NGS Solution for Tumor Detection

N G S

S o l u t i o n

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T u m o r

D e t e c t i o n

2022

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Science and Technology Make a Healthier Life

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About Vazyme

Founded in 2012, Vazyme is now a leading biotechnology company in China, conducting research and development both in technology and products focusing on functional proteins, such as enzymes, antigens, antibodies, and polymer organic materials. Relying on an in-house generic technology platform, Vazyme has successively moved into various business areas ranging from biological research, in vitro diagnosis (IVD) to bio-pharmaceutical. Equipped with both independent technology development and terminal products manufacturing capabilities, Vazyme is now ready to power the biotechnology industry.

Development of Core Technology

Since its establishment, Vazyme has always adhered to the business philosophy—— R&D is the core. Through years of relentless efforts, Vazyme has achieved a lot in biomedical science. For instance, we have developed various kinds of biological preparations, covering but not limited to high-throughput sequencing library series, PCR, qPCR, molecular clone, reverse transcription and 8 sets of POCT diagnostic reagents used to detect heart and cerebral vessels, inflammation, sound child rearing, and gastric function, etc. Now Vazyme has expanded the customer portfolio to a wider range, including scientific research institutions, high-throughput sequencing service companies, molecular diagnostic reagent manufacturers, pharmaceutical companies, CRO companies, hospitals and other medical institutions.

Innovation & Reservation of Talents

Based on self-established core technologies, Vazyme has built an independent generic technology platform to meet the needs of large-scale research and development of products quickly and efficiently. Now we have over 200 kinds of genetic engineering recombinases, more than 1000 kinds of high-performance antigens, mAb and other critical materials. In addition, Vazyme owns above 500 terminal products that are widely applied in science research, high-throughput sequencing, IVD, pharmaceutical and vaccine research development, animal quarantine, etc.

Vazyme's powerful R&D strength is supported by a strong research and innovation team with over 400 multi-disciplinary experts majoring in molecular biology, enzymology, immunology, bioinformatics, organic chemistry and materials science, etc., more than half of which have a master's degree or above. ***We have been mentioned in CNS and sub-journals over 180 times and more than 1500 times in various other journals. The total citation of papers so far has reached to 10000.***

Staying True to the Original Aspiration & Fulfill the Mission

On the way to deepen and broaden the entire product and technology chain, Vazyme stays true to the orignial aspiraton —— "Science and Technology Make a Healthier Life", explores new methods for disease discovery, diagnosis, prevention and treatment, and provides quality products and professional services to creat value for clients.

In the past few years, Vazyme has actively engaged in the construction of public health programs, and played a vital role in fighting against African swine fever and COVID-19. ***So far we have business cooperation with more than 300 IVD kit manufacturers by providing raw materials and premixes for over 800 million population covering more than 30 countries.*** In the future, we will continue to contribute to the development of biosafety, and help mankind to overcome the threats posed by major infectious diseases, tumors, and autoimmune diseases!

Product Catalogue

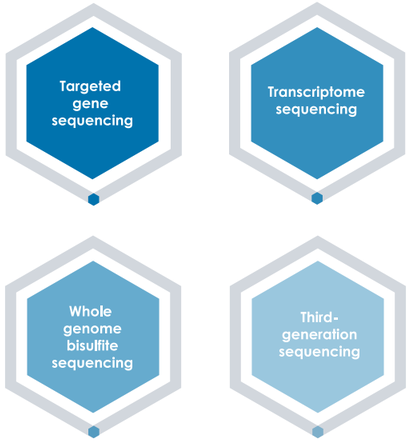
Science and Technology Make a Healthier Life

Contents

Multiomics Tumor Gene Sequencing

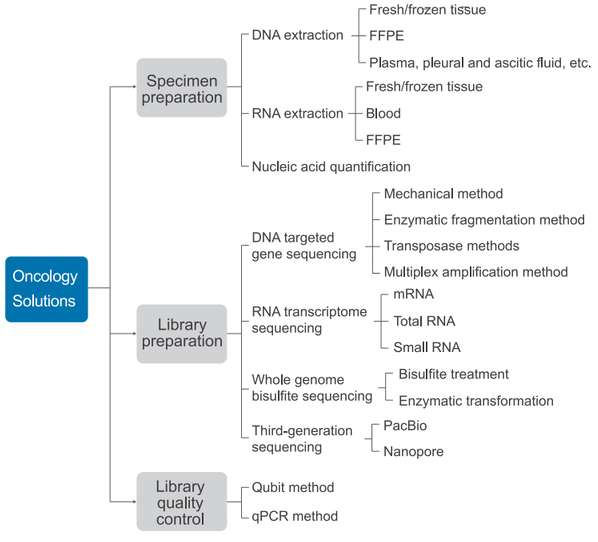
In China, widespread use of NGS (Next-Generation Sequencing, Second-Generation Genetic Sequencing) in clinical settings began with NIPT (Non-Invasive Prenatal Testing). After the great success of NIPT, oncology is the next field for which NGS applications hold even greater potential.

Tumorigenesis and progression of malignant tumors is a complex process, and genomic mutations, epigenetic modification changes, aberrant gene expression levels, etc. can all be important factors contributing to tumorigenesis. Genomic mutations factors should generally be given priority in the explorations of tumor mechanisms and screening for pathogenic targets. However, it is now difficult for single omics studies to meet the needs of scientific research, and multiomics research methods have become mainstream and play an important role in pathogenesis studies, screening tumor markers and pathogenic targets, as well as early diagnosis and treatment.



