



ChIP-Atlas Update

Bisulfite-seq と ATAC-seq データを統合しエピゲノム制御の全貌に迫る

京都大学 医学研究科

鄒 兆南 (ZOU Zhaonan)

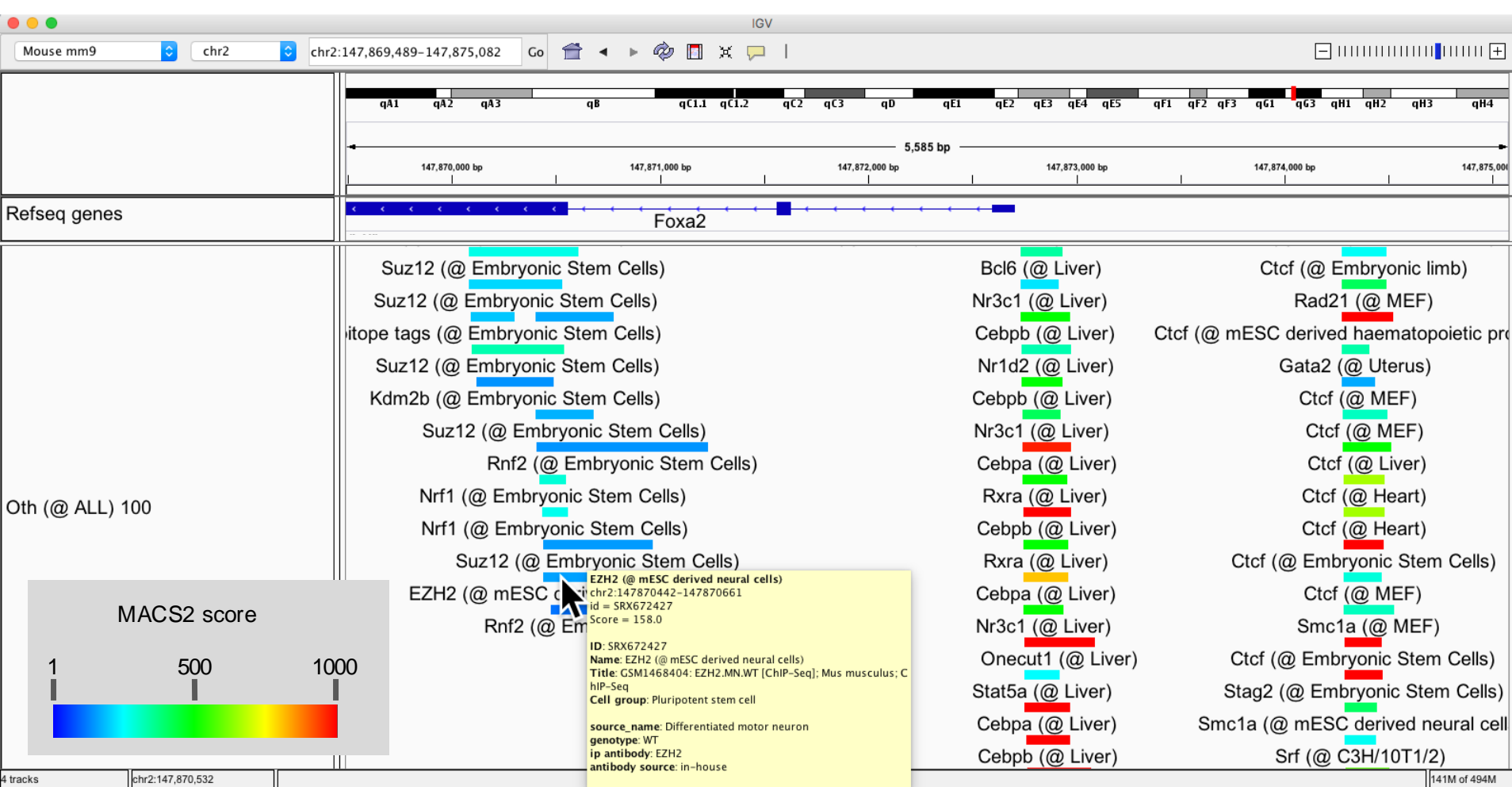


京都大学
KYOTO UNIVERSITY



京都大学大学院医学研究科
創薬医学講座
Department of Drug Discovery Medicine

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



データ処理・公開しているデータ



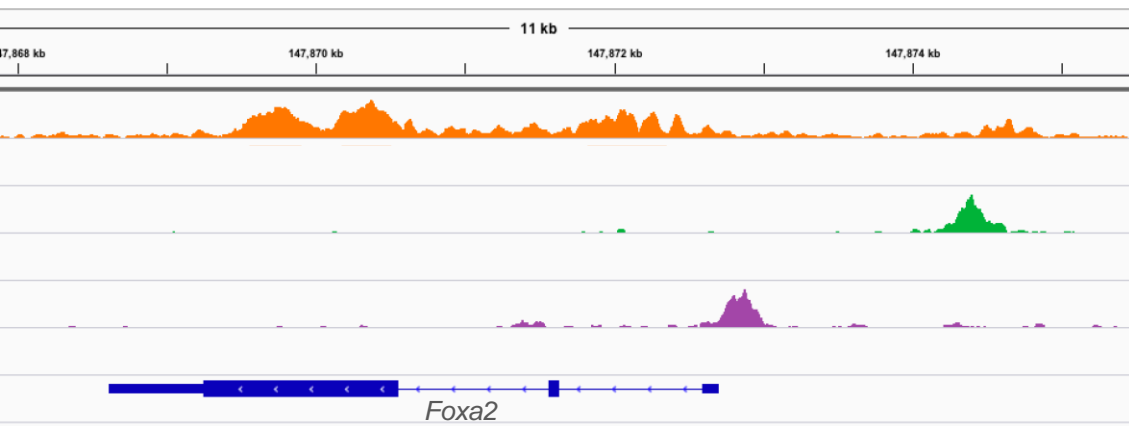
FASTQ (配列生データ)

データ処理・公開しているデータ



FASTQ (配列生データ)

