NGS Library Preparation

Product List

DNA Sequencing

DNA Library Kit (Apply to Illumina platform)

Product Name	Size	Cat.No.#	Price (USD)
HOT VAHTS Universal DNA Library Prep Kit for Illumina V4	24 rxns/96 rxns	ND610-01/02	588/2200
VAHTS AmpSeq Library Prep Kit V3	24 rxns/96 rxns	NA210-01/02	840/2880
HOT VAHTS Universal Plus DNA Library Prep Kit for Illumina V2	24 rxns/96 rxns	ND627-01/02	625/2300
VAHTS ssDNA Library Prep Kit for Illumina	24 rxns/96 rxns	ND620-01/02	884/3150

DNA Library Kit (Apply to Ion Torrent platform)

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Universal DNA Library Prep Kit for Ion Torrent V2	24 rxns/96 rxns	ND702-01/02	588/2200
VAHTS AmpSeq Library Prep Kit V3	24 rxns/96 rxns	NA210-01/02	840/2880

DNA Library Kit (Apply to MGI platform)

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Universal Plus DNA Library Prep Kit for MGI V2	24 rxns/96 rxns	NDM627-01/02	625/2300
Upcoming VAHTS Universal DNA Library Prep Kit for MGI V4	24 rxns/96 rxns	NDM610-01/02	588/2200

DNA Library Preparation Module

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Circularization Kit For MGI	16 rxns/48 rxns	NM201-01/02	348/938
VAHTS HiFi Universal Amplification Mix for MGI (SI)	24 rxns/96 rxns	NM618-01/02	77/268
VAHTS Universal End Preparation Module for Illumina V2	24 rxns/96 rxns	N203-01/02	216/816
VAHTS Universal Adapter Ligation Module for Illumina V2	24 rxns/96 rxns	N204-01/02	360/1345
VAHTS Universal Plus Fragmentation,End Preparation & dA-Tailing Module for Illumina V2	24 rxns/96 rxns	N219-01/02	264/960
VAHTS HiFi Universal Amplification Mix for Illumina	24 rxns/96 rxns	N618-01/02	77/268
VAHTS AmpSeq Multi-PCR Module V3	24 rxns/96 rxns	NA215-01/02	120/412

DNA Library Preparation Single Enzyme

Product Name	Size	Cat.No.#	Price (USD)
T4 DNA Polymerase	2,000 U	N101-01	446
T4 Polynucleotide Kinase	10,000 U	N102-01	583
T4 DNA Ligase (Rapid)	600,000 U	N103-01	936
DNA Polymerase I Klenow Fragment	5,000 U	N104-01	790
DNA Polymerase I Klenow Fragment exo	5,000 U	N105-01	790
Phi29 MAX DNA Polymerase	250 U/1,250 U	N106-01/02	48/191
Phanta Uc Super-Fidelity DNA Polymerase for Library Amplification	100 U/500 U	P507-01/02	200/800

DNA Library Adapter

Product Name	Size	Cat.No.#	Price (USD)
VAHTS DNA Adapters Set 1-Set 2 for Illumina	10 μl each/40 μl each	N801/N802-01/02	165/605
VAHTS DNA Adapters Set 3-Set 6 for Illumina	20 μl each	N805/N806/ N807/N808	315
VAHTS Multiplex Oligos Set 4/Set 5 for Illumina	192 rxns each	N321/N322	739
VAHTS Dual UMI UDI Adapters Set 1 - Set 4 for Illumina	96 rxns each	N351/N352/ N353/N354	499
VAHTS Maxi Unique Dual Index DNA Adapters Set1-Set4 for Illumina	384 rxns each	N34201/N34202/ N34203/ N34204	1920
TruePrep Index Kit V4 for Ilumina	192 rxns each	TD204/TD205/ TD206/TD207	384
TruePrep Index Kit V2 for Illumina	192 rxns	TD202	422
TruePrep Index Kit V3 for Illumina	768 rxns	TD203	1536
VAHTS AmpSeq Adapters for Illumina	2 × 10 rxns each	NA111-01/02	384
	24 × 10 rxns each	NA111-03/04/05	720
VAHTS AmpSeq Adapters for Ion Torrent	12 × 10 rxns each	NA121-01/02	384
	524 × 10 rxns each	NA121-03/04/05	720
VAHTS DNA Adapters Set 8 for MGI	10 μl each/ 40 μl each	NM108-01/02	614/2304
VAHTS PCR-Free DNA Adapters Set 1-Set 4 for MGI	20 μl each	NM10901-NM10904	317
VAHTS Dual UMI UDB Adapters Set 1-Set 8 for MGI	96 rxns each	NM35101-NM35108	499
TruePrep Index Kit for MGI	192 rxns each	TDM101-TDM104	384

RNA Sequencing

RNA Library Kit (Apply to Illumina platform)

Product Name	Size	Cat.No.#	Price (USD)
HOT VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina	24 rxns/96 rxns	NR605-01/02	840/2880

RNA Library Kit (Apply to MGI platform)

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Universal V8 RNA-seq library Prep Kit for MGI	24 rxns/96 rxns	NRM605-01/02	840/2880

RNA Library Preparation Module

Product Name	Size	Cat.No.#	Price (USD)
VAHTS mRNA Capture Beads	24 rxns/96 rxns	N401-01/02	65/235
Ribo-off rRNA Depletion Kit (Human/Mouse/Rat)	24 rxns/96 rxns	N406-01/02	1123/3975
Ribo-off rRNA Depletion Kit (Plant)	12 rxns/24 rxns	N409-01/02	550/972
Ribo-off rRNA Depletion Kit V2 (Bacteria)	12 rxns/24 rxns	N417-01/02	550/972
Ribo-off Globin & rRNA Depletion Kit (Human/Mouse/Rat)	24 rxns/96 rxns	N408-01/02	1123/3975
Ribo-MagOff rRNA Depletion Kit (Human/Mouse/Rat)	12 rxns/24 rxns	N420-01/02	562/994

RNA Library Adapter

Product Name	Size	Cat.No.#	Price (USD)
VAHTS RNA Adapters Set 1-Set 2 for Illumina	10 μl each/40 μl each	N803/N804-01/02	131/492
VAHTS RNA Adapters Set 3-Set 6 for Illumina	20 μl each	N809/N810/ N811/N812	252
VAHTS RNA Multiplex Oligos Set 1-Set 2 for Illumina	192 rxns each	N323/N324	592
TruePrep Index Kit V4 for Illumina	192 rxns each	TD204/TD205/ TD206/TD207	384
TruePrep Index Kit V2 for Illumina	192 rxns each	TD202	422
TruePrep Index Kit V3 for Illumina	796 rxns	TD203	1536
VAHTS RNA Adapters Set 8 for MGI	10 μl each/ 40 μl each	NM208-01/02	499/1843

Single-Cell Seq Series

Product Name	Size	Cat.No.#	Price (USD)
Discover-sc Single Cell WGA Kit	24 rxns/96 rxns	N603-01/02	648/2150
Discover-sc WTA Kit V2	12 rxns/24 rxns/ 96 rxns	N711-01/02/03	432/768/2592

Epigenetics Series

DNA Methylation

Product Name	Size	Cat.No.#	Price (USD)
EpiArt DNA Methylation Library Kit for Illumina V3	24 rxns/96 rxns	NE103-01/02	1560/5568
2 × EpiArt HS Taq Master Mix	1 ml/5 ml/15 ml	EM201-01/02/03	32/140/384
2 × EpiArt HS Taq Master Mix (Dye Plus)	1 ml/5 ml/15 ml	EM202-01/02/03	32/140/384

Nucleic Acid-Protein Interaction

Product Name	Size	Cat.No.#	Price (USD)
Hyperactive pA-MNase for CUT&RUN	200 U/400 U	S701-01/02	900/1600
Hyperactive pG-MNase for CUT&RUN	200 U/400 U	S702-01/02	900/1600

Beads Series

DNA Clean-Up Beads

Product Name	Size	Cat.No.#	Price (USD)
HOT VAHTS DNA Clean Beads	5 ml/60 ml/450 ml	N411-01/02/03	145/950/3785
VAHTS RNA Clean Beads	5 ml/40 ml/450 ml	N412-01/02/03	175/680/4950

Magnetic Rack

Product Name	Size	Cat.No.#	Price (USD)
0.2 ml Magnetic rack	32 hole (200 μl/ hole)	CM101	280
1.5 ml Magnetic rack	24 hole (1.5 ml/ hole)	CM103	280

Quantification Series

qPCR library Quantification

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Library Quantification Kit for Illumina	500 rxns each (20 μl/rxn)	NQ101/NQ102/ NQ103/NQ104	350
DNA Standard 1-6	8 rxns	NQ105	429
Library Dilution Buffer	50 ml	NQ106	95

Qubit Quantification

Product Name	Size	Cat.No.#	Price (USD)
HOT Equalbit 1 × dsDNA HS Assay Kit	100 assays/ 500 assays	EQ121-01/02	95/280
Equalbit RNA HS Assay Kit	100 assays/ 500 assays	EQ211-01/02	100/300

Capture Series

Product Name	Size	Cat.No.#	Price (USD)
VAHTS Target Capture Core Exome Panel	24 rxns/96 rxns	NC001-01/02	2184/8640
VAHTS Target Capture Universal Blockers and Post-PCR Primer Mix for Illumina-TS	24 rxns/96 rxns	NC101-01/02	1320/4378
VAHTS Target Capture Universal Blockers and Post-PCR Primer Mix for MGI-SI	24 rxns/96 rxns	NCM101-01/02	1320/4378
VAHTS Target Capture Hybridization and Wash Kit	24 rxns/96 rxns	NC103-01/02	576/1968