Vazyme Offers a Variety of Oncology Solutions

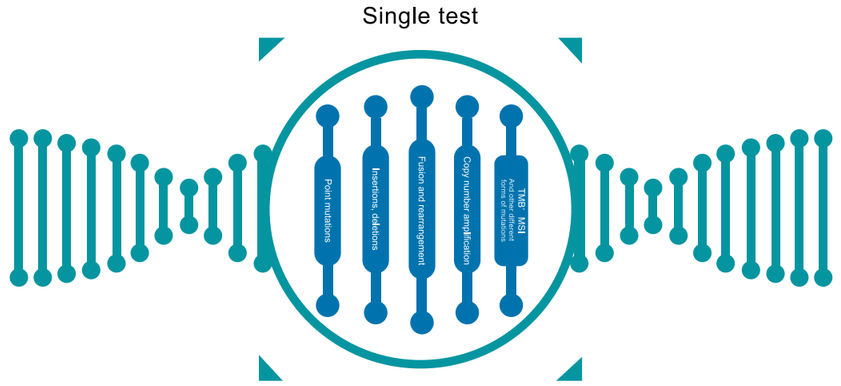
Illumina, MGI and Ion Torrent are companies that supply upstream sequencing instruments in the field of NGS tumor detection Vazyme offers comprehensive solutions for different sequencing platforms. At the same time, there are solutions for all types of specimens used in tumor detection, including gDNA extracted from fresh or frozen tissues, FFPE specimens, and cfDNA from plasma, pleural and ascitic fluid, etc. Vazyme, a supplier of gene sequencing reagents, is committed to providing oncology scientists and clinicians with high-quality, multi-protocol, easy to operate, automation-friendly solutions that facilitate advances in oncology research as well as the diagnosis, treatment, prognosis and early screening of tumors.



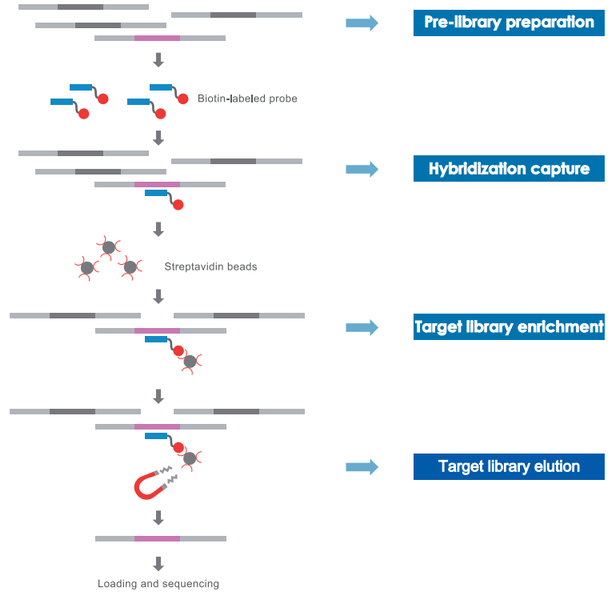
Targeted Gene Sequencing of Tumors

Targeted gene sequencing is a method of focusing only on specific regions of a genome that are used for targeted enrichment and analysis, enabling accurate detection of somatic and reproductive cell mutations in tumor specimens. It is used in clinical research and diagnosis of key genes and key variants associated with tumorigenesis and tumor progression, individual medication, post-operative recurrence monitoring, etc. Targeted sequencing has a deeper sequencing depth and higher detection sensitivity, making for more accurate detection of mutations.

The use of targeted sequencing has become a widely used technique for the detection of tumorous genomic mutations. It can detect all types of mutations, such as mononucleotide mutations, translocations, structural variations, insertions and deletions, and copy number variations in a single test, providing guidance for clinical applications such as targeted treatment and immunotherapy.



Technical Track 1—Hybridization Capture Target Sequencing

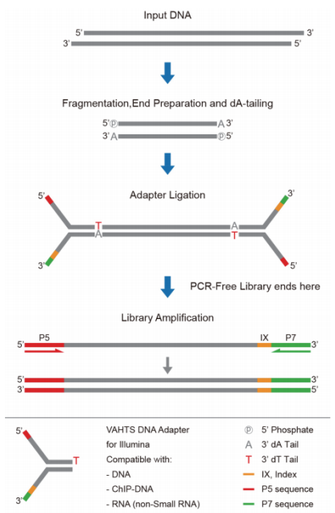


Vazyme Biotech Offers a Variety of Capture Sequencing Pre-library Solutions

Hybridization capture sequencing protocols require the prior preparation of an entire genome library, which is then enriched with a target-specific probe. Vazyme offers a variety of pre-library preparation solutions to help protect your subsequent target enrichment process.

Enzymatically fragmented DNA library preparation

Technical Procedure



Library preparation flow chart (Vazyme #ND617 / #ND627)

Product Features

Wide Compatibility

Easily handles sources from different species, different initial input quantities, and different template types

Ease of Operation

The required library can be achieved simply by adjusting the fragmentation time according to the size of the target insert fragment

High Library Yield

Excellent library conversion rates and better library quality

► VAHTS® Universal Plus DNA Library Prep Kit for Illumina (Vazyme #ND617) is a reagent kit for genome library preparation based on enzymatic fragmentation for the preparation of a complete genome library that is compatible with fresh/frozen tumor tissue and FFPE specimens.

► VAHTS Universal Plus DNA Library Prep Kit for Illumina V2 (Vazyme #ND627) specifically optimized and upgraded the system on the basis of ND617 to reduce the false-positive mutation in the construction of library by fragment enzyme method from the source. Matching with double ended UDI UMI adapters VAHTS dual UMI adapters Set 1 - Set 4 for Illumina (Vazyme #N351-N354) can reduce false positive mutations and make the detection results more accurate and reliable.

ND617 prepares a complete genome pre-library with whole exome panel capture data presentation:

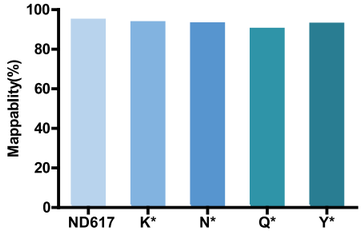


Figure 1. Higher match rates. 100 ng standard NA12878 was added and different brands of enzymatically fragmented library preparation kits with a whole exome capture panel were used. Vazyme #ND617 has the highest match rate with the same sequencing throughput in the same sequencer compared to other brands.

