admera health

Biopharma Services 2021 Catalog

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WHO WE ARE

The Biopharma Services Department (BPS) at Admera Health provides genomics and bioinformatic services for researchers working on projects ranging from exploratory to clinical. Our team of experts offer clients comprehensive support from initial project consultation to post completion.

Our facilities have all the latest equipment and instruments to facilitate your research requirements. BPS operates in a CLIA certified and CAP-accredited laboratory for the delivery of laboratory developed tests (LDTs) as well as RUO (Research Use Only) services. We are committed to maintaining compliance with all clinical regulations and upholding the highest quality standards on all projects.

Admera Health is an advanced molecular diagnostics and research service provider. Utilizing genomic and proteomic technology platforms (such as next generation sequencing), together with advanced bioinformatics, Admera Health strives to provide the best solutions for all researchers and biopharma companies. Maximizing efficiency in laboratory services and practices allows Admera to offer substantial competitive pricing to our customers.

All data is secured behind biometrically restricted laboratory access, biometrically restricted data room, and closed loop data behind firewall.

If you would like more information about genomics and bioinformatics business opportunities or if you have any general questions, please feel free to contact us through our website **www.admerahealth.com/genomics-and-bioinformatics.**

GENOMICS AND BIOINFORMATICS SERVICES

RNA-SEQ

Transcriptome profiling 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 is capable of detecting the presence of novel isoforms, alternatively spliced transcripts; Potential gene fusion events can also be detected through analysis of RNA-seq data.

DELIVERABLES

- Raw data as FASTQ files
- Quality control results
- Complete data analysis available*

**please inquire for more details*

FLEXIBLE STARTING INPUT

- Total RNA
- FFPE
- Blood
- Fresh frozen tissue
- Cell pellet
- Preserved cells
- Fresh cells*

**Please inquire for more details*

SEQUENCING PLATFORMS

- High depth of coverage available, please inquire for details

ESTIMATED TURNAROUND TIME

- 28-42* days

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

DISCOVER

- Novel transcripts
- Mutations SNPs
- Gene sequence annotation

DETECT

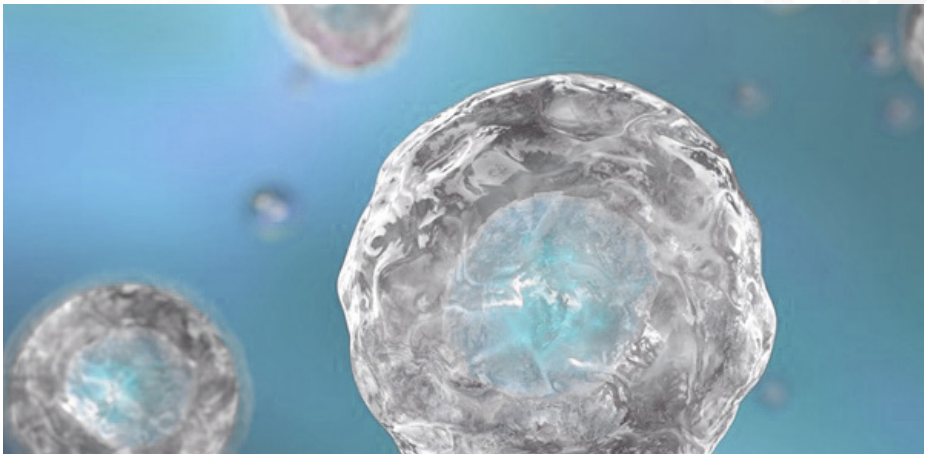
- Changes in gene expression
- Changes from cancer alteration

DETERMINE

- Splicing patterns and potential gene fusion events

SINGLE-CELL RNA SEQUENCING (scRNA-SEQ)

While studying transcriptome profiling through RNA-seq, 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 at single cell resolution and to undiscovered regulatory functions of these cells.



