

<http://dbkero.hgc.jp/>
DBKERO
 Database of Human Genomes for Researches of multi-Omics data

Quick-start: For the beginners

 日本人多層オーミクス
 日本人由来細胞株多層オーミクス
 新規技術データ

 鈴木 穰
 東京大学新領域創成科学研究科

We recommend to use Edge (ver. 40 or above), Google Chrome (ver. 81 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Viewer [How to use]

Multi-Omics-Viewer [Help video 1,2,3 (Japanese)], [GitHub]:
 Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

TSS-Viewer [Help video (Japanese)]:
 Find out transcriptional start sites and compare promoter usage.

Mutation Enriched Genes [Help video (Japanese)]:
 Find out which gene is mutated most in our data.

TF Binding Site Search [Help video (Japanese)]:
 Find out TF binding sites in a region of genome of various organism.
 Powered by [ChIP-Atlas*](#) and [GGGenome*](#).

Pathway Map [Help video (Japanese)]:
 Find out the level of expression or modification of genes within a Pathway

Chromatin-status Data Summary [Help video (Japanese)]:
 Get an overall view of expression and modification of a genome region among our entire data sets.

Featured Dataset

Single cell dataset [Download processed data]:
 Single cell dataset

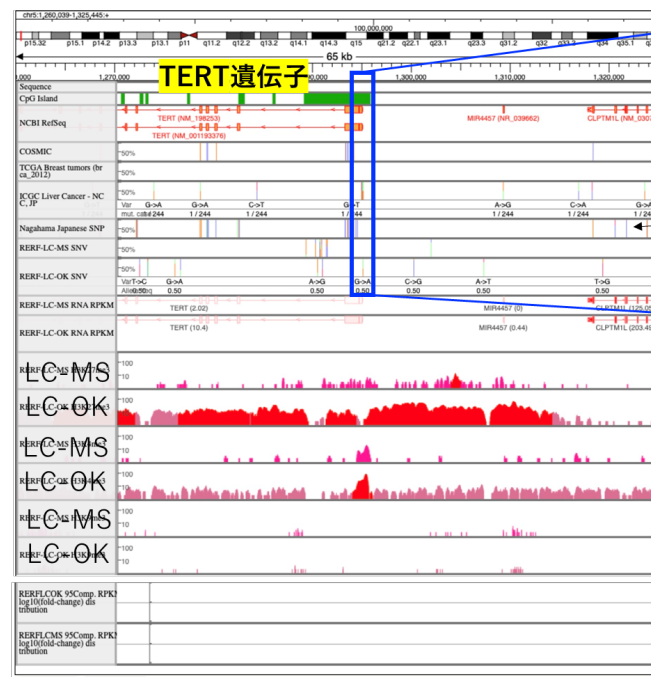
Cancer SV dataset New
 Japanese lung adenocarcinoma sequenced by PromethION(Oxford Nanopore Technologies).

Visium dataset New
 Spatial Gene Expression dataset (10x Genomics Visium system).
 Spaceranger output files for loupe browser and Seurat analysis.

Cancer LongRNA Dataset New
 Aberrant splicing isoforms in non-small cell lung cancer sequenced by MinION (Oxford Nanopore Technologies)

Download

- [Data Portal](#) [Help video (Japanese)]
- [Data Portal PAGS:Genome Shien\(ゲノム支援\)](#)



COSMIC

TCGA_乳癌

ICGC_肝癌

日本人正常ゲノム

LC-MS

LC-OK

H3K27me3(TERT-)

H3K27me3(TERT+)

H3K4me3(TERT-)

H3K4me3(TERT+)

H3K9me3(TERT-)

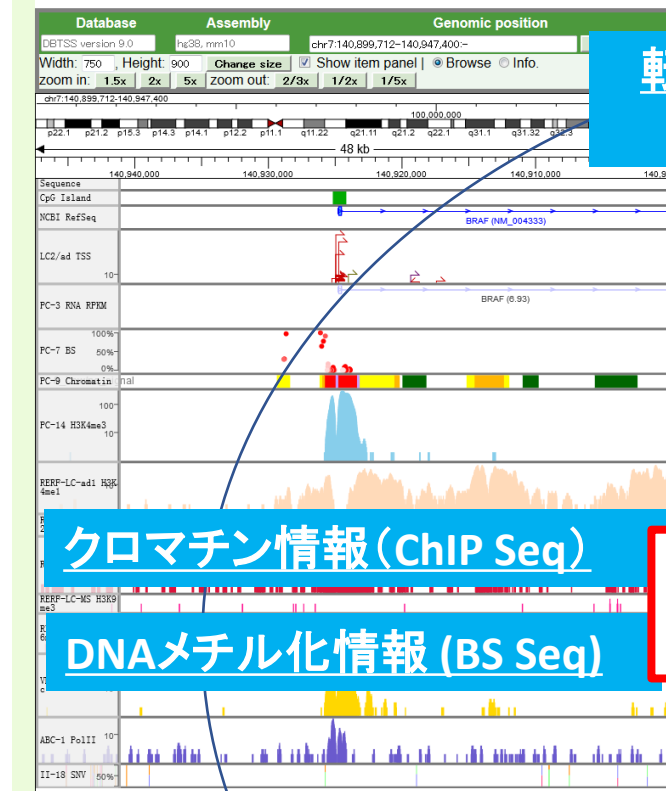
H3K9me3(TERT+)

TERTプロモータの変異
悪性葉状腫瘍 62%¹⁾

- 自分のゲノム情報をアップすることができる
- 例えばTERTプロモーターの変異(葉状腫瘍)
- TCGAなどではどれくらいの頻度であるのか
- 培養細胞のマルチオミクスのデータがあるので、培養細胞のオミクスデータを参照することでこの変異をもつことによって、どんな発現状態(mRNA、メチル化)になるか、自身で実験せずとも参照が可能

 ご質問は:
ysuzuki@hgc.jp
 まで。

Genome viewer (Multi-omics Data)



転写開始点/トランスクリプトーム情報
(TSS/RNA Seq)

(発現量と転写開始点)

クロマチン情報 (ChIP Seq)

DNAメチル化情報 (BS Seq)

多層オミクス情報の
ヒトゲノム変異情報への統合

統合DB (DBKERO)

Clinical Sequencing

(それぞれの検体での変異部位)

パスウェイマップ (文献情報) からの検索

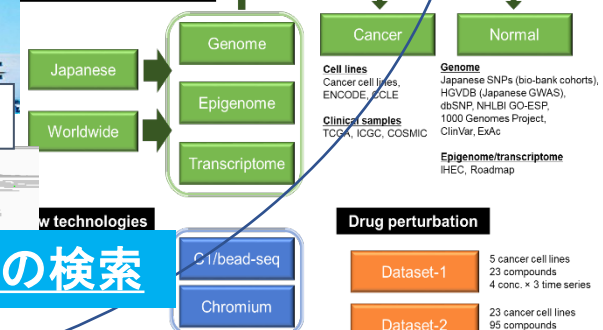
(該当集団中の遺伝子変異頻度を
赤の濃さで示す)

Single Cell Viewer

オミクス新解析技術

- Single cell 解析
- Long read 解析

Standard multi-omics data



何ができるか(1)

日本人正常オーミクスデータ (IHEC)

