

**Services and tools available through
the Advanced Cell Exploration Core
to advance your research**

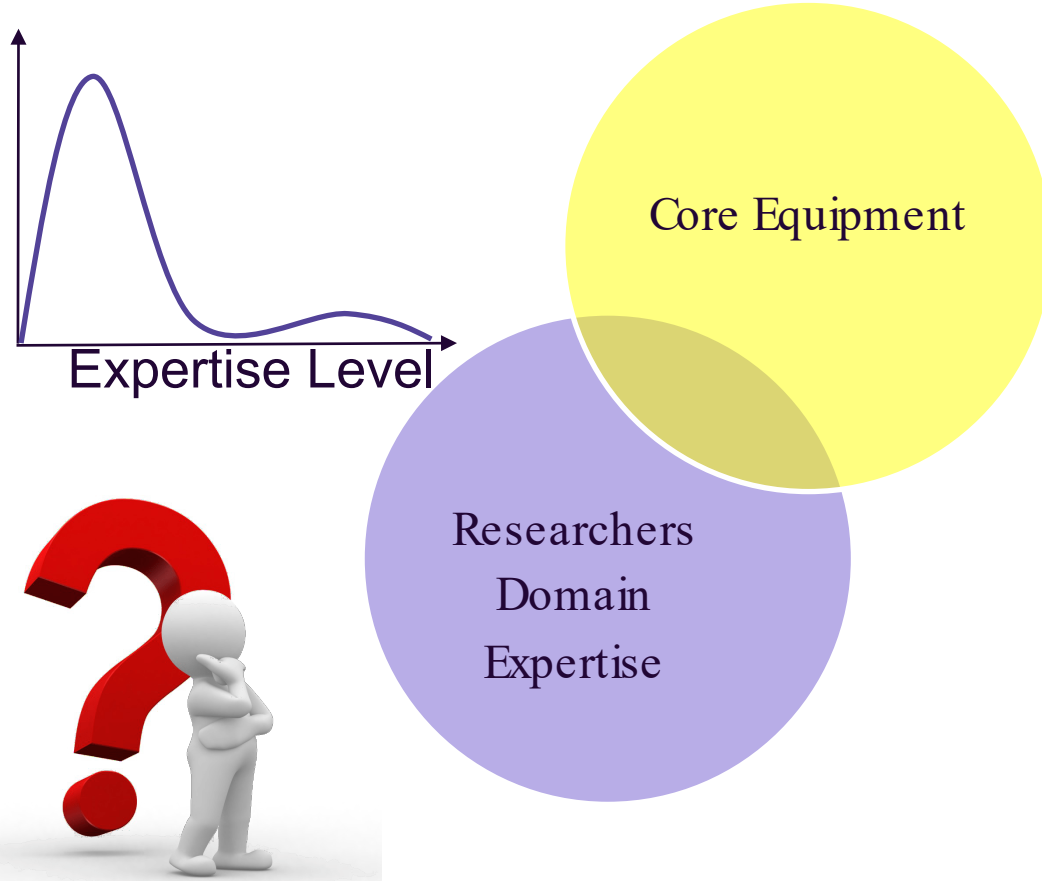
**Mike Wong
Director –ACE Core
uAlberta**

Advanced Cell Exploration Core

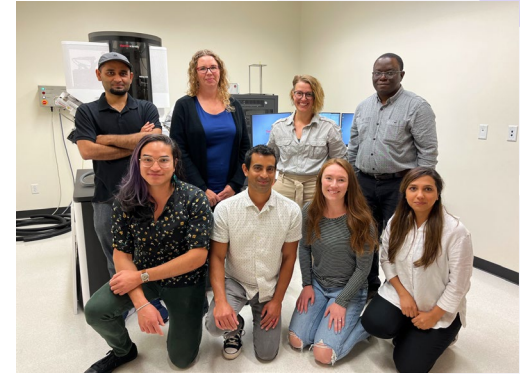
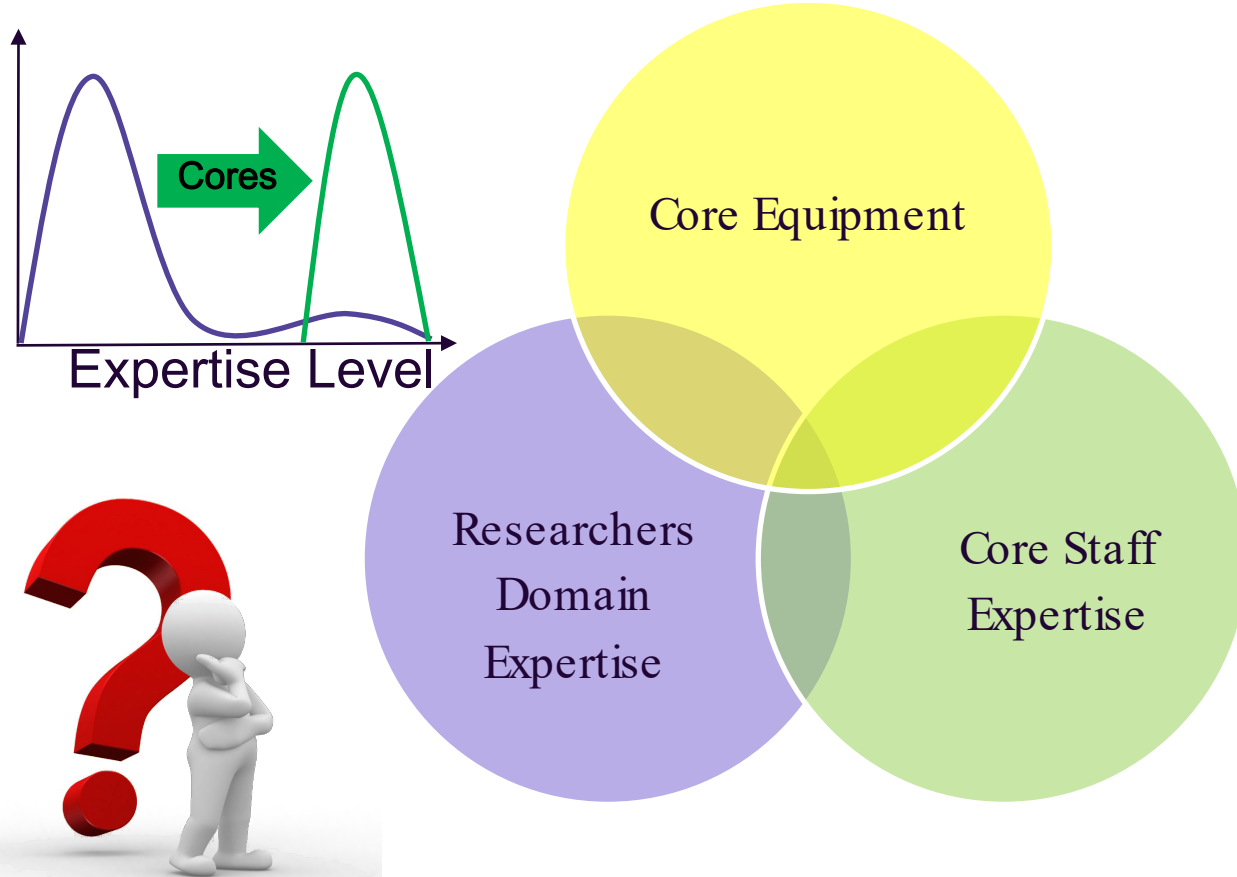


