

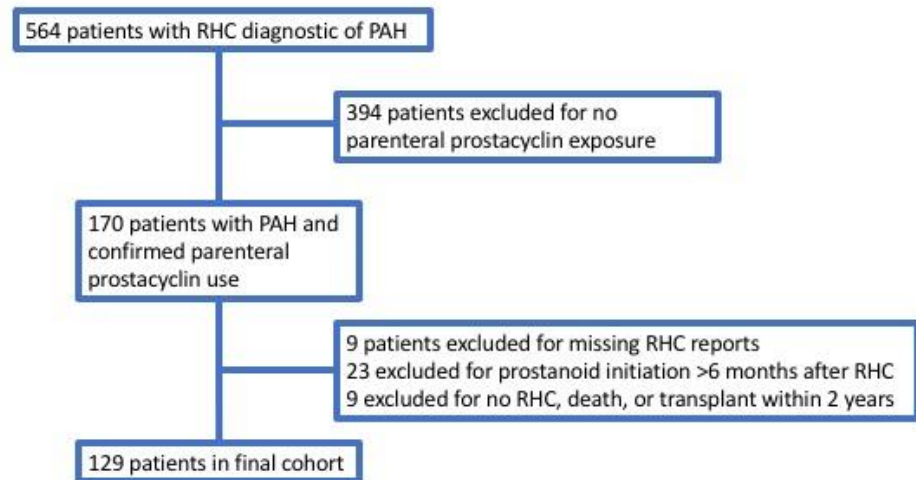
Supplement:**Supplemental Methods:***Genetics Data and Analysis:*

The GTEx project has established that many SNVs correlate with mRNA expression levels of specific genes. The GTEx database is comprised of significant SNV-gene pairs as determined by expression quantitative loci (eQTL) mapping of SNVs to gene transcription levels adjusted for age, genotype platform, sex, and principal components 1-3. SNVs from our GWAS with a p value < 0.01 were mapped to their gene pairs in the GTEx database (Affymetrix 6.0 eQTL annotation) using the website <http://www.scandb.org/newinterface/about.html>. Subsequently, these gene names were submitted to FUMAgwas GENE2FUNC for differentially expressed gene (DEG) analysis.³⁷ DEG sets are pre-calculated sets of differentially expressed genes across the tissue types in the GTEx database. The hypergeometric test was used to determine if the genes are significantly over/under expressed in a given tissue compared to all other tissues.

e-Table 1: Variables Included in Logistic Regression Model of 5 Year Survival

[illegible]

E Fig. 1



E Fig. 2