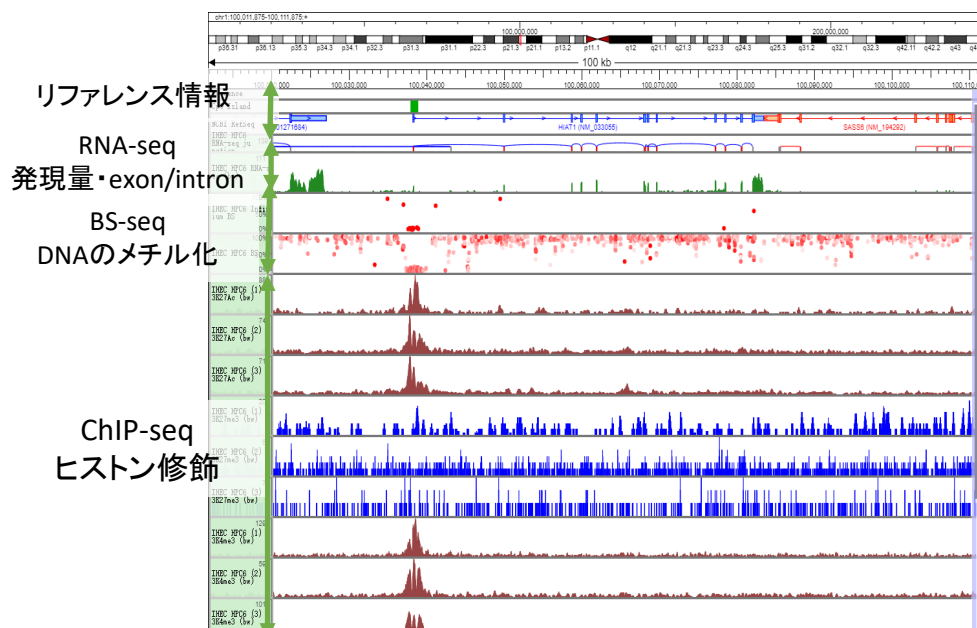
国際エピゲノムコンソシアム (IHEC)

で日本CRESTチームが収集した日本人標準エピゲノムが検索できます。

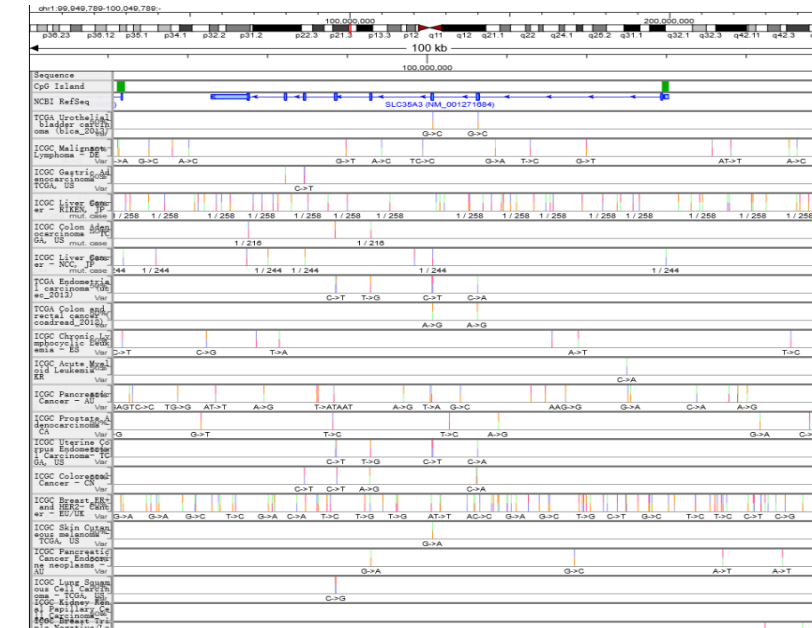
CREST-IHECデータの統合(日本人標準エピゲノム)

IHEC(国際エピゲノムコンソーシアム)データの公開

マルチオミクス情報の表示



TCGA/ICGC変異情報の表示



IHECデータとしてゲノムブラウザから閲覧可能なオープンデータ一覧

Sample	individuals	Expression		DNA methylation	Histone modifications					
		RNA-seq		BS-seq	H3K4me1	H3K4me3	H3K27ac	H3K27me3	H3K36me3	H3K9me3
		Read depth	Exon/intron junction							
Liver	8	8	8	8	13	13	13	13	13	13
Colon	11	11	11	11	11	11	11	11	11	11
Endometrial	15	30	0	13	14	15	15	15	15	15
Vascular endothelial	33	26	0	0	19	27	27	19	27	26

Human Genome Variation DB (旧徳永グループ)との統合

日本人ゲノム多型

DBKERO Release 9.0 Updated (July 9, 2015)
Based on UCSC hg18, ref8

Database Search

Welcome to DBTSS (Database of Transcriptional Start Sites)

To support transcriptional regulation studies, we have constructed the DBTSS (Database of Transcriptional Start Sites), which represents exact positions of transcriptional start sites (TSSs) in the genome based on our unique experimentally validated TSS sequencing method, TSS-seq.

This database includes TSS data of a major part of human adult and embryonic tissues are covered. DBTSS now contains 481 million TSS tag sequences for collected from a total of 20 tissues and 7 cell cultures. We also integrated our newly generated RNA-seq data of subcellular-fractionated RNAs and ChIP-seq data of histone modifications, RNA polymerase II and several transcriptional regulatory factors in cultured cell lines. We also included recently accumulating external epigenomic data, such as chromatin map of the ENCODE project.

In this update, we further associated those TSS information with public and original SNV data, in order to identify single nucleotide variations (SNVs) in the regulatory regions.

It is believed that single nucleotide variations (SNVs) in the transcriptional regulatory regions are responsible for many human diseases, including cancers. However, it remains difficult to identify functionally relevant SNVs from those having no explicit biological consequences. In this version of DBTSS, we attempt to associate SNVs with the omics information of the surrounding regions. We used SNVs which we identified from genomic analyses of various types of cancers, including somatic mutations of 100 lung adenocarcinoma and lung small cell carcinoma. For germline variations, we used SNVs in dbSNP as well as our unique dataset of variations in 1000 Japanese individuals. We integrated those SNV information with our original datasets of TSS-seq, RNA-seq, ChIP-seq of representative histone modifications and Biofire Sequencing of cytosine methylations of DNA. Particular, we present multi-omics data of 20 lung adenocarcinoma cells line for which TSS-seq, RNA-seq, ChIP-seq and BS-seq together with whole genome sequencing are collected from the same materials. We further connected the multi-omics data of model organisms by genome-genome alignment. We provide a unique data resource to investigate what genomic features are observed in a particular genomic coordinates in a wide variety of samples.

Human Chromatin Features

Search from Genomic Position:
chr1:75,787,000

Search from SNP (dbSNP rsID):
rs7522989

Search from SNV (COSMIC):

Search

Human Genome Variation DB Release 9.0 Updated (July 9, 2015)
Based on UCSC hg18, ref8

Database Search

Species: H. sapiens

Keyword: NM_

Search

Font size: 15

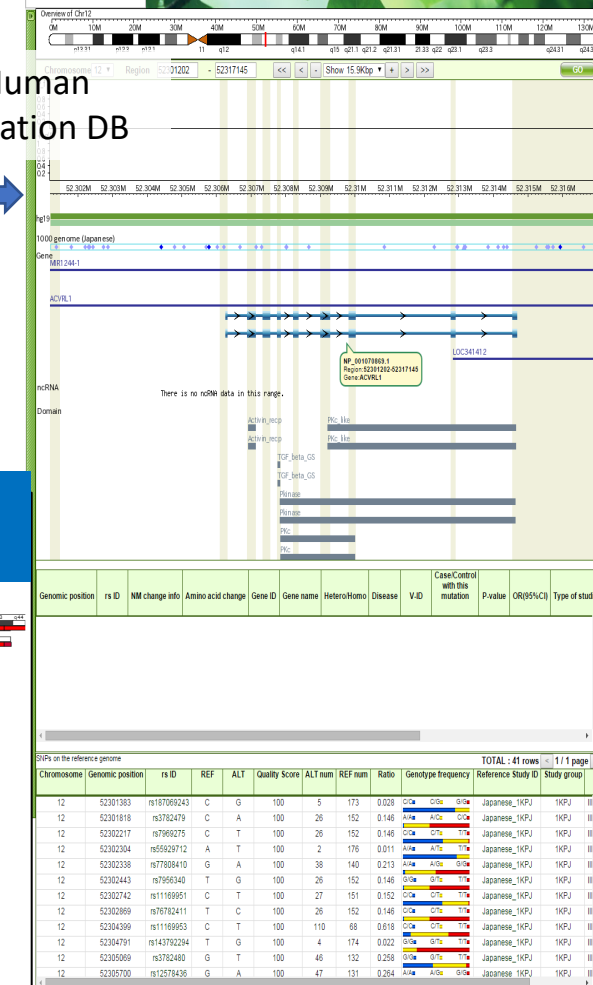
Search from Genomic Position:
chr1:75,787,000

