



# PROSTATE CANCER **BIOREPOSITORY NETWORK**

Datasheet No: 001 - 456 Case Race-Matched TMA

Washington University School of Medicine

<b>TMA Name</b>	Drake Prostate TMA Set (1 through 10, A and B [duplicate])		
<b>Description</b>	A tissue microarray set was created for testing biomarkers strongly associated with known prognostic factors. This TMA contains tumor samples from prostate cancer cases. All cases were obtained from the Washington University Prostate Cancer Biorepository Network and collected under institutional review board approval. (# 201105388)		
<b>Cases</b>	Total of 456 prostate cancer samples = (152 African American Males matched 1:2 to Caucasian Male controls)		
<b>Sample Selection</b>	Tumor cores are sampled from surgical prostate specimens. Each case was reviewed by one pathologist to ensure the best area of tumor to select.		
<b>Construction</b>	The TMAs are assembled using the Beecher Tissue Arrayer and constructed over 10 blocks (Block A and B). Each case selected for the cohort is represented in duplicate (Once on Block A and once on Block B). There is one tumor core per case in each duplicate block.		
<b>Replicates</b>	Each case was arrayed in duplicate. Total of 2 tumor cores per case over TMA set.		
<b>Cores</b>	Blocks 1 through 9- Total 50 cores- 5 control cores (Tonsil for orientation [A1], Ovary [B1], Appendix [C1], Placenta [D1], and Breast [E1]) and 45 individual patient cores. Block 10- Total 57 cores- 6 control cores (Tonsil for orientation [A1], Ovary [B1], Appendix [C1], Placenta [D1], Breast [E1, F1] and 51 individual patient cores.		
<b>Diameter</b>	2.0mm	<b>Thickness</b>	5µm
<b>Layout</b>	Blocks 1 through 9 5 rows x 10 cores Block 10 6 rows, 5 rows x 10, 1 row x 7		
<b>Quality Control</b>	All "A" blocks have had a slide stained with hematoxylin and eosin (H & E) and reviewed for tissue availability. Scanned H & E's of each TMA block ARE available.		
<b>TMA Slide Types</b>	H & E quality control review demonstrated 502 of the 507 (99%) of cores represented in this TMA set.		
<b>Data</b>	Initial and follow-up data extracted from electronic medical records and participant survey data. The survey data includes demographics, family history of cancer, as well as diet and physical activity measures. Recurrence is obtained from clinical records; vital status is updated every 2 years.		

**Race-Matched TMA**



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<b>Age (yrs)</b>	Mean (Std. Dev.)	59.22 (6.86)	
<b>PSA at diagnosis (ng/mL)</b>	Mean (Std. Dev.)	6.98 (5.84)	
		<b>Number (n)</b>	<b>Percentage (%)</b>
<b>Clinical T stage</b>	T1	304	81.15
	T2	85	18.85
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<b>Pathological T stage</b>	pT2	354	77.64
	pT3	34	22.37
<b>Gleason Sum</b>	6	135	29.61
	7	312	68.42
	8	3	0.66
	9	6	1.32
<b>Seminal vesicle Invasion</b>	Negative	420	92.72
	Positive	33	7.28
<b>Outcome</b>	Nil Relapse	387	84.87
	Relapse*	69	15.13
<b>Vital Status</b>	Alive	429	94.08
	Dead	27	5.92
		<b>Mean</b>	<b>Range</b>
<b>Length of Follow-up (months)</b>	Mean (months)	56.03	0-192
<b>Period Disease Free (months)</b>	Mean (months)	28.52	0-84
<i>Frequencies calculated from December 2020</i>			
* - Relapse includes Biochemical Recurrence & Biochemical + Clinical Recurrence			