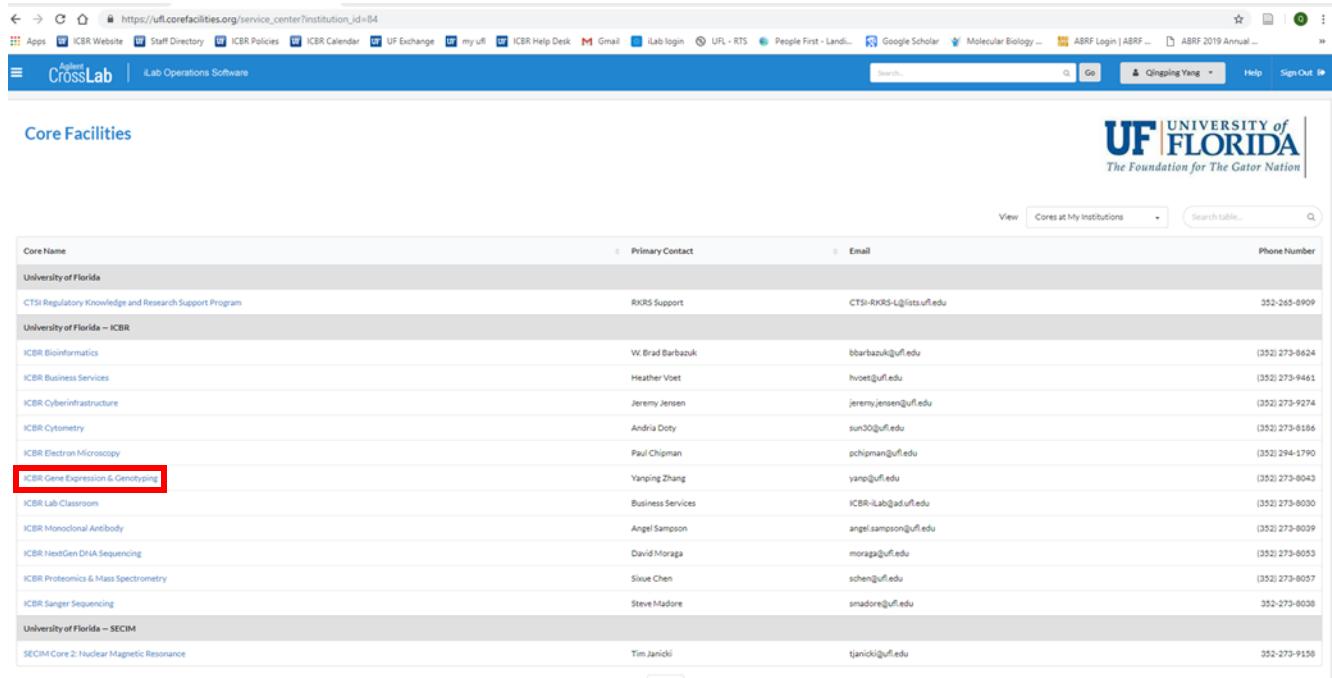


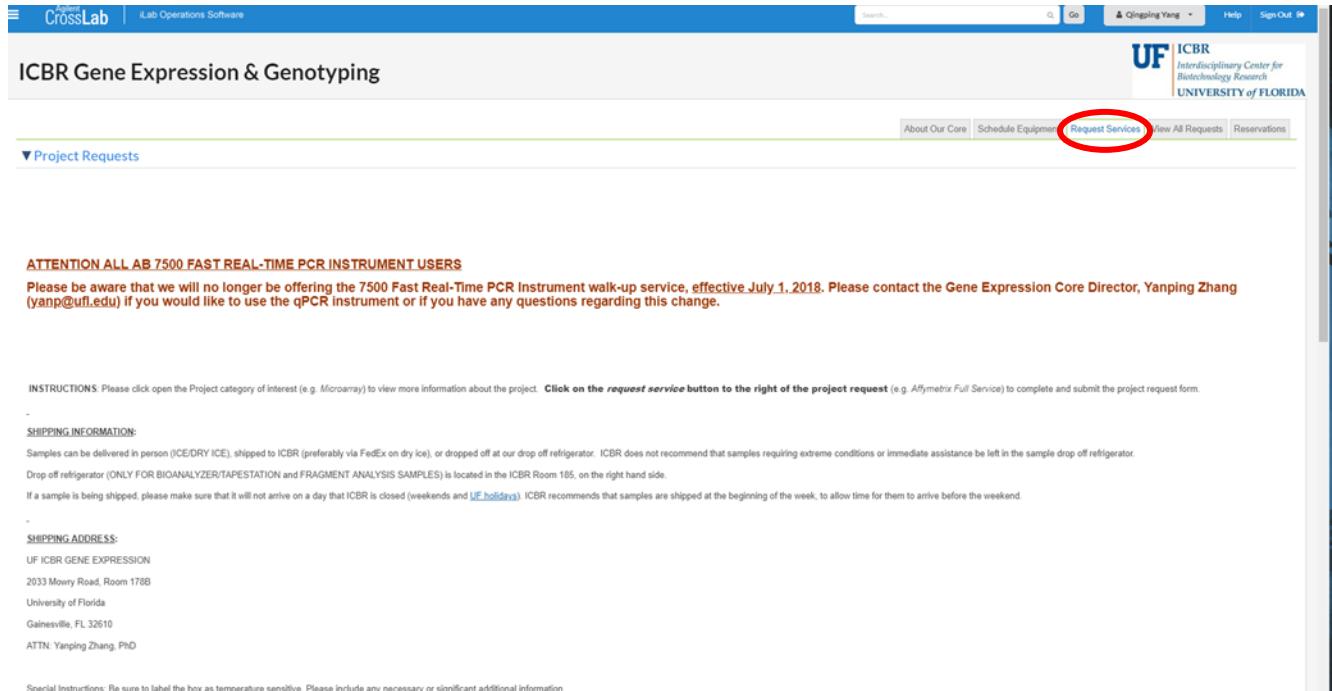
**Featured Project: 16s Library\_Bravo Automation**

1. After creating an account and logging in, navigate to our core by clicking “list all cores”, then selecting ICBR Gene Expression & Genotyping.



Core Name	Primary Contact	Email	Phone Number
University of Florida			
CTSI Regulatory Knowledge and Research Support Program	RKRS Support	CTSI-RKRS-L@lists.ufl.edu	352-265-8909
University of Florida – ICBR			
ICBR Bioinformatics	W. Brad Barbazuk	bbarbazuk@ufl.edu	(352) 273-8624
ICBR Business Services	Heather Voet	hvoet@ufl.edu	(352) 273-9461
ICBR Cyberinfrastructure	Jeremy Jensen	jeremy.jensen@ufl.edu	(352) 273-9274
ICBR Cytometry	Andria Doty	sun30@ufl.edu	(352) 273-8186
ICBR Electron Microscopy	Paul Chipman	pchipman@ufl.edu	(352) 294-1790
ICBR Gene Expression & Genotyping	Yanping Zhang	yanp@ufl.edu	(352) 273-8043
ICBR Lab Classroom	Business Services	ICBR-iLab@ad.ufl.edu	(352) 273-8000
ICBR Monoclonal Antibody	Angel Sampson	angel.sampson@ufl.edu	(352) 273-8039
ICBR NextGen DNA Sequencing	David Moraga	moraga@ufl.edu	(352) 273-8053
ICBR Proteomics & Mass Spectrometry	Sixue Chen	schen@ufl.edu	(352) 273-8057
ICBR Sanger Sequencing	Steve Madore	smadore@ufl.edu	(352) 273-8008
University of Florida – SECIM			
SECIM Core 2: Nuclear Magnetic Resonance	Tim Janicki	tjanicki@ufl.edu	352-273-9158

