

2021.01.13

NBDC AJACS ONLINE5

マルチオミクス解析(DBKERO)

Part II: 実践篇

東京大学新領域創成科学研究所
鹿島幸恵

Introduction

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Viewer [How to use]

- Multi-Omics-Viewer** [Help video^{1,2,3} (Japanese)], [GitHub]: Browse mutations, transcripts and epigenetic modifications along the genome coordinates.
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- SNV Summary in Cancers** [Help 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 [Help video (Japanese)]
- SV viewer^{New}

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.

Download

- Data Portal [Help video (Japanese)]
- Data Portal (PAGS)

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.)

How to use genome browser (Basic)

How to use genome browser (Track selection)

(<https://kero.hgc.jp/>)

DBTSS/DBKERO

:実験学的に保証された5'端配列(TSS)

- Oligo capping method
- CAP tapper method

現在利用可能なツール

- Single cell dataset
- Cancer SV dataset ←new !
- Visium dataset ←new !
- Data Portal
- Data Portal (PAGS)
- Multi-Omics-Viewer
- TSS viewer
- Mutation enriched gene
- TF-bind site search
- Pathway map
- Chromatin-status Data summary
- SNV summary in cancers
- RDF gate(Trial)
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本日ご紹介するツール

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- SNV summary in cancers
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- Single cell viewer
- SV viewer

統合オミクスデータベースDBKEROの具体的な操作方法を解説します

I, Data Portal

- IHEC (International Human Epigenome Consortium)のデータを利用する
- 国内の研究データを利用する

II, Multi-Omics Viewer

- 多階層のデータを一覧する
- 解析例: TERT (promoterの変異と関連するomicsデータの俯瞰)

III, Pathway MAP

- Pathway上に様々な情報を反映させる

IV, SV viewer

V, Summary

I, Data Portal

DBKERO
Database of Keio Encyclopedia for Researches of multi-Omics data

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

Click !!!

I, Data Portal - Part 1: IHEC -

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Other tools

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- [SV viewer](#)^{New}

DBKERO Data Portal

2579 Hits
[Batch download](#)
[TSV](#)

Matrix
List

Assay>>>		Single cell	Nanopore	GWAS	Cancer Cell Line	Drug Perturbation
IHEC						
Total	583	1163	3	20	478	332
ChIP-Seq	423	0	0	0	216	0
RNA-Seq	105	1163	0	0	53	226
BS-Seq	55	0	0	0	26	0
Resequencing	0	0	3	0	78	0
GWAS	0	0	0	20	0	0
ChromHMM	0	0	0	0	27	0
TSS-Seq	0	0	0	0	26	0
CNV	0	0	0	0	26	0
SV	0	0	0	0	26	0
ATAC-Seq	0	0	0	0	0	106

I, Data Portal - Part 1: IHEC -

IHEC: International Human Epigenome Consortium > 左のメニューからデータの絞り込みが可能です

Race:

- Japanese (583)
- Worldwide (0)

Omics Category:

- Epigenome (478)
- Transcriptome (105)
- Genome (0)

Reference Genome:

- hg38 (583)

Data Category:

- IHEC (583)
- Lung adenocarcinoma 26 cell lines (0)
- GWAS (0)
- Drug perturbation (0)

Assay:

- ChIP-Seq (423)
- RNA-Seq (105)
- BS-Seq (55)
- Resequencing (0)
- GWAS (0)
- ChromHMM (0)
- TSS-Seq (0)
- CNV (0)
- SV (0)
- ATAC-Seq (0)

File Format:

- BigWig (read depth) (481)
- BigWig (read depth) x2 (15)
- TSV (BS) (42)
- BigWig (BS) (13)
- TSV (exon/intron junction) (32)
- TSV (expression level) (0)
- TSV (expression distribution) (0)
- BAM (0)
- TSV (GWAS) (0)
- TSV (ChromHMM) (0)
- TSV (TSS) (0)
- TSV (SNP/SNV) (0)
- TSV (read depth) (0)
- TSV (CNV) (0)
- TSV (translocation) (0)
- TSV (expression fold-change) (0)

583 Hits [Batch download](#) [TSV](#)

Matrix List

Track ID	Project	Race	Omics Category	Object ID	Object Description	Reference Genome	Data Category	Assay	File Format	Download
1	IHEC	Japanese	Epigenome	COC11_H3K27Ac_hg38	IHEC COC11 H3K27Ac (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
2	IHEC	Japanese	Epigenome	COC11_H3K27me3_hg38	IHEC COC11 H3K27me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
3	IHEC	Japanese	Epigenome	COC11_H3K36me3_hg38	IHEC COC11 H3K36me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
4	IHEC	Japanese	Epigenome	COC11_H3K4me1_hg38	IHEC COC11 H3K4me1 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
5	IHEC	Japanese	Epigenome	COC11_H3K4me3_hg38	IHEC COC11 H3K4me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
6	IHEC	Japanese	Epigenome	COC11_H3K9me3_hg38	IHEC COC11 H3K9me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
7	IHEC	Japanese	Transcriptome	COC11_rnaseq_bw_hg38	IHEC COC11 RNA-seq (bw)	hg38	IHEC	RNA-Seq	BigWig (read depth)	Download
8	IHEC	Japanese	Epigenome	COC14_H3K27Ac_hg38	IHEC COC14 H3K27Ac (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
9	IHEC	Japanese	Epigenome	COC14_H3K27me3_hg38	IHEC COC14 H3K27me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
10	IHEC	Japanese	Epigenome	COC14_H3K36me3_hg38	IHEC COC14 H3K36me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
11	IHEC	Japanese	Epigenome	COC14_H3K4me1_hg38	IHEC COC14 H3K4me1 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
12	IHEC	Japanese	Epigenome	COC14_H3K4me3_hg38	IHEC COC14 H3K4me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download
13	IHEC	Japanese	Epigenome	COC14_H3K9me3_hg38	IHEC COC14 H3K9me3 (bw)	hg38	IHEC	ChIP-Seq	BigWig (read depth)	Download

I, Data Portal - Part 2: PAGS -

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Release 1.2.5 Updated (Dec. 05, 2020)
Based on UCSC hg38, mm10
Formerly DBTSS

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Top > Data portal

DBKERO Data Portal

Project: 292 Hits Batch download TSV

Organism: Matrix List

Omics Category:

Reference Genome:

Data Category:

Assay:

File Format:

Read Type:

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- [Data Portal \(PAGS\)](#)

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Assay>>>	Ooshima Masanobu	Tamura Tomohiko	Yasuyuki Onodera	Suzuki Ayako	Matsuhashita Tomonao	Mino Takashi	Fujita Toshitsugu	Shigyo Masayoshi	Iwama Atsushi
Total	18	20	6	75	7	20	11	60	39
RNA-Seq	18	18	6	0	0	20	0	60	4
ChIP-Seq	0	2	0	0	0	0	7	0	29
WGS	0	0	0	2	0	0	0	0	0
TSS-Seq	0	0	0	27	7	0	0	0	0
Exome	0	0	0	46	0	0	0	0	0
enChIP-seq	0	0	0	0	0	0	4	0	0
RRBS	0	0	0	0	0	0	0	0	6

I, Data Portal - Part 2: PAGS -

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Featured

- Single cell**
Single cell
- Cancer S**
Japanese I
Nanopore
- Visium d**
Spatial Gen
Spacerang

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Matrix List

Project>>>

	Oshima Masanobu	Tamura Tomohiko	Yasuyuki Onodera	Suzuki Ayako	Matsuhashita Tomonao	Mino Takashi	Fujita Toshitsugu	Shigyo Masayoshi	Iwama Atsushi
Total	18	20	6	75	7	20	11	60	39
RNA-Seq	18	18	6	0	0	20	0	60	4
ChIP-Seq	0	2	0	0	0	0	7	0	29
WGS	0	0	0	2	0	0	0	0	0
TSS-Seq	0	0	0	27	7	0	0	0	0
Exome	0	0	0	46	0	0	0	0	0
enChIP-seq	0	0	0	0	0	0	4	0	0
RRBS	0	0	0	0	0	0	0	0	6

Assay>>>

Ooshima Masanobu

Total	18	20
RNA-Seq	18	18
ChIP-Seq	0	2
WGS	0	0
TSS-Seq	0	0
Exome	0	0
enChIP-seq	0	0
RRBS	0	0

Tamura Tomohiko

Total	18	20
RNA-Seq	18	18
ChIP-Seq	0	2
WGS	0	0
TSS-Seq	0	0
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I, Data Portal - Part 2: PAGS -

国内の研究データを様々な項目から検索できます

>Project:

- ▼Project:
 - Ooshima Masanobu (18)
 - Tamura Tomohiko (20)
 - Yasuyuki Onodera (6)
 - Suzuki Ayako (75)
 - Matsushita Tomonao (7)
 - Mino Takashi (20)
 - Fujita Toshitsugu (11)
 - Shigyo Masayoshi (60)
 - Iwama Atsushi (39)
 - Kuroyanagi Hidehito (4)
 - Goto Yukiko (1)
 - Kuba Keiji (1)
 - Mitsuya Shiro (12)
 - Sawabe Tomoo (9)
 - Matsuno Keita (3)
 - Mitsuhashi Satomi (6)

>Organism:

- ▼Organism:
 - Mus musculus (87)
 - Spinacia oleracea (6)
 - Homo sapiens (100)
 - Arabidopsis thaliana (7)
 - Gallus gallus (7)
 - Allium fistulosum (60)
 - Caenorhabditis elegans (4)
 - Oryza sativa (12)
 - Vibrio haloticoli (3)
 - Vibrio tritonius (6)

>Omics Category:

- ▼Omics Category:
 - Transcriptome (200)
 - Epigenome (44)
 - Genome (48)

>Reference Genome:

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 - Mus musculus (87)
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 - Oryza sativa (12)
 - Vibrio haloticoli (3)
 - Vibrio tritonius (6)

>Data Category:

- ▼Assay:
 - RNA-Seq (162)
 - ChIP-Seq (38)
 - WGS (2)
 - TSS-Seq (34)
 - Exome (46)
 - enChIP-seq (4)
 - RRBS (6)

>Assay:

>File Format:

- ▼File Format:
 - FASTQ (290)
 - TSV (GEO expression) (2)

