Cell-free nucleic acid sequencing

Shorter time to better results from cell-free nucleic acids

Speed up the development of your liquid biopsy assays

> "Your ThruPLEX Plasma-seq kit is the easiest to follow and has the most streamlined protocol (importantly with the fewest clean-up steps). We successfully made libraries from 1 ng input in this trial."
> *—Dr. Charlie Massie, UNIVERSITY OF CAMBRIDGE*

ThruPLEX Plasma-Seq kit for cell-free DNA (cfDNA)

When it comes to assay development, a streamlined protocol means faster results, a need for less starting material, and less hands-on time—leading to lower variability between samples, runs, and operators, and therefore more reproducible and reliable results.

The ThruPLEX Plasma-Seq kit was developed and optimized for cell-free DNA. Its innovative chemistry offers many advantages:

- **Single-tube workflow:** no transfers or purification steps required
- **Ultra-fast protocol:** three steps; two hours to complete
- **Optimized reagents:** no titration of adapter concentration
- **Superior performance:** high-complexity NGS libraries and reproducible results

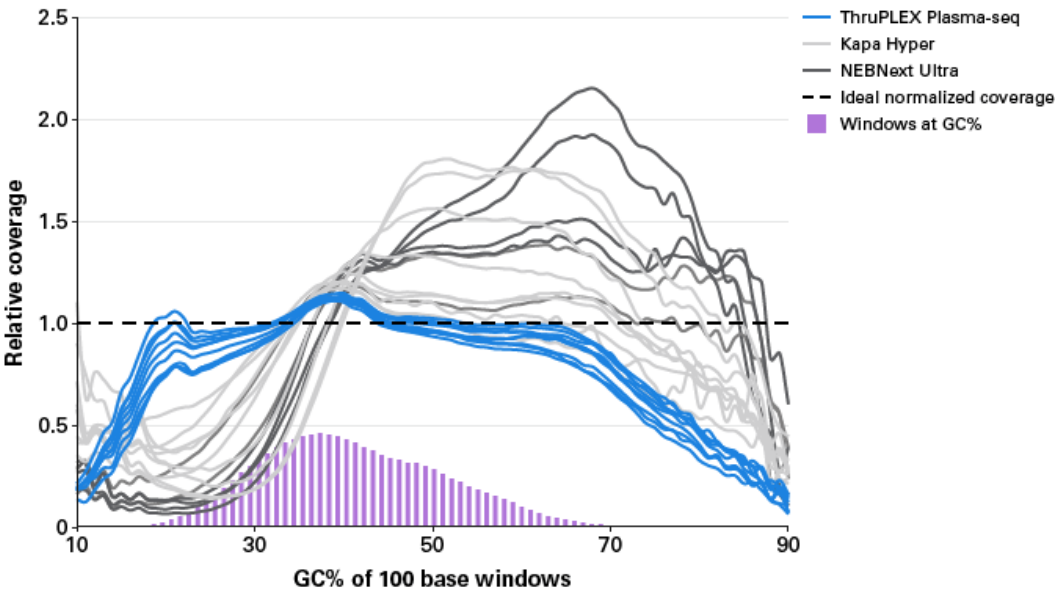

Figure 1. Fewer steps and pipetting operations translate to higher sensitivity and reproducibility. The ThruPLEX Plasma-Seq kit provided the most reproducible and unbiased GC coverage across the human genome, showing minimal variability across the nine plasma samples tested. Libraries were prepared from cell-free DNA isolated from an equivalent of 1 ml of plasma sample and sequenced on an Illumina NextSeq® 500 instrument. Four separate plasma samples were used to construct the NEBNext Ultra libraries.

ThruPLEX technology's high performance has enabled scientists to address challenges in obtaining insights from cell-free DNA samples, advancing the frontier of liquid biopsies to demonstrate clinical utility. Kitzman et al. prepared NGS libraries from cfDNA extracted from maternal plasma samples using a ThruPLEX Plasma-seq kit to demonstrate, for the first time, the non-invasive determination of a fetal genome sequence. Murtaza et al. used a ThruPLEX Plasma-seq kit to perform whole-exome analysis on ctDNA to monitor patients' tumor evolution before and after treatment, demonstrating the first use of NGS to non-invasively identify mutations by sequencing the cfDNA from patients.

