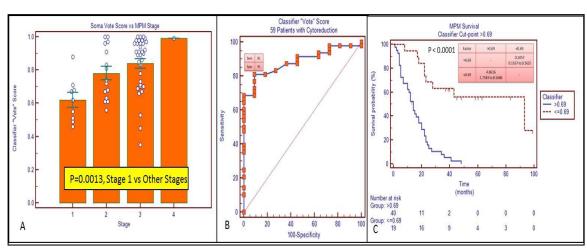
Aim 1: Develop a novel SOMAmer based proteomic platform in order to validate plasma and pleural effusion diagnostic and prognostic biomarkers

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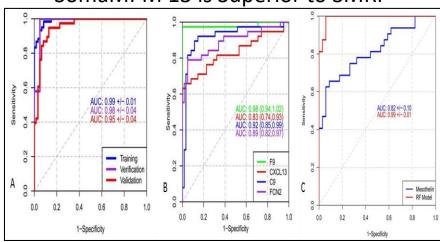
Gene Name	Gene ID	Protein Target	SwissProt ID	Function	MM vs Asbestos*	KS test p-value	t test p-value
APOA1	335	Apo A-I	P02647	Lipid transport	Down	2.99E-08	6.32E-11
C9	735	C9	P02748	Adaptive immune response	Up	6.47E-07	1.1 4 E-07
CCL23	6368	Ck-b-8-1	P55773	Cellular ion homeostasis, inflammatory response	Up	2.81E-06	4.00E-08
CDK5/CDK5R1	1020/8851	CDK5/p35	Q00535/Q15078	Cell morphogenesis	Up	1.22E-06	8.64E-09
CXCL13	10563	BLC	043927	Immune system development	Up	1.67E-09	6.31E-08
F9	2158	Coagulation Factor IX	P00740	Coagulation cascade	Up	2.46E-07	9.61E-09
FCN2	2220	FCN2	Q15485	Immune effector	Up	3.38E-09	6.09E-11
FN1	2335	Fibronectin	P02751	Cell morphogenesis	Down	9.23E-06	9.41E-06
ICAM2	3384	sICAM-2	P13598	Cell adhesion	Up	2.67E-05	1.75E-06
кіт	3815	SCF sR	P10721	Immune system development, receptor tyrosine kinase	Down	3.83E-06	1.14E-08
MDK	4192	Midkine	P21741	Regulation of cell division	Up	2.99E-08	8.54E-02
SERPINA4	5267	Kallistatin	P29622	Serine protease inhibitor	Down	2.05E-07	4.56E-07
TNFRSF8	943	CD30	P28908	Regulation of cytokines & cell proliferation	Up	8.02E-08	3.94E-06

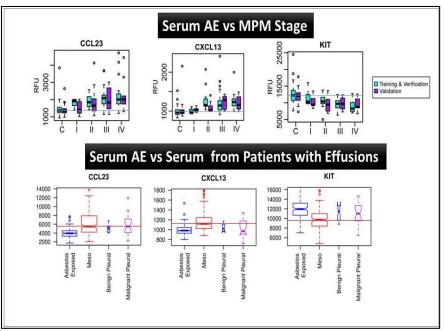
Proteins detected by SOMAscan to separate AE from MPM serum. Yellowed serum markers were also the most significant in separating individuals with MPM effusions from those with non-MPM effusions.



Prognosis of MPM with SOMAmer technology. A)Classifier vote increases with Stage of MPM, B) ROC curve separates living vs dead from the time of serum harvest. C) Dichotomous separation of survival by classifier cut-point. Kolmogorov–Smirnov test

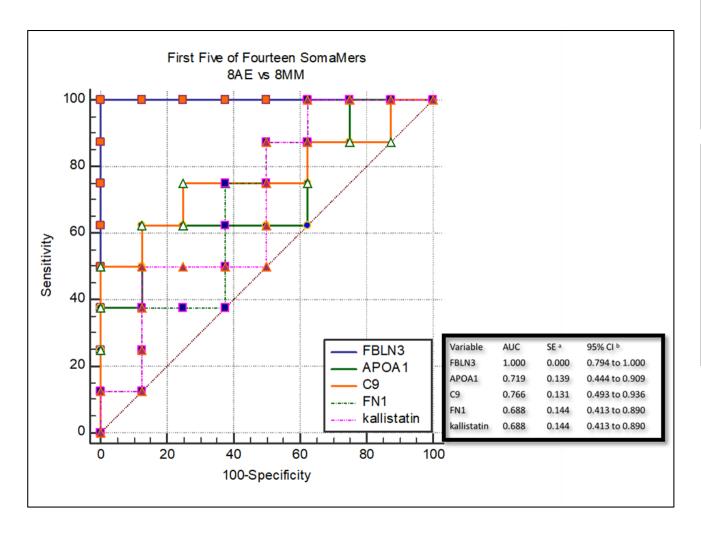
SomaMPM 13 is Superior to SMRP

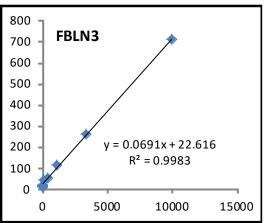


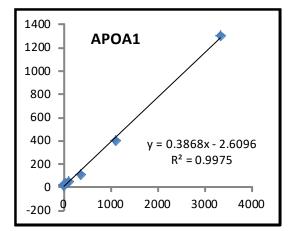


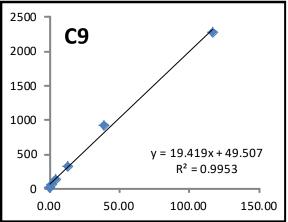
SOMAmer diagnosis of MPM vs AE. A)ROC curves for discovery and validation, B) ELISA validation of selected SOMAmer data, C) Head to head comparison of SMRP and SOMA 13 panel shows better characteristics for the latter. LOWER PANEL. Serum levels of patients with MPM effusions compared to those with non-MPM effusions suggests that 3 markers may have specificity capabilities.