- ▼Read Type:
 - Single-end (178)
 - Paired-end R1 (56)
 - Paired-end R2 (56)
 - NA (2)

I, Data Portal - Part 2: PAGS -

Listには関連する情報へのリンクが貼られています

Project主宰者ラボHPへのlink

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Matrix List **Click !!!**

Track ID	Project	Organism	Omics Category	Project Title	Study Title	Object Description	Reference Genome	Data Category	Assay	File Format	Read Type	DRA Accession	Sample Accession	Web URL	DOI	Download
1	Ooshima Masanobu	Mus musculus	Transcriptome	Analysis on colon cancer malignant progression using novel mouse models	Expression analysis of intestinal tumor organoids derived from different driver gene genotypes	Sample: A1E, Strain: C57BL/6	Mus musculus	PAGS	RNA-Seq	FASTQ	Single-end	DRA005647	DRX083302	http://genetics.w3.kanazawa-u.ac.jp/	10.1158/0008-5472.CAN-17-3303	Download
2	Ooshima Masanobu	Mus musculus	Transcriptome	Analysis on colon cancer malignant progression using novel mouse models	Expression analysis of intestinal tumor organoids derived from different driver gene genotypes	Sample: A2E, Strain: C57BL/6	Mus musculus	PAGS	RNA-Seq	FASTQ	Single-end	DRA005647	DRX083303	http://genetics.w3.kanazawa-u.ac.jp/	10.1158/0008-5472.CAN-17-3303	Download
3	Ooshima Masanobu	Mus musculus	Transcriptome	Analysis on colon cancer malignant progression using novel mouse models	Expression analysis of intestinal tumor organoids derived from different driver gene genotypes	Sample: A3E, Strain: C57BL/6	Mus musculus	PAGS	RNA-Seq	FASTQ	Single-end	DRA005647	DRX083304	http://genetics.w3.kanazawa-u.ac.jp/	10.1158/0008-5472.CAN-17-3303	Download
4	Ooshima Masanobu	Mus musculus	Transcriptome	Analysis on colon cancer malignant progression using novel mouse models	Expression analysis of intestinal tumor organoids derived from different driver gene genotypes	Sample: AK1E, Strain: C57BL/6	Mus musculus	PAGS	RNA-Seq	FASTQ	Single-end	DRA005647	DRX083305	http://genetics.w3.kanazawa-u.ac.jp/	10.1158/0008-5472.CAN-17-3303	Download
5	Ooshima Masanobu	Mus musculus	Transcriptome	Analysis on colon cancer malignant progression using novel mouse models	Expression analysis of intestinal tumor organoids derived from different driver gene genotypes	Sample: AK2E, Strain: C57BL/6	Mus musculus	PAGS	RNA-Seq	FASTQ	Single-end	DRA005647	DRX083306	http://genetics.w3.kanazawa-u.ac.jp/	10.1158/0008-5472.CAN-17-3303	Download

II, Multi-Omics-Viewer

DBKERO
 DataBase of Keio Encyclopedia for Researches of multi-Omics data

Quick-start: For the beginners

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.

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.
 - [Search from Genomic Position](#)
 - [Search from SNP \(dbSNP rsID\)](#)
 - [Search from SNV \(COSMIC: somatic mutation\)](#)
- SNV Summary in Cancers** [Help 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](#) [Help video (Japanese)]
 - [SV viewer](#)^{New}

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.

Download

- [Data Portal](#) [Help video (Japanese)]
- [Data Portal \(PAGS\)](#)

Documents

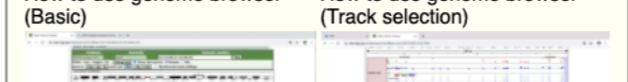
- [Experimental Procedures](#)
- [Data Contents](#)
- [Tutorial](#)
- [Download bulk data](#)
- [References](#)

Movie (For Japanese)

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



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



Click !!!

II, Multi-Omics-Viewer

Multi-Omics-Viewer

Multi-Omics-Viewer:

Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: Keyword:

H. sapiens (hg38) NM_* Search

Genome version or Liftover: Genomic position:

H. sapiens (hg38) chr1:99,950,000-100,050,000:- Search

Font size: 16 Change font size

Show 50 entries

Term	Genomic position
NM_000014	chr12:9,067,708-9,115,962:-
NM_000015	chr8:18,391,245-18,401,213:+
NM_000016	chr1:75,724,347-75,763,678:+
NM_000017	chr12:120,725,768-120,740,008:+
NM_000018	chr17:7,219,831-7,225,267:+
NM_000019	chr11:108,121,531-108,148,164:+
NM_000020	chr12:51,907,418-51,923,361:+
NM_000021	chr14:73,136,435-73,223,691:+
NM_000022	chr20:44,619,522-44,651,735:-
NM_000023	chr17:50,166,005-50,175,932:+
NM_000024	chr5:148,826,593-148,828,634:+
NM_000025	chr8:37,962,996-37,966,666:-

[上段]

Species

- hg38/mm10

Keyword

- NM_*
- Gene symbol

[下段]

Genome versions or Leftover

- hg38, hg19 to hg38, mm10

Genomic position

- locationからも検索ができる

[TSS viewer](#)

[Multi-Omics-Viewer](#)

Click !!!

II, Multi-Omics-Viewer : Ex) TERT

TERTのプロモーター変異と周辺のデータをMulti-Omics-Viewerを使って解析する

DBKERO
Database of Koshien Encyclopedia for Researches of multi-Omics data

Quick-start: For the beginners

Release

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 anymore.

[Viewer](#) | [Tutorial](#)

Viewer [How to use]

Click !!! 

- Multi-Omics-Viewer** [Help video1,2,3 (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)]:

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.

Download

- **Data Portal** [[Help video](#) (Japanese)]
- **Data Portal (PAGS)**

II, Multi-Omics-Viewer : Ex) TERT

1) Multi-Omics-ViewerでTERTを検索する

Multi-Omics-Viewer:

Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: Keyword: 解析したい遺伝子のsymbol(“TERT”)を入力

H. sapiens (hg38) ▼ TERT Search

Genome version or Liftover: Genomic position:

H. sapiens (hg38) ▼ chr1:99,950,000-100,050,000:- Search

2) Go to “Multi-Omics-Viewer”を選択する

Multi-Omics-Viewer:

Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: Keyword:

H. sapiens (hg38) ▼ TERT Search

Genome version or Liftover: Genomic position:

H. sapiens (hg38) ▼ chr1:99,950,000-100,050,000:- Search

Font size: 16 Change font size

Show 50 ▼ entries

Search:

Term ▲

Genomic position

Go to

Go to

TERT

chr5:1,253,172-1,295,047:-

[TSS viewer](#)

[Multi-Omics-Viewer](#)

Showing 1 to 1 of 1 entries

Click !!!

Previous

1

Next

II, Multi-Omics-Viewer : Ex) TERT

3) defaultでは下記のようなデータが表示される



II, Multi-Omics-Viewer : Ex) TERT

4) 臨床データを追加して表示してみる

Multi-Omics-Viewer:
Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: H. sapiens (hg38) Keyword: keyword (e.g. EGFR, NM) Search

Genome version or Liftover: H. sapiens (hg38) Genomic position: chr5:1,260,150-1,288,068: Search

Multi-Omics-Viewer

Database: DBTSS version 10.0 Assembly: hg38 Genomic position: chr5:1,260,150-1,288,068: View

Width: 926, Height: 500 Change size: Show item panel | Browse Info.

zoom in: 1.5x 2x 5x zoom out: 2/3x 1/2x 1/5x Synchronize track settings

chr5:1,260,150-1,288,068: 1,280,000 1,270,000 1,260,000

Your Query Sequence CpG Island NCBI RefSeq IHEC HPC8 H3K e3 (bw) IHEC COC15 H3 me3 (bw) PC-9 Chromium Gefitinib ppm distribution PC-7 GemCode assing Pattern PC-9 GemCode assing Pattern

>500ppm Haplotype 1 Haplotype 2 Unphased Haplotype 1 Haplotype 2 Unphased Haplotype 1

Add separator Clear all tracks Show basic public data (Sequence+RefSeq+CpG)

Tracks

Basic Items

Sequence CpG Island NCBI RefSeq UCSC gene
 Human vs Mouse Human vs Chimp Human vs Macaque Human vs Rat Human vs Zebrafish

Datasets

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input checked="" type="radio"/> Genome	<input checked="" type="radio"/> Normal cell	<input type="radio"/> Cell lines	<input type="checkbox"/> Others	
<input type="radio"/> Worldwide	<input type="radio"/> Epigenome	<input type="radio"/> Cancer cell	<input checked="" type="radio"/> Clinical samples	<input type="checkbox"/> SCLC	
	<input type="radio"/> Transcriptome	<input type="radio"/> Unphased		<input type="checkbox"/> TCGA	<input checked="" type="checkbox"/> SNP_SNV
					<input checked="" type="checkbox"/> ICGC

ICGC Liver Cancer - NCC, JP
 ICGC Liver Cancer - RIKEN, JP
 ICGC Biliary tract cancer - JP

4-1) 日本人のがんのデータ(臨床)を追加

Japanese → Genome → Cancer cell → Clinical samples
 → ICGC → SNP_SNV

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input checked="" type="radio"/> Genome	<input type="radio"/> Normal cell	<input type="radio"/> Cell lines	<input type="checkbox"/> Others	
<input type="radio"/> Worldwide	<input type="radio"/> Epigenome	<input type="radio"/> Cancer cell	<input checked="" type="radio"/> Clinical samples	<input type="checkbox"/> SCLC	
	<input type="radio"/> Transcriptome	<input type="radio"/> Unphased		<input type="checkbox"/> TCGA	<input checked="" type="checkbox"/> SNP_SNV
					<input checked="" type="checkbox"/> ICGC

- ICGC Liver Cancer - NCC, JP
 ICGC Liver Cancer - RIKEN, JP
 ICGC Biliary tract cancer - JP

