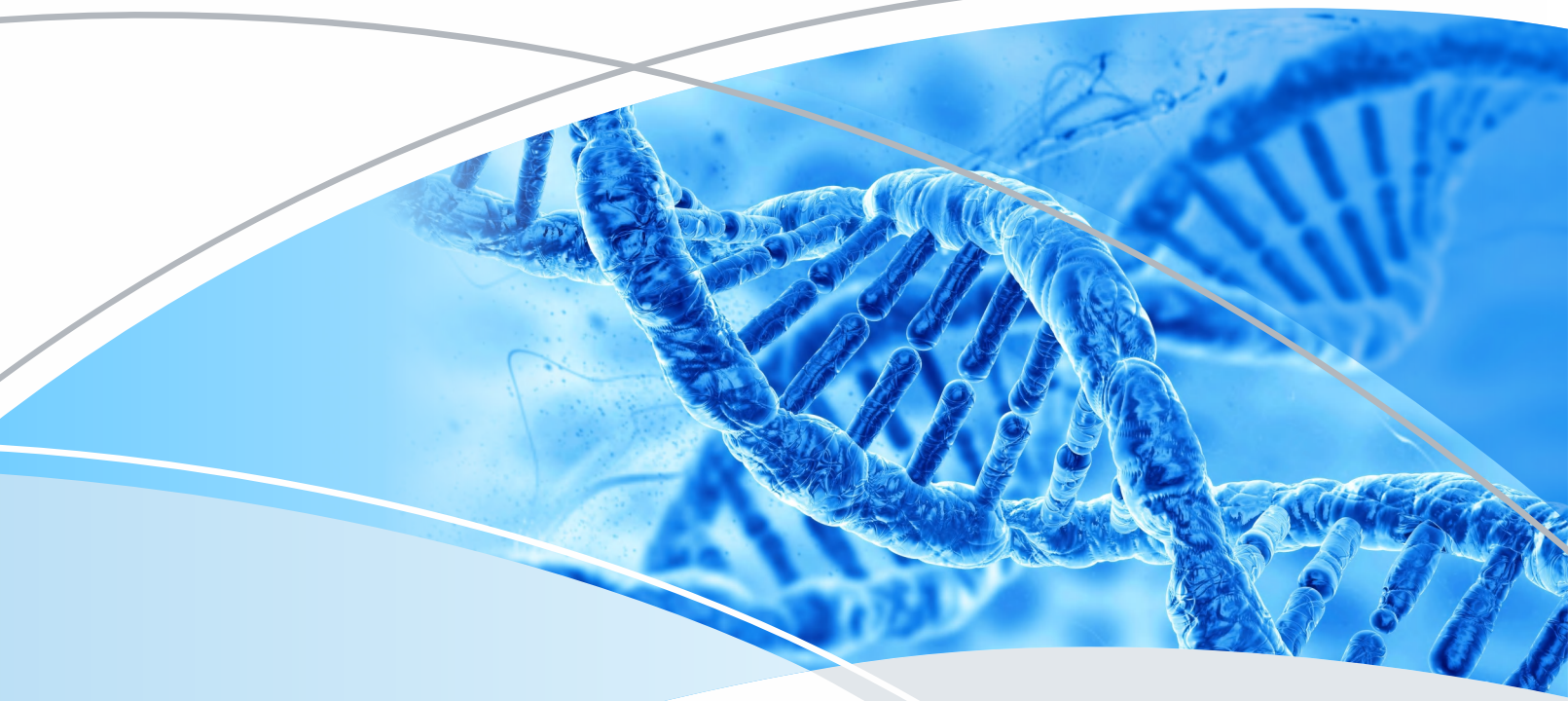
BiOri BIOTECH



2026

NGS LIBRARY SERIES

Next-Generation Solutions

Zhuhai Biori Biotechnology Co.,Ltd

Pursuing Excellence in Quality
Providing Prompt and Thorough Service

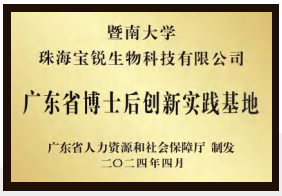
ABOUT US

Founded in 2012, Zhuhai Biori Biotechnology Co., Ltd. provides biological raw materials and reagent solutions for life science research, in vitro diagnostics (IVD), and biopharmaceutical applications. The company builds on established capabilities in protein engineering, recombinant expression, process development, and application-focused research to support both research and industrial customers worldwide.

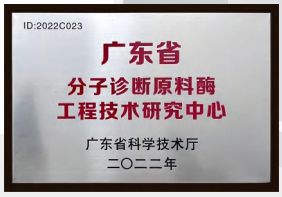
Biori operates under ISO 13485 and ISO 9001 certified quality management systems and maintains GMP and GMP-grade manufacturing facilities to ensure consistent quality and reliable supply. With a long-term focus on innovation and quality, Biori aims to support customer success, foster sustainable team growth, and contribute to the advancement of life science and healthcare technologies.

ational Level Specialized, Refined, Differentiated, and Innovative Little Giant Enterprise

National High-Tech Enterprise



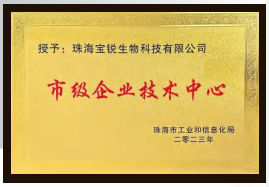
Postdoctoral Innovation and Practice Base



Molecular Diagnostic Raw Materials Technology Center of Guangdong Province

ISO 9001:2015

ISO 13485:2016



Municipal Enterprise Technology Center

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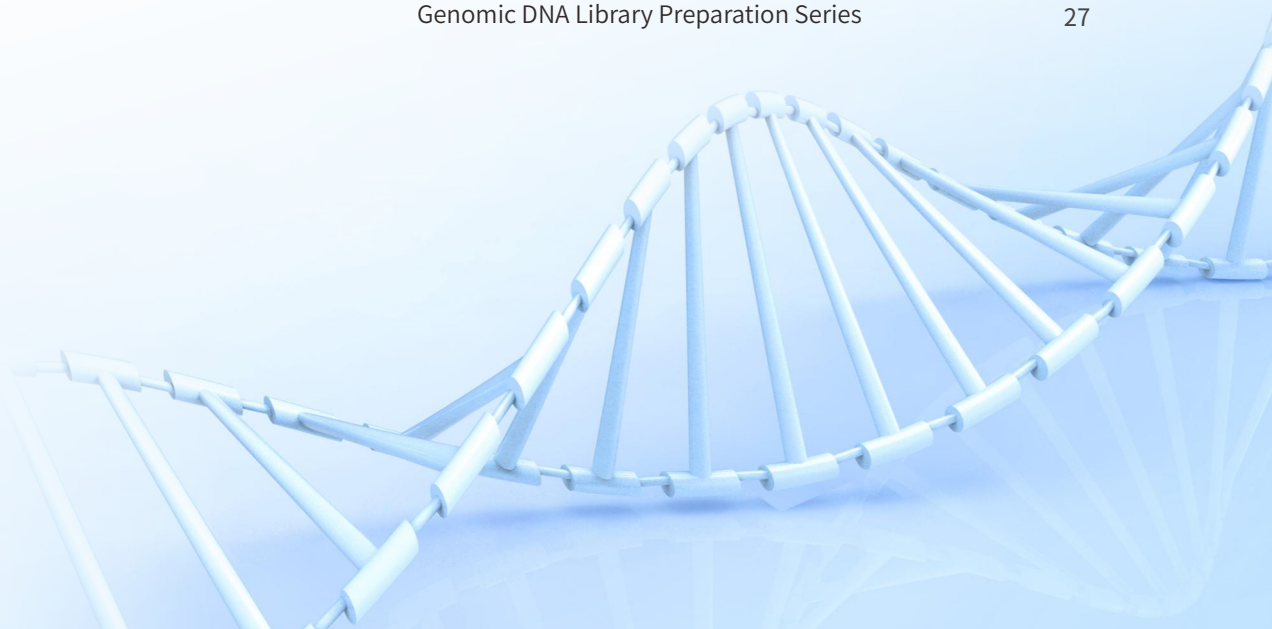


01 Tool Enzymes

Product Type	Product Name	Cat.No.	Feature
Single Enzyme	AmpHifi HS DNA Polymerase Ⅰ	BR3P101	❶ PFU origin. ❷ Fidelity:71 times higher fidelity than Taq polymerase. ❸ Amplification rate: 30
	AmpHifi HS DNA Polymerase III	BR3P103	❶ KOD origin. ❷ Fidelity:154 times higher fidelity than Taq polymerase. ❸ Amplification rate: 5 s/kb.
	T4 DNA Ligase	BR3P301	Double-stranded DNA sticky-end TA ligation.
	T4 DNA Polymerase	BR3P302	Overhang trimming, end-blunting.
	T4 Polynucleotide kinase	BR3P303	5'-phosphorylation, 3'-dephosphorylation.
	phi29 DNA Polymerase	BR3P104	❶ Strand displacement DNA polymerase. ❷ Whole-genome isothermal amplification.
	Vent(exo-)DNA Polymerase	BR3P107	❶ Thermostable strand displacement DNA polymerase. ❷ Whole-genome thermal cycling amplification.

Single Enzyme

AmpHifi HS DNA Polymerase I

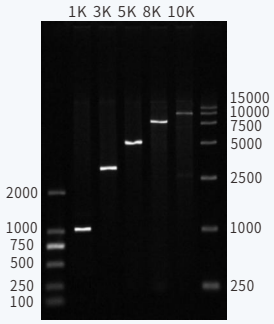
Cat.No.BR3P101

Product Features »

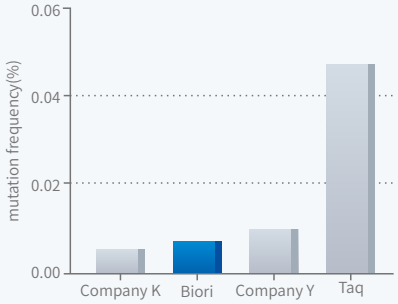
- Stable and Efficient
- Hot Start
- High Fidelity

Product Applications »

- Gene Cloning: Routine gene fragment amplification, recombinant gene amplification validation, first-generation sequencing.
- Long- Fragment Amplification: Gene long-fragment amplification, species identification, SNV identification, third-generation sequencing.



Stable and Efficient: Using the human genome as a template, it efficiently amplifies fragments ranging from 0.1 kb to 10 kb.



High Fidelity: Low mismatch rate ensures accurate results.

T4 DNA Polymerase

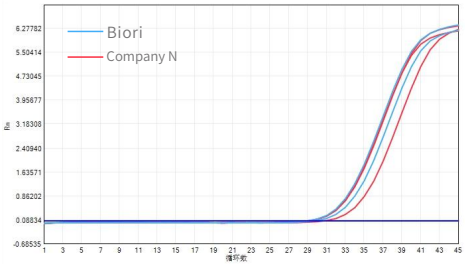
Cat.No.BR3P302

Product Features »

- **Stable and Efficient**
  Strong Inhibitor Resistance
- **High Fidelity, Bias-Free**
  Processes All Types of Nucleic Acids
- **High Salt Tolerance**
  Adaptable to Wide Range of Ion Strength Environments

Product Applications »

- DNA end processing: Overhang trimming, end blunting.
- Probe labeling: Labeled DNA probe synthesis.
- Site-directed mutagenesis: Gene site-directed mutation, PCR amplification.



More Efficient End Processing: DNA ends with overhangs and truncated substrates were treated with BR3P302 and Company N, respectively, followed by qPCR validation. BR3P302 demonstrated superior DNA end processing efficiency.

AmpHifi HS DNA Polymerase III

Cat.No.BR3P103

Product Features »

Stable and Efficient
Strong anti-inhibitor ability

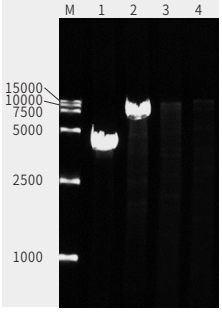
High speed, high yield
1kb/10s, less enzyme usage, higher yield

Hot-start high fidelity
Higher specificity, greater fidelity

Wide adaptability
Conventional PCR, multiplex PCR, specialized PCR, etc.

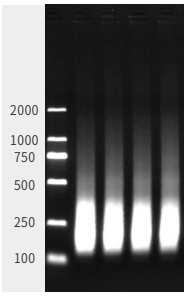
Product Applications »

- **Gene Cloning**
  Routine gene fragment amplification, recombinant gene amplification validation, first-generation sequencing.
- **Ultra-Long Fragment Amplification**
  Long gene fragment amplification, species identification, SNV identification, third-generation sequencing.
- **Multiplex Amplification**
  Exome multiplex amplification, complex template amplification, target gene variant detection, second-generation sequencing, third-generation sequencing.
- **Universal Library Amplification**
  Library amplification compatible with all sequencing platforms.

