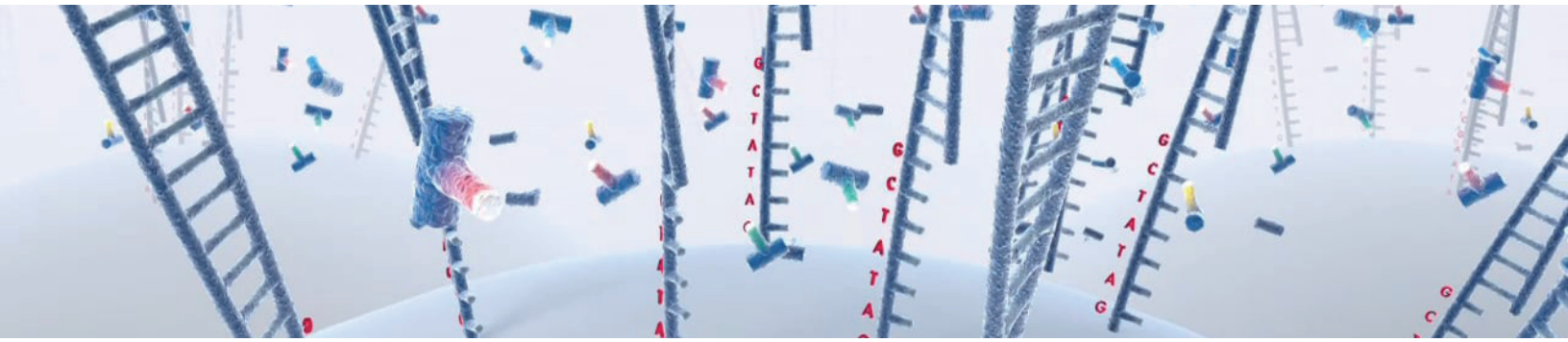
LIFESCT
Life Scientists' Service Center



NGS Research Services

RNA-Seq

Single-cell RNAseq

Whole Exome Sequencing

Whole Genome Sequencing

Whole Genome Bisulfite Sequencing

Chromatin Immunoprecipitation Sequencing

Metagenomics

Content

RNA-Seq

Service description:

Transcriptome profling with RNA-Seq is a powerful tool for analyzing gene expression levels within an individual sample as well as for comparing differential gene expression between multiple samples. Additionally, RNA-Seq can detect the presence of novel isoforms, alternatively spliced transcripts; potential gene fusion events can also be detected through analysis of RNA-seq data.

Advantages:

Complete solution from RNA extraction to bioinformatics analysis
Variable sample type: mRNA, whole transcriptome, targeted RNA, miRNA, low input, ribosomal profling
Ability to detect transcripts with low expression levels
Low cost and short TAT

Service grade:

Research Use Only (RUO) in a CLIA environment

Deliverables:

Raw data as FASTQ files
Quality control results
Complete data analysis available*
* Please inquire for more details

Estimated turnaround time: 28-42 days*

* Varies based on services required; expedited services available (please inquire)

Sample requirements*:

Extracted RNA, Fresh frozen tissue or cell pellet, FFPE tissue on slides (extra QC may be needed)
1µg or more**
* Extraction services provided (please inquire)
** Low input protocols available

Sequencing platforms:

High depth of coverage and long reads available, please inquire for details.

Library preparation options*:

NEBNext® Ultra™ RNA Library Prep Kit for Illumina
NEBNext® Ultra™ Directional RNA Library Prep Kit
NEBNext® Multiplex Small RNA Library Prep Kit
TruSeq Small RNA Library Preparation Kits
SMARTer Stranded Total RNA-Seq Kit - Pico Input Mammalian
SMART-Seq V4 Ultra Low Input RNA Kit
KAPA RNA HyperPrep with RiboErase (HMR)
KAPA Stranded RNA-seq with RiboErase (HMR)
Lexogen QuantSeq 3'mRNA-Seq
* Additional preparation available, please inquire for more details

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loor data behind firewall

Single-cell RNAseq (scRNA-seq)

Service description:

While studying transcriptome profiling through RNAseq, many have reported subpopulations of cells which expressed its genes at various levels despite originating from a single tissue. The rising popularity in single cell sequencing has given insight to the extent of heterogeneity between cells as well as undiscovered regulatory functions of these cells.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Deliverables:
Raw data as FASTQ files
Quality control results
Complete data analysis available*
* Please inquire for more details

