TRANSGEN BIOTECH

Next Generation Sequencing

Next Generation Sequencing

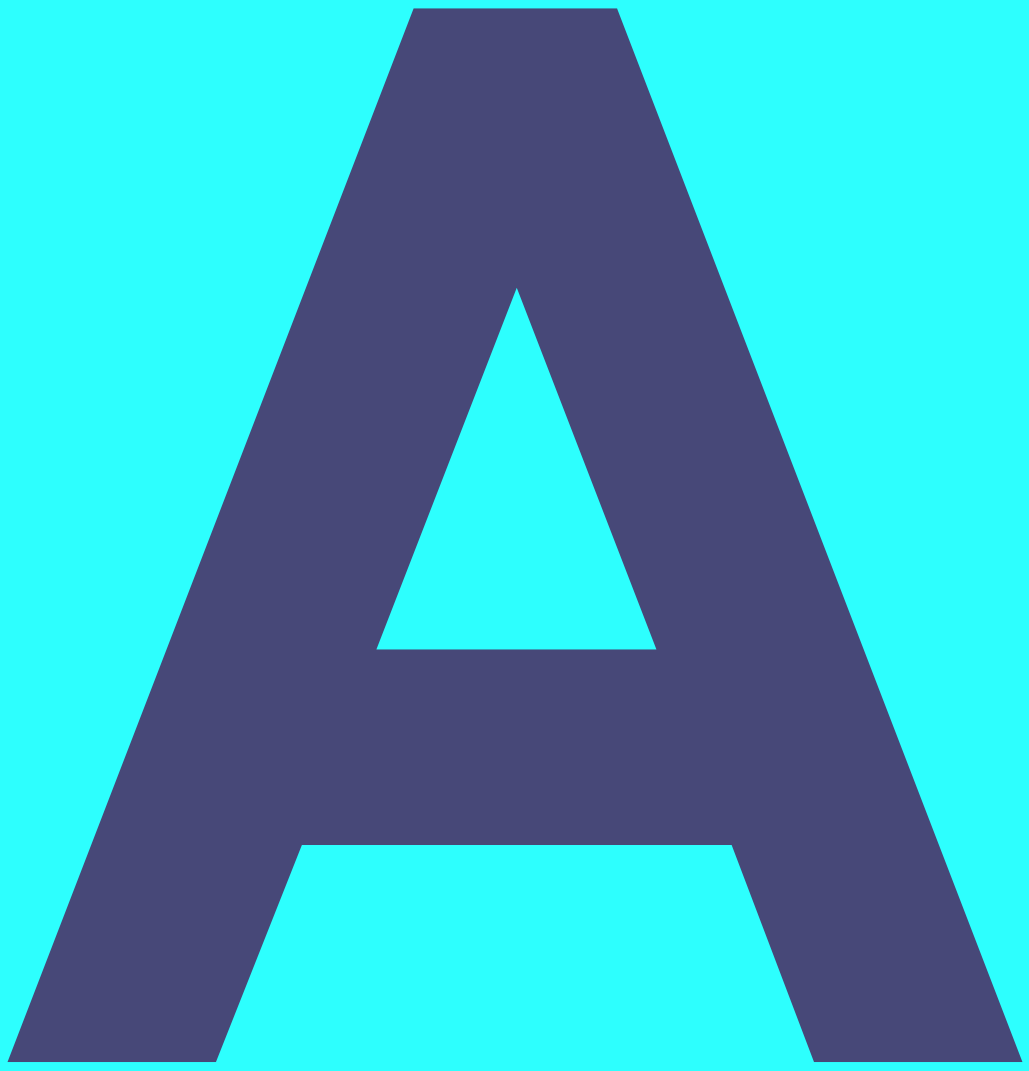
Providing Innovative Reagents for Life Sciences since 2006

CONTEN

NTS

TRANSGEN

DNA Library Prep



01 Library Preparation using Transposase

*Trans*NGS® Tn5 DNA Library Prep Kit for Illumina® (for 5 ng/50 ng/1 ng DNA) (Patent Pended)

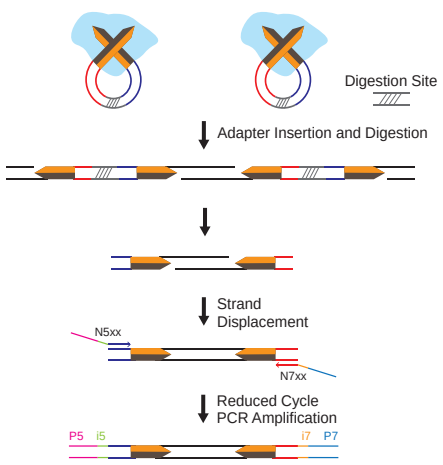
Features

- Easy operation and time-saving.
- High efficiency with minimal amount of input DNA.

Product Details

Construct libraries suitable for the Illumina high-throughput sequencing platform from genomes (animal, plant, fungus, bacterium, archaea, double-stranded DNA virus, etc.), plasmids, and PCR amplicons (greater than 300 bp).

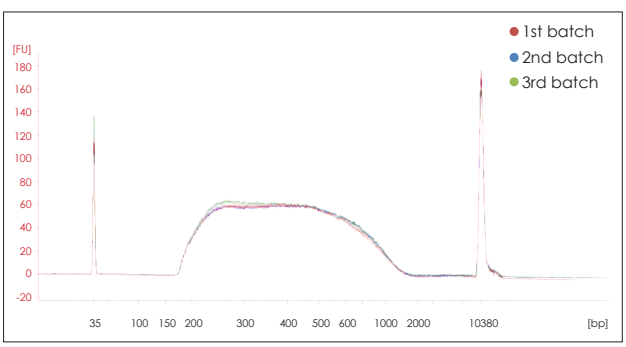
Schematic Diagram of Library Preparation

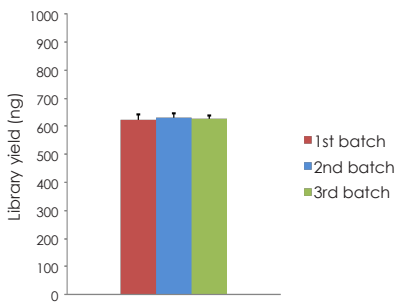


High Stability

Whole-genome libraries are constructed from 5 ng of human genomic DNA using kits of different batches. After 9 PCR cycles, the products are purified using 1.0× DNA magnetic beads (TransGen, EC401) (without size selection). The libraries are then analyzed using an Agilent High Sensitivity DNA chip, showing consistent fragment size distributions, primarily ranging between 200–2000 bp. The library concentrations are measured by Qubit, demonstrating consistent yields across batches. The uniformity in peak profiles and yields confirms the high batch-to-batch consistency of the product.

Peak Patterns and Yields Across Library Batches

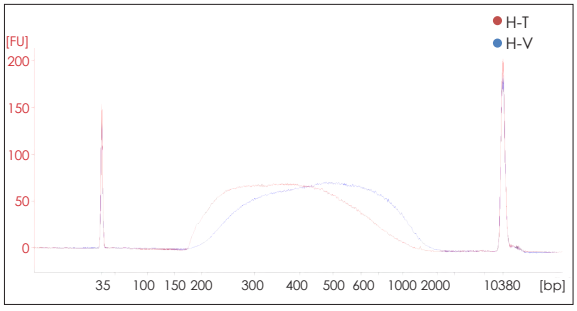


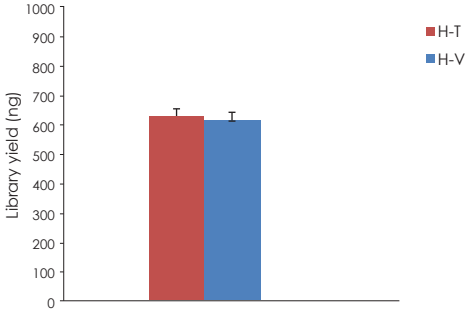


Comparison with Competitors

Using 5 ng of human genomic DNA as input, whole-genome libraries are prepared with TransGen and Competitor V's products, followed by library sequencing and analysis. The results demonstrate that TransGen's product exhibits comparable performance to the competitor in terms of library peak profile, yield, sequencing data quality, GC distribution, and correlation.

Library Peak Patterns and Yields

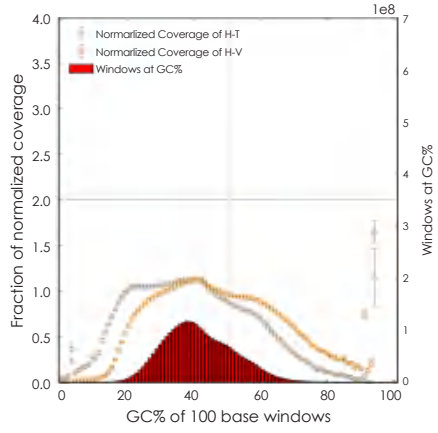




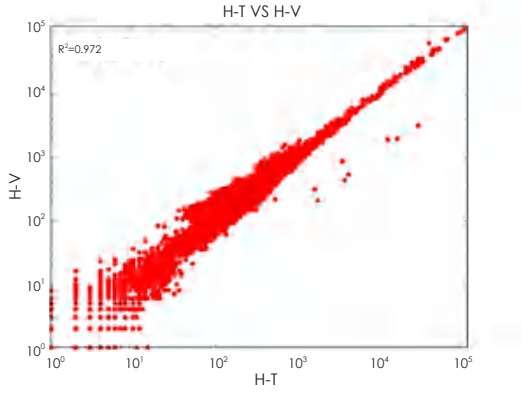
Sequencing Data Quality

Sample	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Coverage-1× (%)	Coverage-4× (%)	Duplication Rate (%)	Depth (×)
H-T	98.14	94.42	39.51	99.8	90.67	53.04	16.67	4.62
H-V	97.84	93.68	40.80	99.74	90.70	53.64	17.48	4.68

GC Distribution



Relativity



*Trans*NGS® Tn5 Plasmid DNA Library Prep Kit for Illumina® (for ≤3 ng Plasmid DNA)

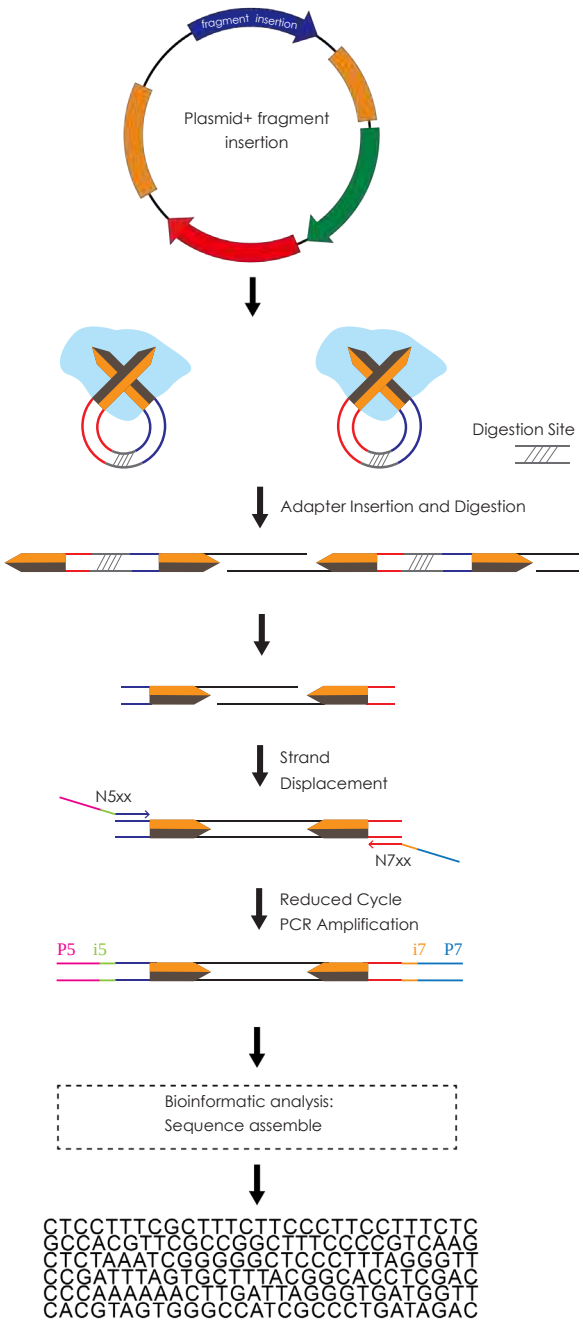
Features

- Next Generation Sequencing.
- Fast library preparation.
- User friendly.
- High-through, 96×96 plasmids sequencing at once.

Product Detail

*Trans*NGS® Tn5 Plasmid DNA Library Prep Kit for Illumina® contains buffers and enzymes to generate next generation sequencing libraries for Illumina® high-throughput sequencing platform for purified plasmid DNA. This kit is suitable for vector construction and screening of point mutation.

Schematic Diagram of Library Preparation



02 Conventional Library Preparation

*Trans*NGS® DNA Library Prep Kit for Illumina® (KP201)

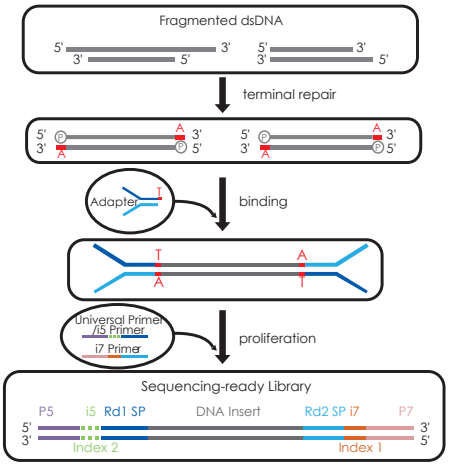
Features

- High Library Conversion Efficiency
- Suitable for diverse sample types

Applications

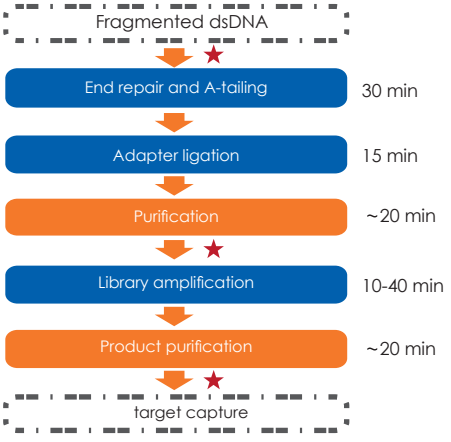
- Whole genome sequencing.
- Target gene sequencing.
- Exon sequencing / other targeted capture sequencing.
- Metagenomic sequencing.
- Co-immunoprecipitation sequencing.

Schematic Diagram of Library Preparation



The i5 position is indicated by a dotted line, which means that some libraries do not have this Index

Workflow Diagram



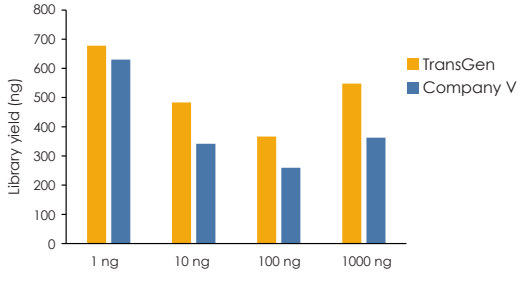
not included in the kit

★ Steps where fragments size selection can be performed

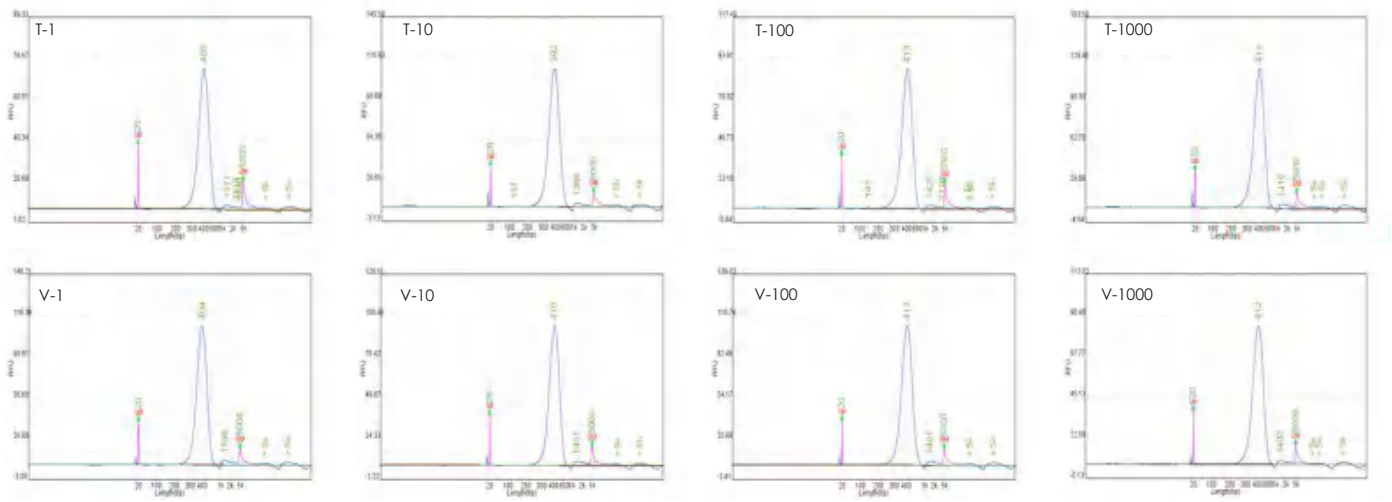
Comparison with Competitors

Sonicated DNA from HeLa cells is used for library construction with input amounts of 1 ng, 10 ng, 100 ng, and 1000 ng, employing TransGen and Company V's DNA library preparation kits. The TransGen kit demonstrates superior library yield compared to the competitor's product, while the library peak profiles are consistent between the two kits. Sequencing analysis reveals no significant differences between TransGen and the competitor in key metrics such as Q20/Q30 scores, GC content, duplicate rates, alignment rates, and GC distribution. The sequencing results show a high correlation ($R^2 > 0.95$) between the two kits.

Library Yield (after fragments selection)



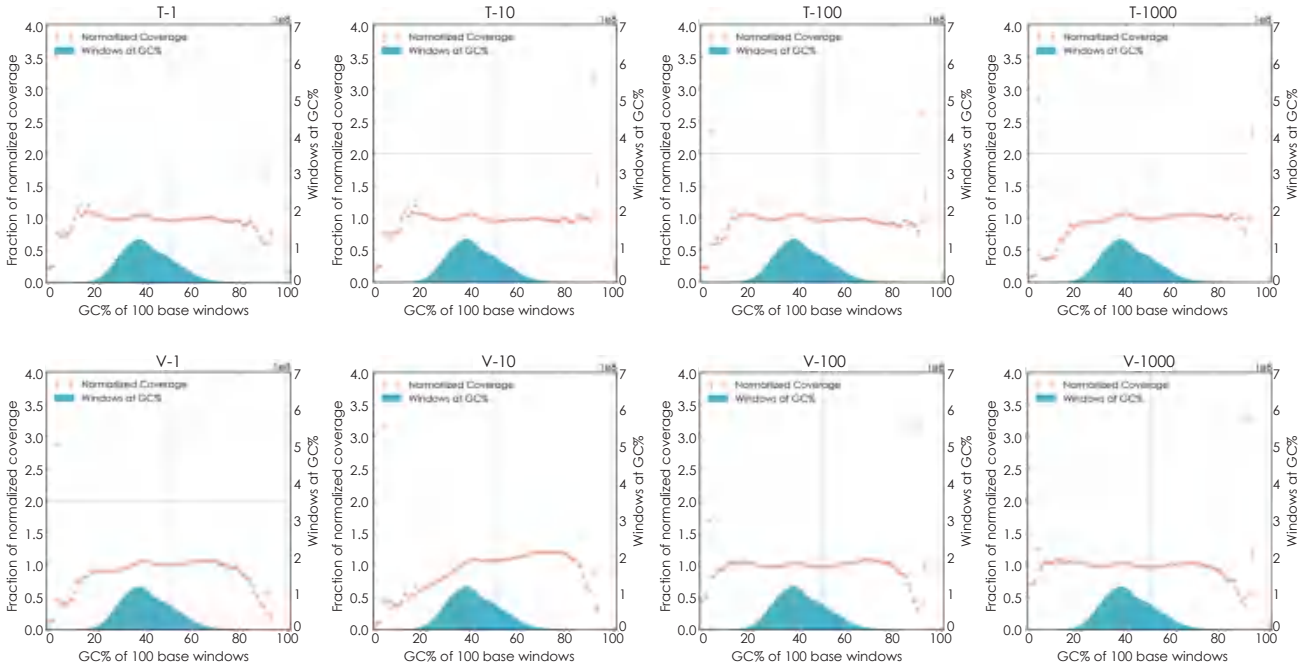
Library Peak Profile



Sequencing Data Quality

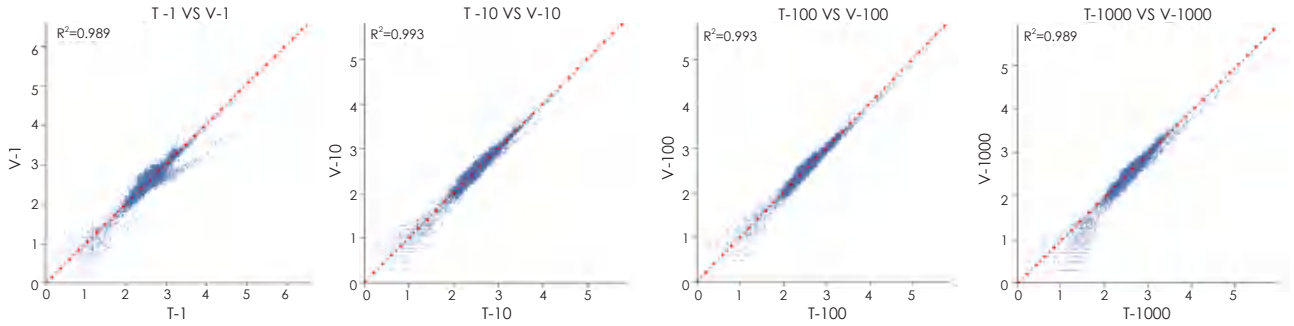
Sample	Error Rate(%)	Q20(%)	Q30(%)	GC Content(%)	Optical/PCR duplicate(%)	Unmapped reads(%)
T-1	0.03	96.17	91.18	42.11	25.38	0.71
T-10	0.03	97.85	92.78	43.26	20.22	0.63
T-100	0.03	97.93	93.71	40.63	17.89	0.53
T-1000	0.03	97.67	92.14	40.72	17.20	0.67
V-1	0.03	96.45	90.79	42.82	24.37	0.64
V-10	0.03	97.33	92.86	43.42	20.23	0.54
V-100	0.03	97.60	93.22	41.00	16.36	0.46
V-1000	0.03	97.45	92.83	40.92	17.50	0.45

GC Distribution



Chromosomal Coverage Depth Distribution

Correlation Analysis



*Trans*NGS® DNA Library Prep Kit for MGI® (KP221)

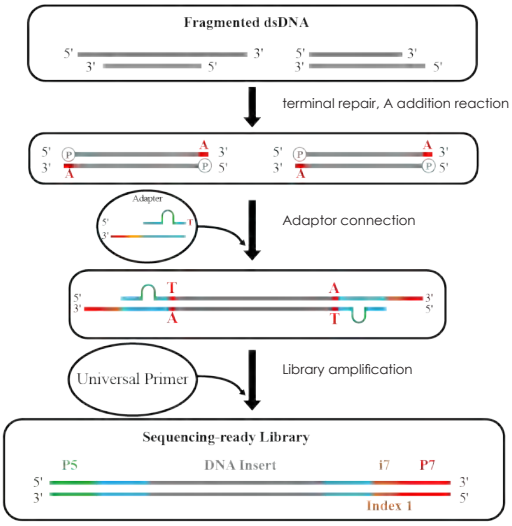
Features

- Suitable for diverse sample types
- High Library Conversion Efficiency
- High-quality sequencing data

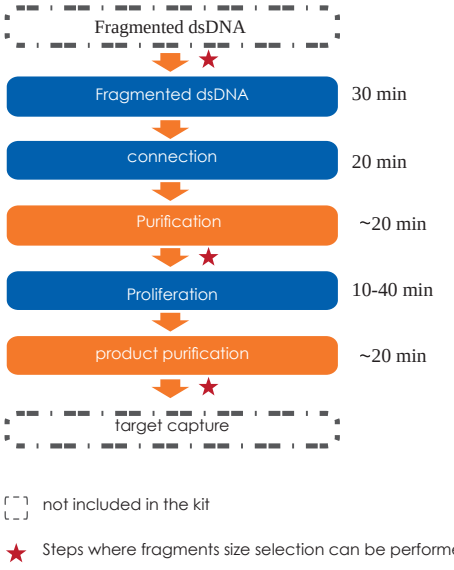
Applications

- Whole genome sequencing
- Target gene sequencing
- Exon sequencing / other targeted capture sequencing
- Metagenomic sequencing
- Co-immunoprecipitation sequencing

Schematic Diagram of Library Preparation



Workflow Diagram

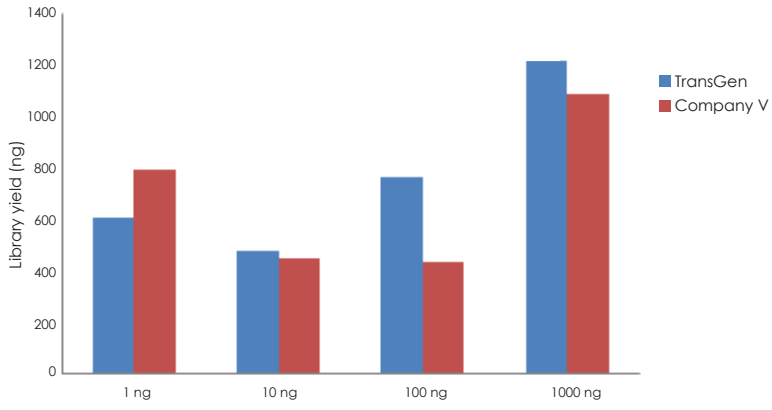


Comparison with Competitors

(1) Library Yield with Different Input Amounts

Using TransGen and Company V's kits, fragmented dsDNA derived from human HeLa cells is subjected to library construction with identical PCR cycles across varying input amounts (1 ng to 1 μg). Results demonstrate that the TransGen kit achieve consistently high library preparation efficiency across the entire input range (1 ng–1 μg).