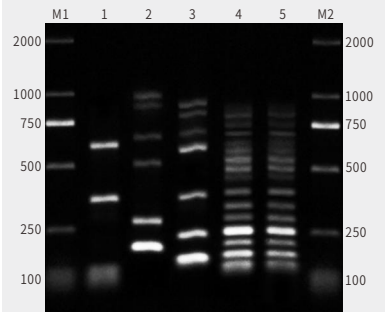


M: DL 15,000 Marker
1: 5K
2: 8K
3: 10K
4: 15K

- **Stable and High-Speed:** Using human genomic DNA as a template, extension for 1 minute can yield up to 8 kb products with high specificity.

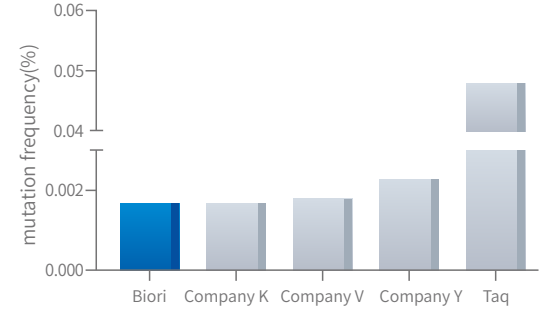


- **High Efficiency and High Yield:** From-scratch library preparation of 50 ng human genomic DNA, amplified over 8 cycles, yielding over 1000 ng of library.



M1: DL 2, 000 Marker
1: 3-plex PCR
2: 6-plex PCR
3: 7-plex PCR
4: 15x PCR
5: 15x PCR
M2: DL 2, 000 Marke

- **Broad Compatibility and High Uniformity:** Using human genomic DNA as a template, it stably and uniformly amplifies diverse amplicons with GC content ranging from 30% to 80%.



- **Enhanced Fidelity:** High-depth sequencing of genomes with varying GC content, with calculated amplification-induced mutation rates matching the fidelity of internationally renowned Company K.

02 Module Reagents

- DNA Multiplexing/Amplification Reagents
- RNA Multiplexing/Amplification Reagents
- NGS Library Preparation Reagents

DNA Multiplexing/Amplification Reagents

Product Name	Cat.No.	Feature
2×Multiplex PCR Master Mix	BR3M101	❶ Taq DNA polymerase. ❷ High amplification efficiency. ❸ Suitable for multiplex amplification of 10-1000 pathogen DNA samples.
2×Multiplex PCR Master Mix V2	BR3M106	❶ Taq DNA polymerase. ❷ High amplification efficiency (enhanced uniformity and amplification efficiency). ❸ Suitable for multiplex amplification of 10–1000 pathogen DNA samples. fragments.
AmpHiFi Mul-PCR Mix	BR3M104	❶ High-fidelity DNA polymerase (fidelity++). ❷ Pre-mixed solution. ❸ Compatible with multiplex amplification of 10–3000 DNA samples.
AmpHifi XL Premix	BR3M401	❶ High-fidelity DNA polymerase (fidelity +++). ❷ High-efficiency long-fragment DNA amplification (0.1-15k). ❸ Amplification rate: 30 s/kb.
2×AmpHifi EXL Premix	BR3M402	❶ High-fidelity DNA polymerase (fidelity ++++). ❷ High-efficiency long-fragment DNA amplification (1–20 kb). ❸ Amplification rate: 10 s/kb.
2×Super-Fidelity Master Mix (Dye Plus)	BR3M121	❶ High-fidelity DNA polymerase (fidelity ++++). ❷ Dye-containing premix (convenient to use). ❸ Simple templates up to 30 kb. ❹ Complex templates up to 20 kb. ❺ Amplification rate: 5 s/kb. ❻ Wider compatibility (dye-free option available).

RNA Multiplexing/Amplification Reagents

Product Name	Cat.No.	Feature
One step RT PCR Mix	BR3M301	❶ Taq DNA polymerase. ❷ One-step RT-PCR. ❸ Compatible with multiplex amplification of DNA & RNA templates.
Multiple PCR Mix for DNA&RNA	BR3M302	❶ Taq DNA polymerase. ❷ One-step RT-PCR. ❸ Compatible with multiplex amplification of DNA & RNA templates. ❹ Higher specificity.
One step RT PCR Mix V2	BR3M322	❶ Blended enzyme for enhanced fidelity. ❷ One-step RT-PCR. ❸ Compatible with multiplex amplification of DNA & RNA templates.
NeoScript One Step RT-PCR Kit	BR3M321	❶ Blended enzyme, balancing amplification efficiency and fidelity. ❷ One-step RT-PCR. ❸ Amplification of 1-10 kb RNA long fragments. ❹ Amplification rate: 20-60 s/kb

NGS Library Preparation Reagents

Product Name	Cat.No.	Feature
Script Max 1st Strand c DNA Synthesis Kit	BR3N701	❶ High-efficiency reverse transcription. ❷ Compatible with reverse transcription temperatures of 42-55°C.
Rapid End Repair/dA-Tailing Module	BR3N601	End repair with A-addition.
Universal DNA Fragmentation Module	BR3N602	Enzyme digestion for DNA fragmentation and end repair with A-addition.
AmpSeq Library Prep Kit	BR3M103	❶ High-fidelity DNA polymerase (fidelity +++). ❷ High-efficiency library amplification. ❸ Two-component system.
AmpSeq Library Amplification Mix	BR3M105	❶ High-fidelity DNA polymerase (fidelity ++++). ❷ High-efficiency amplification with high uniformity. ❸ Single-component premix.
Biori ® NGS DNA Clean Beads	BR3N401	❶ High-efficiency nucleic acid recovery and purification. ❷ Enables purification and fractionation of products with varying fragment lengths.

DNA Multiplexing/Amplification Reagents

2×Multiplex PCR Master Mix

Cat.No.BR3M101

Product Features »

Stable and efficient

Produced in clean environments by professionals;Strictly controlled background bacteria, supporting pathogen tNGS

High-Efficiency, High-Yield

Compatible with 10-1000 multi-pathogen panel amplification

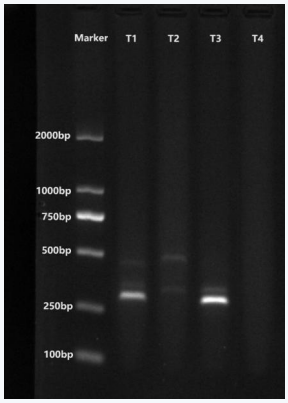
Hot-Start High Fidelity

Demonstrates excellent detection rates and specificity across panels of varying sizes

Product Applications »

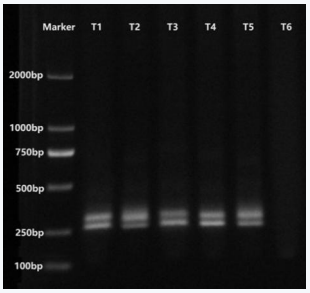
- Microbial Targeted Sequencing
- Environmental Microbial Identification
- Food Safety Testing

Number	Clinical Sample	First-Round Multiplex Amplification (BR3M101)	Second-Round Library Amplification (BR3M105)	Concentration (ng/μL)
T1	Neocryptococcus 1	20cycle	12cycle	4.02
T2	Neocryptococcus 2	20cycle	12cycle	1.57
T3	Negative sample	20cycle	12cycle	5.44
T4	NTC	20cycle	12cycle	0.30
Experimental Protocol	T1 Sample: mNGS detection of 2000 reads from Cryptococcus neoformans positive samples; T2: 2.5-fold dilution of T1 samples ptNGS Methodology:Biori Multi-Primer Chain Reaction (MPR) Panel Size: Biori 268-plex DNA panel Purification Method: No purification required after first-round multiplex amplification; proceed directly to second-round library amplification.			



Note: Whether post-multiplex amplification product purification is required before second-round library amplification depends on the specific tNGS methodology employed.

- **Low Primer Dimer:**
  Exceptional primer dimer control, with no detectable dimer bands even in negative clinical samples.
- **High Specificity Amplification:**
  Clear target amplicon bands with no significant non-specific amplification bands.



Number	Input Amount	Multiple Amplification (BR3M101)	Second-Round Library Amplification (BR3M105)	Concentration (ng/μL)
T1	0.5 ng clinically positive sample	20cycle	12cycle	6.06
T2	5 ng clinically positive sample	20cycle	12cycle	8.20
T3	20 ng clinically positive sample	15cycle	12cycle	10.34
T4	50 ng clinically positive sample	15cycle	12cycle	16.22
T5	500 ng clinically positive sample	15cycle	12cycle	19.70
T6	NTC	15cycle	12cycle	0.59
Experimental Protocol	Sample: Add 2.5 ng of standard Klebsiella pneumoniae nucleic acid and 2.5 ng of standard Mycobacterium tuberculosis nucleic acid to 995 ng of human genomic DNA, mix thoroughly, and use 0.5 ng to 500 ng for the experiment. ptNGS Methodology: Bora Multi-Primer Chain Reaction (PCR) Panel Size: Bora 268 Multi-DNA Panel Purification Method: No purification required after first-round multiplex amplification; proceed directly to second-round library amplification.			

Note: Whether purification of multiplex amplification products is required before second-round library amplification depends on the specific tNGS methodology employed.

- **Excellent amplification reproducibility:**
  Positive pathogens at varying input amounts exhibit consistent amplification with reliable reproducibility.
- **Wide compatibility:**
  Easily accommodates nucleic acid input ranging from 0.5 to 500 ng, with a minimum detection limit as low as 0.1 ng.

2×Multiplex PCR Master Mix V2

Cat.No.BR3M106

2× Multiplex PCR Master Mix V2 is an ultra-multiplex PCR amplification reagent developed for ptNGS technology, representing an iterative version of BR3M101.

Compared to BR3M101, it offers higher amplification efficiency and superior amplification uniformity, with products suitable for library amplification, qPCR validation, and other applications.

Product Features »

Strict Background Contamination Control

Produced in a clean environment by specialized personnel;
Rigorous background contamination control supports pathogen tNGS.

Multiplex Amplification

Compatible with 10-1000-plex pathogen panel amplification.

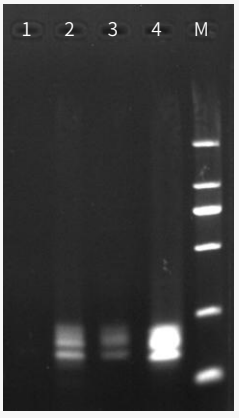
Superior Amplification Performance

Demonstrates excellent detection rates and specificity across panels of varying sizes.

Product Applications »

- Microbial Targeted Sequencing
- Environmental Microbial Identification
- Food Safety Testing

• BR3M106 exhibits higher amplification efficiency and Compatible with lower input amounts

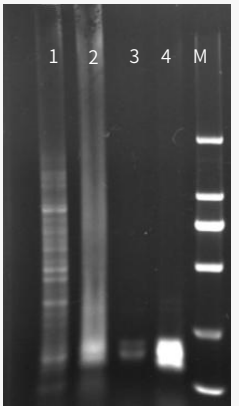


M: Marker (100-2000 bp)
1: Human genomic DNA 0.1 ng, BR3M101
2: Human genomic DNA 0.1 ng, BR3M106
3: Human genomic DNA 10 ng, BR3M101
4: Human genomic DNA 10 ng, BR3M106

• Experimental Setup:

For a challenging human exon 20 multiplex panel (targets with GC content ranging from 27% to 80%, amplicon lengths 150-210 bp), two different versions of multiplex .

• BR3M106 demonstrated superior amplification consistency across varying GC contents, outperforming comparable commercial products.



