

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

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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# 共局在因子を探す

chip-atlas.org

ChIP-Atlas | Target genes

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

View Colocalization Data

Download (TSV)

Download (GML)

クリック



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

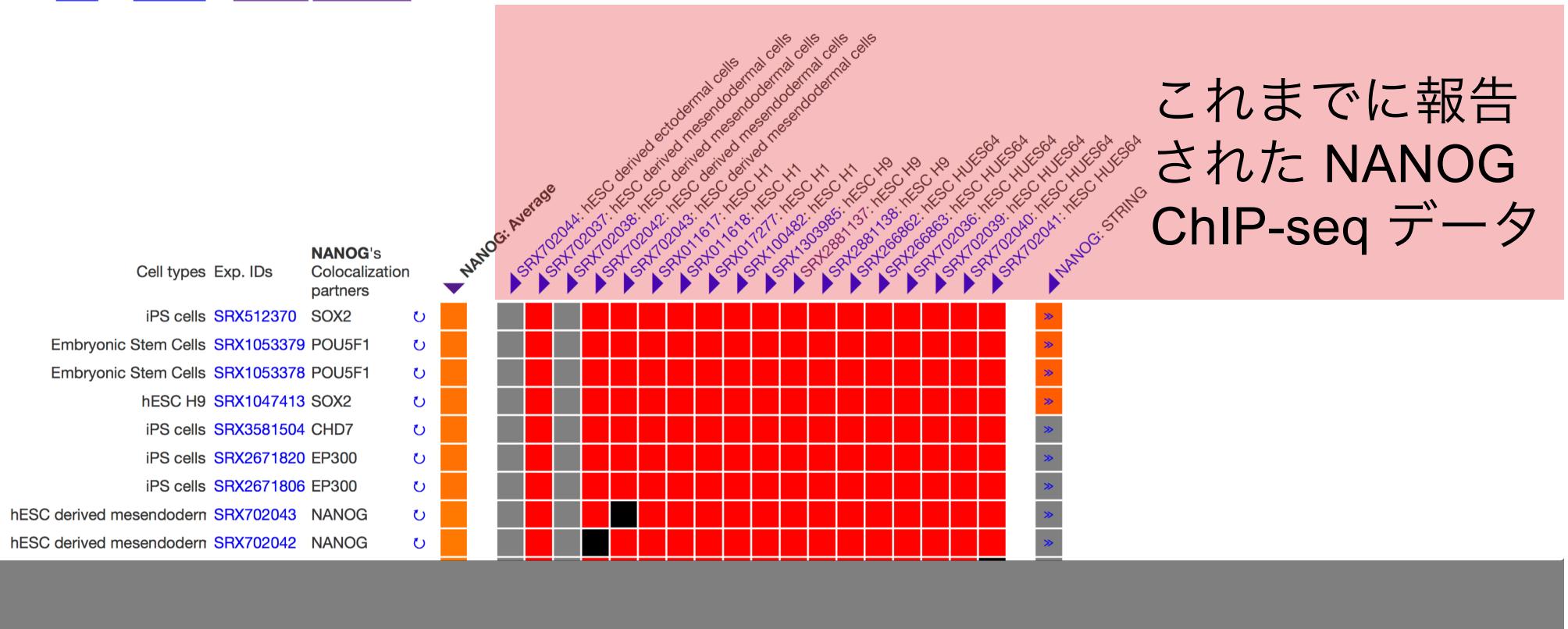
#### Color legends

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

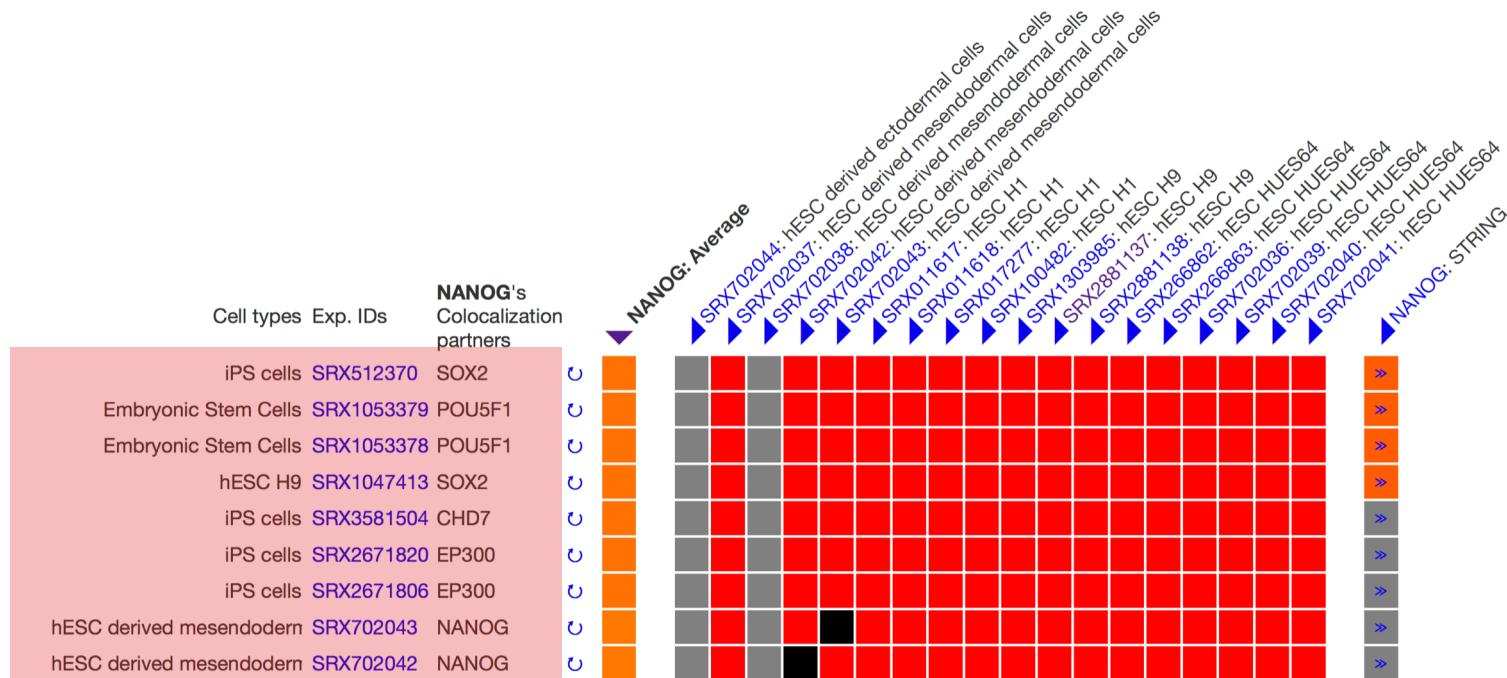
#### Color legends

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)

