



Genomics & Systems Biology Core
 Co-Director: Jianhua Luo, MD, PhD
 Co-Director and Core Manager: Silvia Liu, PhD
 Associate Director: Yanping Yu, MD, PhD

REQUEST FORM

Date of Request: _____

PRINCIPLE INVESTIGATOR INFORMATION

Study Title: _____

Grant Number: _____

Contact Name: _____ Contact Email: _____

PI Name: _____ PI Email: _____

Department: _____ PLRC member: Yes No

Address: _____

Phone: _____ Fax: _____

SERVICE(S) REQUESTED

PRIMARY GENOME ANALYSIS PLATFORM

	U133 2.0 array
	R230 2.0 array
	R430 2.0 array
	CLARIOM array
	SNP 6.0 array
	CytoscanHD array
	OncoScan array
	Human exon 1.0 ST array
	Expression arrays for porcine, bovine, Drosophila, etc.
	AVITI/Illumina sequencing (library ready)
	AVITI/Illumina sequencing (library prep from raw sample or DNA)
	AVITI/Illumina sequencing (library prep for whole genome from raw sample or DNA)
	AVITI/Illumina sequencing (library prep for exome from raw sample or DNA)
	AVITI/Illumina sequencing (library prep for methylation from raw sample or DNA)
	AVITI/Illumina sequencing (library Visium Spatial Cytassist sequencing with spatial molecule barcoded for FFPE sample)
	AVITI/Illumina sequencing (library Visium Spatial sequencing with spatial molecule barcoded)

	AVITI/Illumina sequencing (library prep single cell sequencing with individual molecule barcoded)
	Oxford Nanopore MinION targeted sequencing (library prep from raw sample)
	Single cell 10x genomics transcriptome and ATAC multi-omic prep

DATA ANALYSIS COLLABORATION

	mRNA Microarray: gene quantification, differential expression analysis, pathway analysis, clustering
	SNP array/ CyoscanHD/ OncoScan array: SNP, deletion, amplification and LOH detection
	RNA-seq analysis: gene/isoform quantification, differential expression analysis, pathway analysis, clustering
	ChIP-seq/ATAC-seq analysis: peak calling, peak annotation, differential peak calling and known TF enrichment
	WES/WGS analysis: SNP calling, mutation calling, copy number variation (CNV) and structural variation (SV) detection
	microRNA-seq analysis: differential expression and pathway analysis
	Single-cell sequencing analysis: Quantification and clustering
	Spatial transcriptomics analysis
	Long-read sequencing data analysis
	Regulatory network analysis (mRNA/miRNA, chromatin/expression)
	Predictive models for phenotypes and outcomes
	Causal modeling across data modalities
	Consultation / research design
	Actionable targets and biomarkers / preparing for filing IP
	Other (please provide a brief description below)

OTHER SERVICES (please provide description below):

RESEARCH SYNOPSIS

Please provide 1-2 sentences on your project:

Please note:

1. Sample will **not** be processed without valid account number.
2. Bioinformatics and biostatistics analyses are for collaboration only. Recipients agree to recognize those members of the PLRC Genomics & Systems Biology Core who contribute to the analyses as co-authors in the publication(s) resulting from such analyses.
3. The GSBC is funded by the NIH/NIDDK P30-grant #DK120531 and use of these services should be acknowledged in publications and presentations of the data.

Please email completed form and any attachments to luoj@upmc.edu (Dr. Jianhua Luo) and shl96@pitt.edu (Dr. Silvia Liu).