

Resource Summary Report

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University of Florida ICBR Gene Expression and Genotyping Core Facility

RRID:SCR_019145

Type: Tool

Proper Citation

University of Florida ICBR Gene Expression and Genotyping Core Facility
(RRID:SCR_019145)

Resource Information

URL: <http://www.biotech.ufl.edu/cores/gene-expression-genotyping/>

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Description: Core provides services and consultation on Single Cell RNA-Seq, RNA-Seq, 16s metagenomics and Affymetrix gene expression arrays. High-throughput RNA-seq libraries, 16s libraries and sequencing capture libraries can be done by using Agilent Bravo robot. QuantiGene RNA Assays measure up to 80 gene targets directly with degraded and cross-linked RNA in FFPE tissues and blood, with no RNA purification required. BioRad QX200 AutoDG Droplet Digital PCR System provides absolute quantification of target DNA or RNA molecules with greater precision and sensitivity than qPCR, sensitivity of ddPCR System can facilitate expanded analysis of single cells. Genotyping services include fragment analysis using AB3730, 96 capillary technology, development of microsatellite libraries using Illumina sequence data, and genotyping using mouse tails or ear punches.

Synonyms: University of Florida ICBR Gene Expression and Genotyping, UF ICBR Gene Expression & Genotyping

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

Keywords: USEDB, gene expression, genotyping, single cell RNAseq, PCR, qPCR, analysis, ABRF

Resource Name: University of Florida ICBR Gene Expression and Genotyping Core Facility

Resource ID: SCR_019145

Alternate IDs: ABRF_647

Alternate URLs: <https://coremarketplace.org/?FacilityID=647>

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260905T133418+0000

Ratings and Alerts

No rating or validation information has been found for University of Florida ICBR Gene Expression and Genotyping Core Facility.

No alerts have been found for University of Florida ICBR Gene Expression and Genotyping Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 68 mentions in open access literature.

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

Luo YE, et al. (2026) Fibro-adipogenic progenitor cells from murine SMA muscles are intrinsically adipogenic. Proceedings of the National Academy of Sciences of the United States of America, 123(13), e2525423123.

Perez Taboada V, et al. (2026) Bacterial Schlafen proteins mediate phage defence. Nature microbiology, 11(4), 1037.

Collins JM, et al. (2026) Knockdown of RNA editing proteins reshapes the HepaRG transcriptome and pharmacogene expression. Scientific reports, 16(1).

Tantawy M, et al. (2026) Atorvastatin Protects Against Deleterious Carfilzomib-Induced Transcriptional Changes in Human Induced Pluripotent Stem Cell-Derived Cardiomyocytes. International journal of molecular sciences, 27(3).

Medina-Serpas MA, et al. (2026) Spatial transcriptomics from pancreas and local draining lymph node tissue reveals a lymphotoxin-? signature in human type 1 diabetes. Cell reports, 45(4), 117144.

Canal R, et al. (2026) Enhanced Pro-Osteogenic Regulatory Modulation in Mesenchymal Stem Cells Derived from the Periosteum Under Simulated Microgravity. Cells, 15(11).

Kolling Iv FW, et al. (2026) Multisite Assessment of Methods for Cell Preservation Upstream of Single-Cell RNA Sequencing. Journal of biomolecular techniques : JBT, 37(2), 9.

McMahon S, et al. (2026) Non-canonical histone H3.3 and its chaperones HIRA and DAXX participate in the regulation of KSHV latency. *bioRxiv : the preprint server for biology*.

Irfan M, et al. (2026) A CRISPR array orchestrates virulence and host response in *Porphyromonas gingivalis*. *Microbiology spectrum*, 14(4), e0283425.

Semel M, et al. (2026) Mitochondrial Permeability Transition in Skeletal Muscle Phenocopies Muscle Alterations seen in Cancer Cachexia and other Wasting Conditions. *bioRxiv : the preprint server for biology*.

Abdullah M, et al. (2026) Osteosarcoma cells promote intracellular iron detoxification to mitigate GPX4-mediated ferroptosis. *Cancer gene therapy*, 33(5), 547.

Maldonado MBC, et al. (2026) Alterations in gene expression and DNA methylation in the bovine blastocyst in response to choline supplementation during culture†. *Biology of reproduction*, 114(5), 1568.

Montalvo RN, et al. (2026) Sex Differences in Response to Acute Doxorubicin Cardiorespiratory Muscle Dysfunction and Preconditioning Exercise. *Medicine and science in sports and exercise*, 58(1), 47.

Brummel BR, et al. (2026) Natural Products Inspired Scaffold Diversification Leads to Unnatural Molecular Warhead and Covalent Strategy to Modulating Protein Function through Electrophilic Bromine Transfer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(42), e12849.

Xu P, et al. (2026) Pre-operative Serum Hepatocyte Growth Factor and Inflammatory Prognostic Score as Prognostic Markers in Oral Squamous Cell Carcinoma. *Journal of visualized experiments : JoVE*(230).

Mercado-Rodriguez C, et al. (2026) Defined bacterial consortium highlights the impact of intestinal bacteria on DNA methylation and tumorigenesis. *Genome biology*, 27(1).

Simonovich JA, et al. (2026) Circulating PEG-indoleamine 2,3-dioxygenase ameliorates diverse inflammatory diseases without toxicity or compromising immunocompetence. *Proceedings of the National Academy of Sciences of the United States of America*, 123(28), e2602536123.

Madrid G, et al. (2025) An improved nuclei isolation protocol from leaf tissue for single-cell transcriptomics. *PloS one*, 20(9), e0302118.

Chitre S, et al. (2025) A defined bacterial consortium and spatial transcriptomics highlight the complex interaction between *Campylobacter jejuni* and the murine intestine. *Gut microbes*, 17(1), 2600053.

Diedrick WA, et al. (2025) Molecular Assessment of Genes Linked to Honeybee Health Fed with Different Diets in Nuclear Colonies. *Insects*, 16(4).