

RNA expression differences in prostate tumors and tumor-adjacent stroma between Black and White Americans

SUPPLEMENTARY MATERIALS

Supplementary Dataset 1: RNA sequencing analysis of TAS of Black American (BA) and White American (WA) prostate cancer (PCa) patients. See Supplementary Dataset 1

Supplementary Table 1A: 3550 differentially transcribed genes in 7 BA prostate TAS cases versus 7 WA prostate TAS cases; corrected $p < 0.05$; FC ≥ 2.5 in both directions.

Supplementary Table 1B: Canonical pathways of 1706 significantly differentially downregulated transcribed genes in 7 BA prostate TAS cases versus 7 WA prostate TAS cases; corrected $p < 0.05$.

Supplementary Table 1C: Canonical pathways of 1844 significantly differentially upregulated transcribed genes in 7 BA prostate TAS cases versus 7 WA prostate TAS cases; corrected $p < 0.05$.

Supplementary Dataset 2: Analysis of published RNA sequencing data of prostate cancer tissue samples from BA and WA patients. See Supplementary Dataset 2

Supplementary Table 2A: 1408 differentially transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$; FC ≥ 1.5 in either direction.

Supplementary Table 2B: Canonical pathways of 932 significantly differentially upregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 2C: Canonical pathways of 476 significantly differentially downregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 2D: Diseases and functions associated with 932 significantly differentially upregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 2E: Diseases and functions associated with 476 significantly differentially downregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 2F: Gene network analysis of 476 significantly differentially downregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 2G: Gene network analysis of 932 significantly differentially upregulated transcribed genes in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Dataset 3: Transcriptome analysis of BA versus WA PCa patients in tumor and TAS. See Supplementary Dataset 3

Supplementary Table 3A: 2500 differentially transcribed genes with the highest significance in 7 BA prostate TAS cases versus 7 WA prostate TAS cases; corrected $p < 0.05$.

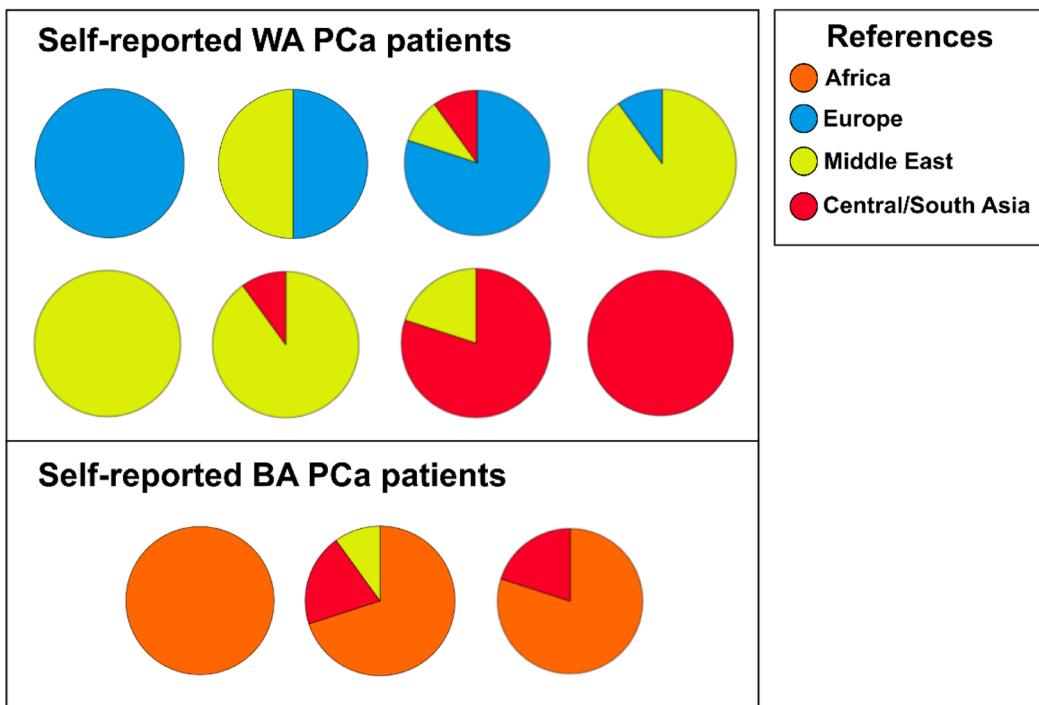
Supplementary Table 3B: 2500 differentially transcribed genes with the highest significance in 15 BA prostate tumor cases versus 30 WA prostate tumor cases; corrected $p < 0.05$.