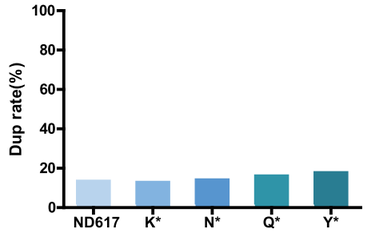


Figure 2. Low dup rate. Vazyme #ND617 has a lower Dup rate than other brands.

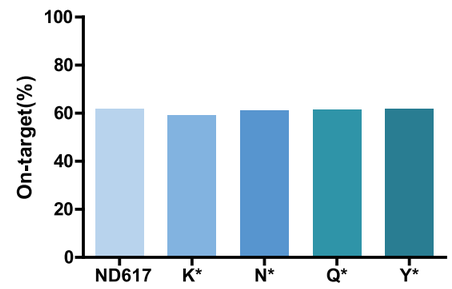


Figure 3. Efficient capture. Vazyme #ND617 has a higher capture efficiency than other brands.

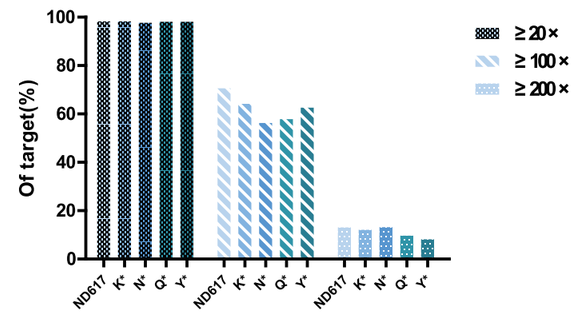


Figure 4. More uniform coverage. Compared to other brands, Vazyme #ND617 has a higher coverage and greater uniformity at several different mean sequencing depths (≥20X; ≥100X; ≥200X).

The ND617 prepares a whole genome prep library equipped with a pan-tumor small panel capture data presentation:

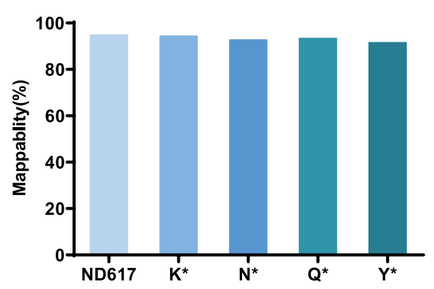


Figure 1. High match rate. 50 ng pan-tumor gDNA standard (GW-OGTM005) was added. Different brands of enzyme digestion fragment library preparation kits, with an NCC tumor diagnosis panel were used. Comparison with other brands under the same sequencer and the same sequencing throughput conditions Vazyme #ND617 compares favorably with K* and is better than other brands.

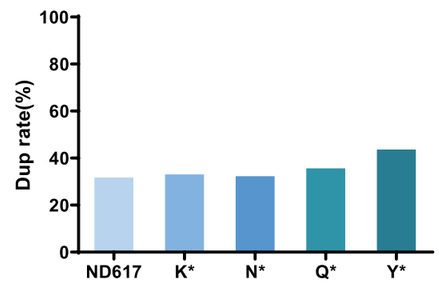
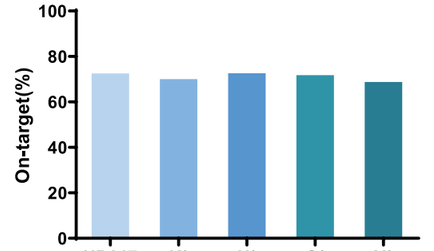


Figure 2. Low dup rate. Vazyme #ND617 has a lower dup rate than other brands.



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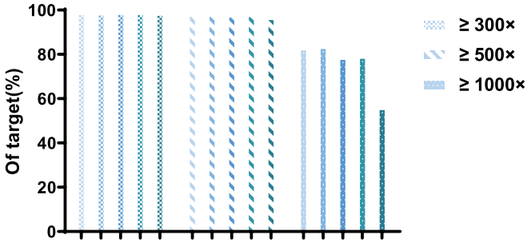


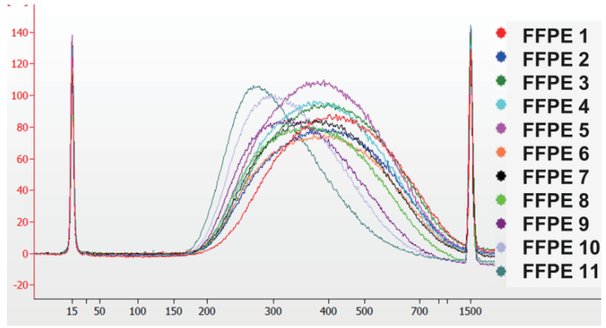
Figure 4. More uniform coverage. Vazyme #ND617 has a higher coverage and greater uniformity than other brands at several different mean sequencing depths (≥300 X; ≥500 X; ≥1000 X).

Table 1: SNP detection rate - pan tumor 800 standard

Gene Name	Chr	AA.change	Ref	Alt	Cosmic_id	Expected (%)	Alt_Frequency (%)				
							ND617	K*	N*	Q*	Y*
EGFR	chr7	p.L858R	T	G	COSM6224	1	1.38	1.4	0.99	1.61	/
EGFR	chr7	p.T790M	C	T	COSM6240	2	2.11	1.82	1.9	1.86	2.55
EGFR	chr7	p.G719S	G	A	COSM6252	4	3.51	4.28	4.92	4.01	3.55
KRAS	chr12	p.G12D	C	T	COSM1135366,COSM521	2	1.9	2.61	1.97	2.16	1.11
KRAS	chr12	p.G13D	C	T	COSM532,COSM1140132	4	3.82	4.04	4.02	3.59	4.38
KRAS	chr12	p.A146T	C	T	COSM19404,COSM1165198	1	1.16	2.01	0.83	0.99	0.7
NRAS	chr1	p.Q61K	G	T	COSM580	1	1.06	0.74	1.06	1.31	0.86
KIT	chr4	p.D816V	A	T	COSM1314	2	1.84	2.6	2.07	1.28	3.05
BRAF	chr7	p.V600E	A	T	COSM476	7	6.43	5.45	4.18	5.3	6.29
PIK3CA	chr3	p.H1047R	A	G	COSM775,COSM94986	7	6.84	5.81	6.91	6.81	6.13

