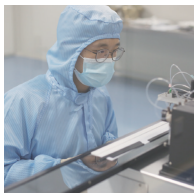Vazyme

2020

**2020 Product Catalogue**

**Reagents for NGS Library Preparation**

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# Overview of Vazyme

## Vazyme: InoVation in Enzyme Technology

With the faith of "InnoVation in Enzyme Technology", Vazyme Biotech Co., Ltd. has passionately focused on developing enzyme and antibody technologies and products for years. The Vazyme Biotech is now staffed by more than 1,000 employees. The headquarter is located in Nanjing of China with a R&D / manufacturing base that covers 25,000 m² and a GMP workshop of 4,000 m². Vazyme has developed a powerful sales network in China and is expanding into international markets.



## Vazyme Technologies and Products

With years of experience, Vazyme has developed six technology platforms that can be commonly used for R&D and manufacturing, including (1) directed enzyme evolution, (2) buffer optimization, (3) chemical synthesis, (4) high cell-density fermentation, (5) protein analysis, and (6) bioinformatics.

Based on the above platforms, Vazyme now provides a variety of products, solutions, and services, which fall into three major product lines, including (1) solutions for molecular biology research, (2) solutions for Next-Generation Sequencing (NGS) library preparation, and (3) enzymes as raw materials for industrial use.
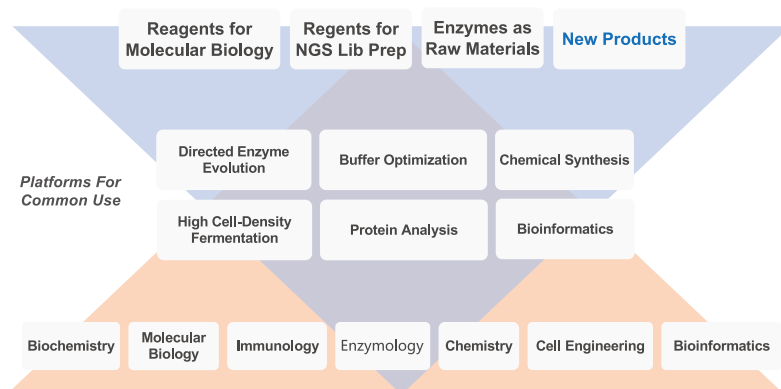


## Developing Technologies to Improve Human Health

Fascinated by the enzyme and antibody technologies, we regard enzymes and antibodies as the key factor of the biotechnology industry. Vazyme's vision is to develop technology to improve human health.

*Experts for Experts*

# 2020 Vazyme Product Catalogue

## Reagents for NGS Library Preparation

## Contents

Contents

# DNA-Seq

## ■ DNA Library Prep (for Illumina®)

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| **HOT** Transposase-based DNA Lib Prep Kits | TruePrep DNA Library Prep Kit V2 for Illumina® (50 ng) | TD501 | 24 rxn/96 rxn |
| | TruePrep DNA Library Prep Kit V2 for Illumina® (5 ng) | TD502 | 24 rxn/96 rxn |
| | TruePrep DNA Library Prep Kit V2 for Illumina® (1 ng) | TD503 | 24 rxn/96 rxn |
| | TruePrep Homo-N7 DNA Library Prep Kit for Illumina® | TD511/TD512/TD513 | 96 rxn |
| Single-Indexed Adapters | TruePrep Index Kit V4 for Illumina® | TD204/TD205/TD206/TD207 | 192 rxn |
| Dual-Indexed Adapters | TruePrep Index Kit V2 / V3 for Illumina® | TD202/TD203 | 96 kinds/384 kinds |
| **HOT** **New** Universal DNA Lib Prep Kits | VAHTS Universal DNA Library Prep Kit for Illumina® V3 | ND607-01/02 | 24 rxn/96 rxn |
| | VAHTS Universal DNA Library Prep Kit for Illumina® V3 (PCR-Free) | ND607-03/04 | 24 rxn/96 rxn |
| | VAHTS Universal DNA Library Prep Kit for Illumina® V5 | ND610-01/02 | 24 rxn/96 rxn |
| DNA Lib Prep Kits for Enzymatic Fragmentation | VAHTS Universal Plus DNA Library Prep Kit for Illumina® | ND617-01/02 | 24 rxn/96 rxn |
| FFPE DNA Lib Prep Kits | VAHTS Universal Pro DNA Library Prep Kit for Illumina® | ND608-01/02 | 24 rxn/96 rxn |
| **New** ssDNA Lib Prep Kits | VAHTS ssDNA Library Prep Kit for Illumina® | ND620-01/02 | 24 rxn/96 rxn |
| MP DNA Lib Prep Kits | VAHTS Mate Pair Library Prep Kit for Illumina® | ND104-01 | 48 rxn |
| Single-Indexed Adapters | VAHTS DNA Adapters Set1 / Set 2 for Illumina® | N801/N802-01/02 | 10 µl each/40 µl each |
| | VAHTS DNA Adapters Set 3 - Set 6 for Illumina® | N805/N806/N807/N808 | 20 µl each |
| Dual-Indexed Adapters | VAHTS Multiplex Oligos Set 4 / Set 5 for Illumina® | N321/N322 | 192 rxn |
| UMI Adapters | VAHTS Dual Index UMI DNA Adapters Set 1 - Set 4 for Illumina® | N331/N332/N333/N334 | 20 µl each |
| **New** Amplicon Lib Prep Kits | VAHTS AmpSeq Library Prep Kit V2 | NA201-01/02 | 24 rxn/96 rxn |
| | VAHTS AmpSeq Library Prep Kit V3 | NA210-01/02 | 24 rxn/96 rxn |
| Amplicon Lib Prep Adapters | VAHTS AmpSeq Adapters 1 - 24 for Illumina® | NA111-01/02 | 12 ×10 rxn |
| | VAHTS AmpSeq Adapters 25 - 96 for Illumina® | NA111-03/04/05 | 24 ×10 rxn |
| Cancer Panels | VAHTS AmpSeq Cancer HotSpot Panel | NA102-01 | 24 rxn |

## ■ DNA Library Prep (for Ion Torrent®)

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Universal DNA Lib Prep Kits | VAHTS Universal DNA Library Prep Kit for Ion Torrent® | ND701-01/02 | 24 rxn/96 rxn |
| Amplicon Lib Prep Kits | VAHTS AmpSeq Library Prep Kit V2 | NA201-01/02 | 24 rxn/96 rxn |
| **New** | VAHTS AmpSeq Library Prep Kit V3 | NA210-01/02 | 24 rxn/96 rxn |
| Amplicon Lib Prep Adapters | VAHTS AmpSeq Adapters 1 - 24 for Ion Torrent® | NA121-01/02 | 12 ×10 rxn |
| | VAHTS AmpSeq Adapters 25 - 96 for Ion Torrent® | NA121-03/04/05 | 24 ×10 rxn |

## ■ DNA Library Prep (for MGI®) **New**

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Universal DNA Lib Prep Kits | VAHTS Universal DNA Library Prep Kit for MGI® | NDM607-01/02 | 24 rxn/96 rxn |
| | VAHTS Universal DNA Library Prep Kit for MGI® V5 | NDM610-01/02 | 24 rxn/96 rxn |
| DNA Lib Prep Kits for Enzymatic Fragmentation | VAHTS Universal Plus DNA Library Prep Kit for MGI® | NDM617-01/02 | 24 rxn/96 rxn |
| FFPE DNA Lib Prep Kits | VAHTS Universal Pro DNA Library Prep Kit for MGI® | NDM608-01/02 | 24 rxn/96 rxn |
| Single-Indexed Adapters | VAHTS DNA Adapters Set 8 for MGI® | NM108-01/02 | 10 µl each/40 µl each |
| Dual-Indexed UMI Adapters | VAHTS Dual UMI Adapters for MGI® | NM301-01/02 | 10 µl each/40 µl each |
| Circularization Kit | VAHTS Circularization Kit for MGI® | NM201-01/02 | 16 rxn/48 rxn |
| Amplification Module | VAHTS HiFi Amplification Mix for MGI® | NM616-01/02 | 24 rxn/96 rxn |
| Amplicon Lib Prep Kits | VAHTS AmpSeq General Library Prep Kit for MGI® | NAM203-01/02 | 24 rxn/96 rxn |

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## Modules for DNA Library Prep

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| TurePrep Lib Amplification | TruePrep Amplify Enzyme | TD601 | 96 rxn |
| FFPE Repair | VAHTS DNA Damage Repair Kit | N208-01/02 | 24 rxn/96 rxn |
| Enzymatic Fragmentation | VAHTS Universal Plus Fragmentation Module | N209-01/02 | 24 rxn/96 rxn |
| DNA Lib Prep Modules | VAHTS Universal End preparation Module for Illumina® | N203-01/02 | 24 rxn/96 rxn |
| | VAHTS Universal Adapter Ligation Module for Illumina® | N204-01/02 | 24 rxn/96 rxn |
| | VAHTS HiFi Amplification Mix | N616-01/02 | 24 rxn/96 rxn |
| AmpSeq Multi-PCR | VAHTS AmpSeq Multi-PCR Module V2 | NA205-01/02 | 24 rxn/96 rxn |
| T4 DNA Polymerase | T4 DNA Polymerase | N101-01 | 2,000 U |
| T4 Polynucleotide Kinase | T4 Polynucleotide Kinase | N102-01 | 10,000 U |
| T4 DNA Ligase (Rapid) | T4 DNA Ligase (Rapid) | N103-01 | 600,000 U |
| Klenow DNA Polymerase | DNA Polymerase I Klenow Fragment | N104-01 | 5,000 U |
| | DNA Polymerase I Klenow Fragment exo- | N105-01 | 5,000 U |
| Phi29 DNA Polymerase | Phi29 MAX DNA Polymerase | N106-01/02 | 250 U/1,250 U |
| Amplification Module | Phanta Uc Super-Fidelity DNA Polymerase for Library Amplification | P507-01/02 | 100 U/500 U |

New (FFPE Repair), New (Enzymatic Fragmentation)

# RNA-Seq

## RNA Library Prep (for Illumina®)

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Total RNA Lib Prep Kits (rRNA Depletion) | VAHTS Total RNA-Seq (H/M/R) Library Prep Kit for Illumina® | NR603-01/02 | 24 rxn/96 rxn |
| Ultra Fast & Universal RNA Lib Prep Kits | VAHTS Universal V6 RNA-Seq Library Prep Kit for Illumina® | NR604-01/02 | 24 rxn/96 rxn |
| | VAHTS Universal V8 RNA-Seq Library Prep Kit for Illumina® | NR605-01/02 | 24 rxn/96 rxn |
| Single-Indexed Adapters | VAHTS RNA Adapters Set 1 / Set 2 for Illumina® | N803/N804-01/02 | 10 µl each/40 µl each |
| | VAHTS RNA Adapters Set 3 - Set 6 for Illumina® | N809/N810/N811/N812 | 20 µl each |
| Dual-Indexed Adapters | VAHTS RNA Multiplex Oligos Set 1 / Set 2 for Illumina® | N323 / N324 | 192 rxn each |
| Small RNA Lib Prep Kits | VAHTS Small RNA Library Prep Kit for Illumina® | NR801-01/02 | 24 rxn/96 rxn |
| Small RNA Lib Prep Adapters | VAHTS Small RNA Index Primer Kit for Illumina® | N813/N814/N815/N816 | 48 rxn each |

HOT, New (Ultra Fast & Universal RNA Lib Prep Kits)