Supplementary Table 3C: Comparative pathway analysis on top differentially transcribed genes downregulated in BA versus WA patients between prostate TAS and tumors; corrected $p < 0.05$.

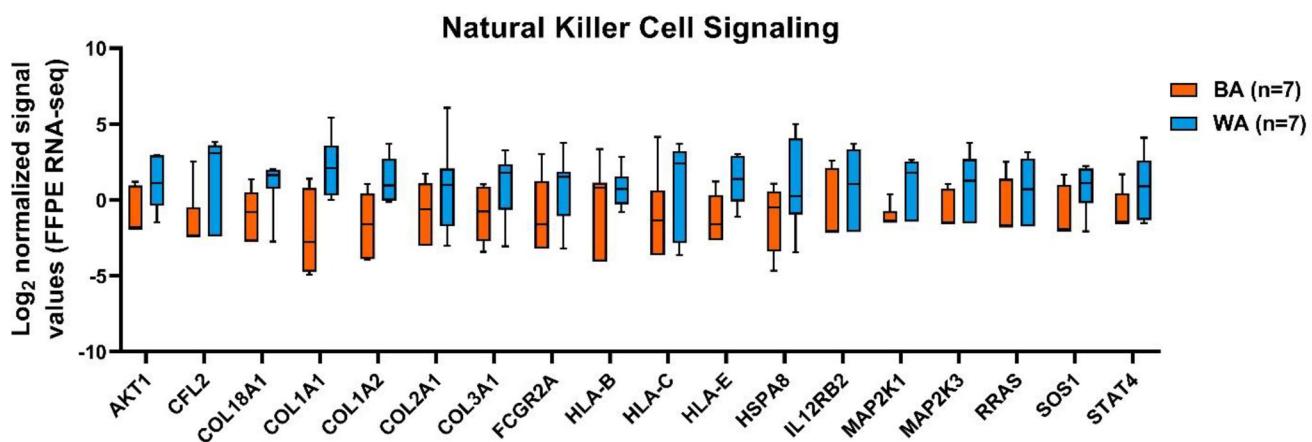
Supplementary Table 3D: Comparative pathway analysis on top differentially transcribed genes upregulated in BA versus WA patients between prostate TAS and tumors; corrected $p < 0.05$.

Supplementary Table 3E: Gene network analysis of 149 discordant genes in prostate TAS and tumors of BA versus WA patients; corrected $p < 0.05$.

