CROWN BIOSCIENCE

Genomics and High-Throughput Sequencing Capabilities

Comprehensive solutions delivering high quality genomics results and advanced data analysis

A JSR Life Sciences Company

FACTSHEET

V1.0

Crown Bioscience At a Glance

Solution

- A cutting-edge drug discovery and development services company providing services for **oncology, immuno-oncology and immune-mediated inflammatory disease research**

Capacity

- **Global reach:** USA, Europe, and APAC
- Capacity to simulate **clinical trials in a preclinical setting**

Experience

- **Contributed to 7 out of 17 FDA approved oncology drugs in 2020**
- Extensive **experience** working with *in vivo* and *in vitro* model systems for drug development
- Historical **data collection**

Breadth

- Exclusive services using the **HUB organoid platform**
- World's **largest commercial collection of PDX models**
- Comprehensive **I/O platform** including syngeneics and humanized models

Knowledge

- 50+ **research articles and conference posters** published each year
- 60+ **peer reviewed papers**
- A **unique source of characterized model data**, fully searchable for PDX, cell lines, xenografts, mouse cancer models, and tumor organoid models

Besides the conventional PCR/qPCR- and Sanger sequencing based genomics assays, Crown Bioscience has introduced industry-leading second and third generation high-throughput sequencing platforms and an optical genome mapping platform to provide our customers with comprehensive solutions for genomics analysis.

We utilize our expertise in bioinformatics, to provide customers with informative and reliable data analysis and reporting, and have also launched some of our own exclusive services, such as the first commercial Cell Line Authentication with Deep Sequencing service, and the Mouse I/O RNA-Seq Panel, a murine immuno-oncology focused RNA-Seq panel to understand the tumor immunity profile effectively and efficiently.

Integrate our genomics services with your *in vivo* or *in vitro* studies with us, or use it as standalone service

- Explore and validate drug mechanism with advanced genomic analysis
- Identify genetics features associated with drug response through genomics profiling
- Understand drug resistance by interrogating the immunogenomics of tumor-immune interactions
- Take advantage of our proprietary tools and model data including of our database of NGS-characterized models

Comprehensive Translational Genomics Services

Conventional Genomics Services

- Sample preparation:
  - DNA/RNA extraction
  - mRNA purification
  - microRNA extraction
- Conventional assays:
  - Target gene expression assay
  - Virus copy number assay
  - Gene copy number variation analysis
  - Gene mutation validation
  - Gene fusion validation

Standard Next Generation Sequencing (NGS) Services

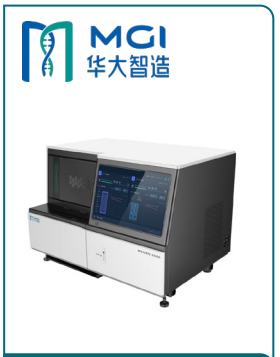
- RNA-Seq
- WES
- WGS
- WBGS
- LncRNA-Seq
- Single cell sequencing
- PacBio: Long read sequencing
- Bionano: Structural variation (SV) detection
- Microbiome sequencing
  - Full length 16S sequencing
  - Metagenomics sequencing
  - Metatranscriptomics sequencing
- Nanostring services

Our Unique NGS services

- Mouse I/O RNA-Seq panel
- Cell line authentication with deep sequencing

Our High-Throughput Sequencing Services

Thermo KingFisher Flex
QIAGEN QIAsynphony SP
Fully Automated Workflow
Reproducible Results



MGI MGISEQ-2000

Medium-Throughout
Flexible Low Cost

Illumina Novaseq 6000

Illumina's Most Powerful
Production-Scale Sequencer

Pacbio Sequel II

Third-Generation Sequencing
Highly Accurate Long Reads

Bionano Saphyr® II

Next-Generation Cytogenetics
with Optical Genome Mapping

RNA-Seq

Applications

- Differential gene expression
- Functional annotation, pathway and network analysis
- Driver mutation prediction
- Tumor purity analysis
- Molecular subtyping analysis
- Comparative analysis with published human tumor samples
- Options to accommodate other analyses

