



*Welcome To The  
Advanced Molecular Era*

**Comprehensive solutions from extraction to analysis**

Transcriptomics | Single-cell | Spatial Biology | WGS/WES  
Epigenomics | Premade Library Sequencing | Bioinformatics



## Advanced Genomic & Bioinformatic Research Services in a CAP/CLIA Environment

Admera Health combines expert scientific support, advanced laboratory processes, stringent quality control measures, and proven project management to deliver superior service.

Synergizing with BioEcho Life Sciences, experts in nucleic acid extraction solutions, Admera Health expands upon their comprehensive NGS offerings, providing customers with innovative nucleic acid extraction technologies that support diverse research initiatives and downstream applications.

All projects are handled with expert care, operating in a CLIA/CLEP certified and CAP accredited lab environment in South Plainfield, New Jersey.

### Why Customers Choose Admera Health



Timely Deliveries  
Quality Service



1:1 Support with  
Our Experts



State-of-the-Art  
Technology



CLIA/CLEP & CAP  
Accreditation



US-based  
Operations

## What Our Customers Say



### Tahoe Therapeutics

"Admera Health has been a great partner for us and has continuously delivered.

Their single-cell sequencing projects have played a big role in helping us build a large single-cell dataset. This has been a key part of moving our pipeline forward and training our AI models for virtual cell platforms.

Their collaborative team works closely with us to make sure the data they deliver is the right fit for what we need. This partnership has helped us to scale our efforts with confidence. With their support, we've been able to speed up our research and development timeline and explore thousands of drug-patient interactions.

We value the work and support from the Admera team and look forward to continuing the collaboration."



### AI Drug Discovery Biotech

"Our group recently transitioned from in-house sequencing to outsourcing, and the experience has been seamless, thanks to Admera. We greatly value their quick turnaround time.

Partnering with Admera has been a game-changer for our sequencing needs, and we couldn't be more pleased with their exceptional service."



## Our Certified Partnerships

### Our Commitment to Excellence: Certified Partnerships

Next-generation sequencing (NGS) has revolutionized genomics research, permitting high-throughput and economical analysis of nucleic acids from diverse sample types.

While the technology of NGS is becoming more accessible, it is still critical to trust that the testing is performed correctly and adheres to the highest quality of standards.

This is where the significance of certification and preferred provider status comes into play.

Certified partnerships require requisite training and are designed to ensure clients receive experimental results they can trust.

The logo for 10x Genomics, featuring the number '10' in a large blue font, followed by a stylized 'x' composed of four colored lines (red, yellow, green, blue), and the word 'GENOMICS' in a smaller blue font to the right.The logo for PacBio, with 'PacBio' in a bold, magenta sans-serif font, followed by a solid magenta circle.The logo for Parse Biosciences, featuring a stylized purple arrow icon on the left, followed by the word 'PARSE' in a bold purple font and 'BIOSCIENCES' in a smaller purple font below it.The logo for Twist Bioscience, with the letters 'T W I S T' in a large, spaced-out, black font, and 'BIOSCIENCE' in a smaller green font below it, flanked by green dots.The logo for TakaRa, with the name 'TakaRa' in a bold, blue, sans-serif font.The logo for New England Biolabs, featuring a stylized orange and black monarch butterfly on the left, followed by the text 'NEW ENGLAND' in a small black font and 'Biolabs®' in a large, black, cursive font.The logo for IDT, featuring a stylized blue DNA double helix on the left, followed by 'IDT' in a large, bold, blue font and 'INTEGRATED DNA TECHNOLOGIES' in a smaller blue font below it.The logo for STOmics, with the name 'STOmics' in a bold, purple, sans-serif font.

# Table of Contents

<b><u>Genomics</u></b>	5
• <u>Whole Genome Sequencing</u>	5
• <u>Long-reads Whole Genome Sequencing</u>	6
• <u>Clinical Whole Genome Sequencing</u>	7
• <u>Whole Exome Sequencing</u>	8
• <u>Targeted Sequencing</u>	8
• <u>Metagenomics</u>	9
<b><u>Transcriptomics</u></b>	10
• <u>RNA Sequencing</u>	10
• <u>Long-read RNA Sequencing</u>	11
• <u>High-throughput RNA Sequencing</u>	12
• <u>Metatranscriptomics</u>	12
<b><u>Single-Cell Sequencing</u></b>	13
<b><u>Spatial Transcriptomics</u></b>	16
<b><u>Amplicon Sequencing</u></b>	18
• <u>16s rRNA Gene Sequencing &amp; ITS Sequencing</u>	18
• <u>CRISPR Screening</u>	19
• <u>Long-read Amplicon sequencing</u>	20
<b><u>Epigenomics</u></b>	21
• <u>WGBS &amp; EM-seq</u>	21
• <u>Targeted Methyl-seq</u>	22
• <u>RRBS</u>	22
• <u>ChIP-seq</u>	23
• <u>CUT&amp;RUN</u>	23
• <u>ATAC-seq</u>	24
• <u>Hi-C Assay</u>	24
<b><u>Sequencing-Only</u></b>	25
<b><u>Bioinformatic Analysis</u></b>	26
<b><u>Products: Nucleic Acid Extraction</u></b>	28
• <u>EchoLUTION™ Cell Culture RNA Kit</u>	29
• <u>EchoLUTION™ FFPE RNA Kit</u>	30
• <u>EchoLUTION™ Plant DNA Kit</u>	31



## Whole Genome Sequencing

Whole genome sequencing (WGS) studies the DNA sequence over an organism's entire genome. WGS provides a broad range of variant identification in a single assay, enabling more uniform coverage of protein-coding and non-coding regions. WGS is becoming a tool for rare genetic disorders, where the detection of variant types can be correlated with disease risk or used as molecular biomarkers for disease diagnosis.