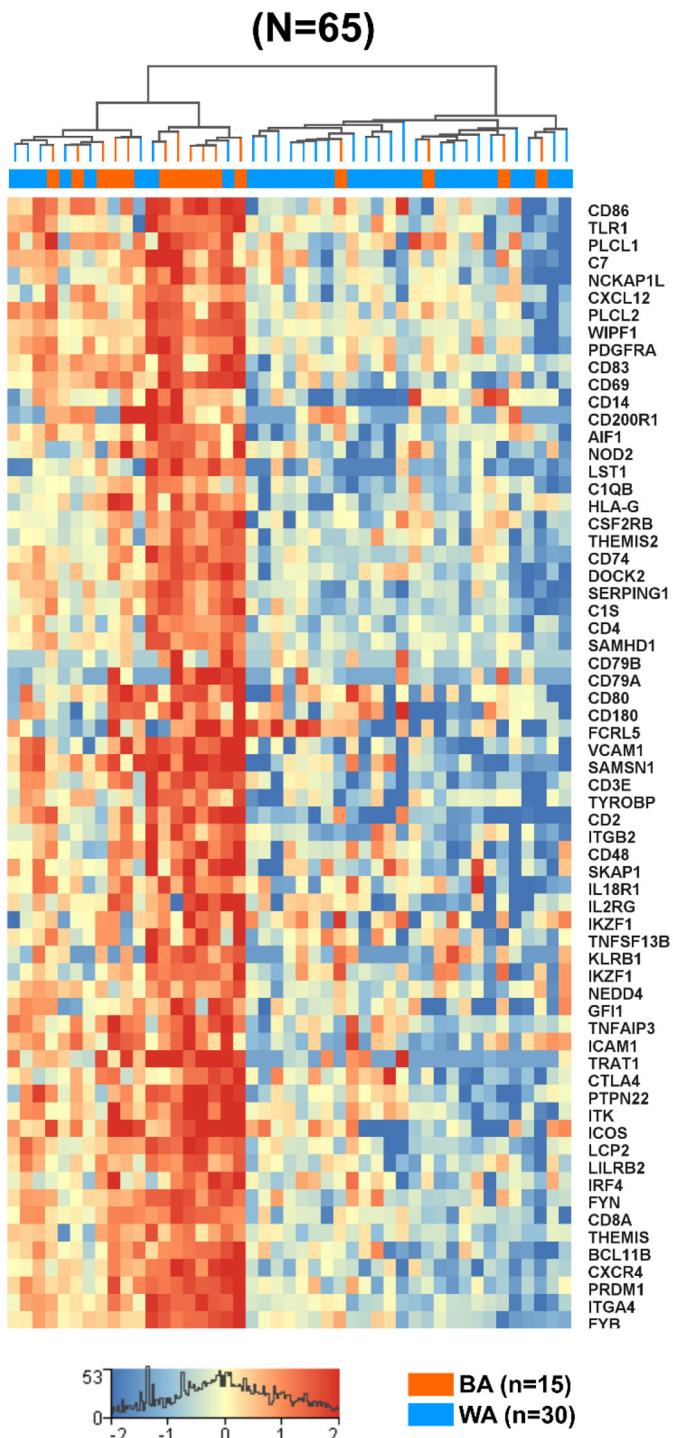
Supplementary Table 3F: Gene network analysis of 94 concordant genes in prostate TAS and tumors of BA versus WA patients; corrected $p < 0.05$.



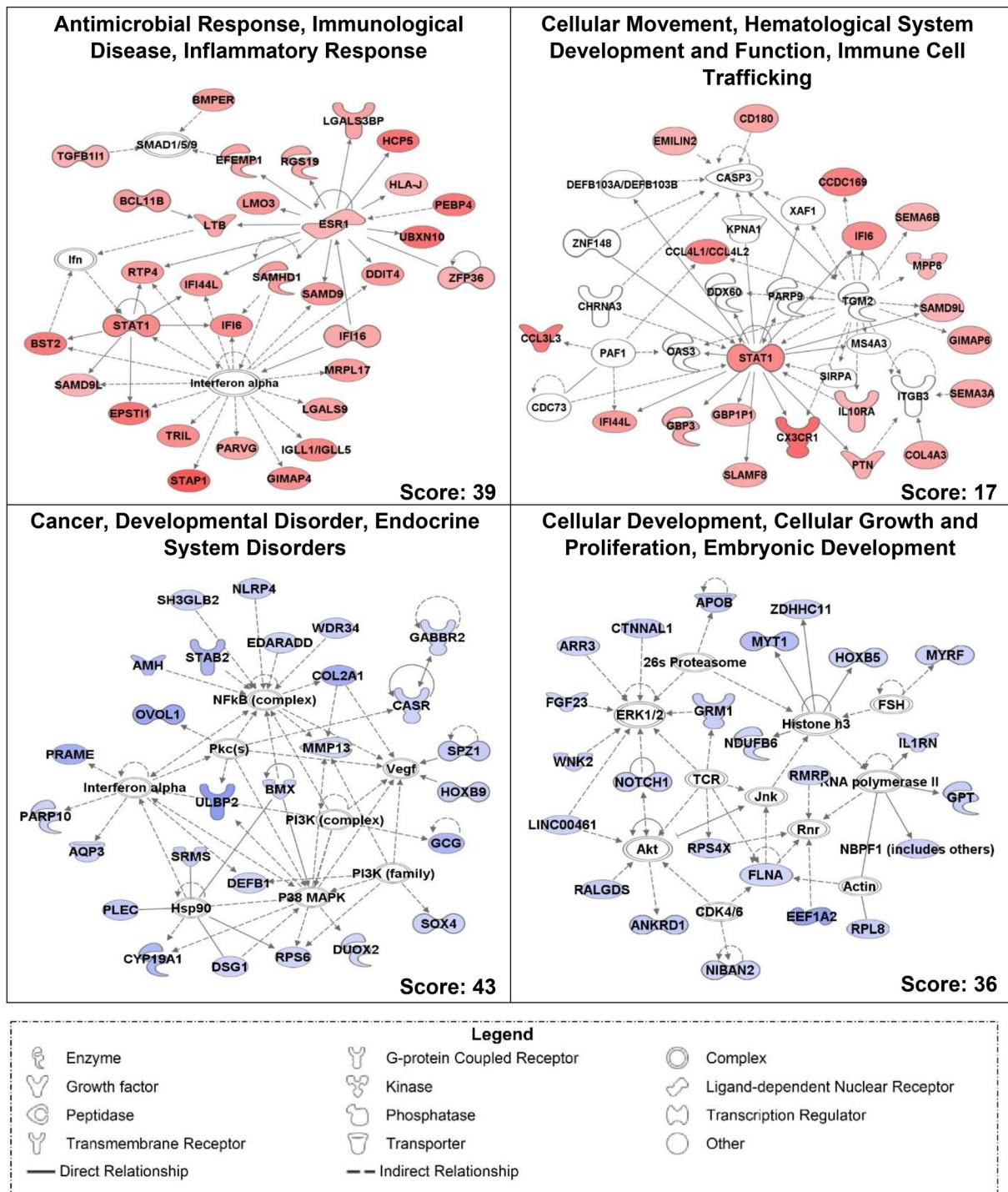
Supplementary Figure 1: Venn diagrams of the different ancestry compositions identified using LASER in 99 FFPE samples from BA and WA PCa patients (GSE54460).



