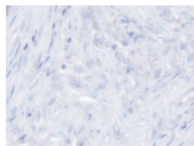
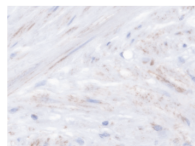
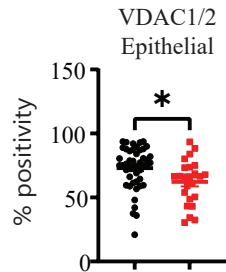
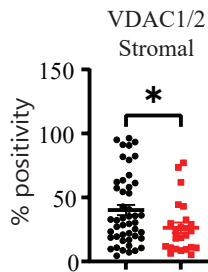
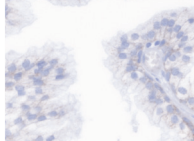
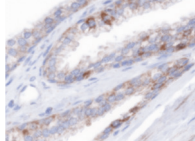


VDAC1/2

Stromal

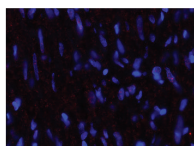
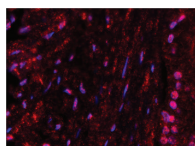


Epithelial

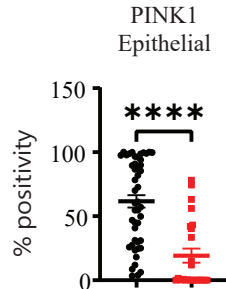
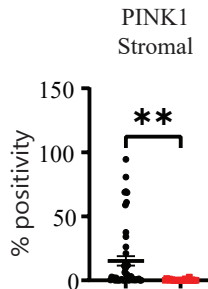
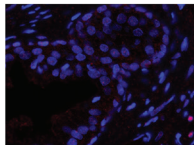
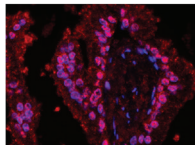


PINK1

Stromal

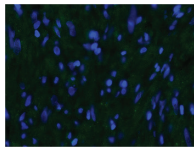
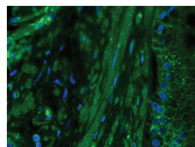


Epithelial

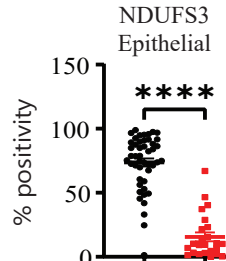
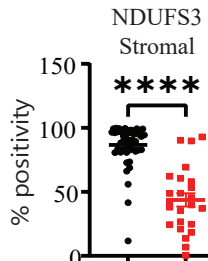
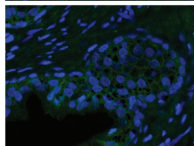
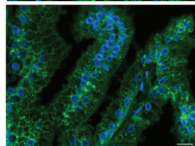


NDUFS3

Stromal



Epithelial



Normal

BPH

Supplemental Figure 1: Reduced accumulation of various markers of mitochondrial function in BPH prostate.

VDAC1/2 (brown), PINK1 (red), and NDUFS3 (green) were all measured using IHC on normal adjacent and BPH prostate tissue samples (BPT=48, BPH=24). Using the Inform software, tissues were segmented into epithelial and stroma, scored to determine a positivity threshold, and calculated as percent positive of total cells (DAPI). Images were taken at 20x magnification and zoomed 2x post-imaging. The scale bar is 10 microns (* $p < 0.05$, ** $p < 0.01$, **** $p < 0.0001$).

Supplemental Table 1

Gene Symbol	BPH vs Normal	P-Value
<i>DDX6</i>	-378.60	0.05
<i>HLA-DRB5///HLA-DRB4///HLA-DRB3///HLA-DRB1</i>	-55.16	0.03
<i>FBXL5</i>	-28.32	0.03
<i>ROM1</i>	-26.51	0.03
<i>SLC12A2</i>	-23.55	0.00
<i>VAT1</i>	-23.55	0.01
<i>PTPN3</i>	-19.75	0.00
<i>TM4SF1</i>	-13.77	0.01
<i>PBX3</i>	-12.43	0.00
<i>SPIN1</i>	-9.36	0.00
<i>ASNA1</i>	-8.49	0.03
<i>CDK7</i>	-8.36	0.02
<i>CHMP4B</i>	-7.31	0.03
<i>EPS8</i>	-6.73	0.01
<i>ZMYM6</i>	-5.94	0.02
<i>MLIP///PIGA</i>	-4.82	0.00
<i>TNFSF12-TNFSF13///TNFSF12///TNFSF13</i>	-4.44	0.03
<i>PCM1</i>	-4.26	0.00
<i>PGM2</i>	-3.92	0.01

