that's GOOD science!

Discover more RNA biomarkers with Pico v2 RNA-seq

RNA-seq is an important tool for uncovering biomarkers that can be important in understanding the onset or progression of a disease, such as cancer. SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input (Pico v2) from Takara Bio has unrivaled sensitivity that can help researchers extract these biomarkers from a broad range of sample types, including FFPE RNA, cell-free RNA, and extracellular vesicles.

- Unmatched sensitivity to find and uncover relevant **biomarkers**
- Robust performance with challenging **FFPE** and **cell-free RNA** samples
- Random-priming approach to detect **coding** and **noncoding** transcripts
- Built-in patented **rRNA depletion** technology
- Up to 384 **unique dual indexes** for use on the NovaSeq™ system
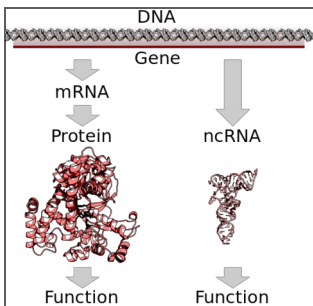
Detect coding and noncoding transcripts with high sensitivity

With the Pico v2 kit, short, overlapping reads originating from the different strands of genomic DNA can be distinguished, enabling more accurate detection of noncoding RNAs that can overlap coding regions and often may not have polyadenylation. Thus, in addition to accurate and sensitive detection of mRNAs, this kit can also detect lncRNAs, tRNAs, and snoRNAs. More information »
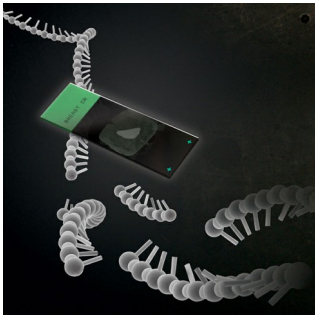

Get high-quality data from degraded FFPE samples

Obtaining good-quality sequencing data from FFPE samples can be a challenge since FFPE RNA integrity can range from high quality to highly degraded. The Pico v2 kit enables good representation of desirable RNA types in a single sequencing experiment, allowing researchers to detect a broad range of different biomarkers from both coding and noncoding RNAs. Get the most out of FFPE RNA with SMARTer chemistry. More information »


Accurately detect RNA transcripts from extracellular vesicles

In a landmark study, researchers from the Center for Medical Genetics at Ghent University and Biogazelle, Zwijnaarde (Belgium) assessed the performance of the Pico v2 kit for RNA-seq analysis of the contents of extracellular vesicles derived from different biofluids. In this extensive assessment, they demonstrated that the kit provided an accurate, precise, and sensitive method to quantify total RNA in human biofluids. More information »
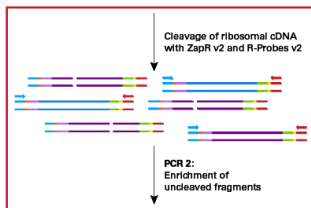
Remove unwanted transcripts with ZapR™

Numerous strategies are available to avoid wasting reads on unwanted transcripts, like rRNA, when doing RNA-seq. Unfortunately, most are very sample-hungry and are ineffective on small quantities of RNA or on degraded RNA. The Pico v2 kit includes a fully integrated method for removal of unwanted transcripts at the cDNA level—so you don't need to go through costly, time-consuming depletion steps and lose your precious RNA before you even get started with library prep. More information »
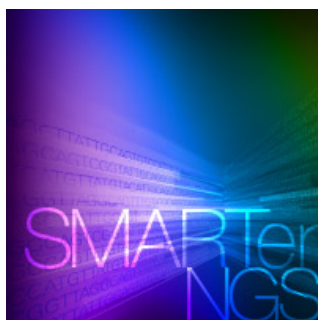
Use unique dual indexes to mitigate index hopping on the NovaSeq system

In order to capitalize on the low cost per sample on the NovaSeq system, experimental design is critical, down to the type of indexes used for sample multiplexing. Unique dual indexes (UDIs) are a requirement to mitigate "index hopping" that can lead to read misassignment on the NovaSeq system. Take the best care of your hard-earned reads using SMARTer unique dual indexes for high-throughput sequencing. More information »

Related products (visit takarabio.com/picov2 for additional configurations)

Cat. #	Product	Size	License	Quantity	Details
634411	SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian	12 Rxns	↗	*	⌃

The SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian is used to generate strand-specific RNA-seq libraries for Illumina sequencing from 250 pg–10 ng inputs of purified total RNA. This kit incorporates Takara Bio's proprietary SMART (Switching Mechanism at the 5' end of RNA Template) technology and includes refinements to the SMARTer method for stranded RNA-seq that simplify the library preparation workflow and improve sequencing performance. This method was developed to work with either high- or low-quality total RNA, does not require additional rRNA removal methods or kits, and produces sequencing libraries that retain strand-of-origin information. The integrated removal of cDNAs derived from rRNA—typically present in high abundance following cDNA synthesis from total RNA inputs—makes the workflow extremely sensitive, yielding data that is highly reproducible with low mapping to rRNA. The new library design featured in the SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian improves sequencing performance compared to the original SMARTer Stranded Total RNA-Seq Kit - Pico Input Mammalian, particularly for NextSeq® and MiniSeq™ instruments carrying the two-channel SBS technology. This kit includes the Indexing Primer Set HT for Illumina v2; for your convenience, we also offer the SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian Components (Cat. #s 634418 and 634419) without indexing primers.

⌄

Documents	Components	Image Data

Cat. #	Product	Size	License	Quantity	Details
634412	SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian	48 Rxns	↗	*	⌃
634413	SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian	96 Rxns	↗	*	⌃
634414	SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian	192 Rxns	↗	*	⌃

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