# 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 off 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:** core facility, access service resource, service resource

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

**Funding:**

**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:** 20250426T060745+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 33 mentions in open access literature.

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

Duarte PM, et al. (2024) Distinctive genes and signaling pathways associated with type 2 diabetes-related periodontitis: Preliminary study. PloS one, 19(1), e0296925.

Schnitzler CE, et al. (2024) The genome of the colonial hydroid Hydractinia reveals that their stem cells use a toolkit of evolutionarily shared genes with all animals. Genome research, 34(3), 498.

Kok HJ, et al. (2024) Transcriptomics reveals transient and dynamic muscle fibrosis and atrophy differences following spinal cord injury in rats. Journal of cachexia, sarcopenia and muscle, 15(4), 1309.

Mitchell DG, et al. (2024) The ctenophore Mnemiopsis leidyi deploys a rapid injury response dating back to the last common animal ancestor. Communications biology, 7(1), 203.

Zhou M, et al. (2024) Light has a principal role in the Arabidopsis transcriptomic response to the spaceflight environment. NPJ microgravity, 10(1), 82.

Viggars MR, et al. (2024) Skeletal muscle BMAL1 is necessary for transcriptional adaptation of local and peripheral tissues in response to endurance exercise training. Molecular metabolism, 86, 101980.

Gutierrez-Monreal MA, et al. (2024) Targeted Bmal1 restoration in muscle prolongs lifespan with systemic health effects in aging model. JCI insight, 9(22).

Febres VJ, et al. (2024) Dissection of transcriptional events in graft incompatible reactions of "Bearss" lemon (Citrus limon) and "Valencia" sweet orange (C. sinensis) on a novel citrandarin (C. reticulata × Poncirus trifoliata) rootstock. Frontiers in plant science, 15, 1421734.

Jin Z, et al. (2024) ANGPTL4 Suppresses Clear Cell Renal Cell Carcinoma via Inhibition of Lysosomal Acid Lipase. Cancer research communications, 4(8), 2242.

Poole B, et al. (2024) Sirtuin3 promotes the degradation of hepatic Z alpha-1 antitrypsin through lipophagy. Hepatology communications, 8(2).

Brinley AR, et al. (2024) Morphological and genetic characterization of the muscadine fruit abscission zone. Horticulture research, 11(10), uhae227.

Lin C-Y, et al. (2024) An insect virus differentially alters gene expression among life stages of an insect vector and enhances bacterial phytopathogen transmission. Journal of virology, e0163024.

Zhou M, et al. (2024) Single-molecule long-read methylation profiling reveals regional DNA methylation regulated by Elongator Complex Subunit 2 in Arabidopsis roots experiencing spaceflight. Biology direct, 19(1), 33.

Pelosi JA, et al. (2024) An efficient and effective RNA extraction protocol for ferns. Applications in plant sciences, 12(6), e11617.

Romero-Carramiñana I, et al. (2024) Ablation of Atp5if1 impairs metabolic reprogramming and proliferation of T lymphocytes and compromises mouse survival. iScience, 27(6), 109863.

Marini S, et al. (2024) Oral Cannabidiol Treatment Is Associated with an Anti-Inflammatory Gene Expression Signature in Myeloid Cells of People Living with HIV. Cannabis and cannabinoid research.

Li Q, et al. (2023) N-hydroxypipecolic acid triggers systemic acquired resistance through extracellular NAD(P). Nature communications, 14(1), 6848.

Viggars MR, et al. (2023) Muscle Bmal1 is necessary for normal transcriptomic and metabolomic adaptation to endurance exercise training. bioRxiv : the preprint server for biology.

Schnitzler CE, et al. (2023) The genome of the colonial hydroid Hydractinia reveals their stem cells utilize a toolkit of evolutionarily shared genes with all animals. bioRxiv : the preprint server for biology.

Ferl RJ, et al. (2023) Transcriptomic dynamics in the transition from ground to space are revealed by Virgin Galactic human-tended suborbital spaceflight. NPJ microgravity, 9(1), 95.