SEQUENCING DEPTH

- High depth of coverage available*

**Please inquire for more details*

LIBRARY PREPARATION OPTIONS

- SMART-Seq HT
- 10x Chromium 3'/5'/VDJ/ADT

** Additional library preparation options available, please inquire for details*

DELIVERABLES

- Raw data as FASTQ files
- Quality control results including cell viability check
- 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*

- **Fresh frozen tissue, cryopreserved cells, cell pellet**
- **Fresh cells, cryopreserved †**

** Only accept cells for processing on Tues/Wed*

† Give one week advanced notice of incoming project

SEQUENCING PLATFORM

- **Illumina Platforms**

DISCOVER

- **Gene expression at single cell level**

DETECT

- **Single cell resolution of heterogeneity**

WHOLE EXOME SEQUENCING (WES)

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. Admera provides a cost-effective solution to studying the exome.

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.

SAMPLE REQUIREMENTS*

- Genomic DNA, FFPE, Blood, fresh frozen tissue, cell pellet
- Extracted genomic DNA: a minimum of 250 nanograms as quantified by Qubit 2.0

* *Extraction services provided (please inquire)*

LIBRARY PREPARATION OPTIONS

- xGen® Exome Research Panel v2.0
- TruSeq DNA Exome
- Nextera DNA Exome (additional charges apply, please inquire for details)
- SureSelect Exon V6, V6 + UTR, V7, Mouse All Exon

* *Additional library preparation options available, please inquire for details*

BIOINFORMATIC ANALYSIS AVAILABLE*

- QC + Mapping + Markdup + BQSR + Germline Variant Analysis

* *Additional analyses such as Somatic Mutation Analysis or Tumor Only Analysis available please inquire for details*

ADVANTAGES

- **Competitive pricing**
- **Flexible coverage**

DISCOVER

- **Disease-related rare variants**

DETECT

- **Variants for diagnosis**

DETERMINE

- **Underlying genetic cause**

SEQUENCING DEPTH

- Mean depth of coverage*: ≥ 100x90% of exons covered at ≥ 20x depth*

* *Higher depth of coverage available for additional charges, please inquire for details*

SEQUENCING PLATFORMS

- Illumina HiSeq and NovaSeq

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

ESTIMATED TURNAROUND TIME

- 28-35* days

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

WHOLE GENOME SEQUENCING (WGS)

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.

SEQUENCING PLATFORMS

- Illumina Miseq, Nextseq, HiSeq, and NovaSeq platforms

BIOINFORMATIC ANALYSES

- Standard Analysis:
- QC & Alignment
- Mapping
- Markdup
- BQSR
- Germline Variant Analysis

Additional Bioinformatic Analysis Available:

- Detailed Annotation
- Germline Structural Variation
- Germline CNV Detection
- TRIOS/Joint VCF

ADVANTAGES

- Flexible sample input
- Competitive pricing
- High coverage depth and uniformity

SURVEY

- Genome for known disease

PERSONALIZE

- Tailor treatments based on individual genome

DETERMINE

- Mutations driving disease
- De novo assembly

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

SEQUENCING DEPTH

- Starting at 90Gb raw data per sample
- Higher depth of coverage available for additional charges, please inquire for details

ESTIMATED TURNAROUND TIME

- 28-35* days

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

SAMPLE REQUIREMENTS

- **FFPE Unstained Slides**
- **Blood samples**
- **Tissue**
- **Saliva (please request sample collection supplies)***
- **Genomic human DNA: a minimum of 100 nanogram as quantified by Qubit 2.0**
- **Amplicon**

Inquire for more details

LIBRARY PREPARATION OPTIONS

- **KAPA Hyper Prep Kits**
- **Swift Accel-NGS® 1S Plus DNA**
- **Nextera XT DNA**
- **Nextera DNA**

Additional kits available

WHOLE GENOME BISULFITE SEQUENCING (WGBS)

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
- Flexible input
- High coverage depth and uniformity
- Short TAT

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

EXAMINE

- Epigenomic modifications

INTERROGATE

- Abnormal methylations and epigenetic regulation

DETERMINE

- Mutations driving disease

SEQUENCING DEPTH

- Illumina 2x150 112.5GB raw data with 20% PhiX, 90GB data without PhiX

Deeper sequencing available, please inquire for details

SEQUENCING PLATFORMS

- Illumina HiSeq and NovaSeq

ESTIMATED TURNAROUND TIME

- 28-35* days

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

SAMPLE REQUIREMENTS

- **Types of samples accepted:High quality genomic human DNA: 500 nanogram as quantified by Qubit 2.0**
- **FFPE Formalin-Fixed, Paraffin-Embedded (FFPE) Unstained Slides***
- **Bisulfite Treated gDNA**

