

Early Detection of Oral Lesions with Dysplasia at High-Risk of Cancer Development Using a Proteomic Signature Image Analysis Based StraticyteTM Ranju Ralhan^{1,2,4,5}, Russell Gu⁵, Jason T.K. Hwang⁵, Paul G. Walfish^{1,2,3,5}, and Ken Pritzker⁵

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Background

Detection of oral lesions with epithelial dysplasia at high-risk of cancer development yet remains an unmet clinical challenge. Biomarkers that allow identification of high-risk oral lesions are urgently needed. Using tissue proteomics and bioinformatics, we identified and verified a biomarker signature comprising of a panel of proteins that distinguishes oral lesions with dysplasia from oral cancers and from normal tissues. The potential of this molecular signature for identification of oral dysplastic lesions at high-risk of cancer development was evaluated using immunohistochemistry and correlation with clinical outcome. Based on these findings, we developed a protein biomarker-based prognostic test, Straticyte, to better stratify oral lesions for predicting the risk of cancer development.

Methods

Oral dysplasia cases with long term follow up from Mount Sinai Hospital were immunostained for various candidate potential cancer marker (PCM) proteins identified by Liquid chromatography-Tandem Mass spectrometry and bioinformatics using specific antibodies, evaluated by two observers blinded to clinical outcomes, image analysis performed and risk prediction algorithm developed from data analysis using the R package.

Homogenates of cancer, oral lesion or normal tissue Digest with trypsin and add mass tags (iTRAQ) Run 1 µL of each fraction on a 2-hour reverse phase gradient $(C_{18} \text{ column})$ into a mass spectrometer, acquiring a CID spectrum of each peptide in the solution Identify using Proteinpilot and Non-redundant human protein database

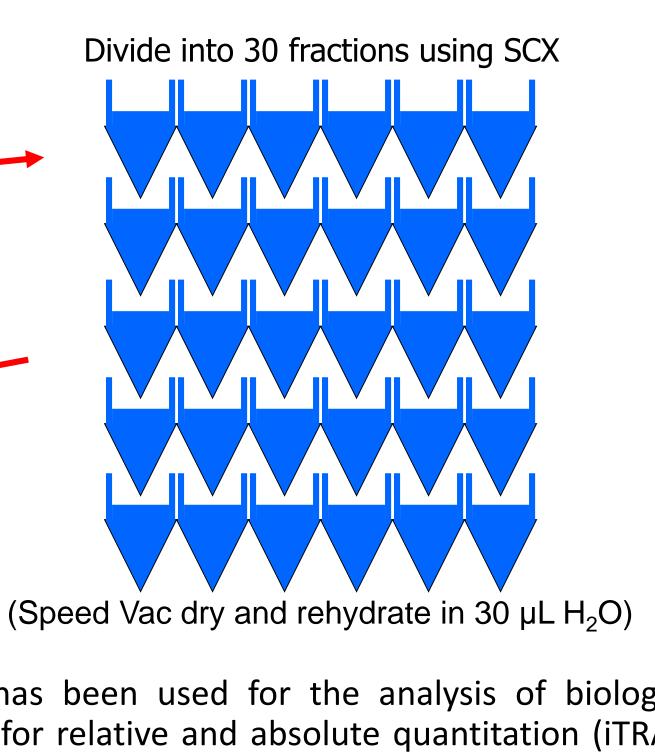


Figure 1. Multidimensional LC-MS/MS has been used for the analysis of biological samples labeled with isobaric mass tags for relative and absolute quantitation (iTRAQ) to identify proteins that are differentially expressed in human oral squamous cell carcinomas (OSCCs) in relation to oral lesions with dysplasia and non-cancerous oral tissues for cancer biomarker discovery.

