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 **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

Please submit this service request form to sequencing@mednet.ucla.edu prior to delivering your samples

on dry ice to CHS 38-123.

**If you need your RNA/libraries back after sequencing, please collect it from us within 2 weeks after we deliver data.**

**Samples AND sequencing libraries will be automatically DISCARDED 2 weeks after sequencing data delivery.**

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| **REQUESTOR INFORMATION** |
| Principal Investigator:  | Phone:  | Email:  |
| Institution/Department:  | Dept. Code: |
| Street Address:  |
| City:  | State:  | Zip Code:  |
| Contact Person: | Phone:  | Email:  |
| Is PI a JCCC Member? ◻ Yes ◻ No  |
| **Payment Info** **(Internal Users Only)** | **(Include any applicable Project Code and/or Source Code)****Full Accounting Unit (FAU):** | Invoice Recipient Email: |
| **Payment Info** **(External Users Only)** | **PO Number:** |

Please fill out completely to avoid processing delays.

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| **EXPERIMENTAL INFORMATION** |
|  Date of Request:  |
|  Project Name:  |
|  Project Description:  |
| **SAMPLE SUBMITTED** |
|  **# of Samples**: \_\_\_\_\_\_\_\_\_\_ **Species:** \_\_\_\_\_\_\_\_\_\_\_  **Sample Type**: [ ]  Frozen Tissue [ ]  Blood [ ]  FFPE Tissue [ ]  Cell Pellet [ ]  Total RNA [ ]  gDNA [ ]  Other (please specify): \_\_\_\_\_\_\_\_  [ ]  slide for GeoMx (see page #3 for slide requirement)  **Library Type:** [ ]  DNA Library [ ]  RNA Library [ ]  ChIP Library [ ]  10x Library, please specify library type: \_\_\_\_\_\_\_\_\_\_\_\_\_ [ ]  Pooled Library (Specify Library Type, nM Concentration & if you want us to QC your pool again): \_\_\_\_\_\_\_\_ [ ]  Other, please specify: \_\_\_\_\_\_\_\_\_\_ If libraries are submitted, please indicate if you need Custom primers (specify concentration):\_\_\_\_\_\_\_ , if you need phix spike-in:\_\_\_\_\_\_\_%, and provide barcode sequences in sample info section or send as an excel file. |
| **SERVICE REQUESTED** |
|  **Nucleic Acid Extraction:** [ ]  DNA [ ]  RNA  |
|  **QC:** [ ]  NanoDrop [ ]  Qubit [ ]  PicoGreen [ ]  TapeStation (If you need specific tape, please specify here):\_\_\_\_\_\_\_\_\_\_\_\_\_  |
| **Sonication**: [ ]  Please specify desired size:\_\_\_\_\_\_\_bp  |
|  **Library Construction:** [ ]  RNASeq [ ]  RNASeq with rRNA Depletion [ ]  Chipseq [ ]  Methyseq [ ]  WGS [ ]  Human WES [ ]  Mouse WES   If for 10X Single Cell: [ ]  Cell Counting & Viability assay [ ]  3’GEX [ ]  ATAC [ ]  5’GEX + FB [ ]  5’GEX + TCR  [ ]  5’GEX + BCR [ ]  Multiome (3’GEX + ATAC) [ ]  hTCR [ ]  mTCR  If for 10X Spatial GEX: [ ]  Visium Tissue Optimization [ ]  Visium Whole Transcription Analysis (WTA)  If for GeoMx DSP: [ ]  hWTA [ ]  mWTA [ ]  hCTA [ ]  Protein Panel (Specify):\_\_\_\_\_\_\_\_\_\_\_\_\_If you need custom antibody for cell staining, please specify name/s and dilution factor for staining: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_If you do not know dilution factor, we can do dry run to determine. Please check the box if you need dry run. [ ]  Dry Run  |
| **Sequencing:** Application System: [ ]  MiSeq [ ]  NextSeq500 Mid Output (130M) [ ]  NextSeq500 High Output (400M) [ ]  Hiseq3000 (300M/lane)  [ ]  Novaseq SP (325-400M/lane) [ ]  Novaseq S1 (650-800M/lane) [ ]  Novaseq S2 (1650-2050M/lane) [ ]  Novaseq S4 (2000-2500M/lane) [ ]  Oxford Nanopore (10-50GB/floecell) Sequencing Type (e.g., 1X50, 1x75, 2X50, 2x75, 2X100, 2x150, 2x250, 2X300): \_\_\_\_\_\_\_\_\_\_  Sequencing Depth Requirements (e.g., 30M from each direction/sample, 2 lanes for all samples, etc.): \_\_\_\_\_\_\_\_\_\_\_\_ |
|  **Data Analysis:** [ ]  Partial Data Analysis [ ]  Full Data Analysis [ ]  10X Single Cell Data Analysis [ ]  Other (Specify): \_\_\_\_\_\_\_\_\_\_\_ Data Analysis Requirements & Details (e.g., normalized gene counts, comparison groups, differential expression statistics, etc.): |
|  **Other Service (Specify): \_\_\_\_\_\_\_\_\_\_** |

If samples submitted have not been QC’d, additional charges will apply. If traces are available, please attach to this form.

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| **SAMPLE INFORMATION** |  |
| Sample # | Sample Name | Concentration (ng/L) | 260/280 Ratio | Volume (L) | Additional Info (e.g., barcode sequence) |
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**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.

• 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.

**Shipping Considerations**

• FFPE unstained sections should be packed securely, preferably in a slide box. 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.

• Ship the contents of the order at room temperature.

**Bio-Safety Level 2 Facility Questionnaire - Mandatory**

The CMC 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: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**