

SUPPLEMENTARY DATA

Comparative Blood-Based Transcriptomic Profiles of Prostate Cancer Patients from South Africa and the USA: A Cross-Sectional Pilot Study

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Supplementary Tables

Supplementary Table 1. Peripheral blood evaluation of top 10 tissue-expressed DEGs between Caucasian and Black men

Upregulated (Black PCa tissue)	PCa blood samples			Control blood samples	
	B:W fold- change	<i>p</i> -value	Same	B:W fold- change	<i>p</i> -value
<i>ANPEP</i>	-3.07	2.57E-09	No	-3.70	7.71E-13
<i>IGKV2D-29</i>	+4.39	1.04E-03	Yes	+2.76	7.72E-05
Down- regulated (Black PCa tissue)					
<i>ANKRD36B</i>	+1.97	1.03E-05	No	+1.48	1.87E-03
<i>RPS24</i>	+1.80	8.09E-15	No	+1.78	1.03E-08
<i>SEC11C</i>	+1.79	1.02E-08	No	+2.05	6.78E-07
<i>SH3KBP1</i>	-1.26	1.16E-03	Yes	-1.46	2.57E-04
<i>STEAP4</i>	-1.44	6.47E-03	Yes	-1.72	3.98E-03

Supplementary Table 2. Peripheral blood evaluation of top 10 tissue-expressed TFs between Caucasian and Black men

Activated (Black PCa tissue)	PCa blood samples			Control blood samples	
	B:W fold- change	<i>p</i> -value	Same	B:W fold- change	<i>p</i> -value
<i>CTCF</i>	-1.27	7.52E-03	No	-1.52	8.97E-07
<i>EP300</i>	-2.19	2.24E-11	No	-2.99	2.23E-15
<i>ESR1</i>	ND			-1.85	9.16E-03
<i>NR3C1</i>	-1.38	1.47E-04	No	-1.54	3.36E-04
<i>SMARCA4</i>	-1.68	2.75E-05	No	-1.69	9.02E-05

ND = no difference between samples

Supplementary Table 3. Peripheral blood evaluation of candidate genes associated with racial differences between Caucasian and Black men

Family	Gene	PCa blood samples		Control blood samples	
		B:W fold-change	p-value	B:W fold-change	p-value
<i>CYP3A – testosterone regulation</i>	CYP3A5	1.78	1.52E-03	ND	
<i>HSD17B - Estrogen & androgen regulation</i>	HSD17B8	1.93	3.98E-02	3.44	1.51E-04
	HSD17B10	1.42	1.72E-05	1.55	6.49E-04
	HSD17B11	1.34	3.31E-03		
<i>Growth factor</i>	EPHB1	-1.56	2.50E-03	-1.73	7.89E-03
<i>BCL - apoptosis</i>	BCL2	-1.49	1.99E-03	ND	
	BCL3	ND		-1.51	8.49E-04
	BCL6	-1.52	7.01E-03	-2.86	3.72E-07
	BCL9	-1.91	8.75E-05	ND	

ND = no difference between samples

Supplementary Table 4. Peripheral blood evaluation of candidate genes associated with racial differences between Caucasian and Black men

Family	Gene	PCa blood samples		Control blood samples	
		B:W fold-change	p-value	B:W fold-change	p-value
<i>Fatty Acid Metabolism</i>	CPT1B	-1.93	4.38E-03	ND	
	CPT2	-1.27	2.87E-02	-1.35	8.30E-03
	FABP5	+2.15	1.61E-02	+3.02	1.58E-04
	FTO	-1.36	1.03E-02	ND	
	LPCAT1	-1.29	7.99E-03	-1.42	9.72E-03