Library Yield (after fragments selection)



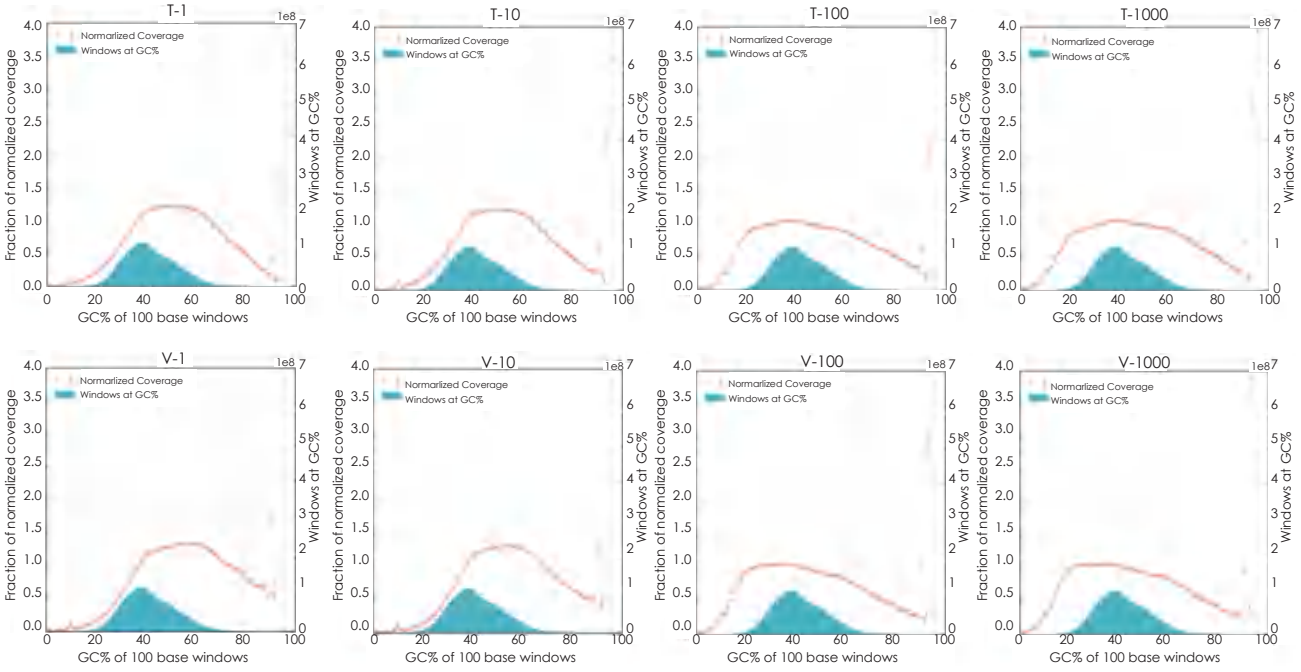
(2) comparison of sequencing result

TransGen and Company V products were used for dsDNA library construction using different amount of fragmented Hela cell DNA. The results showed that the quality of sequencing result, GC distribution and correlation generated by TransGen is as good as competing products.

Comparison of sequencing results

Sample	Clean reads	Optical/PCR duplicate(%)	Unmapped reads(%)	Total mapped(%)	Multiple mapped(%)	Uniquely mapped(%)	Q20(%)	Q30(%)	GC Content(%)
T-1	42720938	1.60	0.54	97.86	5.75	92.11	96.12	90.99	43.11
T-10	42715766	0.29	0.50	99.21	5.79	93.41	96.19	91.14	43.19
T-100	42720042	0.09	0.92	98.98	5.13	93.85	96.43	91.66	40.78
T-1000	42720058	0.11	0.85	99.04	5.21	93.83	96.54	91.89	41.02
V-1	42711428	2.14	0.48	97.38	6.00	91.38	96.27	91.34	44.00
V-10	42710566	0.29	0.44	99.26	6.09	93.18	95.96	90.63	43.90
V-100	42710232	0.10	0.98	98.92	5.10	93.83	96.15	91.04	40.49
V-1000	42704112	0.09	0.98	98.92	5.06	93.86	96.06	90.82	40.48

GC Distribution



03 Fragmentase Library Preparation

*Trans*NGS® Fragmentase DNA Library Prep Kit for Illumina® (KP231)

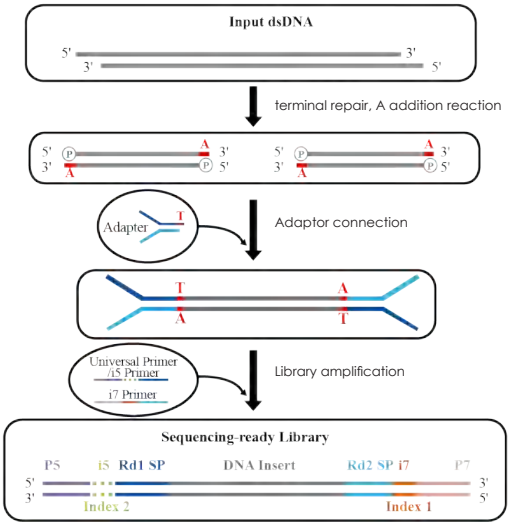
Features

- Suitable for diverse sample types
- High library conversion efficiency

Applications

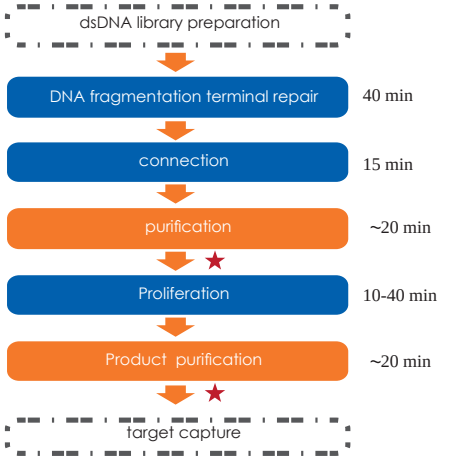
- Whole genome sequencing
- Target gene sequencing
- Exon sequencing / other targeted capture sequencing
- Metagenomic sequencing

Schematic Diagram of Library Preparation



The i5 position is indicated by a dotted line, which means that some libraries do not have this Index

Workflow Diagram



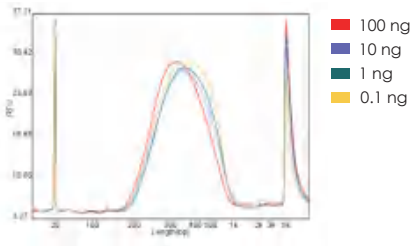
not included in the kit

★ Steps where fragments size selection can be performed

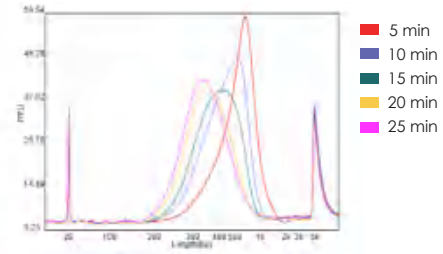
Comparison with competitors

Genomic DNA from HeLa cells is used to construct libraries with TransGen and Company V kits separately. Results show that libraries generated by the TransGen kit exhibit consistent peak profiles across input amounts (0.1 ng, 1 ng, 10 ng, and 100 ng). When fragment size is modulated by adjusting fragmentation time (50 ng input), the TransGen kit demonstrates more sensitive peak profile shifts compared to Company V's. Additionally, at inputs of 1 ng, 10 ng, 100 ng, and 1000 ng, the TransGen kit achieves comparable or superior library yields relative to Company V.

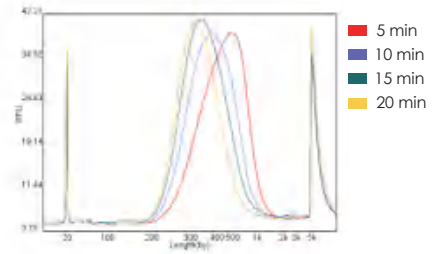
With Different Input Amounts



With Different Fragmentation Time

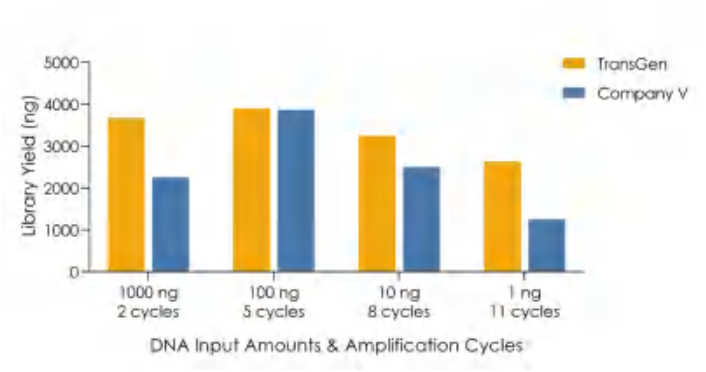


TransGen



Company V

Library Yield with Different Input Amounts



Sequencing Data Quality

Comparative evaluation of TransGen and Company V kits for library construction performance across diverse animal, plant, and microbial samples demonstrates comparable performance in key metrics, including sequencing quality, alignment rate, coverage uniformity, and GC distribution.

Animal Samples

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-Human Blood	97.68	94.30	40.62	99.53	24.10	6.73	6.37	95.87	79.33
V-Human Blood	94.95	94.75	41.22	99.70	23.70	6.62	6.33	95.39	77.20
T-Mouse	97.26	93.05	40.95	99.29	27.30	8.51	7.83	92.86	82.64
V-Mouse	94.68	93.42	41.15	99.49	29.87	8.24	7.46	92.39	79.81

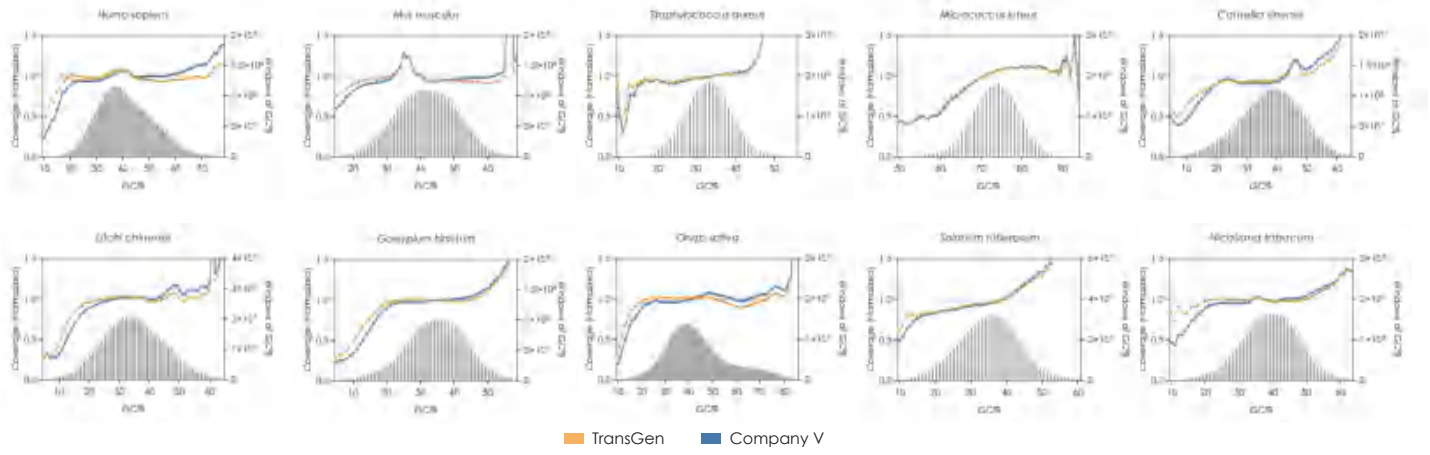
Microorganism

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-*Staphylococcus aureus*	98.60	93.68	32.99	88.74	22.74	2.33	286.09	89.02	88.83
V-*Staphylococcus aureus*	93.67	94.63	33.02	88.82	24.02	2.29	269.15	88.93	88.71
T-*Micrococcus luteus*	97.53	94.64	73.28	82.05	27.47	0.52	543.76	81.09	80.94
V-*Micrococcus luteus*	97.43	95.09	73.29	82.27	27.89	0.51	548.44	81.06	80.91

Plant Samples

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-Tea	97.90	92.95	39.08	99.03	24.39	35.11	6.40	77.16	59.28
V-Tea	95.36	93.48	39.43	99.21	24.39	33.17	6.30	75.87	57.58
T-Litchi	97.88	93.40	37.87	77.10	18.70	16.46	4.84	84.81	63.74
V-Litchi	97.03	94.37	38.35	77.35	20.20	16.15	4.70	83.68	61.90
T-Cotton	97.87	93.98	35.43	97.61	25.20	15.35	9.68	98.26	94.53
V-Cotton	95.13	94.37	35.83	97.93	24.80	14.47	9.56	97.89	93.07
T-Rice	97.51	93.77	43.31	96.83	18.64	18.90	10.75	84.30	78.39
V-Rice	95.24	94.24	44.10	97.06	20.30	18.92	10.33	83.96	77.34
T-Potato	97.87	93.81	36.53	93.68	19.03	17.59	8.09	88.91	69.17
V-Potato	96.18	94.13	36.70	93.89	18.91	17.32	8.09	88.57	68.39
T-Tobacco	97.66	93.56	39.02	99.77	18.66	14.55	5.77	94.37	74.18
V-Tobacco	96.56	94.09	39.31	99.84	20.09	13.10	5.64	93.85	72.61

GC Distribution



*Trans*NGS® Fragmentase DNA Library Prep Kit for Illumina® (SuperMix Version) (KP232)

This product is a pre-mixed version of the *Trans*NGS® Fragmentase DNA Library Prep Kit for Illumina®, designed for efficiently and rapidly constructing Illumina-compatible DNA libraries from input DNA ranging from 1 ng to 1 μg.

Features

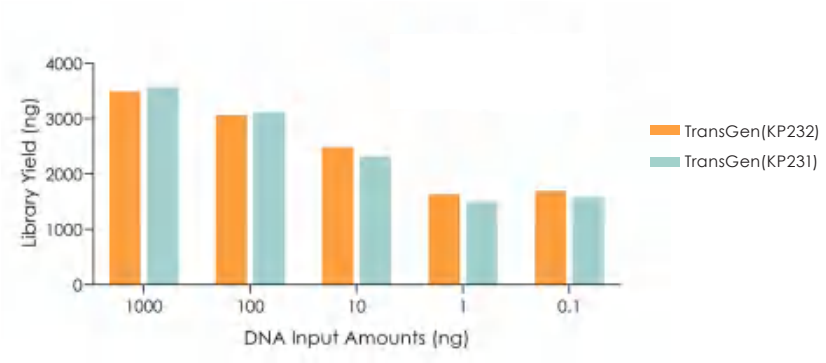
- Suitable for diverse sample types
- High library conversion efficiency
- The pre-mixed format makes the workflow more convenient

Applications

- Whole genome sequencing
- Target gene sequencing
- Exon sequencing / other targeted capture sequencing
- Metagenomic sequencing

Pre-mixed (SuperMix) vs. Non-Pre-mixed (Standard) DNA Library Prep Kits

Equivalent library yields are obtained with both pre-mixed (KP232) and non-pre-mixed (KP231) versions across all input amounts (0.1 ng – 1000 ng HeLa cell genome).



Sequencing data from various animal, plant, and microbial samples shows no significant differences between the pre-mixed and non-pre-mixed versions in terms of sequencing quality, alignment rate, coverage, GC distribution, and other metrics.

Animal Samples

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
KP232-Human Blood	97.80	94.31	40.46	99.48	20.07	6.91	6.78	96.10	82.48
KP231-Human Blood	97.68	94.30	40.62	99.53	24.10	6.73	6.37	95.87	79.33
KP232-Mouse	97.31	93.25	40.86	99.32	28.78	8.48	7.63	92.83	81.92
KP231-Mouse	97.26	93.05	40.95	99.29	27.30	8.51	7.83	92.86	82.64

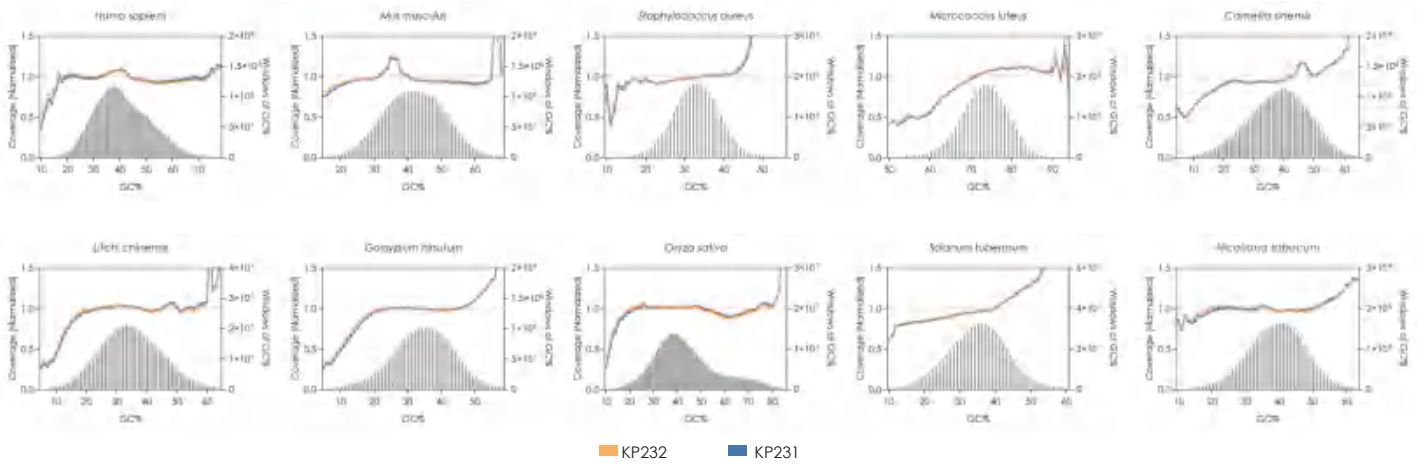
Microorganism

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
KP232-*Staphylococcus aureus*	98.64	93.36	33.03	88.68	22.50	2.44	286.92	89.05	88.85
KP231-*Staphylococcus aureus*	98.60	93.68	32.99	88.74	22.74	2.33	286.09	89.02	88.83
KP232-*Micrococcus luteus*	97.29	94.12	73.29	81.96	28.90	0.53	523.19	81.08	80.94
KP231-*Micrococcus luteus*	97.53	94.64	73.28	82.05	27.47	0.52	543.76	81.09	80.94

Plant Samples

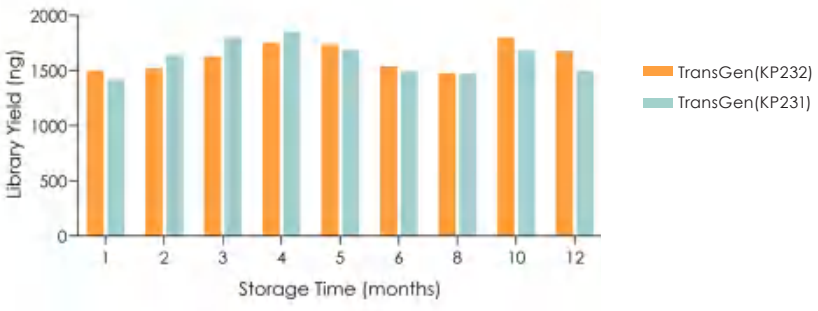
Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
KP232-Tea	97.61	92.24	39.05	98.97	23.40	35.59	6.45	77.24	59.24
KP231-Tea	97.90	92.95	39.08	99.03	24.39	35.11	6.40	77.16	59.28
KP232-Litchi	97.76	93.33	37.72	77.28	20.74	16.08	4.67	84.48	63.26
KP231-Litch	97.88	93.40	37.87	77.10	18.70	16.46	4.84	84.81	63.74
KP232-Cotton	97.95	93.60	35.33	97.60	25.25	15.37	9.68	98.29	94.56
KP231-Cotton	97.87	93.98	35.43	97.61	25.20	15.35	9.68	98.26	94.53
KP232-Rice	97.34	93.80	43.14	96.85	19.32	18.71	10.62	84.29	78.18
KP231-Rice	97.51	93.77	43.31	96.83	18.64	18.90	10.75	84.30	78.39
KP232-Potato	97.78	93.44	36.45	93.60	18.37	17.68	8.16	88.98	69.47
KP231-Potato	97.87	93.81	36.53	93.68	19.03	17.59	8.09	88.91	69.17
KP232-Tobacco	97.68	93.46	38.91	99.75	18.34	14.70	5.79	94.45	74.47
KP231-Tobacco	97.66	93.56	39.02	99.77	18.66	14.55	5.77	94.37	74.18

GC Distribution



High Stability

The product stored at -20°C for one year shows no significant difference in library construction yield compared to the non-pre-mixed version.



