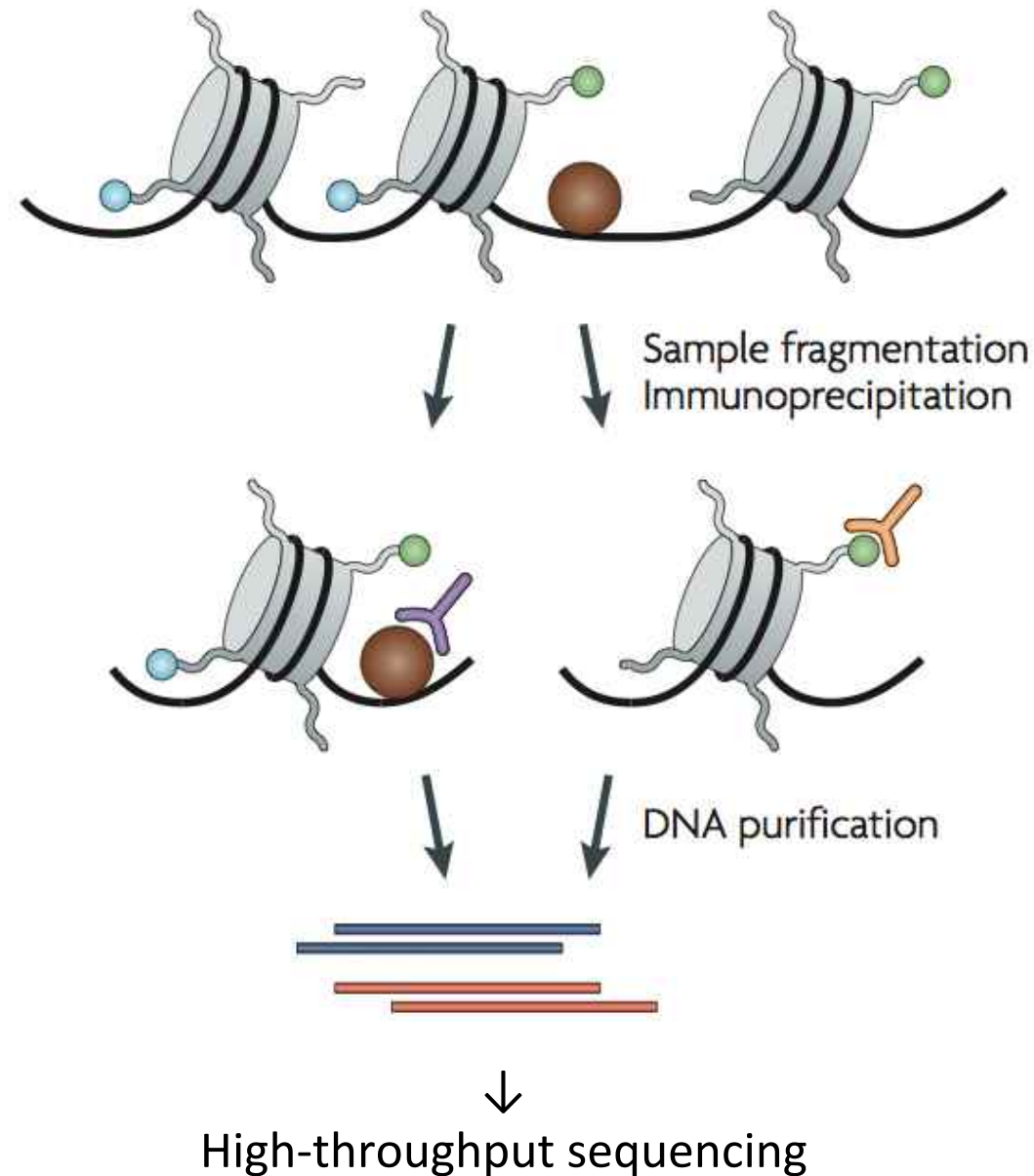


ChIP-seq SRA の統合的可視化と バイオデータベースとの連携

九州大学大学院 医学研究院
発生再生医学分野

沖 真弥





001010
010001
110110
1110

SRA (= Sequenced Read Archive)
+ メタ情報 (抗原・細胞名)

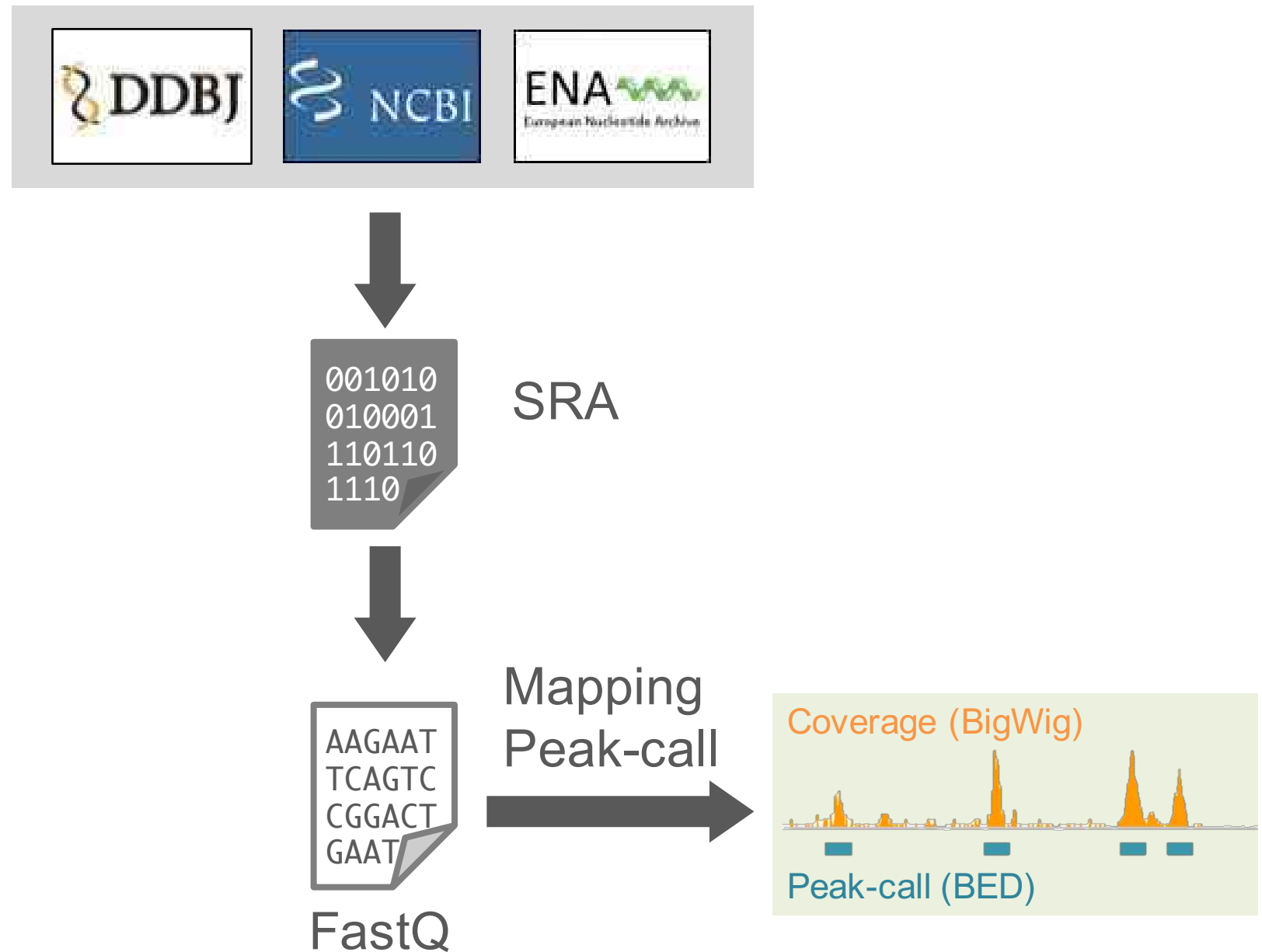
AAGAAT
TCAGTC
CGGACT
GAAT

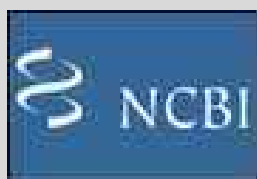
FastQ



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ChIP-seq SRA の利活用は難しい





001010
010001
110110
1110

SRA (= Sequenced Read Archive)
+ メタ情報 (抗原・細胞名)

属性	属性値
ID	SRX213809
Title	AntiGFP KD Oct4; Mus musculus; ChIP-Seq
source_name	Anti-GFP KD mESCs
strain	129S4/Svjae
phenotype	agouti
gender	male
cell type	ESC
genotype	Anti-GFP shRNA KD
chip antibody	Oct4(N-19)(sc-8628), Santa Cruz Biotechnology

AAGAAT
TCAGTC
CGGACT
GAAT

FastQ



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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 30,000 experiments.