4-2) 日本人のNormal cellのデータ(臨床)を追加

Japanese → Genome → Normal cell → Clinical samples
 → HGVD/JapanPGx → SNP_SNV

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input checked="" type="radio"/> Genome	<input checked="" type="radio"/> Normal cell	<input type="radio"/> Cell lines	<input type="checkbox"/> GWAS	
<input type="radio"/> Worldwide	<input type="radio"/> Epigenome	<input type="radio"/> Cancer cell	<input type="radio"/> Clinical samples	<input checked="" type="checkbox"/> HGVD	<input checked="" type="checkbox"/> SNP_SNV
	<input type="radio"/> Transcriptome	<input type="radio"/> Unphased		<input checked="" type="checkbox"/> JapanPGx	

- Nagahama Japanese SNP
 Japan PGx (Japanese SNP)

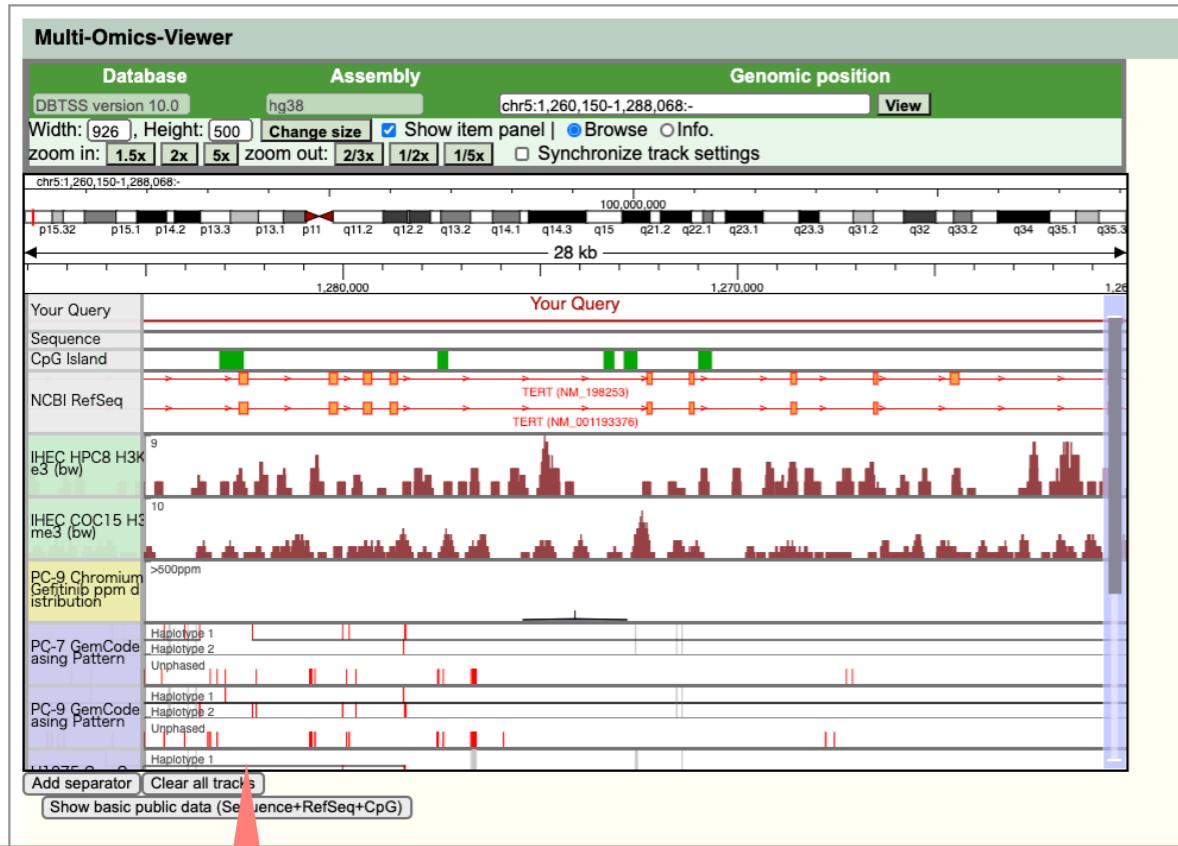
II, Multi-Omics-Viewer : Ex) TERT

5) セルラインのデータを追加して表示する

Multi-Omics-Viewer:
Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: H. sapiens (hg38) Keyword: keyword (e.g. EGFR, NM) Search

Genome version or Liftover: H. sapiens (hg38) Genomic position: chr5:1,260,150-1,288,068: Search



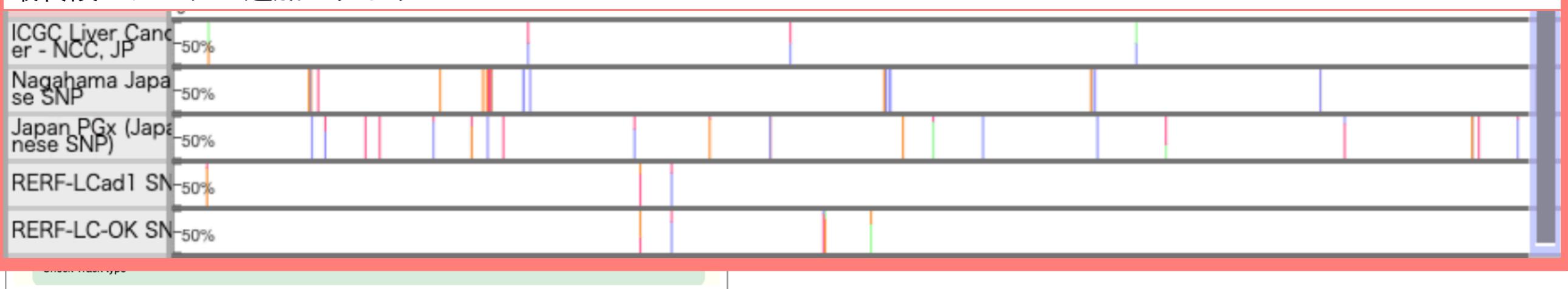
4-3) cell lineのデータを追加

Japanese → Genome → Cancer cell → Clinical samples
→ ICGC → SNP_SNV

Standard multi-omics data

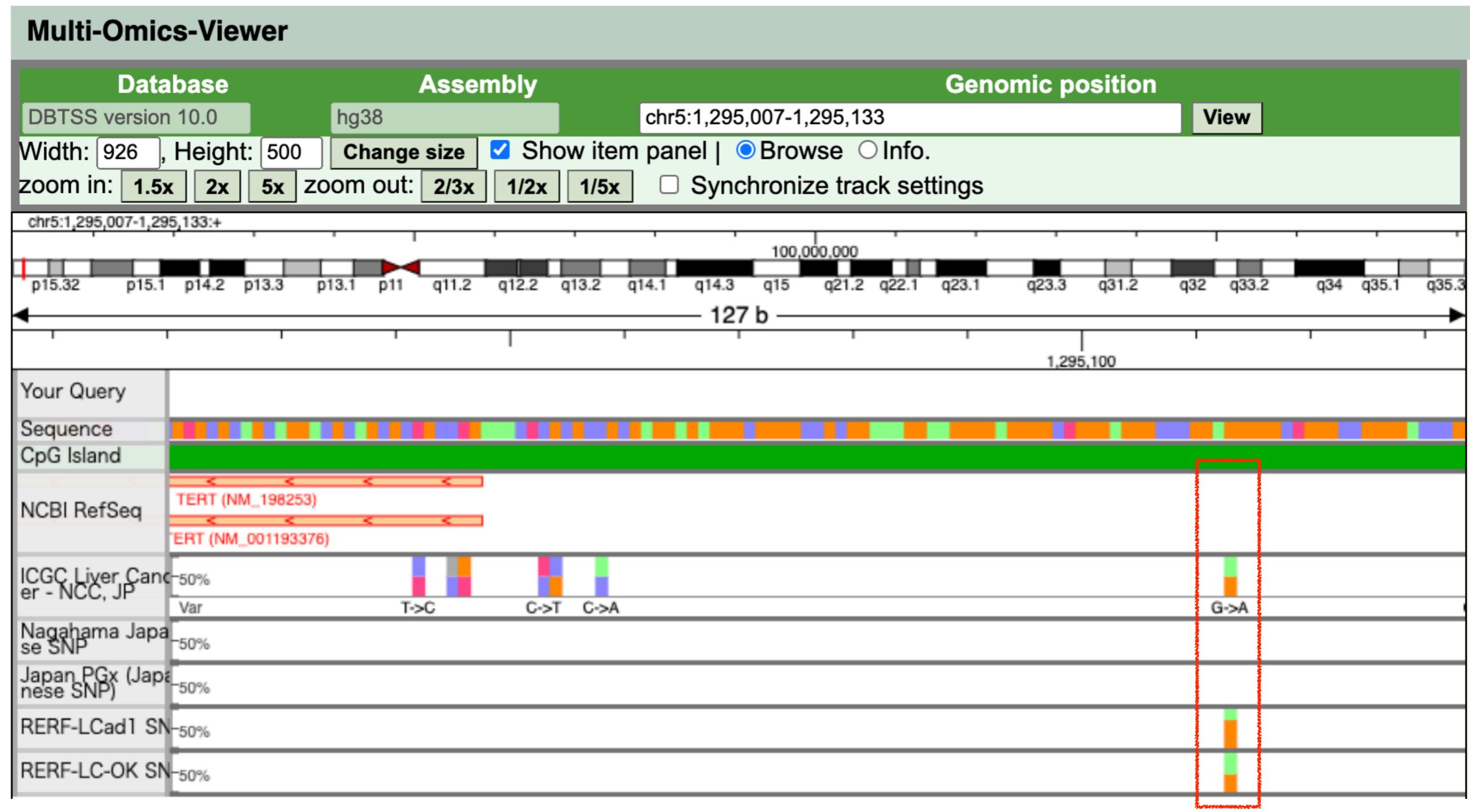
Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese <input type="radio"/> Worldwide	<input checked="" type="radio"/> Genome <input type="radio"/> Epigenome <input type="radio"/> Transcriptome	<input type="radio"/> Normal cell <input checked="" type="radio"/> Cell lines <input checked="" type="radio"/> Cancer cell <input type="radio"/> Clinical samples	<input checked="" type="checkbox"/> Cell_lines	<input checked="" type="checkbox"/> SNP_SNV <input type="checkbox"/> ChIP_bw <input type="checkbox"/> BAM <input type="checkbox"/> CNV <input type="checkbox"/> Gene_Fusion	
<input type="checkbox"/> 26 lung adenocarcinoma cell lines <input type="checkbox"/> LC2/ad SNV <input type="checkbox"/> PC-3 SNV <input type="checkbox"/> PC-7 SNV <input type="checkbox"/> PC-9 SNV <input type="checkbox"/> PC-14 SNV <input checked="" type="checkbox"/> RERF-LCad1 SNV <input type="checkbox"/> RERF-LCad2 SNV <input type="checkbox"/> RERF-LC-KJ SNV <input type="checkbox"/> RERF-LC-MS SNV <input checked="" type="checkbox"/> RERF-LC-OK SNV <input type="checkbox"/> VMRC-LCD SNV <input type="checkbox"/> ABC-1 SNV <input type="checkbox"/> II-18 SNV					
less					