**** Inquire for more details***

BIOINFORMATIC ANALYSES AVAILABLE*

- **QC + Mapping + Remove Duplicates + Extract Methylation**
- **Differentially Methylated Region with MethylKit**
- **Non-CpG (CHH + CHG) differential sites detection**

****Inquire for more details***

LIBRARY PREPARATION OPTIONS

- **EZ DNA Methylation-Gold™ Kit**
- **Accel-NGS MethylSeq kit**

SEQUENCING ONLY

Researchers looking for sequencing only solutions will find that Admera Health 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, Admera Health performs comprehensive quality control steps which are detailed in reports that are sent to you within 24 hours. Admera's QC entails Qubit, Tapestation, and qPCR.

PLATFORMS

- Miseq
- Nextseq
- Hiseq
- Novaseq

CUSTOMIZED SEQUENCING PRIMERS

- Options available, please inquire

DATA TRANSFER*

- Basespace
- sFTP

** Others upon request*

LIBRARY REQUIREMENTS

- Individual Pre-Made Final Libraries
- Pooled Final Libraries
- Based on library type and platform, please inquire

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

ESTIMATED TURNAROUND TIME

- 14-21* days

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

HI-C ASSAY

High Throughput Chromosome Conformation Capture (Hi-C) assay is an extension of chromosome conformation capture (3C) assay studying chromosomal interactions. While 3C and its subsequent adaptations require the choice of a set of target loci, Hi-C employs high-throughput sequencing and can identify genome-wide unbiased long-range interactions. Hi-C results reveal chromosomal interactions such as compartmentations, topologically associating domains (TADs) and chromatin loops.

SAMPLE REQUIREMENT

(need two replicates per sample)

- Minimum 100mg frozen tissue
- 5 million frozen cell pellet per sample
- Snap frozen cells
- Crosslinked samples

HI-C ASSAY & LIBRARY PREPARATION KITS

- Arima Hi-C kit with Roche KAPA Hyper prep

SEQUENCING PLATFORMS

- Illumina HiSeq
- Illumina NovaSeq

ESTIMATED TURNAROUND TIME

- 28-35* days

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

DATA DELIVERY FORMAT

- FASTQ format files

DATA ANALYSIS SUPPORT

- In-house bioinformatics analysis available, please inquire for details.

SUGGESTED SEQUENCING DEPTH

- 1200 M PE reads per biological condition*† (biological replicates combined)

** 1200 M PE reads for human, mouse samples. Sequencing depth requirements may vary for other species*

† Customized sequencing depth available, please inquire for details

ChIP-SEQ

Studying regulatory processes can be accomplished by employing ChIP-seq. Chromatin Immunoprecipitation Sequencing (ChIP-seq) is used to map DNA binding sites on a genome-wide basis for transcription factors and related proteins without prior knowledge, profiling epigenetic modifications of biological processes and disease states. Gaining intricate knowledge on regulators, targeted therapies can be explored and developed.

SAMPLE REQUIREMENTS*

- Immuno-precipitated DNA: a minimum of 100 nanogram as quantified by Qubit 2.0 (recommend input samples included in study)

** Extraction services provided (please inquire)*

INVESTIGATE

- Epigenetic patterns

IDENTIFY

- Protein interactions
- Binding sites

ADVANTAGES

- Low cost
- High coverage depth and uniformity
- Short TAT

DELIVERABLES

- FASTQ files
- Bioinformatic Analysis available upon request

GENES/REGIONS COVERED

- Immuno-precipitated DNA

SEQUENCING DEPTH

- Starting at 40M Total reads*

** Specific depth of coverage available, please inquire for details*

ESTIMATED TURNAROUND TIME

- 28-35* days

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

PREPARATION OPTIONS

- **KAPA Hyper Prep**

Additional library preparation options available, please inquire for details

SEQUENCING PLATFORMS

- **Illumina HiSeq & NovaSeq platforms**

ATAC-SEQ

A good alternative to ChIP-seq 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.

