Purpose: To characterize the inflammatory cells and associated signaling network in incipient and advanced BPH

Approach: We used single cell RNAseq of CD45+ leukocytes, to generate cellular transcriptomes describing the leukocytes present in the transition zones of small and large prostates. CITEseq was used to confirm cell surface marker expression adding confidence to cluster identification. Bioinformatic approaches were used to identify and impute cell signaling pathways active between leukocyte populations.
Findings and future directions

Identification of targetable pathways that contribute to BPH pathogenesis will yield novel therapeutic strategies to limit progression of this disease.

This study will be expanded to incorporate interactions between leukocytes, stromal cells and epithelium to provide a clearer overall picture of cellular interaction in prostate growth.