Resource Summary Report

Generated by RRID on May 17, 2025

YanHuang Project

RRID:SCR_006077
Type: Tool

Proper Citation

YanHuang Project (RRID:SCR_006077)

Resource Information

URL: http://yh.genomics.org.cn

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Description: This database presents the entire DNA sequence of the first diploid genome sequence of a Han Chinese, a representative of Asian population. The genome, named as YH, represents the start of YanHuang Project, which aims to sequence 100 Chinese individuals in 3 years. It was assembled based on 3.3 billion reads (117.7Gbp raw data) generated by Illumina Genome Analyzer. In total of 102.9Gbp nucleotides were mapped onto the NCBI human reference genome (Build 36) by self-developed software SOAP (Short Oligonucleotide Alignment Program), and 3.07 million SNPs were identified. The personal genome data is illustrated in a MapView, which is powered by GBrowse. A new module was developed to browse large-scale short reads alignment. This module enabled users track detailed divergences between consensus and sequencing reads. In total of 53,643 HGMD recorders were used to screen YH SNPs to retrieve phenotype related information, to superficially explain the donor's genome. Blast service to align query sequences against YH genome consensus was also provided.

Synonyms: YH1

Resource Type: data or information resource, database

Keywords: genome, genetic, adult, chromosome, clinical, control, genomic, human, normal, FASEB list

Funding:

Resource Name: YanHuang Project

Resource ID: SCR_006077

Alternate IDs: nif-0000-03654

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250507T060349+0000

Ratings and Alerts

No rating or validation information has been found for YanHuang Project.

No alerts have been found for YanHuang Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Chai P, et al. (2021) Clinical characteristics and germline mutation spectrum of RB1 in Chinese patients with retinoblastoma: A dual-center study of 145 patients. Experimental eye research, 205, 108456.

Jin JY, et al. (2020) Novel Compound Heterozygous DST Variants Causing Hereditary Sensory and Autonomic Neuropathies VI in Twins of a Chinese Family. Frontiers in genetics, 11, 492.

Chen X, et al. (2019) CRB2 mutation causes autosomal recessive retinitis pigmentosa. Experimental eye research, 180, 164.

Wang Y, et al. (2019) Targeted next-generation sequencing extends the mutational spectrums for OPA1 mutations in Chinese families with optic atrophy. Molecular vision, 25, 912.

Kong L, et al. (2019) Identification of two novel COL10A1 heterozygous mutations in two Chinese pedigrees with Schmid-type metaphyseal chondrodysplasia. BMC medical genetics, 20(1), 200.

Zhong Z, et al. (2019) Seven novel variants expand the spectrum of RPE65-related Leber congenital amaurosis in the Chinese population. Molecular vision, 25, 204.

Wang Q, et al. (2019) Whole exome sequencing identifies a novel variant in an apoptosis-inducing factor gene associated with X-linked recessive hearing loss in a Chinese family. Genetics and molecular biology, 42(3), 543.

Chai P, et al. (2019) Clinical characteristics and mutation Spectrum of NF1 in 12 Chinese families with orbital/periorbital plexiform Neurofibromatosis type 1. BMC medical genetics, 20(1), 158.

Gong B, et al. (2019) Mutation screening in the FBN1 gene responsible for Marfan syndrome and related disorder in Chinese families. Molecular genetics & genomic medicine, 7(4), e00594.

Jia Z, et al. (2018) DNA methylome profiling at single-base resolution through bisulfite sequencing of 5mC-immunoprecipitated DNA. BMC biotechnology, 18(1), 7.

Ai H, et al. (2018) GenomeLandscaper: Landscape analysis of genome-fingerprints maps assessing chromosome architecture. Scientific reports, 8(1), 1026.

Chen X, et al. (2018) Distinct mutations with different inheritance mode caused similar retinal dystrophies in one family: a demonstration of the importance of genetic annotations in complicated pedigrees. Journal of translational medicine, 16(1), 145.

Luo Q, et al. (2018) Algorithms designed for compressed-gene-data transformation among gene banks with different references. BMC bioinformatics, 19(1), 230.

Pang M, et al. (2018) A novel APC mutation identified in a large Chinese family with familial adenomatous polyposis and a brief literature review. Molecular medicine reports, 18(2), 1423.

Wang D, et al. (2017) A large family with inherited optic disc anomalies: a correlation between a new genetic locus and complex ocular phenotypes. Scientific reports, 7(1), 7799.

Tan L, et al. (2017) Severe congenital microcephaly with 16p13.11 microdeletion combined with NDE1 mutation, a case report and literature review. BMC medical genetics, 18(1), 141.

Qi YH, et al. (2017) Next-Generation Sequencing-Aided Rapid Molecular Diagnosis of Occult Macular Dystrophy in a Chinese Family. Frontiers in genetics, 8, 107.

Chen X, et al. (2017) GUCA1A mutation causes maculopathy in a five-generation family with a wide spectrum of severity. Genetics in medicine : official journal of the American College of Medical Genetics, 19(8), 945.

Gu S, et al. (2016) Targeted next-generation sequencing extends the phenotypic and mutational spectrums for EYS mutations. Molecular vision, 22, 646.

Xu DL, et al. (2016) Novel 6-bp deletion in MEF2A linked to premature coronary artery disease in a large Chinese family. Molecular medicine reports, 14(1), 649.