2. After clicking on the core, navigate to the “Request Services” tab where you will see a list of our services offered.



**ATTENTION ALL AB 7500 FAST REAL-TIME PCR INSTRUMENT USERS**  
Please be aware that we will no longer be offering the 7500 Fast Real-Time PCR Instrument walk-up service, **effective July 1, 2018**. Please contact the Gene Expression Core Director, Yanping Zhang (yanp@ufl.edu) if you would like to use the qPCR instrument or if you have any questions regarding this change.

**INSTRUCTIONS:** Please click open the Project category of interest (e.g. Microarray) to view more information about the project. **Click on the request service button to the right of the project request** (e.g. Affymetrix Full Service) to complete and submit the project request form.

**SHIPPING INFORMATION:**  
Samples can be delivered in person (ICE/DRY ICE), shipped to ICBR (preferably via FedEx on dry ice), or dropped off at our drop off refrigerator. ICBR does not recommend that samples requiring extreme conditions or immediate assistance be left in the sample drop off refrigerator.  
Drop off refrigerator (ONLY FOR BIOANALYZER/TAPESTATION AND FRAGMENT ANALYSIS SAMPLES) is located in the ICBR Room 105, on the right hand side.  
If a sample is being shipped, please make sure that it will not arrive on a day that ICBR is closed (weekends and [UF holidays](#)). ICBR recommends that samples are shipped at the beginning of the week, to allow time for them to arrive before the weekend.

**SHIPPING ADDRESS:**  
UF ICBR GENE EXPRESSION  
2033 Mowry Road, Room 178B  
University of Florida  
Gainesville, FL 32610  
ATTN: Yanping Zhang, PhD

Special Instructions: Be sure to label the box as temperature sensitive. Please include any necessary or significant additional information

3. Scroll to the category of the project you want, and click the triangle to drop down more information. Select “Initiate Request” after reviewing the description and ensuring this is the correct project.

► [Antibody Sequencing \(1\)](#)  
 ▾ [Bravo Automations \(2\)](#)

**Bravo 16s and RNAseq Library Automation (Bravo Automations)**

16s ribosomal RNA sequencing can be used to identify and compare bacteria present within a given sample.

RNA-Seq is a powerful research tool for expression and variant analysis. Its application includes quantifying mRNA abundance, determining the transcriptional structure of genes, start sites, 5' and 3' ends, and splicing patterns, comparably detecting the changing expression levels of each transcript during development and under different conditions. It picks up all sequences that are present in the cell, regardless of their annotation status.

Gene Expression Core offers library preparation automation by Agilent Bravo Automation Workstation. The constructed libraries can be run on all NextGen sequencing platforms: Illumina HiSeq, MiSeq, and NextSeq. Sequence can be done by ICBR NextGen Sequencing Core.

We also offer Agilent's SureSelect Target Enrichment platform which allows you to focus your NextGen sequencing workflow on key genomic regions of interest while reducing cost per sample. Other NextGen relative services include cDNA library construction, normalization and rRNA depletion (Ribominus). If requested, we will directly deliver the libraries to our ICBR NextGen Sequencing Core with an e-mail notification to you. Otherwise the library will be return to you.

**Custom Bravo Run (Bravo Automations)**

The service includes the Bravo consumables and run assistance.

