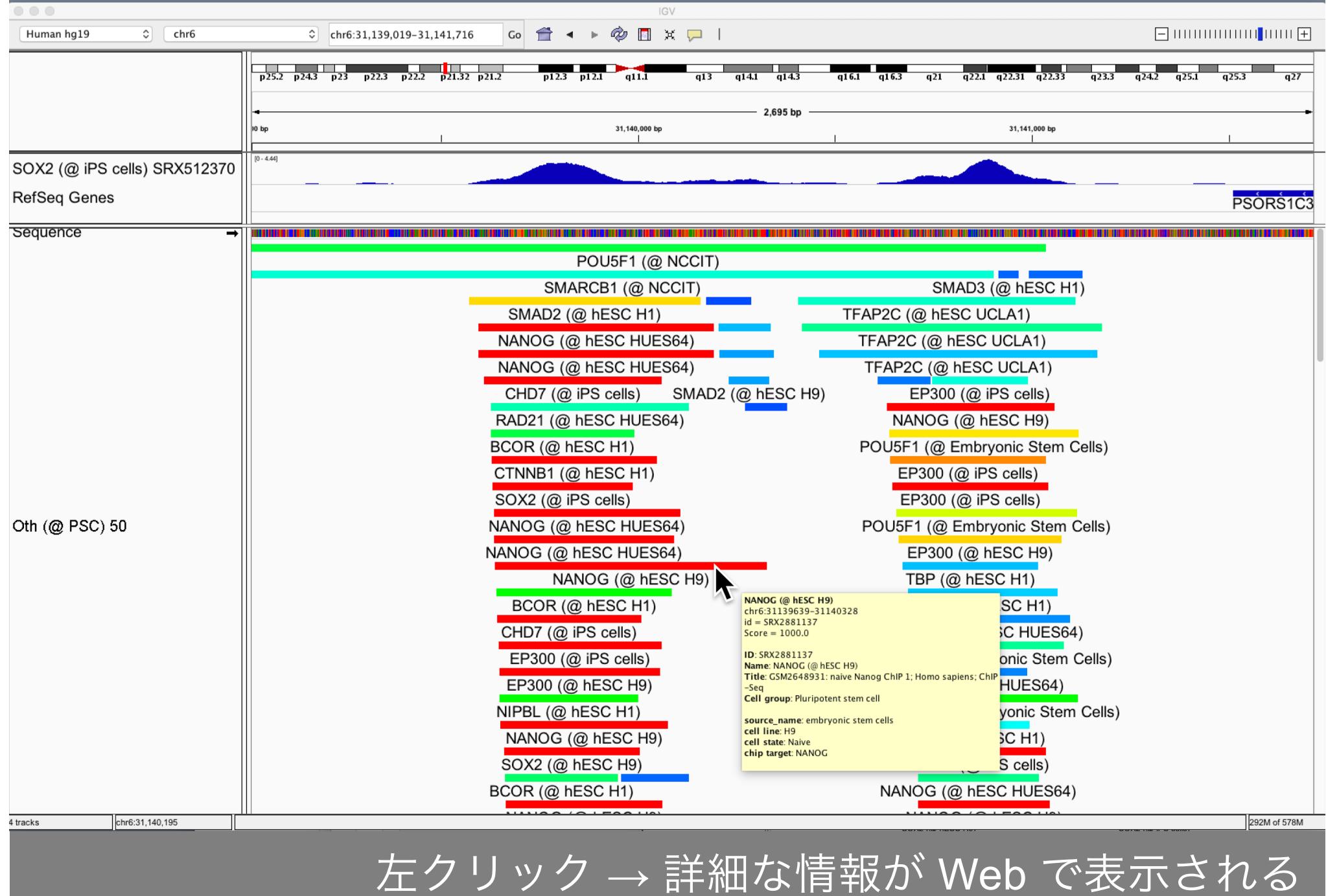
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MACS2 score = $-10 \times \log_{10}[\text{Q-val}]$ (100 以上だとほぼ信頼できる)

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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

クリック

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 pluripotent stem cells; 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', with values like 'hg19', 'TFs and others', 'NANOG', 'Pluripotent stem cell', and 'hESC H9' respectively.