*Trans*NGS® Fragmentase DNA Library Prep Kit for MGI®

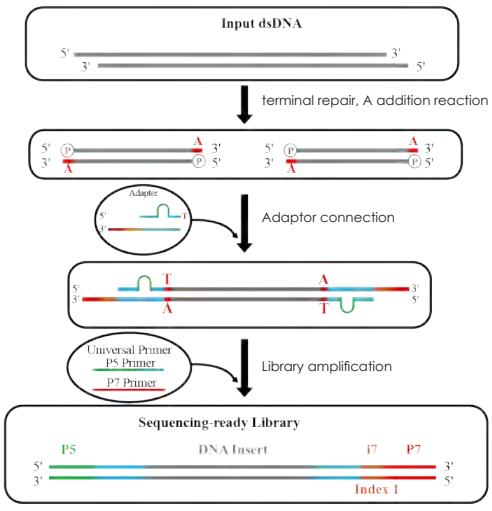
Features

- Suitable for diverse sample types
- High library conversion efficiency

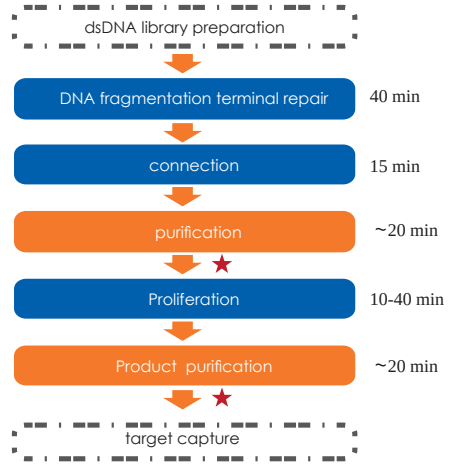
Applications

- Whole genome sequencing
- Target gene sequencing
- Exon sequencing / other targeted capture sequencing
- Metagenomic sequencing

Schematic Diagram of Library Preparation



Workflow Diagram



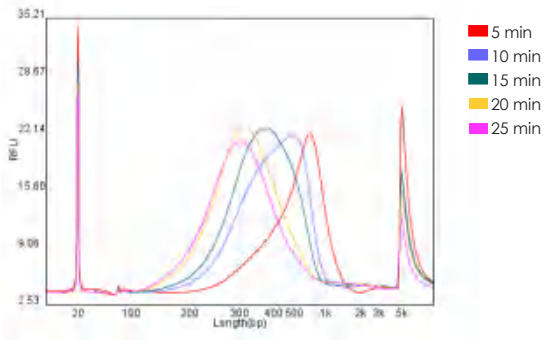
not included in the kit

Steps where fragments size selection can be performed

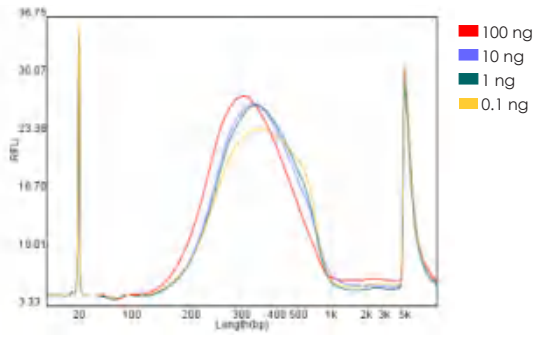
Comparison with Competitors

Construct library using TransGen and Company V kits with varying input amounts (0.1 ng, 1 ng, 10 ng, and 100 ng) of HeLa cell genomic DNA. The TransGen kit demonstrates comparable or superior yields compared with Company V's across all input ranges.

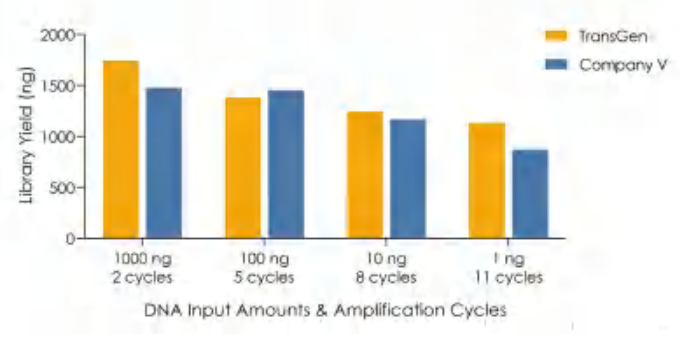
With Different Fragmentation Time



With Different Input Amounts



Library Yield



Comparative analysis across animal, plant and microbial samples shows equivalent sequencing quality to the competitor kits.

Animal Samples

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-Human Blood	98.25	97.28	40.14	99.77	0.84	7.53	7.42	95.96	84.15
V-Human Blood	96.81	97.56	40.24	99.78	1.03	7.15	7.39	95.70	82.97
T-Mouse	97.38	97.26	41.14	99.64	5.59	9.37	6.17	91.54	72.19
V-Mouse	97.48	97.51	41.47	99.64	5.87	9.35	6.26	90.92	70.85

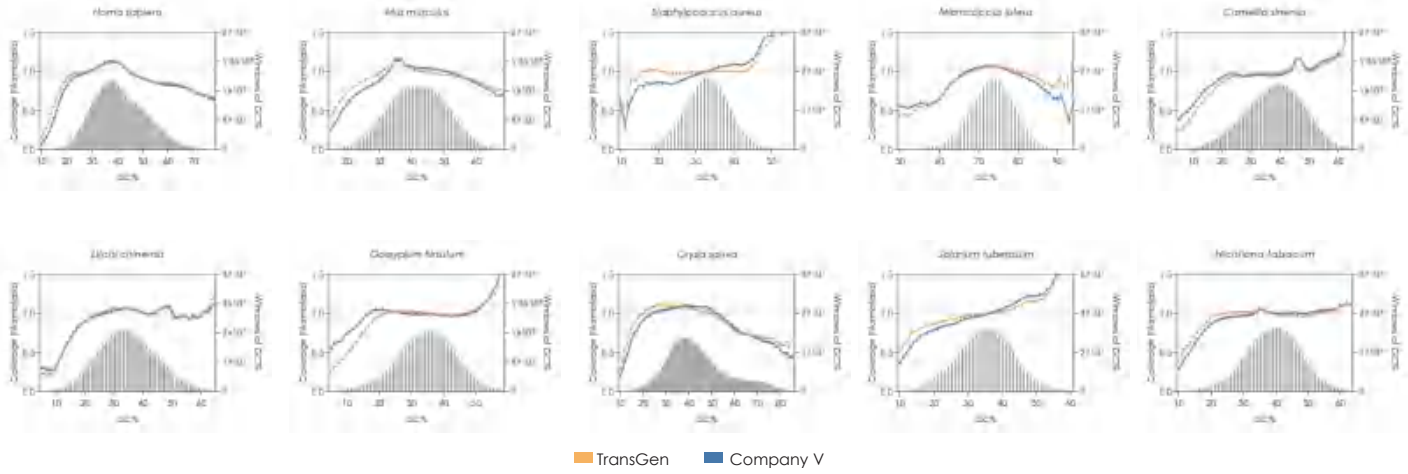
Microorganism

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-*Staphylococcus aureus*	98.82	97.48	32.88	88.74	1.69	2.32	542.69	89.05	88.87
V-*Staphylococcus aureus*	98.82	97.87	33.21	89.24	2.43	2.32	548.77	88.96	88.81
T-*Micrococcus luteus*	97.15	93.93	72.56	81.03	1.39	0.75	501.95	81.11	80.90
V-*Micrococcus luteus*	99.06	94.13	72.51	80.96	2.19	0.82	513.03	81.14	80.93

Plant Sample

Sample	Clean data(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Average depth(×)	Coverage at least 1×(%)	Coverage at least 4×(%)
T-Tea	98.93	97.12	38.92	99.15	2.33	42.07	6.92	77.74	56.41
V-Tea	98.13	97.43	38.91	99.24	2.49	39.88	6.87	77.08	55.91
T-Litchi	98.90	97.35	37.69	77.17	1.05	18.46	5.84	85.83	64.07
V-Litchi	98.19	97.48	37.65	78.05	1.31	18.09	5.83	85.57	63.76
T-Cotton	98.85	97.29	35.10	98.00	0.62	16.94	8.44	98.07	89.48
V-Cotton	97.40	97.52	37.13	86.48	0.94	26.38	6.30	96.86	75.25
T-Rice	98.60	97.24	41.89	97.09	0.59	21.04	11.23	84.22	77.99
V-Rice	98.11	97.37	42.17	97.28	0.84	21.05	11.28	84.01	77.52
T-Potato	97.95	96.64	35.98	94.84	1.14	20.15	10.84	90.38	77.43
V-Potato	97.97	97.40	36.42	94.78	1.35	19.88	10.92	90.18	77.23
T-Tobacco	98.61	97.33	38.89	99.91	0.83	15.69	5.51	94.17	64.47
V-Tobacco	98.63	97.42	39.19	99.90	1.03	14.37	5.51	93.91	65.10

GC Distribution



04 Supportive Products

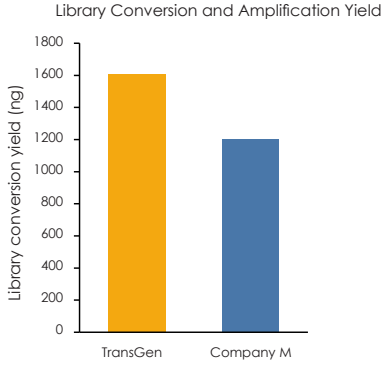
*Trans*NGS® Transformation Kit For MGI®(KC301)

Features

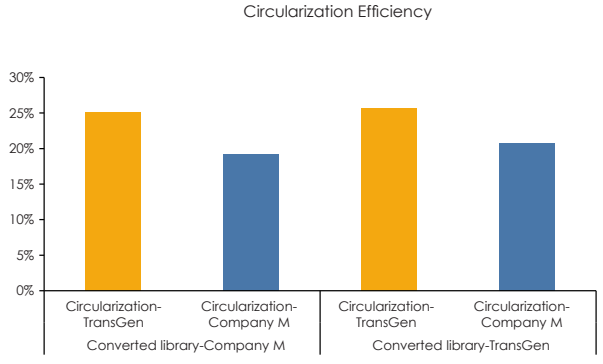
- Library conversion with high stability and good reproducibility.
- High circularization efficiency and short circularization time.
- Suitable for conversion from the linear dsDNA library prepared by non-MGI library prep kits to the single stranded circular DNA library compatible with MGI sequencing platform.

Comparison with competitive product

TransGen's conversion and amplification module and Company M's product are used for conversion and amplification of Illumina DNA library. Qubit is used to measure the amplification yield. The results show that the TransGen's product achieves higher yields.



Circularization of 300 ng DNA library (after conversion and amplification) is performed using TransGen and Company M's products. Qubit is used to measure the MGI library concentration and calculate circularization efficiency. The results demonstrate that TransGen's product achieves higher circularization efficiency.



aCircularization Efficiency = Mass of cyclized product (ng) ÷ Mass of input sample (ng) Efficiency

*Trans*NGS® Universal Circularization Kit For MGI® (KC401)

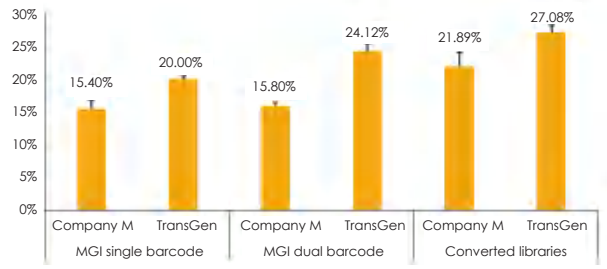
Features

- High circularization efficiency: up to 30%.
- Short operation time: only around 28 minutes.
- Suitable for efficient and rapid preparation of single-stranded circular DNA library from MGI dual/single barcode(s) library or library undergone conversion.

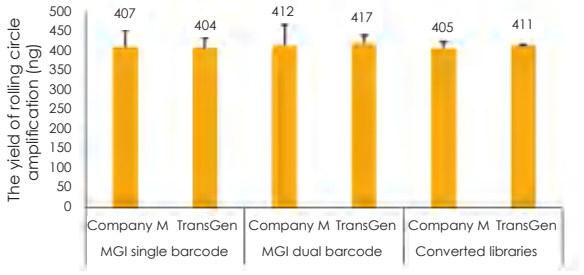
Comparison with competitive product

The TransGen Universal Circularization Kit and Company M's Single-type Circularization Kit are respectively used to circularize three types of library dsDNA: MGI platform single-end barcode libraries, MGI platform paired-end barcode libraries, and Illumina libraries converted using the TransGen-KC301 library conversion module. Comparative evaluation demonstrates superior circularization yield with TransGen's product, while RCA efficiency remained comparable.

Circularization efficiency



The yield of circularization product after rolling circle amplification



Circularization efficiency = circularization product mass (ng)÷ input mass (ng)

MagicPure® Size Selection DNA Beads (EC401)

Features

- Easy operation, compatible with automated workstations.

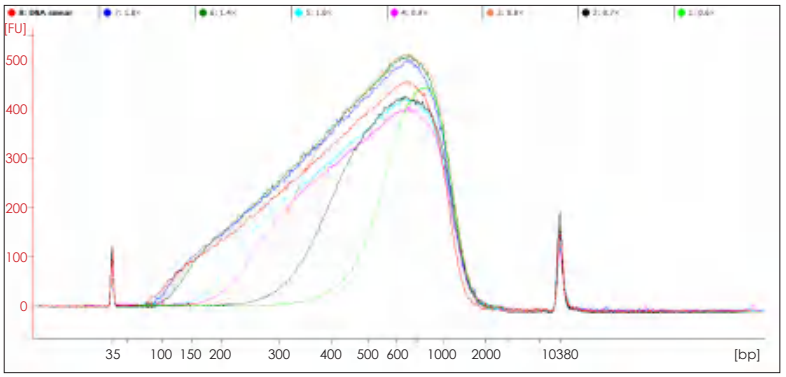
Applications

- DNA purification
- DNA condensation
- DNA fragment sorting in high-throughput sequencing library construction

DNA purification and size selection

DNA samples are performed with purification and size selection using TransGen's products. The results identified by Agilent's high-sensitivity DNA chip shows high efficiency and accuracy of TransGen's product.

DNA Purification

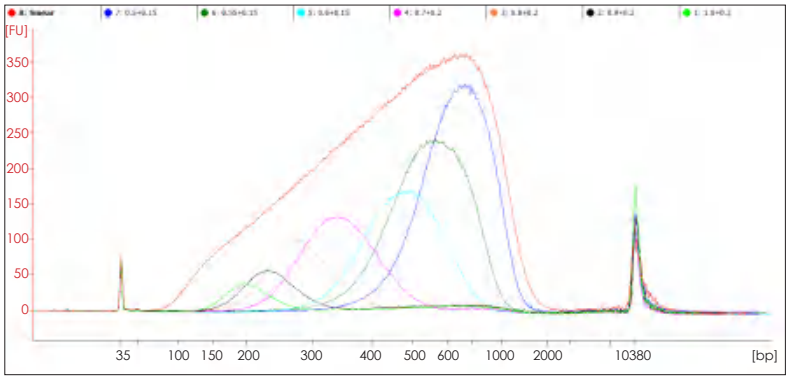


Agilent high-sensitivity DNA electropherogram

Smear - Control dissolved in Nuclease-free Water; 0.6×~1.8× - DNA sample purified by the corresponding magnetic bead ratio

DNA size selection

Average length of sorted fragments (bp)						
190~220	220~250	250~300	300~400	400~500	500~600	600~750
1st volume ratio (DNA Beads:DNA)						
1.0×	0.9×	0.80×	0.70×	0.60×	0.55×	0.50×
2nd volume ratio (DNA Beads:DNA)						
0.20×	0.20×	0.20×	0.20×	0.15×	0.15×	0.15×



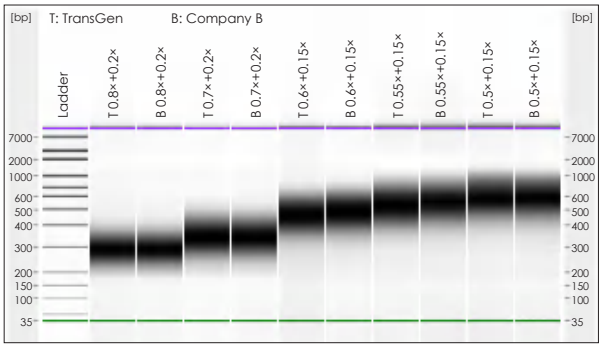
Agilent high-sensitivity DNA electropherogram

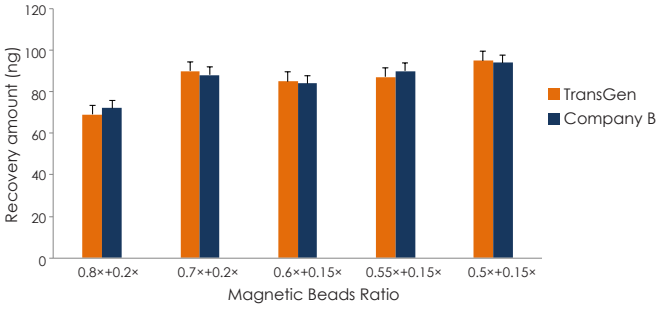
Smear - Control dissolved in Nuclease-free Water; 1.0+0.2~0.5+0.15 - DNA sample purified by the corresponding magnetic bead ratio

Comparison with Competitors

(1) Size Selection

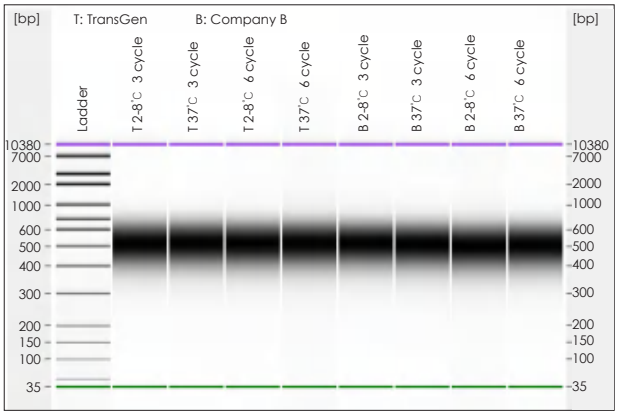
Perform size selection using TransGen and Company B's products respectively. Selected fragments are analyzed by Agilent high-sensitivity DNA chips and the concentration is measured using Qubit. The results show that under the same conditions, the length and recovery amount of the product gives no significant difference.

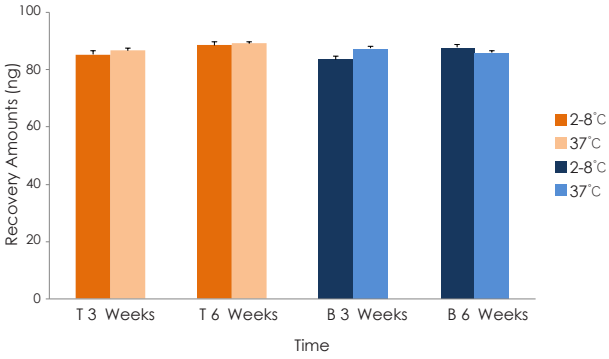




(2) Stability of the Product

The products from TransGen and Company B are stored at 37°C for 3 weeks and 6 weeks (with storage at 2-8°C as the control). The same DNA samples are then subjected to size selection (0.6× + 0.1×). The results analyzed using an Agilent High Sensitivity DNA Chip and Qubit show that after the high-temperature stress test, there was no significant difference in fragment size distribution and recovery yield compared to the competitor's product, demonstrating good stability.





TRANSGEN

RNA Library Prep

B

01 rRNA Removal mRNA Capture

*Trans*NGS® rRNA Depletion Kit (Human/Mouse/Rat) (KD101)

Features

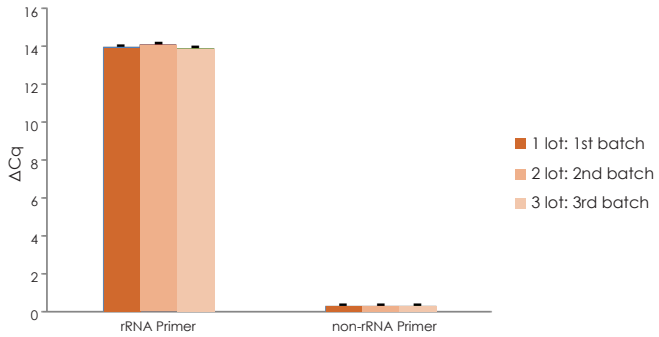
- Remove up to 99% of rRNA in humans/mouse/rats effectively .
- Provide Control qPCR Primer Sets which are able to detect changes in rRNA and non-ribosomal RNA content before and after removal.

Sample Requirements

- Human/mouse/rat total RNA (100 ng-1 μg) samples
- Completely or partially degraded (e.g. FFPE RNA) RNA samples

Stability of the Product

Different batches of the product are used to remove rRNA from 1 μg of total RNA (HepG2 cells). Both untreated and rRNA-depleted RNA samples are then analyzed by qRT-PCR using rRNA-specific primers and non-rRNA primers. The stability between product batches is assessed based on the ΔCq value (Cq value of the depleted sample minus the Cq value of the untreated sample). No significant differences in ΔCq values are observed between different batches, indicating good batch-to-batch consistency.



Comparison with Competitors

For 1 μg of total RNA samples from human (H), mouse (M), and rat (R), rRNA is removed using products from TransGen and Company K. The rRNA-depleted RNA is then used for library preparation (TransGen, KP601). The results demonstrate that TransGen's product performs comparably to—and in some aspects even outperforms—the competitor's product in terms of sequencing data quality, rRNA removal efficiency, detection levels of circRNA and lncRNA, as well as correlation metrics.

