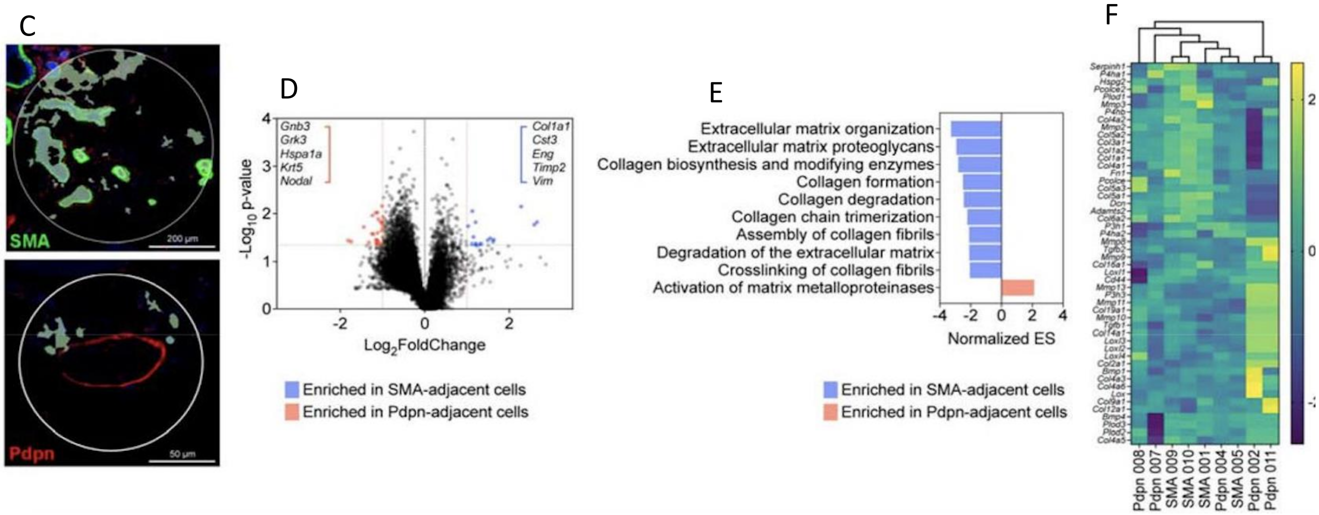
Successful of NanoString GeoMx Digital Spatial Profiler (DSP) service launch

In 2021 we added the NanoString GeoMx DSP, an advanced analytic platform to our instrumentation portfolio via an ETF purchase. The GeoMx DSP enables spatially resolved, high-plex (10s -10,000s) digital quantitation of proteins and mRNA in tissue. The distribution of protein or gene expression can be visualized across multiple tissue compartments. It also provides a complete analyses system for identifying biomarkers and pathway analyses to understand disease mechanisms of action and identify novel targets. We took delivery of this equipment in May 2021, the GeoMx DSP instrument has been installed in June 2021. Trial runs on GeoMx DSP for both protein and RNA assays were successful. The GeoMx RNA assay for Dudley lab on Periostin$^+$ stromal cells guide lymphovascular invasion by cancer cells was published (Jamie L. Null, Dae Joong Kim, James V. McCann, Pankaj Kumar, Lincy Edatt, Chad V. Pecot, Andrew C. Dudley, doi: https://doi.org/10.1101/2022.05.19.492742) and GeoMx protein assay for Dr.Fox on snake envenomation site immune microenvironment in time and space was also successful (manuscript is in preparation).

Below is example of GeoMx RNA assay : Periostin-expressing cells surround tumor-naïve mammary ducts and blood vessels and are enriched at the lymphatic vessel periphery (Null, et all, doi: https://doi.org/10.1101/2022.05.19.492742).



(C) Representative images of regions of interest (ROIs) used to select ZSGreen$^+$ periostin-expressing cells for spatial RNA profiling (n = 4-5 ROIs per group, from the mammary glands of 3 mice). (D) Volcano plot of differential gene expression in ZSGreen$^+$ cells located near ducts and blood vessels (SMA-adjacent) and ZSGreen$^+$ cells located near lymphatic vessels (Pdpn-adjacent). Green line represents a p-value of 0.05 and red line represents the significance threshold. (E) Gene Set Enrichment Analysis (GSEA) showing upregulated pathways in spatially-defined ZSGreen$^+$ populations. (F) Cluster analysis of ZSGreen$^+$ cells from individual ROIs based on collagen-related genes.