[Watch movie introduction](#)

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](#)

in silico ChIP

predicts proteins bound to given genomic loci and genes.

[Watch Movie](#)



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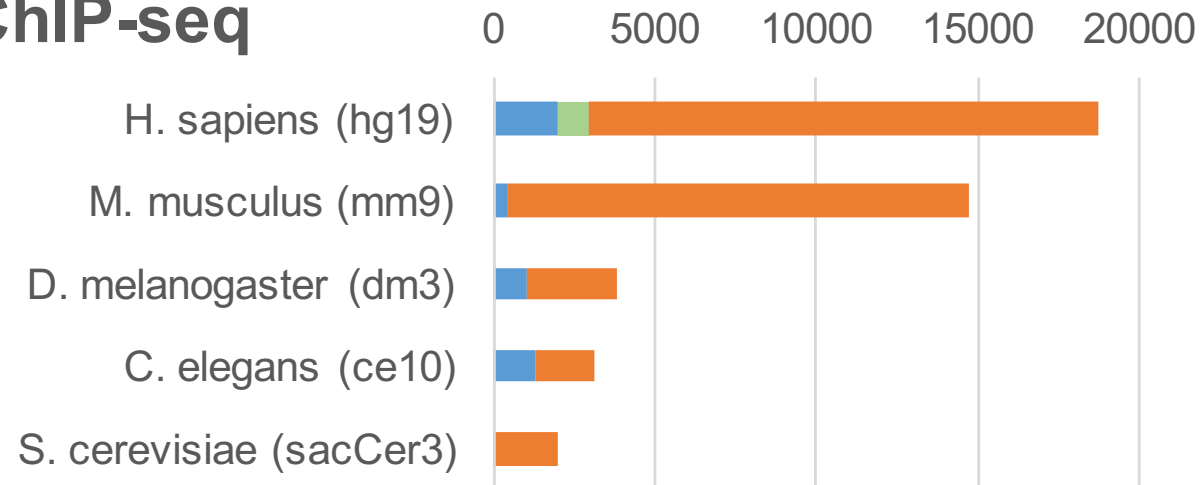
THIS WORK IS SUPPORTED BY NIG SUPERCOMPUTER SYSTEM AND NATIONAL BIOSCIENCE DATABASE CENTER.

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

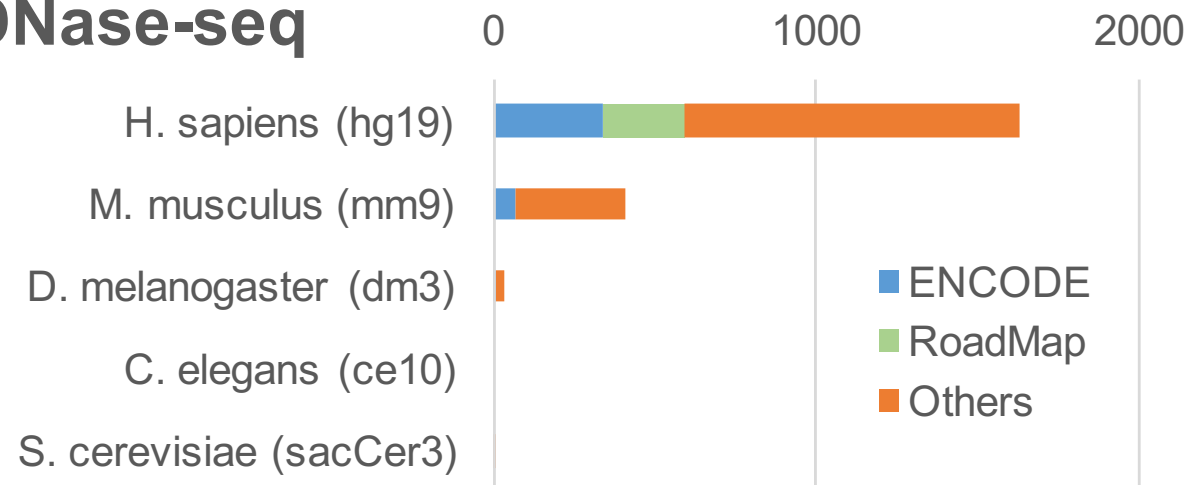
構想: 塩井 剛 氏 (RIKEN)

SRAとして登録されている ChIP-seq と DNase-seq 実験

ChIP-seq



DNase-seq





001010
010001
110110
1110

SRA

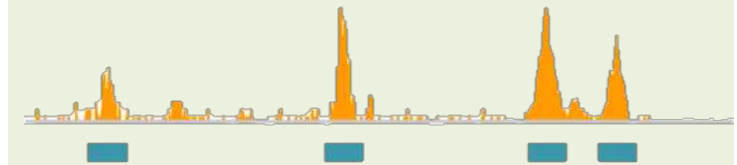
AAGAAT
TCAGTC
CGGACT
GAAT

FastQ

Mapping (bowtie2)
Peak-call (MACS2)



Coverage (BigWig)



Peak-call (BED)

BigWig

BED

サーバの提供:
畠中秀樹氏 (NBDC)



- + シーケンス 生データ
- + メタデータ

属性	属性値
ID	SRX213809
Title	AntiGFP KD Oct4; Mus musculus; ChIP-Seq
source_name	Anti-GFP KD mESCs
strain	129S4/Svjae
phenotype	agouti
gender	male
cell type	ESC
genotype	Anti-GFP shRNA KD
chip antibody	Oct4(N-19)(sc-8628), Santa Cruz Biotechnology

抗原 : Pou5f1

細胞 : Embryonic Stem Cells

属性の絞り込み

抗原 (82)

hgn
chip antibody
factor
ip antibody
ChIP
chip epitope
antibody target
target
chip antibody 1
chip antibody 2
transcription factor
antigen
chip antibody target
chip_target
epitope
chip target
antibodies
chip_or_input
modification
lymphoblast antibody
chromatin ip antibody
Immunoprecipitate
ChIPtarget

細胞 (113)

cell line
cell
ArrayExpress-CellType
CellLine
Cell type abbr.
cell_line
strain
line name
cel_line
cell-line
cells
cell lines
cell line background
cell line id
cell_line_name
cell line
cell line
cell type abbreviation
cell line/clone
Cell line
source_name
cell type
LINE

属性の絞り込み

	属性	属性値
	ID	SRX213809
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属性値の取得・結合

	属性	属性値
	ID	SRX213809
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	gender	male
細	cell type	ESC
	genotype	Anti-GFP shRNA KD
抗	chip antibody	Oct4(N-19)(sc-8628), Santa Cruz Biotechnology

↓ 結合・修正

細 129S4/Svjae | Anti-GFP KD mESCs | ESC

➡ Embryonic stem cells

抗 Oct4(N-19)(sc-8628), Santa Cruz Biotechnology | Anti-GFP KD mESCs

➡ Pou5f1

作業風景 (Google Refine)

Show as: **rows** records Show: 5 10 **25** 50 rows

« first < previous **1 - 25** next > last »