Sequencing Data Quality

Sample	rRNA Rate(%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped (%)	Uniquely Mapped (%)
H-CK	76.4	30611582	96.36	90.37	48.10	81.39	69.91
H-T	3.13	33860104	97.28	91.69	44.52	89.98	88.30
H-K	4.10	25323776	96.97	87.72	45.30	89.37	87.41
M-CK	82.2	31734716	96.37	90.39	50.52	82.77	75.32
M-T	3.37	26782378	97.13	89.71	44.91	87.90	79.78
M-K	5.70	28705540	97.05	88.71	45.11	87.23	79.53
R-CK	76.1	29980720	96.92	91.45	47.73	79.48	67.86
R-T	0.60	36024365	97.09	89.21	45.01	86.93	80.45
R-K	1.47	38587178	97.07	88.96	45.06	86.99	79.98

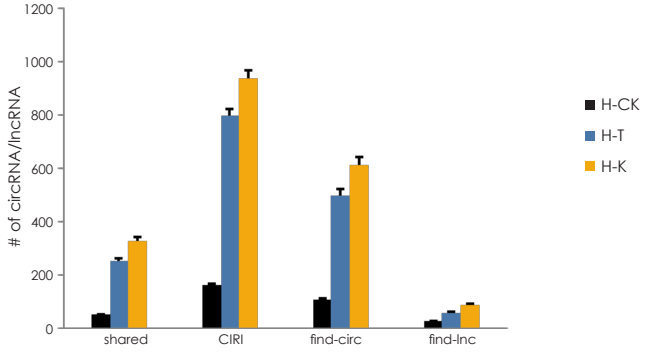
H-CK/M-CK/R-CK: Samples without rRNA removal

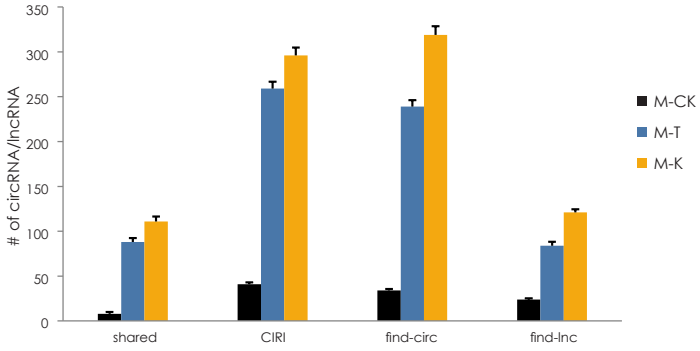
rRNA Residue

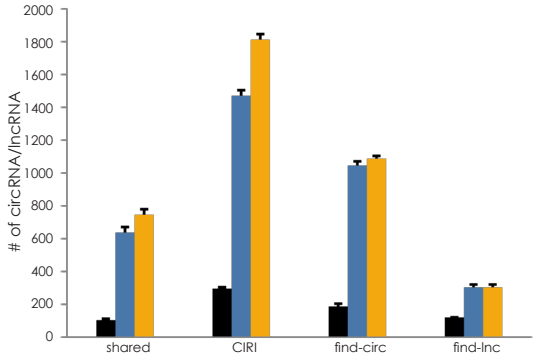
Species	Sample	rRNA Removal (%)	rRNA Rate (%)
Human	H-T	99.88	3.13
	H-K	99.54	4.10
Mouse	M-T	99.79	3.37
	M-K	98.82	5.70
Rat	R-T	99.58	0.60
	R-K	99.03	1.47

rRNA removal is analyzed by Mirabait software, rRNA rate is compared using nt library. The analysis results from Mirabait software are more accurate.

circRNA/lncRNA Analysis







shared: Number of circRNA intersections predicted by different software

CIRI: Number of circRNA intersections predicted byCIRI

find-circ: Number of circRNA intersections predicted by find-circ

find-lnc: Number of lncRNA intersections predicted byfind-lnc

H-CK/M-CK/R-CK: Samples without rRNA removal

MagicPure® mRNA Kit (EC511)

Features

- High mRNA capture efficiency
- Excellent sample compatibility
- High-quality sequencing data
- Compatible with a wide range of species

Sample requirements

- 0.01–10 μg of high-integrity total RNA post-purification (RIN ≥3, optimal RIN ≥8)

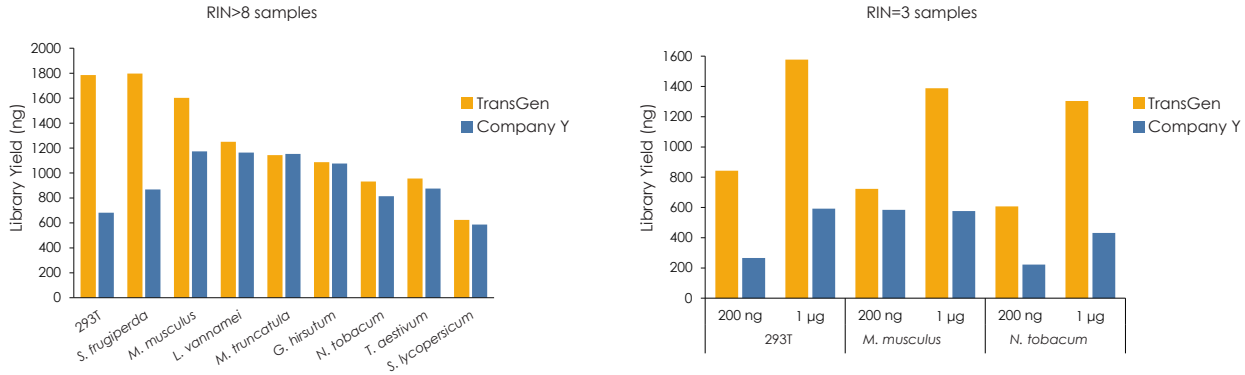
Applications

- The isolated mRNA is suitable for various applications, including RT-PCR, qRT-PCR, and second-generation sequencing, etc.

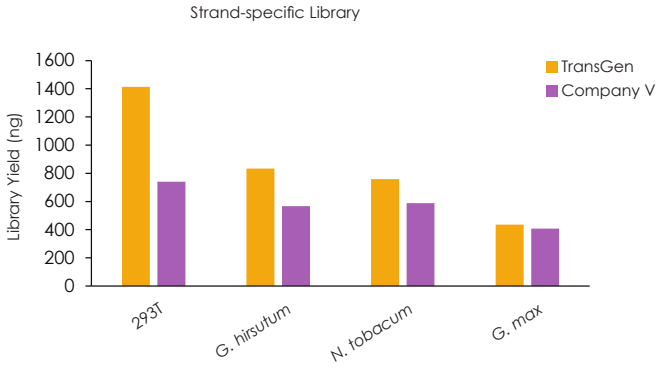
Comparison with Competitors

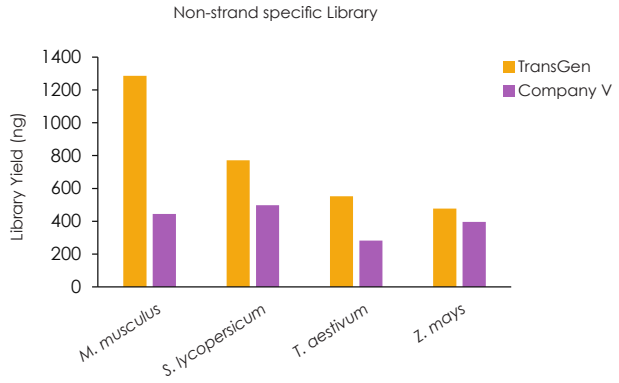
The TransGen mRNA Purification Kit (EC511) and comparable products from Company V and Company Y are used to capture mRNA from varying input amounts and different species for library preparation. The results demonstrate that TransGen's product delivers higher mRNA yield and purity. When paired with library prep kits, it generates higher library yields and superior sequencing data quality compared to competitor's products.

Comparison with Competitors



Sample	Library Prep solution	Kit	Input	rRNA Rate(%)	Q30 (%)	Total mapped (%)	Duplicate (%)	Exon (%)	Gene
O. sativa	Strand-specific Library Preparation	TransGen	100 ng	0.37	95.35	95.44	30.82	93.02	32175
		Company Y		/	/	/	/	/	/
N. tabacum		TransGen	100 ng	0.45	96.36	97.95	24.44	89.17	35928
		Company Y		1.72	96.23	96.75	25.17	88.16	35436
T. aestivum		TransGen	100 ng	0.54	95.03	95.91	29.59	83.44	46979
		Company Y		4.20	96.12	95.22	30.35	80.89	47522
HeLa		TransGen	100 ng	1.56	95.88	98.35	28.79	84.65	15037
		Company Y		5.59	95.73	98.00	29.62	82.10	14426





Sample	Library Prep solution	Kit	Input	rRNA Rate(%)	Q30 (%)	Total mapped (%)	Duplicate (%)	Exon (%)	Gene
293T	Strand-specific Library Prep	TransGen	1 μg	0.92	94.56	97.94	31.06	85.56	14234
		Company V		0.68	94.79	98.22	32.72	84.51	14231
G. hirsutum		TransGen	1 μg	0.69	96.17	98.84	22.89	89.70	38156
		Company V		1.01	96.12	99.19	24.60	89.01	38008
N. tabacum		TransGen	1 μg	0.31	94.37	94.76	31.36	86.59	36637
		Company V		0.34	94.38	87.79	31.43	80.94	36238
G. max		TransGen	1 μg	0.68	96.30	96.30	26.80	81.20	28361
		Company V		0.63	96.20	97.70	28.10	80.10	28653
M. musculus	Non-strand specific Library Prep	TransGen	500 ng	0.67	94.77	95.94	33.78	84.01	14158
		Company V		1.59	96.35	97.36	33.07	83.26	14060
S. lycopersicum		TransGen	1 μg	0.49	94.49	97.81	26.73	92.99	15563
		Company V		0.79	96.22	98.23	27.89	92.02	15361
T. aestivum		TransGen	500 ng	1.91	94.99	94.29	31.05	79.85	43574
		Company V		4.63	94.68	93.86	31.64	79.39	43297
Z. mays		TransGen	1 μg	0.85	94.71	91.79	33.24	87.54	19523
		Company V		1.29	96.16	92.00	32.48	87.41	19481

02 Library Preparation

*Trans*NGS® Fast RNA-Seq Library Prep Kit for Illumina® (KP701)

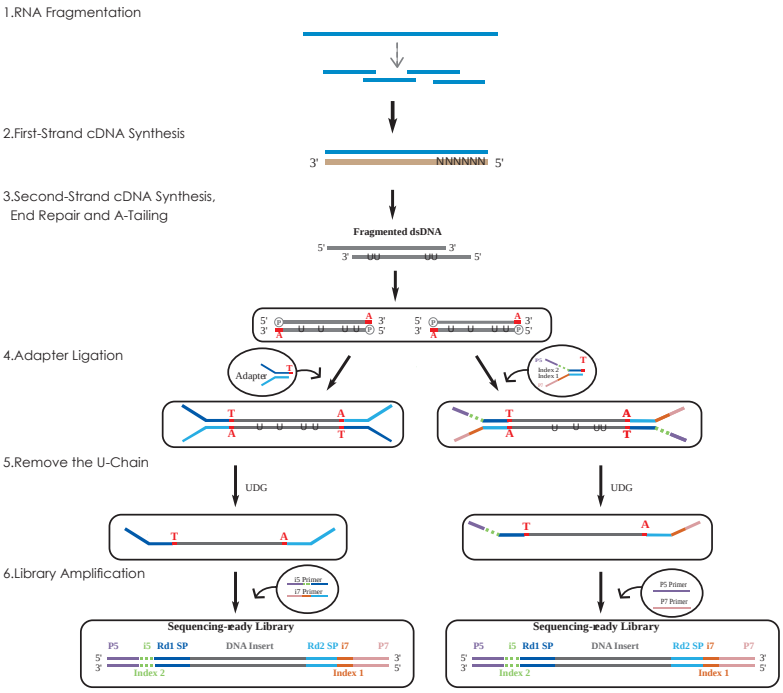
Features

- High library yield
- High library conversion efficiency: Robust performance even with partially degraded RNA (RIN ≥ 3).
- Safe handling: Strand-specific reverse transcription components are actinomycin D-free, requiring no light protection. Low toxicity and odorless.
- Flexible fragmentation conditions: Achieve consistent results across varying fragmentation parameters.
- Broad species compatibility: Suitable for RNA isolated from animals, plants, and microorganisms.
- Versatile upstream compatibility: Compatible with multiple RNA preprocessing methods (e.g., mRNA capture or rRNA depletion).

Applications

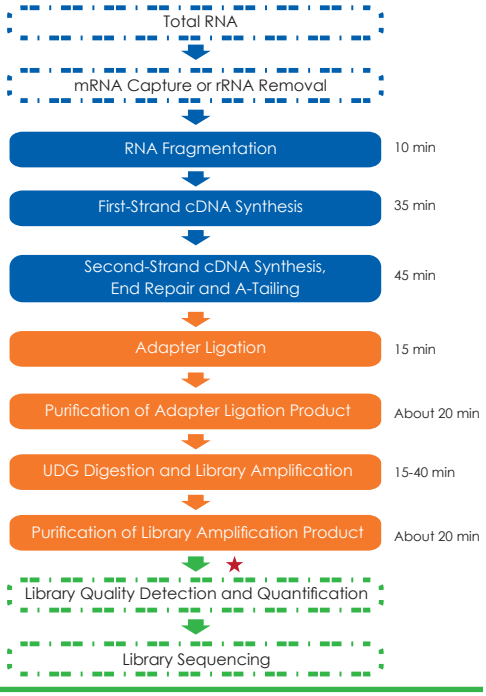
- Whole transcriptome sequencing
- Gene expression analysis
- Single nucleotide variation analysis
- Alternative Splicing Detection
- Fusion Gene Detection
- Analysis of non-coding RNA and RNA precursor

Schematic Diagram of Library Preparation



Principle chart of strand-specific library construction
(No dUTP incorporation and UDG digestion steps in second-strand synthesis of non-strand-specific library)

Workflow Diagram



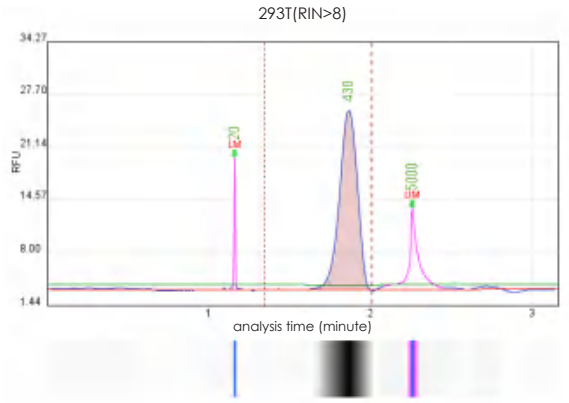
The dotted lines are not included in this kit flow

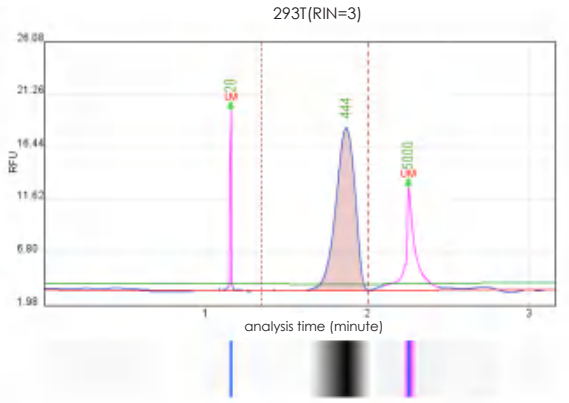
Steps where fragments size selection can be performed

Flow chart of strand-specific library construction
(No dUTP incorporation and UDG digestion steps in second-strand synthesis of non-strand-specific library)

Library Peak Profile

Using 293T RNA samples with varying RIN values (high vs. low integrity), we perform mRNA capture and library construction. TransGen libraries exhibit normal peak profiles (no aberrant size distribution).





Using rRNA-depleted Staphylococcus aureus RNA, we construct both strand-specific and non-strand-specific libraries with TransGen's kits. The sequencing data shows high quality.

Library Prep Solution	Clean data (%)	rRNA (%)	Q30 (%)	GC (%)	Total mapped (%)	Duplicate (%)	Multiple mapped (%)	Exon (%)	Gene
Strand-specific Library	91.95	0.86	95.15	34.7	94.95	27.59	0.24	92.04	2639
Non-strand-specific Library	85.23	0.90	94.99	34.85	94.62	23.91	0.24	91.15	2657

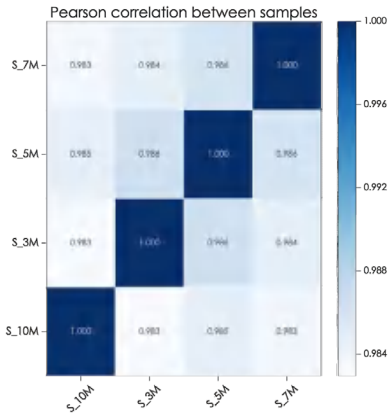
We construct both strand-specific and non-strand-specific libraries with TransGen's technology using mouse fecal microbial RNA post rRNA depletion. The results show highly concordant taxonomic profiles between the two library types.

Taxonomic Annotation of rRNA-Depleted Mouse Fecal RNA Libraries

Classification	Non-strand-specific Library	Strand-specific Library
s__Ligilactobacillus_murinus	0.14395	0.1334
s__Duncaniella_dubosii	0.03768	0.03752
s__Bacteroides_sp._KGMB10229	0.03804	0.037
s__Staphylococcus_aureus	0.0167	0.03449
s__Bacteroides_uniformis	0.02367	0.02409
s__Muribaculum_gordoncarteri	0.02314	0.02315
s__Pusillimonas_faecalis	0.01763	0.01746
s__Muribaculum_intestinale	0.01649	0.01675
s__Roseburia_intestinalis	0.01675	0.01551
s__Duncaniella_sp._B8	0.01537	0.01623
s__Flavonifractor_plautii	0.01546	0.01574
s__Murine_astrovirus	0.01527	0.01521
s__Pseudomonas_aeruginosa	0.01508	0.01537
s__Vescimonas_coprocola	0.01421	0.01376
s__Plasmodium_knowlesi	0.01494	0.01265
s__Dysosmobacter_sp._Marseille-Q4140	0.01306	0.01333
s__Oscillibacter_sp._NSJ-62	0.01314	0.01324
s__Lachnoclostridium_sp._YL32	0.01244	0.01275
s__Roseburia_hominis	0.01023	0.0094
s__Acutalibacter_muris	0.00956	0.00964

Compatible with Variable Fragmentation Durations

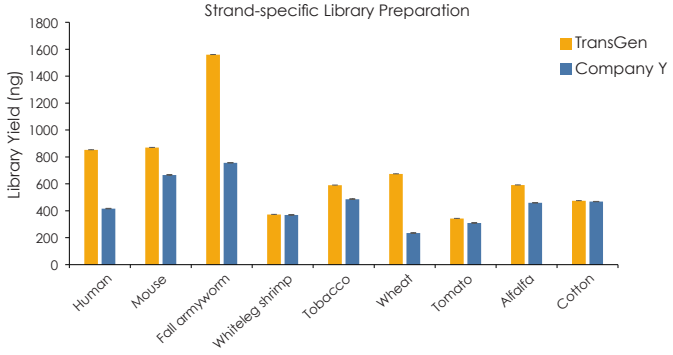
Using 500 ng of 293T total RNA, we test fragmentation time of 3, 5, 7, and 10 minutes, followed by mRNA capture and library construction. Correlation analysis demonstrate Pearson correlation >98% between groups.

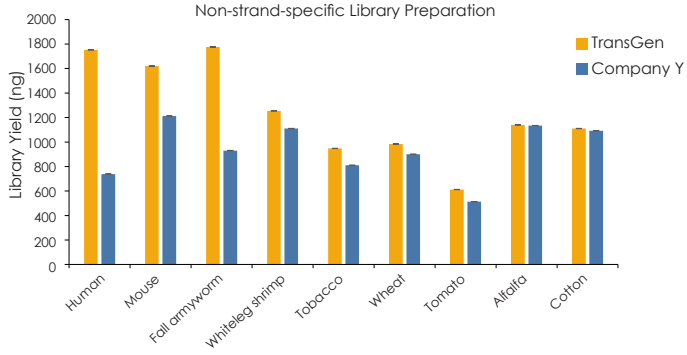


Comparison with Competitors

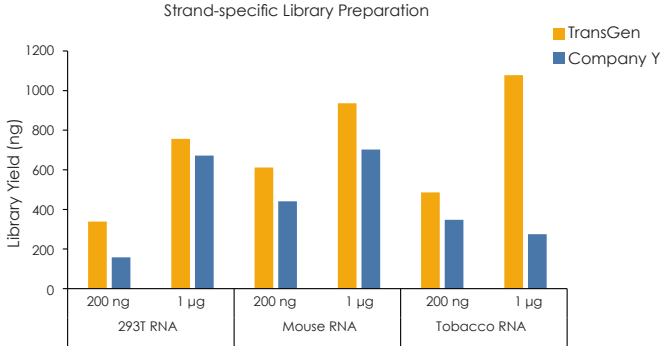
Library Yield

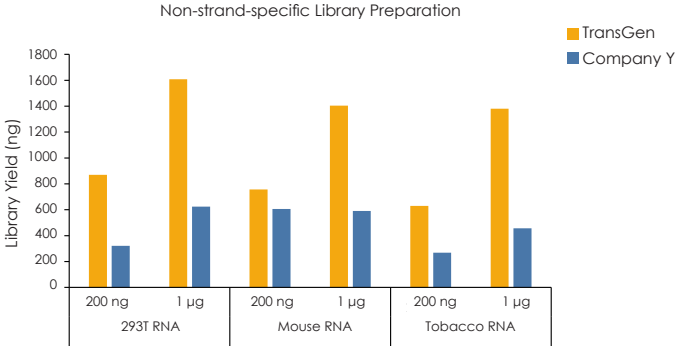
Using high-quality RNA samples (RIN > 8) from nine different species, we perform mRNA capture and subsequent library preparation. The results demonstrate that TransGen's strand-specific and non-strand-specific library preparation kits consistently generated higher library yields compared to those of Company Y.





Using severely degraded RNA (RIN = 3) from human (293T cells), mouse, and tobacco, we perform mRNA capture followed by library construction with high (1 µg) and low (200 ng) input amounts. The results demonstrate that the TransGen's kit (both strand-specific and non-strand-specific) consistently outperforms Company Y in library yield across all species and input amounts.





Sequencing Data Quality

Comparative analysis of sequencing data across multiple species reveal that RNA libraries using TransGen kit significantly outperform Company Y's in percentage of clean data, number of reliably detected genes.

