BIO ECHO

An admera Company

Product Catalog

Reveal the Unseen.
Echoing True Biology.

BioEcho Life Sciences GmbH
Biocampus Cologne E04, 5th Floor
Nattermannallee 1
50829 Cologne
Germany
contact@bioecho.de
www.bioecho.com

Discover EchoLUTION™

WELCOME TO BIOECHO LIFE SCIENCES, AN ADMERA COMPANY

We're thrilled to share our innovations in nucleic acid purification with you. Inside this catalog, you'll discover how our enablement technology helps you achieve Nucleic Acids As Nature Intended, simplifying discovery and accelerating research.

By setting new standards for quality in life science, we're committed to empowering scientists like you to achieve truly transformative & breakthrough results, ultimately Echoing True Biology.

Joining forces with our parent company, Admera Health, and advanced next-generation sequencing & multiomics provider, BioEcho preserves the integrrity of your nucleic acids to enhance diverse downstream applications, including NGS.

EchoLUTION™ Supports Diverse Research Areas

- Infectious Disease
- Agricultural Biotechnology
- Biopharmaceutical Research & Development
- Academic Research

Contact Us:
contact@bioecho.de
www.bioecho.com

BIO ECHO
An admera Company

Reveal the Unseen.
Echoing True Biology.

BioEcho Life Sciences specializes in advanced nucleic acid purification and analysis. Founded in Cologne, Germany (2016), our molecular biology experts are dedicated to minimizing nucleic acid loss. Our innovative EchoLUTION™ technology dramatically enhances recovery, yielding more reliable results with speed and convenience. EchoLUTION™ enables rapid, single-step DNA/RNA extraction, reducing plastic use significantly.

Now part of Admera Health, our focus on maximizing nucleic acid capture is amplified by their extensive research services.

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 similicity of the whole process.

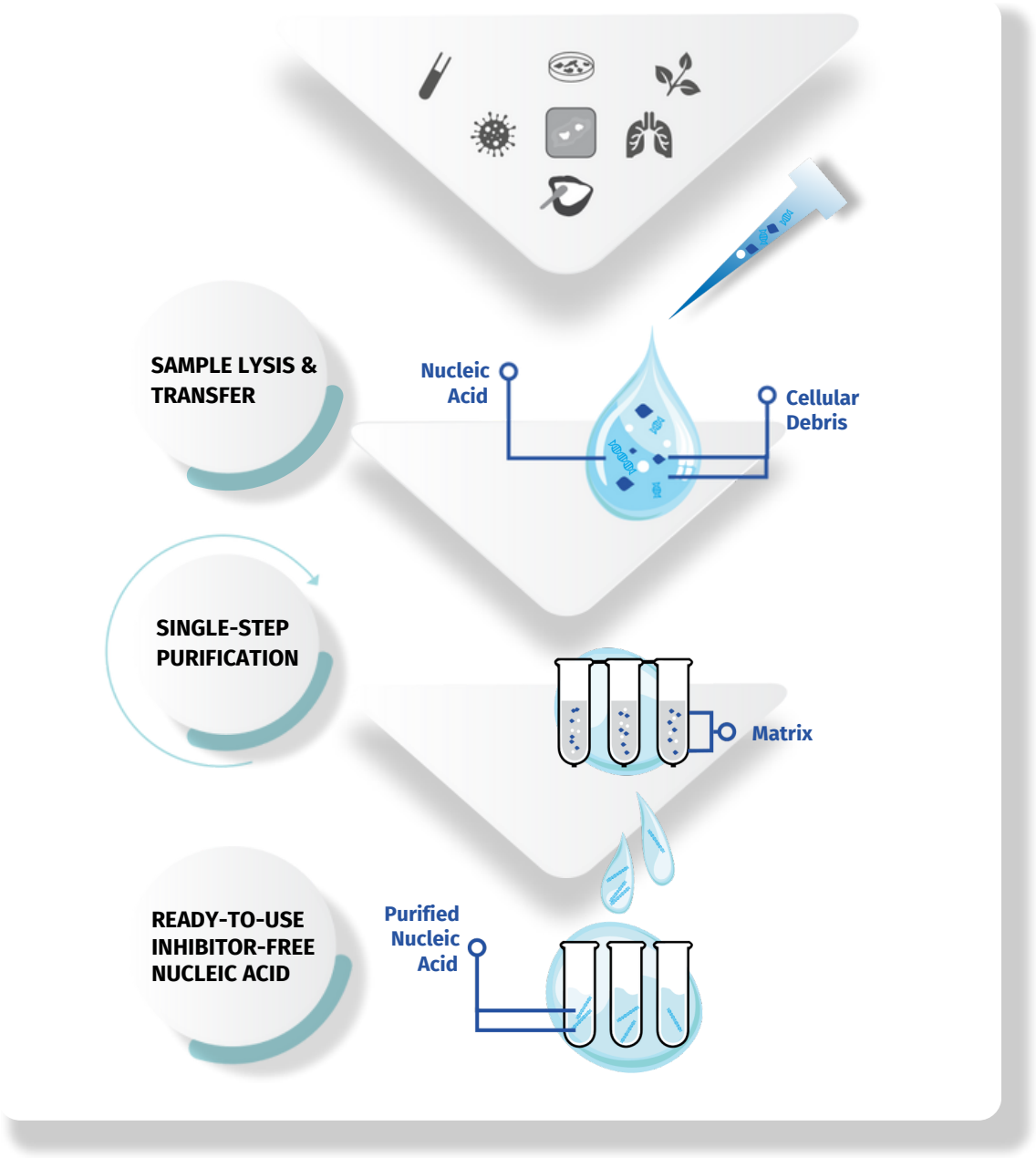
contact@bioecho.de
www.bioecho.com

Table of Contents

Technology

OUR GENTLE EchoLUTION™ TECHNOLOGY goes beyond simple extraction, preserving the natural state and integrity of your nucleic acids.

By echoing true biology, this innovative approach delivers pristine, high-quality material, allowing you to experience the clarity of unaltered biology from cell to insight, ensuring reliable and accurate results for all your downstream applications.



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 RNA-seq, 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: orders@bioecho.de

Product	Quantity	Product no.
EchoLUTION™ Cell Culture RNA Kit (50) EchoLUTION™ Cell Culture RNA Kit (250)	50 250	011-014-050 011-014-250
EchoLUTION™ Cell Culture RNA Kit (2 x 96) EchoLUTION™ Cell Culture RNA Kit (8 x 96)	2 x 96 8 x 96	011-114-002 011-114-008
EchoLUTION™ Cell Culture RNA Kit (2 x 384) EchoLUTION™ Cell Culture RNA Kit (8 x 384)	2 x 384 8 x 384	011-314-002 011-314-008
gDNA Removal Mix*	50 250 2 x 96 8 x 96	011-901-050 011-901-250 011-901-002 011-901-008
Conditioning Plates 96 (2 plates) Conditioning Plates (8 plates) Conditioning Plates (2 plates) Conditioning plates (8 plates)	2 plates 8 plates 2 plates 8 plates	060-001-002 060-001-008 060-006-002 060-006-008

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 from FFPE tissues 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: orders@bioecho.de

Product	Quantity	Product no.
EchoLUTION™ FFPE RNA Kit (10) EchoLUTION™ FFPE RNA Kit (50) EchoLUTION™ FFPE RNA Kit (250)	10 rxn 50 rxn 250 rxn	011-005-010 011-005-050 011-005-250
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: orders@bioecho.de

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 (250)	250	010-003-250
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
Steel Beads, 4 mm (2,000 beads)*	2,000 beads	050-006-002
Steel Beads, 4 mm (10,000 beads)*	10,000 beads	050-006-010
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

*Steel beads, Tubes & Cap Strips, and Lysis Plate 96, Type 1 are not included in the kit. These components are used for sample homogenization and can be purchased separately.
** For sustainability, reasons, Conditioning Plates are not included in our kits. These plates are reusable and can be purchased separately.

Advanced Genomic & Bioinformatic Research Services in a clinical 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 clinical lab environment (CLIA/CLEP certified and CAP accredited) 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

custom-services@admerahealth.com www.admerahealth.com

What Our Customers Say

Cell Signaling in Metabolism
Johns Hopkins All Children's Hospital

"I have worked with Admera since 2019. [Admera Health] is reliable and very professional. I always recommend Admera H. to my coworkers in Colombia, Peru, Bolivia, and USA"

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."

admera health

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.

Our Certified Partnerships

10x GENOMICS

IDT INTEGRATED DNA TECHNOLOGIES

NEW ENGLAND Biolabs®

PARSE BIOSCIENCES

Singleron

STOmics

TWIST BIOSCIENCE

Genomics

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
cFDNA
Cells
Tissue
FFPE samples
& more

Turnaround Time

10-15 Business Days

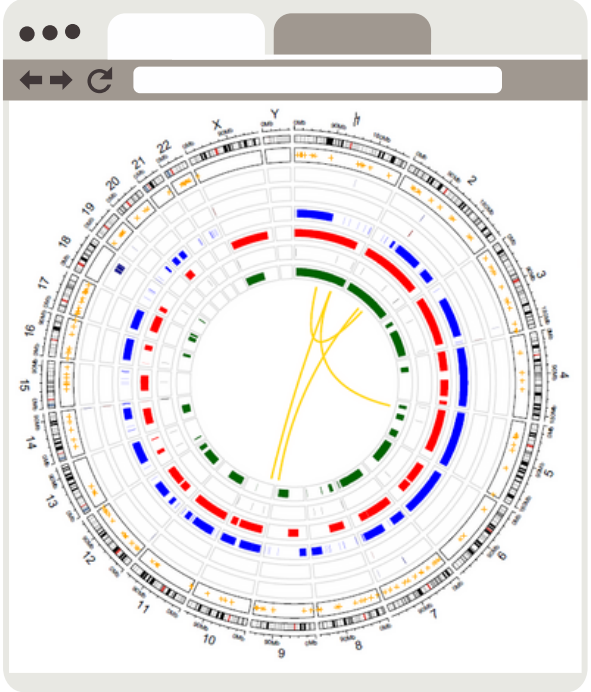
Sequencing Platforms

Illumina NovaSeq X Plus

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



Genomics

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*

Genomics

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

Accepted Sample Types

gDNA
Cells
Tissue
FFPE samples & more

Turnaround Time

10-15 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

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 our customers 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

dsDNA
cDNA
Cells
Tissue
FFPE samples & more

Turnaround Time

10-15 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

Genomics

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

Accepted Sample Types

Microbial DNA
gDNA
Environmental samples
FFPE samples

Turnaround Time

10-15 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

Bioinformatics

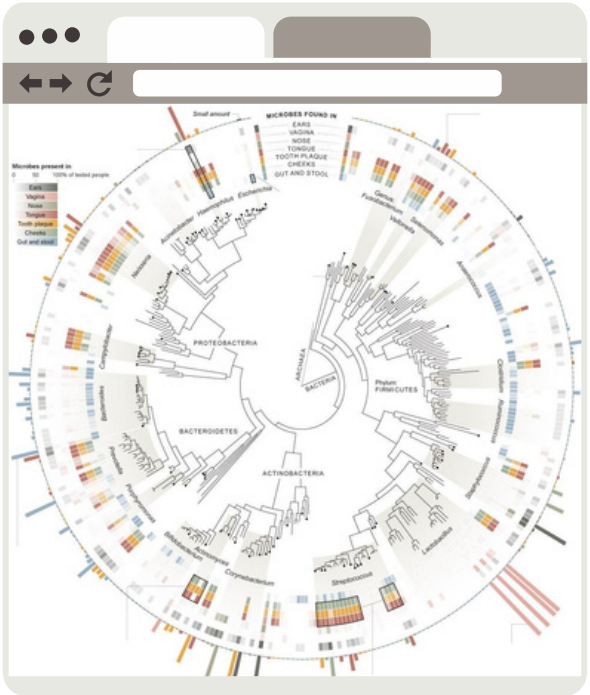
Metagenomics

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



Transcriptomics

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

Turnaround Time

10-15 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

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

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

Transcriptomics

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

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

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
TotalRNA
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

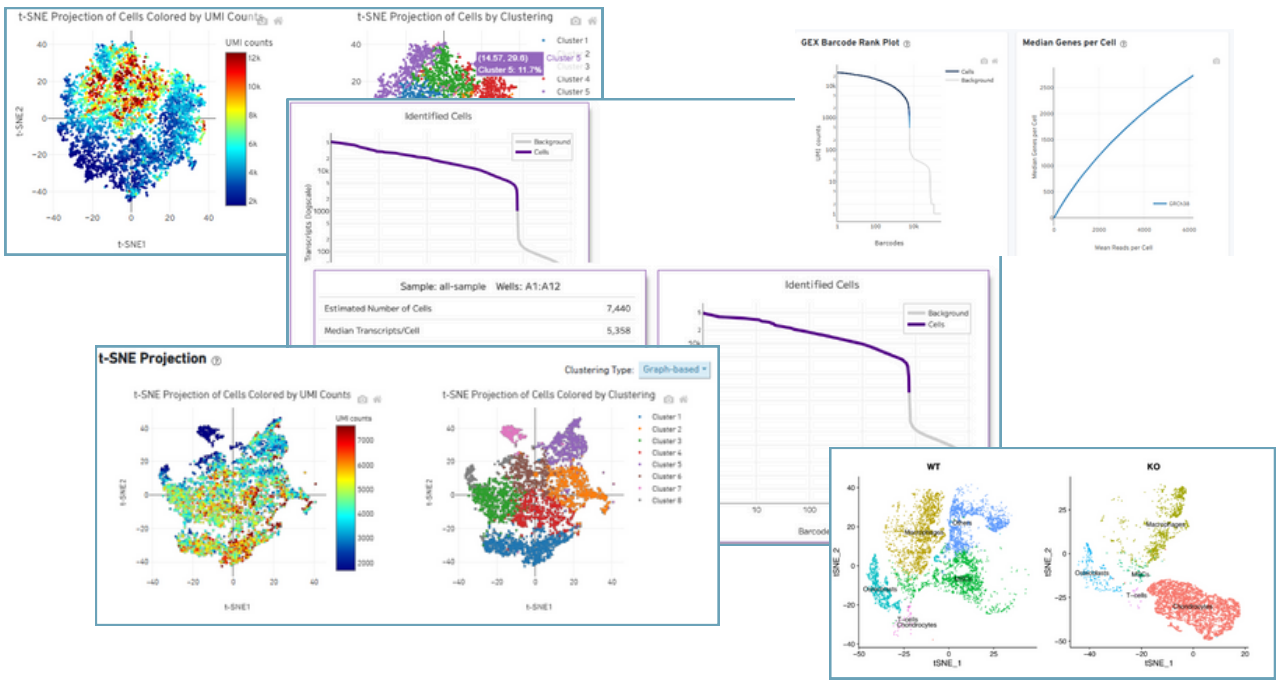
Live cells*
Cryopreserved Cells*
Live Tissue*
Cryopreserved Tissue*
FFPE samples
**Inquire for more details*

Turnaround Time

10-15 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus



Single-Cell Sequencing

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

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

---

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

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

---

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

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

---

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
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

Spatial Transcriptomics

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

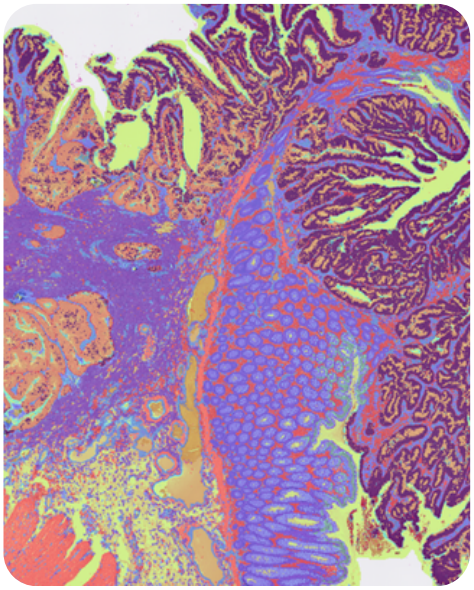
Fresh Frozen
FFPE

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

Spatial Transcriptomics Platforms

10x Genomics Visium HD

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

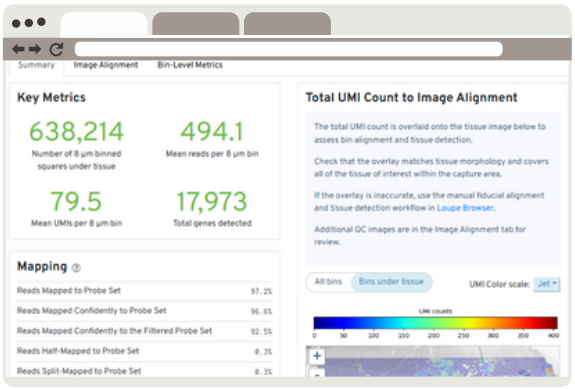
Bioinformatics

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

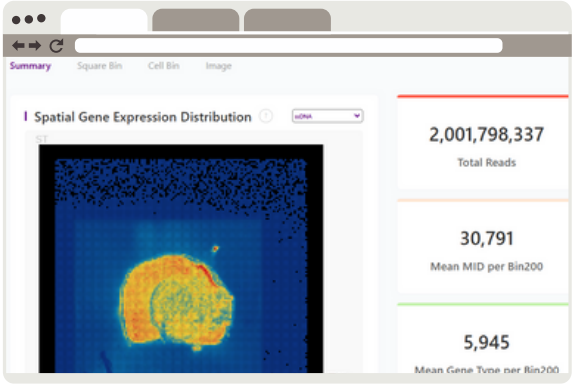
Bioinformatics

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

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 rRNA Gene & ITS 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 Platforms
Other*
**Inquire for more details*

Amplicon Sequencing

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

Accepted Sample Types

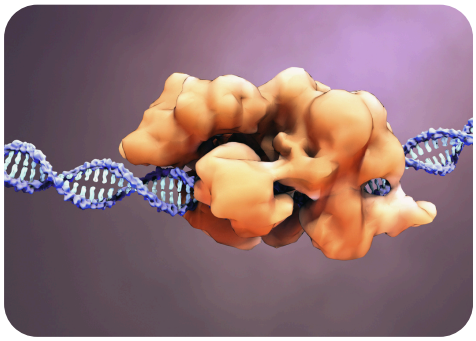
Amplicons	Tissue
Plasmids	gDNA
Cell Pellet	

Turnaround Time

5-7 Business Days
Expedited Service Available

Sequencing Platforms

Illumina Platforms
Other*
**Inquire for more details*



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*

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
Other*
**Inquire for more details*

Epigenomics

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

Accepted Sample Types

FFPE samples
Blood
gDNA
Cell-free DNA
Tissue
Cells

Turnaround Time

20-25 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

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

gDNA
Tissue
Blood

Turnaround Time

20-25 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

Epigenomics

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

Accepted Sample Types

Immunoprecipitated DNA

Turnaround Time

20-25 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

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

Cells
Tissue*
**Per request*

Turnaround Time

20-25 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

Epigenomics

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

Accepted Sample Types

Cells
Transposed DNA

Turnaround Time

20-25 Business Days

Sequencing Platforms

Illumina NovaSeq X Plus

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, 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

Sequencing Only

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) and qPCR (Applied Biosystems) instrumentation to provide accurate quantification prior to sequencing.

Accepted Libraries

Individual Libraries
Pre-pooled Libraries
Customized Libraries

Turnaround Time

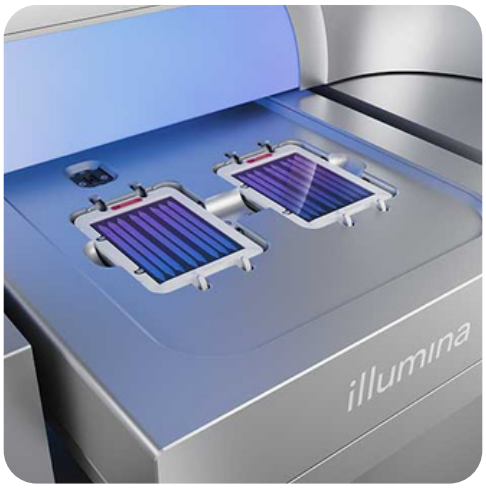
5-10 business days
*Expedited Services Available

Deliverables

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

Sequencing Platforms

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



Bioinformatic Analysis

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)

Transcriptomic Analysis

- Bulk RNAseq
- small RNAseq (smRNA)/micro RNAseq (miRNA)
- De novo Transcriptome Analysis

Epigenomics Analysis

- Whole Genome Bisulfite Sequencing (WGBS)
- Reduced Representation Bisulfite
- Targeted Methylation sequencing
- ATACseq
- ChIPseq
- CUT&RUN
- Hi-C Assay

Bioinformatic Analysis

Bioinformatic Analysis

Single-Cell Analysis

- Single-cell RNAseq
- Single-cell Immune Profiling (VDJ)
- Single Cell ATACseq
- CRISPR Screening

Spatial Transcriptomics Analysis

- STOmics Stereoseq
- 10x Genomics Visium HD

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

BIO ECHO

An admera Company

Reveal the Unseen.
Echoing True Biology.

BIO ECHO

contact@bioecho.de

www.bioecho.com