admera health

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admera health Biopharma Services

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WHO WE ARE

Biopharma Services Department (BPS) offers comprehensive support from the initial project consultation and continues even beyond completion of project. Our facilities have all the latest equipment and instruments to facilitate your 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 and aptamer), together with advanced bioinformatics, Admera Health strives to provide the best solutions for all researchers and biopharma companies.

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

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BIOPHARMA SERVICES

16S rRNA-seq (FLORACHECK™)

The goal of 16S Ribosomal RNA Sequencing 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.

SAMPLE REQUIREMENT

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

GENES/ REGIONS

- V3, V4, V5 Hyper variable regions
- V1-V9 regions are available per request

DELIVERABLES

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

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ATAC-SEQ

An alternative to ATAC-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, does not need antibodies, or sensitive digestion.

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

SEQUENCING DEPTH

- Starting at 40M Total reads*

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

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)*

SAMPLE REQUIREMENTS

- 100,000 cells Cryopreserved in Single Cell Suspension

INVESTIGATE

- Genome wide chromatin accessibility

DISCOVER

- Nucleosome mapping

ChIP-seq

Studying regulatory processes can be accomplished by employing ChIP-seq. Chromatin Immunoprecipitation (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 REQUIREMENT

- Immuno-precipitated DNA

INVESTIGATE

- Epigenetic patterns

IDENTIFY

- Protein interactions
- Binding sites

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

SEQUENCING DEPTH

- Starting at 40M Total reads*

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

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)*

Preparation Options

- **KAPA Hyper Prep**

Additional library preparation options available, please inquire for details

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:

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

Inquire for more details

GENES/ REGIONS

- Target up to 1000 genes

PERSONALIZE

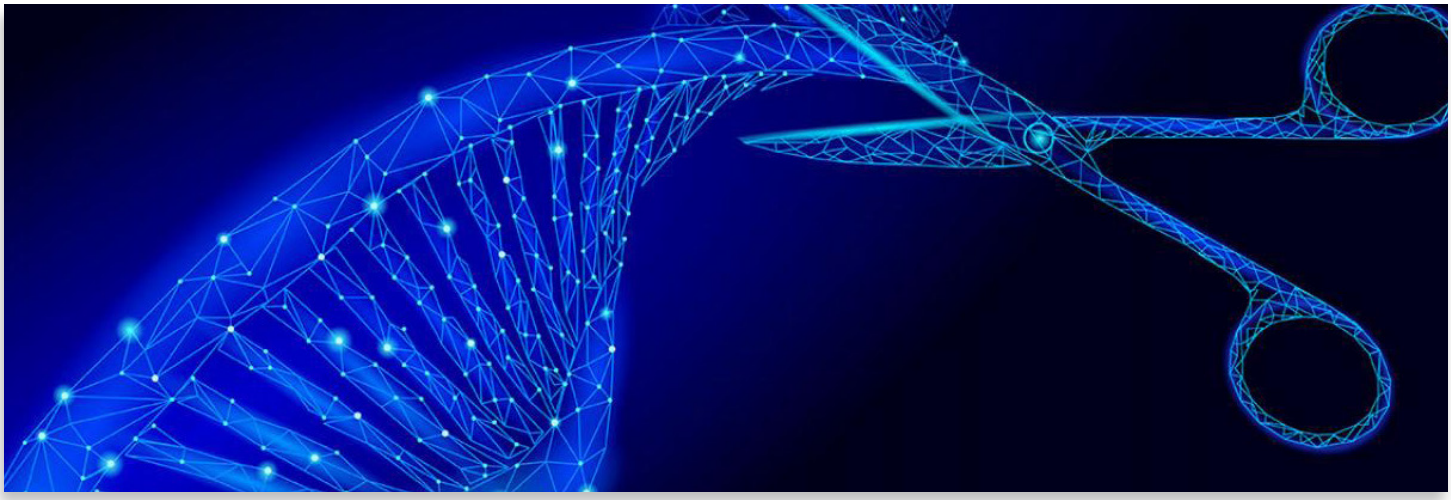
- Tailor panels to research goals

ADVANTAGES

- High coverage depth and uniformity
- Short TAT
- Accurate results

DDRAD-SEQ PANELS

In most sequencing data analysis, prior genomic knowledge is required for studies. Double digest restriction site associated DNA sequencing, or ddRAD-seq, is a new technique can be used for SNP discovery and genotyping without a reference genome. This is a step from RAD-seq 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.



