

2021.12.02

第44回日本分子生物学会年会

生命科学のデータベース活用法

ChIP-Atlas update:

Bisulfite-seq と ATAC-seq データを統合

使い方と沖の遊び方



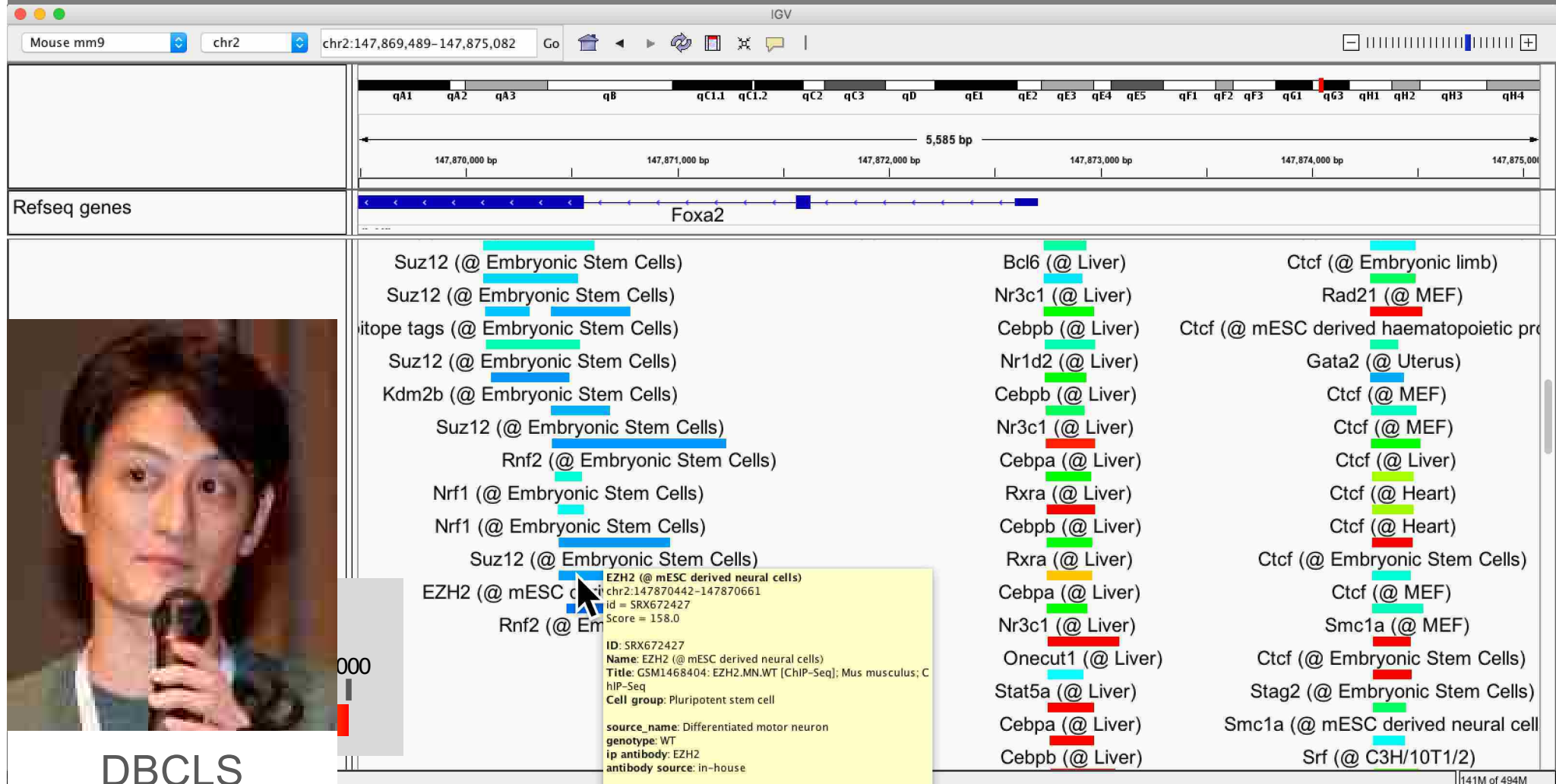
京都大学大学院 医学研究科
創薬医学講座・特定准教授

沖 真弥 (Oki, Shinya)



ChIP-Atlas とは

既報 ChIP-seq データを統合的に活用できる

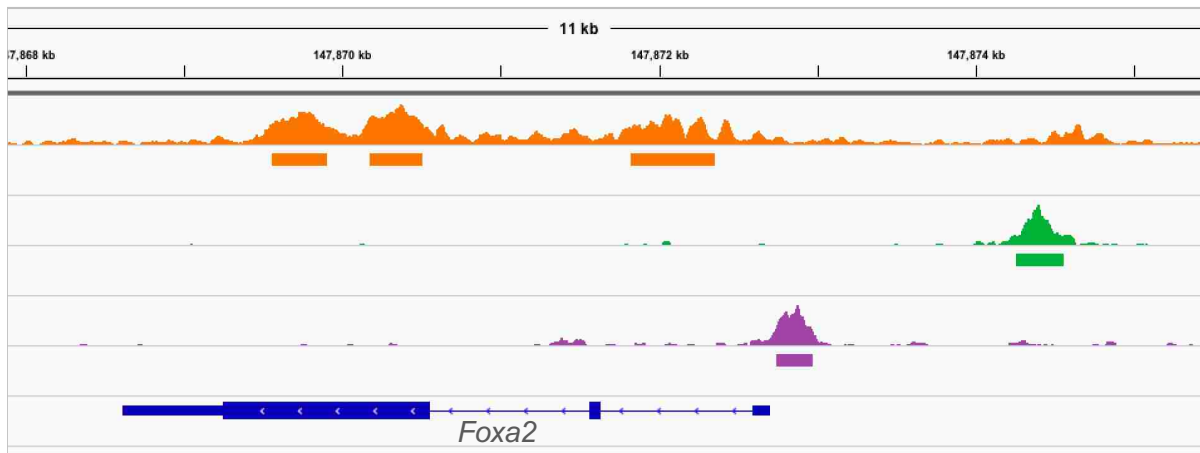


データ処理・公開しているデータ



FastQ (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

データ統合・データマイニング

個々のデータを探す

ChIP-Atlas

Peak Browser

Target Genes

Colocalization

Enrichment Analysis

Publications

Docs

Find By ID

GSM469863

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ChIP-Atlas

An integrative, comprehensive database to explore public Epigenetic dataset, including ChIP-Seq, DNase-Seq, ATAC-Seq, and Bisulfite-Seq data: ChIP-Atlas covers almost all public data archived in Sequence Read Archive of NCBI, EBI, and DDBJ with over 224,000 experiments.

[Watch movie introduction](#)

Advanced

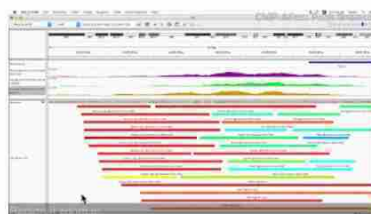
What's new

- Added **ATAC-Seq and Bisulfite-Seq**, together with UI improvement including 'peak' icon! (2021/10/04)
- Updated site design: (2021/01/04)
 - [Dataset search](#) is available as a standalone function
 - ID search at the top right corner now accepts GEO Sample ID (e.g. GSM469863) along with SRA Experiment ID (e.g. SRX018625)
 - New information layout for individual experiment list
- Added new genome assemblies: hg38, mm10, dm6, ce11. Happy holidays! (2020/12/01)

Peak Browser

Visualizes protein binding on given genomic loci with [IGV genome browser](#)

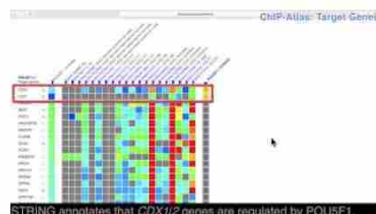
[Watch tutorial movie](#)



Target Genes

Predict target genes bound by given transcription factors

[Watch tutorial movie](#)



Colocalization

Predict partner proteins colocalizing with given transcription factors

[Watch tutorial movie](#)



Enrichment Analysis

Predict proteins bound to given genomic loci and genes

[Watch tutorial movie](#)



個々のデータを探す

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ChIP-Atlas: Dataset Search

Search for data by keywords

[Simple search](#)[Detailed search](#)

Show entries

Search:

Showing 1 to 10 of 224,659 entries

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX019491	SRA012529	GSM534464	hg19, hg38	Input control	Input control	Adipocyte	Adipose stromal cell
SRX019492	SRA012529	GSM534465	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
SRX019493	SRA012529	GSM534466	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell
SRX019494	SRA012529	GSM534467	hg19, hg38	Histone	H3K4me1	Adipocyte	Adipose stromal cell
SRX019495	SRA012529	GSM534468	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
SRX019496	SRA012529	GSM534469	hg19, hg38	Histone	H3K27me3	Adipocyte	Adipose stromal cell
SRX019497	SRA012529	GSM534470	hg19, hg38	Histone	H3K36me3	Adipocyte	Adipose stromal cell
SRX019498	SRA012529	GSM534471	hg19, hg38	TFs and others	CTCF	Adipocyte	Adipose stromal cell
SRX019499	SRA012529	GSM534472	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
SRX019500	SRA012529	GSM534473	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell

[Previous](#)[1](#)[2](#)[3](#)[4](#)[5](#)[...](#)[22466](#)[Next](#)

個々のデータを探す

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Show entries

Search:

Showing 1 to 10 of 12 entries (filtered from 224,659 total entries)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX359953	SRA104261	GSM1239521	hg19, hg38	TFs and others	SALL4	Digestive tract	LoVo
SRX1284248	SRA300875	GSM1892432	mm9, mm10	TFs and others	Sall4	Gonad	Spermatogonia
SRX1284249	SRA300875	GSM1892434	mm9, mm10	TFs and others	Sall4	Gonad	Spermatogonia
SRX1284250	SRA300875	GSM1892435	mm9, mm10	TFs and others	Sall4	Gonad	Spermatogonia
SRX3888135	SRA682432	GSM3082674	hg19, hg38	TFs and others	SALL4	Liver	SNU-398
SRX702073	SRA184799	GSM1505732	hg19, hg38	TFs and others	SALL4	Pluripotent stem cell	hESC HUES64
SRX702074	SRA184799	GSM1505733	hg19, hg38	TFs and others	SALL4	Pluripotent stem cell	hESC derived mesendodermal cells
ERX1399946	ERA582745	-	mm9, mm10	TFs and others	Sall4	Pluripotent stem cell	ES cells

Sall4 in Spermatogonia

Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Publications Docs Find By ID GSM469863 Go Advanced

Visualize

SRX1284250

GSM1892435: SALL4 ChIP - Chromatin sample 3; Mus musculus; ChIP-Seq

Visualize ▾

Analyze ▾

Download ▾

Link Out ▾

Install and launch IGV before selecting data to visualize

For mm10

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

For mm9

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

Error connecting to IGV?