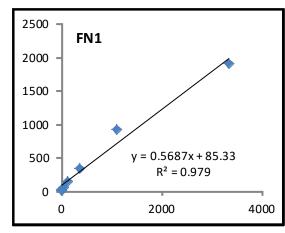
The Other SomaMers

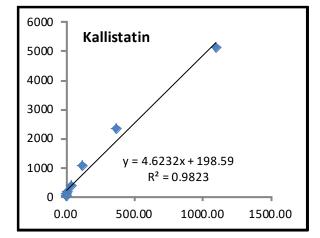






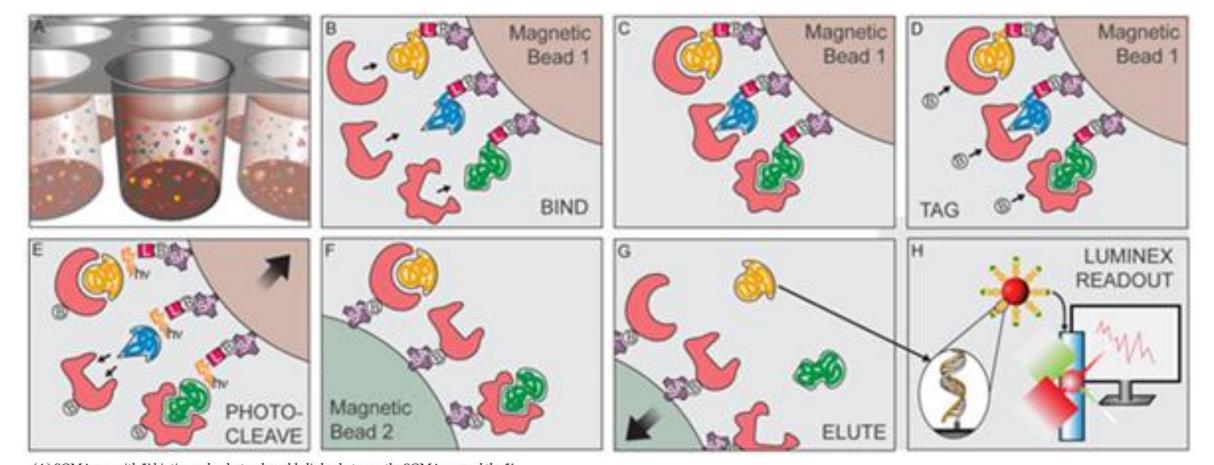




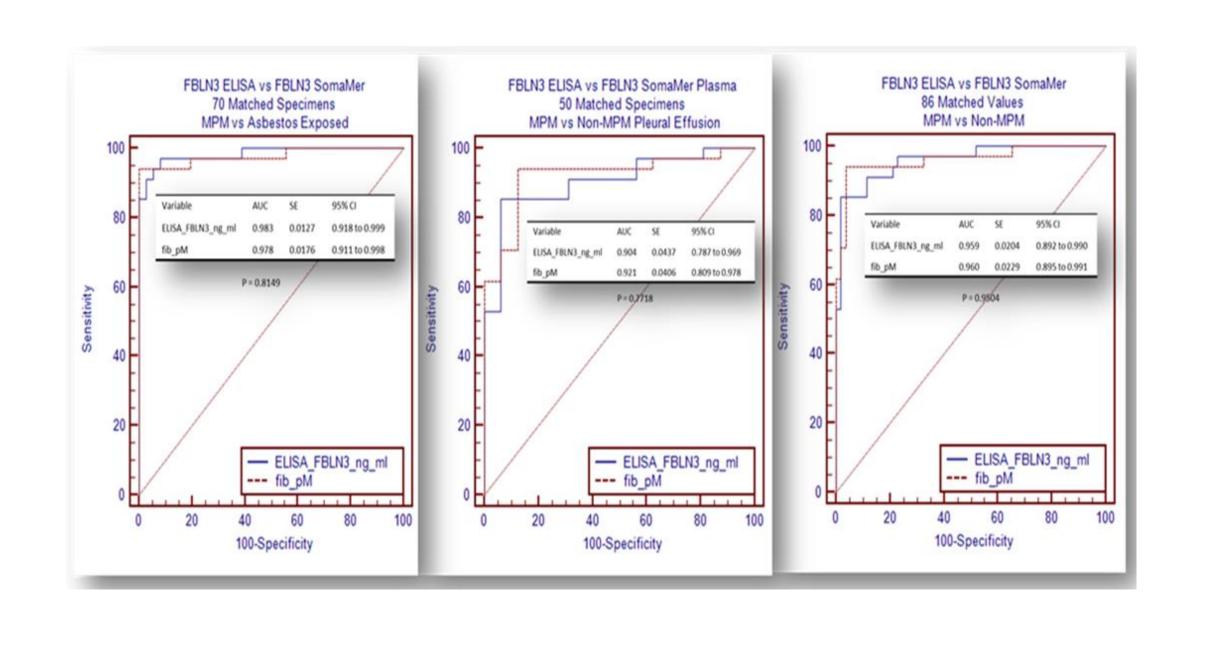


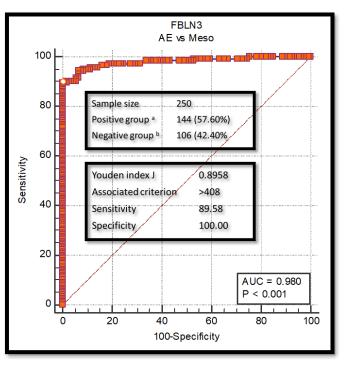
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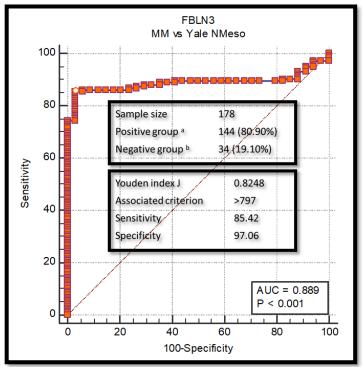
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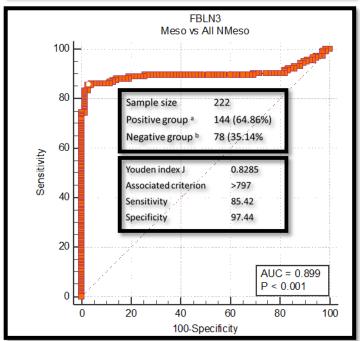


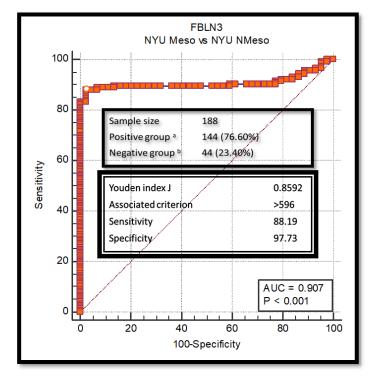
(A) SOMAmer with 5' biotin and a photo-cleavable linker between the SOMAmer and the 5' biotin are pre-bound to streptavidin coated beads (either magnetic or agarose beads can be used) and beads are added to samples in microwells (B-H) Schematic sequence of assay steps leading to quantitative readout of target proteins. (B) Proteins, shown as different shapes, and beads with SOMAmers are mixed in solution (C) SOMAmers attached to magnetic beads bind to proteins specifically (gold and green) and some non-specifically (blue). Unbound proteins are washed away (Catch 1) (D) Tagging: Proteins bound to SOMAmers are tagged with NHS-biotin. (E) Photocleavage and kinetic challenge: UV light (hv) cleaves the linker (L) between the SOMAmer and the 5' biotin, releasing SOMAmers into solution. Taking advantage of a SOMAmer's slow-off rate from its target protein, further specificity of a SOMAmer to its protein target is derived from a kinetic