Vazyme #ND617 mutation detection rates are generally consistent with the standard

ND617 fragment compatibility testing for FFPE specimens:



Different qualities FFPE number	Main peak position (Unit: bp)	Wide distribution (Unit: bp)
FFPE 1	8801	1000-17134
FFPE 2	4594	500-16386
FFPE 3	4050	400-17053
FFPE 4	3066	363-16182
FFPE 5	2300	306-14310
FFPE 6	1956	254-14095
FFPE 7	1598	200-10380
FFPE 8	1307	158-10380
FFPE 9	838	50-10380
FFPE 10	473	40-10380
FFPE 11	275	32-10380

Figure 1.**Peak diagram for ND617 library prepared with FFPE specimens of different classes**
Agilent 2100 was used to detect FFPE specimens of different quality classes. 100 ng was separately added and the library was prepared using ND617, and fragment at 37°C for 15 min. Once the library was built, Agilent 2100 was used to detect the library peak type. The size of libraries prepared with the same fragmentation time are basically of the same size for FFPE samples of different quality classes, excluding the poor quality FFPE specimens (numbers 10 & 11, i.e. Those with FFPE sample main peak below 1 kb).

ND627 optimized for low frequency mutations

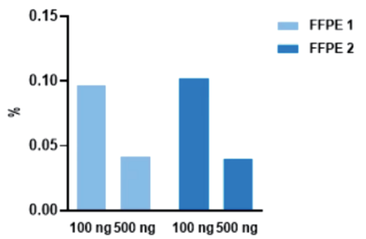


Figure 1.**Test to background noise ratio analysis.**
Analyze the proportion of artifact reads of the tested samples. After the library is constructed with Vazyme #ND627, the proportion of artifact reads can be as low as 0.1%, which greatly reduces the false positive detection of SNV/Indel.

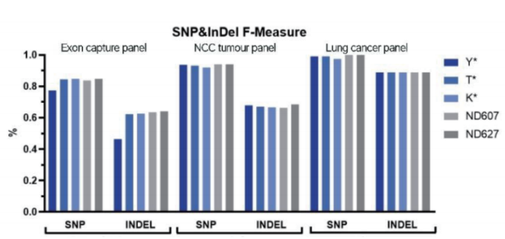
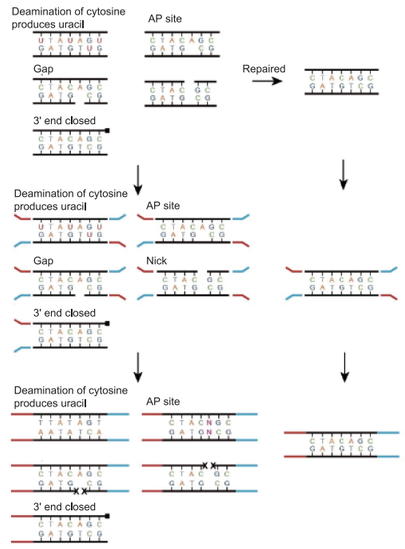


Figure 2.**Comparison of conversion rate of each product library.**
The sensitivity and accuracy of comprehensive SNP and indel detection were F-measure scored, and Vazyme #ND627 outperformed other company products slightly in SNP and indel detection.

Preparation of FFPE, cfDNA specimen DNA damage repair library

Technical Procedure



Schematic diagram of repaired library after DNA damage (Vazyme #ND608)

Product Features

01 Efficient repair of base damage

02 Superior library conversion rates, superior library amplification efficiency

03 Does not alter DNA sequences, significantly improving the quality of sequencing data

▶ VAHTS® Universal Pro DNA Library Prep Kit for Illumina (Vazyme #ND608) is a library preparation kit containing a repair module for compatibility with gDNA, FFPE DNA, and cfDNA specimens extracted from fresh/frozen tumor tissue for preparation of a whole genome library.

The ND608 builds a whole genome prep library with small tumor panel capture data presentation:

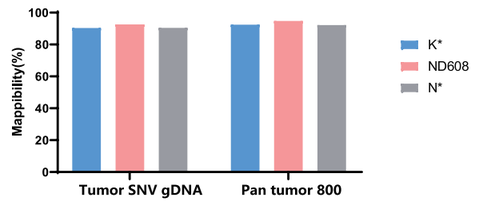


Figure 1. **Higher match rates.** Standard Genewell-Tumor SNV gDNA (1–25%) and Genewell-Pan Tumor 800, using different brands of DNA libraries to reagent kits equipped with custom panels (target region approx. 80 kb). Vazyme's ND608 has the highest match rate for the same sequencer and the same sequencing throughput compared to other brands.

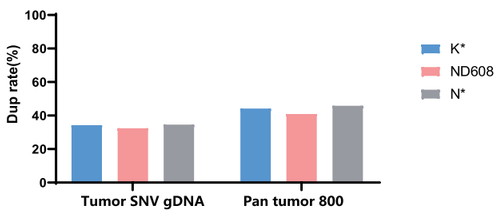


Figure 2. **Low dup rate.** Vazyme #ND608 has a lower dup rate than other brands.

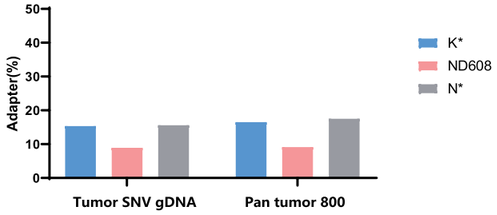


Figure 3. **Low adapter residue.** Vazyme #ND608 has a significantly lower ratio of adapter residue than other brands.