Sequencing depth:
Starting at 40M PE reads*
* Specific depth of coverage available, please inquire for details

Estimated turnaround time: 35-42 days

Sample requirements*:
Extracted RNA, Fresh frozen tissue or cell pellet, FFPE tissue on slides (extra QC may be needed)
Purity of samples:
OD260/280 ratio is between 1.8 to 2.0
OD260/230 ratio is between 1.5 to 2.0
* Extraction services provided (please inquire)

Library preparation options*:
SMART-Seq V4 Ultra Low Input
10× Chromium
* Additional library preparation options available, please inquire for details

Sequencing platforms:
Illumina NextSeq, Illumina HiSeq

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loor data behind firewall

Whole Exome Sequencing (WES)

Service description:

Whole Exome Sequencing (WES) is aimed to sequence all the protein-coding regions or exons in a genome collectively known as exome. There are approximately 180,000 exons which represent less than 2% of the human genome. As most of the disease-related variants are found in the exons, WES is thought to be an efficient way to understand the genetic cause of diseases or conditions. We provide a very cost-effective, high quality WES service.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Human exons in approximately 22,000 genes

Deliverables:
FASTQ, BAM, and VCF files
Variant annotation

Sequencing depth:
Mean depth of coverage*: ≥100×
90% of exons covered at ≥20× depth
* Higher depth of coverage available for additional charges, please inquire for details

Estimated turnaround time: 28-35 days

Sample requirements*:
Extracted genomic DNA: a minimum of 500 ng as quantified by Qubit 2.0
* Extraction services provided (please inquire)

Library preparation options*:
xGen® Exome Research Panel v1.0
TruSeq Exome Library Prep kit
Nextera® Rapid Capture Expanded Exome Kit (additional charges apply, please inquire for details)
SeqCap EZ Exome v3
SureSelect Focused Exome, Exon V5, Exon V6
* Additional library preparation options available, please inquire for details

Sequencing platforms:
Ilumina NextSeq, Illumina HiSeq

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Whole Genome Sequencing (WGS)

Service Description:

Human whole genome sequencing allows for detection of variations to discover potential correlations to Certain disease risks, and it can also play a role as molecular biomarkers for disease diagnosis and prediction. De novo sequencing is typically performed without prior knowledge of the sequencing data. *De novo* sequencing has proven successful for confirming and expanding upon results from database searches, and providing excellent resources for understanding a species. Some of the most crucial information, obtained by resequencing of organism's genome DNA, are the individual variations in the genome, such as single nucleotide polymorphism (SNP), copy number variation (CNV), and structural variation.

Advantages:
Low cost & short TAT
High coverage depth and uniformity

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Human whole genome or other species*
* Please inquire

Deliverables:
FASTQ, BAM, and VCF files (optional)

Sequencing depth:
Mean depth of coverage: ≥30x
Higher depth of coverage available for additional charges, please inquire for details.

Estimated turnaround time: 30-42 days

Sample requirements:
FFPE Formalin-Fixed, Paraffin-Embedded (FFPE) Unstained Slides*
Blood samples*
Saliva (please request sample collection supplies)
High quality genomic human DNA: a minimum of 1.0 microgram as quantified by Qubit 2.0
* Inquire for more details

Sequencing platforms:
Illumina MiSeq, Illumina NextSeq, Illumina HiSeq X Ten Platform

Library preparation options:
KAPA Hyper Prep Kits
Nextera XT DNA
Nextera DNA
* Additional kits available

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Whole Genome Bisulfite Sequencing (WGBS)

Service Description:

Naturally-occurring methylation of DNA at the cytosine residues is an important component in many studies including that of epigenetic studies. With this occurrence in mind, converting and studying these sites is referred to as whole genome bisulfite sequencing (WGBS). This technology is a genome-wide profiling of DNA methylation sites. WGBS is a comprehensive cytosine modification profiling method which provides insight topics relating to epigenomic mapping, patterns of epigenetic marks, aberrant methylation characterized by cancers, and much more.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Human whole genome

Deliverables:
FASTQ, BAM and VCF files

Sequencing depth:
Mean depth of coverage :≥30×
Higher depth of coverage available for additional charges, please inquire for details.