Strand-specific Library Preparation (after mRNA capture)

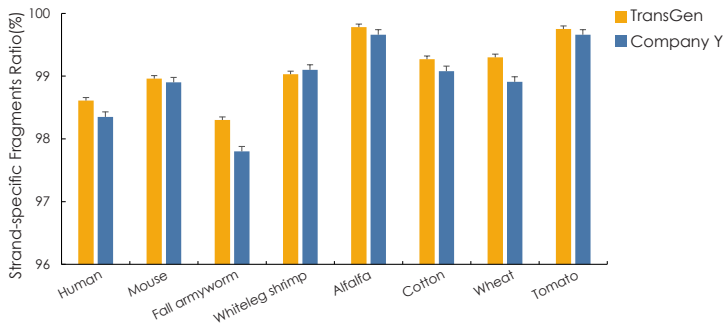
Sample (500 ng total RNA)	Library Prep Solution	Clean data (%)	rRNA (%)	Q30 (%)	GC (%)	Total mapped (%)	Duplicate (%)	Multiple mapped (%)	Exon (%)	Gene
Human	TransGen	91.7	0.21	95.29	48.66	98.24	23.64	7.17	85.88	15421
	Company Y	82.22	0.47	95.7	49.46	98.34	30.56	7.76	84.70	14410
Mouse	TransGen	93.10	0.55	95.73	48.76	97.47	19.62	7.60	89.83	12817
	Company Y	83.19	0.31	96.03	49.48	97.83	20.64	7.73	88.13	12706
Fall armyworm	TransGen	87.52	0.85	94.06	45.29	86.26	24.47	4.15	82.64	7607
	Company Y	84.88	0.58	94.6	47.55	84.81	32.95	4.05	83.67	7503
Whiteleg shrimp	TransGen	83.65	2.76	94.24	47.98	90.77	24.15	14.61	80.25	11858
	Company Y	82.76	3.30	94.65	49.52	90.67	27.88	15.92	78.69	11405
Alfalfa	TransGen	84.66	0.25	95.98	43.65	61.49	28.77	3.17	69.46	15387
	Company Y	81.98	0.21	94.37	43.19	59.25	28.42	2.92	68.50	15231
Cotton	TransGen	87.94	0.98	94.65	43.88	98.23	20.30	4.84	90.65	45809
	Company Y	85.63	0.41	94.63	43.77	98.35	26.50	5.05	88.37	44705
Wheat	TransGen	85.62	1.31	95.58	52.3	95.39	21.53	5.66	87.22	46235
	Company Y	56.42	1.40	94.78	57.74	94.85	28.15	6.66	87.24	47038
Tomato	TransGen	85.6	1.33	93.48	44.34	97.75	25.32	1.56	94.56	17704
	Company Y	83.8	1.34	94.68	44.16	97.76	35.41	1.67	93.71	17563

Non-strand-specific Library Preparation (after mRNA capture)

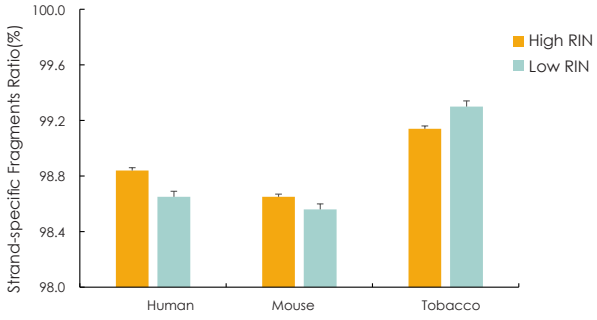
Sample (500 ng total RNA)	Library Prep Solution	Clean data (%)	rRNA (%)	Q30 (%)	GC (%)	Total mapped (%)	Duplicate (%)	Multiple mapped (%)	Exon (%)	Gene
Human	TransGen	93.20	0.71	95.88	47.11	98.35	20.79	7.52	87.15	15037
	Company Y	91.97	0.80	95.71	48.55	98.00	29.62	7.93	85.58	14426
Mouse	TransGen	93.35	0.59	95.79	48.39	96.13	23.79	7.77	93.41	12777
	Company Y	91.24	0.47	95.84	49.35	97.36	25.35	8.14	93.56	12530
Fall armyworm	TransGen	87.22	1.07	93.82	44.88	81.45	22.89	3.39	82.12	7771
	Company Y	83.97	0.52	94.5	45.4	82.45	32.45	3.96	80.11	7668
Whiteleg shrimp	TransGen	83.89	2.61	94.13	46.83	90.2	23.95	19.42	82.17	11783
	Company Y	80.49	3.55	94.83	48.22	90.84	26.69	17.77	83.90	11474
Alfalfa	TransGen	86.11	0.28	93.49	42.3	59.06	21.45	4.33	69.21	15535
	Company Y	80.77	0.22	94.71	42.5	58.21	24.83	4.78	68.35	15639
Cotton	TransGen	85.46	1.07	93.89	43.00	96.91	20.76	4.99	89.40	45096
	Company Y	80.90	1.26	94.6	43.23	98.23	26.93	5.39	87.46	44908
Wheat	TransGen	86.11	1.17	93.98	52.08	87.81	19.59	5.37	84.61	46979
	Company Y	85.39	0.82	94.94	54.73	95.22	30.35	6.44	85.88	47522
Tomato	TransGen	82.82	0.98	93.82	43.73	91.67	27.27	1.58	94.91	17639
	Company Y	79.06	0.96	94.52	43.55	97.64	34.09	1.56	93.73	17412

Higher strand-specific Fragments Ratio

Using high-integrity RNA samples (RIN > 8) from eight diverse species, we perform mRNA capture and library preparation. The results demonstrate that TransGen's libraries consistently achieve higher strand-specific fragments ratio compared to Company Y's across all species tested.



Using high-quality (RIN > 6) and degraded (RIN = 3) RNA samples from human, mouse, and tobacco, we perform mRNA capture and library preparation. TransGen strand-specific libraries maintain high strand specificity regardless of RNA degradation level.



*Trans*NGS® Fast Stranded RNA-Seq Library Prep Kit for MGI® (KP801)

Features

- High library yield
- High library conversion efficiency: Robust performance even with partially degraded RNA (RIN ≥ 3).
- Safe handling: Strand-specific reverse transcription components are actinomycin D-free, requiring no light protection. Low toxicity and odorless.
- Flexible fragmentation conditions: Achieve consistent results across varying fragmentation parameters.
- Broad species compatibility: Suitable for RNA isolated from animals, plants, and microorganisms.
- Versatile upstream compatibility: Compatible with multiple RNA preprocessing methods (e.g., mRNA capture or rRNA depletion).

Applications

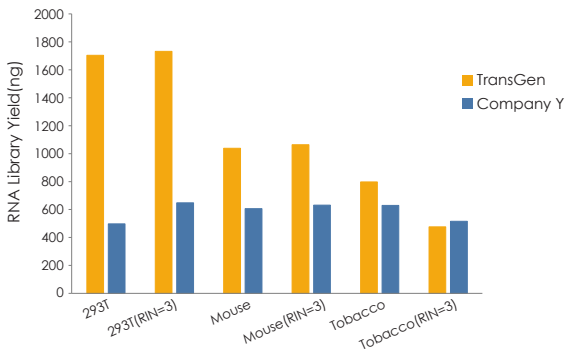
- Whole transcriptome sequencing
- Gene expression analysis
- Single nucleotide variation analysis
- Alternative Splicing Detection
- Fusion Gene Detection
- Analysis of non-coding RNA and RNA precursor

Comparison with Competitors

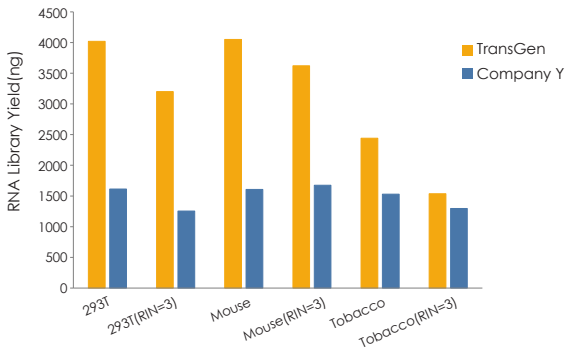
The RNA library construction performance is compared between TransGen and Company Y's products using RNA samples with different input amounts, varying integrity levels and from various species. The TransGen's products demonstrate significantly higher yields compared to competitors, achieve over 98% strand specificity across all types of strand-specific libraries, and consistently produce high-quality sequencing data, showing excellent compatibility with different species and RNA quality levels, strong adaptability to fragmentation conditions.

Library Yield (amplification after size selection)

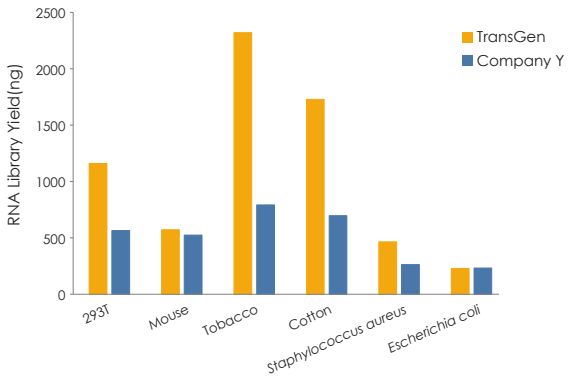
Strand-specific Library Preparation (after mRNA capture)



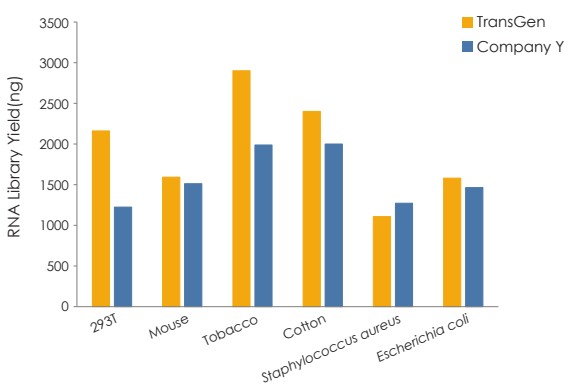
Non-strand-specific Library Preparation (after mRNA capture)



Strand-specific Library Preparation (after rRNA depletion)

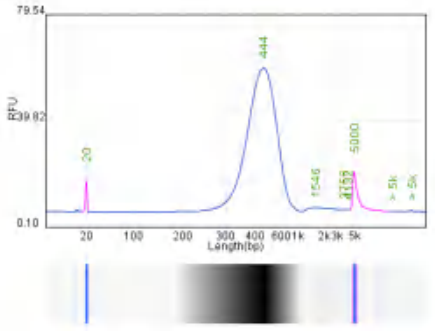


Non-strand-specific Library Preparation (after rRNA depletion)

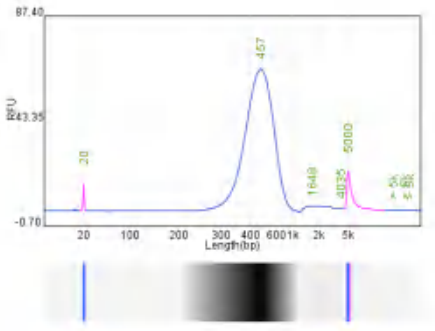


Library Peak Profile

High-integrity RNA Sample (293T-RNA)



Degraded RNA Sample(293T-RNA)



Sequencing Data Quality

Library Preparation using 500 ng of High-integrity/degraded 293T RNA (after mRNA capture)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
293T RNA	Strand-specific	TransGen	95.71	0.60	97.72	49.67	96.53	6.59	7.88	88.38	14944
		Company Y	94.44	0.61	96.91	50.53	91.79	7.49	7.65	87.52	14657
RIN3 293T RNA	Strand-specific	TransGen	95.52	0.68	97.37	49.55	94.96	8.11	7.99	87.89	15340
		Company Y	96.38	0.70	97.92	51.13	91.97	13.29	8.16	86.79	14236
293T RNA	Non-strand-specific	TransGen	96.47	0.64	97.94	47.74	96.08	6.07	6.74	86.49	15709
		Company Y	93.09	0.65	96.52	48.59	91.03	8.33	6.94	85.08	14855
RIN3 293T RNA	Non-strand-specific	TransGen	94.79	0.72	97.24	47.33	94.18	8.10	7.69	85.01	15759
		Company Y	96.55	0.68	97.87	49.98	93.86	14.21	8.13	83.20	14074

Library Preparation using 500 ng of High-integrity/degraded mouse RNA (after mRNA capture)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
Mouse RNA	Strand-specific	TransGen	94.18	0.31	97.00	49.91	94.98	15.58	6.97	81.11	12896
		Company Y	92.78	0.40	96.43	49.80	92.34	15.58	7.08	81.08	12798
mouse RNA (RIN=3)	Strand-specific	TransGen	94.03	0.28	96.84	50.25	92.60	14.92	6.77	80.96	12986
		Company Y	96.18	0.38	97.77	50.56	91.69	19.39	7.78	80.35	12507
Mouse RNA	Non-strand-specific	TransGen	96.87	0.37	98.09	48.81	95.34	13.95	7.22	82.45	13241
		Company Y	93.97	0.42	96.92	49.41	93.64	19.46	7.37	82.27	12907
mouse RNA (RIN=3)	Non-strand-specific	TransGen	95.57	0.48	97.39	49.23	92.94	15.72	7.56	82.97	12986
		Company Y	96.67	0.46	97.92	50.08	93.64	21.05	8.19	82.41	12397

Library Preparation using 500 ng of High-integrity/degraded tobacco RNA (after mRNA capture)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
Tobacco RNA	Strand-specific	TransGen	96.48	0.28	97.93	43.64	96.01	4.58	2.99	83.94	35354
		Company Y	94.37	0.37	97.00	43.75	93.58	6.91	3.01	84.01	35310
Tobacco RNA (RIN=6)	Strand-specific	TransGen	95.44	1.07	97.43	44.51	93.15	8.63	3.70	82.91	35668
		Company Y	96.81	1.03	98.05	44.50	93.00	8.12	3.48	83.08	35528
Tobacco RNA	Non-strand-specific	TransGen	96.37	0.43	97.95	43.17	95.20	4.44	6.06	85.07	35928
		Company Y	93.72	0.30	96.75	43.47	92.58	5.17	6.75	84.48	35486
Tobacco RNA (RIN=6)	Non-strand-specific	TransGen	95.57	1.36	97.54	44.08	93.52	9.69	12.04	84.67	36459
		Company Y	96.69	1.73	97.96	44.29	91.28	8.72	13.55	83.02	35871

Library Preparation using 500 ng of Animal RNA (after rRNA depletion)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
293T RNA	Strand-specific	TransGen	92.33	0.40	95.85	44.29	97.83	5.85	5.73	76.91	15496
		Company Y	95.13	1.03	96.46	49.60	96.99	16.01	7.62	71.98	15478
Mouse RNA	Strand-specific	TransGen	95.42	1.99	97.23	47.70	95.97	12.66	6.56	70.04	13701
		Company Y	94.51	4.12	96.48	50.02	93.57	16.11	9.78	68.31	13651
293T RNA	Non-strand-specific	TransGen	93.89	0.47	96.50	44.94	97.73	8.87	6.09	78.36	16931
		Company Y	93.04	0.87	96.15	48.54	96.86	16.62	7.70	72.10	16840
Mouse RNA	Non-strand-specific	TransGen	95.52	1.35	97.36	47.17	96.25	12.37	6.59	70.94	14660
		Company Y	93.44	3.50	96.14	50.19	93.83	18.30	12.10	68.02	14464

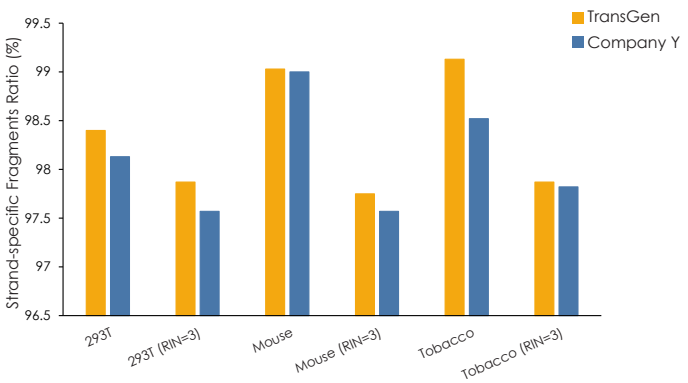
Library Preparation using 500 ng of Microorganism RNA (after rRNA depletion)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
Staphylococcus aureus RNA	Strand-specific	TransGen	96.38	1.41	97.59	35.16	91.83	25.36	0.56	84.17	2477
		Company Y	96.98	3.63	98.04	37.24	88.72	24.93	1.46	76.16	2467
Escherichia coli RNA	Strand-specific	TransGen	94.60	5.42	96.82	50.35	81.49	25.63	1.72	75.08	3952
		Company Y	96.19	5.67	97.81	51.24	86.56	35.24	2.07	71.93	3893
Staphylococcus aureus RNA	Non-strand-specific	TransGen	96.22	1.49	97.77	35.27	91.83	25.46	0.60	86.77	2647
		Company Y	96.04	2.76	97.71	36.33	89.93	24.88	0.97	83.77	2625
Escherichia coli RNA	Non-strand-specific	TransGen	94.02	2.20	96.59	49.71	88.21	28.72	1.11	81.76	4074
		Company Y	96.96	3.68	97.62	50.44	87.51	31.14	1.38	76.35	4010

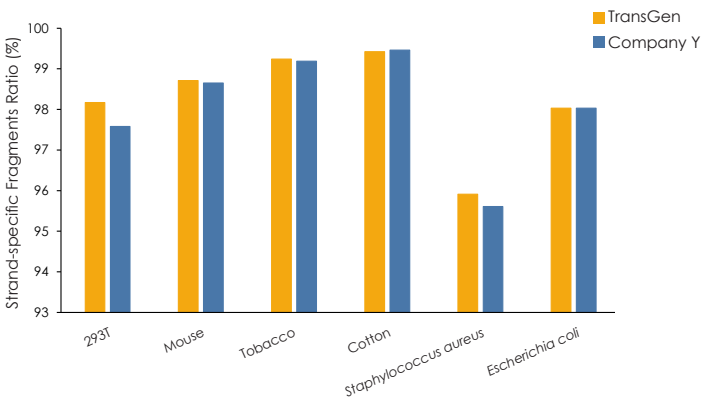
Library Preparation using 500 ng of Plant RNA (after rRNA depletion)

Sample	Library Prep Solution	Kit	Clean data(%)	rRNA(%)	Q30(%)	GC(%)	Total mapped(%)	Duplicate(%)	Multiple mapped(%)	Exon(%)	Gene
Tobacco RNA	Strand-specific	TransGen	96.16	1.18	97.01	41.88	98.05	21.06	22.54	82.44	33638
		Company Y	93.17	1.57	96.50	42.65	94.66	23.23	22.40	79.64	33157
Cotton RNA	Strand-specific	TransGen	96.14	2.55	97.70	42.25	98.03	27.64	19.29	83.37	42221
		Company Y	95.44	3.78	97.36	43.45	96.42	27.22	27.62	80.61	41919
Tobacco RNA	Non-strand-specific	TransGen	94.81	1.43	96.90	41.79	97.44	29.26	20.21	83.47	34865
		Company Y	93.97	1.77	96.47	42.37	95.74	30.31	21.77	79.28	34024
Cotton RNA	Non-strand-specific	TransGen	95.94	1.80	97.74	42.08	97.78	25.68	18.04	84.70	42566
		Company Y	95.60	2.72	97.54	43.06	97.16	26.86	26.17	78.99	42223

Strand-specific Fragments Ratio (after mRNA capture)



Strand-specific Fragments Ratio (after rRNA depletion)



TRANSGEN

Epigenetics

*Trans*NGS® ATAC-Seq Library Prep Kit for Illumina® (KP171)

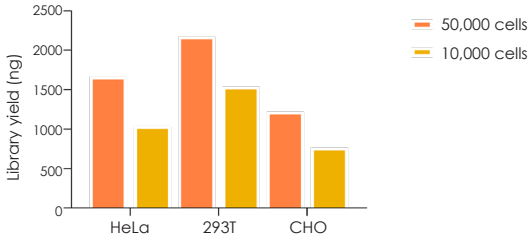
Features

- Minimal cell input requirement. A starting amount from 50 to 50,000 cells can yield high-resolution sequencing maps.
- Time saving and simple operation: For 5,000 cells or fewer, library preparation time can be reduced to under 2 hours.
- High library yield.
- Good library peak pattern: Library peak at 200 to 2,000 bp, with no significant adapter peaks.
- No sorting needed: Sorting can be skipped if there are no specific requirements for library length distribution.

Data

High library yield

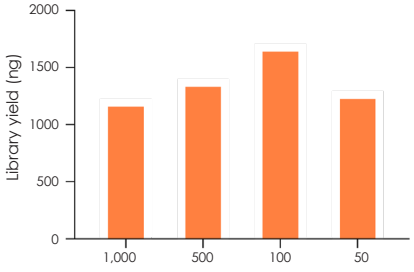
ATAC libraries were constructed from three types of mammalian cells starting with 50,000 and 10,000 cells. Results show that TransGen product can construct high-yield libraries for different cells and inputs.



Minimal cell input requirement

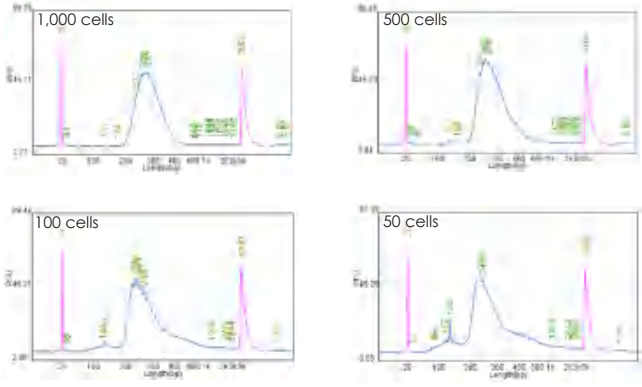
ATAC library construction was performed on HeLa cells with different cell inputs (50 to 1,000 cells). The number of amplification cycles for different cell inputs are shown in the table below. Results show that TransGen product can be used to construct ATAC libraries from a low starting amount (50 cells), with high library yield and good peak pattern.

Library yield



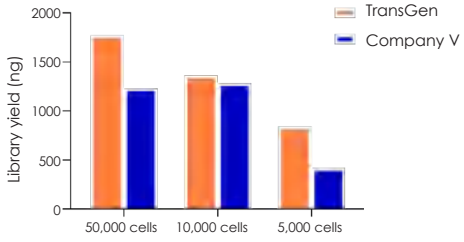
Number of cells	1,000	500	100	50
Cycles	20		25	

Peak pattern



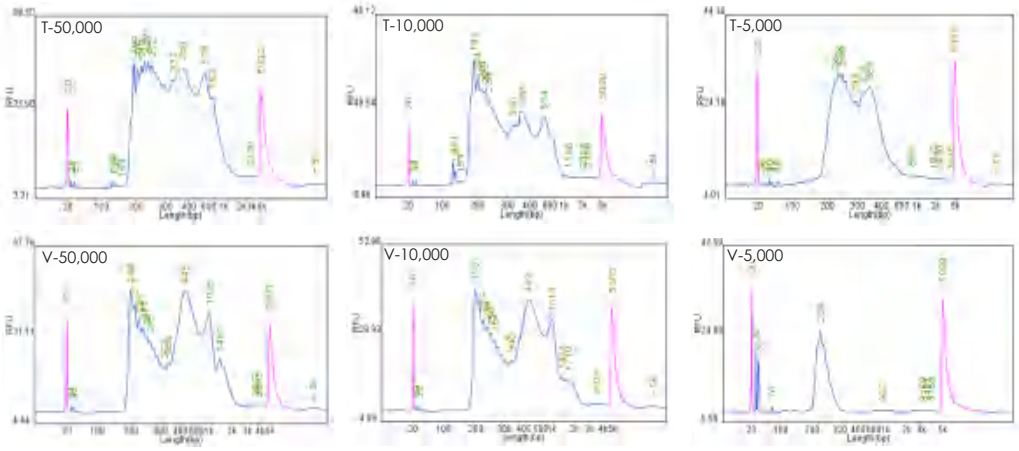
Comparison with competitive product

Library yield



Peak pattern

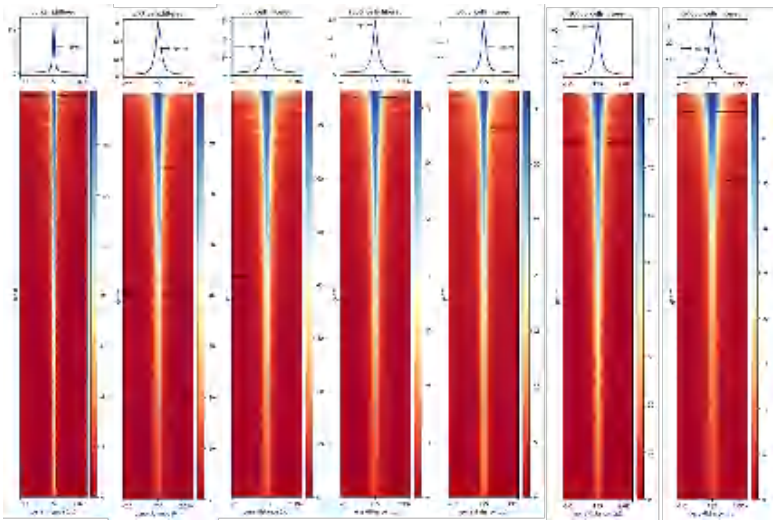
ATAC libraries were constructed from HeLa cells with different cell inputs (5,000 to 50,000 cells) using reagents from TransGen and Company V respectively.



