Resource Summary Report

Generated by dkNET on May 16, 2025

Japanese Genotype-phenotype Archive (JGA)

RRID:SCR_003118
Type: Tool

Proper Citation

Japanese Genotype-phenotype Archive (JGA) (RRID:SCR_003118)

Resource Information

URL: https://www.ddbj.nig.ac.jp/jga/index-e.html

Proper Citation: Japanese Genotype-phenotype Archive (JGA) (RRID:SCR_003118)

Description: A service for permanent archiving and sharing of all types of personally identifiable genetic and phenotypic data resulting from biomedical research projects. The JGA contains exclusive data collected from individuals whose consent agreements authorize data release only for specific research use or to bona fide researchers. Strict protocols govern how information is managed, stored and distributed by the JGA. Once processed, all data are encrypted. The JGA accepts only de-identified data approved by JST-NBDC. The JGA implements access-granting policy whereby the decisions of who will be granted access to the data resides with the JST-NBDC. After data submission the JGA team will process the data into databases and archive the original data files. The accepted data types include manufacturer-specific raw data formats from the array-based and new sequencing platforms. The processed data such as the genotype and structural variants or any summary level statistical analyses from the original study authors are stored in databases. The JGA also accepts and distributes any phenotype data associated with the samples. For other human biological data, please contact the NBDC human data ethical committee.

Abbreviations: JGA

Synonyms: JGA, Japanese Genotype-phenotype Archive (JGA), Japanese Genotype-phenotype Archive

Resource Type: service resource, data or information resource, database, storage service resource, data repository

Keywords: biomedical, genetic, phenotype, gene, data sharing, genotype

Funding:

Availability: Application required, Account required

Resource Name: Japanese Genotype-phenotype Archive (JGA)

Resource ID: SCR_003118

Alternate IDs: nlx_156741

Old URLs: http://trace.ddbj.nig.ac.jp/jga/, http://trace.ddbj.nig.ac.jp/jga/index_e.html

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250516T053656+0000

Ratings and Alerts

No rating or validation information has been found for Japanese Genotype-phenotype Archive (JGA).

No alerts have been found for Japanese Genotype-phenotype Archive (JGA).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Guccione C, et al. (2025) Incomplete human reference genomes can drive false sex biases and expose patient-identifying information in metagenomic data. Nature communications, 16(1), 825.

Nishijima A, et al. (2024) Integrated genomic/epigenomic analysis stratifies subtypes of clear cell ovarian carcinoma, highlighting their cellular origin. Scientific reports, 14(1), 18797.

Guccione C, et al. (2024) Incomplete human reference genomes can drive false sex biases and expose patient-identifying information in metagenomic data. Research square.

Akiyama M, et al. (2023) Genome-wide association study reveals BET1L associated with survival time in the 137,693 Japanese individuals. Communications biology, 6(1), 143.

Muto K, et al. (2022) Semibulk RNA-seq analysis as a convenient method for measuring gene expression statuses in a local cellular environment. Scientific reports, 12(1), 15309.

Wanifuchi-Endo Y, et al. (2022) Discovering novel mechanisms of taxane resistance in human breast cancer by whole-exome sequencing. Oncology letters, 23(2), 60.

Namba S, et al. (2021) Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. Communications biology, 4(1), 1320.

Nagano M, et al. (2021) Comprehensive molecular profiling of pulmonary pleomorphic carcinoma. NPJ precision oncology, 5(1), 57.

Yang XY, et al. (2021) Tracing the Genetic Legacy of the Tibetan Empire in the Balti. Molecular biology and evolution, 38(4), 1529.

Iguchi E, et al. (2021) Author Correction: DNA methyltransferase 3B plays a protective role against hepatocarcinogenesis caused by chronic inflammation via maintaining mitochondrial homeostasis. Scientific reports, 11(1), 14037.

Togi S, et al. (2021) Application of Combined Long Amplicon Sequencing (CoLAS) for Genetic Analysis of Neurofibromatosis Type 1: A Pilot Study. Current issues in molecular biology, 43(2), 782.

Nakatake Y, et al. (2020) Generation and Profiling of 2,135 Human ESC Lines for the Systematic Analyses of Cell States Perturbed by Inducing Single Transcription Factors. Cell reports, 31(7), 107655.

Nakanishi H, et al. (2020) Significance of gene mutations in the Wnt signaling pathway in traditional serrated adenomas of the colon and rectum. PloS one, 15(2), e0229262.

Hashimoto A, et al. (2020) Proteogenomic analysis of granulocyte macrophage colony-stimulating factor autoantibodies in the blood of a patient with autoimmune pulmonary alveolar proteinosis. Scientific reports, 10(1), 4923.

Iguchi E, et al. (2020) DNA methyltransferase 3B plays a protective role against hepatocarcinogenesis caused by chronic inflammation via maintaining mitochondrial homeostasis. Scientific reports, 10(1), 21268.

Oga T, et al. (2019) Genomic profiles of colorectal carcinoma with liver metastases and newly identified fusion genes. Cancer science, 110(9), 2973.

Nomura M, et al. (2019) DNA demethylation is associated with malignant progression of lower-grade gliomas. Scientific reports, 9(1), 1903.

Namba S, et al. (2019) Differential regulation of CpG island methylation within divergent and unidirectional promoters in colorectal cancer. Cancer science, 110(3), 1096.

Sai E, et al. (2019) Identification of candidates for driver oncogenes in scirrhous-type gastric

cancer cell lines. Cancer science, 110(8), 2643.

Hirata M, et al. (2019) Integrated exome and RNA sequencing of dedifferentiated liposarcoma. Nature communications, 10(1), 5683.