## RNA Library Prep (for MGI®) New

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Non-Stranded mRNA Lib Prep Kits | VAHTS mRNA-Seq V3 Library Prep Kit for MGI® | NRM611-01/02 | 24 rxn/96 rxn |
| Total RNA Lib Prep Kits (rRNA Depletion) | VAHTS Total RNA-Seq (H/M/R) Library Prep Kit for MGI® | NRM603-01/02 | 24 rxn/96 rxn |
| Ultra Fast & Universal RNA Lib Prep Kits | VAHTS Universal V6 RNA-Seq Library Prep Kit for MGI® | NRM604-01/02 | 24 rxn/96 rxn |
| | VAHTS Universal V8 RNA-Seq Library Prep Kit for MGI® | NRM605-01/02 | 24 rxn/96 rxn |
| Single-Indexed Adapters | VAHTS RNA Adapters Set 8 for MGI® | NM208-01/02 | 10 µl each/40 µl each |

## Modules for RNA Library Prep

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| mRNA Capture Beads | VAHTS mRNA Capture Beads | N401-01/02 | 24 rxn/96 rxn |
| RNA Fragmentation | VATHS 2 × Frag / Prime Buffer | N402-01 | 96 rxn |
| rRNA Depletion Kits | Ribo-off rRNA Depletion Kit (Human / Mouse / Rat) | N406-01/02 | 24 rxn / 96 rxn |
| | Ribo-off rRNA Depletion Kit (Bacteria) | N407-01/02 | 12 rxn / 24 rxn |
| | Ribo-off rRNA Depletion Kit (Plant) | N409-01/02 | 12 rxn / 24 rxn |

HOT, New (rRNA Depletion Kits)

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# Epigenetics

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Methylation Bisulfite Kit | EpiArt DNA Methylation Bisulfite Kit | EM101-01/02 | 50 rxn/200 rxn |
| Amplification Kit | 2 × EpiArt HS Taq Master Mix | EM201-01/02/03 | 1 ml/5 ml/15 ml |
| | 2 × EpiArt HS Taq Master Mix (Dye Plus) | EM202-01/02/03 | 1 ml/5 ml/15 ml |
| Methylation Lib Prep Kit | EpiArt DNA Methylation Library Kit | NE101-01/02 | 24 rxn/96 rxn |
| pG/pA-Tn5 for CUT&Tag | Hyperactive pG-Tn5 Transposase for CUT&Tag | S602-01/02 | 10 ug/20 ug |
| | Hyperactive pA-Tn5 Transposase for CUT&Tag | S603-01/02 | 10 ug/20 ug |
| pG/pA-Tn5 for CUT&Tag (Pre-loaded with Adapters) | Hyperactive pG-Tn5 Transposon for Illumina (4 μM) | S612-01/02 | 10 ug/20 ug |
| | Hyperactive pA-Tn5 Transposon for Illumina (4 μM) | S613-01/02 | 10 ug/20 ug |
| CUT&Tag Lib Prep Kit (Pre-loaded with Adapters) | Hyperactive In-Situ ChIP Library Prep Kit for Illumina (pG-Tn5) | TD901-01/02 | 12 rxn/48 rxn |
| | Hyperactive In-Situ ChIP Library Prep Kit for Illumina (pA-Tn5) | TD902-01/02 | 12 rxn/48 rxn |
| CUT&RUN | Hyperactive pA-MNase for CUT&RUN | S701-01/02 | 10 ug/20 ug |

# Single Cell-Seq

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| Single Cell WGA | Discover-sc Single Cell Kit | N601-01/02 | 24 rxn/96 rxn |
| | Discover-sc Single Cell WGA Kit | N603-01/02 | 24 rxn/96 rxn |
| Single Cell WTA | Single Cell Full Length mRNA-Amplication Kit | N712-01/02/03 | 12 rxn/24 rxn/96 rxn |

# Beads & Library Quantification

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| DNA Clean-up & Size-Selection | VAHTS DNA Clean Beads | N411-01/02/03 | 5 ml/60 ml/450 ml |
| RNA Clean-up | VAHTS RNA Clean Beads | N412-01/02/03 | 5 ml/40 ml/450 ml |
| Library Quantification Kits | VAHTS Library Quantification Kit for Illumina® | NQ101/102/103/104 | 500 rxn |
| | DNA Standard 1-6 | NQ105 | 8 rxn |
| | Library Dilution Buffer | NQ106 | 50 ml |
| Equalbit Assay Kits | Equalbit dsDNA HS Assay Kit | EQ111-01/02 | 100 / 500 assays |
| | Equalbit 1x dsDNA HS Assay Kit | EQ121-01/02 | 100 / 500 assays |
| | Equalbit RNA HS Assay Kit | EQ211-01/02 | 100 / 500 assays |
| | Equalbit RNA BR Assay Kit | EQ212-01/02 | 100 / 500 assays |

# cfDNA

| Application | Product Name | Cat. No.# | Size |
|---|---|---|---|
| cfDNA Preservation | VAHTS Blood Collection Tube for Cell-Free DNA Preservation | N901 | 10 ml tube |
| cfDNA Isolation | VAHTS Serum / Plasma Circulating DNA Kit | N902-01/02 | 50 rxn / 200 rxn |

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● TruePrep DNA Library Prep Kit V2 for Illumina (**Vazyme, #TD501/502/503**)
Transposase (Tn5)-based Ultra-Fast DNA Library Prep Kit

| | | |
|---|---|---|
| ■ **Easy to Use** | One-step enzymatic reaction. | |
| ■ **Ultra-Fast** | Library prep within **90 min**. | |
| ■ **Versatile** | Applicable for genomic DNA, single cell-seq, and epigenetics (i.e. ATAC-Seq). | |
| ■ **Reliable** | Optimized polymerase and buffer to achieve high efficiency and uniformity. | |
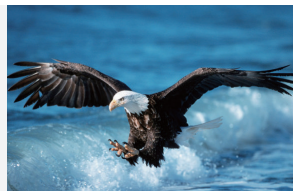
● VAHTS Universal Plus DNA Library Prep Kit for Illumina (**Vazyme, #ND617**)
DNA Library Prep Kit with Enzymatic Fragmentation

| | |
|---|---|
| ■ **Universal** | Applicable for 100 pg - 1 μg of input DNA from many species. |
| ■ **Easy** | Enzymatic fragmentation with no need for physical shearing / sonication. |
| ■ **Time-Saving** | Fragmentation, end repair, dA-tailing are performed in one step. |
| ■ **Reliable** | Generate high-quality DNA libraries with high yields. |

● VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina (**Vazyme #NR604**)
Fast & Effective RNA Library Prep Kit

| | |
|---|---|
| ■ **Fast** | The 2nd strand cDNA synthesis, end-repair, and dA-Tailing in one reaction! High-quality library prepared from enriched RNA within **4 hours**. |
| ■ **Flexible** | Compatible with a variety of RNA enrichment modules. |
| ■ **Universal** | Options for the preparation of stranded or non-stranded RNA-Seq libraries. |

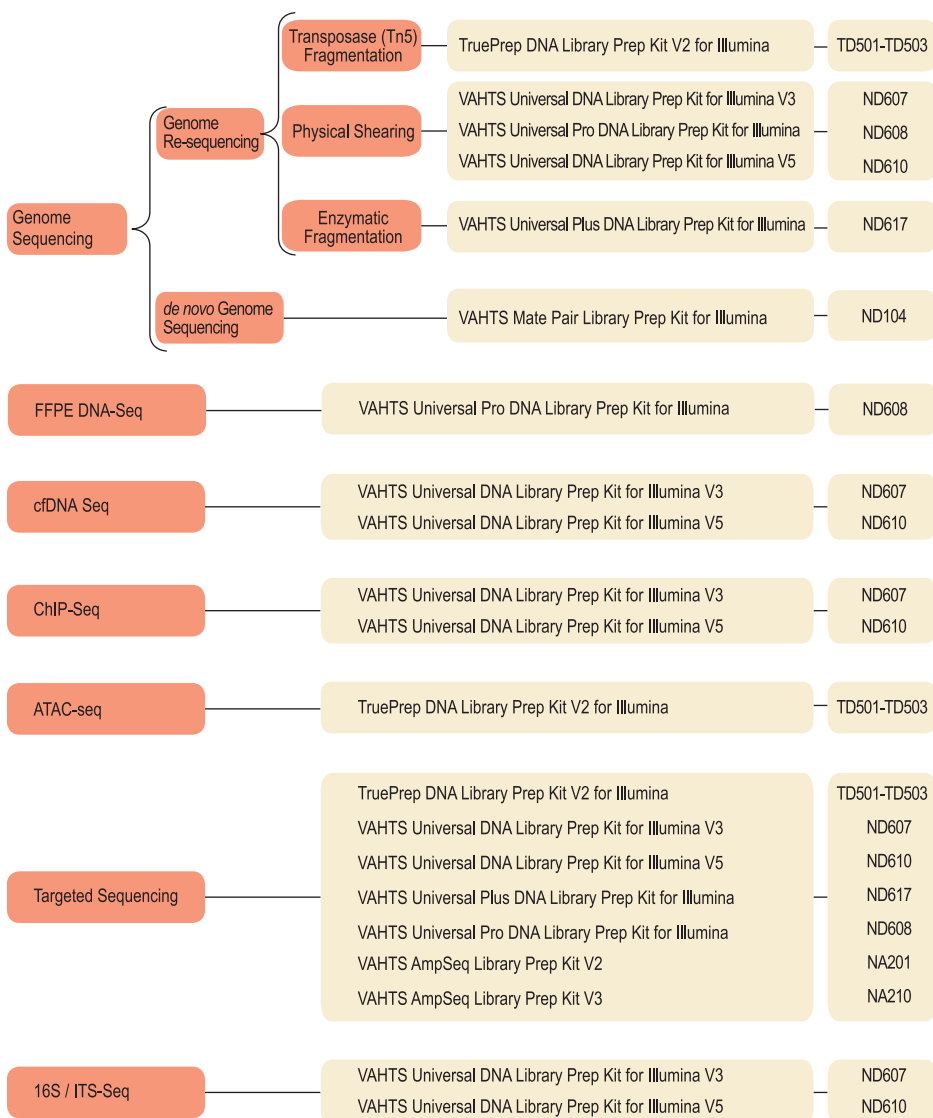● Hyperactive In-Situ ChIP Library Prep Kit for Illumina (pG/pA-Tn5) **(Vazyme, #TD901/902)**
An revolutionary technology that can replace CUT&RUN and ChIP-Seq.