<input type="checkbox"/> All	<input type="checkbox"/> SRA	<input type="checkbox"/> SRX	<input type="checkbox"/> old	<input type="checkbox"/> new	
<input type="checkbox"/> <input type="checkbox"/>	1.	216	2716	NoAb	NoD@ NA
<input type="checkbox"/> <input type="checkbox"/>	2.	55	1018	DNase-seq	DNS@ DNase-Seq
<input type="checkbox"/> <input type="checkbox"/>	3.	1	225	LoVo	NoD@ NA
<input type="checkbox"/> <input type="checkbox"/>	4.	3	162	Anti H3K27me3	His@ H3K27me3
<input type="checkbox"/> <input type="checkbox"/>	5.	3	162	Anti H3K4me3	His@ H3K4me3
<input type="checkbox"/> <input type="checkbox"/>	6.	1	86	FC-0077	NoD@ NA
<input type="checkbox"/> <input type="checkbox"/>	10.	59	59	H3K27ac AB4729 Lymphoblastoid cell lines	His@ H3K27ac
<input type="checkbox"/> <input type="checkbox"/>	11.	51	51	H3K27Ac Lymphoblastoid Cell Lines	His@ H3K27ac
<input type="checkbox"/> <input type="checkbox"/>	12.	49	49	H3K27me3 Lymphoblastoid Cell Lines	His@ H3K27me3
<input type="checkbox"/> <input type="checkbox"/>	13.	47	47	CTCF Lymphoblastoid Cell Lines	Oth@ CTCF
<input type="checkbox"/> <input type="checkbox"/>	14.	3	46	CTCF	Oth@ CTCF
<input type="checkbox"/> <input type="checkbox"/>	15.	1	46	Anti-trimethyl-Histone H3 (Lys4) RAMOS	His@ H3K4me3
<input type="checkbox"/> <input type="checkbox"/>	16.	45	45	H3K4me3 Lymphoblastoid Cell Lines	His@ H3K4me3
<input type="checkbox"/> <input type="checkbox"/>	17.	44	44	H3K4me1 Lymphoblastoid Cell Lines	His@ H3K4me1
<input type="checkbox"/> <input type="checkbox"/>	18.	1	41	Pol II (8WG16) Lymphoblastoid Cells	Pol@ RNA polymerase II
<input type="checkbox"/> <input type="checkbox"/>	19.	40	40	H3K36me3 Lymphoblastoid Cell Lines	His@ H3K36me3
<input type="checkbox"/> <input type="checkbox"/>	20.	39	39	SA1 Lymphoblastoid Cell Lines	Oth@ STAG1
<input type="checkbox"/> <input type="checkbox"/>	21.	4	38	None	InP@ Input control
<input type="checkbox"/> <input type="checkbox"/>	22.	38	38	NFB p65 (C-20) rabbit polyclonal antibody Lymphoblastoid Cells	Oth@ RELA
<input type="checkbox"/> <input type="checkbox"/>	23.	6	34	lymphoblastoid cells	NoD@ NA
<input type="checkbox"/> <input type="checkbox"/>	26.	23	23	anti-ER (SC-543, Santa Cruz Biotechnologies) Human tumour tissue	Oth@ ESR1
<input type="checkbox"/> <input type="checkbox"/>	28.	21	21	normal mouse IgG Lymphoblastoid Cells	InP@ Input control
<input type="checkbox"/> <input type="checkbox"/>	29.	20	20	normal rabbit IgG Lymphoblastoid Cells	InP@ Input control

ルール（転写因子名）

Official gene symbol に統一

ヒト	HUGO
マウス	MGI
ハエ	FlyBase
線虫	WormBase
酵母	SGD

例：Oct4 → Pou5f1

ルール (細胞名)

Official symbol がないので、以下の表記に準拠

Yu 2014 Nature

Cell line nomenclature の提唱

ATCC

世界最大の cell line バンク

ENCODE

MeSH

米国国立医学図書館の生命科学用語集

MDA-MB-231

MDA-MB231

MDAMB-231

MDAMB231



MDA-MB-231

Curator for ChIP-Atlas

Select a curation type

Antigens ▾

hg19 ▾

Intial settings:

Judge settings:

Excluded strings:

Result:

Manual annotation

TFs and others ▾

Search from histories

Serach from: After Before Resource

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 30,000 experiments.

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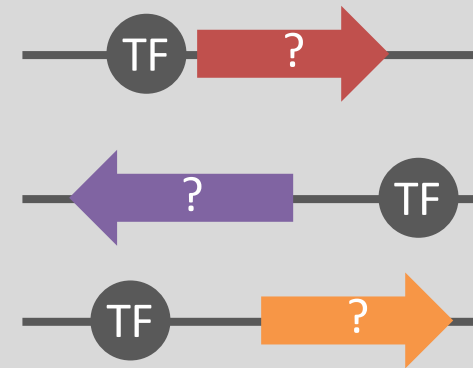
Web UI, そのほか多方面での協力: 大田達郎 氏 (DBCLS)

Peak Browser

① Peak Browser
どこに何が結合する？

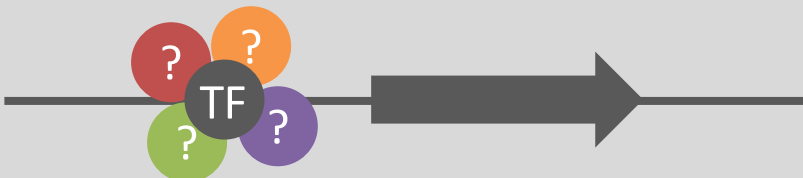


② Target Genes
標的遺伝子は？

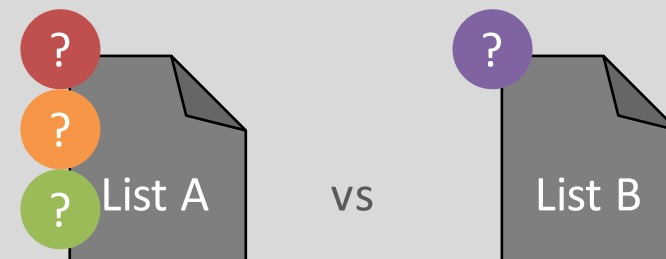


ChIP-Atlas

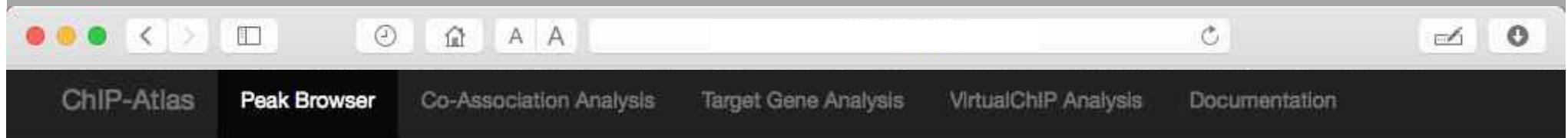
③ Colocalization
共局在パートナーは？



④ in silico ChIP
ユーザデータの解析



Peak Browser



ChIP-Atlas

[Tutorial movies ▾](#)

Visualize All Peaks from Published ChIP-Seq data.

[H. sapiens](#)
[M. musculus](#)
[D. melanogaster](#)
[C. elegans](#)
[S. cerevisiae](#)

Antigen Class

- All antigens (13732)
- DNase-seq (910)
- Histone (3117)
- RNA polymerase (532)
- TFs and others (4321)**
- Input control (1669)
- Unclassified (302)
- No description (2881)