Whole Genome Sequencing (WGS)

Applications

- Gene mutation identification
- Copy number variants
- Large structural variants

Whole Exome Sequencing (WES)

Applications

- Identify genomic variants at DNA level, such as gene mutation, and copy number variants
- Co-expression network analysis
- Comparative analysis with published human tumor samples
- Options to accommodate other analyses

Whole Genome Bisulfite Sequencing (WGBS)

Applications

- Epigenomics
- Gene methylation analysis

Single Cell Sequencing

Assays

- Single cell RNA-Seq
- T Cell Receptor (TCR) Sequencing

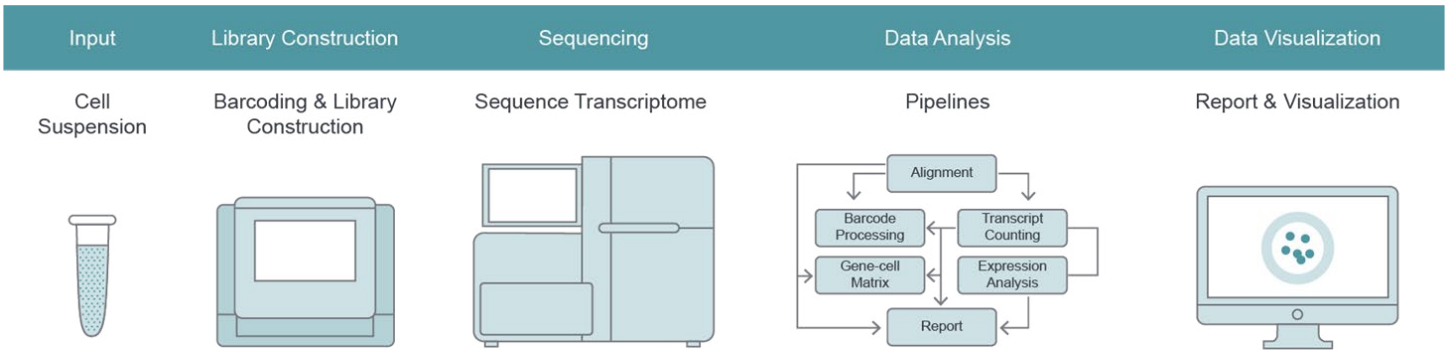
Applications

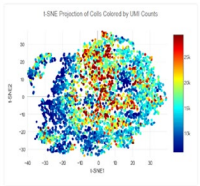
- Characterize and identify heterogeneous cell populations
- Discover new cell markers and regulatory pathways
- Uncover novel cell types, cell states and rare cell types
- Reconstruct developmental hierarchies and reveal lineage relationships
- Profiling healthy and diseased tissue and organs

Data Analysis

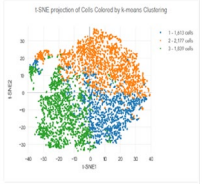
- QC and cell/gene filtering
- Cluster analysis on integrated samples
- Explore known cell type markers
- Identification of cluster-specific markers
- Functional analysis on cluster-specific markers
- Further customized analysis upon request