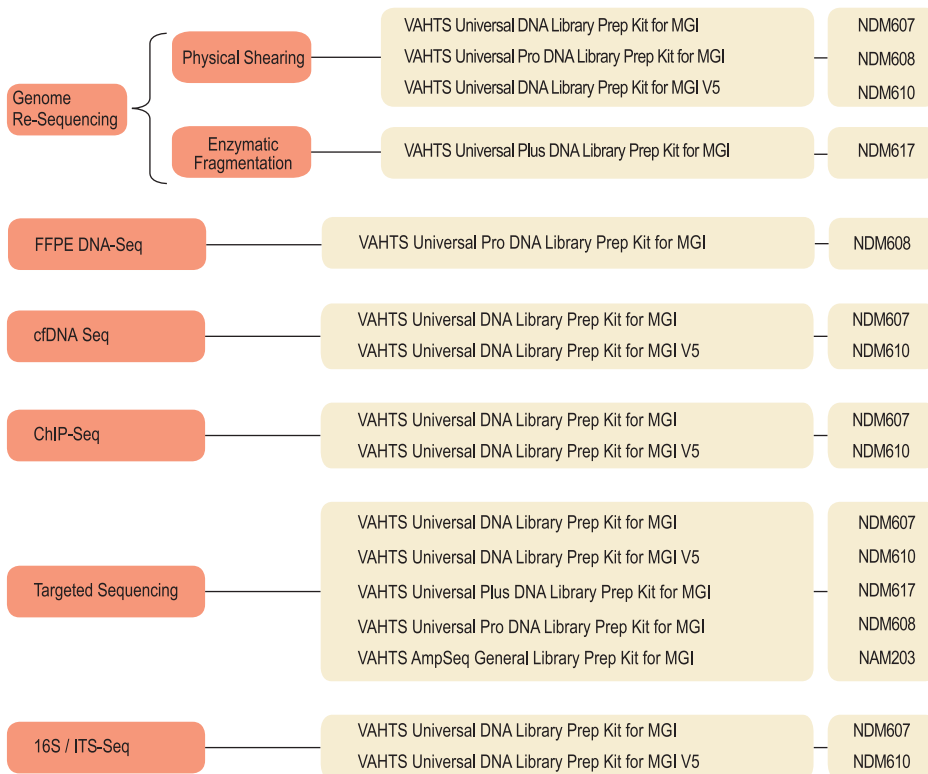| | |
|---|---|
| ■ **Easy to Operate** | DNA tagmentation and adapters ligation in one step. Sequencing-ready libraries can be generated from live cells within only **9 hours**. |
| ■ **Hyperactive** | pG/A & Tn5 transposase with hyper activity results in high efficiency of DNA tagmentation. |
| ■ **Low Input** | Starting from 60 cells or even single cells. |
| ■ **High Purity** | Proteins with high purity and extra low residual amount of nucleic acid. |

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## DNA-Seq Library Prep for Illumina®

| | | | | |
|---|---|---|---|---|
| Genome Sequencing | Genome Re-sequencing | Transposase (Tn5) Fragmentation | TruePrep DNA Library Prep Kit V2 for Illumina | TD501-TD503 |
| | | Physical Shearing | VAHTS Universal DNA Library Prep Kit for Illumina V3 | ND607 |
| | | | VAHTS Universal Pro DNA Library Prep Kit for Illumina | ND608 |
| | | | VAHTS Universal DNA Library Prep Kit for Illumina V5 | ND610 |
| | | Enzymatic Fragmentation | VAHTS Universal Plus DNA Library Prep Kit for Illumina | ND617 |
| | *de novo* Genome Sequencing | | VAHTS Mate Pair Library Prep Kit for Illumina | ND104 |

| FFPE DNA-Seq | VAHTS Universal Pro DNA Library Prep Kit for Illumina | ND608 |
|---|---|---|

| cfDNA Seq | VAHTS Universal DNA Library Prep Kit for Illumina V3 | ND607 |
|---|---|---|
| | VAHTS Universal DNA Library Prep Kit for Illumina V5 | ND610 |

| ChIP-Seq | VAHTS Universal DNA Library Prep Kit for Illumina V3 | ND607 |
|---|---|---|
| | VAHTS Universal DNA Library Prep Kit for Illumina V5 | ND610 |

| ATAC-seq | TruePrep DNA Library Prep Kit V2 for Illumina | TD501-TD503 |
|---|---|---|

| Targeted Sequencing | TruePrep DNA Library Prep Kit V2 for Illumina | TD501-TD503 |
|---|---|---|
| | VAHTS Universal DNA Library Prep Kit for Illumina V3 | ND607 |
| | VAHTS Universal DNA Library Prep Kit for Illumina V5 | ND610 |
| | VAHTS Universal Plus DNA Library Prep Kit for Illumina | ND617 |
| | VAHTS Universal Pro DNA Library Prep Kit for Illumina | ND608 |
| | VAHTS AmpSeq Library Prep Kit V2 | NA201 |
| | VAHTS AmpSeq Library Prep Kit V3 | NA210 |

| 16S / ITS-Seq | VAHTS Universal DNA Library Prep Kit for Illumina V3 | ND607 |
|---|---|---|
| | VAHTS Universal DNA Library Prep Kit for Illumina V5 | ND610 |

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## DNA-Seq Library Prep for MGI®

**Genome Re-Sequencing**

**Physical Shearing**

| VAHTS Universal DNA Library Prep Kit for MGI | NDM607 |
| VAHTS Universal Pro DNA Library Prep Kit for MGI | NDM608 |
| VAHTS Universal DNA Library Prep Kit for MGI V5 | NDM610 |

**Enzymatic Fragmentation**

| VAHTS Universal Plus DNA Library Prep Kit for MGI | NDM617 |

**FFPE DNA-Seq**

| VAHTS Universal Pro DNA Library Prep Kit for MGI | NDM608 |

**cfDNA Seq**

| VAHTS Universal DNA Library Prep Kit for MGI | NDM607 |
| VAHTS Universal DNA Library Prep Kit for MGI V5 | NDM610 |

**ChIP-Seq**

| VAHTS Universal DNA Library Prep Kit for MGI | NDM607 |
| VAHTS Universal DNA Library Prep Kit for MGI V5 | NDM610 |

**Targeted Sequencing**

| VAHTS Universal DNA Library Prep Kit for MGI | NDM607 |
| VAHTS Universal DNA Library Prep Kit for MGI V5 | NDM610 |
| VAHTS Universal Plus DNA Library Prep Kit for MGI | NDM617 |
| VAHTS Universal Pro DNA Library Prep Kit for MGI | NDM608 |
| VAHTS AmpSeq General Library Prep Kit for MGI | NAM203 |

**16S / ITS-Seq**

| VAHTS Universal DNA Library Prep Kit for MGI | NDM607 |
| VAHTS Universal DNA Library Prep Kit for MGI V5 | NDM610 |

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## TruePrep DNA Library Prep (Transposase-based)

### TruePrep DNA Library Prep Kit V2 for Illumina®
### (#TD501, #TD502, #TD503)

| Rapid & Easy | **Time-Saving**: Library prepared within **90 min**.<br>**Easy-to-Use**: one-step enzymatic reaction, no need for physical shearing / sonication. |
|---|---|

| High Adaptability to Input DNA | Applicable for genomic DNA, cDNA, and amplicons from multiple species.<br>**Input DNA**: **1 ng - 50 ng**. |
|---|---|

| High Amplification Uniformity | Optimized polymerase and buffer to achieve high efficiency and uniformity in library amplification. |
|---|---|

### Selected Product Citations of TruePrep Kits (#TD501, #TD502, #TD503)

Wang J, et al. Asymmetric expression of LincGET biases cell fate in two-cell mouse embryos. *Cell*, 2018, 175(7):18871-1901.

Han X, *et al.* Mapping the Mouse Cell Atlas by Microwell-Seq. *Cell*, 2018, 172(5):1091-107.

Zhang L, et al. Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. *Nature*, 2018, 564(7735):268-72.

Wu J, *et al*. Chromatin analysis in human early development reveals epigenetic transition during ZGA. *Nature*, 2018, 557(7704):256-60.

Zheng C, *et al*. Landscape of Infiltrating T Cells in Liver Cancer Revealed by Single-Cell Sequencing. *Cell*, 2017, 169(7):1342-56.

Huang X, *et al*. Genomic architecture of heterosis for yield traits in rice. *Nature*, 2016, 537(7622):629-33.

Wu J, *et al.* The landscape of accessible chromatin in mammalian preimplantation embryos. *Nature*, 2016, 534(7609):652-7.

Guo X, et al. Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. *Nature Medicine*, 2018, 24(7):978-85.

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## Mechanism of TruePrep DNA Library Prep

TruePrep Tagment Enzyme Mix (TTE Mix) contains transposase and two kinds of adapters (Adapter 1 and Adapter 2) with equal molar. Input DNA are fragmented and linked with adapters on both ends just by mixing with TTE Mix, followed by a 10-minute incubation at 55°C. The tagged DNA fragments can be further amplified with two pairs of primers N5 (N5XX) / N7 (N7XX) and P5 / P7 (PCR Primer Mix, PPM). After size selection and clean-up, the library is ready for sequencing on Illumina platforms.
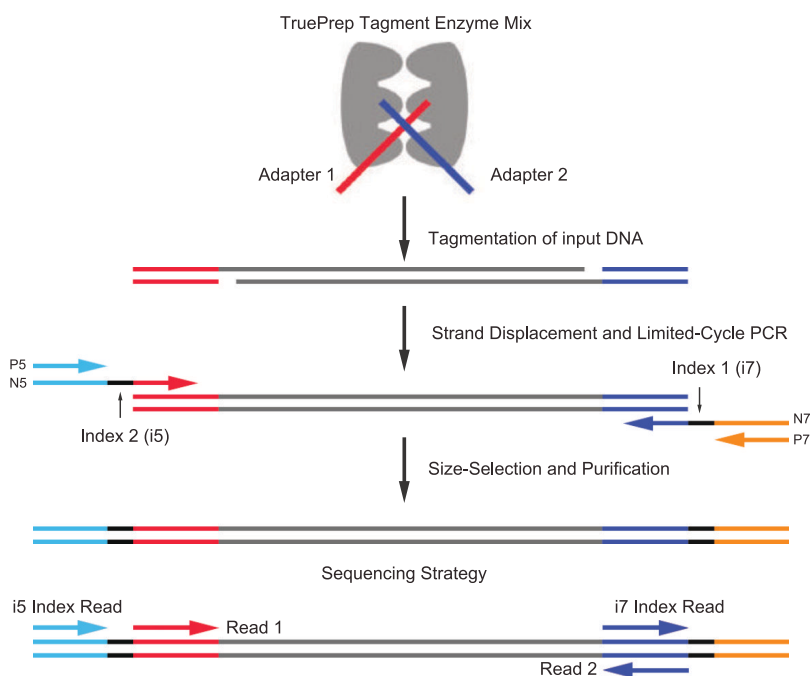


Adapter 1 and Adapter 2, two oligos embedded in TruePrep Tagment Enzyme

P5 and P7, two universal PCR Primers

N5 and N7, two index primers containing index 2 (i5) and index 1 (i7) respectively

Index 2 (i5) 5'-AATGATACGGCGACCACCGAGATCTACAC||||||||TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-NNNNNN-CTGTCTCTTATACACATCTCCGAGCCCACGAGAC||||||||ATCTCGTATGCCGTCTTCTGCTTG-3' Index 1 (i7)

|||||||: Index 2 (i5), 8 bases      ||||||||: Index 1 (i7), 8 bases     -NNNNNN-: insert sequence

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# VAHTS Universal Plus DNA Library Prep Kit for Illumina® (#ND617) (for Enzymatic Fragmentation)

**Universal** — Applicable for 100 pg-1 µg of input DNA (e.g. genomic DNA, FFPE DNA) from many species.

**Easy** — Enzymatic fragmentation with a single protocol, with no need for physical shearing / sonication.

**Time-Saving** — Fragmentation, end repair, dA-tailing are performed in one step. No clean-ups needed before adapter ligation.

**Reliable** — Generate high-quality DNA libraries with high yields.

## 1. Broad Input Amount Compatibility
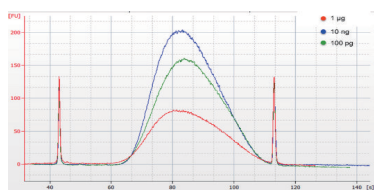


*Size distribution of library fragments constructed with different DNA input. For different input mounts of salmon sperm gDNA (100 pg, 10 ng, 1 ug, respectively) with the same fragmentation time, the size distribution of these libraries were identical.*

## 2. Extensive Species Compatibility
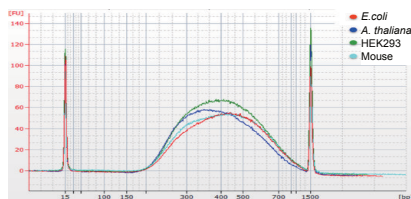


*Size distribution of library fragments constructed by gDNA of different species. For the same input of 100 ng, the size distribution of these libraries from different species were identical.*



Input DNA

Fragmentation, End Repair, dA-Tailing

Adapter Ligation

PCR-free library prep ends here.

