



# PROSTATE CANCER **BIOREPOSITORY NETWORK**

Datasheet No: 007 - **119 Case NYU HGPIN TMA** (119HGPINTMA)

Version No: 1.0 September 2013

<b>TMA Name (# cases, abbreviated name)</b>	<b>119 Case NYU HGPIN TMA</b>		
<b>Description (options: intermediate/ high density; use: eg for comparing ---- among</b>	An intermediate-density tissue microarray for comparing high-grade prostatic intraepithelial neoplasia among patients who have been diagnosed with prostate cancer. This TMA contains tumor and HGPIN samples from localized prostate cancer cases. A subset of the cases have histologically non-neoplastic tissue samples (not HGPIN, not tumor represented). 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 (CDEs PROVIDED for the TMA)</b>	Total of 119 cases – with HGPIN and cancer from radical prostatectomy (RP). Each case is provided with the following data: <ol style="list-style-type: none"> <li>1. Gleason Sum</li> <li>2. Gleason Primary</li> <li>3. Gleason Secondary</li> <li>4. Gleason Tertiary</li> <li>5. Lobe laterality of tumor</li> <li>6. Pathological T Stage</li> </ol>		
<b>Sample Selection</b>	HGPIN cores were sampled from foci of HGPIN usually >1mm away from tumor. A few cores of HGPIN may have cancer on same core. Cancer cores were sampled from areas of largest grade and focus.		
<b>Construction (INSTRUMENT used; # of blocks)</b>	The TMA was assembled using a motorized version of the MTA1 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>	HGPIN for each case was arrayed in quadruplicate to address tissue heterogeneity and to assure representation. A single core of tumor was represented.		
<b>Cores (# of cores)</b>	Block 1 – total 250 cores (4x orientating liver, 49x prostate cell lines, 201x HGPIN cores, 6x cell lines); _ cases Block 2 – total 262 cores (3x orientating liver, 49x normal tissues, 50x tumor, 154x HGPIN cores, 6x cell lines); _ cases Block S – total 145 cores (4x nL LN, 10x NI prostate cell lines, 25x normal tissues, 25x tumor, 75x HPIN cores, 6x cell lines): _ cases		
<b>Diameter of cores / section thickness</b>	0.6mm	<b>Thickness</b>	5µm
<b>Layout (distribution)</b>	Block 1: 23 col x 17 rows ( <i>row 1 has liver in first 2 columns as orientating cores; row 6 has cell lines in first 6 columns with remainder of row left blank, while rows 16, and 21 intentionally left entirely blank</i> ). Column F		





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	<p>has cell line in row 6 with remainder left blank. Columns L and R are intentionally left blank</p> <p>Block 2: 23 cols x 18 rows (<i>row 1 has liver in first 3 columns as orientating cores; row 7 has cell lines in first 6 columns with remainder of row left black, while row 13 intentionally left entirely blank</i>) Column G has cell line in row 7 with remainder left black. Columns M and S are intentionally left blank</p> <p>Block S: 17 cols x 12 rows (<i>row 6 has cell lines in first 6 columns with remainder of row left blank</i>) Column F has cell line in row 6 with remainder of row left blank.</p>
<b>TMA Slide Types (unstained/ which were stained)</b>	<p>Unstained: unstained paraffin TMA slide for final analysis (&gt;90% cores present).</p> <p>Trial: unstained paraffin TMA slide for trial analysis (titrating Ab and experiment conditions) or control (10-25% cores missing)</p> <p>Trial: unstained paraffin TMA slide for trial analysis (titrating Ab and experiment conditions) or control (10-25% cores missing)</p>

