



Spatially Resolved Transcriptomics Deconvolutes Prognostic Histological Subgroups in Patients with Colorectal Cancer and Synchronous Liver Metastases

Background

50% of CRC patients experience liver metastasis (CRLM) which remains a large contributor to death. Four consensus molecular subtypes for CRC have been defined but have failed to project prognosis into the metastatic setting.

Research Questions

- Is “stromal noise” observed with bulk transcriptional analysis potentially concealing biological pathway discovery and intratumoral heterogeneity characterization?
- What can spatial transcriptomics reveal about the functional biology underlying clinically relevant subtypes in matched primary and CRLM?
- Does bulk transcriptional analysis on nCounter correlate with spatial transcriptional analysis with GeoMx?

“Spatial transcriptomics has potential to deepen our understanding of tumor immune interactions and may result in an armamentarium of biomarkers.”

-Wood et. al.

Experimental Setup

Instrument	nCounter®, GeoMx® with nCounter® readout
Sample Type	FFPE tissue Primary, matched metastasis, subtyped
Tissue Type	Colorectal cancer specimens
Assay	PanCancer IO 360™, Cancer Transcriptome Atlas
Analyte	RNA

Spatially Resolved Transcriptomic Analysis Using NanoString Cancer Transcriptome Atlas Gene Sets

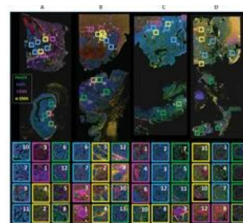
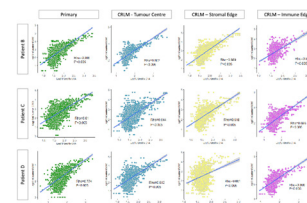


Figure 4: Topographic regions are annotated and each box represents hand-selected area of tumor.

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Comparison of nCounter® IO 360™ and GeoMx® CTA Gene Expression in Matched Samples



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“IO 360 bulk transcriptome panel and GeoMx CTA data in matched samples were correlated and grouped by region.” —Wood et. al.

Results & Conclusions

- Spatial transcriptomics uncovers heterogeneity between patients, lesions, and within individual lesions to identify drivers of metastatic progression in colorectal cancer.
- Specific regions in CRC influence outcome more than others. These regions offer a treasure trove of possible biomarkers & drug targets.
- nCounter and GeoMx together enable the study of existing bulk transcriptomic signatures, molecular subtypes and explore the biology within these groups spatially.

Wood CS, Pennel K, Leslie H, Legrini A, Cameron A, Melissourgou-Syka L, Quinn JA, C. van Wyk H, Hay J, Roseweir AK, Nixon C, Roxburgh CSD, McMillan DC, Biankin AV, Sansom OJ, Horgan PG, Edwards J, Steele CW, Jamieson NB; Spatially Resolved Transcriptomics Deconvolutes Prognostic Histological Subgroups in Patients with Colorectal Cancer and Synchronous Liver Metastases. Cancer Res 15 April 2023; 83 (8): 1329-1344. <https://doi.org/10.1158/0008-5472.CAN-22-2794>

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