Researchers
Domain
Expertise

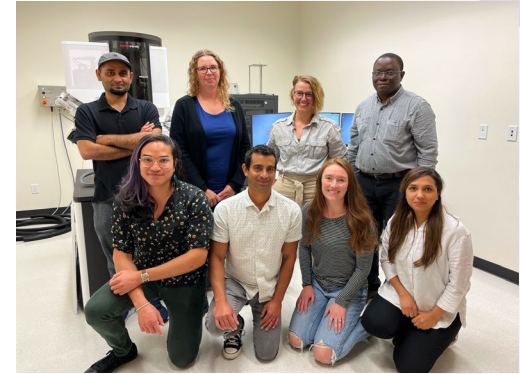
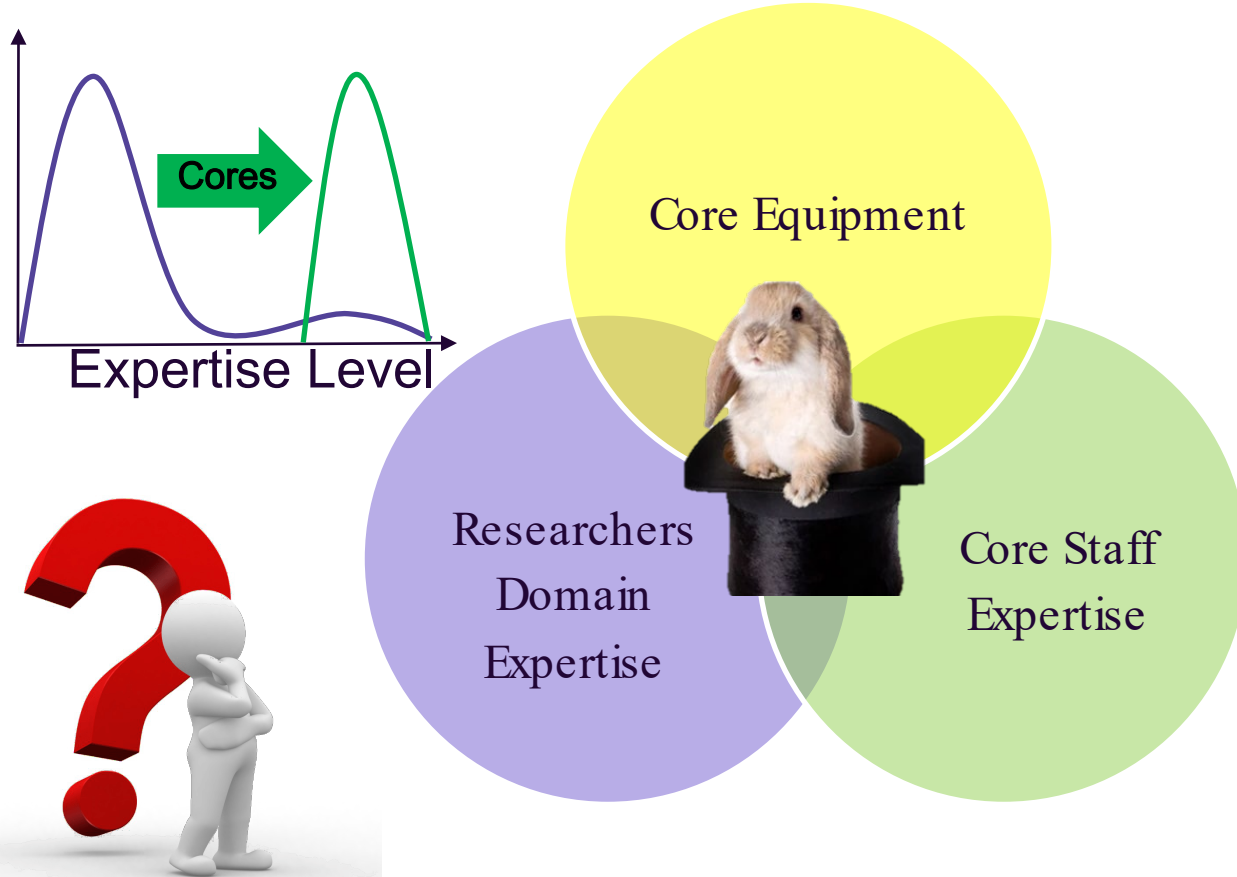
Advanced Cell Exploration Core