challenge, by adding excess anionic competitor ("random" SOMAmers) to the SOMAmer-protein complex in solution; cognate complexes (gold and green) dissociate slowly, but non-cognate complexes (blue SOMAmer) dissociate rapidly and competitor prevents re-binding. (F) Catch 2: The SOMAmer-protein complexes that remain after the kinetic challenge are captured onto new streptavidin (SA) coated magnetic beads by the biotin tag on the protein from the NHS-biotin labeling of the protein (D) and unbound SOMAmers are washed away. (G) Elution: SOMAmers are eluted into solution by disrupting complexes (e.g. proteins denatured with sodium perchlorate) (H) Readout: Eluted SOMAmers are hybridized to complimentary probe sequences on coded Luminex beads and quantified by flow cytometry on Luminex











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 - Validated the new Fibulin 3 SomaMer Assay
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 - Nope, we developed a new Fibulin 3 ELISA

New Antibodies

Published OnlineFirst November 16, 2017; DOI: 10.1158/1078-0432.CCR-17-1628

Cancer Therapy: Preclinical

Development of a Function-Blocking Antibody Against Fibulin-3 as a Targeted Reagent for Glioblastoma

Mohan S. Nandhu^{1,2}, Prajna Behera^{1,2}, Vivek Bhaskaran¹, Sharon L. Longo³, Lina M. Barrera-Arenas², Sadhak Sengupta⁴, Diego J. Rodriguez-Gil⁵, E. Antonio Chiocca¹, and Mariano S. Viapiano^{1,2,3}



