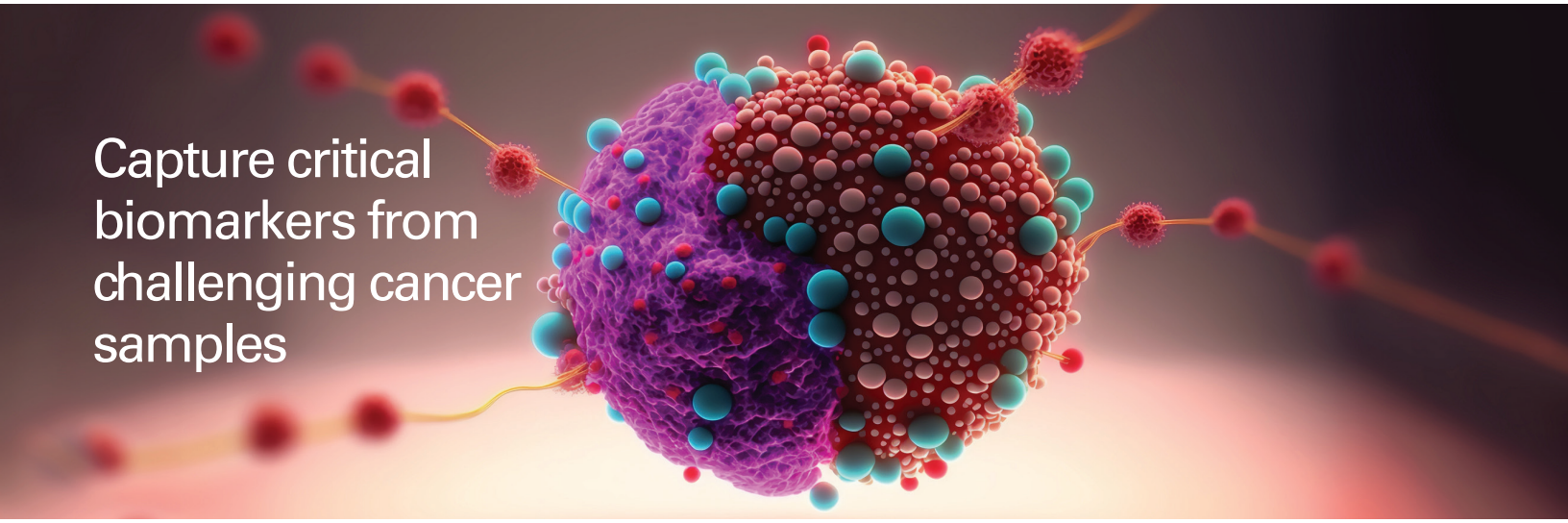
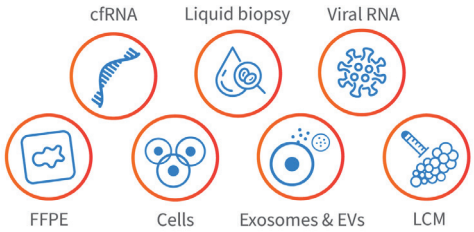
RNA biomarker analysis

TaKaRa

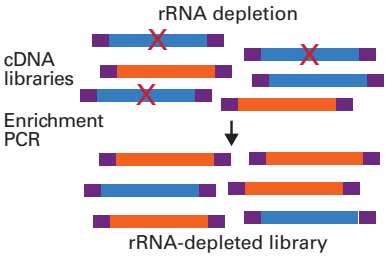


Low input, high-/low-quality, FFPE RNA-seq solutions



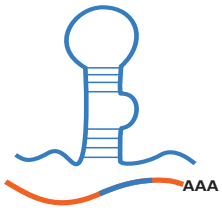
High-quality libraries from a range of samples types and quality (RIN 3-10)

- Including fresh, fresh frozen, and highly degraded FFPE samples
- Compatible with even < 1 ng RNA



All-in-one kit for library prep and ribosomal RNA depletion

- Streamlined, single day protocol ~7h



Capture coding and non-coding transcripts with high sensitivity & specificity

- Detect mRNA,non-PolyA RNA, long non-coding RNA (lncRNA) species
- Prepare stranded libraries

Improve data accuracy with unique molecular identifiers (UMIs) and unique dual indexes (UDIs)

Learn more at takarabio.com/totalrna-seqkits

that's GOOD science!

RNA biomarker analysis

High-quality data from even highly degraded FFPE samples across a wide range of inputs