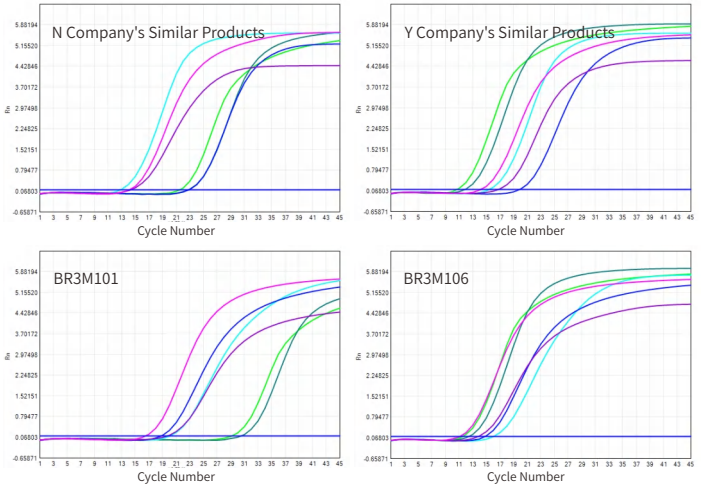
M: marker (100-2000 bp)
1: Human genomic DNA 10 ng, N Company's comparable product
2: Human genomic DNA 10 ng, Y Company's comparable product
3: Human genomic DNA 10 ng, BR3M101
4: Human genomic DNA 10 ng, BR3M106

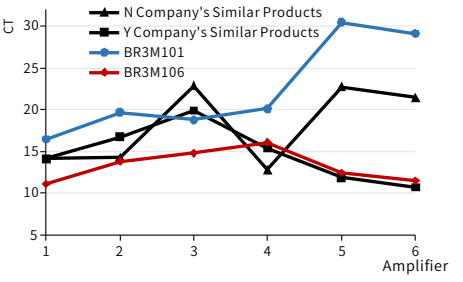
Note: Enzyme amount 2.5 U, 28 cycles. After 2000-fold dilution of the product, 6 randomly selected amplicons underwent qPCR detection

• Experimental Setup:

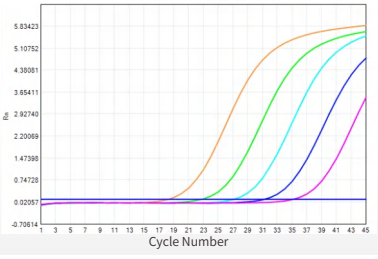
For a difficult-to-amplify human exon 20 multiplex panel (target GC content range 27–80%, amplicon length 150-210 bp), amplified using comparable products from Companies N and Y. After 2000-fold dilution of amplification products, 6 targets with different GC contents were selected for qPCR identification.

BR3M106 demonstrated superior amplification consistency across varying GC contents, outperforming comparable commercial products.





BBR3M106 exhibits high amplification sensitivity.



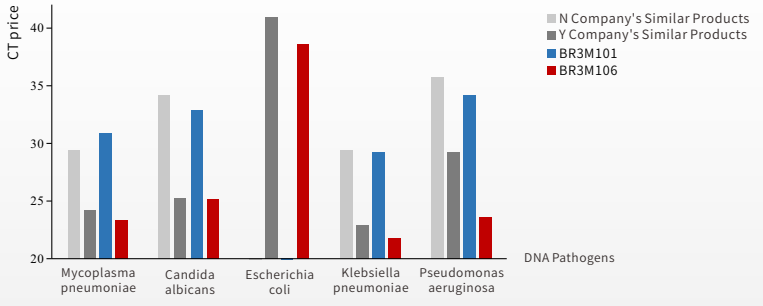
No.	Template input (copies/reaction)	Ct value
1	7.25	35.12
2	7.25E1	31.25
3	7.25E2	27.11
4	7.25E3	22.80
5	7.25E4	18.25

- Experimental setup: Client-provided viral DNA underwent gradient dilution followed by dye-based qPCR amplification. Amplified fragment length: 900 bp.

BR3M106 demonstrates superior uniformity and detection rate in pathogen multiplex amplification.

Sample Detection Limit Reference Material L2 (Including Human Background)
Panel 500x Respiratory DNA & RNA Targeted Product
Number of Amplification Cycles 20

Multiplex Amplification Reagent	qPCR Validation CT Value after 100-fold Dilution of Multiplex Product				
	Mycoplasma pneumoniae	Candida albicans	Escherichia coli	Klebsiella pneumoniae	Pseudomonas aeruginosa
N Company's Similar Products	29.4	34.13	NoCt	29.44	35.69
Y Company's Similar Products	24.15	25.25	40.93	22.88	29.21
BR3M101	30.85	32.85	NoCt	29.18	34.17
BR3M106	23.27	25.14	38.57	21.75	23.57



Product Features »

Super-multiple amplification

Compatible with 10- to 3000-plex gene amplification.

High Fidelity

Maximizes preservation of original genetic information.

High amplification uniformity

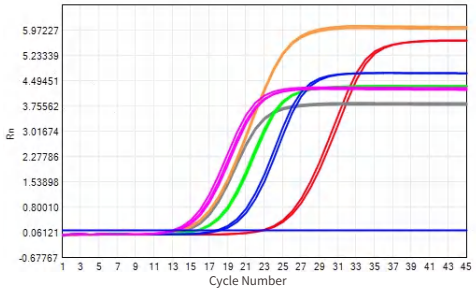
Maintains relatively consistent amplification efficiency across amplificons with varying GC content.

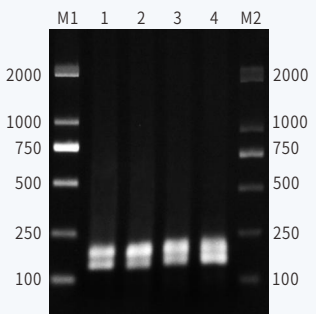
Broad GC compatibility

30%-80%

Product Applications »

- Targeted Sequencing.
- Gene Function Research, Full-Length Gene Amplification.
- Hypermultiplex amplification compatible with genomes, exomes, variant-enriched genomes, etc.

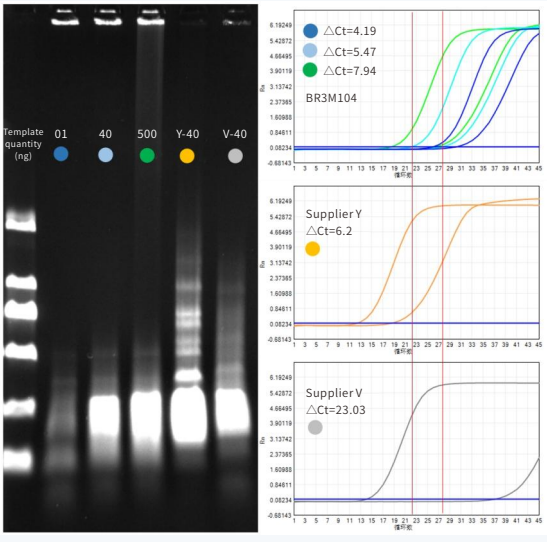




M1: DL2,000 Marker
1: Enzyme concentration 1U/50μL
2: Enzyme concentration 2U/50μL
3: Enzyme concentration 3U/50μL
4: Enzyme concentration 4U/50μL
M2: DL2,000 Marker

- **Wi compatibility with high GC content:**
  qPCR validation of targets with 25%-85% GC content selected from 34-fold amplification products detected all targets.

- **Stable and Efficient:**
  Under varying enzyme concentrations, stable amplification of 34-plex panels spanning 25%-85% GC content with no significant dimer formation.



BR3M104 template compatibility ranges from 0.1-500 ng/25μL. Lower template quantities yield stronger uniformity.

Supplier Y exhibits comparable uniformity to BR3M104 but inferior specificity.

Supplier V demonstrates specificity between Yeasen and BR3M104, yet exhibits poor uniformity.

- **Combined uniformity and specificity:**
  Among 34 amplified products, targets with 25%-85% GC content selected for qPCR validation were all detected.

AmpHifi XL Premix

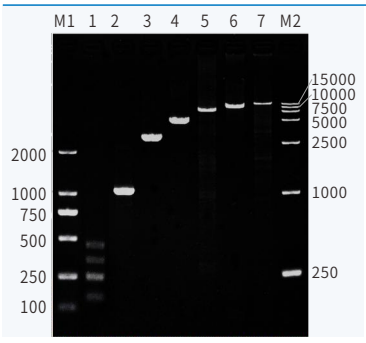
Cat.No.BR3M401

Product Features »

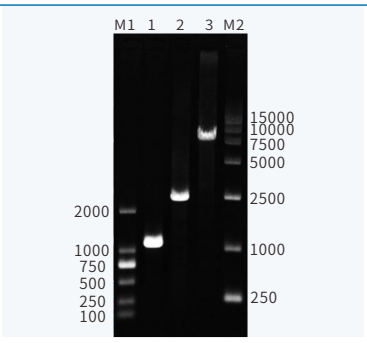
High-Fidelity DNA Polymerase (Fidelity+++)

High-Efficiency Long-Fragment DNA Amplification (0.1-15 kb)

Amplification Rate: 30 s/kb



M1:DL2,000Marker
1:Quadruple PCR
2: 1K
3: 3K
4: 5K
5: 8K
6: 10K
7: 15K
M2: DL15,000Marker



M1:DL2,000Marker
1: 74% GC
2: 73% GC
3: 72% GC
M2: DL15,000Marker

- **Stable and Efficient:** Using the human genome as a template, it efficiently amplifies 15Kb fragments.
- **High Compatibility:** Efficiently amplifies long fragments with local GC content exceeding 80% and overall GC content exceeding 70%.

2×AmpHifi EXL Premix

Cat.No.BR3M402

Product Features »

Stable and efficient

Extended amplification duration, supporting up to 15 hours of amplification; compatible with low-purity templates.

Hot-start and Easy to Operate

Room-temperature operation with ready-to-use 2× premix.

High-Speed Long-Distance Amplification

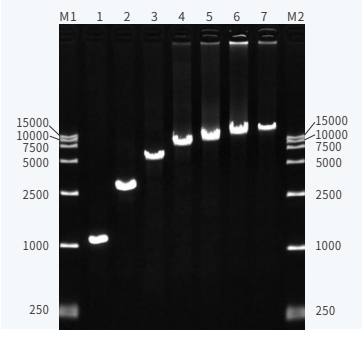
Compatible with 1kb-20kb long fragment amplification, achieving speeds up to 1kb/10s.

Wide GC tolerance

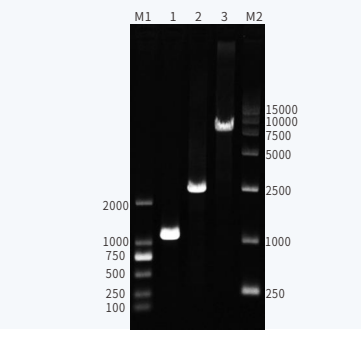
30%-80%

Product Applications »

- Long-read PCR, compatible with first-generation sequencing, second-generation sequencing, and third-generation sequencing.
- Colony PCR, Strain Identification
- Genotype Identification



M1:DL15,000Marker
1:1K
2:3K
3:5K
4:8K
5:10K
6:15K
7:20K
M2:DL15,000Marker



M1:DL2,000Marker
1:74% GC
2:73% GC
3:72% GC
M2:DL15,000Marker

- **Stable and Efficient:** Efficiently amplifies 20Kb fragments using human genomic DNA as template.
- **High Compatibility:** Efficiently amplifies long fragments with localized GC content exceeding 80% and overall GC content exceeding 74%.

2×Super-Fidelity Master Mix (Dye Plus)

Cat.No.BR3M121

2× Super-Fidelity Master Mix (Dye Plus) contains a genetically engineered hot-start high-fidelity DNA polymerase with exceptional DNA affinity and continuous synthesis capability. It demonstrates excellent compatibility with complex and partially degraded templates, offering approximately 96 times the fidelity of Taq polymerase.

This product contains hot-start high-fidelity DNA polymerase, dNTPs, and an optimized buffer system. Simply add primers and template to initiate amplification, reducing pipetting steps while enhancing throughput and reproducibility.

Product Features »

Bwide Template Compatibility

Compatible with genomic DNA from various species, bacterial cultures, crude nucleic acid extracts, and more.

Wide Amplification Length Compatibility

Supports amplification of target fragments ranging from 0.1 kb to 20 kb.

Higher Sensitivity

Stable amplification achievable with as little as 1 pg of plasmid template.