### Common Applications

- Detect SNVs, CNVs, indels, SVs, mitochondrial variants & repeat expansions
- Identify mutations driving tumorigenesis in humans or other species
- De novo genome assembly and annotation

### Accepted Sample Types

dsDNA	Tissue
cFDNA	FFPE samples
Cells	& more

### Turnaround Time

10-15 Business Days

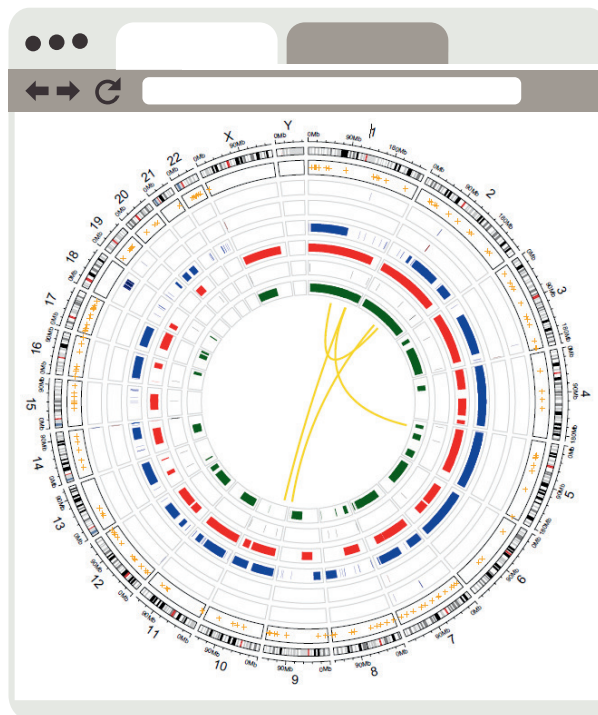
### Sequencing Platforms

Illumina NovaSeq X Plus  
PacBio Revio

## Bioinformatic Analysis

### WGS/Hybrid-capture (WES & Panel)

Preliminary QC, alignment and duplicate detection, downstream QC, somatic and germline variant detection, variant annotation, CNV and SV detection, tumor mutation burden (TMB), HLA-typing, waterfall plot, and Circos plot





## Long-reads Whole Genome Sequencing

PacBio HiFi whole-genome sequencing delivers the clarity today's research and development workflows demand. Unlike short-read WGS, which struggles with structural variants and complex regions, long-read HiFi data provides complete, highly accurate views of the genome—including repeats, large rearrangements, and haplotype structure. With the power of the Revio system, teams gain the resolution needed to make confident decisions in discovery, engineering, and quality assessment.

### Accepted Sample Types

High-molecular weight (HMW) DNA  
Cells  
Tissue & more

### Turnaround Time

4 - 5 weeks

### Sequencing Platforms

PacBio Revio

## Common Applications

- Comprehensive structural variant profiling across the full genome, including large insertions, deletions, inversions, and complex rearrangements.
- Repeat and difficult-region analysis, such as tandem repeats, segmental duplications, and GC-rich or highly repetitive loci.
- Haplotype-resolved genomics, enabling allele-specific interpretation, phasing of variants, and cis/trans determination.
- Full-length gene and isoform characterization, supporting transcript-aware variant interpretation and mechanistic studies.
- Genome integrity and stability assessment for engineered cell lines, biologics production systems, and synthetic constructs.

## Bioinformatics

Variant discovery (QC, mapping, variant calling, annotation, structural variation, and insertion-site analysis) as well as genome assembly for both small and large genomes. Deliverables include assembled FASTA files, reference-based gene annotation, online genome browsing, and haplotype-resolved sequences for complex mammalian genomes.



## Clinical Whole Genome Sequencing

A robust clinical-grade whole genome sequencing (cWGS) service to advance research initiatives with an added layer of confidence. With cWGS, we can unveil novel genomic information to accelerate drug discovery, therapeutic development, and biomarker discovery.

### Accepted Sample Types

Saliva	Cells
Tissue	gDNA
Blood	FFPE

- **Clinical-Grade WGS:** Our cWGS service provides a comprehensive assay for clients who require higher-quality laboratory practices adhering to rigorous quality control procedures and recordkeeping upheld by CLIA-trained personnel with verified equipment.
- **Standard WGS:** Our standard WGS service provides a cost-effective whole genome sequencing service operating in a CAP/CLIA environment.

## Our Optimized Workflow



### High-Purity DNA Extraction

Our high-throughput isolation protocol ensures reproducible, contaminant-free DNA for extracts with high yields



### Superior Library Preparation

Streamlined DNA library preparation enables the construction of high-quality libraries over a wide range of sample inputs & qualities



### High-Throughput Sequencing

cWGS samples are sequenced on the Illumina NovaSeq X Plus, a CLIA-validated platform providing ultra-high-throughput results



### Comprehensive Data Analysis

Our team of expert bioinformaticians analyze sequencing data using established pipelines for accurate, efficient, & comprehensive genomic investigations



### Lab Director Sign-off

Lab Director signing of clinical report  
*\*Available for select variants*



## Whole Exome Sequencing

Whole exome sequencing (WES) investigates the protein coding regions - or exomes - of an organism's genome, where an estimated 85% of disease-causing mutations are suspected to originate. WES identifies variant types including SNVs, indels, runs of homozygosity and mosaic variants. WES is a more cost-efficient alternative to WGS.

### Bioinformatic Analysis

Preliminary QC, alignment and duplicate detection, downstream QC, somatic and germline variant detection, variant annotation, CNV and SV detection, tumor mutation burden (TMB), HLA-typing, waterfall plot, and Circos plot

## Targeted Sequencing

Targeted sequencing allows for analysis at subsets of the genome to discover and validate novel variants, examine specific genes involved in signaling pathways, or used as a follow-up to genome-wide association studies (GWAS). Based on prior knowledge of the region of interest, targeted sequencing leverages the power of NGS to offer higher coverage at reduced costs compared to WGS/WES. At Admera, we offer the flexibility to target 10-1000 genes.

### Bioinformatic Analysis

Suitable to detect low frequency somatic mutations:  
Deduplication, somatic and germline variant detection, variant annotation, CNV and SV detection, tumor mutation burden (TMB), waterfall plot, and Circos plot

### Accepted Sample Types

gDNA  
Cells  
Tissue  
FFPE samples & more

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

### Accepted Sample Types

dsDNA  
cDNA  
Cells  
Tissue  
FFPE samples & more

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus  
PacBio Revio



## Metagenomics

Shotgun metagenomic sequencing analyzes microbial DNA contained within a sample, providing in-depth insight into community structure and function across all domains of life. Metagenomics is a powerful lens for viewing the microbial world revolutionizing our understanding across the entire living world.