Library Amplification

VAHTS DNA Adapter for Illumina
Compatible with:
- DNA
- ChIP-DNA
- RNA (non-Small RNA)

⑫ 5' Phosphate
A 3' dA Tail
T 3' dT Tail
IX, Index
—— P5 sequence
—— P7 sequence

## 3. Excellent Library Conversion Rate



*Comparison of library conversion rates. For different input amount of gDNA libraries, Vazyme #ND617 has a higher library conversion rate than that of other competitors.*
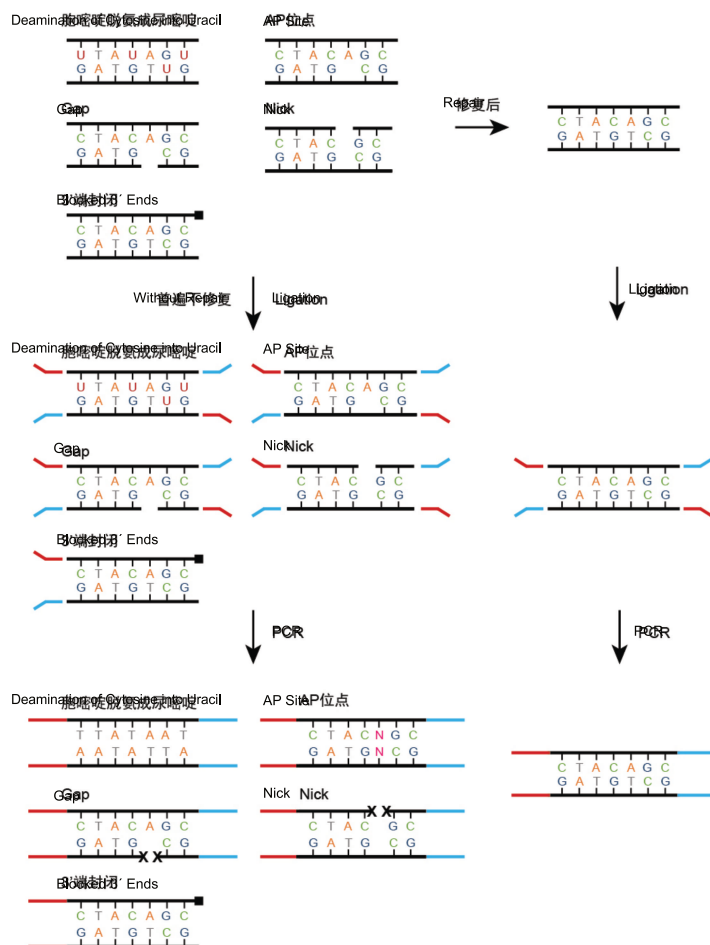
## 4. High Sequencing Data Quality
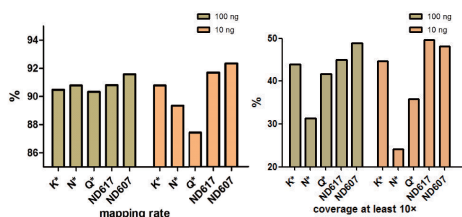


*Comparison of sequencing data quality. The Arabidopsis thaliana gDNA library constructed using Vazyme ND617, followed by sequencing on Hiseq X10 PE150.*

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## Mechanism of FFPE DNA Library Prep

VAHTS Universal Pro DNA Library Prep Kit for Illumina (Vazyme, #ND608) is specially designed for library preparation from 100 pg - 1 μg of input DNA for NGS on Illumina® platforms. This kit contains a DNA damage repair module that can effectively repair DNA damage caused by formalin-fixed paraffin-embedded (FFPE), including deamination of cytosine, nicks and gaps, oxidized bases, blocked 3′ ends, compatible with common DNA samples without affecting the quality of normal DNA sample libraries. The overall optimization of the module of end-repair, ligation and library amplification leads to excellent library conversion rate and amplification output. It is widely applicable to PCR or PCR-Free library construction of multiple samples, and is compatible with targeted capture process.



DNA Library Prep without or with DNA Damage Repair

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→ **VAHTS Universal Pro DNA Library Prep Kit for Illumina®(#ND608)**

## Repairable Types of DNA Damage

| Types of DNA Damage in FFPE Samples | Deamination of Cytosine into Uracil | Nicks & Gaps | Oxidized Bases | Blocked 3´ Ends | DNA Fragmentation | DNA-Protein Crosslinks |
|---|---|---|---|---|---|---|
| Whether Can Be Repaired by #ND608 | YES | YES | YES | YES | NO | NO |

## Validation Data

### 1. Efficient Repair of Base Damage
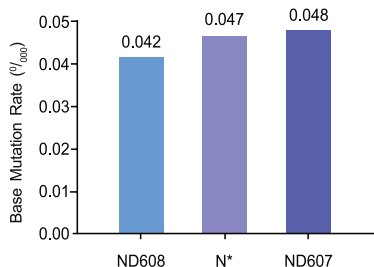


The DNA Repair Module of the ND608 has the ability to repair base damage efficiently, significantly reducing the number of base aberrant mutations introduced during FFPE sample preparation and storage.

### 2. Efficient Library Conversion
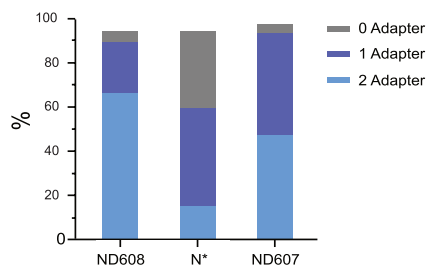


The library conversion rate of ND608 is higher than that of N* company and VAHTS Universal Plus DNA Library Prep Kit for Illumina (Vazyme, #ND607, without FFPE repair module), and the library conversion rate is as high as 67%.

### 3. Excellent Library amplification Efficiency
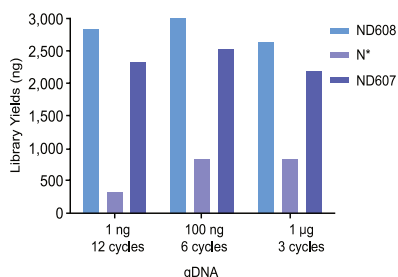


For amplification, the yield of the library constructed by ND608 is increased by 3-9 times compared with other kits under the same cycle number; the number of cycles required for competing products is reduced by 2-3 cycles under the same yield.

### 4. Excellent Raw Data Quality
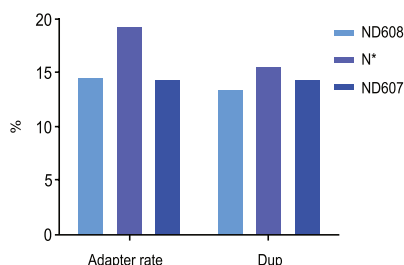


ND608 can effectively improve the data quality of samples, with lower Adapter rate and Duplication rate.

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## VAHTS Universal DNA Library Prep Kit for Illumina® V3 (#ND607) (for physical fragmentation)

| **Time-Saving** | Library prepared within **75 min**. |
| **High Adaptability to Input Amount** | Effective library preparation from **100 pg - 4 μg** of Input DNA. |
| **Applicable to Most Samples** | Genomic DNA, cfDNA, ctDNA, FFPE DNA, ChIP DNA, and Amplicons. |
| **Excellent Adapter Ligation Efficiency** | Suitable for library preparation with PCR or PCR-free. |

## VAHTS HiFi Amplification Mix (#N616)

**Excellent Template Adaptability**
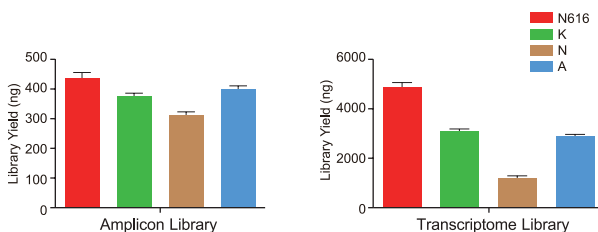


The amplification performance of *VAHTS HiFi Amplification Mix (Vazyme, #N616)* in multiple samples is significantly better than that of competitors. Amplicon library (80 ng) and transcriptome library (5 ng) was used as template and amplified for 4 and 13 cycles, respectively. The library concentrations were determined by Qubit.

**Super High Plateau of Amplification**
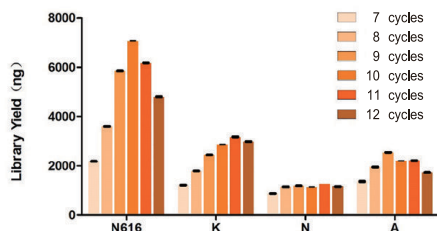


The amplification plateau of *VAHTS HiFi Amplification Mix (Vazyme, #N616)* can reach 7 μg, which is significantly superior to that of competitors. Fragmented DNA (50 ng, approximately 350 bp) was ligated with adapters and then amplified. The library concentrations were determined by Qubit.

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## RNA-Seq Library Prep for Illumina®

### Ultra Fast & Universal RNA-Seq

**Kit**
VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina — NR604
VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina — NR605

**Adapter**
VAHTS RNA Adapters Set 1-Set 6 for Illumina — N803/N804 & N809-N812
VAHTS RNA Multiplex Oligos Set 1-Set 2 for Illumina — N323/N324

**Module**
VAHTS mRNA Capture Beads — N401
Ribo-off rRNA Depletion Kit (Human/Mouse/Rat) — N406
Ribo-off rRNA Depletion Kit (Bacteria) — N407
Ribo-off rRNA Depletion Kit (Plant) — N409

### Non-Stranded mRNA-Seq

**Kit**
VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina — NR604
VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina — NR605

**Adapter**
VAHTS RNA Adapters Set 1-Set 6 for Illumina — N803/N804 & N809-N812
VAHTS RNA Multiplex Oligos Set 1-Set 2 for Illumina — N323/N324

**Module**
VAHTS mRNA Capture Beads — N401

### Stranded mRNA-Seq

**Kit**
VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina — NR604
VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina — NR605

**Adapter**
VAHTS RNA Adapters Set 1-Set 6 for Illumina — N803/N804 & N809-N812
VAHTS RNA Multiplex Oligos Set 1-Set 2 for Illumina — N323/N324

**Module**
VAHTS mRNA Capture Beads — N401

### Total RNA-Seq (rRNA Depletion)

**Kit**
VAHTS Total RNA-Seq (H/M/R)Library Prep Kit for Illumina — NR603
VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina — NR604
VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina — NR605

**Adapter**
VAHTS RNA Adapters Set 1-Set 6 for Illumina — N803/N804 & N809-N812
VAHTS RNA Multiplex Oligos Set 1-Set 2 for Illumina — N323/N324

**Module**
Ribo-off rRNA Depletion Kit (Human/Mouse/Rat) — N406
Ribo-off rRNA Depletion Kit (Bacteria) — N407
Ribo-off rRNA Depletion Kit (Plant) — N409