Recently, researchers from the Medical College of Wisconsin and the Mayo Clinic used ThruPLEX technology to identify cfDNA biomarkers for

prostate, lung, and colon cancer. Watch the webinar (located below).

SMARTer Stranded Total RNA-Seq Kit v2 for cell-free RNA (cfRNA)

For sensitive detection of transcripts from Illumina-ready stranded NGS libraries generated from cell-free RNA, we offer the SMARTer Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian (Pico v2). This kit features a streamlined six-hour workflow that generates high-quality, stranded NGS libraries from 250 pg to 10 ng of purified total RNA isolated from cell-free RNA derived from plasma and other biofluids. The data shown below demonstrates the sensitivity of the kit in detecting transcripts from as little as 150 pg of input, in comparison to the ideal recommended input amount of 1 ng.

Read our tech note to learn more.

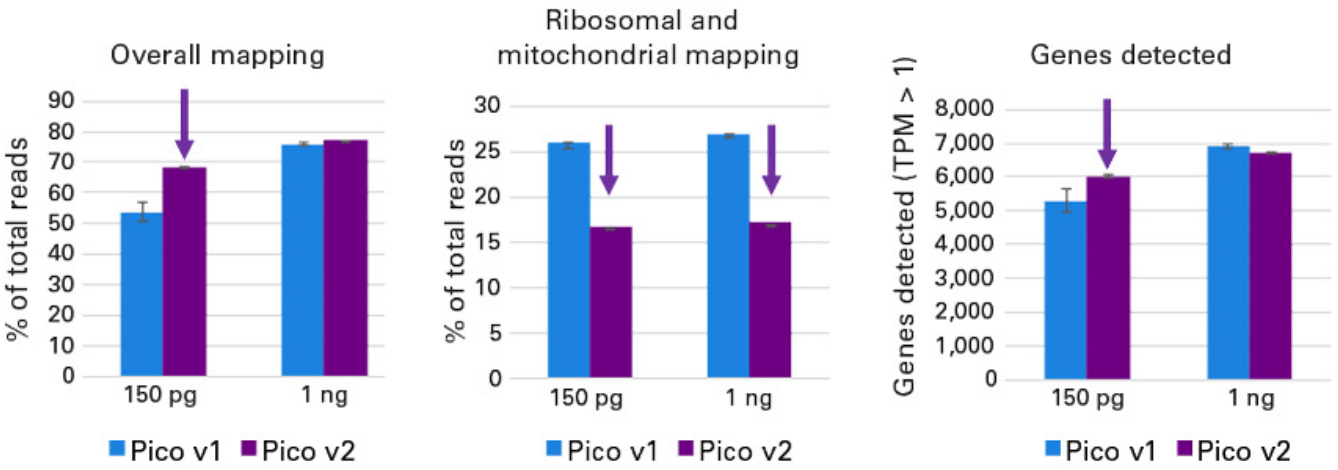

Figure 2. Sensitive detection of transcripts at picogram inputs of cell-free RNA with the Pico v2 kit. While the ideal input of cfRNA for the SMARTer Stranded Total RNA-seq Kit starts at 1 ng, the kit is sensitive enough to generate high-quality NGS libraries from smaller amounts of cfRNA. The data here shows the performance metrics generated using the Pico v1 kit compared to the Pico v2 kit using input amounts of 150 pg and 1 ng. The Pico v2 kit provided improved performance, yielding a low percentage of ribosomal and mitochondrial reads and a high number of genes detected.

References

Kitzman, J.O. *et al.* Noninvasive Whole-Genome Sequencing of a Human Fetus. *Sci. Transl. Med.* **4,** 137–176 (2012).

Murtaza, M. *et al.* Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nature* **497,** 108–112 (2013).

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