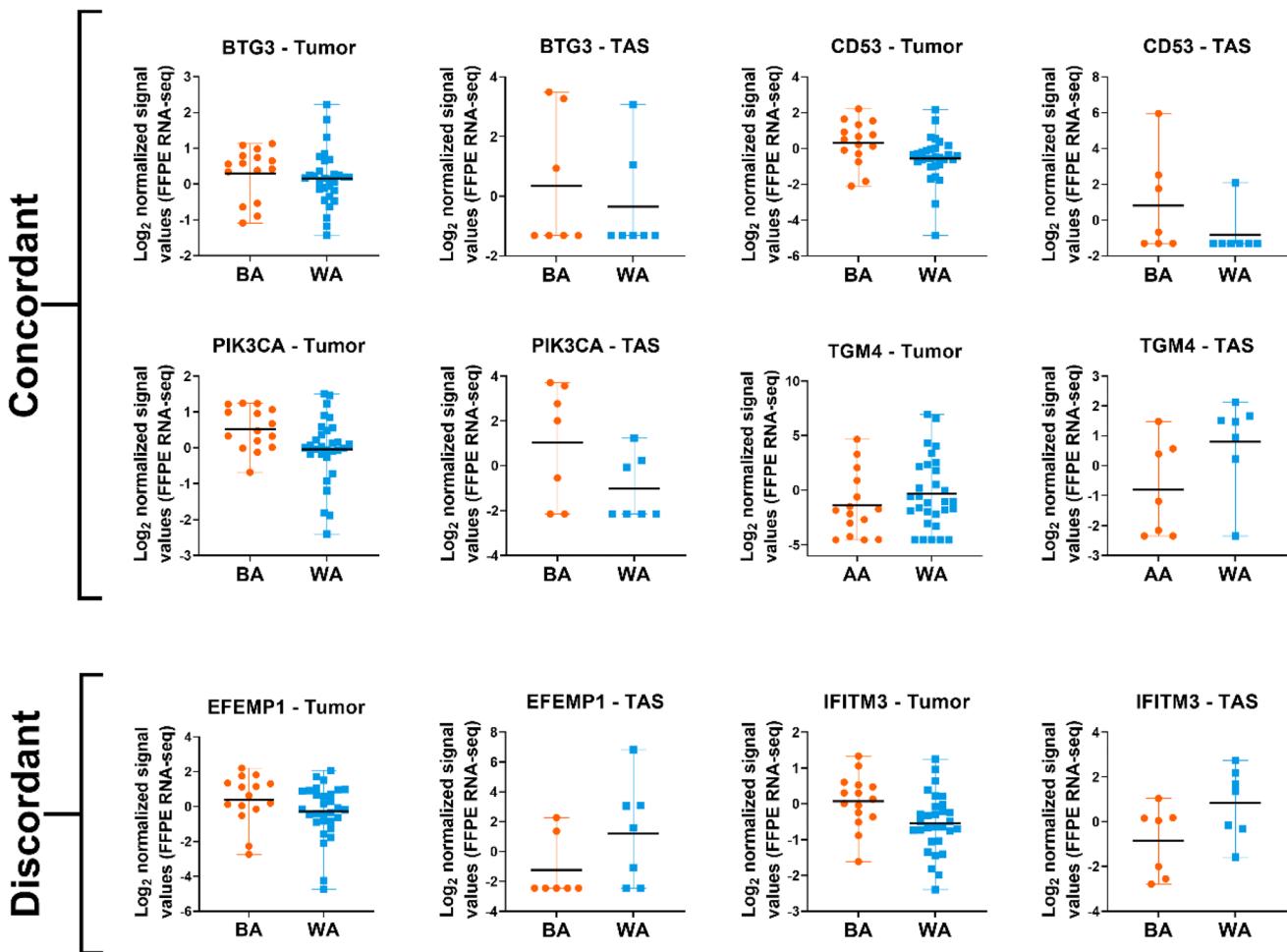
Supplementary Figure 2: Natural killer cell signaling genes significantly downregulated in the TAS of BA ($n = 7$) compared to WA ($n = 7$) prostate cancer samples. Y axis represents normalized \log_2 signal values (normalized reads) ($p_{adj} < 0.05$). Each dot represents a patient.