最終段にデータが追加されます



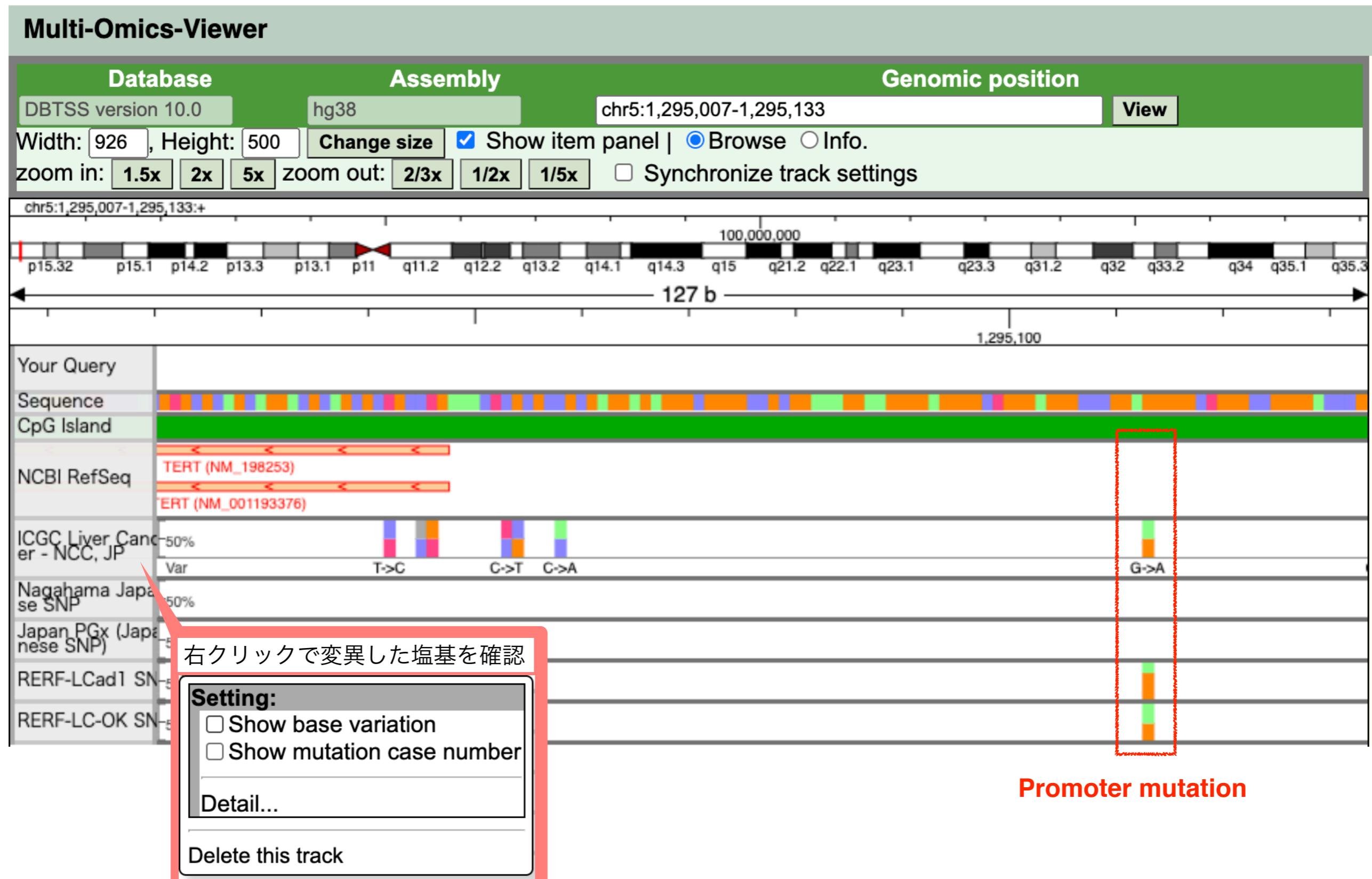
II, Multi-Omics-Viewer : Ex) TERT

6) TERTのpromoter領域にZoom inする



II, Multi-Omics-Viewer : Ex) TERT

7) 変異した塩基を確認する



II, Multi-Omics-Viewer : Ex) TERT

8) Promoterの変異が確認できたので、データを追加して一覧で確認してみる

Multi-Omics-Viewer:

Browse mutations, transcripts and epigenetic modifications along the genome coordinates.

Species: Keyword:

H. sapiens (hg38) ▾ TERT

Genome version or Liftover: Genomic position:

H. sapiens (hg38) ▾ chr1:99,950,000-100,050,000:-

再度、TERTを”search”するところからスタート。

II, Multi-Omics-Viewer : Ex) TERT

9) セルラインのデータを追加して表示する(Genome)

Datasets “Japanese” → “Genome”→ “Cancer cell”→“Cell lines” → “SNP_SNV”

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese <input type="radio"/> Worldwide	<input checked="" type="radio"/> Genome <input type="radio"/> Epigenome <input type="radio"/> Transcriptome	<input type="radio"/> Normal cell <input checked="" type="radio"/> Cancer cell	<input checked="" type="radio"/> Cell lines <input type="radio"/> Clinical samples	<input checked="" type="checkbox"/> Cell_lines	<input checked="" type="checkbox"/> SNP_SNV <input type="checkbox"/> ChIP_bw <input type="checkbox"/> BAM <input type="checkbox"/> CNV <input type="checkbox"/> Gene_Fusion
<ul style="list-style-type: none"><input type="checkbox"/> 26 lung adenocarcinoma cell lines<input type="checkbox"/> LC2/ad SNV<input type="checkbox"/> PC-3 SNV<input type="checkbox"/> PC-7 SNV<input type="checkbox"/> PC-9 SNV					
<p>more...</p> <div style="border: 2px solid red; padding: 10px; margin-top: 10px;"><ul style="list-style-type: none"><input type="checkbox"/> 26 lung adenocarcinoma cell lines<input type="checkbox"/> LC2/ad SNV<input type="checkbox"/> PC-3 SNV<input type="checkbox"/> PC-7 SNV<input checked="" type="checkbox"/> PC-9 SNV<input type="checkbox"/> PC-14 SNV<input checked="" type="checkbox"/> RERF-LCad1 SNV<input type="checkbox"/> RERF-LCad2 SNV<input type="checkbox"/> RERF-LC-KJ SNV<input type="checkbox"/> RERF-LC-MS SNV<input checked="" type="checkbox"/> RERF-LC-OK SNV<input type="checkbox"/> VMRC-LCD SNV<input type="checkbox"/> ABC-1 SNV<input type="checkbox"/> II-18 SNV<p>less</p></div>					

“more...”でcell lineを表示
→ 3つの系列を選択

II, Multi-Omics-Viewer : Ex) TERT

10) セルラインのデータを追加して表示する(epigenome/ChIP-seq, H3K4me3)

Datasets

“Japanese” → “Epigenome” → “Cancer cell” → “Cell lines” → “ChIP_H3Kme3”

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input type="radio"/> Genome	<input type="radio"/> Normal cell	<input checked="" type="radio"/> Cell lines	<input checked="" type="checkbox"/> Cell_lines	<input type="checkbox"/> ChromHMM
<input type="radio"/> Worldwide	<input checked="" type="radio"/> Epigenome	<input type="radio"/> Cancer cell	<input type="radio"/> Clinical samples		<input type="checkbox"/> BS
	<input type="radio"/> Transcriptome				<input checked="" type="checkbox"/> ChIP_H3K4me3
					<input type="checkbox"/> ChIP_H3K4me1
					<input type="checkbox"/> ChIP_H3K27me3
					<input type="checkbox"/> ChIP_PolII
					<input type="checkbox"/> ChIP_H3ac
					<input type="checkbox"/> ChIP_H3K9me3
					<input type="checkbox"/> ChIP_H3K36me3
					<input type="checkbox"/> ChIP_H3K27ac
<hr/>					
<div style="border: 1px solid red; padding: 5px;"><input type="checkbox"/> SAEC H3K4me3 <input type="checkbox"/> LC2/ad H3K4me3 <input checked="" type="checkbox"/> PC-9 H3K4me3 <input type="checkbox"/> ABC-1 H3K4me3 <input type="checkbox"/> II-18 H3K4me3 <input type="checkbox"/> PC-14 H3K4me3 <input type="checkbox"/> PC-3 H3K4me3 <input type="checkbox"/> PC-7 H3K4me3 <input type="checkbox"/> RERF-LC-KJ H3K4me3 <input type="checkbox"/> RERF-LC-MS H3K4me3 <input checked="" type="checkbox"/> RERF-LC-OK H3K4me3 <input checked="" type="checkbox"/> RERF-LC-ad1 H3K4me3 <input type="checkbox"/> RERF-LC-ad2 H3K4me3 <input type="checkbox"/> VMRC-LCD H3K4me3</div>					
<hr/>					
<p>“more...”でcell lineを表示 → 3つの系列を選択 PC-9 H3K4me3, RERF-LC-OK H3K4me3, RERF-LC-OK H3K4me3</p>					

II, Multi-Omics-Viewer : Ex) TERT

11) セルラインのデータを追加して表示する(epigenome/ChIP-seq, ChIP_PolIII)

Datasets

“Japanese” → “Epigenome” → “Cancer cell” → “Cell lines” → “ChIP_PolIII”