### Small RNA-Seq

**Kit**
VAHTS Small RNA Library Prep Kit for Illumina — NR801

**Adapter**
VAHTS Small RNA Index Primer Kit for Illumina — N813-N816

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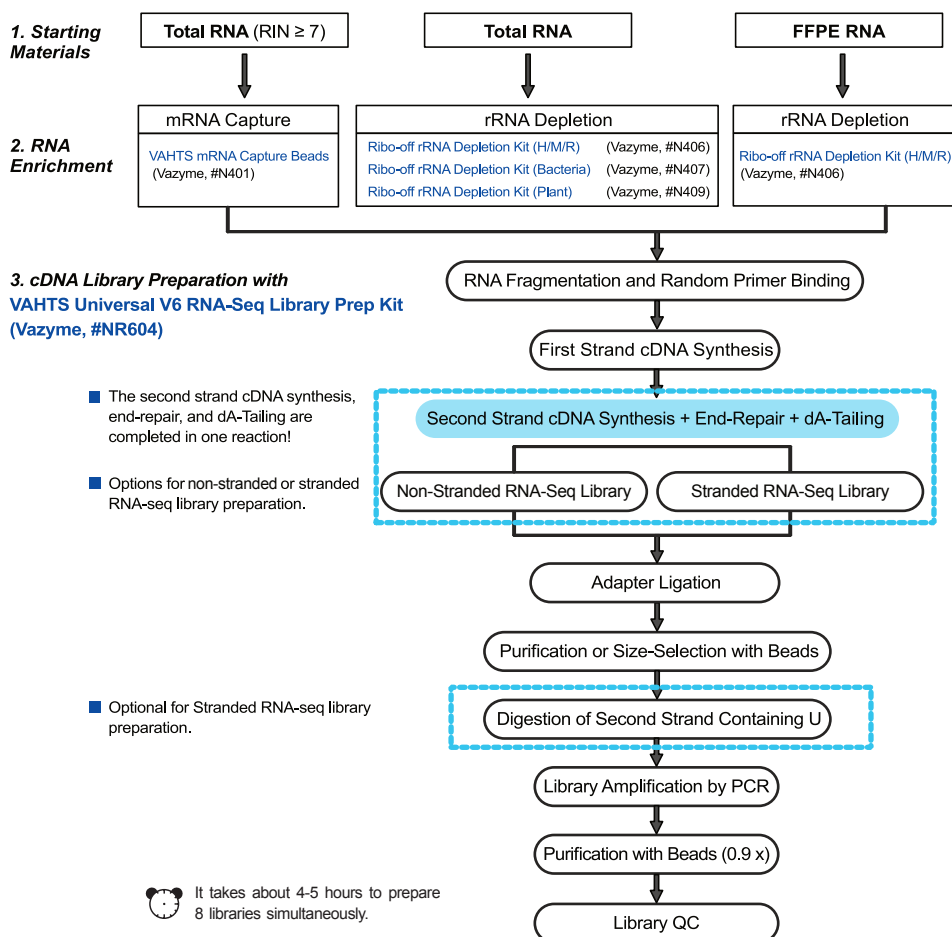Innovation in Enzyme Technology

## RNA-Seq Library Prep for MGI®

**Ultra Fast & Universal RNA-Seq**

| Kit | VAHTS Universal V6 RNA-seq Library Prep Kit for MGI<br>VAHTS Universal V8 RNA-seq Library Prep Kit for MGI | NRM604<br>NRM605 |
|---|---|---|
| Adapter | VAHTS RNA Adapters Set 8 for MGI | NM208 |
| Module | VAHTS mRNA Capture Beads<br>Ribo-off rRNA Depletion Kit (Human/Mouse/Rat)<br>Ribo-off rRNA Depletion Kit (Bacteria)<br>Ribo-off rRNA Depletion Kit (Plant) | N401<br>N406<br>N407<br>N409 |

**Non-Stranded mRNA-Seq**

| Kit | VAHTS Universal V6 RNA-seq Library Prep Kit for MGI<br>VAHTS Universal V8 RNA-seq Library Prep Kit for MGI | NRM604<br>NRM605 |
|---|---|---|
| Adapter | VAHTS RNA Adapters Set 8 for MGI | NM208 |
| Module | VAHTS mRNA Capture Beads | N401 |

**Stranded mRNA-Seq**

| Kit | VAHTS Universal V6 RNA-seq Library Prep Kit for MGI<br>VAHTS Universal V8 RNA-seq Library Prep Kit for MGI | NRM604<br>NRM605 |
|---|---|---|
| Adapter | VAHTS RNA Adapters Set 8 for MGI | NM208 |
| Module | VAHTS mRNA Capture Beads | N401 |

**Total RNA-Seq (rRNA Depletion)**

| Kit | VAHTS Total RNA-Seq (H/M/R)Library Prep Kit for MGI<br>VAHTS Universal V6 RNA-seq Library Prep Kit for MGI<br>VAHTS Universal V8 RNA-seq Library Prep Kit for MGI | NRM603<br>NRM604<br>NRM605 |
|---|---|---|
| Adapter | VAHTS RNA Adapters Set 8 for MGI | NM208 |
| Module | Ribo-off rRNA Depletion Kit (Human/Mouse/Rat)<br>Ribo-off rRNA Depletion Kit (Bacteria)<br>Ribo-off rRNA Depletion Kit (Plant) | N406<br>N407<br>N409 |

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## Solutions of RNA-Seq Library Preparation

VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina® (Vazyme, #NR604) is specially designed for the preparation of transcriptome libraries for NGS platforms of Illumina®. This kit combines 2nd Strand cDNA synthesis, end-repair, and dA-Tailing into one step, with no need of clean-ups, which greatly simplifies the process of library construction and shortens the operation time. The kit also can be used for non-stranded or stranded transcriptome analysis.

*1. Starting Materials*

| Total RNA (RIN ≥ 7) | Total RNA | FFPE RNA |
|---|---|---|

*2. RNA Enrichment*

| mRNA Capture | rRNA Depletion | rRNA Depletion |
|---|---|---|
| VAHTS mRNA Capture Beads (Vazyme, #N401) | Ribo-off rRNA Depletion Kit (H/M/R)   (Vazyme, #N406)<br>Ribo-off rRNA Depletion Kit (Bacteria)  (Vazyme, #N407)<br>Ribo-off rRNA Depletion Kit (Plant)    (Vazyme, #N409) | Ribo-off rRNA Depletion Kit (H/M/R) (Vazyme, #N406) |

*3. cDNA Library Preparation with*
**VAHTS Universal V6 RNA-Seq Library Prep Kit (Vazyme, #NR604)**

RNA Fragmentation and Random Primer Binding

First Strand cDNA Synthesis

- The second strand cDNA synthesis, end-repair, and dA-Tailing are completed in one reaction!

Second Strand cDNA Synthesis + End-Repair + dA-Tailing

- Options for non-stranded or stranded RNA-seq library preparation.

| Non-Stranded RNA-Seq Library | Stranded RNA-Seq Library |
|---|---|

Adapter Ligation

Purification or Size-Selection with Beads

- Optional for Stranded RNA-seq library preparation.

Digestion of Second Strand Containing U

Library Amplification by PCR

Purification with Beads (0.9 x)

It takes about 4-5 hours to prepare 8 libraries simultaneously.

Library QC

Mechanism of VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina® (Vazyme, #NR604)

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## VAHTS Universal V6 RNA-seq Library Prep Kit for Illumina® (#NR604)

**Fast**

The second strand cDNA synthesis, end-repair, and dA-Tailing are completed in one reaction! High-quality library prepared from enriched RNA within **4 hours**.
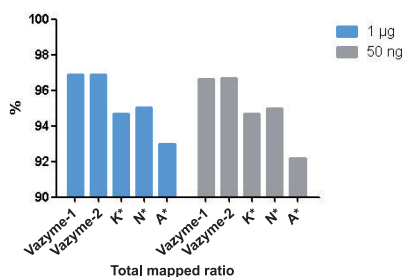
**Flexible**

Compatible with a variety of RNA enrichment modules.

**Universal**

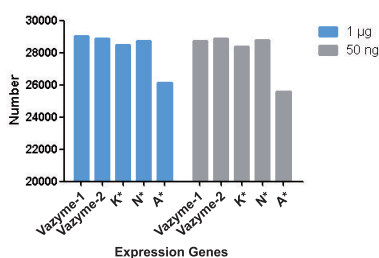Options for the preparation of stranded or non-stranded RNA-Seq libraries.
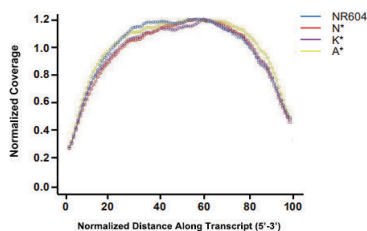
## Validation Data

### 1. High Mapped Rate



Compared with several similar kits, Vazyme, #NR604 performed better in mapped ratio.

### 2. High Gene Detection Number



Compared with several similar kits on the market, Vazyme, #NR604 showed higher gene detection number.

### 3. Excellent Uniformity



The data of library prepared using Vazyme, #NR604 was evenly distributed, with no 5'- or 3'- preference, and is highly consistent with several similar kits.

### 4. High Expression Repeat Correlation
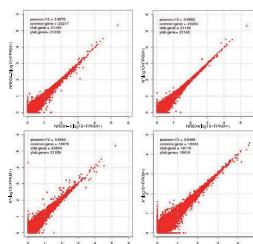


The correlation coefficient $r^2$ between Vazyme, #NR604 and several similar kits on the market is higher than 0.94.

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# Total RNA-Seq Library Prep

## VAHTS Total RNA-seq (H/M/R) Library Prep Kit for Illumina® (#NR603)

| | |
|---|---|
| **Extensive Species Compatibility** | Compatible with human, mouse, rat, and many other species. |
| **High rRNA Removal Efficiency** | rRNA removal efficiency up to 99.9%. |
| **Low Template Input Amount** | As low input as 100 ng total RNA. |
| **Optimized Fragmentation & Size-Selection** | Provides fragmentation and size selection solutions for four different fragments. |

### Selected Product Citations

He Y, et al. Transitory presence of myeloid-derived suppressor cells in neonates is critical for control of inflammation. *Nature Medicine*, 2018, 24(2):224-31.

