Reminder

If you have any questions, please contact us by customer service hot line +86-400-898-0321

About us

- We Provide High Quality Products for Life Science.
- We Provide Simple and Efficient Methods.
- We Provide New Concept for Scientific Research.

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TRANS
TRANSGEN BIOTECH

Next Generation Sequencing Series Products

ABOUT US

TransGen Biotech Co., Ltd.

TransGen Biotech Co., Ltd. is a national high-tech enterprise specializing in the development, manufacture, sales of molecular and cellular biology products. Its headquarters is located in the research and development base of Beijing high-tech industry -Zhongguancun Dongsheng International Science Park. The headquarters covers an area of nearly 10,000 square meters, equipped with GMP facilities and gene amplification detection labs. The company has been certified by ISO9001 and ISO13485 quality management systems, and is committed to providing raw materials for molecular diagnostic industry and CRO services according to customized needs from customers.

CONTENTS

TransNGS® DNA Library Prep Kit for Illumina®

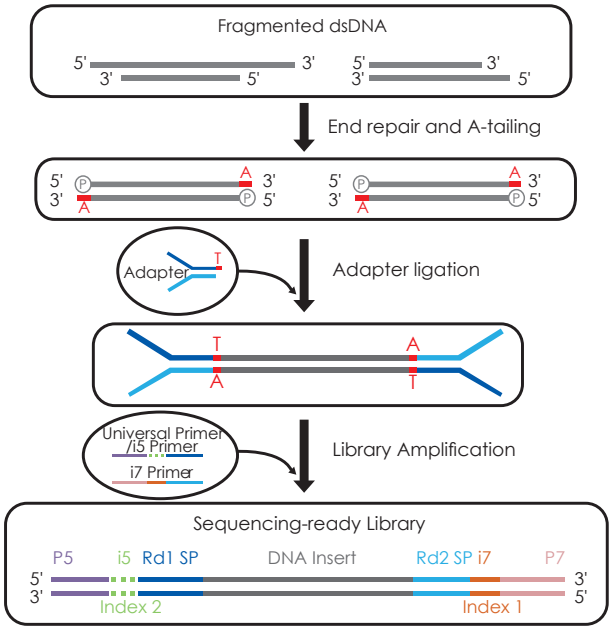
Features

- High library conversion rate
- Diverse applicable sample type

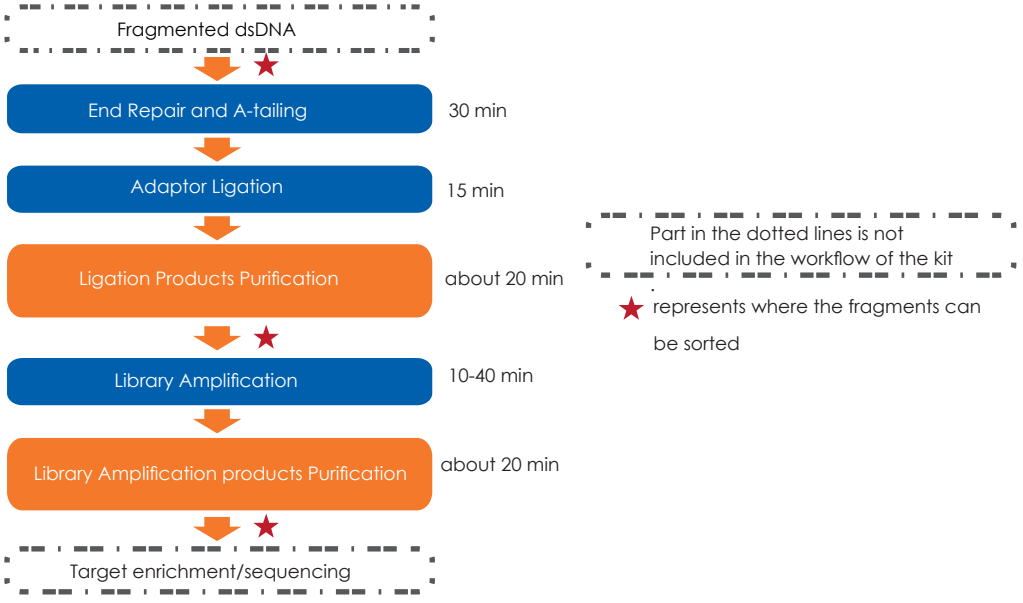
Application

- Whole genome sequencing.
- Target gene sequencing.
- Exon sequencing / other target capture sequencing.
- Metagenomic sequencing.
- Immunoprecipitation sequencing.

Principle of Library Preparation



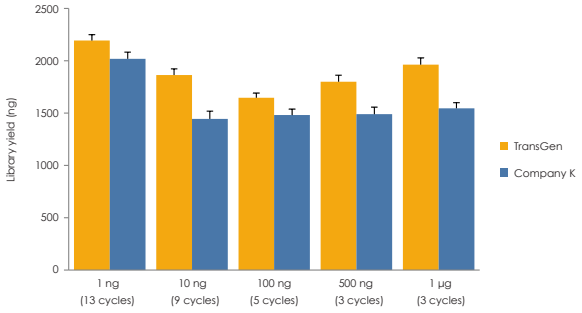
Operation Flow Chart



Comparison with Competitors

(1) Comparison of library yields of different initial sample inputs

Libraries were prepared with different initial sample inputs of dsDNA derived from fragmented human blood genome DNA, using TransGen, company K products. The results show that TransGen products have a higher efficiency in library preparation for the initial sample inputs of 1 ng-1 μg.



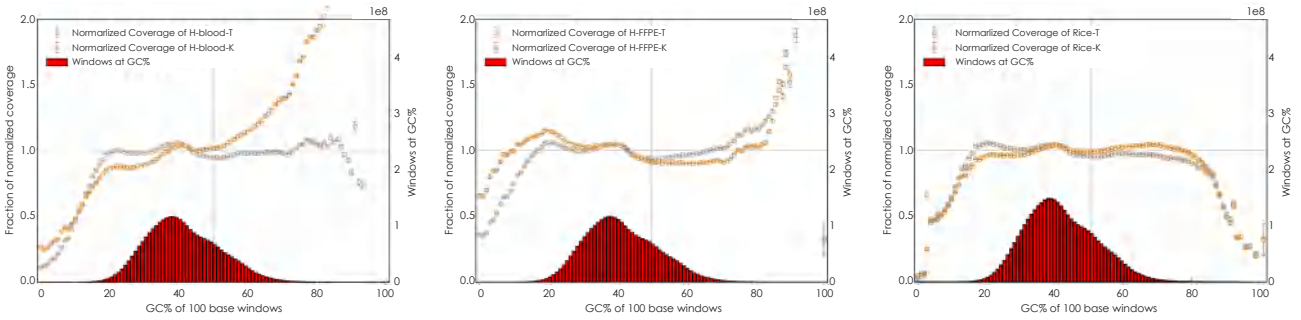
(2) Comparison of sequencing results

Libraries were prepared with 100 ng fragmented dsDNA derived from genomic DNA of human blood, human lung FFPE samples, and rice leaf samples, using TransGen and company K products respectively. Then they were sequenced and analyzed. The results of sequencing data quality, GC distribution, and correlation show that TransGen product performed similarly to competitor's product.

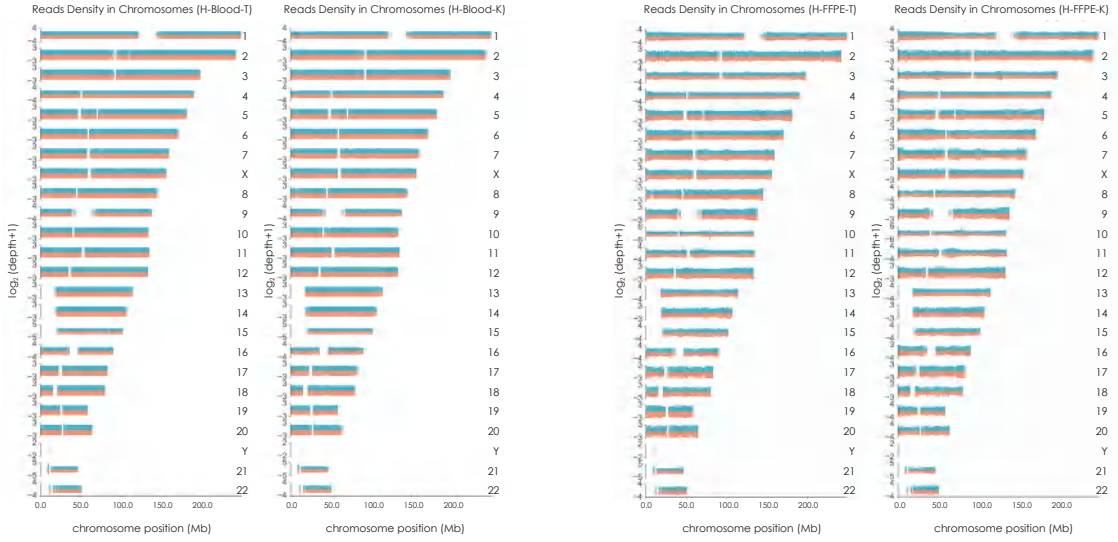
Sequencing Data Quality

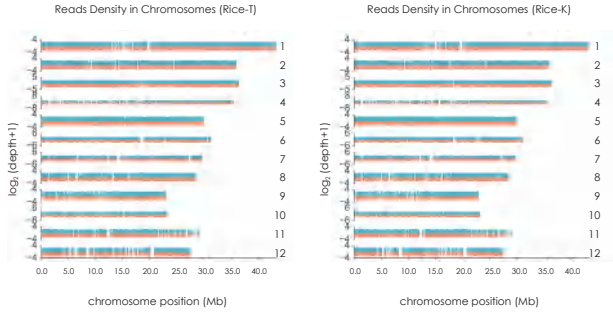
Sample	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped (%)	Coverage-1× (%)	Coverage-4× (%)	Duplication Rate (%)	Depth
H-Blood-T	97.74	91.67	40.53	98.47	96.29	89.45	11.17	8.06
H-Blood-K	97.56	91.62	41.56	98.49	96.13	89.46	11.27	8.04
H-FFPE-T	97.83	91.66	41.59	97.56	96.18	84.68	10.31	8.09
H-FFPE-K	97.64	91.23	43.32	97.51	96.15	84.67	10.41	8.05
Rice-T	97.64	91.62	43.76	94.54	88.18	80.78	9.56	11.43
Rice-K	97.63	91.63	44.02	94.52	88.07	80.72	10.47	11.56

GC Distribution



Chromosome Coverage Depth Distribution



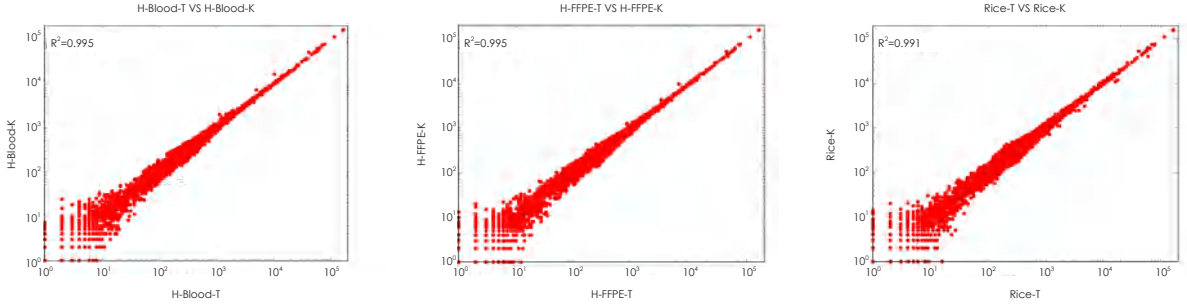


SNP Analysis

Sample	Total	ts	tv	ts/tv	Het rate (‰)
H-Blood-T	3644082	2428172	1215910	1.997	0.661
H-Blood-K	3536253	2352768	1183485	1.988	0.718
H-FFPE-T	2922527	1962117	960410	2.043	0.771
H-FFPE-K	2969375	1998991	970384	2.06	0.76
Rice-T	4061849	2917666	1144183	2.55	4.394
Rice-K	4201744	3021147	1180597	2.559	4.657

ts: SNP transitions tv: SNP transversions tv: SNP transversions Het rate(‰): Heterozygosity rate

Correlation Analysis



TransNGS® DNA Library Prep Kit for MGI®

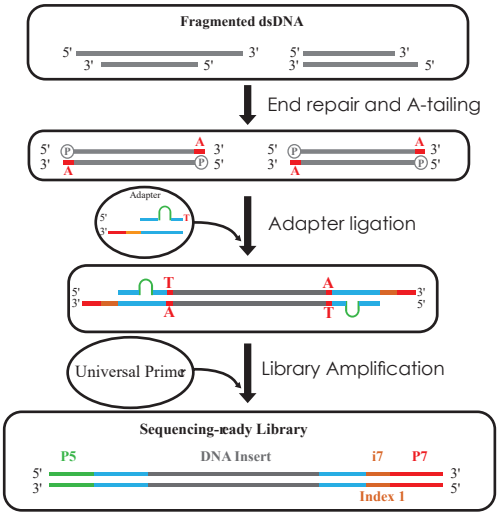
Features

- Diverse applicable sample type
- High conversion rate
- High data quality

Application

- Whole genome sequencing.
- Target gene sequencing.
- Exon sequencing / other target capture sequencing.
- Metagenomic sequencing.
- Immunoprecipitation sequencing.