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input type="radio"/> Genome	<input type="radio"/> Normal cell	<input checked="" type="radio"/> Cell lines	<input checked="" type="checkbox"/> Cell_lines	<input type="checkbox"/> ChromHMM
<input type="radio"/> Worldwide	<input checked="" type="radio"/> Epigenome	<input checked="" type="radio"/> Cancer cell	<input type="radio"/> Clinical samples		<input type="checkbox"/> BS
	<input type="radio"/> Transcriptome				<input type="checkbox"/> ChIP_H3K4me3
					<input type="checkbox"/> ChIP_H3K4me1
					<input type="checkbox"/> ChIP_H3K27me3
					<input checked="" type="checkbox"/> ChIP_PolIII
					<input type="checkbox"/> ChIP_H3ac
					<input type="checkbox"/> ChIP_H3K9me3
					<input type="checkbox"/> ChIP_H3K36me3
					<input type="checkbox"/> ChIP_H3K27ac
<input type="checkbox"/> SAEC PolIII		<input type="checkbox"/> SAEC PolIII			
<input type="checkbox"/> LC2/ad PolIII		<input type="checkbox"/> LC2/ad PolIII			
<input type="checkbox"/> PC-9 PolIII		<input checked="" type="checkbox"/> PC-9 PolIII			
<input type="checkbox"/> ABC-1 PolIII		<input type="checkbox"/> ABC-1 PolIII			
<input type="checkbox"/> II-18 PolIII		<input type="checkbox"/> II-18 PolIII			
<input type="checkbox"/> PC-14 PolIII		<input type="checkbox"/> PC-14 PolIII			
<input type="checkbox"/> PC-3 PolIII		<input type="checkbox"/> PC-3 PolIII			
<input type="checkbox"/> PC-7 PolIII		<input type="checkbox"/> PC-7 PolIII			
<input type="checkbox"/> RERF-LC-KJ PolIII		<input type="checkbox"/> RERF-LC-KJ PolIII			
<input type="checkbox"/> RERF-LC-MS PolIII		<input type="checkbox"/> RERF-LC-MS PolIII			
<input checked="" type="checkbox"/> RERF-LC-OK PolIII		<input checked="" type="checkbox"/> RERF-LC-OK PolIII			
<input checked="" type="checkbox"/> RERF-LC-ad1 PolIII		<input checked="" type="checkbox"/> RERF-LC-ad1 PolIII			
<input type="checkbox"/> RERF-LC-ad2 PolIII		<input type="checkbox"/> RERF-LC-ad2 PolIII			
<input type="checkbox"/> VMRC-LCD PolIII		<input type="checkbox"/> VMRC-LCD PolIII			

“more...”でcell lineを表示

→ 3つの系列を選択

PC-9 PolIII, RERF-LC-OK PolIII, RERF-LC-OK PolIII

II, Multi-Omics-Viewer : Ex) TERT

12) セルラインのデータを追加して表示する(transcriptome/TSS-seq and RNA-seq)

“Japanese” → “Transcriptome” → “Cancer cell” → “Cell lines” → “TSS”, “RPKM”

Standard multi-omics data

Ethnic	Omics Category	Tissue Type	Sample Type	Dataset	Track Type
<input checked="" type="radio"/> Japanese	<input type="radio"/> Genome	<input type="radio"/> Normal cell	<input checked="" type="radio"/> Cell lines	<input checked="" type="checkbox"/> Cell_lines	<input checked="" type="checkbox"/> TSS
<input type="radio"/> Worldwide	<input type="radio"/> Epigenome	<input checked="" type="radio"/> Cancer cell	<input type="radio"/> Clinical samples		<input type="checkbox"/> RNA_Junction
	<input checked="" type="radio"/> Transcriptome				<input checked="" type="checkbox"/> RPKM

LC2/ad TSS

PC-3 TSS

PC-7 TSS

PC-9 TSS

PC-14 TSS

[more...](#)

LC2/ad TSS

PC-3 TSS

PC-7 TSS

PC-9 TSS

PC-14 TSS

RERF-LC-ad1 TSS

RERF-LC-ad2 TSS

RERF-LC-KJ TSS

RERF-LC-MS TSS

RERF-LC-OK TSS

VMRC-LCD TSS

ABC-1 TSS

II-18 TSS

[less](#)

