GENOMICS CORE BLDG. 37







Genomics Core Bldg. 37 Room 2135

INA CCR

Providing open access to multiple genomics platforms

Personnel:

Liz Conner, Manager Val Bliskovsky Steve Shema Qin Wei



CORE STATISTICS

808 Registered iLab Members
260 Principal Investigators/Lab groups
10 ICs (NIAID, NHLBI, NIDDK, NEI, NIAMS, NIMH, NINDS, NIAAA, NIA, NICHD)

54, 468 Samples processed/year across all platforms



Platforms:

NGS: MiSeq (2012) NextSeq500 (2015)

NGS-related:

Tape Station (2012) BioRad ddPCR QX200 (2014) Agilent Bravo (2014) SAGE Sci Pippin HT (2015) Fluidigm C1 (2014) Keyence BZX700 (2016) Illumina NeoPrep (2016)

Others:

Sanger Sequencing (1997) Nanostring (2009)



Next-Generation Sequencing – 2 platforms







BioRad QX200 Droplet Digital PCR System



Automated Droplet Generator

QX200 Droplet Reader



- Provides absolute quantification of target molecules without the use of standard curves
- PCR becomes "digital" through sample partitioning and the subsequent statistical analysis of target detection across the partitions
- Advanced microfluidics technology to generate 20,000 nanoliter-sized droplets per sample

BioRad QX200 Droplet Digital PCR System





– EvaGreen

Probe

- Common applications:
 - Expression
 - Mutation
 - Copy number variation



 Cost recovery service (\$5/sample)

Illumina NeoPrep™ Automated Library Preparation System

illumina®





Agilent 2200 TapeStation



- QC platform for quality/quantity assessment of RNA and DNA as well as NGS library preparations
- Obtain size distribution and concentration estimates

• Cost recovery service (\$3-4.00/sample)

Fluidigm C₁ Single-Cell Auto Prep System Prepare Sequence Analyze Library Lyse, RT Wash, Load Enrich Stain & Capture Amplify Image **RNA-Seq on any** Illumina System Amplify Transfer Load & Detect **Gene Expression Profiling:** Fluidigm C₁ Single-Cell Auto **BioMark System Prep System** Chips optimized to isolate cells by cell size: 5-10 micron: stem cells and WBC Self-service following training

OSTR Subsidy available (50%)

10-17 micron: iPS, progenitor cells, and others

17-25 micron: fibroblasts, keratinocytes, and others



How to obtain our services:

iLab website: https://nci.corefacilities.org/account/login



A part of Agilent Technologies

Internal NCI user :

Click here to login or register using your institute login and password.

Not a NCI user?

Login using iLab credentials

If you don't have an account, please <u>register</u> for an iLab account.

✿ home	CCR Genomics Core								
(3619)			About Our Core	Schedule Equipment	Request Services	View All Requests	Reservations		
CCR Genomics Core	ANNOUNCEMENTS								
my reservations view requests my centers list all cores	LAST Core billing for FY16 will be Tuesday, August 23.								
🏜 reporting									
manage groups my labs									
my core National Cancer Institute people search Purchase Orders	Overview of Services								
	Welcome to the CCR Genomics Core								
	The mission of the CCR Genomics Core is to provide CCR investigators with "open access" to genomic technologies, with the goal of providing efficiency and quality of a centralized facility with the speed and conver facility has been in operation since 1997, primarily as a DNA sequencing facility averaging over 200 samples per day with the usual time between submission of samples and delivery of data typically less than one d and Technology Resources (OSTR) to acquire and make available new genomic technologies and instrumentation.								

Key technologies:

- Sanger Sequencing
- NanoString Technologies nCounter® Analysis System
- Ilumina Next Generation Sequencing
- Fluidigm C1 Single-cell Autoprep System
- BioRad Qx200 Digital Droplet PCR System
- · Agilent TapeStation 2200 for quantitate and qualitative nucleic acid analysis

Sanger Sequencing Request

- Rapid and accurate sequencing of DNA samples
- Expertise in the use of software for sequencing data
- Troubleshooting sequencing reactions

Samples are accepted in which sequencing reactions are completed by the user, as well as samples in which the sequencing reaction and clean-up are performed by the core.

Data will be transferred to a data destination folder on group drive, NCI GP-DNACore-Access (\\nciis-p001.nci.nih.gov\dnacore\). If you are unable to map the group drive to your computer please contact NIH Help Desk for support. The files transferred from the Genetic analyzer to your data destination folder on the DNACore group drive are read-only and deleted after 4 weeks. You are responsible for copying your data to storage of your own. The data generated by the Genetic Analyzers is backed up and kept indefinitely.

NOTE: iLab charges per sample so BULK-AS-IS sample requests (96 well MicroAmp plates completely ready to be placed on capillary sequencer) costs will be modified by Core Staff to reflect the correct pricing.

Sanger Request Types

ELECTROPHORESIS ONLY \$2.00/sample SEQUENCING RX And Electrophoresis \$7.00/sample SEQ REACTIONS, CLN-UP & ELECTOPHORESIS (96 SBP) \$440.00 Bulk capillary As-Is Run (SEQ RX & CLN-UP performed by customer): (0-16 samples) \$22.00 (16-32 samples) \$44.00 (33-48 samples) \$44.00 (49-64 samples) \$40.0 (65-80 samples) \$10.00 (81-96 samples) \$132.00

Agilent 2200 TapeStation

📫 initiate request 🛛 🖌

initiate request

Automates RNA, DNA and protein sample QC, including sample loading, separation, and imaging.

1. What is it? It is an automatic electrophoresis system that provides qualitative and quantitative characteristics of the sample

1 Why would I want to use it?

How to obtain an Office of Science and Technology Resources (OSTR) subsidy:

https://ostr.cancer.gov/STARS

The total amount of subsidy available to each principal investigator for each fiscal year is capped at \$10,000.

General Information		Subsidy For				
PI *		Service Type *				
- Select -	¥	Digital Gene Expression Profi 💌				
PI Email Address *		Service Company *				
		NanoString Technologies •				
Lab/Branch *		NCI Internal Core				
- Select -	T	Items Ordered *				
Lab Location *						
- Select -	¥					
CAN/PID *						
		Totals				
AO		Total Cost of Order *				
Email Address *						
		Calculated Subsidy *				
First Name *						
		Submit				
Last Name *						



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Please remember to....

- Acknowledge the CCR Genomics Core in all publications that include data derived from the facility
- Provide us with a PDF of any publications in which the CCR Genomics Core is acknowledged



Method	\$ system	\$ per cells	No. cells	Doublets	Transcript type	UMIs
DROP-seq	\$50000	\$0.65	up to 50000	0.36-11.3%	3' mRNA	Yes
Fluidigm C1	\$150,000	\$1.5-10	96, 800 (10k?)	10-23%	mRNA	No
10X Genomics	\$125,000	\$0.20-1.00	1000-6000	1-5%	3' mRNA	Yes
Wafergen	\$200,000	\$1.5-2.5	~1800	1-5%?	3' mRNA	Yes