Single Cell Sequencing Workflow by 10x Genomics

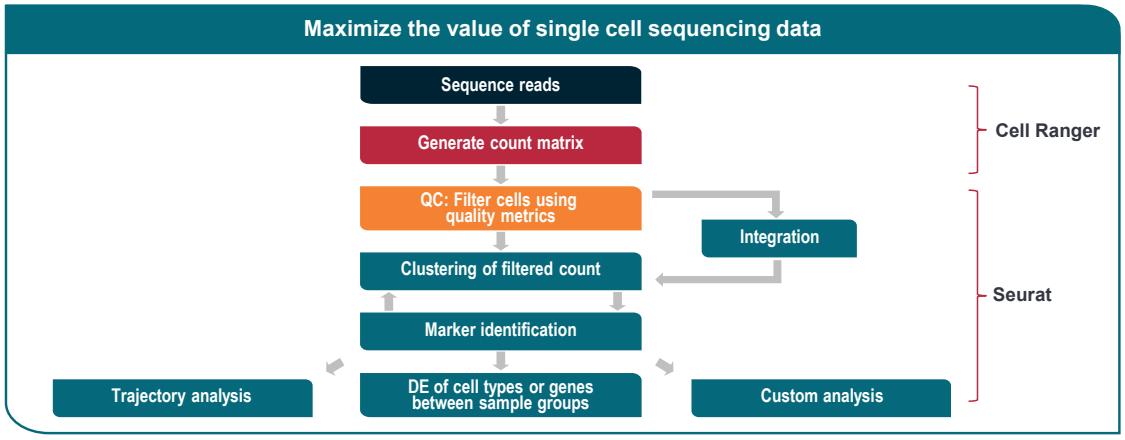




Cellular RNA content

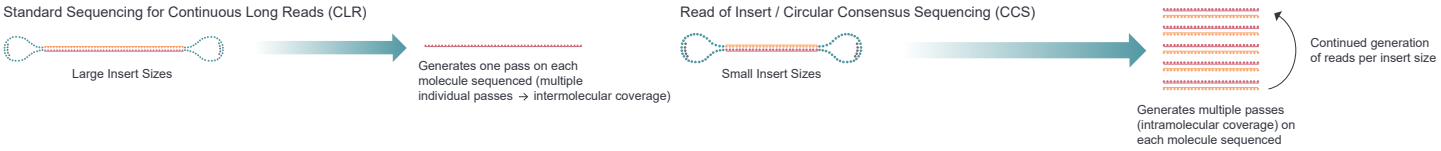


Clustering by gene expression



Third Generation Sequencing – PacBio Sequel II Platform

Single Molecule, Real-Time (SMRT) Sequencing



Applications

Whole Genome Sequencing
- *De novo* assembly
- Variant detection
- Structural variant detection

RNA Sequencing
- Full-length transcripts for whole transcriptome and genome annotation

Complex Populations
- Full-length 16S
- Metagenomic functional profiling
- Shotgun metagenomic assembly

HiFi Sequencing Benefits

Long Reads
Readily assemble complete genomes and sequence full-length transcripts

High Accuracy
>99.999% consensus accuracy

Uniform Coverage
Sequence through regions inaccessible to other technologies

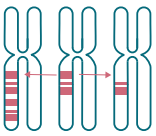
Single-Molecule Resolution
Capturing sequence data from native DNA or RNA molecules

Epigenetics
Base modifications are directly detected during sequencing

Bionano Saphyr® Platform - Optical Genome Mapping

Applications
Resolve large-scale structural variations

- Undiagnosed genetic disorders
- Solid tumor research
- Cell line stability

				
Homozygous insertions/deletions larger than 500 bp	**Balanced and unbalanced translocations** larger than 50 kbp	**Inversions** larger than 30 kbp	**Duplications** larger than 30 kbp	**Copy number variations** larger than 30 kbp
99% sensitivity	**95% sensitivity**	**99% sensitivity**	**97% sensitivity**	**97% sensitivity**
False positives below 2%				

Microbiome Analysis

Services

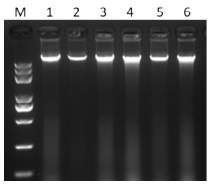
- Microbiome culture
- Metagenomic sequencing
- Metatranscriptomic sequencing
- Full Length 16S rRNA sequencing

Sequencers

- PacBio Sequel II
- Illumina NovaSeq 6000

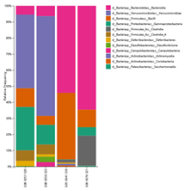
Shotgun Metagenomic Sequencing

DNA QC

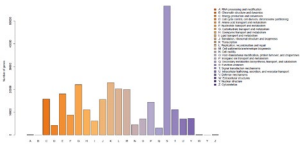


Metagenome assembled genome

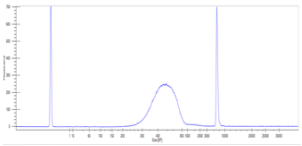
Taxonomy abundance



Unigene function description

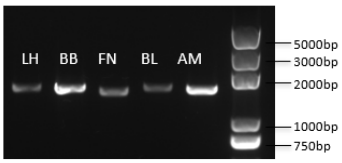


Sequencing Library QC



Full Length 16S rRNA sequencing

DNA Extraction → PCR Amplification (barcoding) → Sample Pooling and Library Construction → CCS Sequencing on Sequel II → Data Analysis