Product Introduction

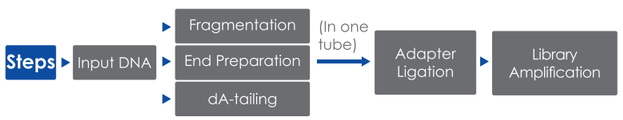
DNA Library Kit (Apply to Illumina platform)

Applications	Products (Cat.No.#)	Features	Applicable for
Enzymatic Fragmentation Library Preparation	VAHTS Universal Plus DNA Library Prep Kit for Illumina V2 (ND627)	The false positives of SNV and InDel detection are greatly reduced; improving the accuracy of mutation detection.	Animals, plants, microorganisms source of genomic DNA, FFPE DNA, etc.
Mechanical Method Library Preparation	VAHTS Universal DNA Library Prep Kit for Illumina V4 (ND610)	Higher conversion rate; Higher compatibility; Higher Sequencing depth; Better mutation detection.	Genomic DNA, cfDNA, ChIP-seq, target region capture, 16S/ITS-seq
Single-stranded DNA Library Preparation	VAHTS ssDNA Library Prep Kit for Illumina (ND620)	Compatible with single and double stranded mixed DNA Library; compatible with DNA samples as short as 40 bp.	Genomic DNA, FFPE DNA, ChIP DNA, cfDNA, microbial DNA, paleontological DNA, etc.
Multiplex Amplification Library Preparation	VAHTS AmpSeq Library Prep Kit V3 (NA210)	With different initial input (1 - 100 ng); the library can be built efficiently; Compatible with both Illumina & Ion Torrent platforms.	gDNA, FFPE DNA, cfDNA etc.

Enzymatic fragmentation Library Preparation

Universal Plus DNA library Prep Kit for Illumina V2 (#ND627)

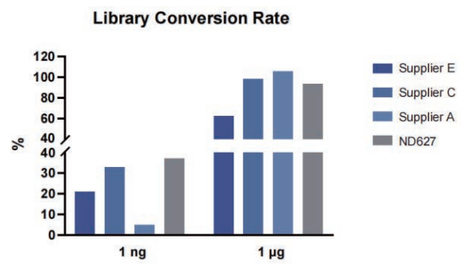
Workflow



Validation Data

1.High library conversion

The PCR free library was constructed with salmon genomic DNA as a template, and the input amount was 1 ng and 1 ug. Compared with similar products of other companies, Vazyme #ND627 has basically the same library conversion rate and a higher conversion rate when the input amount is low.

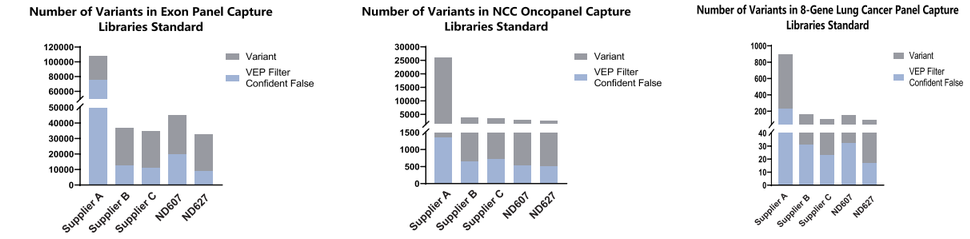


Features

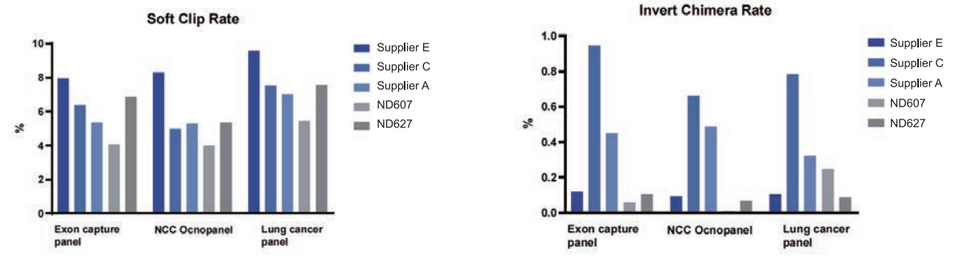
- Reduce "false positives", greatly reduce the false positives detected by SNP and InDel, and improve the accuracy rate of mutation detection
- High library yield, excellent library conversion rate, and higher library quality.

2.Reduced SNV detection background noise.

Use the standard for library preparation. Vazyme #ND627 greatly reduces the false positive Variant detection results without affecting the detection of true Variants.

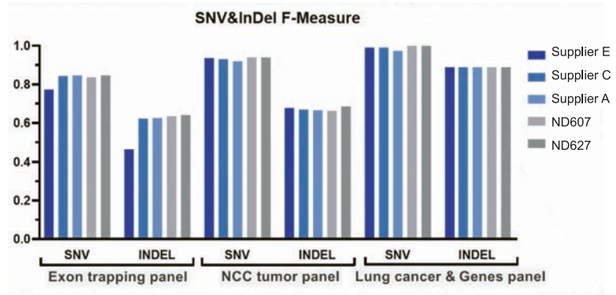


Use the standard for library construction. Vazyme #ND627 is not significantly different from the product of Supplier C in terms of Soft Clip detection but has a lower detection rate of Invert Chimera when compared with similar products.



3.Superior SNP and InDel detection

The sensitivity and accuracy of SNP and indel are evaluated by F-measure, and Vazyme #ND627 out performed other company products slightly in SNP and Indel detection.



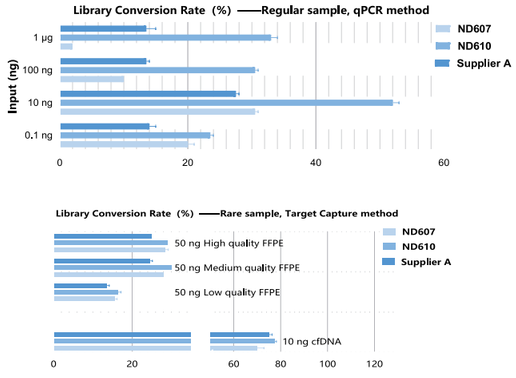
Mechanical Method Library Preparation

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

Workflow

Validation Data

1.Higher conversion rate

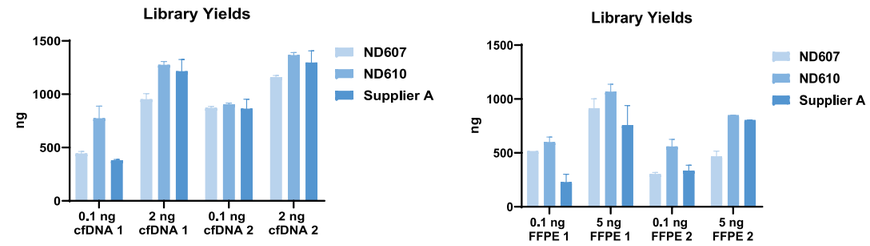


Use conventional samples of varying amounts and rare clinical samples of different quality to construct libraries. ND610 generates an obviously higher library conversion rate than the similar products of other companies under the same conditions.

Features

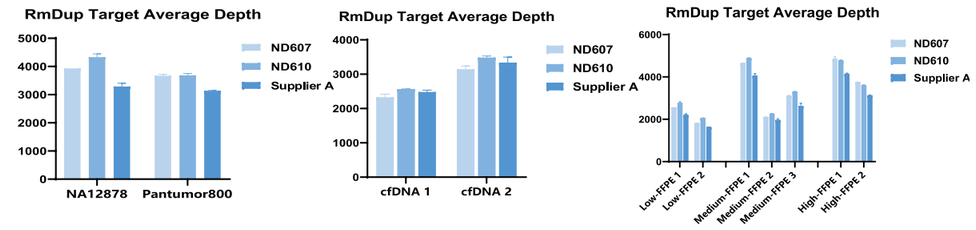
- Wide sample compatibility in addition to conventional samples, compatible with low quality FFPE, cfDNA samples.
- High library Preparation efficiency and higher library conversion rate.
- Mutation detection Accurate low frequency mutation detection rate.

2.Applicable to FFPE, cfDNA, and Other Samples of Low Quality



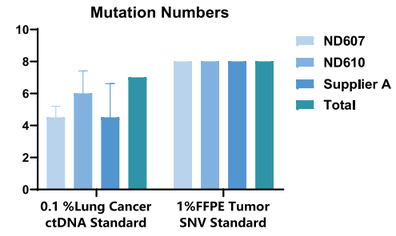
After the same number of amplification cycles, ND610 generates an obviously higher library yield than the similar products of other companies

3.Better Effective Sequencing Depth



Use clinical cfDNA and FFPE DNA of varying degrees of degradation to construct libraries. After normalizing the data volume, libraries constructed with ND610 have better sequencing depth after de-duplication.

4.More Accurate Detection of Low-Frequency Mutations



For the 1% FFPE tumor SNV standard, the detection of low-frequency mutations using the library constructed with ND610 is equivalent to that constructed by the similar products of other companies; for the 0.1% lung cancer ctDNA standard, the detection of low-frequency mutations using libraries constructed with ND610 is superior to that constructed by the similar products of other companies.