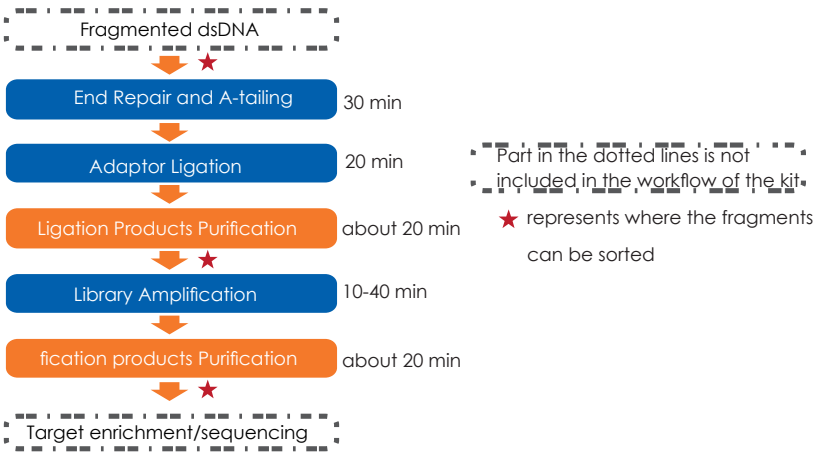
Principle of Library Preparation



Schematic diagram of the strand-specific library preparation principle

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

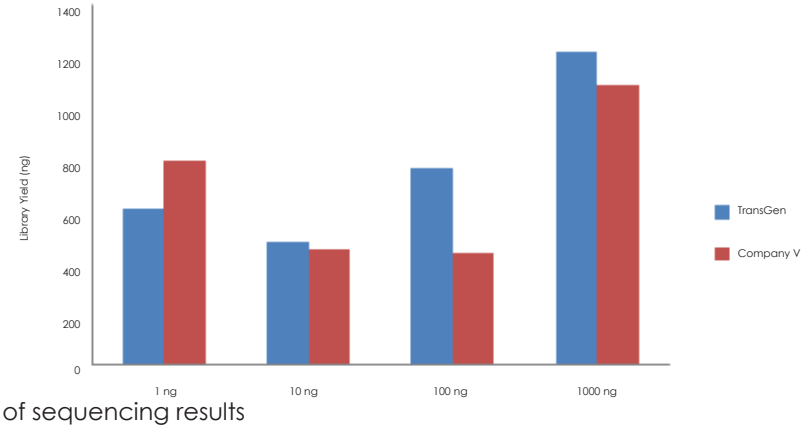
Operation Flow Chart



Comparison with Competitors

(1) Comparison of library yields of different initial sample inputs

Libraries were prepared with fragmented dsDNA derived of different initial sample inputs from human HeLa cells by the same number of cycles, using TransGen and company V products. The results show that TransGen products have a higher efficiency for library preparation for the initial sample input of 1 ng-1 μg.



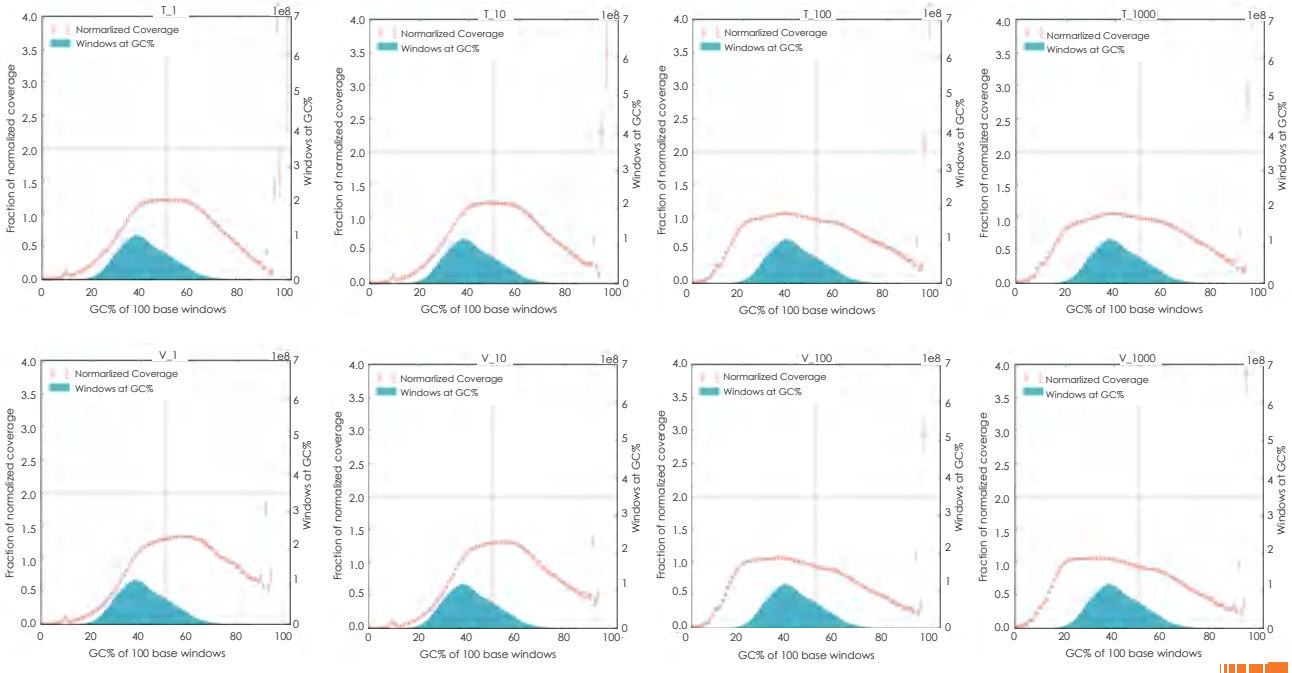
(2) Comparison of sequencing results

Libraries were prepared with fragmented dsDNA derived of different initial sample inputs from human HeLa cells, using TransGen and company K products. Then they were sequenced and analyzed. The results of sequencing data quality, GC distribution, and correlation show that TransGen products performed similarly to competitor's product.

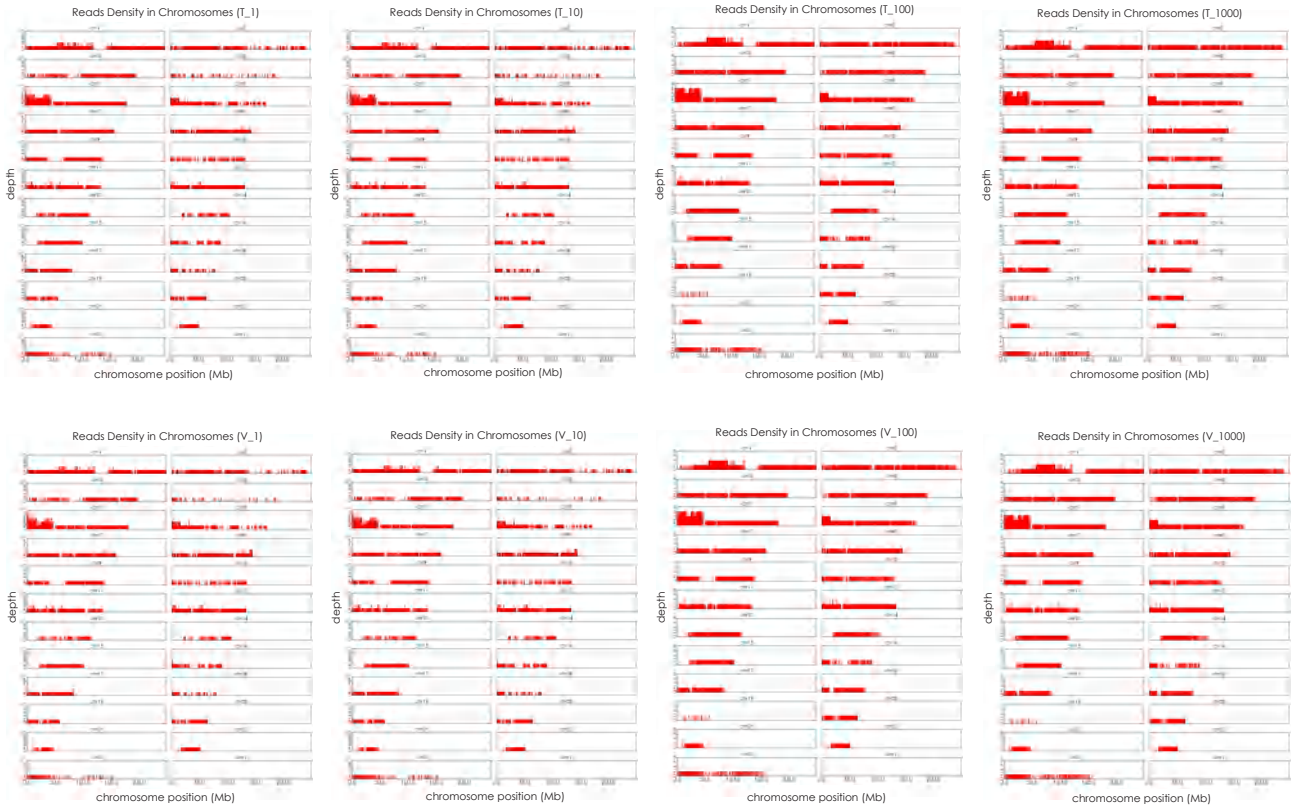
Sequencing Data Quality

Sample	Clean reads	Optical/PCR duplicate	Unmapped reads	Total mapped	Multiple mapped	Uniquely mapped	Q20(%)	Q30(%)	GC Content(%)
T_1	42720938	684528 (1.60%)	230611 (0.54%)	41805799 (97.86%)	2456018 (5.75%)	39349781 (92.11%)	96.12	90.99	43.11
T_10	42715766	123735 (0.29%)	215356 (0.50%)	42376675 (99.21%)	2474022 (5.79%)	39902653 (93.41%)	96.19	91.14	43.19
T_100	42720042	40336 (0.09%)	395135 (0.92%)	42284571 (98.98%)	2191110 (5.13%)	40093461 (93.85%)	96.43	91.66	40.78
T_1000	42720058	48045 (0.11%)	363641 (0.85%)	42308372 (99.04%)	2225122 (5.21%)	40083250 (93.83%)	96.54	91.89	41.02
V_1	42711428	914214 (2.14%)	205217 (0.48%)	41591997 (97.38%)	2560892 (6.00%)	39031105 (91.38%)	96.27	91.34	44
V_10	42710566	124841 (0.29%)	189493 (0.44%)	42396232 (99.26%)	2599217 (6.09%)	39797015 (93.18%)	95.96	90.63	43.9
V_100	42710232	41899 (0.10%)	418119 (0.98%)	42250214 (98.92%)	2176671 (5.10%)	40073543 (93.83%)	96.15	91.04	40.49
V_1000	42704112	40522 (0.09%)	420547 (0.98%)	42243043 (98.92%)	2159708 (5.06%)	40083335 (93.86%)	96.06	90.82	40.48

GC Distribution



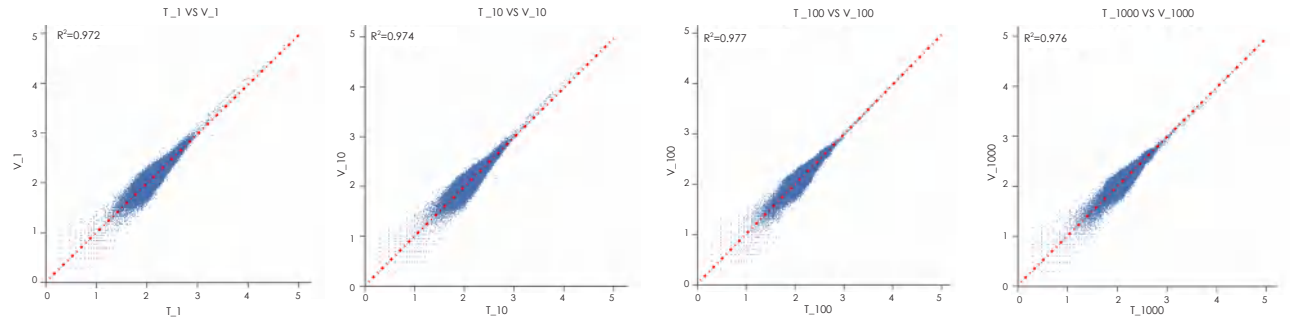
Chromosome Coverage Depth Distribution



SNP Analysis

Sample	Total	ts	tv	ts/tv	Het rate(‰)
T_1	370121	248048	122073	2.032	0.056
T_10	385539	258593	126946	2.037	0.059
T_100	346836	229439	117397	1.954	0.052
T_1000	351188	232588	118600	1.961	0.053
V_1	387938	259987	127951	2.032	0.06
V_10	395365	265578	129787	2.046	0.061
V_100	330186	217375	112811	1.927	0.049
V_1000	331440	218787	112653	1.942	0.049

Correlation Analysis



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

Features

• Remove up to 99% ribosomal RNA from human/mouse/rat total RNA.

• Control qPCR Primer Sets are provided to monitor the depletion efficiency of ribosomal RNA and the retention rate of non-ribosomal RNA.

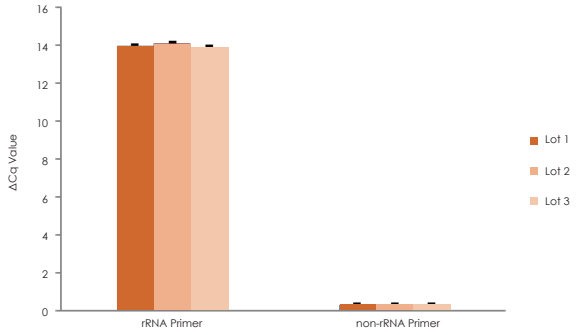
Application

• Human/ Mouse/ Rat total RNA samples (100 ng-1 μg).

• Suitable to both intact and degraded RNA samples (e.g. FFPE RNA).