Estimated turnaround time: 30-42 days

Sample requirements:
Types of samples accepted:
Saliva (please request sample collection supplies)
High quality genomic human DNA: a minimum of 1.0 microgram as quantified by Qubit 2.0
FFPE Formalin-fixed, Paraffin-Embedded (FFPE) Unstained Slides*
* Inquire for more details

Sequencing platforms:
Ilumina HiSeqX Platform

Library preparation options:
EZ DNA Methylation-Gold™ Kit
Accel-NGS MethylSeq kit
TruSeq DNA Methylation Kit*
* Additional kits available

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Sequencing Only

Service Description:

Researchers looking for sequencing only solutions will find that LifeSct offers a quick and supportive team to reach your goals! We work with both individually-barcoded libraries or any pre-pooled libraries. Upon receipt of your samples, LifeSct performs comprehensive quality control steps which are detailed in reports that are sent to you within 24 hours. Our QC entails Qubit, Tapestation, and qPCR.

Library requirements:
Based on library type and platform, please inquire

Customized sequencing primers:
Option available, please inquire

Platforms:
Miseq
Nextseg
Hiseq
Novaseq

Data transfer:
Basespace
FTP
Other, please inquire

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Chromatin Immunoprecipitation Sequencing (ChIPseq)

Service Description:

Studying regulatory processes can be accomplished by employing ChIP and next generation sequencing technologies. Chromatin Immunoprecipitation (ChIP) sequencing is essentially used to identify DNA binding sites for transcription factors and related proteins without prior knowledge. Profiling epigenetic modifications on a genome-wide basis allows for a deeper understanding of biological processes and disease states. Gaining intricate knowledge on regulators, targeted therapies can be explored and developed.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Immuno-precipitated DNA

Deliverables:
FASTQ files

Sequencing depth:
Starting at 40M PE reads*
* Specific depth of coverage available, please inquire for details

Estimated turnaround time: 28-35 days

Sample requirements*:
Immuno-precipitated DNA: a minimum of 100 nanogram as quantified by Qubit 2.0
* Extraction services provided (please inquire)

Sequencing platforms:
Illumina NextSeq, Illumina HiSeq

Library preparation options:
KAPA Hyper Prep*
* Additional library preparation options available, please inquire for details

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Assay for Transposase-Accessible Chromatin using sequencing (ATAC- seq)

Service Description:

A good alternative to ChIPseq when beginning epigenetic studies is Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq). ATAC-seq is a common assay being utilized to landscape genome-wide of chromatin assembly, understand accessibility to regions, discover transcription factor binding sites, gene regulation, and more. ATAC-seq has an advantage over other epigenomic assays as it requires a small number of starting input.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Immuno-precipitated DNA

Deliverables:
FASTQ files

Sequencing depth:
Starting at 50M PE reads*
* Specific depth of coverage available, please inquire for details

Estimated turnaround time: 30-42 days

Sample requirements:
TA: a minimum of 500 nanogram as quantified by Qubit 2.0
Other sample types accepted*
* Please inquire for further details; extraction services also provided

Sequencing platforms*:
Illumina NextSeq, Illumina HiSeq, Illumina Novaseq
* Availability may vary, please inquire

Library preparation options:
Laboratory developed test with Nextera
* Additional library preparation options available, please inquire for details

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Human T-Cell Receptor (TCR) Profiling

Service Description:

T-cells are central in its role during an immune response. When encountering Human T-Cell Receptor (TCR) Profiling allows researchers to study the diverse TCRs in cells and in the context of adaptive immune response in cancer. With the limitless number of TCR variations, research challenges are met quite often when attempting to characterize T-cell repertoires. High-throughput profiling grants the study of low-abundance variants with challenging sample input.

Advantages:
Low cost
High coverage depth and uniformity
Short TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Genes/regions covered: Immuno-precipitated DNA

Deliverables:
FASTQ files

Sequencing depth:
Starting at 40M PE reads*
* Specific depth of coverage available, please inquire for details

Estimated turnaround time: 30-42 days

Sample requirements:
Total RNA: a minimum of 500 nanogram as quantified by Qubit 2.0
Other sample types accepted*
Purity of samples:
OD260/280 ratio is between 1.8 to 2.0
OD260/230 ratio is between 1.5 to 2.0
* Please inquire for further details; extraction services also provided

Sequencing platforms:
Illumina NextSeq, Illumina HiSeq

Library preparation options:
Laboratory developed test with Clontech SMARTScribe™ Reverse Transcriptase
SMARTerO Human TCR a/b Profiling Kit
* Additional library preparation options available, please inquire for details

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

RADseq

Service Description:

Restriction site associated DNA sequencing (RAD-Seq) investigates selective regions of the genome based on the restriction enzyme of choice for digestion. This allows for a variety of population-scale studies to be performed at the fraction of the cost of a typical genome-wide association study.