Alignment

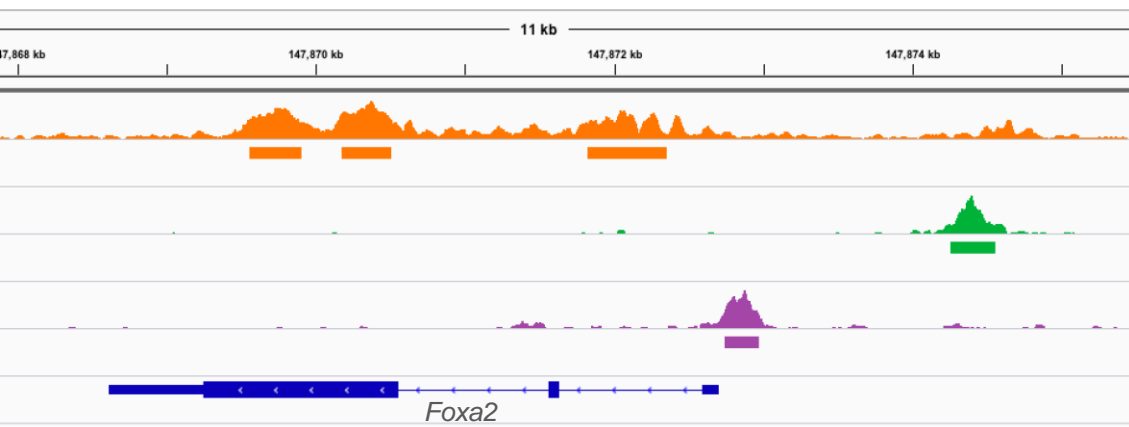


データ処理・公開しているデータ



FASTQ (配列生データ)

Alignment
Peak-call



データ処理・公開しているデータ

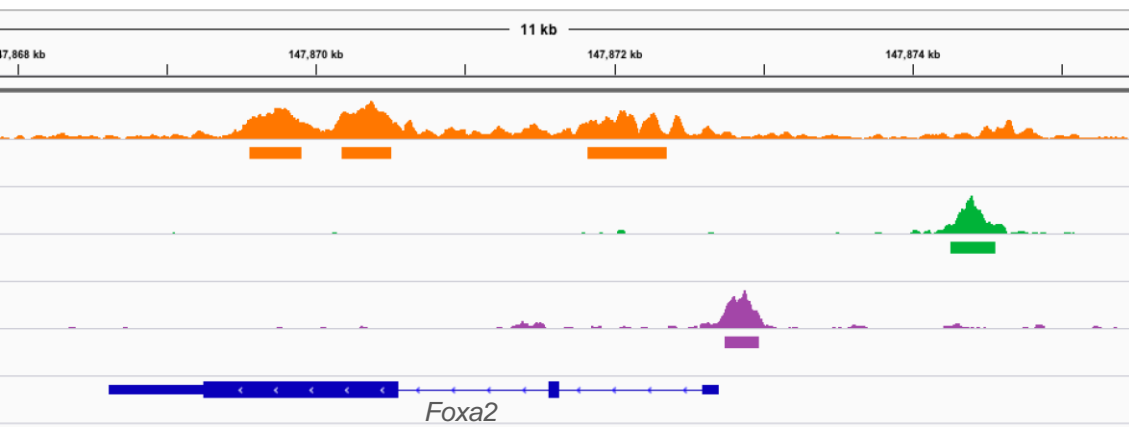


FASTQ (配列生データ)

Sample metadata

Alignment
Peak-call

Curation



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

データ処理・公開しているデータ

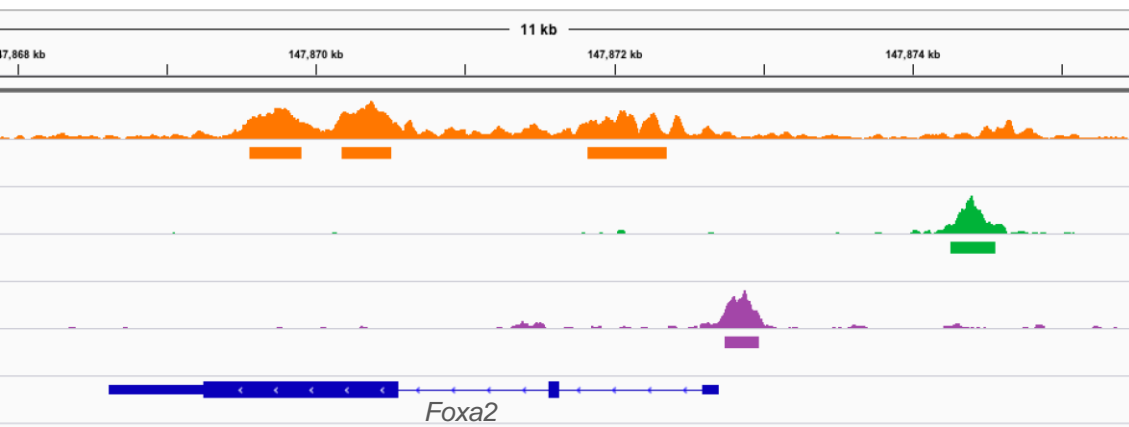


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データ統合・データマイニング



ChIP-Atlas

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[Watch movie introduction](#)

What's new

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- **New publication** on the NAR web server issue! <https://doi.org/10.1093/nar/gkac199> (2022/03/24)
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- 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](#)

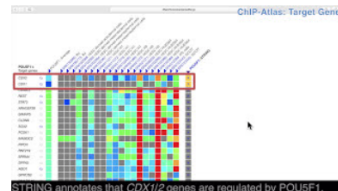
[Watch tutorial movie](#)



Target Genes

Predict target genes bound by given transcription factors

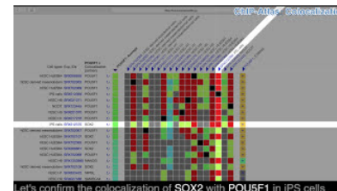
[Watch tutorial movie](#)



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

ChIP-Atlas Peak Browser Target Genes Colocalization Enrichment Analysis Publications Docs Find By ID SRX018625 Go Q Advanced

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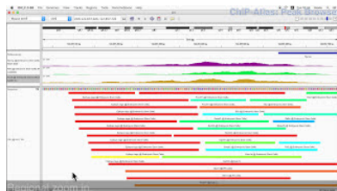
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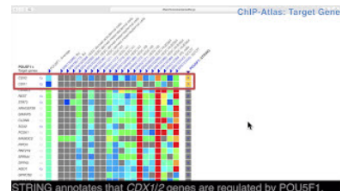
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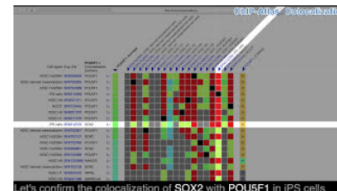
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個々のデータを探す

ChIP-Atlas: Dataset Search

Search for data by keywords

Simple search

Detailed search

Show entries

Search:

Showing 1 to 20 of 224,659 entries

Copy

TSV

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
SRX019501	SRA012529	GSM534474	hg19, hg38	Histone	H3K4me1	Adipocyte	Adipose stromal cell
SRX019502	SRA012529	GSM534475	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
SRX019503	SRA012529	GSM534476	hg19, hg38	Histone	H3K27me3	Adipocyte	Adipose stromal cell
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ゲノム