SEQUENCING PLATFORMS

- Illumina NextSeq
- Illumina HiSeq
- Illumina NovaSeq

Availability may vary, please inquire

SEQUENCING DEPTH

- Starting at 50M PE reads*

** Specific depth of coverage available, please inquire for details*

DELIVERABLES

- FASTQ files
- Bioinformatic Analysis available upon request

ESTIMATED TURNAROUND TIME

- 28-35* days

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

LIBRARY PREPARATION OPTIONS

- **Laboratory developed test with Nextera**

Additional library preparation options available, please inquire for details

ADVANTAGES

- **Low cost**
- **High coverage depth and uniformity**
- **Short TAT**

SAMPLE RECEIPT TYPES

- **Live cells**
- **Cryopreserved cells (pre-counted 1M cells; two replicates per sample)**
- **Snap frozen tissue 5-50mg with intact nuclei**
- **Other sample types accepted***

**** Please inquire for further details***

INVESTIGATE

- **Genome wide chromatin accessibility**

DISCOVER

- **Nucleosome mapping**

CUT&RUN ASSAY

CUT&RUN is a method used to study epigenetic regulation and analyze the protein interactions in DNA. This technology, similar to ChIPseq, isolates protein-DNA complex of interest. The technology can handle low number of cells and reduce non-specific signals in data.

ADVANTAGES

- **High coverage depth and uniformity**
- **Short TAT**
- **Experienced scientific support team**

DELIVERABLES

- FASTQ files

SAMPLE RECEIPT TYPES

- Treated DNA

** Please inquire for further details*

SEQUENCING PLATFORMS

- Illumina NextSeq
- Illumina HiSeq
- Illumina NovaSeq

** Availability may vary, please inquire*

ESTIMATED TURNAROUND TIME

- 28-35* days

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

LIBRARY PREPARATION OPTIONS

- KAPA Adapted LDT

SEQUENCING DEPTH

- Starting at 20M PE reads*

** Specific depth of coverage available, please inquire for details*

HUMAN T-CELL RECEPTOR (TCR) PROFILING

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
- Short TAT

SEQUENCING DEPTH

- Starting at 40M PE reads*

** Specific depth of coverage available, please inquire for details*

LIBRARY PREPARATION OPTIONS

- Laboratory developed test with Clontech SMARTScribe™ Reverse Transcriptase
- SMARTer® Human TCR a/b Profiling Kit
- QIAseq Immune Repertoire RNA Library

** Additional library preparation options available, please inquire for details*

SAMPLE REQUIREMENTS

- Total RNA: 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

ESTIMATED TURNAROUND TIME

- 28-35* days

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

RAD-SEQ/ddRAD-SEQ

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.

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 non-targeted approach.

ADVANTAGES

- Low cost
- High coverage depth
- Flexible enzyme combination
- Superb technical support

SAMPLE REQUIREMENTS*

- Genomic DNA: a minimum of 1 microgram as quantified by Qubit 2.0

* *Extraction services provided (please inquire)*

SEQUENCING DEPTH

- Starting at 1M reads per sample*

* *Coverage adjustable per enzyme choice and customer preference*

LIBRARY PREPARATION OPTIONS

- Laboratory Developed Test*

* *Proprietary to Admera Health*

ESTIMATED TURNAROUND TIME

- 28-35* days

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

SEQUENCING PLATFORMS

- Illumina MiSeq, Illumina NextSeq, Illumina HiSeq

DELIVERABLES

- FASTQ files

CUSTOMIZED GENE PANELS

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.

SAMPLE REQUIREMENTS

- Extracted genomic DNA: a minimum of 100 nanogram as quantified by Qubit 2.0

** Extraction services provided (please inquire)*

LIBRARY PREPARATION OPTIONS

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

SEQUENCING DEPTH*

- Mean depth of coverage: ≥ 250x
- 90% of exons covered at ≥ 50x depth*

** Higher depth of coverage available for additional charges, please inquire for details*

GENES/ REGIONS COVERED

- Flexibility to target 1-1000 genes

DELIVERABLES

- FASTQ, BAM and VCF files
- Variant annotation

ESTIMATED TURNAROUND TIME

- 35-42* days

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

SEQUENCING PLATFORMS

- Illumina NextSeq
  Illumina HiSeq

16S rRNA-SEQ (FLORACHECK™)

