Amaras Genomics LLC
15011 Ventura Blvd
Sherman Oaks, CA 91403
Phone: 818-946-8177
Email: services@amarasgenomics.com

Amaras Genomics Laboratory
Service Request Form

Before delivering your samples, please e-mail us the copy of the request form to **services@amarasgenomics.com**
Also, please print a copy of the request form when you deliver your samples in person.

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		
Requestor Name:	Phone:	Email:
Company/Institution Name:		Dept. Code:
Street Address:		
City:	State:	Zip Code:
Contact Person who delivers samples:	Phone (Required):	Email:
If Amaras Genomics Member? ☐ Yes ☐ No		

BILLING INFORMATION	
Internal Users: FAU REQUIRED. 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
☐ Singe Cell Suspension ☐ Single Nuclei Suspension ☐ Fixed Cells
☐ slide for 10X Visium
☐ 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 or DNAzol)

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
☐ 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)

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)
☐ 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 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
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.					

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.

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 ship 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.

BIO-SAFETY LEVEL 2 FACILITY QUESTIONNAIRE - MANDATORY

The Amaras Genomics 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. Services cannot be granted until approval is obtained. Contact Amaras Genomics if you have questions or e-mail at **services@amarasgenomics.com**.

Exempt. 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.

Requestor Signature: ____ Date: ___________________

Company Representative Signature: ____________________________ Date: ___________________