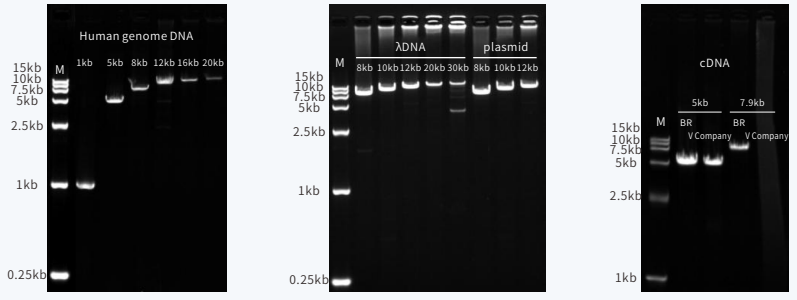
Extensive GC Content Tolerance

20%-80%

Product Applications »

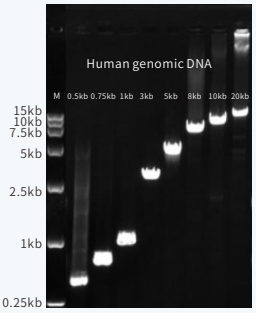
- Pathogenic Microorganism Detection, suitable for PCR, qPCR, or DNA library construction.
- Functional Gene Research (Scientific Research)
- Gene Cloning or Gene Expression Analysis
- Gene Analysis, Transgenic Analysis, etc.

Broad Template Compatibility



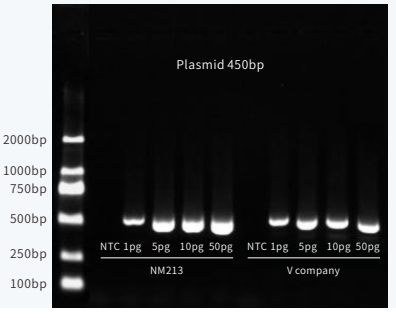
- Using BR3M121 for PCR amplification of four distinct DNA template types, the results shown above demonstrate excellent amplification performance across all four templates (also compatible with other diverse templates such as rice leaves, corn cobs, yeast, and blood DNA).

Broad Amplification Length Compatibility



- BR3M121 demonstrates excellent amplification capabilities for both long and short DNA fragments.

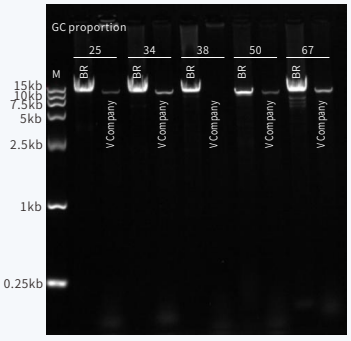
High Sensitivity



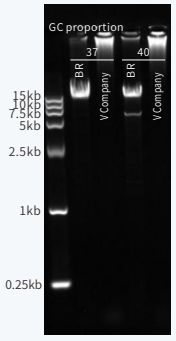
- When amplifying plasmids with varying input amounts using BR3M121 and Company V's product, the results shown in the figure above indicate that BR3M121 exhibits high sensitivity comparable to Company V's product.

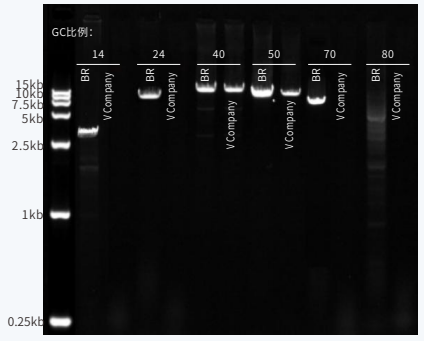
Broad GC compatibility

Human genome 10kb template GC proportion



Human genome 20kb template GC proportion

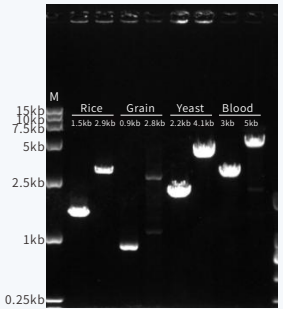




- Figure 1—Using BR3M121 and V Company to amplify DNA fragments from complex regions with 10kb GC content ranging from 25% to 67%, and 20kb GC content ranging from 37% to 40%.
- Figure 2: Amplification of DNA fragments from simple regions with GC content ranging from 14% to 80% using BR3M121 and V Company.

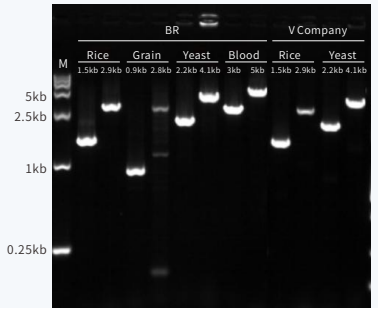
Analysis of the results indicates that BR3M121 exhibits excellent amplification performance across templates with varying GC ratios, outperforming Company V and demonstrating compatibility with GC ratios ranging from 20% to 70%.

Stable Crude Sample Amplification Capability



- Using rice leaves, corn cobs, yeast, and blood as DNA templates, BR3M121 demonstrated excellent amplification performance across four distinct crude samples.

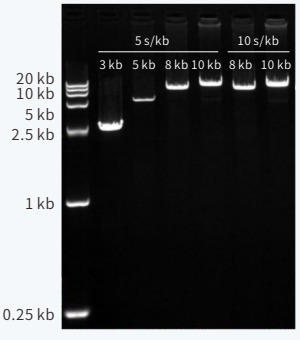
Stable Crude Sample Amplification Capability



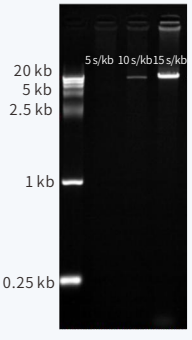
- Repeatability testing of PCR amplification across the four crude samples was conducted and compared with reagents from Company V. Both demonstrated good amplification performance, with BR3M121 exhibiting superior amplification efficiency compared to Company V.

High-Efficiency Amplification Rate

Human Gene DNA



Human Gene DNA: 20kb



- For targets under 10 kb, the amplification rate reaches up to 5s/kb; for targets over 10 kb, the amplification rate reaches up to 10s/kb.

RNA Multiplexing/Amplification Reagents

One step RT PCR Mix

Cat.No.BR3M301

Product Features »

RNA & DNA Co-Amplification

Compatible with 10-600x RNA & DNA mixtures for simultaneous amplification.

Single-Tube Reaction

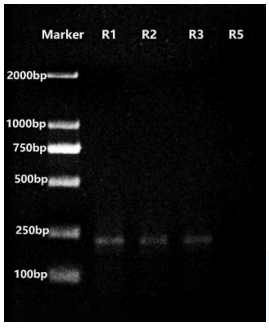
No prior reverse transcription required; completes cDNA synthesis and multiplex PCR amplification in a single step within one tube.

Strict Background Contamination Control

Produced in a clean environment by specialized personnel; rigorously controlled background contamination.

Product Applications »

- Targeted Sequencing of Pathogenic Microorganisms; PCR Detection of Pathogenic Microorganisms
- Environmental Microbial Identification
- Food Safety Testing; Functional Gene Research (Scientific Research)



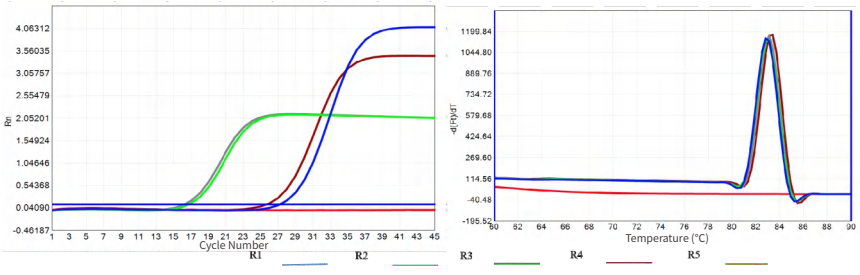
- **Excellent dimer control:** No significant dimer formation observed in 50x multiplex RT-PCR amplification in a single tube.

Note: R4 reaction does not undergo secondary library amplification and does not require gel electrophoresis.

One Step RT-PCR Mix (BR3M301) Library Construction Test in 50-Sample RNA Pathogen Panel.

No.	Template	Reverse Transcription & 1st Round PCR Multiplex Amplification BR3M301	Second Round Library Amplification	Concentration (ng/μL)	qPCR Detection CT Value	
					Human Total RNA	COVID-19 Pseudovirus
R1	50ng Human Total RNA + COVID-19 (10 copies)	15cycle	10cycle	3.00	2.05	29.03
R2	50ng Human Total RNA + COVID-19 (50 copies)	15cycle	10cycle	2.56	2.07	16.68
R3	50ng Human Total RNA + COVID-19 (100 copies)	15cycle	10cycle	2.78	1.70	16.21
R4	50ng Human Total RNA + COVID-19 (100 copies)	15cycle	0	/	7.26	25.68
R5	NTC	15cycle	10cycle	0.848	-	-

COVID-19 Pseudovirus qPCR Detection Results.



- **Superior sensitivity assurance:** 50-fold single-tube reverse transcription multiplex PCR amplification enables easy detection of 10 copies of COVID-19 pseudovirus via qPCR.

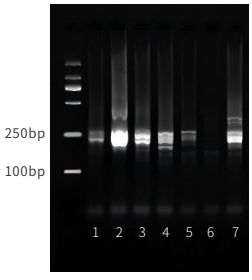
Multiple PCR Mix for DNA&RNA

Cat.No.BR3M302

Product Features »

- Taq DNA Polymerase, High Efficiency
- RT-PCR—Step Method
- Enhanced Specificity
- Compatible with DNA & RNA Templates for Multiplex Amplification

tNGS 400+ multiplex amplification, diverse samples, excellent specificity, no significant dimers.



No.	Sample	panel	Multiplex Amplification	Library Amplification	Library Concentration
1	Fs026+ External Reference	BR	BR3M302	BR	19.0
2	Sp015+ External Reference				TH
3	Bf026+ External Reference				38.0
4	Negative Quality Control Sample				30
5	External				12.1
6	Water				3.74
7	Positive Control P2+External Reference				44.4

One step RT PCR Mix V2

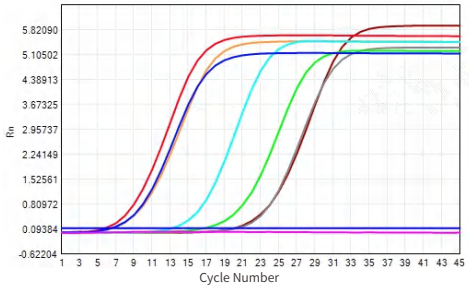
Cat.No.BR3M322

Product Features »

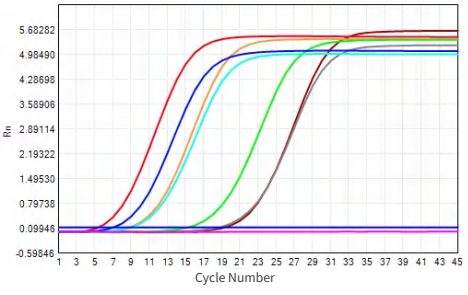
- Mixed Enzymes, Enhanced Fidelity
- RT-PCR—Step Method
- Compatible with DNA & RNA Templates for Multiplex Amplification

BR3M302 exhibits multiplex amplification efficiency comparable to single-target amplification.

Single-Target Amplification Results for 7 Targets



Multiplex Amplification Results for 7 Targets (BR3M322)



Target 1 :ΔCT=0.3
Target2 :ΔCT=-0.48
Target3 :ΔCT=-2.18
Target4 :ΔCT=4.18
Target5 :ΔCT=1.0
Target6 :ΔCT=1.05
Target7 :ΔCT=1.26

NeoScript One Step RT-PCR Kit

Cat.No.BR3M321

Neoscript One Step RT-PCR Kit is an endpoint PCR qualitative detection reagent for RNA templates. Using gene-specific primers, cDNA synthesis and PCR amplification are performed consecutively in the same reaction system without requiring additional liquid additions, simplifying experimental procedures. This kit incorporates a high-temperature reverse transcriptase, novel hot-start enzyme, and RNase inhibitor, combined with an optimized buffer system, enabling amplification of fragments up to 10 kb or longer.

Product Features »

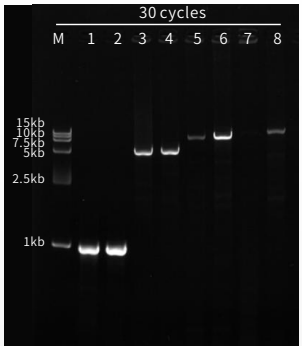
Single-tube reactions minimize contamination risks, enabling accurate and straightforward amplification of target genes from RNA starting materials.

High-temperature reverse transcription at 50°C; PCR extension time: 20 sec–1 min/kb.

Accommodates a wide range of total RNA input quantities.