Lot to Lot Consistency

rRNA depletion for 1 μg total RNA (HepG2 cell) was performed using TransNGS® rRNA Depletion Kit (Human/Mouse/Rat) of 3 different lots, and qRT-PCR was performed using rRNA Primer and Non-rRNA Primer for treated and non-treated samples. △ Ct (Ct of treated sample minus Ct of non-treated sample) kept consistent for 3 different lots, which indicated that *Trans*NGS® rRNA Depletion Kit (Human/Mouse/Rat) has very good stability.



△ Ct of 3 different lots

Comparison with Competitors

rRNA depletion for 1 μg total RNA of human (H), mouse (M), Rat (R) was performed using TransNGS® rRNA Depletion Kit (Human/Mouse/Rat) and Company K rRNA depletion kit. Then library was prepared (TransGen, KP601), sequenced, and analyzed. The results of sequencing data quality, rRNA depletion rate, circRNA and lncRNA detection amount, and correlation show that TransGen product performed similarly to competitor's product, and even better.

Sequencing Aata Quality

Sample	rRNA Rate(%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
H-CK	76.4	30611582	96.36	90.37	48.1	24914766 (81.39%)	21400556 (69.91%)
H-T	3.13	33860104	97.28	91.69	44.52	30467321 (89.98%)	29898471 (88.3%)
H-K	4.1	25323776	96.97	87.72	45.3	22631858 (89.37%)	22135512 (87.41%)
M-CK	82.2	31734716	96.37	90.39	50.52	26266824 (82.77%)	23902588 (75.32%)
M-T	3.37	26782378	97.13	89.71	44.91	23541710 (87.9%)	21366981 (79.78%)
M-K	5.7	28705540	97.05	88.71	45.11	25039842 (87.23%)	22829515 (79.53%)
R-CK	76.1	29980720	96.92	91.45	47.73	23828676 (79.48%)	20344916 (67.86%)
R-T	0.6	36024365	97.09	89.21	45.01	31315980 (86.93%)	28981601 (80.45%)
R-K	1.47	38587178	97.07	88.96	45.06	33566986 (86.99%)	30862024 (79.98%)

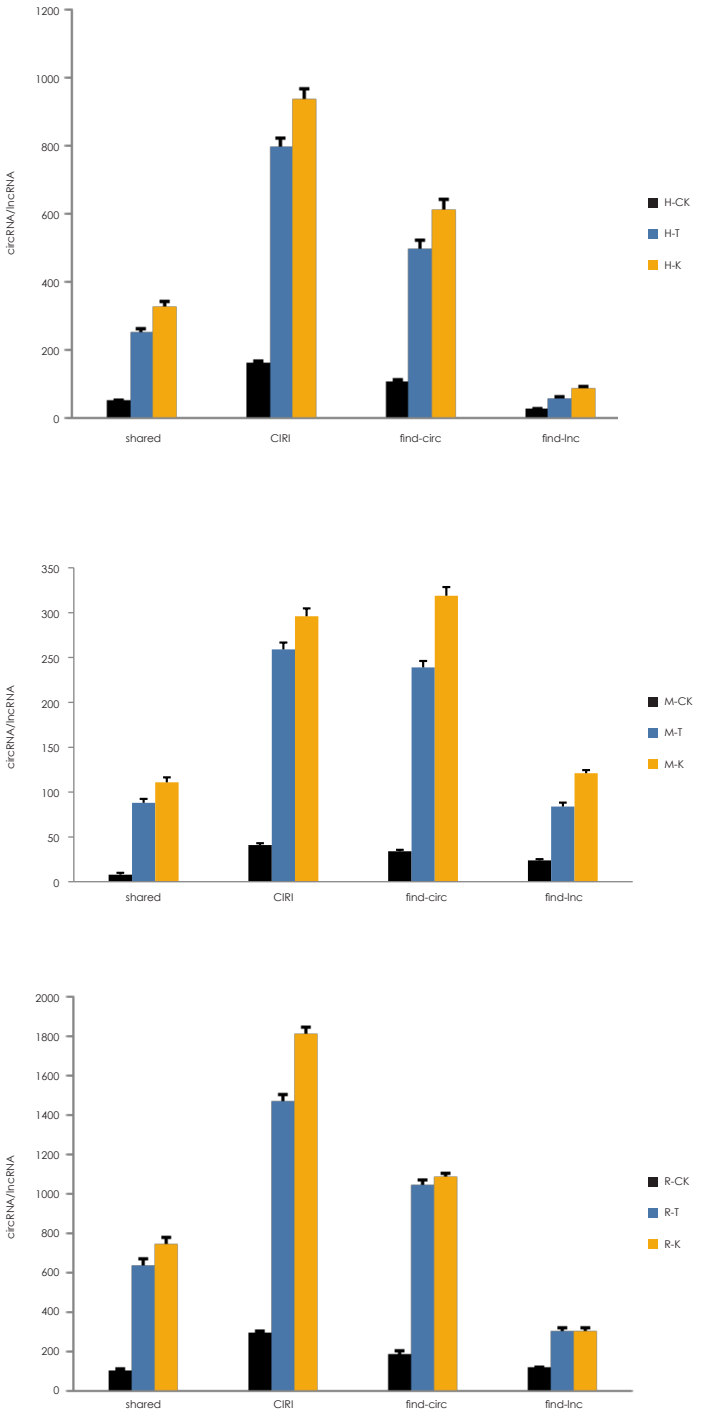
*H-CK/M-CK/R-CK: Samples without rRNA removal.

rRNA Content Analysis

Species	Sample	rRNA Removal (%)	rRNA Rate (%)
Human	H-T	99.88	3.13
	H-K	99.54	4.1
Mouse	M-T	99.79	3.37
	M-K	98.82	5.7
Rat	R-T	99.58	0.6
	R-K	99.03	1.47

*rRNA Removal is the result of analysis using Mirabait software and rRNA Rate is the result of comparison using nt library. The analysis result of Mirabait software is more accurate.

circRNA/lncRNA Analysis



shared: The number of circRNA intersections predicted by different software.

CIRI: The number of circRNA predicted by CIRI.

find-circ: The number of circRNA predicted by find-circ.

find-lnc: The number of lncRNA predicted by find-lnc.

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

*Trans*NGS® rRNA Depletion Kit (Bacteria)

Features

- Remove up to 99% ribosomal RNA from various bacteria.
- Simple workflow.

Application

- Gram-positive and Gram-negative bacteria RNA samples.
- Total bacterial RNA (200 ng~2 μg) sample.
- Complete or partially degraded RNA sample.

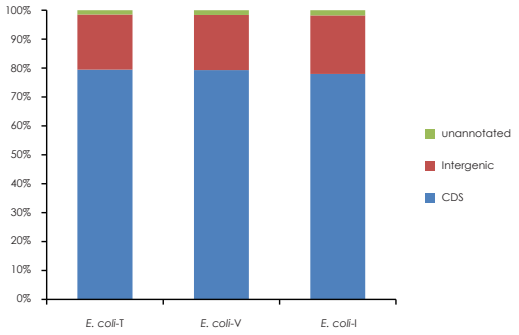
Comparison with Competitors

rRNA depletion for 2 μg total RNA of Escherichia coli (E. coli) was performed using *Trans*NGS® rRNA Depletion Kit (Bacteria), Company V and Company I rRNA depletion kits. Then library was prepared (TransGen, KP601), sequenced, and analyzed. The results of sequencing data quality, gene expression level and correlation show that TransGen products performed similarly to competitor products.

Sequencing Data Quality

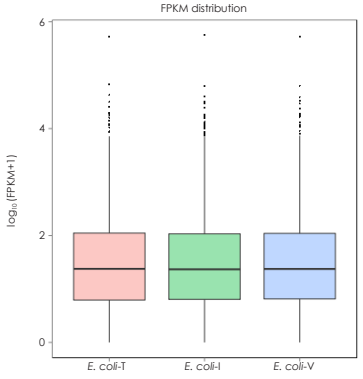
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
E. coli-T	0.56	15359560	97.79	93.71	50.94	14574686 (94.89%)	13685367 (89.1%)
E. coli-V	0.62	17633274	97.69	93.525	50.84	16652800 (94.44%)	15418534 (87.44%)
E. coli-I	0.58	15964872	97.72	93.585	50.83	15089492 (94.52%)	14127315 (88.49%)

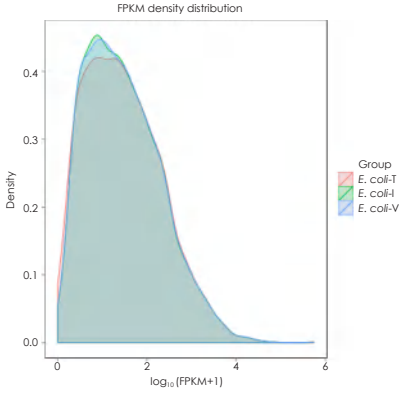
Aligned Region Distribution

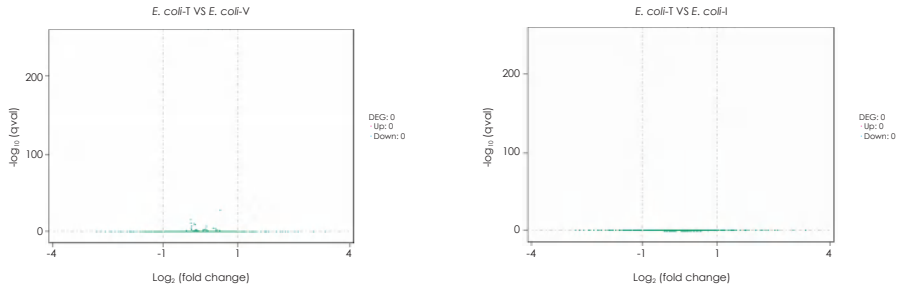


Gene Expression and Variation Analysis

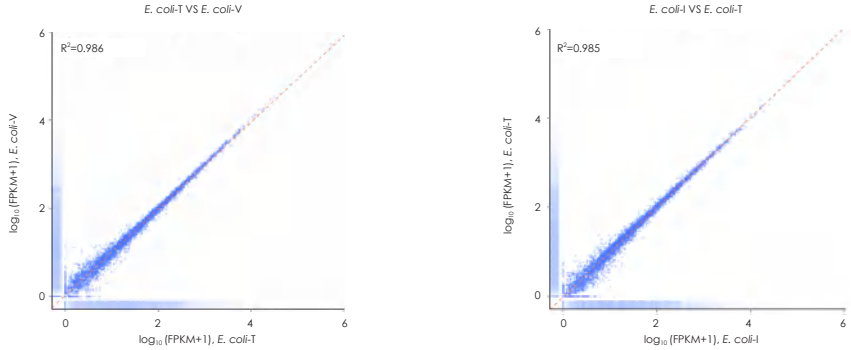
FPKM interval	*E. coli*-T	*E. coli*-V	*E. coli*-I
0~1	869 (19.84%)	800 (18.26%)	790 (18.03%)
1~3	437 (9.97%)	472 (10.77%)	463 (10.57%)
3~15	931 (21.25%)	986 (22.51%)	999 (22.80%)
15~60	872 (19.90%)	866 (19.77%)	879 (20.06%)
>60	1272 (29.03%)	1257 (28.69%)	1250 (28.53%)







Correlation Analysis



Strains that Have been Successfully Tested (rRNA Rate <5%)

Bacillus coagulans	Bacillus subtilis	Escherichia coli	Helicobacter pylori
Lactobacillus plantarum	Mycobacterium paratuberculosis	Mycobacterium smegmatis	Pseudomonas aeruginosa
Salmonella typhimurium	Sphingomonas mali	Staphylococcus aureu	Streptococcus
Streptomyces coelicolor			

*Trans*NGS® rRNA Depletion Kit (Animal)

Features

- Remove up to 99% ribosomal RNA from various animals.
- Simple workflow.

Application

- Animal total RNA (200 ng~2 μg) sample.
- Complete or partially degraded RNA sample.

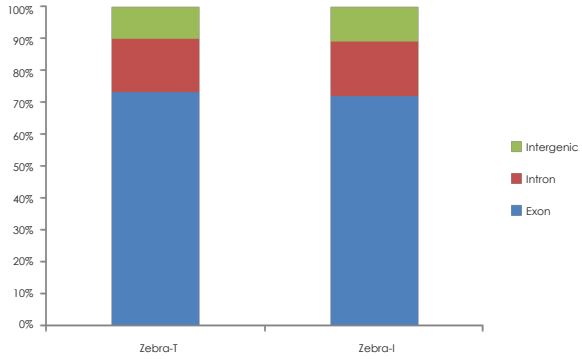
Comparison with Competitor Products

rRNA depletion for 2 μg total RNA of Zebra fish was performed using *Trans*NGS® rRNA Depletion Kit (Animal) and Company I rRNA depletion kits. Then library was prepared (TransGen, KP601), sequenced, and analyzed. The results of sequencing data quality, gene expression level and correlation show that TransGen product performed similarly to competitor's product.