Supplementary Figure 3: Comparison of published regulation status of genes in BA vs WA PCa samples and our gene list. A study by Hardiman et al. from 10 self-reported BA and 17 self-reported WA PCa patients identified 242 upregulated genes [21]. We identified 65 overlapping genes with our list of 1408 genes, at 98% concordance. The heat map shows the expression levels of those 65 overlapping concordant genes in 15 BA compared to 30 WA prostate cancer patients. Red depicts up- and blue depicts downregulation. N is the number of genes.



Supplementary Figure 4: Gene network analysis of statistically significant (corrected p value < 0.05) up- and downregulated genes in BA ($n = 15$) versus WA ($n = 30$) PCa samples. The networks shown are among those with the highest significance of connections between molecules in the network as indicated by their score. Blue nodes indicate downregulated gene expression and red nodes indicate upregulated gene expression. Darker shades of the nodes indicate higher regulation ratios. Dotted lines represent indirect interactions while solid lines represent direct interactions. White colored notes are in the pathway, but not in our dataset.



Supplementary Figure 5: Overlapping genes in tumor and TAS of BA versus WA PCa patients with concordant and discordant regulations.

Supplementary Table 1: Transcriptome analysis and clinical characteristics of TAS of self-reported BA (*n* = 9) and WA (*n* = 11) PCa patients