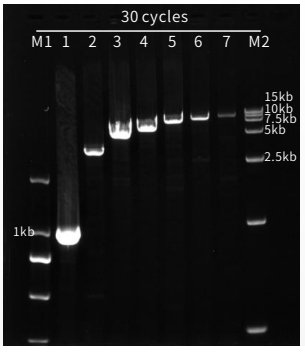
Product Applications »

- Suitable for life science research fields including gene structure and function studies, transcript diversity analysis, and more.
- Genetic Disease Research
- Viral Genome Research
- Tumor diagnosis and detection, such as studies on gene rearrangements and gene fusions.



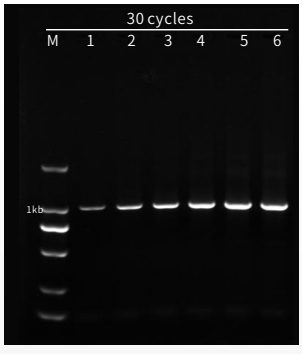
Template:
HEK293-derived total RNA,
100 ng/25 μL reaction volume.
Size-Extension speed:
1:1kb-20 sec/kb
2:1kb-1 min/kb
3:5kb-20 sec/kb
4:5kb-1 min/kb
5:8kb-20 sec/kb
6:8kb-1 min/kb
7:10.5kb-20 sec/kb
8:10.5kb-1 min/kb

- **Extension Speed Measurement:**
  PCR extension speed can be set to 20 sec/kb. When the amplification length exceeds 5 kb, extension time may be increased. Generally, extending the extension time helps improve amplification yield.



Template:
HEK293-derived total RNA,
100 ng/25 μL reaction.
Target:
1:CDK/1kb
2:GAPDH/3.5kb
3:UTRN/5kb
4:UTRN/6kb
5:UTRN/8kb
6:UTRN/9kb
7:UTRN/10.5kb

- **Amplification Fragment Length:**
  Can amplify fragments ranging from 1 kb to 10.5 kb.



Template Amount
(HEK293-derived total RNA)
1:10pg
2:0.1ng
3:1ng
4:10ng
5:100ng
6:1μg

- **Detection Sensitivity:**
  Detection is achievable with 10 pg of total RNA, with sensitivity reaching 10 pg.

NGS Library Preparation Reagents

Script Max 1st Strand cDNA Synthesis Kit

Cat.No.BR3N701

Script Max 1st Strand cDNA Synthesis Kit includes reverse transcriptase and an optimized reaction buffer. The reverse transcriptase is derived from M-MLV, with RNase H activity removed and enhanced thermal stability. This enables high-temperature reverse transcription, effectively eliminating adverse effects of RNA higher-order structures and non-specific factors on cDNA synthesis, resulting in greater stability and reverse transcription capacity. This product enables single-stranded cDNA synthesis. The resulting product can undergo double-stranded synthesis for downstream applications such as PCR and transcriptome library construction.

Product Features »

Stable and Efficient Reverse Transcription Efficiency

The reverse transcriptase enables extended reactions at temperatures as high as 55°C, overcoming complex RNA structures to yield cDNA and full-length cDNA more efficiently and uniformly.

Broad Template Compatibility

Compatible with total RNA ranging from 0.5ng to 3000ng.

Strict Background Contamination Control

Produced in a clean environment by specialized personnel; background contamination is strictly controlled.

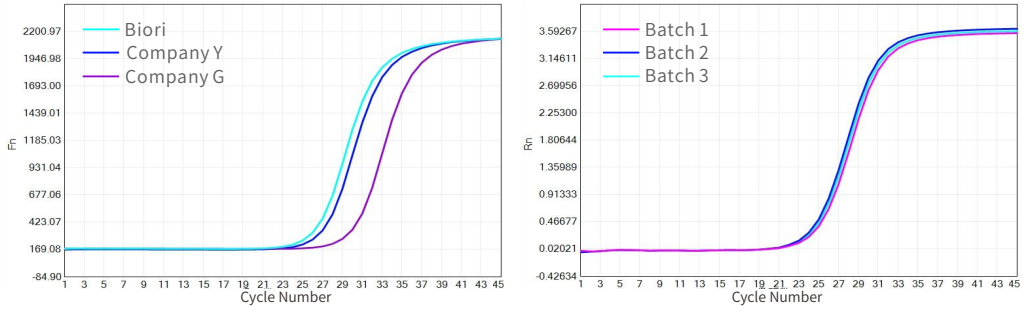
Flexible Primer Usage

Different types of reverse transcription primers can be flexibly used according to varying experimental requirements.

Product Applications »

- Pathogenic Microorganism Detection: Suitable for PCR, qPCR, or DNA library construction.
- cDNA Synthesis.
- Functional Gene Research (Scientific Research)

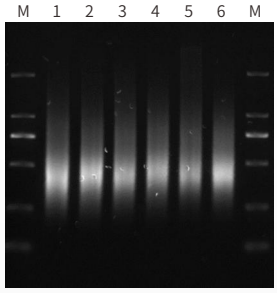
Experiments
Sample: Human Total RNA Reverse transcription temperature: 50°C Reverse transcription time: 15min



- **High Temperature:** Capable of high-temperature reverse transcription, withstanding up to 55°C.
- **High Efficiency:** Demonstrates superior reverse transcription efficiency compared to competitors under identical conditions.
- **Stability:** Exceptional batch-to-batch stability.

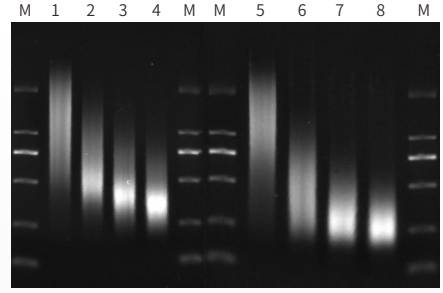
Universal DNA Fragmentation Module

Cat.No.BR3N602



M: DL2,000 marker
1: 50 ng E. coli gDNA fragmentation for 10 min
2: 50 ng Thermus thermophilus gDNA fragmentation for 10 min
3: 50 ng phi29 DNA polymerase amplification product fragmentation for 10 min
4: 50 ng λ DNA fragmentation 10 min
5: 50 ng high-fidelity DNA polymerase 10Kb gene amplification product fragmentation 10 min
6: 50 ng 293T gDNA fragmentation 10 min

- Suitable for nucleic acids from different sources and species.



M: DL2,000 marker
1: 50 ng 293T gDNA fragmentation 1 min
2: 50 ng 293T gDNA fragmentation 5 min
3: 50 ng 293T gDNA fragmentation 10 min
4: 50 ng 293T gDNA fragmentation 15 min
5: 250 ng 293T gDNA fragmentation 1 min
6: 250 ng 293T gDNA fragmentation 5 min
7: 250 ng 293T gDNA fragmentation 10 min
8: 250 ng 293T gDNA fragmentation 15 min

- Insert size is controlled by reaction time.

AmpSeq Library Amplification Mix

Cat.No.BR3M105

Neoscript One Step RT-PCR Kit is an endpoint PCR qualitative detection reagent for RNA templates. Using gene-specific primers, cDNA synthesis and PCR amplification are performed consecutively in the same reaction system without requiring additional liquid additions, simplifying experimental procedures. This kit incorporates a high-temperature reverse transcriptase, novel hot-start enzyme, and RNase inhibitor, paired with an optimized buffer system, enabling amplification of fragments up to 10 kb or longer.

Product Features »

Stable and Efficient
Suitable for all types of library amplification.

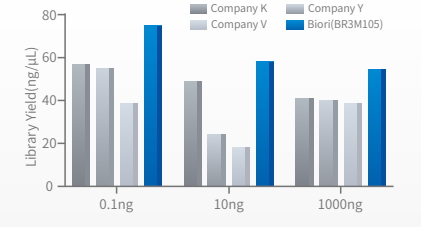
Hot-Start High Fidelity
Operates at room temperature with exceptional fidelity.

High Speed and High Yield
Fewer cycles, higher library yield.

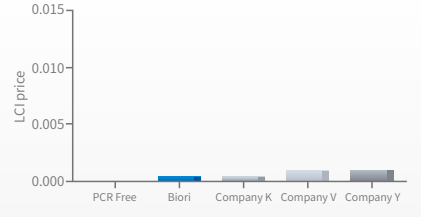
Simple and User-Friendly
Ready-to-use premix.

Product Applications »

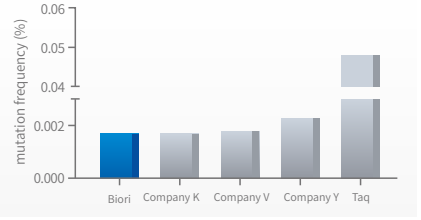
- Amplification of libraries with intact adapters.



- **Stable High Yield:** Consistent library amplification across varying input levels, achieving higher yields at identical cycle numbers.



- **Low Bias, High Uniformity:** Enhanced coverage uniformity, with LCI matching international K company standards.



- **Superior Fidelity:** High-depth sequencing of genomes with varying GC content, with calculated amplification-induced mutation rates matching fidelity levels of internationally renowned K company.

Biori ® NGS DNA Clean Beads

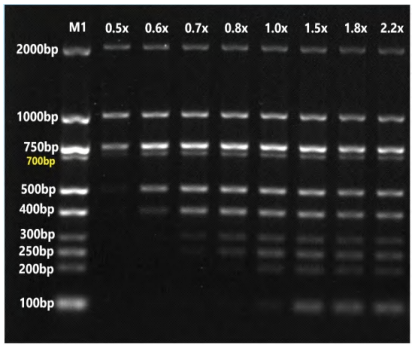
Cat.No.BR3N401

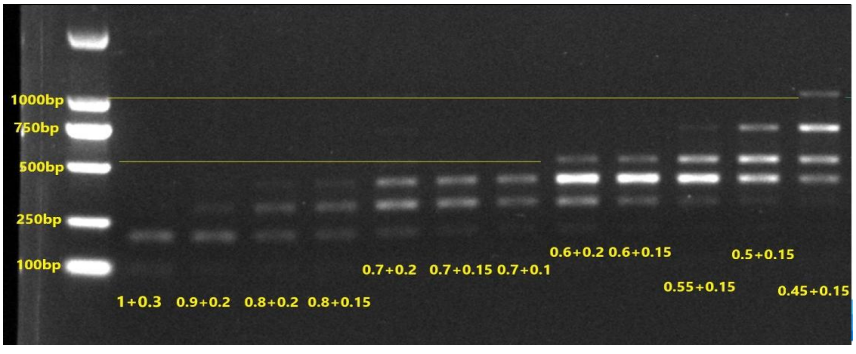
Biori® NGS DNA Clean Beads recover DNA fragments of varying molecular weights with a specific bead-to-sample ratio, which are based on superparamagnetic microparticles and an optimized buffer system.. This product is compatible with DNA and RNA library preparation kits from all major suppliers and is used in the same manner as the widely adopted AMPure XP Beads. It is suitable for both manual laboratory procedures and high-throughput processing on automated liquid handling workstations.

- **Exceptional library recovery efficiency:**
  Biori Magnetic Beads achieve recovery rates among the highest globally (greater than 85%).

Test ID	Bead Ratio	Input Sample	Recovered Concentration	Total Recovery	Recovery Rate
Manufacturer A-1	1.8×	2195ng	64.4	1932	88.02%
Manufacturer A-2	1.8×	2195ng	62.6	1878	85.56%
Manufacturer B-1	1.8×	2195ng	59	1770	80.64%
Manufacturer B-2	1.8×	2195ng	60.7	1821	82.96%
Manufacturer C-1	1.8×	2195ng	63.4	1902	86.65%
Manufacturer C-2	1.8×	2195ng	64.6	1938	88.29%
Manufacturer D-1	1.8×	2195ng	53	1590	72.44%
Manufacturer D-2	1.8×	2195ng	54.4	1632	74.35%
BR-1	1.8×	2195ng	64.2	1926	87.74%
BR-2	1.8×	2195ng	63.8	1914	87.20%

- **Superior product selection capability:** By adjusting the bead ratio, users can flexibly recover single-stranded DNA or selectively isolate target products.