Sequencing Data Quality

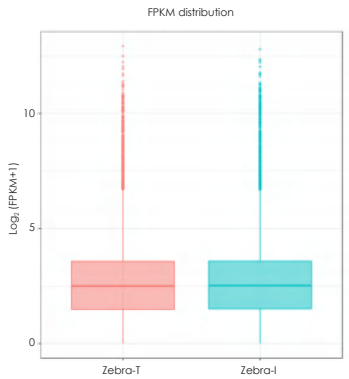
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
Zebra-T	2.21	64491476	98.64	95.14	43.18	59551428 (92.34%)	57939142 (89.84%)
Zebra-I	1.97	64508688	98.66	95.22	42.68	60773634 (94.21%)	54858188 (85.04%)

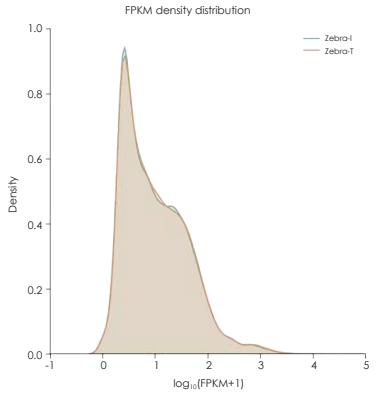
Aligned Region Distribution

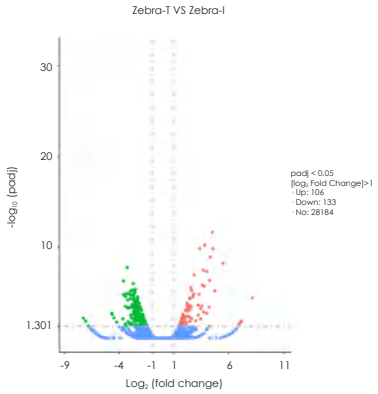


Gene Expression and Variation Analysis

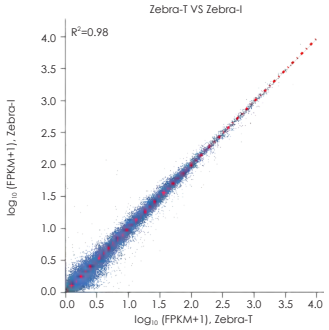
FPKM interval	Zebra-T	Zebra-I
0~1	21,729 (39.11%)	19,747 (35.54%)
1~3	8,965 (16.13%)	10,800 (19.44%)
3~5	10,310 (18.56%)	10,801 (19.44%)
5~15	7,367 (13.26%)	6,863 (12.35%)
15~60	5,577 (10.04%)	5,597 (10.07%)
>60	1,615 (2.91%)	1,755 (3.16%)







Correlation Analysis



Species that Have been Successfully Tested (rRNA Rate <10%)

Cattle	Pig	Chicken
Goat	Grouper	Zebra fish
Tilapia	Gold pomfret	Rosella Shrimp

MagicPure® mRNA Kit

Features

- High-yield and high-purity isolated mRNA.
- Simple workflow.

Sample Requirement

- 0.1-10 μg total RNA with good integrity after purification (RIN value≥8).

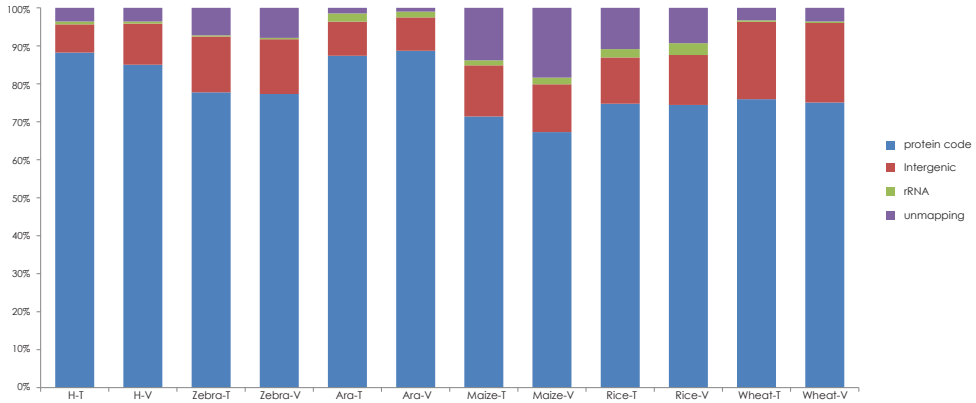
Comparison with Competitors

mRNA was enriched from 1 μg total RNA of human (H), Zebra fish (Zebra), Wheat, Rice, Arabidopsis thaliana, Maize, using MagicPure® mRNA Kit and Company V product. Then library was prepared (TransGen, KP601), sequenced, and analyzed. The results of sequencing data quality, rRNA depletion rate, aligned region distribution, gene expression level and correlation show that TransGen product performed similarly to competitor's product, and even better.

Sequencing Data Quality

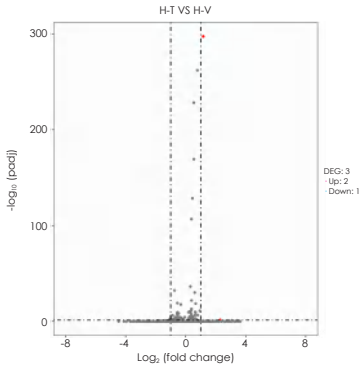
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
H-T	0.6	29615492	98.13	93.62	49.25	28552295 (96.41%)	26464135 (89.36%)
H-V	0.59	32450902	97.95	93.19	48.48	31295649 (96.44%)	29053281 (89.53%)
Zebra-T	0.37	21441766	98.7	95.21	48.85	19897958 (92.80%)	18158657 (84.69%)
Zebra-V	0.42	19191744	98.53	94.75	47.96	17677515 (92.11%)	16223630 (84.53%)
Ara-T	2.11	31324630	98.09	93.5	45.27	30923674 (98.72%)	29901890 (95.46%)
Ara-V	1.46	25838478	98.14	93.65	45.33	25618850 (99.15%)	24870854 (96.26%)
Maize-T	1.33	20537236	98.68	95.2	55.38	17787300 (86.61%)	17006473 (82.81%)
Maize-V	1.77	22089200	98.58	94.91	54.01	18084428 (81.87%)	17231916 (78.01%)
Rice-T	2.13	37310272	98.15	93.76	52.95	33609093 (90.08%)	32282747 (86.53%)
Rice-V	3.06	38700400	98.1	93.63	52.32	35352815 (91.35%)	33424624 (86.37%)
Wheat-T	1.78	23587858	98.48	94.66	57.44	22821252 (96.75%)	21598625 (91.57%)
Wheat-V	2.95	26945610	98.52	94.76	57.11	25980957 (96.42%)	24620014 (91.37%)

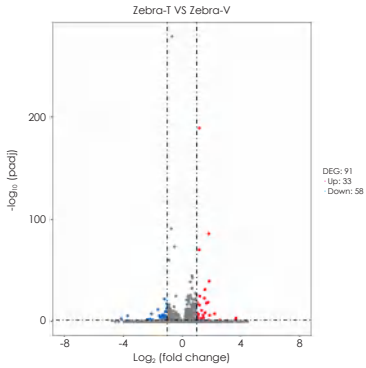
Aligned Region Distribution

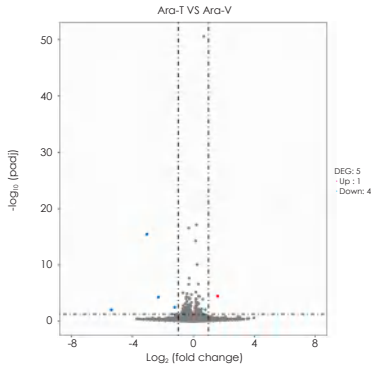


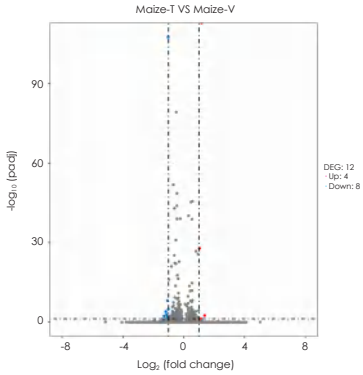
Gene Expression Level and Variation Analysis

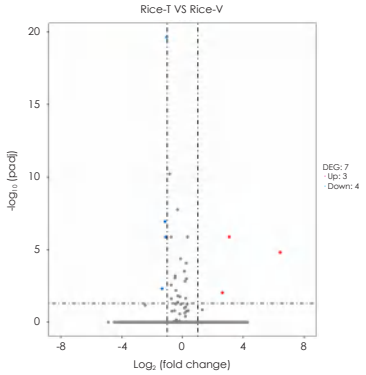
FPKM Interval	H-T	H-V	Zebra-T	Zebra-V	Ara-T	Ara-V	Maize-T	Maize-V	Rice-T	Rice-V	Wheat-T	Wheat-V
0~1	45,606 (76.40%)	45,200 (75.72%)	20,010 (50.32%)	19,886 (50.01%)	13,411 (40.54%)	13,437 (40.62%)	31,019 (57.72%)	30,208 (56.21%)	70,025 (75.01%)	70,042 (75.03%)	85,993 (63.09%)	85,745 (62.91%)
1~3	3,013 (5.05%)	3,140 (5.26%)	6,852 (17.23%)	6,950 (17.48%)	2,900 (8.77%)	2,891 (8.74%)	6,694 (12.46%)	7,259 (13.51%)	5,442 (5.83%)	5,585 (5.98%)	22,276 (16.34%)	21,681 (15.91%)
3~5	1,281 (2.15%)	1,300 (2.18%)	2,236 (5.62%)	2,058 (5.18%)	1,982 (5.99%)	1,922 (5.81%)	2,859 (5.32%)	2,942 (5.47%)	2,610 (2.80%)	2,505 (2.68%)	8,867 (6.51%)	9,177 (6.73%)
5~15	3,177 (5.32%)	3,223 (5.40%)	4,133 (10.39%)	4,070 (10.24%)	6,207 (18.76%)	6,211 (18.78%)	6,633 (12.34%)	6,763 (12.58%)	6,007 (6.43%)	6,018 (6.45%)	12,404 (9.10%)	12,936 (9.49%)
15~60	4,364 (7.31%)	4,512 (7.56%)	4,450 (11.19%)	4,708 (11.84%)	6,591 (19.93%)	6,681 (20.20%)	4,678 (8.70%)	4,767 (8.87%)	6,494 (6.96%)	6,487 (6.95%)	5,151 (3.78%)	5,172 (3.79%)
>60	2,253 (3.77%)	2,319 (3.88%)	2,083 (5.24%)	2,092 (5.26%)	1,987 (6.01%)	1,936 (5.85%)	1,861 (3.46%)	1,805 (3.36%)	2,780 (2.98%)	2,721 (2.91%)	1,614 (1.18%)	1,594 (1.17%)