DNA Single stranded library Preparation

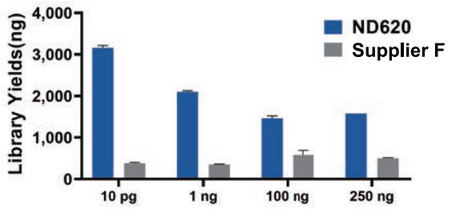
VAHTS ssDNA Library Prep Kit for Illumina (#ND620)

Workflow

Steps ▸ Input DNA ▸ 3'Adapter Ligation ▸ Extension ▸ 5'Adapter Ligation ▸ Library Amplification

Validation Data

1.Input compatible as low as 10 pg

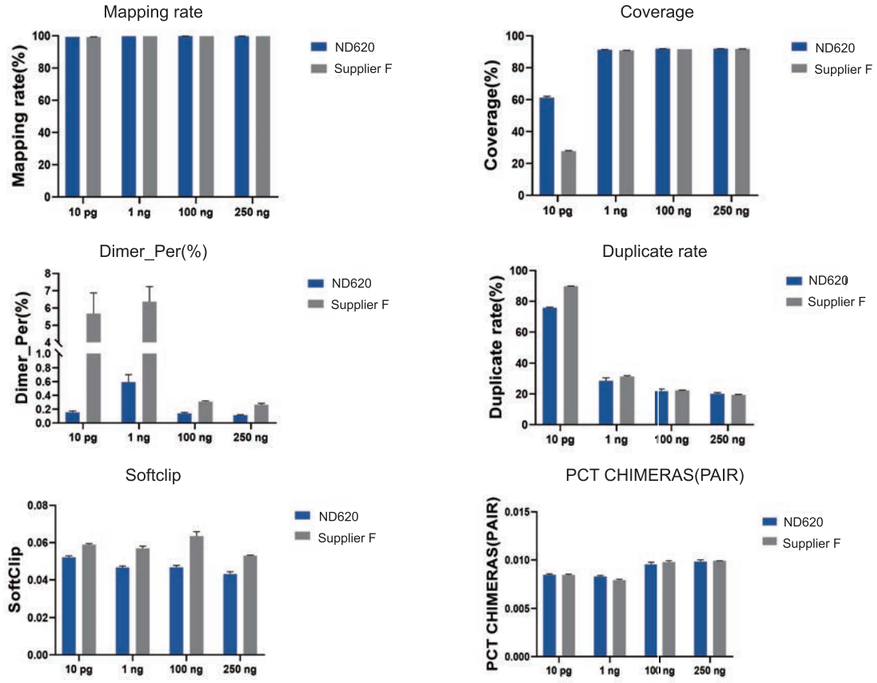


The fragment mouse gDNA was used as the starting template, and the Input DNA volume was 10 pg, 1 ng, 100 ng, and 250 ng, respectively. The library was constructed according to the standard library preparation process of Vazyme # ND620 and similar products of Supplier F. The results show that Vazyme # ND620 can build libraries efficiently. Compared with the similar products of Supplier F, the library has higher yield and better peak shape.

Features

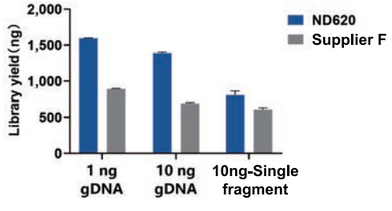
- Easy to operate, a single sample database only takes 2 hours;
- Compatible with single and double strand mixed DNA library. compatible with DNA samples as short as 40 bp.
- Libraries with different starting sizes (10 pg - 250 ng) had excellent sequencing data quality.

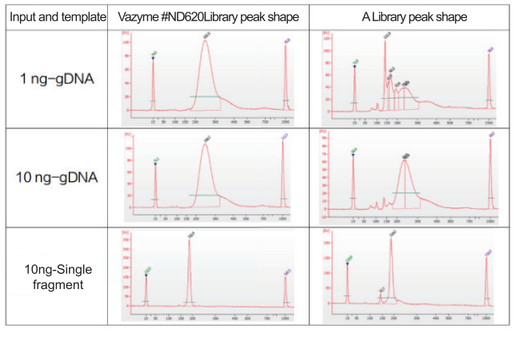
2.Good quality of sequencing data



Vazyme #ND620 in terms of sequencing data quality, compared with similar products of Supplier F, the Mapping rate/ Coverage/Duplicate rate/Softclip/Dimer - Per are better than similar products of Supplier F, especially under low input amount.

3.Compatible with segments as short as 40 bp



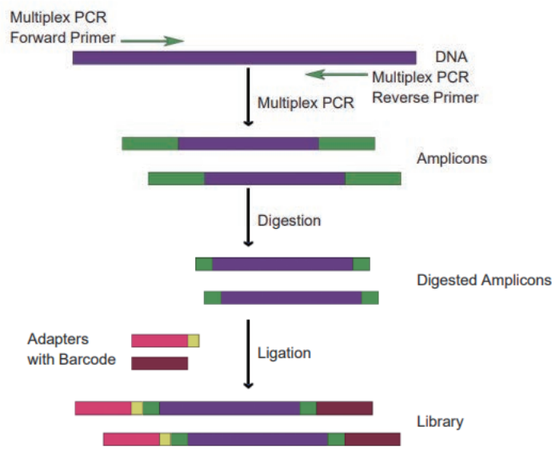


Two short fragment models were used as templates (fragmented mouse gDNA was sorted to the main peak of 90 bp, and a single fragment of 40 bp was synthesized). The library was constructed according to the standard library building process of Vazyme #ND620 and similar products of Supplier F. The results show that Vazyme # ND620 was compatible with the template as short as 40 bp. Compared with the similar products of Supplier F, the library has higher yield and better peak shape.

Multiple Amplification Library Preparation

VAHTS AmpSeq Library Prep Kit V3(#NA210)

Mechanism



Features

- **High output of library**
  The library can be built efficiently under different initial inputs (1-100 ng).
- **Sequencing data quality**
  High coverage and high uniformity.
- **Extensive template compatibility**
  gDNA, FFPE DNA, cfDNA samples.
- **Dual platform compatibility**
  Illumina & Ion Torrent.

DNA Library Kit (for MGI platform)

Applications	Cat.No.#	Features	Applicable for
Mechanical Method Library Preparation	VAHTS Universal DNA library Prep Kit for MGI V4 (NDM610)	Higher conversion rate; Higher compatibility; Higher Sequencing depth; Better mutation detection	Genomic DNA, cfDNA, ChIP-seq, target region capture, 16S/ ITSseq
Enzymatic Fragmentation Library Preparation	VAHTS Universal Plus DNA library Prep Kit for MGI V2 (NDM627)	Compatible with MGI platform, reduce the "false positive", improve the mutation detection accuracy	genomic DNA, FFPE DNA, etc.
Single-strand Cyclic DNA Libraries	VAHTS Circularization Kit For MGI (NM201)	The cyclization time is as low as 70 min; High cyclization efficiency can reach 60%.	Applicable to all MGI high-throughput sequencing platforms

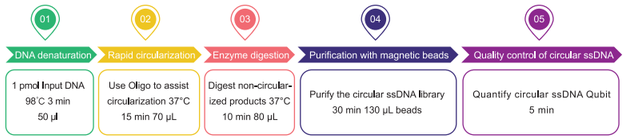
RNA Library Kit (for Illumina&MGI platform)

Applications	Cat.No.#	Features	Applicable for
Rapid Transcriptome Library Preparation	VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina (NR605)	For low initial amount and degraded samples, it has a higher success rate of database construction	Compatible with the total RNA of all kinds of samples
RNA Multiple PCR Library Preparation	VAHTS RNA Multi-PCR library Prep Kit (NA210)	Different starting amounts (1-100 ng) can effectively prepare the library. Compatible with both Illumina & Ion Torrent platform	gDNA, FFPE DNA, cfDNA etc.
rRNA Depletion Kit	Ribo-off Globin & rRNA Depletion Kit(Human/ Mouse/Rat)(N408)	High deplete efficiency of low-quality RNA samples.Start as low as 10 ng	Globin mRNA and rRNA were depleted
rRNA Depletion Kit	Ribo-off rRNA Depletion Kit V2 (Bacteria)(N417)	Species coverage increased; It applies to a wider range of species.	Gram-positive bacteria and gram-negative bacteria of rRNA depletion
rRNA Depletion Kit	Ribo-off rRNA Depletion Kit (Plant)(N409)	Strong compatibility, low rRNA residual rate	Plants to deplete rRNA
Rapid Transcription Library Preparation	VAHTS Universal V8 RNA-seq library Prep Kit for MGI (NRM605)	For low-quality samples, it has a higher success rate of database construction; Gene detection rate is high, the transcription of this region of uniform coverage.	Rapid and highly detectable RNA library construction of the MGI platform

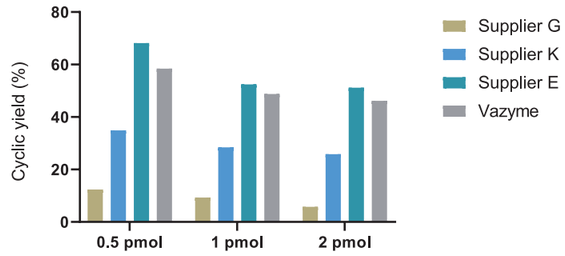
VAHTS Circularization Kit for MGI (#NM201)

Validation Data

1.Operation quickly



2.Broad library input compatibility



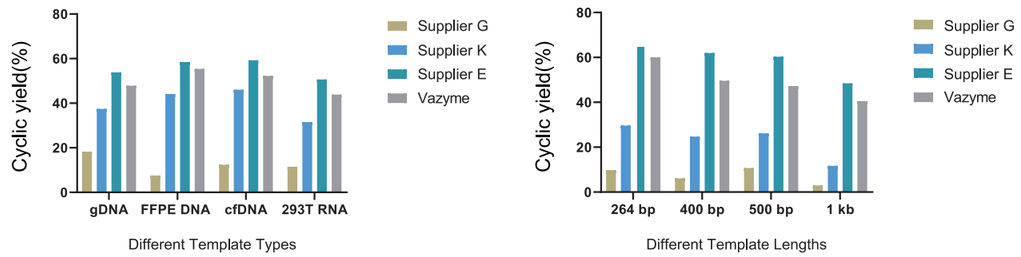
Compared with the similar products from Supplier G and Supplier K, NM201 a higher cyclization yield.