**LETTERS**

nature medicine

### Transitory presence of myeloid-derived suppressor cells in neonates is critical for control of inflammation

Yu-Mei He[1,2,9], Xing Li[1-3,9], Michela Perego[4,9], Yulia Nefedova[4], Andrew V Kossenkov[4], Erik A Jensen[5], Valerian Kagan[6], Yu-Feng Liu[1], Shu-Yu Fu[1], Qing-Jian Ye[3], Yan-Hong Zhou[7], Lai Wei[8], Dmitry I Gabrilovich[1,2,4,10] & Jie Zhou[1,2,7,10]

PMN-MDSCs and M-MDSCs from spleens of neonatal (7 d old) and adult mice (6 to 8 weeks old) were enriched with CD11b-beads and then sorted on a FACSAria cell sorter (BD Bioscience), on the basis of the CD11b+Ly6CintLy6G+phenotype for PMN-MDSCs and CD11b+Ly6ChighLy6G− for M-MDSCs. The sorting purity was >95%. RNA sequencing was performed on the Illumina Hiseq 2500 platform. A VAHTS Total RNA-Seq Library Preparation Kit (Vazyme Biotech) was used for library preparation. Single-end-read runs were used with read lengths up to 50 bp in high-output mode and 30 million total read counts. Data were analyzed in RSEM v1.2.12 software30 against the mm10 genome, and genelevel read counts and RPKM values on the gene level were estimated for the ensemble transcriptome.
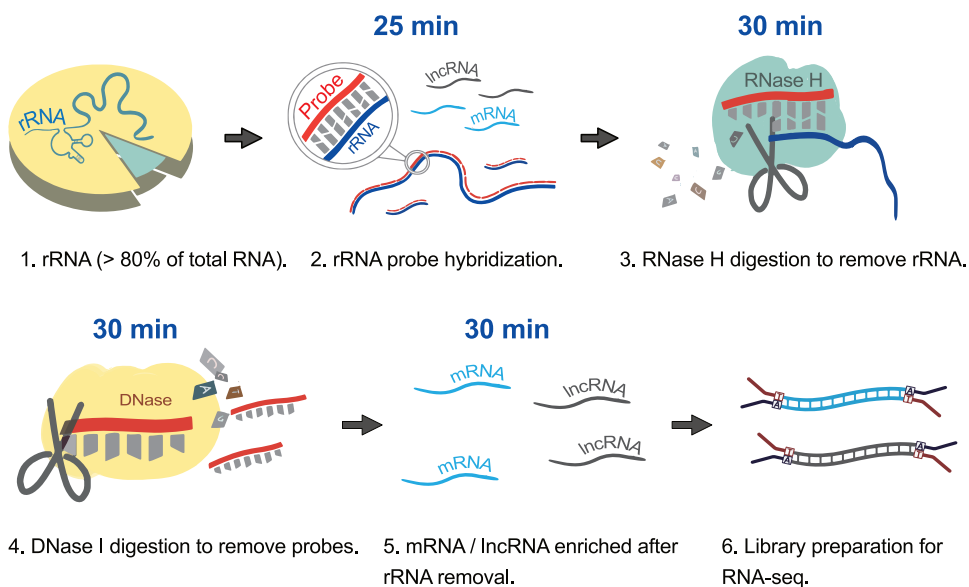
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## Ribo-off rRNA Depletion Kits

| Ribo-off Modules | Cat# | In-put Total RNA | Species |
|---|---|---|---|
| Ribo-off rRNA Depletion Kit (H/M/R) | #N406 | 50 ng - 1 μg | Human, mouse, rat, etc.* |
| Ribo-off rRNA Depletion Kit (Bacteria) | #N407 | 1 μg - 5 μg | Bacteria. |
| Ribo-off rRNA Depletion Kit (Plant) | #N409 | 1 μg - 5 μg | Plants. |

* Validated species of #N406: human, mouse, rat, cattle, dog, horse, chicken, monkey, pig, zebrafish, etc.

**Complete rRNA removal within 2 hours.**

**25 min** **30 min**



1. rRNA (> 80% of total RNA). 2. rRNA probe hybridization. 3. RNase H digestion to remove rRNA.

**30 min** **30 min**



4. DNase I digestion to remove probes. 5. mRNA / lncRNA enriched after rRNA removal. 6. Library preparation for RNA-seq.

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## Ribo-off rRNA Depletion Kit (Plant) (#N409)

| | |
|---|---|
| **Extensive Species Compatibility** | Compatible with Arabidopsis, cotton, corn, soybean, rice, tomato, peanut, apple, wheat, Selaginella, Cuscuta, etc. |
| **High rRNA Removal Efficiency** | Effective removal of cytoplasmic rRNA, mitochondrial rRNA, and chloroplast rRNA. |
| **Wide Range of Input Compatibility** | 1 μg - 5 μg total RNA. |
| **Easy & Fast Procedures** | Using with #NR604, library preparation and quality control can be completed within one day. |

## Validation Data

The transcriptome libraries of Arabidopsis thaliana, rice, tomato, and maize were prepared using Vazyme, #N409 and RNA-Seq library prep kit, respectively. The quality-controlled libraries were sequenced using an Illumina Hiseq X10 platform for PE150 sequencing. High-quality clean reads obtained from the raw data was analyzed.

### 1. Excellent Data Quality
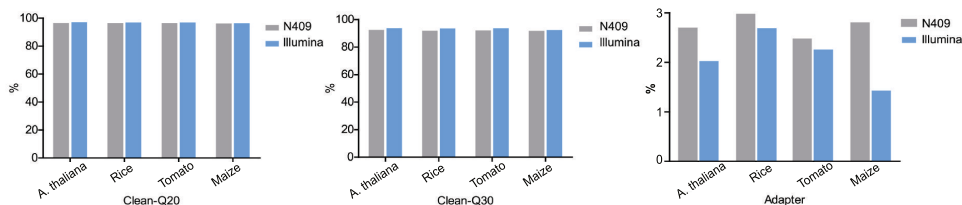


*Compared with several similar kits on the market, Vazyme, #NR604 showed higher gene detection number.*

### 2. High rRNA Removal Efficiency
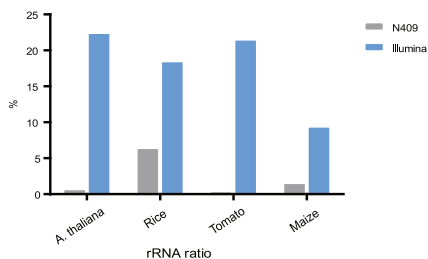


*For different species, N409 can effectively remove rRNA and minimize the waste of data caused by rRNA residues.*

### 3. High Mapped Ratio
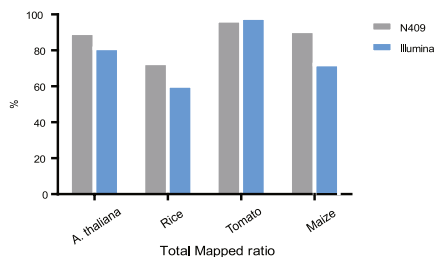


*The data obtained by sequencing the library prepared using Vazyme, #N409 and RNA-Seq library prep kit showed high mapped ratio.*

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## Library Prep for Epigenetics

**Bisulfite Sequencing**

EpiArt DNA Methylation Bisulfite Kit — EM101
2 × EpiArt HS Taq Master Mix — EM201
2 × EpiArt HS Taq Master Mix (Dye Plus) — EM202
EpiArt DNA Methylation Library Kit — NE101

**CUT&Tag**

Hyperactive pG-Tn5 Transposase for CUT&Tag — S602
Hyperactive pA-Tn5 Transposase for CUT&Tag — S603
Hyperactive pG-Tn5 Transposon for Illumina (4 μM) — S612
Hyperactive pA-Tn5 Transposon for Illumina (4 μM) — S613
Hyperactive In-Situ ChIP Library Prep Kit for Illumina(pG-Tn5) — TD901
Hyperactive In-Situ ChIP Library Prep Kit for Illumina(pA-Tn5) — TD902

**CUT&RUN**

Hyperactive pA-MNase for CUT&RUN — S701

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## Methylation Bisulfite Kit

### EpiArt DNA Methylation Bisulfite Kit (#EM101)

| Short Operating Time | Combines DNA denaturation and bisulfite conversion into one step, and the conversion reaction time is only 140 min. |
|---|---|

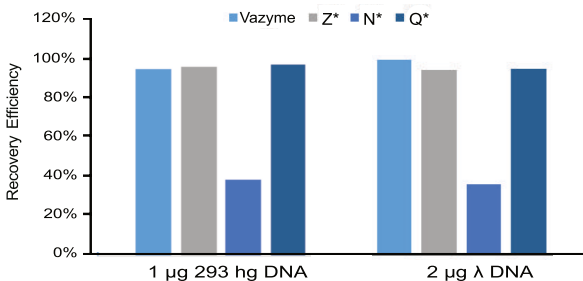| High Conversion Efficiency | Compatible with 100 pg-2 μg of input genomic DNA. The recovery efficiency is ≥ 80% and the unmethylated cytosine conversion efficiency is ≥ 99%. |
|---|---|

| Wide Range of Compatibility | Efficient conversion of DNA, cfDNA, and purified PCR products from animals, plants, and microorganisms. |
|---|---|

| Suitable for Many Downstream Applications | The bisulfite converted product is suitable for downstream applications such as PCR amplification and NGS sequencing. |
|---|---|

## Validation Data

### 1. High Recovery Efficiency



### 2. High Conversion Efficiency

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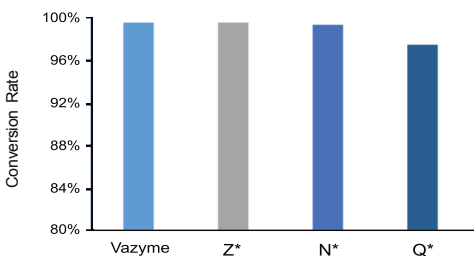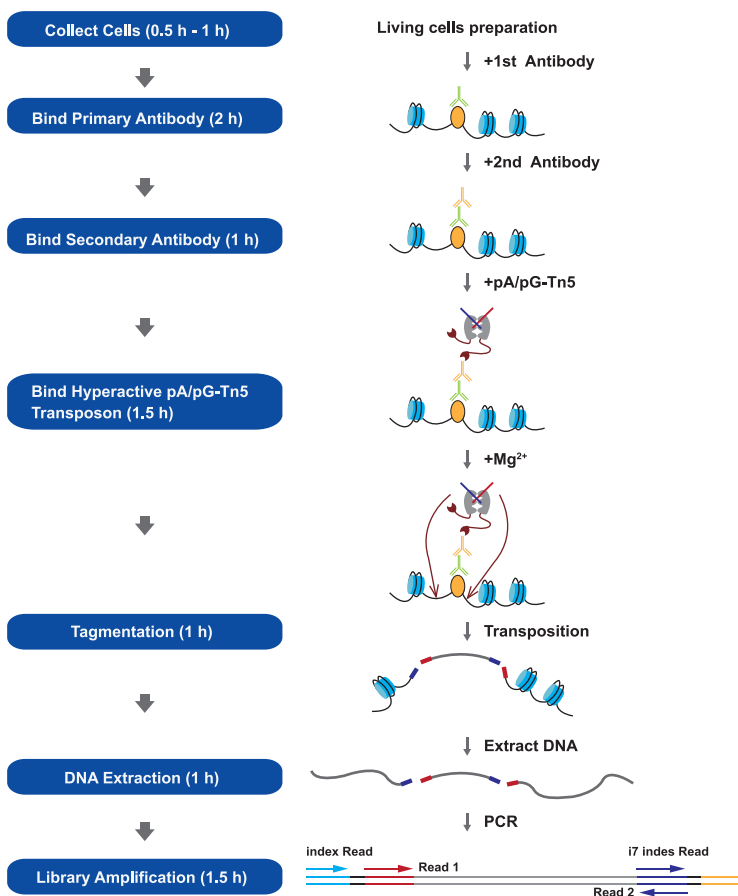
## CUT&Tag

Cleavage Under Targets and Tagmentation (CUT&Tag) is a specific technology designed for the study of protein-genomic interaction that can seamlessly replace the traditional ChIP-Seq. Compared with ChIP-Seq, the CUT&Tag has several significant advantages, including high signal-to-noise ratio, excellent repeatability, short operation time (generate sequencing-ready libraries beginning with live cells within one day), and low cell input. This technology will facilitates the research in epigenetics, tumors, and stem cells.