SRX2881137

GSM2648931: naive

pluripotent stem cells; 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

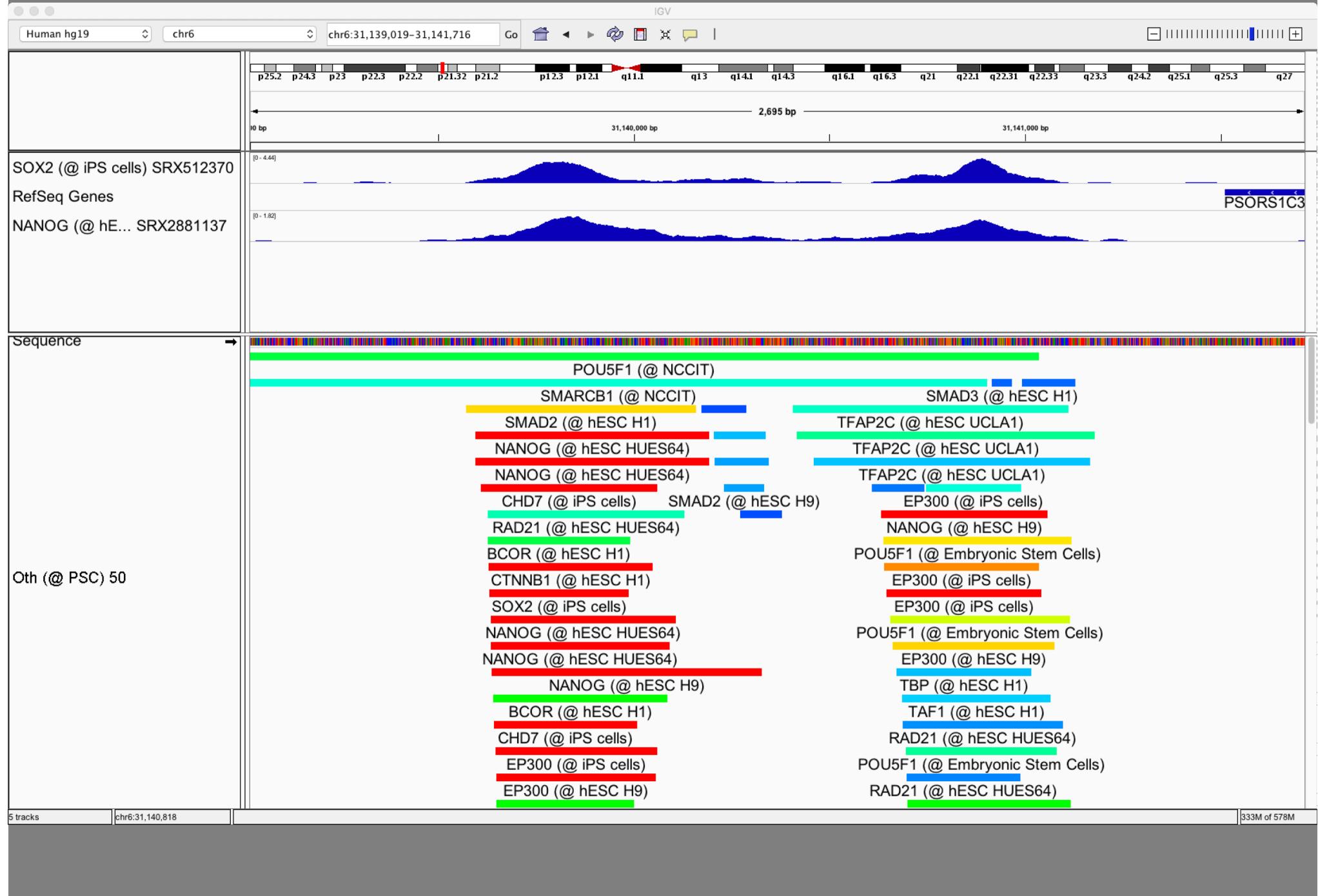
NA

NA

Attributes by Original Data Submitter

source_name	embryonic stem cells
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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 ⓘ

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クリック

View on IGV

Download BED file

Histone

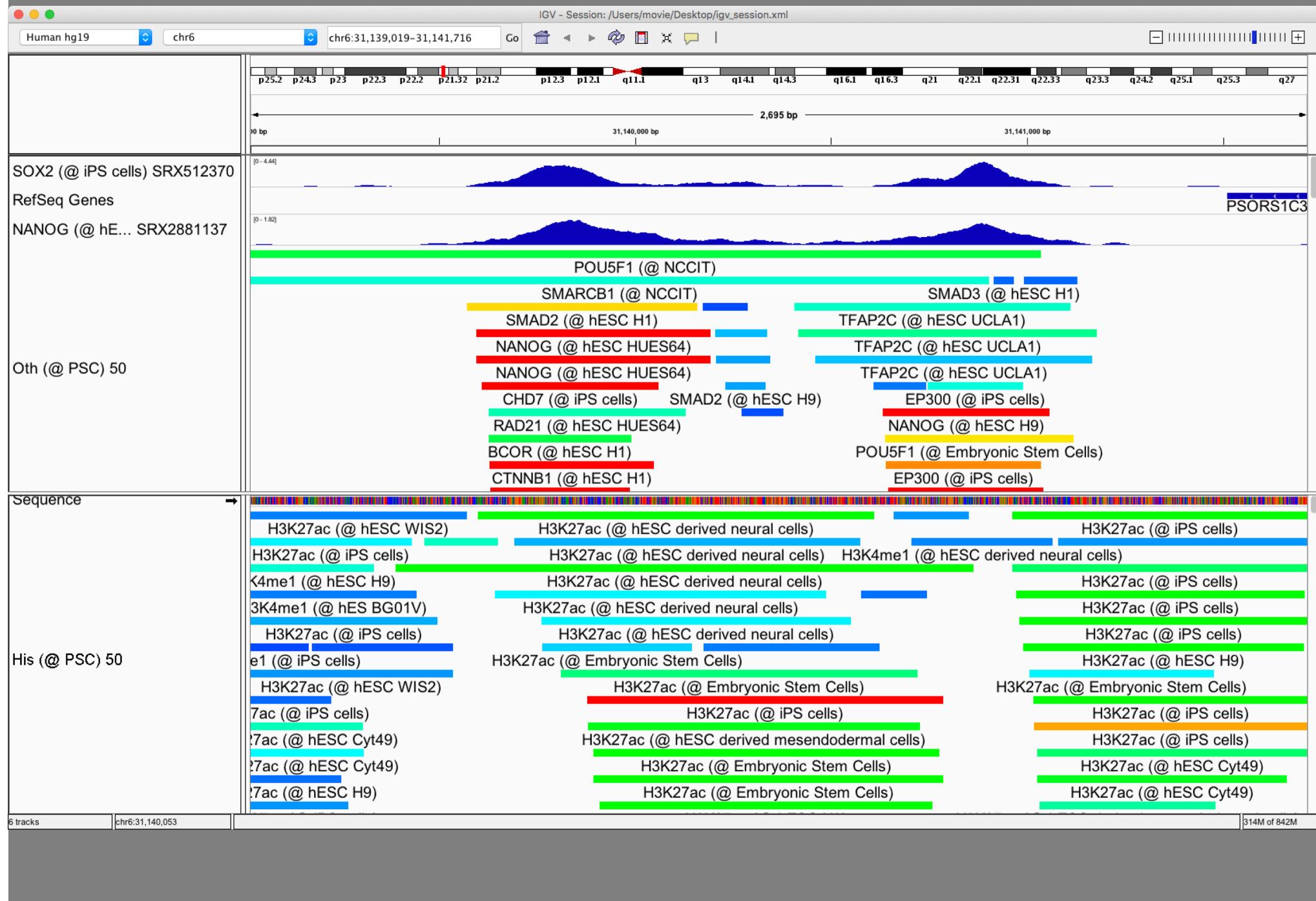
Pluripotent stem cell

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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.