PCa-TAS	Reported Race	Location	Relapse Definition	Follow-up (months)	Gleason Score	Total Gleason Score	Given Age	Race Ratio	Race Breakdown	Number of Reads	Aligned Reads
<i>TAS1</i> *	Black	MUSC	R	24	3+5	8	60	7:2:1	Africa: C/S Asia: Middle East	58,353,208	9,146,862
<i>TAS2</i> *	Black	MUSC	N	59	3+4	7	61	10:0	Africa	17,275,140	9,540,061
<i>TAS3</i> *	Black	MUSC	R	1	3+4	7	66	10:0	Africa	100,431,162	28,995,535
<i>TAS4</i> *	Black	MUSC	R	73	3+3	6	60	6:2:2	Africa: C/S Asia: Middle East	14,218,314	8,651,441
<i>TAS5</i> *	Black	UCI	R	11	4+5	9	57	10:0	Africa	46,529,804	22,448,895
<i>TAS6</i> *	Black	MUSC	R	23	4+5	9	64	7:2:1	Africa: C/S Asia: Middle East	13,857,852	5,685,592
<i>TAS7</i> *	Black	MUSC	N	36	3+4	7	62	5:3:2	Africa: C/S Asia: Middle East	9,567,576	3,693,855
<i>TAS8</i>	Black	MUSC	R	89	3+4	7	56	6:4	Middle East: C/S Asia	34,398,988	4,202,710
<i>TAS9</i>	Black	UCI	N	13	3+4	7	66	6:4	Middle East: C/S Asia	175,188,492	65,452,830
<i>TAS10</i> *	White	UCI	R	95	4+4	8	62	10:0	Middle East	8,702,216	5,104,814
<i>TAS11</i> *	White	UCI	N	82	3+4	7	66	10:0	Middle East	60,372,832	35,386,525
<i>TAS12</i> *	White	UCI	R	24	3+4	7	53	8:1:1	Europe: Middle East: C/S Asia	19,391,098	11,692,864
<i>TAS13</i> *	White	UCI	R	19	4+4	8	43	10:0	Europe	3,800,718	1,053,081
<i>TAS14</i> *	White	UCI	R	16	4+5	9	63	10:0	Europe	18,000,216	6,707,433
<i>TAS15</i> *	White	UCI	R	17	4+4	8	68	8:2	Europe: Middle East	49,658,208	17,847,446
<i>TAS16</i> *	White	UCI	R	22	4+3	7	66	10:0	Europe	5,539,412	1,309,553
<i>TAS17</i>	White	UCI	N	61	3+3	6	60	10:0	C/S Asia	31,396,544	17,660,670
<i>TAS18</i>	White	UCI	R	90	3+4	7	63	9:1	C/S Asia: Europe	26,390,916	8,587,454
<i>TAS19</i>	White	UCI	R	2	4+5	9	59	7:3	C/S Asia: America	14,017,038	3,781,150
<i>TAS20</i>	White	UCI	R	15	4+5	9	67	9:1	C/S Asia: Europe	5,513,162	1,008,259

Abbreviations: TAS: Tumor adjacent stroma; PCa: Prostate cancer; UCI: University of California, Irvine; MUSC: Medical University of South Carolina; C/S: Central/South; R: Relapse; N: Non-relapse. (*) denotes patients selected for gene expression analysis.

Supplementary Table 2: Clinical characteristics and geographical ancestry of GSE54460 PCa patients