### Metagenomics Common Applications

- Identify functionally important microbes in the context of human disease
- Analyze microbial community structure at the species and strain-level
- De novo genome assembly and annotation

## Bioinformatics

### Metagenomics

Raw read QC & pre-processing, taxonomic assignment, de novo assembly, binning, alpha/beta diversity analysis, differential abundance analysis, tree visualization

\*Custom analysis available upon request

### Bacterial Isolates Assembly

Read trimming & QC, de novo genome assembly, taxonomic identification using Kraken2/RDP Classifier, multi-locus sequence typing (MLST), pangenome analysis, determination of antimicrobial resistance, virulence gene identification & visualization, plasmid replicon screening, fimH typing, serotyping

### Accepted Sample Types

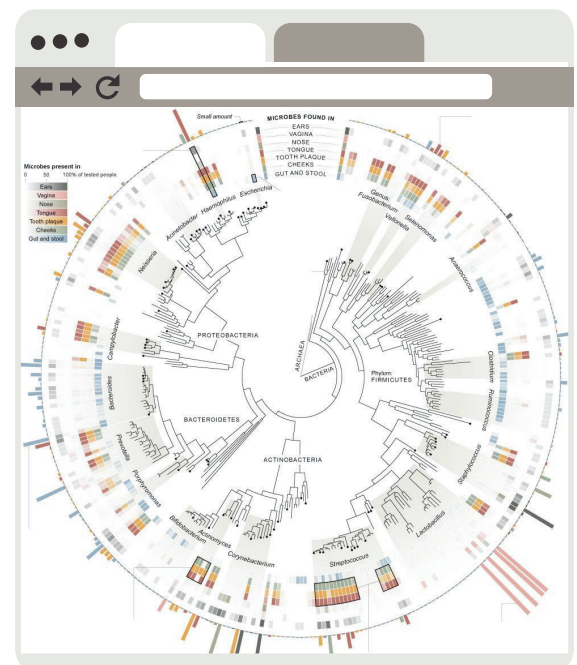
Microbial DNA  
gDNA  
Environmental samples  
FFPE samples

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus  
PacBio Revio





## RNA Sequencing

RNA sequencing (RNA-seq) has become an essential tool to analyze the transcriptome. Bulk mRNA-seq analyzes gene expression levels, identifies alternative splicing, novel isoforms or potential gene fusion events. Bulk total RNA-seq surveys both coding and non-coding RNA. These techniques provide a comprehensive view of the cellular RNA landscape.

### Accepted Sample Types

FFPE samples  
Blood  
Fresh Frozen Tissue  
Total RNA  
Cells (pellet, preserved, & fresh\*)  
\*Please inquire for more details

## RNA-seq Workflows

### **Bulk RNA-seq**

Investigate the transcriptome to quantify protein-coding genes, reveal mRNA splicing, study alternative polyadenylation, and evaluate the regulation of gene expression by non-coding RNAs

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus  
PacBio Revio\*  
*\*see next page*

### **Bioinformatics**

Bulk RNA-seq:

Trimming & QC, STAR mapping, HTSeq Count, Picard QC Analysis, counting/normalization, differential expression (DE) analysis (MA-plot, PCA, sample or gene level heatmaps, volcano plots) & functional enrichment analysis

De novo Transcriptome:

Trimming & QC, Trinity assembly, Trinotate annotation, DE analysis, and GO enrichment analysis

Custom analysis available upon request

### **smRNA-seq**

Analyze the critical regulatory roles of small RNAs in RNA interference (RNAi), cell differentiation, cell proliferation, cell death & embryonic development

### **Bioinformatics**

Trimming and QC, miRNA count & hair-pin structure, counts for: piRNA, tRNA, snoRNA, snRNA, and circRNA, & DE analysis



## RNA-seq Workflows continued

### PacBio Iso-Seq

The Iso-Seq method sequences the entire RNA molecules including untranslated regions, exons, and polyadenylated tails—without fragmentation, and the need for bioinformatics transcript assembly, so you can characterize novel genes and isoforms in bulk and single-cell transcriptomes.

#### Bioinformatics

Generate HiFi reads. Demultiplex samples. Cluster full-length isoforms. Map isoforms to the genome. Classify transcripts as known or novel.

#### Downstream Analysis (optional)

Compare gene and isoform expression, gene set enrichment (GSEA), GO enrichment, or KEGG pathway analysis. Analyze splicing variants.

### Common Applications

- Characterize alternative splicing (AS) events, including alternative start sites, end sites, intron retention, and exon-skipping events
- Detect differentially expressed isoforms and isoform switching events
- Predict functional impact of novel isoforms through open reading frame (ORF) prediction
- Find gene fusions in tumor samples
- Identify allele-specific isoforms

#### Accepted Sample Types

Blood  
Fresh Frozen Tissue  
Total RNA  
Cells (pellet, preserved, & fresh\*)  
\*Please inquire for more details

#### Turnaround Time

20-25 Business Days

#### Sequencing Platforms

PacBio Revio





## RNA-seq Workflows continued

### **circRNA-seq**

Examine circular RNAs impact on the regulation gene expression to characterize immune responses, development, tumorigenesis, and neurogenesis

### **Bioinformatics**

Trimming and QC, STAR mapping, chimeric identification, CIRCexplorer2/3, circRNA detection, circular & linear comparison

### **High-Throughput RNA-seq\*\***

#### **DRUG-seq or BRB-seq**

Rapid, affordable, and comprehensive transcriptome analysis for high-throughput screening, useful for identifying genetic & chemical perturbations in drug discovery

*\*\*Request more information*

## Metatranscriptomics

Shotgun metagenomics and 16S rRNA gene sequencing have broadened our understanding of microbial communities, but distinguishing active from inactive members remains difficult. Metatranscriptomics addresses this by analyzing the community's collective transcriptome, revealing active microbes and their functions, and can be combined with host transcriptomics to explore host-microbe interactions across diverse environments like human, soil, and aquatic systems.

### **Metatranscriptomics Common Applications**

- Explore gene expression community-wide
- Identify active community members and their function

### **Bioinformatics**

De Novo Transcriptome

### Accepted Sample Types

FFPE samples  
Blood  
Fresh Frozen Tissue  
Total RNA  
Cells (pellet, preserved, & fresh\*)  
\*Please inquire for more details

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

### Accepted Sample Types

FFPE samples  
Blood  
Fresh Frozen Tissue  
Total RNA  
Cells (pellet, preserved, & fresh)

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

# Single-Cell Sequencing



## Single-Cell Sequencing

Single-cell sequencing has revolutionized our understanding of cellular heterogeneity by enabling the measurement of DNA, RNA, and proteins at the individual cell level. This powerful approach has unveiled a level of biological complexity previously unattainable. Single-cell RNA-seq (scRNA-seq) has been instrumental in identifying novel cell types, dissecting intricate gene regulatory networks, and illuminating key processes involved in cell development, differentiation, and responses to environmental cues.

To address this, single-cell multiomic technologies integrate multiple data types within a single assay. This integrated analysis provides a more comprehensive view of cell identity and function, revealing the interplay between different molecular layers within individual cells.