Table 1: SNP detection rate—tumor SNV standard

Gene Name	Chr	AA.change	Ref	Alt	Cosmic_id	Expected (%)	Alt_Frequency (%)		
							ND608	N*	K*
NRAS	chr1	p.Q61K	G	T	COSM580	12.5	11.68	11.52	10.12
BRAF	chr7	p.V600E	A	T	COSM476	10.5	8.93	8.72	8.08
EGFR	chr7	p.L858R	T	G	COSM6224	3	3.12	2.76	3.04
PIK3CA	chr3	p.E545K	G	A	COSM125370,COSM763	9	7.83	11.27	7.62
KRAS	chr12	p.G13D	C	T	COSM532,COSM1140132	15	13.97	14.99	13.73
KRAS	chr12	p.G12D	C	T	COSM1135366,COSM521	6	6.21	6.69	8.92
PIK3CA	chr3	p.H1047R	A	G	COSM775,COSM94986	17.5	16.31	17.6	15.91
EGFR	chr7	p.G719S	G	A	COSM6252	24.5	23.84	21.78	22.68
EGFR	chr7	p.T790M	C	T	COSM6240	1	0.93	0.63	0.85

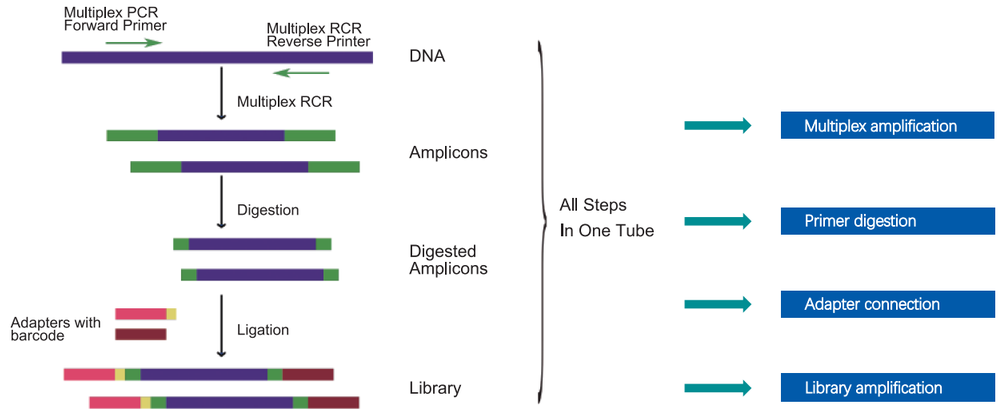
Table 2: SNP detection rate - pan tumor 800 standard

Gene Name	Chr	AA.change	Ref	Alt	Cosmic_id	Expected (%)	Alt_Frequency (%)		
							ND608	N*	K*
EGFR	chr7	p.L858R	T	G	COSM6224	1	0.95	1.16	0.86
EGFR	chr7	p.T790M	C	T	COSM6240	2	1.85	2.5	1.84
KRAS	chr12	p.G13D	C	T	COSM532,COSM1140132	4	3.81	3.36	4.76
KRAS	chr12	p.A146T	C	T	COSM19404,COSM1165198	1	1.14	1.06	1.7
KRAS	chr12	p.G12D	C	T	COSM1135366,COSM521	2	1.99	3.02	2.19
NRAS	chr1	p.Q61K	G	T	COSM580	1	1.01	0.66	0.9
KIT	chr4	p.D816V	A	T	COSM1314	2	1.89	1.25	1.69
EGFR	chr7	p.G719S	G	A	COSM6252	4	3.94	3.98	2.81
BRAF	chr7	p.V600E	A	T	COSM476	7	6.39	5.67	6.09
PIK3CA	chr3	p.H1047R	A	G	COSM775,COSM94986	7	6.45	7.94	7.18

Vazyme #ND608 mutation detection rates are generally consistent with the standard

Technical Track 2 - Multiplex Amplification Targeted Sequencing

Technical Procedure



Multiplex amplification targeted gene sequencing flow chart for tumors (Vazyme #NA210)

Multiplex Amplification DNA Library Preparation

Compatible with low input

Easily handle sources from different species and different types of template with a minimum compatible input of 1 ng

Wide range of applications

Suitable for 20 – 5,000 pairs of primers

Flexible

Compatible with Illumina and Ion Torrent sequencing platforms, with customized services available

VAHTS® AmpSeq Library Prep Kit V3 (Vazyme #NA210) is based on super multiplex PCR, including core technologies such as end primer digestion. An amplicon library kit is used to connect adapters to create a library. Used for analyzing genetic mutations in specific genomic regions.

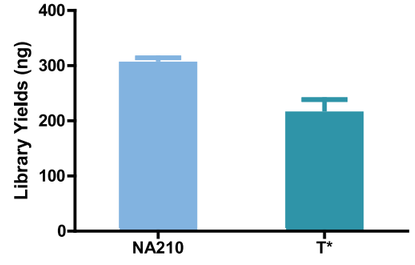
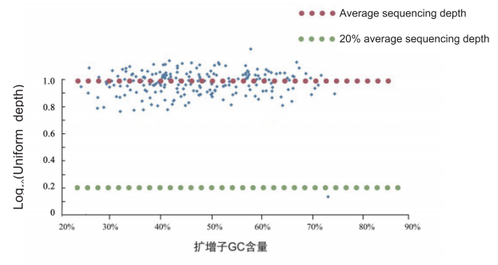


Figure 1. **High library yield.** 10 ng human whole blood gDNA was added. The same multiplex amplicon kit as NA210 and T* products were used in combination with the human tumor-related gene hotspot mutation region VAHTS AmpSeq Cancer HotSpot Panel (Vazyme #NA102). The library yield of Vazyme #NA210 is higher.

Figure 2. **Good uniformity.** When Vazyme #NA210 amplifies 207 amplicons of different GC content, most of the amplicon sequencing depths are concentrated near the average sequencing depth, showing excellent GC compatibility and uniformity of amplification.