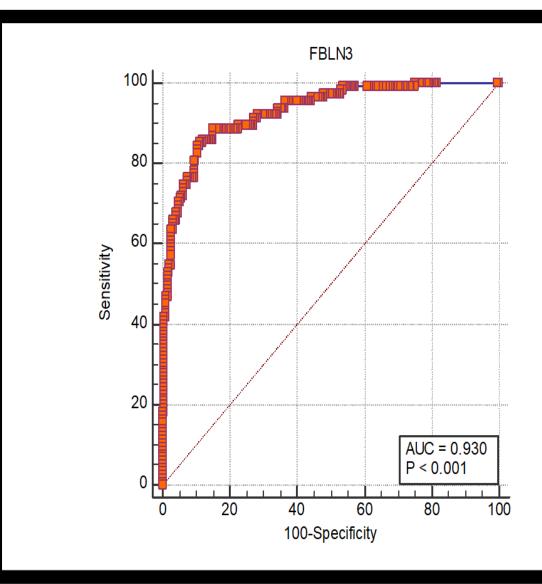


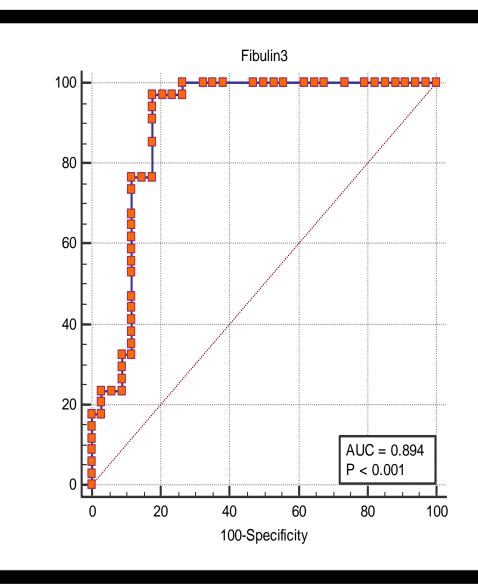
A Theranostic Antibody-Cytokine Reagent				
for Diagnosis and Multipronged Therapy of				Institution: NEW YORK, STATE UNIVERSITY
Malignant Mesothelioma	VIAPIANO, MARIANO S	CA170319	W81XWH-18-1-0183	OF, UPSTATE MEDICAL UNIVERSITY
Engineering T Cells Against the Tumor				
Extracellular Matrix for Enhanced				Institution: NEW YORK, STATE UNIVERSITY
Immunotherapy of Mesothelioma	VIAPIANO, MARIANO S	CA160356	W81XWH-17-1-0444	OF, UPSTATE MEDICAL UNIVERSITY

So what happened to the Biomarker??

- Our lab made a new ELISA using the Viapiano antibody mAB428.2
- But we had to answer basic questions
 - Any difference between serum and plasma?
 - Any difference between arterial (OR Blood) and venous (Clinic Blood)
 - Any difference between blood plasma FBLN3 levels between
 - Asbestos exposed vs MM
 - Patients with non MM effusions and Patients with MM

Blinded Validation University Pennsylvania MM (61) vs Non Meso High Risk (34)





Sensitivity

Plans for Fibulin 3, Aim 1

 Blinded mutual validation of Fibulin3 by Institute for Prevention and Occupational Medicine of the German Social Accident Insurance and Calretinin by the NYU Mesothelioma Biomarker Discovery Lab

MATERIAL TRANSFER AND COLLABORATION AGREEMENT

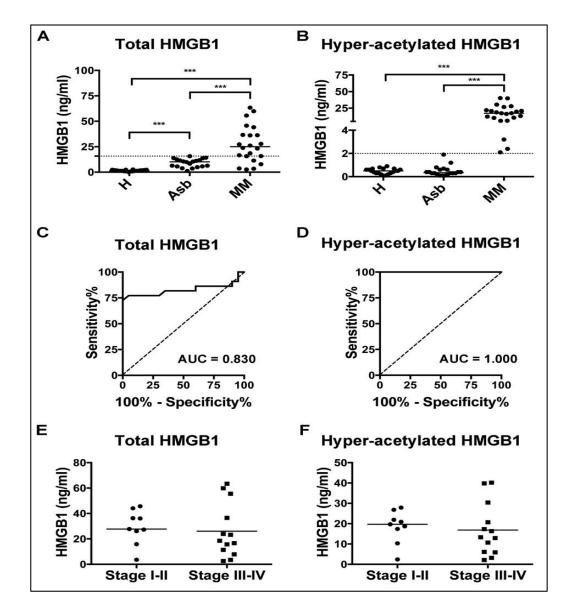
This Material Transfer and Collaboration Agreement (the "Agreement") between NYU Grossman School of Medicine, an administrative unit of New York University, an education corporation organized and existing under the laws of the State of New York and having a place of business at 70 Washington Square South, New York, New York 10012 (hereinafter "NYU"), and Berufsgenossenschaft Rohstoffe und chemische Industrie (BG RCI) located at Kurfuersten-Anlage 62, 69115 Heidelberg, Germany, acting for the Institute for Prevention and Occupational Medicine of the German Social Accident Insurance, Institute of the Ruhr University Bochum (IPA), Bochum, Germany (hereinafter "Collaborator"). NYU and Collaborator may hereinafter be referred to individually as a "Party", and/or collectively as the "Parties". The effective date of this Agreement shall be the date of execution (the "Effective Date").

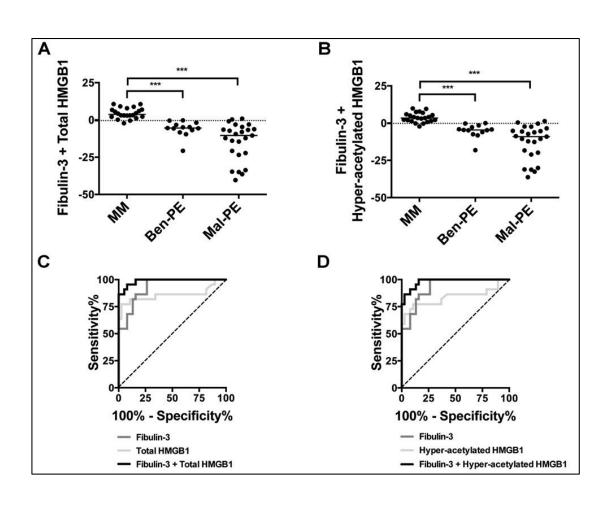
Provider	Background Materials
NYU	Plasma from: 120 mesotheliomas, 50 asbestos-exposed individuals, and 30 individuals with pleural effusions not mesothelioma.
COLLABORATOR	Plasma from: • 80 patients with mesothelioma (including 16 duplicate samples with 5-10 freeze/thaw cycles), and • 75 asbestos-exposed patients

- CORE funds for Specificity of Fibulin 3 in Patients with Pleural Effusions
 - Thoracic Surgery Oncology Group: American Association for Thoracic Surgery
 - 23 member institutions
 - MPM Centers: Baylor, Duke, MDA, Pittsburgh, Toronto, MSKCC
 - Prospective collection of blood and pleural effusion for patients presenting with pleural effusion
 - Hopefully conducted through DMCC
- Humanized Fibulin 3 antibody
 - Three lots of antibodies being tested for dilutions and sensitivity/specificity

Aim 2: Investigate HMGB1 and its Isoforms in the Diagnosis of the MPM Pleural Effusion

Total and hyper-acetylated HMGB1 are biomarkers for asbestos exposure and MM





Harvey I. Pass (PI)
Haining Yang (co-PI)

 The major goal of this project is to evaluate whether by measuring total HMGB1 and its isoforms, we can accurately differentiate pleural effusions that are MPM from non-MPM effusions.