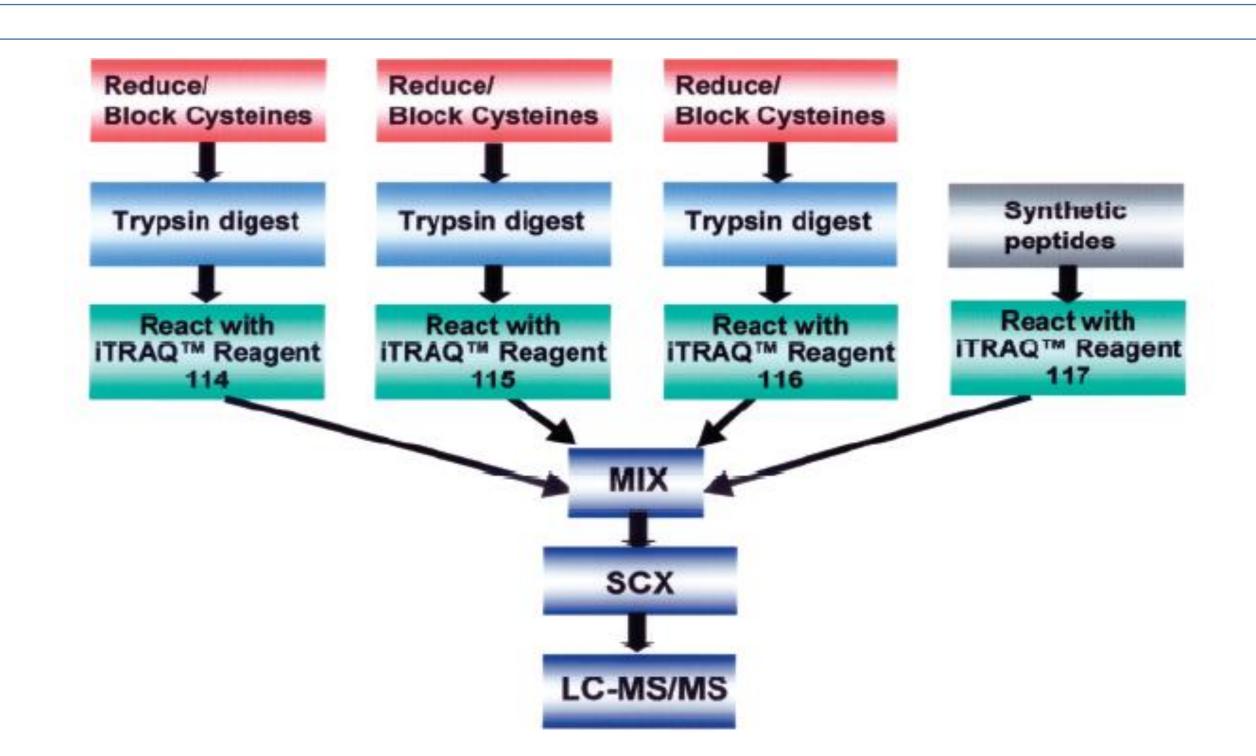


Figure 2. Work flow of iTRAQ-LC-MS/MS analysis of normal oral tissues and OSCC or oral lesions with dysplasia.

Protein I	D1	D2	D3	D4	D5	D6	N1	N2	N3
PCM 69	0.74	2.15	1.94	1.53	1.77	1.63	0.88	0.74	0.75
PCM 70	1.02	3.07	1.19	1.88	0.81	1.5	1.18	0.84	0.99
PCM 72	9.86	1.14	1.13	1.71	1.25	1.5	1.04	1.24	1.1
PCM 10	2.86	1.65	1.46	3.38	0.8	0.99	1.16	1.19	0.61
PCM 12	0.64	0.61	1.19	1.53	3.91	3.54	0.69	0.91	1.57
PCM 28	NQ	NQ	NQ	3.97	2.35	2.89	NQ	NQ	0.81
PCM 31	2.97	1.25	1.73	0.87	1.96	1.52	1.2	0.82	1.83
PCM 74	1.2	0.96	1.56	1.66			0.77	0.97	
PCM 76	1.22	1.55	0.86	1.35	0.92	1.11	1.15	0.78	1.11
PCM 78	NQ	1.2			1.15	1.12	NQ		0.96
PCM 11	0.78	1.14	0.36	0.39	0.54	0.78	0.96	0.29	0.82
PCM 73	0.67	0.5	0.57	0.61	0.72	0.6	0.56	0.57	0.83
PCM 75	1.63	0.29			0.5	0.53	0.43		0.75
PCM 81	0.45	0.57	0.67	0.85	1.36	0.99	0.92	0.77	0.79
PCM 77	0.89	0.72	0.62	0.63	0.64	0.47	0.99	0.7	0.69
PCM 84	0.78	1.43	0.79	0.67	0.58	0.66	0.89	0.97	0.87
PCM 79	1.13	0.58	1.15	0.67			1.11	1.24	
PCM 80	0.48	0.45			0.84	1.18	0.51		1.19
PCM 81					4.09	1.77			0.95
PCM 82	7.77	4.35					0.97		
PCM 83					1.34	1.51			1.23
PCM 85	1.04	1.37	1.26	1.66	1.09	1.12	1.12	0.94	1.09
PCM 86	1.3	1.7	1.16	1.25	0.9	1.87	0.81	1.33	1.04
PCM 87	1.17	1.88	0.78	1.27	1.13	2.35	0.96	1.17	0.83
PCM 88	1.13	1.27	1.45	2.06	1.17	1.17	0.73	0.93	1.05
PCM 89	1.37	1.55	0.75	1.5	1.13	1.12	1.39	0.62	1.36
PCM 90	0.93	1.7	1.35	1.17	1.1	1.25	0.93	1.06	1.24
PCM 91	1.26	1.47			1.35	1.28	1.03		1.34
PCM 92	NQ	NQ	1.3	1.4			NQ	0.88	
PCM 93					1.4	1.57			1.05
PCM 94	1.25	0.97	1.15	1.15			0.89	1	0.89

