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Vazyme

Scientific Service NGS Solutions

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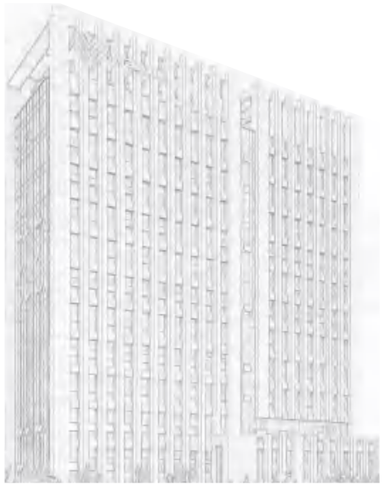
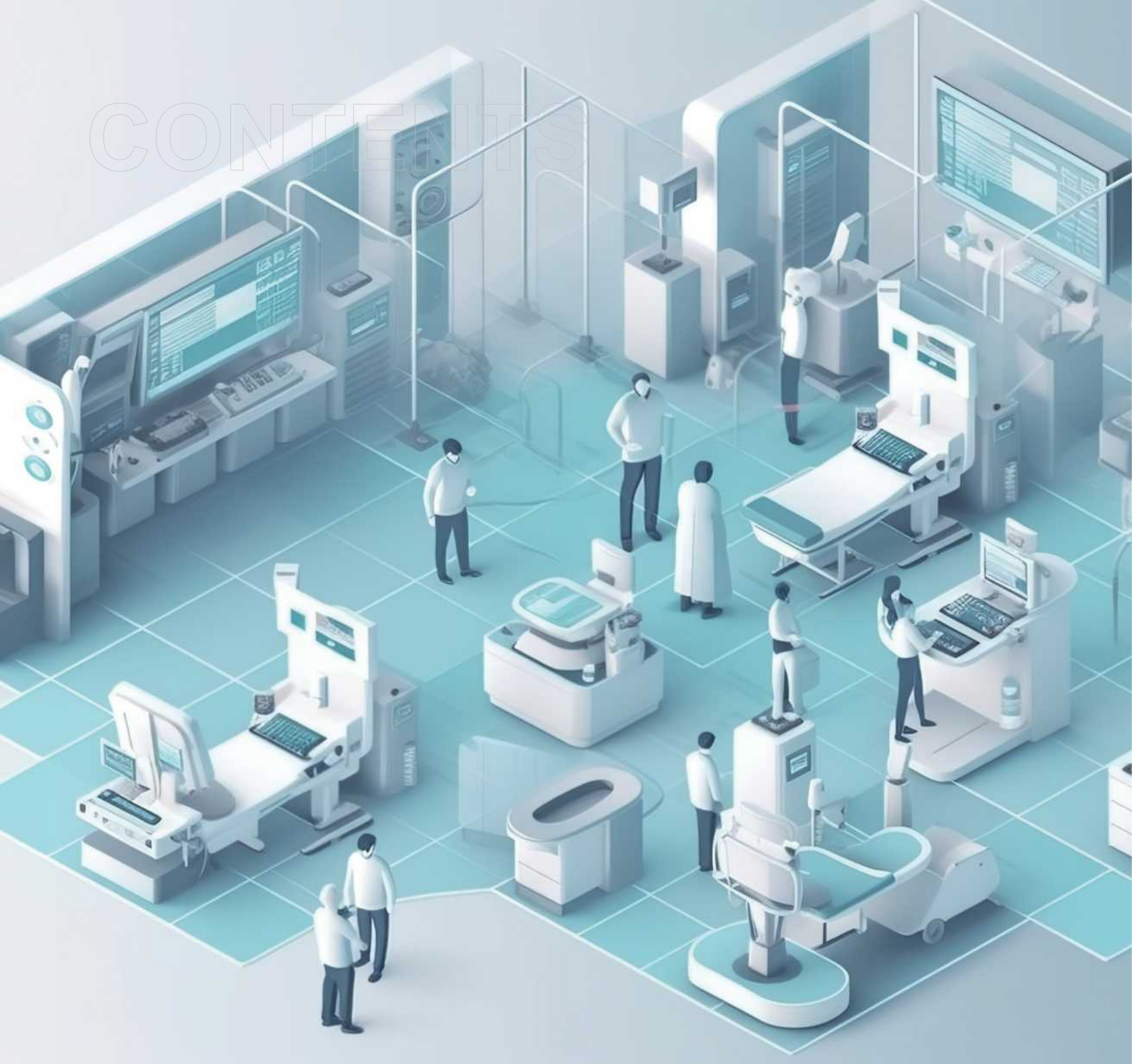
For Science For Health

Vazyme (688105.SH) is a global technology and service providerthat has been digging deep into the field of bioactive compoundssince 2012.We specialize in the design,manufacture,andapplication of functional proteins like enzymes, antigens,andantibodies,as well as high-polymer organic materials. Our R&Defforts have allowed us to expand into a wide range of industries,including life sciences, in vitro diagnostics, bio-medicine,andexploratory business. We strive to deliver comprehensive solutionsthat are tailored fo the diverse needs of our customers. Ourcommitment to excellence has propelled us to become a publiclylisted company on the Shanghai Stock Exchange in 2021.



InnoVation in Enzyme Technology



Contents

Next-Generation Sequencing

Genome Sequencing

1.1 Whole Genome Sequencing

Whole genome sequencing (WGS) is the process of determining the DNA sequence of a species with a known genomic make-up, from which individual or population analyses can be performed. Through sequence alignment, WGS is capable of detecting a large number of variants, including single nucleotide polymorphisms (SNPs), insertions and deletions (InDels), structural variants (SVs), and copy number variations (CNVs). The detected variants enable researchers to examine animal and plant species traits, study population evolution, and map trait loci of interest.

With the decrease in sequencing costs and increase in species with known genome sequences, WGS has become one of the most rapid and effective methods for research on molecular breeding and population evolution in animals and plants. WGS facilitates rapid discovery of genetic variants associated with key traits in animals and plants, which helps accelerate the breeding process when applied to molecular breeding.

/ Advantages

Compre–hensive

Enables comprehensive detection of genomic variants, including SNPs, InDels, CNVs, and SVs;
Enables comprehensive detection of coding and non-coding genetic variants;
Facilitates research on the evolutionary history, environmental adaptability, natural selection, and trait mapping of species in population samples.

/ Applications

WGS can be applied for research on complex diseases, rare diseases, de novo mutations, pharmacogenomics, molecular subtyping of diseases, population cohort databases, and population evolution. By leveraging WGS data on non-coding variants and SVs, scientists are able to uncover genome-wide pathogenic variant sites.

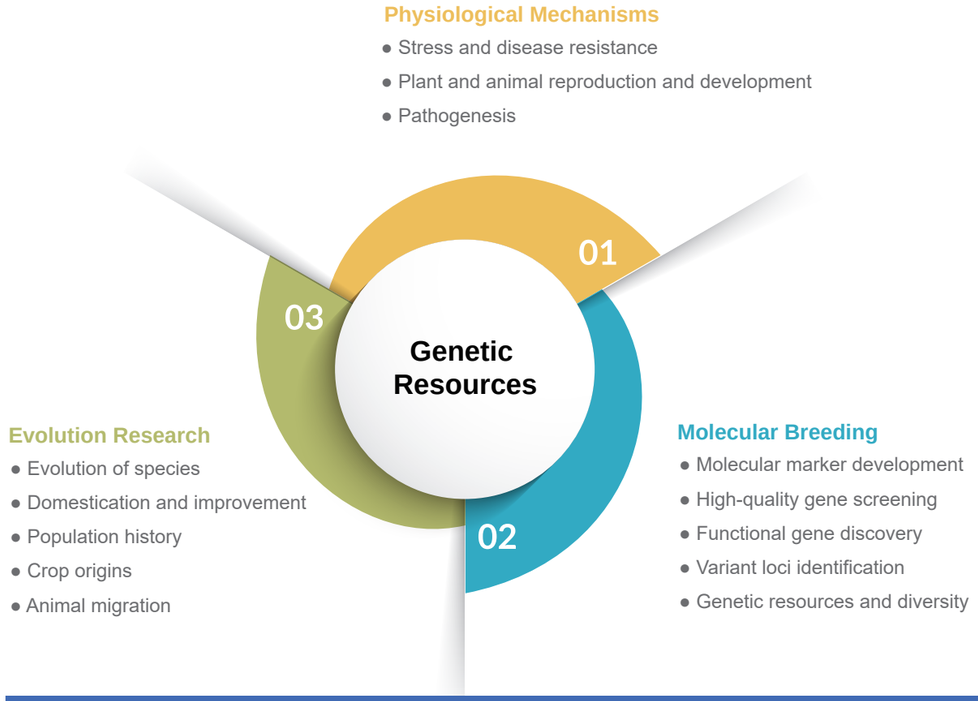
WGS is widely applied in disease research, including cancer, genetic diseases, epidemics and infectious diseases. It also supports in exploring individual susceptibility and biological evolution

Genetic diseases
Identify new mutants and pathogenic mechanisms of genetic diseases

Oncology
Tumor discovery, risk factors, prognosis, treatment, and drug resistance mechanisms

Infectious diseases
Antimicrobial resistance mechanisms

Epidemiology
Epidemiological investigations and drug resistance studies for infectious diseases such as malaria and tuberculosis; determination of individual susceptibility



/ Recommended Products

Platform	Technical Routes	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	Mechanical	ND610	N805-N808, N342 N321/N322, N351-N354	N411	EQ121
	Enzymatic fragmentation	UND637			
		ND627			
	Transposase	TD501	TD202-TD207		
		TD502			
		TD503			
		TD504			
MGI	Mechanical	NDM607	NM108, NM109, NM351		
	Enzymatic fragmentation	NDM637			
		NDM627			
	Transposase	TDM501	TDM101-TDM104 TDM201-TDM202		
		TDM502			
		TDM503			
		TDM504			
Ion Torrent	Mechanical	ND702	NA121		

1.2 Whole Exome Sequencing

Whole exome sequencing (WES) is the most frequently used genomic sequencing method. DNA from exons, the protein-coding regions in the human genome, can be captured and enriched using sequence capture technology. Although exonic regions account for only about 1% of the whole genome, they contain 85% of pathogenic mutations. WES is less costly and more efficient than WGS. It is primarily used to identify and analyze variations in coding regions and UTRs that are associated with diseases and population evolution. The abundant exome data available in public databases facilitates better understanding of the relationship between identified variants and diseases.

/ Advantages

Cost-effective

Directly sequences protein-coding regions, narrowing the scope and reducing data volume

In-depth

Enables analysis of common, rare, and low-frequency variants

/ Applications

Compared to WGS, WES sequences a smaller portion of the genome (about 1%), thus allowing detection of more low-frequency and rare variants with deeper sequencing, while reducing sequencing costs and storage space. This feature determines the important role of WES in genetic disease and oncology research, especially in tumor heterogeneity. Tumor heterogeneity gives rise to multiple subclones in a tumor, some at very low frequencies. Deep WES enables faster and Deep WES enables faster and cost-effective detection of somatic mutations that are difficult to detect with conventional sequencing depths. detection of somatic mutations that are hard to discover at regular sequencing depths.

/ Recommended Products

Platform	Capture Probes	Capture Blockers and Amplification Primers	Hybridization and Wash	Beads	Qubit Quantification
Illumina	NC001	NC101	NC103	N411	EQ121
MGI		NCM101			

1.3 Target Capture Sequencing

Target region sequencing (TRS) hybridizes customized probe to genomic DNA, enriching genomic regions of interest for high-throughput sequencing.

/ Advantages

Focused

Targeted detection of genetic variants within genomic regions of interest

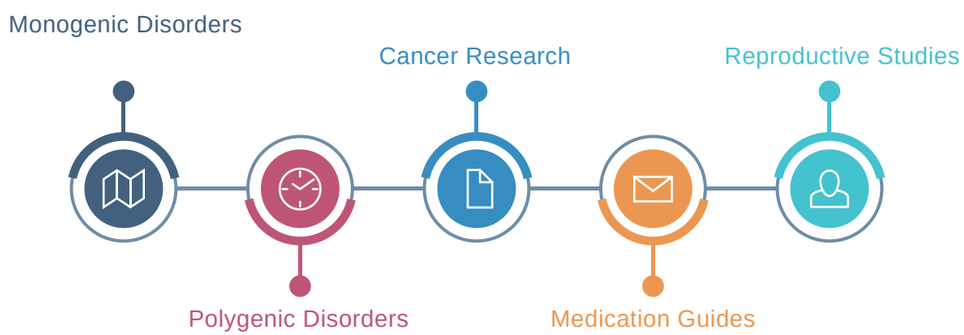
Cost-effective

Lower cost and higher throughput, suitable for large sample sizes

Accurate

Deeper coverage and higher accuracy, improving the detection of rare variants

/ Applications



/ Recommended Products

■ Hybridization capture-based library preparation

Platform	Technical Routes	Library Preparation	Adapters	Beads	Qubit Quantification	Capture reagents
Illumina	Mechanical	ND610	N805-N808, N342 N321/N322, N351-N354	N411	EQ121	See Compatible Products in 1.2
	Enzymatic fragmentation	ND627				
	Transposase	TD501	TD202-TD207			
		TD502				
		TD503				
		TD504				
MGI	Mechanical	NDM607	NM108, NM109, NM351			
	Enzymatic fragmentation	NDM627				

■ Multiplex targeted amplicon library preparation

Platform	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	NA210	NA111	N411	EQ121
Ion Torrent		NA121		

1.4 Single Cell Genome Sequencing

Rapid advancement in next-generation sequencing (NGS) and third-generation sequencing (TGS) have driven revolutionary changes in biological research. in the past, sequencing required large number of cells in order to obtain sufficient amount of DNA; therefore, the results represented cells in bulk. However, significant genetic differences may exist across phenotypically identical cells due to cellular heterogeneity. When cells are sequenced in bulk, significant amount of ow abundance genetic information is lost. As a solution to these limitations, single cell sequencing technologies were developed. conventional DNA sequencing produces result that are an average of many cells, obscuring differences between individual cells. Such methods are unsuitable for rare, precious samples, that are amenable only to single cell sequencing techniques. It is also challenging to apply conventional NGS for the research on fastidious microbes, circulating tumor cell (CTC) transcriptomics, differentiation profiling in early human embryogenesis, tumor heterogeneity, and microevolution. By amplifying and sequencing the genomes of individual cells, single cell sequencing overcomes challenges such as the lack of single cell heterogeneity data from tissue samples or inability to conduct conventional sequencing on low-quantity samples. This novel approach enables scientists to study individual cell behaviors, mechanisms, and cell-organism relationships, thereby support the identification of early detection, diagnosis early detection, diagnosis, and personalized treatment of diseases.

/ Advantages

01

Enables parallel multi-omics studies at single-cell resolution

02

Studies on functional states of single cells allow unbiased inference and discovery of new cell types

03

Enables construction of differentiation trajectories and molecular atlases for cell lineages

04

Better detection of new genes without prior sequence information, and higher sensitivity for quantifying rare variants and transcripts

/ Applications

Single cell sequencing can rapidly determine precise gene expresion profiles of thousands to millions of cells, enabling analysis of genetic heterogeneity among phenotypically identical cells. This technique has been applied in a wide range of fields, including neurobiology, organ development, cancer biology, clinical diagnosis, immunology, microbiology, embryology, and prenatal genetic diagnosis.

- Construction of single-cell DNA molecular atlas in oncology
- Metastasis
- Relapse mechanisms
- Identification of single-cell biomarkers for cancer diagnosis
- Minimal residual disease detection
- Drug resistance in cancer
- Pinpoint validation of genome editing for heterozygous and concurrent mutations

/ Compatible Products

Platform	Amplification	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	N603	TD502	TD202-TD207	N411	EQ121

1.5 Metagenomic Sequencing

Microbes inhabit nearly every corner of the earth and have an immense impact on ecosystems and host health. NGS combined biological data with potential genetic associations, rapidly advancing the understanding of microbiota biodiversity. although metagenomic squencing provides insight into omplex microbiome, the resulting data may be incomplete or limited. Therefore objectivity on metagenomi sequencing is vital when employing this technique in scientific research.

Metagenomics employs NGS to study the genomes of microbial communities inhabiting particular environments. expanding microbial diversity, population structure, and evolutionary relationships, metagenomics reveals biologically meaningful insights into microbiota by further exploring their functional activity, interactions, and relationships with the environment. Compared to traditional microbiological techniques, metagenomic sequencing circumvents issues such as inability to detect trace microbes or culture most microorganisms. Therefore, this approach has been widely adopted in environmental microbiology in recent years.

/ Advantages

01

Viruses can be directly sampled from the environment, eliminating the need for isolation and culture; enables comprehensive analysis and identification of dispersed, low-abundance viruses.

/ Applications

Medicine
Metabolic diseases and cancer research

Animal Husbandry
Digestive tract and rumen microbiota (e.g., methanogens) and animal health/nutrition

Agriculture
Microbe-plant interactions, tillage, fertilizer application, and soil microbiota

Environment
Smog mitigation, wastewater treatment, oil spill bioremediation, acid mine drainage treatment, and marine ecosystem research

Bioenergy
Development of strains with specialized functions, genome mining, microbial engineering

Extreme Environments
Profiling microbiota in extreme environments

/ Recommended Products

Platform	Series	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	Mechanical	ND610	N805-N808, N342 N321/N322, N351-N354	N411	EQ121
	Enzymatic fragmentation	UND637 (non-diagnostic, no background microbe QC requirement)			
	Transposase	TD501-TD504	TD202-TD207		

1.6 Environmental DNA Sequencing

Analysis of microbiota dynamics in complex samples by NGS has become a key research focus in microbiology. 16S/18S/ITS amplicon sequencing involves extraction of DNA from environmental samples and amplifying full-length (TGS) or targeted (NGS) 16S/18S/ITS regions with suitable universal primers. By detecting sequence variations and abundance in the regions of interest, this approach provides insights into environmental microbial biodiversity and differences in microbiota composition. 16S sequencing is most commonly used.

/ Advantages

Species-level resolution
High resolving power for microbial diversity profiling

Variable region amplification sequencing
Longer sequences and more accurate identification

Low cost
Higher throughput and lower costs than conventional colony-based methods

/ Applications

Human microbiota
Characterization of microbiota composition in different human tissues and association analysis between disease and microbiota diversity to inform disease prevention and diagnosis

Host environment
Research on the functional interactions between hosts (animals or plants) and microbiota and the mechanisms underlying symbiosis

Environmental samples
Research on microbiota diversity in different environmental samples (e.g., soil, water, activated sludge, air, oceans, mine drainage, hot springs) for applications in biogeochemistry, biogeography and microbial ecology

/ Recommended Products

Platform	Technical Routes	Amplification/Library Preparation	Kit	Beads	Qubit Quantification
Illumina	Two-round PCR	Taq DNA polymerase	P111, P112	N411	EQ121
		High-fidelity DNA polymerase	P510, P515		
		DNA library amplification module (polymerase only)	N618		
		Multiplex amplification module	NA301 (with background microbe QC)		
	One-round PCR + Library preparation	Taq DNA polymerase	P111		
		High-fidelity DNA polymerase	P510, P515		
		DNA library amplification module (polymerase only)	N618		
		Mechanical method library preparation	ND610		

RNA-seq

2.1 Eukaryotic RNA-Seq

The transcriptome provides the essential link between genetic information and biological function. Eukaryotic RNA-seq is an NGS-based approach that enables rapid acquisition of the full set of transcripts of a particular cell or tissue of a species in a given state, which can be used for the study of gene structure and function, alternative splicing, and prediction of novel transcripts. With the advancement in sequencing technology, RNA-seq has become foundational to virtually all areas of biological research, from regulation of growth and development, adaptation to environmental stress, evolutionary patterns, critical mechanisms of pathogenesis, to discovery of key regulatory targets for genes implicated in diseases.

/ Advantages

01

Whole genome analysis without the need for pre-designed specific probes, enabling expression profiling for all genes at the same time

02

Simultaneous profiling of known and unknown genes and discovery of novel transcripts and alternative splicing events

03

High sensitivity allowing detection of transcripts expressed at very low levels

/ Applications

Plant research

Eukaryotic RNA-seq enables analysis of gene expression, developmental processes, and cell types in plants. For example, researchers can analyze the RNA-seq data of medicinal plants to gain useful insights into functional genes and regulatory mechanisms that help improve selective breeding and cultivation techniques.

Medicine

Transcriptomics is a powerful tool in medical research. For example, it assists in the detection of early cancer biomarkers, and provides species or tissue transcripts that facilitate discovery of novel genes.

/ Compatible Products

Platform	Technical Routes	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	**mRNA enrichment:** N403 (eukaryotes) **rRNA depletion:** N406 (human/mouse/rat, enzymatic) N417 (bacteria, enzymatic) N408 (blood, enzymatic) N409 (plant, enzymatic) N420 (human/mouse/rat, beads)	NR606	N803/N804 N809-N812 N323/N324	N411 N412	EQ121
MGI		NRM606	NM208		

2.2 Single Cell RNA-Seq

Cellular heterogeneity is a critical challenge in cancer research, diagnosis, and treatment. Single cell sequencing (SCS) was developed to address this issue. Single cell RNA sequencing (scRNA-seq) is a novel technique for RNA-seq at single-cell resolution, enabling the analysis of gene expression within individual cells. By overcoming cellular heterogeneity challenges that cannot be resolved with bulk tissue sequencing, scRNA-seq facilitates analysis of individual cell behaviors, mechanisms, and cell-organism relationships.

/ Advantages

Low input

Compatible with single cell input, suitable for samples that cannot meet the starting material requirements for 10x Genomics and other platforms

High coverage

Covers full-length cDNA sequences, each cell enabling expression profiling of tens of thousands of genes

Extensive data

Besides gene expression, data can also be used for analysis on alternative splicing, cSNPs, and lncRNAs with poly(A) structures

/ Applications

- Stem cell differentiation and tissue/organ development
- Disease subtyping and medication guidance
- Tumor heterogeneity
- Immunology
- Neurodevelopment

/ Compatible Products

Platform	Amplification	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	N711 (standalone reverse transcriptase)	TD503	TD202-TD207	N411	EQ121

2.3 Small RNA Sequencing

Small RNAs inhibit target mRNA expression at transcriptional and translational levels by specific recognition and binding of RNA-induced silencing complexes (RISCs). As a key member of the highly complex RNA regulatory network in cells, small RNAs play important regulatory roles in nearly all cellular events involved in ontogenesis, proliferation, differentiation, tumorigenesis, and antiviral response. Large-scale sequencing of small RNAs generates genome-wide small RNA atlases, enabling the discovery of novel small RNA enabling the discovery of novel small RNA molecules, predict and identify their target genes, of their target genes, differential expression analysis across samples, small RNA clustering, and expression profiling.

/ Advantages

01

Nucleotide-level examination of small RNA molecules without fluorescence crosstalks or background noise common in conventional microarray hybridization, greatly facilitating the discrimination of highly similar small RNAs from the same family

02

High-throughput analysis for any species without requiring prior sequence or secondary structure information

03

High sensitivity and sequencing throughput provide remarkable coverage and depth for small RNA discovery and research, enabling detection of rare, extremely low-abundance transcripts

04

Annotation and expression analysis of known small RNA with public small RNA databases; further analysis of unmapped data provides deeper research insights and allows discovery of novel types and isoforms of small RNA

/ Applications

Plants

Environmental adaptation, stress response, ontogeny, genetic traits

Fungi

Mechanisms, applications, edible and medicinal properties

Animals

Agricultural traits, adaptability, ontogeny, genetic traits, regulatory mechanisms in model animals treated with interventions

/ Compatible Products

Platform	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	NR811	N813-N816	N411	EQ121

2.4 Metatranscriptomic Sequencing

Metatranscriptomics is a discipline that studies the genome-wide transcription and transcriptional regulation within a microbial community inhabiting a specific environment at a given time.

Metatranscriptomic sequencing enables in situ characterization of active strain composition and gene expression within a microbial community in a specific niche under given environmental conditions. Metatranscriptomics provides significant advantages over metagenomics in research, because the presence of a gene in DNA does not necessarily indicate the gene is transcriptionally active and functional, especially in complex environments like soil, where microbes typically do not proliferate in large numbers at the same time. Besides taxonomic identification, metatranscriptomics allows investigation of the composition and active gene expression of microbial communities that are active under specific environmental conditions.

/ Advantages

Allows multi-sample analysis of differences in active composition between microbial communities under different environmental conditions (location and time) due to physicochemical and other differences;

Examination of active microbes, transcripts, and functions in samples and comparison of differentially expressed genes and functional pathways between environments, which reveal adaptive mechanisms of microbes under varied environmental stresses and provide insight into interactions between environments and microbes.

/ Applications

Medicine

Viral identification, relationships between human microbiota and diseases/cancer, identification and screening of molecular biomarkers and drug targets

Ecology

Microbial response mechanisms under stressful environments

Industry

Bioactive microbial metabolites, bioenergy, environmental pollution monitoring and bioremediation

Platform	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	NR606	N803/N804, N809-N812 N323/N324	N411	EQ121
	TR501-TR503	TD202-TD207		
MGI	NRM606	NM208		

2.5 lncRNA Sequencing

Long non-coding RNAs (lncRNAs) are RNAs > 200 nt in size. They play regulatory roles in cell proliferation, differentiation, migration, apoptosis, and immunity via epigenetic modifications of the genome, post-transcriptional regulation of gene expression, and competing endogenous RNA (ceRNA) and enhancer RNA (eRNA) activity.

/ Advantages

Library optimization

Ribosomal depletion and strand-specific library preparation protocols retain full lncRNA and mRNA sequences, including sequence orientation

Extensive sequencing

Identification and analysis of almost all lncRNA and mRNA sequences in a sample; in-depth analyses of lncRNA regulatory networks via association analysis of lncRNAs and mRNAs

/ Applications

■ lncRNA sequencing is suitable for studying various stages, tissues, or aspects of an organism's growth and development.

Animal

Embryonic, gonadal, and muscular development and immunological regulations in human, mice, and zebrafish

Plant

Stress response, organ development, reproduction and growth, and viral infection

Tomor and other diseases

Pathogenesis and management of cancer, psychiatric disorders, metabolic diseases, cardiovascular diseases, and immune disorders

/ Compatible Products

Platform	Technical Routes	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	**rRNA depletion:** N406 (human/mouse/rat, enzymatic) N417 (bacteria, enzymatic) N408 (blood, enzymatic) N409 (plant, enzymatic) N420 (human/mouse/rat, beads)	NR606	N803/N804 N809-N812 N323/N324	N411 N412	EQ121
MGI		NRM606	NM208		

2.6 circRNA Sequencing

circular RNA (circRNA) is a special class of non-coding RNA molecules that are becoming increasingly popular in RNA research. Unlike linear RNAs containing 5' and 3' ends, circRNAs form closed loop structures, making them resistant to RNA exonucleases, more stable, and less susceptible to degradation. Recent studies indicate that circRNAs play important regulatory roles in growth, development, and environmental responses. circRNAs demonstrate a range of functions, serving as miRNA sponges to competitively bind miRNA, and as ceRNA to regulate gene expression. Their close associations with disease etiology and progression also suggest promising applications as disease biomarkers.

/ Advantages

Analysis of circRNA offers in-depth understanding of circRNA functions in transcriptional regulation.

/ Applications

■ circRNA sequencing is suitable for studying various stages, tissues, or aspects of an organism's growth and development.

Growth and development
Cellular and tissue growth and development in humans, mice, and drosophila

Cancer and other diseases
Pathogenesis and management of cancer, metabolic diseases, and immune disorders

Plant
Stress response and genetic breeding

/ Compatible Products

Platform	Technical Routes	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	**rRNA depletion:** N406 (human/mouse/rat, enzymatic) N417 (bacteria, enzymatic,) N408 (blood, enzymatic) N409 (plant, enzymatic) N420 (human/mouse/rat, beads)	NR606	N803/N804 N809-N812 N323/N324	N411 N412	EQ121
MGI		NRM606	NM208		

Epigenomic Sequencing

3.1 CUT&Tag Sequencing

DNA-protein interactions are pivotal in biological research, as they are involved in virtually all processes of life, such as gene expression, regulation, replication, recombination, and repair, as well as RNA translocation, translation, and regulation. Current methods for studying DNA-protein interactions include traditional ChIP-Seq, optimized CUT&RUN, and newer approaches like CUT&Tag. In ChIP-Seq, DNA fragments are obtained by lysis of formaldehyde-crosslinked cells, random chromatin shearing by sonication, and antibody-mediated immunoprecipitation, followed by library preparation and sequencing. This approach requires a high sample input and yields data with high background signal. In contrast, CUT&Tag utilizes transposons for in situ cleavage of chromatin near binding sites of the target protein in intact cells or cell nuclei. The resulting DNA fragments can be prepared into sequencing libraries with a simple PCR reaction. Compared to ChIP-Seq, CUT&Tag requires a lower sample input, offers a higher signal-to-noise ratio, and employs a simple workflow. CUT&Tag allows genome-wide detection of DNA fragments interacting with histones, transcription factors, and other proteins of interest, representing a new generation of ultra low-input techniques. CUT&Tag shows potential to transform protein-chromatin DNA interaction studies into a routine procedure like PCR, which would have important implications for research on gene regulation and epigenetics.

/ Advantages

Compatible with low sample input	Compatible with lower cell input
Saves time	Streamlined workflow takes less time than conventional ChIP
High signal-to-noise ratio	Does not require formaldehyde crosslinking, reducing background noise and demanding less sequencing depth
Good experimental repeatability	Consistent results across replicate experiments

/ Applications

CUT&Tag has been applied to animal, plant, and yeast samples in basic life science research, agricultural innovation, and translational medicine, providing a novel approach for epigenetics.

- Protein-DNA interactions
- Detection of histone modifications across the genome
- Identification of genome-wide transcription factor binding sites
- Identification of super enhancers

/ Compatible Products

Platform	Library Preparation	Beads	Qubit Quantification
Illumina	TD904	N411	EQ121

3.2 CUT&RUN Sequencing

Protein-DNA interaction assays, such as chromatin immunoprecipitation (ChIP) and ChIP-Seq, have increased the understanding that epigenetic dysregulation can cause diseases. Cleavage under targets and release using nuclease (CUT&RUN) is a novel technique for chromatin analysis applicable to study early embryogenesis, stem cells, cancer, and epigenetics. Compared to traditional ChIP-Seq methods, CUT&RUN offers advantages such as fast turnaround, low cell input, low background signals, and good repeatability, promising revolutionary impact on epigenetics and gene regulation research.

/ Advantages

01

CUT&RUN has lower cost than CUT&Tag. It enables unbiased cleavage of euchromatin and heterochromatin, and has better cleavage efficiency than CUT&Tag for target sites on heterochromatin.

/ Applications

CUT&RUN and CUT&Tag share the same application areas, including research on histone modifications, transcription factors, and chromatin-associated complexes.

/ Compatible Products

Cat. No.	Technical Routes
HD101	PCR/qPCR
HD102	Illumina Library Preparation

3.3 ATAC Sequencing

As chromatin undergoes dynamic remodeling, its global regulation is associated with the dynamic positioning of nucleosomes. Therefore, efficient, precise detection of genome-wide open chromatin regions (OCRs) and dynamic changes in nucleosome positioning provides important cues and effective means for discovering genomic regulatory elements and elucidating regulatory mechanisms of gene expression. In medicine, chromatin accessibility techniques represent a new generation of powerful tools for new drug R&D and for studying pathogenesis of major diseases, drug mechanisms of action, and biomarker functions.

Assay for transposase accessible chromatin using sequencing (ATAC), which requires only a small number of cells, leverages transposase-mediated cleavage of OCRs to obtain active transcription regulatory sequences (TRSs) across the genome under given conditions. It has broad applications in epigenetic research on transcription factor binding sites, nucleosome positioning, and distribution of active regulatory elements.

/ Advantages

01

Low sample input: Requires as little as a few hundred cells or lower for library preparation, suitable for rare samples

02

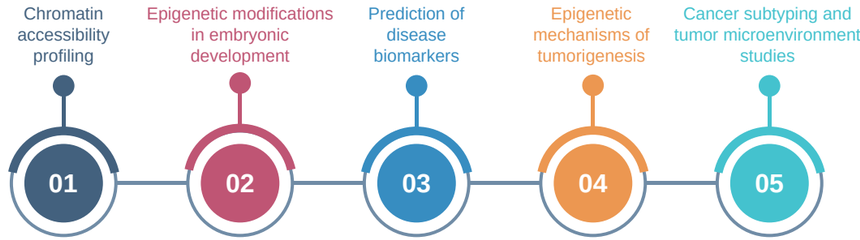
ATAC-seq has a simple workflow without ultrasonication or phenol-chloroform extraction steps and takes less time with transposase-based library preparation.

03

Faster sample preparation: Compared to other methods that require complex sample preparation, ATAC-seq samples can be prepared in simple, fast steps, reducing instability from prolonged handling

/ Applications

ATAC-seq yields rich epigenetic data, including open chromatin profiles, nucleosome positioning, and transcription factor binding sites. By identifying transcription factor binding sites within OCRs, it can be used to examine transcription factors and regulatory regions. ATAC-seq can be applied to the following areas:



/ Compatible Products

Platform	Library Preparation	Adapters	Beads	Qubit Quantification
Illumina	TD711	TD202-TD207	N411	EQ121

3.4 Whole Genome Bisulfite Sequencing (WGBS)

Epigenetic modifications can alter phenotypes without changing the DNA sequence. Changes in epigenetic modification are closely associated with gene function and cellular states, development, aging, and disease. DNA methylation is the most important and widely studied epigenetic modification, and whole genome bisulfite sequencing (WGBS) is undoubtedly the most effective approach. DNA methylation is a post-replication epigenetic modification commonly found in prokaryotic and eukaryotic genomes. It regulates genomic functions without altering the primary DNA structure, and plays crucial roles in gene expression, transposon silencing, chromatin interactions, cell differentiation, and growth and development.

/ Advantages

Easy operation

Enzymatic conversion options effectively prevent issues with degradation

Wider range

Compatible with third-generation sequencing, enabling analysis of complex, highly repetitive genomic regions such as centromeres that are hard to detect with short-read sequencing

Powerful functions

Identification of allele-specific methylation

Wide application

One set of data can be used for SNP, SV, methylation, and genome assembly analysis

/ Applications

Whole-genome methylation

HiFi sequencing of single samples helps profile genome-wide methylation patterns (e.g., hypomethylation of transcription start sites), characterize differential methylation between tissues/organs, and construct whole-genome methylation maps

Whole genome methylation

Identifies differential methylation between strains by sequencing multiple samples

/ Compatible Products

Platform	Technical Routes	Solution
Illumina	Conversion -> Library preparation	Conversion: Bisulfite conversion: EM102 (column-based)/EM103 (bead-based); Enzymatic: EM301 Library preparation: NE103
	Library preparation -> Conversion	End-repair + adapter module: ND610 Conversion: Bisulfite conversion: EM102 (column-based)/EM103 (bead-based); Enzymatic: EM301 (recommended)

3.5 Reduced Representation Bisulfite Sequencing (RRBS)

Reduced representation bisulfite sequencing (RRBS) is a technique that uses restriction enzymes to enrich genomic DNA fragments rich in CCGG, followed by bisulfite treatment and high-throughput sequencing to examine methylation in CpG-rich genomic regions at single-base resolution. Compared to WGBS, RRBS is a more cost-effective option with significantly reduced sequencing volume, making it widely applicable for large-scale studies of clinical samples.

RRBS converts unmethylated cytosines (C) to thymines (T) with bisulfite while leaving methylated cytosines unchanged. Methylation rate at individual C sites can then be derived from sequencing data of the bisulfite-converted genome by calculating the ratio of reads with unconverted C to the total sequenced reads. This technique has significant applications in research on the epigenetic mechanisms of embryonic development, aging, and pathogenesis, as well as screening for epigenetic markers associated with diseases.

/ Advantages

Accurate

Single base resolution enables accurate analysis of methylation state at each cytosine

Cost-effective

Enables analysis of DNA methylation in promoters and CpG islands with smaller amounts of sequencing data

/ Applications

Cohort studies

Disease and risk factors, genetic traits, biomarkers

Cancer and other diseases

Cancer, psychiatric disorders, metabolic diseases, and immune diseases

Animal development

Muscle development, breeding, and reproduction

/ Compatible Products

Platform	Technical Routes	Restriction Enzyme	Conversion	Library Preparation	Beads	Qubit Quantification
Illumina	Conversion -> Library preparation	N/A (NEB recommended)	Bisulfite conversion: EM103 Enzymatic conversion: EM301	NE103	N411	EQ121

Third-Generation Sequencing

1.1 Third-Generation Sequencing

Third-generation sequencing (TGS) refers to single-molecule real-time sequencing (SMRT), also known as de novo sequencing. Compared to previous sequencing technologies, its key feature is single-molecule sequencing, which enables sequencing of individual DNA molecules without PCR amplification. At present, short-read NGS still dominates the market, but rapid advances in TGS in recent years have facilitated its application in a number of research areas, including genome sequencing, methylation, and variant identification.

/ Advantages

Ultra-long reads	Average 10 - 12 kb, up to > 30 kb
No GC bias	Does not require PCR amplification, avoiding biases and non-uniform coverage caused by PCR
High accuracy	Up to 99.999% accuracy (QV50) with completely random sequencing errors
High sensitivity	Detects mutations with frequencies below 0.1%
Direct detection of modified bases	

/ Applications

Large genome assembly

Previous short-read assembly of certain animal or plant genomes could be challenging due to polyploidy, highly repetitiveness, and high heterozygosity. Long reads in TGS facilitate assembly of large genomes and significantly enhance completeness.

Iso-Seq

Previous RNA-seq techniques cannot sequence RNA directly without extra steps like mRNA fragmentation and reverse transcription, which prevents acquisition and analysis of full-length transcripts. TGS generates long reads and allows accurate identification of multiple isoforms of the same gene.

Structural variation of large fragments

Structural variations of large genomic fragments (e.g., deletions, inversions, and translocations) are often related to human diseases. Unlike short-read sequencing, long-read TGS is capable of detecting these variabts, therefore offers promising potential for the extensive application in disease research.

Fast microbial identification

Rapid, real-time TGS enables sequencing straight at the sample collection site, which allows real-time taxonomic classification based on sequencing data for fast microbial identification

/ Compatible Products

Platform	DNA Repair	End Repair	Adapter Ligation	Library Preparation	
PacBio	/			TS101	Upcoming
Nanopore	N208	N203	N204	TS201	Upcoming