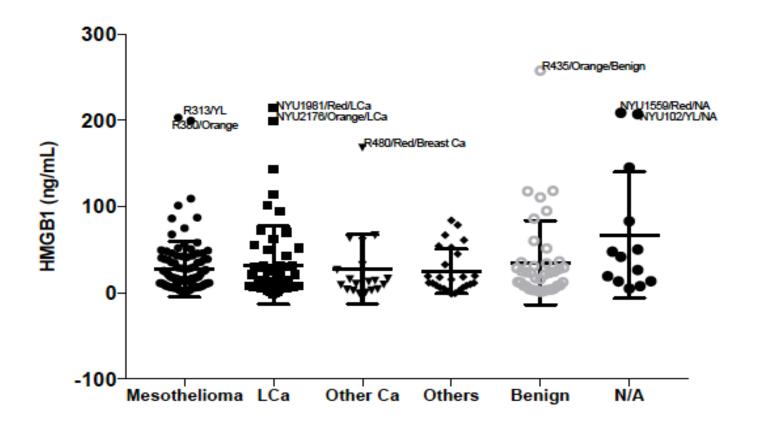
- Develop clinically applicable MS based quantitative assay for:
 - Total HMGB1
 - Acetylated HMGB1
 - Redox HMGB1
- *In collaboration with Dr. <u>Justyna Fert-Bober, Weston Spivia and Dr.</u> <u>Jennifer Van Eyk</u> at Cedars-Sinai Medical Center.

HMGB1 Mass Spec measurement in pleural effusion and serum samples

Total HMGB1 measured by the mass spec assay for the NYU pleural effusion and serum samples gives the overall concentration of HMGB1 with these samples. The amount of fully acetylated, as well as unacetylated, HMGB1 relative to standard gives the proportion of post-translationally modified HMGB1 in serum.

Study ID	ELISA	PE MS	Serum	Total HMGB1	Unacetyl	Acetylated
	HMGB1	results of	(ng/ml)	Relative Quant	HMGB1	HMGB1 Relative
	(ng/mL)	total	MS results	by GluC - DMA	Relative Quant	Quant
NIV/1.14	110.26	HMGB1	600.20	1 1016	(Serum)	(Serum)
NYU1	118.36	16.62	689.38	1.1916	64.8084	Below LOD
NYU1295	49.69	15.55	56.95	0.12885	0.1554	Below LOD
NYU1306	51.68	17.65	29.18	0.0651	0.08535	Below LOD
NYU1318	1.86	-2.85	64.7	0.1735	0.21945	Below LOD
NYU1336	4.73	-1.66	31.99	0.0729	0.0992	Below LOD
NYU1338	52.48	10.52	36.06	0.1318	0.2094	Below LOD
NYU1353	22.88	1.01	95.23	0.06585	0.1061	Below LOD
NYU1373	5.44	-1.8	58.22	0.11955	0.15015	Below LOD
NYU1621	5.13	-0.39	132.63	0.432	0.38535	Below LOD
NYU1660	117.96	3.5	44.6	0.0967	0.08965	Below LOD
NYU1661	15.71	5.7	53.15	0.1132	0.1562	Below LOD
NYU181	18.52	13.66	145.35	0.2772	0.30785	Below LOD
NYU1937	26.89	12.21	17.29	0.0118	0.02415	Below LOD
NYU207	86.11	24.11	48.66	0.1275	0.194	Below LOD
NYU2190		-2.25	25.6	0.0789	0.0952	Below LOD
NYU250	8.78	23.82	111.82	0.18655	0.2493	Below LOD
NYU540	16.5	-0.87	70.05			Below LOD
NYU754	203.3	75.26	139.05	0.2525	0.3103	Below LOD
Α						
NYU754 B	60.1	21.73	35.51	0.0818	0.1214	Below LOD
NYU826	38.87	20.65	138.2	0.2599	0.3296	Below LOD
NYU851	4.66	-2.63	53.41	0.1338	0.19775	Below LOD
NYU872	6.89	3.29	330.66	0.5827	0.59475	Below LOD
NYU93	52.11	24.81	108.12	0.23295	0.4012	Below LOD
NYU937	6.15	0.58	62.22	0.1478	0.19035	Below LOD
R489	17.41	6.54	69.1	0.1853	0.22295	_

HMGB1 ELISA assays on 263 pleural effusion samples

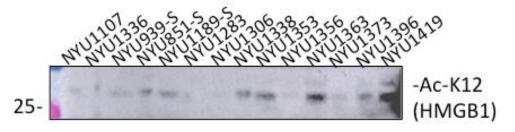


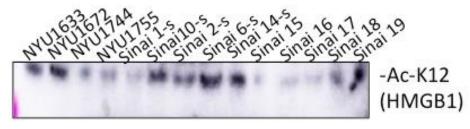
Total HMGB1 levels measured by ELISA assay using patients' pleural effusions samples obtained from patients with different disease status.

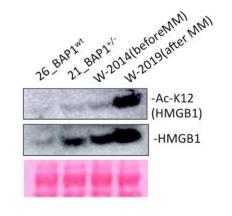
(Note: We labeled the color of the samples with relatively high HMGB1 levels, as it has been reported that hemolyzed red blood cells could release HMGB1 into the fluid, which might contribute to the relatively high levels of HMGB1 measured in those samples.