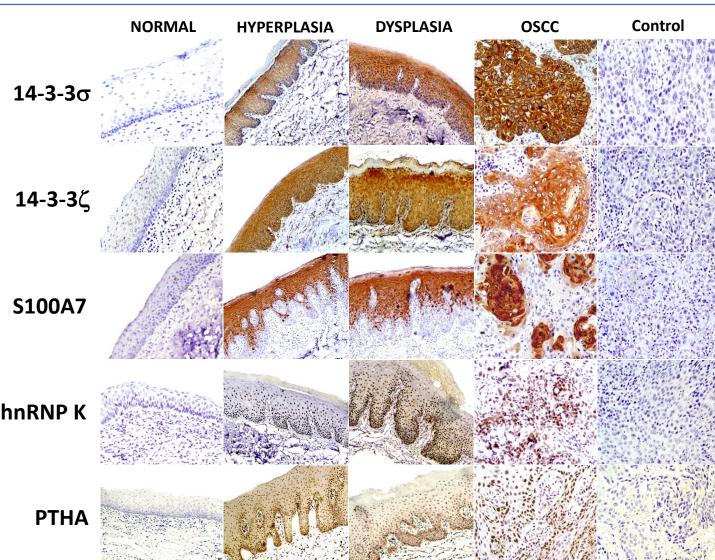
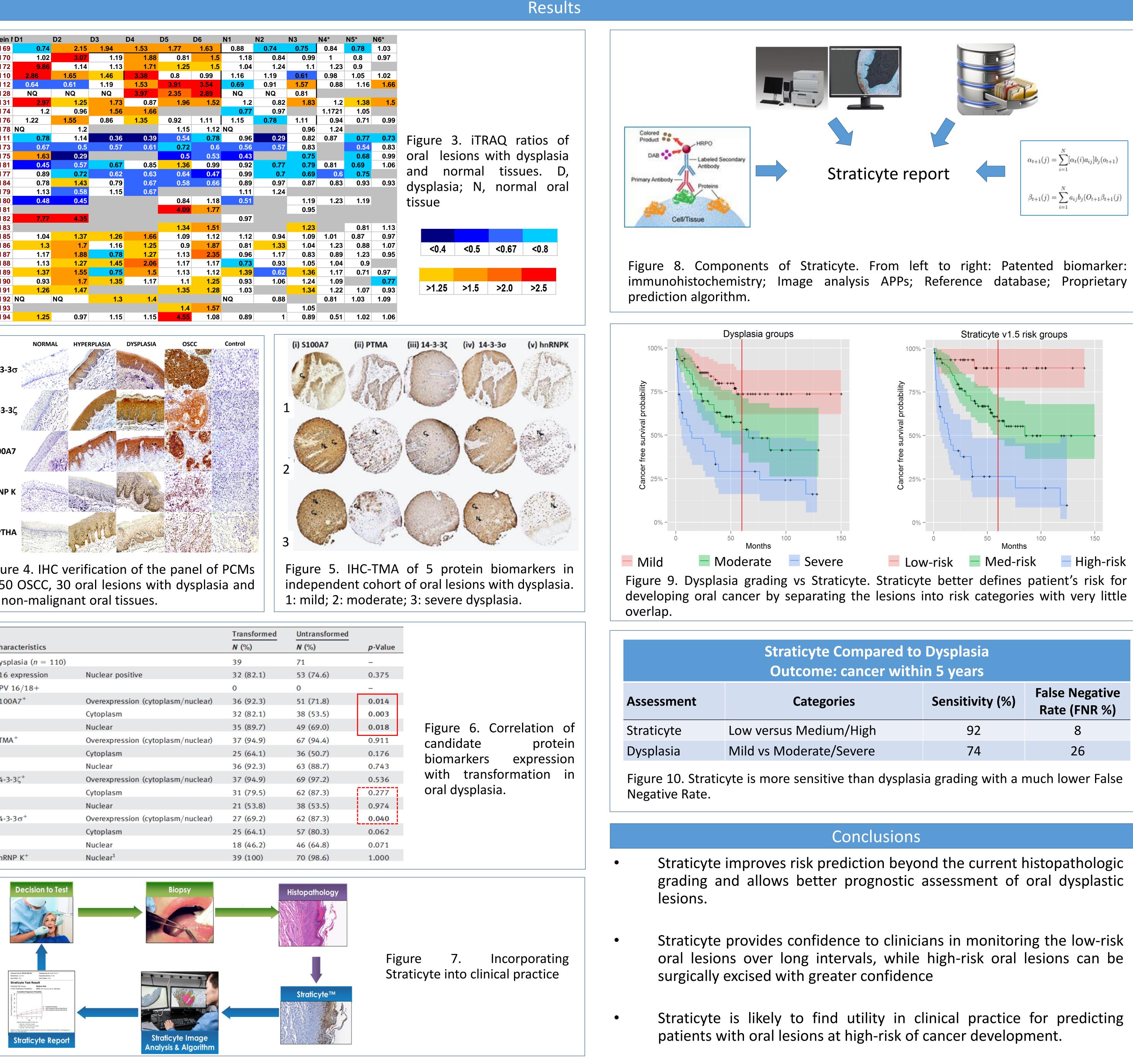
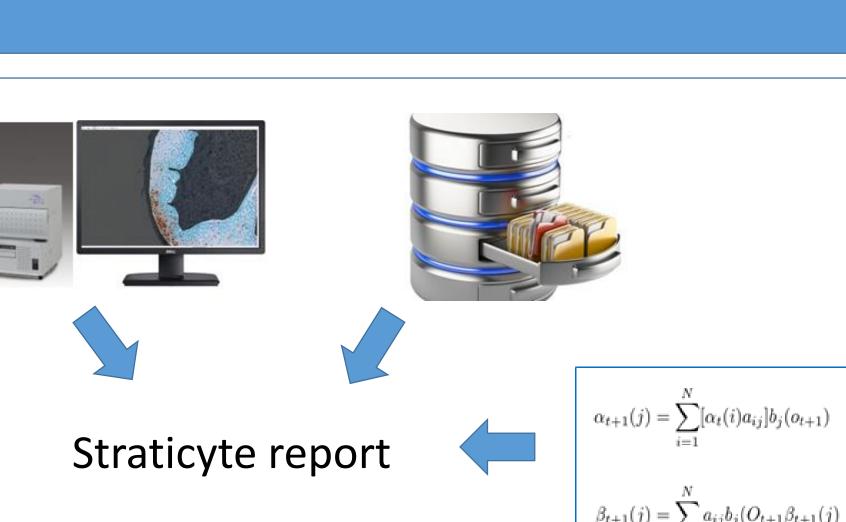