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](#)

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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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dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

Query protein: NANOG

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

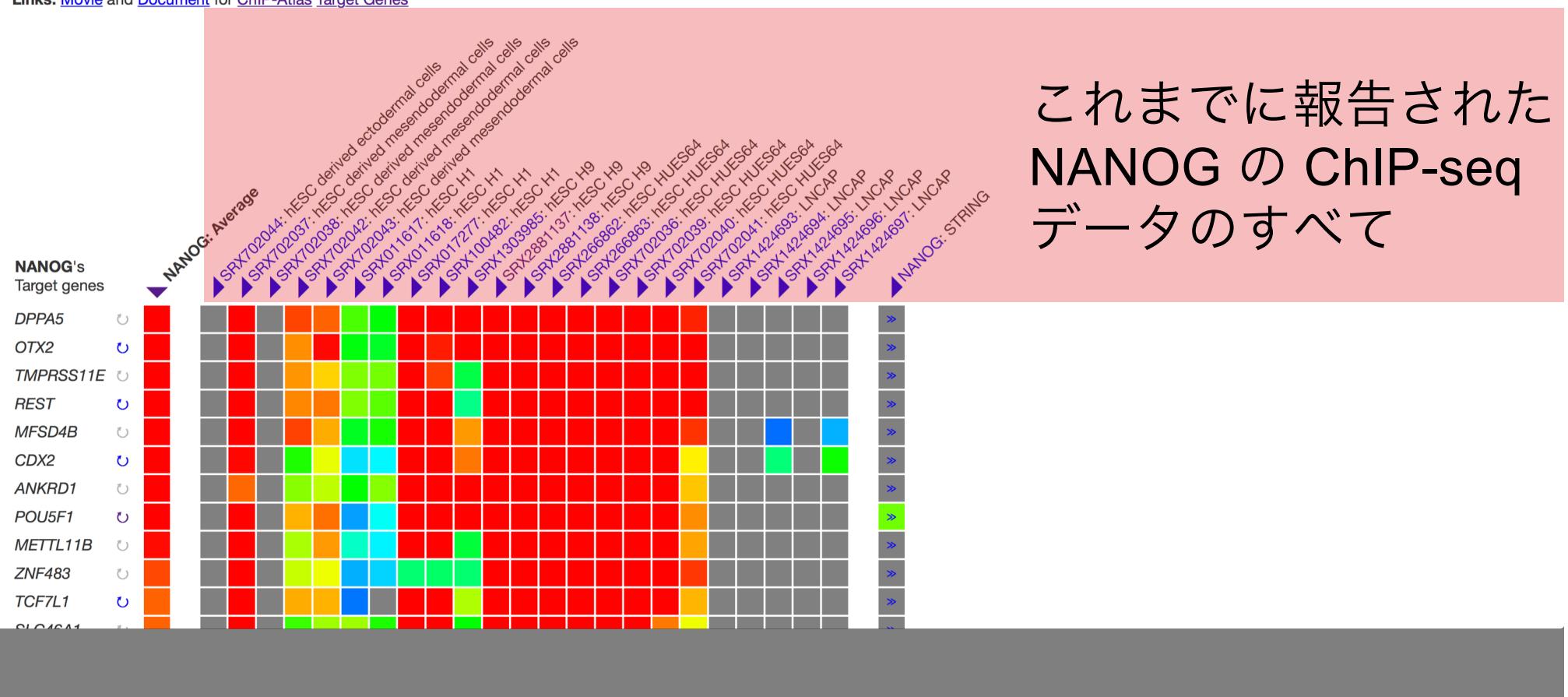
Sort key: NANOG | Average

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



標的遺伝子を探す

dbarchive.biosciencedbc.jp

ChIP-Atlas: Target genes

Potential target genes for NANOG

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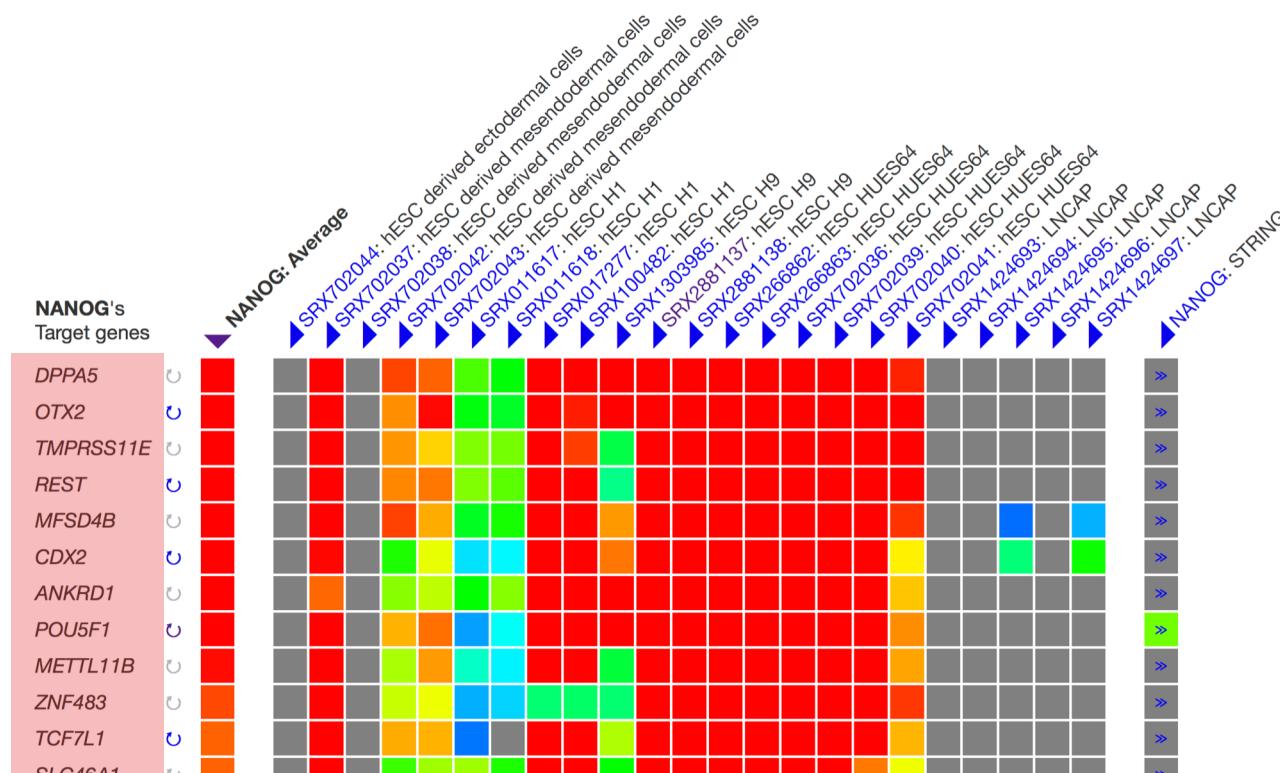
Sort key: NANOG | Average