Search from SNP (dbSNP rsID):
rs7522989

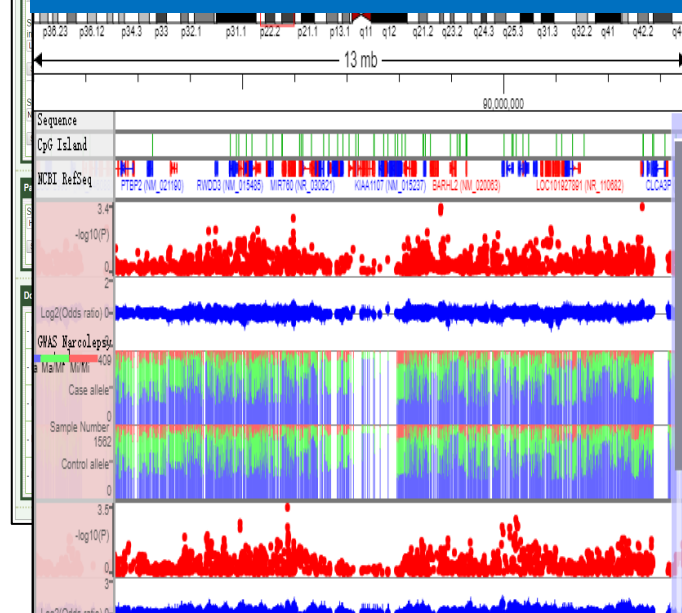
Search from SNV (COSMIC):

HGVDBへのリンク機能

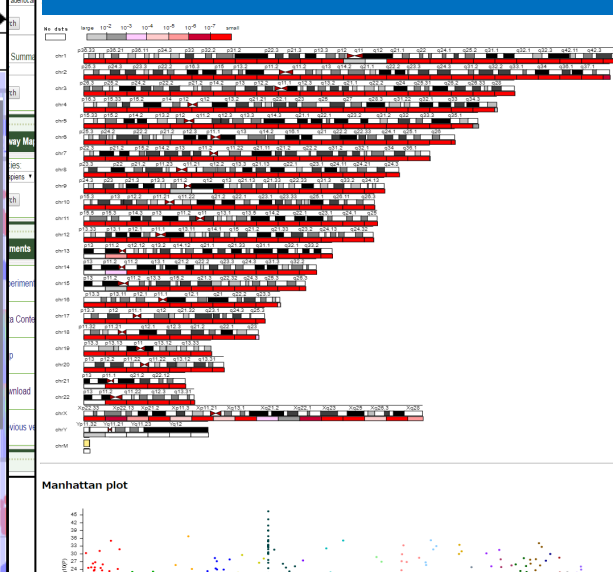
Human
Variation DB



Genome browserへGWAS情報の可視化



Whole genome viewer, Manhattan viewer



NBDC ヒトDBとの 連携へ

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©2021鈴木穰（東京大学新領域創成科学研究科）



何ができるか(2)

どの培養細胞をモデルにするのか？
を選ぶオーミクスデータ

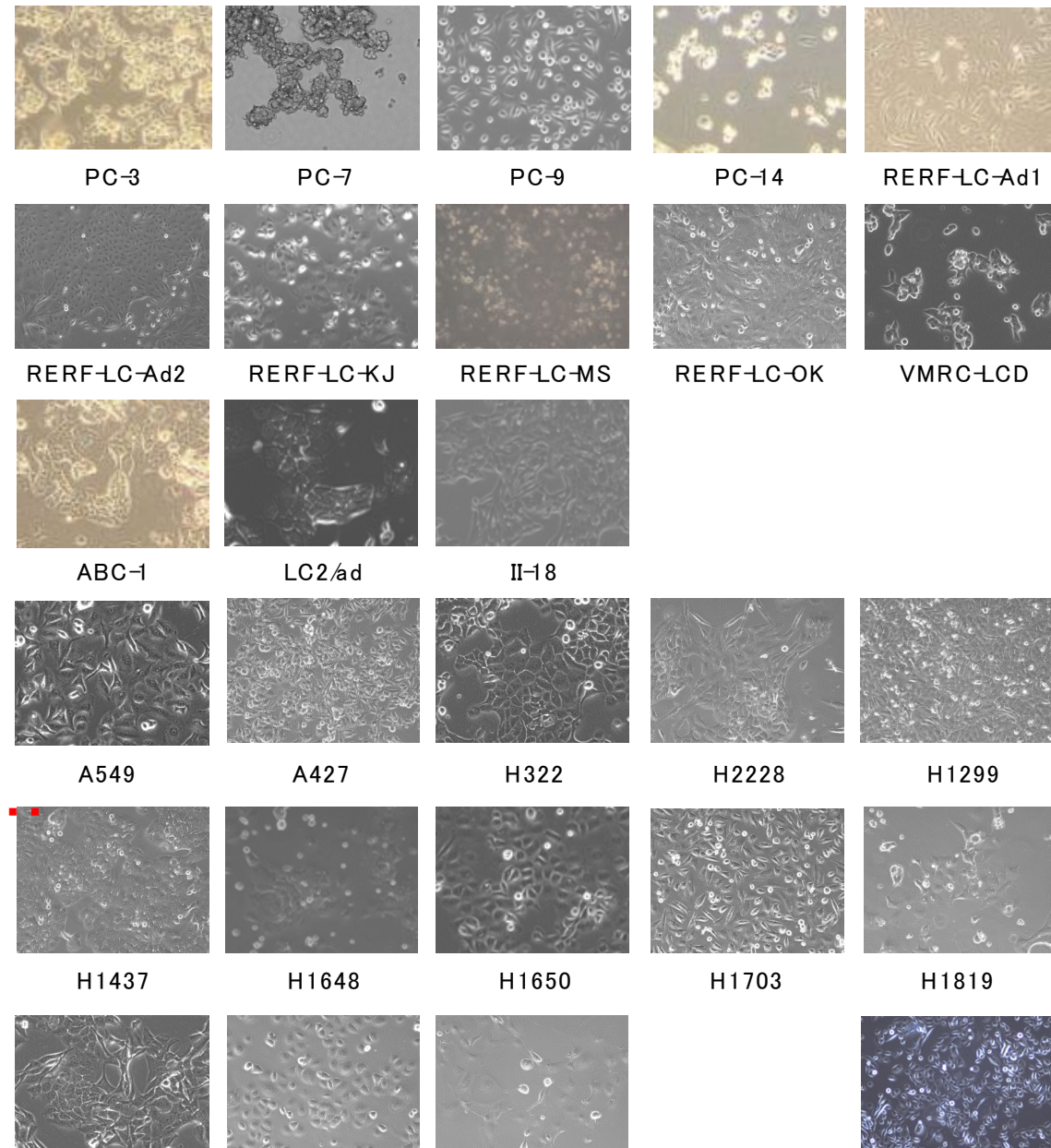
肺腺癌細胞株等で日本人由来のオーミクスデータが充実しています。

培養細胞オーミクス

26 lung adenocarcinoma cell lines

Cell line	Origin
PC-3	日本人由来
PC-7	
PC-9	
PC-14	
RERF-LC-Ad1	
RERF-LC-Ad2	
RERF-LC-KJ	
RERF-LC-MS	
RERF-LC-OK	
VMRC-LCD	
ABC-1	
LC2/ad	
II-18	
A427	Non-Japanese
A549	
H322	
H2228	
H1299	
H1437	
H1648	
H1650	
H1703	
H1819	
H1975	
H2126	

もちろん、ENCODE/CCLEにもありますが...