SAEC RNA RPKM

LC2/ad RNA RPKM

ABC-1 RNA RPKM

II-18 RNA RPKM

PC-14 RNA RPKM

PC-3 RNA RPKM

PC-7 RNA RPKM

PC-9 RNA RPKM

RERF-LC-KJ RNA RPKM

RERF-LC-MS RNA RPKM

RERF-LC-OK RNA RPKM

RERF-LC-ad1 RNA RPKM

RERF-LC-ad2 RNA RPKM

VMRC-LCD RNA RPKM

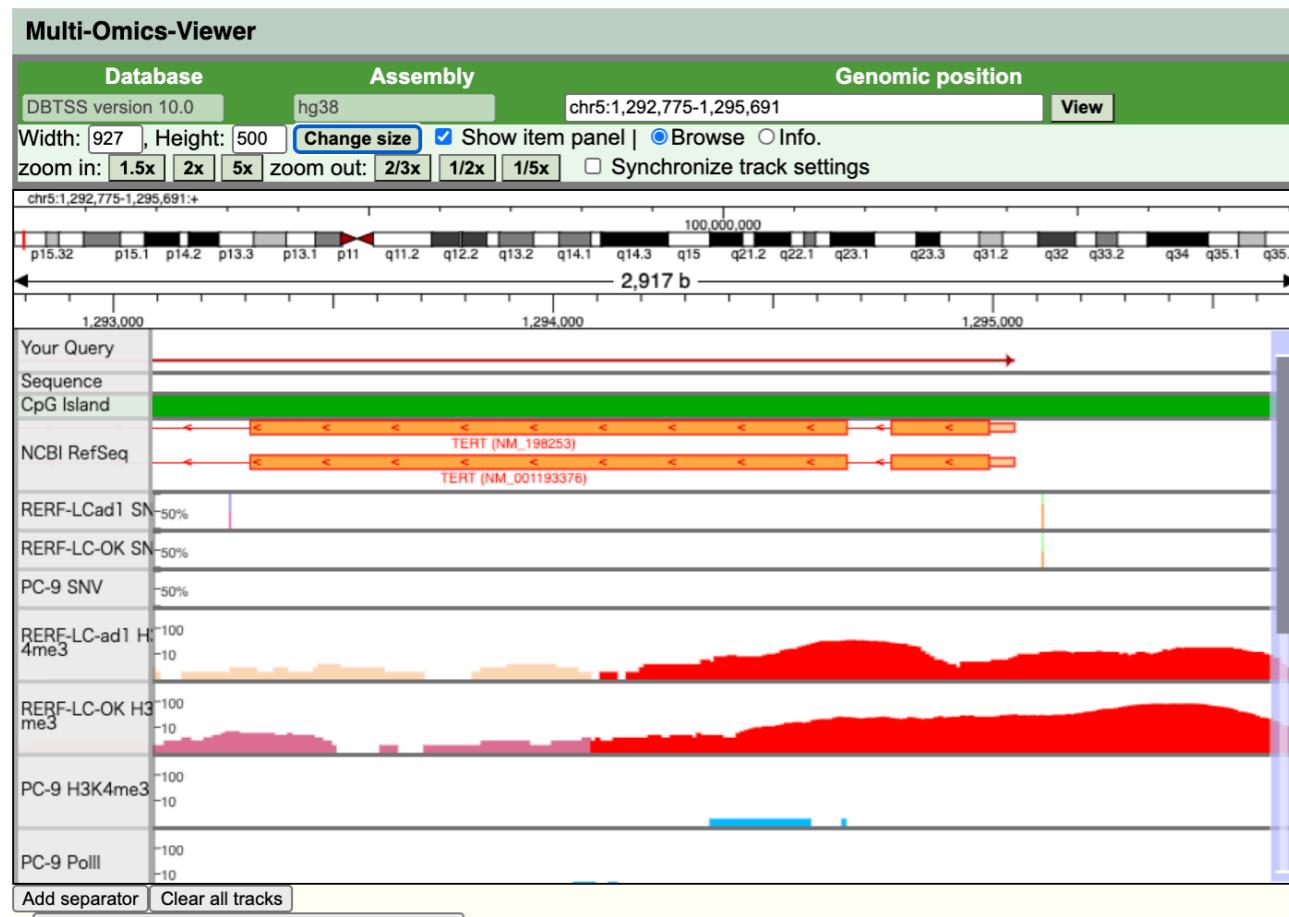
“more...”でcell lineを表示→3つの系列を選択

PC-9 TSS, RERF-LC-OK TSS, RERF-LC-OK TSS

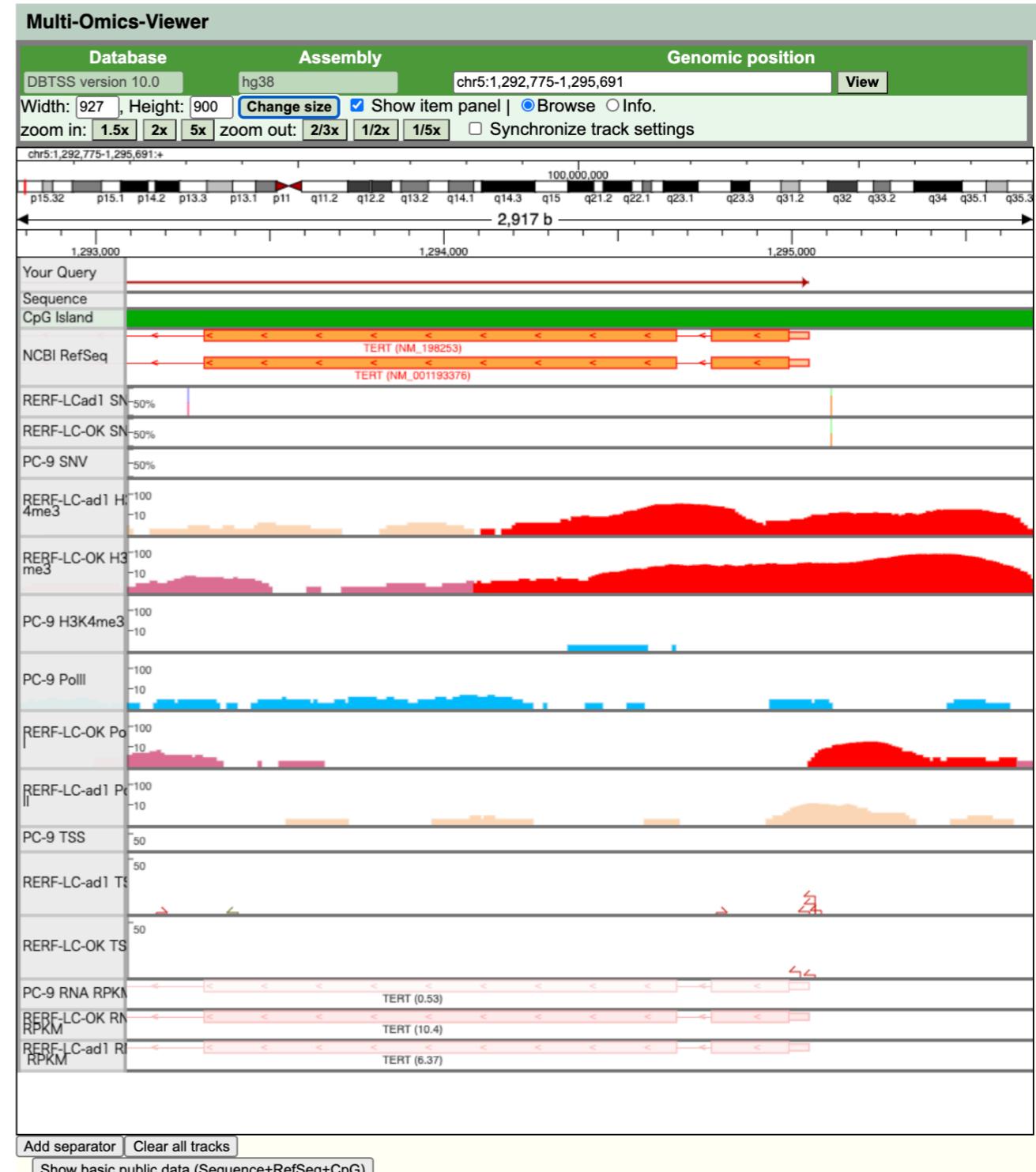
PC-9 RNA RPKM, RERF-LC-OK RNA RPKM, RERF-LC-OK RNA RPKM

II, Multi-Omics-Viewer : Ex) TERT

13) 画面表示を調整する

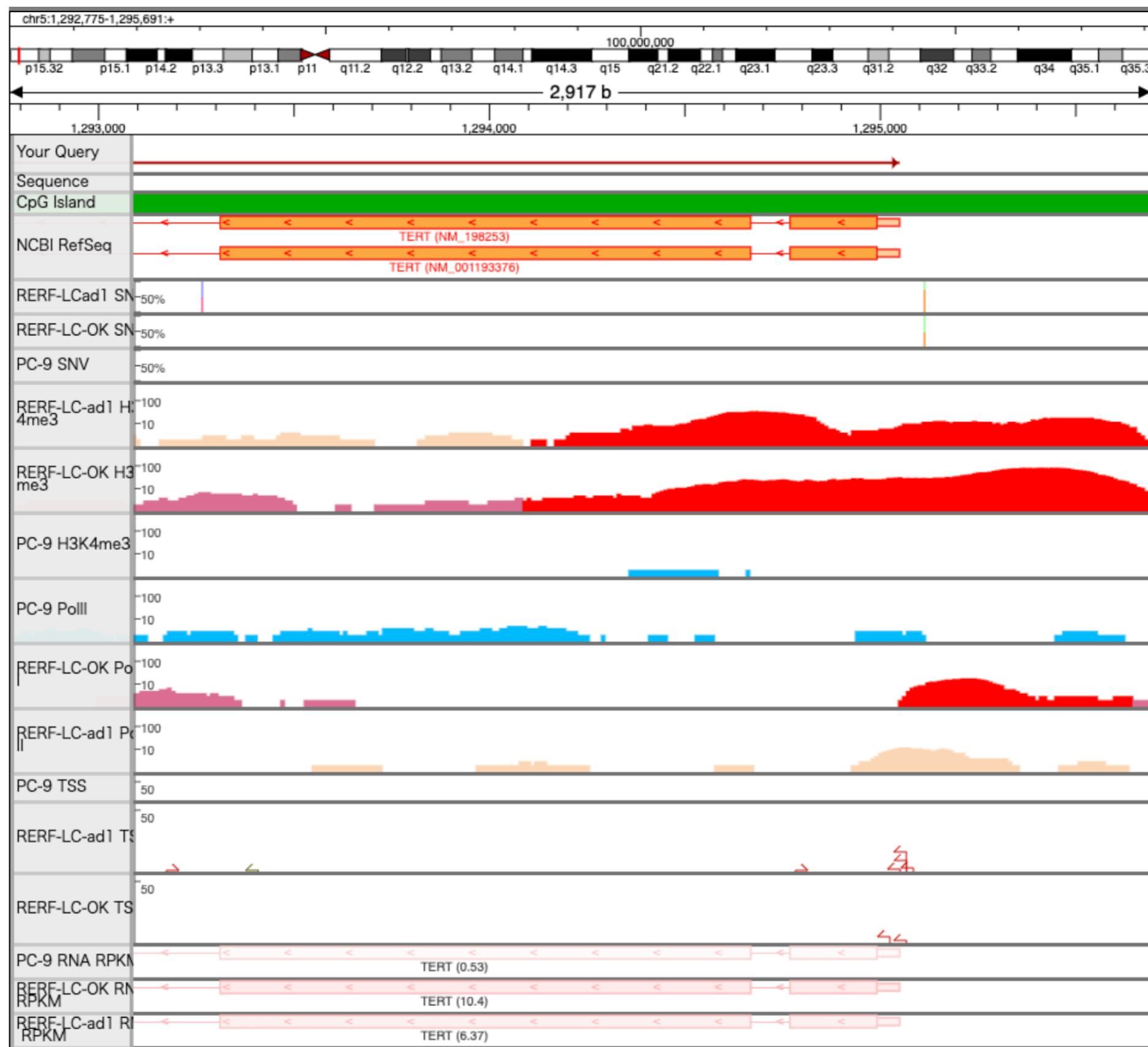


height: 500 → 900



II, Multi-Omics-Viewer : Ex) TERT

promoter mutation周辺のmulti-omicsデータを俯瞰することが可能



III, Pathway MAP

Pathway map: Cell Signaling Technologyのマップと、KEGGが利用可能

DBKERO
Database of Keio Encyclopedia for Research of multi-Omics data

Quick-start: For the beginners

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.

Viewer [How to use]

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- Whole-genome Data Summary** [Help video (Japanese)]: Overall view of expression and modification of a genome region including our entire data sets.
 - Search from Genomic Position
 - Search from SNP (dbSNP rsID)
 - Search from SNV (COSMIC: somatic mutation)
- SNV Summary in Cancers** [Help 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 [Help video (Japanese)]
- SV viewer^{New}

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.

Download

- Data Portal [Help video (Japanese)]
- Data Portal (PAGS)

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.)

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

Pathway Map

Find out the level of expression or modification of genes within a Pathway

Illustration reproduced courtesy of Cell Signaling Technology, Inc. <http://www.cellsignal.com/>

Pathways (Map)

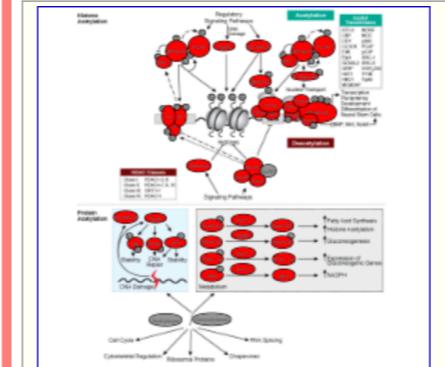
Click !!!

Pathways (List)