The cyclization production rate of similar products of Supplier E is higher than that of NM201 and Supplier K. However, subsequent data analysis shows that the cyclization products of Supplier E's products contain more non-cyclization fragments. As a result, when using ssDNA Qubit (which cannot distinguish between linear and circular DNA molecules) for quantitative cyclization products, the detection value is inflated.

Features

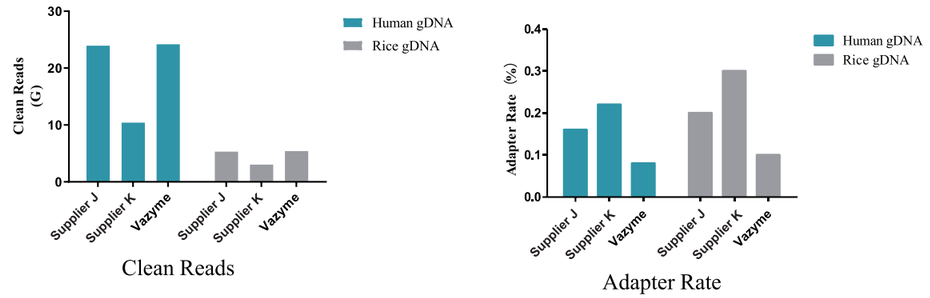
- **The cyclization time is as low as 70 min**
- **The maximum cyclization efficiency can reach 60%**
- **Compatible with different library preparation methods, library inputs, and template types.**

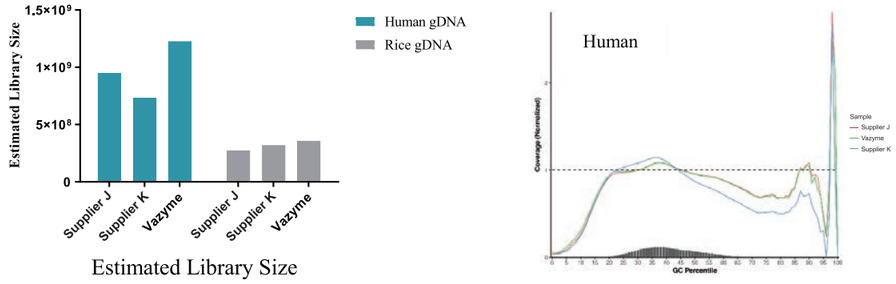
3.High cyclization rate and wide compatibility



NM201 has a wide range of template types and template length compatibility, and the cyclization yield is more than 40%, and the highest cyclization yield can reach 60%. The cyclization production rate of NM201 is higher than that of Supplier G and Supplier K.

4.The quality of the data is excellent



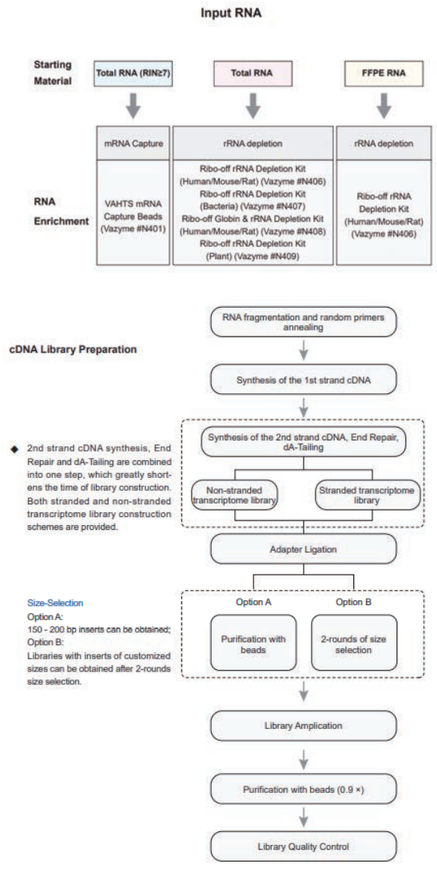


In terms of data quality, Clean reads and Adapter Rate of Vazyme #NM201 are superior to similar products from Supplier J and Supplier K, and data analysis show that Vazyme #NM201 has an even larger estimated library size.

Rapid Transcriptome Library preparation Library

VAHTS Universal V8 RNA-seq library Prep Kit for Illumina (#NR605)

Mechanism&workflow



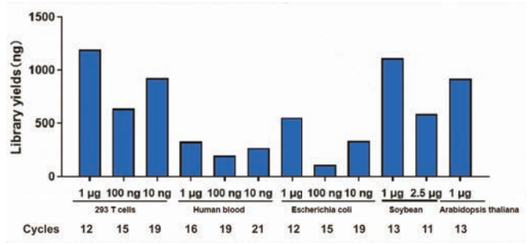
Features

- **Fast**
  Extremely simple operational process, shortening the transcriptome library preparation time to 3 h
- **Compatible**
  Higher success rate of library preparation for low initial input and degraded specimens
- **High quality**
  Excellent sequencing data quality, resulting in more uniform coverage of the transcript regio

Validation Data

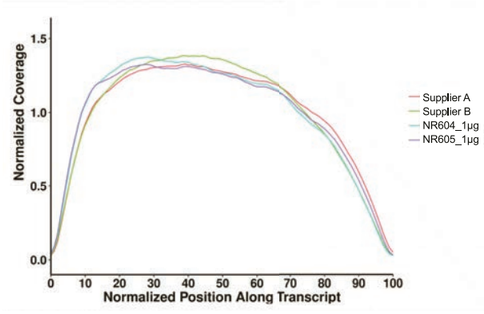
1.Compatible with low quality samples

The stranded transcriptome library was constructed according to the library construction process of NR605. The results show that libraries can be successfully constructed for different samples, and the yield is normal.



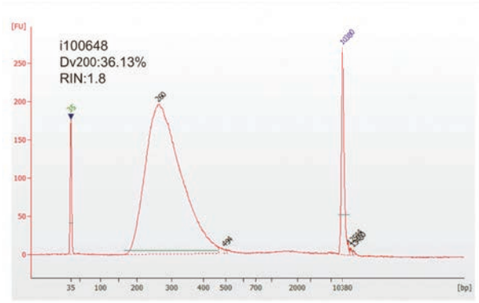
2.High data uniformity

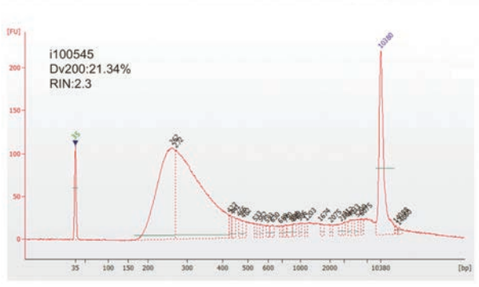
Sequencing results show that the libraries prepared by different transcriptome library kits are highly consistent in the uniformity of sequencing.



3.High success rate

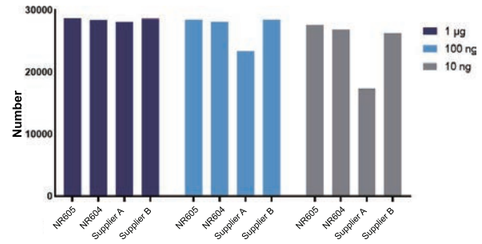
The stranded transcriptome library is constructed according to the library construction process of NR605. The results show that NR605 can be successfully used to build library for FFPE samples of different quality.





4.More abundant genes were detected

The sequencing results show that for the same sequencing quantity, the libraries constructed by using different transcriptome library preparation products can obtain a relatively rich number of genes detected. However, for low initial input, NR605 have more abundant gene detection numbers.