**Living cells preparation**

**Collect Cells (0.5 h - 1 h)**

**Bind Primary Antibody (2 h)** — +1st Antibody

**Bind Secondary Antibody (1 h)** — +2nd Antibody

**Bind Hyperactive pA/pG-Tn5 Transposon (1.5 h)** — +pA/pG-Tn5

+Mg$^{2+}$

**Tagmentation (1 h)** — Transposition

**DNA Extraction (1 h)** — Extract DNA

**Library Amplification (1.5 h)** — PCR

index Read / Read 1 / i7 indes Read / Read 2

**Workflow of CUT&Tag**

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# Hyperactive In-Situ ChIP Library Prep Kit for Illumina (pG-Tn5/pA-Tn5) (#TD901 / #TD902)

| Easy to Operate | DNA tagmentation and adapters ligation can be achieved in one step. |
|---|---|
| **Low Input Amount** | Starting from 60 cells or even single cells. |
| **Hyperactive** | Protein G/A & Tn5 transposase with hyper activity results in high efficiency of DNA tagmentation. |
| **High S/N Ratio** | Higher signal-to-noise ratio than ChIP-Seq. |
| **Excellent Reproducibility** | Good reproducibility among sample replicates. |
| **Time-Saving** | Sequencing-ready libraries can be generated from live cells within **only 9 hours**. |

## Validation Data

### 1. Low Input Amount of Cells
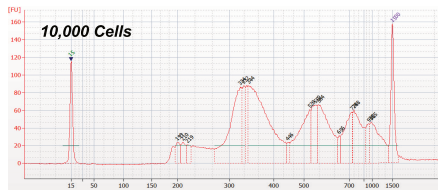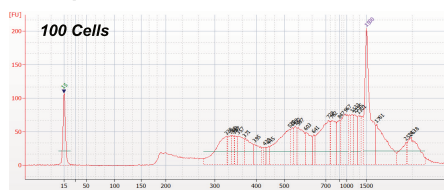


Size distribution of CUT&Tag library fragments prepared from 100 cells (left) or 10,000 cells (right). One hundred or 10,000 cells of HEK293 was used for CUT&Tag and library preparation using *Vazyme, #TD901*, respectively. The final concentration of pG-Tn5 transposon was 0.04 μM. The 1st antibody was H3K27me3 (CST, #9733), the 2nd antibody was Goat anti Rabbit (Bioworld, #BS13271). Size distribution of library fragments was detected using an Agilent 2100 Bioanalyzer. The results showed that, using **#TD901**, CUT&Tag libraries were prepared successfully from both 100 and 10,000 cells.
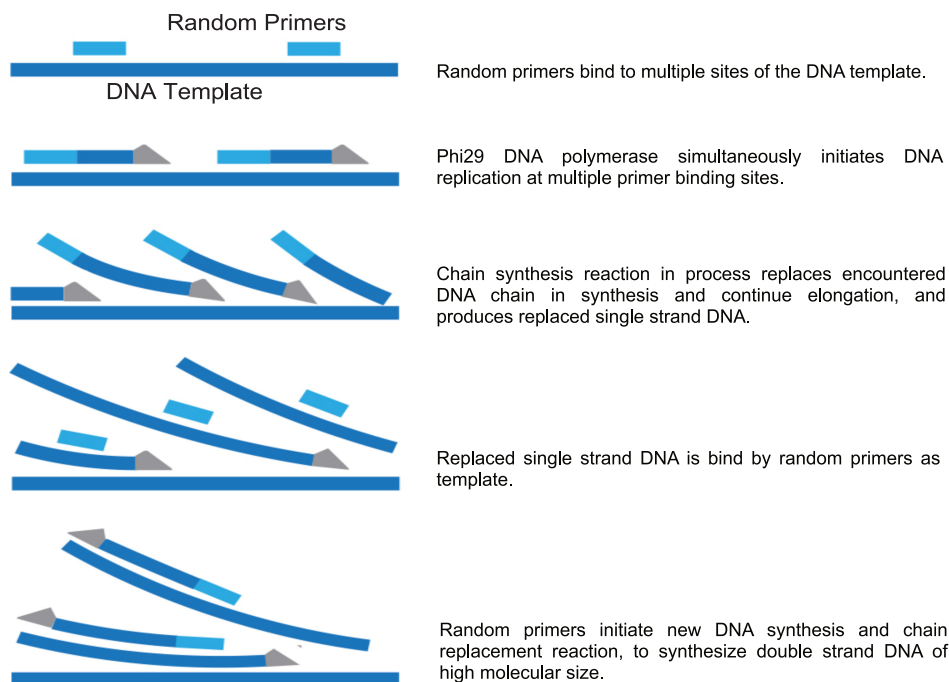
### 2. High Signal-to-Noise Ratio
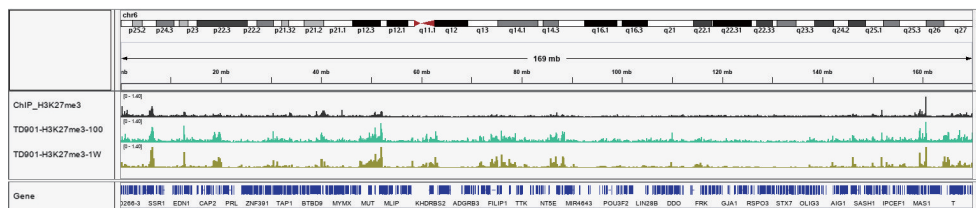


Peak enrichment of libraries that compared with different methods and different cell inputs. (The 1st row - ChIP-Seq; the 2nd row - CUT&Tag from 100 cells using #TD901; the 3rd row - CUT&Tag from 10,000 cells using #TD901). CUT&Tag libraries were sequenced on a Hiseq X10 PE150, respectively. The raw data was filtered and then subjected to Peak Calling analysis. The results showed that the peak enrichment of CUT&Tag library from 100 cells is similar to that of 10,000 cells, and the signal-to-nose ratio (S/N) of both CUT&Tag libraries was significantly better than that of traditional ChIP-Seq library.

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# Single Cell Whole Genome Amplification (WGA) Kit

Discover-sc Single Cell WGA Kit (#N603) is an isothermal amplification system based on the multiple displacement amplification (MDA) using Phi29. The Phi29 DNA polymerase is cloned from phage and has extremely strong strand-displacement activity and can be used for in vitro MDA polymerization at a constant temperature, with no need for thermal cycling. One single polymerization reaction using Phi29 can achieve continuous polymerization extension up to 100 kb. This kit is suitable for the whole genome amplification (WGA) from a single cell, small amount of tissues, or even trace purified genomic DNA, to obtain a large amount of genomic DNA with high coverage.

**Random Primers**

**DNA Template**

Random primers bind to multiple sites of the DNA template.

Phi29 DNA polymerase simultaneously initiates DNA replication at multiple primer binding sites.

Chain synthesis reaction in process replaces encountered DNA chain in synthesis and continue elongation, and produces replaced single strand DNA.

Replaced single strand DNA is bind by random primers as template.

Random primers initiate new DNA synthesis and chain replacement reaction, to synthesize double strand DNA of high molecular size.

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

| Wide Sample Compatibility | Applicable to animal and plant cells, bacteria or blastomeres, trophectoderm cells, sperm and other samples. |
|---|---|

| High Coverage | Single cell genome can reach more than 95% coverage after amplification. |
|---|---|

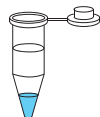| High Uniformity | Chromosome copy number variation analysis from > 1 Mb of the read depth. |
|---|---|

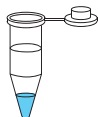| High Fidelity | The fidelity of Phi29 DNA polymerase is 1000 folds than Taq polymerase. |
|---|---|

| Easy Operation | React at single tube, operate within 10 min, not required for purification of amplification product. |
|---|---|

Cell Lysis　　　　　　　　Termination of Lysis　　　　　　Isothermal Amplification

10 min　　　　　　　　　　　　　　2 hr　　　Analysis
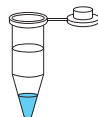
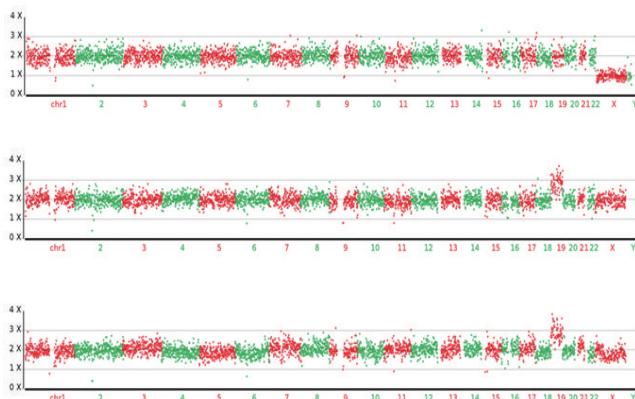| Step 1: Cell Lysis | Step 2: Termination of Lysis | Step 3: MDA Amplification |
|---|---|---|
| 1. Prepare a mixture of cell lysis buffer. 2. Add the cell to lysis buffer. 3. Incubate at 65℃ for 10 min. | Add a neutral solution to stop the reaction from previous step. | 1. Prepare the mixture of amplification. 2. Add the mixture of amplification to the system from Step 2. 3. Amplify at 30℃ for 2 hours. |



Single cell (using trophectoderm cells and sperm as a template, respectively) genomic amplification was performed using *Vazyme #N603*. Then libraries were prepared for sequencing, which was performed in Illumina MiniSeq after pooling according to the effective concentration and the 0.01X of sequencing depth. The data showed that the distribution of the reads was uniform in all parts of the genome, indicating that the amplification uniformity of *Vazyme #N603* was excellent.
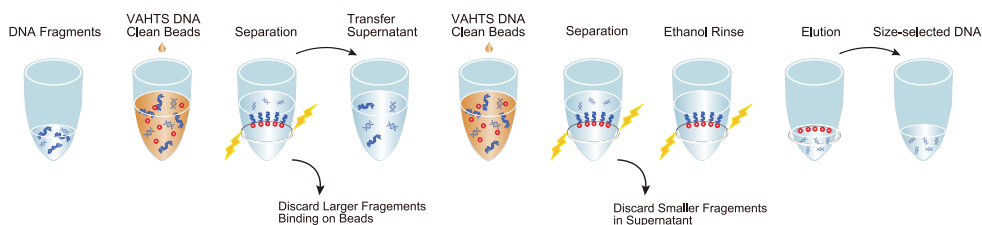
Scatter plots of whole genome copy numbers.

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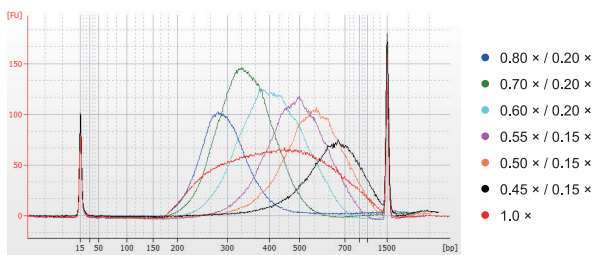
## Beads

### → VAHTS DNA Clean Beads (#N411)
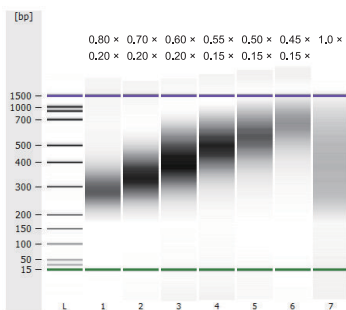
♡ Applicable for DNA purification and size selection in NGS library preparation.

♡ Compatible with almost all library prep protocols provided by all manufacturers.

