**MULTI-OMICS DATA IN THE PREDICTION OF KIDNEY CANCER SUBGROUPS**

**ANNOTATION 7**

(1) Eliana Marostica, Rebecca Barber, Thomas Denize, Isaac S. Kohane, Sabina Signoretti, Jeffrey A. Golden, Kun-Hsing Yu; **Development of a Histopathology Informatics Pipeline for Classification and Prediction of Clinical Outcomes in Subtypes of Renal Cell Carcinoma**. Clin Cancer Res 15 May 2021; 27 (10): 2868–2878. <https://doi.org/10.1158/1078-0432.CCR-20-4119>

(2) In this study, they developed informatics pipelines to connect Renal cell carcinoma (RCC) histopathology images with genomic information, clinical profiles, and biomarkers of response to immune checkpoint blockade. (3) The authors obtained whole-slide histopathology images and demographic, genomic and clinical data from The Cancer Genome Atlas (TCGA), the Clinical Proteomic Tumor Analysis Consortium, Brigham and Women’s Hospital (Boston, MA), and developed fully automated convolutional neural networks to diagnose renal cancers and connect quantitative pathology patterns with patients’ genomic profiles and prognoses. (4) Their research focused on predict the subtypes, prognoses, and genomic aberrations of patients with RCC using histopathology images to guide clinical decision making, improve patients’ outcomes, and reduce the cost of cancer management. (5) The article is useful to our research topic, as authors suggested that integrated information from multiple modalities, including multi-omics are extensible to the histopathology evaluation of other complex diseases. (6) The main limitation of this article is that even they employed a large dataset in this study, may not capture the full spectrum of morphology heterogeneity in RCC, (7) authors indicated that further the performance needs to be evaluated in tumors with atypical histology manifestations. (8) This research used omics data of kidney cancer from TCGA data like our research for even subtyping a particular kidney cancer subgroup, where we are subgrouping the kidney cancer.