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



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

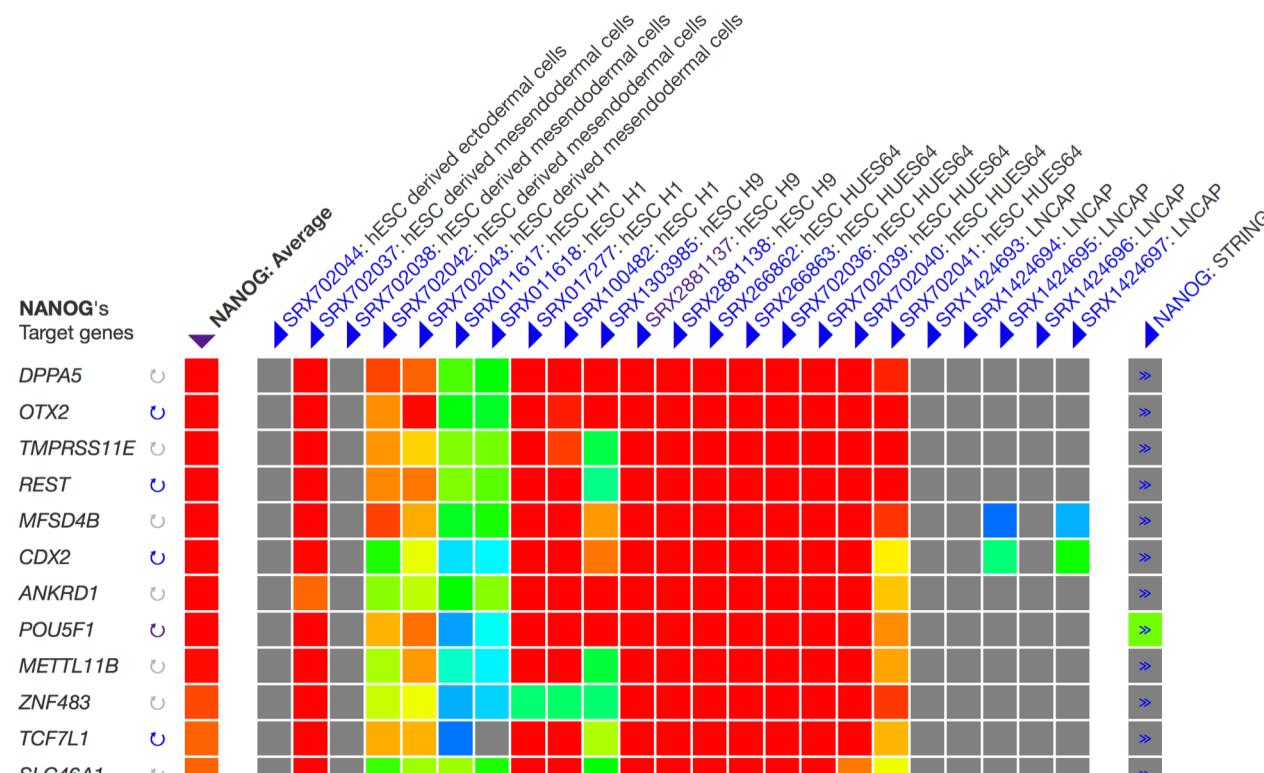
Color legends

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

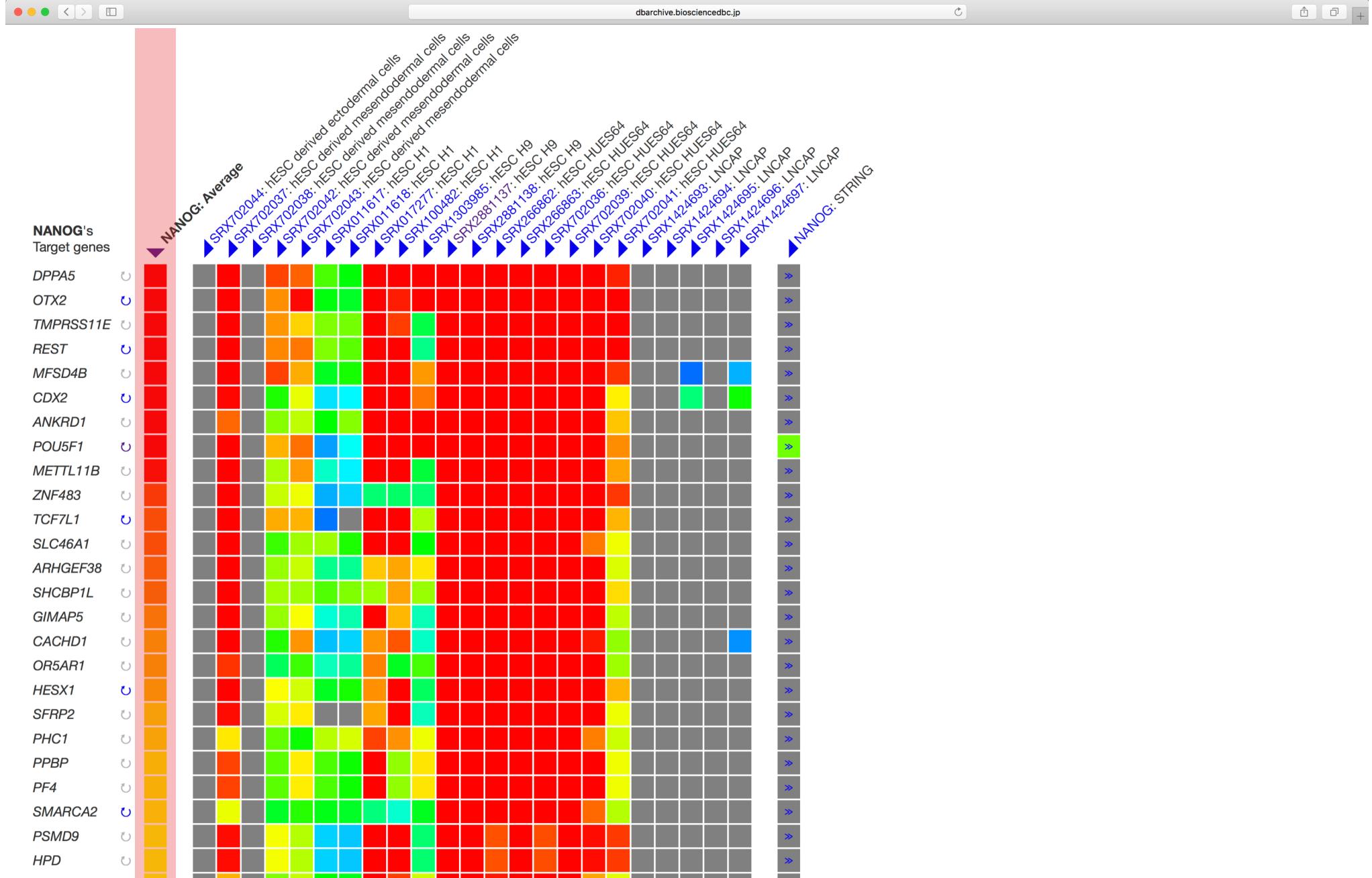
MACS2 score

Download: [TSV](#) (text)