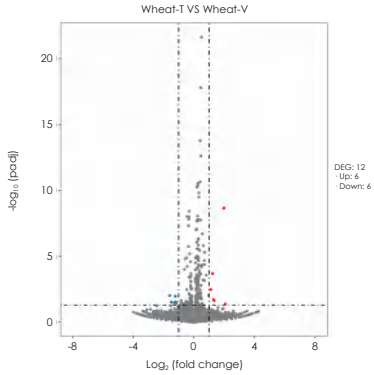




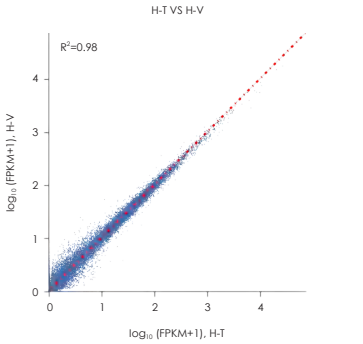


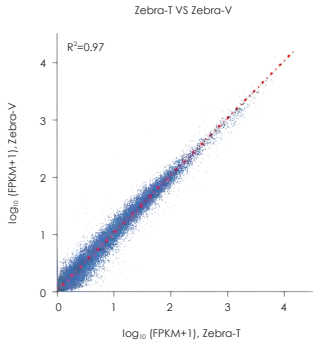


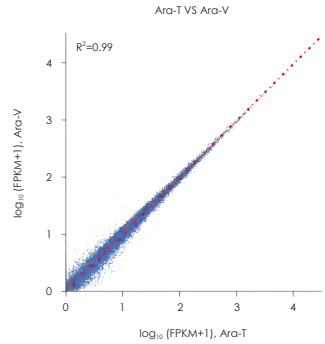


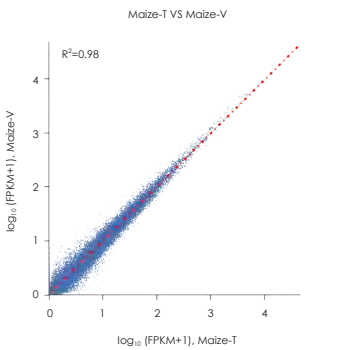


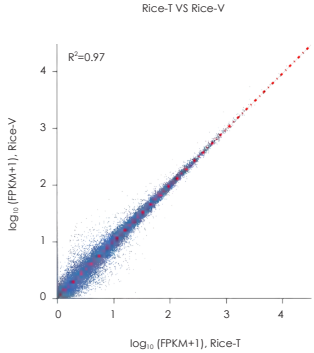
Correlation Analysis

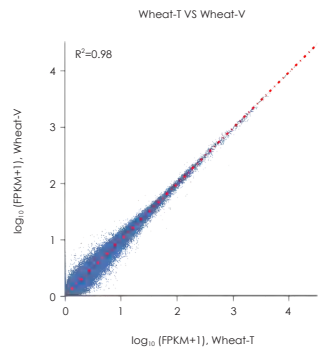












TransNGS® RNA-Seq Library Prep Kit for Illumina®

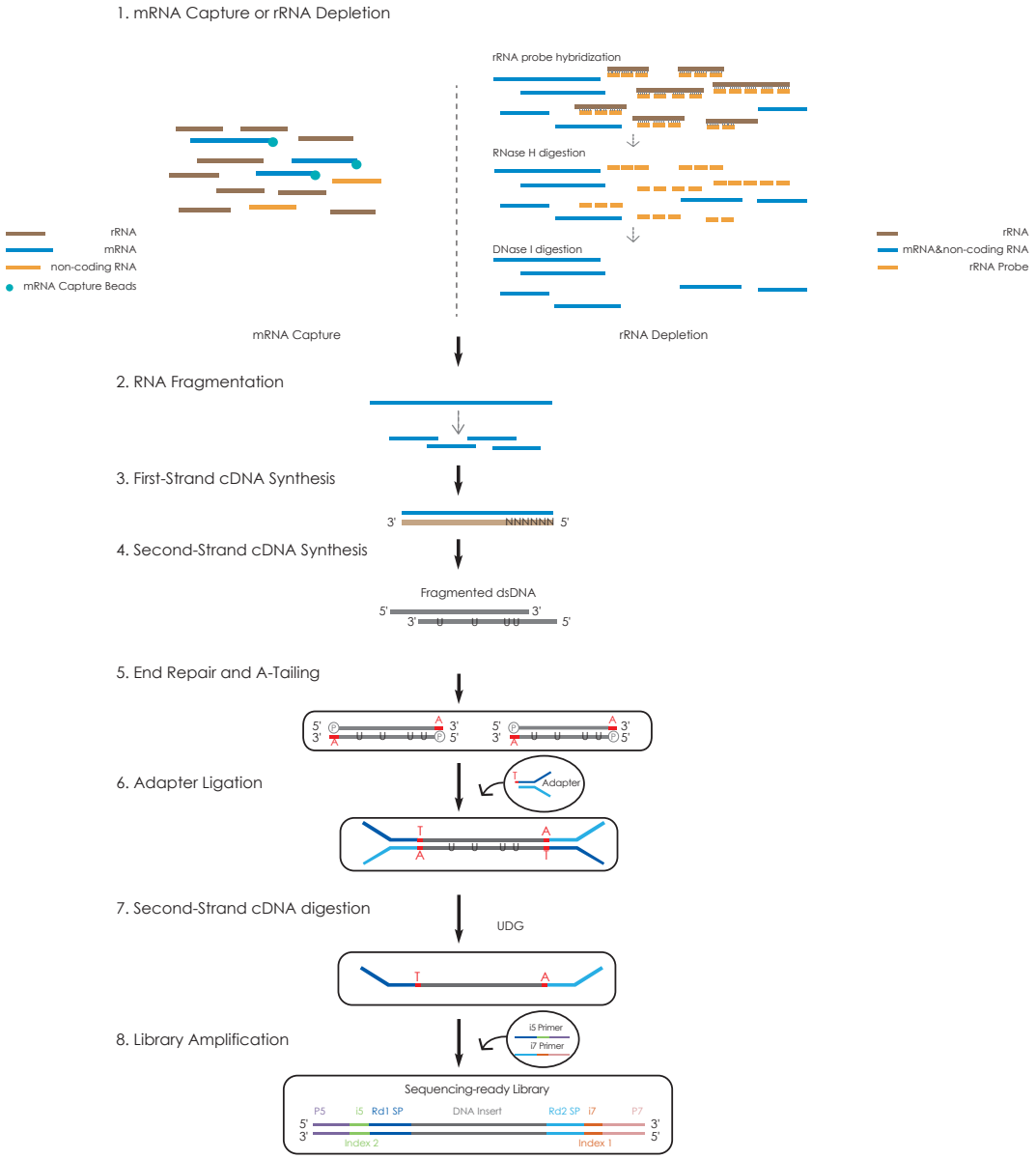
Features

- High conversion rate.
- High data quality.

Application

- Whole transcriptome sequencing.
- Gene expression analysis.
- Single Nucleotide Variation Analysis
- Variable shear detection.
- Fusion gene detection.
- Non-coding RNA and RNA precursor analysis.

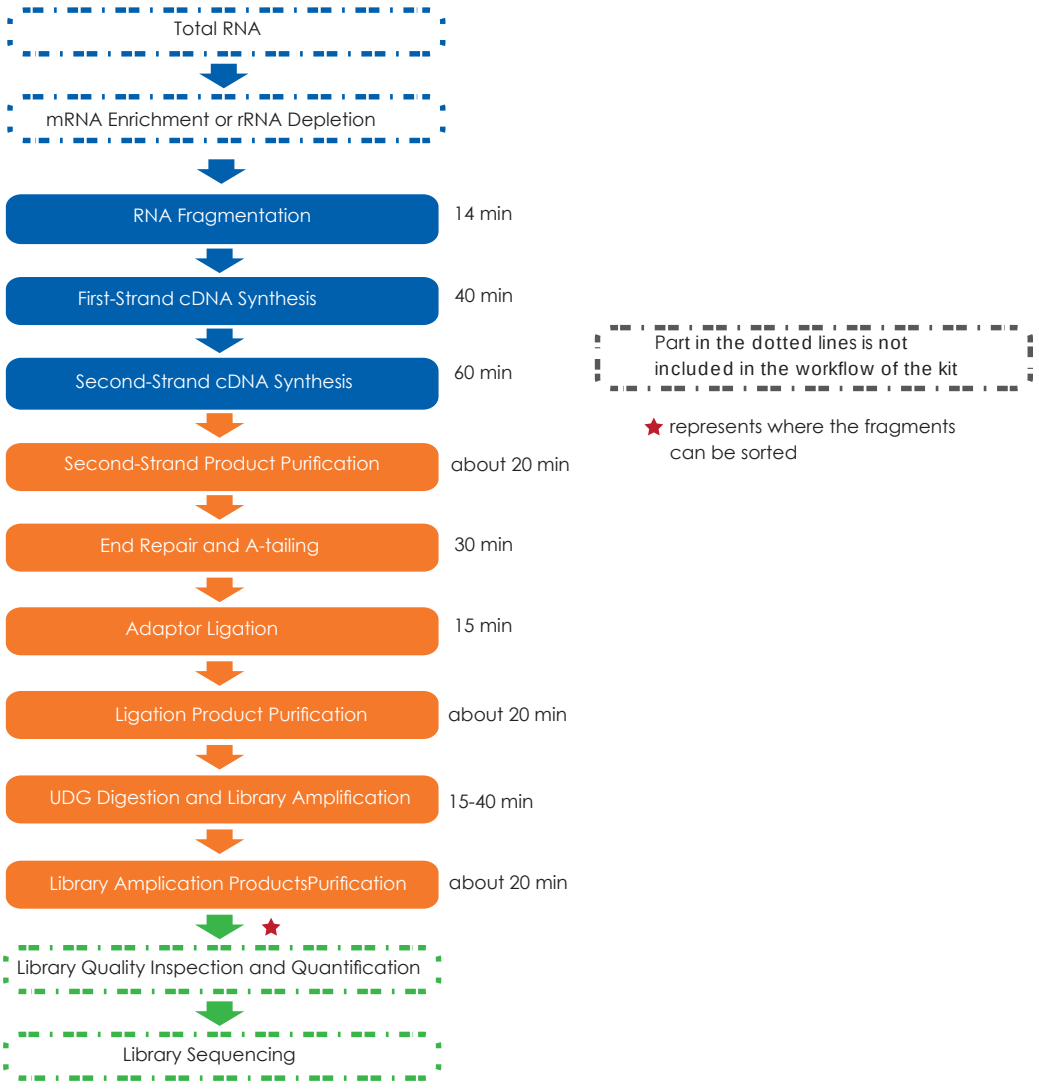
Principle of Library Preparation



Schematic diagram of the strand-specific library preparation principle

(There is no dUTP incorporation during the second-strand synthesis of non-strand-specific libraries, and no UDG enzyme digestion steps)

Operation Flow Chart



Schematic diagram of strand-specific library preparation process
(There is no dUTP incorporation during the second-strand synthesis of non-strand-specific libraries, and no UDG enzyme digestion steps)

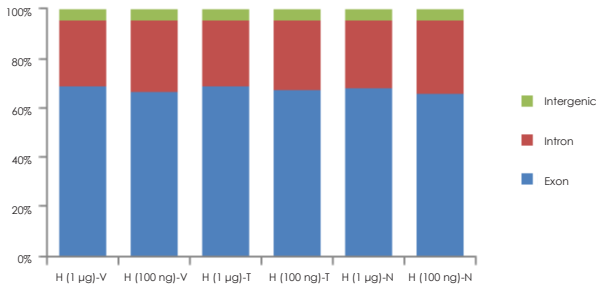
Comparison with Competitors

(1) After removing the rRNA from the 1 μg and 100 ng human blood total RNA samples (TransGen, KD101), TransGen, Company N and Company V library preparation products were used for library preparation, sequencing and analysis. The results show that the performance of TransGen product is comparable in terms of sequencing data quality, gene expression and correlation, compared with competitors' products.

Sequencing Data Quality

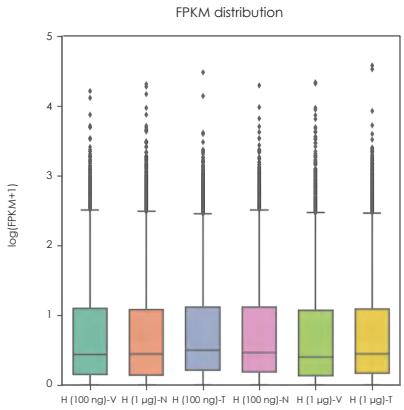
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
H (1 μg)-T	0.78	27709932	98.85	95.67	49.03	25146763 (90.75%)	23079602 (83.29%)
H (100 ng)-T	2.31	24376592	98.96	95.99	48.57	21702480 (89.03%)	20093625 (82.43%)
H (1 μg)-V	0.88	24545480	98.92	95.85	46.92	22486114 (91.61%)	20961840 (85.40%)
H (100 ng)-V	2.91	26241828	98.94	95.57	49.11	23575658 (89.84%)	21841073 (83.23%)
H (1 μg)-N	0.69	19833710	98.72	95.22	50.75	17,980,295 (90.66%)	16,545,319 (83.42%)
H (100 ng)-N	2.55	20951360	98.65	95.00	47.95	19,036,259 (90.86%)	17,730,696 (84.63%)

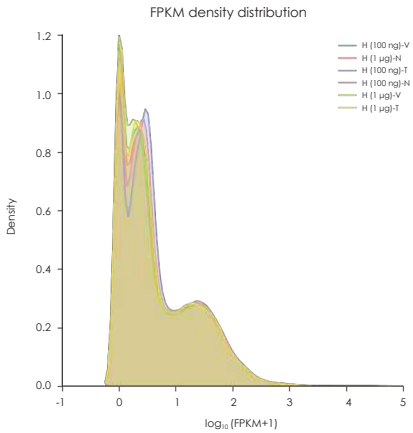
Aligned Region Distribution

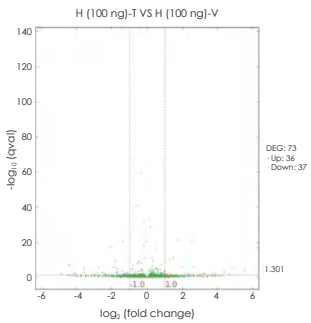


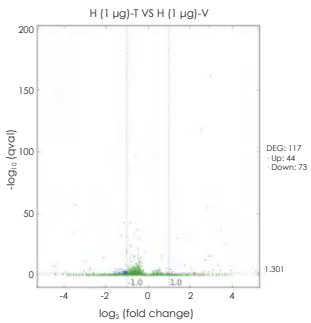
Gene Expression Level and Variation Analysis

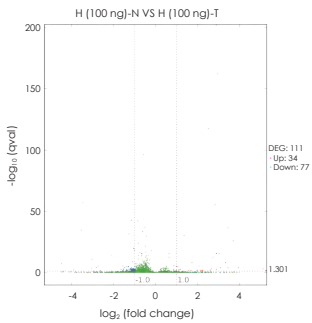
FPKM interval	H (1 μg)-V	H (100 ng)-V	H (1 μg)-T	H (100 ng)-T	H (1 μg)-N	H (100 ng)-N
0~1	51,114 (69.59%)	50,586 (68.87%)	52,346 (71.27%)	52,782 (71.86%)	51,300 (70.95%)	50,587 (69.96%)
1~3	8,588 (11.69%)	8,842 (12.04%)	6,098 (8.30%)	5,929 (8.07%)	8,161 (11.29%)	8,606 (11.90%)
3~5	3,397 (4.62%)	3,347 (4.56%)	3,784 (5.15%)	3,470 (4.72%)	1,893 (2.62%)	1,975 (2.73%)
5~15	3,765 (5.13%)	3,640 (4.96%)	4,043 (5.50%)	4,133 (5.63%)	3,679 (5.09%)	3,595 (4.97%)
15~60	4,582 (6.24%)	4,715 (6.42%)	4,870 (6.63%)	4,830 (6.58%)	5,031 (6.96%)	5,185 (7.17%)
>60	2,004 (2.73%)	2,320 (3.16%)	2,309 (3.14%)	2,306 (3.14%)	2,245 (3.10%)	2,361 (3.27%)

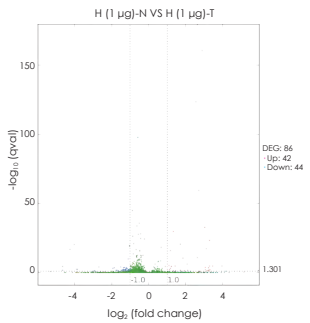




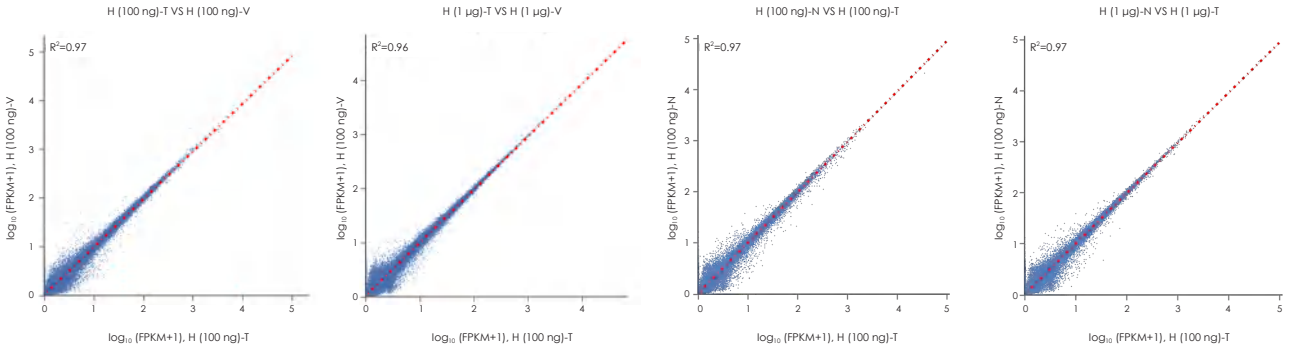








Correlation Analysis

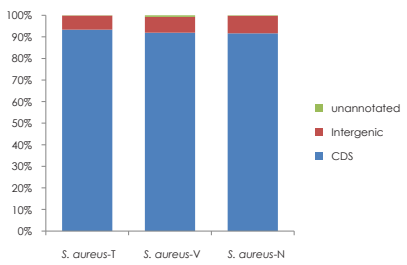


(2) After removing rRNA (TransGen, KD201) from 2 μg of Staphylococcus aureus (S. aureus) total RNA sample, TransGen, Company N, and Company V library products were used for library preparation, sequencing and analysis. The results show that the performance of TransGen product is comparable in terms of sequencing data quality, gene expression level and correlation, compared with competitors' products.