The goal of 16S Ribosomal RNA Sequencing (16S rRNA-SEQ) is to determine the type and relative abundance of bacterial and archaeal species in heterogeneous samples, such as soil, marine, or gut microbiome. Floracheck™ is a proprietary assay that improves upon current 16S metagenomics techniques with significant sensitivity and specificity. Side-by-side comparison with the most commonly used 16S metagenomics assays reveals that Floracheck™ can detect more bacterial and archaeal genera with a lower limit of detection for both environmental and mammalian species.

Admera's technology improves the sensitivity so to detect the low abundant bacteria. Floracheck can amplify a much broader range of bacteria and archaea with minimum bias.

ADVANTAGES

- Higher sensitivity
- Low bias
- Cost-effective
- Fast TAT

SAMPLE REQUIREMENTS

- Extracted genomic DNA: a minimum of 50 nanogram as quantified by Qubit 2.0

REGION COVERAGE

- Floracheck™ Environmental (V3, V4, and V5 hypervariable regions)
- Floracheck™ Mammalian (V3 and V4 hypervariable regions)
- Floracheck™ Essential (V4 hypervariable region)
- V1-V9 Hypervariable regions

SEQUENCING DEPTH

- Illumina 2x250 with 0.1M PE Reads (50K in each direction)

DELIVERABLES

- Raw data as FASTQ files
- Chart detailing the type and relative abundance of bacterial and archaeal genera in each sample
- Deeper analysis available per request

ESTIMATED TURNAROUND TIME

- 28-35* days

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

FUNGAL ITS SEQUENCING

Biopharma Services offers opportunity to help identify fungal species through ITS1 and ITS2 amplification. Our team offers experience and fast turnaround for those studying environmental diversity.

ADVANTAGES

- Higher sensitivity
- Low bias
- Cost-effective
- Fast TAT

DELIVERABLES

- Raw data as FASTQ files

SAMPLE REQUIREMENTS

- Extracted genomic DNA: a minimum of 200 nanogram as quantified by Qubit 2.0

SEQUENCING DEPTH

- Illumina 2x250 with 0.1M PE Reads (50K in each direction)

REGION COVERAGE

- ITS1 and ITS2 Regions

ESTIMATED TURNAROUND TIME

- 28-35* days

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

METAGENOMICS

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.

FEATURES

- High sensitivity
- Cost-effective & fast

ESTIMATED TURNAROUND TIME

- 28-35* days

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

DELIVERABLES

- Raw data as FASTQ file

REGION COVERAGE

- Whole Genome

SAMPLE SUBMISSION

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

METATRANSCRIPTOMICS

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

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

SEQUENCING DEPTH*

- Mean depth of coverage: ≥ 250x
- 90% of exons covered at ≥ 50x depth*

** Higher depth of coverage available for additional charges, please inquire for details*

ESTIMATED TURNAROUND TIME

- **35-42* days**

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

SEQUENCING PLATFORMS

- **High depth of coverage and long reads available**

Price upon request

HUMAN LEUKOCYTE ANTIGEN (HLA) TYPING

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

- HLA-A 4th field Full Gene
- HLA-B 4th field Full Gene
- HLA-C 4th field Full Gene
- HLA-E 4th field Full Gene
- HLA-F 4th field Full Gene
- HLA-G 4th field Full Gene
- HLA-H 4th field Full Gene
- DRB1 3rd field Full Exon
- DRB3/4/5 3rd field Full Exon
- DQA1 3rd field Full Exon
- DQB1 3rd field Full Exon
- DPA1 3rd field Full Exon
- DPB1 3rd field Full Exon
- MICA 2nd field Full Exon
- MICB 2nd field Full Exon

SEQUENCING DEPTH

- Illumina 2x150 0.1 M total reads
- Mean depth of coverage: ≥ 300x

ESTIMATED TURNAROUND TIME

- 28-35* days

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

SEQUENCING PLATFORMS

- Illumina MiSeq
- Illumina NextSeq
- Illumina HiSeq
- Illumina NovaSeq

DELIVERABLES

- FASTQ, BAM, and VCF files
- Variant annotation
- Technical report
- Software & Reporting available upon request

SAMPLE REQUIREMENTS*

- Extracted genomic DNA: a minimum of 1 microgram as quantified by Qubit 2.0

** Extraction services provided (please inquire)*

LIBRARY PREPARATION

- AlloSeq Tx 17
- Illumina's TruSight™ HLA v2 Sequencing Panel
- AllType FastPlex

Other kits available please inquire for more details

QUANTITATIVE REAL-TIME PCR (qPCR)

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.