Cell type Class

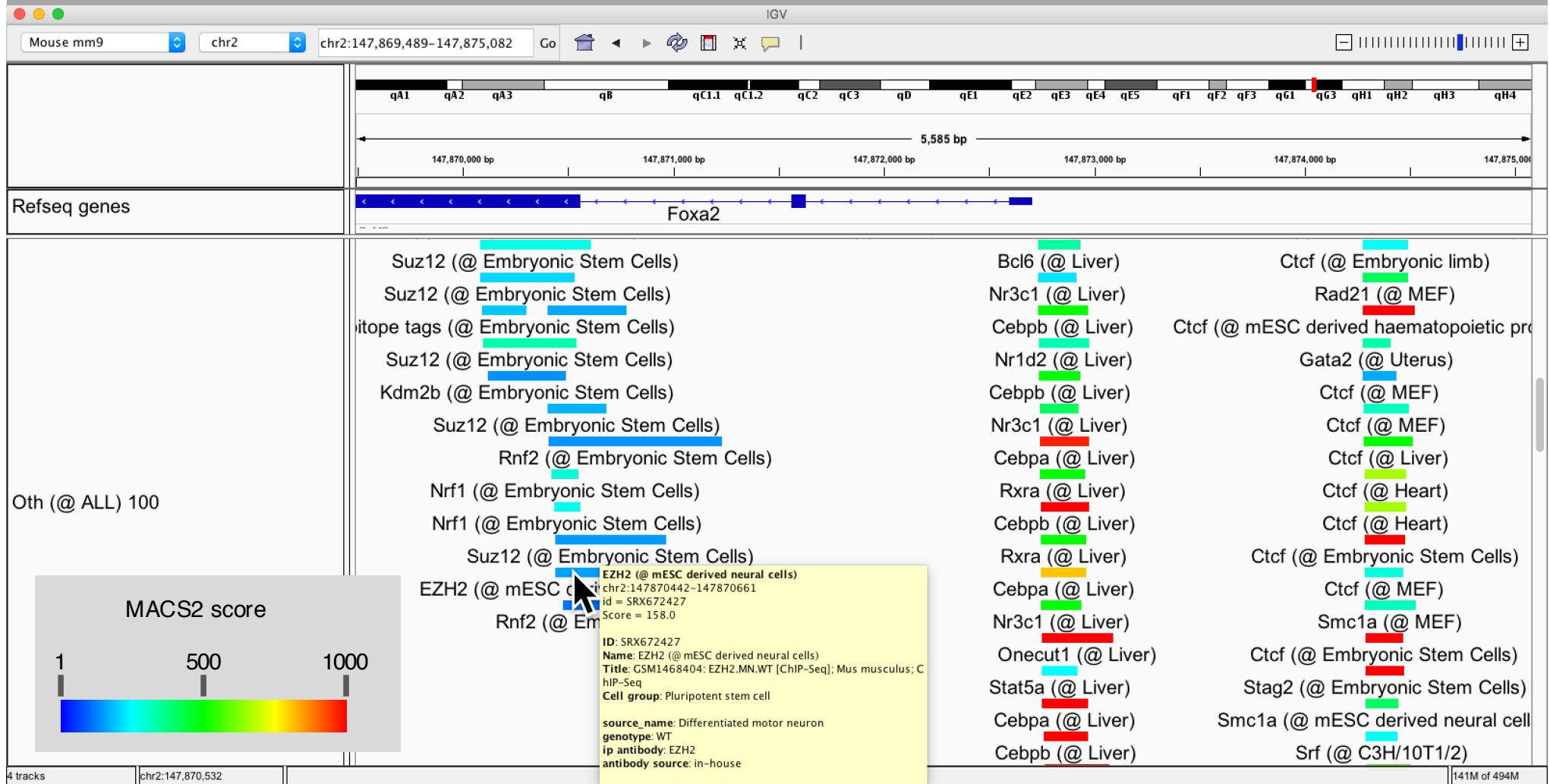
- All cell types (13732)**
- Adipocyte (80)
- Blood (3737)
- Bone (180)
- Breast (1362)
- Cardiovascular (480)
- Digestive tract (1106)
- Epidermis (391)

Threshold for Significance

- 50
- 100**
- 200
- 500

[View on IGV](#)

Peak Browser



SRX015142
GSM487427: K562 Myc ChIPSeq

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

Curated Sample Data

Genome	hg19
Antigen Class	TFs and others
Antigen	MYC
Cell type Class	Blood
Cell type	K-562

Cell type information

Primary Tissue	Blood
Tissue Diagnosis	Leukemia Chronic Myelogenous

Attributes by Original Data Submitter

source_name	K562
biomaterial_provider	cellBiology
growth_properties	Suspension Morphology
lymphoblast_antibody	Myc

Metadata from Sequence Read Archive

Library Description

library_name	K562_Myc_ChIPSeq
library_strategy	ChIP-Seq
library_source	GENOMIC
library_selection	ChIP

Platform Information

instrument_model	Illumina Genome Analyzer
------------------	--------------------------

External Database Query

Query antigen: MYC [WikiGenes](#) [PubMed](#) [PDB](#)

Query cell-type: K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)

Logs in read processing pipeline

Number of total reads	11974409
Reads aligned (%)	85.3
Duplicates removed (%)	3.8
Number of peaks	13041 (qval < 1E-05)

Sequence Quality Data from DBCLS SRA

SRR032509_fastqc SRR032510_fastqc

Curated Sample Data

Genome	hg19
Antigen Class	TFs and others
Antigen	MYC
Cell type Class	Blood
Cell type	K-562

SRX015142

GSM487427: K562 Myc ChIPSeq

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Curated Sample Data

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Antigen MYC
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Cell type K-562

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Primary Tissue Blood
Tissue Diagnosis Leukemia Chronic Myelogenous

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growth_properties Suspension Morphology
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library_source GENOMIC
library_selection CHIP

Platform Information

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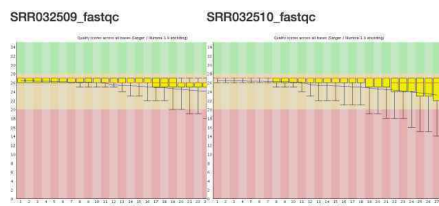
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Query cell-type: K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)

Logs in read processing pipeline

Number of total reads 11974409
Reads aligned (%) 85.3
Duplicates removed (%) 3.8
Number of peaks 13041 (qval < 1E-05)

Sequence Quality Data from DBCLS SRA



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source_name K562
biomaterial_provider cellBiology
growth_properties Suspension Morphology
lymphoblast_antibody Myc

SRX015142

GSM487427: K562 Myc ChIPSeq

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

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Antigen MYC
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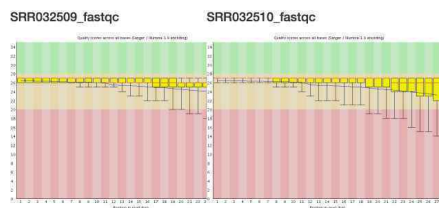
External Database Query

Query antigen MYC [WikiGenes](#) [PosMed](#) [PDBj](#)
Query cell-type K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)

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SRX015142

GSM487427: K562 Myc ChIPSeq

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library_selection ChIP

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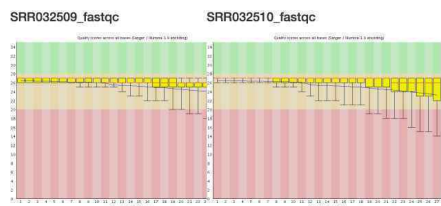
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Sequence Quality Data from DBCLS SRA



External Database Query

Query antigen MYC [WikiGenes](#) [PosMed](#) [PDBj](#)
Query cell-type K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)

統合化推進プログラムの データベース

SRX015142
GSM487427: K562 Myc ChIPSeq

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Curated Sample Data

Genome hg19
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Antigen MYC
Cell type Class Blood
Cell type K-562

Cell type information

Primary Tissue Blood
Tissue Diagnosis Leukemia Chronic Myelogenous

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biomaterial_provider cellBiology
growth_properties Suspension Morphology
lymphoblast antibody Myc

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library_selection ChIP

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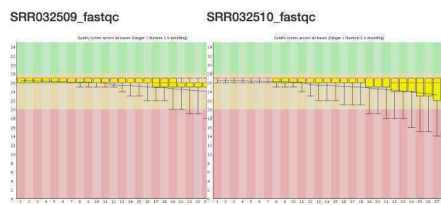
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External Database Query

Query antigen: MYC [WikiGenes] [PosMed] [PDBj]
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<http://pdbj.org/mine/search?query=MYC>

The screenshot shows the PDBj search results for the query 'MYC'. The search bar contains 'MYC' and the results are filtered to show 151 PDB entries, 1 webpage, 2 status searches, and 2 compound searches. Two results are highlighted:

- 1NKP: CRYSTAL STRUCTURE OF MYC-MAX RECOGNIZING DNA**
分子名称: Myc proto-oncogene protein/Max protein/DNA
著者: Nair, S.K., Burley, S.K.
登録日: 2003-01-03
公開日: 2003-02-04
最終更新日: 2009-02-24
実験手法: X-RAY DIFFRACTION (1.8 Å)
主引用文献: X-ray structures of Myc-Max and Mad-Max recognizing DNA: Molecular bases of regulation by proto-oncogenic transcription factors Cell(Cambridge,Mass.), 112, 2003
- 1MVO: NMR STRUCTURE OF THE TUMOR SUPPRESSOR BIN1: ALTERNATIVE SPLICING IN MELANOMA AND INTERACTION WITH C-MYC**
分子名称: Myc box dependent interacting protein 1, C-MYC
著者: Pineda-Lucena, A., Arrowsmith, C.H.
登録日: 2002-09-24
公開日: 2003-09-30
最終更新日: 2009-12-08
実験手法: SOLUTION NMR
主引用文献: A structure-based model of the c-Myc/Bin1 protein interaction shows alternative splicing of Bin1 and c-Myc phosphorylation are key binding determinants. J.Mol.Biol., 351, 2005