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

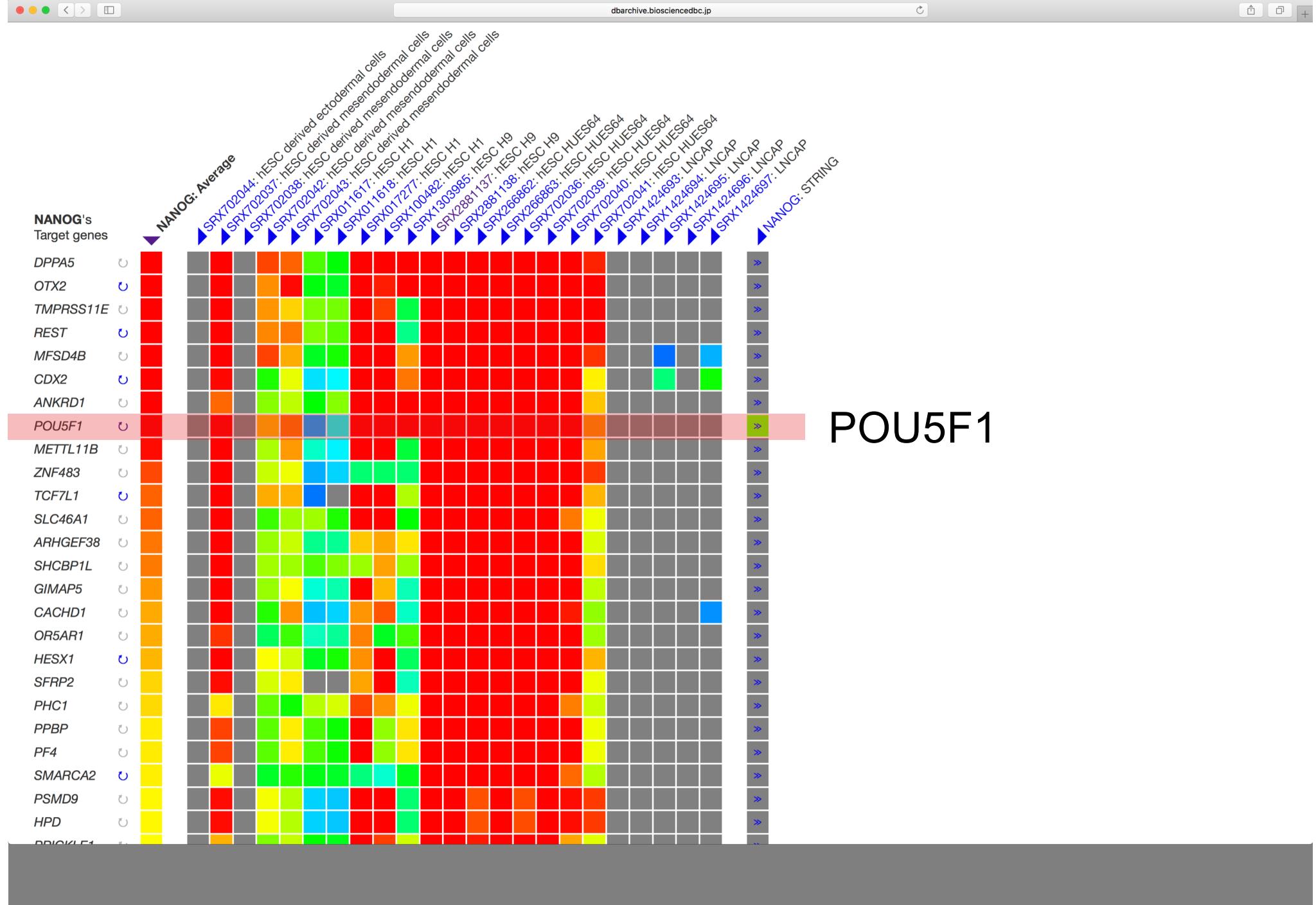


標的遺伝子を探す

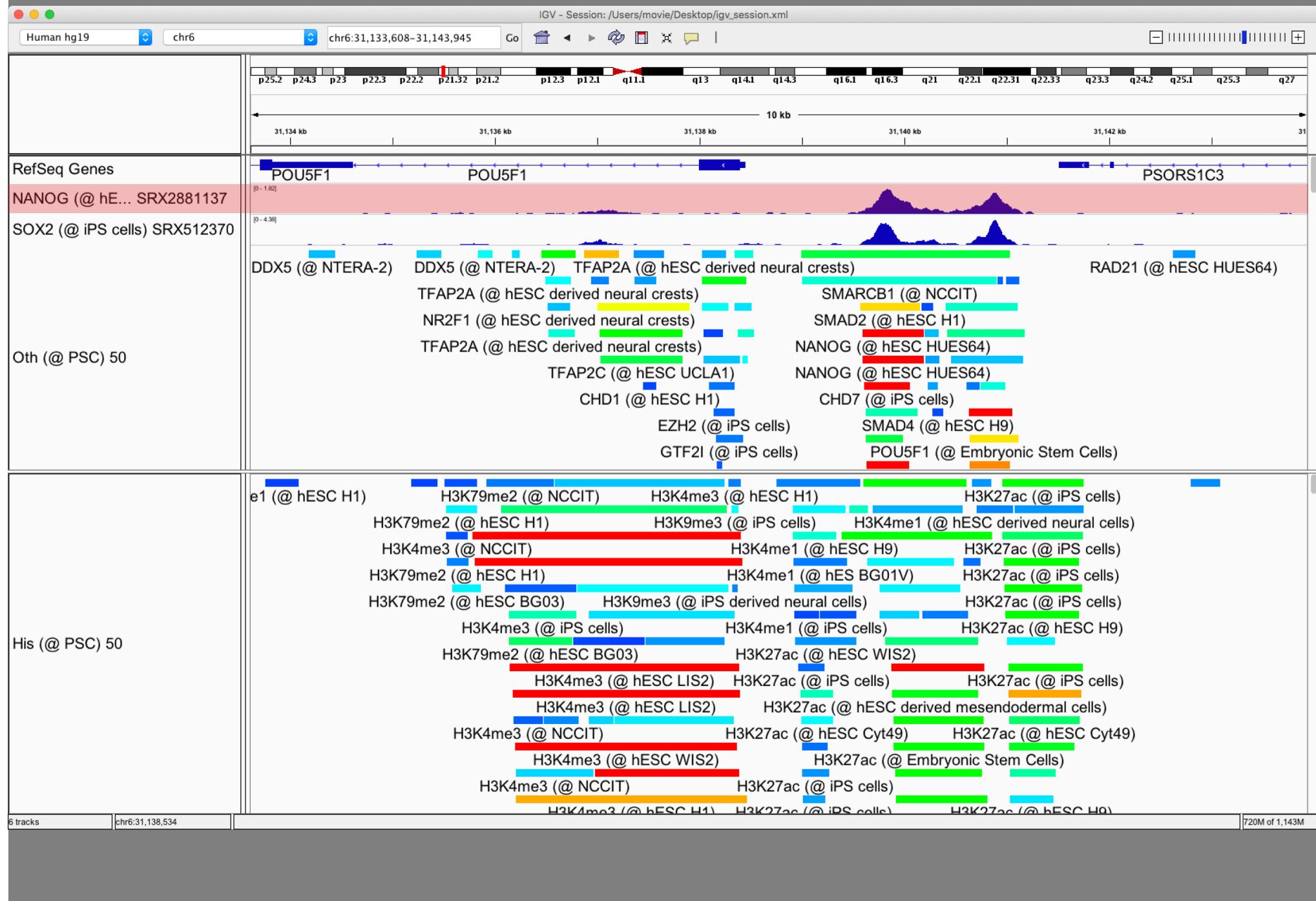