Gene Symbol	BPH vs Normal	P-Value
<i>GATAD2B</i>	-3.79	0.02
<i>SUSD4</i>	-3.75	0.01
<i>GM2A</i>	-3.19	0.03
<i>FLNB</i>	-2.98	0.04
<i>MAPK8</i>	-2.97	0.05
<i>AGK</i>	-2.91	0.02
<i>KLF6</i>	-2.76	0.02
<i>RHOA</i>	-2.75	0.04
<i>NDUFS4</i>	-2.73	0.04
<i>POLDIP3</i>	-2.73	0.01
<i>GNAS</i>	-2.67	0.02
<i>ZFYVE19</i>	-2.56	0.02
<i>SLC12A2</i>	-2.42	0.00
<i>WNK1</i>	-2.37	0.01
<i>ZMYND11</i>	-2.35	0.03
<i>DMXL1</i>	-2.26	0.00
<i>PRKARIA</i>	-1.95	0.02
<i>OSBPL10</i>	-1.88	0.01
<i>IL1R1</i>	-1.86	0.00
<i>EFEMP2</i>	1.80	0.04
<i>SGK1</i>	2.12	0.04

Gene Symbol	BPH vs Normal	P-Value
<i>ACSS3</i>	2.13	0.01
<i>HSPB8</i>	2.18	0.03
<i>ACTA2</i>	2.21	0.04
<i>TGFBR3</i>	2.32	0.02
<i>LAMB2</i>	2.32	0.02
<i>MYADM</i>	2.33	0.01
<i>MCL1//EPAS1</i>	2.42	0.05
<i>GUCY1A3</i>	2.44	0.03
<i>PTPN11</i>	2.44	0.05
<i>GSN-AS1//GSN</i>	2.46	0.03
<i>BBX</i>	2.46	0.04
<i>MYL9</i>	2.52	0.03
<i>MBD1//HLF</i>	2.61	0.03
<i>EIF4EBP2</i>	2.63	0.04
<i>MEG3</i>	2.69	0.00
<i>MAL2</i>	2.70	0.00
<i>FNBP1L</i>	2.77	0.04
<i>PMP22</i>	2.82	0.05
<i>MSN</i>	2.86	0.03
<i>MYADM</i>	2.94	0.02
<i>CCND2</i>	2.95	0.01
<i>LOC100129846//RBPMS</i>	2.97	0.05

Gene Symbol	BPH vs Normal	P-Value
<i>SORBS1</i>	2.99	0.04
<i>SLMAP</i>	2.99	0.01
<i>CPQ</i>	3.29	0.04
<i>NARR//RAB34</i>	3.39	0.00
<i>C1R</i>	3.49	0.04
<i>PRELP</i>	3.57	0.00
<i>CTSL</i>	3.66	0.03
<i>FBN1</i>	3.67	0.01
<i>PKD2</i>	3.86	0.01
<i>MAPRE1</i>	3.91	0.04
<i>MAPK10</i>	3.96	0.03
<i>CDC42BPA</i>	4.12	0.04
<i>SSBP2</i>	4.15	0.02
<i>FGFR1</i>	4.23	0.00
<i>KLHL42</i>	4.34	0.05
<i>FAAH</i>	4.40	0.04
<i>IQCK</i>	4.42	0.02
<i>ENPP4</i>	4.43	0.01
<i>C9orf3//DSTN</i>	4.54	0.03
<i>COL4A2-AS1//COL4A2</i>	4.56	0.03
<i>ITM2A</i>	4.65	0.00
<i>CLDN4</i>	4.78	0.00

Gene Symbol	BPH vs Normal	P-Value
<i>FBLN1</i>	4.87	0.00
<i>GABBR1</i>	5.38	0.01
<i>PNISR</i>	5.39	0.03
<i>ADAM22</i>	5.47	0.00
<i>MAPK1</i>	5.98	0.00
<i>BBX</i>	6.39	0.01
<i>MAMLD1</i>	6.86	0.00
<i>NPTN</i>	7.40	0.04
<i>RAB11FIP2</i>	8.12	0.02
<i>TSPAN3</i>	8.46	0.04
<i>VIM</i>	8.76	0.01
<i>COL3A1</i>	9.46	0.02
<i>PIAS1</i>	9.64	0.01
<i>ALCAM</i>	9.72	0.00
<i>RSU1///ABCD3</i>	9.97	0.00
<i>SLC39A6</i>	11.37	0.01
<i>TST</i>	11.59	0.00
<i>PLOD3</i>	11.69	0.01
<i>YAPI</i>	11.74	0.00
<i>PLGLA///PLG</i>	15.53	0.02
<i>LDB2</i>	16.68	0.02
<i>CRTC3</i>	21.77	0.02

Gene Symbol	BPH vs Normal	P-Value
<i>PEA15</i>	21.92	0.04
<i>BPTF</i>	24.74	0.02
<i>IL10RA</i>	25.30	0.03
<i>NEDD4L</i>	25.49	0.01
<i>SEPP1</i>	29.61	0.00
<i>CCDC80</i>	66.25	0.01
<i>ARPC4-TTLL3///ARPC4</i>	98.33	0.03
<i>SRSF3</i>	169.61	0.05

Supplemental Table 2

YWHAZ	F	TGATCCCCAATGCTTCACAAG
	R	GCCAAGGTAACGGTAGTAATCT
TBP	F	CCACTCACAGACTCTCACAAC
	R	CTGCGGTACAATCCCAGAACT
COL1A1	F	GAGGGCCAAGACGAAGACATC
	R	CAGATCACGTCATCGCACAAC
COL3A1	F	GCCAAATATGTGTCTGTGACTCA
	R	GGGCGAGTAGGAGCAGCAGTTG