抗原

組織・細胞

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SRX019495	SRA012529	GSM534468	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
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SRX019499	SRA012529	GSM534472	hg19, hg38	Histone	H3K4me3	Adipocyte	Adipose stromal cell
SRX019500	SRA012529	GSM534473	hg19, hg38	Histone	H3K4me2	Adipocyte	Adipose stromal cell
SRX019501	SRA012529	GSM534474	hg19, hg38	Histone	H3K4me1	Adipocyte	Adipose stromal cell
SRX019502	SRA012529	GSM534475	hg19, hg38	Histone	H3K27ac	Adipocyte	Adipose stromal cell
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Detailed search

Show **20** entries

Search:

検索

Showing 1 to 20 of 224,659 entries

Copy

TSV

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個々のデータを探す

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Search for data by keywords

Simple search

Detailed search

Show entries

Search:

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

Copy

TSV

Sall4

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	GSM1892433	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
ERX1399947	ERA582745	-	mm9, mm10	TFs and others	Sall4	Pluripotent stem cell	ES cells
ERX1399948	ERA582745	-	mm9, mm10	TFs and others	Sall4	Pluripotent stem cell	ES cells

個々のデータを探す

ChIP-Atlas: Dataset Search

Search for data by keywords

Simple search

Detailed search

Show entries

Sall4

Search:

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

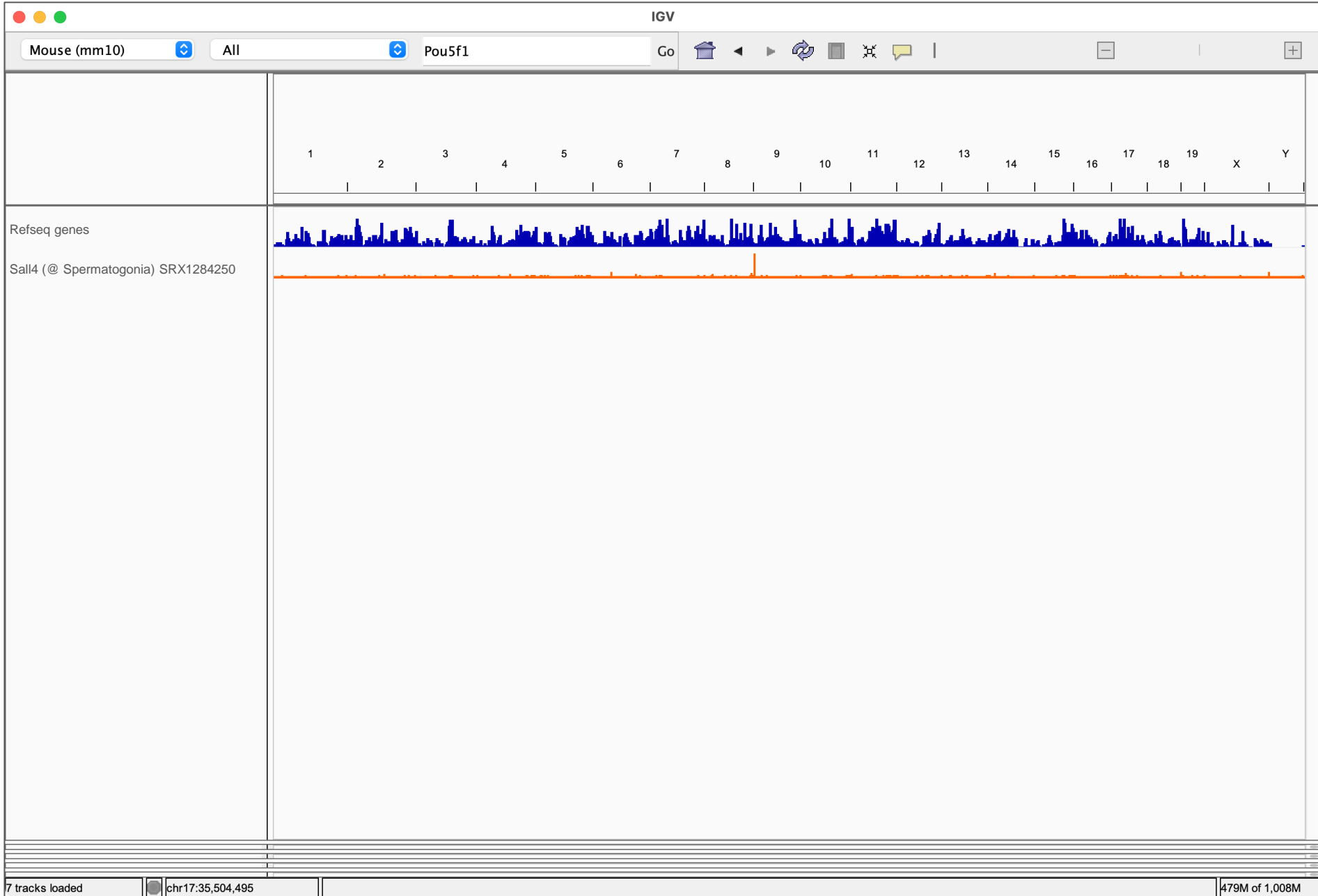
Copy

TSV

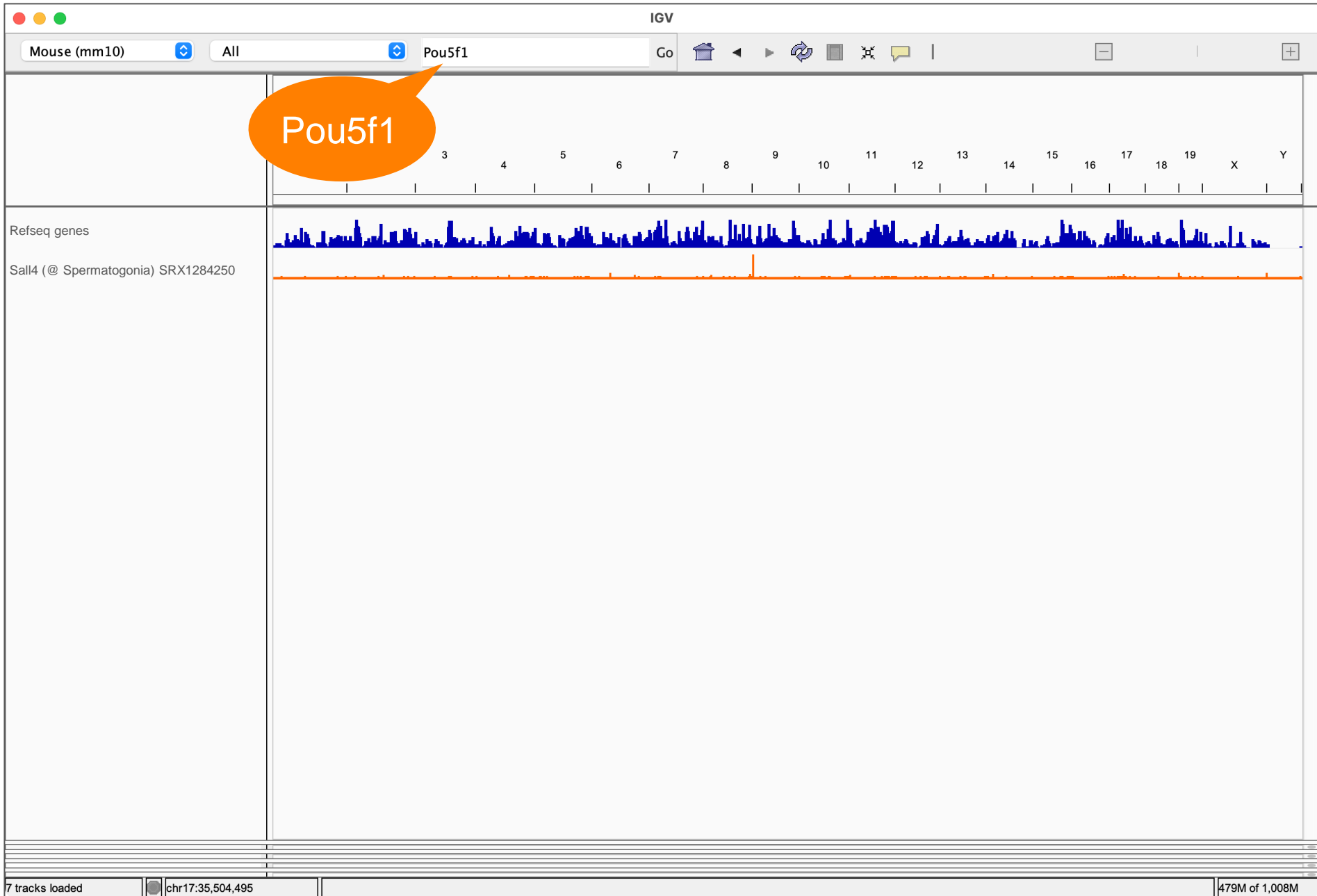
SRX1284250

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
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ERX1399948	ERA582745	-	mm9, mm10	TFs and others	Sall4	Pluripotent stem cell	ES cells

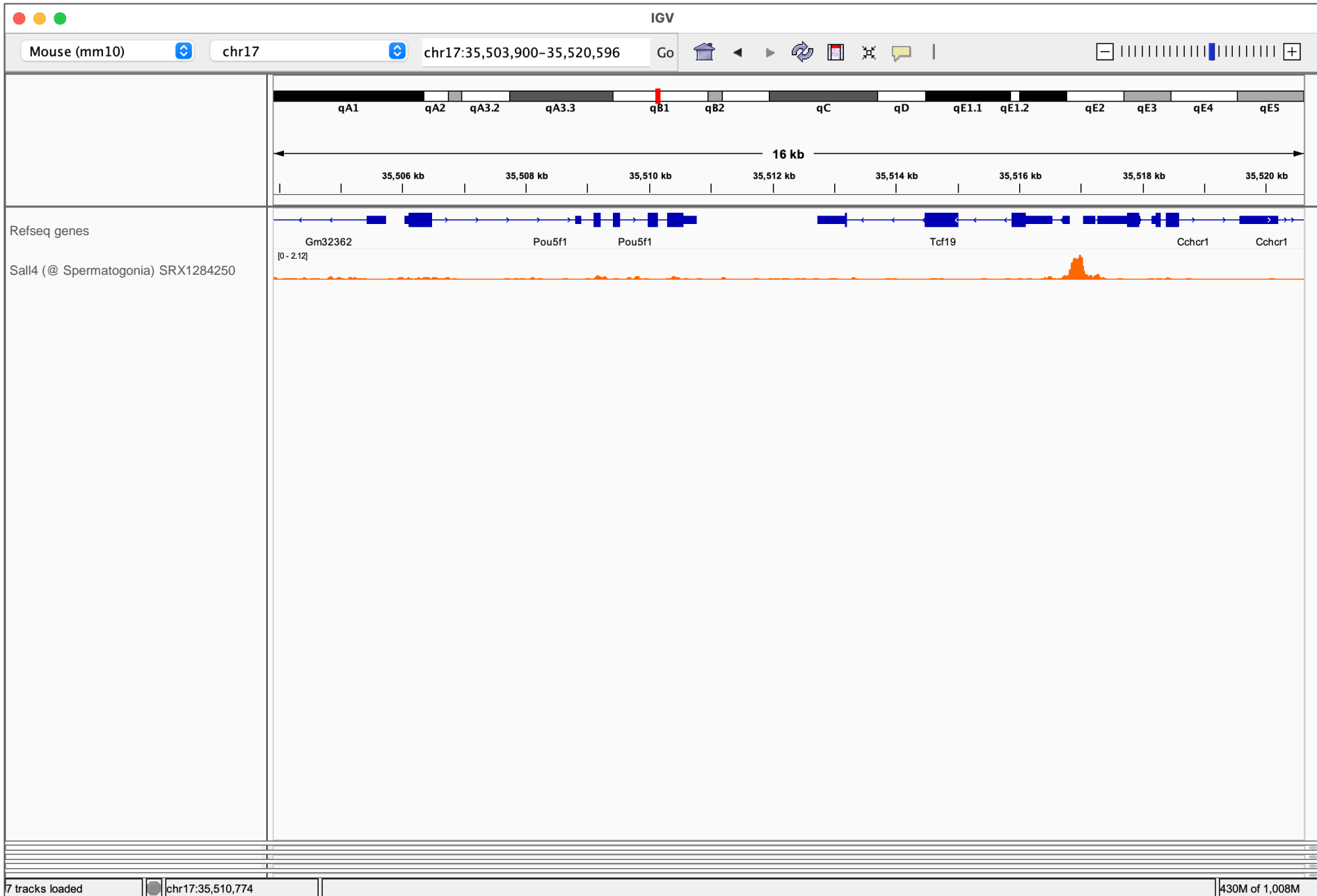
Sall4 in Spermatogonia



Sall4 in Spermatogonia



Sall4 in Spermatogonia



複数の ChIP-seq データをまとめて閲覧する

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- Added new genome assembly, hg38, hg19, hg18, hg17, hg16, hg15, hg14, hg13, hg12, hg11, hg10, hg9, hg8, hg7, hg6, hg5, hg4, hg3, hg2, hg1, hg0. Happy holidays! (2020/12/01)

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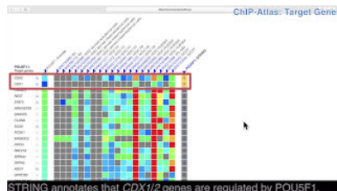
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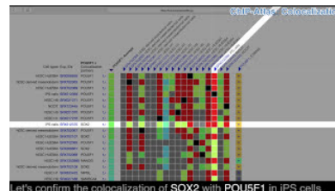
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ChIP-Atlas: Peak Browser

Tutorial movies ▾

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

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

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

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

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

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

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

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

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

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

1. Experiment type

ChIP: Histone (25969)
ChIP: RNA polymerase (2497)
ChIP: TFs and others (13156)
ChIP: Input control (7641)
ATAC-Seq (23627)
DNase-seq (1040)
Bisulfite-Seq (13409)

2. Cell type Class

Embryo (450)
Embryonic fibroblast (1067)
Epidermis (98)
Gonad (321)
Kidney (117)
Liver (940)
Lung (54)
Muscle (288)

3. Threshold for Significance ⓘ

50
100
200
500

ChIP Antigen (optional)

type to search

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

Cell type (optional)

type to search

Round spermatids (13)
Sertoli Cells (1)
Sperm (19)
Spermatids (4)
Spermatocytes (30)
Spermatogonia (25)
Testicular germ cells (8)
Testis (185)

[View on IGV](#)

Error connecting to IGV?