Sequencing Data Quality

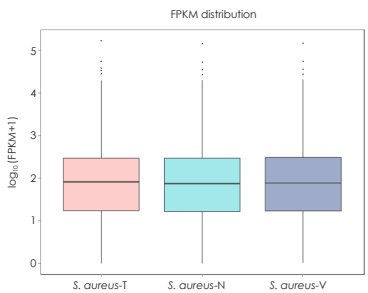
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
S. aureus-T	0.78	42568676	98.14	94.27	35.15	41551285 (97.61%)	40172060 (94.37%)
S. aureus-V	0.93	46495960	97.87	92.68	34.37	45224260 (97.26%)	43260173 (93.04%)
S. aureus-N	0.68	44678992	98.18	93.92	34.88	43687118 (97.78%)	42078675 (94.18%)

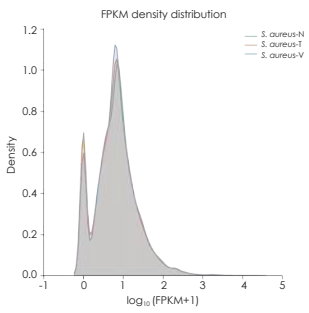
Aligned Region Distribution

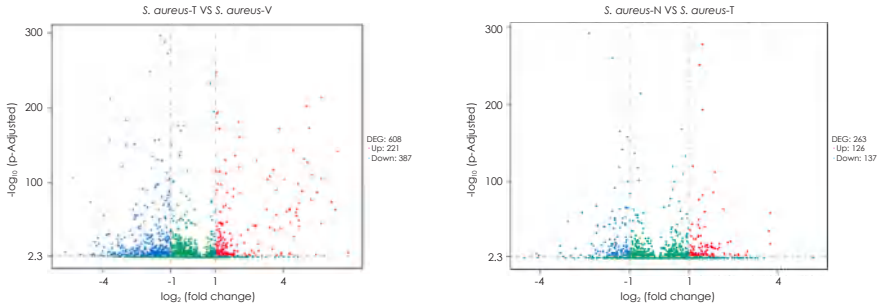


Gene Expression Level and Variation Analysis

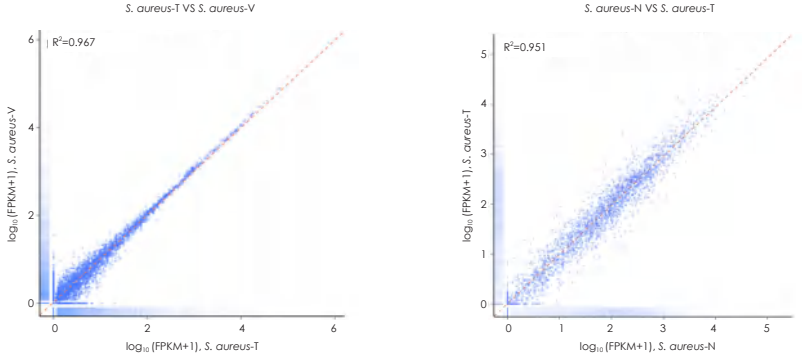
FPKM interval	*S. aureus*-T	*S. aureus*-V	*S. aureus*-N
0~1	516 (18.43%)	472 (16.88%)	477 (17.04%)
1~3	157 (5.61%)	151 (5.43%)	155 (5.54%)
3~15	355 (12.68%)	357 (12.78%)	378 (13.50%)
15~60	507 (18.11%)	502 (17.96%)	490 (17.50%)
>60	1265 (45.18%)	1315 (46.95%)	1300 (46.43%)







Correlation Analysis

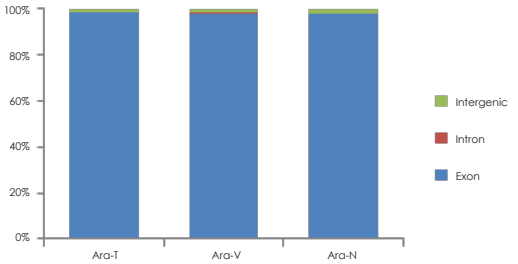


(3) After mRNA was enriched (TransGen, EC511) from 1 μg of Arabidopsis thaliana total RNA sample, the library preparation products of TransGen, Company N and Company V were used for library preparation, sequencing and analysis. The results show that the performance of TransGen product is comparable in terms of sequencing data quality, gene expression level and correlation, compared with competitors' products.

Sequencing Data Quality

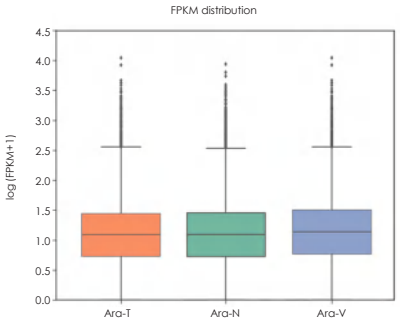
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
Ara-T	1.5	31749892	98.85	95.44	45.59	29736948 (93.66%)	28432028 (89.55%)
Ara-V	1.73	30337494	98.8	95.3	45.43	28373086 (93.52%)	26966821 (88.89%)
Ara-N	1.99	29649246	98.29	94.1	45.59	27606511 (93.11%)	26543366 (89.52%)

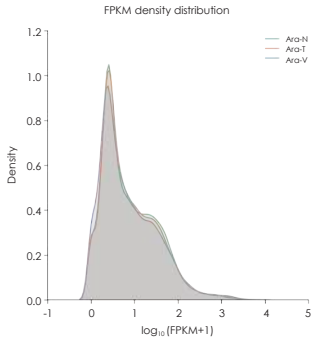
Aligned Region Distribution

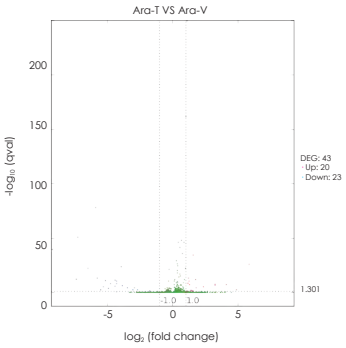


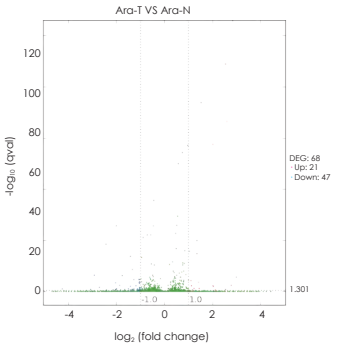
Gene Expression Level and Difference Analysis

FPKM interval	Ara-T	Ara-V	Ara-N
0~1	14,358 (43.40%)	15,374 (46.54%)	14,139 (42.73%)
1~3	2,618 (7.91%)	2,554 (7.73%)	2,688 (8.12%)
3~5	1,771 (5.35%)	1,748 (5.29%)	1,835 (5.55%)
5~15	5,895 (17.82%)	5,501 (16.65%)	6,069 (18.34%)
15~60	6,453 (19.50%)	5,801 (17.56%)	6,414 (19.39%)
>60	1,991 (6.02%)	2,057 (6.23%)	1,941 (5.87%)

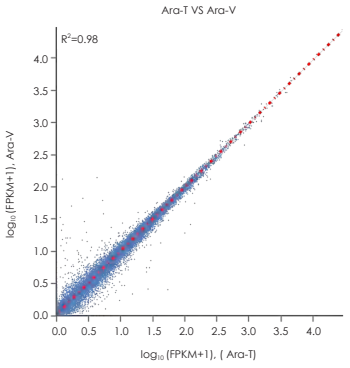


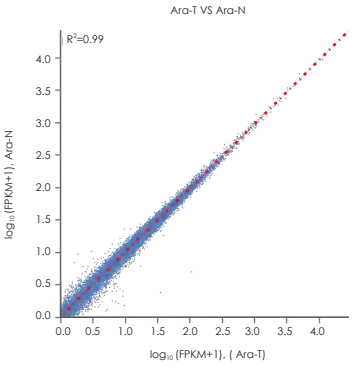






Correlation Analysis



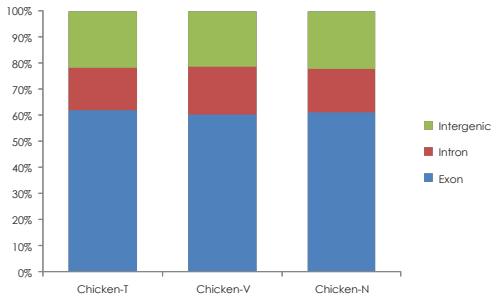


(4) After removing rRNA from 2 μg chicken total RNA sample (TransGen, KD301), TransGen, Company N, and Company V library preparation products were used for library construction, sequencing and analysis. The results show that the performance of TransGen product is comparable in terms of sequencing data quality, gene expression level, and correlation , compared with competitors' products.

Sequencing Data Quality

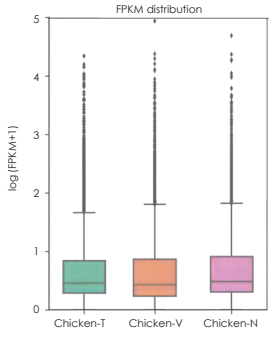
Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped
Chicken-T	0.17	32795560	98.77	95.5	50.63	29250359 (89.19%)	28420632 (86.66%)
Chicken-V	0.09	34135368	98.9	95.75	47.26	30633079 (89.74%)	29639740 (86.83%)
Chicken-N	0.19	33397144	98.73	95.43	51.07	29506376 (88.35%)	28634711 (85.74%)

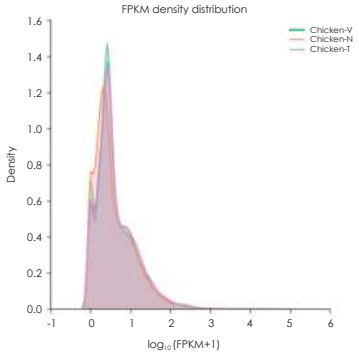
Aligned Region Distribution

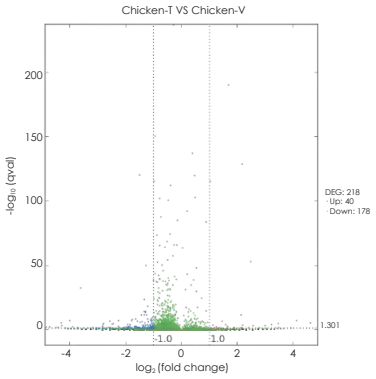


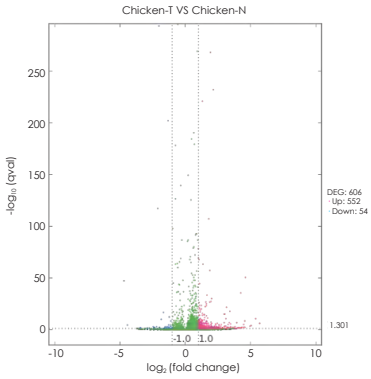
Gene Expression Level and Variation Analysis

FPKM interval	Chicken-T	Chicken-V	Chicken-N
0~1	12,476 (39.74%)	12,883 (41.03%)	14,702 (46.83%)
1~3	8,904 (28.36%)	9,359 (29.81%)	7,352 (23.42%)
3~5	2,178 (6.94%)	2,245 (7.15%)	2,098 (6.68%)
5~15	4,473 (14.25%)	4,061 (12.93%)	4,311 (13.73%)
15~60	2,539 (8.09%)	2,175 (6.93%)	2,223 (7.08%)
>60	826 (2.63%)	673 (2.14%)	710 (2.26%)

