



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



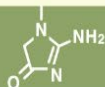
Genome Sequence

トップページ

Welcome to
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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

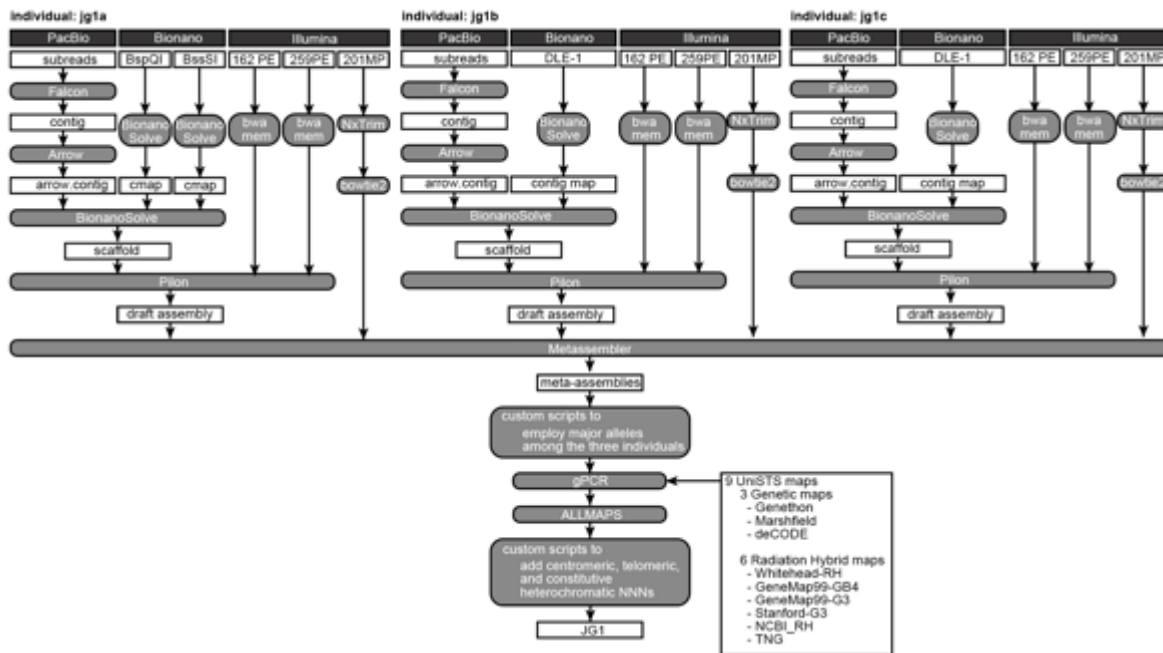


Genome Sequence

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

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

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



ゲノム配列



Genome Sequence

配列+annotationをブラウザで表示

JG1.0 beta
GRCh37
GRCh38

The screenshot displays the jMorp genome browser interface. On the left, there is a sidebar with 'Available Tracks' including Reference sequence, Gene, Annotation, and various minimap2 alignment tracks. The main panel shows a genomic region on chromosome 12 (chr12:11211721..112122900 (11.18)). The interface includes a navigation bar with 'Track', 'View', 'Help', 'Tools', and 'Downloads' menus. A search bar contains the coordinates 'chr12:11211721..112122900 (11.18)'. Below the search bar, there are zoom controls (minus, plus, and a magnifying glass icon) and a 'Compare genomes' button. The main display area shows multiple tracks: 'Reference sequence', 'Gene' (including GENCOD29 LiftOver and Repeat Masker), 'Annotation' (including ALDH2(ENSG0000111275.12)), and several 'minimap2' alignment tracks for different reference panels (JG1.0.0beta to AK1, GRCh37, GRCh38, KOREF1.0, HX1, hg18). A red box highlights the 'Track' menu, and another red box highlights the search bar. A red arrow points from the search bar area down to the text at the bottom of the slide.

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

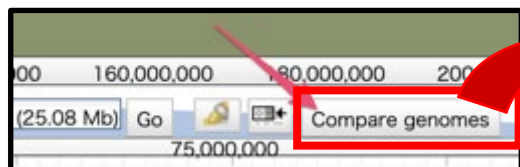


ゲノム配列



Genome Sequence

ページ右上部



3種の配列の同等領域を同時表示