03 Library Preparation Solutions

- DNA/RNA Co-Extraction
- DNA Genomics Library Construction Series
- DNA/RNA Co-Library Construction Series
- Targeted DNA/RNA Co-Library Preparation Series

Product Type	Product Name	Cat.No.	Feature
DNA/RNA Co-Extraction	Magnetic Microbiota DNA&RNA Isolation Kit V2	BR2C102	❶ Compatible with multiple sample types. ❷ Simultaneous DNA & RNA extraction. ❸ One-step lysis + two-step washing, zirconia bead-free.
DNA/RNA Co-Library Construction Series	DNA&RNA Library Prep Kit For Illumina V2	BR3C102	❶ Specifically designed for pathogen detection. ❷ Simultaneous RNA and DNA library preparation. ❸ Illumina platform.
	DNA&RNA Library Prep Kit For MGI V2	BR3C103	❶ Specifically engineered for pathogen detection. ❷ Simultaneous RNA and DNA library preparation. ❸ MGI platform.
Targeted DNA/RNA Co-Library Preparation Series	Multiplex Pathogen Targeted Library Preparation Kit for Infectious Diseases	BR3C202	❶ Specifically developed for tNGS pathogen detection. ❷ Simultaneous RNA and DNA library preparation. ❸ Illumina platform.
DNA Genomics Library Construction Series	Low input DNA Library Prep Kit For Illumina	BR3D501	❶ Developed for PGS/PGT testing, compatible with DNA metagenomics. ❷ Low-input DNA/single-cell template library preparation. ❸ Illumina platform.
	Low input DNA Library Prep Kit For MGI	BR3D502	❶ Developed for PGS/PGT testing, compatible with DNA metagenomics. ❷ Library preparation for low-input DNA/single-cell templates. ❸ MGI platform.
	Universal DNA Library Prep Kit	BR3D201	DNA Fragmentation and 3' End A-Adding in One Step (Illumina and MGI Dual Platforms)
	One-Step Tn5 DNA Library Prep Kit	BR3D301 (1ng)	❶ Tn5 transposase-based library preparation. ❷ Compatible with diverse nucleic acid samples. ❸ Low bias.
		BR3D301 (5ng)	
		BR3D301 (50ng)	

DNA/RNA Co-Extraction

Magnetic Microbiota DNA&RNA Isolation Kit v2

Cat.No.BR2C102

Product Features »

Strict Background Contamination Control

Produced in clean environments by specialized personnel; Rigorous background contamination control supports pathogen detection.

Wide Sample Compatibility

Compatible with biological fluid samples (blood, swabs, sputum, bronchoalveolar lavage fluid, etc.) and bacterial cultures.

Stable and Efficient

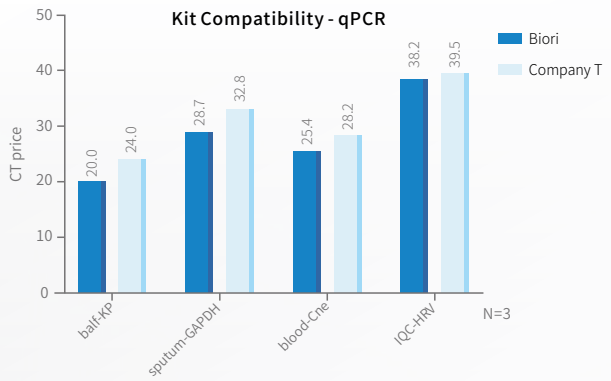
Highly efficient extraction of difficult-to-lyse microorganisms, including Gram-positive bacteria, fungi, and tuberculosis, enhancing detection rates.

Co-Extraction

Simultaneous DNA & RNA extraction, accommodating RNA viruses.

Product Applications »

- Pathogenic Microorganism Detection, Environmental Microbial Identification.
- DNA&RNA Co-Library Preparation, PCR, qPCR.
- Food Safety Testing.



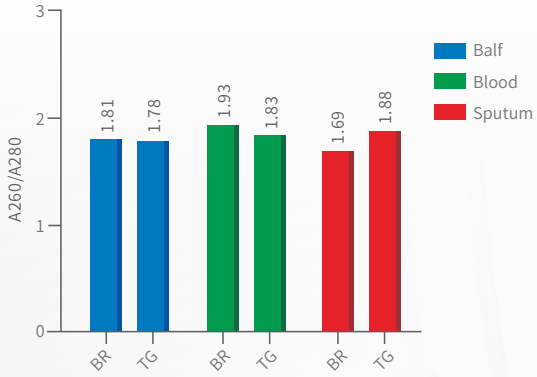
DNA & RNA Co-Extraction Experiment

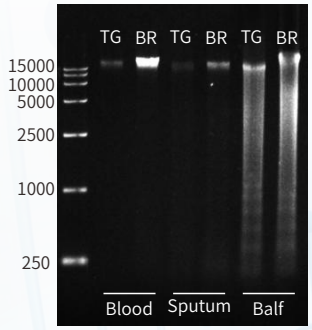
Clinical Sample Types: Bronchoalveolar lavage fluid, sputum, blood, RNA quality control material.

Pathogen Types: Klebsiella pneumoniae (bacteria), Cryptococcus neoformans (fungus), human internal reference RNA, rhinovirus (RNA virus) for DNA & RNA co-extraction.

Result Validation: Identical volumes tested via qPCR.

- **High Extraction Efficiency:** Excellent for bacteria, fungi, and viruses.
- **wide compatibility:** Superior extraction efficiency with diverse clinical sample types.





- **High Purity:** Exceptionally high extraction purity with various clinical sample types.
- **High Integrity:** Superior extraction integrity compared to competitors with different clinical sample types.

Real-world testing: Respiratory tNGS analysis is performed on various clinical samples after extraction.

Code	Sample type	Concentration ng/μL	A260/A280	tNGS Detected Pathogens
1	Secretions	19.80	2.01	G-; G+; DNA Viruses
2	Alveolar Lavage Fluid	37.30	1.81	G-; G+; DNA Viruses; Mycoplasma
3	Sputum	33.90	1.86	G-; G+; DNA Viruses; Fungi; Tuberculosis
4	Sputum	94.67	1.82	G-; G+; DNA Viruses; RNA Viruses
5	Sputum Alveolar Lavage Fluid	133.41	1.75	G-; G+; DNA viruses; fungi; RNA viruses
6	Cerebrospinal Fluid	24.24	2.15	G-; G+
7	Sputum	486.12	1.94	G-; G+; DNA viruses; RNA viruses
8	Sputum Alveolar Lavage Fluid	54.44	1.87	G-; G+; DNA viruses; Chlamydia; fungi
9	Sputum Alveolar Lavage Fluid	44.90	1.99	G-; G+; DNA viruses; fungi
10	Sputum Alveolar Lavage Fluid	1006.70	1.86	G-; G+; DNA viruses; fungi; Mycoplasma
11	Sputum Alveolar Lavage Fluid	63.70	1.85	G-; G+; DNA viruses; fungi; tuberculosis

DNA/RNA Co-Library Preparation Series

DNA&RNA Library Prep Kit For Illumina

Cat.No.BR3C102

Product Features »

Strict Background Contamination

Produced in clean environments by specialized personnel; high-purity enzymes with stringent background contamination control.

Minimal Workflow

No separate cDNA synthesis required; no intermediate purification needed. Single-tube, one-step co-library preparation for true DNA & RNA co-libraries.

Greater Efficiency

Stable library construction achievable with nucleic acids from clinical samples ranging from as low as 0.5 ng to as high as 100 ng.

Greater Sensitivity and Uniformity

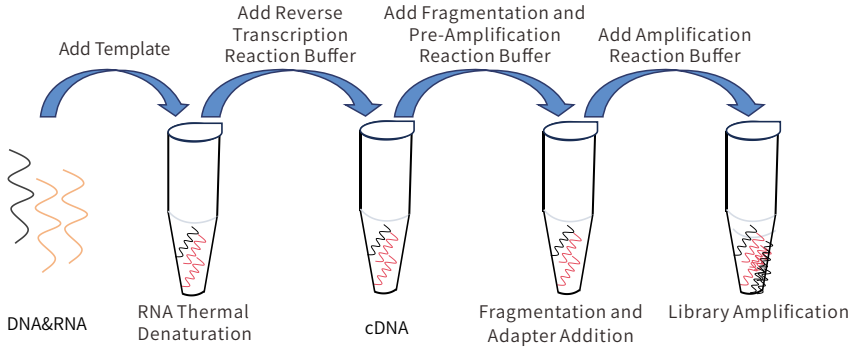
Enhanced detection of both high- and low-abundance species.

Automation

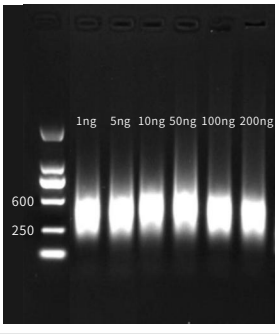
Compatible with pipetting workstations or digital microfluidic automated library preparation.

Product Applications »

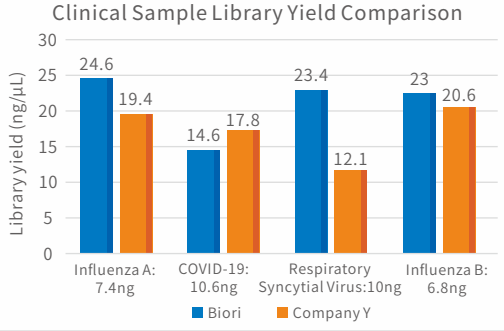
- Pathogenic Microorganism Detection, mNGS, Third-Generation Sequencing



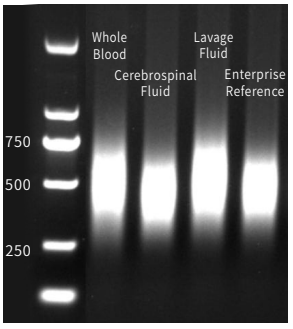
- **Minimalist Workflow:** Multi-step integrated single-tube sequential reactions eliminate intermediate purifications, simplifying complex procedures.



- Compatible with 1-200 ng template input.



- Higher library yield.



Sample Type	Template Input (ng)	Total Library (ng)	Theoretical Sequencing Pooling Data Volume	Sequencing Output Reads
Whole Blood	76ng	1112	10M	13,438,382
Cerebrospinal Fluid	0.72ng	1192	10M	13,812,644
Bronchoalveolar Lavage Fluid	224ng	1353	10M	15,100,801
Enterprise Reference Materials	0.86ng	1028	10M	12,545,691

- Compatible with different sample types.

• High concordance with qPCR for pathogen detection.

Sample Type	Sample qPCR Quantification Ct Value	Detection Status (resds)	Remarks
Positive Reference Samples	Mycoplasma pneumoniae (27.50) Bacteroides fragilis (28.46) Escherichia coli (28.17) Klebsiella pneumoniae (27.96) Pseudomonas aeruginosa (34.71) Respiratory Syncytial Virus (RSV) (30.37) COVID-19 (31.30) Human Herpesvirus 5 (HHV-5) Porcine Rhinovirus Prevotella intestinalis	Pneumococcus (1560) Staphylococcus aureus (151602) Escherichia coli (6418) Klebsiella pneumoniae (9156) Pseudomonas aeruginosa (1299) Respiratory Syncytial Virus (28) COVID-19 (14) Herpesvirus 5 (41) Atiplasma pleuropneumoniae (24823) Prevotella intestinalis (17313)	Sequencing Mode: SE75bp Sequencing Data Volume: 15M
Detection limit L1 2μL	Pneumoniae (32.90) Porcine rhinovirus Bacillus (34.19) Escherichia coli (33.34) Klebsiella pneumoniae (32.59) Pseudomonas aeruginosa (/) Respiratory syncytial virus (36.15) COVID-19 (33.79)	Pneumococcus (149) Swine-nose pathogen (154965) Staphylococcus (4288) Escherichia coli (15404) Klebsiella pneumoniae (259) Pseudomonas aeruginosa (41) Respiratory syncytial virus (1) COVID-19 (1)	

Name	Sample	Total Data Volume	Human Origin Proportion	Non-Human Origin Proportion	Microbial Share of Non-Human Origin	Viral Species	Bacterial Species	Eukaryotic Species	Total Microbial Count
B6 (Biori)	Reference L2	5,856,697	96.81%	3.19%	12.44%	2	93	4	99
B6 (Biori)	Reference P2	32,489,019	89.22%	10.78%	0.94%	1	110	12	123
Y6 (Control)	Reference L2	2,061,565	87.09%	12.91%	4.40%	4	66	6	76
Y6 (Control)	Reference P2	22,976,622	96.70%	3.30%	0.35%	0	75	14	89

Name	qPCR Positive	Escherichia coli	Candida albican	Mycoplasma pneumoniae	Klebsiella pneumoniae	Pseudomonas aeruginosa	Respiratory Syncytial Virus	COVID-19
B6 (Biori)	Mycoplasma pneumoniae (32.9) Candida albicans (34.19) Escherichia coli (33.34) Klebsiella pneumoniae (32.59) Pseudomonas aeruginosa (36.45) Respiratory syncytial virus (RSV) (36.15) COVID-19 (33.79)	21	776	20942	75	7	12	9
B6 (Biori)	Mycoplasma pneumoniae (27.5) Staphylococcus aureus (28.46) Escherichia coli (28.17) Klebsiella pneumoniae (27.96) Pseudomonas aeruginosa (34.71) Respiratory Syncytial Virus (RSV) (30.37) COVID-19 (31.3)	6418	151602	1560	9155	1299	28	41
Y6 (Control)	Pneumococcus (32.9) Staphylococcus aureus (34.19) Escherichia coli (33.34) Klebsiella pneumoniae (32.59) Pseudomonas aeruginosa (36.45) Respiratory Syncytial Virus (RSV) (36.15) COVID-19 (33.79)	6	57	11352	35	15	6	4
Y6 (Control)	Pneumococcus (27.5) Staphylococcus aureus (28.46) Escherichia coli (28.17) Klebsiella pneumoniae (27.96) Pseudomonas aeruginosa (34.71) Respiratory syncytial virus (30.37) COVID-19 (31.3)	3231	9787	676	4531	796	15	28

• Sequencing results from different types of authentic clinical samples.