Advantages:
Low cost
High coverage depth
Flexible enzyme combination
Superb technical support

Service grade: Research Use Only (RUO) in a CLIA environment

Deliverables:
FASTQ files

Sequencing depth:
Starting at 1M reads per sample*
* Coverage adjustable per enzyme choice and customer preference

Estimated turnaround time: 35-42 days

Sample requirements:
Genomic DNA: a minimum of 1 microgram as quantified by Qubit 2.0
* Extraction services provided (please inquire)

Sequencing platforms:
Illumina Miseq, Illumina NextSeq, Illumina HiSeq

Library preparation options:
Laboratory Developed Test*
* Proprietary to LifeSct

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Double Digest RADseq

Service Description:

In most sequencing data analysis, prior genomic knowledge is required for studies. Double digest restriction site associated DNA sequencing, or ddRADseq, is a new technique can be used for SNP discovery and genotyping without a reference genome. This is a step from RADseq by adding another restriction enzyme for digestion. Although it is a reduced representation, the sampling of genome wide enzyme digestion offers an insight on SNP marker development. This method of genotyping is feasible because of its cost-effective approach.

Advantages:
Low cost
High coverage depth
Flexible enzyme combination
Superb technical support

Service grade: Research Use Only (RUO) in a CLIA environment

Deliverables:
FASTQ files

Sequencing depth:
Starting at 1M reads per sample*
* Coverage adjustable per enzyme choice and customer preference

Estimated turnaround time: 35-42 days

Sample requirements*:
Genomic DNA: a minimum of 1 microgram as quantified by Qubit 2.0
* Extraction services provided (please inquire)

Sequencing platforms:
Illumina Miseq, Illumina NextSeq, Illumina HiSeq

Library preparation options:
Laboratory Developed Test*
* Proprietary to LifeSct

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Customized Gene Panels

Service Description:

Targeted resequencing allows researchers to analyze a specific subset of the genome to discover and validate novel variants, examine specific genes in pathways, or as a follow-up to GWAS data. Based on prior knowledge of the region of interest, custom targeted sequencing aims to only sequence the specified subset of the genome to enable maximum utilization of the NGS platform by giving the deepest genetic analysis compared to WGS and Exome-Seq. Depending on the genes for your target, we can design up to 40 million base pairs and perform the gene sequencing for your specific project. Each project is given special attention and designed exclusively.

Advantages:
High coverage depth and uniformity
Short TAT
Accurate results

Service grade: Research Use Only (RUO) in a CLIA environment

Deliverables:
FASTQ, BAM and VCF files
Variant annotation

Sequencing depth:
Mean depth of coverage: ≥250×
90% of exons covered at ≥50× depth
* Higher depth of coverage available for additional charges, please inquire for details

Estimated turnaround time: 35-42 days

Sample requirements*:
Extracted genomic DNA: a minimum of 100 nanogram as quantified by Qubit 2.0
* Extraction services provided (please inquire)

Sequencing platforms:
Lllumina NextSeq, llumina HiSeq

Library preparation options:
xGen® target capture products
Agilent Sureselect Custom Bait
TruSeq Custom Amplicon Low Input Library Prep Kit
Powered by the SmartChip™ technology, WaferGen technology based singleplex PCR

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

16S rRNA sequencing

Service Description:

Targeted resequencing allows researchers to analyze a specific subset of the genome to discover and validate novel variants, examine specific genes in pathways, or as a follow-up to GWAS data. Based on prior knowledge of the region of interest, custom targeted sequencing aims to only sequence the specified subset of the genome to enable maximum utilization of the NGS platform by giving the deepest genetic analysis compared to WGS and Exome-Seq. Depending on the genes for your target, we can design up to 40 million base pairs and perform the gene sequencing for your specific project. Each project is given special attention and designed exclusively.

