UCLA Technology Center for Genomics & Bioinformatics
Service Request Form

Mailing address: 650 Charles E Young Drive South, CHS 38-123
Los Angeles, CA 90095-1735
Phone: (310) 206-3945

Before delivering your samples, please e-mail us the copy for the request form at sequencing@mednet.ucla.edu.
Also, please print a copy of the request form when you deliver your samples at CHS 38-123.

If you need your samples back, please collect them from us within 2 weeks after you receive the data.
ALL samples will be automatically DISCARDED 2 weeks after the data delivery.

REQUESTOR INFORMATION		
Principal Investigator (**one PI only**):	Phone:	Email:
Institution/Department:		Dept. Code:
Street Address:		
City:	State:	Zip Code:
Contact Person who delivers samples:	Phone (Required):	Email:
Is PI a JCCC Member? ☐ Yes ☐ No		

BILLING INFORMATION	
Internal Users: FAU REQUIRED. Include any applicable Project Code and/or Source Code Full Accounting Unit (FAU)**:**	Fund Manager Email:
External Users: PO# REQUIRED. Quote will be created after submitting the request form. PO #: Tax ID #:	

Please fill out completely to avoid processing delays.

EXPERIMENTAL INFORMATION
Date of Request:
Project Name:
Project Information:

SAMPLE SUBMITTED (What You Give us)

# of Samples: _____ **Species:** _____

Sample Type: ☐ Frozen Tissue ☐ Blood ☐ FFPE Tissue/slide ☐ Cell Pellet (in 1.5 mL Tubes) ☐ Total RNA ☐ gDNA
☐ Single Cell Suspension ☐ Single Nuclei Suspension ☐ Fixed Cells
☐ slide for GeoMx ☐ slide for CosMx ☐ slide for 10X Xenium ☐ slide for 10X Visium ☐ slide for Stereoseq
☐ Library (please specify library type): ____ ☐ 10x Library (please specify library type): ____
☐ Pooled Libraries (Specify Library Type, nM Concentration & if you want us to QC your pool again): _____
☐ Other (please specify): _____

SERVICE REQUESTED (What You Want us to Do)

Nucleic Acid Extraction: ☐ DNA ☐ RNA (Please specify, if your samples are in Trizol.)

QC (for DNA/RNA QC, check Nanodrop and Tapestation; for library QC, check Qubit and Tapestation):
Quantitative: ☐ NanoDrop ☐ Qubit
Qualitative: ☐ TapeStation (If you need specific tape, please specify here): _____

Library Construction:

Bulk Sequencing: ☐ RNASeq ☐ RNASeq with rRNA Depletion ☐ miRNASeq ☐ Chipseq ☐ Methyseq (WGBS) ☐ Methyseq (RRBS)
☐ Human WES ☐ Mouse WES ☐ WGS ☐ Other (please specify): ____

Single Cell: ☐ Cell Counting & Viability assay ☐ 3'GEX ☐ 5'GEX ☐ TCR ☐ BCR ☐ FB ☐ ATAC
☐ Multiome (3'GEX+ATAC) ☐ FFPE/Fixed ☐ BD Rhapsody
☐ Other (please specify): ____

10X Visium: ☐ Visium Tissue Optimization ☐ Visium Whole Transcription Analysis (WTA)
☐ Visium Whole Transcription Analysis + protein expression (WTA+PEX) ☐ Other (please specify): ____

10X Visium HD: ☐ Human Whole Transcription Analysis (WTA) ☐ Mouse Whole Transcription Analysis (WTA)

10X Xenium: ☐ Fresh 10X Xenium ☐ FFPE 10X Xenium (Users need to provide the panel.): Please specify: _____

GeoMx DSP: ☐ Dry Run ☐ hWTA ☐ mWTA ☐ hCTA ☐ Protein Panel (Specify):____ ☐ Other (please specify): ____

CosMx SMI: ☐ Human Universal Panel (1000 genes) ☐ Human Immuno-Oncology (100 genes) ☐ Mouse Neuro Panel (1000 genes)
☐ Human Immuno-Oncology protein panel (64 proteins) ☐ Other (please specify): ____

StereoSeq: ☐ StereoSeq (1 cm x 1 cm) ☐ Tissue Optimization

If you need custom antibody for cell staining, please specify name/s and dilution factor for staining: _____

Sequencing:

Application System: ☐ Novaseq X Plus **1.5B** (750M/lane) ☐ Novaseq X Plus **10B** (1250M/lane) ☐ Novaseq X Plus **25B** (3125M/lane)
☐ MiSeq ☐ NextSeq500 Mid Output (130M) ☐ NextSeq500 High Output (400M) ☐ Oxford Nanopore (10-50GB/flow cell)
☐ DNBseq T7 (5000M/flow cell) – 50, 200 and 300 cycle flow cell

Sequencing Type (e.g., 2X50, 2X100, 2x150): _____

Sequencing Depth (e.g., 30M from each direction/sample, 2 lanes for all samples, etc.): _____

If you are submitting customer constructed libraries:
- If you need custom primers for sequencing, please specify and submit at 100 uM at 50 uL.
- If you need Phix spike-in, please let us know what percentage at: _____%.
- If you are not requesting QC, please provide 50ul of 3nM pooled libraries and TapeStation trace file or average bp size.
- Please provide barcode sequences (i7 and/or i5) in an excel file.

Data Analysis: ☐ Partial Data Analysis ☐ Full Data Analysis ☐ 10X Single Cell Data Analysis ☐ Spatial Data Analysis
☐ Other (Specify): _____

Data Analysis Requirements & Details (e.g., normalized gene counts, comparison groups, differential expression statistics, etc.)

Other Custom Service (Specify): _____

SAMPLE GUIDELINES:

- If you are submitting extracted DNA and/or RNA
  - If you have more than 6 samples, please put them into a PCR strip.
  - If you have more than 16 samples, please put them into 96 well plates.
  - Please plate in the order of Sample 1=A1, Sample 2=B1, Sample 3=C1… Sample 9=A2…Sample 96=H12.

- Please label the tube caps with Sample Number (1, 2, 3…) that corresponds the table below.

SAMPLE INFORMATION					
Sample #	**Sample Name** (Avoid any spaces, decimals, dashes, slashes, parentheses, etc.) Underscore "_" is acceptable.	**Concentration (ng/uL)**	**260/280 Ratio**	**Volume (uL)**	**Additional Info** (%DV200, RIN, Date of block created, etc.)
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
15					
16					
If you have more than 16 samples, please attach an Excel file.					

VOLUME RECOMMENDATIONS:

- QC:
  - Quantitative Measure
    - NanoDrop: 2 uL
    - Qubit: 3 uL
  - Quality Measure
    - TapeStation: 3 uL
  - Example: NanoDrop + TapeStation= 5 uL

- Library Construction:
  - 20 ng/uL to 200 ng/uL in 50 uL
  - If you are planning to bring us less than 15 uL, please let us know before sample submission.

- Sequencing:
  - Concentration needed for sequencing: >2 nM in 50 uL~ 100 uL.
  - Volume will vary depending on the sequencer.

SHIPPING CONSIDERATIONS FOR FFPE SLIDES

• FFPE unstained sections should be packed securely in a slide box and shipped at room temperature. Bubble wrap or foam wrap may be inserted to prevent the slides from breaking during transport.

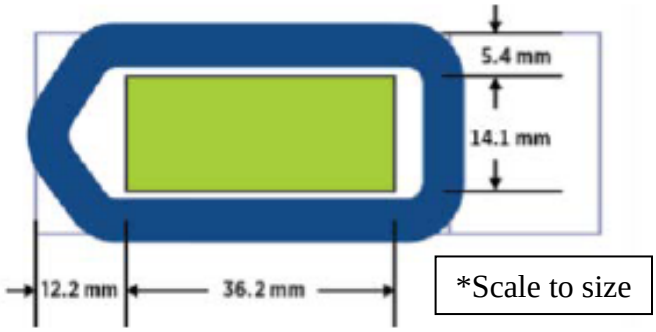
• If sending FFPE tissue blocks, care should be taken to prevent scraping of tissue surface during transport.

ADDITIONAL SAMPLE GUIDELINES FOR GEOMX DSP:

Sample Guidelines

• 4 µm-6 µm unstained sections mounted on adhesive/positively charged slides are required, e.g., Superfrost Plus; Leica X-tra-adhesive (Cat#: 3800050). For TMA, bone marrow tissue and mRNA DSP samples, Leica Bond plus slides (Cat#: S21.2113.A) are recommended.

• Dry sectioned slides at 42C with a vent for at least 4 hours to overnight. Bake at 65C for 1 hour.



