

Resource Summary Report

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Perlegen/NIEHS National Toxicology: Mouse Genome Resequencing Project

RRID:SCR_000726

Type: Tool

Proper Citation

Perlegen/NIEHS National Toxicology: Mouse Genome Resequencing Project
(RRID:SCR_000726)

Resource Information

URL: <http://mouse.perlegen.com/mouse/index.html>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, Documented on August 12, 2014. Data, grouped by chromosome, available as flat files for download, of identified DNA polymorphisms (SNPs) in 15 commonly used strains of inbred laboratory mice. Perlegen's SNP, genotype (empirical and imputed), haplotype, trace, and PCR primer data has been compiled with NCBI Mouse Build information to produce data files for public use. Using high-density oligonucleotide array technology, the study identified over 8 million SNPs and other genetic differences between these strains and the previously sequenced C57BL/6J reference strains (Phase 1). By leveraging data provided by Mark Daly's research team at the Broad Institute, genotypes were also predicted for 40 other common strains (Phase 2). Under an extension to the contract, Eleazar Eskin's group at UCLA has used this data to evaluate SNP associations with phenotypes from the Mouse Phenome Project (the Mouse Phenome Database), and to construct haplotype maps for a total of 94 inbred strains (the Mouse HapMap Project). SNP and genotype positions have been mapped from their original reference coordinates to NCBI Mouse Build 37 coordinates. Note that C57BL6/J strain was not selected for re-sequencing as this data would have been almost entirely redundant with the NCBI reference sequence. Since we did not actually determine genotypes for C57BL6/J, we did not submit genotypes for this strain to dbSNP. However, implicit genotypes for C57BL6/J can be obtained from the reference sequence at each SNP position (the reference allele is the first allele in the ALLELES column). The data is available for download in two different compressed file formats. The files are saved as both PC .zip files and Unix compressed .gz files. At this website, you can: * Learn more about the goals of the Perlegen mouse resequencing project. * Learn more about the array-based resequencing technology used in the project. * Download the SNPs, genotypes, and other data generated by the project, plus sequences of the long-

range PCR primers used for SNP discovery. * Browse the mouse genome for SNPs. * View the haplotype blocks within the mouse genome. Mouse Genome Browser The Mouse Genome Browser can be used to visualize genes and the SNPs discovered in this study of genome-wide DNA variation in 15 commonly used, genetically diverse strains of inbred laboratory mice. The reference genome is the C57BL/6J strain NCBI build 37 mouse sequence. In addition to the experimentally-derived genotypes for the original 15 strains, the imputed genotypes for 40 additional inbred mouse strains can also be accessed. Mouse Haplotype Analysis The sequences of 16 commonly used, genetically diverse strains of inbred laboratory mice were analyzed to determine their haplotype structure. The Ancestry Browser shows which ancestral sequence each inbred strain most resembles, along with statistics on the pairwise similarity between the ancestral strains. The Haplotype Viewer shows the haplotype block boundaries and the pairwise similarity for all 56 strains: the 15 used for SNP discovery, the reference strain (C57BL/6J), and the 40 additional strains for which the genotypes were imputed.

Abbreviations: Mouse Resequencing Project

Resource Type: data or information resource, data set

Keywords: genetic variation, chromosome, dna, genome, genotype, haplotype, oligonucleotide, inbred mouse strain, polymorphism, sequence, single-nucleotide polymorphism, c57bl6/j

Funding: NIEHS ;
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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Perlegen/NIEHS National Toxicology: Mouse Genome Resequencing Project

Resource ID: SCR_000726

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Record Creation Time: 20220129T080203+0000

Record Last Update: 20260808T190544+0000

Ratings and Alerts

No rating or validation information has been found for Perlegen/NIEHS National Toxicology: Mouse Genome Resequencing Project.

No alerts have been found for Perlegen/NIEHS National Toxicology: Mouse Genome Resequencing Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Li X, et al. (2010) Expression genetics identifies spinal mechanisms supporting formalin late phase behaviors. *Molecular pain*, 6, 11.

Ahn SH, et al. (2010) Two genes on A/J chromosome 18 are associated with susceptibility to *Staphylococcus aureus* infection by combined microarray and QTL analyses. *PLoS pathogens*, 6(9), e1001088.

Ghazalpour A, et al. (2008) High-resolution mapping of gene expression using association in an outbred mouse stock. *PLoS genetics*, 4(8), e1000149.