[Download BED file](#)

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Visualizes protein binding on given genomic loci with IGV genome browser **mm10**

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

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TFs

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Gonad

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Spermatogonia

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Gonad

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クリック

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Testicular germ cells (8)
Testis (185)

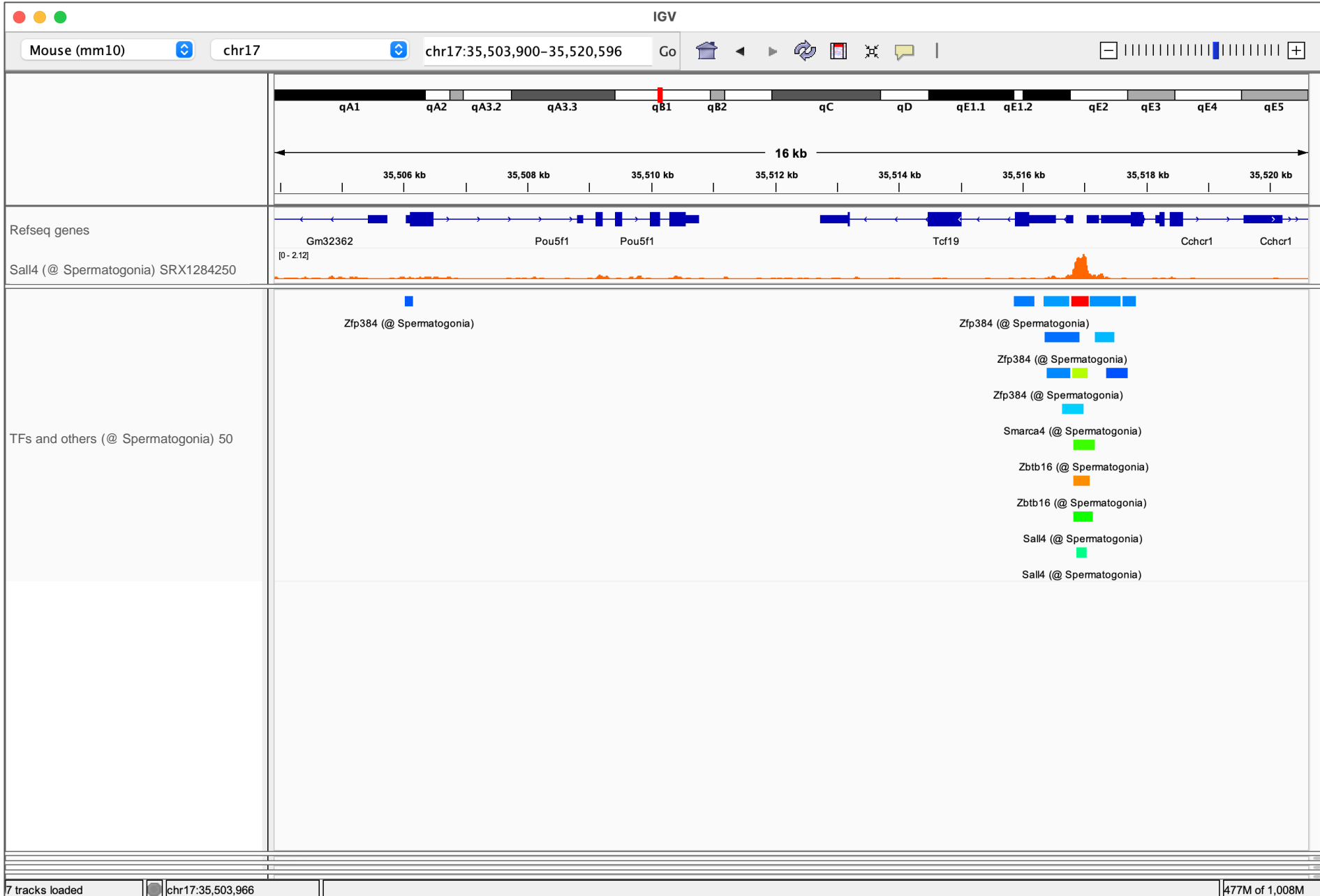
Spermatogonia

[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する



ChIP-Atlas とは

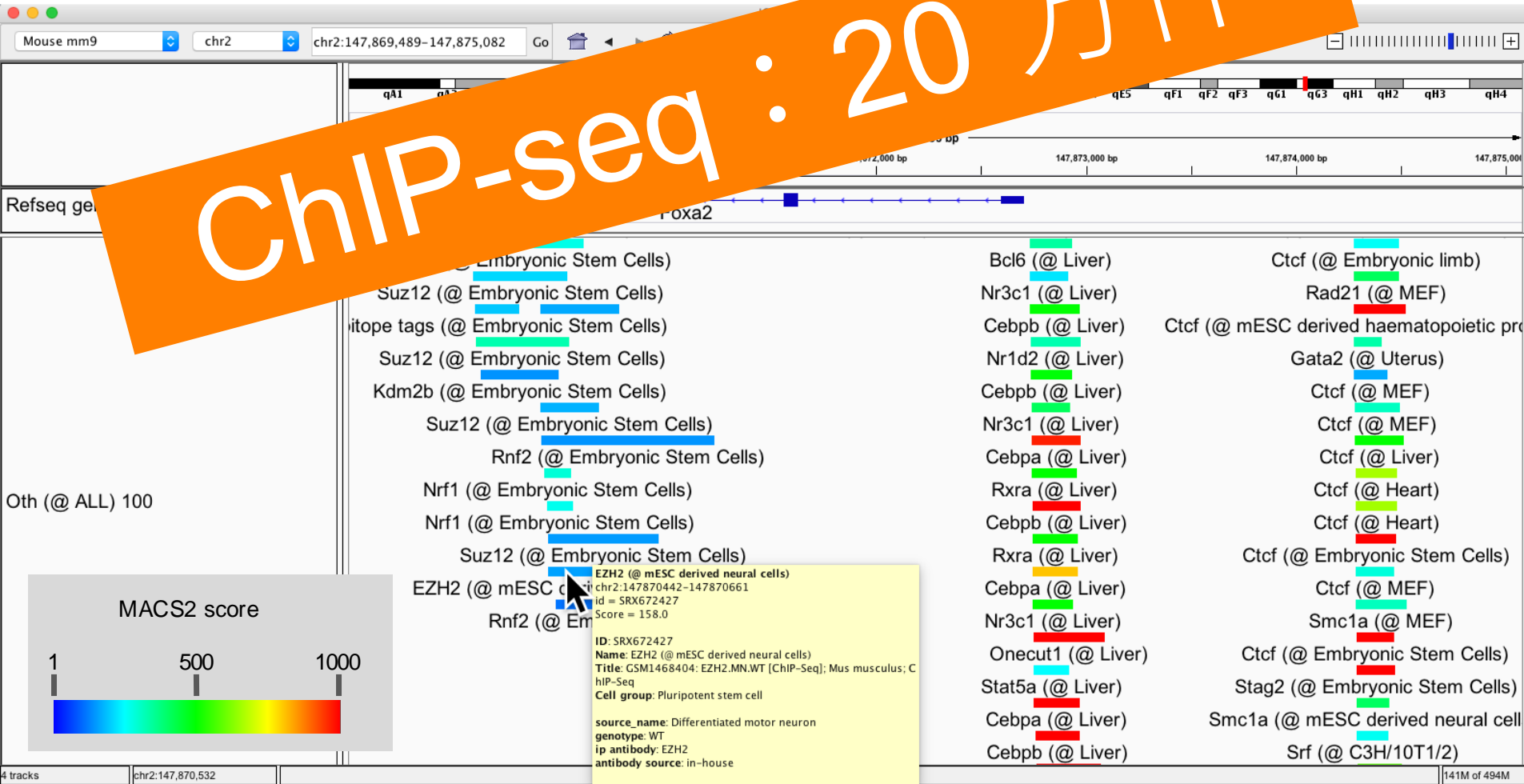


ChIP-Atlas



既報 ChIP-seq データを統合的に活用

ChIP-seq : 20 万件



ChIP-Atlas とは



ChIP-Atlas



既報 ChIP-seq データを統合的に活用

ChIP-seq : 20 万件

Bisulfite-seq : 5 万件



ChIP-Atlas とは



ChIP-Atlas



既報 ChIP-seq データを統合的に活用

ChIP-seq : 20 万件

Bisulfite-seq : 5 万件

ATAC-seq : 7 万件



ChIP-Atlas とは



ChIP-Atlas



既報 ChIP-seq データを統合的に活用

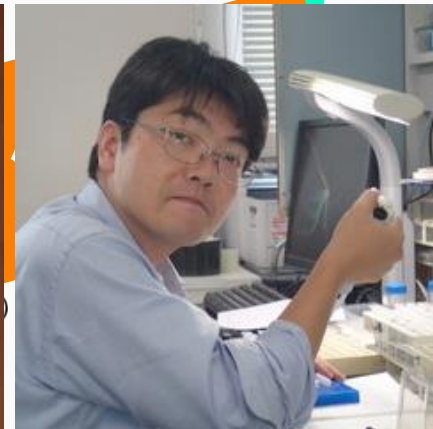
ChIP-seq : 20 万件

Bisulfite-seq : 5 万件

ATAC-seq

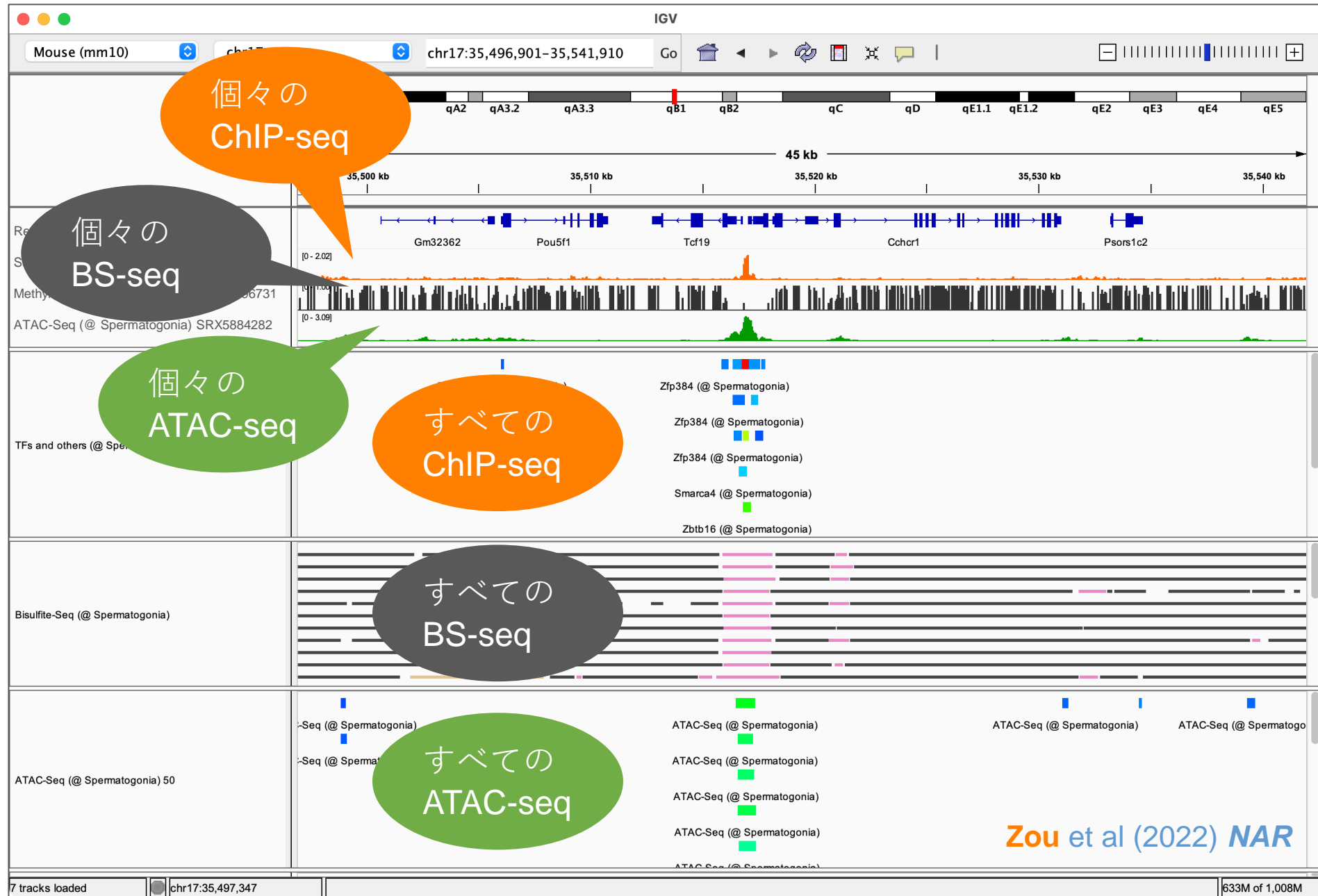


大田 達郎
(DBCLS)

