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

**ANNOTATION 2**

[1] Marquardt, André et al. “Subgroup-Independent Mapping of Renal Cell Carcinoma-Machine Learning Reveals Prognostic Mitochondrial Gene Signature Beyond Histopathologic Boundaries.” Frontiers in oncology vol. 11 621278. 15 Mar. 2021, doi:10.3389/fonc.2021.621278

[2] This research article mainly focused on establishing histopathologic subgroups in renal cell carcinoma (RCC) and finding treatments with drug sequencing for affected patients. [3] Required data for the research is obtained from Internationally recognized sources like the GDC portal and t-SNE plotting with Random Forest Learning is used to train a model for the Machine learning approach. [4] Scope of this article is to observe most common Renal Cell Carcinomas and find out them in early stage. [5] One of the main properties of this article is kidney cancer subgrouping which is mainly related to our topic. [6] Among many kidney cancers, this article only considers three main subtypes of kidney cancers due to its complexity. [7] The authors revealed that overall survival possibility is low in ccRCC and high in chRCC. [8] Our research is mainly depending on Multi-omics data and this article only considered a single omic data for its functions.