Advanced Cell Exploration Core



Advanced Cell Exploration Core



Advanced Cell Exploration (ACE) Core

Genomic
Tech

Single Cell
Tech

Screening
Libraries

Auxiliary
Platforms

Spatial
Genomics

- ◆ Flexible nodes to adapt to new technologies
- ◆ Since have grown to a team of 4
 - ◆ Mike Wong
 - ◆ Dr. Mackenzie Brandon Coatham
 - ◆ Dr. Rene Dicipulo
 - ◆ Sudip Subedi

[ACE Core Google Drive](#)

acecore@ualberta.ca



Advanced Cell Exploration (ACE) Core

Mission:

To act as a hub that enables scientists to successfully access advanced genomics, spatial and screening techniques to propel their research.

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To act as a hub that enables scientists to successfully access advanced genomics, spatial and screening techniques to propel their research.

For researchers, the ACE Core provides deep technical expertise, professional partnerships, friendly customer service and collaboration to generate high quality data using cutting edge techniques.

Genomics Node- Sequencing



\$\$\$\$\$/base



\$/base



\$/base

ACE Core

Illumina MiSeq
Up to 25M read pairs
15Gb total

Hopefully soon! – Mid
Capacity Seq 1-2B read
pairs

Small genome (\$)
16s rRNA metagenomics
mRNA
Single Cell
WGS

GIFS/ OPAL (Carla Protsko)



\$/base



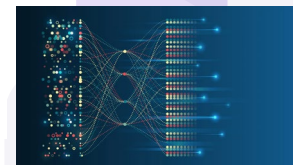
UBC-Seq (Tara Stach)



\$/base



Genomics Node- Sequencing



\$\$\$\$\$/base



\$/base



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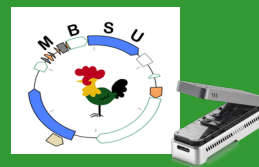


\$/base



MBSU

- Anthony Cornish
- Sophie Dang
- Anh Dao
- Troy Locke



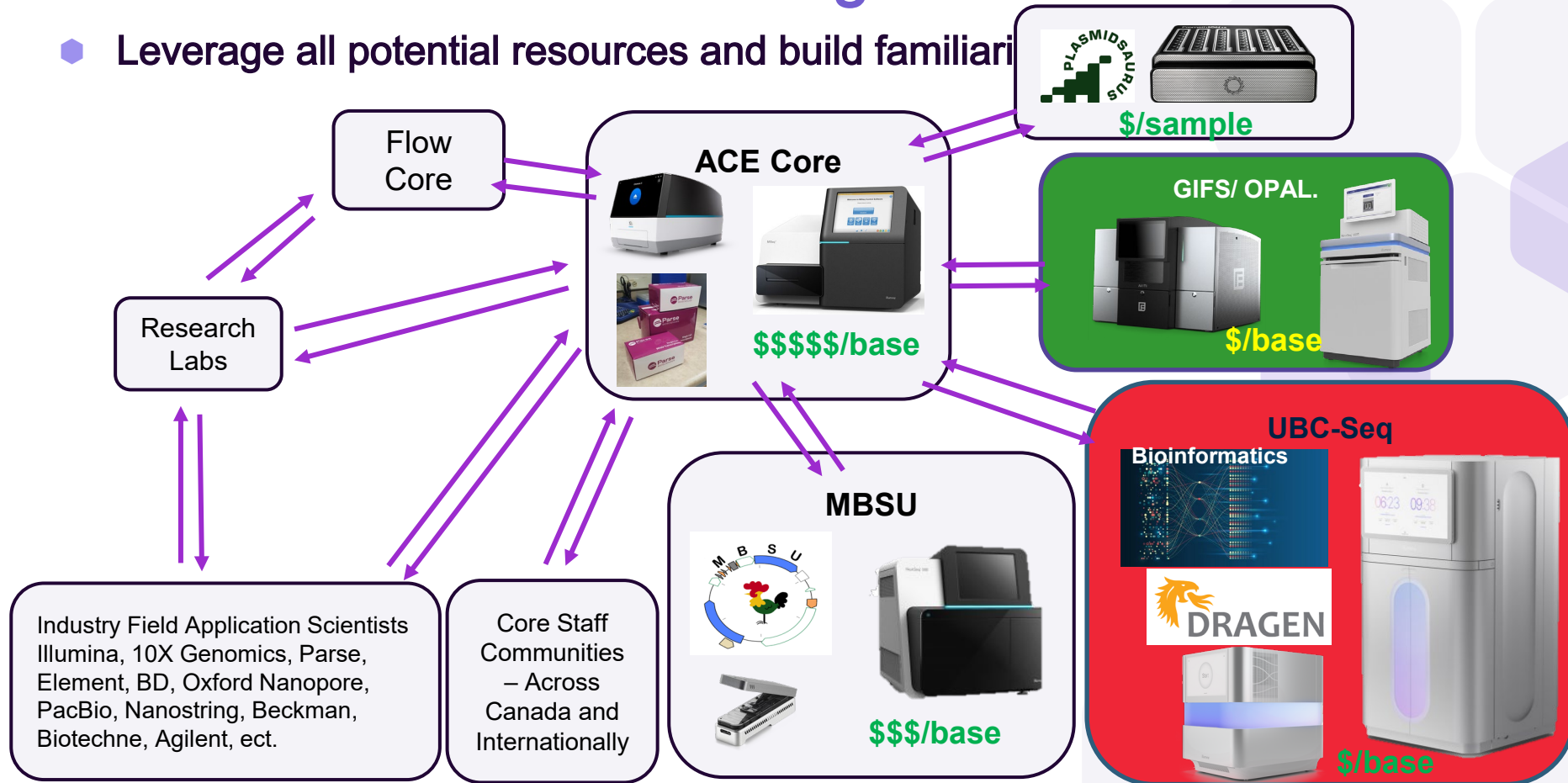
\$\$\$\$/base



Dropbox Services
Multiplexed, budget ONT seq pass-through
services.
Small genome, plasmids, amplicons, etc.

