Revelo™ RNA-Seq High Sensitivity

for Human .

Robust and streamlined library preparation for low-input and challenging human samples

Suitable for

FFPE SAMPLES

NASAL SWABS

BLOOD SAMPLES

Produce high quality libraries from samples with ultra-low or degraded RNA

Optimized for degraded, low input samples such as FFPE RNA

Revelo RNA-Seq High Sensitivity is a whole transcriptome solution that is optimized for the detection and characterization of rare and low abundance transcripts from degraded samples. Revelo RNA-Seq High Sensitivity is built with proven and proprietary technologies created for an end-to-end processing of degraded samples with inputs as low as 250 pg.

- **DimerFree® technology** — eliminate adaptor dimers without the need for adaptor titration, regardless of sample input
- **SPIABoost™ technology** — suppress human rRNA and globin mRNA to maximize informative sequencing reads
- **NuQuant® library quantification** — quantify libraries in minutes by a simple fluorescent and avoid additional quantification methods such as qPCR
- **Unique Dual Indexed Adaptors** — maximize sequencing capacity by multiplexing

Product Highlights

- **Co-infection detection** — identify co-infective agents in the same sample without *a priori* knowledge
- **Scale your assay throughput** — complete an NGS workflow from RNA sample to data in under 24 hours with Revelo RNA-Seq High Sensitivity's 6.5 hour library preparation and quantification workflow. Further scale with our DreamPrep™ automated sample prep platform
- **Reduce the noise** — sequence only the informative transcripts and suppress nuclear rRNA, mitochondrial rRNA and adult globin transcripts
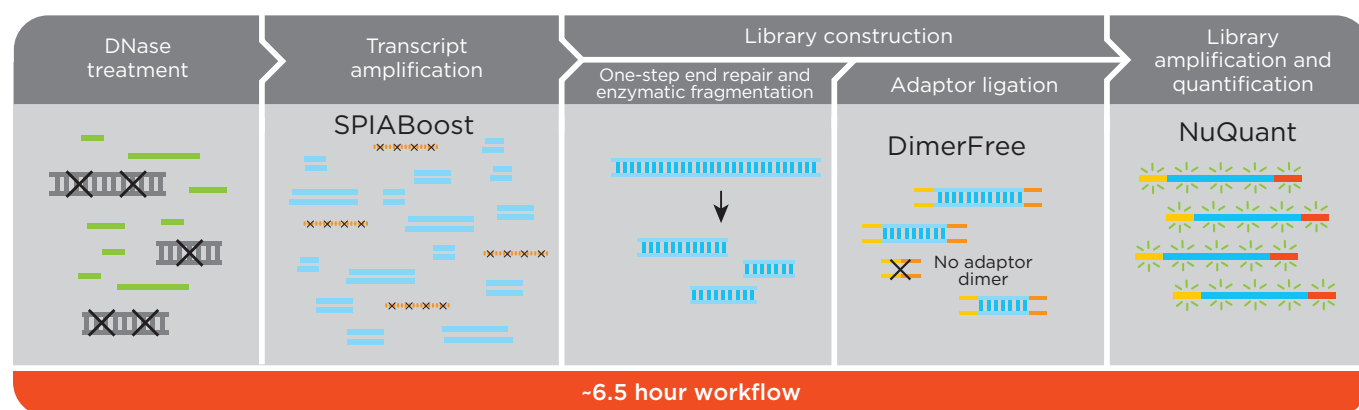

Figure 1: **Save time and resources with Revelo RNA-Seq High Sensitivity, an one-day sample-to-sequencer workflow optimized for degraded sample types.**

Consistent high quality data from degraded sample types and low input ranges

Robust conversion of low quality RNA from FFPE samples to informative reads

RNA degradation, such as in FFPE samples, provides an additional challenge for RNA-Seq library preparation. With Revelo RNA-Seq High Sensitivity, more transcripts from the low quality inputs are enriched, allowing more of the sample to be converted to libraries. Figure 2 shows a successful generation of high quality libraries from total RNA extracted from normal human liver FFPE sample using Revelo RNA-Seq High Sensitivity.
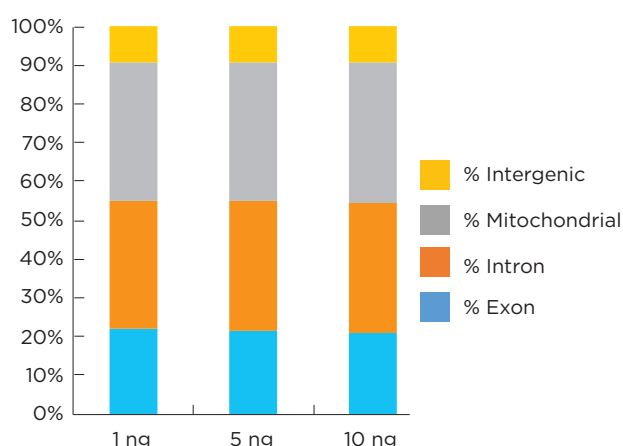

Figure 2: **Distribution of reads in libraries from inputs of 1 ng, 5 ng and 10 ng of human liver FFPE RNA (RIN 2.4).**