Admera Health, 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.

SAMPLE ACCEPTANCE CRITERIA

- gDNA Concentration starting from as little as 20ng per sample
- RNA Concentration starting from as little as 100ng per sample

DELIVERABLES

- RAW data
- Exported excel file

ADVANTAGES

- Fast Turnaround Times
- Affordable pricing

PLATFORM

- QuantStudio® 5

ESTIMATED TURNAROUND TIME

- 1-2* weeks

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

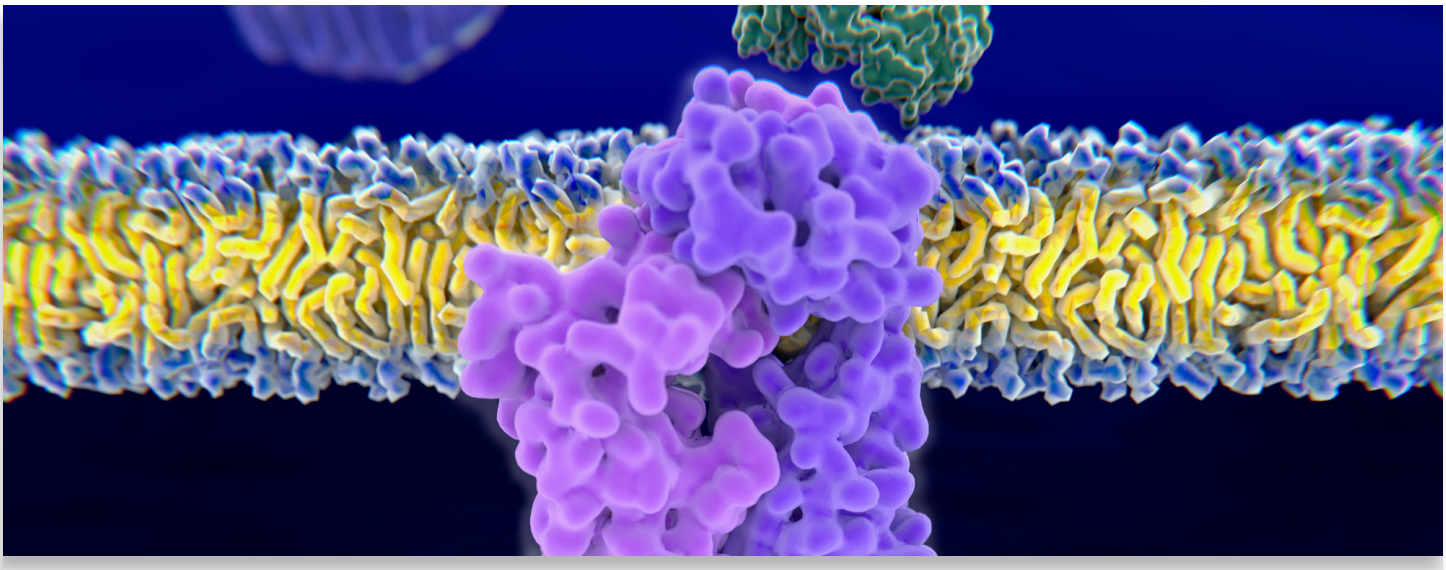
IMMUNOGENOMICS SERVICES

NEOANTIGEN IDENTIFICATION

Mutations in protein coding genes of cancer cells are a source of potential neoantigens that the immune system can target. Characterization of expressed neoantigens has contributed to development of personalized cancer therapeutics. NGS has enabled the predictive selection of novel tumor antigens that can be applied to elicit a tumor-specific response.

