

Evercode™ WT FFPE

True Whole Transcriptome Single Cell from Archival Samples

Formalin-fixed, paraffin-embedded (FFPE) tissue represents the largest source of clinically annotated samples, but has historically been incompatible with whole transcriptome single cell analysis. Evercode WT FFPE enables single cell RNA sequencing from archived FFPE tissue using reverse transcription-based chemistry, capturing gene expression without predefined panels and supporting discovery-driven analysis across cohorts.

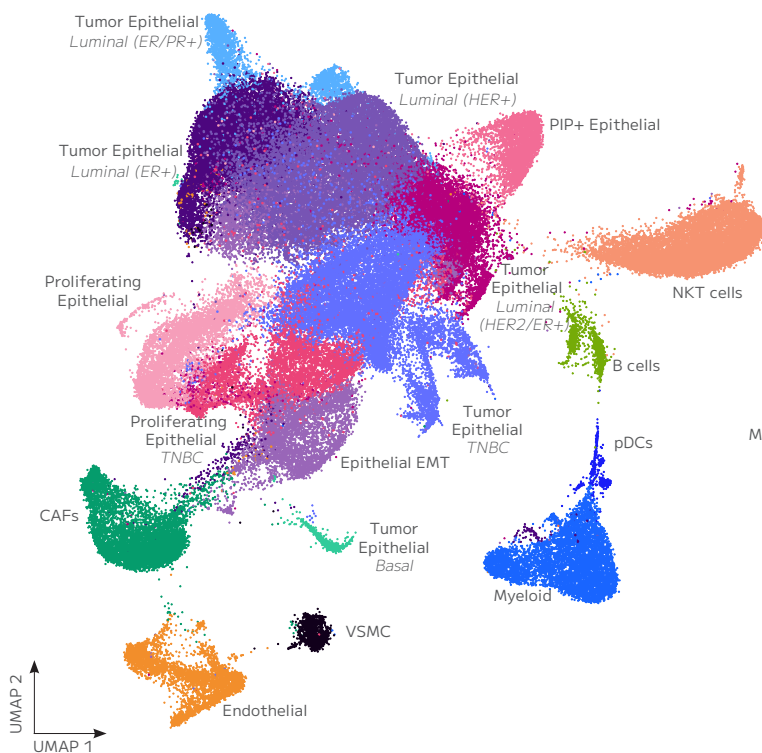
Unbiased Whole Transcriptome Profiling

High-Fidelity Data from FFPE Samples

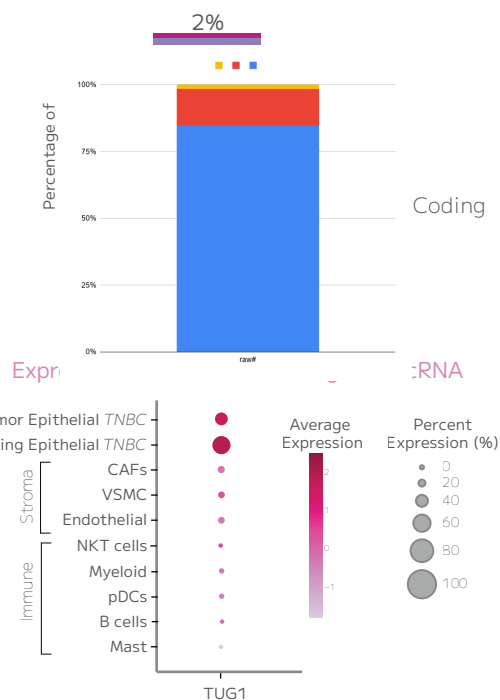
Exponentially Scalable

Instrument-Free, Automation-Compatible

Unbiased Profiling Captures Complete Cellular Context

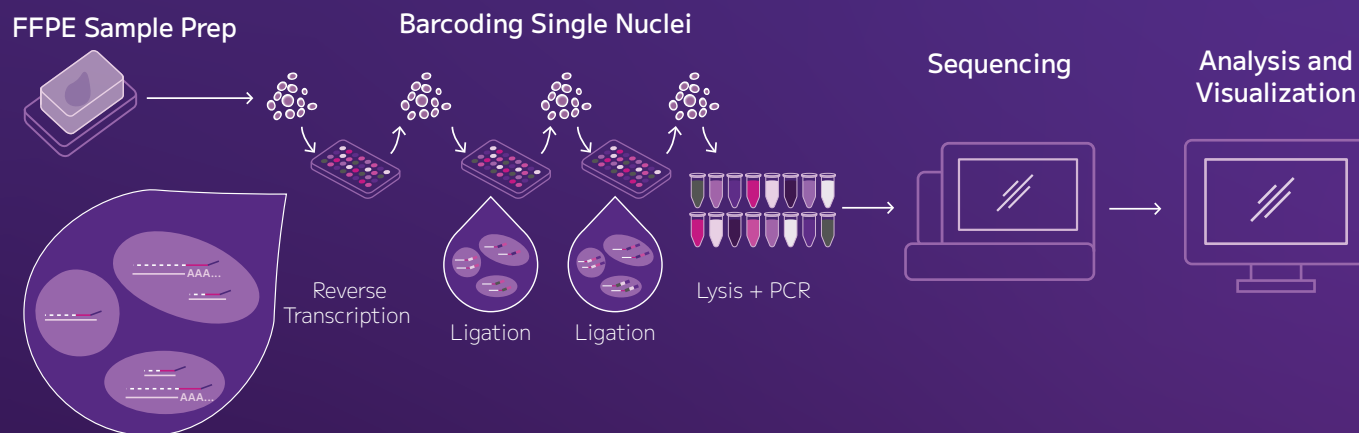


Comprehensive RNA Biotype Detection



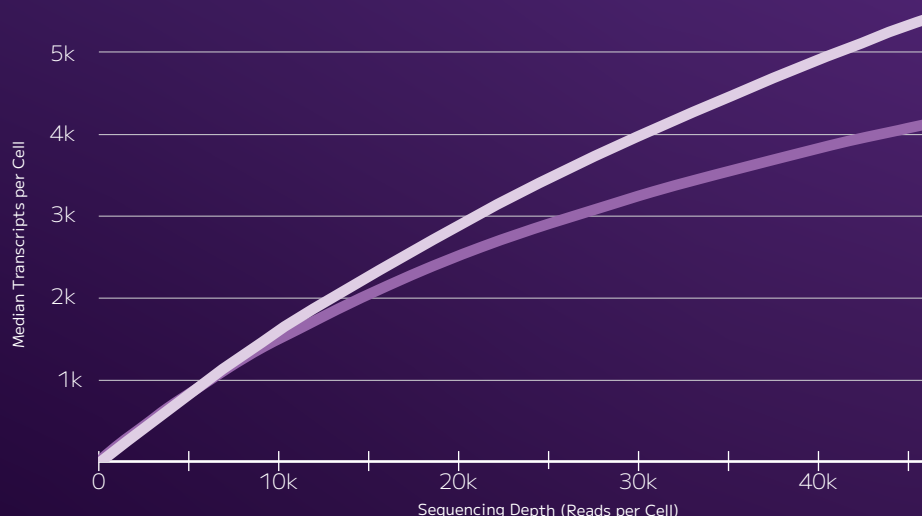
Nuclei from human breast cancer FFPE samples were profiled, capturing diverse tumor epithelial states alongside stromal and immune populations. Robust detection of coding and noncoding transcripts reveals that lncRNAs comprise 14% of total transcripts, with the oncogenic lncRNA TUG1 enriched in proliferating and TNBC epithelial cells, highlighting the power of unbiased profiling to resolve gene expression and the regulatory landscape.

Instrument-Free, Automation-Compatible



Sensitive Transcript Detection in FFPE Tissue

Optimized chemistry for degraded RNA enables accurate measurement of gene expression from FFPE samples. Higher transcript recovery per cell supports reliable identification of cell states, and expression profiles can be compared with fresh tissue datasets. The two lines represent samples from different donors, reflecting biological and FFPE preparation variation across samples.



Built to Scale to Cohort-Level Studies

**Evercode
MAX WT FFPE**

**Evercode
WT FFPE Penta**

**Build Your
Experiment**



For research use only. Not for use in diagnostic procedures.

Evercode WT FFPE Product Sheet - Version 2.0

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