



Welcome to  
Japanese Multi Omics  
Reference Panel.

日本人基準ゲノム配列 (JRGA)

# 第二版 (JG2) 利用ガイド

ゲノム配列



Genome Sequence

トップページ

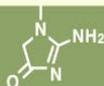


Welcome to  
Japanese Multi Omics  
Reference Panel.



Phenome

To be provided



Metabolome



Proteome



Transcriptome

Iwate Medical Megabank Organization; iMethyl



Methylome

Iwate Medical Megabank Organization; iMethyl



Genome Variation



Genome Sequence

jMorp release 201911

November, 1st, 2019

GWAS summary statistics datasets and Japonica Array NEO marker list

We have added [GWAS summary statistics page](#), which is a list of Genome-Wide Association Studies performed by TMM project. Users can download summary statistics data for**代謝物 25K**

Array NEO is available from Downloads page.

[More](#)**タンパク質 500**

Tadaka S, Saigusa D, Motoike IN, Inoue J, Aoki Y, Shiota M, Koshiba S, Yamamoto M, Kinoshita K.  
"jMorp: Japanese Multi Omics Reference Panel"  
Nucleic Acids Research. 2018 Jan 4;46(D1):D551-D557. [↗](#)

Tadaka S, Katsuoka F, et al.,  
"3.5KJPNv2, An allele frequency panel of 3,552 Japanese Individuals including the X chromosome"  
Human Genome Variation, 2019 Jun 18;6:28. doi: 10.1038/s41439-019-0059-5. [↗](#)

Saigusa D, Matsukawa N, Tadaka S, Motoike IN, Koshiba S.  
"Metabolome Analysis of Human Plasma by GC-MS/MS in a Large-scale Cohort"  
Proteome Letters, 2019 Volume 4 Issue 1 Pages 31-40. doi: 10.14889/jpros.4.1\_31. [↗](#)

[More](#)**ゲノムバリエント 8.3K****ゲノム配列 JG2**

ゲノム配列



Genome Sequence

## 日本人基準ゲノムJG2: 日本人男性3人6ゲノムのデータの統合

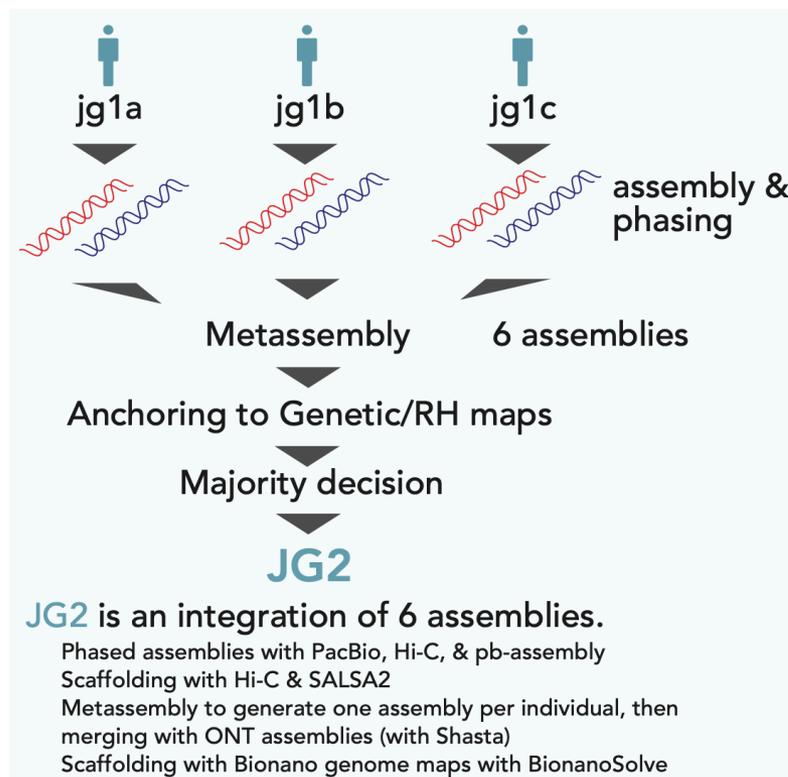
PacBio + Bionano + Illumina + Hi-C + Nanopore