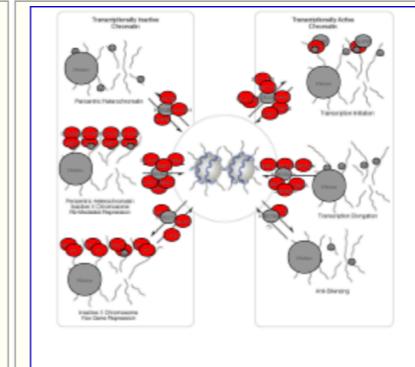
KEGG

Chromatin Regulation / Acetylation

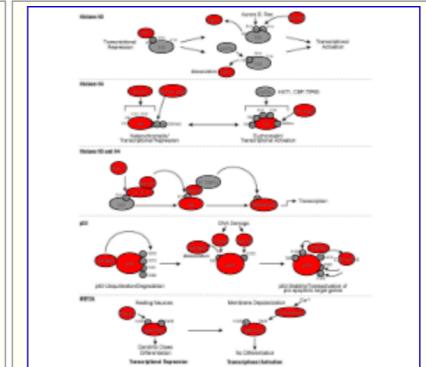
Protein Acetylation



Histone Methylation

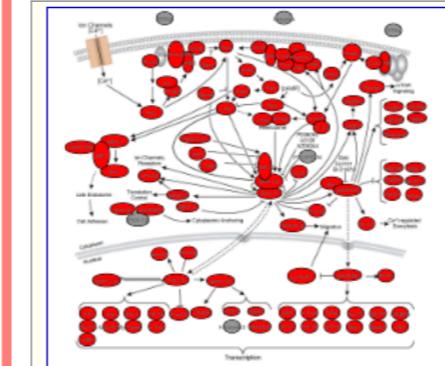


Examples of Crosstalk Between Post-translational Modifications

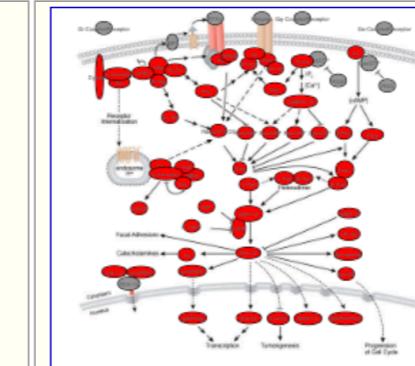


Mitogen-Activated Protein Kinase (MAPK) Cascades

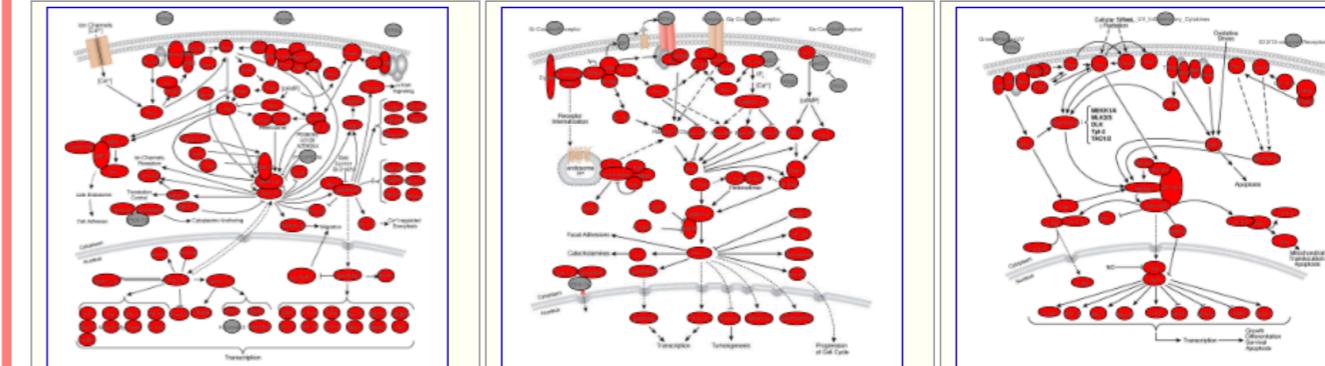
MAPK/Erk in Growth and Differentiation



G-Protein-Coupled Receptors Signaling to MAPK/Erk



SAPK/JNK Signaling Cascades



III, Pathway MAP, Ex) Pathway of lung cancer

Pathway_map> Pathway of lung cancer > 26 cell lines > LC2/ad

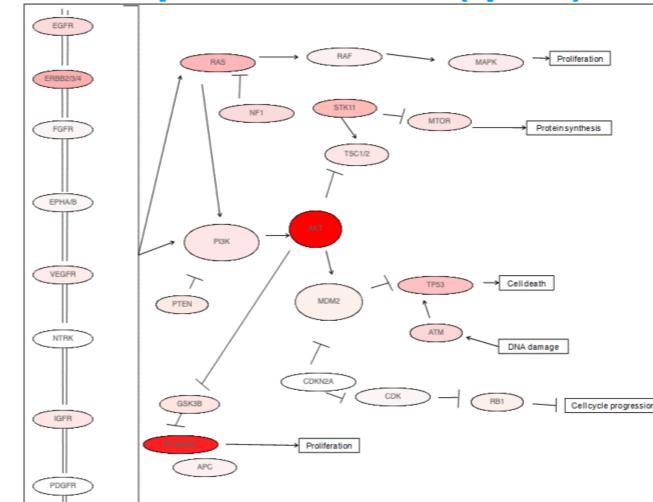
● Pathways (List)

Show 25 entries

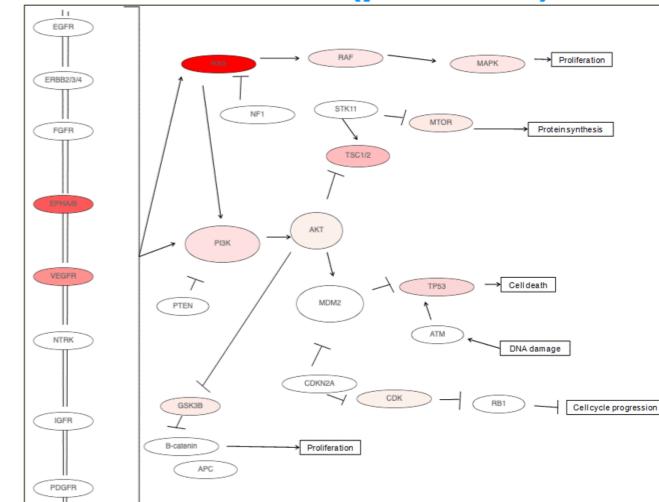
Search:

Category	Title
Adhesion	Adherens Junction Dynamics
Angiogenesis	Angiogenesis
Apoptosis	Death Receptor Signaling
Apoptosis	Inhibition of Apoptosis
Apoptosis	Mitochondrial Control of Apoptosis
Apoptosis	Overview
Autophagy	Autophagy Signaling
Ca, cAMP & Lipid Signaling	Phospholipase Signaling
Ca, cAMP & Lipid Signaling	Protein Kinase C Signaling
Cancer cell	Pathway of lung cancer
Cell Cycle and Checkpoint Control	G1/S Checkpoint
Cell Cycle and Checkpoint Control	G2M/DNA Damage Checkpoint
Chromatin Regulation / Acetylation	Examples of Crosstalk Between Post-translational Modifications
Chromatin Regulation / Acetylation	Histone Methylation
Chromatin Regulation / Acetylation	Protein Acetylation
Cytoskeletal Signaling	Regulation of Actin Dynamics
Cytoskeletal Signaling	Regulation of Microtubule Dynamics
Glucose Metabolism	AMPK Signaling
Glucose Metabolism	Insulin Receptor Signaling
Glucose Metabolism	Warburg Effect
Jak/Stat Pathway	IL-6 Receptor Signaling
Lymphocyte Signaling	B Cell Receptor Signaling
Lymphocyte Signaling	T Cell Receptor Signaling
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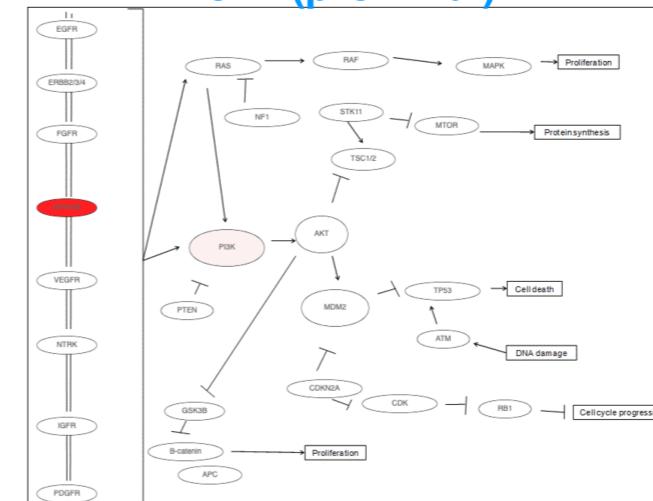
Expression level (rpkm)



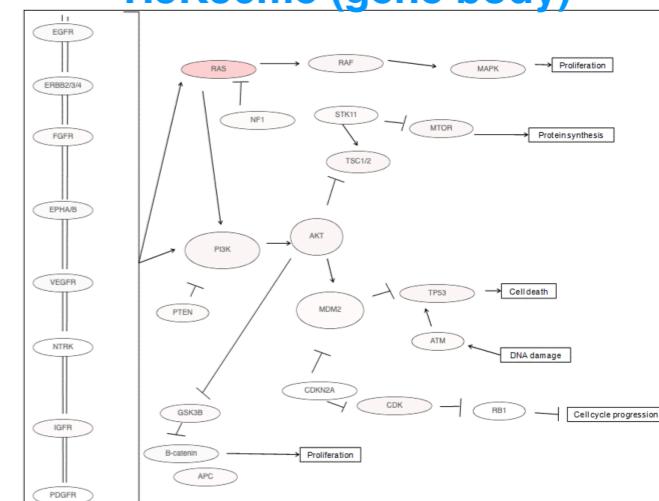
H3K4me3 (proximal)



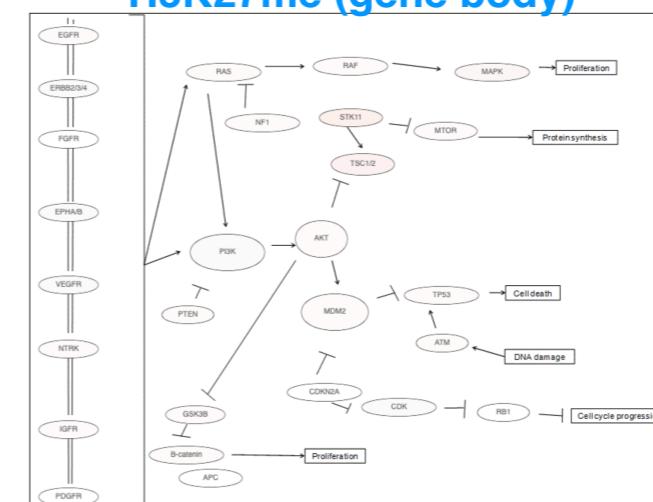
Pol II (proximal)



H3K36me (gene body)

