<u>Narrative</u>

We aim to investigate the genomic cause of racial disparities in renal cell carcinoma, focusing on two known kidney cancer genes, *VHL* and *MET.* We will perform whole-genome sequencing of African Americans with clear cell renal cell carcinoma to complete a missing aspect of The Cancer Genome Atlas, and then identify and validate a set of variants that are both associated with kidney cancer and racially disparate. Finally, we will perform functional characterization of our prioritized, high-confidence list of genetic variants using a CRISPR/Cas platform.