BigWig

Sample information curated by ChIP-Atlas

Antigen

Antigen Class TFs and others
Antigen Sall4

Cell type

Cell type Class Gonad
Cell type Spermatogonia
MeSH Description Euploid male germ cells of an early stage of SPERMATO onset of puberty, spermatogonia at the basement memb then meiotic divisions and give rise to the haploid SPERMATOCYTES.

Attributes by original data submitter

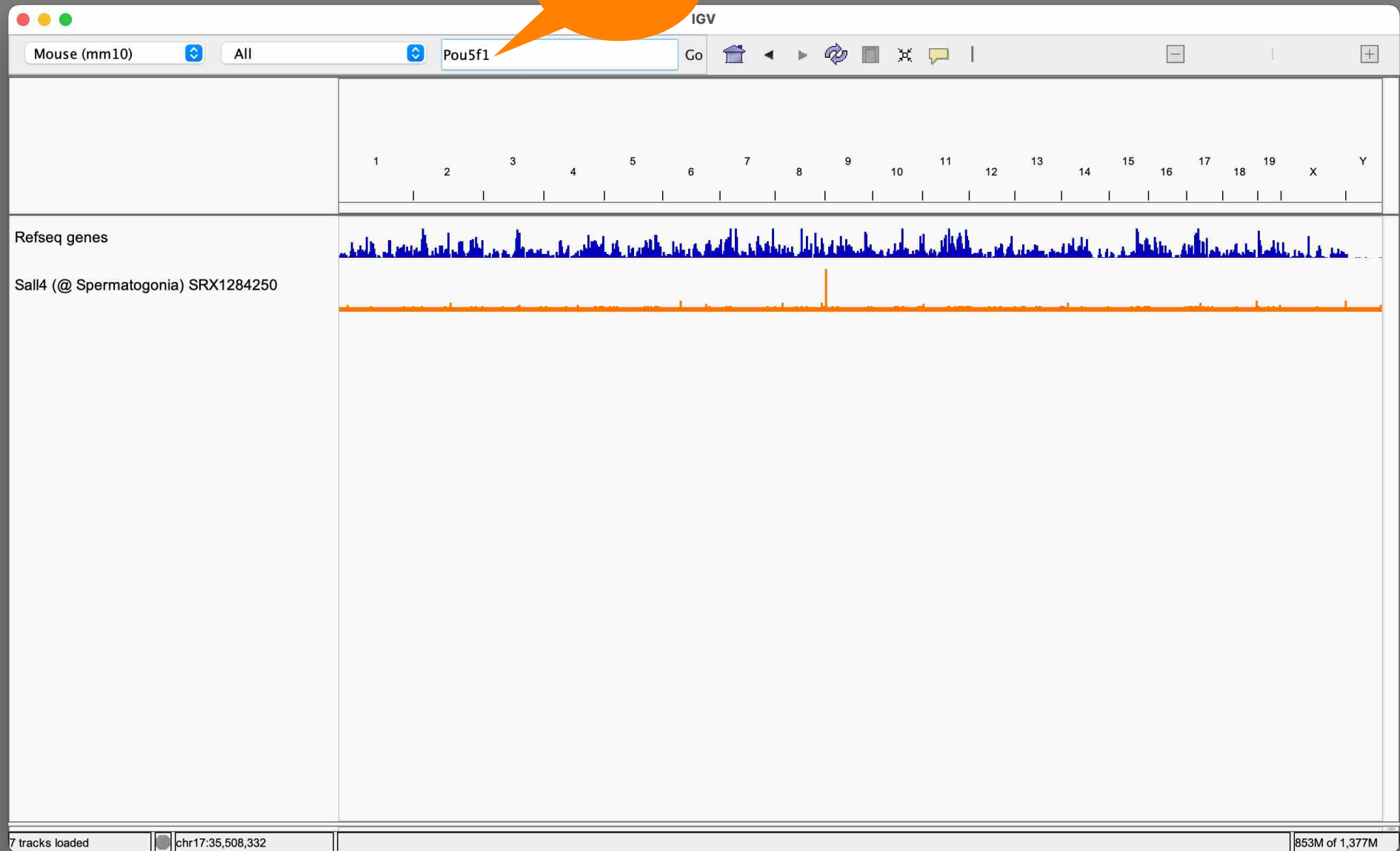
Sample

source_name THY1+ spermatogonia

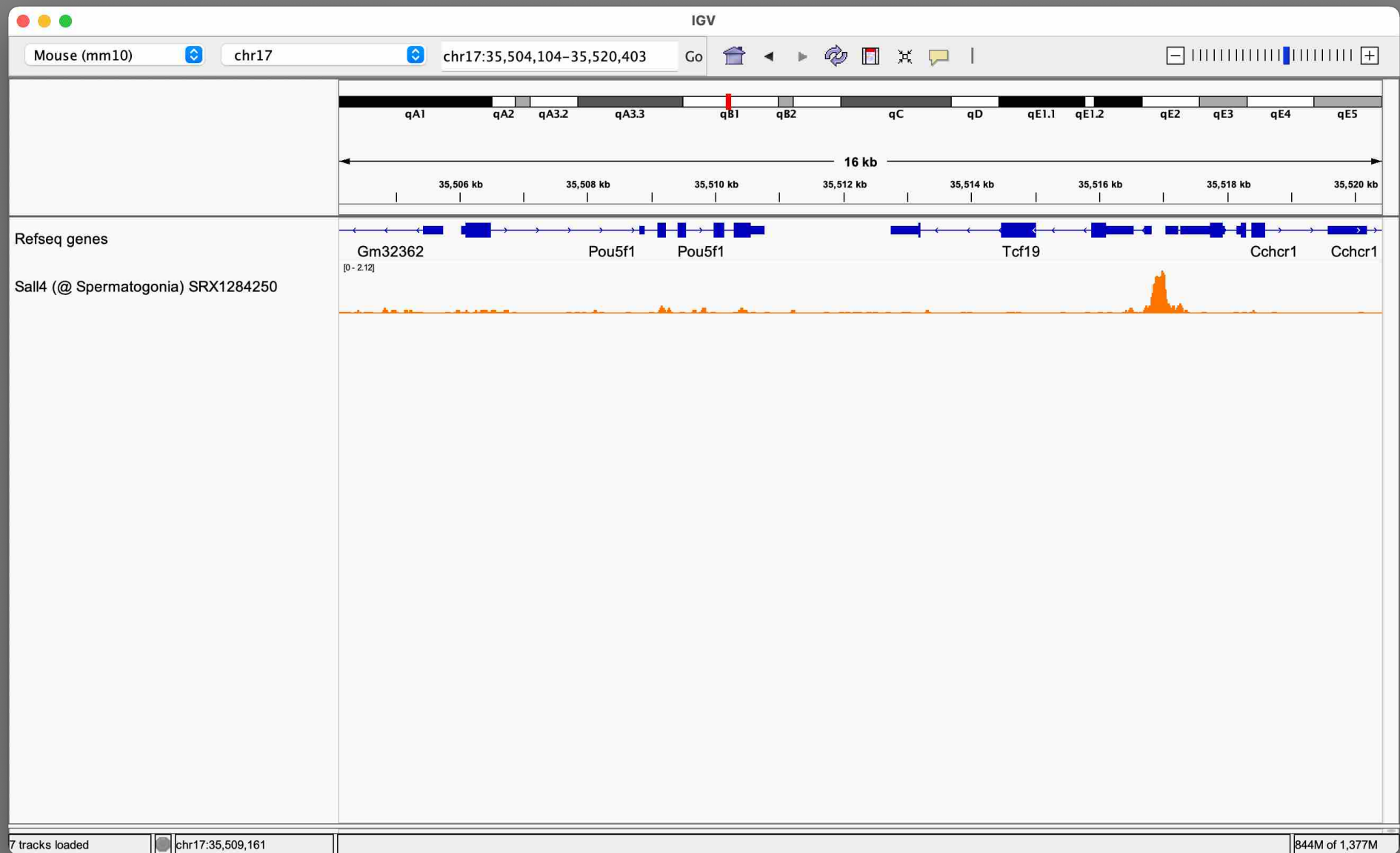
ig=http://dbarchive.biosciencedbc.jp/auxiliary/mm10/eachData/bw/SRX1284250.bw&genome=mm10&name=Sall4%20(%20Spermatogonia)%20SRX1284250を新規タブで開く

Sall4 in Spermatogonia

Pou5f1



Sall4 in Spermatogonia



複数の ChIP-seq データをまとめて閲覧

▲ ChIP-Atlas

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 - New info [individual experiment list](#)
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Peak
Browser

Peak Browser

Visualizes protein binding on given genomic loci with [IGV genome browser](#)

[Watch tutorial movie](#)



Target Genes

Predict target genes bound by given transcription factors

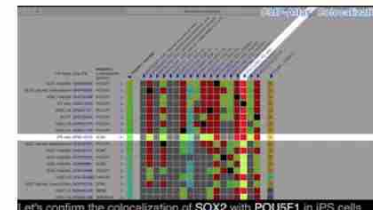
[Watch tutorial movie](#)



Colocalization

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[Watch tutorial movie](#)



Enrichment Analysis

Predict proteins bound to given genomic loci and genes

[Watch tutorial movie](#)



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[H. sapiens \(hg19\)](#)

[H.sapiens \(hg38\)](#)

[M. musculus \(mm9\)](#)

[M. musculus \(mm10\)](#)

[R. norvegicus \(rn6\)](#)

[D. melanogaster \(dm3\)](#)

[D. melanogaster \(dm6\)](#)

[C. elegans \(ce10\)](#)

[C. elegans \(ce11\)](#)

[S. cerevisiae \(sacCer3\)](#)

Experiment type

TFs

ChIP: Histone (25639)
ChIP: RNA polymerase (2497)
ChIP: TFs and others (13156)
ChIP: Input control (7641)
ATAC-Seq (23627)
DNase-Seq (1040)
Bisulfite-Seq (13409)