SRX015142

GSM487427: K562 Myc ChIPSeq

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Curated Sample Data

Genome hg19
Antigen Class TFs and others
Antigen MYC
Cell type Class Blood
Cell type K-562

Cell type information

Primary Tissue Blood
Tissue Diagnosis Leukemia Chronic Myelogenous

Attributes by Original Data Submitter

source_name K562
biomaterial_provider cellBiology
growth_properties Suspension Morphology
lymphoblast antibody Myc

Metadata from Sequence Read Archive

Library Description

library_name K562_Myc_CHIPSeq
library_strategy ChIP-Seq
library_source GENOMIC
library_selection ChIP

Platform Information

instrument_model Illumina Genome Analyzer

External Database Query

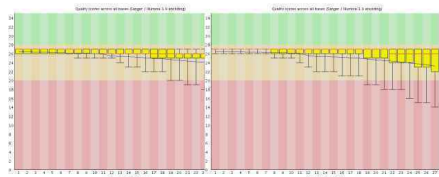
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Sequence Quality Data from DBCLS SRA

SRR032509_fastqc SRR032510_fastqc



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Query cell-type: K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)



<http://www2.brc.riken.jp/lab/cell/list.cgi?key=K-562>

CELL SEARCH SYSTEM

Items 2

[Search](#)

細胞番号	細胞名
RCB1197	P2UR/K-562
RCB1635	K-562

[ページTOP](#)

[View Cart](#)



Search キーワード K-562

[検索](#)

[クリア](#)

[← back](#)

RIKEN BioResource Center
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当HP掲載の記事・写真の無断転載を禁じます。

SRX015142

GSM487427: K562 Myc ChIPSeq

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growth_properties Suspension Morphology
lymphoblast_antibody Myc

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Library Description

library_name K562_Myc_ChIPSeq
library_strategy ChIP-Seq
library_source GENOMIC
library_selection CHIP

Platform Information

instrument_model Illumina Genome Analyzer

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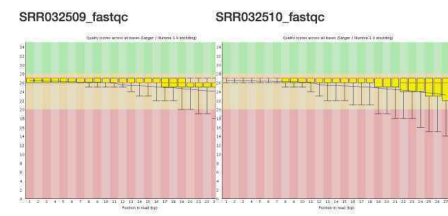
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Number of total reads 11974409
Reads aligned (%) 85.3
Duplicates removed (%) 3.8
Number of peaks 13041 (qval < 1E-05)

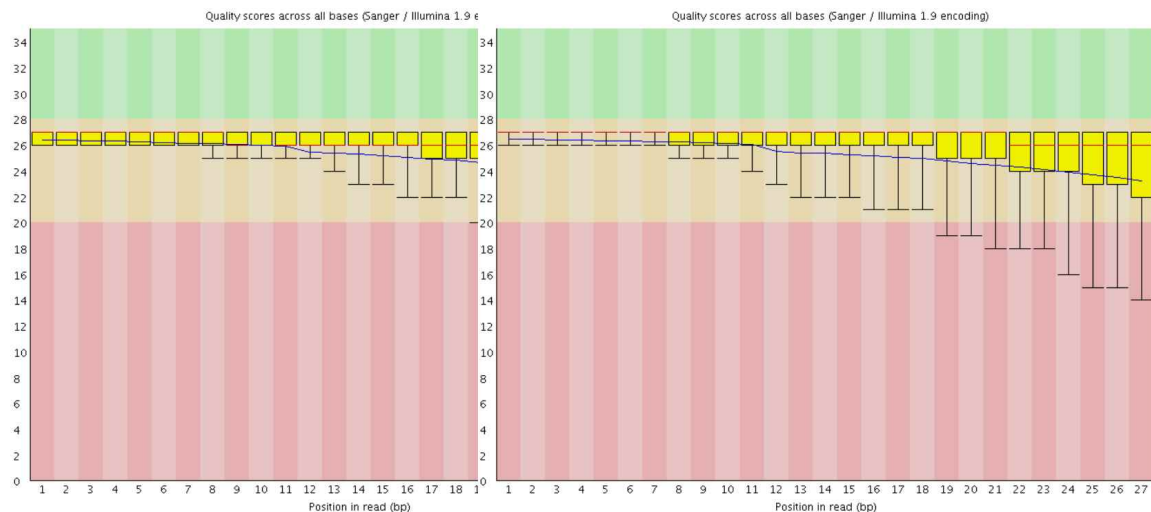
Sequence Quality Data from DBCLS SRA



Sequence Quality Data from DBCLS SRA

SRR032509_fastqc

SRR032510_fastqc



SRX015142

GSM487427: K562 Myc ChIPSeq

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

Curated Sample Data

Genome hg19
Antigen Class TFs and others
Antigen MYC
Cell type Class Blood
Cell type K-562

Cell type information

Primary Tissue Blood
Tissue Diagnosis Leukemia Chronic Myelogenous

Attributes by Original Data Submitter

source_name K562
biomaterial_provider cellBiology
growth_properties Suspension Morphology
lymphoblast_antibody Myc

Metadata from Sequence Read Archive

Library Description

library_name K562_Myc_ChIPSeq
library_strategy ChIP-Seq
library_source GENOMIC
library_selection ChIP

Platform Information

instrument_model Illumina Genome Analyzer

External Database Query

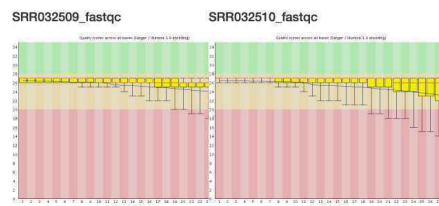
Query antigen: MYC [WikiGenes](#) [PubMed](#) [PDB](#)

Query cell-type: K-562 [ATCC](#) [MeSH](#) [RIKEN BRC](#)

Logs in read processing pipeline

Number of total reads 11974409
Reads aligned (%) 85.3
Duplicates removed (%) 3.8
Number of peaks 13041 (qval < 1E-05)

Sequence Quality Data from DBCLS SRA



[View on IGV](#)

[View Analysis](#)

[Download](#)

[Link Out](#)

BigWig

Peak-call (q < 1E-05)

Peak-call (q < 1E-10)

Peak-call (q < 1E-20)

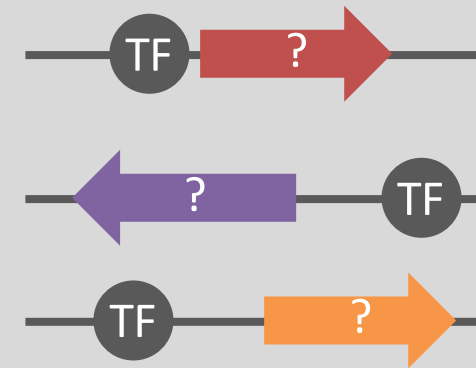
Genome hg19
Antigen Class TFs and others
Antigen MYC
Cell type Class Blood
Cell type K-562

Target Genes

① Peak Browser どこに何が結合する？

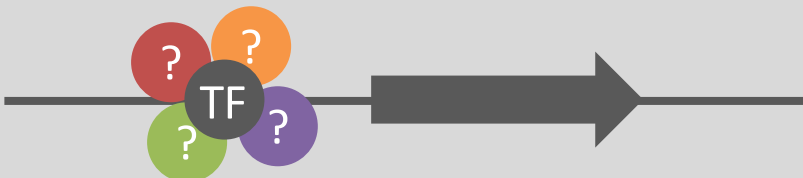


② Target Genes 標的遺伝子は？

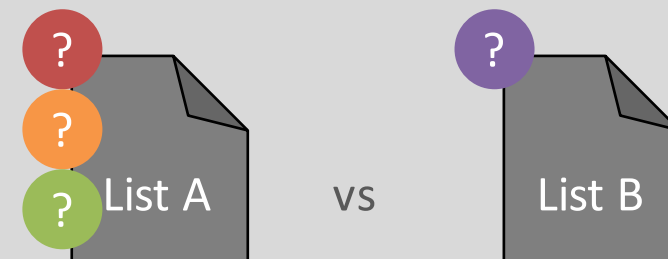


ChIP-Atlas

③ Colocalization 共局在パートナーは？



④ in silico ChIP ユーザデータの解析



Target Genes

例: POU5F1 の標的遺伝子は？

[ChIP-Atlas](#)[Peak Browser](#)[Target Genes](#)[Colocalization](#)[in silico ChIP](#)[Documentation](#)

ChIP-Atlas - Target Genes

Predict potential target genes of TFs.