Multi-omics sequencing data of lung cancer cell lines

Suzuki *et al.* 2014 *Nucleic Acids Research*

Suzuki *et al.* 2015 *Nucleic Acids Research DB issue*

26 NSCLC cell lines

13 Japanese
13 non-Asian
+ normal (SAEC)

Genome

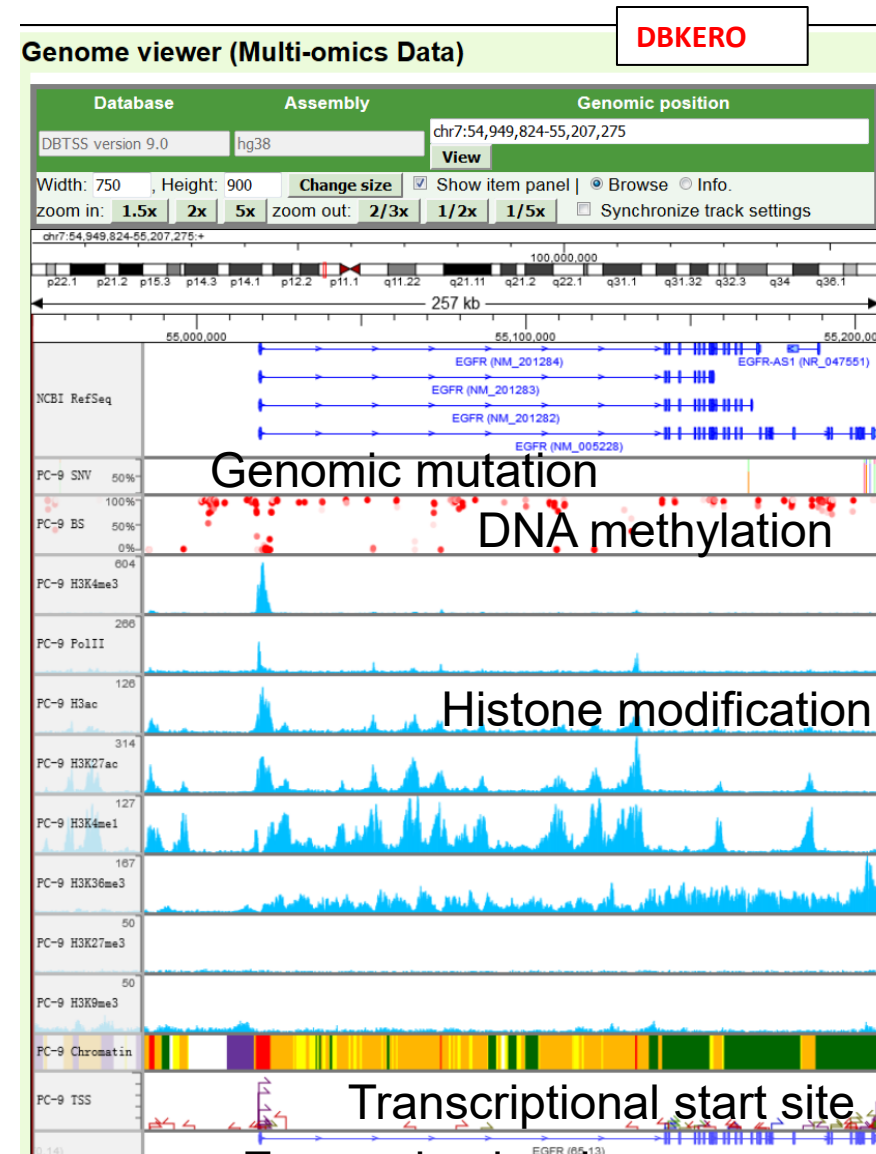
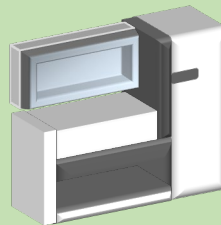
- Whole-genome sequencing
- Long-read sequencing (MinION/PromethION)

Epigenome

- Bisulfite seq/**EM seq** (not yet)
- ChIP-Seq
- ATAC-Seq

Transcriptome

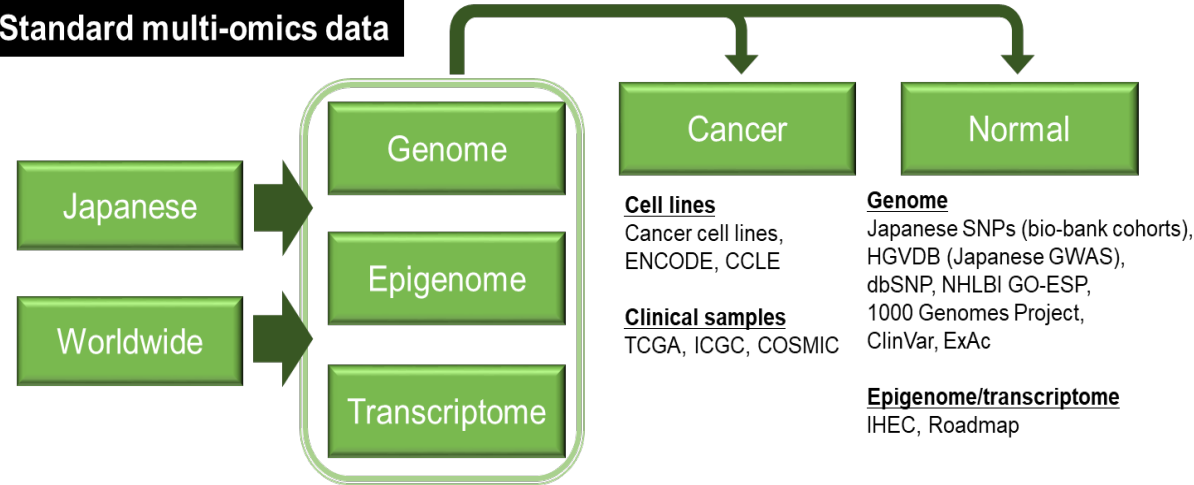
- TSS-Seq
- RNA-Seq
- miRNA-seq



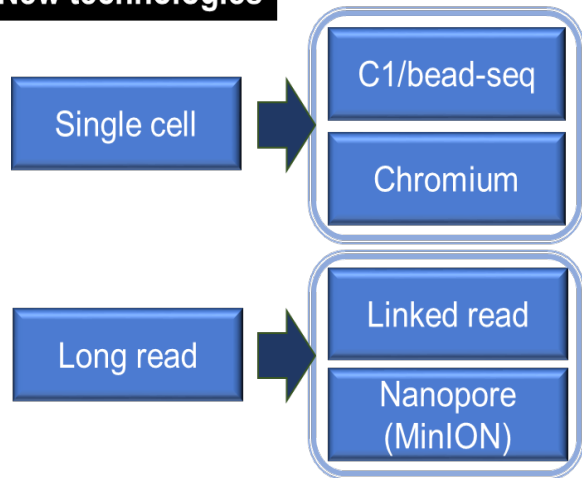
データコンテンツの選択と表示

KEROデータコンテンツ

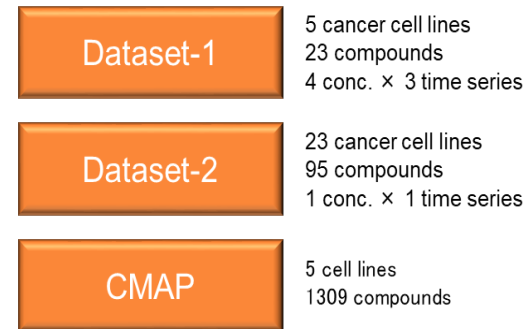
Standard multi-omics data



New technologies



Drug perturbation



DBKEROのデータ構造の全体像。日本人の臨床オミックス情報がモデルシステムからの包括的オミックス情報とどのように関連しているかを示す。

New technologiesとして、近年新たに産出可能となったシングルセルとロングリードのデータやDrug perturbationとして、化合物によるマルチオミックス摂動の情報を含んでいる。

異なるカテゴリーのデータセットは、異なる色のボックスとして示した。

DBKERO
Database of Korean Encyclopedia for Research of multi-Omic data

Quick-start: For the beginners Release 1.2.3 Updated (Aug. 19, 2020)
Based on UCSC hg38, mm10
Formerly DBTSS

We recommend to use Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Top | Multi-Omics-Viewer | Tutorial