Admera Health's biopharma services characterize DNA and RNA across all ~20,000 genes in a tumor and matched normal sample configuration by exome sequencing and transcriptome sequencing to provide an extensive evaluation of candidate neoantigens derived from SNVs, indels, and/or fusions.

Based on Admera Health's proprietary bioinformatics analysis method, experts provide accurate and comprehensive neoantigen detection, characterization and prioritization.



ADVANTAGES

- Advanced pipelines and integrated framework
- Comprehensive analysis covering ranging from neoantigen identification to peptide evaluation
- Competitive pricing and turnaround

Extensive experience in sample sequencing with low input or FFPE

OUR TECHNOLOGIES

- DNA-seq
- RNA-seq
- Proprietary bioinformatics analysis methods

DELIVERABLES

- Identification and ranking of neoantigens based on information such as HLA typing, MHC-binding prediction, peptide processing, similarity-to-self, similarity-to-known antigens, and immunogenicity
- Peptide ordering optimization for DNA vector–based vaccine design
- Allelic fraction and gene- and variant-level expression
- Phasing for allele-specific expression determination

IMMUNE REPERTOIRE ANALYSIS

The adaptive immune system recognizes pathogens by binding their antigens to specific surface receptors expressed on B and T cells. The immense diversity of B-cell receptors (BCR) and T-cell receptors (TCR), generated through recombination of the variable (V), diversity (D), and joining (J) loci, is key to the adaptive immune system. Our Immuno-Profiling service uses high-throughput sequencing and sophisticated bioinformatics to measure diversity and provide comprehensive characterization of the entire BCR or TCR repertoire.

ADVANTAGES

- Complete V(D)J sequence information - obtain full-length sequences for variable regions
- TRA/TRB or Heavy/light/kappa chain pairing with single cell technology
- Exceptional sensitivity and excellent reproducibility
- Competitive Pricing & Short TAT

DELIVERABLES

- Our interactive HTML reports include following:
- Repertoire Properties analysis
- CDR3 Amino Acid Length Distribution
- CDR3 Amino Acid Abundancy Analysis
- Gene Segments Usage analysis
- Top V(D)J combination
- Clonal Frequency and Distribution
- CDR Diversity and Motif analysis
- Repertoire Dynamics analysis
- Differential analysis to detect the clonotypes whose abundance significantly changed among conditions
- Clone Tracking and Analysis
- Compare and track clones across multiple samples and conditions
- Clustering analysis

APPLICATION

- BCR/TCR repertoire profiling
- Antibody discovery
- Hybridoma screening

TECHNOLOGIES

- Bulk Immuno-Profiling
- Single-Cell Immuno-Profiling
- Human and Mouse for TCRA, TCRB, TCRD, TCRG, TCL, IGH, IGL, IGK

VACCINE DEVELOPMENT

PERSONALIZED CANCER VACCINE

The adaptive immune system employs an immensely diverse repertoire of lymphocyte receptors to recognize and neutralize pathogen or tumor-associated antigens. Analyzing the neoantigen can provide insight into diseases and aid the development of vaccines. At Admera Health, our immunogenomics service adopts high-throughput sequencing, molecular profiling, and sophisticated bioinformatics to facilitate the vaccine development. We can provide accurate neoantigen detection, characterization, and prioritization to use in the development of either an 'off-the-shelf' or personalized vaccine as well as peptide ordering optimization for DNA vector vaccine design, peptide synthesis assessment and peptide toxicity evaluation. Our TCR screening capabilities also have the potential to guide the design and development of next-generation vaccines by characterizing the immunogenicity and monitoring early signs of antigen-specific T cell responses.