Primer	Sequence	Product Size	Reference
PB_F	AGRGTTYGATYMTGGCTCAG	1510bp	PacBIo
PB_R	RGYTACCTTGTTACGACTT	1510bp	PacBIo

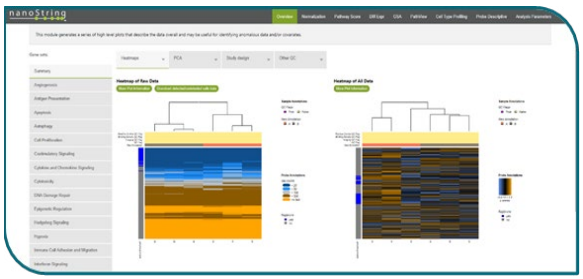
Nanostring Services

Applications

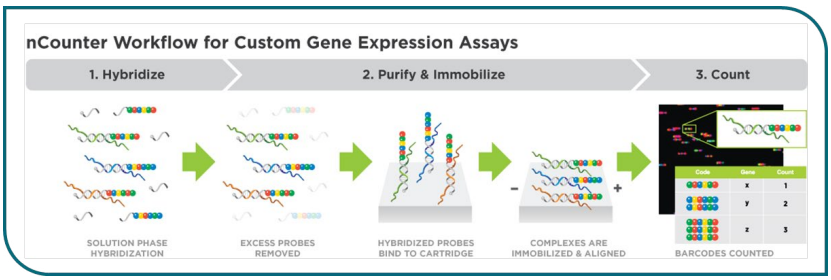
- Gene expression analysis
- Solid tumor profiling
- Immuno-oncology profiling
- Gene fusion analysis
- Single cell gene expression analysis
- miRNA expression analysis
- Copy number variation analysis
- lncRNA expression analysis
- ChIP-String expression analysis

nCounter Analysis Platform

- Array-based multiplex analysis of up to 800 RNA, DNA, or protein targets
- Flexible sample types including FFPE, tissue, lysates, and biofluid samples
- Panels available:
  - PanCancer IO 360 Panel
  - PanCancer Immune Profiling Panel
  - PanCancer Pathways Panel
  - PanCancer Progression Panel
  - Check other available panels here



Check other available panels on Nanostring website



Cell Line Authentication (CLA) with Deep Sequencing

The first commercial deep sequencing-based CLA service

Outperforms Conventional PCR-based STR/SNP Assays

- Increased Accuracy
- Increased Sensitivity
- Higher Throughput
- Extensive Information
- Lower Cost per Sample
- Rapid Turnaround

Suitable Sample Types:
Human and mouse examples
(cell lines, tissues, organoids, and xenografts)

Cell Line Authentication (CLA) Assay Comparison	CLA with Deep Sequencing	CLA with STR Profiling	CLA with SNP Profiling
Technology	Barcode Deep NGS	Multiplex PCR & capillary electrophoresis	Multiplex PCR/qPCR
Readout Type	Digital (clean,near-zero quantification error)	Analog (noisy,high quantification error)	Analog (noisy, high quantification error)
Human Cell Authentication	Yes	Yes	Yes
Mouse Cell Authentication	Yes	Limited	No
MMR Deficient Cell lines Identification	Yes	No	Yes
Contamination-Detecting Sensitivity	High (1%)	Low to medium (5-20%)	Low to medium (3-20%)
Accuracy	High	Low to medium	Low to medium
Throughput	High	Low	Low
Contaminant Identification	Yes	No	No
Quantification of Contamination Ratio	Yes	No	No

Check other infomation available from this analysis on our website.