Tools

- TSS-Viewer** [Video (Japanese)]:
Find out transcriptional start sites and compare promoter usage.
- Multi-Omics-Viewer** [Video 1.2.3 (Japanese)] [GitHub]:
Browse mutations, transcripts and epigenetic modifications along the genome coordinates.
- Mutation Enriched Genes** [Video (Japanese)]:
Find out which gene is mutated most in our data.
- TF Binding Site Search** [Video (Japanese)]:
Find out TF binding sites in a region of genome of various organism. Powered by ChIP-Atlas* and GGGenome*.
- Pathway Map** [Video (Japanese)]:
Find out the level of expression or modification of genes within a Pathway
- Chromatin-status Data Summary** [Video (Japanese)]:
Get an overall view of expression and modification for a genome region among our entire data sets.
- Search from Genomic Position**
- Search from SNP (dbSNP rsID)**
- Search from SNV (COSMIC; somatic mutation)**
- SNV Summary in Cancer** [Video (Japanese)]:
Find out mutation frequency of a gene among our cancer data sets.
- RDF gate (Trial)**
Lung adenocarcinoma 26 cell lines: RNA-seq, ChIP-seq, SNV, BS-seq, TSS-seq
- RDF Schema**
- RDF Browser**
- SPARQL Endpoint**
- Other tools**
- Single cell viewer** [Video (Japanese)]
- SV viewer** new

Download

- Data Portal** [Video (Japanese)]

Documents

- Experimental Procedures**
- Data Contents**
- Tutorial**
- Download bulk data**
- References**

Movie (For Japanese)

Overview movie 1 in Japanese (9 min.) Overview movie 2 in Japanese (53 min.)

疾患ヒトゲノム
ヒト統合オミクスデータベース

How to use genome browser (Basic) How to use genome browser (Track selection)

How to use genome browser (Comparative viewer) How to use data portal

News

各種使い方のチュートリアルビデオヘリンク

ブラウザの使い方
Quick-start: For the beginners

Release 1.2.3 Updated (Aug. 19, 2020)
Based on UCSC hg38, mm10
Formerly DBTSS

We recommend to use Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Top | Tutorials | Multi-Omics-Viewer (Basic)

マルチオミクスビューの使い方 (基本)

転写因子結合領域予測の使い方
Quick-start: For the beginners

Release 1.2.3 Updated (Aug. 19, 2020)
Based on UCSC hg38, mm10
Formerly DBTSS

We recommend to use Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Top | Tutorials | TF binding site search

転写因子結合領域の予測検索

データポータルの使い方
Quick-start: For the beginners

Release 1.2.3 Updated (Aug. 19, 2020)
Based on UCSC hg38, mm10
Formerly DBTSS

We recommend to use Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Top | Tutorials | Data portal

DBKEROデータポータルの使い方

Search for genomic position

2022 info. Batch download

Category	ChIP-seq	RNA-seq	BS-seq	TSS-seq	SNV	SV
Total	583	1363	3	14	479	
ChIP-seq	0	0	0	0	279	
RNA-seq	1363	0	0	0	53	
BS-seq	0	0	0	0	26	
TSS-seq	0	0	0	0	79	
SNV	0	0	0	14	0	
SV	0	0	0	0	27	
Chromatin	0	0	0	0	26	
ChIP-seq	0	0	0	0	26	
RNA-seq	0	0	0	0	26	
BS-seq	0	0	0	0	26	
TSS-seq	0	0	0	0	0	

先進ゲノム支援(文科省新学術領域):
"PAGS"= Platform for Advanced Genome Sciences

<http://www.genome-sci.jp/>

Google “ゲノム支援”

文部科学省科学研究費助成事業「新学術領域研究『学術研究支援基盤形成』」

先進ゲノム解析研究推進プラットフォーム

先進ゲノム支援

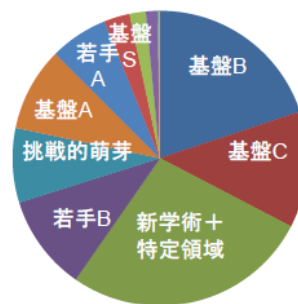
ホーム 先進ゲノム支援とは 公募要項 支援申請の流れ 支援申請 公募支援に関するFAQ お問い合わせ



新学術領域研究「先進ゲノム解析システム」の提供することにより様々な

この過程でゲノム解析システムを用いては生命科学のさまざまな研究が進みます。この支援にふさわ

② 支援採択課題の元科研費

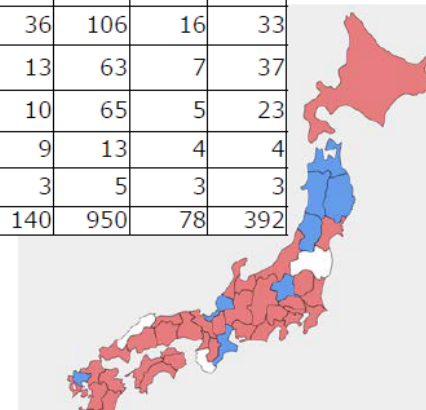


全期間の応募・採択数

年度	H22	H23	H24	H25	H26	H27
応募数	166	237	200	172	161	211
採択数	60	62	81	88	91	74

③ 支援依頼者所在機関 (H26まで)

	応募		採択	
	機関	件数	機関	件数
国立大学	53	662	38	282
公立大学	16	36	5	10
私立大学	36	106	16	33
国立研究所	13	63	7	37
独法研究所	10	65	5	23
公立研究所	9	13	4	4
財団研究所	3	5	3	3
合計	140	950	78	392



DBKEROデータポータル of 構築

DBKERO Data Portal

▼Project:

- ☐ IHEC (583)
- ☐ Single cell (1163)
- ☐ Nanopore (3)
- ☐ Cancer Cell Line (478)

▼Race:

- ☐ Japanese (1677)
- ☐ Worldwide (550)

▼Omics Category:

- ☐ Epigenome (747)
- ☐ Transcriptome (1347)
- ☐ Genome (133)

▼Reference Genome:

- ☐ hg38 (2227)

▼Data Category:

- ☐ IHEC (583)
- ☐ Lung adenocarcinoma (1644)

▼Assay:

- ☐ ChIP-Seq (639)
- ☐ RNA-Seq (1321)
- ☐ BS-Seq (81)
- ☐ Resequencing (81)
- ☐ ChromHMM (27)
- ☐ TSS-Seq (26)
- ☐ CNV (26)
- ☐ SV (26)

▼File Format:

- ☐ BigWig (read depth) (854)
- ☐ BigWig (read depth) x2 (14)
- ☐ TSV (BS) (68)
- ☐ BigWig (BS) (13)
- ☐ TSV (exon/intron junction) (27)
- ☐ TSV (expression level) (27)
- ☐ TSV (expression distribution) (27)
- ☐ BAM (481)
- ☐ TSV (ChromHMM) (27)
- ☐ TSV (TSS) (26)
- ☐ TSV (SNP/SNV) (26)
- ☐ TSV (read depth) (216)
- ☐ TSV (CNV) (26)
- ☐ TSV (translocation) (26)

データ
カテゴリ
選択

Matrix List

Project>>>

	IHEC	Single cell	Nanopore	Cancer Cell Line
Total	583	1163	3	478
ChIP-Seq	423	0	0	216
RNA-Seq	105	0	0	53
BS-Seq	55	0	0	26
Resequencing	0	3	78	0
ChromHMM	0	0	27	0
TSS	2227	0	0	0

Assay>>>

Batch download TSV

マトリクス
画面

バッチダウンロード

各データダウンロード

リスト画面

Object ID	Object Description	Reference Genome	Data Category	Assay	File Format	Download
11_H3K27Ac	IHEC COC11 H3K27Ac (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_H3K27me	IHEC COC11 H3K27me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_H3K36m	IHEC COC11 H3K36me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_H3K4me	IHEC COC11 H3K4me1 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_H3K4me	IHEC COC11 H3K4me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_H3K9me	IHEC COC11 H3K9me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11_maseq_b	IHEC COC11 RNA-seq (bw)	hg38	IHEC	RNA-Seq	BigWig (read depth)	Download
14_H3K27Ac	IHEC COC14 H3K27Ac (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download