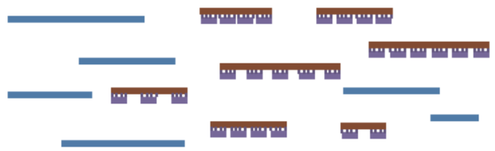


rRNA Depletion Kit

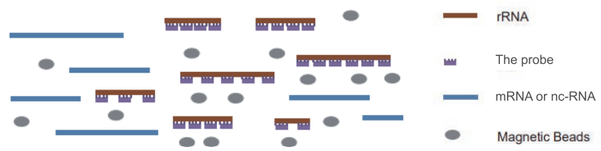
Ribo-MagOff rRNA Depletion Kit (Human/Mouse/Rat)(#N420)

Mechanism

1.RNA probe hybridization



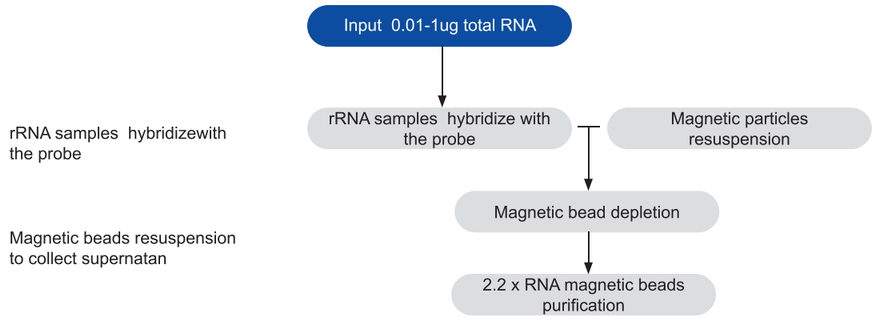
2.beads hybridization



3. rRNA depletion

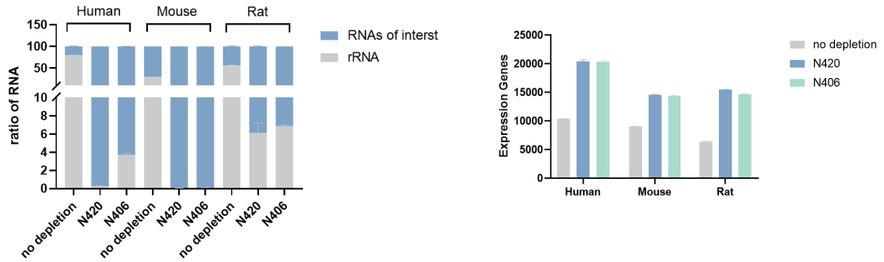
Features

- **Fast**
  Easy to operate, the whole process only takes 1 h
- **Compatibility**
  Compatible with low starting quantity and low quality samples
- **High efficiency**
  High rRNA depletion efficiency, rRNA residual rate <10 %

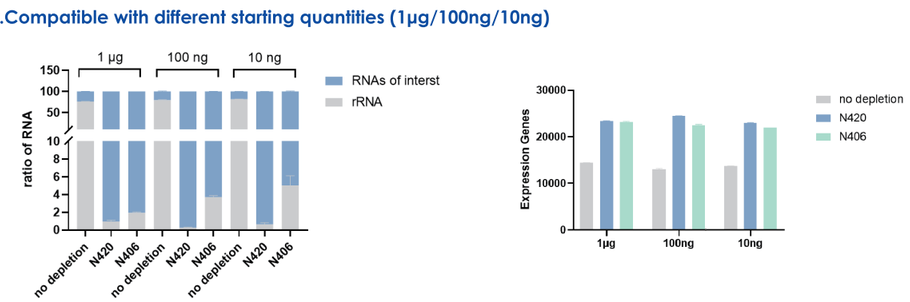


Validation Data

1.Compatible with different species (human/rat/mouse)

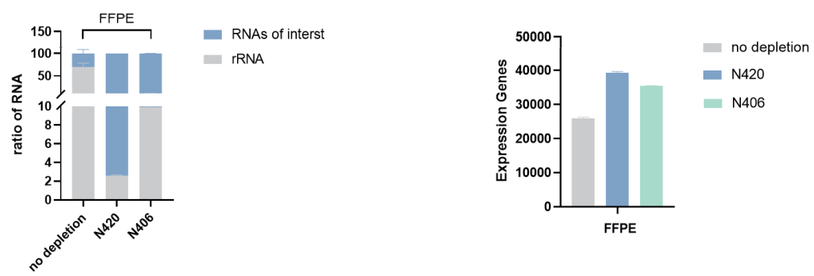


2.Compatible with different starting quantities (1μg/100ng/10ng)



According to different starting quantity samples (1μl / 100 ng / 10 ng), in the aspect of library output, Vazyme # N420 compatible efficient build library module, to ensure the good library output

3.Compatible with FFPE samples



Vazyme #N420 has a rich number of gene detections. In terms of correlation, the correlation between Vazyme #N420 and Vazyme #N406 is >0.9.

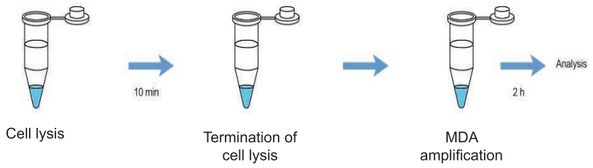
Single-Cell Seq Series

Applications	Cat.No.#	Features	Applicable for
Single Cell Genome Sequencing	Discover-scSingle Cell WGA Kit (N603)	It can be used for copy number variation analysis of chromosomes >1 Mb. Phi29 DNA polymerase is 1000 times higher in fidelity than Taq enzyme.	Applicable to animal and plant cells, bacteria or blastomere, trophoblast cells, sperm and other samples
Single-cell Transcriptome Sequencing	Discover-sc WTA Kit V2 (N711)	The full-length cDNA was amplified by two-terminal primers, and the whole transcriptome information was obtained, avoiding the 5' and 3' preference	Single cell or 10 pg Total RNA

Single cell Genome Sequencing

Discover-scSingle Cell WGA Kit (#N603)

Workflow



Validation Data

A small number of cells were amplified with N603 for single cell genome amplification and library construction.Finally, Illumina MiniSeq sequencing was performed according to the effective concentration and sequencing depth Pooling of 0.01X. The sequencing data showed that reads were evenly distributed in all parts of the genome, indicating good homogeneity of N603 amplification.

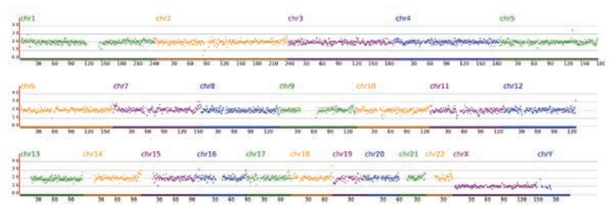


Figure Genome-wide copy number scatter distribution

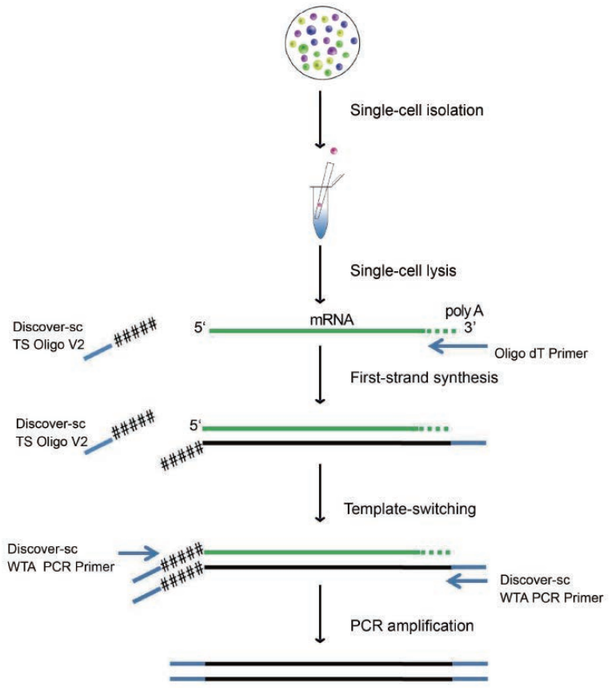
Features

- **High coverage**
  Single cell genome amplification can reach more than 95% coverage.
- **High average degree**
  It is suitable for analysis of chromosome aneuploidy, insertion/deletion variants and SNV >0.5 Mb.
- **The operation is simple**
  Single tube reaction, operation time less than 10 min, amplification products without purification can be used for a variety of downstream reactions.

Single-cell Transcriptome Sequencing

Discover-sc WTA Kit V2 (#N711)

Mechanism



Features

- **High amplification sensitivity**

Use LNA locked nucleotide technology carefully optimized reaction system, greatly increases the detection number of low-expressed genes.

- **Great product integrity**

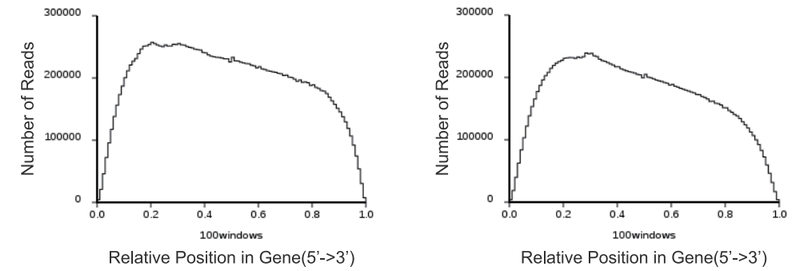
The full-length mRNA sequence information is obtained, avoiding 3' and 5' end bias.

- **Low template input amount**

A single cell or a small amount of RNA can be used as a starting template.

Validation Data

1. The data are uniformly distributed and unbiased



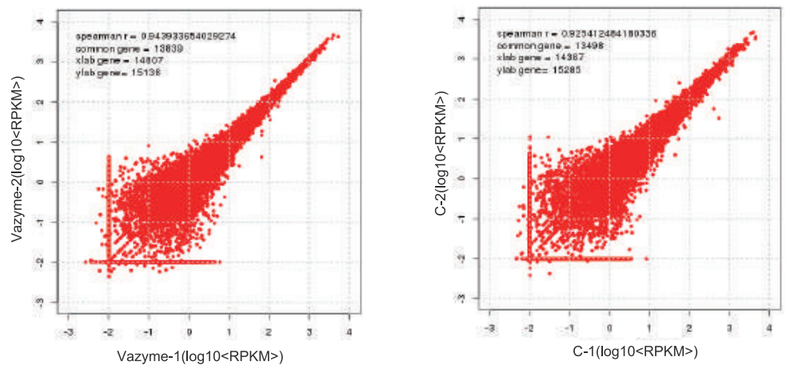
The left figure shows the distribution results of Vazyme-1 sequencing fragment on genes, and the right figure shows the distribution results of Supplier J-1 sequencing fragment on genes. Data showed that the amplification of Discover-scWTA Kit V2 well ensured the coverage of genes 5 'and 3'.