Sensitive detection of viral sequences from highly degraded nasal swab samples

RNA-Seq libraries were prepared using 500 pg K562 human RNA spiked with synthetic SARS-CoV-2 genome at 100, 1,000, and 100,000 viral copies. Revelo RNA-Seq High Sensitivity libraries show significantly better viral coverage and greater detection sensitivity compared to a competitor kit (Figure 3).
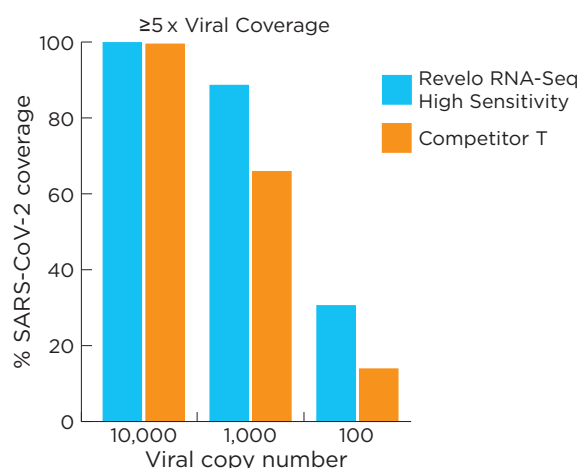

Figure 3: **Revelo RNA-Seq High Sensitivity demonstrates increased viral genome coverage at ≥5 x compared to a competitor kit at 100 and 1,000 copies (Illumina NovaSeq 6000, 20 million (M) reads/sample).** The increased detection sensitivity achieved with Revelo RNA-Seq High Sensitivity enables access to high-quality data from as little as 100 viral copies and uncovers previously inaccessible information from as little as 500 pg total RNA input. ≥1 x and ≥10 x showed a similar trend of increased viral genome coverage.

Next, Revelo RNA-Seq High Sensitivity was used to successfully generate libraries from nasal swab samples which ranged in RIN values as low as 2.20 and viral titer from several hundred to millions of viral copies. Table 1 shows superior sensitivity of Revelo RNA-Seq High Sensitivity compared to

CoV Sample ID	Viral copies per sample	Avg Ct value	RIN values	Revelo RNA-Seq High Sensitivity				Competitor T			
				Viral coverage			Viral reads	Viral coverage			Viral reads
				≥1 x	≥5 x	≥10 x		≥1 x	≥5 x	≥10 x	
Sample 1	537	32	2.6	42.55 %	24.72 %	14.59 %	1293	1.33 %	0.0 %	0.0 %	13
Sample 2	647	32	*	48.75 %	31.54 %	23.21 %	2797	0.0 %	0.0 %	0.0 %	5
Sample 3	1052	31	2.5	42.24 %	19.37 %	8.80 %	639	0.48 %	0.0 %	0.0 %	14
Sample 4	17638	30	2.5	97.57 %	73.13 %	40.07 %	1995	4.37 %	0.0 %	0.0 %	37
Sample 5	216827	23	5.9	100.00 %	99.99 %	99.99 %	688987	13.90 %	0.0 %	0.0 %	33
Sample 6	7026072	19	2.4	100.00 %	100.00 %	99.99 %	843342	99.87 %	38.57 %	5.81 %	717

*Too low to measure

Table 1: **Revelo RNA-Seq High Sensitivity achieves greater detection sensitivity across a range of viral load (500–7 M) compared to the competitor kit.** The Revelo RNA-Seq High Sensitivity libraries provided increased number of viral reads even at a shallow sequencing depth (1M reads/sample) resulting in better viral coverage and increased detection sensitivity. Revelo RNA-Seq High Sensitivity performed better than a competitor kit regardless of RNA quality or viral titer.

the competitor kit in detecting SARS-CoV-2 even with limited sequencing depth (Illumina MiniSeq, 1M reads/sample).

Applications

- Multi-modal cancer assays
- Virus research and surveillance from challenging and degraded samples
- RNA-Seq from degraded and mixed samples such as FFPE and nasal swabs
- Gene expression from rare and transient signals
- Rare transcript detection
- Whole transcriptome profiling

Description	Specs
Sample input	250 pg-10 ng total RNA
rRNA depletion	Human rRNA
Total workflow time	~ 6.5 hours
Multiplexing	Up to 96 single index and 96 UDI
Automation	• DreamPrep NGS (Fluent® 780 workstation). • Automation on other platforms available
Compatible platforms	Illumina HiSeq®, MiSeq®, NextSeq®, MiniSeq, NovaSeq

Table 2: **Revelo RNA-Seq High Sensitivity product specifications.**

Ordering information

Product Name	Part number	No. of reactions
Revelo RNA-Seq High Sensitivity Core Module 32	30201358	32
Revelo RNA-Seq High Sensitivity Core Module A01	30201359	96 (Automation fill)
Revelo SPIABoost Human 32	30201370	32
Revelo SPIABoost Human A01	30201372	96 (Automation fill)
Adaptor Plate L2V23 32	S02317-FG	32
Adaptor Plate L2V2896 PLEX UDI	30184203	96

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