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

**ANNOTATION 5**

(1) Hu F, Zeng W, Liu X. A **Gene Signature of Survival Prediction for Kidney Renal Cell Carcinoma by Multi-Omic Data Analysis**. International Journal of Molecular Sciences. 2019; 20(22):5720. https://doi.org/10.3390/ijms20225720

(2) In this paper, they performed a multi-omics analysis to build a multi-gene prognosis signature for Kidney renal cell carcinoma (KIRC). (3) The authors downloaded multiplatform genomics datasets from The Cancer Genome Atlas (TCGA), identified 863 differentially expressed genes (DEGs) with an altered DNA methylation status, found 189 methylated differentially expressed genes (MDEGs) as prognosis-related genes, selected 7 and generate a risk score to predict prognosis based on the expression of the seven genes on KIRC patient. (4) Their research focused on methylation and expression profiles to provide a reliable prognostic model for KIRC patients. (5) The article is useful to our research topic, as authors suggested seven-MDEG signature for predicting survival in KIRC patients. (6) The main limitation of this paper is that the signature was only validated on the TCGA cohort. Thus authors indicate that this signature needs to be further investigated in multiple datasets with different populations. (7) Their results showed that their signature is an independent prognostic factor in KIRC patients and can more accurately predict overall survival in KIRC patients than a tumor stage system. (8) This study is on one of the kidney cancer subgroups, hence gives an idea on kidney cancer related studies such as DEGs and MDEs.