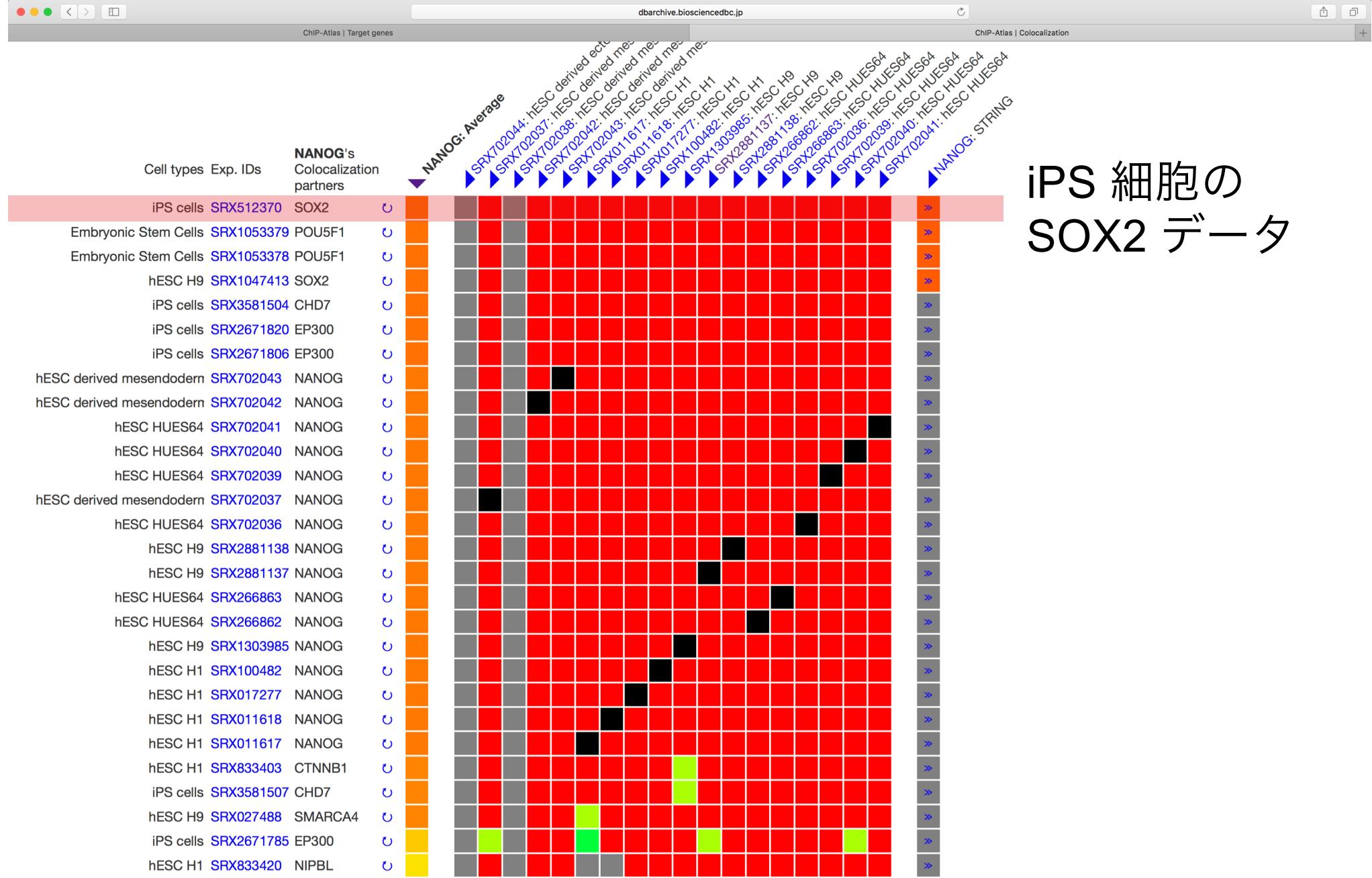
Downloads: [TSV](#) (text), [GML](#) (Cytoscape)