2. Higher gene detection rates

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-1	15138	88.2%	3.06%	86.9%	9.4%	3.72%
Supplier J-1	14367	84.6%	1.76%	85.9%	10.3%	3.77%
Supplier J-2	15285	84.7%	2.27%	82.0%	13.5%	4.56%

From the results, it can be seen that the detection sensitivity of the amplification products of the Discover-sc WTA Kit V2 kit is high, and the number of genes detected by a single 293T cell is up to 15000.

3.Repeated high correlation expression



The left figure shows the repetitive correlation analysis of Vazyme-1 and Vazyme-2, and the right figure shows the correlation analysis of the expression repeatability of Supplier J-1 and Supplier J-2. The data shows that the expression repeatability is higher than that of Supplier J.

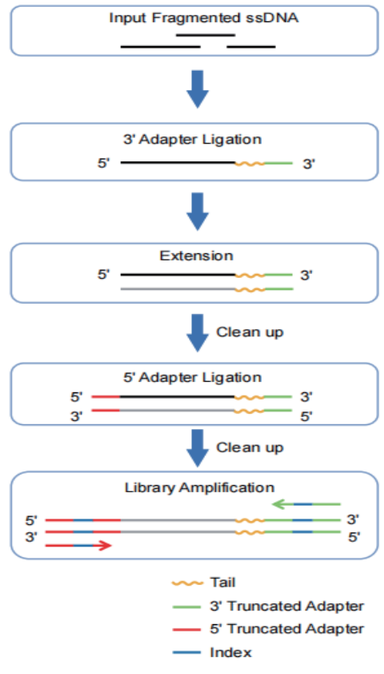
Epigenetics

Applications	Products (Cat.No.#)	Features	Applicable for
Methylation Library Preparation	EpiArt DNA Methylation library Kit for Illumina V3 (NE103)	Based on the single-strand library construction method, it is compatible with as low as 10 pg DNA	Genomic DNA, FFPE DNA, ChIP DNA, cfDNA, ctDNA, microbial DNA, etc.
Amplification Enzyme After Methylation Transformation	2 × EpiArt HS Taq Master Mix (EM201) 2 × EpiArt HS Taq Master Mix (Dye Plus)(EM202)	Better amplification efficiency, sensitivity and specificity	It is suitable for PCR reaction of bisulfite transformation processing DNA
DNA - Protein Interactions	Hyperactive pA-MNase for CUT&RUN (S701) Hyperactive pG-MNase for CUT&RUN(S702)	Using enzyme digestion instead of ultrasonic fragmentation, DNA fragmentation activity is higher.Compatible with as few as 50 cells.	CUT&Run library Preparation single enzyme

Methylation Library Preparation

EpiArtDNA Methylation Library Kit for Illumina V3 (#NE103)

Workflow

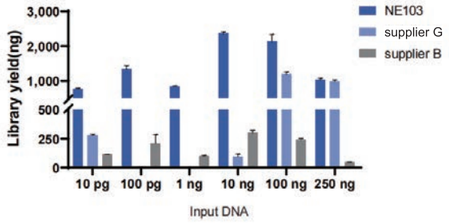


Features

- The fast and minimal operation process reduces the transcription library construction time to 3 hours
- High quality, excellent sequencing data quality, resulting in more uniform coverage of transcript region

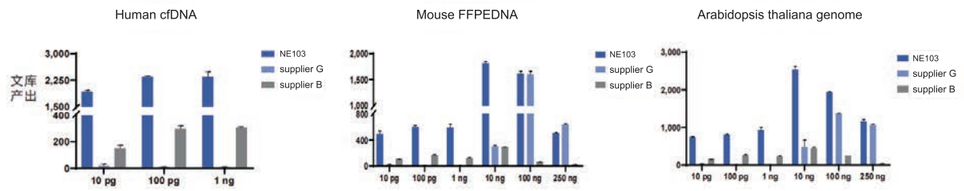
Validation Data

1. The input amount is compatible with 10 pg - 250 ng.



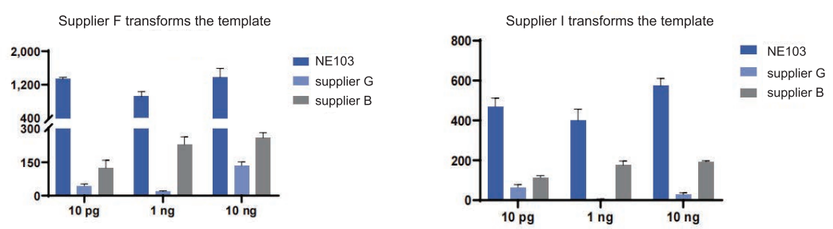
Using 293 cell gDNA as template, Vazyme #EM101 was used for methylation transformation after fragmentation. The results show that Vazyme #NE103 can efficiently build library under different initial input amounts (10 pg, 100 pg, 1 ng, 10 ng, 100 ng, 250 ng). Compared with similar products of Supplier G and Supplier B, the library yield is higher and the quality of offline data is better.

2. Compatible with different template types



Use a different template type (FFPE cfDNA, mice, arabidopsis thaliana genome DNA, DNA), after the fragmentation Vazyme # EM101 methylation transformation, the product of the converted reference Vazyme # NE103 and Supplier G and Supplier B standard database construction process of the same kind of library preparation, the results show that the Vazyme # NE103 can efficiently build library.

3. Compatible with different conversion kits

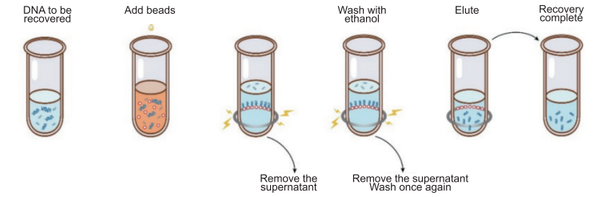


The gDNA of 293 cells was used as A template, and after fragmentation, it was methylated and transformed by bisulfite conversion and enzymatic conversion kit (Supplier F and Supplier I conversion kit). The transformed products were constructed according to the standard library preparation process of Vazyme #NE103, Supplier G and Supplier B similar products. Vazyme # NE103 can efficiently prepare library

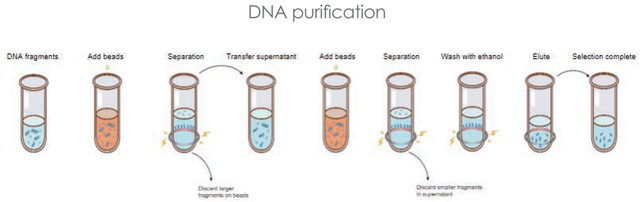
Beads Series

VAHTS DNA Clean Beads (#N411)

Workflow



DNA purification



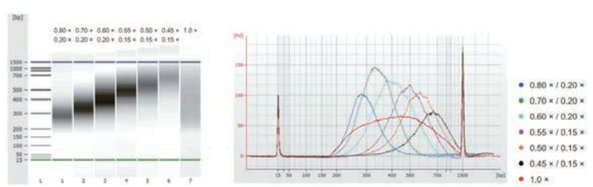
DNA size selection

Validation Data

1.Flexible and Accurate Size Selection

Use the VAHTS DNA Clean Beads to conduct size selection using conditions in the following table to get different sizes of libraries, which are then analyzed with the Agilent 2100 Bioanalyzer.

First-round volume ratio (beads: DNA)	0.80 ×	0.70 ×	0.60 ×	0.55 ×	0.50 ×	0.45 ×	1.0 ×
Second-round volume ratio (beads: DNA)	0.20 ×	0.20 ×	0.20 ×	0.15 ×	0.15 ×	0.15 ×	
Average library length (bp)	300	350	400	500	600	700	200-1500

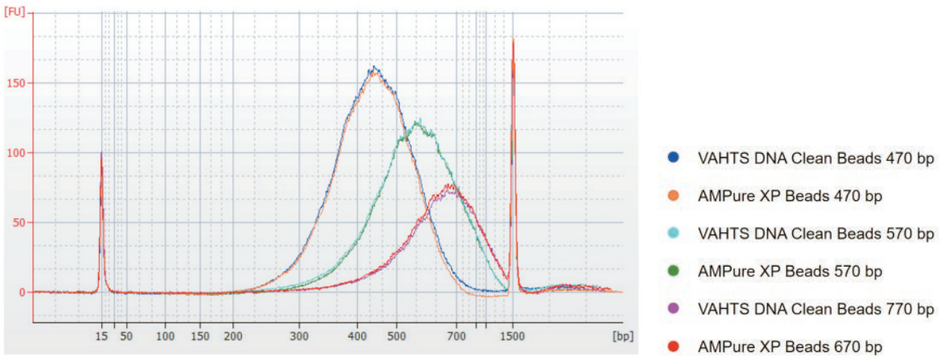


Features

- The ideal alternative to AMPure XP Beads and SPRIselect;
- Compatible with automatic platforms;
- Compatible with various types of DNA and RNA library construction kits;
- Purification and sorting of integrated magnetic beads.