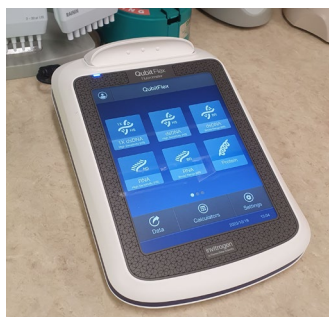
Build a Network of Knowledge and Resources

- Leverage all potential resources and build familiarity



Genomics Node- QC

Upgrade and acquisition
of (almost) all QC
platforms



**Qubit Flex
(Quantification)**



**Nanodrop 8
(Purity)**



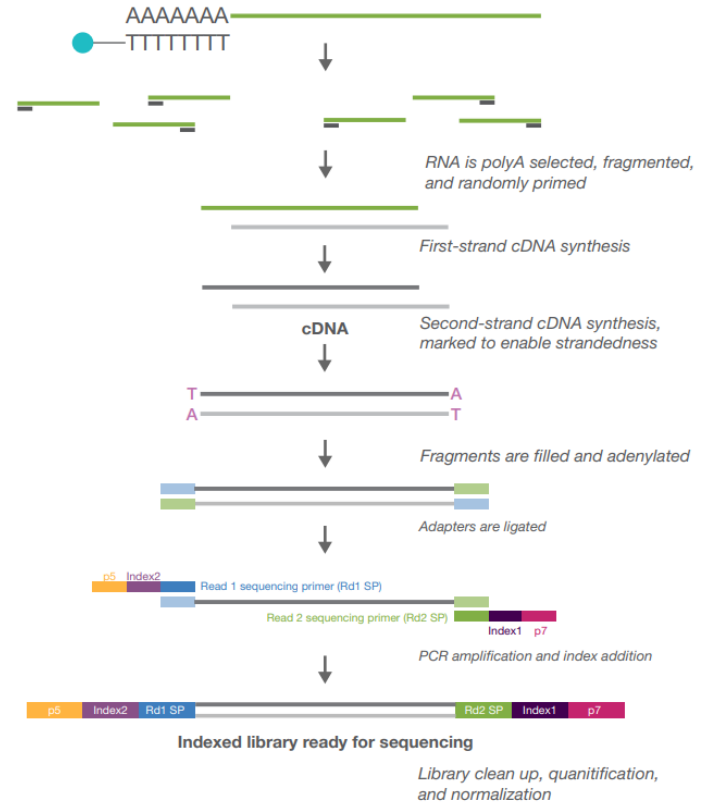
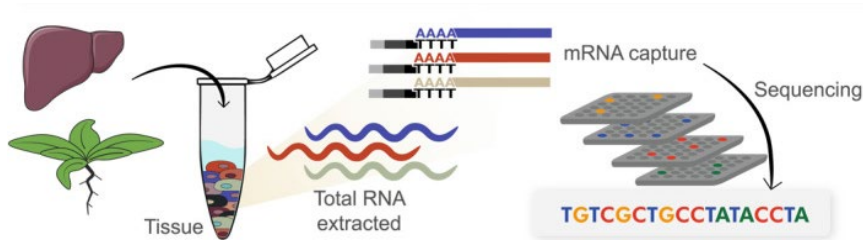
**Bioanalyzer 2100
Tapestation 4200
(Fragment distribution)**



**Logos LunaFX
Automated Cell Counter**

Bulk RNA Seq Service

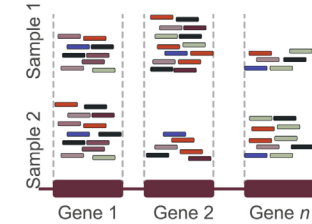
- Drop off your sample and let us handle the rest
- Stranded chemistry (mapping of overlapping genes)
- PolyA tail selection
- Randomly primed
- Full transcript coverage
 - Splice variant and SNP data available



Bulk RNA Seq Service

- Drop off your sample and let us handle the
- Stranded chemistry (mapping of overlapping genes)
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Sequence alignment to reference



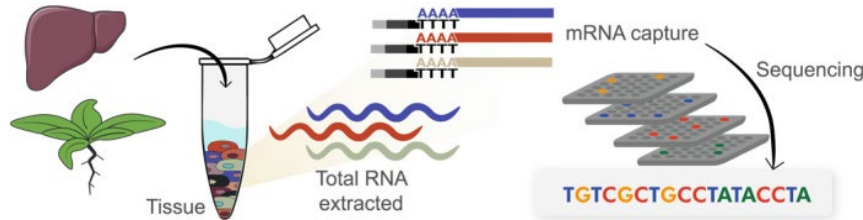
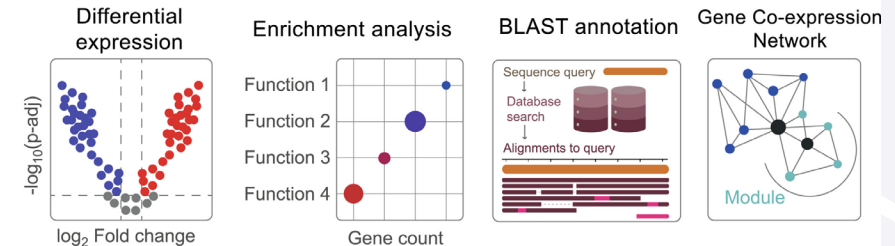
Raw count matrix