	<i>LPCAT2</i>	-1.62	1.98E-04	-1.95	5.58E-04
	<i>LPCAT3</i>	<i>ND</i>		-1.50	5.68E-03
	<i>LPL</i>	+2.24	4.28E-02	+2.98	9.30E-04
	<i>PPARA</i>	-1.44	5.08E-05	-1.35	8.14E-03
	<i>PPARD</i>	-1.49	3.60E-03	-1.49	1.59E-03
	<i>PPARGC1B</i>	-1.73	1.07E-04	-1.43	3.79E-02
	<i>SCD</i>	-1.87	8.91E-03	-1.53	2.49E-02
<i>NFK1B</i>	<i>NFKB1</i>	-1.33	4.73E-04	-1.50	1.09E-04
	<i>NFKB2</i>	-1.72	3.14E-06	-1.76	4.29E-05
	<i>NFKBID</i>	-1.31	3.13E-02	<i>ND</i>	
	<i>NFKBIL1</i>	+1.50	4.52E-03	+1.44	2.65E-02
	<i>NFKBIZ</i>	-1.41	7.05E-03	-1.43	5.06E-03
<i>Interleukins</i>	<i>IL10RB</i>	-1.51	3.80E-04	-2.14	7.54E-09
	<i>IL11RA</i>	-1.89	6.38E-03	<i>ND</i>	
	<i>IL13RA1</i>	-1.26	4.12E-02	-1.81	6.78E-03
	<i>IL15</i>	<i>ND</i>		+1.34	3.85E-02
	<i>IL16</i>	-1.13	4.69E-02	-1.41	2.28E-03
	<i>IL17RA</i>	-1.61	1.16E-03	-2.46	3.71E-08
	<i>IL18</i>	<i>ND</i>		-1.44	2.56E-02
	<i>IL18BP</i>	-1.49	3.10E-07	<i>ND</i>	
	<i>IL18RAP</i>	+2.22	1.25E-02	<i>ND</i>	
	<i>IL1R1</i>	-1.69	3.98E-03	-2.01	1.10E-02
	<i>IL1RL1</i>	-2.46	8.09E-03	-3.11	2.76E-03
	<i>IL2RA</i>	-1.42	2.23E-02	<i>ND</i>	
	<i>IL2RB</i>	-1.87	3.26E-03	<i>ND</i>	
	<i>IL23A</i>	<i>ND</i>		+1.98	2.55E-03
	<i>IL31RA</i>	<i>ND</i>		-4.30	4.23E-04
	<i>IL32</i>	+1.93	3.90E-07	+2.68	2.48E-08
	<i>IL4R</i>	<i>ND</i>		-1.38	2.17E-02
	<i>IL5RA</i>	-1.53	1.56E-02	-2.23	7.67E-03
	<i>IL6R</i>	-1.42	3.62E-03	-1.92	8.01E-07
	<i>IL7R</i>	+1.39	4.03E-02	<i>ND</i>	

<i>Chemokine signaling</i>	CCL28	<i>ND</i>		+1.46	1.53E-02
	CCL3L1	<i>ND</i>		+2.46	4.16E-02
	CCL4	+1.67	1.14E-02	+1.85	1.10E-03
	CCL4L2	+3.68	2.28E-07	+3.22	2.14E-05
	CCL5	+1.71	4.78E-05	+1.43	1.24E-02
<i>Innate immune system</i>	<i>NLRP1</i>	-2.05	8.78E-12	-2.16	5.92E-07
	<i>NLRP12</i>	<i>ND</i>		-1.93	1.52E-06
	<i>NLRP2</i>	<i>ND</i>		-2.46	1.32E-04
	<i>NLRP3</i>	-2.05	1.14E-04	-1.86	2.69E-05
	<i>NLRP6</i>	-1.47	1.06E-02	-2.43	1.47E-03
<i>COX2</i>	<i>PTGS2</i>	-2.44	1.37E-05	-1.77	1.10E-03
<i>Regulation of Cytokine signaling</i>	SOCS2			+1.37	4.59E-02
	<i>SOCS4</i>	-1.39	8.12E-03		
	<i>SOCS6</i>	-1.62	8.55E-03	-1.45	4.60E-02
	<i>SOCS7</i>	-1.47	3.89E-05		

ND = no difference between samples

Supplementary Figures and Legends

Supplementary Figure 1. GO analysis of DEGs in RSA-PCa vs USA-PCa.

Supplementary Figure 2. GO analysis of DEGs in RSA-Controls vs USA-Controls.

Supplementary Figure 3. Gene expression analysis: PCa vs. controls.

3A. Venn diagram showing common genes between RSA and USA population, without statistical filtering, where show. More 90% of the genes were common to both groups.

3B. Venn diagram showing commonly expressed genes after applying a fold change (FC) >2 and $p < 0.05$ filter. Only <10% of genes were commonly expressed.

Supplementary Figure 4.

4A. Hierarchical clustering (heatmap) showing the clustering of gene expression profiles in blood samples from RSA-PCa vs RSA-controls.