Cell type Class

Gonad

Digestive (91)
Embryo (91)
Embryonic fibroblast (3896)
Epidermis (1190)
Gonad (3259)
Kidney (1242)
Liver (5449)
Lung (1644)

Threshold for Significance ①

50
100
200
500

クリック

ChIP Antigen

type to search

All
5-hmC (3)
Ar (13)
Arid4b (1)
Atf7 (8)
Bmi1 (1)
Brd4 (1)
Crotonyl lysine (3)

Cell type

type to search

Round spermatid (1)
Sertoli Cells (1)
Sperm (19)
Spermatids (4)
Spermatocytes (30)
Spermatogonia (25)
Testicular germ cells (8)
Testis (185)

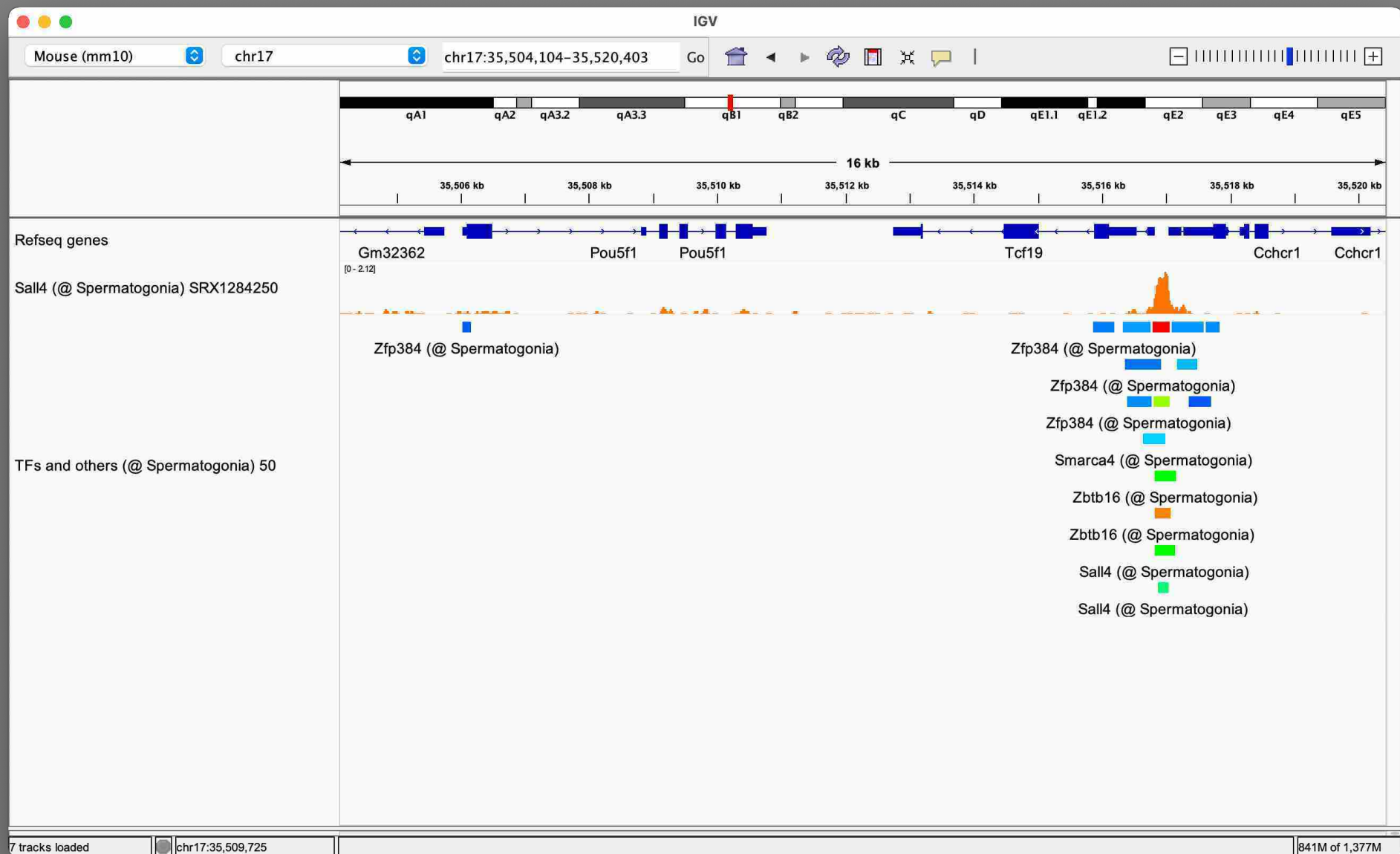
Spermatogonia

View on IGV

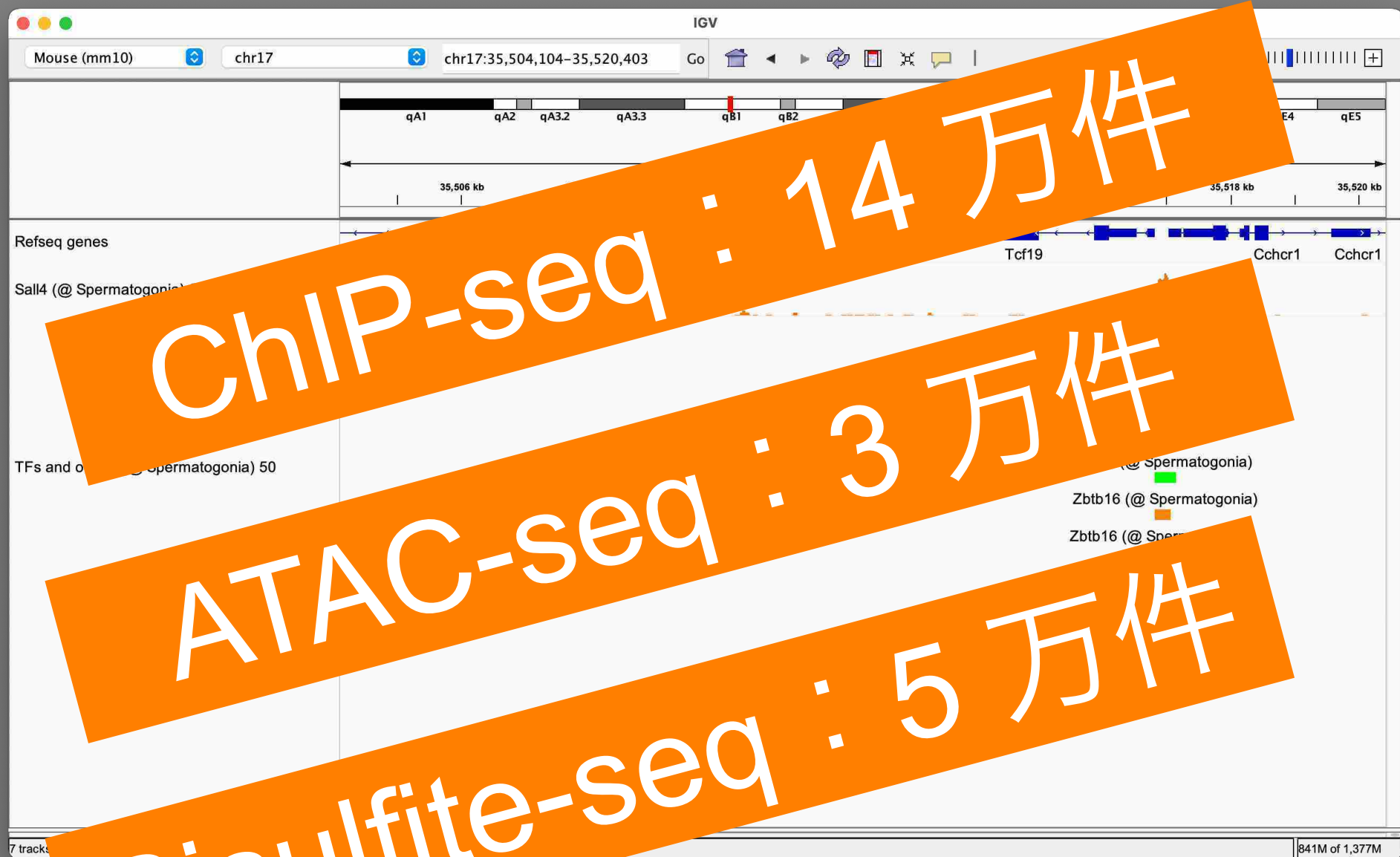
Error connecting to IGV?