何ができるか(3)

新しい手法でどんなデータが出てくるのか？

シングルセルデータ、空間トランスクリプトームデータ、
ナノポアデータ等がおちています。

ブラウザはなくとも、まずはデータだけでも・・・

The image shows a screenshot of the DBKERO website. At the top, the DBKERO logo is displayed with the tagline "Database of Cancer Genomics for Researchers of multi-Omic data". Below the logo is a red banner that reads "Quick-start: For the beginners". The website is divided into two main columns. The left column contains sections for "Selected Dataset", "Documents", and "Movie (For Japanese)". The right column contains a "Download" section and several tool links. Annotations with blue arrows point from text boxes to specific parts of the website:

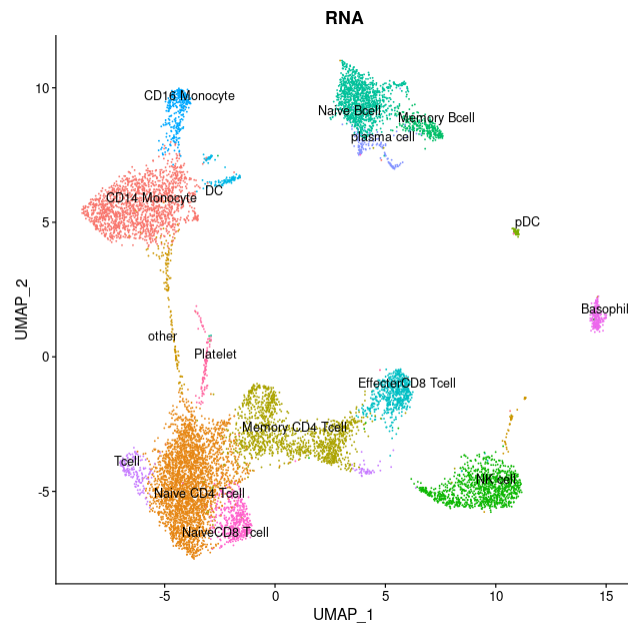
- シングルセルデータ** (Single-cell data) points to the "Selected Dataset" section.
- シングルセルデータ加工の Tutorial動画** (Tutorial video for single-cell data processing) points to the "Movie (For Japanese)" section.
- VISIUMのデータ (空間トランスクリプトーム解析)** (VISIUM data (spatial transcriptome analysis)) points to the "Documents" section.
- Longリードデータ (日本人肺腺がんのSV)** (Long-read data (SV of Japanese lung adenocarcinoma)) points to the "Download" section.
- データポータル (2500程度の多層オミクスデータセット; 細胞株が多いです)** (Data portal (2500+ multi-omic datasets; many cell lines)) points to the "Data Portal" link in the "Download" section.

The "Selected Dataset" section lists several datasets, including "Single-cell dataset" and "Gene Expression dataset". The "Documents" section lists links for "Experimental Procedures", "Data Contents", "Tutorial", "Download bulk data", and "References". The "Movie (For Japanese)" section features two overview movies and two tutorial videos. The "Download" section includes links for "Data Portal", "Mutation Enriched Genes", "TF Binding Site Search", "Pathway Map", "Chromatin-status Data Summary", "Search from Genomic Position", "Search from SNP", "Search from SNV", "SNV Summary in Cancers", and "RDF gate".

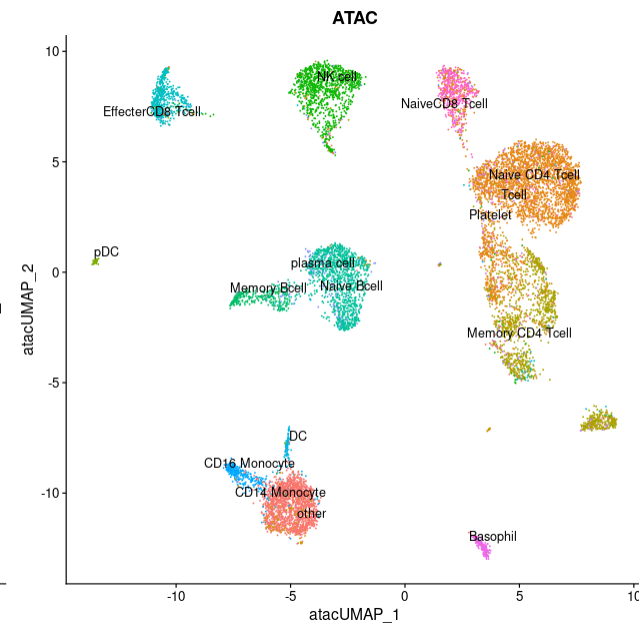
scMulti-Ome

UMAP Analysis

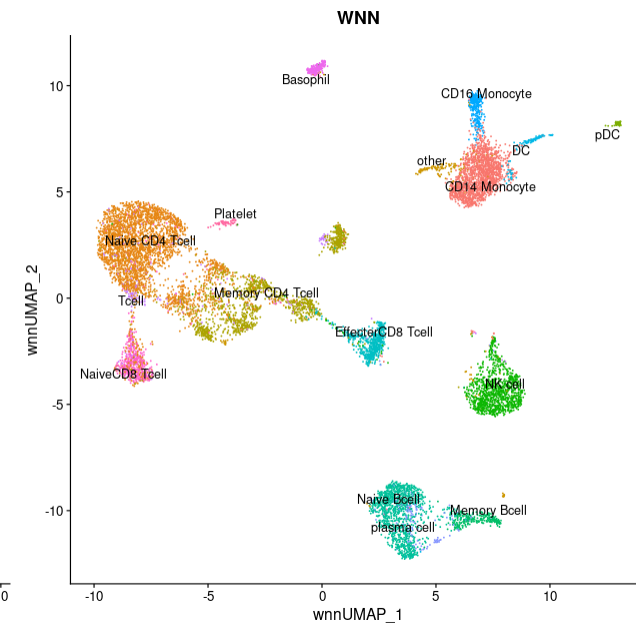
RNA



ATAC



ATAC & RNA



本書ではシングルセル解析初心者の方がテストデータを用いて、一通りのデータ解析が出来るようになることを目的としています。

リンク：シングルセル解析の必要性

ここでは、10x Genomics社のChromiumプラットフォームを用いた配列データの解析方法について説明します。

この文書にある処理は東京大学医科研究所ヒトゲノム解析センターのスーパーコンピュータ(HGC)で動作を確認しています。HGCをご利用になる場合は、以下

Rをご使用する場合は、R3.6以上のバージョンが必要です。HGCをご利用の場合は、以下のように使用するRを指定してください。

リンク・シングルセル解析の様々なプラットフォーム

ここではマウス肺正常細胞のncRNA-seqデータと、解析ツールとしては10x GenomicsのCell RangerとSeuratを用いて解析した。

2. Cell Rangerによる解析

Chromiumで取得したデータの解析を行うツール



テストデータの準備

データセットは https://ker0.hgc.jp/tutorials/learning/data/10X_RNAv3_Lung.tar からダウンロードできます。

```
od ~/data/ #データをダウンロードするディレクトリに移動
```

下記コマンドでCell Rangerを実行することが可能です。先ほど用意したfastqファイルを解析してみましょう。

※ 本表は、本誌掲載の各記事の掲載ページを掲載しています。

ラスタリング、発現変動遺伝子 (DEG) 解析) コマンド) を実行し

セットを展開したディレクトリを指定

※—localmen: 使用メモリ量 (GB) (ご自身の環境に合わせてなるべく大きな値にしてください)

Cell Ranger の処理が完了したら、出力ファイルを確認しましょう。

```

$ cd /usr/local/src/openssl-1.0.2g
$ ls

```

```
% ed outs
```

```
filtered_feature_bo_matrix  molecule_info.h5          raw_feature_bo_matrix
```

File Name	Description
-----------	-------------

21 鈴木 瑛 (東京大学新領域創成科学研究科)

Quick-start: For the beginners

recommend to use Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for the DBKERO browsing. We do not support Internet Explo