4B. Circos plot identifying statistically significant gene expression in RSA-PCa vs RSA-Controls. Chromosome hotspots identified in Chromosome 1, 15, 16 and 17.

4C. Volcano plot displaying the significantly differentially expressed genes ($p < 0.05$) between RSA-PCa vs RSA-Control populations.

4D. Major pathways regulating ribosomal and hematopoietic cell lineages enriched in RSA-PCa samples.

Supplementary Figure 5.

5A. Hierarchical clustering (heatmap) showing the clustering of gene expression profiles in blood samples from USA-PCa vs USA-controls.

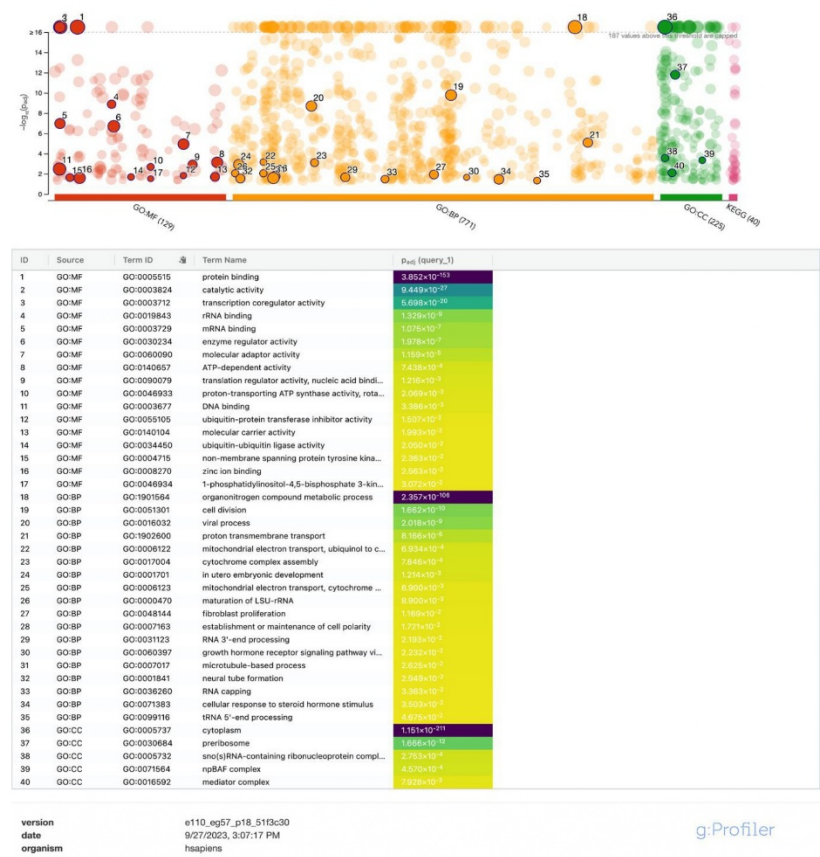
5B. Circos plot identifying statistically significant gene expression in USA-PCa vs USA-Controls. Chromosome hotspots identified in Chromosomes 1, 5, 6, 15 and 19.

5C. Volcano plot displaying the significantly differentially expressed genes ($p < 0.05$) between USA-PCa vs USA-Control populations.

5D. Pathways significantly enriched in USA-PCa samples include protein export and endoplasmic reticulum pathways.