*Scale to size

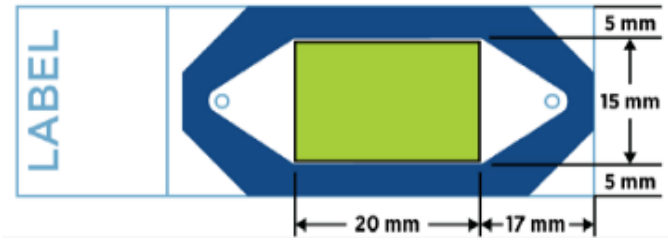
• Ideally, tissue sections should be placed in the center of the slide and be no larger than 36.2 mm wide by 14.1 mm high. If sections are larger than this size or placed off center, it is possible that the tissue located in blue area cannot be measured.

• Tissue less than 3 years old is preferred. We recommend cutting sections fresh for best performance with RNA. Protein samples can be fresh cut or previously slide mounted.

ADDITIONAL SAMPLE GUIDELINES FOR COSMX SMI:

Sample Guidelines

• 4 µm-6 µm unstained sections mounted on adhesive/positively charged slides are required, e.g., Superfrost Plus; Leica X-tra-adhesive (Cat#: 3800050). For TMA, bone marrow tissue and mRNA DSP samples, Leica Bond plus slides (Cat#: S21.2113.A) are recommended.



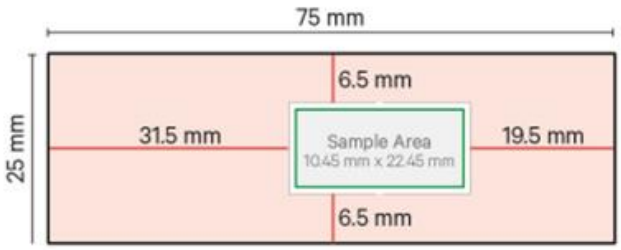
*Scale to size

• Ideally, tissue sections should be placed in the center of the slide and be no larger than 20 mm wide by 15 mm high. If sections are larger than this size or placed off center, it is possible that the tissue located in blue area cannot be measured.

• Tissue less than 3 years old is preferred. We recommend cutting sections fresh for best performance with RNA. Protein samples can be fresh cut or previously slide mounted.

ADDITIONAL SAMPLE GUIDELINES FOR XENIUM SLIDE:

Sample Guidelines



*Scale to size

- Use the following diagram to verify that freshly placed tissue sections are compatible with the Xenium Slide. Reference the image below to draw the sample area on the back of blank slides.
- Practice correct section placement within the representative frames using non-experimental blocks.

BIO-SAFETY LEVEL 2 FACILITY QUESTIONNAIRE - MANDATORY

The TCGB BSL2 Facility accommodates researchers using biological materials from various sources that may contain known or unknown human pathogens. In order to insure safe and appropriate working conditions for all users of the facility, accurate and complete information about the agents you propose to use is needed to maintain appropriate biosafety standards.

Please fill out this form COMPLETELY and have it signed by the principal investigator before experiments begin. The CMC staff will review the form as part of the training and facility access process, and keep it on file. IF NEW BIOHAZARDS ARE ADDED at a future date, IT IS YOUR RESPONSIBILITY TO UPDATE THIS FORM.

Do you have current Institutional Biosafety Committee (IBC) approval or Institutional Review Board (IRB) approval for this project? (Check all that apply)

Yes. Attach a copy of the IBC and/or IRB approval letter.

IBC and/or IRB Approval Pending. Access cannot be granted until approval is obtained. Contact the EH&S Biosafety Office at extension x63929 or e-mail at biosafety@ehs.ucla.edu.

Exempt. Verify exemption with EH&S. Attach copy of IBC letter of exemption.

No ICB/IRB Approval Needed.

List type of materials to be used, and sources (i.e., mouse spleen cells, human peripheral blood mononuclear cells, cells from an animal en-grafted with human cells, viruses etc.); for cell lines, describe cell origin.

Does the sample contain any known infectious agent(s)? Yes No

If yes, list infectious agents (*must be listed on your IBC approval letter with the proper containment indicated)*:

Were the cells genetically engineered? Yes ___ No ___

If yes, how were they genetically engineered? Was a gene therapy virus (adenovirus, retrovirus, lentivirus, herpesvirus, etc.) used to transfer genetic information to the cells?

If yes, describe method in detail, attach vector map and show packaging cell line.

I have read above questions carefully and certify the information provided to be correct.

PI or Supervisor Signature: _____ Date: _____

Researcher Signature: _____ Date: _____