各行の平均値でソート

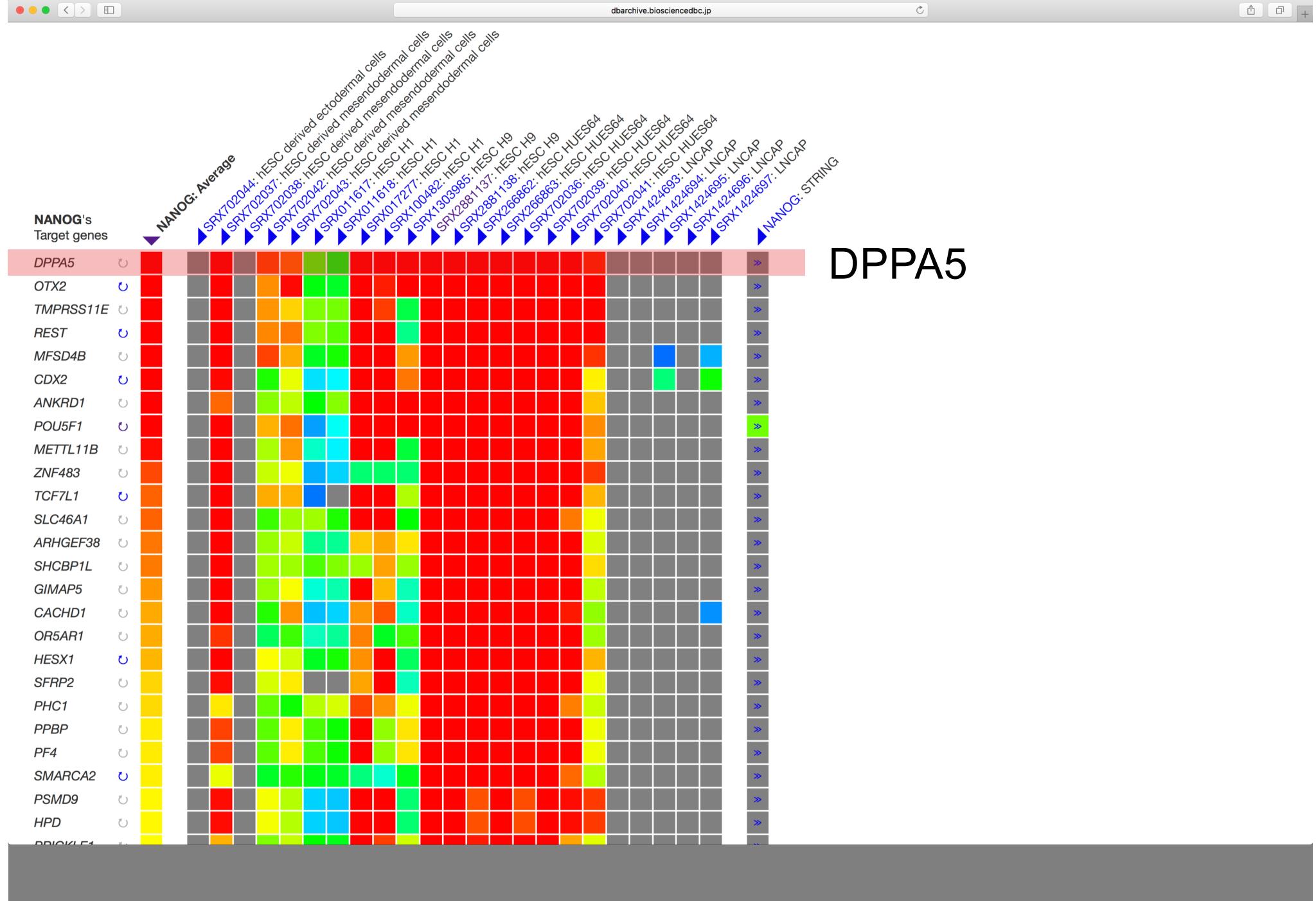
標的遺伝子を探す



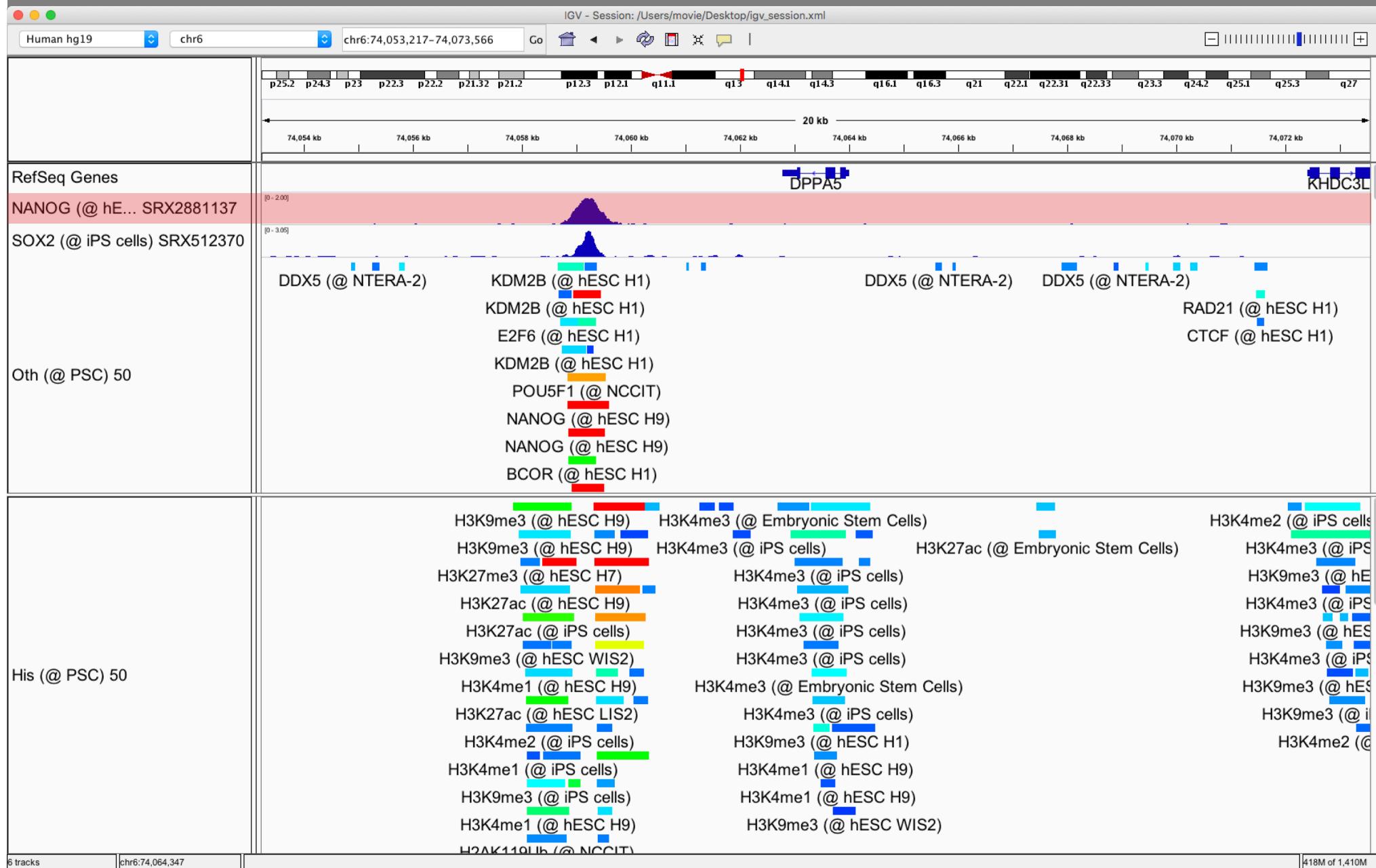
標的遺伝子を探す



標的遺伝子を探す