PCa-Tumor	Reported Race	Location	Given Age	BCR (months)	Gleason Score	Total Gleason Score	Follow-up (months)	Race Ratio	Race Breakdown
<i>BA1*</i>	Black	VA	63	NA	5+3	8	59.5	10:0	Africa
<i>BA2*</i>	Black	VA	62	NA	3+4	7	61.5	10:0	Africa
<i>BA3*</i>	Black	VA	69	NA	3+4	7	67.9	10:0	Africa
<i>BA4*</i>	Black	VA	70	NA	3+4	7	106.6	10:0	Africa
<i>BA5*</i>	Black	VA	47	NA	3+4	7	69.8	10:0	Africa
<i>BA6*</i>	Black	VA	56	NA	3+3	6	51.5	10:0	Africa
<i>BA7*</i>	Black	VA	62	NA	3+4	7	71.9	10:0	Africa
<i>BA8*</i>	Black	VA	54	NA	3+4	7	73.8	10:0	Africa
<i>BA9*</i>	Black	VA	50	NA	3+4	7	77.3	10:0	Africa
<i>BA10*</i>	Black	VA	53	1.6	3+4	7	1.6	10:0	Africa
<i>BA11*</i>	Black	VA	66	26.6	4+3	7	26.6	10:0	Africa
<i>BA12*</i>	Black	VA	55	0.7	4+5	9	0.7	10:0	Africa
<i>BA13*</i>	Black	VA	58	60.5	3+4	7	60.5	10:0	Africa
<i>BA14*</i>	Black	VA	52	26	3+4	7	26	10:0	Africa
<i>BA15*</i>	Black	VA	62	2.2	4+4	8	2.2	9:1	Africa: C/S Asia
<i>BA16</i>	Black	VA	69	NA	3+4	7	69.5	8:2	Africa: C/S Asia
<i>BA17</i>	Black	VA	56	NA	3+4	7	68	8:2	Africa: C/S Asia
<i>BA18</i>	Black	VA	56	NA	3+4	7	118.3	9:1	Africa: C/S Asia
<i>BA19</i>	Black	VA	50	NA	3+4	7	96.6	10:0	Africa
<i>BA20</i>	Black	VA	57	NA	4+3	7	89.3	7:2:1	Africa: C/S Asia: Middle East
<i>BA21</i>	Black	VA	60	26.6	4+3	7	26.6	7:2:1	Africa: C/S Asia: Middle East
<i>BA22</i>	Black	VA	58	101.1	3+4	7	101.1	8:2	Africa: C/S Asia
<i>BA23</i>	NA	MCC	43	NA	3+4	7	50	10:0	Africa
<i>BA24</i>	NA	UTP	55	0	3+4	7	50	10:0	Africa
<i>BA25</i>	NA	UTP	71	0	3+4	7	54	10:0	Africa
<i>BA26</i>	NA	UTP	51	0	4+3	7	100	10:0	Africa
<i>BA27</i>	NA	VA	59	36	4+4	8	36	10:0	Africa
<i>WA1*</i>	White	VA	62	NA	4+3	7	62.4	10:0	Europe
<i>WA2*</i>	White	VA	52	NA	3+4	7	50.4	10:0	Europe
<i>WA3*</i>	White	VA	51	NA	3+3	6	64.2	10:0	Europe
<i>WA4*</i>	White	VA	64	NA	4+4	8	171.1	10:0	Europe
<i>WA5*</i>	White	VA	69	NA	3+4	7	48.6	10:0	Europe
<i>WA6*</i>	White	VA	70	NA	3+4	7	116.5	10:0	Europe
<i>WA7*</i>	White	VA	65	NA	3+4	7	148.2	10:0	Europe
<i>WA8*</i>	White	VA	67	NA	3+4	7	116.9	10:0	Europe
<i>WA9*</i>	White	VA	64	NA	3+4	7	155.1	10:0	Europe
<i>WA10*</i>	White	VA	61	NA	4+3	7	31.8	10:0	Europe
<i>WA11*</i>	White	VA	50	NA	3+4	7	100.2	8:1:1	Europe: Middle East: C/S Asia
<i>WA12*</i>	White	VA	54	NA	3+4	7	95.9	10:0	Europe
<i>WA13*</i>	White	VA	61	NA	3+4	7	83	9:1	Middle East: C/S Asia
<i>WA14*</i>	White	VA	54	NA	3+4	7	64.3	10:0	Europe
<i>WA15*</i>	White	VA	55	NA	3+4	7	82.3	10:0	Middle East
<i>WA16*</i>	White	VA	66	NA	4+3	7	55.6	10:0	Middle East