New data developed recently

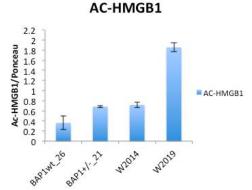
1. We are able to detect acetylated HMGB1 by Western blot, and we are setting up the ELISA assay

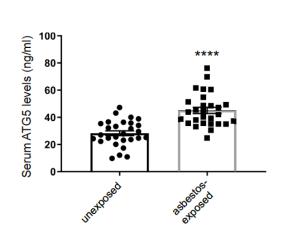


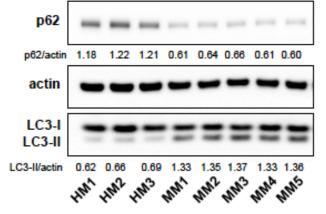


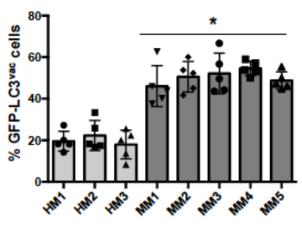


2. We found that autophagy levels are increased in asbestos exposed individuals and MPM patients, which can be the new marker.









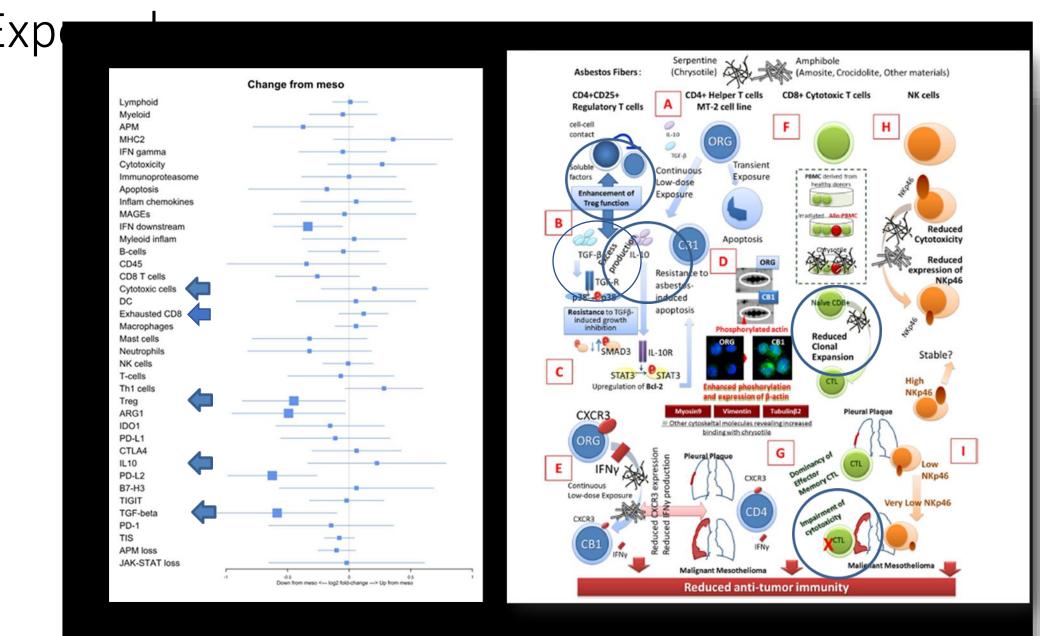
Aim 3: To determine whether buffy coat immuno-oncologic RNA expression can define asbestos exposure and diagnose MPM

- **Subaim 3a:** Further refine and validate Nanostring Immuno-oncology profiles in the diagnosis of asbestos exposure and MPM
- **Subaim 3b:** Blindly validate locked in Nanostring Immuno-oncology profiles for healthy, non-AE vs AE, AE vs MPM, and MPM vs non-MPM using buffy coat from the Princess Margaret Cancer Center

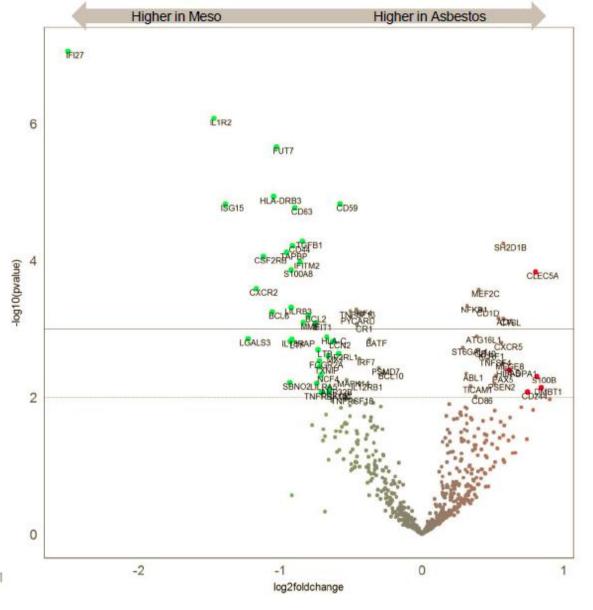
Buffy Coat Immunotranscriptomics: Mesothelioma

- Patient samples
 - 40 mesothelioma patients (NYU#)
 - 44 asbestos exposure patients (SINAI#)
- Gene expression panel
 - NanoString PanCancer Immune Profiling panel V1.1 (730 IO targets + 40 HK references)
- Analysis objectives
 - Perform data QC and normalization
 - Perform differential expression (DE) analysis
 - Perform gene set analysis (GSA)
 - Perform immune cell type profiling
 - Identify a gene expression signature relating to diagnosis