Genes	Sample 1	Sample 2	Sample n
Gene 1	9	13	x_n
Gene 2	14	6	x_n
Gene n	6	10	x_n

D Data normalization and gene expression

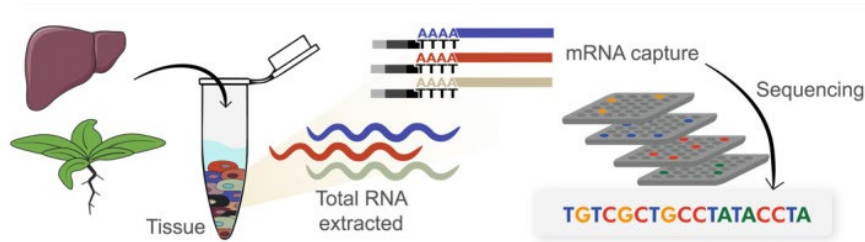


E Downstream analyses



Bulk RNA Seq Service

- Drop off your sample and let us handle the rest
- Stranded chemistry (mapping of overlapping genes)
- PolyA tail selection
- Randomly primed
- Full transcript coverage
 - Splice variant and SNP data available



Your Bulk RNA-seq projects, Simplified.

The ACE Core has revamped our bulk RNA sequencing services to be as researcher-friendly as possible; leveraging our expertise, rigorous quality control and sample handling procedures, and external partnerships.

Drop off your extracted total RNA samples and let us handle the rest!



All Inclusive Service,
Receive ONE Bill



Expert Staff Coordination
and Hands-On Support



Coordinated Sequencing at
UBC-Seq (NovaSeq X or NextSeq 2000)



Basic Bioinformatics Analysis Included!
Additional Analysis Available.

Starting At

\$228

Per Sample for
Internal Academics



More Information and
Submission Form

Base Price Includes:

- ✓ Sample QC
- ✓ Library Construction
- ✓ Sample Shipment to UBC-Seq and Coordination of Sequencing
- ✓ Sequencing 20M read pairs/sample
- ✓ Differential Expression Report

Questions? Contact Us
acecore@ualberta.ca

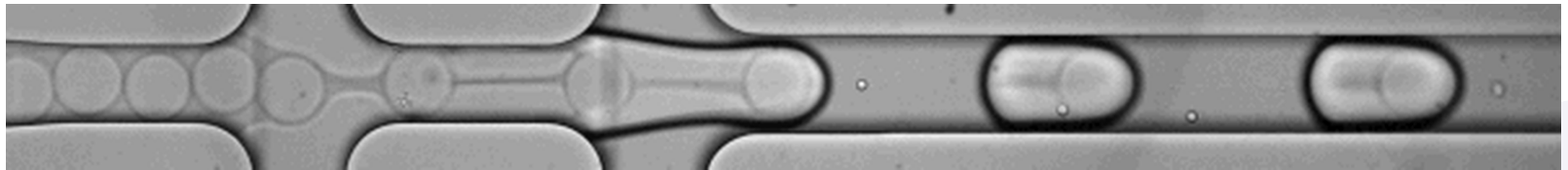
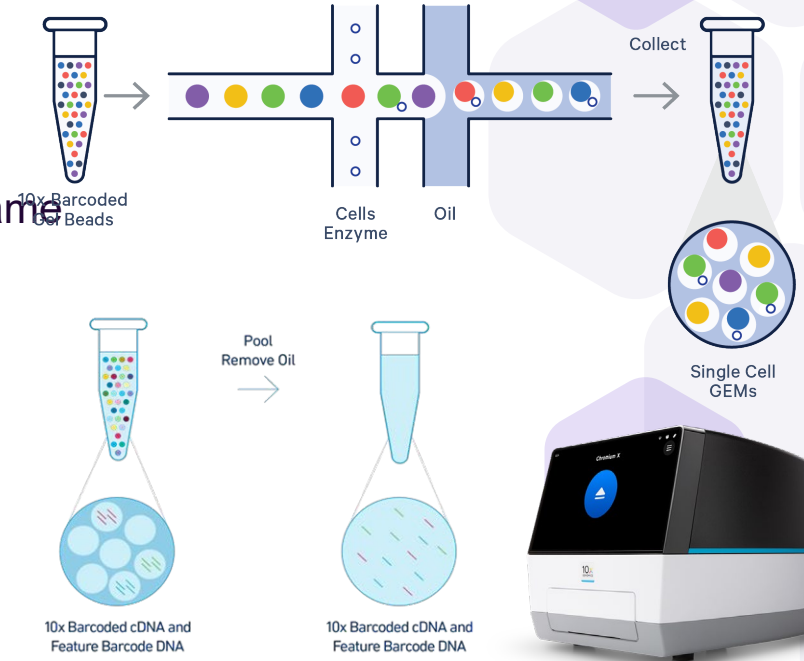
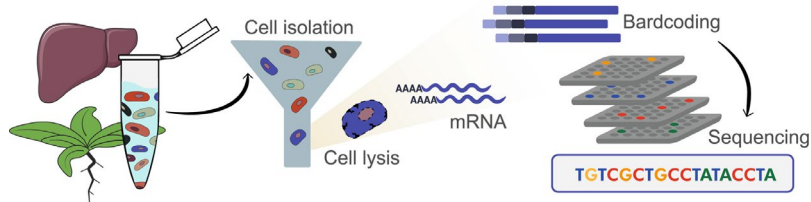
2026April01