Download BED file

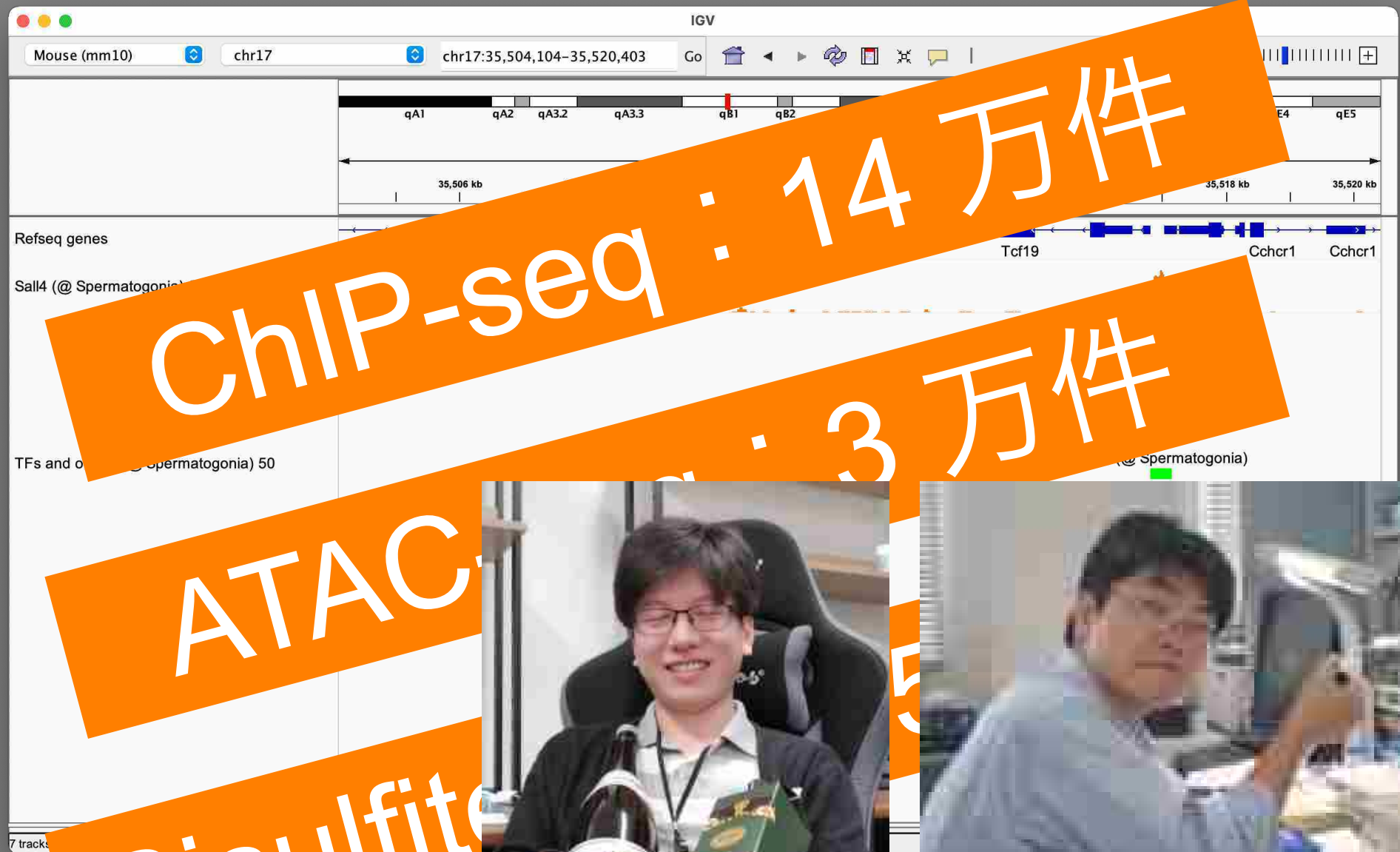
複数の ChIP-seq データをまとめて閲覧



Bisulfite-seq と ATAC-seq も閲覧できる



Bisulfite-seq と ATAC-seq も閲覧できる



鄒 兆南 (DC2)
1P-0692



九大・三浦史仁

Bisulfite-seq と ATAC-seq も閲覧できる

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Search for data by keywords

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Show entries

Search:

Showing 11 to 20 of 39 entries (filtered from 224,659 total entries)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX332325	SRA096819	GSM1202740	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX332326	SRA096819	GSM1202741	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX6874358	SRA965083	GSM4086441	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX6874359	SRA965083	GSM4086442	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX688590	SRA096819	GSM1489487	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX688591	SRA096819	GSM1489488	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia
SRX688592	SRA096819	GSM1489489	mm9, mm10	Bisulfite-Seq	Bisulfite-Seq	Gonad	Spermatogonia

Bisulfite +
Spermatogonia

Bisulfite-seq と ATAC-seq も閲覧できる

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Show entries

Search:

Showing 1 to 10 of 28 entries (filtered from 224,659 total entries)

SRX ID	SRA ID	GEO ID	Genome	Antigen class	Antigen	Cell type class	Cell type
SRX2416286	SRA502502	GSM2425094	hg19, hg38	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX2416287	SRA502502	GSM2425095	hg19, hg38	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX2416288	SRA502502	GSM2425096	hg19, hg38	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX2416289	SRA502502	GSM2425097	hg19, hg38	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX3114871	SRA601871	GSM2751121	mm9, mm10	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX3114872	SRA601871	GSM2751122	mm9, mm10	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX3114873	SRA601871	GSM2751123	mm9, mm10	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX3114874	SRA601871	GSM2751124	mm9, mm10	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia
SRX3114875	SRA601871	GSM2751125	mm9,	ATAC-Seq	ATAC-Seq	Gonad	Spermatogonia

ATAC +
Spermatogonia

Bisulfite-seq と ATAC-seq も閲覧できる

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ChIP-Atlas: Peak Browser

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[M. musculus \(mm10\)](#)

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[D. melanogaster \(dm3\)](#)

[D. melanogaster \(dm6\)](#)

[C. elegans \(ce10\)](#)

[C. elegans \(ce11\)](#)

[S. cerevisiae \(sacCer3\)](#)

Experiment type

ChIP: Histone (25988)
ChIP: RNA pol II (1040)
ChIP: TFs and co-factors (1040)
ChIP: Input control (1040)
ATAC-Seq (2200)
DNase-Seq (1040)
Bisulfite-Seq (13409)

Bisulfite-seq

Cell type Class

Embryo (9150)
Embryonic fibroblast (3896)
Epidermis (1190)
Gonad (3259)
Kidney (1242)
Liver (5449)
Lung (1644)
Muscle (1869)

Threshold for Significance ⓘ

NA

ChIP Antigen

type to search

NA

Cell type

type to search

Oocytes (920)
Prospermatogonia (10)
Sertoli Cells (1)
Sperm (155)
Spermatids (5)
Spermatocytes (7)
Spermatogonia (27)
Testis (22)

View on IGV

Error connecting to IGV?

Download BED file

Bisulfite-seq と ATAC-seq も閲覧できる

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ChIP-Atlas: Peak Browser

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ChIP: Histone
ChIP: RNA polymerase
ChIP: TFs and co-factors (13156)
ChIP: Input control (7641)
ATAC-Seq (23627)
DNase-Seq (1040)
Bisulfite-Seq (13409)

ATAC-seq

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Gonad (3259)
Kidney (1242)
Liver (5449)
Lung (1644)
Muscle (1869)

Threshold for Significance ⓘ

50
100
200
500

ChIP Antigen

NA

Cell type

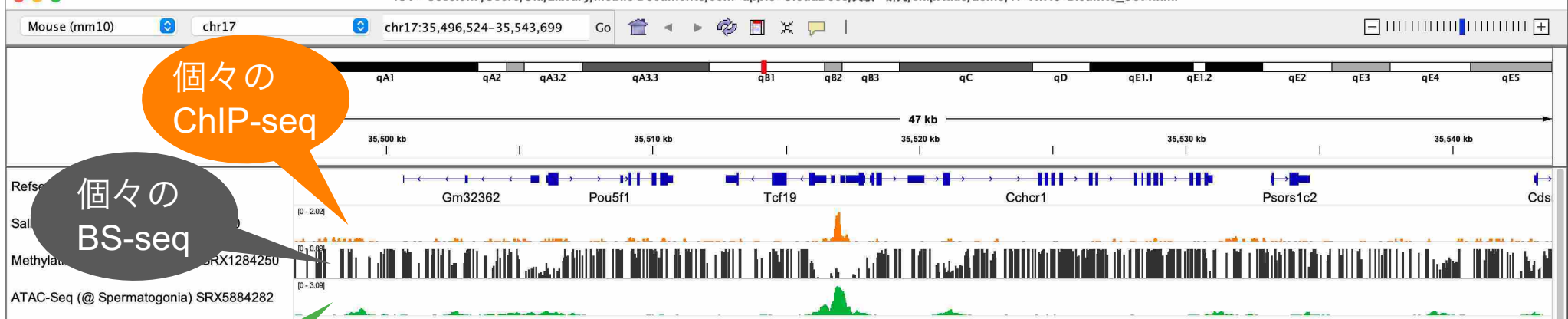
Round spermatids (6)
SK-OV-3 (3)
Sperm (44)
Spermatids (24)
Spermatocytes (7)
Spermatogenic cells (2)
Spermatogonia (24)
Testis (1)

[View on IGV](#)

Error connecting to IGV?

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ChIP-seq + Bisulfite-seq + ATAC-seq



個々の
ChIP-seq

個々の
BS-seq

個々の
ATAC-seq

ChIP-seq + Bisulfite-seq + ATAC-seq



複数の遺伝子の制御機構を探る

ChIP-Atlas

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複数の遺伝子の制御機構を探る

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[Q. Advanced](#)[H. sapiens \(hg19\)](#)[H.sapiens \(hg38\)](#)[M. musculus \(mm9\)](#)[M. musculus \(mm10\)](#)[R. norvegicus \(rn6\)](#)[D. melanogaster \(dm3\)](#)[D. melanogaster \(dm6\)](#)[C. elegans \(ce10\)](#)[C. elegans \(ce11\)](#)[S. cerevisiae \(sacCer3\)](#)

1. Experiment type

ChIP: Histone (16612)
ChIP: RNA polymerase (2099)
ChIP: TFs and others (15155)
ChIP: Input control (8078)
ATAC-Seq (27318)
DNase-Seq (1642)
Bisulfite-Seq (15000)

2. Cell type Class

All cell types (103765)
Adipocyte (392)
Blood (36245)
Bone (1501)
Breast (7459)
Cardiovascular (2336)
Digestive tract (6151)
Embryo (728)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

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

GPRC5B
GRID2
HDAC9
HES3
ICMT
KIAA1919
LEFTY1
LFNG
LINC01

ファイル
Choose

Hepatocyte で
特異的に発現

5. Enter dataset B

- ☐ Refseq coding genes (excluding dataset A) ⓘ
☒ Gene list (Gene symbols) ⓘ

RBM4B
RGPD2
RNASE4
RPS19
RPS29
RRAS
SACM1L
SCAF1
SCML1

ファイル
Choose

その他の細胞で
発現する遺伝子

6. Analysis description

Analysis title ⓘ

Dataset A title ⓘ

Dataset B title ⓘ

Distance range from TSS ⓘ

- bp ≤ TSS ≤ + bp

Estimated run time: 2 mins

複数の遺伝子の制御機構を探る

Atlas Peak Browser Target hg19 hg38 Enrichment Analysis Publications Docs Find By ID GSM469863 Go Q Advanced

H. sapiens (hg19) H.sapiens (hg38) M. musculus (mm9) M. musculus (mm10) R. norvegicus (rn6) D. melanogaster (dm3) D. melanogaster (dm6)
C. elegans (ce10) C. elegans (ce11) S. cerevisiae (sacCer3)

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ChIP: Input control (8078)
ATAC-Seq (27318)
DNase-Seq (1642)
Bisulfite-Seq (15000)

TFs

2. Cell type Class

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Blood (36245)
Bone (1501)
Breast (7459)
Cardiovascular (2336)
Digestive tract (6151)
Embryo (728)

All cell types

3. Threshold for Significance ①

50
100
200
500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ①
☒ Gene list (Gene symbols) ①