Mouse Visium Dataset

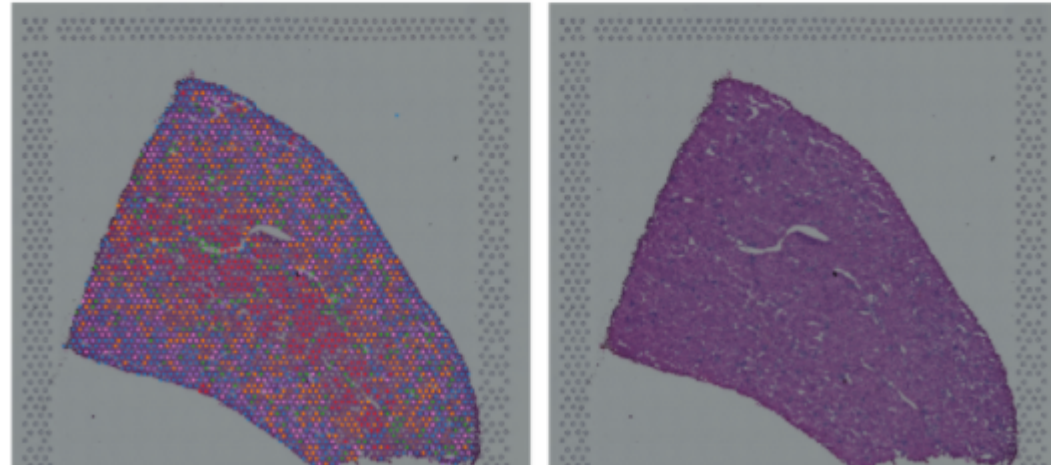
We prepared mouse kidney spatial gene expression dataset (10x Genomics visium system).
Sequenced by Novaseq 6000.

You can download the dataset from the link below.

These datasets are processed by spaceranger v1.0.0 (refdata-cellranger-mm10-3.0.0).

- [Summary.html \(by spaceranger\)](#)
- [Dataset for loupe* visualization](#)
- [Dataset for Seurat analysis](#)

*loupe is visualization software released by 10x genomics.
please download from [10x genomics web site](#) (Registration required).



独自にも進める技術開発

肺がんゲノムのLong read解析

構造多型は時として非常に複雑: 従来のシーケンサーでは検出困難

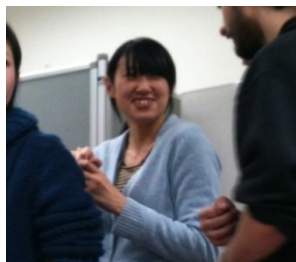
Research

Long-read sequencing for non-small-cell lung cancer genomes

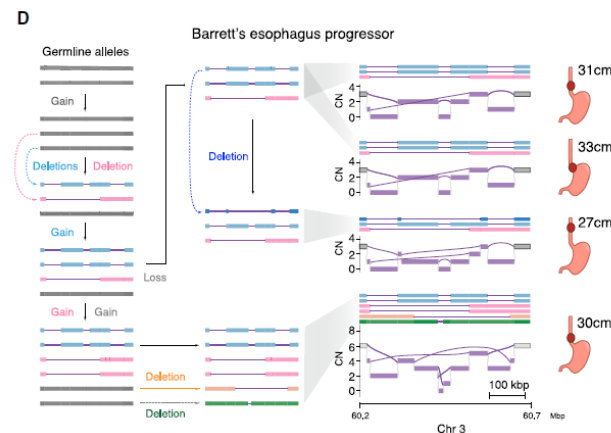
Yoshitaka Sakamoto,¹ Liu Xu,¹ Masahide Seki,¹ Toshiyuki T. Yokoyama,¹ Masahiro Kasahara,¹ Yukie Kashima,^{2,3} Akihiro Ohashi,³ Yoko Shimada,⁴ Noriko Motoi,⁵ Katsuya Tsuchihara,² Susumu S. Kobayashi,³ Takashi Kohno,⁴ Yuichi Shiraishi,⁶ Ayako Suzuki,^{1,2} and Yutaka Suzuki¹

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Genome Res. published online September 4, 2020
Access the most recent version at doi:[10.1101/gr.261941.120](https://doi.org/10.1101/gr.261941.120)



鈴木絢子准教授
(CBMS, 東大新領域)



肺がんTranscriptomeのLong read解析

がんのスプライス異常がネオ抗原の母地になっている可能性

Oka et al. Genome Biology (2021) 22:9
<https://doi.org/10.1186/s13059-020-02240-8>

Genome Biology

RESEARCH

Open Access

Aberrant splicing isoforms detected by full-length transcriptome sequencing as transcripts of potential neoantigens in non-small cell lung cancer

Miho Oka^{1,2†}, Liu Xu^{1†}, Toshihiro Suzuki^{3,4}, Toshiaki Yoshikawa⁴, Hiromi Sakamoto⁵, Hayato Uemura⁶, Akiyasu C. Yoshizawa⁶, Yutaka Suzuki^{1*}, Tetsuya Nakatsura⁴, Yasushi Ishihama⁶, Ayako Suzuki¹ and Masahide Seki^{1*}



NMDのおこらないガンが多い?