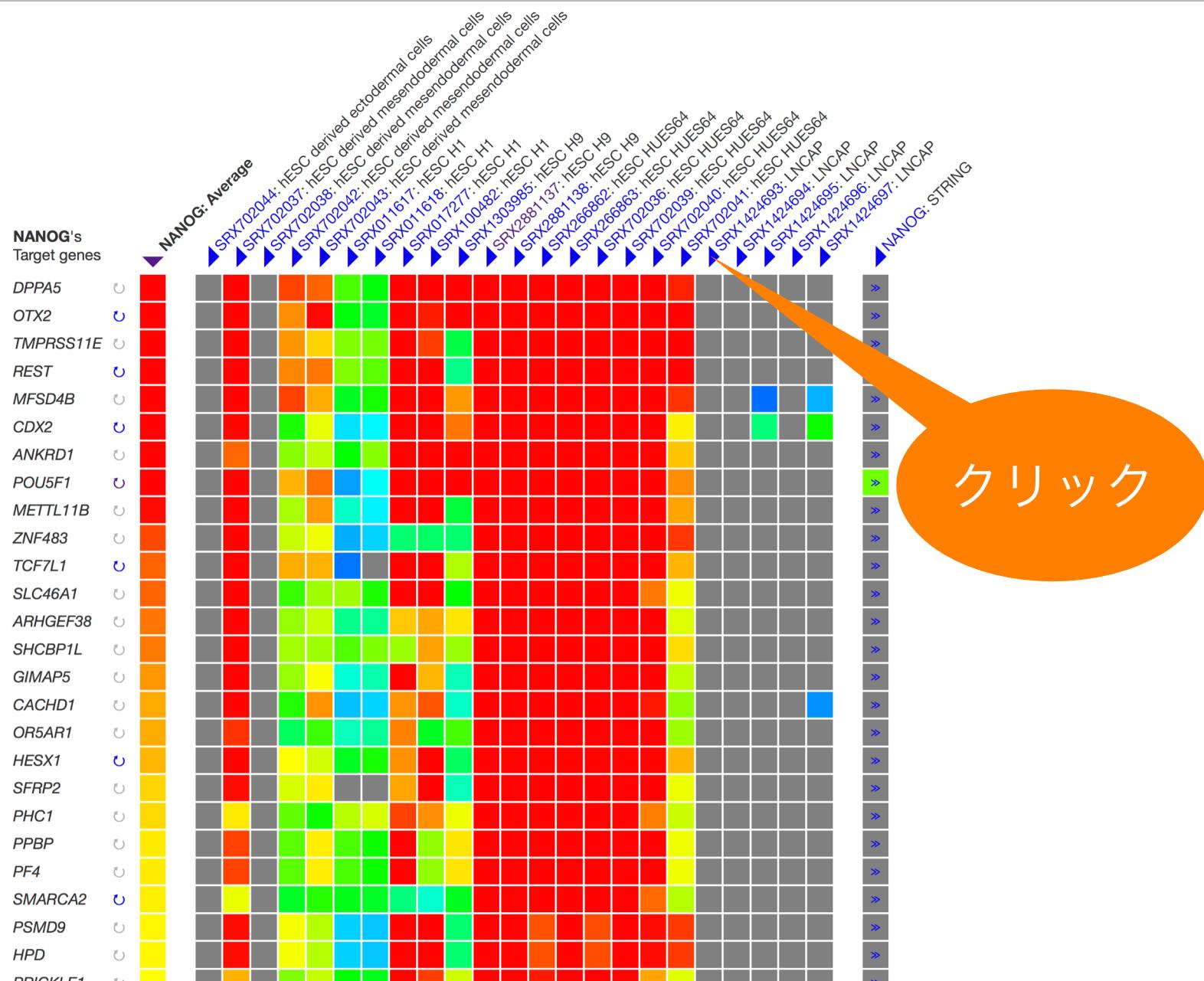


標的遺伝子を探す



標的遺伝子を探す

dbarchive.biosciencedbc.jp



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