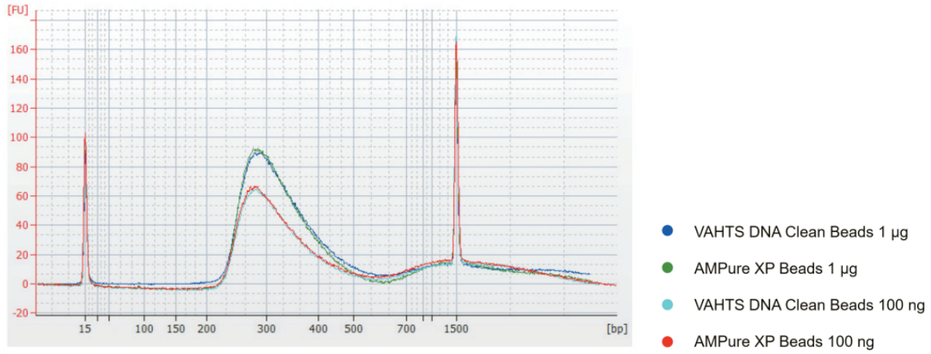
2.DNA Library Construction, Compared with AMPure XP Beads

Using DNA Library Prep Kit for Illumina (Vazyme) to construct DNA Library with 50 ng human DNA template. Using VAHTS DNA Clean Beads and AMPure XP Beads to select the average length of about 470, 570, 670 bp library in the same conditions (corresponding insert size is 350, 450, 550 bp). Using the Agilent 2100 Bioanalyzer to analyze.



3.RNA Library Construction, Compared with AMPure XP Beads

Using TruSeq RNA Sample Prep Kit V2(Illumina #RS-122-2001)to construct RNA Library with 1 μg or 100 ng Universal Human Reference RNA (UHRR) template. Using VAHTS DNA Clean Beads and AMPure XP Beads to select the average length of about 280 bp library in the same conditions (corresponding insert size is 160 bp). Using the Agilent 2100 Bioanalyzer to analyze.



Quantitative series

Applications	Cat.No.#	Features	Applicable for
qPCR Library Quantifcation	VAHTS library Quantifcation Kit for Illumina (NQ101-NQ104) DNA Standard 1-6 (NQ105) Library Dilution Buffer (NQ106)	Contains quantitative all required components; Compatible with all mainstream quantitative PCR instruments.	Library absolute quantitative kit; Library quantitative standard; Library diluention.
Qubit Quantification	Equalbit 1 × dsDNA HS Assay Kit (EQ121)	Accurate quantification of 0.2-100 ng dsDNA	dsDNA high sensitivity test kit
Qubit Quantification	Equalbit RNA HS Assay Kit (EQ211)	Accurate quantification of total RNA, rRNA, and mRNA samples	RNA high sensitivity test kit

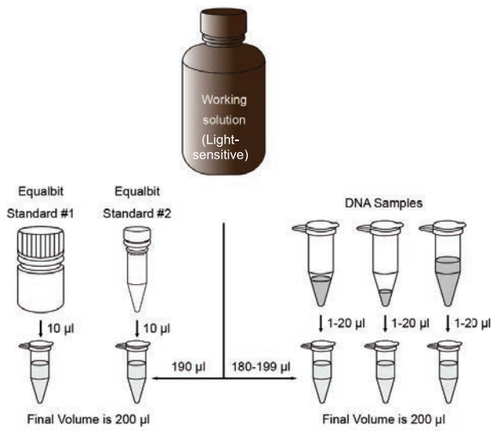
Quantitative Series

Equalbit 1 × dsDNA HS Assay Kit (#EQ121)

Features

- **Simple operation**
The ready-to-use pre-mix simplifies operation steps by eliminating the need to prepare the working solution.
- **Precise and sensitive**
Precisely quantifies 0.2 - 100 ng of dsDNA.
- **High specificity**
Specifically detects dsDNA and well tolerates some common contaminants.
- **Rapid binding of the dye**
Achieves saturation within 2 minutes.
- **High stability**
The production process of standards is strictly controlled to ensure lot-to-lot stability.

Mechanism & Work flow

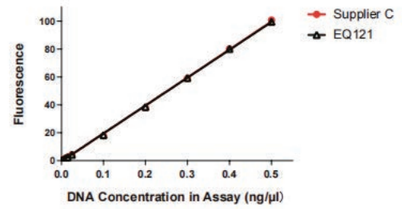


There is no need to prepare the working solution during the assay. Directly aliquot the pre-mix to a 500 µl tube, add the standard or the specimen, and read the result from a Qubit 2.0, 3.0, or 4.0 fluorometer.

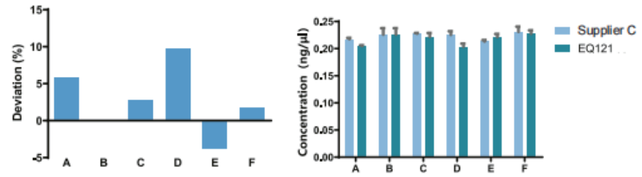
Validation Data

1.High Sensitivity

The total dsDNA sample size has a good linear relationship in the 0.2 - 100 ng range. Low concentrations (0.2 - 1 ng) as well as high concentration measurements are on a linear curve.

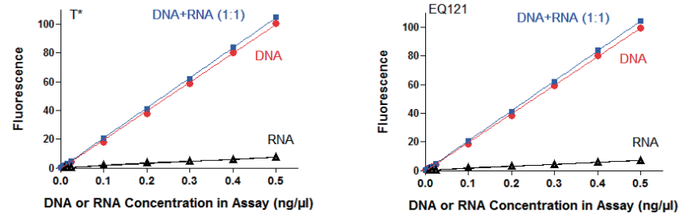


Dilute Standard 2 at 10 ng/µl in gradient to a theoretical concentration of 0.2 ng/µl. Let six operators simultaneously perform the assay. The deviation in results from the similar product of Supplier C is less than 10% at the near-critical level.



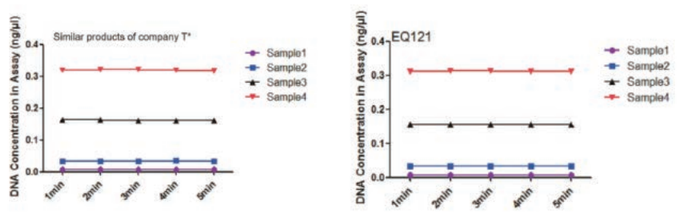
2.High Specificity

The results show that Equalbit 1 × dsDNA HS Assay Kit could specifically bind dsDNA, and even in the presence of RNA, it could still accurately quantify dsDNA, and its performance was comparable to that of similar products of supplier C.



3.Dyes Bind Quickly

The results show that the deviation between the test results of the two kits after adding samples for 5 min and 1 min was within 10%, indicating that the binding speed of the two kits to dsDNA samples was the same, and saturation could be achieved within 2 min.



Selected Product Citations

DNA library Preparation

[1]Wu J, Xu J, Liu B, Yao G, Wang P, Lin Z, Huang B, Wang X, Li T, Shi S, Zhang N, Duan F, Ming J, Zhang X, Niu W, Song W, Jin H, Guo Y, Dai S, Hu L, Fang L, Wang Q, Li Y, Li W, Na J, Xie W, Sun Y.(2018). Chromatin analysis in human early development reveals epigenetic transition during ZGA. .Nature. 557(7704):256-260. IF:40.137 (Vazyme #TD202)

[2]Jiang Liudan., Yin Jiayong., Qian Maoxiang., Rong Shaoqin., Zhang Shengqi., Chen Kejing., Zhao Chengchen., Tan Yuanqing., Guo Jiayin., Chen Hao., Gao Siyun., Liu Tingting., Liu Yi., Shen Bin., Yang Jian., Zhang Yong., Meng Fei-Long., Hu Jinchuan., Ma Honghui., Chen Yi-Han.(2022). UdgX-Mediated Uracil Sequencing at Single-Nucleotide Resolution. J Am Chem Soc, 144(3), 1323-1331. IF:15.419 (Vazyme #P507)

[3]Fu Aikun., Yao Bingqing., Dong Tingting., Chen Yongyi., Yao Jia., Liu Yu., Li Hang., Bai Huiru., Liu Xiaoqin., Zhang Yue., Wang Chunhui., Guo Yajing., Li Nan., Cai Shang.(2022). Tumor-resident intracellular microbiota promotes metastatic colonization in breast cancer. Cell, 185(8), 1356-1372.e26.IF:41.584 (Vazyme #TD203)

[4]Chang Dehui., Xing Qi., Su Yang., Zhao Xiaohong., Xu Wei., Wang Xiaohu., Dong Chen. (2020). The Conserved Non-coding Sequences CNS6 and CNS9 Control Cytokine-Induced Rorc Transcription during T Helper 17 Cell Differentiation. Immunity, 53(3), 614-626.e4. IF:22.55 (Vazyme #TD202)

[5]Zhang Ke., Wu Dan-Ya., Zheng Hui., Wang Yao., Sun Qiao-Ran., Liu Xin., Wang Li-Yan., Xiong Wen-Jing., Wang Qiujun., Rhodes James D P., Xu Kai., Li Lijia., Lin Zili., Yu Guang., Xia Weikun., Huang Bo., Du Zhenhai., Yao Yao., Nasmyth Kim A., Klose Robert J., Miao Yi-Liang., Xie Wei.(2020). Analysis of Genome Architecture during SCNT Reveals a Role of Cohesin in Impeding Minor ZGA. Mol Cell, 79(2), 234-250.e9. IF:15.584 (Vazyme #TD202)

