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

**ANNOTATION**

[1] Terrematte, P.; Andrade, D.S.; Justino, J.; Stransky, B.; de Araújo, D.S.A.; Dória Neto, A.D. A Novel Machine Learning 13-Gene Signature: Improving Risk Analysis and Survival Prediction for Clear Cell Renal Cell Carcinoma Patients. Cancers 2022, 14, 2111. https:// doi.org/10.3390/cancers14092111

[2] This article was used to analyze the survival rate for Clear Cell RCC patients. [3] It evaluated a linear survival model of Cox regression with 14 signatures and 6 methods of feature selection and performed a functional analysis and differential gene expression approaches by using ccRCC cohorts of the Cancer Genome Atlas (TCGA-KIRC) and International Cancer Genome Consortium (ICGC-RECA). [4] It considered the major Kidney Cancer subgroup known as Clear Cell Renal Cell Carcinoma. [5] This article used a multi-omics data approach and a machine learning method for data analysis. [6] It only focused on the major Kidney Cancer subgroup for its analysis. [7] It identified two clusters of genes within one subtypr of kidney cabcer (renal cell carcinoma) with a high and low expressionlevels. [8] This article is related to our topic as they used multi-omics data of kidney cancer with different machine learning model.