Dissecting neuroendocrine mixed tumors by single cell RNA-seq

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Neuroendocrine tumors (NET) are composed of diverse malignant, immune and stromal cells that interact with one another and collectively determine tumor biology and clinical phenotypes. We are using single cell RNA-seq (scRNA-seq) to comprehensively characterize the cellular diversity of NETs and to compare them to other tumors and to normal tissues. This approach will help us uncover the composition of the tumor microenvironment, the impact of hormonal secretion, the differences between tumors and the corresponding healthy tissues, and the exact cellular states of the malignant neuroendocrine cells. In addition to NETs, we are also interested in profiling "mixed" tumors, known as Mixed Adeno-neuroendocrine Carcinomas (MANECs). Recent profiling of a MANEC tumor from the lung demonstrates the co-existence of two malignant and proliferating components and suggests potential insights into their emergence and interactions.