Mouse I/O RNA-Seq Panel

- Comprehensive profiling of 1080 genes associated with tumor immunity from a single sample
- Rapid transcriptomic insights into key immune cell populations and I/O pathways and process in the tumor microenvironment (TME)

Panel Includes Key Immune Cell Signatures

- B cells*
- Dendritic cells*
- Tolerogenic DCs
- Macrophages
- Tumor-associated macrophages
- G-MDSCs*
- M-MDSCS*
- Neutrophils
- Natural killer cells*
- CD4 T cells*
- CD8 T cell*
- Naïve T cells
- Memory T cells*
- h1 cells
- h2 cells
- h17 cells
- Treg cells
- iTreg cells

*Strain specific gene signatures available for C57BL/6 and BALB/c

Assay Comparison	Mouse I/O RNA-Seq Panel	Array-based I/O profiling*
Technology	Targeted deep sequencing	Target mRNA (cDNA) hybridize with DNA probes
Target molecules	mRNAs	mRNAs
Throughput	High (1080 genes)	High (hundreds to thousands of genes, depending on vendor)
Accuracy	High	Low-medium
Sensitivity on low expressing genes	High	Low-medium
Mouse strain discrimination	Yes	No
Turnaround time	2-3 weeks	3-10 weeks, depending on vendor
Cost	Low	Medium

*** Such as Nanostring nCounter PanCancer IO 360 panel**

Streamline Your *In Vivo* Study Sample Analysis Workflow

3 Weeks

Sample generation

- Integrate into existing syngeneic, tumor homograft (MuPrime™), and human target knock-in model (HuGEMM™/ HuCell™) studies
- In-house or externally generated murine samples
- Suitable for large-scale immunotherapy screening such as MuScreen™

Sample submission

- Accepted murine samples types include*:
  - Extracted RNA (recom. 2µg, Min. 500ng)
  - Frozen tissue
  - Whole blood
  - Immune cell pellets

* See sample Collection and Preparation Guide for more detail

Sequencing

- Targeted RNA-Seq of 1080 genes
- ≥ 2GB data

Data analysis

- Raw and normalized data
- Comprehensive report with up to 6 comparisons
- Additional comparisons available
- Consultation for follow up studies

Global Headquarters

San Diego
16550 West Bernardo Drive
Building 5, Suite 525
San Diego, CA 92127
USA
T: +1 858 622 2900

Europe

UK
Hillcrest, Dodgeford Lane
Belton, Loughborough
LE12 9TE
UK
T: +44 1530 234871

Netherlands
J.H. Oortweg 21
2333 CH Leiden
The Netherlands
T: +31 71 3322 875

Yalelaan 42
3584 CM Utrecht
The Netherlands
T: +31 71 3322 875

APAC

Beijing
6th Floor, Yilan Building
No.28 Huojü Street
Zhong Guan Cun Science Park
Changping District
Beijing
P.R. China 102200
T: +86 10 5633 2600

Shanghai
3rd Floor, Building 10
Changtai Square
Zhangjiang Hi-Tech Park
Pudong New Area
Shanghai
P.R. China 201203
T: +86 21 8016 8666

Suzhou
Room 303, Building A6
No. 218 Xinghu Street
Industrial Park
Suzhou City
Jiangsu Province
P.R. China 215000
T: +86 512 6799 3717

Taicang
Science & Technology
Innovation Park
No. 6 Beijing West Road
Taicang City
Jiangsu Province
P.R. China 215400
T: +86 512 5387 9999

Taipei
333 Keelung Road
Xinyi District
Taipei 11012
Taiwan
T: +886 2 7718 1690

Zhongshan
No. 1 Lipson Science Park
Yangfan Road
Cuiheng New District
Zhongshan City
Guangdong Province
P.R. China 528400
T: +86 760 8670 8888

Get in touch

Sales
busdev@crownbio.com
www.crownbio.com

Science
consultation@crownbio.com