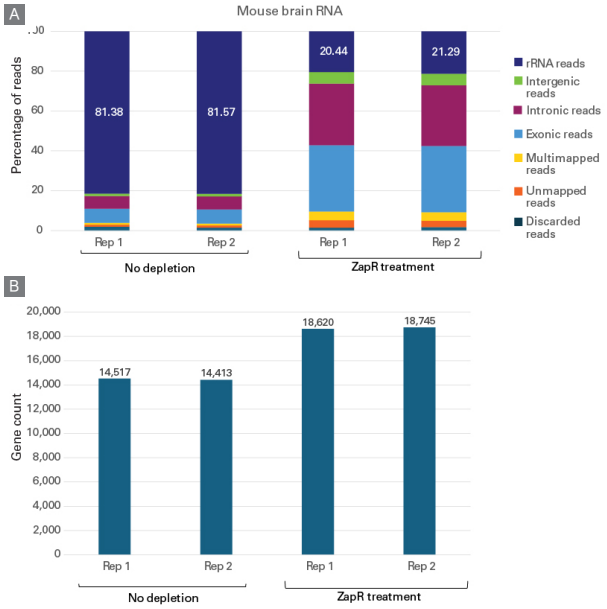
NGS 데이터 Zip

SMART-Seq® Total RNA Pico Input with UMIs (ZapR® Mammalian) 적용 데이터

TaKaRa

Input 종류와 양에 상관없이 ZapR® Mammalian rRNA Depletion Kit의 높은 rRNA 제거 능력과 일관된 유전자 수 검출

■ Mouse brain total RNA input 결과

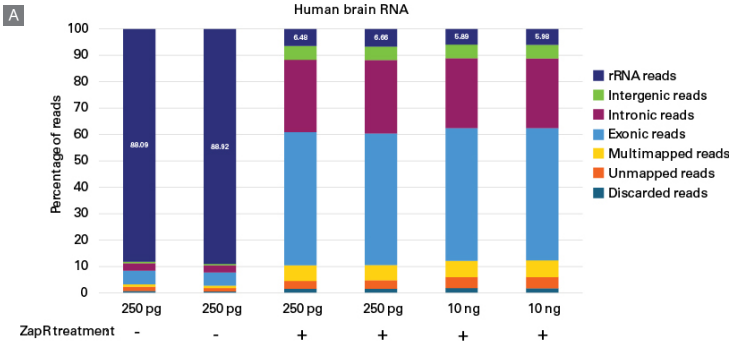


C

	No depletion		ZapR treatment	
	Replicate 1	Replicate 2	Replicate 1	Replicate 2
Discarded reads (%)	1.92	1.53	1.50	1.69
Unmapped reads (%)	1.06	1.04	3.76	3.23
Multimapped reads (%)	0.93	0.94	4.31	4.31
Exonicreads (%)	7.04	7.09	33.24	33.24
Intronic reads (%)	6.38	6.53	30.91	30.48
Intergenic reads (%)	1.29	1.29	5.85	5.77
rRNA reads (%)	81.38	81.57	20.44	21.29
No. of UMIs	64,006	63,952	65,418	65,423
Gene count	14,517	14,413	18,620	18,745
Strand specificity (%)	0.967	0.967	0.968	0.969

Figure 1. Ribosomal rRNA depletion and gene and transcript counts for mouse brain total RNA-seq libraries.
SMART-Seq Total RNA Pico Input with UMIs was used to prepare libraries from 250 pg of mouse brain RNA. Libraries were then either treated with the ZapR Mammalian rRNA Depletion Kit (sold as part of SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian)) and enriched through PCR amplification or left untreated. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. Read distribution (**Panel A** and **Panel C**) and gene count (**Panel B** and **Panel C**) are shown for libraries treated with the ZapR Mammalian rRNA Depletion Kit compared to untreated libraries.