[6]Liu Bofeng., Xu Qianhua., Wang Qiujun., Feng Su., Lai Fangnong., Wang Peizhe., Zheng Fangyuan., Xiang Yunlong., Wu Jingyi., Nie Junwei., Qiu Cui., Xia Weikun., Li Lijia., Yu Guang., Lin Zili., Xu Kai., Xiong Zhuqing., Kong Feng., Liu Ling., Huang Chunyi., Yu Yang., Na Jie., Xie Wei.(2020). The landscape of RNA Pol II binding reveals a stepwise transition during ZGA. Nature, 587(7832), 139-144. IF:38.138 (Vazyme #TD502)

RNA library Preparation

[1] Xu Wenqi., Li Jiahui., He Chenxi., Wen Jing., Ma Honghui., Rong Bowen., Diao Jianbo., Wang Liyong., Wang Jiahua., Wu Feizhen., Tan Li., Shi Yujiang Geno., Shi Yang., Shen Hongjie.(2021). METTL3 regulates heterochromatin in mouse embryonic stem cells. Nature, 591(7849), 317-321. IF:42.77 (Vazyme #N406)

[2]Zhang Hongchen., Shao Shipeng., Zeng Yong., Wang Xiaotian., Qin Yizhi., Ren Qiunan., Xiang Shengqi., Wang Yuxin., Xiao Junyu., Sun Yujie.(2022). Reversible phase separation of HSF1 is required for an acute transcriptional response during heat shock. Nat Cell Biol, 24(3), 340-352. IF:28.82 (Vazyme #NR605)

[3]Yu Runxian., Sun Chenyu., Zhong Yan., Liu Ying., Sanchez-Puerta M Virginia., Mower Jeffrey P., Zhou Renchao.(2022). The minicircular and extremely heteroplasmic mitogenome of the holoparasitic plant Rhopalocnemis phalloides. Curr Biol, 32(2), 470-479.e5. IF:10.83 (Vazyme #NR605)

Single Cell-Seq Series

[1]Sheng Xiaoqiang., Liu Chuanming., Yan Guijun., Li Guangyu., Liu Jingyu., Yang Yanjun., Li Shiyuan., Li Zhongxun., Zhou Jidong., Zhen Xin., Zhang Yang., Diao Zhenyu., Hu Yali., Fu Chuanhai., Yao Bin., Li Chaojun., Cao Yu., Lu Bin., Yang Zhongzhou., Qin Yingying., Sun Haixiang., Ding Lijun.(2022). The mitochondrial protease LONP1 maintains oocyte development and survival by suppressing nuclear translocation of AIFM1 in mammals. EBioMedicine, 75(undefined),103790. IF:21.53 (Vazyme #N711)

[2]Huang Yumei., Shang Rui., Lu Guang-An., Zeng Weishun., Huang Chenglong., Zou Chuangchao., Tang Tian.(2022). Spatiotemporal Regulation of a Single Adaptively Evolving Trans-Regulatory Element Contributes to Spermatogenetic Expression Divergence in Drosophila. Mol Biol Evol, 39(7), undefined. IF:15.33 (Vazyme #N711)

[3]Liu Chuanming., Li Shiyuan., Li Yifan., Tian Jiao., Sun Xiaoling., Song Tianran., Yan Guijun., Ding Lijun., Sun Haixiang.(2021). Growth hormone ameliorates the age-associated depletion of ovarian reserve and decline of oocyte quality via inhibiting the activation of Fos and Jun signaling. Aging (Albany NY), 13(5), 6765-6781. IF:11.43 (Vazyme #N711)

Epigenetics Series

[1]Snaurova Renata., Vdovin Alexander., Durech Michal., Nezval Jakub., Zihala David., Jelinek Tomas., Hajek Roman., Simicek Michal.(2022). Deubiquitinase OTUD1 Resolves Stalled Translation on polyA and Rare Codon Rich mRNAs. Mol Cell Biol, undefined(undefined), e0026522. IF:3.611 (Vazyme #EM201)

[2]Pan Chun., Zhang Ling., Meng Xiannan., Qin Haixiang., Xiang Zou., Gong Wenyue., Luo Wenxin., Li Dongmei., Han Xiaodong.(2021). Chronic exposure to microcystin-LR increases the risk of prostate cancer and induces malignant transformation of human prostate epithelial cells. Chemosphere, 263(undefined), 128295. IF:5.778 (Vazyme #P507)

Beads Series

[1]Ye, F., Zhang, G., E, W., Chen, H., Yu, C., Yang, L., Fu, Y., Li, J., Fu, S., Sun, Z., Fei, L., Guo, Q., Wang, J., Xiao, Y., Wang, X., Zhang, P., Ma, L., Ge, D., Xu, S., Caballero-Pérez, J., … Guo, G. (2022). Construction of the axolotl cell landscape using combinatorial hybridization sequencing at single-cell resolution. Nature communications, 13(1), 4228. IF:14.92 (Vazyme #N411)

[2]Liang Zhenwei., Yuan Liangbing., Xiong Xiangyu., Hao Yuanhao., Song Xin., Zhu Tao., Yu Yaoguang., Fu Wei., Lei Yawen., Xu Jianqu., Liu Jun., Li Jian-Feng., Li Chenlong.(2022). The transcriptional repressors VAL1 and VAL2 mediate genome-wide recruitment of the CHD3 chromatin remodeler PICKLE in Arabidopsis. Plant Cell, 34(10), 3915-3935. doi:10.1093/plcell/koac217.IF: 11.28 (Vazyme #N411)

[3]Yu, Y., Fu, W., Xu, J., Lei, Y., Song, X., Liang, Z., Zhu, T., Liang, Y., Hao, Y., Yuan, L., & Li, C. (2021). Bromodomain-containing proteins BRD1, BRD2, and BRD13 are core subunits of SWI/SNF complexes and vital for their genomic targeting in Arabidopsis. Molecular plant, 14(6), 888–904. IF: 13.16 (Vazyme #N411)

[4]Liu, J., Huang, T., Chen, W., Ding, C., Zhao, T., Zhao, X., Cai, B., Zhang, Y., Li, S., Zhang, L., Xue, M., He, X., Ge, W., Zhou, C., Xu, Y., & Zhang, R. (2022). Developmental mRNA m5C landscape and regulatory innovations of massive m5C modification of maternal mRNAs in animals. Nature communications, 13(1), 2484.IF: 14.92 (Vazyme #N411)

[5]Fei, L., Chen, H., Ma, L., E, W., Wang, R., Fang, X., Zhou, Z., Sun, H., Wang, J., Jiang, M., Wang, X., Yu, C., Mei, Y., Jia, D., Zhang, T., Han, X., & Guo, G. (2022). Systematic identification of cell-fate regulatory programs using a single-cell atlas of mouse development. Nature genetics, 54(7), IF: 38.33 (Vazyme #N411)

[6]Chen Qiuxia., Li You., Lin Chunrong., Chen Liu., Luo Hao., Xia Shuai., Liu Chuan., Cheng Xuemin., Liu Chengzhong., Li Jin., Dou Dengfeng.(2022). Expanding the DNA-encoded library toolbox: identifying small molecules targeting RNA. Nucleic Acids Res, 50(12), e67.IF:16.971 (Vazyme #N412)

[7]Hu Yanyan., Yang Yuanyuan., Tan Pengcheng., Zhang Yuxia., Han Mengxia., Yu Jiawei., Zhang Xin., Jia Zeran., Wang Dan., Li Yinqing., Ma Tianhua., Liu Kang., Ding Sheng.(2022). Induction of mouse totipotent stem cells by a defined chemical cocktail. Nature, undefined(undefined), undefined. IF:49.96 (Vazyme #N411)

[8]Ma Xiaojie., Lu Yunkun., Zhou Ziyu., Li Qin., Chen Xi., Wang Weiyun., Jin Yan., Hu Zhensheng., Chen Guo., Deng Qian., Shang Weina., Wang Hao., Fu Hongxing., He Xiangwei., Feng Xin-Hua., Zhu Saiyong.(2022). Human expandable pancreatic progenitor-derived β cells ameliorate diabetes. Sci Adv, 8(8), eabk1826. IF:14.14 (Vazyme #N411)

Quantitative Series

[1]Yu Qiong., Liu Shun., Yu Lu., Xiao Yu., Zhang Shasha., Wang Xueping., Xu Yingying., Yu Hong., Li Yulong., Yang Junbo., Tang Jun., Duan Hong-Chao., Wei Lian-Huan., Zhang Haiyan., Wei Jiangbo., Tang Qian., Wang Chunling., Zhang Wutong., Wang Ye., Song Peizhe., Lu Qiang., Zhang Wei., Dong Shunqing., Song Baoan., He Chuan., Jia Guifang.(2021). RNA demethylation increases the yield and biomass of rice and potato plants in field trials. Nat Biotechnol, 39(12), 1581-1588. .IF:54.908 (Vazyme #EQ211)

[2]Cao Shangtao., Yu Shengyong., Li Dongwei., Ye Jing., Yang Xuejie., Li Chen., Wang Xiaoshan., Mai Yuanbang., Qin Yue., Wu Jian., He Jiangping., Zhou Chunhua., Liu He., Zhao Bentian., Shu Xiaodong., Wu Chuman., Chen Ruiping., Chan Waiyee., Pan Guangjin., Chen Jiekai., Liu Jing., Pei Duanqing.(2018). Chromatin Accessibility Dynamics during Chemical Induction of Pluripotency. Cell Stem Cell, 22(4), 529-542.e5. IF:23.394 (Vazyme #NQ101-106)