WA17*	White	VA	62	NA	3+4	7	34.7	10:0	Europe
WA18*	White	VA	65	NA	3+3	6	63.4	10:0	Middle East
WA19*	White	VA	58	3.6	4+3	7	3.6	10:0	Europe
WA20*	White	VA	64	0.8	4+4	8	0.8	10:0	Europe
WA21*	White	VA	67	3.6	3+4	7	3.6	10:0	Europe
WA22*	White	VA	52	1	4+4	8	1	10:0	Europe
WA23*	White	VA	67	95	3+4	7	95	10:0	Europe
WA24*	White	VA	67	18.3	4+3	7	18.3	10:0	Europe
WA25*	White	VA	65	1.6	4+4	8	1.6	10:0	Europe
WA26*	White	VA	62	3.5	3+4	7	3.5	10:0	Europe
WA27*	White	VA	67	11.8	3+4	7	11.8	9:1	Middle East: Europe
WA28*	White	VA	62	48.9	4+3	7	48.9	10:0	Middle East
WA29*	White	VA	59	2.8	4+3	7	2.8	9:1	Europe: Middle East
WA30*	White	VA	57	39.9	3+4	7	39.9	10:0	Europe
WA31	White	VA	68	NA	3+4	7	63.6	7:3	Europe: Middle East
WA32	White	VA	65	NA	3+4	7	160.3	8:2	Europe: Middle East
WA33	White	VA	72	NA	3+4	7	97.9	8:2	Europe: Middle East
WA34	White	VA	65	NA	3+4	7	76.8	8:2	Middle East: Europe
WA35	White	MCC	78	NA	3+4	7	119	10:0	Europe
WA36	White	MCC	61	NA	3+3	6	114	10:0	Europe
WA37	White	MCC	63	NA	3+3	6	87	7:3	Middle East: Europe
WA38	White	MCC	57	NA	3+4	7	69	10:0	Europe
WA39	White	MCC	54	NA	3+4	7	57	10:0	Europe
WA40	White	MCC	66	26.5	3+3	6	104.05	10:0	Europe
WA41	White	MCC	61	22.13	3+3	6	74.24	10:0	Middle East
WA42	White	MCC	60	154.22	3+2	5	180.56	10:0	Europe
WA43	White	UTP	58	18	3+4	7	43	10:0	Europe
WA44	White	UTP	72	0	4+4	8	112	10:0	Europe
WA45	NA	MCC	58	NA	3+4	7	98	10:0	Europe
WA46	NA	UTP	57	NA	4+3	7	72	10:0	Europe
WA47	NA	UTP	66	NA	4+4	8	85	10:0	Europe
WA48	NA	UTP	50	NA	3+3	6	63	10:0	Europe
WA49	NA	UTP	69	NA	3+4	7	82	10:0	Europe
WA50	NA	UTP	71	38.2	5+4	9	38	10:0	Europe
WA51	NA	UTP	50	23	3+4	7	68	10:0	Europe
WA52	NA	UTP	68	27.6	4+3	7	82	10:0	Middle East
WA53	NA	UTP	55	0	3+4	7	49	8:2	Europe: Middle East
WA54	NA	UTP	65	8	3+4	7	128	10:0	Europe
WA55	NA	UTP	62	21.4	3+3	6	116	10:0	Europe
WA56	NA	UTP	58	0	3+4	7	102	10:0	Europe
WA57	NA	UTP	67	0	4+5	9	26	5:5	Europe: Middle East
WA58	NA	UTP	70	0	4+4	8	35	10:0	Europe
WA59	NA	UTP	59	0	4+3	7	88	10:0	Europe
WA60	NA	UTP	53	43.4	5+4	9	75	10:0	Middle East
WA61	NA	UTP	60	29.8	3+4	7	43	10:0	Europe
WA62	NA	UTP	60	48.5	3+4	7	49	7:3	Europe: Middle East

<i>WA63</i>	NA	UTP	65	27.6	4+3	7	101	10:0	Europe
<i>WA64</i>	NA	UTP	74	18.2	3+4	7	79	10:0	Europe
<i>WA65</i>	NA	UTP	66	49.5	3+4	7	125	10:0	Europe
<i>WA66</i>	NA	UTP	57	27.5	3+4	7	112	9:1	Europe: Middle East
<i>WA67</i>	NA	UTP	66	0	4+3	7	72	10:0	Europe
<i>WA68</i>	NA	UTP	72	9.6	4+3	7	36	5:5	Europe: Middle East
<i>AS1</i>	White	VA	64	NA	3+3	6	97.3	10:0	C/S Asia
<i>AS2</i>	White	VA	64	NA	4+3	7	96.1	8:2	C/S Asia: Middle East
<i>AS3</i>	NA	UTP	64	21.6	4+3	7	89	10:0	C/S Asia
<i>AS4</i>	NA	UTP	58	29.9	4+3	7	61	10:0	C/S Asia

Abbreviations: BA: Black American; WA: White American; AS: Asian; VA: Atlanta Veterans Administration Medical Center; MCC: Moffitt Cancer Center; UTP: University of Toronto Sunnybrook Health Sciences Center; C/S: Central/South; BCR: biochemical relapse; NA: Not applicable. (*) denotes patients selected for gene expression analysis.

Supplementary Table 3: Summary of clinically matched BA (*n* = 15) and WA (*n* = 30) FFPE PCa tumor-enriched samples (GSE54460)

	<i>n</i>	No BCR: BCR	Average Age	Gleason Score 6	Gleason Score 7	Gleason Score 8	Gleason Score 9	Average Follow-Up (Months)	80-90% Ancestry	100% Ancestry
BA	15	9:6	59	1	11	2	1	50	1	14
WA	30	18:12	61	2	24	4	0	59	4	26

Abbreviations: BA: Black American; WA: White American; BCR: biochemical relapse.