複数検体の  
デノボアセンブリ

複数アセンブリの  
統合

遺伝地図等を用いた  
染色体構築

多数決による  
レアアレル排除



JG2上の遺伝子領域定義ファイル(GENCODE34),  
GRCh37, GRCh38との座標変換用ファイルも提供



# ゲノム配列



# Genome Sequence

## 配列+annotationをブラウザで表示

JG2.0.0 beta  
GRCh37  
GRCh38

拡大/縮小

表示位置(遺伝子名可)

表示配列種別

ユーザが選択したファイル(vcf, bam)を同軸で表示可能  
(ToMMoにデータは送られません)



# ゲノム配列



# Genome Sequence

ページ右上部

ToMMo JG2.0.Obeta

100,000,000

Go **Compare genomes**

157,500

選んだ基準ゲノムの同等領域を  
同時表示

jMorp | JG2.0.Obeta | GRCh38 | Swap Genome | OK | Report Issue

Track View Help Tools | ToMMo JG2.0.Obeta | Share

0 50,000,000 100,000,000 150,000,000 200,000,000

chr1 | chr1:6694507..9330237 (2.64 Mb) | Go

7,000,000 7,500,000 8,000,000 8,500,000 9,000,000

Reference sequence | Zoom in to see sequence

GENCODE34 LiftOver

Available Tracks

- filter tracks
- Reference sequence
- Annotation
  - N-Gap
  - Repeat Masker
- Gene
  - GENCODE34 LiftOver
  - GENCODE34 Basic LiftOver
- minimap2 to
  - minimap2 from JG2.0.Obeta to hg18 difference VCF
  - minimap2 from JG2.0.Obeta to AK1 difference VCF
  - minimap2 from JG2.0.Obeta to hg18 alignment
  - minimap2 from JG2.0.Obeta to GRCh38.p13 alignment
  - minimap2 from JG2.0.Obeta to GRCh38.p13 difference VCF
  - minimap2 from JG2.0.Obeta to KOREF1.0 difference VCF
  - minimap2 from JG2.0.Obeta to KOREF1.0 alignment
  - minimap2 from JG2.0.Obeta to HX1 alignment
  - minimap2 from JG2.0.Obeta to GRCh37\_primary\_assembly alignment
  - minimap2 from JG2.0.Obeta to JG1.0.Obeta alignment
  - minimap2 from JG2.0.Obeta to JG1.0.Obeta difference VCF
  - minimap2 from JG2.0.Obeta to AK1 alignment

Track View Help Tools | GRCh38.p12 | Share

0 50,000,000 100,000,000 150,000,000 200,000,000

chr1 | chr1:7191483..9812734 (2.62 Mb) | Go

7,500,000 8,000,000 8,500,000 9,000,000 9,500,000

Reference sequence | Zoom in to see sequence

GENCODE29 Basic

Available Tracks

- filter tracks
- Reference sequence
- N-Gap
- Annotation
  - GENCODE29
  - GENCODE29 Basic
  - dbSNP build 151
  - GENCODE29 LiftOver failed (JG1)
  - Repeat Masker
- Reference Sequence Comparison - minimap2 to
  - minimap2 from GRCh38 to AK1 alignment
  - minimap2 from GRCh38 to AK1 difference VCF
  - minimap2 from GRCh38 to GRCh37 alignment
  - minimap2 from GRCh38 to GRCh37 difference VCF
  - minimap2 from GRCh38 to KOREF1.0 alignment
  - minimap2 from GRCh38 to KOREF1.0 difference VCF
  - minimap2 from GRCh38 to HX1 alignment
  - minimap2 from GRCh38 to HX1 difference VCF
  - minimap2 from GRCh38 to hg18 alignment
  - minimap2 from GRCh38 to hg18 difference VCF
  - minimap2 from GRCh38 to JG1.0.Obeta alignment
  - minimap2 from GRCh38 to JG1.0.Obeta difference VCF