

Resource Summary Report

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University of North Carolina Systems Genetics Core Facility

RRID:SCR_016401

Type: Tool

Proper Citation

University of North Carolina Systems Genetics Core Facility (RRID:SCR_016401)

Resource Information

URL: <http://csbio.unc.edu/CCstatus/index.py>

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Description: Core focused on systems genetics approach to understanding diseases, development, aging, and fertility in mouse. Projects range from development of new community resources, such as Collaborative Cross, to development of tools and assays for measuring genetic diversity and discerning genomic structure. Collaborative Cross is reference population for mapping multigenic traits that would be free of population structure and it is new panel of recombinant inbred lines generated by randomizing genetic diversity of existing inbred mouse resources.

Synonyms: University of North Carolina, Chapel Hill - Systems Genetics Core, UNC Systems Genetics

Resource Type: access service resource, core facility, service resource

Keywords: system, genetic, core, mouse, structure, disease, development, aging, fertility

Availability: Restricted

Resource Name: University of North Carolina Systems Genetics Core Facility

Resource ID: SCR_016401

Alternate IDs: SCR_017240

Alternate URLs: <http://www.findmice.org/repository>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260813T055130+0000

Ratings and Alerts

No rating or validation information has been found for University of North Carolina Systems Genetics Core Facility.

No alerts have been found for University of North Carolina Systems Genetics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Darville T, et al. (2026) Genetic diversity of collaborative cross mice enables the establishment of a novel Chlamydia muridarum female genital tract infection model. Infection and immunity, 94(6), e0074625.

Schoenrock SA, et al. (2025) Genetic mapping in collaborative cross mouse strains identifies loci that affect initial sensitivity to cocaine. Psychopharmacology.

Blanchard MW, et al. (2024) The updated mouse universal genotyping array bioinformatic pipeline improves genetic QC in laboratory mice. G3 (Bethesda, Md.), 14(10).

Allayee H, et al. (2023) Systems genetics approaches for understanding complex traits with relevance for human disease. eLife, 12.

Alugupalli KR, et al. (2023) Identification of collaborative cross mouse strains permissive to Salmonella enterica serovar Typhi infection. Scientific reports, 13(1), 393.

He L, et al. (2023) Genetic architecture of the acute and persistent immune cell response after radiation exposure. Cell genomics, 3(11), 100422.

Zhang T, et al. (2023) Multi-omics analysis identifies drivers of protein phosphorylation. Genome biology, 24(1), 52.

Jensen IJ, et al. (2022) Novel Mouse Model of Murine Cytomegalovirus-Induced Adaptive NK Cells. ImmunoHorizons, 6(1), 8.

Mosedale M, et al. (2021) Human-relevant mechanisms and risk factors for TAK-875-Induced liver injury identified via a gene pathway-based approach in Collaborative Cross mice. Toxicology, 461, 152902.

He L, et al. (2021) Genetic background influences the effect of thirdhand smoke exposure on anxiety and memory in Collaborative Cross mice. Scientific reports, 11(1), 13285.

Jin X, et al. (2021) Gut microbiome partially mediates and coordinates the effects of genetics on anxiety-like behavior in Collaborative Cross mice. *Scientific reports*, 11(1), 270.

Nunes-Freitas AL, et al. (2021) Prenatal exposure to nicotine in mice is associated with alterations in development and cellular and synaptic effects of alcohol in a brainstem arousal nucleus. *Neurotoxicology and teratology*, 87, 106980.

Matsushita K, et al. (2021) The role of Sp140 revealed in IgE and mast cell responses in Collaborative Cross mice. *JCI insight*, 6(12).

Keenan BT, et al. (2021) The dihydropyrimidine dehydrogenase gene contributes to heritable differences in sleep in mice. *Current biology : CB*, 31(23), 5238.

Jarmas AE, et al. (2021) Progenitor translational changes coordinated by Tsc1 increase perception of Wnt signals to end nephrogenesis. *Nature communications*, 12(1), 6332.

Sigmon JS, et al. (2020) Content and Performance of the MiniMUGA Genotyping Array: A New Tool To Improve Rigor and Reproducibility in Mouse Research. *Genetics*, 216(4), 905.

Binenbaum I, et al. (2020) Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. *BMC genomics*, 21(1), 761.

Mao JH, et al. (2020) Genetic and metabolic links between the murine microbiome and memory. *Microbiome*, 8(1), 53.

Lor?? NI, et al. (2020) Collaborative Cross Mice Yield Genetic Modifiers for *Pseudomonas aeruginosa* Infection in Human Lung Disease. *mBio*, 11(2).

Price A, et al. (2020) Transcriptional Correlates of Tolerance and Lethality in Mice Predict Ebola Virus Disease Patient Outcomes. *Cell reports*, 30(6), 1702.