GPRC5B
GRID2
HDAC9
HES3
ICMT
KIAA1919
LEFTY1
LFNG
LINC01

HNF4A
FOXA2

Hepatocyte で
特異的に発現

5. Enter dataset B

☐ Refseq coding genes (excluding dataset A) ①
☒ Gene list (Gene symbols) ①

RBM4B
RGPD2
RNASE4
RPS19
RPS29
RRAS
SACM1L
SCAF1
SCML1

その他の細胞で
発現する遺伝子

6. Analysis description

Analysis title ①

My project

Dataset A title ①

dataset A

Dataset B title ①

Control

Distance range from TSS ①

- 5000 bp ≤ TSS ≤ + 5000 bp

TSS ±
5,000 bp

Submit

submit

Estimated run time: 2 mins

Hepatocyte 特異的遺伝子の制御因子

ID	Antigen	Cell class	Cell	Num of peaks	Overlaps / Hepatocyte	Overlaps / Other enhancers	Log P-val	Fold Enrichment
SRX100544	EP300	Liver	Hep G2	24334	80/286	1147/20509	-32.1	5.00
SRX190321	MAX	Liver	Hep G2	40220	90/286	1497/20509	-31.9	4.31
SRX100552	SP1	Liver	Hep G2	19032	64/286	755/20509	-29.7	6.08
SRX100449	HNF4G	Liver	Hep G2	15919	54/286	507/20509	-29.3	7.64
SRX100497	RXRA	Liver	Hep G2	13022	54/286	557/20509	-27.5	6.95
SRX100493	HEY1	Liver	Hep G2	26412	69/286	984/20509	-27.5	5.03
SRX100538	HDAC2	Liver	Hep G2	16071	58/286	676/20509	-27.0	6.15
SRX100505	HNF4A	Liver	Hep G2	21259	54/286	585/20509	-26.5	6.62
SRX190332	MYBL2	Liver	Hep G2	15213	55/286	637/20509	-25.7	6.19
SRX190264	CREB1	Liver	Hep G2	26690	68/286	1092/20509	-24.3	4.47
SRX100448	FOXA2	Liver	Hep G2	45130	67/286	1138/20509	-22.6	4.22
SRX150360	TBP	Liver	Hep G2	10293	38/286	327/20509	-21.7	8.33
SRX100506	FOXA1	Liver	Hep G2	50941	70/286	1295/20509	-21.7	3.88
SRX1165097	CREB1	Liver	Hep G2	21856	58/286	899/20509	-21.2	4.63
SRX1902		Liver	Hep G2	18201	48/286	605/20509		5.69

転写因子

組織・細胞

P-value

Hepatocyte 特異的遺伝子の制御因子

ID	Antigen	Cell class	Cell	Num of peaks	Overlaps / Hepatocyte	Overlaps / Other enhancers	Log P-val	Fold Enrichment
SRX100544	EP300	Liver	Hep G2	24334	80/286	1147/20509	-32.1	5.00
SRX190321	MAX	Liver	Hep G2	40220	90/286	1497/20509	-31.9	4.31
SRX100552	SP1	Liver	Hep G2	19032	64/286	755/20509	-29.7	6.08
SRX100449	HNF4G	Liver	Hep G2	15919	54/286	507/20509	-29.3	7.64
SRX100497	RXRA	Liver	Hep G2	13022	54/286	557/20509	-27.5	6.95
SRX100493	HEY1	Liver	Hep G2	26412	69/286	984/20509	-27.5	5.03
SRX100538	HDAC2	Liver	Hep G2	16071	58/286	676/20509	-27.0	6.15
SRX100505	HNF4A	Liver	Hep G2	21259	54/286	585/20509	-26.5	6.62
SRX190332	MYBL2	Liver	Hep G2	15213	55/286	637/20509	-25.7	6.19
SRX190264	CREB1	Liver	Hep G2	26690	68/286	1092/20509	-24.3	4.47
SRX100448	FOXA2	Liver	Hep G2	45130	67/286	1138/20509	-22.6	4.22
SRX150360	TBP	Liver	Hep G2	10293	38/286	327/20509	-21.7	8.33
SRX100506	FOXA1	Liver	Hep G2	50941	70/286	1295/20509	-21.7	3.88
SRX1165097	CREB1	Liver	Hep G2	21856	58/286	899/20509	-21.2	4.63
SRX190266	NR2F2	Liver	Hep G2	18201	48/286	605/20509	-20.9	5.69

複数の遺伝子の制御機構を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

H. sapiens (hg19)

H.sapiens (hg38)

M. musculus (mm9)

M. musculus (mm10)

R. norvegicus (rn6)

D. melanogaster (dm3)

D. melanogaster (dm6)

C. elegans (ce10)

C. elegans (ce11)

S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (16612)

ChIP: RNA polymerase (2099)

ChIP: TFs and others (15155)

ChIP: Input control (8078)

ATAC-Seq (27318)

DNase-Seq (1642)

Bisulfite-Seq (15000)

2. Cell type Class

All cell types (103765)

Adipocyte (392)

Blood (36245)

Bone (1501)

Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

Choose local file

[Try with example](#)

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

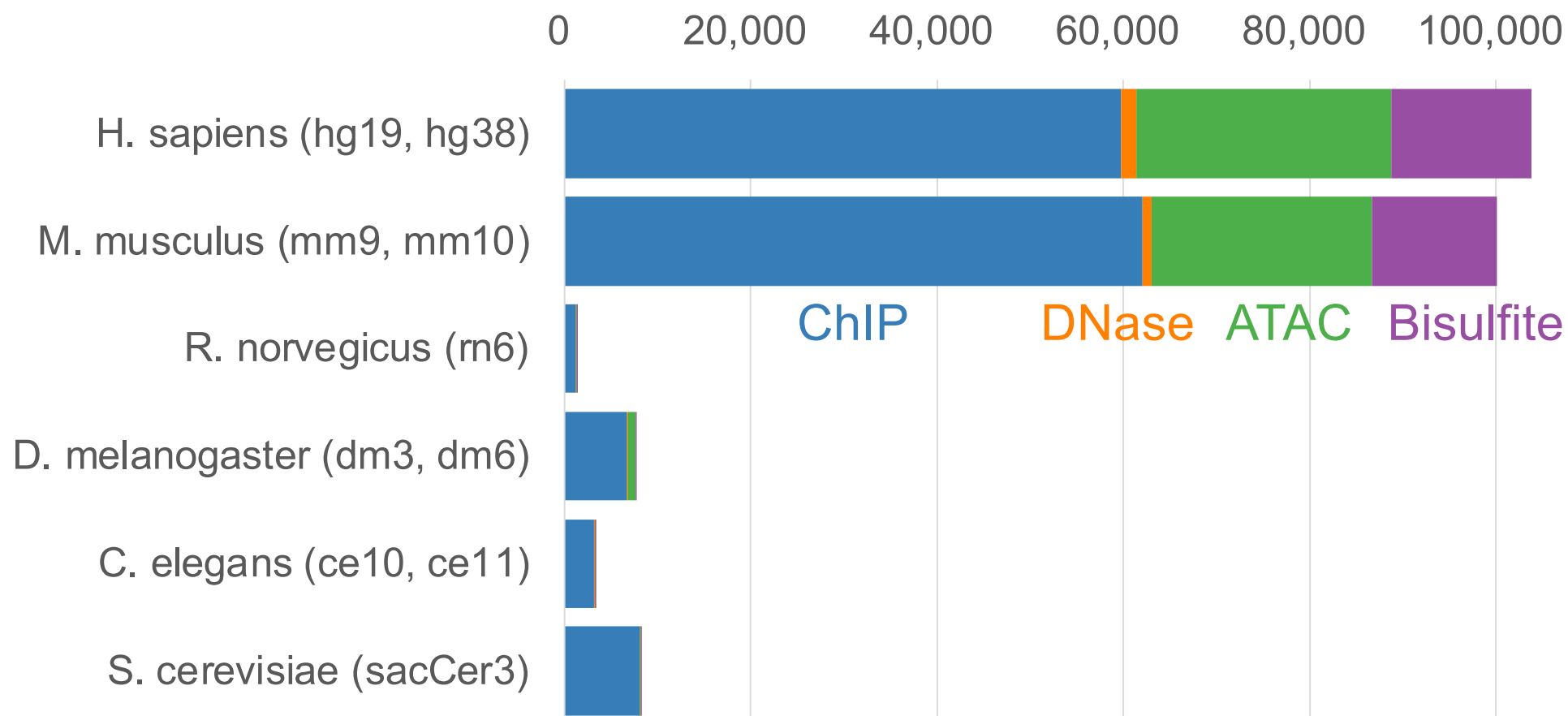
Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