Targeted Sequencing Solutions for Tumors

DNA Preservation and Extraction

Product application	Product name	Cat. #
Blood genome DNA extraction kit	FastPure® Blood DNA Isolation Mini Kit V2	DC111
Cell/Tissue DNA extraction kit	FastPure® Cell/Tissue DNA Isolation Mini Kit	DC102
Blood/Cell/Tissue/Bacteria DNA extraction kit	FastPure® Blood/Cell/Tissue/Bacteria DNA Isolation Mini Kit	DC112

DNA Library Preparation (for Illumina Platforms)

Product application	Product name	Cat. #
Routine DNA library preparation kit	VAHTS® Universal DNA Library Prep Kit for Illumina V3	ND607
Enzymatically fragmented DNA library preparation kit	VAHTS® Universal Plus DNA Library Prep Kit for Illumina	ND617
Enzymatically fragmented DNA library preparation kit	VAHTS® Universal Plus DNA Library Prep Kit for Illumina V2	ND627
FFPE DNA library preparation kit	VAHTS® Universal Pro DNA Library Prep Kit for Illumina	ND608
Dual-end index adapter	VAHTS® Dual UMI UDI Adapters for Illumina	N351-N354
Multiplex amplicon library preparation kit	VAHTS® AmpSeq Library Prep Kit V3	NA210

DNA Library Preparation (for Ion Torrent Platforms)

Product application	Product name	Cat. #
Routine DNA library kit	VAHTS® Universal DNA Library Prep Kit for Ion Torrent V2	ND702
Multiplex amplicon library kit	VAHTS® AmpSeq Library Prep Kit V3	NA210

DNA Library Preparation (for MGI Platforms)

Product application	Product name	Cat. #
Routine DNA library preparation kit	VAHTS® Universal DNA Library Prep Kit for MGI	NDM607
Enzymatically fragmented DNA library preparation kit	VAHTS® Universal Plus DNA Library Prep Kit for MGI	NDM617
Enzymatically fragmented DNA library preparation kit	VAHTS® Universal Plus DNA Library Prep Kit for MGI V2	NDM627
FFPE DNA library preparation kit	VAHTS® Universal Pro DNA Library Prep Kit for MGI	NDM608
Dual-end UMI adapters	VAHTS® Dual UMI Adapters for MGI	NM301
Circularization kit	VAHTS® Circularization Kit for MGI	NM201

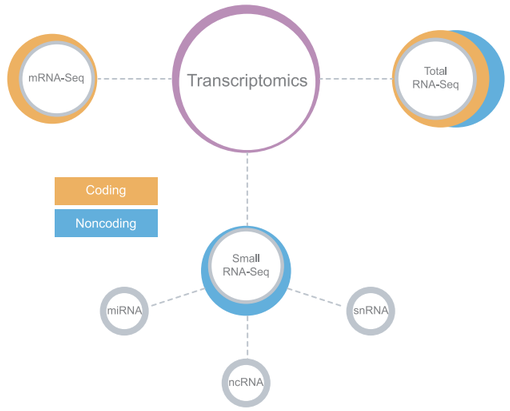
Magnetic Beads and Library Quantification

Product application	Product name	Cat. #
DNA purification and selection beads	VAHTS® DNA Clean Beads	N411
Library absolute quantification kit	VAHTS® Library Quantification kit for Illumina	NQ101-106
dsDNA high-sensitivity assay kit	Equalbit® 1 x dsDNA HS Assay Kit	EQ121

Tumor Transcriptome Sequencing

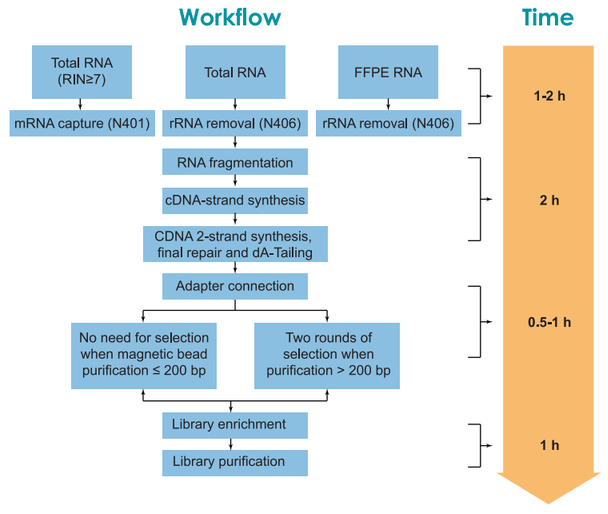
The transcriptome is broadly defined as a collection of all the products of gene transcription in a cell, and is often referred to as a collection of all mRNAs in the narrow sense. Transcriptome sequencing (RNA-seq) is typically used to sequence mRNA and non-coding RNA (ncRNA) in cells using high-throughput gene sequencing technologies. The transcriptome is rich in gene expression and sequence information compared to genome sequencing, and has a unique advantage in the analysis of gene fusion, splice variants and gene expression profiles. Consequently there is increasing interest in the use of transcriptomics in tumor detection for a more comprehensive assessment of tumorigenesis and tumor progression.

Transcriptome Solutions from Vazyme



Vazyme Biotech Offers a Variety of Capture Sequencing Pre-library Solutions

Technical Procedure



Rapid transcriptome RNA library preparation flow chart (Vazyme #NR604)

Product Features

Rapid

The simplicity of the process reduces the preparation time by 2 h

Compatible

Compatible with a wide range of RNA enrichment modules for your choice

General purpose

Flexible and free choice of strand-specific or non-strand-specific libraries

Performance Demonstration

VAHTS® Universal V6 RNA-seq Library Prep Kit for Illumina (Vazyme #NR604) is a rapid transcriptome library kit that is perfectly compatible with mRNA transcriptome preparation and total RNA library preparation. The kit combines two-strand synthesis, end repair and dA-tailing in one step, with no intermediate purification steps required, greatly simplifying the process and reducing preparation time.