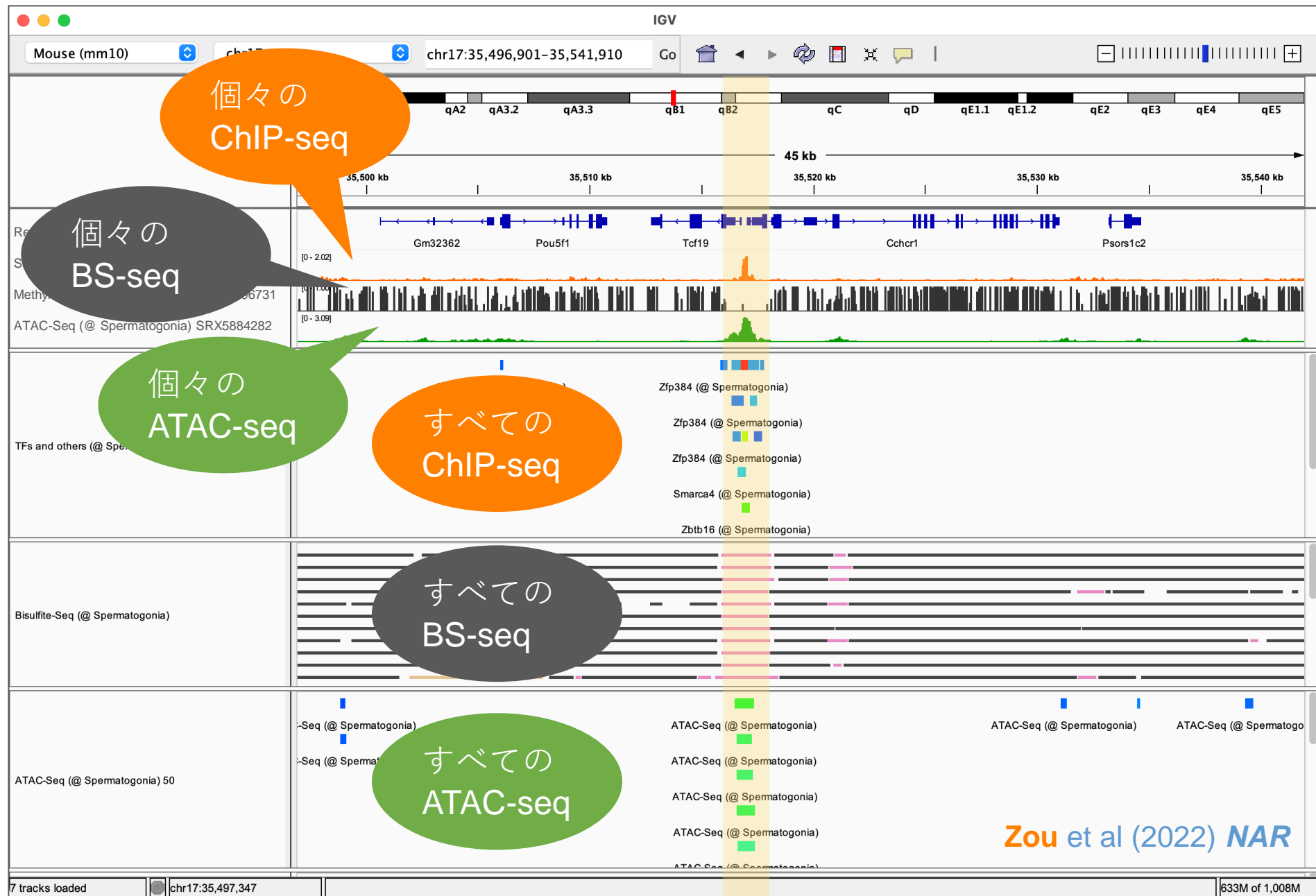


三浦 史仁
(九大)

複数のデータをまとめて見る



複数のデータをまとめて見る



個々の
ChIP-seq

個々の
BS-seq

個々の
ATAC-seq

すべての
ChIP-seq

すべての
BS-seq

すべての
ATAC-seq

Zou et al (2022) *NAR*

複数の遺伝子の制御機構を探る

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 324,000 experiments.

[Watch movie introduction](#)

What's new

- Data updated! (2022/11/30)
- **New publication** on the NAR web server issue! <https://doi.org/10.1093/nar/gkac199> (2022/03/24)
- Minor bug fix: Peak Browser / Enrichment Analysis UI updates the number of experiments by selecting experiment type (2022/03/01)
- Updated the order of the genome assembly tabs, now GRCh38 is default. And some minor fixes came together! (2022/02/08)
- 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 experiment ID
 - New information layout for individual experiment list
- Added new genome assemblies: hg38, mm10, dm6, ce11. Happy holidays! (2020/12/01)

Enrichment Analysis

Peak Browser

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

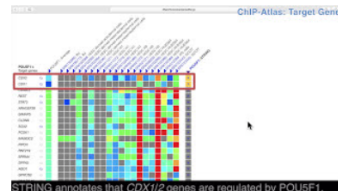
[Watch tutorial movie](#)



Target Genes

Predict target genes bound by given transcription factors

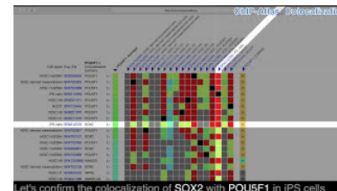
[Watch tutorial movie](#)



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](#)



複数の遺伝子の制御機構を探る

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

Predict proteins bound to given genomic loci and genes

H.sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

S. cerevisiae (sacCer3)

1. Experiment type

ChIP: Histone (16612)
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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 (15155)
Adipocyte (79)
Blood (3513)
Bone (276)
Breast (2911)
Cardiovascular (312)
Digestive tract (882)
Epidermis (427)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

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

ATP6V0E2
RARRES2
TMEM176A
SLC4A2
PRKAG2
SHH
GATA4
DLC1

好きな
遺伝子

Choose File no file selected

Choose local file

[Try with example](#)

5. Enter dataset B

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

その他の
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

submit

複数の遺伝子の制御機構を探る

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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Choose File no file selected

Choose local file

Try with example

好きな
遺伝子

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マスターレギュレーター

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 Gene list (Gene symbols) ⓘ

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Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

DEG

RNA-seq で得られた DEG の上流制御因子がわかる

薬剤の作用機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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Choose File no file selected

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 Gene list (Gene symbols) ⓘ

6. Analysis description

Analysis title ⓘ

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Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

Distance range from TSS ⓘ

薬剤投与による DEG

RNA-seq で得られた DEG の上流制御因子がわかる

薬剤の作用機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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2. Cell type Class

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Blood (3513)
Bone (276)
Breast (2911)
Cardiovascular (31)
Digestive tract (88)
Epidermis (427)