Circulating microenvironment: MPM vs Asbestos

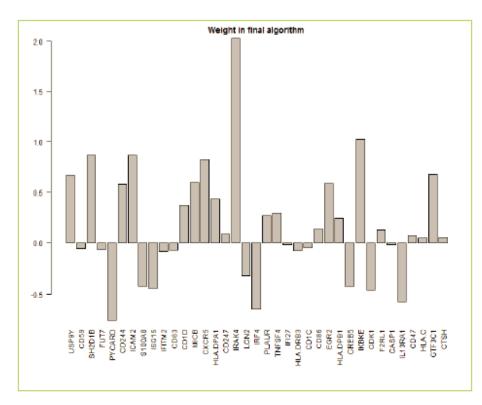


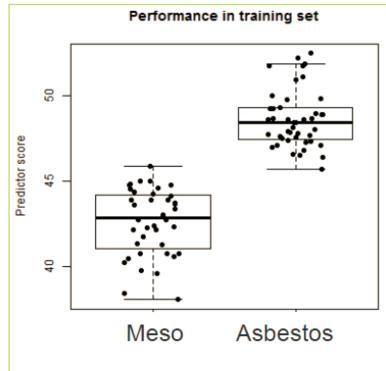
Circulating microenvironment: MPM vs Asbestos Exposed

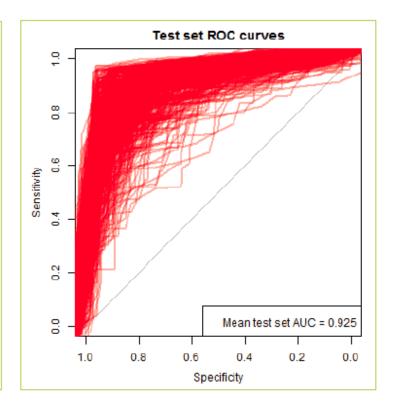


		Log2 fold change	P-value	Gene.sets
	IFI27-mRNA	-2.5	4.86E-07	Chemokines
	MEF2C-mRNA	0.486	8.64E-07	
	IL1R2-mRNA	-1.45	3.70E-06	Cytokines
	FUT7-mRNA	-1.1	4.52E-06	Leukocyte Functions
	CD59-mRNA	-0.616	2.12E-05	
	CD1D-mRNA	0.443	2.37E-05	B-Cell Functions, Cell Functions, T-Cell Functions
	SH2D1B-mRNA	0.604	2.75E-05	Leukocyte Functions
	ISG15-mRNA	-1.32	3.98E-05	,
< 0.001	CD63-mRNA	-0.846	5.39E-05	
< 0.01	CLEC5A-mRNA	0.779	6.33E-05	
	HLA-DR83-mRNA	-0.98	7.11E-05	Antigen Processing
	CD44-mRNA	-0.872	0.00014	Senescence, Transporter Functions
	TAPBP-mRNA	-0.929	0.000144	Antigen Processing
	TGFB1-mRNA	-0.775	0.000159	Interleukins, Regulation
	PIK3CG-mRNA	0.236	0.000182	
	NFKB1-mRNA	0.309	0.000231	
	IFITM2-mRNA	-0.855	0.000247	
	KLRF1-mRNA	0.531	0.000251	Cell Functions, NK Cell Functions
	CSF2RB-mRNA	-1.07	0.000303	Chemokines
	HLA-DPA1-mRNA	0.733	0.000355	Antigen Processing

Modeling Differences between MPM and AE BC Immunogenes



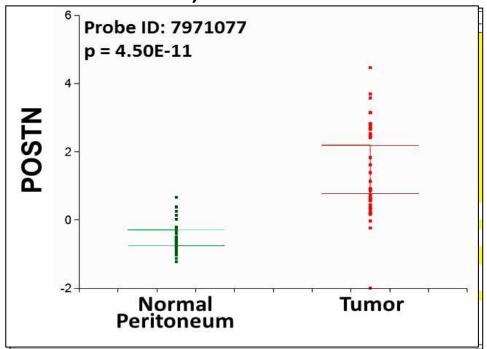


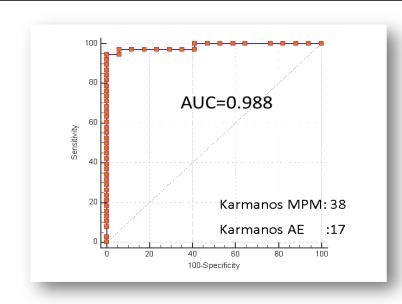


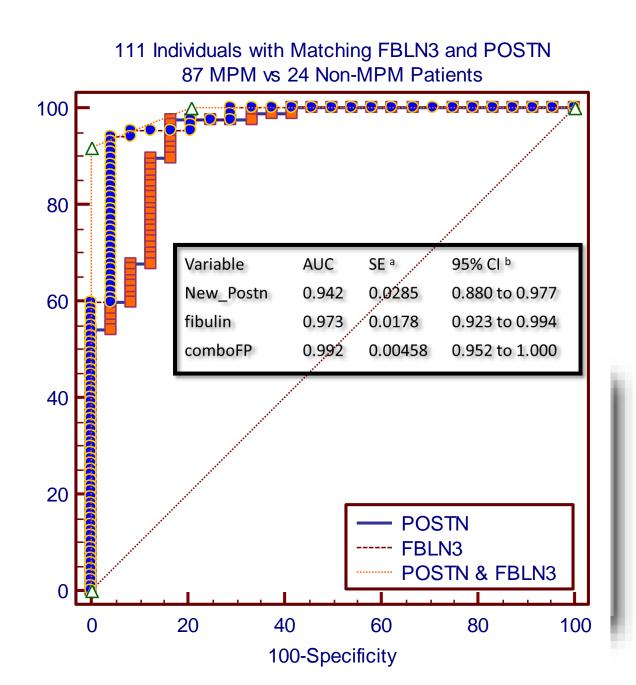
Set-Asides

- Year 1: Wasted on the proposed LPT3 Prognostic Project
- Year 2: Periostin
- Year 3: BC and Lung Cancer

