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

**ANNOTATION 6**

(1) He, Z., Liu, H., Moch, H. et al. Machine learning with autophagy-related proteins for discriminating renal cell carcinoma subtypes. Sci Rep 10, 720 (2020). <https://doi.org/10.1038/s41598-020-57670-y>

(2) In this paper, they tested the possibility of using numeric data acquired from software-based quantification of certain marker proteins, key autophagy proteins (ATGs), obtained from immunohistochemical (IHC) images of renal cell carcinomas (RCC). (3) The authors found a Tissue microarray (TMA) containing 237 RCCs from untreated patients and 18 normal kidney tissues from healthy donors belongs to Department of Pathology and Molecular Pathology, University and University Hospital Zurich and analyzed data using different data cleaning and machine learning techniques to classify the subtypes of RCCs. (4) Their research focused on indicating the potential for bioinformatics approaches in tumor classification based on the expression levels of certain ATGs in RCC. (5) The article is useful to our research topic, as authors suggested that histone methyltransferases and microRNA-145 may have diagnostic value for discrimination of certain subtypes of RCC. (6) The main limitation of this article is that most of the tested proteins could not differentiate papillary renal cell carcinomas (pRCC) from normal tissue, (7) thus the authors suggested that evaluation of autophagy and/or ATGs are less sufficient for pRCC prediction as compared with other subtypes. (8) Here authors did the same research as ours and only difference is using autophagy-related proteins instead of multi-omics data.