Advantages:
Higher sensitivity
Low bias
Cost-effective
Fast TAT

Region coverage:
Floracheck™ Environmental (V3, V4, and V5 hypervariable regions)
Floracheck™ Mammalian (V3 and V4 hypervariable regions)
Floracheck™ Essential (V4 hypervariable region)

Deliverables:
Raw data as FASTQ files
Chart detailing the type and relative abundance of bacterial and archaeal genera in each sample

Sequencing depth:
Guaranteed 50MB data, deep coverage per request

Estimated turnaround time: 2 weeks

Sample requirements* :
Extracted genomic DNA: a minimum of 100 nanogram as quantified by Qubit 2.0
Purity of genomic DNA samples:
OD260/280 ratio is between 1.8 to 2.0
OD260/230 ratio is between 1.5 to 2.0
* Extraction services provided (please inquire)

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Metagenomics

Service Description:

Metagenomics is the study of genetic material recovered directly from environmental samples. The broad field may also be referred to as environmental genomics, ecogenomics or community genomics. While traditional microbiology and microbial genome sequencing and genomics rely upon cultivated clonal cultures, early environmental gene sequencing cloned specific genes (often the 16S rRNA gene) to produce a profile of diversity in a natural sample. Such work revealed that most of microbial biodiversity had been missed by cultivation-based methods. Recent studies use either "shotgun" or PCR directed sequencing to get largely unbiased samples of all genes from all the members of the sampled communities. Because of its ability to reveal the previously hidden diversity of microscopic life, metagenomics offers a powerful lens for viewing the microbial world that has the potential to revolutionize understanding of the entire living world. As the price of DNA sequencing continues to fall, metagenomics now allows microbial ecology to be investigated at a much greater scale and detail than before.

Advantages:
Higher sensitivity
Low bias
Cost-effective & fast Estimated Turnaround Time

Estimated turnaround time: 28-35 days

Region coverage: Whole Genome

Sample submission:
Cell pellets
High quality genomic DNA (a minimum of 100ng as quantified by Qubit 2.0)

Deliverables:
Raw data as FASTQ files
Assembly and *de novo* per request

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Metatranscriptomics

Service Description:

Metatranscriptomics has been developed to help understand how communities respond to changes in their environment. Metagenomic studies provided a snapshot of the genetic composition of the community at any given time. However, short-timescale studies investigating the response of communities to rapid environmental changes (e.g. pollution events or diurnal light availability) require analysis of changes in the abundance and composition of the active fraction of the community. Metatranscriptomics enables researchers to investigate the actively transcribed ribosomal and messenger RNA from a community. It has been applied to environments as diverse as soil and seawater.

Advantages:
Complete solution from RNA extraction to bioinformatics analysis
Ability to detect transcripts with low expression levels
Low cost and fast TAT

Service grade: Research Use Only (RUO) in a CLIA environment

Estimated turnaround time: 35-42 days

Deliverables:
FASTQ files
Gene expression analysis (FPKM in both gene and transcript levels)
Alternative splicing/novel isoform analysis
List of potential gene fusion events if detected
* Additional charges may apply

Sample requirements (internal QC upon receipt):
Extracted RNA, Fresh frozen tissue or cell pellet, FFPE tissue on slides (extra QC may be needed)*
* Extraction services provided (please inquire)

Sequencing platforms:
High depth of coverage and long reads available*
* Price upon to request

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Human Leukocyte Antigen (HLA) typing

Service Description:

Human leukocyte antigen (HLA genes are the most polymorphic in the human genome). They play a pivotal role in the immune response and have been implicated in numerous human pathologies, especially autoimmunity and infectious diseases. When a mutation occurs in any of the 11 HLA loci, our body loses the ability to distinguish between self-cells and nonself-cells. Furthermore, mutations can cause transplant rejection, autoimmune responses, promotion of cancer, and drug sensitivity.