Sample	Split Reads	Human Proportion	Non-Human Proportion	Microbial Share of Non-Human	Viral Count	Bacterial Count	Eukaryotic Count	Total Microbial Count	Viral Species	Bacterial Species	Eukaryotic Species	Total Microbial Count
Sputum	13,794,411	99.77%	0.23%	19.76%	4	6,053	103	6,160	1	138	5	144
Bronchoalveolar Lavage Fluid	14,537,695	99.81%	0.19%	18.46%	0	3,962	1,174	5,136	0	50	9	59
Swab	12,471,602	76.12%	23.88%	23.52%	9	647,533	52,929	700,471	3	313	24	340
Blood	10,608,211	98.72%	1.28%	14.16%	0	10	19,270	19,280	0	9	17	26
Sputum	12,162,397	99.68%	0.32%	26.79%	7	10,436	30	10,473	1	153	5	159
Swab	15,568,578	66.11%	33.89%	19.42%	5	661,018	363,427	1,024,450	3	303	41	347

Targeted DNA/RNA Co-Library Preparation Series

Multiplex Pathogen Targeted Library Construction Kit for Infectious Diseases

Cat.No.BR3C202

Product Features »

Strict Background Contamination Control

Produced in clean environments by specialized personnel; high-purity enzymes ensure strict control of background contaminants.

Minimal Workflow

No separate cDNA synthesis step is required; intermediate purification optional. Single-tube, one-step DNA & RNA co-targeting library preparation.

Enhanced Efficiency

Compatible with diverse clinical samples including bronchoalveolar lavage fluid, cerebrospinal fluid, sputum, and swabs. Efficient library construction achievable with input ranging from 1ng to 500ng.

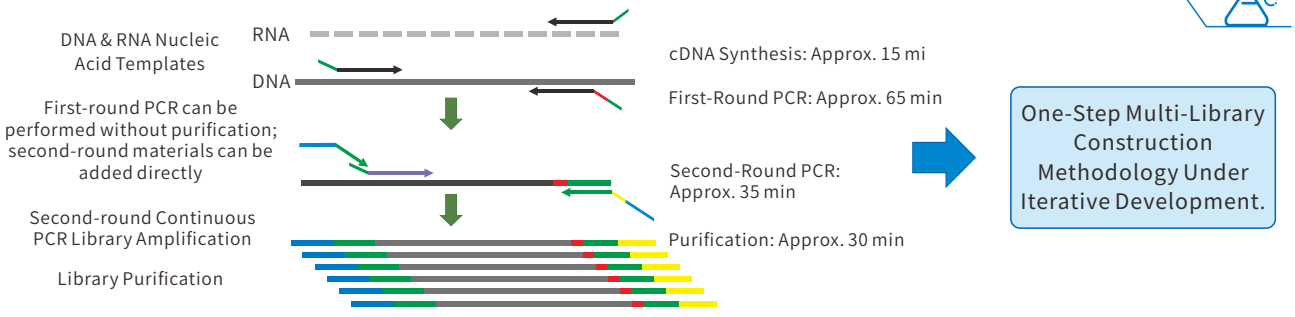
Compatible with Automated Library Construction

Customized Multiplex Amplification Library Preparation Services.

Product Applications »

- Pathogen Targeted Sequencing
- Methylation Targeted Sequencing
- Other Targeted Sequencing

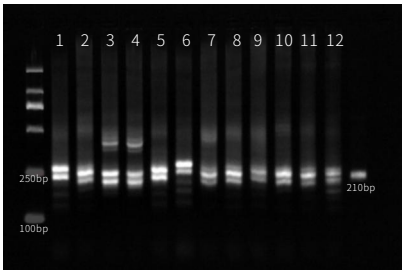
• Biori tNGS library construction principle: multi-primer chain Amplification Method.



No.	Syndrome	Detection Range				
		Bacteria	Fungi	Viruses	Others (Parasites, Mycoplasma, etc.)	Drug resistance gene
1	Respiratory Tract	105 types	23 types	71 types	15 types	17 types
2	Bloodstream Infection	72 types	22 types	17 types	5 types	/
3	Neurological Infection	67 types	26 types	45 types	22 types	/
4	Generalized Infection	124 types	26 types	106 types	39 types	21 types

- **The above syndrome products can be customized according to customer requirements:** adding or removing pathogen types, or adding/removing antimicrobial resistance gene detection.

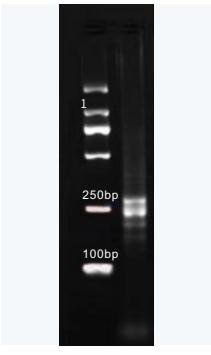
• Real-World Detection: 300+ multiplex tNGS assays, undeterred by primer dimers.



• Real-World Testing: Respiratory tNGS performed on various clinical sample types post-extraction.

Category	FS026	BF015	SP015	SP028	BF032	CF051	SP050	BF043	BF033	PU015	BF026	
	Secretions	Bronchoalveolar Lavage Fluid	Sputum	Sputum	Bronchoalveolar Lavage Fluid	Cerebrospinal Fluid	Sputum	Bronchoalveolar Lavage Fluid	Bronchoalveolar Lavage Fluid	Bronchoalveolar Lavage Fluid	Bronchoalveolar Lavage Fluid	Negative Control Materials
Total Reads	1895714	1823835	677526	695989	1366495	2934966	913226	1070761	1312804	1437945	1739851	2992934
low_quality	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
human	2.81%	57.38%	5.20%	7.09%	23.14%	0.18%	63.20%	45.33%	22.60%	55.00%	47.82%	9.02%
primer|adapter	21.84%	9.48%	3.72%	4.26%	17.80%	19.58%	9.67%	17.25%	23.80%	5.07%	12.23%	16.42%
Target	75.03%	32.97%	90.95%	88.58%	58.81%	79.85%	27.05%	37.24%	53.35%	39.87%	39.79%	74.22%
unmap	0.33%	0.17%	0.12%	0.07%	0.25%	0.39%	0.09%	0.18%	0.26%	0.06%	0.16%	0.34%

• Unpurified system prevents aerosol contamination.



- Purified system: Purify first-round amplification products before library amplification.

- Unpurified system: Use 30% and 50% of products for second-round library amplification.

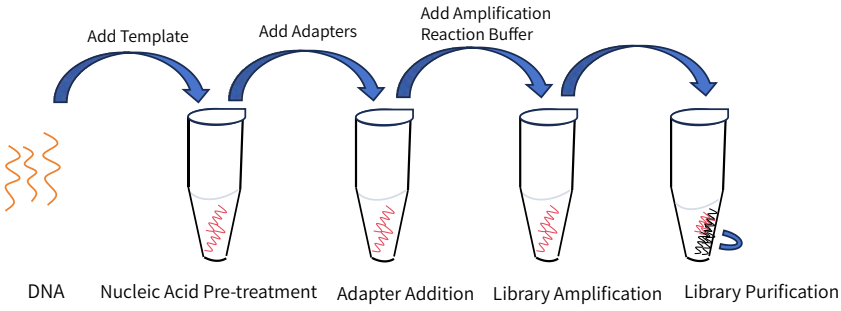
Pathogens (qPCR CT values)	Experiment ID		
	1	2	3
	Purified	30% amplified product	50% amplified product
	Positive control	Positive control	Positive control
	100k reads normalized data (0.1M)		
Mycoplasma pneumoniae (30.4)	430	689	716
Escherichia coli (31.5)	1923	184	133
Klebsiella pneumoniae (31.4)	3316	1923	1799
Pseudomonas aeruginosa (40)	259	279	241
SARS-CoV-2 (31.9)	100	68	48
Candida albicans (31.8)	1991	1467	766
External control (33)	55685	8565	6745

DNA Gene Construction Library Series

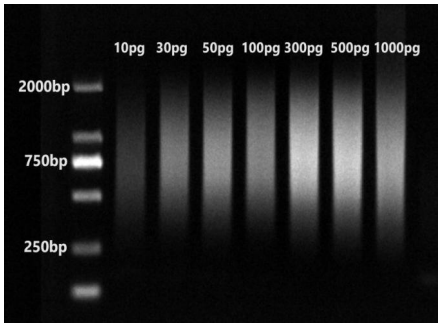
Low input DNA Library Prep Kit For Illumina

Cat.No.BR3D501

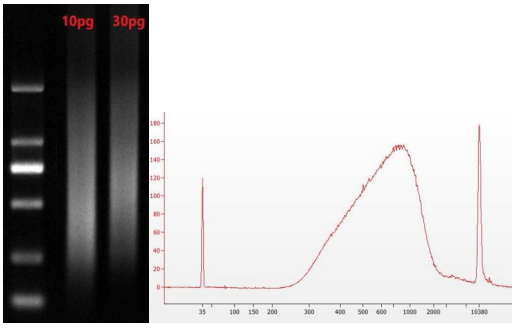
Minimalist Workflow: Multi-step integrated single-tube reaction with no intermediate purification, eliminating complex operations.



Library Fragment Distribution: 250–2000 bp.



Biori

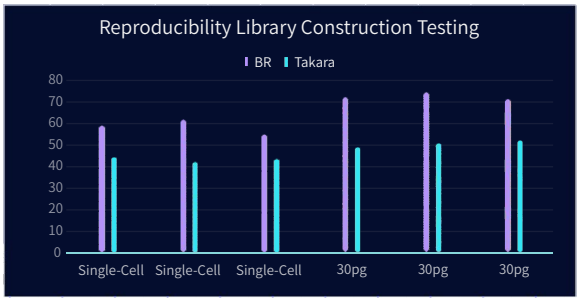


Takara

- Compatible with template inputs ranging from 10 pg to 1000 pg.

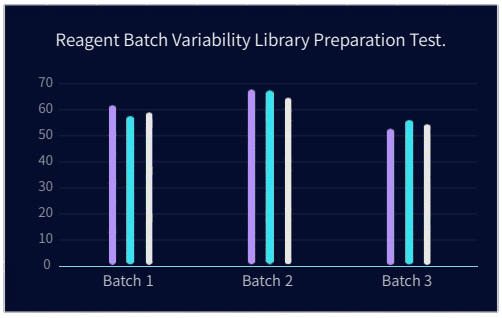
Cell Sample Reproducibility Library Construction Testing.

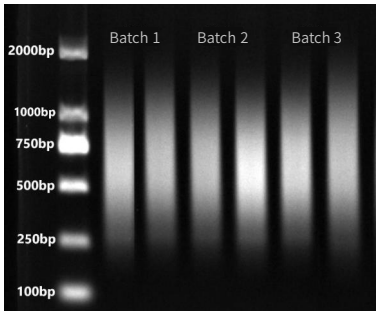
Template	BR (ng/μL)	CV	Takara (ng/μL)	CV
Single-Cell	59.4	6.04%	44.8	2.99%
Single-Cell	62.4		42.2	
Single-Cell	55.3		43.6	
30pg	73.2	2.17%	49.5	2.95%
30pg	75.4		51.2	
30pg	72.3		52.5	



- Higher library yield from cell templates and nucleic acid templates.

Reagent Batch Variability Library Preparation Test.





- Excellent repeatability across different reagent batches.