[H. sapiens](#)[M. musculus](#)[D. melanogaster](#)[C. elegans](#)[S. cerevisiae](#)

1. Choose Antigen

PIAS4
PLAG1
PML
POU2F1
POU2F2
POU5F1
PPARA
PPARG

2. Choose Distance from TSS

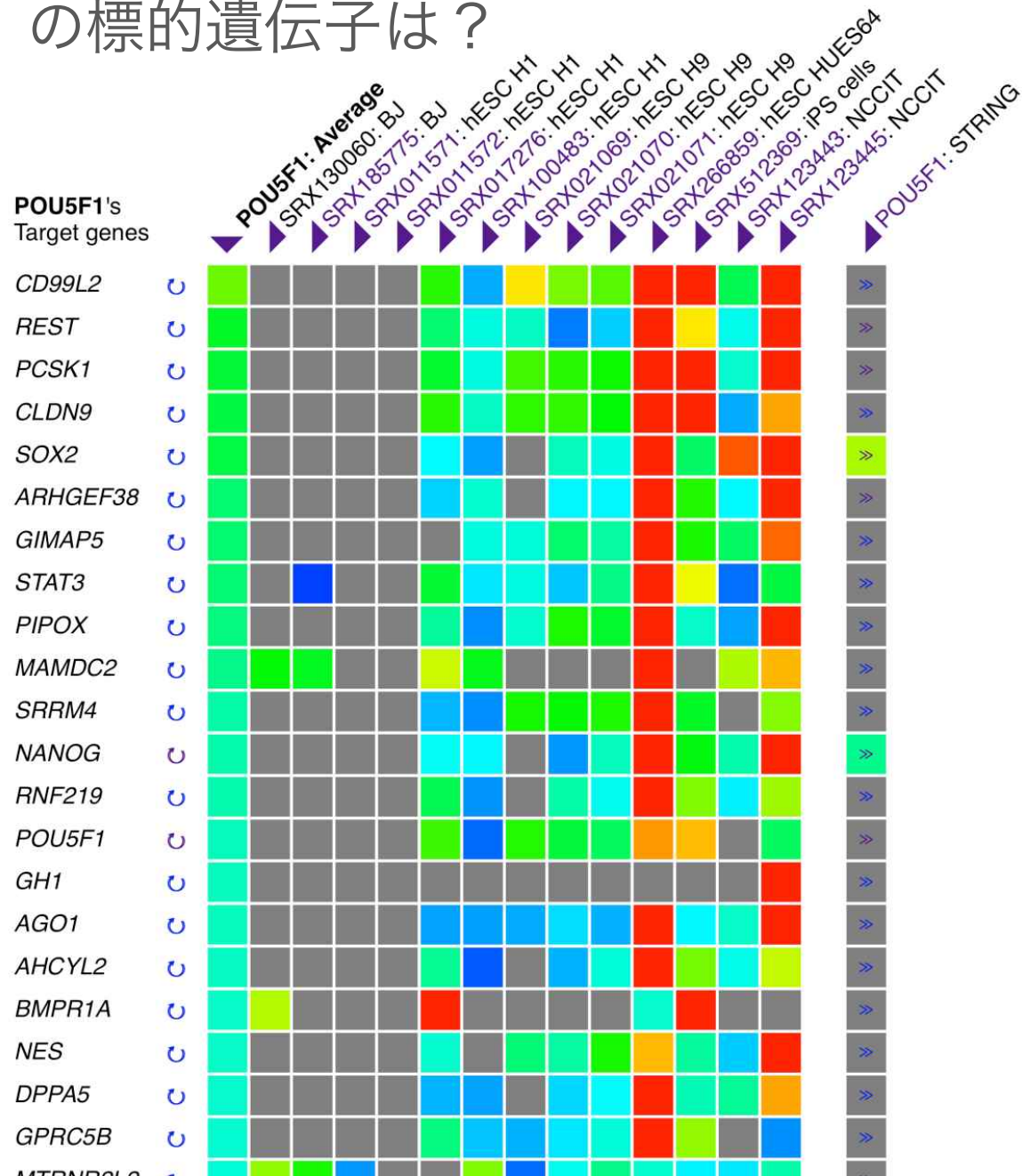
- ±1k
 ±5k
 ±10k

[View Potential Target Genes](#)