■ Human brain total RNA input 결과

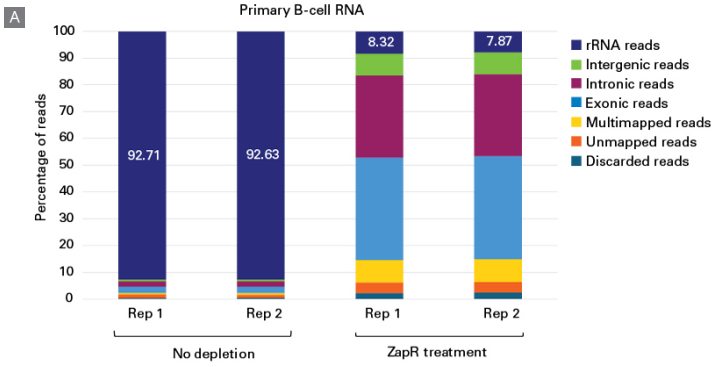


B

	No depletion		ZapR treatment		ZapR treatment	
	250 pg: rep 1	250 pg: rep 2	250 pg: rep 1	250 pg: rep 2	10 ng: rep 1	10 ng: rep 2
Discarded reads (%)	0.81	0.58	1.60	1.61	1.87	1.77
Unmapped reads (%)	1.60	1.31	3.03	3.22	4.13	4.27
Multimapped reads (%)	0.95	0.90	5.89	5.77	6.20	6.33
Exonic reads (%)	5.14	5.03	50.40	49.87	50.21	50.06
Intronic reads (%)	2.80	2.69	27.43	27.71	26.47	26.37
Intergenic reads (%)	0.61	0.58	5.17	5.16	5.22	5.22
rRNA reads (%)	88.09	88.92	6.48	6.66	5.89	5.98
No. of UMIs	61,920	61,518	65,441	65,453	65,494	65,491
Strand specificity (%)	96.8	96.7	97.2	97.3	97.4	97.5
Gene count	13,461	13,362	19,344	19,557	21,493	21,409
Transcripts (TPM≥0.1)	20,098	19,883	35,848	36,632	40,232	40,165
Transcripts (TPM≥1)	20,092	19,874	34,438	35,158	38,506	38,465

Figure 2. Ribosomal rRNA depletion and gene and transcript counts for human brain total RNA-seq libraries.
SMART-Seq Total RNA Pico Input with UMIs was used to prepare libraries from 250 pg and 10 ng of human brain RNA. Libraries were then either treated with the ZapR Mammalian rRNA Depletion Kit (sold as part of SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian)) and enriched through PCR amplification or left untreated. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The bar graph (**Panel A**) and table (**Panel B**) show the read distribution of 250 pg-input and 10 ng-input libraries treated with the ZapR Mammalian rRNA Depletion Kit compared to 250 pg-input untreated libraries.

■ Primary B-cell total RNA input 결과



B

	No depletion		ZapR treatment	
	Replicate 1	Replicate 2	Replicate 1	Replicate 2
Discarded reads (%)	0.49	0.52	2.35	2.48
Unmapped reads (%)	1.23	1.15	3.97	3.93
Multimapped reads (%)	0.66	0.68	8.36	8.53
Exonicreads (%)	2.34	2.40	38.21	38.56
Intronic reads (%)	1.95	1.98	30.71	30.57
Intergenic reads (%)	0.62	0.64	8.09	8.06
rRNA reads (%)	92.71	92.63	8.32	7.87
No. of UMIs	57,616	57,679	65,496	65,487
Strand specificity (%)	95.4	95.6	95.7	95.7
Gene count	9,474	9,481	16,960	17,037
Transcripts (TPM≥0.1)	13,319	13,258	31,207	31,293
Transcripts (TPM≥1)	13,317	13,258	29,792	29,843

Figure 3. Ribosomal rRNA depletion and gene and transcript counts for primary B-cell total RNA-seq libraries.
SMART-Seq Total RNA Pico Input with UMIs was used to prepare libraries from 1 ng of human primary B-cell RNA. Libraries were then either treated with the ZapR Mammalian rRNA Depletion Kit (sold as part of SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian)) and enriched through PCR amplification or left untreated. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The bar graph (**Panel A**) and table (**Panel B**) show the read distribution for libraries treated with the ZapR Mammalian rRNA Depletion Kit compared to untreated libraries.

Total RNA 및 primary cell input에서 일관된 성능

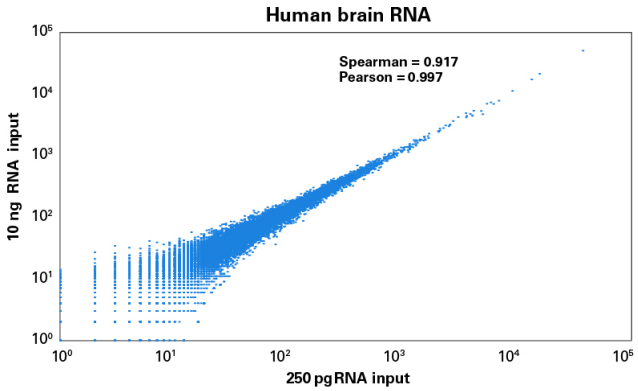


Figure 5. Transcript expression correlation across input amounts for human brain total RNA-seq libraries.
SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian) was used to prepare libraries from 250 pg and 10 ng of human brain RNA. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The scatterplot illustrates the high correlation between the 10 ng-input libraries and 250 pg-input libraries.

