Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 8, 2025

Mouse HapMap Imputation Genotype Resource

RRID:SCR_002576
Type: Tool

Proper Citation

Mouse HapMap Imputation Genotype Resource (RRID:SCR_002576)

Resource Information

URL: http://mouse.cs.ucla.edu/mousehapmap/

Proper Citation: Mouse HapMap Imputation Genotype Resource (RRID:SCR_002576)

Description: Genetic maps for 94 inbred strains of mouse and imputed genotypes using the NIEHS / Perlegen resequencing resource. Combining with the 13,094 Wellcome Trust SNPs (Single-nucleotide polymorphisms), a set of 132,285 SNPs was compiled and is available for download. Using the mouse HapMap resource, it is possible to accurately impute the genotypes of the 94 strains at the 8 million SNPs discovered by the NIEHS/Perlegen mouse resequencing project. They imputed the genotypes at the NIEHS/Perlegen SNPs from the mouse HapMap SNPs and an additional set of 7,570 gap-filling SNPs provided by NIEHS/Perlegen. Since each NIEHS/Perlegen SNP probe has different quality, they classified roughly half of the SNPs as "high-quality" SNPs, which do not have missing genotype at any of the 15 resequenced strains. The imputed genotypes are available for the high-quality SNPs, which has estimated error rate of 0.27% for high-confidence imputed genotypes. In addition, the imputed genotypes for all 8 million SNPs are also available for download. Their estimated error rate is 0.37% for high-confidence imputed genotypes.

Abbreviations: Mouse HapMap

Resource Type: data or information resource, data set

Keywords: genetic variation, genotype, haplotype, imputed genotype, inbred mouse strain, imputed, phenotype, single-nucleotide polymorphism

Funding: NIEHS

Resource Name: Mouse HapMap Imputation Genotype Resource

Resource ID: SCR_002576

Alternate IDs: nif-0000-21752

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250407T215329+0000

Ratings and Alerts

No rating or validation information has been found for Mouse HapMap Imputation Genotype Resource.

No alerts have been found for Mouse HapMap Imputation Genotype Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Rudy RF, et al. (2019) A Genome-Wide Analysis of the Penumbral Volume in Inbred Mice following Middle Cerebral Artery Occlusion. Scientific reports, 9(1), 5070.

Zhou Y, et al. (2019) Integrative system genetic analysis reveals mRNA-lncRNA network associated with mouse spontaneous lung cancer susceptibility. Oncotarget, 10(3), 339.

Rau CD, et al. (2015) High-Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping. G3 (Bethesda, Md.), 5(10), 2021.

Adams A, et al. (2013) Presphenoidal synchondrosis fusion in DBA/2J mice. Mammalian genome : official journal of the International Mammalian Genome Society, 24(1-2), 54.

Park CC, et al. (2011) Gene networks associated with conditional fear in mice identified using a systems genetics approach. BMC systems biology, 5, 43.