Target Genes

例: POU5F1 の標的遺伝子は？

Lo  Hi

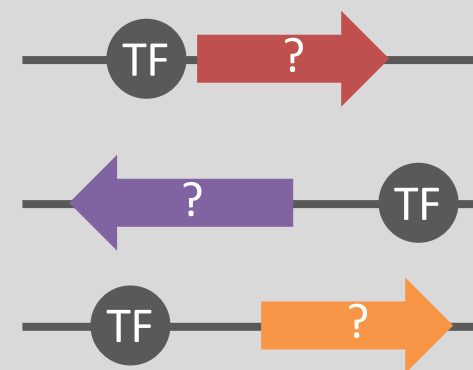


Colocalization

① Peak Browser どこに何が結合する？

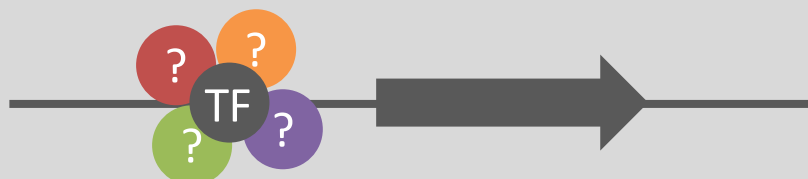


② Target Genes 標的遺伝子は？

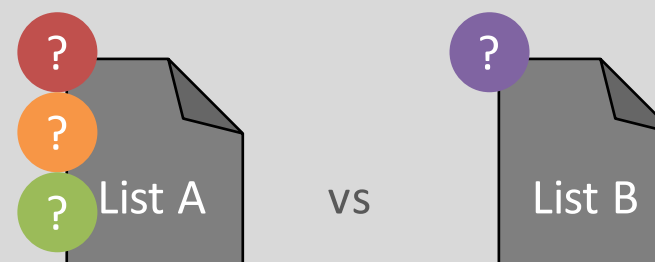


ChIP-Atlas

③ Colocalization 共局在パートナーは？



④ in silico ChIP ユーザデータの解析



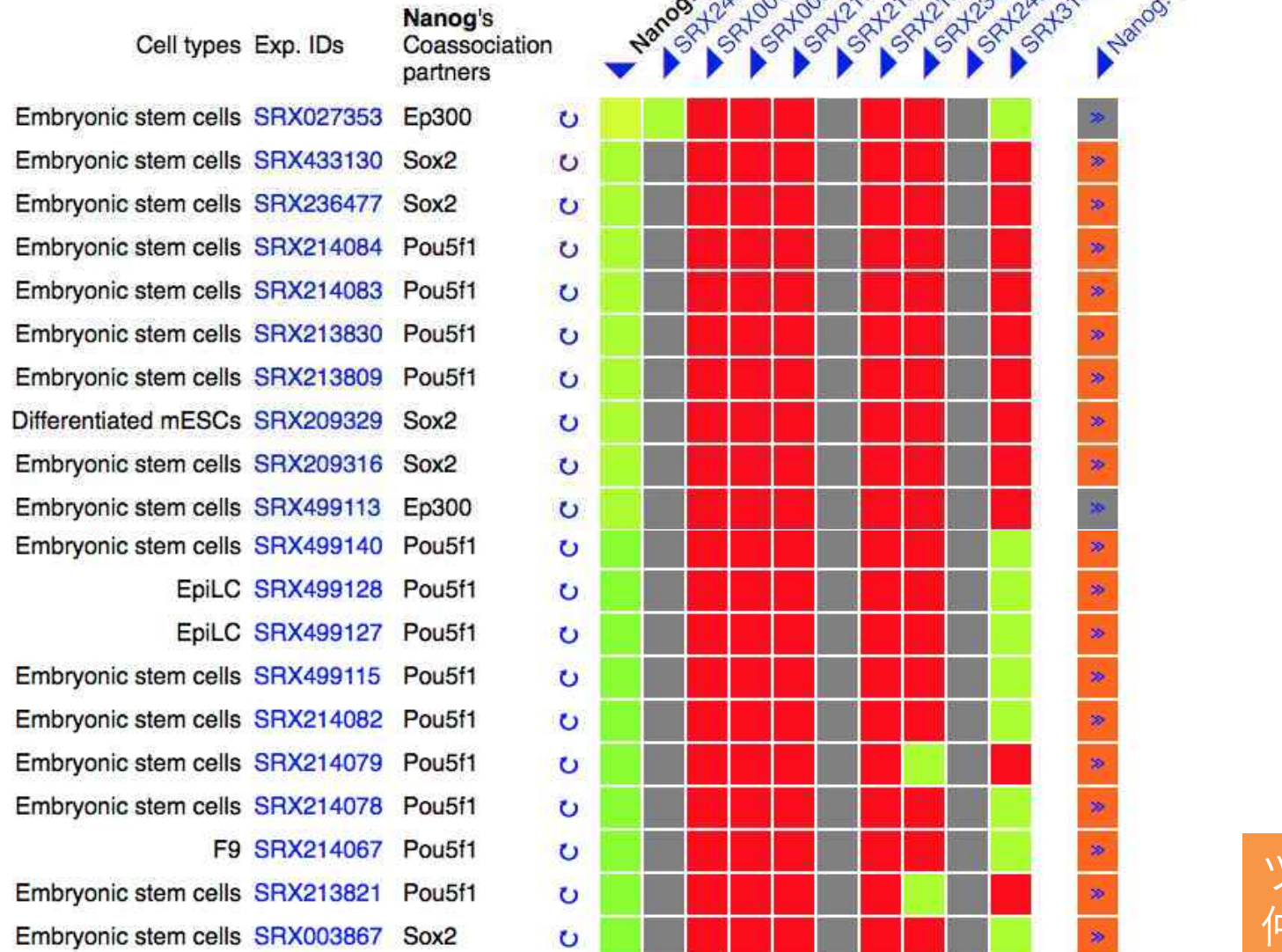
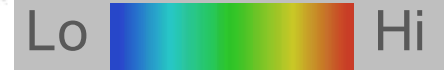
Colocalization

例: NANOG と共局在する因子は？

The screenshot shows the ChIP-Atlas Colocalization tool interface. At the top, there is a navigation bar with links for ChIP-Atlas, Peak Browser, Target Genes, Colocalization (selected), *in silico* ChIP, and Documentation. Below the navigation bar, the title "ChIP-Atlas - Colocalization" is displayed, followed by the subtitle "Predict colocalization partners of TFs." The interface is divided into three main sections: 1. Search mode, 2. Choose Antigen, and 3. Choose Cell Type Class. In the Search mode section, the "Antigens → Cell Type" option is selected. In the Choose Antigen section, "Nanog" is entered in the search box, and a dropdown menu shows a list of genes including Myog, Myt1l, Nanog (highlighted), Nbn, Ncapd3, Ncapg, Ncaph2, and Ncoa2. In the Choose Cell Type Class section, "Pluripotent stem cell" is entered in the search box. At the bottom of the interface, there is a large blue button labeled "View Colocalization Data".

Colocalization

例: Nanog と共局在する因子は？



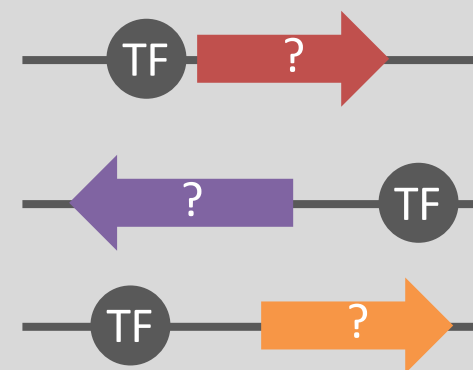
ツール (CoLo) 提供:
仲木 竜 氏 (東大)

in silico ChIP

① Peak Browser どこに何が結合する？

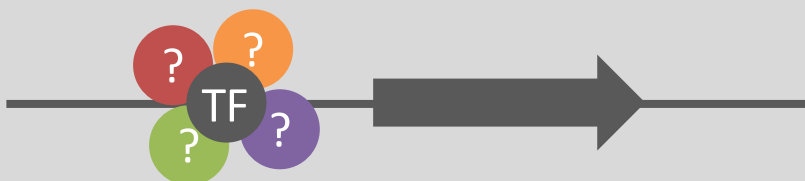


② Target Genes 標的遺伝子は？

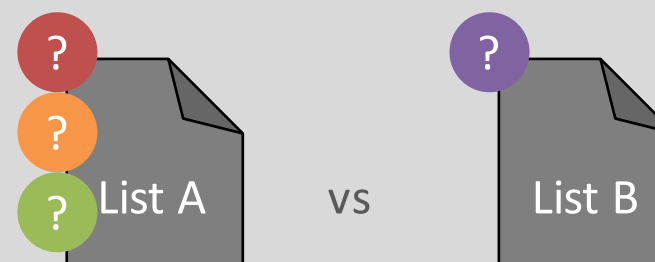


ChIP-Atlas

③ Colocalization 共局在パートナーは？



④ in silico ChIP ユーザデータの解析



in silico ChIP

例: 肝臓特異的遺伝子の制御を司る因子は？

ChIP-Atlas Peak Browser Target Genes Colocalization in silico ChIP Documentation Find an experiment ▾

ChIP-Atlas - in silico ChIP

Analyze your data with public ChIP-seq data.

H. sapiens
M. musculus
D. melanogaster
C. elegans
S. cerevisiae

1. Antigen Class

- All antigens (16138)
- DNase-seq (1024)
- Histone (3824)
- RNA polymerase (629)
- TFs and others (5088)
- Input control (1956)
- Unclassified (596)
- No description (3021)

2. Cell type Class

- All cell types (16138)
- Adipocyte (120)
- Blood (4559)
- Bone (200)
- Breast (1712)
- Cardiovascular (498)
- Digestive tract (1205)
- Epidermis (431)

3. Threshold for Significance

50

100

200

500

4. Select your data

Genomic regions (BED) or sequence motif ⓘ

Gene list (Gene symbols) ⓘ

ADI1

AGO1

AHCYL2

AJAP1

APOBEC3C

APOBEC3D

ARHGEF38

ATPAF2

...

肝臓特異的
遺伝子

Choose File no file selected
Choose local file Try with example

5. Select dataset to be compared

Refseq coding genes (excluding user data) ⓘ

Gene list (Gene symbols) ⓘ

AGBL5

ALOXE3

AMZ2

ANG

APBB3

ARID2

ASF1A

ATP5O

...

その他の
遺伝子

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

Distance range from TSS ⓘ

- bp ≤ TSS ≤ + bp

submit

Estimated run time: 1 mins

in silico ChIP

例: 肝臓特異的遺伝子の制御を司る因子は？

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Liver	Overlaps / Other RefSeq genes	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21259	624/1023	4555/17599	-114.8	-111.1	2.36	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15919	574/1023	3926/17599	-112.1	-108.7	2.52	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	460/1023	3027/17599	-87.1	-83.9	2.61	TRUE
SRX100544	TFs and others	EP300	Liver	Hep G2	24334	596/1023	4983/17599	-82.6	-79.5	2.06	TRUE
SRX150698	TFs and others	HNF4A	Liver	Hep G2	10069	447/1023	2972/17599	-82.5	-79.5	2.59	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45130	688/1023	6974/17599	-66.6	-63.6	1.70	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	674/1023	6764/17599	-65.8	-62.9	1.71	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50941	710/1023	7765/17599	-56.0	-53.2	1.57	TRUE
SRX018625	TFs and others	HNF4A	Liver	Hep G2	2654	179/1023	705/17599	-55.0	-52.2	4.37	TRUE
SRX100538	TFs and others	HDAC2	Liver	Hep G2	16071	539/1023	5045/17599	-54.1	-51.4	1.84	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19032	616/1023	6313/17599	-52.4	-49.8	1.68	TRUE
SRX018626	TFs and others	HNF4A	Liver	Hep G2	1639	131/1023	446/17599	-45.4	-42.8	5.05	TRUE
SRX190331	TFs and others	TEAD4	Liver	Hep G2	10956	311/1023	2260/17599	-44.9	-42.3	2.37	TRUE
SRX190234	TFs and others	CEBPB	Liver	Hep G2	12482	376/1023	3106/17599	-44.0	-41.4	2.08	TRUE
SRX150355	TFs and others	ARID3A	Liver	Hep G2	13508	336/1023	2822/17599	-36.8	-34.3	2.05	TRUE
SRX190197	TFs and others	NFIC	Liver	Hep G2	13273	425/1023					

Showing 1 to 100 of 5,158 entries

WABI 作製:
小笠原 理 氏・奥田喜広 氏 (DDBJ)

in silico ChIP

例: 肝臓特異的エンハンサーの制御を司る因子は？

ChIP-Atlas
Peak Browser
Target Genes
Colocalization
in silico ChIP
Documentation
Find an experiment ▾

ChIP-Atlas - *in silico* ChIP

Analyze your data with public ChIP-seq data.