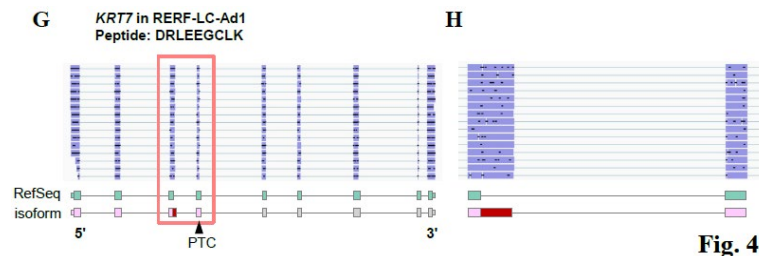


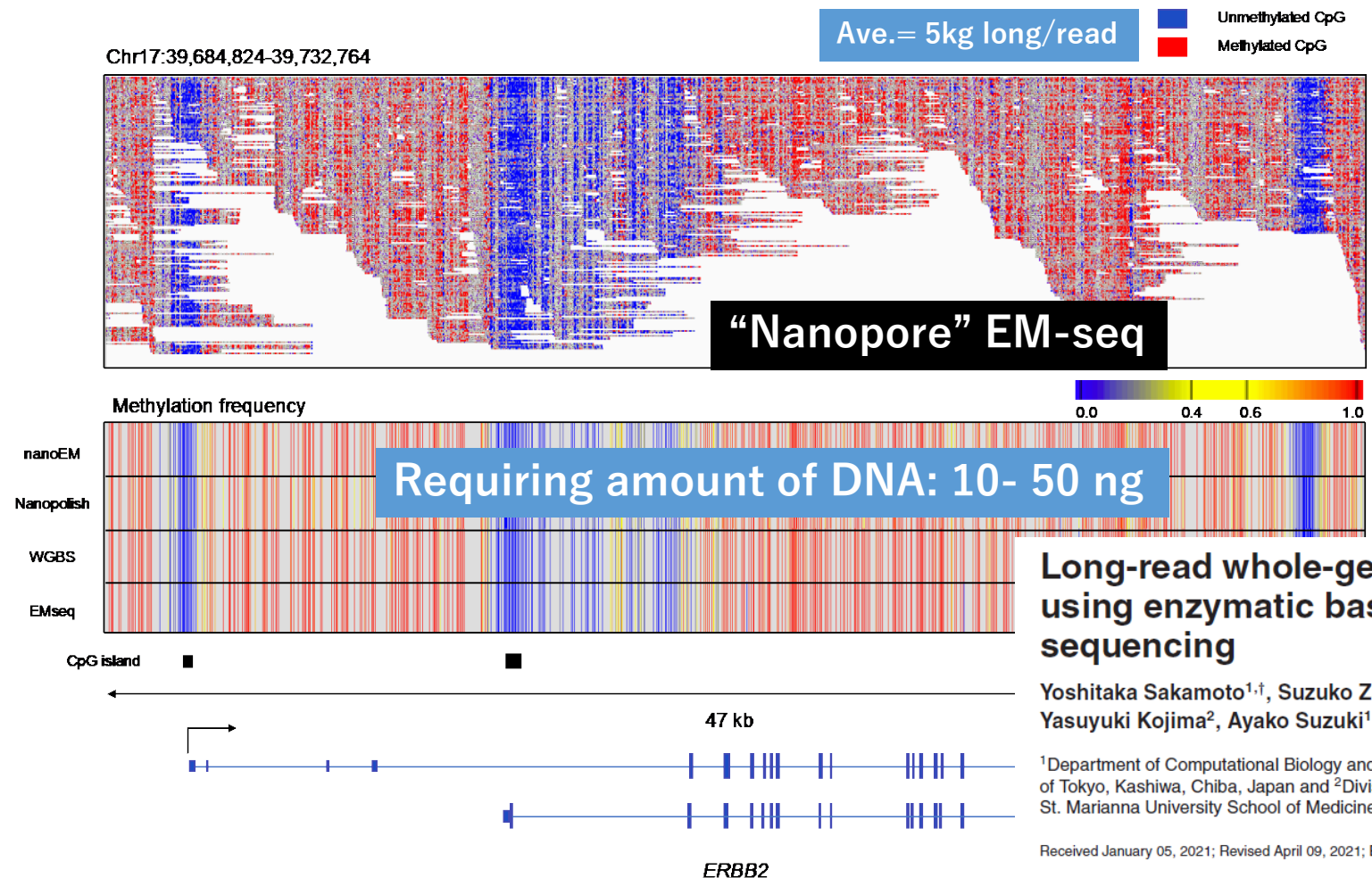
Fig. 4



岡実穂 DSTEP博士課程学生
(小野薬品工業/CBMS, 東大新領域)

エピゲノム（DNAメチル化）の長鎖解析

Long read Methylation Analysis using nanoEM-seq



関真秀DSTEP特任准教授
(CBMS, 東大新領域)

Sakamoto et al. NAR 2021

Long-read whole-genome methylation patterning using enzymatic base conversion and nanopore sequencing

Yoshitaka Sakamoto^{1,†}, Suzuko Zaha^{1,†}, Sato Nagasawa¹, Shuhei Miyake¹, Yasuyuki Kojima², Ayako Suzuki¹, Yutaka Suzuki^{1,*} and Masahide Seki^{1,*}

¹Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, The University of Tokyo, Kashiwa, Chiba, Japan and ²Division of Breast and Endocrine Surgery, Department of Surgery, St. Marianna University School of Medicine, Kawasaki, Kanagawa, Japan

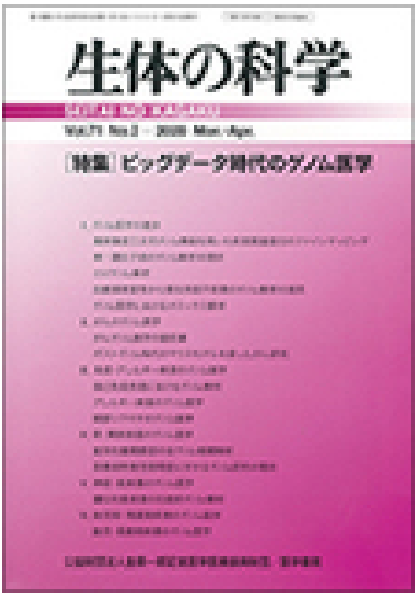
Received January 05, 2021; Revised April 09, 2021; Editorial Decision April 23, 2021; Accepted April 30, 2021

国内総説を用いた広報活動

遺伝子医学34号(2020)



生体の科学(2020)



その他

遺伝子医学35号(2021)

和光純薬時報(2021)

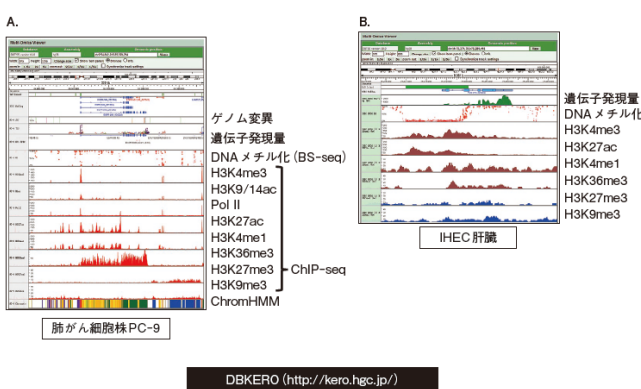
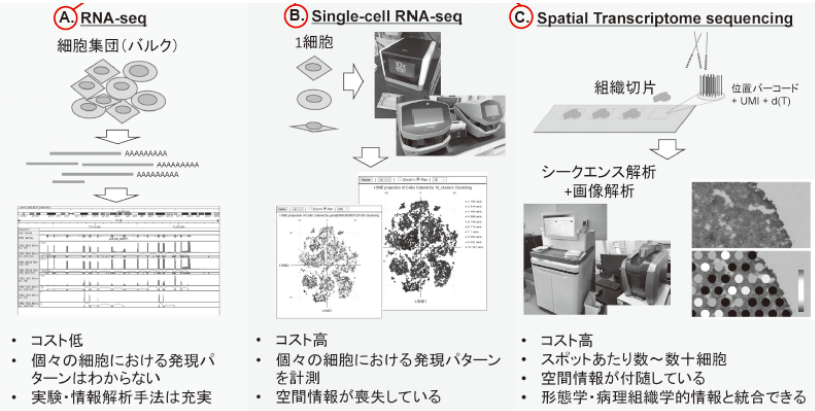


図 2 DBKERO におけるがん細胞および正常組織のエピゲノムおよびマルチオミクスステータス

疾患ヒトゲノム変異の生物学的機能注釈を目指した多階層オーミクスデータの統合

トーゴの日シンポジウム2021

<http://dbkero.hgc.jp/>

まずはデータだけでも見てみたい！

※近日公開

Yamagishi et al
Nat Com 2021

Nagasawa et al
Com Biol 2021

DBKERO
Database of Korean Encyclopedia for Researcher of multi-Omics data

Quick-start: For the beginners

Recommend to use Edge (ver. 40 or above), Google Chrome (ver. 81 or above) or Firefox (ver. 86 or above) for the DBKERO browsing. We do not support Internet Explorer any more.

Viewer [How to use]

- Multi-Omics** [Browse multi-omics data]
- ATLシングルセルデータ** [Single cell dataset]
- シングルセルデータ加工のTutorial動画** [Tutorial video for single cell data processing]
- Mutation Enriched Genes [Help video (Japanese)]:** Find out which gene is mutated most in our data.
- VISIUMのデータ (空間トランスクリプトーム解析)** [Visium dataset]
- Pathway Map [Help video (Japanese)]:** Find out the level of expression or modification of genes within a Pathway.
- Chromatin-status Data Summary [Help video (Japanese)]:** Get an overall view of expression and modification of a genome region among our entire data sets.

Featured Dataset

- Single cell dataset [Download processed data]:** Single cell dataset
- Cancer SV data** [Download processed data]: Japanese lung adenocarcinoma sequenced by PromethION (Oxford Nanopore Technologies).
- Visium dataset New** [Download processed data]: Spatial Gene Expression data sequenced by Visium (Oxford Nanopore Technologies).
- Cancer LongRNA Dataset New** [Download processed data]: Aberrant splicing isoforms in non-small cell lung cancer sequenced by MinION (Oxford Nanopore Technologies).

Download

- Data Portal [Help video (Japanese)]**
- Data Portal PAGS:Genome Shien(ゲノム支援)**

Sakamoto et al
Genome Res 2020

Oka et al
Genome Biol 2021

Sakamoto et al
NAR 2021

日本人健常者末梢血scRNA

健常者が日常生活でどのようにscRNAを変化させるのか？

がんゲノム長鎖Phasingデータ

がん変異の染色体背景は？
(相同染色体は等価か？)

ゲノム支援データポータル

ご質問は:
ysuzuki@hgc.jp
まで。