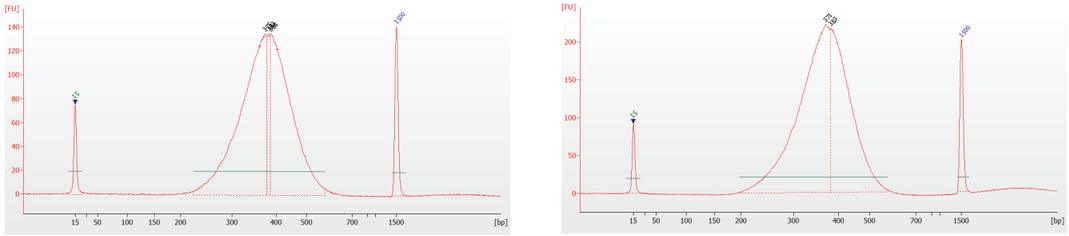


Figure 1. **Normal library peak pattern.** 1 ug and 10 ng of Total RNA from 293T cells of 1 ug and 10 ng, were added separately. RNA Capture Beads (Vazyme #N401) and the rapid transcriptome library kit (Vazyme #NR604) were used to prepare the library. The peak types of libraries prepared using Vazyme's NR604 were all normal at high/low starting volumes. No residual adapter contamination or large fragments are present.

Tumor Transcriptome Sequencing Solution

RNA extraction

Product application	Product name	Cat. #
Cell/Tissue RNA extraction kit	Fastpure® Cell/Tissue Total RNA Isolation Mini Kit	RC101

RNA library preparation (for Illumina Platform)

Product application	Product name	Cat. #
Rapid transcriptome library kit	VAHTS® Universal V6 RNA-seq Library Prep Kit for Illumina	NR604
	VAHTS® Universal V8 RNA-seq Library Prep Kit for Illumina	NR605

RNA library preparation (for MGI platforms)

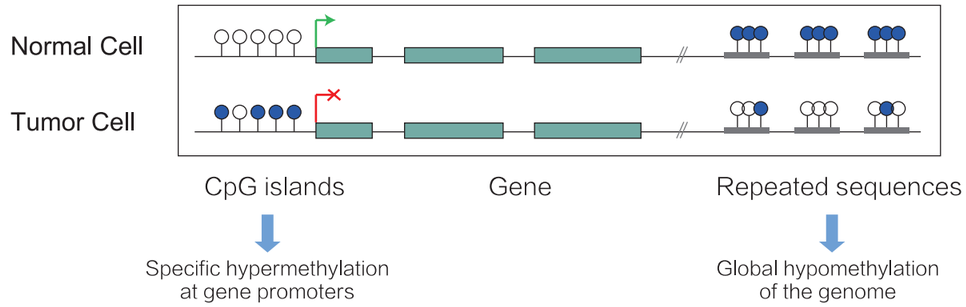
Product application	Product name	Cat. #
Rapid transcriptome library kit	VAHTS® Universal V8 RNA-seq Library Prep Kit for MGI	NRM605

DNA Preservation and Extraction

Product application	Product name	Cat. #
RNA high-sensitivity assay kit	Equabit® RNA HS Assay Kit	EQ211
mRNA enriching beads	VAHTS® mRNA Capture Beads	N401
rRNA removal kit	Ribo-off® rRNA Depletion Kit(Human/Mouse/Rat)	N406
RNA purification beads	VAHTS® RNA Clean Beads	N412
DNA purification and selection beads	VAHTS® DNA Clean Beads	N411

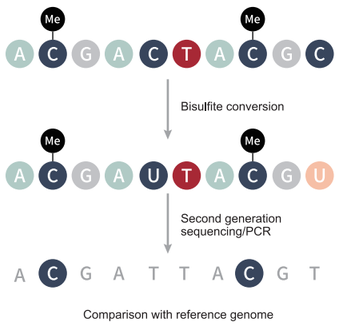
Tumor Whole Genome Methylation Sequencing

Tumorigenesis is not only a type of genetic expression, but is also affected by epigenetic modifications. Current findings in genomic DNA methylation in tumor cells include: extensive genome hypomethylation and CpG island hypermethylation. In many tumor tissues, the previously hypomethylated CPG islands become hypermethylated, resulting in gene silencing, such as tumor suppressor genes. Therefore, by studying DNA methylation, we can gain insight into the molecular mechanisms of tumorigenesis and tumor progression, and provide new evidence for early screening, diagnosis and assessing the prognoses of tumors.



Detecting DNA Methylation With Bisulfite Conversion

The EpiArt™ DNA Methylation Bisulfite Kit (Vazyme #EM101) uses bisulfite to treat DNA in order to convert unmethylated cytosine to uracil, while methylated cytosine remains unchanged during the process. After conversion, DNA methylation can be determined using PCR amplification or NGS sequencing.



Short operation time — The conversion response time is only 140 min

High conversion efficiency — Efficiency of non-methylated cytosine conversion ≥99%

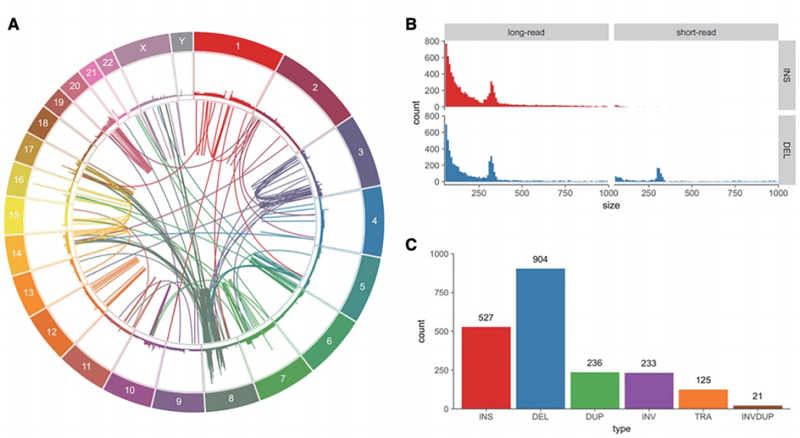
Wide compatibility — Highly efficient conversion of DNA, cfDNA, purified PCR products from cells or tissues of animals, plants, microorganisms, etc. Recovery rate ≥80%

