Using cell-free RNA for biomarker discovery in cancer research

A noninvasive approach for transcriptome-wide assessment of prognostic, diagnostic, and predictive cancer biomarkers

Potential role of the transcriptome in cancer detection

Early cancer diagnosis gives patients access to possible treatments sooner and the best chance for a favorable outcome.¹ With this in mind, scientists globally continue to search for fast, sensitive, accurate screening methods for cancer-relevant prognostic, diagnostic, and predictive biomarkers. Previous studies have shown that circulating tumor DNA (ctDNA) can act as an indicator for early-stage cancers.² ctDNA analysis has proven to have therapeutic and predictive significance correlated to improved outcomes in late-stage cancers. However, the low abundance of ctDNA in early stage or in low-shedder cancers makes it not ideal for use as an analyte in early detection and screening.³ To overcome these challenges, researchers turned to cell-free RNA (cfRNA). In a 2021 publication,³ they:

- Provided evidence that RNA extracted from plasma is stable and usable for sequencing
- Developed a method for extracting cfRNA from plasma and performing differential expression analysis to identify biomarkers
- Identified mRNA signatures specific to lung and breast cancer only and not detectable in healthy individuals
- Discovered "Dark Channel Biomarker" (DCB) genes that are specific to cancer tissue and subtype, with low false-positive rates

Results support the potential use of cfRNA in early cancer detection and cancer research.

Overview of the workflow used to characterize cfRNA





Read the paper

Larson MH, Pan W, Kim HJ, et al. A comprehensive characterization of the cell-free transcriptome reveals tissueand subtype-specific biomarkers for cancer detection. *Nat Commun.* 2021;12(1):2357. Published 2021 Apr 21. doi:10.1038/ s41467-021-22444-1

Learn more

Illumina RNA Prep with Enrichment, illumina.com/products/by-type/sequencing-kits/library-prep-kits/rna-prep-enrichment.html

Illumina sequencing systems, illumina.com/systems.html

References

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- 3. Larson MH, Pan W, Kim HJ, et al. A comprehensive characterization of the cell-free transcriptome reveals tissue- and subtypespecific biomarkers for cancer detection. *Nat Commun*. 2021;12(1):2357. Published 2021 Apr 21. doi:10.1038/s41467-021-22444-1

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