H. sapiens
M. musculus
D. melanogaster
C. elegans
S. cerevisiae

1. Antigen Class

- All antigens (16138)
- DNase-seq (1024)
- Histone (3824)
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- Unclassified (596)
- No description (3021)

2. Cell type Class

- All cell types (16138)
- Adipocyte (120)
- Blood (4559)
- Bone (200)
- Breast (1712)
- Cardiovascular (498)
- Digestive tract (1205)
- Epidermis (431)

3. Threshold for Significance

4. Select your data

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

chr1	100128315	100128440
chr1	103190456	103190612
chr1	107541234	107541357
chr1	108325177	108325403
chr1	110412483	110412583
chr1	111120868	111121001
chr1	111693652	111693799
chr1	112421367	112421483

5. Select dataset to be compared

Random permutation of user data ⓘ
 BED or sequence motif ⓘ

chr1	10488202	10488365
chr1	107973343	107973565
chr1	108293100	108293277
chr1	109370825	109371023
chr1	110319562	110319739
chr1	112298232	112298429
chr1	113351913	113352118
chr1	116524095	116524271

6. Describe datasets

User data title ⓘ

Compared data title ⓘ

Project title ⓘ

Estimated run time: 2 mins

肝臓特異的
エンハンサー

その他の
エンハンサー

in silico ChIP

例: 肝臓特異的エンハンサーの制御を司る因子は？

ID	Antigen class	Antigen	Cell class	Cell	Num of peaks	Overlaps / Hepatocyte	Overlaps / Other enhancers	Log P-val	Log Q-val	Fold Enrichment	FE > 1?
SRX100544	TFs and others	EP300	Liver	Hep G2	24334	80/286	1147/20509	-32.1	-28.5	5.00	TRUE
SRX190321	TFs and others	MAX	Liver	Hep G2	40220	90/286	1497/20509	-31.9	-28.5	4.31	TRUE
SRX100552	TFs and others	SP1	Liver	Hep G2	19032	64/286	755/20509	-29.7	-26.5	6.08	TRUE
SRX100449	TFs and others	HNF4G	Liver	Hep G2	15919	54/286	507/20509	-29.3	-26.2	7.64	TRUE
SRX100497	TFs and others	RXRA	Liver	Hep G2	13022	54/286	557/20509	-27.5	-24.5	6.95	TRUE
SRX100493	TFs and others	HEY1	Liver	Hep G2	26412	69/286	984/20509	-27.5	-24.5	5.03	TRUE
SRX100538	TFs and others	HDAC2	Liver	Hep G2	16071	58/286	676/20509	-27.0	-24.2	6.15	TRUE
SRX100505	TFs and others	HNF4A	Liver	Hep G2	21259	54/286	585/20509	-26.5	-23.7	6.62	TRUE
SRX190332	TFs and others	MYBL2	Liver	Hep G2	15213	55/286	637/20509	-25.7	-22.9	6.19	TRUE
SRX190264	TFs and others	CREB1	Liver	Hep G2	26690	68/286	1092/20509	-24.3	-21.5	4.47	TRUE
SRX100448	TFs and others	FOXA2	Liver	Hep G2	45130	67/286	1138/20509	-22.6	-19.9	4.22	TRUE
SRX150360	TFs and others	TBP	Liver	Hep G2	10293	38/286	327/20509	-21.7	-19.1	8.33	TRUE
SRX100506	TFs and others	FOXA1	Liver	Hep G2	50941	70/286	1295/20509	-21.7	-19.1	3.88	TRUE
SRX1165097	TFs and others	CREB1	Liver	Hep G2	21856	58/286	899/20509	-21.2	-18.6	4.63	TRUE
SRX190266	TFs and others	NR2F2	Liver	Hep G2	18201	48/286	605/20509	-20.9	-18.4	5.69	TRUE
SRX100477	TFs and others	FOXA1	Liver	Hep G2	40732	66/286	1198/20509	-20.8	-18.2	3.95	TRUE

Showing 1 to 100 of 5,184 entries

Previous 1 2 3 4 5 ... 52 Next

in silico ChIP の応用

FANTOM5 Promoter

ある組織で特異的に
発現する遺伝子

VS

その他の
遺伝子



組織特異性を司る
転写因子の探索

FANTOM5 Enhancer

ある組織で特異的な
エンハンサー

VS

その他の
エンハンサー



組織特異性を司る
転写因子の探索

GWAS catalog

ある疾患で特異的な
SNP loci

VS

その他の
SNP loci



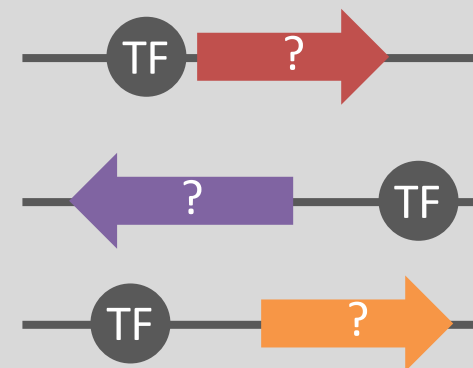
疾患に関わる
転写因子の探索

まとめ

① Peak Browser
どこに何が結合する？

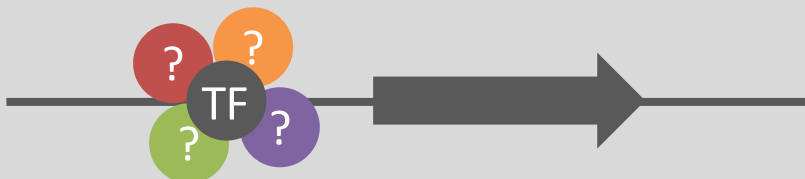


② Target Genes
標的遺伝子は？

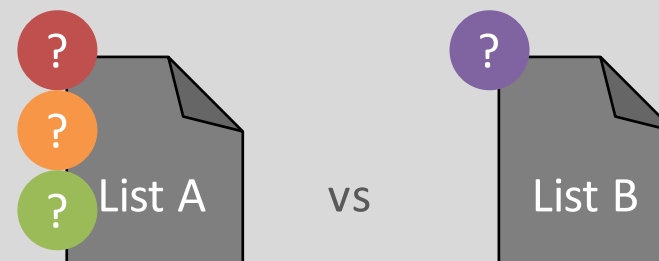


ChIP-Atlas

③ Colocalization
共局在パートナーは？



④ in silico ChIP
ユーザデータの解析



まとめ

- メタデータのクレンジング
- 外部データベースとの連携
PosMed PDBj RIKEN BRC
DBCLS SRA
- 細胞分化や遺伝的疾患を司る転写因子の予測

謝辞

Web UI の作製, 様々な提言
大田 達郎 (DBCLS)

構想, 提案
塩井 剛 (RIKEN)

CoLo の提供
仲木 竜 (東大)

計算機
NIG supercomputer

WABI の作製
小笠原 理
奥田 喜広 (DDBJ)

サーバ提供
畠中 秀樹 (NBDC)

データ考察
目野 主税 (九大)



独立行政法人
科学技術振興機構
Japan Science and Technology Agency
H27 年度 統合化推進プログラム
(統合データ解析トライアル)