Methylation Sequencing Solutions from Vazyme Biotech

Product application	Product name	Cat. #
Methylation kit	EpiAr DNA Methylation Bisulfite Kit	EM101
Amplification after methylation	2x EpiArt HS Taq Master Mix	EM201
	2x EpiArt HS Taq Master Mix (Dye plus)	EM202
Methylated library kit	EpiArt DNA Methylation Library Kit V2	NE102

Third Generation Sequencing of Tumor

Next generation sequencing (NGS) has great advantages such as high throughput, high cost performance and simultaneous detection of a large number of tumor mutations. It has become more and more widely used in clinical practice. Many NGS-based IVD products have gradually been approved. However, the read length of NGS is short, resulting in poor detection sensitivity for structure variations (SVs). However, accurate detection of tumor SVs is a very important step in assisted diagnosis and precise medication, and it has huge research potential. The third generation single-molecule real-time sequencing breaks through the technical bottleneck that NGS cannot accurately measure SVs due to its advantages of long read length.



Nattestad M, Goodwin S, Ng K, et al. Genome research, 2018.
The advantage of PacBio sequencing platform in detection of SVs

Third Generation Sequencing Solutions from Vazyme Biotech

Applicable Platform	Product Type	Product Name	Cat. #
PacBio	DNA Library Preparation Kit	VAHTS® DNA Library Prep Kit for Pacbio	TS101
Nanopore	DNA Damage Repair Module	VAHTS® DNA Damage Repair Kit	N208
	End Preparation Module	VAHTS® Universal End preparation Module for Illumina	N203
	Adapter Ligation Module	VAHTS® Universal Adapter Ligation Module for Illumina	N204

Ordering Information

	Product Type	Product Name	Cat. #	Specification
DNA/RNA Library Preparation (Illumina Platform)	Universal DNA Library Preparation Kit	VAHTS® Universal DNA Library Prep Kit for Illumina V3	ND607-01/02	24 rxn/96 rxn
	DNA Damage Repair Library Preparation Kit	VAHTS® Universal Pro DNA Library Prep Kit for Illumina	ND608-01/02	24 rxn/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS® Universal Plus DNA Library Prep Kit for Illumina	ND617-01/02	24 rxn/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS Universal Plus DNA Library Prep Kit for Illumina V2	ND627-01/02	24 rxn/96 rxn
	Multi-amplicon Library Preparation Kit	VAHTS® AmpSeq Library Prep Kit V3	NA210-01/02	24 rxn/96 rxn
	Single-Indexed Adapters	VAHTS® DNA Adapters set 1/2 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
		VAHTS® Dual UMI UDI Adapters for Illumina	N351-N354	20 μL each
RNA Library Preparation Module (Ion Torrent&MGI Platform)	Universal DNA Library Preparation Kit	VAHTS® Universal DNA Library Prep Kit for Ion Torrent V2	ND702-01/02	24/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS® Universal Plus DNA Library Prep Kit for Ion Torrent	ND711-01/02	24/96 rxn
	Single-Indexed 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
	Universal DNA Library Preparation Kit	VAHTS® Universal DNA Library Prep Kit for MGI	NDM607-01/02	24/96 rxn
	DNA Damage Repair Library Preparation Kit	VAHTS® Universal Pro DNA Library Prep Kit for MGI	NDM608-01/02	24/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS® Universal Plus DNA Library Prep Kit for MGI	NDM617-01/02	24/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS® Universal Plus DNA Library Prep Kit for MGI V2	NDM627-01/02	24/96 rxn
	Enzymatic Fragmentation-based DNA Library Preparation Kit	VAHTS® DNA Adapters set 8 for MGI	NM108-01/02	10 μL each/40 μL each
RNA Library Preparation Module (Illumina Platform)	Fast Transcriptome Library Preparation Kit	VAHTS® Universal V6 RNA-seq Library Prep Kit for Illumina	NR604-01/02	24/96 rxn
		VAHTS® Universal V8 RNA-seq Library Prep Kit for Illumina	NR605-01/02	24/96 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
RNA Library Preparation Module (MGI Platform)	Fast Transcriptome Library Preparation Kit	VAHTS® Universal V6 RNA-seq Library Prep Kit for MGI	NRM604-01/02	24/96 rxn
		VAHTS® Universal V8 RNA-seq Library Prep Kit for MGI	NRM605-01/02	24/96 rxn
	Single-Indexed Adapters	VAHTS® RNA Adapters set 8 for MGI	NM208-01/02	10 μL each/40 μL each
RNA Library Preparation Module	mRNA Enrichment Module	VAHTS® mRNA Capture Beads	N401-01/02	24/96 rxn
	rRNA Depletion Kit	Ribo-off® rRNA Depletion Kit (H/M/R)	N406-01/02	24/96 rxn
		Ribo-off® rRNA Depletion Kit (Bacteria)	N407-01/02	12/24 rxn
		Ribo-off® Globin & rRNA Depletion Kit (Human/Mouse/Rat)	N408-01/02	24/96 rxn
		Ribo-off rRNA depletion Kit (Plant)	N409-01/02	12/24 rxn
	RNA Fragmentation Buffer(containing random primers)	VAHTS® 2 × Frag/Prime Buffer	N402-01	96 rxn
Magnetic Beads and Library Quantification	DNA Purification and Size Selection Magnetic Beads	VAHTS® DNA Clean Beads	N411-01/02/03	5 mL/60 mL/450 mL
	RNA Purification Magnetic Beads	VAHTS® RNA Clean Beads	N412-01/02/03	5 mL/40 mL/450 mL
	dsDNA High Sensitivity Detection Kit	Equalbit® 1 × dsDNA HS Assay Kit	EQ121-01/02	100 assays/500 assays
	RNA High Sensitivity Detection Kit	Equalbit® RNA HS Assay Kit	EQ211-01/02	100 assays/500 assays
	High Sensitivity Detection Kit	Equalbit® RNA BR Assay Kit	EQ212-01/02	100 assays/500 assays

Science and Technology Make a Healthier Life