Supplement:

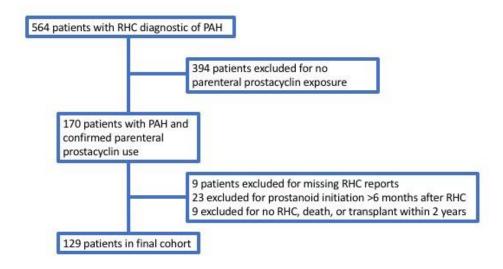
Supplemental Methods:

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						
	25%	75%	Δ	Coefficient	Odds Ratio	95% CI
Intercept				-4.15		
Mean RA Pressure						
(mmHg)	8.5	17	8.5	0.0394	1.397	(0.567 - 3.443)
Cardiac Index (L/min/m ²)	1.54	2.23	0.69	0.535	1.447	(0.561 - 3.728)
Pulmonary Artery O ₂						
saturation	51	63	12	-0.0517	0.538	(0.202 - 1.429)
Heart Rate	73	90	17	0.0151	1.293	(0.603 - 2.770)
Age	38.5	59.1	20.6	0.0775	4.965	(1.517 - 16.255)
Gender (male)				0.3183	1.375	(0.257 - 7.366)
APAH vs. IPAH/HPAH				0.9448	0.389	(0.127 - 1.186)
RA = right atrial; APAH = a	issociated	l pulmona	Iry arterial	hypertension; I	PAH = idiopat	hic PAH; HPAH
= heritable PAH						

E Fig. 1



E Fig. 2