Supplementary Figure 1

RSA-PCa vs USA-PCa

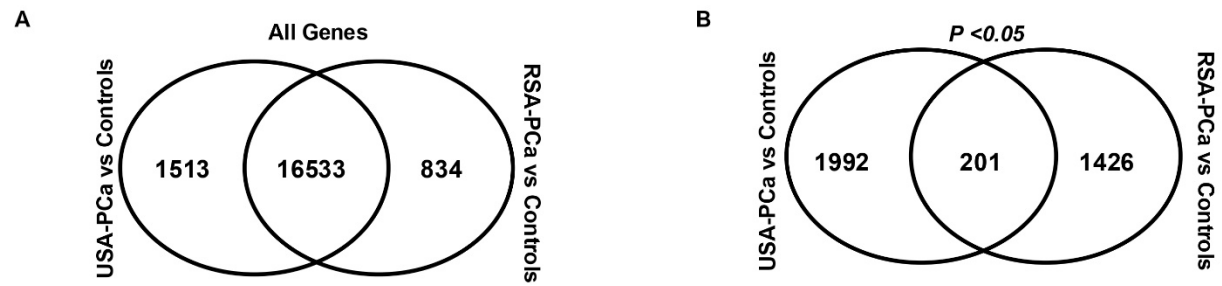


Supplementary Figure 2

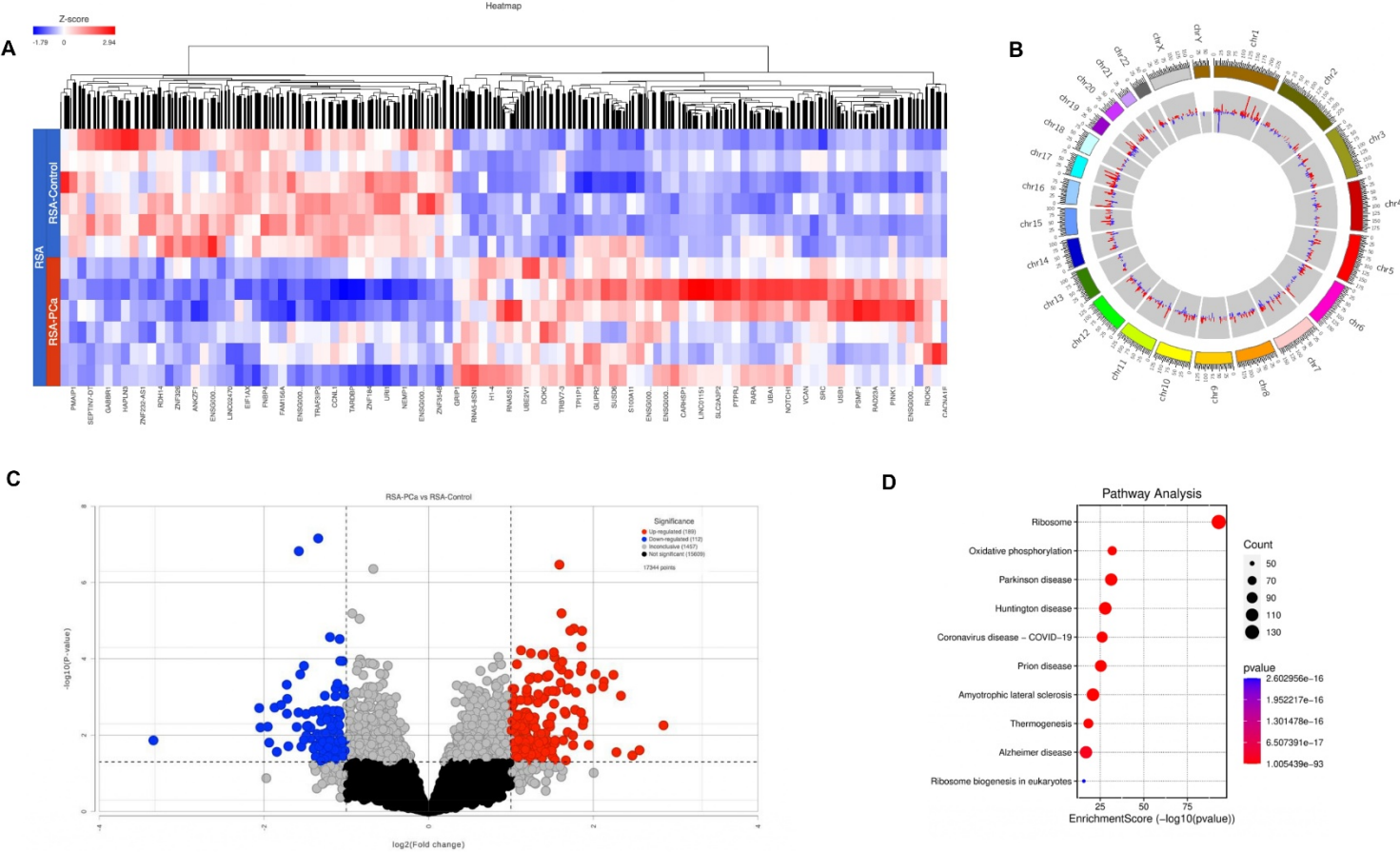
RSA-Controls vs USA-Controls



Supplementary Figure 3 PCa vs Controls



Supplementary Figure 4 RSA-PCa vs Controls



Supplementary Figure 5 USA-PCa vs Controls