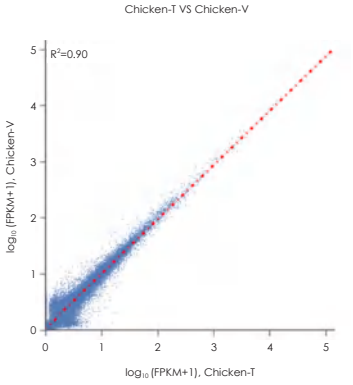


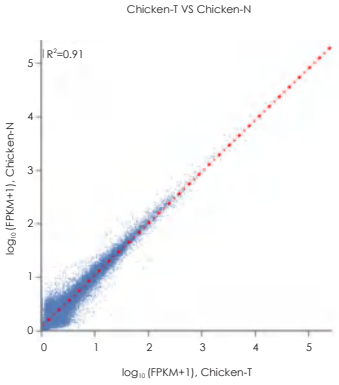






Correlation Analysis





TransNGS® Fast RNA-Seq Library Prep Kit for Illumina®

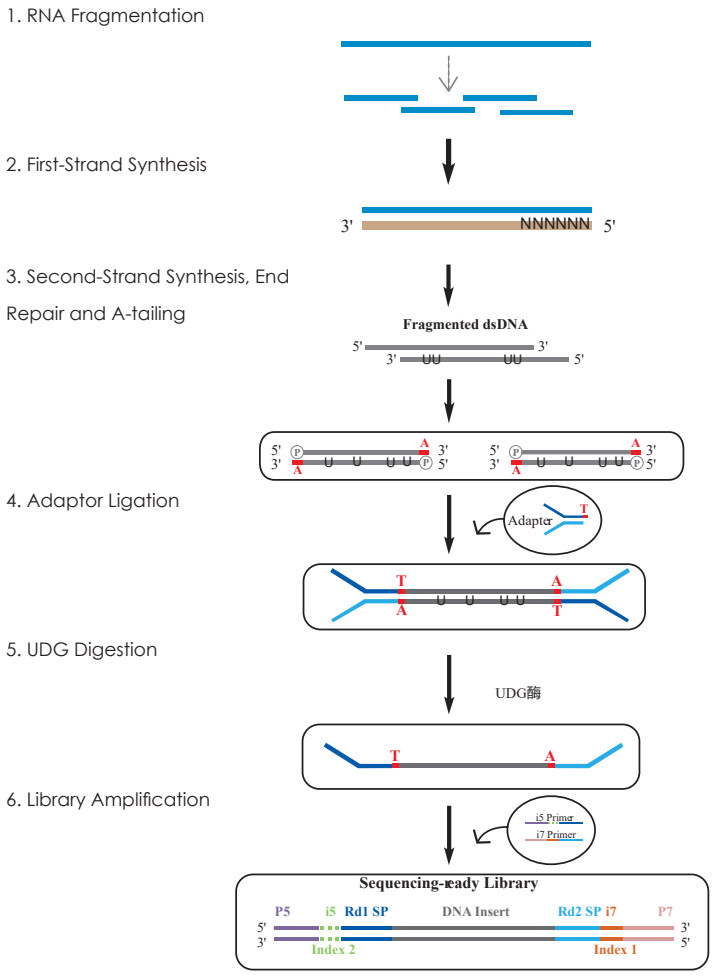
Features

- Fast library preparation.
- High library conversion rate.
- High data quality.

Applications

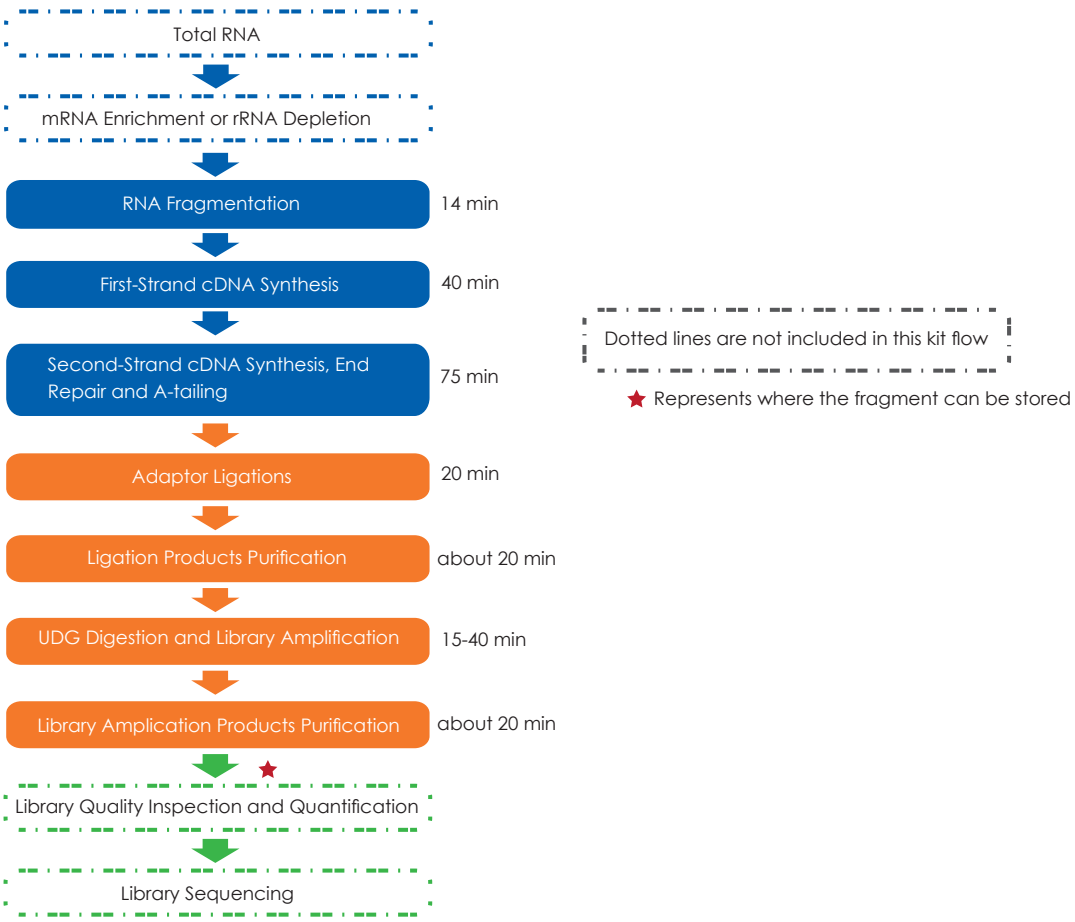
- Whole transcriptome sequencing.
- Gene expression analysis.
- Single Nucleotide Variation Analysis
- Variable shear detection.
- Fusion gene detection.
- Non-coding RNA and RNA precursor analysis.

Principle of Library Preparation



Schematic diagram of the chain-specific library preparation process (There is no dUTP incorporation during the second-strand synthesis of non-strand-specific libraries, and no UDG enzyme digestion steps)

Operation Flow Chart



Schematic diagram of the strand-specific library preparation process
(There is no dUTP incorporation during the second-strand synthesis of non-strand-specific libraries, and no UDG enzyme digestion steps)

Comparison with Competitors

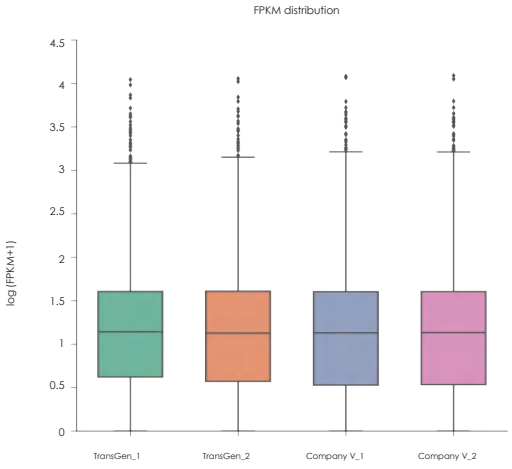
After mRNA enrichment (TransGen, EC411) from 200 ng of Hela cell total RNA samples, the library preparation products of TransGen and Company V were used for library preparation, sequencing and analysis. The results show that performance of TransGen products was comparable with competitors' products in terms of sequencing data quality, gene expression level, and correlation.

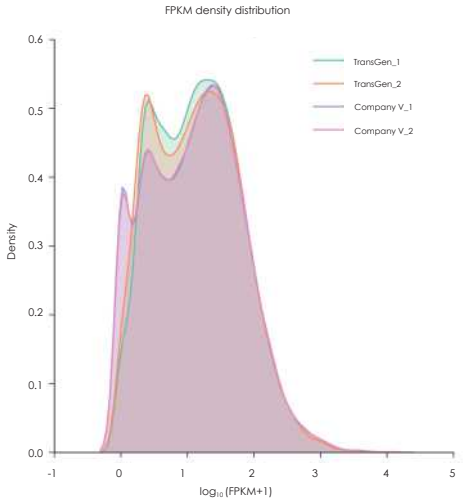
Sequencing Data Quality

Sample	rRNA Rate (%)	Clean reads	Q20 (%)	Q30 (%)	GC content (%)	Total Mapped	Uniquely Mapped	Error_rate(%)
TransGen_1	291072 -0.79%	36,816,940	98.31	94.01	50.45	35,249,092 (95.74%)	32,999,432 (89.63%)	0.03
TransGen _2	320734 -0.92%	34,923,176	97.97	93.21	50.59	33,410,989 (95.67%)	31,259,310 (89.51%)	0.03
Company V_1	233648 -1.06%	21,990,698	98.36	94.25	51.36	21,147,387 (96.17%)	19,666,413 (89.43%)	0.03
Company V_2	268606 -1.18%	22,719,014	98.44	94.44	51.04	21,840,159 (96.13%)	20,300,389 (89.35%)	0.03

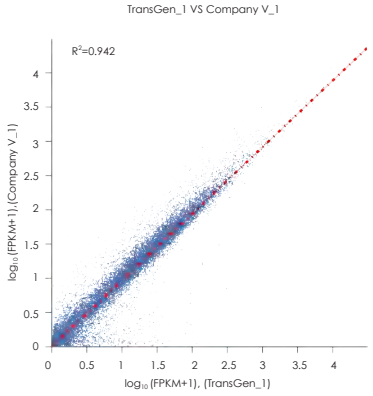
Gene Expression Level and Variation Analysis

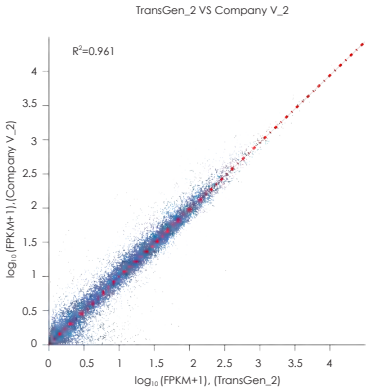
FPKM Interval	TransGen_1	TransGen _2	Company V_1	Company V_2
0	38,435(65.82%)	38,724(66.31%)	40,709(69.71%)	40,522(69.39%)
0~1	6,637(11.37%)	6,720(11.51%)	5,222(8.94%)	5,402(9.25%)
1~3	2,307(3.95%)	2,260(3.87%)	1,994(3.41%)	1,982(3.39%)
3~15	4,254(7.28%)	3,992(6.84%)	3,755(6.43%)	3,773(6.46%)
15~60	4,313(7.39%)	4,233(7.25%)	4,233(7.25%)	4,231(7.25%)
>60	2,449(4.19%)	2,466(4.22%)	2,482(4.25%)	2,485(4.26%)

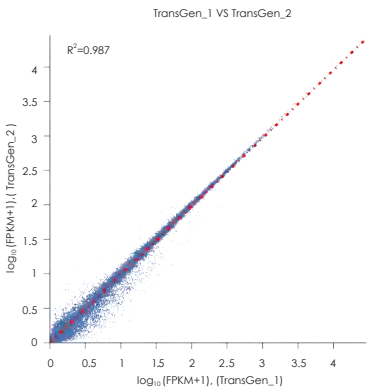




Correlation Analysis







*Trans*NGS® Library Amplification SuperMix

Features

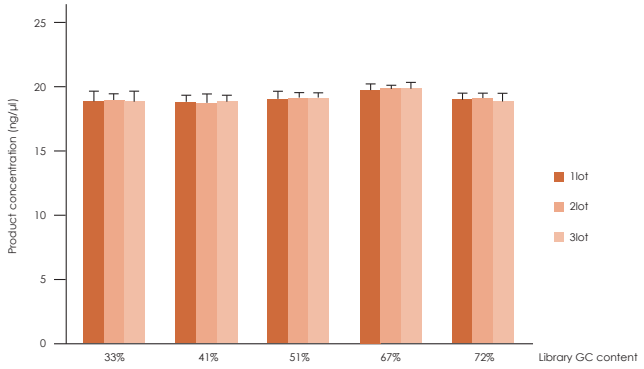
- Ultra-high fidelity.
- Low GC bias.
- High sensitivity and high specificity.
- Hot start.

Application

Next-generation sequencing library amplification

Product Stability

DNA libraries were prepared with 25 ng DNA with different GC content (33%-72%), using *Trans*NGS® Library Amplification SuperMix of different lots respectively. The whole process contained 6 amplification cycles, and PCR products were purified by 1.0× beads. The final concentration was measured using Qubit. The results indicate that the amplification efficiency of different lots keeps consistent for templates with different GC content.

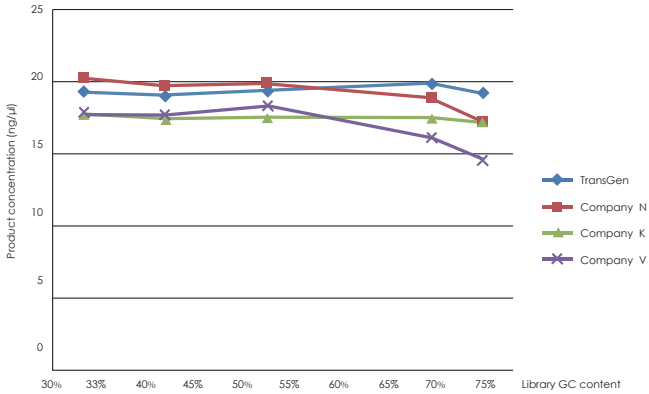


Comparison between amplification efficiency of different lots

Comparison between Amplification Efficiency of Different Lots

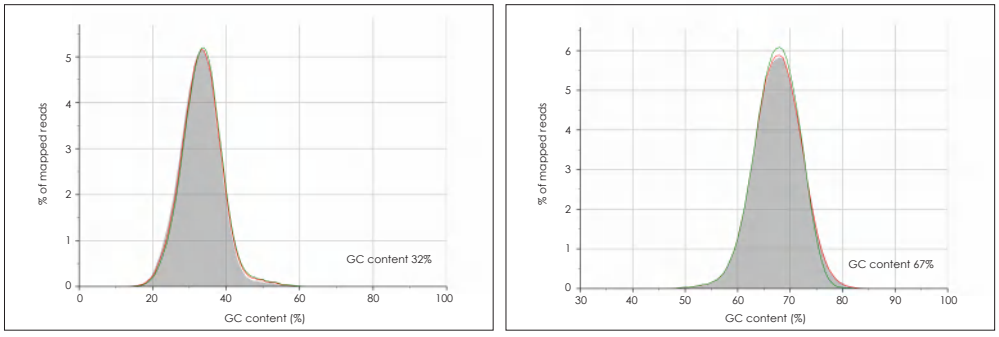
(1) Comparison of library yields of different initial sample sizes

DNA libraries were prepared with 25 ng human genomic DNA with different GC content (33%-72%), using library amplification mixes of TransGen Biotech, Company N, Company K and Company V. The whole process contained 6 amplification cycles, and PCR products were purified by 1.0×beads. The final concentration was measured using Qubit. TransGen Biotech products present higher amplification efficiency and lower GC preference.