[initiate request](#)

► [Cell-Line Authentication \(Human\) \(1\)](#)  
 ► [Custom Project \(1\)](#)  
 ► [Digital PCR Analysis \(1\)](#)

4. Type **your** name into the search bar, your institution/lab should appear as well. Select it and click "Proceed."

**ICBR Gene Expression & Genotyping**



**Bravo 16s and RNAseq Library Automation**

person: **Yanping Zhang** ICBR Gene Expression & Genotyping Core (UF) Lab (+1) yanp@ufl.edu 3522738036

search within:  current customers  this institution  All

lab: ICBR Gene Expression & Genotyping Core (UF) Lab [Proceed](#) (circled in red)

[About Our Core](#) [Schedule Equipment](#) [Request Services](#) [View All Requests](#) [Reservations](#)

[Cancel](#)

5. Fill out the form below and upload sample names in a worksheet format. Do not worry about the request name ICBR-GE-[CID], this will auto-complete upon submission.

[View Form](#) **Bravo Library Automation Form**

Please complete the form below and click 'save completed form' to provide the core with details regarding your request. Required fields are marked by a red star.

[Save Progress](#)

★ Number of Samples:

★ Starting Material:

★ Name of the Species:

★ Please select the service(s) you would like to request:

16 s library Automation Per Sample (batch w/48 samples)  
 16 s library Automation Per Sample (batch w/96 samples)  
 DNASeq library automation per sample (24 samples)  
 DNASeq library automation per sample (48 samples)  
 DNASeq library automation per sample (96 samples)  
 RNASeq library automation per sample (24 samples)  
 RNASeq library automation per sample (48 samples)  
 RNASeq library automation per sample (96 samples)

★ Type of Library:

★ Kit provided:

★ Multiplex for Library Preparation:

★ NextGen Instrument:

★ Sequencing Run Format:

★ # of Cycles:

★ Number of Runs/Lanes:

★ Would you like to request Data Analysis Service?

Sample Sheet Instructions:

Please upload your sample sheet with the specific information requested for each sample: SAMPLE NAME, ORGANISM, OD 260/280, TOTAL RNA CONCENTRATION (ng/μl), VOLUME OF TOTAL RNA, RNA PURIFICATION METHOD, SOLVENT, DNase TREATMENT.

★ Sample Sheet:

Use of ICBR services constitutes acceptance and agreement to abide by ICBR Terms and Conditions.

★ I affirm that I have read and agree to all ICBR Terms and Conditions.  Yes

★ Special Request (such as special Indexes are needed to be used, pooling ratio for each sample, and extra pre-made libraries need to be pooled together with this project) Please write "No" if no special request is needed.

6. Save your form if you have finished it, or save a draft to come back to later. Input your payment information, using the account or credit card that you would like to project billed to. When you are finished, either submit the request to our core, or save a draft if it is not complete.

**Cost**

Please provide the customer with a final quote for this request. The quote will be based on the services and charges you have added above and any "buffer" you have added. The "buffer" amount is for services or charges that you have not yet defined but that you expect to arise during the course of the request.

Add value or percent buffer:  
as percentage  %

Quote (total predicted cost):  
\$ (automatic total of any services, charges or buffer added to this request)

**3 Payment Information**

Please enter the GE-ID or Chartfield:  
 UF Chartfield  Select UF Chartfield

enter additional payment information

Skip approval?

submit request to researcher  save draft request  Cancel



7. You are now finished, and should receive an email from [no-reply@ilabsolutions.com](mailto:no-reply@ilabsolutions.com) with a copy of your form and a GE-ID number which we will use to track your project. Please print the form and bring it with you when you deliver your samples.
8. Drop off your samples and form with GE-ID to ICBR Gene Expression & Genotyping Core, located in CGRC Room 178B. If you are shipping your samples, please be sure to include your name, your institution/lab, and GE-ID. We recommend sending temperature-sensitive samples on dry ice. Please clearly address the package as follows:

UF ICBR GENE EXPRESSION  
2033 Mowry Road, Room 178B  
University of Florida  
Gainesville, FL 32610  
ATTN: Yanping Zhang, PhD

*If you have any additional questions, please feel free to contact our core at (352)-273-8036, or email us at [ICBR-GeneExpression@ad.ufl.edu](mailto:ICBR-GeneExpression@ad.ufl.edu). Thank you!*