DEG

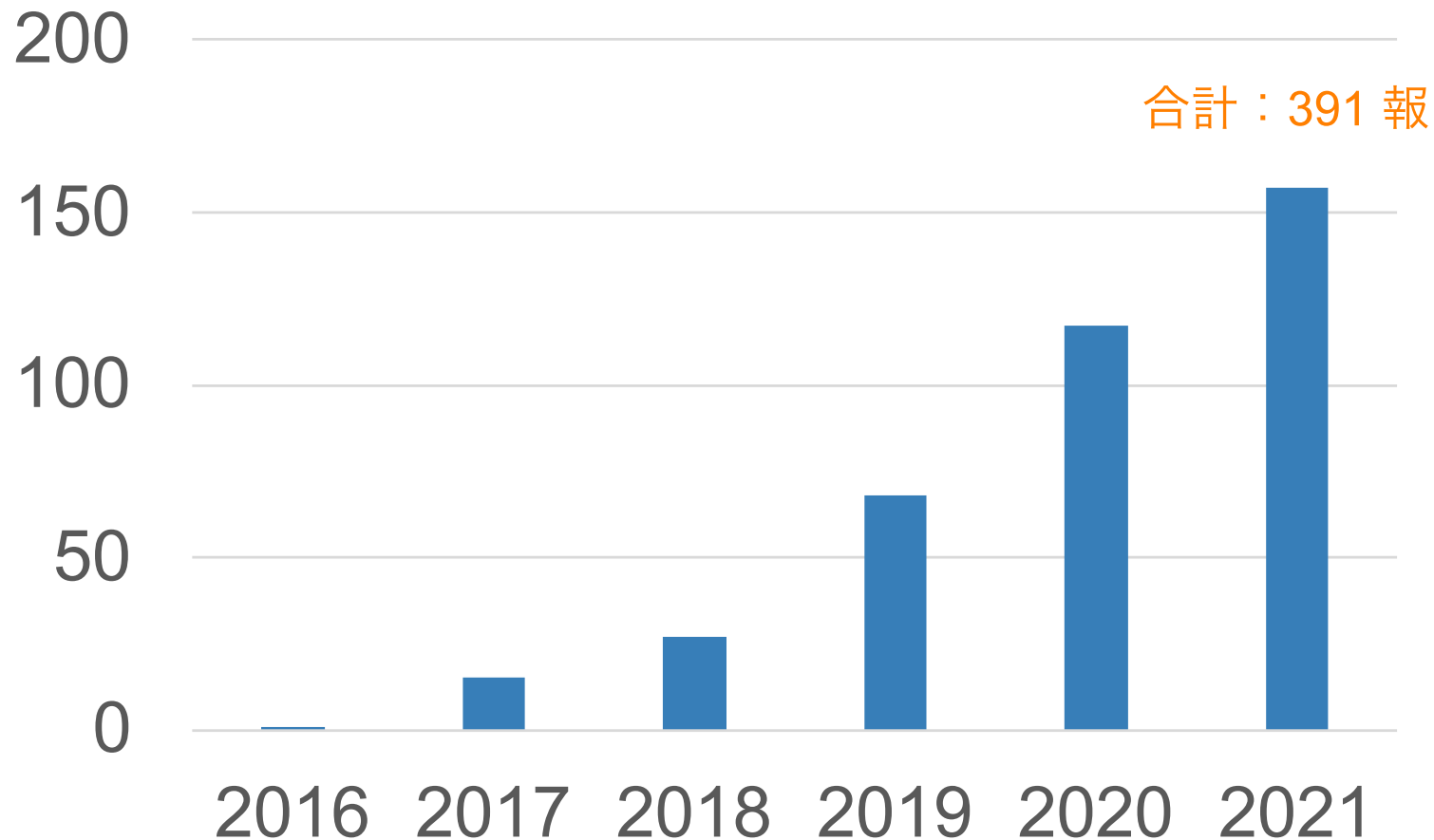
RNA-seq で得られた DEG の制御因子がわかる

実験データ数



引用論文

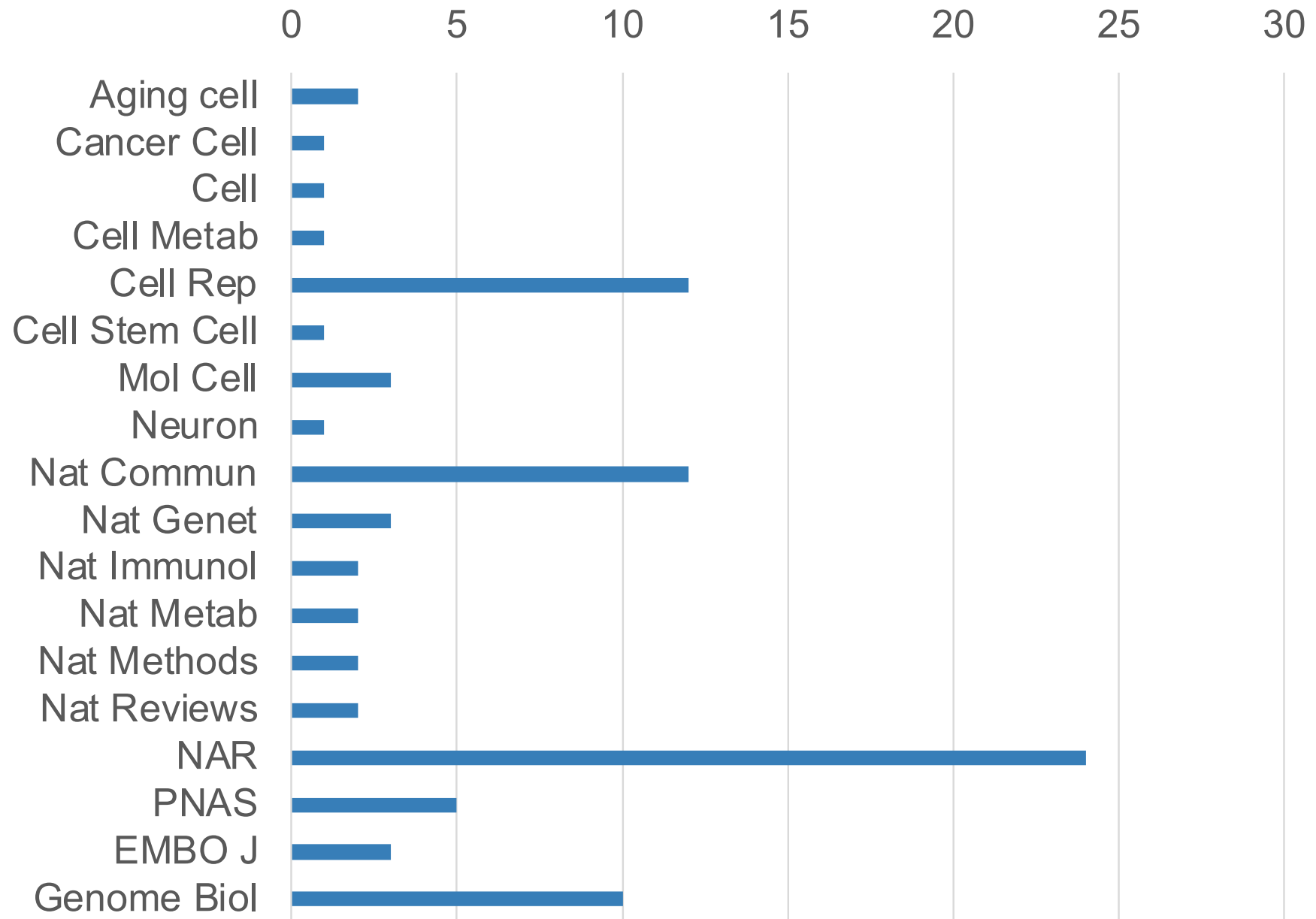
※ Google scholar で “ChIP-Atlas” を全文検索し、内容を精査した。



年々ほぼ倍増。
2/3 が海外グループ

引用論文

High impact journal にも引用されている



自分で
楽しむ

活用事例

その1

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

H. sapiens (hg19)

H.sapiens (hg38)

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Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

ファイル未選択

Choose local file

[Try with example](#)

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

薬剤投与による DEG

制御因子

薬剤投与による DEG の制御因子がわかる

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

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Breast (7459)

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Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

ファイルを選択 ファイル未選択

Choose local file

Try with example

薬剤投与による DEG

5. Enter dataset B



鄒 兆南 (DC2)

1P-0692

6. Analysis description



九州工業大学
山西 芳裕
岩田 通夫

submit

Estimated run time: 9 mins

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

[Tutorial movie ▾](#)

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[S. cerevisiae \(sacCer3\)](#)

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Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

ESR1

Choose local file

[Try with example](#)

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

Tamoxifen で
発現変化

ESR1

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

H. sapiens (hg19)

H.sapiens (hg38)

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DNase-Seq (1642)

Bisulfite-Seq (15000)

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All cell types (103765)

Adipocyte (392)

Blood (36245)

Bone (1501)

Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

ファイルを選択 ファイル未選択

Choose local file

Try with example

Testosterone で
発現変化

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

AR

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

-

5000

bp

≤

TSS

≤

+

5000

bp

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

H. sapiens (hg19)

H.sapiens (hg38)

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M. musculus (mm10)

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D. melanogaster (dm6)

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C. elegans (ce11)

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Blood (36245)

Bone (1501)

Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

ファイルを選択

ファイル未選択

Choose local file

Try with example

抗がん薬で
発現変化

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

P53

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

薬剤の作用機序に関わる因子を探る

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

Tutorial movie ▾

H. sapiens (hg19)

H.sapiens (hg38)

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M. musculus (mm10)

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DNase-Seq (1642)

Bisulfite-Seq (15000)

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All cell types (103765)

Adipocyte (392)

Blood (36245)

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Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic regions (BED) or sequence motif ⓘ