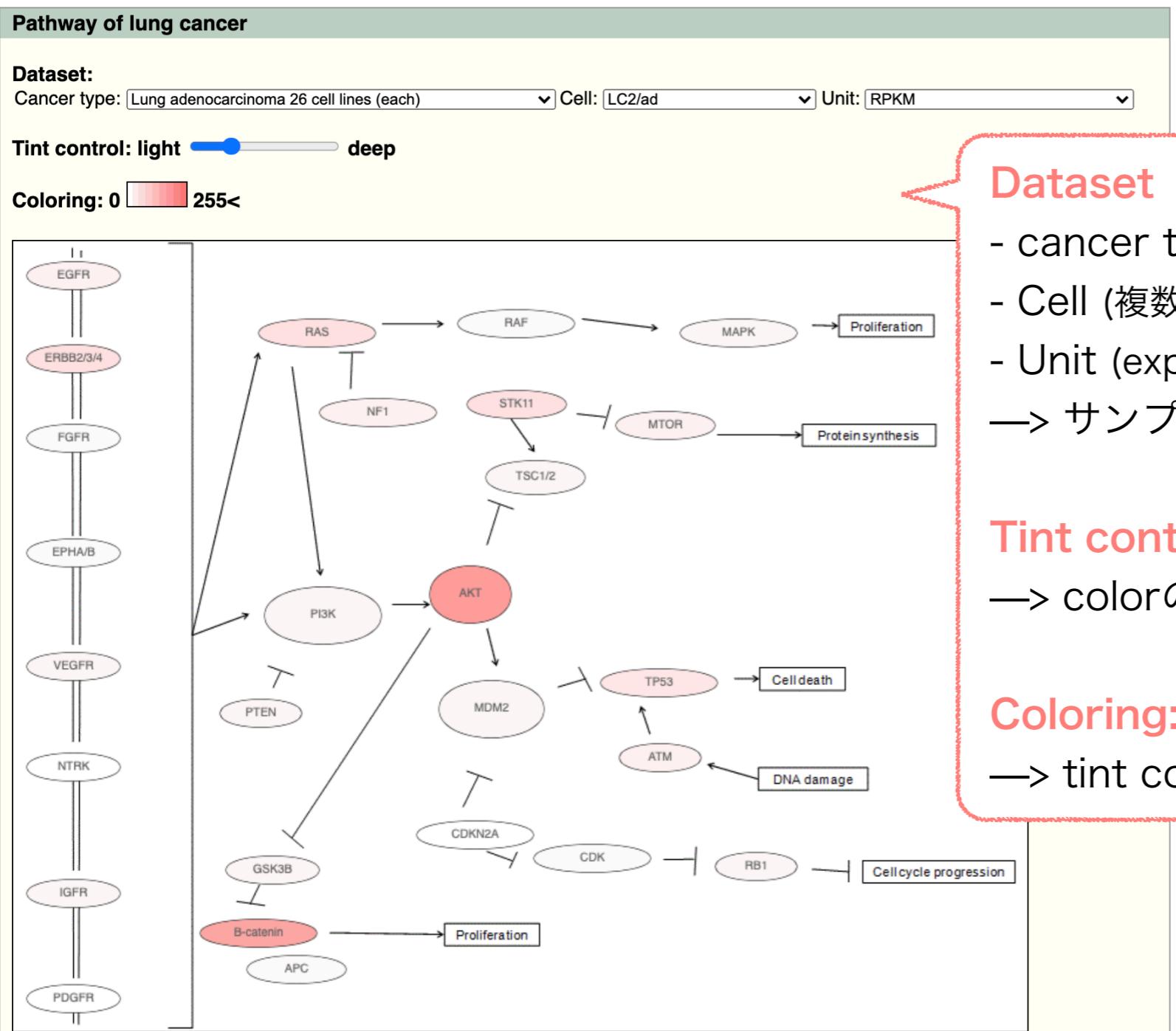


H3K27me (gene body)



III, Pathway MAP, Ex) Pathway of lung cancer

Pathway_map> Pathway of lung cancer > 26 cell lines > LC2/ad



Dataset

- cancer type (実験データ, TCGA, ICGC …etc)
 - Cell (複数のcellが含まれるデータの時のみ表示される)
 - Unit (exp, メチル化, mutation frequency…etc)
- サンプルによって表示できるデータが異なる

Tint control:

- colorのthresholdを変更できる

Coloring:

- tint controlの変化に伴い、上限の数値が変化

VI, SV Viewer

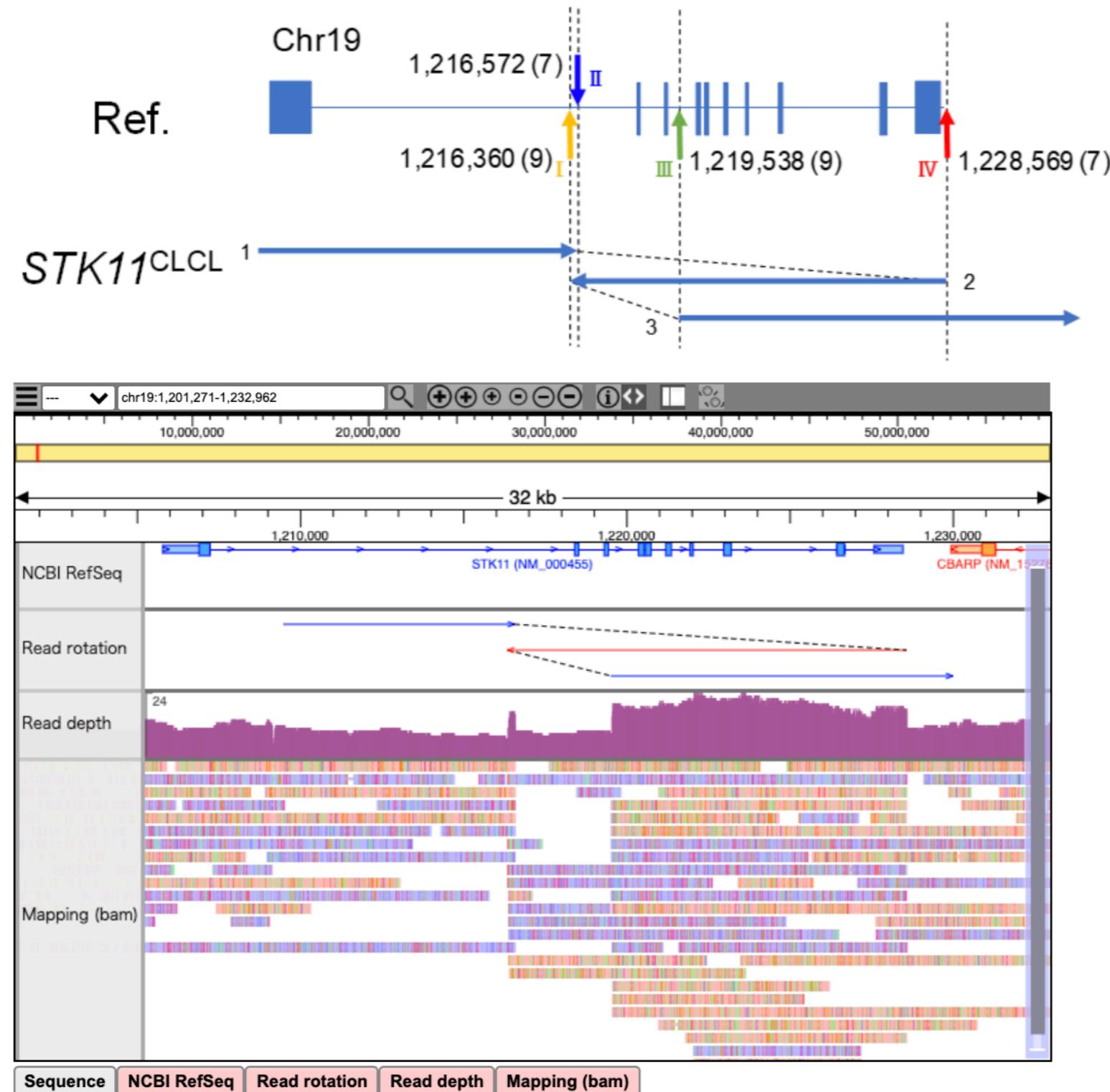
SV viewer ① Cancer SV dataset

sampleID	Tumor			Normal			Number of SVs	Processed data
	Yields(Gb)	Number of reads	Coverage(x)	Yields(Gb)	Number of reads	Coverage(x)		
S1	99	14881240	33	57	11709609	19	7	S1 SV gene candidates.bedpe
S2	94	25379061	31	41	7016159	14	120	S2 SV gene candidates.bedpe
S3	77	15952312	25	48	12971173	15	41	S3 SV gene candidates.bedpe
S5	82	21640571	27	35	6503970	11	11	S5 SV gene candidates.bedpe
S6	76	11336329	25	48	7531078	16	72	S6 SV gene candidates.bedpe
S7	85	13880384	28	46	7555316	15	91	S7 SV gene candidates.bedpe
S8	100	18661003	33	54	8351411	18	67	S8 SV gene candidates.bedpe
S9	96	13179209	32	34	4483001	11	48	S9 SV gene candidates.bedpe
S10	85	12424087	28	42	7029224	14	64	S10 SV gene candidates.bedpe
S11	69	21140772	22	59	7832201	19	42	S11 SV gene candidates.bedpe
S12	73	15634853	24	84	12908975	27	2	S12 SV gene candidates.bedpe
S13	104	30719862	34	38	5506152	12	31	S13 SV gene candidates.bedpe
S14	74	14328017	24	56	6464828	18	53	S14 SV gene candidates.bedpe
S15	75	12278084	24	55	9585959	18	7	S15 SV gene candidates.bedpe
S16	74	20118226	24	55	7924757	18	103	S16 SV gene candidates.bedpe
S17	52	7086616	17	59	6766386	20	3	S17 SV gene candidates.bedpe
S18	62	7091142	20	44	5335320	15	14	S18 SV gene candidates.bedpe
S19	60	6352847	20	37	5025576	12	10	S19 SV gene candidates.bedpe
S20	58	5836744	19	47	5620346	15	87	S20 SV gene candidates.bedpe
S21	63	8985953	21	57	6166961	19	19	S21 SV gene candidates.bedpe

VI, SV Viewer

SV viewer② Viewer (Cell line data)

RERF-LC-KJ: STK11



V, Summary

説明はweb上でも閲覧することができます



<https://kero.hgc.jp/>



DBKERO
Database of Koshin Encyclopedia for Researches of multi-Omics data

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[Top](#) | [Multi-Omics-Viewer](#) | [Tutorial](#)

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 Click !!!

V, Summary

他の解析ツールも是非ご活用ください

The screenshot shows the DBKERO homepage with a red header bar containing the text "Quick-start: For the beginners". Below the header, a message recommends using Edge (ver. 40 or above), Google Chrome (ver. 61 or above) or Firefox (ver. 56 or above) for browsing. It states that Internet Explorer is no longer supported.

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(<https://kero.hgc.jp/>)

DBTSS/DBKERO

:実験学的に保証された5'端配列(TSS)

- Oligo capping method
- CAP tapper method

現在利用可能なツール

- Single cell dataset
- Cancer SV dataset ←new!
- Visium dataset ←new!
- Data Portal
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- TSS viewer
- Mutation enriched gene
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