DELIVERABLES

We aim to help you to identify the most immunogenic antigens for personalized vaccine to advance the next generation of cancer therapy. Admera Health's services include:

- Identification and ranking of neoantigens based on information such as HLA typing, MHC-binding prediction, peptide processing, similarity-to-self, similarity-to-known antigens, and immunogenicity as well as allelic fraction and gene/variant level abundance
- Fusion based neoantigen prediction and vaccine discovery
- Linker analysis, peptide stability and toxicity analysis
- Antigen-specific T cell responses

ADMERA HEALTH'S UNIQUE ADVANTAGES

- Advanced pipelines & integrated framework
- Best-in-class neoantigen prediction algorithm
- Comprehensive analysis covering ranging from neoantigen identification to peptide evaluation
- Competitive pricing and turnaround
- Customized services
- Extensive experience in sample sequencing with low input or FFPE

POTENTIAL APPLICATIONS

- Personalized cancer vaccine discovery
- Vaccine design and development
- Vaccine immunogenicity characterization and monitoring

TECHNOLOGIES

- DNA-seq
- RNA-seq
- Proprietary bioinformatics analysis methods

TUMOR ESCAPE & RESISTANCE

Increasingly apparent from clinical studies across immunotherapies is that at least 30–50% of cancers that initially respond subsequently acquire means of immune escape and relapse. Paradoxically, the patients' cancer immunoediting mechanisms, wherein normally the adaptive immune system recognizes and eliminates immunogenic nascent tumors, may facilitate selection of cancer subclones that acquire new armaments to evade the immune responses elicited by immunotherapies.

Our Immuno-Profiling service couples high-throughput sequencing and sophisticated bioinformatics analysis to study and understand the diverse immunogenomic mechanisms of primary tumor resistance acquired by cancers to escape patients' immune systems —including immune checkpoint profiling as well as deficiencies in antigenicity, immunogenicity, and antigen presentation machinery.

ADVANTAGES

- Comprehensive bioinformatics analysis covering all aspects of tumor escape & resistance mechanisms
- Accurate results
- Competitive pricing and short TAT

DELIVERABLES

Admera Health's customized analysis includes:

- Tumor Microenvironment (TME) Analysis
- Antigen processing and presentation machinery (APM) profiling
- Signaling Pathway Analysis
- Immunogenicity analysis
- Chemokines/Cytokines profiling
- T cell co-stimulation and co-inhibition profiling
- Drug target profiling and mutation analysis
- Gut microbiome analysis

POTENTIAL APPLICATIONS

- **Biomarker discovery & Companion Diagnostics Development**
- **Immune checkpoint inhibitor discovery**
- **Clinical investigations of relapse following immunotherapy**

TECHNOLOGIES

- **RNA-seq**
- **DNA-seq**
- **Single-cell RNA-seq**
- **Metagenomics WGS/16S-seq**

MINIMUM RESIDUAL DISEASE

The clearance of malignant clonal cells significantly correlates with clinical outcomes in many cancers. Accurate and ultra-deep next-generation sequencing for minimal residual disease (MRD) detection have allowed for higher sensitivity analyses and more precise stratification of patients, based on molecular response to therapy. For example, rearrangements of the immunoglobulin heavy chain (IGH) are good biomarkers for MRD monitoring in hematological malignancies while ctDNA profiling have the potential to transform clinical practice via non-invasive monitoring of solid tumor malignancies, residual disease detection at earlier timepoints than standard clinical and/or imaging surveillance, and treatment personalization based on real-time assessment of the tumor genomic landscape.

With expertise in immune repertoire profiling and proprietary liquid biopsy technology LiquidGx™, we will be able to provide multiple approaches for MRD biomarker discovery and non-invasive clinical test development for disease progression monitoring.

ADVANTAGES

- High sensitivity and accuracy
- Competitive pricing and short TAT

TECHNOLOGIES

- Immune Repertoire sequencing, including clonal rearrangements of immunoglobulin/T-cell antigen receptor genes: IGH (VDJ), IGH (DJ), IGK, IGL, TRG, TRA, TRB, TRD, and translocations of BCL1/IGH (J) and BCL2/IGH (J)
- LiquidGx OneTM for circulating tumor DNA (ctDNA) detection

DELIVERABLES

Admera Health's services support biomarker research and development for disease diagnostics and monitoring and can be adapted to suit research and clinical programs.

- Dominant tumor clones of IGH
- The minimal residue disease status in blood cancers
- Survival analysis
- The diversity changes of immune repertoire in solid cancers

POTENTIAL APPLICATIONS

- Post-treatment monitoring of B- and T-cell malignancies
- Drug efficacy biomarker discovery and development
- Disease prognostics test
- Disease progression monitoring

admera health

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