

Resource Summary Report

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University of North Carolina at Chapel Hill Mammalian Genotyping Core Facility

RRID:SCR_022716

Type: Tool

Proper Citation

University of North Carolina at Chapel Hill Mammalian Genotyping Core Facility
(RRID:SCR_022716)

Resource Information

URL: <https://uncch.ilab.agilent.com/sc/5341/mammalian-genotyping-core/?tab=about>

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Description: Core is component of Integrated Genomics Core/High Throughput Sequencing Facility. Supports population, basic, clinical and translational research by providing centralized cost efficient, high quality genotyping and methylation services using Illumina BeadArray and Infinium microarray assay technologies for Single Nucleotide Polymorphism Genotyping, Copy Number Variant, Loss of Heterozygosity, Insertions Deletion (indel), Structural Variant, and DNA Methylation Analysis. Can assist with selecting appropriate arrays to meet your needs.

Abbreviations: MGC

Synonyms: University of North Carolina at Chapel Hill Mammalian Genotyping Core, Mammalian Genotyping Core

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

Keywords: USEdit, ABRF, genotyping and methylation services, Illumina BeadArray assay, Infinium microarray assay, Single Nucleotide Polymorphism Genotyping, Copy Number Variant, Loss of Heterozygosity, Insertions Deletion, Structural Variant, DNA Methylation Analysis

Resource Name: University of North Carolina at Chapel Hill Mammalian Genotyping Core Facility

Resource ID: SCR_022716

Alternate IDs: ABRF_1518

Alternate URLs: <https://coremarketplace.org/?FacilityID=1518&citation=1>

Record Creation Time: 20220830T050156+0000

Record Last Update: 20260731T043117+0000

Ratings and Alerts

No rating or validation information has been found for University of North Carolina at Chapel Hill Mammalian Genotyping Core Facility.

No alerts have been found for University of North Carolina at Chapel Hill Mammalian Genotyping Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hartwell HJ, et al. (2025) Heritable dysregulation of DNA methylation may underlie the diabetogenic effects of paternal preconception exposure to inorganic arsenic in C57BL/6J mice. Toxicology and applied pharmacology, 496, 117242.