Comparison between different lots of library amplification kit

(2)Libraries with different GC content were amplified using TransGen Biotech and company N products. The amplified libraries were DNA fragments ligated with the same adaptors, and then they were sequenced by Illumina sequencing platforms. Distribution of sequencing reads with different GC content was presented by the curves in the following figure, and distribution of libraries amplified by TransGen Biotech products was closer to the expected distribution.



Red curve: TransGen Biotech; Green curve: Company N; Gray shadow: Expected reads distribution.
Comparison of reads distribution of templates with different GC content

MagicPure® Size Selection DNA Beads

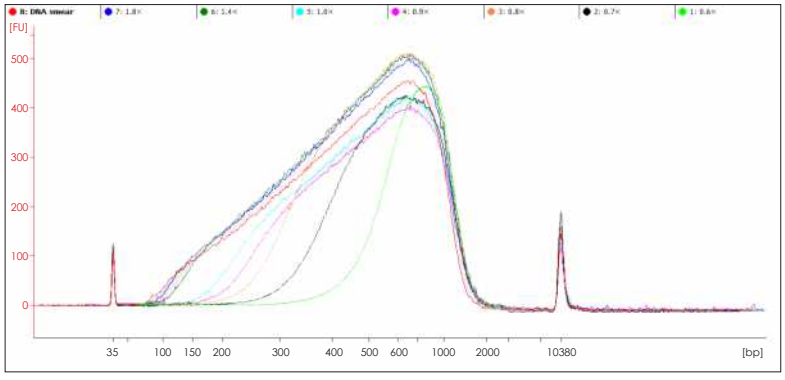
Features

Easy to use. Suitable for automated work station.

DNA Purification and Size Selection

Purification and size selection of DNA samples were performed using TransGen *MagicPure*® Size Selection DNA Beads. The products were detected by Agilent's high-sensitivity DNA chip. The results show that TransGen products can achieve efficient purification and precise sorting.

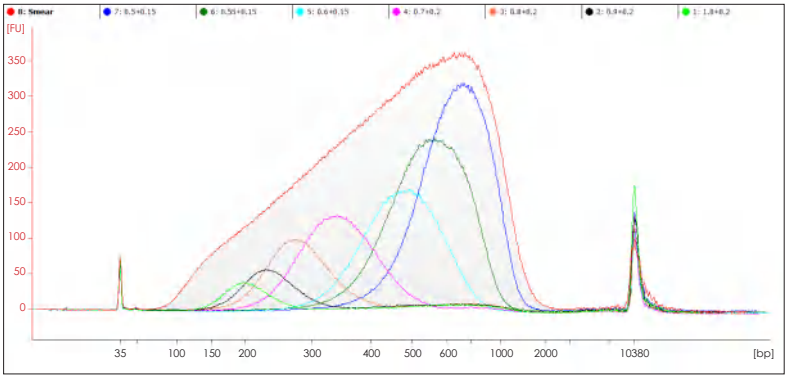
DNA Purification



Agilent high-sensitivity DNA chip electropherogram
Smear-Control DNA sample dissolved in Nuclease-free Water; 0.6×~1.8×-DNA sample purified by the corresponding ratio of magnetic beads.

DNA Size Selection

Average length of sorted fragments (bp)	190~220	220~250	250~300	300~400	400~500	500~600	600~750
Volume ratio in the first round (DNABeads:DNA)	1.0×	0.9×	0.80×	0.70×	0.60×	0.55×	0.50×
Volume ratio in the second round(DNA Beads:DNA)	0.20×	0.20×	0.20×	0.20×	0.15×	0.15×	0.15×

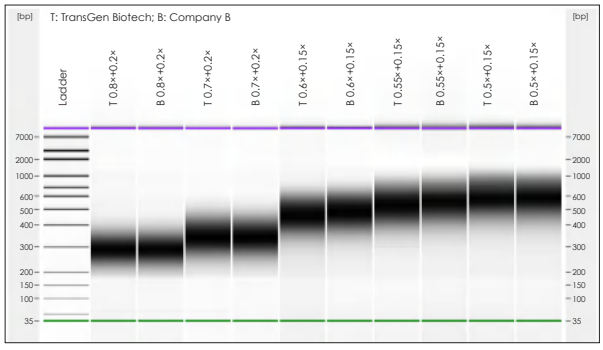


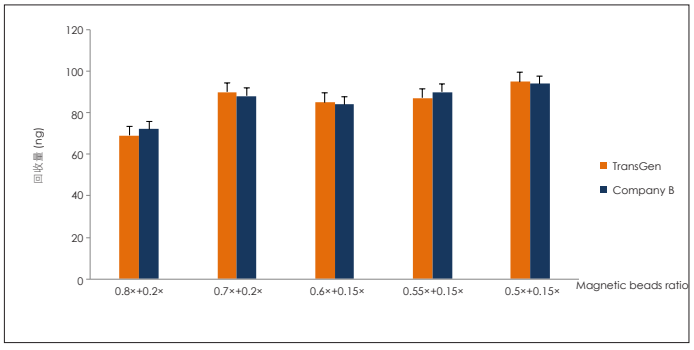
Agilent high-sensitivity DNA chip electropherogram
Smear-Control DNA sample dissolved in Nuclease-free Water; 1.0+0.2~0.5+0.15-DNA sample purified by the corresponding ratio of magnetic beads.

Comparison with Competitors

(1) Size selection

Size selection of the same DNA samples was performed using TransGen Biotech and Company B products. The products were detected by Agilent's high-sensitivity DNA chip and their concentrations were determined using Qubit. The results show that there is no significant difference in product fragment size and recovery amount under the same selection conditions.

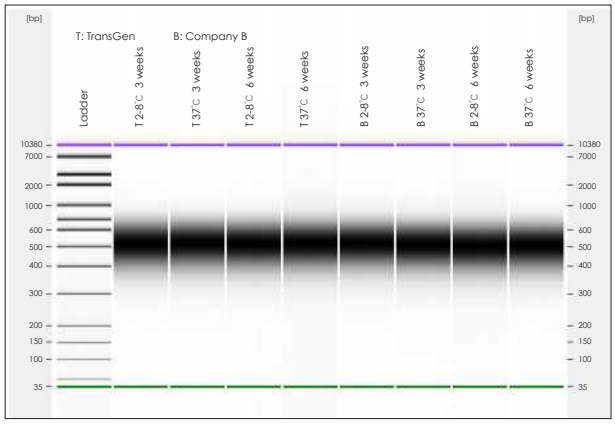


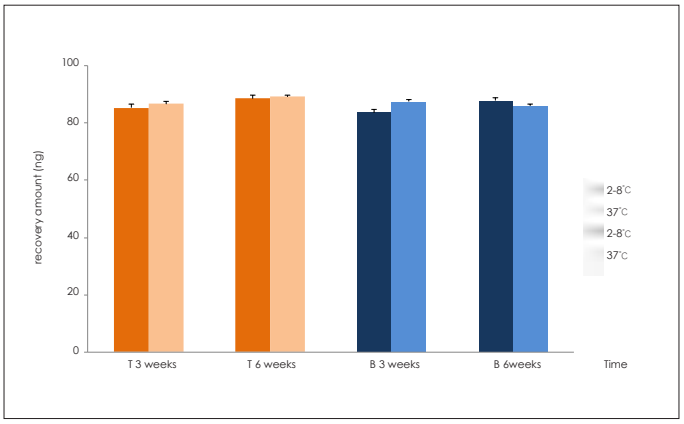


Comparison of size selection results under different size selection conditions

(2) Stability comparison

TransGen and B products were stored at 37°C for 3 weeks / 6 weeks (conserved at 2-8°C as a control). Size selection of the same DNA samples was performed (0.6× +0.1×). The products were detected by Agilent high-sensitivity DNA chip and their concentrations were determined using Qubit. The results show that there is no significant difference in product fragment distribution and recovery amount after high temperature destructive





Comparison of size selection results under different storage temperature conditions

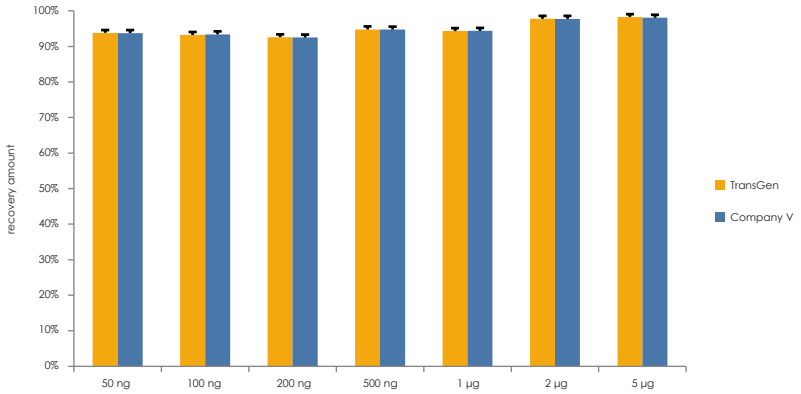
MagicPure® RNA Beads

Features

Easy to use. Suitable for automated work station.

Comparison with Competitors

Different amounts of total human RNA samples were purified by TransGen *MagicPure*® RNA Beads and Company V products. Qubit was used to determine the concentration of RNA before and after purification to determine the recovery rate of RNA Beads. The results show that there is no significant difference in the recovery rate of different RNA Beads.



Comparison of purification recovery rate with competitors' products

Product Name	Cat. No.	Specification
*Trans*NGS® DNA Library Prep Kit for Illumina®	KP201-01	12 rxns
	KP201-02	24 rxns
	KP201-03	96 rxns
*Trans*NGS® DNA Library Prep Kit for MGI®	KP221-01	12 rxns
	KP221-03	96 rxns
*Trans*NGS® rRNA Depletion Kit (Human/Mouse/Rat)	KD101-01	6 rxns
	KD101-02	24 rxns
	KD101-03	96 rxns
*Trans*NGS® rRNA Depletion Kit (Bacteria)	KD201-01	6 rxns
	KD201-02	24 rxns
	KD201-03	96 rxns
*Trans*NGS® rRNA Depletion Kit (Animal)	KD301-01	6 rxns
	KD301-02	24 rxns
	KD301-03	96 rxns
MagicPure® mRNA Kit	EC511-01	24 rxns
	EC511-02	96 rxns
*Trans*NGS® RNA-Seq Library Prep Kit for Illumina®	KP601-01	12 rxns
	KP601-02	96 rxns
*Trans*NGS® RNA-Seq Library Prep Kit for Illumina® (With mRNA	KP611-01	12 rxns
	KP611-02	96 rxns
*Trans*NGS® RNA-Seq Library Prep Kit for Illumina® (With Human/Mouse/Rat rRNA Depletion)	KP621-01	12 rxns
	KP621-02	96 rxns
*Trans*NGS® RNA-Seq Library Prep Kit for Illumina® (With Bacteria rRNA Depletion)	KP631-01	12 rxns
	KP631-02	96 rxns
*Trans*NGS® RNA-Seq Library Prep Kit for Illumina® (With Animal rRNA Depletion)	KP641-01	12 rxns
	KP641-02	96 rxns
*Trans*NGS® Fast RNA-Seq Library Prep Kit for Illumina®	KP701-01	12 rxns
	KP701-02	96 rxns
*Trans*NGS® Library Amplification SuperMix	KA101-01	1 ml
	KA101-02	5×1 ml
*Trans*NGS® Library Quantification Kit for Illumina®	KQ101-01	100 rxns
	KQ101-02	500 rxns

Product Name	Cat. No.	Specification
MagicPure® Size Selection DNA Beads	EC401-01	1 ml
	EC401-02	5 ml
	EC401-03	60 ml
	EC401-04	450 ml
MagicPure® RNA Beads	EC501-01	1 ml
	EC501-02	5 ml
	EC501-03	60 ml
*Trans*NGS® Library Quantification qPCR SuperMix	KQ201-01	1 ml
	KQ201-02	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® Tn5 Index Kit for Illumina®	KI101-01	96 Indices, 48 Samples
	KI101-02	96 Indices, 192 Samples
*Trans*NGS® Single Index Primers Kit for Illumina® (Set 1)	KI201-01	48 rxns
	KI201-02	96 rxns
*Trans*NGS® Single Index Primers Kit for Illumina® (Set 2)	KI211-01	48 rxns
	KI211-02	96 rxns
*Trans*NGS® Single Index Primers Kit for Illumina® (Set 3)	KI221-01	96 rxns
	KI221-02	192 rxns
*Trans*NGS® Dual Index Primers Kit for Illumina®	KI231-01	48 rxns
	KI231-02	96 rxns

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