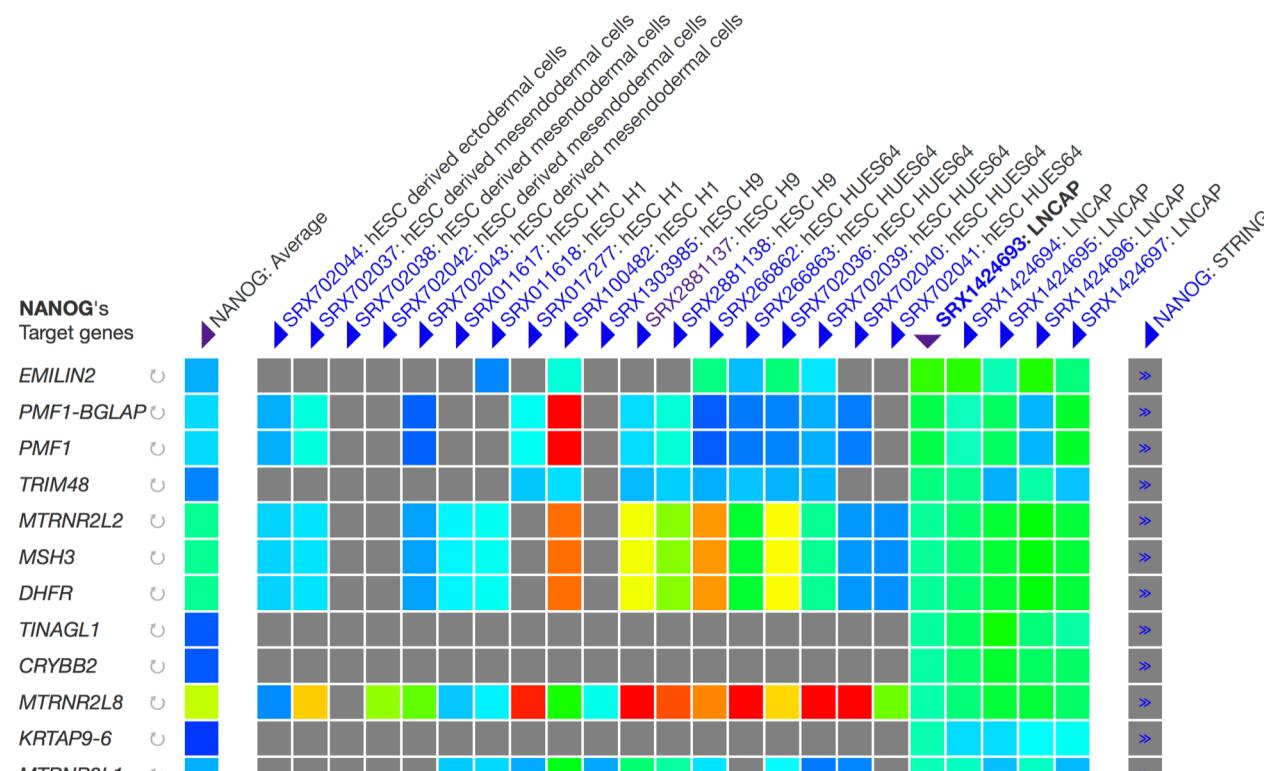
Sort key: SRX1424693 | LNCAP

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