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

ファイルを選択 ファイル未選択

Choose local file

Try with example

抗てんかん薬で
発現変化

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

CHD8
ASD原因遺伝子

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

自分で
楽しむ

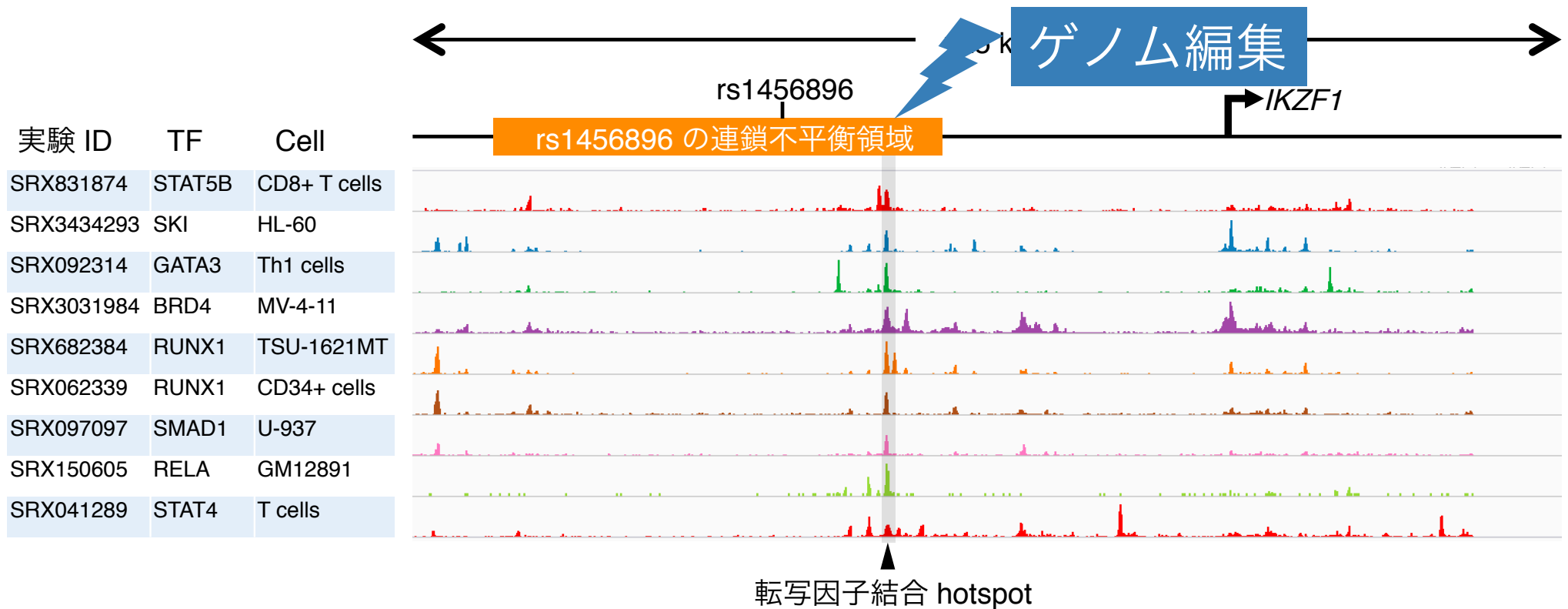
活用事例

その2

疾患の原因 SNP の予測・機能解析

GWAS で同定された疾患関連 SNP

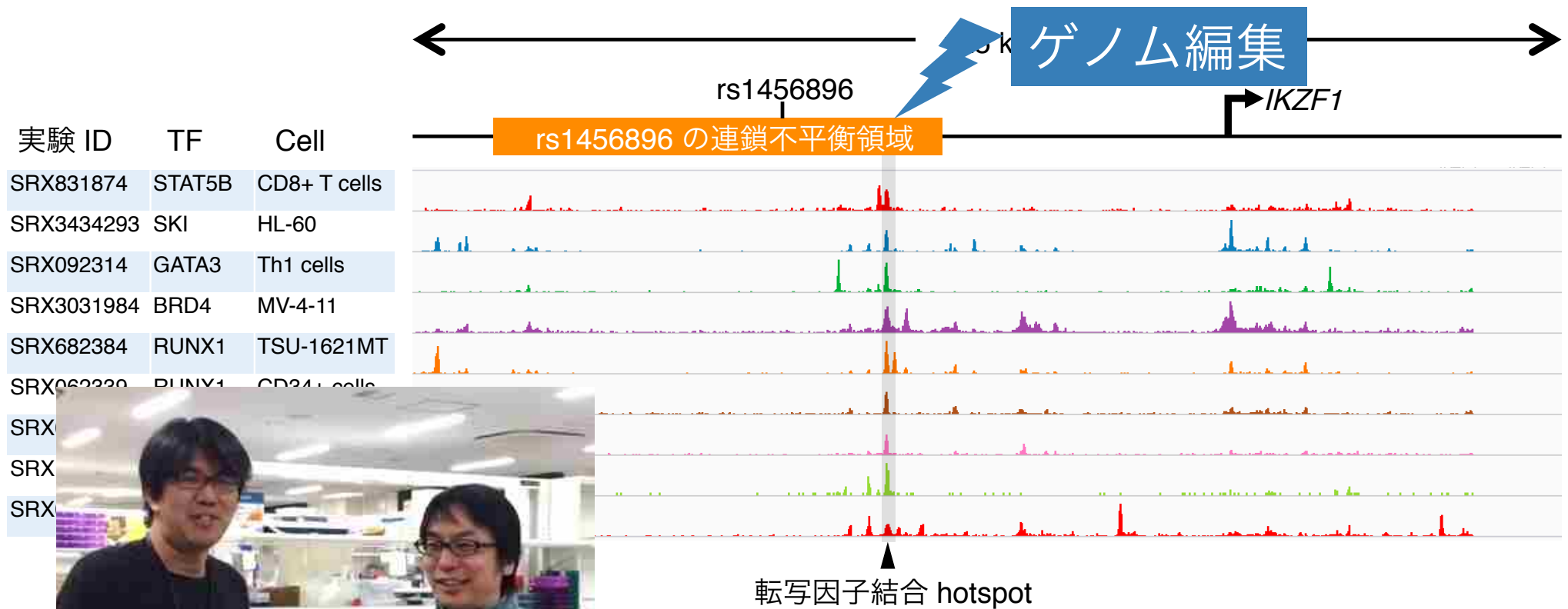
- ・ ほとんどが non-coding 領域にある
- ・ 統計学的に有意な SNP ≠ 真の原因 SNP



疾患の原因 SNP の予測・機能解析

GWAS で同定された疾患関連 SNP

- ・ ほとんどが non-coding 領域にある
- ・ 統計学的に有意な SNP ≠ 真の原因 SNP



竹本 龍也
(徳島大)

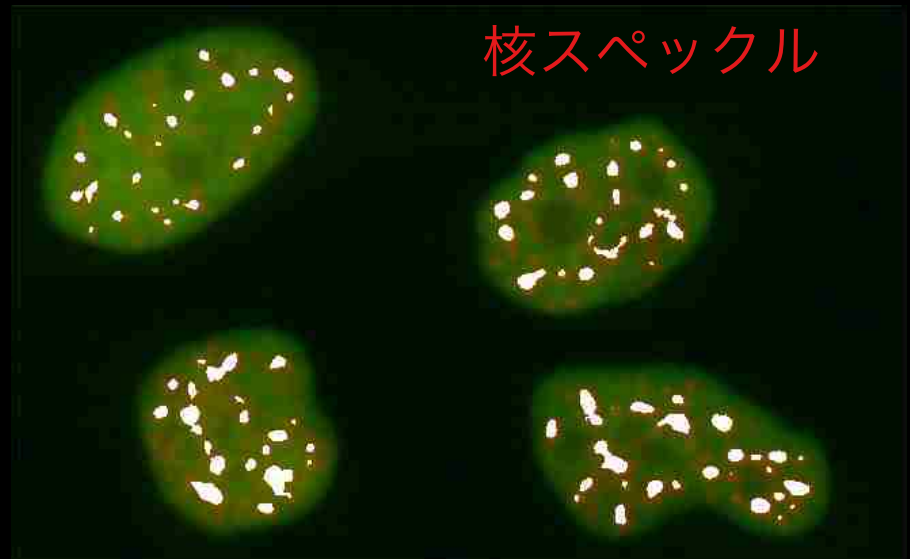
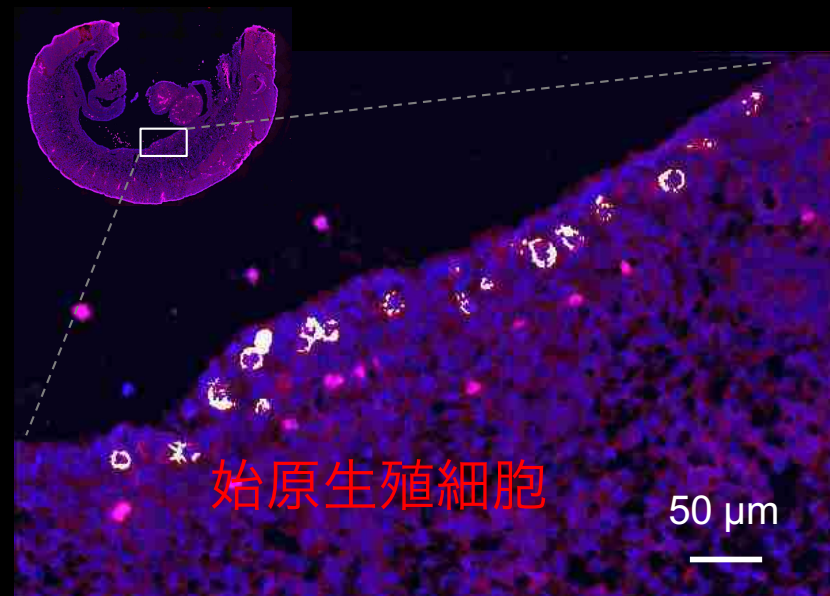
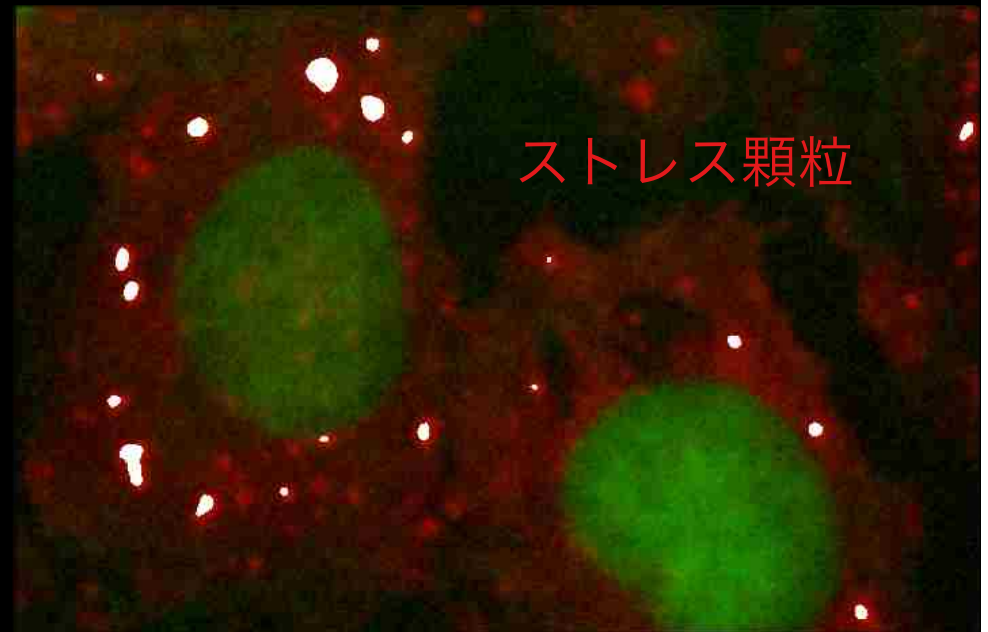
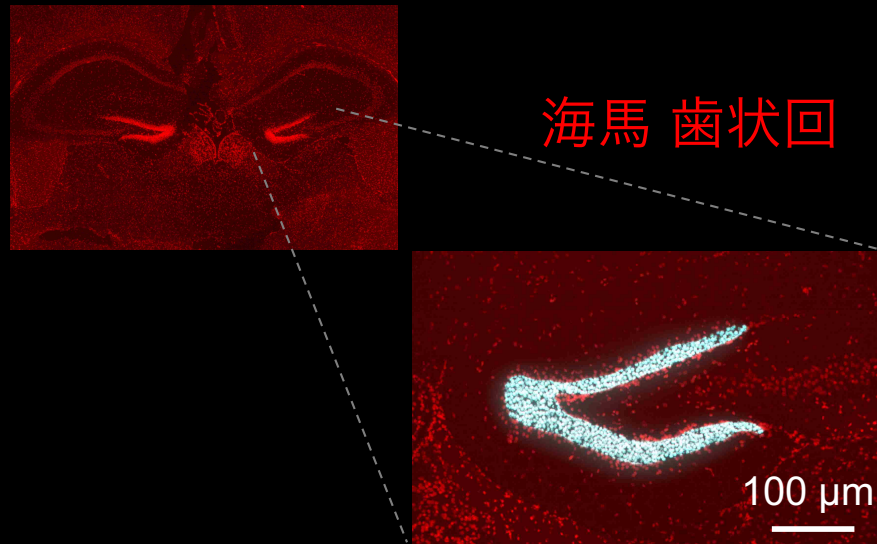
沢津橋 俊
(徳島大)