Single CellSeq

- Isolate cells from each other to barcode transcripts and identify which sequences came from individual cells

single cell RNA-seq

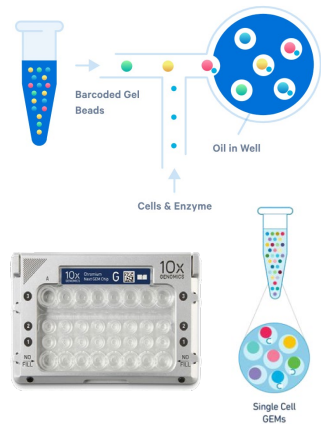
A Sample preparation and sequencing



Single Cell Assays

- Many ways to achieve single cell partitioning

Microfluidic Droplet Based Partitioning



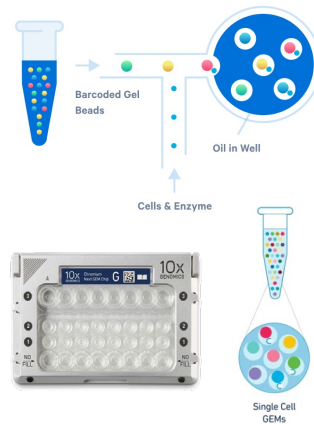
**10X Genomics
Chromium**

**Up to 20 000 cells/
sample***

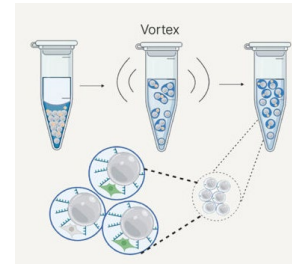
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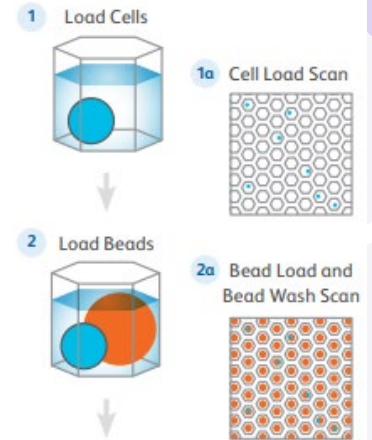


**10X Genomics
Chromium**
Up to 20 000 cells/
sample*



**Illumina single
cell 3' PIP-seq**
Up to 200k cells/ run

Gravity Loaded Nano-well Arrays

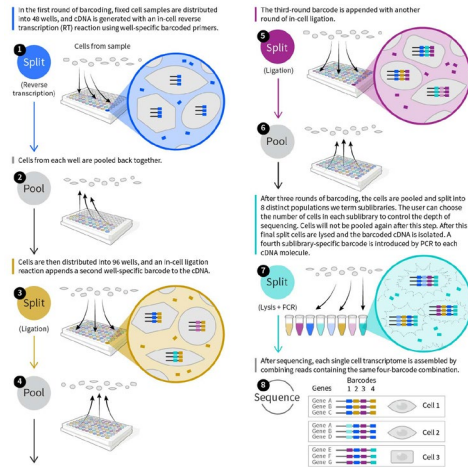


BD Rhapsody
Up to 100 000 cells/run

Single Cell Assays

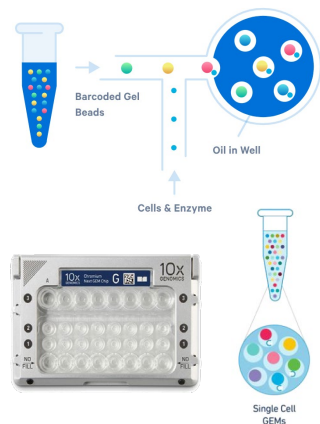
- Many ways to achieve single cell partitioning

Combinatorial Barcoding

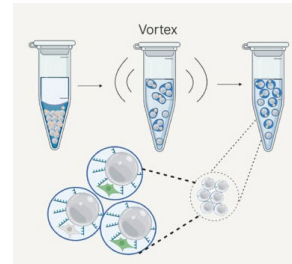


**Parse Biosciences
Evercode WT**
Up to 1 000 000 cells/run

Microfluidic Droplet Based Partitioning

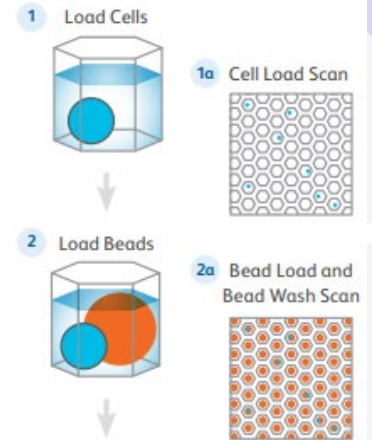


**10X Genomics
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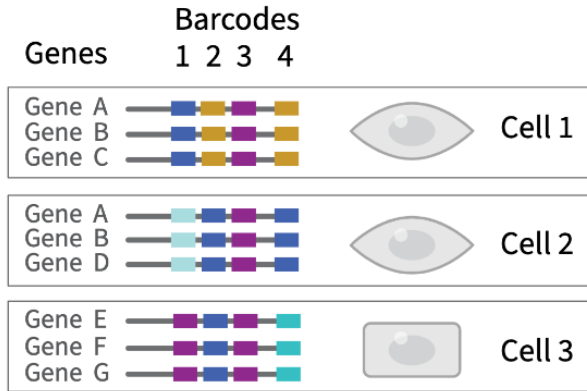
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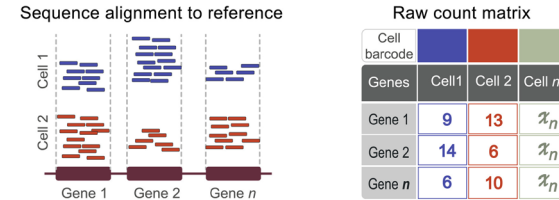