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



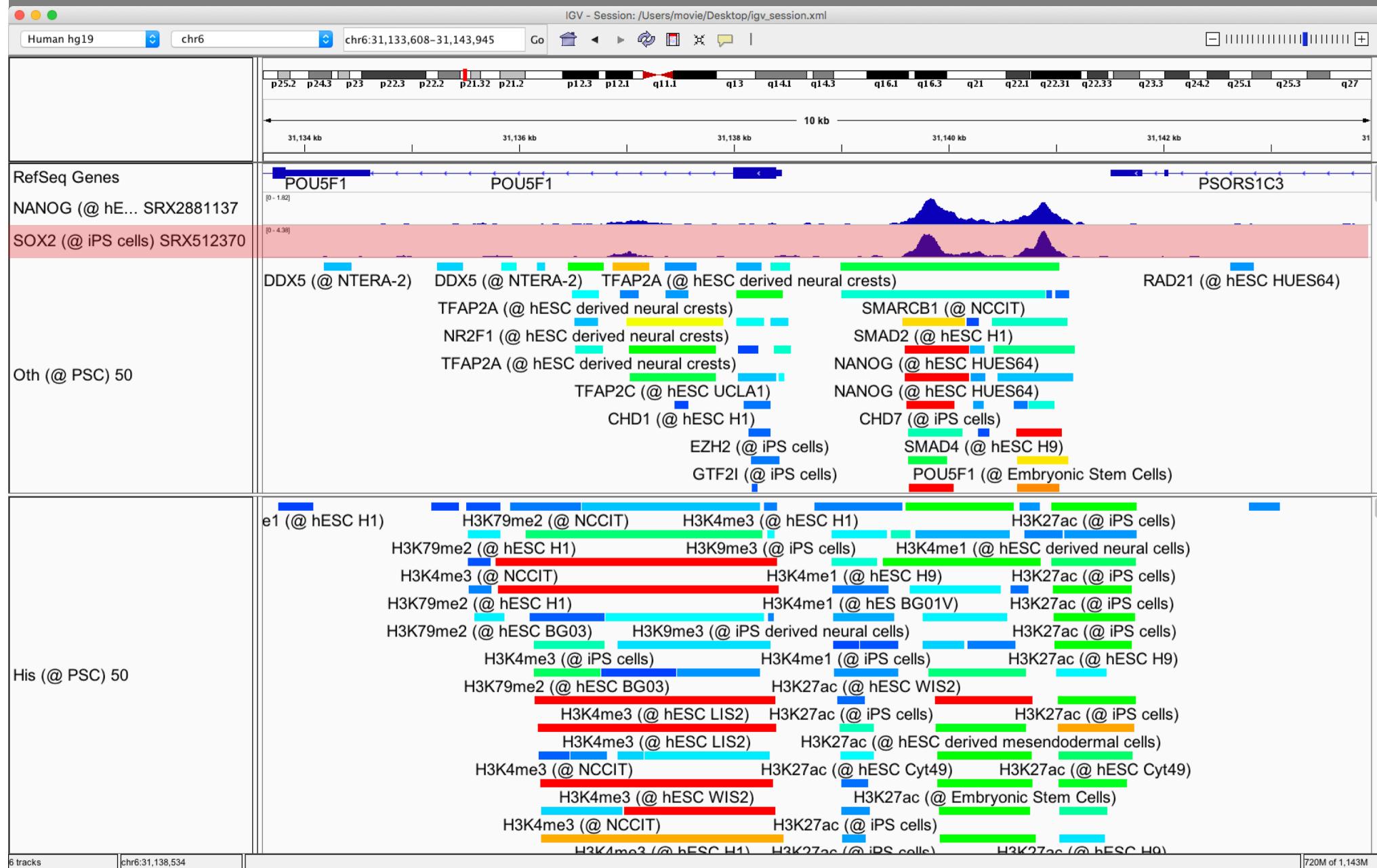
NANOG と同じゲノム領域に結合する ChIP-seq データ

# 共局在因子を探す

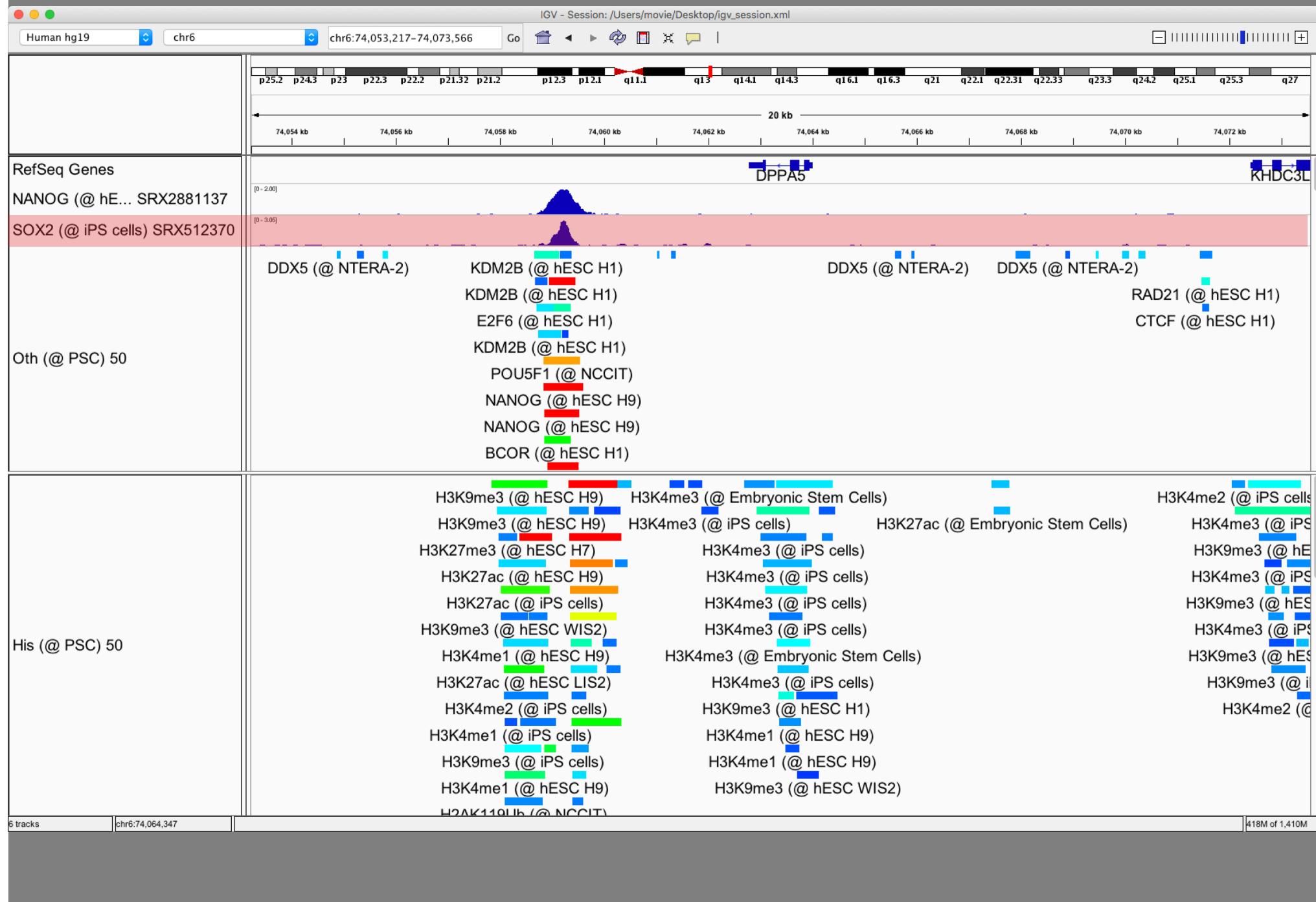


## iPS 細胞の SOX2 データ

# 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

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[Watch movie introduction](#)

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

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<sup>2</sup>Gladstone Institute of Cardiovascular Disease, San Francisco, CA 94158, USA

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<sup>6</sup>Department of Biochemistry and Biophysics

<sup>7</sup>Department of Pediatrics

<sup>8</sup>Department of Epidemiology & Biostatistics and Institute for Human Genetics