3. Threshold for Significance ⓘ

50
100
200

4. Enter dataset A

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 Gene list (Gene symbols) ⓘ

ATP6V0E2
RARRES2
TMEM176A
SLC4A2
PRKAG2
SHH
GATA4
DLC1

Choose File no file selected

5. Enter dataset B

- Refseq coding
 Gene list (Gene symbols)



山西 芳裕
(九工大)



岩田 通夫
(九工大)

薬剤投与による DEG

RNA-seq で得られた DEG の上流制御因子がわかる

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50
100
200
500

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ATP6V0E2
RARRES2
TMEM176A
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PRKAG2
SHH
GATA4
DLC1

Choose File no file selected

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

ER

薬剤の作用機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

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 Gene list (Gene symbols) ⓘ

ATP6V0E2
RARRES2
TMEM176A
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Choose File no file selected

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

Testosterone で
発現変化

AR

薬剤の作用機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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50
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 Gene list (Gene symbols) ⓘ

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Choose File no file selected

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

Valproic acid で
発現変化

CHD8

※ ASD の原因遺伝子

疾患の発症機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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50
100
200
500

4. Enter dataset A

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

```
chr8 134339107 1  
chr15 41548749  
chr15 25207262  
chr1 190561786  
chr3 14220849 142208615  
chr9 115544616 115544762  
chr15 59846350 59846560  
chr15 81109164 81109289
```

疾患 SNP

5. Enter dataset B

- Random permutation of dataset A ⓘ
Permutation times x1 x10 x100
 BED or sequence motif ⓘ

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

submit

疾患の発症機序における中心的な転写因子

疾患の発症機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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疾患 SNP

5. Enter dataset B

- Random permutation of dataset
Permutation times x1 x10
 BED or sequence motif ⓘ



伊藤 薫
(RIKEN)



宮澤 一雄
(RIKEN)

疾患の発症機序における中心的な転写因子

疾患の発症機序に関わる因子

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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chr3 14220849 142208615  
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chr15 59846350 59846560  
chr15 81109164 81109289
```

Choose File no file selected

Choose local file

心房細動
SNP

5. Enter dataset B

- Random permutation of dataset A ⓘ
Permutation times x1 x10 x100
 BED or sequence motif ⓘ

転写因子 X

6. Analysis description

Analysis title ⓘ

My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

Control

submit

Estimated run time: 5 mins

複数の遺伝子の制御機構を探る

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

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DLC1

Choose File no file selected

Choose local file

[Try with example](#)

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- Gene list (Gene symbols) ⓘ

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My project

Dataset A title ⓘ

dataset A

Dataset B title ⓘ

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- 5000 bp ≤ TSS ≤ + 5000 bp

submit

薬剤投与による DEG

薬剤の作用機序

複数の遺伝子の制御機構を探る

ChIP-Atlas: Enrichment Analysis

Tutorial movie ▾

Predict proteins bound to given genomic loci and genes

H.sapiens (hg38)

H. sapiens (hg19)

M. musculus (mm10)

M. musculus (mm9)

R. norvegicus (rn6)

D. melanogaster (dm6)

D. melanogaster (dm3)

C. elegans (ce11)

C. elegans (ce10)

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 (15155)
Adipocyte (79)
Blood (3513)
Bone (276)
Breast (2911)
Cardiovascular (312)
Digestive tract (882)
Epidermis (427)

3. Threshold for Significance ⓘ

50
100
200
500

4. Enter dataset A

- Genomic regions (BED)
- Gene list (Gene symbols)

ATP6V0E2
RARRES2
TMEM176A
SLC4A2
PRKAG2
SHH
GATA4
DLC1

Choose File no file selected

Enter dataset B

- Genomic regions (BED)
- Gene list (Gene symbols) ⓘ

6. Analysis description

My project

Dataset A title ⓘ

dataset A

Distance range from TSS ⓘ

薬剤投与による DEG

薬剤の作用機序

疾患関連 SNP

疾患の発症メカニズム

使い方のバリエーションは無限大！！

ChIP-Atlas の使い方

第6章 実験の結果を解釈する

鄒 兆南, 沖 真弥

発現解析

4. ChIP-Atlas 2.0

—転写制御機構&エピゲノムランドスケープを
可視化する

→ //chip-atlas.org

このツールでできること

- ChIP-seq, ATAC-seq, Bisulfite-seq データを縦覧する
- これらのデータをフル活用したデータマイニングをウェブブラウザ上で行う

はじめに

細胞の運命を決定する遺伝子発現は転写因子による制御を受け、そこに転写調節領域のエピゲノム状態が

(Peak Browser). そのほかに、転写因子の標的遺伝子 (Target Genes) や共局在情報 (Colocalization) を調べる機能に加え、リアルな実験データをフル活用したデータマイニングツールも用意されている (Enrichment Analysis). **2**では、Peak Browser と Enrichment Analysis の使い方について紹介する.

PDF ダウンロード

2 使

<https://is.gd/TT6Gh9>

1) P

ChIP-Atlas の使い方

出張ハンズオンセミナーやっています！！

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企業・アカデミア Welcome

ChIP-Atlas の使い方

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交通費・謝礼は不要！

企業・アカデミア Welcome

intrared: 統合的な転写制御データ基盤

NBDC

2022 年度統合化推進プログラム採択課題

ChIP-Atlas

トランス因子・エピゲノム

ChIP-Seq

転写因子
(トランス因子)
結合領域の統合データ

ATAC-Seq
Bisulfite-Seq

クロマチン状態・
DNAメチル化の情報

ENCODE
IHEC
Roadmap

エピゲノム
機能情報



fanta.bio

シスエレメント

シスエレメント
リファレンス
(ヒト・マウス・
非ヒト霊長類)

細胞種ごとの
シスエレメント活性

近接する変異
(ゲノムバリエーション)

バルク
5' RNA 配列
データ

一細胞遺伝子
発現データ

ゲノム
バリエーション
データ



開発体制

ChIP-Atlas

研究分担：沖 G (京都大)

- トランス因子・エピゲノムデータの収集
- データ更新・機能拡充



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研究代表：粕川 G (理研 IMS)

- 研究開発の取りまとめ
- ヒト・マウスのシスエレメントデータの作成
- インタフェース開発
- データベース運用



研究分担：川路 G (都医学研)

- シスエレメント同定のパイプライン開発
- 非ヒト霊長類のシスエレメントデータの作成



研究分担：梶屋 G (理研 BRC)

- ゲノム変異とシスエレメントの対応づけ
- メタデータの作成



謝辞 ※ 敬称略

ChIP-Atlas

DBCLS 大田 達郎
九大 三浦 史仁

薬効解析

九工大 山西 芳裕
九工大 岩田 通夫

疾患 SNP

RIKEN 伊藤 薫
RIKEN 宮澤 一雄

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Computing



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