SAMPLE REQUIREMENTS*

- Genomic DNA: a minimum of 500ng as quantified by Qubit 2.0

** Extraction services provided (please inquire)*

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment
- Flexible enzyme combination

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)*

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

DELIVERABLES

- Raw data as FASTQ files
- De novo assembly per additional charge

RNA-SEQ

Admera's Biopharma Services team is ready to provide a one-stop solution for RNA-seq projects, including whole transcriptome, smRNA or miRNA, lncRNA, scRNA-seq, metatranscriptomics.

Flexible Starting Input:

Total RNA, FFPE, Blood, fresh frozen tissue, cell pellet, fresh cells

Preparation Options:

- **Lexogen QuantSeq 3' mRNA-Seq**
- **NEBNext® Ultra™ II RNA Library Prep Kit for Illumina, NEBNext® Ultra™ II Directional RNA Library Prep Kit**
- **TruSeq Stranded Total RNA, TruSeq Stranded mRNA Library Preparation Kit**
- **SMARTer Stranded Total RNA-Seq, SMART-Seq V4 Ultra Low Input RNA Kit**
- **KAPA RNA HyperPrep with RiboErase (HMR)**
- **NEBNext Multiplex Small RNA Library Prep Kit**
- **TruSeq Small RNA Library Preparation Kits**
- **10x Chromium Single Cell Library Construction**

Additional preparation options available

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

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 PLATFORMS

- High depth of coverage and long reads available

ESTIMATED TURNAROUND TIME

- 28-42 days*

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

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.

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

SEQUENCING PLATFORMS

- Starting at 40M Total reads*

**please inquire for more details*

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

ESTIMATED TURNAROUND TIME

- 28-42 days*

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

SAMPLE REQUIREMENT

- Extracted RNA, Fresh frozen tissue, cell pellet, FFPE tissue on slides (extra QC may be needed)
- Fresh cells, cryopreserved

PREPARATION OPTIONS

- SMART-Seq V4 Ultra Low Input
- 10x Chromium 3'/5'/VDJ/CNV

Additional preparation options available

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

DATA TRANSFER*

- Basespace
- FTP

** Others upon request*

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

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)*

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 Health provides a very cost-effective, high quality WES service.

ADVANTAGES

- Competitive pricing
- Flexible coverage
- Flexible Starting Input:
  - Genomic DNA
  - FFPE
  - Blood
  - Fresh Frozen Tissue
  - Cell Pellet

PREPARATION OPTIONS

- xGen® Exome Research Panel v1.0
- SureSelect Exon V6, V6 + UTR, V7, Mouse All Exon

Additional preparation options available

DISCOVER

- Disease-related rare variants

DETECT

- Variants for diagnosis

DETERMINE

- Underlying genetic cause

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 PLATFORMS

- High depth of coverage

ESTIMATED TURNAROUND TIME

- 28-35 days*

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

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.

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

SURVEY

- Genome for known disease

PERSONALIZE

- Tailor treatments based on individual genome

DETERMINE

- Mutations driving disease
- De novo assembly

SEQUENCING DEPTH

- Mean depth of coverage: ≥ 30x

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

ESTIMATED TURNAROUND TIME

- 28-35 days*

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

Preparation Options

- **Zymo EZ Gold with**
- **ACCEL-NGS® METHYL-SEQ DNA LIBRARY KIT**

Additional options available upon request

Sample Requirements

- **Saliva (please request sample collection supplies)**
- **High quality genomic human DNA: a minimum of 500ng as quantified by Qubit 2.0**
- **FFPE Formalin-Fixed, Paraffin-Embedded (FFPE) Unstained Slides***

**** Inquire for more details***

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.

SERVICE GRADE

- Research Use Only (RUO) in a CLIA environment

DELIVERABLES

- Raw data as FASTQ files
- Quality control results

SURVEY

- Genome for known disease

PERSONALIZE

- Tailor treatments based on individual genome

DETERMINE

- Mutations driving disease
- De novo assembly

SEQUENCING DEPTH

- Mean depth of coverage: ≥ 30x

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

ESTIMATED TURNAROUND TIME

- 28-35 days*

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

Sample Requirements

- **Saliva (please request sample collection supplies)**
- **High quality genomic human DNA: a minimum of 500ng as quantified by Qubit 2.0**
- **FFPE Formalin-Fixed, Paraffin-Embedded (FFPE) Unstained Slides***

**** Can accommodate lower input***

Preparation Options

- **KAPA Hyper Prep Kits**
- **KAPA Hyper PCR Free**
- **Nextera XT DNA**
- **NEBNext Ultra II DNA**

Additional preparation options available

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