自分で
楽しむ

活用事例

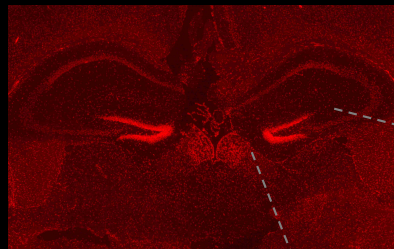
その3

PIC = Photo-Isolation Chemistry

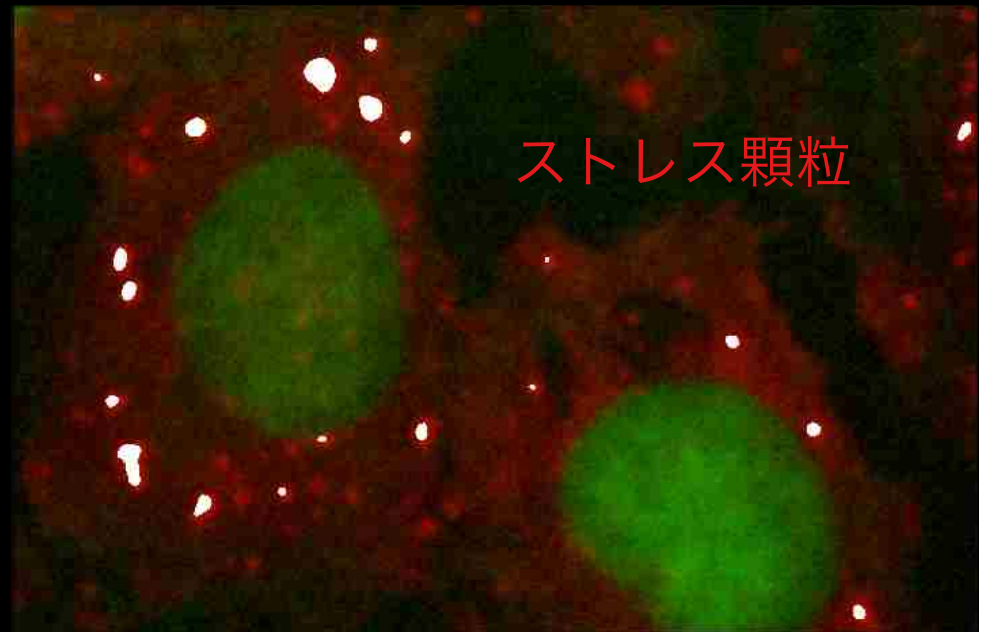
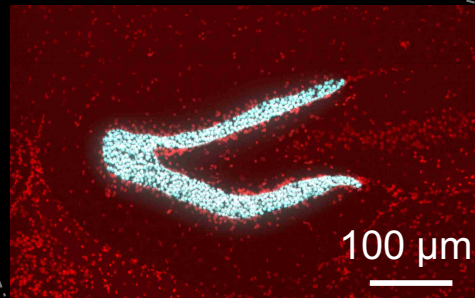


光照射領域に限定可能な RNA-seq 技術

PIC = Photo-Isolation Chemistry



海馬 歯状回



ストレス顆粒



核スペckル



本田瑞季 (助教)
2P-0708



木村龍一 (助教)
3P-0230



大川恭行 (九大)

PIC で得られた DEG の上流因子の特定

ChIP-Atlas: Enrichment Analysis

Predict proteins bound to given genomic loci and genes

[Tutorial movie ▾](#)

[H. sapiens \(hg19\)](#)

[H.sapiens \(hg38\)](#)

[M. musculus \(mm9\)](#)

[M. musculus \(mm10\)](#)

[R. norvegicus \(rn6\)](#)

[D. melanogaster \(dm3\)](#)

[D. melanogaster \(dm6\)](#)

[C. elegans \(ce10\)](#)

[C. elegans \(ce11\)](#)

[S. cerevisiae \(sacCer3\)](#)

1. Experiment type

ChIP: Histone (16612)

ChIP: RNA polymerase (2099)

ChIP: TFs and others (15155)

ChIP: Input control (8078)

ATAC-Seq (27318)

DNase-Seq (1642)

Bisulfite-Seq (15000)

2. Cell type Class

All cell types (103765)

Adipocyte (392)

Blood (36245)

Bone (1501)

Breast (7459)

Cardiovascular (2336)

Digestive tract (6151)

Embryo (728)

3. Threshold for Significance ⓘ

50

100

200

500

4. Enter dataset A

☐ Genomic region

☒ Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

Choose local file

[Try with example](#)

ROI で特異的に
発現する遺伝子

5. Enter dataset B

☒ Refseq coding genes (excluding dataset A) ⓘ

☐ Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

- 5000 bp ≤ TSS ≤ + 5000 bp

局所領域のマスター転写因子が特定できる

クローズアップ 実験法



ChIP-Atlas: 既報の ChIP-seqデータをフル活用 するためのウェブサービス

沖 真弥, 大田達郎

何ができるようになった?

論文などで報告されたすべてのChIP-seqデータ（約10万件）を閲覧できる。また、それらをフル活用したデータ解析も可能であり、転写因子と遺伝子の制御関係を知ることができる。

必要な機器・試薬・テクニックは?

MacやWindowsなどのパソコンをインターネット接続
操作のほとんどがマウスクリックで済むため、シークエン

PDF ダウンロード

https://is.gd/Oki_Lab

空間トランスクリプトームと PIC

生命を科学する 明日の医療を切り拓く

実験医学
Experimental Medicine

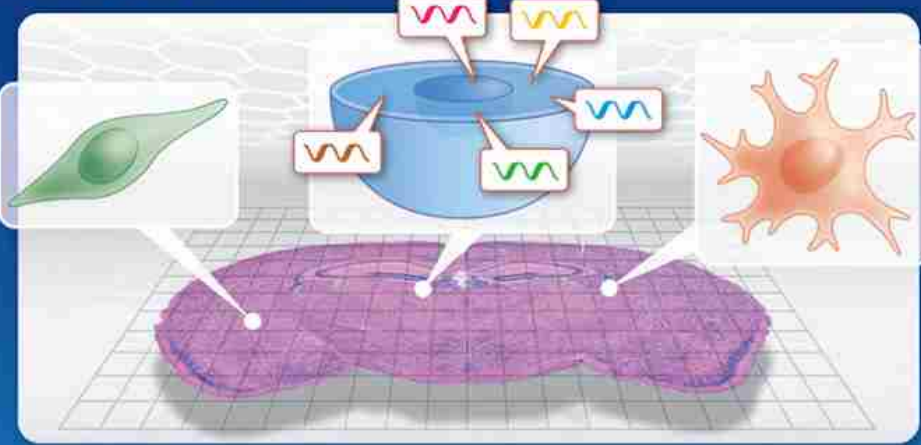
Vol.39 No.14
2021
9

特集
空間トランスクリプトーム

Spatial Transcriptome

細胞内局在から組織構成まで、遺伝子発現の位置情報がわかる!

企画／沖 真弥, 大川 恭行



いま知りたい!!
かじる? 呑み込む?
食食の多様性
トロゴサイトーシスとエフェロサイトーシス

実験法
三次元自動細胞追跡ツール:
3DeeCellTrackerで
解析できることと使い方

羊土社

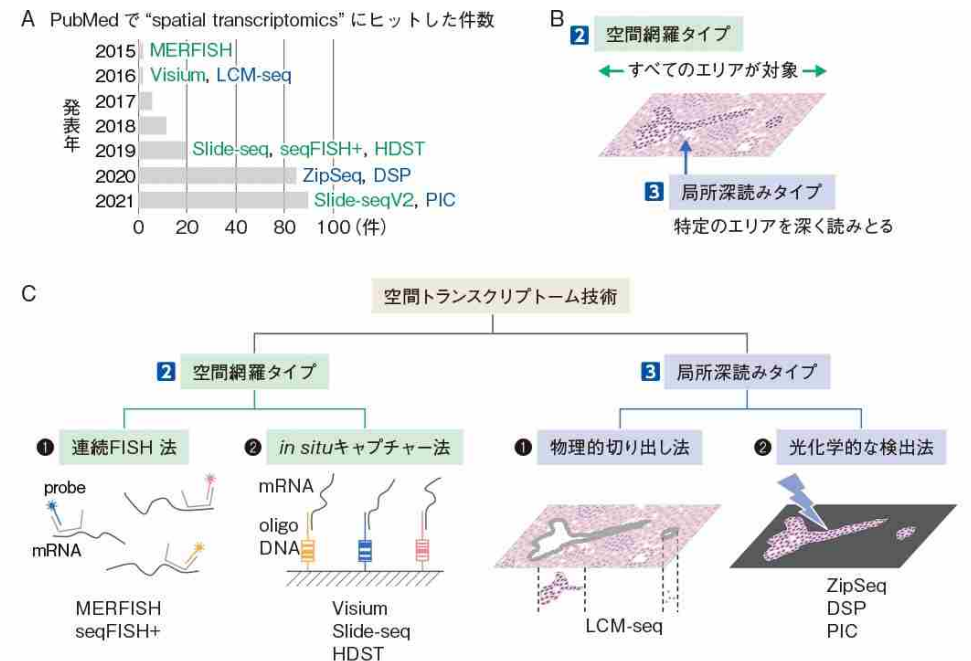


図1 空間トランスクリプトーム技術の歴史と分類

A) PubMedで“spatial transcriptomics”をサーチしたときの、発表年ごとのヒット件数とそのときに開発された技術を示す。B) 空間網羅タイプは組織の全エリアを対象とし、局所深読みタイプは特定のROIだけを対象とする。C) 空間トランスクリプトーム技術の系統。

実験医学 2021年9月号 Vol.39 No.14

PDF ダウンロード

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