

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, service resource, core facility

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: 20260806T054709+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 50 mentions in open access literature.

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

Gurgel BCV, et al. (2025) Comprehensive analysis of transcriptome and pathway interactions in periodontitis. Journal of applied oral science : revista FOB, 33, e20250396.

Sieber KR, et al. (2025) Caste- and environment-associated differential expression of olfactory receptors in pest ants. Scientific reports, 15(1), 31079.

Duran-Pinedo A, et al. (2025) Longitudinal host-microbiome dynamics of metatranscription identify hallmarks of progression in periodontitis. Microbiome, 13(1), 119.

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

Taboada VP, et al. (2025) Bacterial Schlafens mediate anti-phage defense. bioRxiv : the preprint server for biology.

Laforest LC, et al. (2025) A chromosome-level Mitragyna parvifolia genome unveils spirooxindole alkaloid diversification and mitraphylline biosynthesis. The Plant cell, 37(9).

Seo D, et al. (2025) GLARE: discovering hidden patterns in spaceflight transcriptome using representation learning. NPJ microgravity, 11(1), 76.

Kolling FW, et al. (2025) Multi-site Assessment of Methods for Cell Preservation Upstream of Single Cell RNA Sequencing. bioRxiv : the preprint server for biology.

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

Bogale M, et al. (2025) Development of Monoclonal Antibodies for Identifying Plant-Parasitic Nematodes. *Journal of nematology*, 57(1), 20250024.

Enriquez V, et al. (2025) Active *Cryptococcus neoformans* glucuronoxylomannan production prevents elimination of cryptococcal CNS infection in vivo. *Journal of neuroinflammation*, 22(1), 61.

Chitre S, et al. (2025) A defined bacterial consortium and spatial transcriptomics highlight the complex interaction between *Campylobacter jejuni* and the murine intestine. *bioRxiv* : the preprint server for biology.

Dill MN, et al. (2025) Exploring the Unique Extracellular Matrix Composition of *Acomys* as a Potential Key to Resisting Fibrosis. *ACS biomaterials science & engineering*, 11(6), 3616.

Scott KA, et al. (2025) Cardiometabolic and anxiogenic consequences of chronic social defeat stress in male mice. *Neurobiology of stress*, 38, 100752.

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.

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.

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.

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

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.