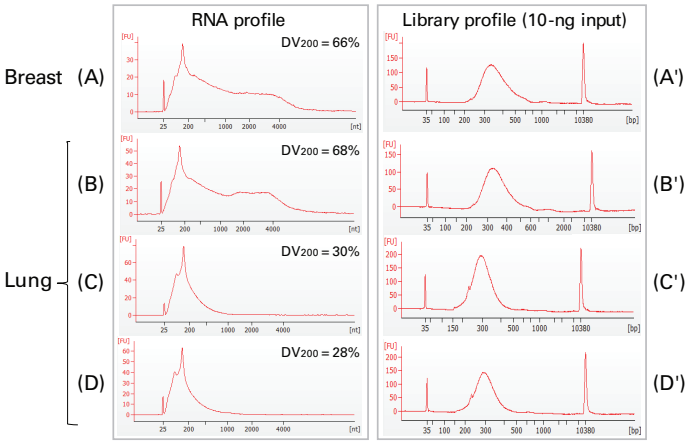
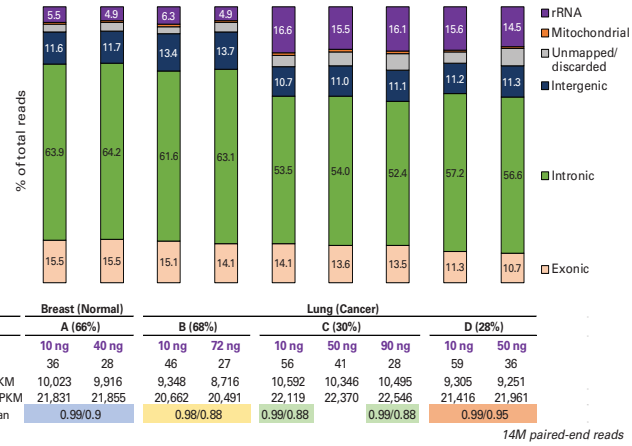


Figure 1. Evaluation of input RNA integrity and NGS library profiles for FFPE samples. Panels A–D. Bioanalyzer traces of RNA inputs obtained from four different samples: one healthy breast tissue sample, and three lung tissue samples obtained from cancer patients. RNA profiles and DV200 values indicate the integrity of each sample. Panels A'-D'. Bioanalyzer traces of sequencing libraries generated from the corresponding RNA inputs. The profile data suggests that high-quality libraries are produced regardless of input RNA integrity.



FFPE tissue	Breast (Normal)		Lung (Cancer)						
Sample (DV 200)	A (66%)		B (68%)		C (30%)			D (28%)	
Input amount	10 ng	40 ng	10 ng	72 ng	10 ng	50 ng	90 ng	10 ng	50 ng
% duplicates	36	28	46	27	56	41	28	59	36
Transcripts ≥1 FPKM	10,023	9,916	9,348	8,716	10,592	10,346	10,495	9,305	9,251
Transcripts ≥0.1 FPKM	21,831	21,855	20,662	20,491	22,119	22,370	22,546	21,416	21,961
Pearson/Spearman	0.99/0.9		0.98/0.88		0.99/0.88		0.99/0.88	0.99/0.95	

14M paired-end reads

Figure 2. Sequencing metrics for FFPE samples show comparable numbers of transcripts identified with fragments per kilobase per million reads mapped (FPKM) >1, and a high degree of correlation across input amounts.

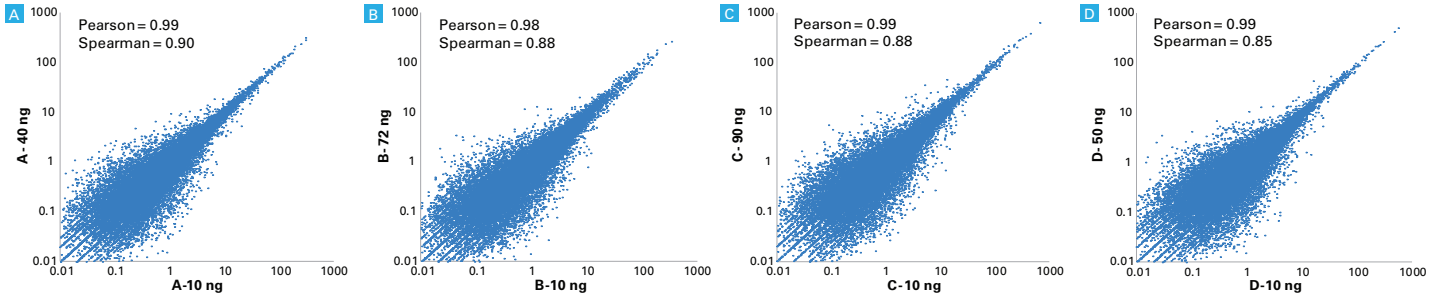


Figure 3. Comparison of transcript expression measurements shows highly reproducible transcript expression across input amounts for samples of varying integrity including two highly degraded samples with DV200 ~30% (C and D). Plots A - D show data from samples with corresponding labels in Figure 1.

Choose the right kit

	SMARTer® Stranded Total RNA-Seq Kit v3 - Pico Input Mammalian	SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian	SMART-Seq® Stranded Kit
Input	250 pg–10 ng, total RNA, 10–1,000 cells	250 pg–10 ng, total RNA	10 pg–10 ng, total RNA, 1–1,000 cells
FFPE compatible	Yes	Yes	No
RNA integrity	RIN 3–10; DV_{200} >25% (including FFPE)	RIN 3–10; DV_{200} >25% (including FFPE)	RIN 3–10
rRNA removal	H/M/R* rRNA	H/M/R rRNA	H/M/R rRNA
UDIs	384 UDIs	384 UDIs	384 UDIs
UMIs	Yes	No	No
Workflow time	~7.5 h	~6 h	~7 h

*H/M/R = human, mouse, rat

Learn more at takarabio.com/totalrna-seqkits

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