Advantages:
Sample-to-report services
High-throughput, high-resolution human leukocyte antigen (HLA) typing results
Definitive, unambiguous results
High coverage depth and uniformity
Short TAT

Genes/regions covered:
Loci Target Sequence

HLA-A 4.1 kb (entire gene)	HLA-DQB1 7.1kb(exon 1-3'UTR)
HLA-B 2.6 kb (exons 1-7 + introns)	HLA-DPB1 9.7 kb(exon 2-3'UTR)
HLA-C 4.2 kb (entire gene)	HLA-DQA1 7.3 kb (entire gene)
HLA-DRB1/3/4/5 4.1 kb (exon 2, intron 4)	HLA-DPA1 10.3 kb(entire gene)

Estimated turnaround time: 28-35 days

Deliverables:
FASTQ, BAM, and VCF files
Variant annotation, Technical report

Sequencing depth: Mean depth of coverage: ≥300×

Sample requirements*:
Extracted genomic DNA: a minimum of 1 microgram as quantified by Qubit 2.0
Purity of genomic DNA samples:
OD260/280 ratio is between 1.8 to 2.0
OD260/230 ratio is between 1.5 to 2.0
* Extraction services provided (please inquire)

Sequencing platforms:
Illumina MiSeq, Illumina NextSeq, Illumina HiSeq

Library preparation:
Illumina's TruSight™ HLA Sequencing Panel

Software & Reporting:
Conexio Genomics

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall

Clinical Biomarker Services

Service Description:

LifeSct discovers, develops, and commercializes non-invasive clinical biomarkers and diagnostic tests. We are a trusted partner to biopharmaceutical companies and biomedical institutions, enabling their efforts to bring the most effective personalized therapies to global markets.

Our Ability to Deliver

- Experiment design
- Feasibility studies
- Novel biomarker discovery
- Clinical validation
- Companion diagnostic development
- Regulatory approval
- CLIA-certified, CAP-accredited laboratory services
- Commercialization of clinical tests to global markets
- Project management and customer service
- Reimbursement

Our Technology Platforms and Advantages

We have set up an array of technology platforms to discover and develop different types of clinical biomarkers, including but not limited to DNA mutation, RNA (mRNA, smRNA, miRNA), protein and metabolite biomarkers.

We have proprietary platforms that are suitable for developing non-invasive clinical biomarkers:

BEST™: this blocker-based enrichment technology preferentially amplifies circulating tumor DNA (ctDNA) in blood and reliably identifies genetic alterations. We offer this technology on both qPCR and NGS platform. An added benefit of using NGS is the ability to accurately quantify ctDNA abundance, thus indicating tumor burden.

CiRiSeg™: this technology incorporates an innovative non-blocker non-probe based method to enrich genes and regions of interest. Its near error-free deep sequencing technology is ideal for novel rare mutation discovery.

UltraD™: this aptamer-based technology uses single-stranded nucleic acid to bind to targets including proteins and small molecules in a similar fashion to antibodies. Compared to traditional antibodies, UtraD™ has advantages such as easy chemical synthesis and modification, short development time,reduced cost, batch consistency, stability, and long shelf-life. Hence, it's more suitable for the development of novel clinical applications.

Key Features & Benefits:

- Complete solutions include biomarker discovery and validation, as well as development and processing of clinically relevant assays and companion diagnostics.
- Expertise with and availability of multiple technology platforms, including liquid biopsy, aptamer, next generation sequencing, and qPCR.
- State-of-the-art CLIA-certified, and CAP-accredited laboratory.
- Pre-designed solutions and CLIA-certified tests for oncology, cardiovascular and pharmacogenomics diagnostics.
- Extensive experience in obtaining regulatory approval and commercialization of Lab Developed Tests (LDTs) globally, especially in US and China.

Quantitative Real-Time PCR(qPCR)

Service Description:

Real Time PCR allows for the enzymatic amplification and fluorescent labeling of a short, specific region or your template. As amplification continues, fluorescence is released in a manner that is directly proportional to the amount of DNA that is amplified. The release of fluorescence during amplification is monitored in real time providing highly sensitive quantitative data. The results gained from performing RT-qPCR have a variety of applications, including identifying microorganisms, genotyping, detecting SNPs, primer efficiency, precise quantitation measures, *etc.*

LifeSct, a molecular diagnostics company, offers qualitative and quantitative real time PCR for all of your NGS based DNA and RNA needs. Run on our QuantStudio® 5, we offer qPCR services using a variety of commercial kits on SYBR Green-based assays.

Advantages:
Fast estimated turnaround times
Affordable pricing

Estimated turnaround time: 1-2 weeks

Deliverables:
RAW data
Exported excel file

Sample acceptance criteria:
gDNA concentration starting from as little as 20ng per sample
RNA concentration starting from as little as 100ng per sample

Platform:
QuantStudio® 5

Data security: biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall