Vazyme | Stock Code 688105.SH

Reagents for

NGS Library Preparation

Product Catalogue

Vazyme

Vazyme (688105.SH) is a global supplier dedicated to design, manufacture and application of bioactive proteins and continuously expands the application fields of core technologies in life science, in vitro diagnostics, bio-medicine,and others.

Strive for Excellence

Catering to Diverse Customer Needs

To meet the varying needs of our customers and partners, we have developed over 600+ types of genetically engineered recombinant enzymes and over 2,500+ types of high-performance materials and over 2,000+ end products.

Commitment to Quality

Pursing Highest Standards of Products and Services

While remaining steadfast to high quality standards, producing all core materials in-house and adhering to GMP quality control standards, we endeavor to maintain a stable and sufficient supply for global customers by establishing subsidiary companies and local warehouses.

Operation in Global Terms

Serving Customers in 60+ Countries

Currently, Vazyme had 9 global subsidiary companies to offer local services in the USA, Canada, Indonesia, Singapore, Germany, the UK, Australia, South Korea, and Hungary.

Our mission is to empower our customers to advance the innovation of science and health.

Our Vision

For Science For Health

Helping our customers unlock new frontiers in scientific exploration and develop innovative solutions is the driving force behind our work at Vazyme. Together, we explore the unknown and push the boundaries of scientific research in the service of healthier life for all.

Our Culture

- We care for our customers
- We strive for excellence
- We live by our principles
- We thrive on innovation
- We own our company
- We achieve as a team

Our Global Operation

We Strive to Connect with Customers and Partners Worldwide

Customers remain our foremost priority. By setting up local customer support teams in major global markets, we are able to directly engage and connect with our users.

We have served customers in over 60 countries and regions, including scientists, researchers, and engineers devoted to human health. Our products have obtained 300+ market accesses. To better cater to our global clientele, we have established global subsidiary companies in USA, Canada, Indonesia, Singapore, Germany, UK, Australia, South Korea and Hungary, creating localized customer service and technical support teams that promptly address customer needs and offer one-stop services. Furthermore, we have set up warehouses in multiple regions worldwide and ensured high quality delivery of products through cold chain transportation.

Vazyme

NGS Library Preparation Product Catalogue

For Science For Health

Content

01

DNA Sequencing

DNA Sequencing

Background

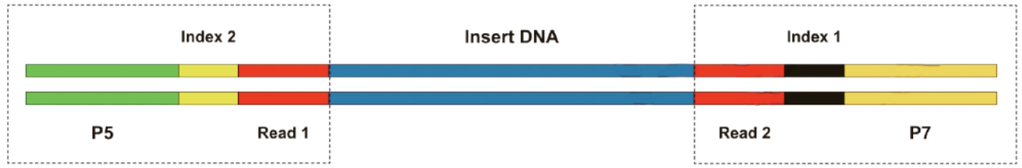
Brief Introduction

Next Generation Sequencing (NGS) is currently the most widely used technology and enables rapid and accurate determination of the genetic sequence of any organism. Supporting a broad range of applications, including gene expression profiling, chromosome counting, pathogen research, reproductive health and oncology diagnosis, NGS is driving discovery and enabling the future of personalized medicine. NGS usually includes the following processes:

NGS Process

DNA Library Preparation

DNA library preparation is the foundation of the NGS technology. A library contains DNA inserts flanked on each side by an adapter as shown below. Insert DNA is the DNA fragment to be sequenced, Read 1/Read 2 are sequencing primers binding sites to initiate sequencing, Index 1/Index 2 sequences are sample identifiers that allow pooling of multiple samples in a single sequencing run or flow cell lane, and P5/P7 sequences that allow the library to bind and generate clusters on the flow cell.



Schematic representation of a dual-index library fragment

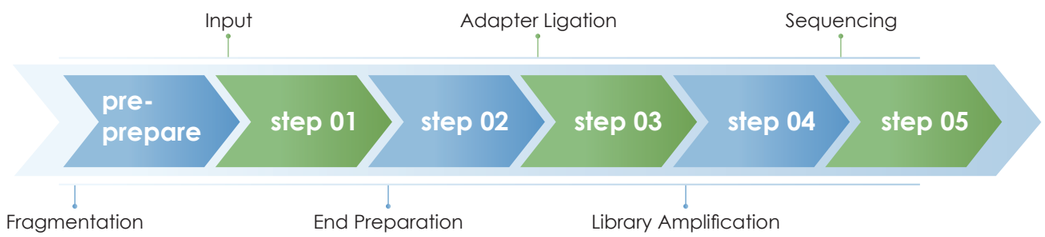
DNA Library Preparation Kit

Library Prep		Sequencer	Product Name	Cat. No.
dsDNA Library Prep	Based on mechanical fragmentation	Illumina	VAHTS Universal DNA Library Prep Kit for Illumina V4	ND610
		MGI	VAHTS Universal DNA library Prep Kit for MGI V3	NDM607
	Based on enzymatic fragmentation	Illumina	VAHTS Universal Plus DNA Library Prep Kit for Illumina V2	ND627
			UltraClean Universal Plus DNA Library Prep Kit for Illumina V3	UND637
		MGI	VAHTS Universal Plus DNA Library Prep Kit for MGI V2	NDM627
			UltraClean Universal Plus DNA Library Prep Kit for MGI V3	UNDM637
	Based on transposase fragmentation	Illumina	TruePrep DNA Library Prep Kit V2 for Illumina	TD501/TD502/ TD503
			TruePrep Flexible DNA Library Prep Kit for Illumina	TD504
		MGI	TruePrep DNA Library Prep Kit for MGI	TDM501/TDM502/ TDM503
			TruePrep Flexible DNA Library Prep Kit for MGI	TDM504
ssDNA Library Prep		Illumina	VAHTS ssDNA Library Prep Kit for Illumina	ND620
Amplicon Library Prep		Illumina/Ion Torrent	VAHTS AmpSeq Library Prep Kit V3	NA210
Third-Generation Sequencing		Nanopore	VAHTS TGS DNA Library Prep Kit for ONT	TS201

VAHTS Universal DNA Library Prep Kit for Illumina V4 (Vazyme #ND610)

VAHTS Universal DNA Library Prep Kit for Illumina V4 (Vazyme #ND610) is a library preparation kit for Illumina. 100 pg -1 μg of fragmented dsDNA can be converted into a dedicated library. The kit can improve the conversion rate of low-quality template libraries and reduce the repetition rate of libraries by optimizing and improving the terminal repair module, ligation module and library amplification module. This kit is widely suitable for PCR or PCR-Free library preparation of a variety of samples, and is compatible with the targeted capture process.

Workflow



Features

• High library conversion rate

Use samples with different inputs for preparing PCR-Free libraries. Compared with similar products, Vazyme #ND610 has significant advantages over Supplier A.

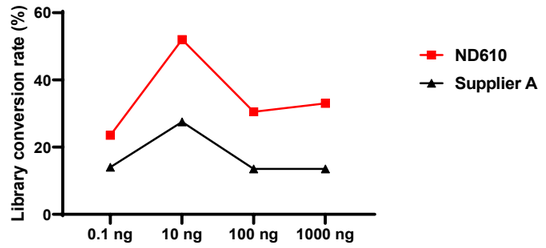


Figure 1 Conversion rate under different inputs

• Wide compatibility with multiple sample types

Use various samples for preparing libraries with ND610 and Supplier A, respectively. Vazyme #ND610 has higher library yield than Supplier A.

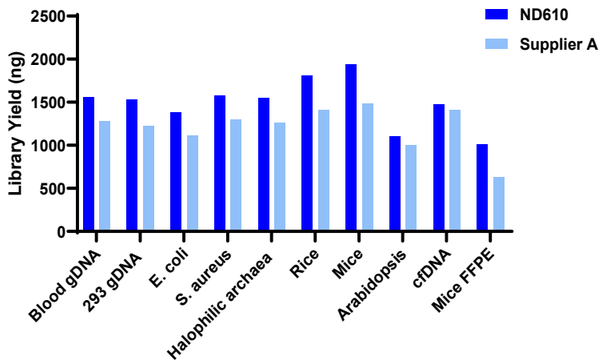


Figure 2 Library yield under different samples

• Accurate detection of low-frequency mutations

Libraries were prepared with human gDNA (0.1% ctDNA), Vazyme #ND610 has more accurate mutation detection rate than Supplier A. When using Pan-tumor 800 (1% FFPE) for preparing libraries, Vazyme #ND610 has consistent mutation detection with Supplier A.

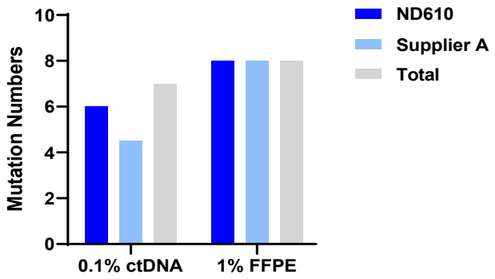
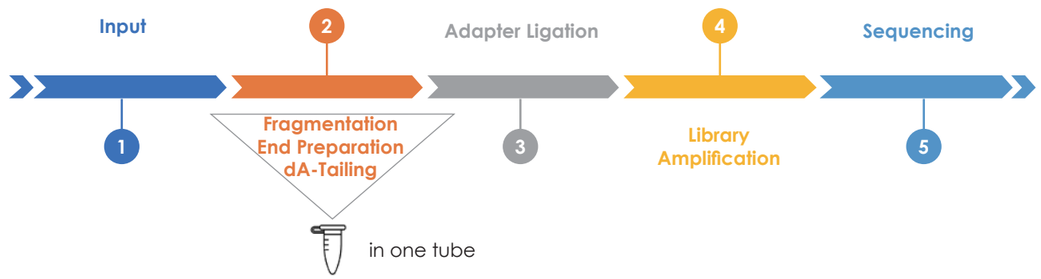


Figure 3 Mutation detection performance

VAHTS Universal Plus DNA Library Prep Kit for Illumina V2 (Vazyme #ND627)

VAHTS Universal Plus DNA Library Prep Kit for Illumina V2 (Vazyme #ND627) can reduce the false-positive mutation in the library preparation by enzymatic fragmentation. The kit combines DNA fragmentation, end repair, and dA-tailing into one step and can prepare PCR-Free libraries. It is perfectly compatible with DNA from different samples and inputs.

Workflow



Features

• High library conversion rate

Using salmon gDNA as the template, PCR-Free libraries were prepared from different manufacturers to evaluate the performance. Compared with similar products, Vazyme #ND627 has basically the same library conversion rate.

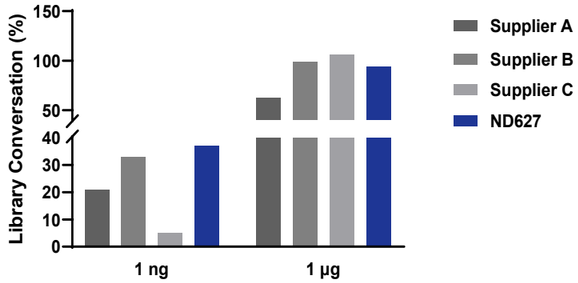


Figure 1 Conversion rate under different inputs

• Lower false positive rate

Vazyme #ND627 is not significantly different from the product of Supplier B in terms of Soft Clip and Invert Chimera detection. And the detection rates are lower than those of similar products form other companies, which demonstrates excellent control of false positive rate.

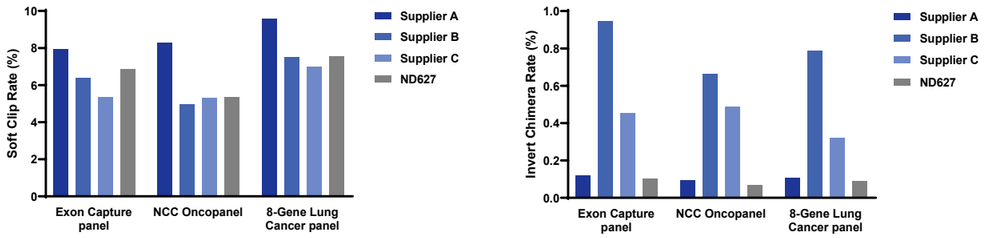


Figure 2 Soft Clip and Invert Chimera detection

• SNP and InDel detection

Use F-measure to evaluate the sensitivity and accuracy of SNP and InDel detection. Compared with similar products, Vazyme #ND627 has has significant advantages in SNP and InDel detection.

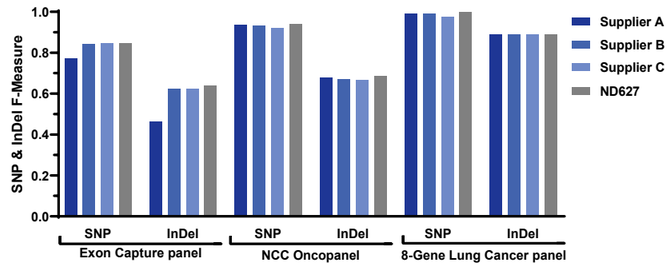
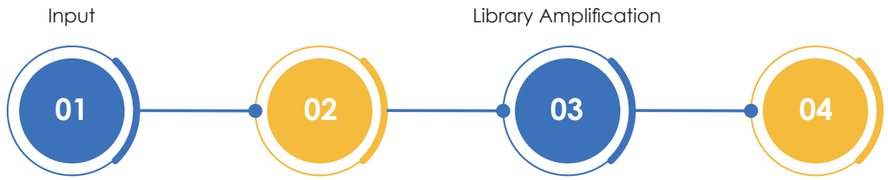


Figure 3 SNP and InDel detection

TruePrep Flexible DNA Library Prep Kit for Illumina (Vazyme #TD504)

TruePrep Flexible DNA Library Prep Kit for Illumina enables the preparation of 100 pg - 500 ng DNA inputs into sequencing libraries dedicated to the Illumina sequencing platform. Compared with conventional transposase library preparation kits, this kit significantly shortens the library preparation time and improves the compatibility of DNA template inputs by chemically coupling the transposase to magnetic beads.

Workflow



Features

• Support a broad DNA input range (100 pg - 500 ng)

Using 293 gDNA as templates, libraries were prepared from different manufacturers with different input DNA. The results show that Vazyme #TD504 has a higher library yield and average size is consistent with Supplier I.

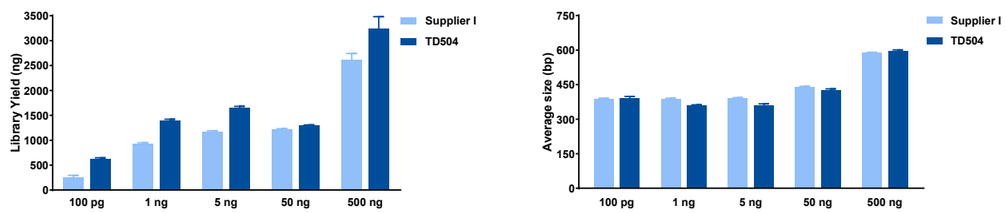


Figure 1 Input DNA and average size

• Wide compatibility with multiple sample types

Using gDNA of different species as templates, libraries were prepared from different manufacturers. Compared with similar products, Vazyme #TD504 can efficiently prepare libraries under various samples and has higher yields than Supplier I.

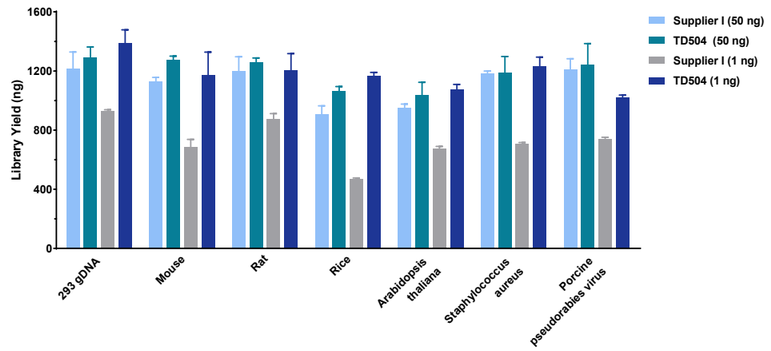


Figure 2 Library yields under various samples

• Microorganism detection

Microorganisml detection models were established: add 10 pg (1/100), 1 pg (1/1,000) and 100 fg (1/10,000) of *E.coli* gDNA and λDNA to 1 ng of 293 gDNA. The same amount of clean reads was intercepted from downstream data and compared with Supplier I. Vazyme #TD504 has higher mapped reads in all models.

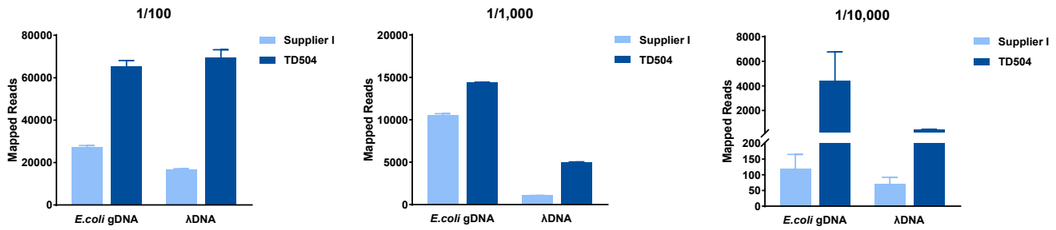
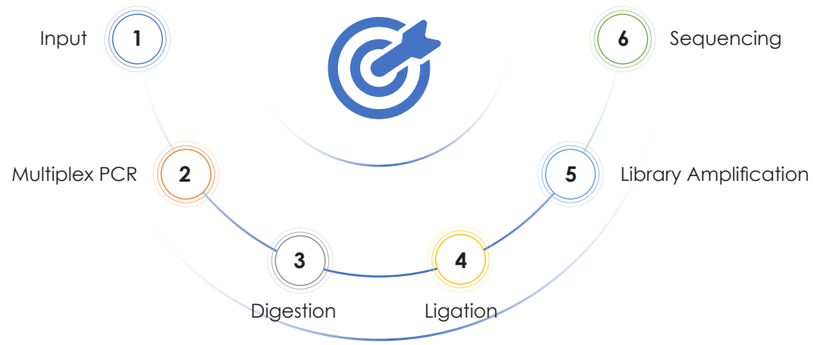


Figure 3 Mapped reads under different models

VAHTS AmpSeq Library Prep Kit V3 (Vazyme #NA210)

VAHTS AmpSeq Lilbrary Prep Kit V3 is based on ultra-multiplex PCR, introducing several core technologies such as end primer digestion and ligating adapters to prepare a library. Compared to the previous generation (Vazyme #NA201), this kit improves the high coverage and high uniformity of the amplicon library. The upgraded digestion module can effectively solve the problem of PCR products contamination and improve data utilization. With this kit, the sequencing results are more stable and reliable, helping researchers to complete high quality library preparation quickly and easily.

Workflow



Features

• High library yield

Using 293 gDNA as the template, libraries were prepared from Vazyme #NA210 and Supplier A. Vazyme #NA210 can efficiently prepare libraries and has higher yields than similar product under various panels and different inputs.

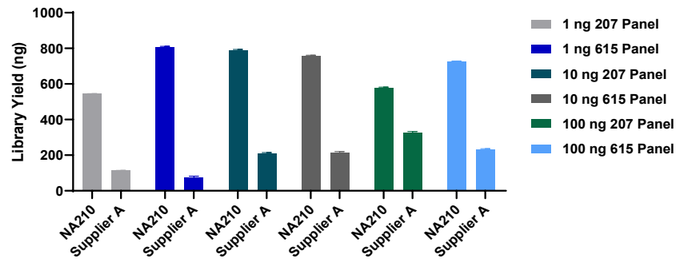


Figure 1 Library yield under different panels

• High coverage rate

Using 293 gDNA as the template, libraries were prepared with Vazyme #NA210 and Supplier A under different inputs and panels, respectively. The results show that the Vazyme #NA210 has higher coverage rate than Supplier A.

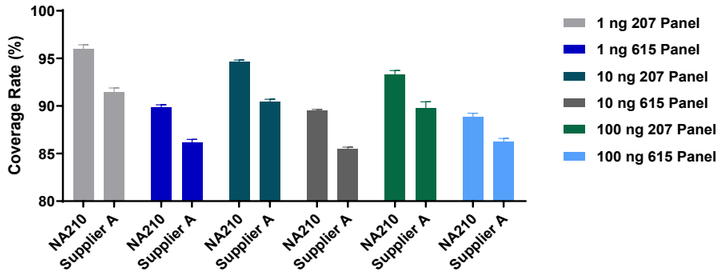


Figure 2 Coverage rate under different inputs and panels

• High uniformity rate

Using 293 gDNA as the template, libraries were prepared with Vazyme #NA210 and Supplier A under different inputs and panels, respectively. The results of uniformity rate show that less than 1% difference between Vazyme #NA210 and Supplier A in relative sequencing depth 0.25-1.75 (%) and <0.2 (%).

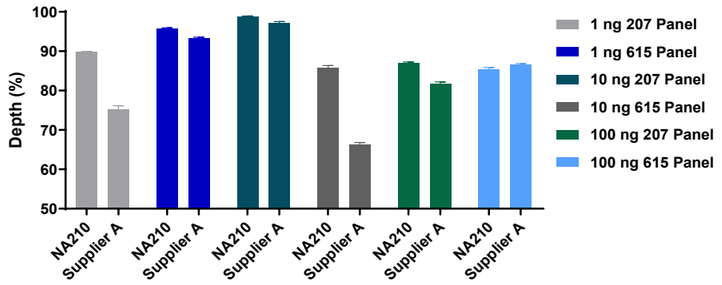


Figure 3 Relative sequencing depth 0.25-1.75 (%)

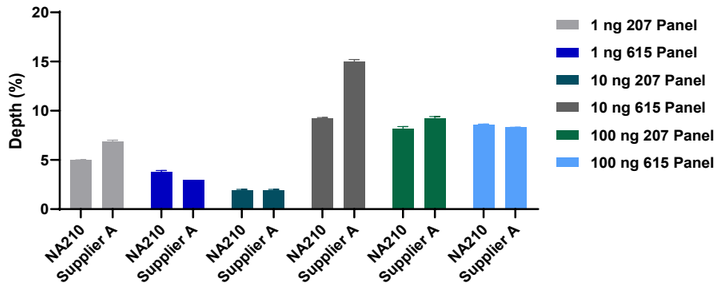


Figure 4 Relative sequencing depth <0.2 (%)

02

RNA Sequencing

RNA Sequencing

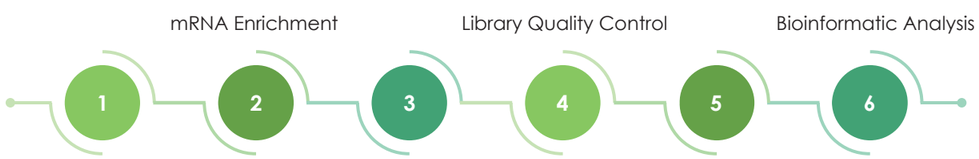
Background

Brief Introduction

RNA-Seq, a tool for tarnscriptomics research, refers to the collection the information of RNA under certain physiological conditions with high-throughput sequencing technology. Transcriptomics refers to the collection of all transcripts information in the cells, including mRNA, rRNA, tRNA and other non-coding RNA.

Transcriptomics is used for gene function and gene structure research, which could reveal specific biological processes and molecular mechanism in the process of disease occurrence. And RNA has been already applied in many fields, such as pathogen gene expression analysis, tumor early screening, drug development, etc.

Experiment Process



RNA Quality Control

RNA quality control is essential before experiment. The total RNA amount and purity of RNA samples must meet the conditions required in the products manual, usually containing RNA amount, integrity (RIN score), OD260/OD280 and OD260/OD230.

mRNA Enrichment

There are two mainly methods to obtain more transcription information from mRNA, mRNA capture and rRNA depletion. mRNA capture is based on the feature of eukaryotic mRNA with poly(A) tail which could be captured by oligo (dT) magnetic beads. rRNA depletion is based on probes hybridization and the complex of rRNA and probes are depleted subsequently. For small RNA-Seq, there is specific way to collect these information.

RNA Library Preparation

The general procedures of RNA library preparation contain RNA fragmentation and random primers annealing, 1nd strand cDNA synthesis, 2nd strand cDNA synthesis, adapter ligation, library amplification, library purification and quality control.

The small RNA library preparation is based on the 3'/5' ends adapter ligation strategy, and the mainly procedures contain 3' adapter ligation, 5' adapter ligation, cDNA synthesis, library amplification, library purification and quality control.

Library Quality Control

For library quantification, two mainly methods based on dsDNA fluorescent dyes or qPCR are used. Library size distribution is usually detected by Aglient 2100 Bioanalyzer.

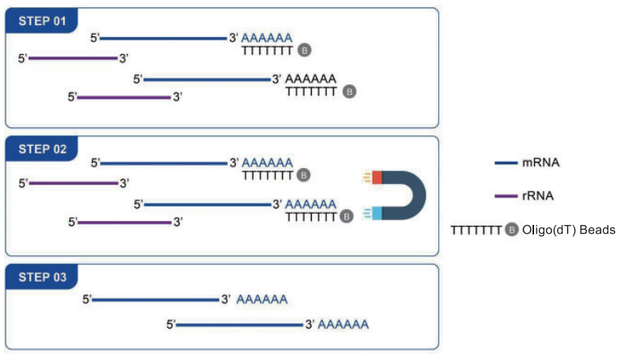
RNA Library Preparation Kit

RNA Quality Control		
Application	**Product Name**	**Cat. No.**
RNA concentration detection	Equalbit RNA HS Assay Kit	EQ211
	Equalbit RNA BR Assay Kit	EQ212
mRNA Enrichment		
Application	**Product Name**	**Cat. No.**
mRNA capture	VAHTS mRNA Capture Beads 2.0	N403
rRNA depletion	Ribo-off rRNA Depletion Kit (Human/Mouse/Rat)	N406
	Ribo-off Globin & rRNA Depletion Kit (Human/Mouse/Rat)	N408
	Ribo-off rRNA depletion kit (Plant)	N409
	Ribo-off rRNA Depletion Kit V2 (Bacteria)	N417
	Ribo-MagOff rRNA Depletion Kit (Human/Mouse/Rat)	N420
	FastSelect rRNA Kit (Human)	N460
RNA purification	VAHTS RNA Clean Beads	N412
RNA Library Preparation		
Application	**Product Name**	**Cat. No.**
RNA Library Preparation	VAHTS Universal V10 RNA-seq Library Prep Kit for Illumina	NR606
	VAHTS Universal V10 RNA-seq Library Prep Kit for MGI	NRM606
	VAHTS Universal V8 RNA-seqLibrary Prep Kit for Illumina	NR605
	VAHTS Universal V8 RNA-seq Library Prep Kit for MGI	NRM605
Small RNA Library Preparation	VAHTS Small RNA Library Prep Kit for Illumina V2	NR811

VAHTS mRNA Capture Beads 2.0 (Vazyme #N403)

VAHTS mRNA Capture Beads 2.0 is 1 μm Oligo(dT)-coupled paramagnetic microspheres intended for the isolation of poly(A)$^+$ RNA from purified total RNA. The magnetic separation technology allows for the isolation of intact mRNA in small sample volumes, eliminating the need for mRNA precipitation.

Workflow



Features

• Short operation time

The whole mRNA capture workflow can be completed in 1 h.

• Wide species and RNA input compatibility

Use 10 ng, 50 ng, 100 ng, 1 μg and 5 μg total RNA of maize and rat as templates for library preparation. Compared to Supplier E-4, Vazyme #N403 has higher library yield.

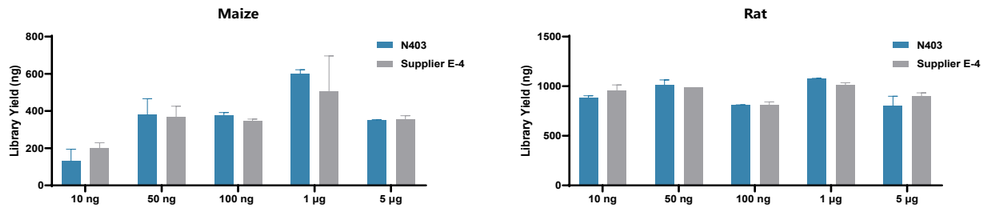


Figure 1 Library yield at different inputs in maize and rat

• Specific mRNA enrichment with lower residual rRNA

Use 1 μg of total RNA from different species as templates for library preparation. Compared to Supplier E-4, Vazyme #N403 has better mRNA ratio and lower residual rRNA.

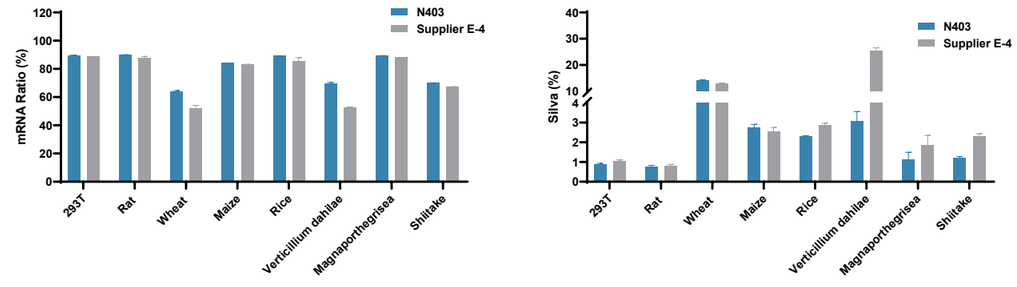


Figure 2 mRNA ratio and residual rRNA ratio at 1 μg input in different species

Ribo-off rRNA Depletion Kit (Human/Mouse/Rat) (Vazyme #N406)

Ribo-off rRNA Depletion Kit (Human/Mouse/Rat) is designed for removing ribosomal RNA (rRNA) (including cytoplasmic 28S, 18S, 5.8S, 5S rRNA, and mitochondrial 16S, 12S rRNA) while retaining mRNA and other non-coding RNA. The kit is applicable to both intact and partially degraded RNA samples (e.g. FFPE RNA), and the resulting rRNA-depleted RNA can be used for the analysis of mRNA and non-coding RNA such as lncRNA.

Workflow

Features

• Short operation time

The whole rRNA depletion workflow can be completed in 2 h.

• Wide RNA input compatibility

Use 50 ng, 100 ng and 1 μg total RNA from 293T cells as templates for library preparation. Compared to Supplier Q, Vazyme #N406 has higher library yield and mapping rate.

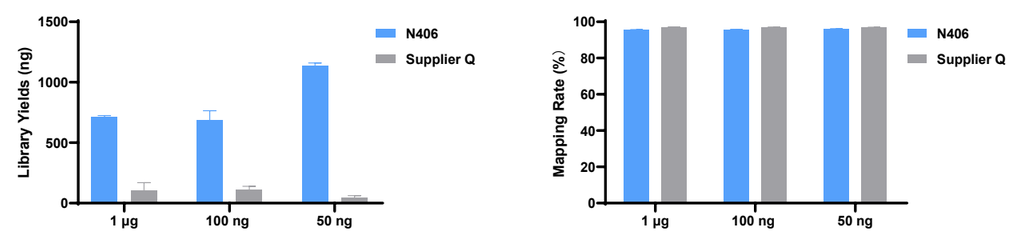


Figure 1 Library yield and mapping rate at different inputs

• Excellent rRNA depletion efficiency

Use 50 ng, 100 ng and 1 μg total RNA from 293T cells as templates. Vazyme #N406 has lower residual rRNA ratio and more expression genes than Supplier Q.

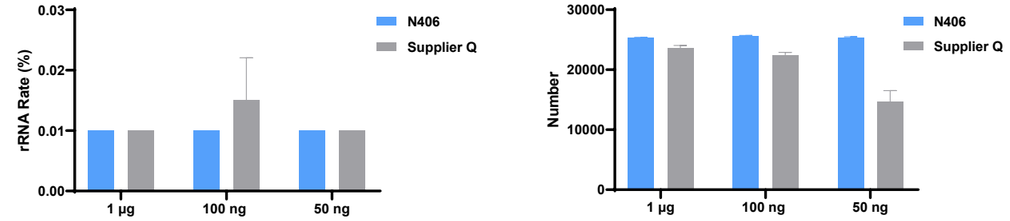
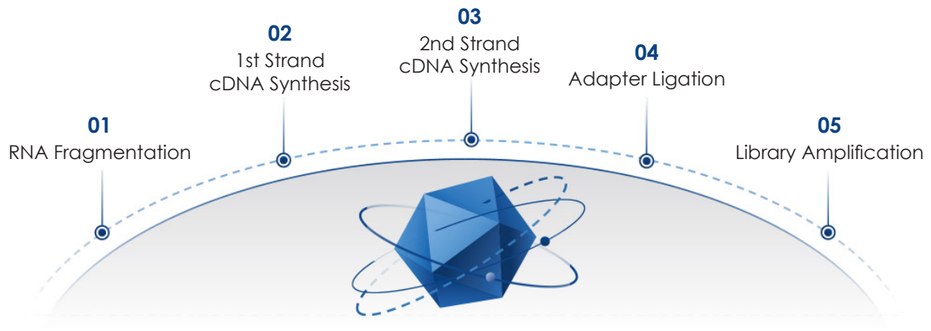


Figure 2 rRNA rate and expression genes at different inputs

VAHTS Universal V10 RNA-seq Library Prep Kit for Illumina (Vazyme #NR606)

VAHTS Universal V10 RNA-seq Library Prep Kit for Illumina is a RNA library preparation kit specifically suitable for Illumina high-throughput sequencing platforms. The kit is applicable to RNA library preparation of total RNA, mRNA from eukaryotes with good integrity that have been enriched by Poly(A) method or RNA have been enriched by rRNA depletion. And two types of 2nd strand cDNA synthesis buffers included in the kit are used for non-strand-specific or strand-specific RNA-seq library preparation.

Workflow



Features

• Short operation time

The whole RNA library preparation workflow can be completed in 3 h.

• Extensive RNA input and species compatibility

Use 10 ng, 100 ng, 500 ng and 1 μg total RNA from 293T cells and 500 ng total RNA from different species as templates for library preparation. Compared to Supplier A, Vazyme #NR606 has higher library yield under various RNA inputs and species.

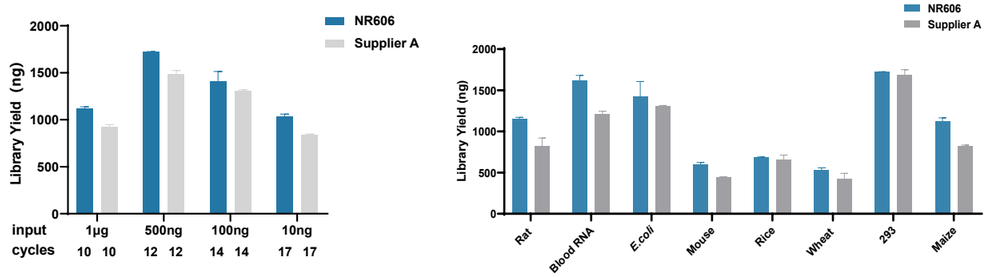


Figure 1 Library yield at different inputs and species

• High mRNA ratio and expression genes

Use 500 ng total RNA from different species as templates for library preparation. Compared to Supplier A, Vazyme #NR606 has higher mRNA ratio and expression genes at different species.

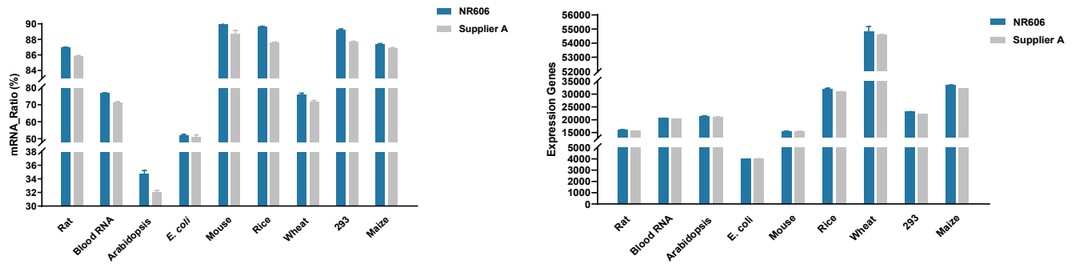


Figure 2 mRNA ratio and expression genes at different species

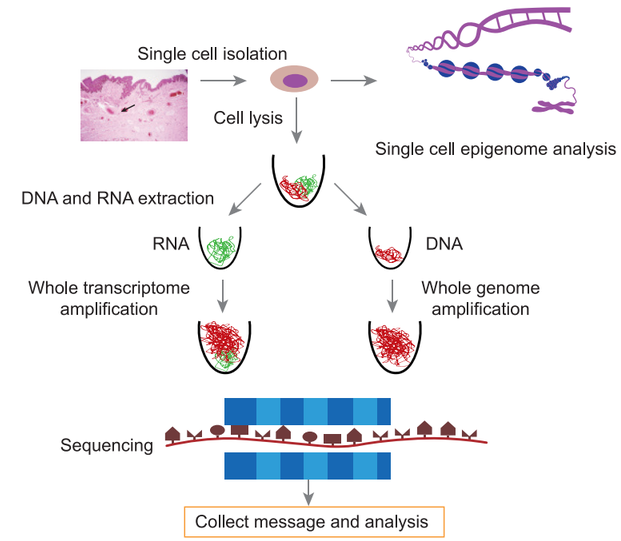
03

Single-cell Sequencing

Single-cell Sequencing

Background

Single-cell sequencing technologies refer to the sequencing of a single-cell genome or transcriptome, so as to obtain genomic, transcriptome or other multi-omics information to reveal cell population differences and cellular evolutionary relationships. In cancer, sequencing the DNA of individual cells can give information about mutations carried by small populations of cells. In development, sequencing the RNA expressed by individual cells can give insight into the existence and behavior of different cell types. In microbial systems, a population of the same species can appear genetically clonal. Still, single-cell sequencing of RNA or epigenetic modifications can reveal cell-to-cell variability that may help populations rapidly adapt to survive in changing environments. Single-cell sequencing usually includes the following processes:



Single-cell Amplification Kit

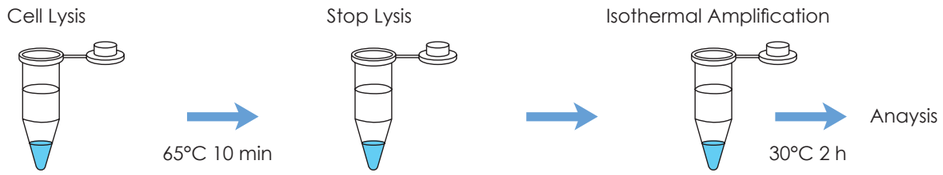
Application	Product Name	Cat. No.
Whole Genome	Discover-sc Single Cell WGA Kit	N603
Full Transcriptome	Discover-sc WTA Kit V2	N711

Note: It's recommended to use Vazyme #TD501-503/TD504 for downstream library preparation after single-cell amplification.

Discover-sc Single Cell WGA Kit (Vazyme #N603)

Discover-sc Single Cell WGA Kit is based on multiple displacement amplification (MDA) and is designed for unbiased whole genome amplification from single cell and other micro samples. The sizes of amplification products are between 2 kb to 100 kb, with a coverage greater than 95% and an average length higher than 15 kb. The products can be widely applied to whole genome sequencing, whole exome sequencing, large fragment copy number variation analysis, microsatellite analysis, qPCR analysis, or gene chip analysis.

Workflow



Features

• High uniformity

1.Use the whole genome amplification product of single 293 cell as a template to perform qPCR. All 16 pairs of qPCR primers could amplify normally and the C_T values are all between 22-28, which indicates that the Vazyme #N603 kit has good amplification uniformity.

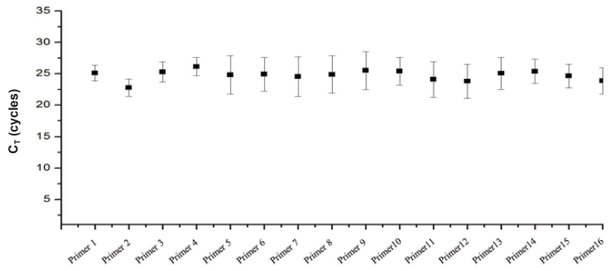


Figure 1 qPCR results

2.Using single cell as a template, genome amplification was performed with Vazyme #N603 kit and libraries were prepared with Vazyme #TD502. The results show that the reads are relatively evenly distributed in different genomes, indicating that Vazyme #N603 has good amplification uniformity and can be used for large fragment copy number variation analysis.

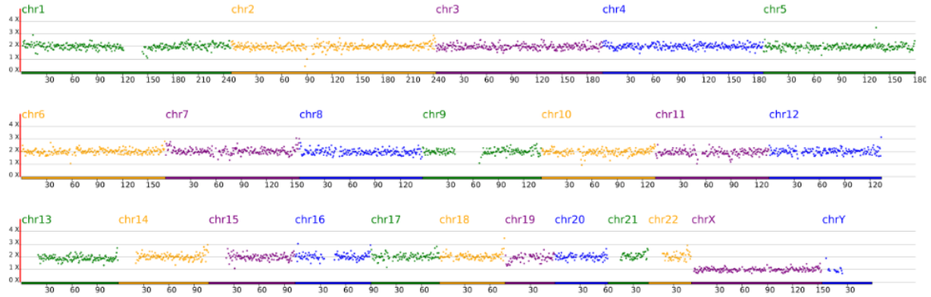


Figure 2 Whole genome copy number scatter plot

• High coverage rate

Vazyme #N603 uses an optimized reaction system that enables whole genome amplification of single cell and genome coverage more than 95%, which is higher than Supplier Q and Y.

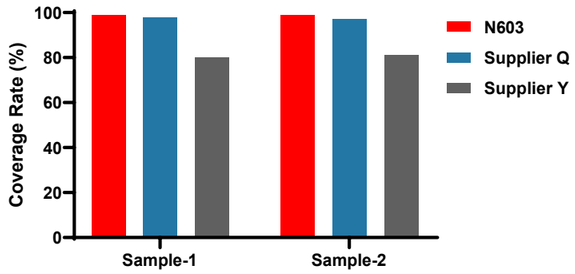
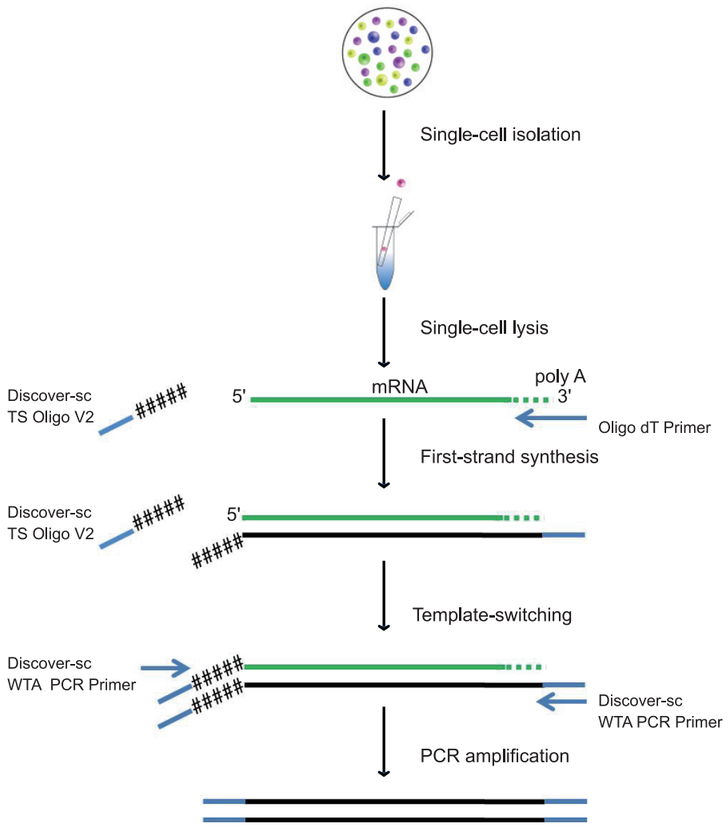


Figure 3 Coverage rate

Discover-sc WTA Kit V2 (Vazyme #N711)

Discover-sc WTA Kit V2 is capable of obtaining sufficient samples for sequence analysis through first-strand cDNA synthesis and amplification using 1 - 1,000 cells or 10 pg - 10 ng of total RNA as templates, thus overcoming the technical difficulty that the conventional mRNA-seq method cannot be used for sequence analysis of trace samples such as single cells due to the low RNA content. The upgraded version features substantially improved detection sensitivity and volume compatibility, and is more suitable for the detection of low-abundance genes and low-concentration templates.

Workflow



Features

• High gene detection rate

Vazyme #N711 detects amplification products with high sensitivity and up to 15,000 genes were detected in a single 293T cell.

Table 1 Mapped rate from different companies

Samples	Expression Genes	Mapped to genome	Mapped to rRNA	Mapped to exon	Mapped to intron	Mapped to intergenic
Vazyme-1	14807	88.4%	1.24%	86.1%	10.5%	3.46%
Vazyme-2	15138	88.2%	3.06%	86.9%	9.4%	3.72%
Supplier C-1	14367	84.6%	1.76%	85.9%	10.3%	3.77%
Supplier C-2	15285	84.7%	2.27%	82.0%	13.5%	4.56%

• High uniformity and no bias

The result shows that Vazyme #N711 ensures good coverage of the 5' and 3' genes.

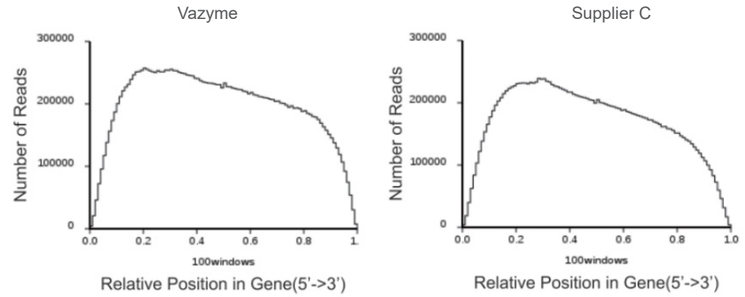


Figure 1 Relative position in gene and number of reads

• High expression replicate correlation

The results show that Vazyme #N711 has higher expression replicate correlation than Supplier C.

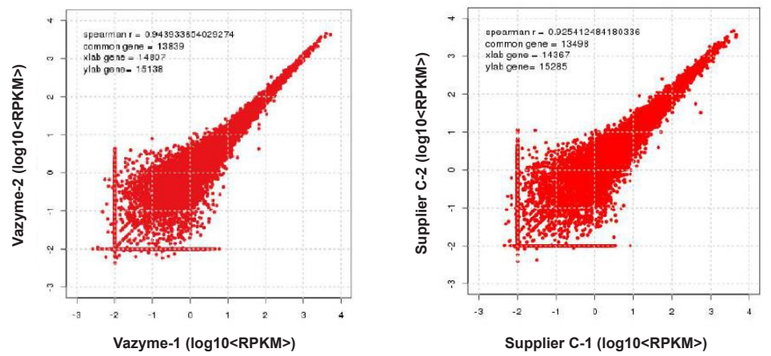


Figure 2 Expression replicate correlation

04

Epigenetics

Epigenetics

Background

Brief Introduction

Epigenetics involves heritable structural and biochemical alterations of the chromatin without altering the DNA sequence. Mechanisms of epigenetics include DNA methylation, chromatin accessibility, histone modifications, non-coding RNAs and more. Disruption of gene expression patterns regulated by epigenetics can lead to autoimmune diseases, cancers, and many other disorders.

Experiment Process

Epigenetic Library Preparation Kit

DNA Methylation		
Application	**Product Name**	**Cat. No.**
DNA Conversion	EpiArt Magnetic DNA Methylation Bisulfite Kit	EM103
	EpiArt DNA Enzymatic Methylation Kit	EM301
Library Preparation	EpiArt DNA Methylation Library Kit for Illumina V3	NE103
Chromatin Accessibility		
Application	**Product Name**	**Cat. No.**
Complete ATAC-Seq Solution	Hyperactive ATAC-Seq Library Prep Kit for Illumina	TD711
Library Preparation Module	TruePrep DNA Library Prep Kit V2 for Illumina	TD501/TD502/TD503
Histone Modifications		
Application	**Product Name**	**Cat. No.**
CUT&Tag	Hyperactive Universal CUT&Tag Assay Kit for Illumina Pro	TD904
	Hyperactive Universal CUT&Tag Assay Kit for Illumina	TD903
	VAHTS Concanavalin A-coated Magnetic Beads Pro	N515
CUT&RUN	Hyperactive pG-MNase CUT&RUN Assay Kit for PCR/qPCR	HD101
	Hyperactive pG-MNase CUT&RUN Assay Kit for Illumina	HD102

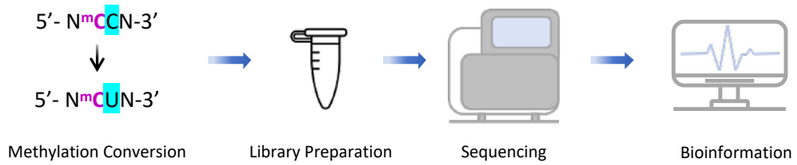
EpiArt DNA Enzymatic Methylation Kit (Vazyme #EM301)
EpiArt DNA Methylation Library Kit for Illumina V3 (Vazyme #NE103)

DNA methylation is a form of chemical modification of DNA that alters genetic expression without changing the DNA sequence. DNA methylation reserach with high-throughput sequencing consists of DNA conversion and library preparation. For DNA conversion, both bisulfite and enzymatic treatment could convert unmethylated cytosine into uracil and methylated cytosine are retained. And the genome-wide DNA methylation information with single base resolution is revealed with high-throughput sequencing.

(Vazyme #EM301)

(Vazyme #NE103)

Workflow and Principle



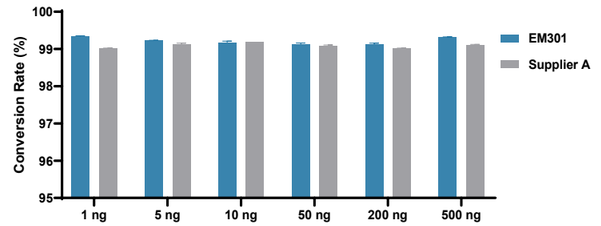
Features

- **Less DNA damage**

Enzymatic conversion causes minimal damage of DNA than chemical conversion.

- **High methylation conversion rate**

Use 1 ng, 5 ng, 10 ng, 50 ng, 200 ng and 500 ng NA12878 gDNA and human HCT116 cell gDNA, human cfDNA, arabidopsis gDNA, maize gDNA as templates for library preparation with Vazyme #NE103. Compared to Supplier A, Vazyme #EM301 has higher conversion rate under different DNA inputs and species.



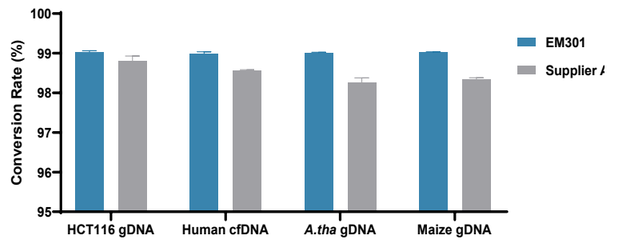
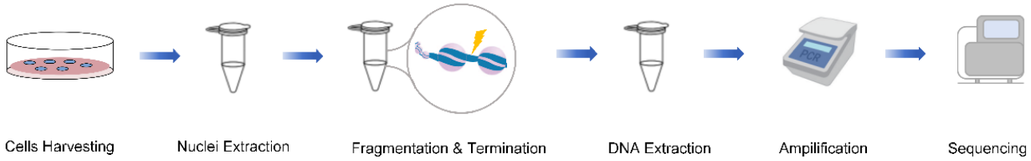


Figure 1 Conversion rate at different inputs and species

Hyperactive ATAC-Seq Library Prep Kit for Illumina (Vazyme #TD711)

Assay for Transposase-Accessible Chromatin with high throughput sequencing (ATAC-Seq) is a tool for chromatin accessibility research. In ATAC-Seq, transposome is used to simultaneously cut and ligate adapters for high-throughput sequencing at chromatin regions of increased accessibility.

Workflow



Features

• Wide cell input compatibility

In terms of cell inputs (among 100-100,000 Hela cells), Vazyme #TD711 has higher library yield under different cell amounts than Supplier A and Supplier B.

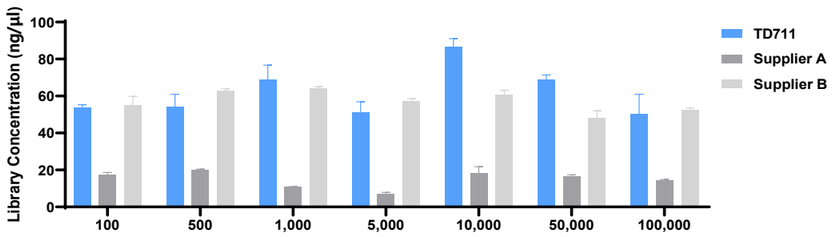


Figure 1 Library yield at different inputs

• High-quality sequencing results

Input 100, 500, 5,000, 10,000, 50,000 and 100,000 Hela cells, respectively. The IGV displays the same gene positions with low background and high signal-to-noise ratio.

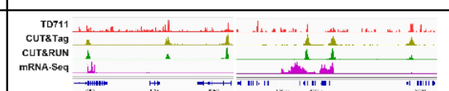
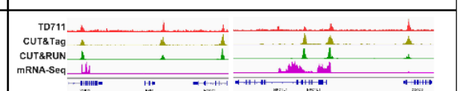
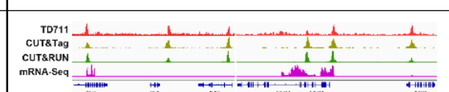
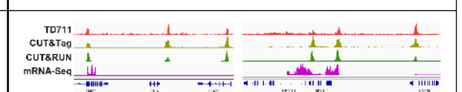
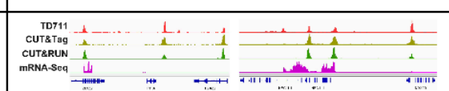
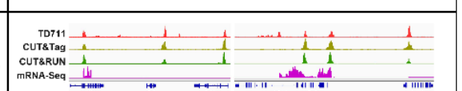
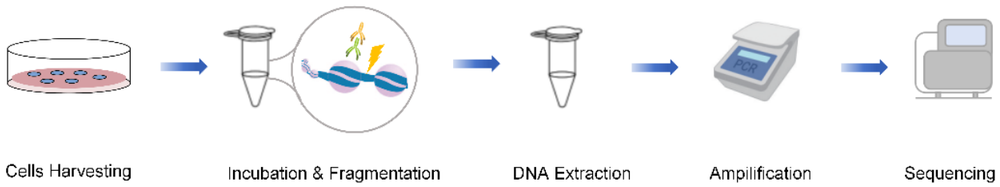
Input amount (cell)	IGV Visualization	Input amount (cell)	IGV Visualization
100		500	
5,000		10,000	
50,000		100,000	

Figure 2 IGV view at different inputs

Hyperactive Universal CUT&Tag Assay Kit for Illumina Pro (Vazyme #TD904)

Cleavage Under Targets & Tagmentation (CUT&Tag) technology is a new method to investigate protein-DNA interactions. In CUT&Tag, chromatin protein is bound in situ by a specific antibody, which then tethers protein A/G-transposome. Activation of the pA/G-transposome efficiently produces fragment libraries with superior resolution and minimal background noise.

Workflow



Features

• Short operation time

Whole CUT&Tag workflow can be completed in 9 h.

• Wide cell input compatibility

Use different cell amounts of 293T cells for library preparation in H3K4me3 system. Vazyme #TD904 is compatible with 10- 100,000 cells with high signal-to-raise ratio.

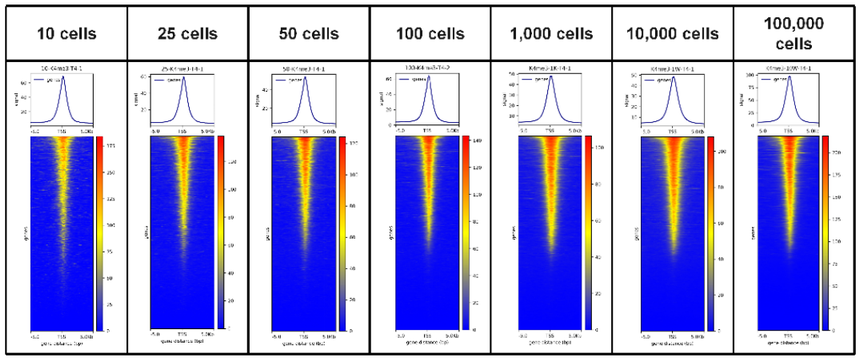


Figure 1 TSS enrichment in H3K4me3 system at 10-100,000 cells

• High-quality sequencing results

The results from CUT&Tag (H3K4me3, RNA PolII and H3K27me3 systems), ATAC-Seq and mRNA-Seq were co-analyzed. As the IGV view shown, Vazyme #TD904 attains valid results with high signal-to-raise ratio.

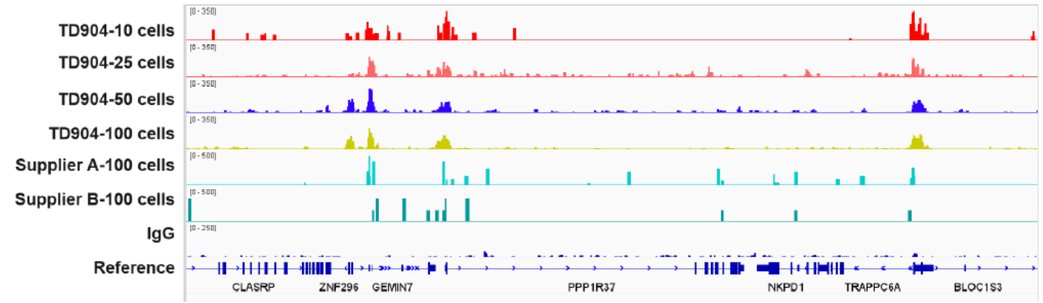
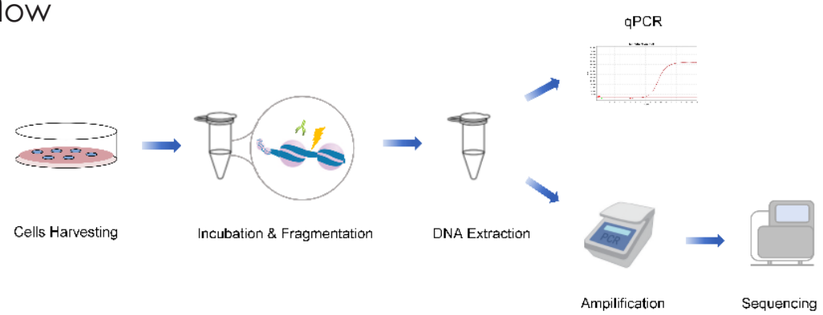


Figure 2 IGV view for multi techniques co-analysis

Hyperactive pG-MNase CUT&RUN Assay Kit for Illumina (Vazyme #HD102)

Cleavage Under Targets and Release Using Nuclease (CUT&RUN) is a new method for studying protein-DNA interactions. In CUT&RUN, cells are incubated with first antibody, which is then bound by a pG-MNase. Upon activation of tethered pG-MNase, the bound complex is excised and released into the supernatant for DNA extraction. The extracted products could be used for qPCR detection and sequencing analysis through library preparation.

Workflow



Features

• Short operation time

Whole CUT&RUN workflow can be completed in 11 h.

• Wide cell input compatibility

Use different cell amounts of 293T cells for library preparation in H3K4me3 system. Vazyme #HD102 is compatible with 5,000- 500,000 cells with high signal-to-raise ratio.

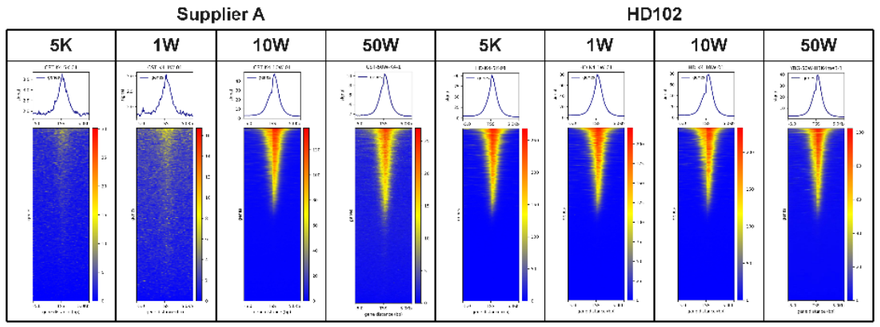


Figure 1 TSS enrichment in H3K4me3 system at 5,000- 500,000 cells

• Accurate Detection

Vazyme #HD102 accurately detects of euchromatin and heterochromatin with high signal-to-noise ratio.

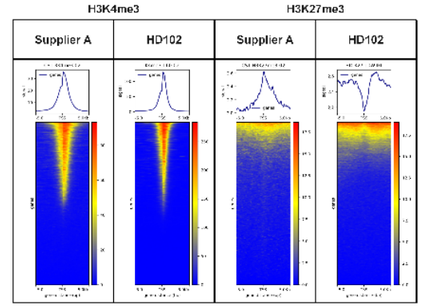


Figure 2 TSS enrichment in H3K4me3 and H3K27me3 systems

05

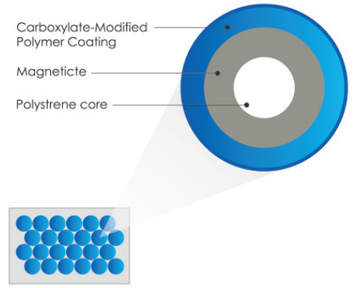
Clean up Beads & Library Quantification

Clean up Beads

Background

Brief Introduction

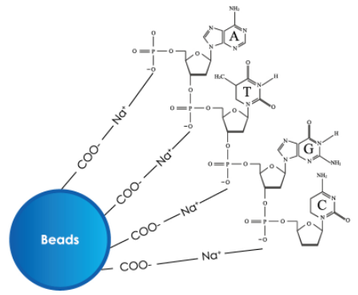
The magnetic beads are usually divided into three layers. The core is generally a support material, such as polystyrene. The intermediate layer is magneticte. The material of the magnetic layer is usually Fe_3O_4, which is mainly used for adsorption with the magnet on the magnetic frame to achieve the purpose of separating nucleic acid and reaction solution. The coat is a functional group modification layer, such as carboxylate group.



Structure of magnetic beads

Purification principle

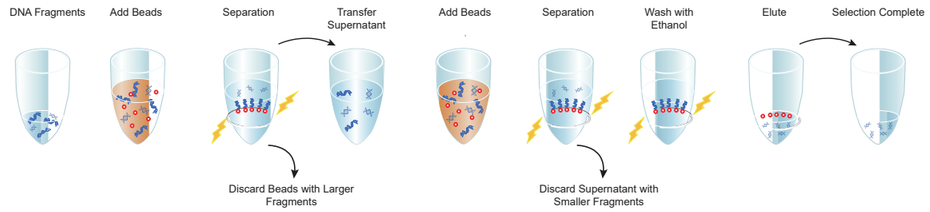
In the buffer environment, DNA molecules will be compressed from linear to spherical, exposing a large number of negatively charged groups on the nucleic acid framework. The cation in buffer connects nucleic acid and magnetic beads to form a structure of anion-cation-anion", also known as "salt bridge". This allows DNA to be specifically adsorbed to the surface of the magnetic beads. After the buffer is removed, aqueous molecules are added, the salt bridge is broken, and the nucleic acid is purified from the reaction solution.



Structure of "salt bridge"

Size selection principle

The magnetic beads will preferentially bind longer nucleic acid fragments. When perform the size selection, the expected size of library fragments can be obtained by controlling the amount of beads added in two rounds. Add the beads in the first round will bind the larger fragments and the unexpected fragments can be removed by discarding the beads. Then, beads are added in the second round to the supernatant. The beads preferentially bind the remaining larger fragments in the supernatant and then the unexpected short fragments are removed by discarding the supernatant. After two rounds beads selection, we can obtain the expected medium-sized fragment.



Principle of size selection

Reagents for Clean up Beads

Product Name	Cat. No.	Application
VAHTS DNA Clean Beads	N411	DNA purification and library selection
VAHTS RNA Clean Beads	N412	RNA purification
VAHTS CA-28 Streptavidin Beads	N512	Streptavidin magnetic beads
Magnetic Separation Rack	CM101	32 well (200 μl/well)
	CM103	24 well (1.5 ml/well)

VAHTS DNA Clean Beads

VAHTS DNA Clean Beads is a SPRI-based (Solid-Phase Reverse Immobilization) chemistry, compatible with DNA purification and size selection for fragment library preparation for Next Generation Sequencing. VAHTS DNA Clean Beads is suitable for all DNA/RNA library preparation protocols currently provided by manufacturers or published in academic journals. The usage of VAHTS DNA Clean Beads is similar to other suppliers. The yield and size distribution of the libraries prepared with VAHTS DNA Clean Beads are highly consistent with those suppliers.

Features

• Flexible and accurate size selection

The initial size of the library is 200-1,500 bp. The libraries were selected with Vazyme #N411 according to the conditions in the table below to obtain different size fragments. Vazyme #N411 can accurately select the fragment size.

Volume of beads for 1st round (Beads: DNA)	0.80 ×	0.70 ×	0.60 ×	0.55 ×	0.50 ×	0.45 ×	1.0 ×
Volume of beads for 2nd round (Beads: DNA)	0.20 ×	0.20 ×	0.20 ×	0.15 ×	0.15 ×	0.15 ×	
Average total length of the library (bp)	300	350	400	500	600	700	200-1,500

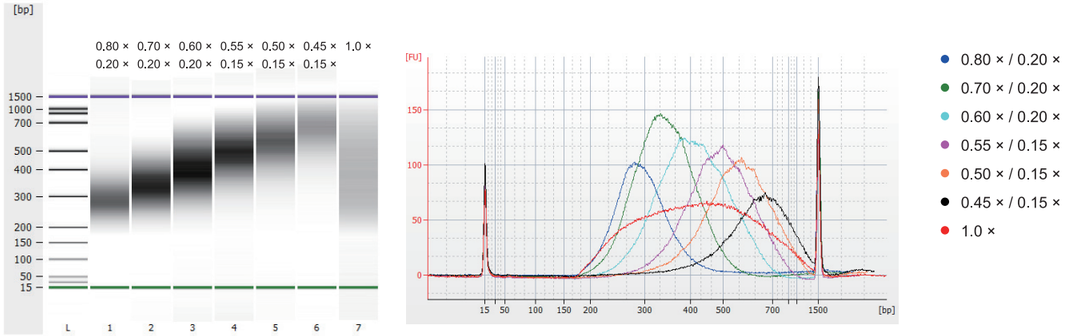


Figure 1 Schematic diagram of analyzing the library size selection with Agilent 2100 Bioanalyzer

Library Quantification

Background

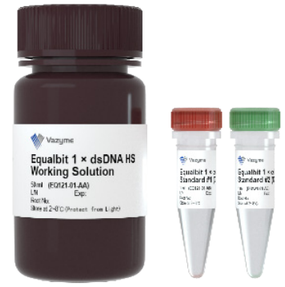
During the NGS process, the amount of input samples directly determines the strategy of library preparation. After library preparation was completed, the concentration of the library is also very important. It will directly affect the amount of sequencing data and the quality of sequencing. There are two methods for quantification, which are the absolute qualitative method based on qPCR and the Qubit quantitative method based on the fluorescence principle. However, the Qubit quantitative method is more convenient and accurate. Qubit Fluorometers is equipped with a high-sensitivity Qubit quantitative analysis kit, which can accurately quantify the concentration of DNA, RNA or protein. Only when fluorescent dyes are pacifically bound to the target molecules, they can emit fluorescent signals and report the concentration of target molecules.

Reagents for Library Quantification

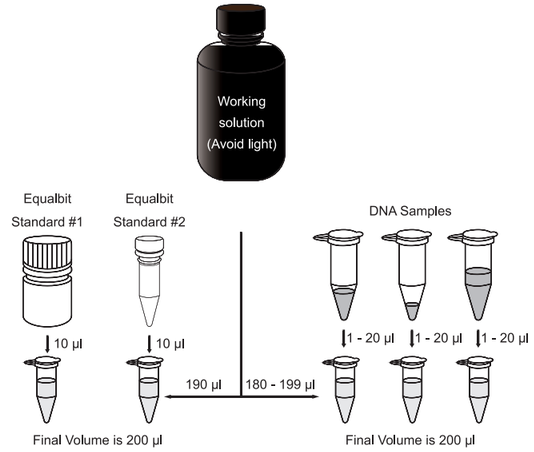
Product Name	Cat. No.	Application
Equalbit 1 × dsDNA HS Assay Kit	EQ121	Qubit Quantification
Equalbit RNA HS Assay Kit	EQ211	
Equalbit RNA BR Assay Kit	EQ212	
VAHTS Library Quantification Kit for Illumina	NQ101 - NQ102	qPCR Library Quantification
VAHTS Library Quantification Kit for Illumina (Low ROX Premixed)	NQ103	
VAHTS Library Quantification Kit for Illumina (High ROX Premixed)	NQ104	
VAHTS Library Quantification Kit for Illumina DNA Standard 1 - 6	NQ105	DNA standards
Library Dilution Buffer	NQ106	Dilution buffer

Equalbit 1 × dsDNA HS Assay Kit

Equalbit 1 × dsDNA HS (High Sensitivity) Assay Kit is a simple, sensitive and accurate double-stranded DNA (dsDNA) fluorescence quantitative detection kit, which contains pre-mixed working solution (with fluorescent dye) and dsDNA standards. It has good linearity in the range of 0.2 - 100 ng dsDNA, allowing accurate quantification of dsDNA concentrations from 10 pg/μl to 100 ng/μl. In addition, it has good impurity tolerance to common contaminants, such as RNA, salts, free nucleotides, proteins, solvents, detergents, etc. This kit provides a ready-to-use working solution so that operators can directly add samples into it, enabling simple dsDNA sample quantification by the Qubit Fluorometer.



Workflow



Features

• High sensitivity

For different concentrations of dsDNA samples, Vazyme #EQ121 and Supplier A were used for linear determination and the fluorescence values were read by Qubit Fluorometer 3.0. The results show that Vazyme #EQ121 has good linearity when the concentrations of dsDNA are in the range of 0.2 - 100 ng comparable to Supplier A.

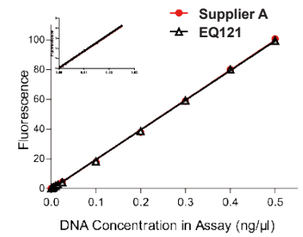


Figure 1 Comparison of linearity from 0.2 - 100 ng

• High specificity

Using 12 kinds of DNA samples, RNA samples and DNA plus RNA mixed samples in the range of 0.2 - 100 ng. Each sample were tested by Vazyme #EQ121 and Supplier A respectively. The results show that Vazyme #EQ121 can specifically bind to dsDNA and accurately quantify dsDNA even in the presence of RNA, which performance is comparable to Supplier A.

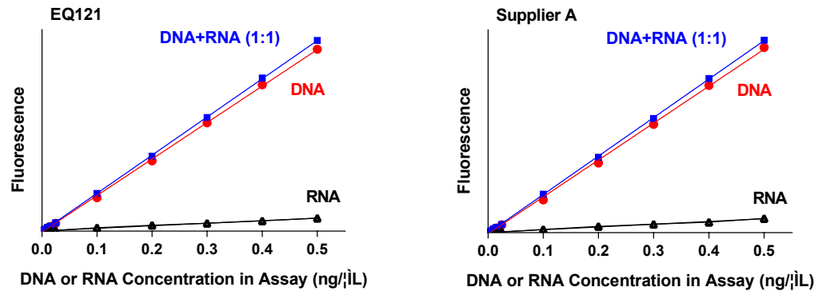


Figure 2 dsDNA specificity detection diagram

• Rapid binding of the dye

The results show that the deviation of the testing results by two kits is within 10% after adding samples for 1 min to 5 min. Indicating that the binding speed of the two kits is the same and saturation could be achieved within 2 min.

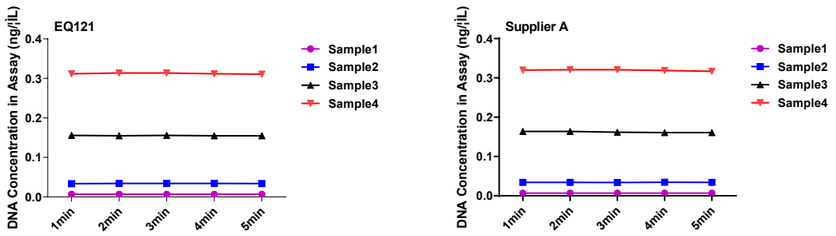


Figure 3 Comparison binding speed with dsDNA dye of E121 and Supplier A

06

Appendix

DNA Adapters

Sequencer	Product Name	Cat. No.
Illumina	VAHTS DNA Adapters Set 3 - Set 6 for Illumina	N805 - N808
	VAHTS Maxi Unique Dual Index DNA Adapters Set 1 - Set 4 for Illumina	N34201 - N34204
	VAHTS Multiplex Oligos Set 4 - Set 5 for Illumina	N321 - N322
	VAHTS Maxi Unique Dual Index Primers Set 1 - Set 4 for Illumina	N34401 - N34404
	VAHTS Dual UMI UDI Adapters Set 1 - Set 4 for Illumina	N351 - N354
	TruePrep Index Kit V2 for Illumina	TD202
	TruePrep Index Kit V3 for Illumina	TD203
	VAHTS AmpSeq Adapters for Illumina	NA111
MGI	VAHTS DNA Adapters Set 8 for MGI	NM108
	VAHTS PCR-Free DNA Adapters for MGI	NM10901 - NM10904
	VAHTS Maxi Unique Dual Barcode Primers Set 1 - Set 4 for MGI	NM34401 - NM34404
	VAHTS Dual UMI UDB Adapters Set 1 - Set 8 for MGI	NM35101 - NM35108
	TruePrep Dual Index Kit V1 for MGI	TDM201
Ion Torrent	VAHTS AmpSeq Adapters for Ion Torrent	NA121

RNA Adapters

Sequencer	Product Name	Cat. No.
Illumina	VAHTS RNA Adapters Set 3 - Set 6 for Illumina	N809 - N812
	VAHTS RNA Multiplex Oligos Set 1 - Set 2 for Illumina	N323 - N324
MGI	VAHTS RNA Adapters Set 8 for MGI	NM208-01/02
Small RNA library prep for Illumina	VAHTS Small RNA Index Primer Kit for Illumina	N813 - N816

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