DNA Fragments | VAHTS DNA Clean Beads | Separation | Transfer Supernatant | VAHTS DNA Clean Beads | Separation | Ethanol Rinse | Elution | Size-selected DNA

Discard Larger Fragments Binding on Beads

Discard Smaller Fragments in Supernatant

## Validation Data

A DNA library (200 bp - 1,500 bp) was prepared using TruePrep DNA Library Prep Kit V2 for Illumina (**Vazyme, #TD501**). Size-selection was performed using VAHTS DNA Clean Beads (Vazyme, #N411) according to the different parameters in the following table, respectively. Size distribution was detected using an Agilent 2100 Bioanalyzer.

| Ratio of 1st-round (Beads: DNA) | 0.80 × | 0.70 × | 0.60 × | 0.55 × | 0.50 × | 0.45 × | 1.0 × |
|---|---|---|---|---|---|---|---|
| Ratio of 2nd-round (Beads: DNA) | 0.20 × | 0.20 × | 0.20 × | 0.15 × | 0.15 × | 0.15 × | |
| Average Size (bp) | 300 | 350 | 400 | 500 | 600 | 700 | 200-1500 |

- 0.80 × / 0.20 ×
- 0.70 × / 0.20 ×
- 0.60 × / 0.20 ×
- 0.55 × / 0.15 ×
- 0.50 × / 0.15 ×
- 0.45 × / 0.15 ×
- 1.0 ×

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## Library Quantification

### ➔ Equalbit 1 × dsDNA HS Assay Kit (#EQ121)

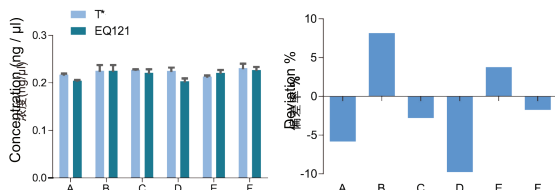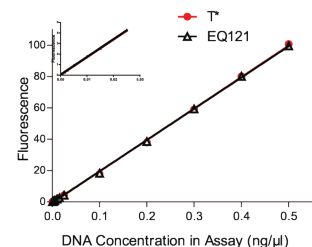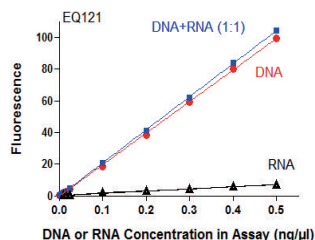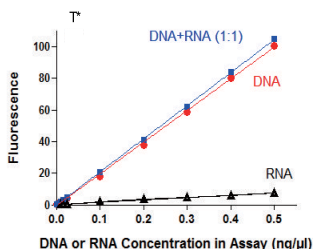| **Easy to Use** | Premixed reagent that is ready-to-use. |
| --- | --- |
| **Hyper Sensitive** | Accurate quantification of 0.2 ng- 100 ng of dsDNA. |
| **Super Specificity** | Excellent specificity to dsDNA. |
| **Excellent Stability** | Strictly quality controlled standards, ensuring batch-to-batch consistency. |

## Validation Data

### 1. Hyper Sensitive



Linearity Analysis (0.2 ng-100 ng): dsDNA samples with 12 different concentrations were tested using **Vazyme, #EQ121** or a similar reagent from vendor T*, respectively. Fluorescence signals were read using a Qubit$^{TM}$ Fluorometer 3.0. The result showed a excellent linear relationship between fluorescence and DNA concentration when the amount of dsDNA ranged from 0.2 ng to 100 ng.



Results and deviation rate obtained from different operators: the standard of **Vazyme, #EQ121** was serial-diluted to 0.2 ng / µl (theoretical concentration), and then tested by 6 different operators (A, B, C, D, E, F), respectively. The results are showed on the left, and the deviation rate, calculated as [result of EQ121 - result of T*] / test result of T* x 100%, are all within 10%.

### 2. Super Specificity to dsDNA

Samples of dsDNA, RNA, and DNA + RNA (1:1) were tested with **Vazyme, #EQ121** and a similar reagent from vendor T*. The results showed that Similar to products from T*, **Vazyme, #EQ121** specifically binds to dsDNA, even in the presence of RNA.

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## Cell-free DNA (cfDNA) Preservation and Isolation

### 👍 → VAHTS Blood Collection tube for cell-free DNA preservation (#N901)

♡ Preserve cfDNA in whole blood for up to **14 days** at room temperature without genomic DNA release or DNase-induced degradation.

♡ Excellent **tolerance to temperature & shaking** benefits the storage and long-distance transport of blood samples.

♡ The extracted cfDNA can be used for library preparation with **excellent efficiency and fidelity**.

♡ User-friendly label design and **flexible volume** for blood collection.

### 👍 → VAHTS Serum / Plasma Circulating DNA Kit (#N902)

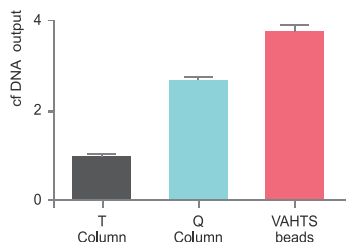| | |
|---|---|
| **cfDNA with Excellent Purity** | Accurate product concentration determination, unaffected by Carrier RNA. |
| **cfDNA with High Coverage** | The extracted cfDNA has no GC preference and is suitable for sequencing (i.e. NGS). |
| **Compatible with Automatic Procedures** | Suitable for manual extraction procedures and most automatic nucleic acid extraction instruments. |

## Validation Data

### 1. Products with High Purity
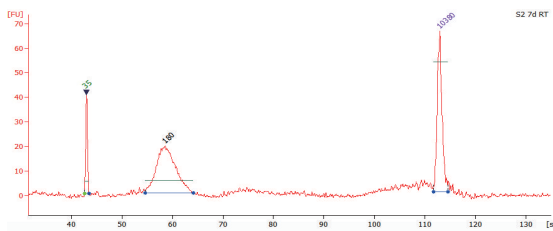


Electropherogram of separated cfDNA in Agilent 2100 analyzer.

### 2. High Yield



Actual yield of cfDNA detected by qPCR.

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# TruePrep DNA Library Prep Kits for Illumina®

Wang J, Wang L, *et al*. Asymmetric Expression of LincGET Biases Cell Fate in Two-Cell Mouse Embryos. *Cell*, 2018, 175(7):18871-1901. **(Vazyme #TD502)**

Han X, Wang R, *et al*. Mapping the Mouse Cell Atlas by Microwell-Seq. *Cell*, 2018, 172(5):1091-107 **(Vazyme #TD513)**

Zhang L, Yu X, et al. Lineage tracing reveals dynamic relationships of T cells in colorectal cancer. *Nature*, 2018, 564(7735):268-72. **(Vazyme #TD502)**

Wu J, Xu J, *et al*. Chromatin analysis in human early development reveals epigenetic transition during ZGA. *Nature*, 2018, 557(7704):256-60 **(Vazyme, #TD502)**

Zheng C, Zheng L, *et al*. Landscape of Infiltrating T Cells in Liver Cancer Revealed by Single-Cell Sequencing. *Cell*, 2017, 169(7):1342-56 **(Vazyme, #TD503)**

Huang X, Yang S, *et al*. Genomic architecture of heterosis for yield traits in rice. *Nature*, 2016, 537(7622):629-33. **(Vazyme, #TD501)**

Wu J, Huang B, *et al*. The landscape of accessible chromatin in mammalian preimplantation embryos. *Nature*, 2016, 534(7609):652-7. **(Vazyme, #TD501)**

Guo X, Zhang Y, et al. Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. *Nature Medicine*, 2018, 24(7):978-85. **(Vazyme, #TD501)**

Liu Z, Yan M, et al. Nucleoporin Seh1 Interacts with Olig2/Brd7 to Promote Oligodendrocyte Differentiation and Myelination. *Neuron*, 2019, pii: S0896-6273(19)30153-9. **(Vazyme, #TD502)**

Li X, Meng D, *et al*. Single nucleus sequencing reveals spermatid chromosome fragmentation as a possible cause of maize haploid induction. *Nature Communications*, 2017, 8(1):991. **(Vazyme, #TD501, #TD503)**

Yang L, Wang W, *et al*. A single-cell transcriptomic analysis reveals precise pathways and regulatory mechanisms underlying hepatoblast differentiation. *Hepatology*, 2017, 66(5):1387-401. **(Vazyme, #TD502, #411)**

# VAHTS Universal DNA Library Prep Kits for Illumina®

Zhang M, Dong Y, *et al*. Transcription factor Hoxb5 reprograms B cells into functional T lymphocytes. *Nature Immunology*, 2018, 19(3):279-90. **(Vazyme, #ND604, #N601)**

Cao S, Yu S, *et al*. Chromatin accessibility dynamics during chemical induction of pluripotency. *Cell Stem Cell*, 2018, 22(4): 529-42. **(Vazyme, #ND102, #NQ101)**

# VAHTS Total RNA-seq (H/M/R) Library Prep Kit for Illumina®

He Y, Li X, *et al*. Transitory presence of myeloid-derived suppressor cells in neonates is critical for control of inflammation. *Nature Medicine*, 2018. 24(2):224-31. **(Vazyme, #NR603)**

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## VAHTS mRNA-seq Library Prep Kits for Illumina®

Tian X, He G, et al. Cryptococcus neoformans sexual reproduction is controlled by a quorum sensing peptide. *Nature Microbiology*, 2018: 3(6):698-707. **(Vazyme, #NR601)**

Han X, Chen H, et al. Mapping human pluripotent stem cell differentiation pathways using high throughput single-cell RNA-sequencing. *Genome Biology*, 2018, 19(1):47. **(Vazyme, #NR601)**

Qin X, Liu S, *et al.* Heterotrimeric G Stimulatory Protein α Subunit Is Required for Intestinal Smooth Muscle Contraction in Mice. *Gastroenterology*, 2017, 152(5):1114-25. **(Vazyme, #NR601)**

Shen C, Wang J, *et al.* Transcriptome Analysis of Differentially Expressed Genes Induced by Low and High Potassium Levels Provides Insight into Fruit Sugar Metabolism of Pear. *Frontiers in Plant Science*, 2017, 8:938. **(Vazyme, #NR601)**

## VAHTS Stranded mRNA-seq Library Prep Kit for Illumina®

Song L, Ma Q, *et al.* Molecular Link between Leaf Coloration and Gene Expression of Flavonoid and Carotenoid Biosynthesis in Camellia sinensis Cultivar 'Huangjinya'. *Frontiers in Plant Science*, 2017, 8:803. **(Vazyme, #NR602)**

## Discover-sc Single Cell Kit

Zhang M, Dong Y, *et al.* Transcription factor Hoxb5 reprograms B cells into functional T lymphocytes. *Nature Immunology*, 2018, 19(3):279-90. **(Vazyme, #ND604, #N601)**

## VAHTS DNA Clean Beads

Yang L, Wang W, *et al.* A single-cell transcriptomic analysis reveals precise pathways and regulatory mechanisms underlying hepatoblast differentiation. *Hepatology*, 2017, 66(5):1387-401. **(Vazyme, #TD502, #N411)**

Wang Y, Zhang X, et al. Bisulfite-free, single base-resolution analysis of 5-hydroxymethylcytosine in genomic DNA by chemical-mediated mismatch. *Chemical Science*, 2018, 10(2): 447-52. **(Vazyme, #N411)**

Tao Z, Zhang X, *et al.* Analysis of long noncoding RNA and mRNA using RNA sequencing during the differentiation of intramuscular preadipocytes in chicken. *PLoS One*, 2017, 12(2):e0172389 **(Vazyme, #N411)**

## VAHTS Library Quantification Kits for Illumina®

Cao S, Yu S, *et al.* Chromatin accessibility dynamics during chemical induction of pluripotency. *Cell Stem Cell*, 2018, 22(4):529-42. **(Vazyme, #ND102, #NQ101)**

Li D, Liu J, *et al.* Chromatin Accessibility Dynamics during iPSC Reprogramming. *Cell Stem Cell*, 2017, 21(6):819-33. **(Vazyme, #NQ101)**

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