

Resource Summary Report

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Kyushu University Definitive Haplotype Database

RRID:SCR_013280

Type: Tool

Proper Citation

Kyushu University Definitive Haplotype Database (RRID:SCR_013280)

Resource Information

URL: <http://orca.gen.kyushu-u.ac.jp>

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Description: D-HaploDB genome-wide definitive haplotypes, determined using a collection of 100 Japanese complete hydatidiform moles (CHMs), each carrying a genome derived from a single sperm. The haplotypes incorporate 281 k (D-Haplo Phase I: D1), 581k (D-Haplo Phase II: D2), or 1M (D-Haplo Phase III: D3) SNPs, genotyped with high throughput array-based oligonucleotide hybridization techniques. The Definitive Haplotype Browser can be used to view various information, such as SNP alleles, haplotype blocks, LD-bins and extended shared haplotypes (ESHs) in our study.

Synonyms: D-HaploDB

Resource Type: data or information resource, database

Keywords: extended shared haplotype, haplotype, haplotype block, high throughput array-based oligonucleotide hybridization, ld-bin, snp allele

Resource Name: Kyushu University Definitive Haplotype Database

Resource ID: SCR_013280

Alternate IDs: nif-0000-02717

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260729T044312+0000

Ratings and Alerts

No rating or validation information has been found for Kyushu University Definitive Haplotype Database.

No alerts have been found for Kyushu University Definitive Haplotype Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Zhang J, et al. (2021) Genetic and Functional Evaluation of the Role of FOXO1 in Antituberculosis Drug-Induced Hepatotoxicity. Evidence-based complementary and alternative medicine : eCAM, 2021, 3185874.

Zhang J, et al. (2019) Genetic polymorphisms in PXR and NF- κ B1 influence susceptibility to anti-tuberculosis drug-induced liver injury. PloS one, 14(9), e0222033.

Wu Y, et al. (2018) Population genomic data reveal genes related to important traits of quail. GigaScience, 7(5).

Li D, et al. (2017) Polymorphic variants in VAX1 and the risk of nonsyndromic cleft lip with or without cleft palate in a population from northern China. Medicine, 96(14), e6550.

Tahira T, et al. (2014) A definitive haplotype map of structural variations determined by microarray analysis of duplicated haploid genomes. Genomics data, 2, 55.

Shimada MK, et al. (2009) VarySysDB: a human genetic polymorphism database based on all H-InvDB transcripts. Nucleic acids research, 37(Database issue), D810.

Higasa K, et al. (2007) D-HaploDB: a database of definitive haplotypes determined by genotyping complete hydatidiform mole samples. Nucleic acids research, 35(Database issue), D685.