Figure 4. IHC verification of the panel of PCMs in 50 OSCC, 30 oral lesions with dysplasia and 50 non-malignant oral tissues.

		Transformed	Untran
Characteristics		N (%)	N (%)
Dysplasia ($n = 110$)		39	71
p16 expression	Nuclear positive	32 (82.1)	53 (74
HPV 16/18+		0	0
S100A7 ⁺	Overexpression (cytoplasm/nuclear)	36 (92.3)	51 (71
	Cytoplasm	32 (82.1)	38 (53
	Nuclear	35 (89.7)	49 (69
PTMA ⁺	Overexpression (cytoplasm/nuclear)	37 (94.9)	67 (94
	Cytoplasm	25 (64.1)	36 (50
	Nuclear	36 (92.3)	63 (88
14-3-3ζ ⁺	Overexpression (cytoplasm/nuclear)	37 (94.9)	69 (97
	Cytoplasm	31 (79.5)	62 (87
	Nuclear	21 (53.8)	38 (53
14-3-3σ ⁺	Overexpression (cytoplasm/nuclear)	27 (69.2)	62 (87
	Cytoplasm	25 (64.1)	57 (80
	Nuclear	18 (46.2)	46 (64
hnRNP K ⁺	Nuclear ¹	39 (100)	70 (98





Straticyte Compared to Dysplasia Outcome: cancer within 5 years								
Categories	Sensitivity (%)	False Negative Rate (FNR %)						
rsus Medium/High	92	8						
Moderate/Severe	74	26						