### Accepted Sample Types

- Live cells\*
- Cryopreserved Cells\*
- Live Tissue\*
- Cryopreserved Tissue\*
- FFPE samples

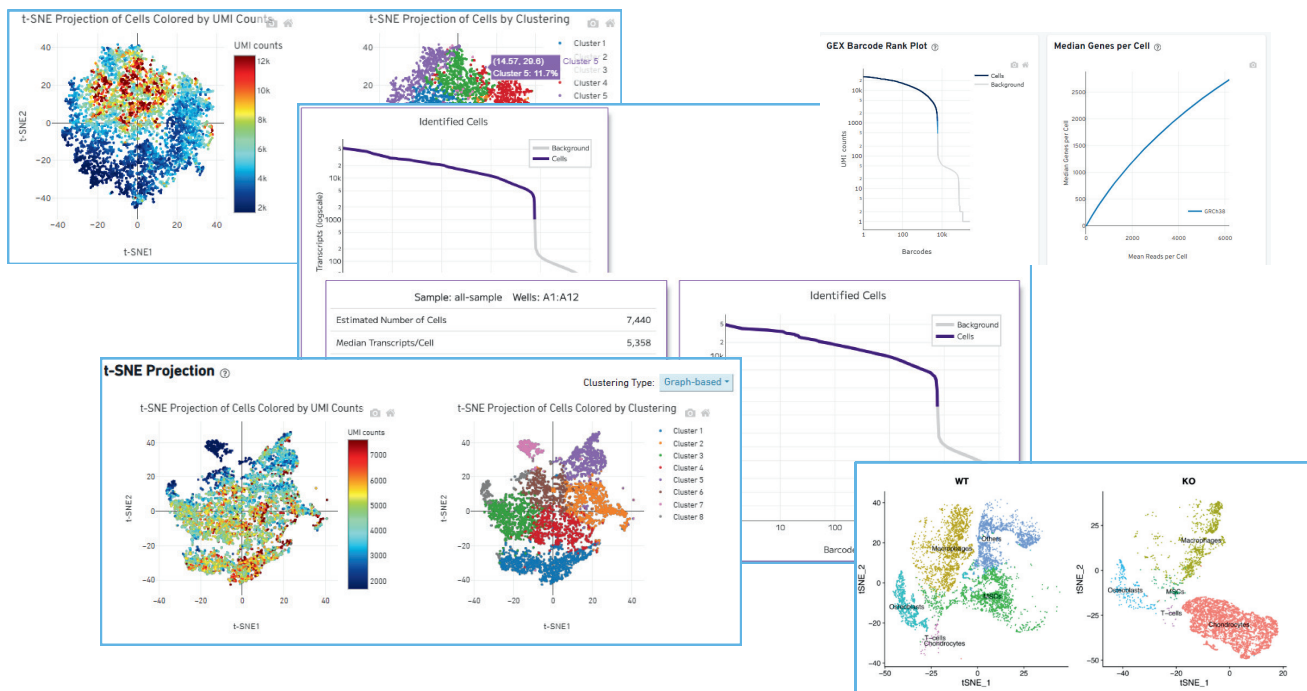
*\*Inquire for more details*

### Turnaround Time

10-15 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus  
PacBio Revio





## scRNA-seq Workflows

### **Whole Transcriptome**

Uncover complete cellular heterogeneity, gene expression, novel targets, and biomarkers from thousands of single cells

### **Whole Transcriptome with Fixed Samples**

Fix, batch, and run samples later for unsurpassed workflow flexibility and affordability to reveal crucial insights at the single-cell level, even from FFPE samples

### **Immune Profiling**

A multiomic solution to simultaneously analyze cell surface protein expression, antigen specificity, and CRISPR edits with 5' gene expression

### **Multiome**

Explore gene expression and chromatin accessibility simultaneously, to discover complex gene regulatory mechanisms and characterize novel cell types

### **CRISPR Screening**

Gather scalable, in-depth readouts of specific CRISPR-driven gene edits or knockdowns to investigate the intricate biology of gene function, development, disease status, & therapeutic responses of individual cells

### **Bioinformatic Analysis**

Explore cellular heterogeneity with plots and visual identification, differential expression analysis, visualization of gene expression patterns, infer cell-cell communication networks, understand or infer ordering of cells along a path

### **Bioinformatic Analysis**

V(D)J counts, clonotype frequency, visualization of immune repertoire and cellular landscape

### **Bioinformatic Analysis**

Identify genes with significant expression differences between cell clusters or conditions, obtain accurate chromatin accessibility profiles, identifying regions of open chromatin, identify cells with both high-quality RNA and ATAC data, identify distinct cell populations

### **Bioinformatic Analysis**

Counting sgRNA in each cell, visualize the statistical significance and magnitude of gene expression changes associated with each sgRNA, gain insights into the functional consequences of gene knockouts or activations

# Single-Cell Sequencing



## scRNA-seq Workflows continued

### PacBio Single-Cell Sequencing

Understanding cell heterogeneity at the isoform level is critical for basic and disease research. Short reads can only capture gene-level information, while other long-read technologies lack the accuracy for accurate UMI/barcode identification. HiFi reads can provide accurate detection of isoforms in your single-cell study: move from gene counting to full-length isoform information, and reveal cell type-specific spliced isoforms and expressed variants

#### Bioinformatic Analysis

Generate HiFi reads. De-concatenate reads. Map reads and classify transcripts. Produce Seurat-ready output.

QC and clustering. Cell type annotation. Differential expression. GSEA, GO, and other enrichment analyses.

#### Accepted Sample Types

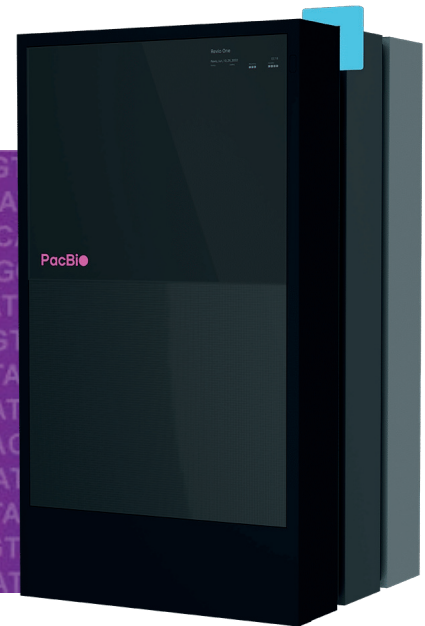
- Live cells\*
  - Cryopreserved Cells\*
  - Live Tissue\*
  - Cryopreserved Tissue\*
  - Single-cell cDNA libraries\*
- \*Inquire for more details*

#### Turnaround Time

20-25 Business Days

#### Sequencing Platforms

PacBio Revio

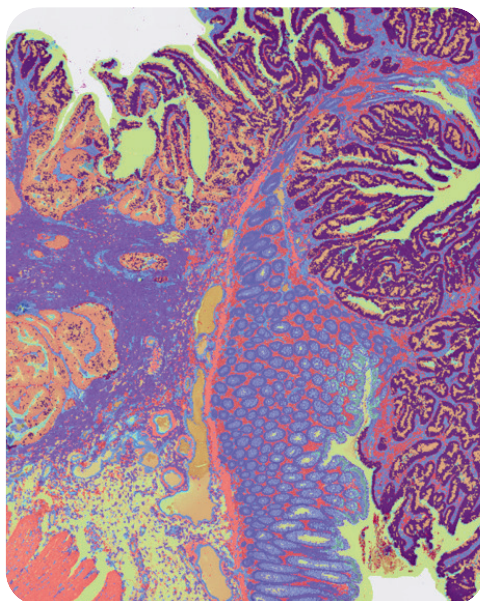




## Spatial Transcriptomics

Spatial transcriptomics adds a crucial layer of information. While single-cell sequencing reveals the diversity of cell types and gene expression within a tissue, spatial transcriptomics maps where those diverse cells are located and how their gene expression varies across space.

Spatial transcriptomics allows researchers to see not just what cell types exist, but also how they are organized and how their gene expression is influenced by their spatial context and neighboring cells. This is powerful when combined with single-cell data, allowing researchers to place the detailed molecular information obtained from single cells within the broader tissue architecture.



### Accepted Sample Types

Fresh Frozen  
FFPE

### Turnaround Time

25-30 business days

### Sequencing Platforms

Illumina NovaSeq X Plus  
Other\*

*\*Inquire for more details*

## Common Applications

- Identify spatially restricted gene expression signatures associated with disease or treatment response
- Map gene expression patterns across tissue sections to understand tissue architecture and function
- Investigate the spatial context of tumor development, progression, and metastasis
- Discover new cell populations for potential biomarkers and complex cell-to-cell interactions
- Visualize the spatial distribution of drug targets within tissues to guide the development of targeted therapies



## Spatial Transcriptomics Platforms

### 10x Genomics Visium HD

Whole transcriptome spatial gene expression with single-cell scale resolution from fresh frozen, PFA-fixed frozen tissue.

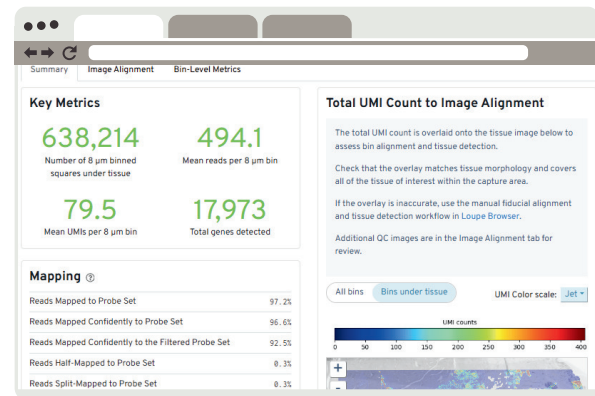
#### Bioinformatics

Space Ranger & Loupe Browser: QC & metrics statistics, Mapping, Tissue/Cell segmentation, Spatial UMAP & tissue clustering, Violin plots for gene & MID

#### Optional Analysis:

Single-Cell RNA-seq related analysis

Customized requests



### Stereo-seq & Stereo-seq OMNI

Stereo-seq: For fresh-frozen tissue, species-agnostic workflow achieves ultra-high-resolution for unprecedented field-of-view (up to 2cm x 3cm), cellular, subcellular, and molecular level analysis

Stereo-seq OMNI: Use precise Stereo-seq technology compatible with FFPE samples

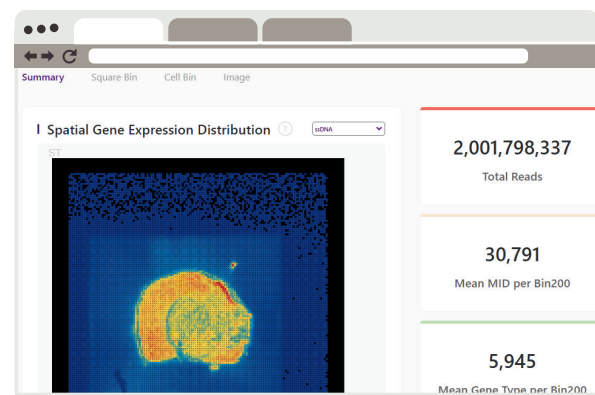
#### Bioinformatics

Stereo-seq Analysis Workflow (SAW): QC & metrics statistics, Mapping, Tissue/Cell segmentation, Spatial UMAP & tissue clustering, Violin plots for gene & MID

#### Optional Analysis:

Single-Cell RNA-seq related analysis

Customized requests





## Amplicon Sequencing

Amplicon sequencing is a highly targeted method for studying genetic variation in specific regions of the genome. The amplicons are generated by PCR, pooled, and sequenced. The sequencing data provides researchers targeted insights with low-level inputs. This approach is particularly useful for applications like identifying specific mutations, analyzing highly variable regions, and detecting rare variants within a complex sample.

## 16S & ITS rRNA Sequencing

Amplicon sequencing using universal primers targeting the 16S ribosomal RNA (rRNA) gene or the internal transcribed spacer region (ITS) of the nuclear rRNA operon, are marker-gene based approaches to profile bacteria/archaea or fungi in samples, respectively. These approaches offer cost-effective methods to analyze community composition, be it human-associated microbiomes, environmental samples, or for understanding fungi's role in nutrient cycling, identification of pathogens, and carbon cycling.

### Bioinformatics

Demultiplexing, DADA2 or deblur analysis, taxonomic assignment, alpha/beta diversity analysis, clustering & visualization

### Accepted Sample Types

gDNA	Blood
Amplicon	FFPE
Cell pellet	Tissue
Environmental Samples	

### Turnaround Time

10-15 Business Days  
Expedited Service Available

### Sequencing Platforms

Illumina Miseq i100  
NextSeq 1000/2000  
NovaSeq X Plus  
PacBio Revio



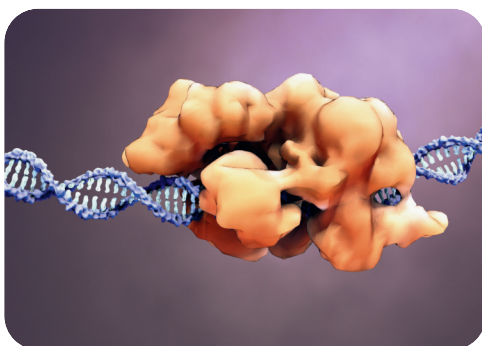
## CRISPR Screening

CRISPR (clustered regularly interspaced short palindromic repeats) screening makes use of the robust CRISPR-Cas genome editing system to identify genes or pathways involved with diverse phenotypes or biological process. It has been widely used including drug discovery to identify targets that either confer sensitivity or resistance to a drug, determine susceptibility to a disease state, discovery of components involved with cellular signaling, and more.

Admera takes this technology a step further. We offer expertly customized CRISPR screening services, tailored to your unique research goals. Our experienced team can design and execute complex screens that go beyond standard offerings, providing insights that are often unattainable with off-the-shelf solutions.

## Common Applications

- Identify genes fundamental to various cellular processes, either targeted or genome-wide
- Explore cancer-specific essential genes for drug development or drug sensitivity/resistance studies



### Bioinformatics

#### CRISPR screening

QC, count table, MAGeCK pair comparison, gene set enrichment (GSEA) analysis

#### CRISPR edit

QC, mapping, indel calling

*\*Custom Analysis available upon request*

### Accepted Sample Types

Amplicons	Tissue
Plasmids	gDNA
Cell Pellet	

### Turnaround Time

5-7 Business Days  
Expedited Service Available

### Sequencing Platforms

Illumina Miseq i100  
NextSeq 1000/2000  
NovaSeq X Plus

# Amplicon Sequencing



## Long-read Amplicon seq

Designed to generate high-accuracy, long-read sequences of targeted genomic regions. HiFi sequencing can span the amplicon in a single read, giving unambiguous haplotype resolution through direct phasing. HiFi amplicon sequencing replaces multiple assays with one fast, easy, scalable, and economical workflow.

Start with high-quality DNA, as low as 50 ng for small amplicons, from 500 bp to kilobase scale. Multiplexing up to 384 samples, and sequence to desired coverage based on project needs.

### Common Applications

- Microbial profiling, HLA typing, and variant detection (from single nucleotide variants and indels, to structural variants).

### Accepted Sample Types

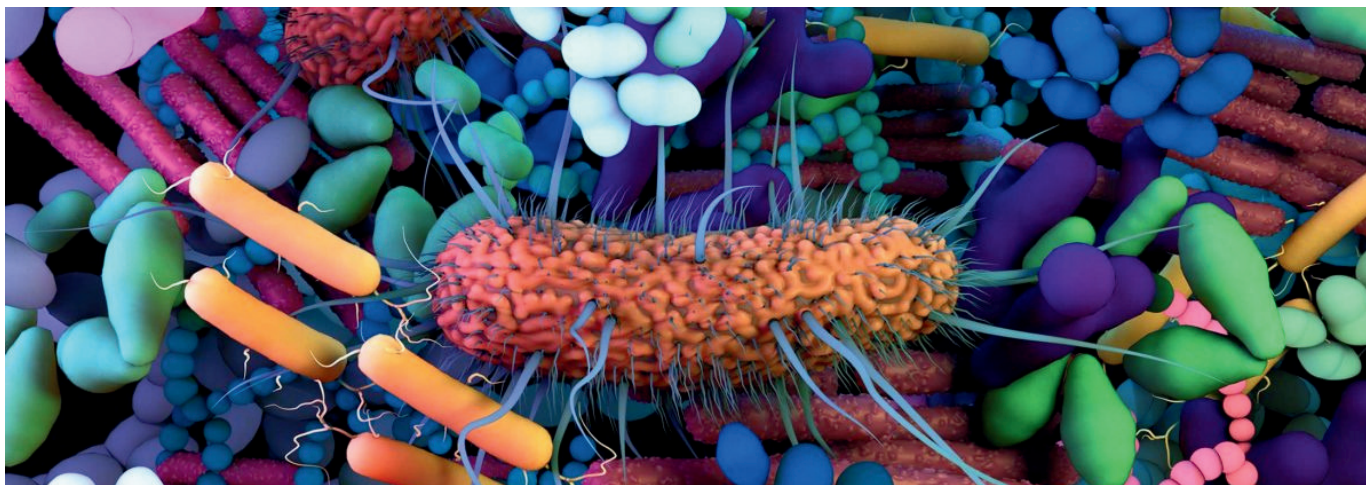
gDNA	FFPE
Amplicon	Environmental samples
Cell pellet	
Blood	
Tissue	

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

PacBio Revio





## Epigenomics

The epigenome plays an important role in gene expression and development of many organisms, providing heritable genomic information outside the DNA sequence, which can be influenced by the environment. The primary epigenomic mechanisms under study include chromatin accessibility, DNA methylation, histone modifications, and nuclear organization .

## WGBS & EM-seq

Whole-genome bisulfite sequencing (WGBS) is the gold-standard method for profiling the DNA methylome at single-nucleotide resolution, enabling the study of gene regulation, aberrant methylation, and embryonic development. Enzymatic methyl-seq (EM-seq) offers an alternative approach, directly detecting methylation patterns without chemical conversion, generating more accurate and unbiased data with higher coverage and less GC content bias.

## Bioinformatics

Preliminary QC, trimming, mapping & methylation calling, bisulfite conversion efficiency, differential methylation analysis (identifying DMR/DMS), annotation, clustering, pathway analysis (GO/KEGG) and visualization

### Accepted Sample Types

FFPE samples	Tissue
Blood	Cells
gDNA	Cell-free DNA

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina Platforms  
PacBio Revio  
Other\*

*\*Inquire for more details*



## Targeted Methyl-seq

Targeted methyl-seq uses hybridization probes to capture and enrich biologically relevant methylated regions within the genome. The targeted nature of this approach reduces sequencing costs and enhances overall coverage depth. Targeted methyl-seq is compatible over a range of input quantities and is highly correlated to WGBS.

### Bioinformatics

Preliminary QC, trimming, mapping & methylation calling, bisulfite conversion efficiency, differential methylation analysis (identifying DMR/DMS), annotation, clustering, pathway analysis (GO/KEGG) and visualization

## RRBS

Reduced representation bisulfite sequencing (RRBS) is a more cost-efficient alternative to WGBS, using methylation-sensitive restriction enzymes to limit sequencing to approximately 20% the genome with high CpG content.

### Bioinformatics

Preliminary QC, trimming, mapping & methylation calling, bisulfite conversion efficiency, differential methylation analysis (identifying DMR/DMS), annotation, clustering, pathway analysis (GO/KEGG) and visualization

### Accepted Sample Types

FFPE samples  
Blood  
gDNA  
Cell-free DNA  
Tissue  
Cells

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

### Accepted Sample Types

gDNA  
Tissue  
Blood

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus



## ChIP-seq

Chromatin immunoprecipitation followed by sequencing (ChIP-seq) is an epigenome-wide approach to investigate histone modifications and chromatin structure, using target specific antibodies to study DNA-protein binding sites without prior knowledge. This is a well-established experimental technique to identify DNA-protein interactions.

### Bioinformatics

Preliminary QC and trimming, genome alignment, duplicate removal, alignment QC, normalization, annotation, enrichment analysis, peak calling & QC, clustering, differential analysis, functional analysis, combined density profile analysis and motif analysis

## CUT&RUN

CUT&RUN (Cleavage Under Targets and Release Using Nuclease) is an epigenomic method using antibodies to target specific protein-DNA complexes and a recombinant micrococcal nuclease to cleave at various chromatin sites at high resolution. CUT&RUN offers advantages like lower cell requirement, reduced sequencing costs, and often delivers data with clearer signal compared to background noise.

### Bioinformatics

Preliminary QC and trimming, genome alignment, duplicate removal, alignment QC, normalization, annotation, enrichment analysis, peak calling & QC, clustering, differential analysis, functional analysis, combined density profile analysis and motif analysis

### Accepted Sample Types

Immunoprecipitated DNA

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

### Accepted Sample Types

Cells  
Tissue\*  
*\*Per request*

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus



## ATAC-seq

The assay for transposase accessible chromatin with sequencing (ATAC-seq) uses an engineered hyperactive Tn5 transposase to cleave open chromatin sites and ligate sequence adapters (tagmentation) to investigate chromatin accessibility, transcription factor binding sites, gene regulation, and more.

### Bioinformatics

Preliminary QC and trimming, genome alignment, duplicate removal, alignment QC, normalization, annotation, enrichment analysis, peak calling & QC, clustering, differential analysis, functional analysis, combined density profile analysis and motif analysis

## Hi-C Assay

The three-dimensional (3D) architecture of the genome, a complex web of folds and compacted DNA, plays an important role in cell differentiation, gene expression, and disease progression. Hi-C is a genome-wide chromatin conformation capture (3C) assay that examines this structure at multiple scales, supplying long-range information of loci pairs megabases apart, but on the same chromosome.

### Bioinformatics

Standard: QC, Alignment (Juicer), Contact statistics, and Contact domains  
Optional Analysis:  
Chromatin Loop Detection and Scaffolding analysis

### Accepted Sample Types

Cells  
Transposed DNA

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus

### Accepted Sample Types

Cells  
Transposed DNA

### Turnaround Time

20-25 Business Days

### Sequencing Platforms

Illumina NovaSeq X Plus



## High-Throughput Premade Library Sequencing

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 and pre-pooled libraries. We also offer customized sequencing runs to meet your specific needs.

Upon receipt of your samples, we perform comprehensive quality control steps that are detailed in reports and sent to you within 24 hours. Admera's library QC utilizes Qubit® (Invitrogen), TapeStation (Agilent), Femto Pulse (Agilent), and qPCR (Applied Biosystems) instrumentation to provide accurate quantification prior to sequencing.

### Accepted Libraries

Individual Libraries  
Pre-pooled Libraries  
Customized Libraries

### Turnaround Time

5-10 business days  
\*Expedited Services Available

### Deliverables

Library QC report  
FASTQ files  
BCL files  
\*other file formats available

## Sequencing Platforms

- > NovaSeq X Plus
- > MiSeq i100
- > NovaSeq 6000
- > NextSeq 1000/2000
- > PacBio Revio





## Bioinformatic Analysis Solutions

Our team of highly experienced bioinformaticians provides comprehensive analysis solutions, designed to empower researchers across diverse scientific disciplines. We go beyond basic data processing, delivering ready-to-interpret reports and offering expert collaborative support to ensure your research objectives are met. From customized pipeline development to in-depth data interpretation, Admera Health provides the expertise needed to maximize the impact of your sequencing data.



### Genomic Analysis

- Whole Genome Sequencing (WGS)
- Bacterial Isolates Assembly
- Whole Exome Sequencing (Hybrid-Capture)
- Hybrid-Capture NGS Assay (including custom gene panels)
- Targeted Sequencing
- De novo Assembly Analysis (i.e. without Reference Genome)
- Long-read Whole Genome Sequencing



### Transcriptomic Analysis

- Bulk RNA-seq
- small RNA-seq (smRNA)/micro RNA-seq (miRNA)
- De novo Transcriptome Analysis
- Iso-Seq



### Epigenomic Analysis

- Whole Genome Bisulfite Sequencing (WGBS)
- Reduced Representation Bisulfite
- Targeted Methylation sequencing
- ATAC-seq
- ChIP-seq
- CUT&RUN
- Hi-C Assay



## Bioinformatic Analysis



### Single-Cell Analysis

- Single-cell RNA-seq
- Single-cell Immune Profiling (VDJ)
- Single Cell ATAC-seq
- CRISPR Screening
- Long-read Single-cell RNA-seq



### Spatial Transcriptomics Analysis

- 10x Genomics Visium HD
- STOmics StereoSeq



### Microbiome Analysis

- 16s rRNA Sequencing
- ITS Sequencing
- Metagenomics
- Metatranscriptomics



### Sequencing-Only

- Short read sequencing data analysis
- Long read sequencing data analysis
- Flexible and customizable options available



### Customized Analysis

We would love to hear about your research so our expert team of scientists can build a pipeline to meet your goals



## Superior Nucleic Acid Extraction Solutions with EchoLUTION™

Admera Health and BioEcho partner to deliver superior NGS support. Combining Admera Health's expertise working with complex samples and BioEcho's advanced EchoLUTION™ technology, researchers benefit with superior results & quality deliverables.

Innovative EchoLUTION™ technology simplifies nucleic acid extraction and overcomes the limitations of conventional methods, resulting in higher yields, efficiency, and downstream results to support diverse research applications.

### Discover the Power of EchoLUTION™



#### Increased Yield & Purity

Highly pure nucleic acids free of inhibitors



#### Quick & Efficient Workflows

Up to 3x faster protocol than conventional methods with single-step purification & one-minute centrifugation



#### Top-tier Results For a Wide Range of Research

Generate diverse populations of nucleic acids to support flexible downstream applications



#### Maximize Sustainability

Up to 70% less plastic consumption with plastic-free packaging & no ecologically hazardous reagents

### What Customers Say



#### University of Southern Denmark

The EchoLUTION™ 96-well plates for RNA purification has been a great addition to our high-throughput screening assays.

The quality of the eluted RNA is very high, and the extraction process is fast and very efficient. By downscaling our transfection reagents and other consumables.



#### Environment and Plant Protection Institute, Chinese Academy of Tropical Agricultural Sciences

We compared the EchoLUTION™ Plant DNA Kit with our established silica-technology based kit. Using the BioEcho kit, we obtained genomics DNA in high yields much faster and easier than before. We were impressed with the simplicity of the whole process.



# Nucleic Acid Extraction



## EchoLUTION™ Cell Culture RNA Kit

The EchoLUTION™ Cell Culture RNA Kit was developed for efficient RNA extraction from human and animal cultured cells. Our EchoLUTION™ technology allows extraction of nucleic acids in a single step after an ultra-fast sample lysis. This revolutionary method purifies RNA with high yield and quality. The isolated total RNA is ready-to-use in standard downstream applications such as RT-PCR, RT-qPCR, and RNAseq, among others. The product delivers dedicated solutions to anyone committed to drug discovery, sequencing, and/or basic research, such as oncology, immunology, and transcriptomics.



### Speed & Convenience

Ultra-fast lysis combined with the single-step purification leading to a protocol 50-70% faster with fewer hands-on steps than established kits on the market



### High Sensitivity, Increased Yield

Highly pure RNA free of contaminants and inhibitors



### Reliable Results

Premium quality RNA perfectly suited for downstream applications such as RT-PCR, RT-qPCR, RNAseq, and others



## Ordering Information

Ordering questions: [products@admerahealth.com](mailto:products@admerahealth.com)

Product	Quantity	Product no.
EchoLUTION™ Cell Culture RNA Kit (10)	10	011-014-010
EchoLUTION™ Cell Culture RNA Kit (50)	50	011-014-050
EchoLUTION™ Cell Culture RNA Kit (2 x 96)	2 x 96	011-114-002
EchoLUTION™ Cell Culture RNA Kit (8 x 96)	8 x 96	011-114-008
EchoLUTION™ Cell Culture RNA Kit (2 x 384)	2 x 384	011-314-002
EchoLUTION™ Cell Culture RNA Kit (8 x 384)	8 x 384	011-314-008
gDNA Removal Mix*	10	011-901-010
	50	011-901-050
	2 x 96	011-901-002
	8 x 96	011-901-008
Conditioning Plates 96 (2 plates)	2 plates	060-001-002
Conditioning Plates (8 plates)	8 plates	060-001-008
Conditioning Plates (2 plates)	2 plates	060-006-002
Conditioning plates (8 plates)	8 plates	060-006-008

\*Lysis and Sealing Foils components can be purchased separately. Inquire for more details.

# Nucleic Acid Extraction



## EchoLUTION™ FFPE RNA Kit

FFPE tissue analysis is crucial for disease research, but current RNA extraction methods are often slow, cumbersome, and involve hazardous chemicals, hindering research progress.

The EchoLUTION™ FFPE RNA Kit simplifies RNA extraction with a streamlined workflow. This kit enables efficient RNA isolation suitable for downstream applications like RT-qPCR and RNA-seq, delivering high-quality results with increased unique mappers and gene counts.

EchoLUTION™ technology streamlines the process by eliminating lengthy incubations and enabling single-step RNA extraction after decrosslinking and paraffin removal. By utilizing this advanced technology, researchers can achieve superior results and high-quality deliverables.



### Speed

Optimized tissue lysis combined with single-step purification leads to a 30% faster protocol than with competing kits



### High Sensitivity, Increased Yield

High purity RNA free of contaminants and inhibitors



### Reliable Results

High purity and competitive RNA integrity perfectly suited for downstream applications such as RT-qPCR, and RNA-seq



## Ordering Information

Ordering questions: [products@admerahealth.com](mailto:products@admerahealth.com)

Product	Quantity	Product no.
EchoLUTION™ FFPE RNA Kit (10)	10 rxn	011-005-010
EchoLUTION™ FFPE RNA Kit (50)	50 rxn	011-005-050
BioEcho Cap Puncher*	1 Piece	050-001-001

\*Optional, for convenient handling of spin columns

# Nucleic Acid Extraction



## EchoLUTION™ Plant DNA Kit

The EchoLUTION™ Plant DNA Kit delivers pure genomic DNA with minimal inhibitors, enabling high yields from various plant species and tissues (leaves, seeds, roots) within 1.5 hours. The EchoLUTION™ Plant DNA Kit delivers superior results to support downstream applications including high-throughput sequencing for KASP and low-pass WGS.



### Speed & Convenience

Single-step purification allows complete extraction of 96 samples within 1.5 hours



### High Compatibility

Suitable for a wide range of plant species such as strawberry, parsley, tomato, potato, wheat, barley, and many others



### Increased Yield & Purity

Extract highly pure nucleic acids free of inhibitors and contaminants



## Ordering Information

Ordering questions: [products@admerahealth.com](mailto:products@admerahealth.com)

Product	Quantity	Product no.
EchoLUTION™ Plant DNA Kit (10)	10	010-003-010
EchoLUTION™ Plant DNA Kit (50)	50	010-003-050
EchoLUTION™ Plant DNA Kit (2 x 96)	2 x 96	010-103-002
EchoLUTION™ Plant DNA Kit (8 x 96)	8 x 96	010-103-008
EchoLUTION™ Plant DNA Kit (2 x 384)	2 x 384	010-303-002
EchoLUTION™ Plant DNA Kit (8 x 384)	8 x 384	010-303-008
Tube & Cap Strips (8 racks of 96)*	8 racks of 96	060-002-008
Lysis Plate 96, Type 1 ( 8 plates)*	8 plates	060-003-008
Conditioning Plate 96 (2 plates)**	2 plates	060-001-002
Conditioning Plate 96 (8 plates)**	8 plates	060-001-008
Conditioning Plate 384 (2 plates)**	2 plates	060-006-002
Conditioning Plate 384 (8 plates)**	8 plates	060-006-008

\* Tube & Cap Strips and Lysis Plate 96 (Type 1) are not included in the kit. These components can be purchased separately.

\*\*For sustainability reasons, Conditioning Plates are not included in our kits. These plates are reusable and can be purchased separately.



*Welcome To The  
Advanced Molecular Era*

# Comprehensive solutions from extraction to analysis

Transcriptomics | Single-cell | Spatial Biology | WGS/WES |  
Epigenomics | Premade Library Sequencing | Bioinformatics

[www.admerahealth.com](http://www.admerahealth.com)  
126 Corporate Blvd  
South Plainfield, New Jersey 08820  
United States  
(908)-222-0533  
[custom-services@admerahealth.com](mailto:custom-services@admerahealth.com)  
CLIA ID: 31D2038676  
© 2026 Admera Health. All rights reserved.

