



# PROSTATE CANCER **BIOREPOSITORY NETWORK**

Datasheet No: 006 - 135 Case NYU RP TMA

Version No: 1.0 November 2017

<b>TMA Name</b>	<b>135 Case NYU RP TMA</b>		
<b>Description</b>	An intermediate-density tissue microarray containing tumor and benign samples from localized prostate cancer cases. All of the cases were obtained from the NYU Site of the Prostate Cancer Biorepository Network, which were collected with institutional review board approval.		
<b>Cases</b>	Total of 145 cases –there are approximately 10 missing cases are which are accounted for. Cores are sampled from cancer and benign tissue from radical prostatectomy (RP) cases. Each case is provided with the following data: <ol style="list-style-type: none"><li>1. Race</li><li>2. Age at Surgery</li><li>3. Gleason Sum</li><li>4. Pathological T Stage</li><li>5. PreOp PSA</li></ol>		
<b>Sample Selection</b>	Tumor cores were sampled from areas of largest grade and focus.		
<b>Construction</b>	The TMA was assembled using a motorized version of the MTAI microarrayer (Beecher Instruments, Sun Prairie, Wisconsin) and constructed over 3 blocks. The cohort was divided into 3 case sets, assembled per block.		
<b>Replicates</b>	Each case was arrayed in duplicates to address tissue heterogeneity and to assure representation.		
<b>Cores</b>	Block 1 – total 257 cores (3x orientating liver, 94x liver cores, 80x tumor cores, 80x benign cores) Block 2 – total 248 cores (3x orientating kidney, 45x kidney cores, 100x tumor, 100x benign cores) Block 3 – total 376 cores (3x orientating kidney, 105x kidney cores, 134x tumor, 134x benign cores)		
<b>Diameter</b>	0.6mm	<b>Thickness</b>	5µm
<b>Layout</b>	<p><b>Block 1:</b> 20 col x 17 rows (rows 1-3 begin with an orienting liver core; rows 1-5 have cores in A-J with the remainder of the rows left blank; row 6 has liver cores in columns A-O with the remainder of the row left blank; rows 7-11 have cores in columns A-O with the remainder of the rows left blank; rows 12-17 have cores in columns A-S with rows 12 and 17 entirely liver cores; row 16 has liver cores in columns P-S. Columns E and J are entirely liver cores, rows 1-17; column O has liver cores in rows 6-12 columns)</p> <p><b>Block 2:</b> 20 cols x 16 rows (rows 1-3 begin with an orienting liver core; rows 1-9 have cores in columns A-S; rows 10- 16 have cores in column A-N with the remainder of the rows left blank; row 6 has kidney cores in columns A, E, J, N, O; row 12 has kidney cores in columns A, E, J, N; columns E and J are entirely kidney cores; column O has kidney cores in rows 1-9 with the remainder of the column left blank)</p> <p><b>Block 3:</b> 24 cols x 17 rows (rows 1-3 begin with an orienting kidney core; rows 6 and 12 are entirely kidney cores; columns E, J, O are entirely kidney cores; column T has kidney cores in rows 4-17 with rows 1-3 left blank; rows 1-3 has cores in columns A-O with the remainder of the rows left blank; rows 4-5 has cores in columns A-T with the remainder of the rows left blank; rows 16-17 has cores in columns A-X)</p>		
<b>Quality Control</b>	Initial section and every 20 <sup>th</sup> section thereafter is stained with hematoxylin and eosin		
<b>TMA Slide Types</b>	Unstained: unstained paraffin TMA slide for final analysis (>90% cores present). Trial: unstained paraffin TMA slide for trial analysis (titrating Ab and experiment conditions) or control (10-25% cores missing)		





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