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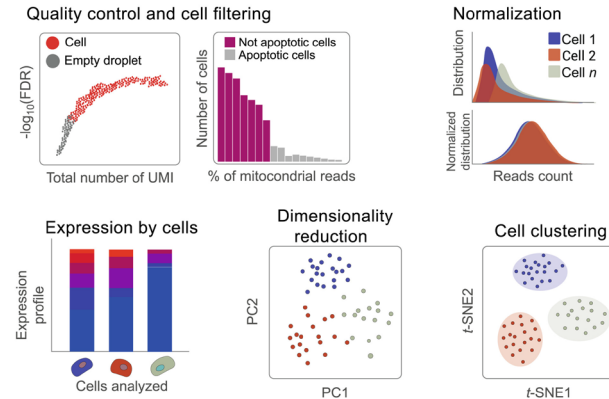
Single Cell Assays



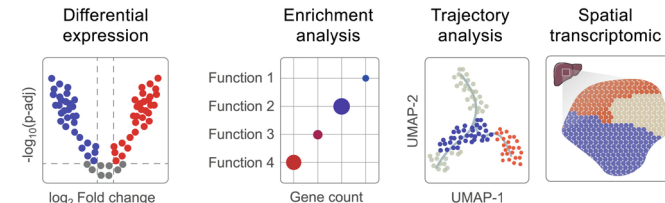
B Sequence alignment and sequence count



C Data normalization and gene expression



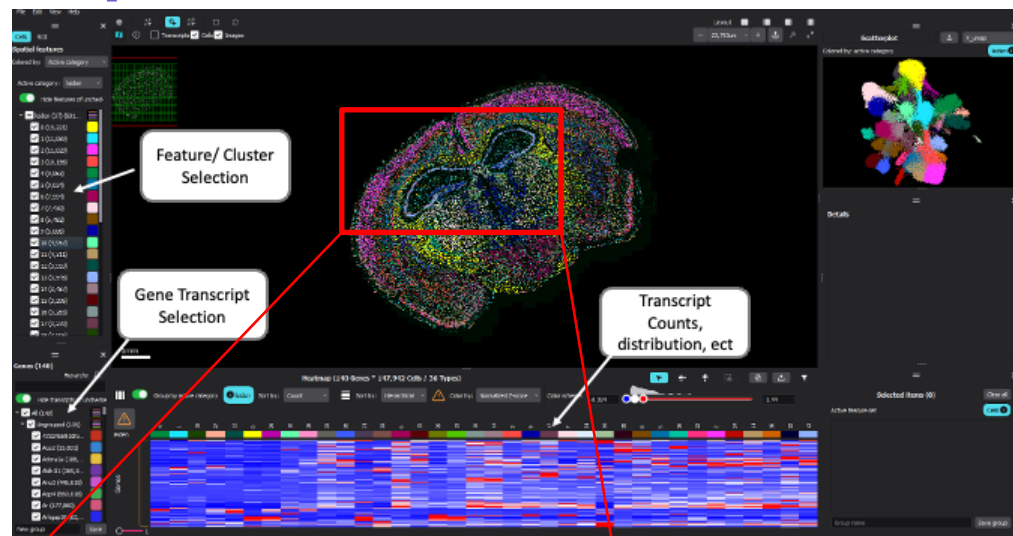
D Downstream analyses



- Count genes on the individual cell level
- Allow much more nuanced analysis
- Good discovery tool to understand population shifts, pathway activation, differentiation, etc.

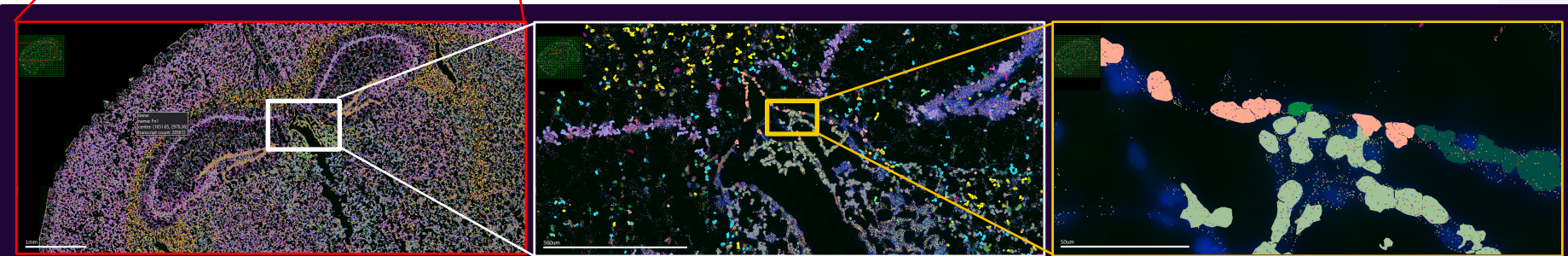
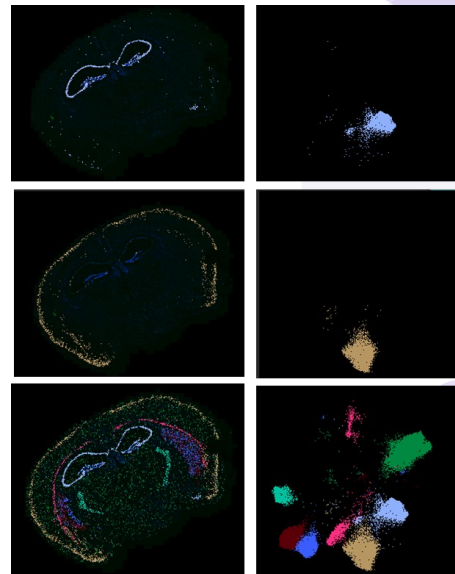
Spatial Node