<sup>9</sup>Cardiovascular Research Institute

University of California, San Francisco, CA 94158, USA

<sup>10</sup>These authors contributed equally to this work

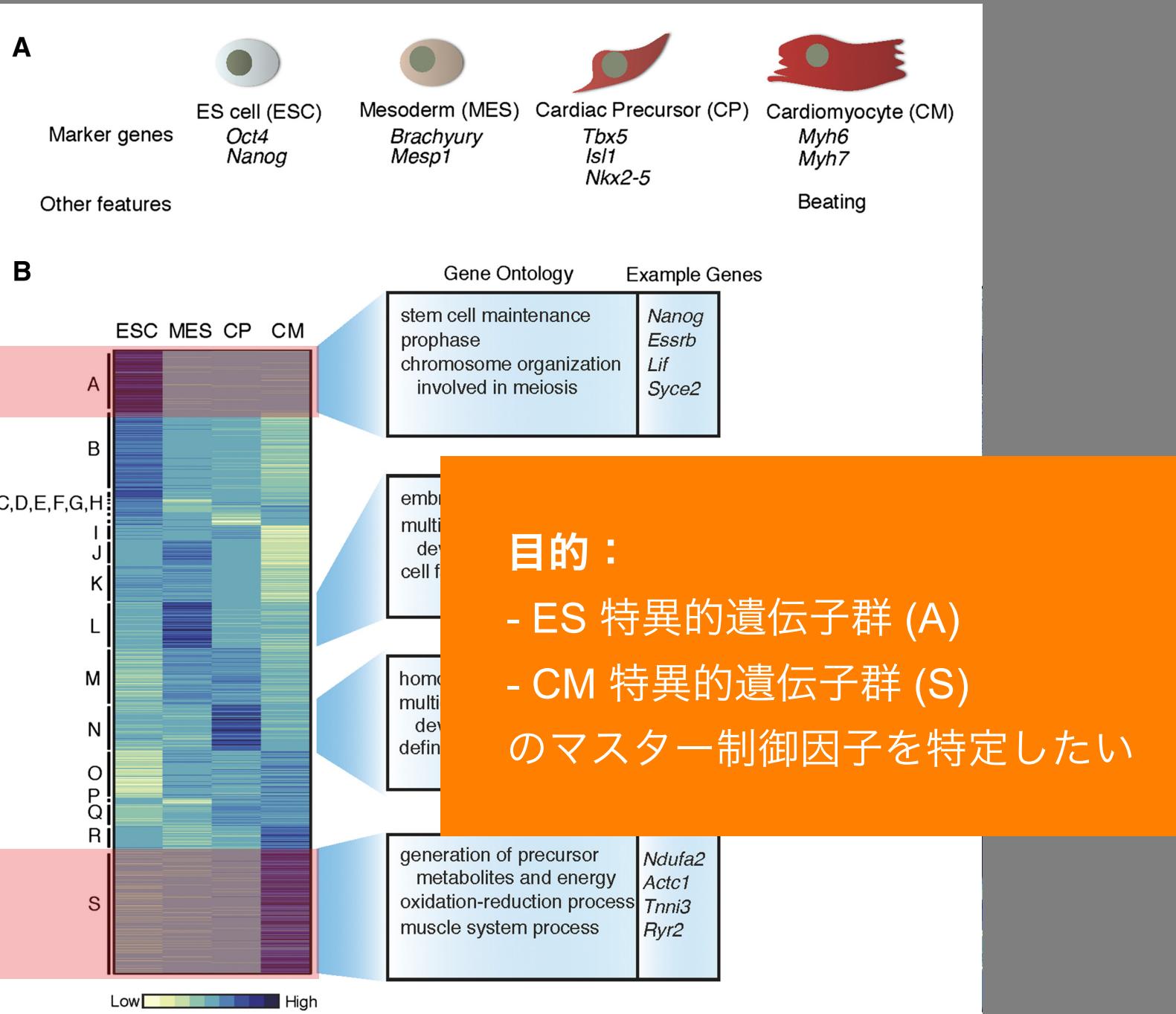
\*Correspondence: lboyer@mit.edu (L.A.B.), bbruneau@gladstone.ucsf.edu (B.G.B.)

<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:	<a href="http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&amp;format=html">http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&amp;format=html</a>
Download TSV:	<a href="http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&amp;format=tsv">http://ddbj.nig.ac.jp/wabi/chipatlas/wabi_chipatlas_2018-1207-1735-03-394-748830?info=result&amp;format=tsv</a>

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
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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 are tabs for ChIP-Atlas, Peak Browser, Target Genes, Colocalization, Enrichment Analysis (which is active), Documentation, Publications, and a search bar for 'Find an experiment'. Below the tabs, there are buttons for different organisms: H. sapiens (selected), M. musculus, R. norvegicus, D. melanogaster, C. elegans, and S. cerevisiae. The main area 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. A large orange speech bubble with the Japanese text 'クリック' (Click) points to the 'All antigens (34390)' button in section 1.

## 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。