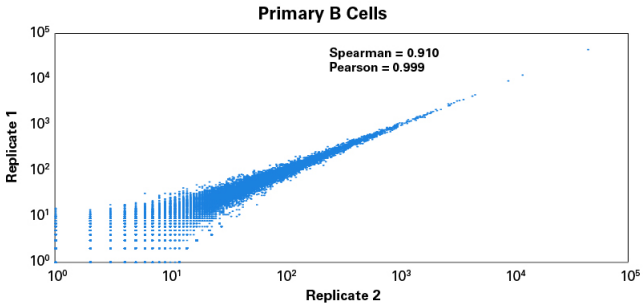
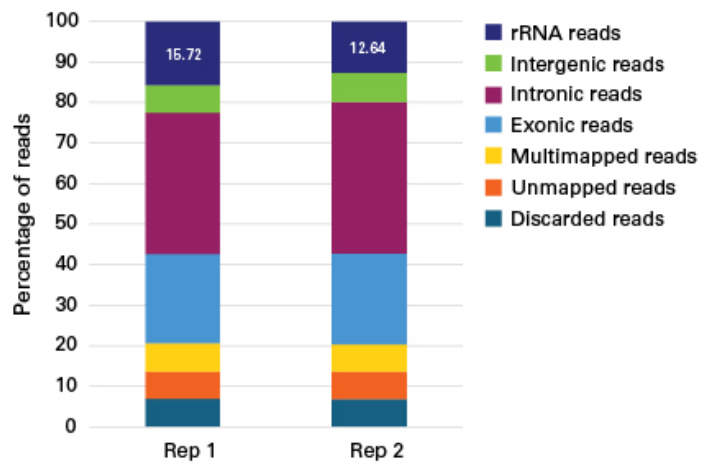


Figure 6. Transcript expression correlation across replicates for primary B-cell RNA-seq libraries.
SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian) was used to prepare libraries from 1 ng of human primary B-cell RNA. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The scatterplot illustrates the high correlation between the two replicates.

FFPE 유래 RNA input에서 ZapR® Mammalian rRNA Depletion Kit의 높은 rRNA 제거 능력과 일관된 검출 유전자 수

A



B

FFPE RNA	Replicate 1	Replicate 2
Discarded reads (%)	6.97	6.94
Unmapped reads (%)	6.68	6.68
Multimappedreads (%)	6.97	6.75
Exonicreads (%)	22.01	22.38
Intronic reads (%)	34.86	37.37
Intergenic reads (%)	6.79	7.23
rRNA reads (%)	15.72	12.64
No. of UMIs	65,007	65,511
Strand specificity (%)	94.4	94.1
Gene count	19,672	19,652
TPM ≥0.1	31,173	31,126
TPM ≥1	30,464	30,433

Figure 4. Ribosomal rRNA depletion and gene and transcript counts for libraries produced from degraded FFPE RNA samples.
SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian) was used to prepare libraries from 10 ng of FFPE RNA (RIN = 3, DV200 = 77%). Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The bar graph (**Panel A**) and table (**Panel B**) show the read distribution for two replicates.

기존의 제품 (SMARTer® Stranded Total RNA-Seq Kit v3 – Pico Input Mammalian) 보다 향상된 성능

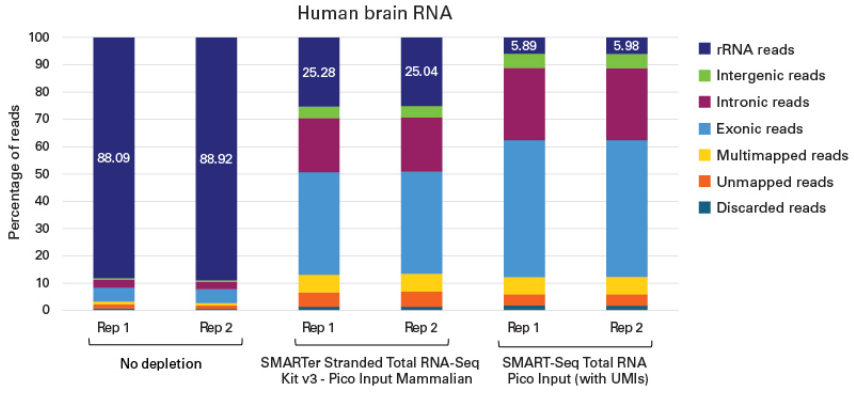


Figure 7. Improved rRNA depletion and enhancement of biologically relevant reads over original SMARTer Stranded Total RNA-Seq Kit v3 – Pico Input Mammalian.
SMART-Seq Total RNA Pico Input with UMIs was used to prepare libraries from 250 pg of human brain RNA. Libraries were then either treated with the ZapR Mammalian rRNA Depletion Kit (sold as part of SMART-Seq Total RNA Pico Input with UMIs (ZapR Mammalian)) and enriched through PCR amplification or left untreated. In addition, SMARTer Stranded Total RNA-Seq Kit v3 - Pico Input Mammalian was used to prepare libraries from 250 pg of human brain RNA. Data analysis was performed with CogentAP using 3 x 10^6 paired-end reads. The read distribution of libraries treated with the ZapR Mammalian rRNA Depletion Kit shows a decreased percentage of rRNA-associated reads and an increased percentage of exonic reads compared to libraries prepared using the SMARTer Stranded Total RNA-Seq Kit v3 - Pico Input Mammalian.