Vizgen MERscope MERFISH



Cell Highlight

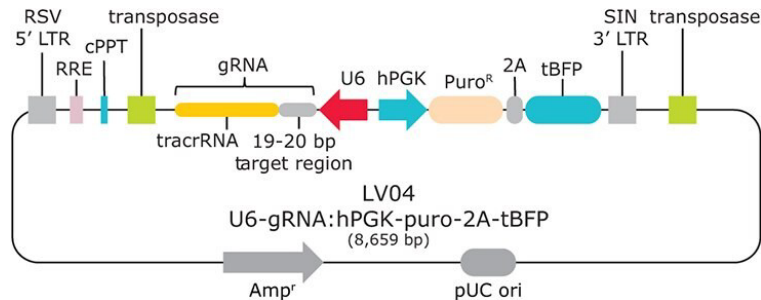
Cluster



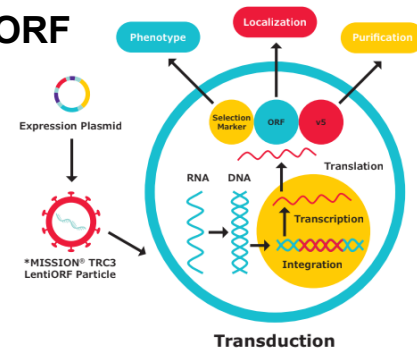
Genomic Expression Tools

- ◆ Frozen stocks of E. coli expressing various constructs (\$15 per culture)
- ◆ ACE core will seed the selected cultures for you to mini prep or propagate
- ◆ shRNA mouse and human TRC01.5
 - ◇ (*current version posted online is 3.0+)
- ◆ MissionTRC3 human LentiORF library
 - ◇ Overexpression or CRISPR rescue
- ◆ Human Sanger CRISPR gRNA library
 - ◇ 2x optimized gRNAs per gene covering 17000 human genes

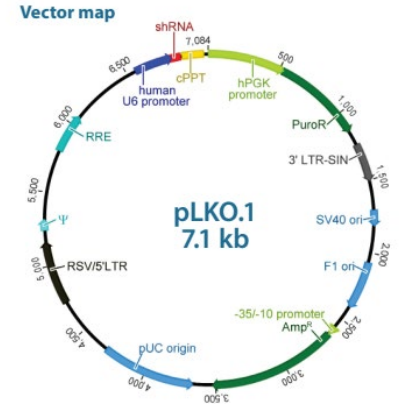
CRISPR gRNA



LentiORF



shRNA



[ACE Core Genomic
Tool Database and
Order Forms](#)

ACE Core

Genomics Node - Sequencing

HCAC

Illumina MiSeq
Up to 25M read pairs
15Gb total

Small genomes (\$\$\$\$)
16s rRNA metagenomics

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Up to 25M read pairs
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Hopefully coming soon: Mid Capacity Seq 1-2B read pairs

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GIFS/ OPAL (Carla Protzko)

\$/base

UBC-Seq (Tara Stach)

\$/base

MBSU
Anthony Cornish
-Sophie Dang
-Anh Dao
-Troy Locke

Dropbox Services
Multiplexed, budget ONT seq pass-through services.
Small genome, plasmids, amplicons, etc.

\$\$\$/\$base

29

Single Cell Node

HCAC

10X Genomics Chromium X
Up to 20,000 cells/ run
Live Poly-A capture
Multiplexing
Fixed (FFPE Human/Mouse)

Hopefully soon!

\$/base

ACE Core

\$1.5 million in reagents processed.
>2.8 million cells profiled

Illumina single cell RNA PIP-seq
100-200K cell input
Poly-A Capture
Multiplexing
Fixed

Parse Evercode WT
100-5M cell input
Poly-A and random hexamer capture
Multiplexing
Fixed

Prerelease testing

BD Rhapsody Demo
Up to 100K cell input
Poly-A
Immediate capture QC

Screening Node

HCAC

Screening Libraries
LOPAC 1280
TimTec Natural Derivatives
Myriasiscreen 10K

Expression Vectors
shRNA TCR 1.0-1.5
siRNA

\$\$\$\$ Tips

Screening Libraries
Enamine BioReference 3600
Tankyrase inhibitors
Wnt/β-Catenin inhibitors

Expression Vectors
Human Lenti-ORF TRC3
Human Sanger CRISPR gRNA

Beckman Echo 650

Hopefully -High grade NGS system -Organoid culturing systems

Screening Libraries
Enamine BioReference 3600
Tankyrase inhibitors
Wnt/β-Catenin inhibitors

Expression Vectors
Human Lenti-ORF TRC3
Human Sanger CRISPR gRNA

opentrons
OpenAI

Genomics Node - QC

Upgrade and acquisition of (almost) all platforms

Qubit Flex (Quantification)

Nanodrop 8 (Purity)

Bioanalyzer 2100 Tapestation 4200 (Fragment distribution)

Logos LunaFX Automated Cell Counter

30

Spatial Node

Vizgen MERSCOPE MERFISH
Up to 1000 plex error robust FISH

Cell Highlights Cluster

UBC-Seq
Potential Passthrough to 10X Genomics Xenium workflows

Hopefully coming soon
10X Genomics
Visium HD Spatial Whole transcriptome

Auxiliary Platforms

"Weird Instruments" Autonomous Use

Agilent Seahorse XFe96 Metabolic Analyzer

ProteinSimple JESS automated Western

FLUORESCENT DETECTION

Quotient Signal

40

Advanced Cell Exploration (ACE) Core

Main Lab: Katz-081

Request service, consultation or training: acecore@ualberta.ca

ACE Core Google Shared Drive

- Policies and other documentation
- Library databases
- Order forms
- Learning materials
- Updated constantly*