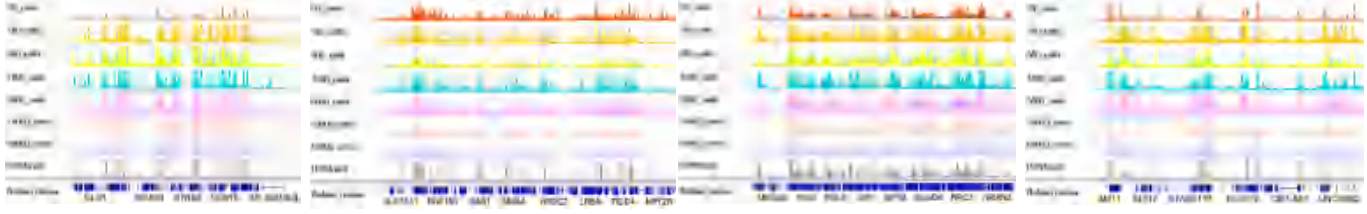
Sequencing data

ATAC libraries were constructed from HeLa cells with varying cell inputs (50 to 50,000 cells), sequenced, and bioinformatics analysis was conducted post-sequencing. Results show that TSS enrichment maps indicate significant enrichment around transcription start sites of genes, and the IGV view confirms that ATAC peaks align with H3K4me3 gene ChIP-seq results, proving the reliability of the experimental results.

Views of TSS with different cell inputs



IGV views with different cell inputs



Note: Four chromatin regions were randomly selected across the entire genome for analysis.

*Trans*NGS® CUT&Tag Library Prep Kit for Illumina® CUT&Tag (KP172)

Features

- Short operation time, library preparation can be completed within 5.5 h.
- Sequencing data with high quality: High yield, good library peak pattern.
- Accurate and reliable sequencing data: high proportion of clean data, more stable mapping rate, accurate and valid peak positions.
- Antibody with good compatibility and high affinity.
- Wide range of cell inputs: Applicable to the library preparation with 10-10^5 mammalian cells or processed cell nucleus, as well as eukaryotic cells without cell wall structures (such as plant cell protoplasts, etc.)

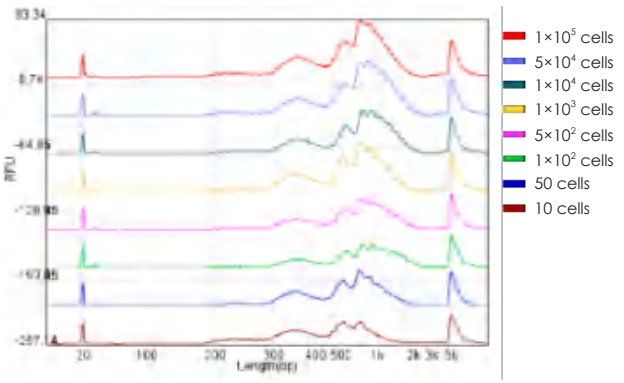
Library preparation with different cell inputs

TransGen product was used to perform CUT&Tag experiments with CTCF antibodies on 293T cells with different inputs. The results showed that the library yield of TransGen product was high, and the library peak pattern and peak position were basically consistent under different cell inputs, and it was compatible with library preparation with low cell input (10 cells).

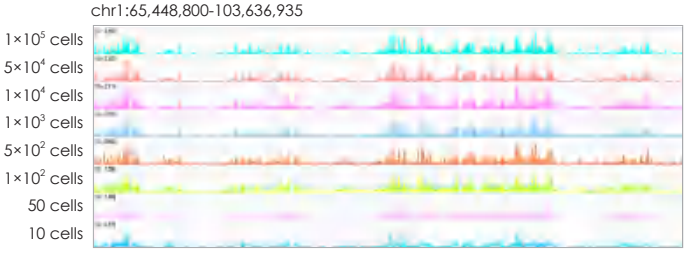
Library yield

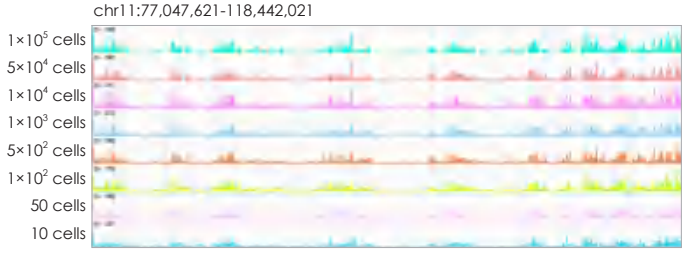
Cell Input	Cycles	Library Yield(ng)
1×10^5	11	2360
5×10^4	12	3896
1×10^4	14	4400
1×10^3	17	3568
5×10^2	18	2796
1×10^2	19	1048
50	21	2256
10	25	3780

Library peak pattern



Accurate and valid peak positions





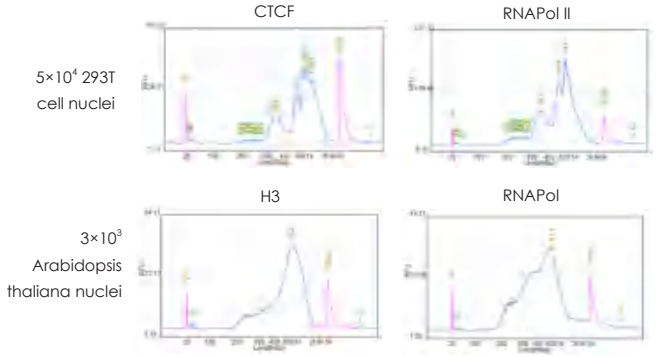
Library preparation of different cell nucleus

TransGen product was used to perform CUT&Tag experiments with different antibodies on 293T cell nuclei and Arabidopsis thaliana nuclei. The results showed that TransGen product have high library yield and standard library peak pattern, which is suitable for the library preparation of animal and plant cell nuclei.

Library yield

Cell Input	Antibody	Cycles	Library Yield(ng)
5×10^4 293T cell nuclei	CTCF	12	2120
	RNAPol II	12	3636
3×10^3 Arabidopsis thaliana nuclei	H3	15	3240
	RNAPol	15	5400

Library peak pattern



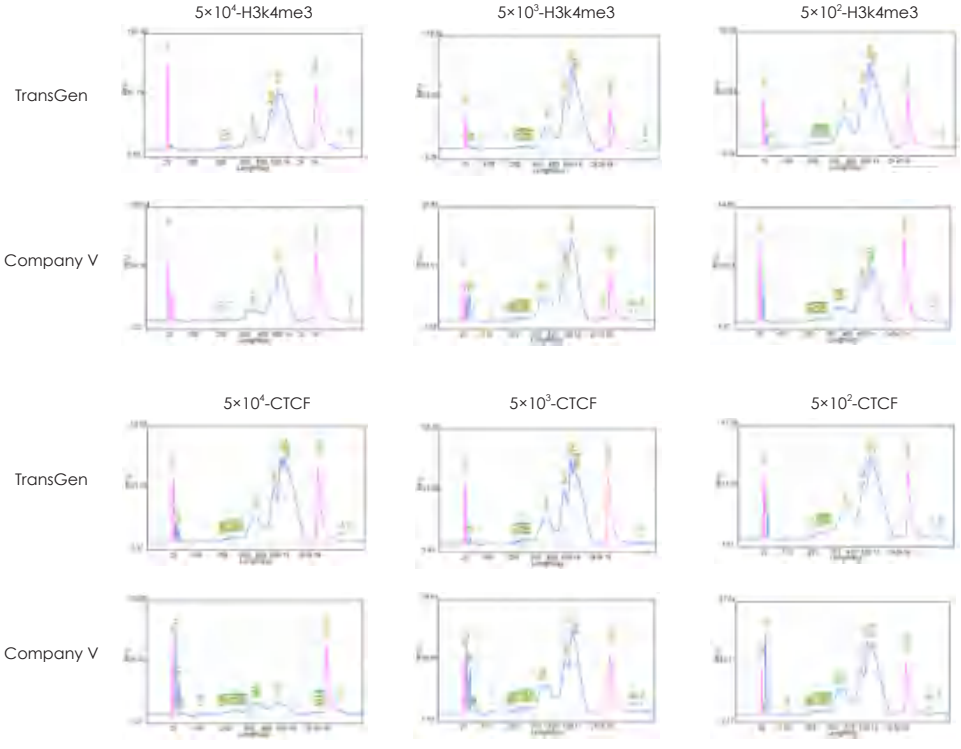
Comparison with competitive product

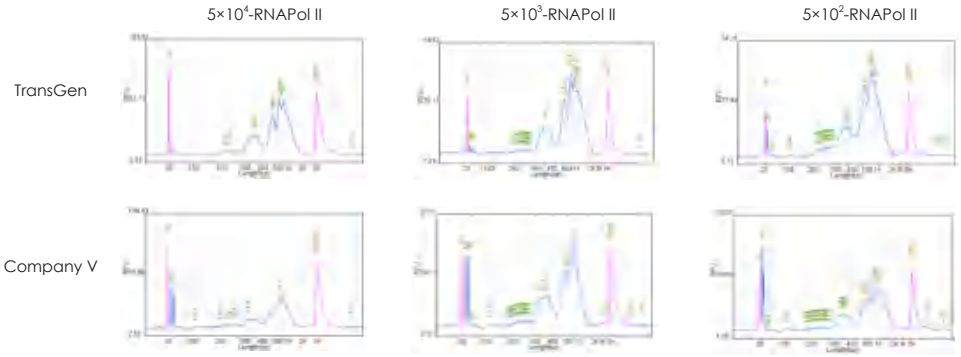
TransGen and Company V products were used to perform CUT&Tag experiments with H3k4me3, CTCF antibodies, and RNAPol II antibodies on 293T cells of different inputs , and the library yield, library peak pattern, and sequencing results were compared.
Compared with Company V, TransGen product has higher library yield, more standardized library peak pattern, and higher quality of sequencing data.

Library yield

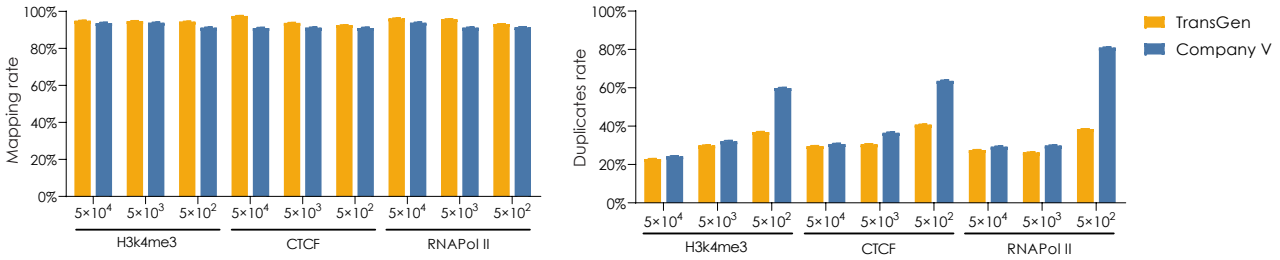
Antibody	Cell Input	Library Yield(ng)	
		TransGen	Company V
H3k4me3	5×10^4	1904	280
	5×10^3	2200	436
	5×10^2	836	376
CTCF	5×10^4	656	532
	5×10^3	1552	208
	5×10^2	646	206
RNAPol II	5×10^4	1240	100
	5×10^3	1644	308
	5×10^2	532	87.6

Library peak pattern



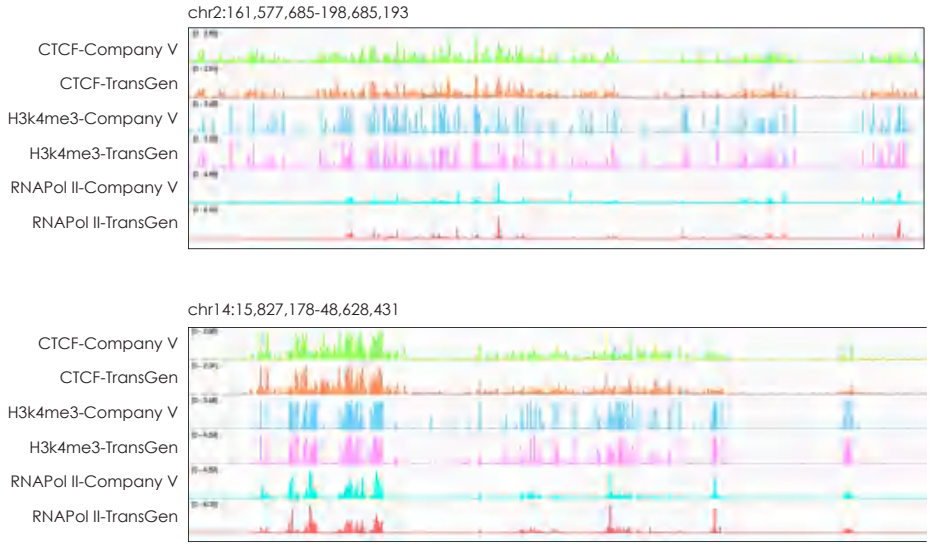


Sequencing data



Accurate and valid peak positions

CUT&Tag libraries generated from different target proteins (CTCF, H3k4me3, RNAPol II) of 5×10^4 293T cells by using TransGen and Company V products, the peak positions of two different chromosome segments were displayed.



Peak comparison picture of DNA interaction regions of different target proteins

TRANSGEN

Single Cell Library Preparation

D

*Trans*NGS® Single Cell Full Length cDNA Synthesis&Amplification Kit (KC901)

Features

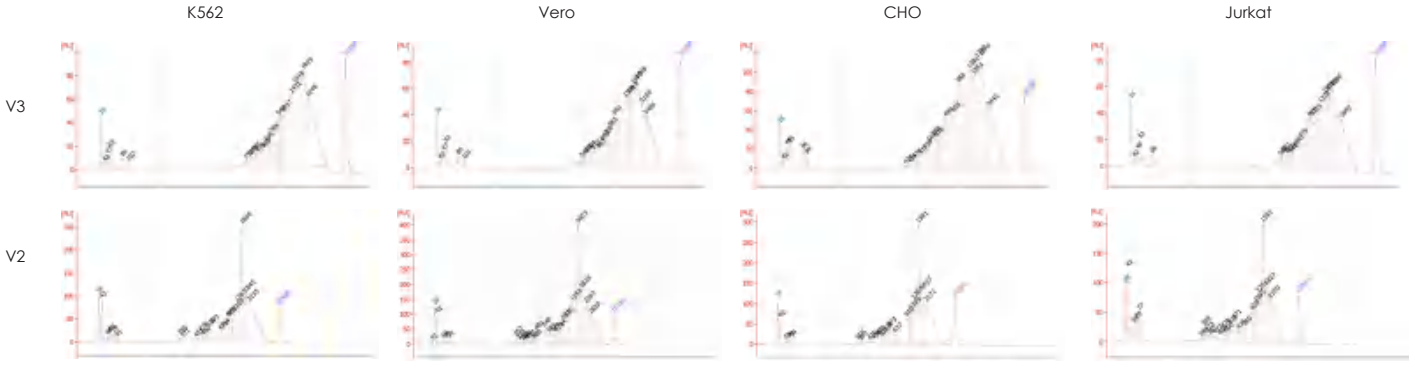
- Broad cell type compatibility – Suitable even for low-RNA-content cells (e.g., immune cells)
- Robust tissue adaptability – Effective for hard-to-dissociate tissues (e.g., brain samples)
- Rapid library prep – Total workflow time ~4 hours
- Streamlined reagent formulation – Simplified pipetting with consolidated components
- Enhanced full-length cDNA products – Improved transcript length coverage
- High-quality sequencing data – Ultra-low rRNA retention in cDNA products

Sample Requirements

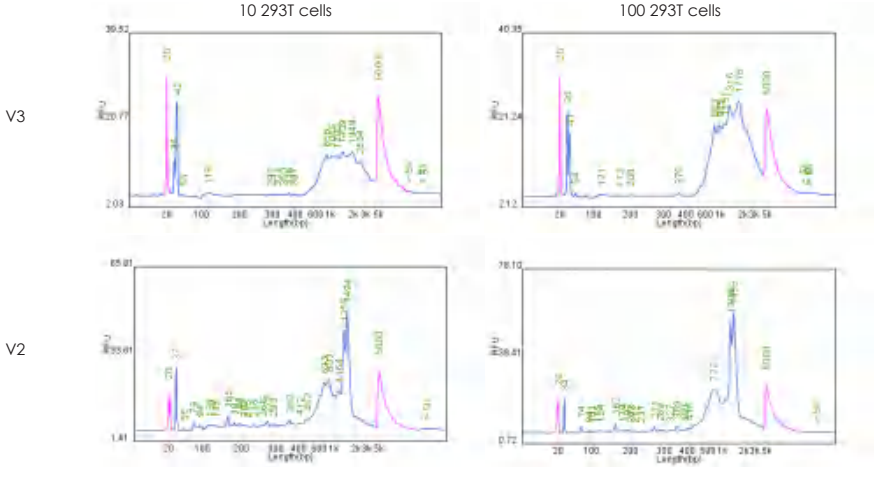
- 1–500 mammalian cells or eukaryotic cells lacking cell walls (e.g., protoplasts)
- 10 pg–10 ng total RNA (requires poly(A)-tailed mRNA)

Data Exhibition

Improved cDNA Fragment Length in Single-cell Outputs



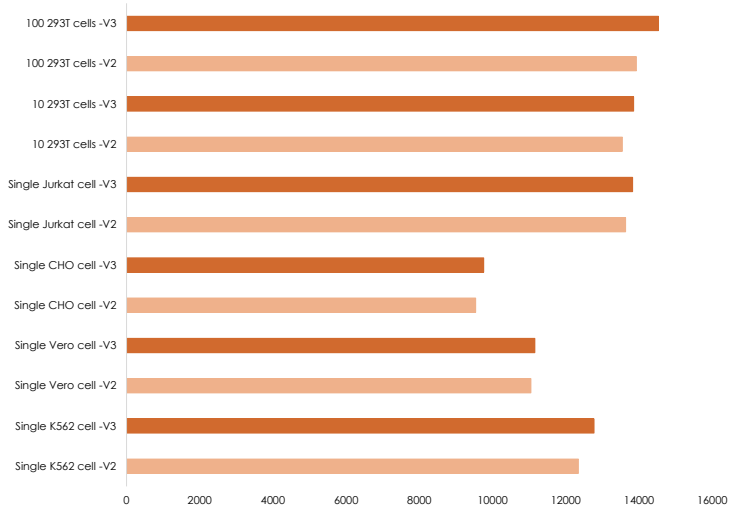
Improved cDNA fragment length in Bulk-cell Outputs



Low Non-specific Product Ratio

Group	Cell Type	Cell Number	rRNA(%)	Total mapped(%)	Exon(%)
1	K562 cell	1	2.60	97.75	71.80
2	Vero cell	1	3.15	98.11	72.50
3	CHO cell	1	2.52	97.25	70.10
4	Jurkat cell	1	2.34	98.07	73.00
5	293T cell	10	3.25	97.82	74.60
6	293T cell	100	3.62	98.13	74.90

Higher Number of Genes Detected



*Trans*NGS® Whole Transcriptome Amplification Kit (KC921)

Features

- Highly compatible with different cell types, suitable for low RNA content (such as immune cells).
- Highly compatible with different tissue types, suitable for tissues that are difficult to dissociate (such as brain tissue).
- High yield in single-cell library preparation, excellent peak shape and large number of genes detected effectively (FPKM>1).
- Short library preparation time, with a total duration of approximately 3 hours.
- The sample volume is up to 6 μl, supporting the amplification of RNA at different concentrations or varying numbers of cells.

Range of application

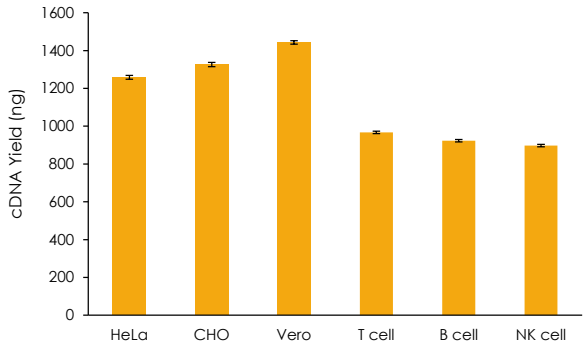
- 1-10^5 mammalian cells or eukaryotic cells without cell walls (such as protoplasts).
- 10 pg-100 ng total RNA (including mRNA with poly(A) sequences)

Data

Applicable to a wide variety of sample types

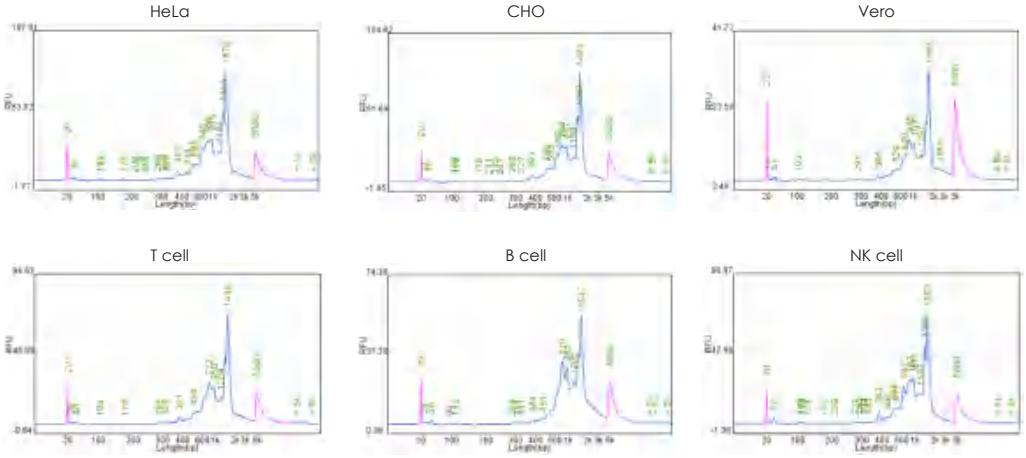
High Library Yield

Using KC921 to construct full-length cDNA libraries from six different types of single cells (with an input of 100 cells), the results show that KC921 is suitable for various cell types, with library yields exceeding 800 ng.



