



Welcome to  
Japanese Multi Omics  
Reference Panel.

日本人基準ゲノム配列 (JGRA)

# 初版 (JG1) 利用ガイド

ゲノム配列



Genome Sequence

トップページ

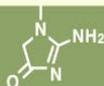


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Phenome

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 15K** 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 4.7K**

**ゲノム配列**



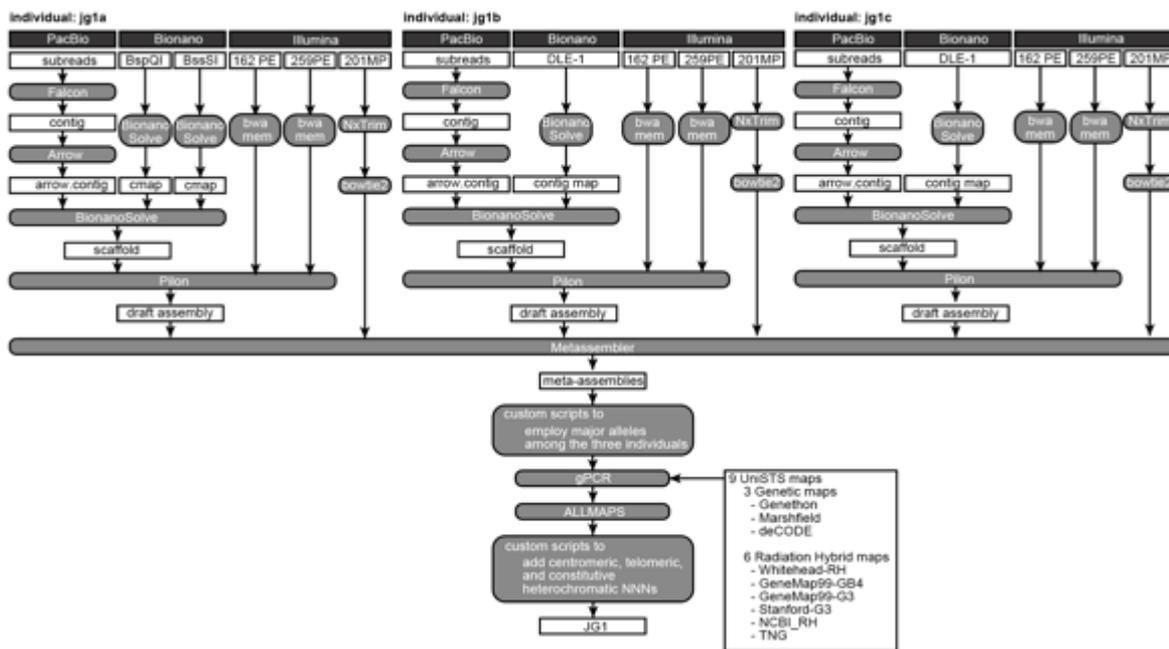
ゲノム配列



Genome Sequence

日本人基準ゲノムJG1:  
日本人男性3人のデータの統合

PacBio + Bionano + illumina



JG1beta上の遺伝子領域定義ファイル(GENCODE29), GRCh37, GRCh38との座標変換用ファイルも提供

複数検体の  
デノボアセンブリ

複数アセンブリの統合

多数決による  
レアアレル排除

遺伝地図等を用いた  
染色体構築



# ゲノム配列



# Genome Sequence

## 配列+annotationをブラウザで表示

JG1.0 beta  
GRCh37  
GRCh38

拡大/縮小

表示位置(遺伝子名可)

表示配列種別

Available Tracks

- filter tracks
- Reference sequence (2)
  - Reference sequence
  - N-Gap
- Gene (2)
  - GENCODE29 LiftOver
  - GENCODE29 Basic LiftOver
- Annotation (1)
  - Repeat Masker
- minimap2 to (12)
  - minimap2 from JG1.0.0beta to AK1 alignment
  - minimap2 from JG1.0.0beta to AK1 difference VCF
  - minimap2 from JG1.0.0beta to GRCh37 alignment
  - minimap2 from JG1.0.0beta to GRCh37 difference VCF
  - minimap2 from JG1.0.0beta to KOREF1.0 alignment
  - minimap2 from JG1.0.0beta to KOREF1.0 difference VCF
  - minimap2 from JG1.0.0beta to GRCh38 alignment
  - minimap2 from JG1.0.0beta to GRCh38 difference VCF
  - minimap2 from JG1.0.0beta to HX1 alignment
  - minimap2 from JG1.0.0beta to HX1 difference VCF
  - minimap2 from JG1.0.0beta to hg18 alignment
  - minimap2 from JG1.0.0beta to hg18 difference VCF
- minimap2 from (14)

Genome Track View Help Tools Downloads

chr12:112111721..112122900 (11.18)

ALDH2(ENSG00000111275.12)

RepeatMasker SINE/Alu MER20-DNA/hAT-Charlie Charlie5a-DNA/hAT-Charlie (TTTA)n-Simple\_repeat AluSx-SINE/Alu AluJr-SINE/Alu (GGCCT)n-Simple\_repeat L1MC2-LINE/L1 AluSx3-SINE/Alu AluSg-SIN

minimap2 from JG1.0.0beta to GRCh37 alignment

minimap2 from JG1.0.0beta to GRCh38 alignment

minimap2 from GRCh37 to JG1.0.0beta alignment

ユーザが選択したファイル(vcf, bam)を同軸で表示可能

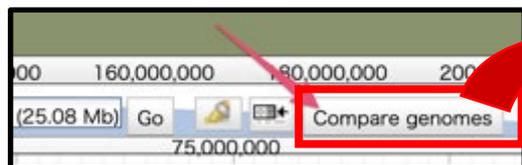


# ゲノム配列



# Genome Sequence

ページ右上部



3種の配列の同等領域を同時表示