Sequencing Performance Comparison (vs. Competitors Using Same Methodology)

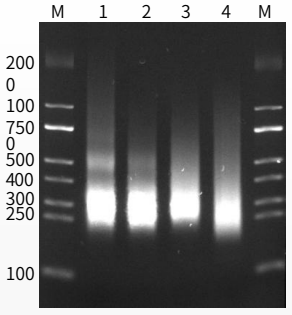
Kit	Sample	Library Concentration	Library Quantification	Unique reads	Mean Depth	GC	Map ratio	Dulication ratio
Takara	Cell 1	29.6	750bp	2552608	5.589	47.26	99.3	5.19
BR		68.5	750bp	6211305	11.021	41.44	98.2	13.57
Takara	Cell 2	27	750bp	6725363	11.378	46.95	99.43	11.52
BR		58.6	750bp	6755430	11.509	40.79	98.76	12.71
Takara	Cell 3	28.6	750bp	17363283	18.107	47	99.29	15.25
BR		55.6	750bp	3745574	5.605	40.65	99.36	11.35

- Sequencing data metrics are largely comparable to competitors.

Sequencing data metrics are largely comparable to competitors.

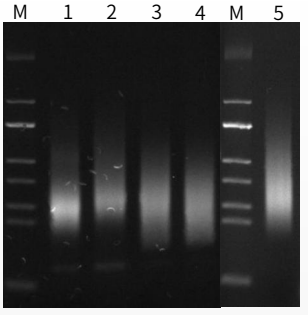
Library Construction Methodology	Sample	Unique reads	Mean Depth	GC	Map ratio	Dulication ratio
MDA Amplification + DNA Library Construction Kit	S1	1156608	2.289	46.26	71	4.86
	S2	1610368	3.141	47.01	74.19	5.44
	S3	1991512	3.744	45.28	71.83	4.73
BR3D501 (DNA Micro Library Construction Kit)	S1	3079412	6.7	39.16	97.93	9.72
	S2	3786855	7.196	39.82	98.19	15.26
	S3	3860131	7.302	39.78	98.76	11.36

- Sequencing Data Map ratio significantly higher than traditional library preparation methods.
- Average GC content more closely aligned with GRCh38.



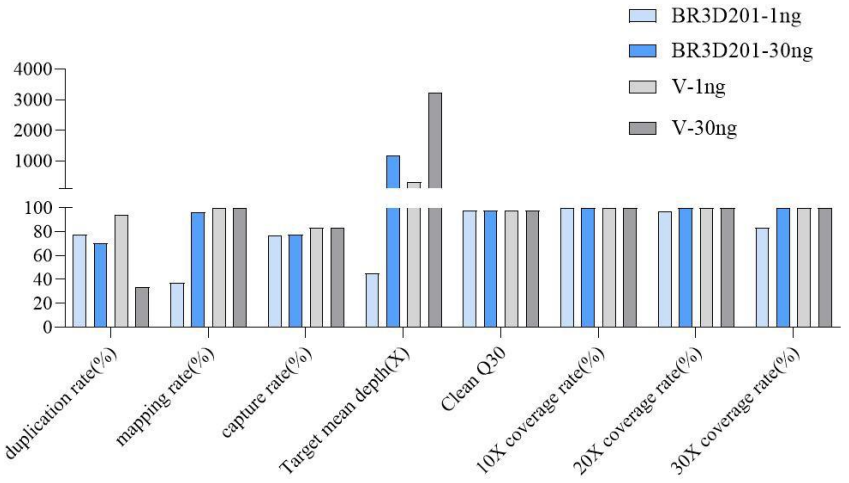
M:DL 2 , 000 marker.
1:0.1 ng of 293T gDNA was fragmented for 7 minutes.
2:1ng 293T gDNA fragmenting for 7 minutes.
3:10 ng of 293T gDNA fragment for 7 minutes.
4:1000ng 293T gDNA fragmenting for 7 minutes.

- Compatible with a wide range of input amounts.

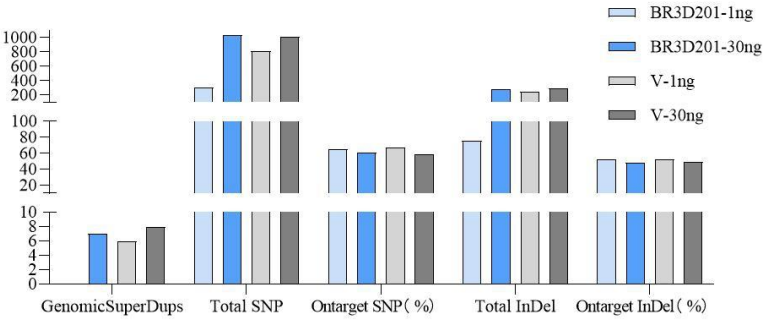


M: DL 2,000 markers
1: BR3D201 library construction with 1 ng pan-cancer standard.
2: BR3D201 library construction with 30 ng pan-cancer standard.
3: Competitor library preparation with 1 ng pan-cancer standard.
4: Competitor library preparation with 30 ng pan-cancer standard.
5: Pan-cancer standard library + hybridization capture.

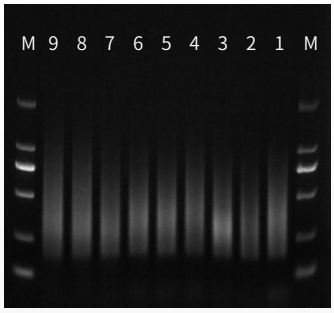
- Fragmentation efficiency is comparable to competitors.



- Tumor hybridization capture data aligns with competitors.

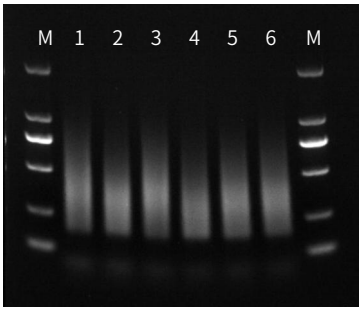


- The tumor hybridization capture assay demonstrates a lower false-positive rate and superior detection of SNPs and InDels.

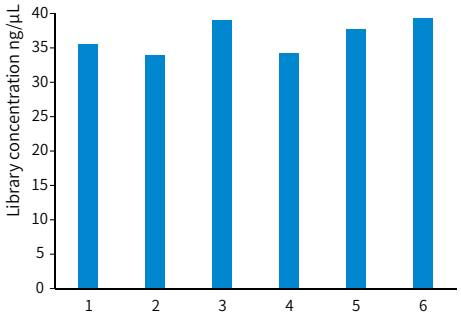


M:DL 2 , 000 marker
1-3:1ng human 293T DNA
4-6:5ng human 293T DNA
7-9:50ng human 293T DNA

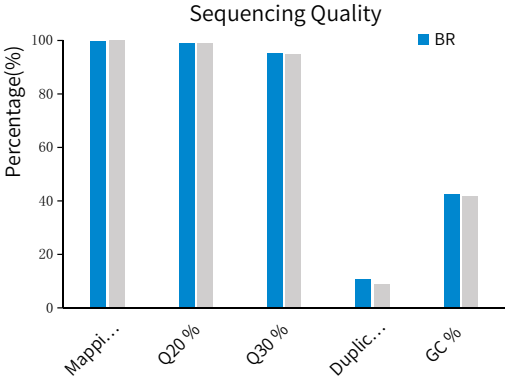
- One-Step Tn5 DNA Library Prep Kit enables library construction from 1ng/5ng/50ng nucleic acids, yielding a library with a distinct main peak and consistent length distribution between 200-1000bp.

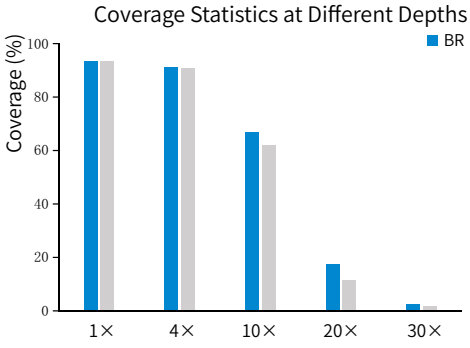


M: DL 2,000 marker
1: 1 ng human 293T DNA
2: 1 ng mouse DNA
3: 1 ng Pseudomonas aeruginosa DNA
4: 1 ng Clinical sample DNA
5: 1 ng λ DNA
6: 1 ng 1-12K length amplicon



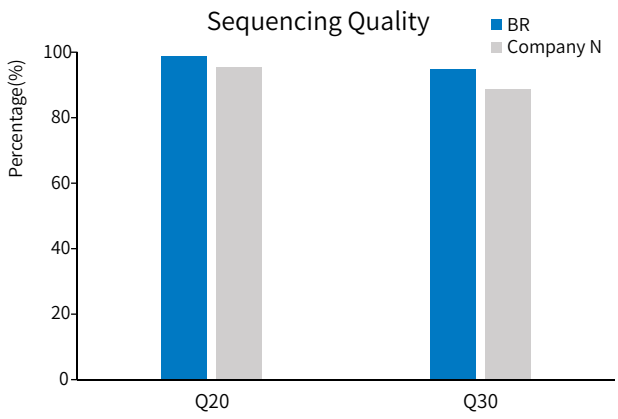
- The One-Step Tn5 DNA Library Prep Kit demonstrates universal compatibility and high efficiency with nucleic acids from a wide range of sources and species.





	Mapping rate %	Q20 %	Q30 %	Duplicate %	GC %	1×	4×	10×	20×	30×
BR	99.85	98.94	95.24	10.8	42.28	93.5	91.11	66.95	17.43	2.57
Company N	99.86	98.84	94.94	8.67	41.86	93.31	90.91	62.03	11.39	1.63

- The tumor hybridization capture assay demonstrates a lower false-positive rate and superior detection of SNPs and InDels.



Product	Company N	BR
Viral Count	159	162
Bacterial Count	139441	135497
Eukaryotic Count	3342	5225
Total Microbial Count	142941	140884
Viral Species	4	4
Bacterial Species	284	308
Eukaryotic Species	21	22
Total Microbial Count	309	334

- Library preparation using clinical samples, metagenomic sequencing analysis.
- Data normalization shows BR pathogen detection rates consistent with competitors.

Pathogens	Company N	BR	Pathogens	Company N	BR
Neisseria subflava	65734	59097	Tannerella forsythia	176	175
Haemophilus influenzae	19502	19876	Terrincoloides variabilis	168	133
Aspergillus flavus	2540	3994	Human gammaherpesvirus 4	154	157
Mycobacterium tuberculosis	2172	1479	Granulicatella adiacens	118	109
Prevotella melaninogenica	2040	3291	Actinomyces durangensis	105	99
Moraxella encephalitidis	1402	1294	Candida albicans	100	128
Veillonella dispar	1337	2033	Porphyromonas gingivalis	99	120
Pseudomonas aeruginosa	664	465	Bifidobacterium dentium	86	52
Streptococcus pneumoniae	660	667	Dolosigranulum pigrum	75	98
Moraxella nonliquefaciens	544	677	Campylobacter rectus	70	58
Prevotella tannerae	308	363	Treponema denticola	63	81
Rothia mucilaginosa	305	280	Veigya	60	50
Bacteroides heparinolyticus	240	281	Gemella haemolysans	58	87
Lautropia mirabilis	224	193	Escherichia coli	55	86
Cutibacterium avidum	216	106	Clostridium moorei	55	66
Pathogens	Company N	BR	Pathogens	Company N	BR
Selenomonas noxia	50	34	Xylanimonas cellulolytica	13	12
Desulfomicrobium orale	47	46	Dialister invisus	13	17
Eikenella corrodens	44	41	Slackia exigua	11	10
Capnocytophaga granulosa	43	92	Parvimonas micra	11	12
Olsenella uli	37	50	Megasphaera micronuciformis	11	10
Catonia segmentans	36	0	Fusobacterium nucleatum	10	14
Lancefieldella parvula	36	45	Eubacterium gingivalis	10	4
Leptotrichia wadei	33	27	Anaerorhabdus furcosa	9	11
Difficilis biforis	30	41	Cardiobacterium valvarum	9	13
Davisella invisibilis	29	32	Cutibacterium acnes	4	20
Kingella denitrificans	25	33	Rhodococcus ruber	1	3555
Piscibacter invisibilis	21	10	Acinetobacter bereziniae	0	20
Streptococcus anginosus	19	21	Bacillus licheniformis	0	11
Abiotrophia defectiva	19	18	Corynebacterium durum	0	39
Phocaeicola abscessus	14	13	Delftia acidovorans	0	67

Corporate Mission

Protecting Life and Health, Creating a Better Life

Corporate Vision

Leader in the Life Sciences Field

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Pursuing Excellence in Quality Providing Prompt and Thorough Service

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