Peak Pattern

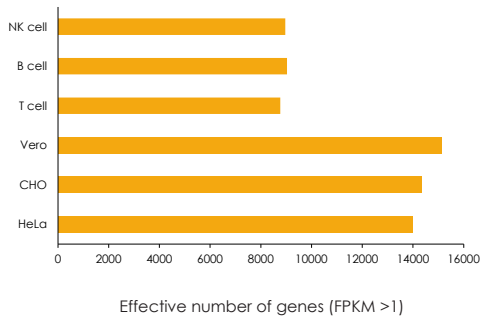
After purification, library peak profiles are analyzed using Qsep100. The results show that the library peak range covers 200-10,000 bp, the cDNA product sizes meet expectations and no abnormal peaks are observed.



High Sequencing Data Quality

The library results using Tn5 transposase enzyme show that the sequencing data quality is high across all cell types, with high gene coverage and a high number of effectively detected genes (FPKM >1)

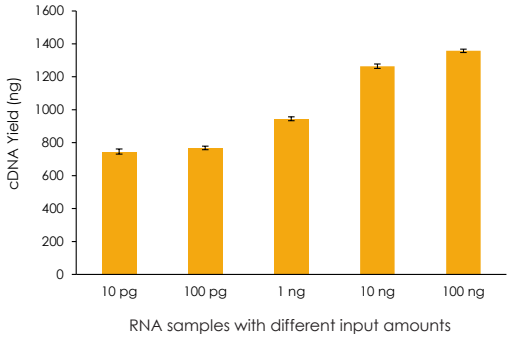
Cell Type	Q30	Total mapped	GC	Exon
HeLa	95.83%	97.98%	50.46%	79.91%
CHO	94.91%	97.54%	50.57%	81.61%
Vero	92.65%	98.10%	50.09%	78.57%
B cell	93.89%	97.67%	49.78%	76.37%
T cell	93.95%	97.77%	50.14%	77.63%
NK cell	93.92%	97.58%	49.39%	75.99%



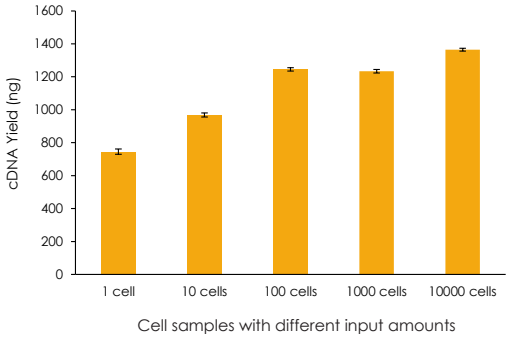
Wide Sample Input Range

Library Yield

Full-length cDNA amplification is performed using KC921 on RNA and cell samples with different input. After purification, library concentration is measured using Qubit. The results show that high library yields are achieved across various input, demonstrating the broad sample input compatibility of KC921.



RNA samples with different input amounts



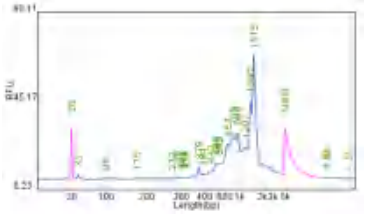
Cell samples with different input amounts

Great Library Peak Profile

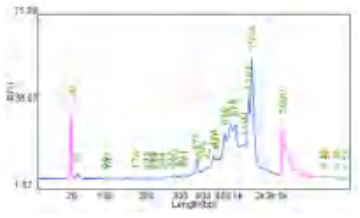
Full-length cDNA amplification is performed using KC921 on RNA and cell samples with different input. After purification, library peak profiles are analyzed using Qsep100. The results show that the library peak range covers 200-10,000 bp, the cDNA product sizes meet expectations and no abnormal peaks are observed.

With different RNA samples input amounts

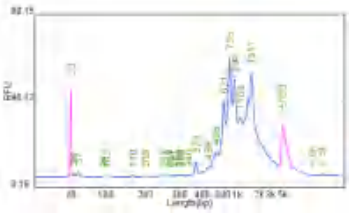
10 pg



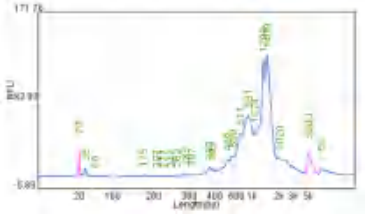
100 pg



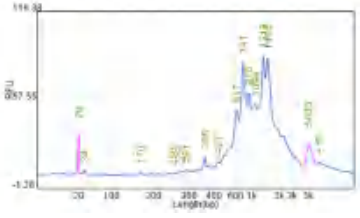
1 ng



10 ng

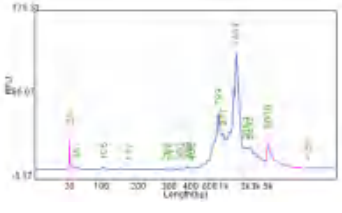


100 ng

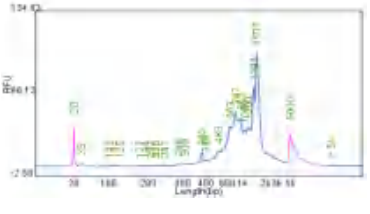


With different cell samples input amounts

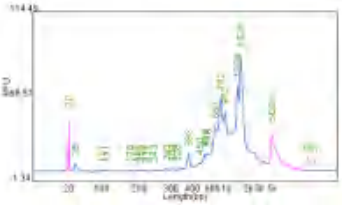
1 cell



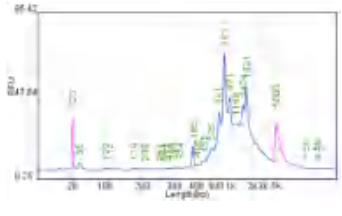
10 cells



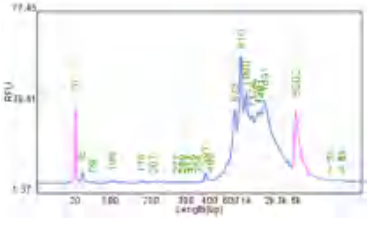
1000 cells



1000 cells



10000 cells

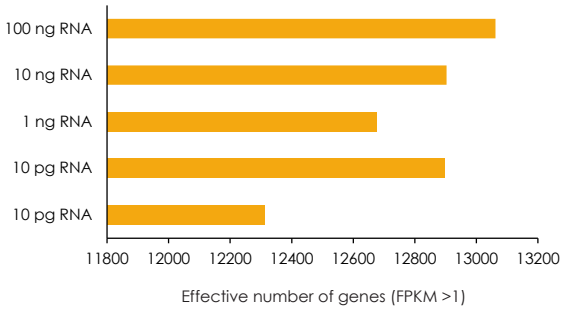


High Sequencing Data Quality

Full-length cDNA amplification is performed using KC921 on RNA and cell samples with different input, followed by library preperation using Tn5 transposase enzyme. The results show that KC921 products perform excellently across different input amounts in terms of Q30, total alignment rate and average number of effectively detected genes (gene FPKM >1), demonstrating high library construction efficiency.

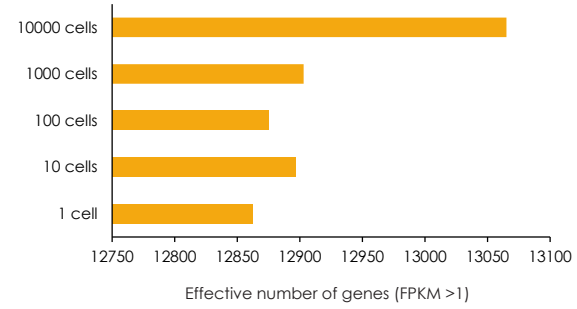
with different RNA samples input

样品投入量	Q30	Total mapped
10 pg RNA	95.63%	97.64%
100 pg RNA	95.91%	97.58%
1 ng RNA	95.78%	98.23%
10 ng RNA	95.89%	97.96%
100 ng RNA	95.95%	98.07%



with different cell samples input

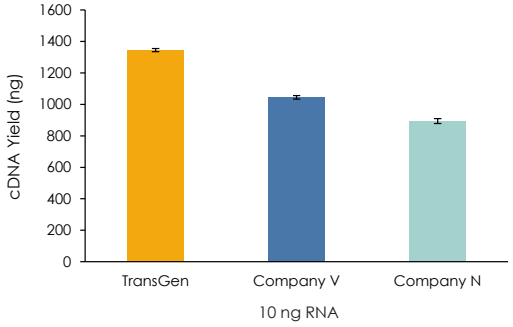
样品投入量	Q30	Total mapped
1 cell	94.76%	98.42%
10 cells	95.08%	98.16%
100 cells	95.23%	98.05%
1000 cells	95.21%	98.22%
10000 cells	95.13%	98.65%

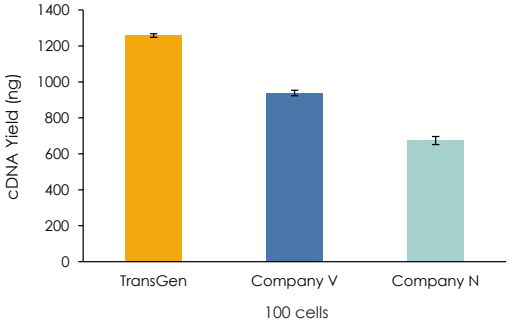


Comparison with Competitors

Higher Library Yield

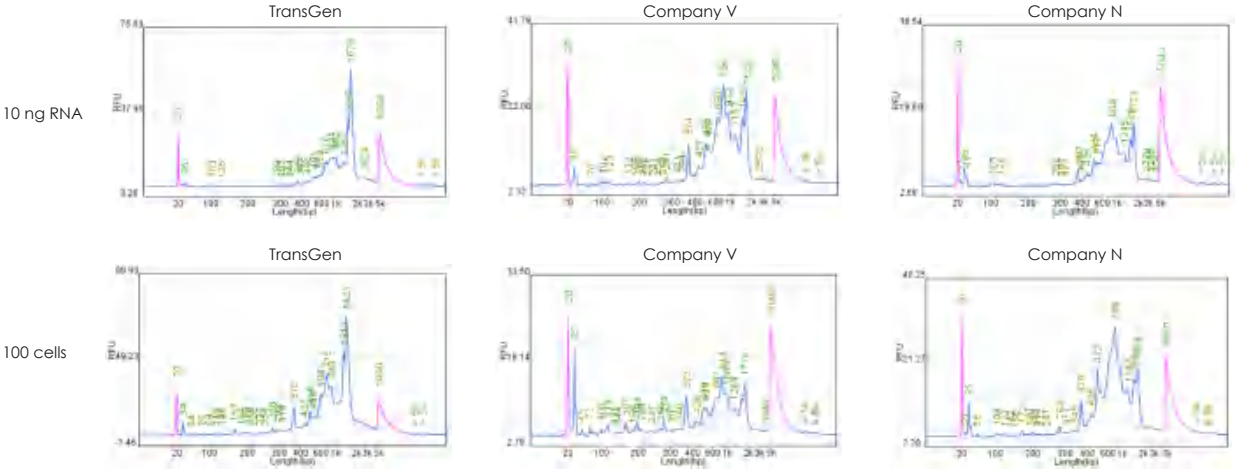
Full-length cDNA amplification is performed on 10 ng RNA and 100 HeLa cell samples using TransGen, Company V and Company N products. After purification, library concentration is measured using Qubit. The results show that TransGen product (KC921) consistently achieves higher library yields compared to competitor products.



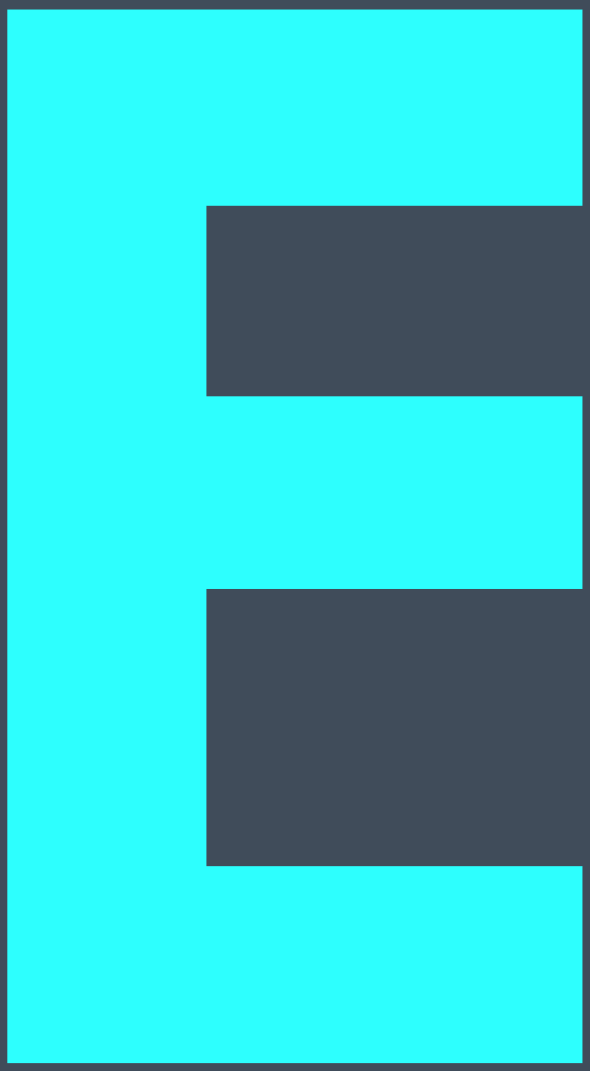


Better Library Peak Profile

Full-length cDNA amplification is performed on 10 ng RNA and 100 HeLa cell samples using TransGen, Company V and Company N products. After purification, library peak profiles are analyzed using Qsep100. The results show that the library peak range covers 200-10,000 bp, the cDNA product sizes meet expectations and no abnormal peaks are observed.



TRANSGEN Pathogenic Microorganism Detection



01 Nucleic Acid Extraction

MagicPure® Stool and Soil Genomic DNA Kit (EC801)

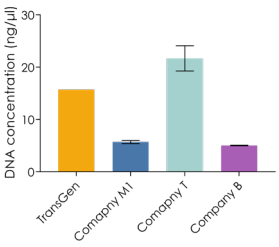
Features

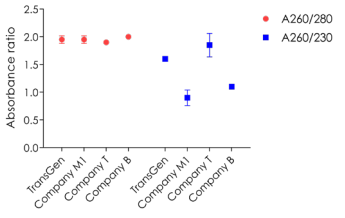
- Simple operation: cumbersome steps such as heating or ice bathing are not required.
- High purity: Humic Acid Removal can efficiently remove inhibitors to produce high-quality DNA.
- Wide range of applications: suitable for various soil and stool samples.

Comparison with competing products

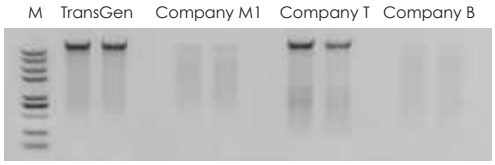
Soil samples

Silt

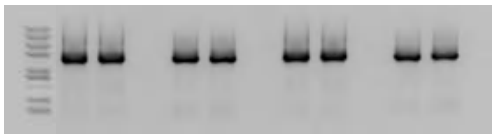




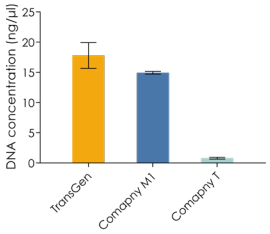
Agarose gel electrophoresis result of extracted gDNA

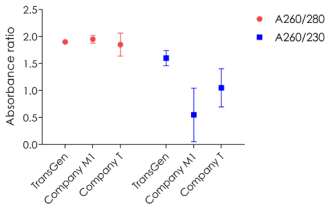


Amplification result of 16S



Farmland soil

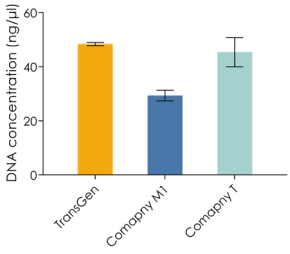


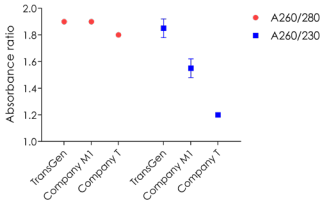


Agarose gel electrophoresis result of extracted gDNA

Amplification result of 16S

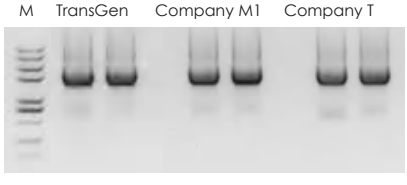
Grassland soil





Agarose gel electrophoresis result of extracted gDNA

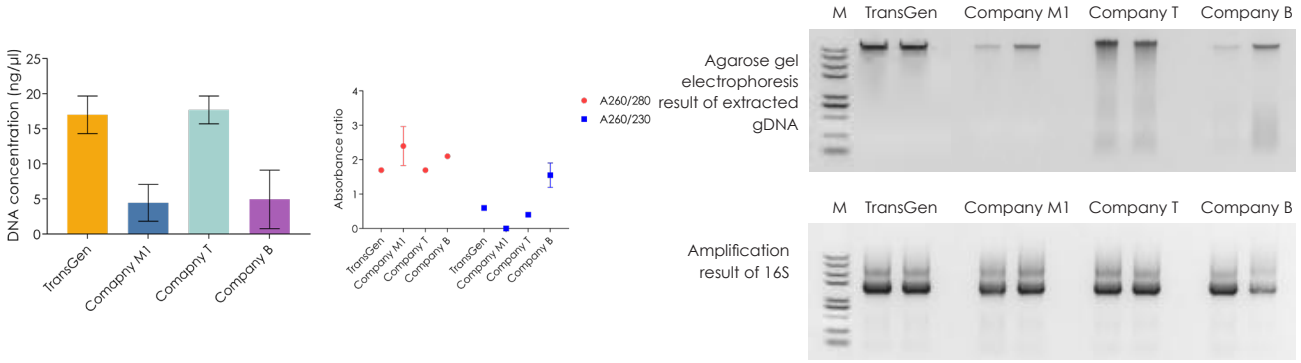
Amplification result of 16S



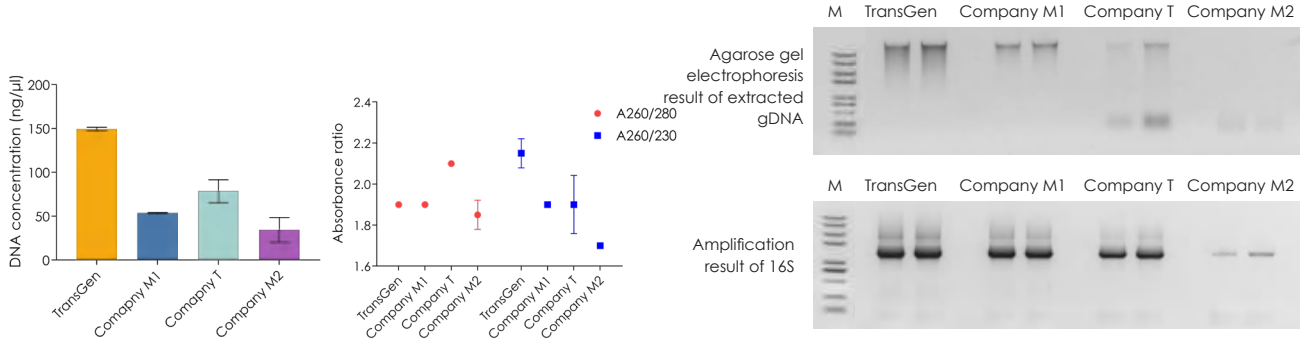
Genomic DNA was extracted from different soil samples using reagents from TransGen and competitors respectively. The extracted gDNAs were detected for DNA concentration, A260/280 ratio, A260/230 ratio, agarose gel electrophoresis, and downstream gene amplification. The results showed that extracted gDNAs using TransGen reagent had high concentration, good quality and no inhibition on downstream gene amplification.

Stool samples

Pig stool



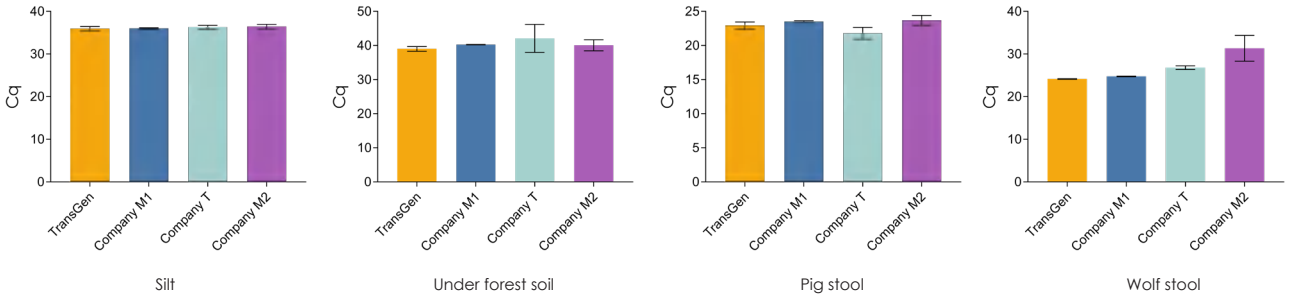
Mouse stool



Genomic DNA was extracted from different stool samples using reagents from TransGen and competitors respectively. The extracted gDNAs were detected for DNA concentration, A260/280 ratio, A260/230 ratio, agarose gel electrophoresis, and downstream gene amplification. The results showed that extracted gDNAs using TransGen reagent had high concentration, good quality and no inhibition on downstream gene amplification.

Downstream application

qPCR detection



Genomic DNA was extracted from different samples using reagents from TransGen and competitors respectively. The extracted gDNAs were used as templates for qPCR. The results showed that extracted gDNAs using TransGen reagent had better amplification performance and exhibits no inhibition in qPCR amplification.

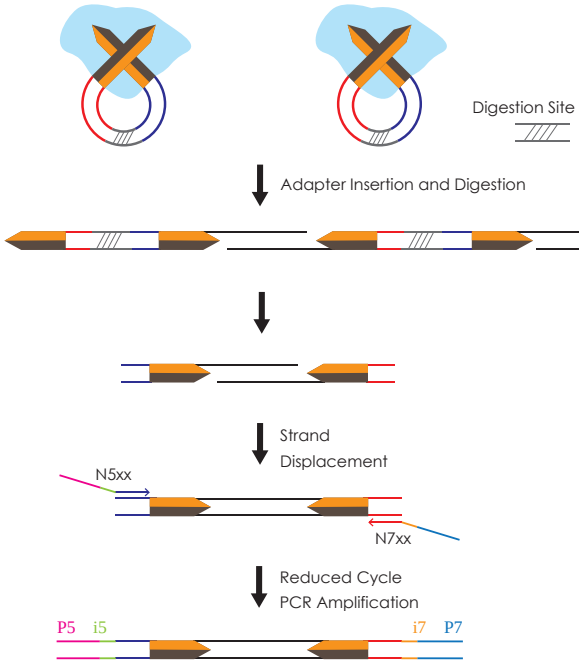
02 Library Preparation

*Trans*NGS® Microbiome DNA Library Prep Kit for Illumina® (KP141)

Features

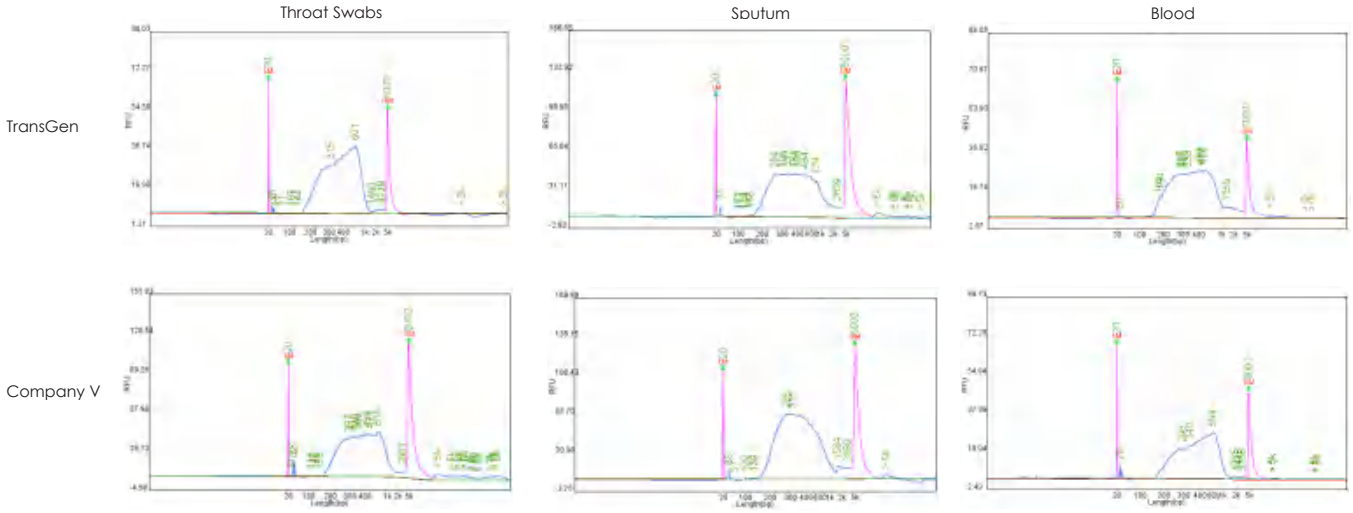
- Fast: no more than 90 minutes.
- Easy to operate: single-tube enzymatic reaction, DNA fragmentation and adapter ligation are synchronized.
- Wide compatibility: the transposase method is suitable for a variety of DNA template library construction requirements.
- Low sample volume: as low as 1 ng.

Schematic diagram of the metagenome library preparation



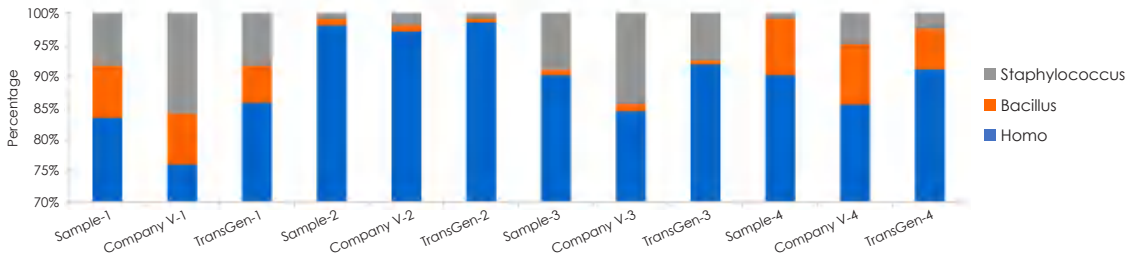
Comparison with Competitors

Library construction is performed using 1 ng of genomic DNA from throat swabs, sputum, and blood samples with TransGen and Company V's products, respectively. The results demonstrate that TransGen's product is suitable for library preparation across diverse sample types.



Library Construction using Clinically Simulated Samples

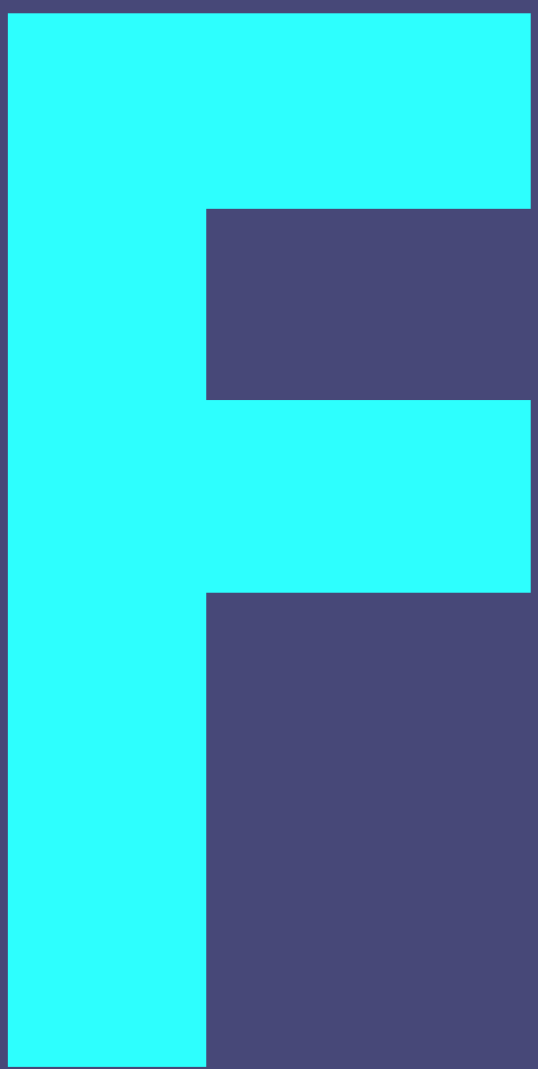
Library construction is performed using in vitro-simulated clinical pathogen samples with TransGen and Company V's products, respectively. The results demonstrate that TransGen's libraries achieve detection rates more closely aligned with the expected simulated proportions.



1:100 pg Bacillus DNA+100 pg Staphylococcus DNA+1 ng Homo DNA;
2:10 pg Bacillus DNA+10 pg Staphylococcus DNA+1 ng Homo DNA;
3:10 pg Bacillus DNA+100 pg Staphylococcus DNA+1 ng Homo DNA;
4:100 pg Bacillus DNA+10 pg Staphylococcus DNA+1 ng Homo DNA;

TRANSGEN

Common Used Enzymes



T4 DNA Ligase for NGS (LL101)

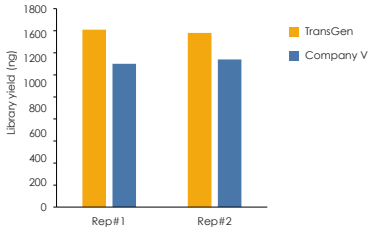
Applications

- This is primarily used for adapter ligation during NGS library construction.
- It can also be used for cloning of restriction enzyme fragments.

Comparison with competing products

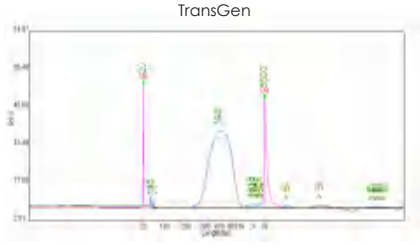
Using both TransGen and Company V products for library adapter ligation in next generation sequencing, the results indicate that the library yield and peak shape of TransGen are consistent with those of Company V products.

Library yield

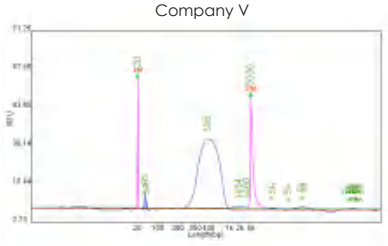


The peak shape of the library construction

TransGen



Company V



DNA polymerase I Klenow Fragment (LE201)

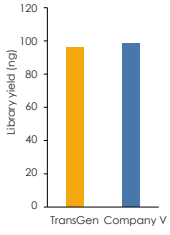
Applications

The complementary filling of the 5' overhang and excision of the 3' overhang in double-stranded DNA.

Comparison with competing products

Using a specific quantity of single-stranded cDNA (GFP gene, approximately 700 bp) as a template, dual-strand synthesis was performed using TransGen and Company N products separately. The reaction was carried out at 25℃ for 10 minutes, and the yield was measured. The results indicate that the performance of TransGen products is consistent with that of Company N products in next-generation sequencing.

Library yield



T4 DNA Polymerase (LP201)

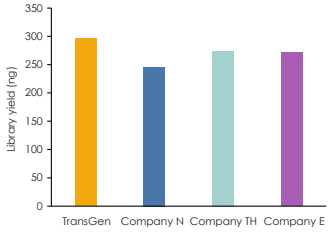
Applications

- Smoothing of DNA 5' or 3' protruding ends.
- Synthesis of labeled DNA probes through displacement reaction.
- Subcloning after single-strand deletion.
- Synthesis of the second strand during gene site-directed mutagenesis process.

Comparison with competing products

Using a certain amount of single-stranded cDNA (GFP gene, approximately 700 bp) as a template, we performed double-stranded synthesis using TransGen products and similar competitors. The reaction was carried out at 25℃ for 10 minutes, and the yield was measured. The results indicate that the performance of TransGen products is consistent with that of the competitors.

Library yield



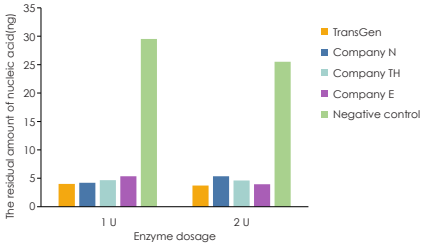
T4 Polynucleotide Kinase (LK101)

Applications

- Oligonucleotide, DNA, or RNA 5' end labeling for use as probes in Southern, Northern, EMSA, DNA sequencing primers, PCR primers, etc.
- Phosphorylation of oligonucleotide, DNA, or RNA 5' ends.
- Removal of 3' end phosphate groups.

Comparison with competing products

Using 1U and 2U TransGen products, as well as similar competitor products, a 50 ng 250 bp PCR fragment was phosphorylated. The resulting product was digested using λ enzyme (with phosphorylated double-stranded DNA as the optimal substrate) and the remaining product was quantified. The results indicate that the phosphorylation efficiency of TransGen products is consistent with that of the competitors.



*Trans*NGS® Library Amplification SuperMix (KA101)

Features

- Ultra high fidelity.
- Low preference.
- High sensitivity and specificity.
- Hot Start.

Applications

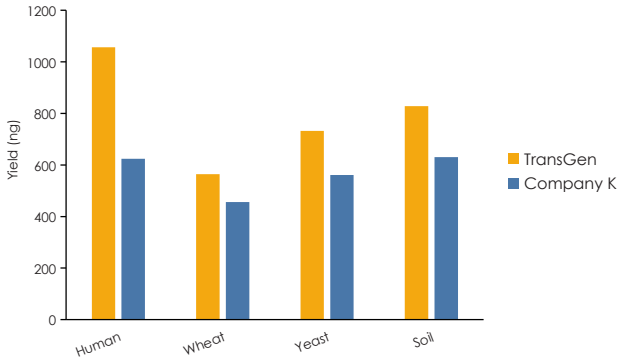
Next-generation sequencing library amplification.

Comparison with Competitors

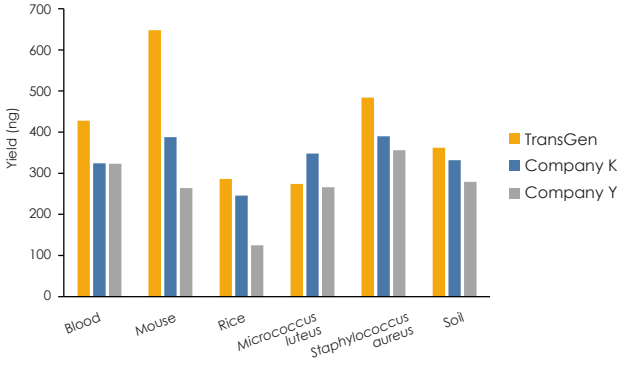
DNA and RNA libraries from species with varying GC content are amplified using TransGen, Company K, and Company Y's products. The results show that TransGen outperform competitors in yield, deliver superior sequencing quality, exhibit uniform GC distribution, and maintain high data correlation with rival products.

Library Yield

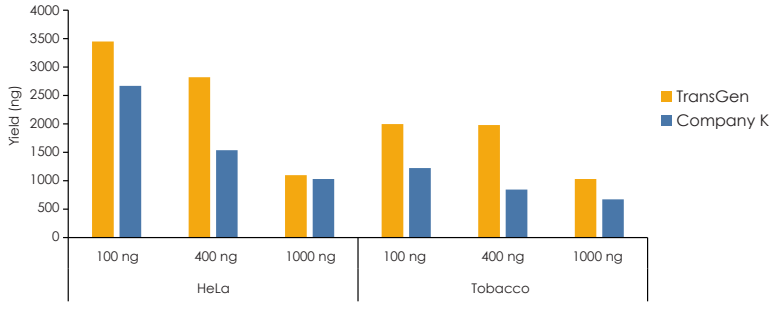
Ultrasonic DNA Fragmentation Library preparation



Enzymatic DNA Fragmentation Library Preparation



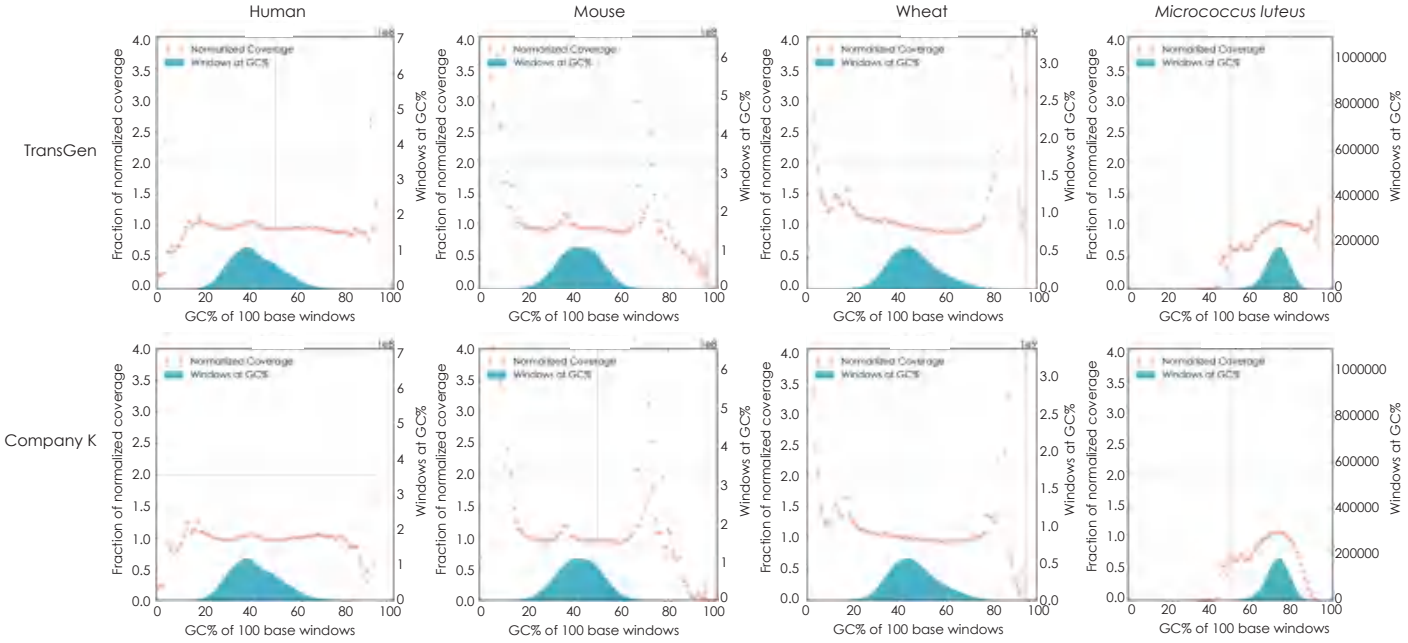
RNA Library Preparation



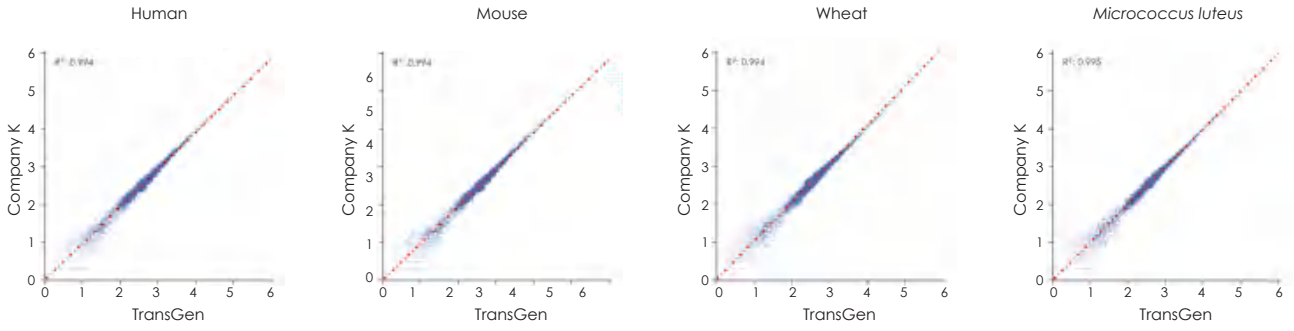
Sequencing Data Quality

Species	Kit	Q30(%)	GC Content(%)	PCR duplicate(%)	Unmapped reads(%)
Human	TransGen	92.51	41.06	27.21	0.39
	Company K	92.30	41.08	27.28	0.43
Wheat	TransGen	91.37	45.91	27.17	0.88
	Company K	91.06	46.13	25.23	0.97
Mouse	TransGen	93.87	41.45	53.12	0.51
	Company K	93.28	41.44	54.99	0.53
Micrococcus luteus	TransGen	95.07	73.03	45.16	17.75
	Company K	95.09	72.64	45.68	18.16

GC Distribution



Correlation Analysis



Category	Product Name	Catalog Number	Specification
DNA Library Preparation	*Trans*NGS® Tn5 DNA Library Prep Kit for Illumina® (for 50 ng DNA)	KP101-11/03	12 rxns / 96 rxns
	*Trans*NGS® Tn5 DNA Library Prep Kit for Illumina®(for 1 ng DNA)	KP111-11/03	12 rxns / 96 rxns
	*Trans*NGS® Tn5 DNA Library Prep Kit for Illumina®(for 5 ng DNA)	KP121-11/03	12 rxns / 96 rxns
	*Trans*NGS® Tn5 Plasmid DNA Library Prep Kit for Illumina® (for ≤3 ng Plasmid DNA)		定制
	*Trans*NGS® DNA Library Prep Kit for Illumina®	KP201-11/03	12 rxns / 96 rxns
	*Trans*NGS® DNA Library Prep Kit for MGI®	KP221-01/02	12 rxns / 96 rxns
	*Trans*NGS® Fragmentase DNA Library Prep Kit for Illumina®	KP231-01/02	12 rxns / 96 rxns
	*Trans*NGS® Fragmentase DNA Library Prep Kit for Illumina® (SuperMix Version)		
	*Trans*NGS® Fragmentase DNA Library Prep Kit for MGI®	KP241-01/02	12 rxns / 96 rxns
	*Trans*NGS® ATAC-Seq Library Prep Kit for Illumina®	KP171-01/02	12 rxns / 96 rxns
	*Trans*NGS® CUT&Tag Library Prep Kit for Illumina®	KP172-01/02	12 rxns / 96 rxns
	*Trans*NGS® Transformation Kit For MGI®	KC301-01/02	12 rxns / 96 rxns
	*Trans*NGS® Universal Circularization Kit For MGI®	KC401-01/02	12 rxns / 96 rxns
	MagicPure® Size Selection DNA Beads	EC401-01/02/03/04	1 mL / 5 mL / 60 mL / 450 mL
RNA Library Preparation	*Trans*NGS® rRNA Depletion Kit (Human/Mouse/Rat)	KD101-11/03	12 rxns / 96 rxns
	MagicPure® mRNA Kit	EC511-01/02	24 rxns / 96 rxns
	*Trans*NGS® Fast RNA-Seq Library Prep Kit for Illumina®	KP701-01/02	12 rxns / 96 rxns
	*Trans*NGS® Fast RNA-Seq Library Prep Kit for MGI®	KP801-01/02	12 rxns / 96 rxns
	MagicPure® RNA Beads	EC501-01/02/03	1 ml / 5 ml / 60 ml
	*Trans*NGS® Single Cell Full Length cDNA Synthesis&Amplification Kit	KC901-01/02/03	12 rxns /24 rxns / 96 rxns
	*Trans*NGS® Whole Transcriptome Amplification Kit	KC921-01/02	12 rxns / 96 rxns
Adapter &Library Quantification	*Trans*NGS® Library Quantification Kit for Illumina®	KQ101-01/02	100 rxns / 500 rxns
	*Trans*NGS® Library Quantification qPCR SuperMix	KQ201-01/02	1 mL / 5×1 mL
	*Trans*NGS® Library Quantification DNA Standards (S1-S6)	KS101-21	50% , 120 μL each
	*Trans*NGS® Library Dilution Buffer	KB101-01	5×1 mL
	*Trans*NGS® UDI Indexed Adapter Kit for Illumina®	KI341-01/02	192 rxns / 384 rxns
	*Trans*NGS® 384 UDI Indexed Adapter Kit for Illumina®	KI351-01/02	192 rxns / 384 rxns
	*Trans*NGS® Indexed Adapter Kit for MGI®	KI401-S_{1-3}-01/02	192 rxns / 384 rxns
	*Trans*NGS® Tn5 Index Kit for Illumina®	KI101-01/02	48 rxns / 192 rxns
	*Trans*NGS® Index Primers (384) Kit for Illumina®	KI241-01/02	96 rxns / 384 rxns
	1×dsDNA HS Assay Kit	GS401-00/01/02	20 rxns /100 rxns / 500 rxns
Pathogenic Microorganism Detection	*TransGuard*® Disposable Virus Sampling Tube	ES101-01	50 rxns
	TransGuard® Fecal DNA Sampling Tube	ES102-01	50 rxns
	TransGuard® Buccal Swab DNA Preservation Buffer	ES103-01	50 mL
	*Trans*NGS® Host DNA Depletion Kit	EH301-01	50 rxns
	EasyPure® Microbiome DNA Isolation Kit	EE401-01	50 rxns
	MagicPure® 32 Microbiome DNA Isolation Kit	EC107-32-11	32 rxns
	EasyPure® Viral DNA/RNA Kit	ER201-01/02	50 rxns / 200 rxns
	MagicPure® Fly 96 Viral DNA/RNA Kit	EC331-96	96 rxns
	MagicPure® Stool and Soil Genomic DNA Kit	EC803-01	50 rxns
	*Trans*NGS® Microbiome DNA Library Prep Kit for Illumina®	KP141-01/02	12 rxns / 96 rxns
Commonly Used Enzymes	T4 DNA Ligase(for NGS)	LL101-01/02	200 μL / 1 mL
	T4 DNA Polymerase	LP201-01/02	150 units / 5×150 units
	T4 Polynucleotide Kinase	LK101-01/02	500 units / 4×500 units
	DNA Polymerase I Klenow Fragment	LE201-01	500 units
	*Trans*NGS® Library Amplification SuperMix	KA101-01/02	1 mL / 5×1 mL

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