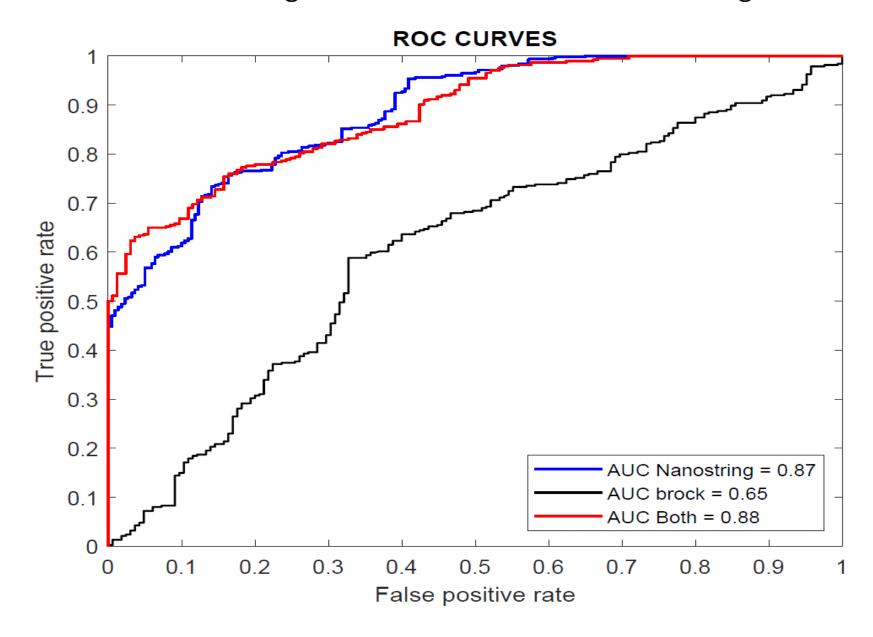
Periostin, son of Fibulin



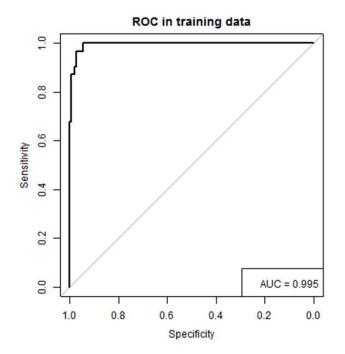


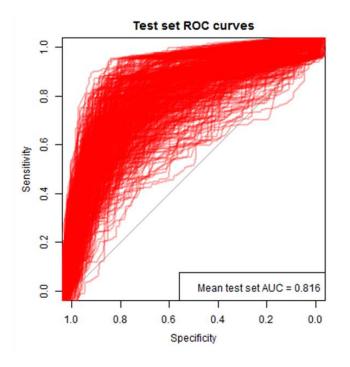


Set Asides: Buffy Coat Immunotranscriptomics for Diagnosis Early Stage Adenocarcinoma: 207 Stage I Adenocarcinomas vs 100 Benign Nodules

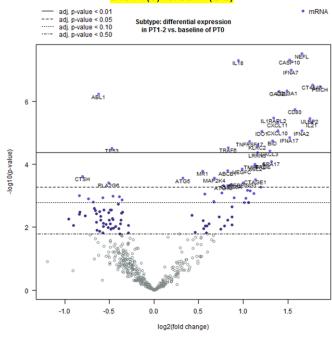


	No Progres	ssion n=148	Progressio	on n=31		
	Mean	SD	Mean	SD	95% CI	P a
Age	68.5068	9.5707	71.9032	8.0844	-0.2425 to 7.0354	0.0672
Gender	109F/39M		17F/14M			
Pack_per_year	26.2588 30.9382		35.4355	29.3345	-2.7794 to 21.1328	0.1316
Predominant	MP/Solid 25		MP/Solid 12		0.1342 to 0.6823	0.0037
Size_cm	1.7568	0.7593	2.1452	0.9081	0.08184 to 0.6950	0.0133
LVI	12		13		0.2120 to 0.4646	<0.0001
Pleural_invasion	15		8		0.02761 to 0.2858	0.0176

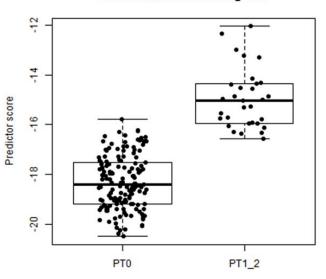


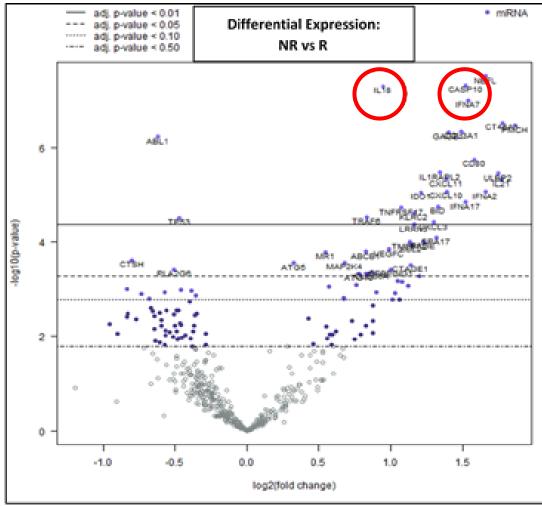


148 PT(0) vs. 31 PT(1-2)

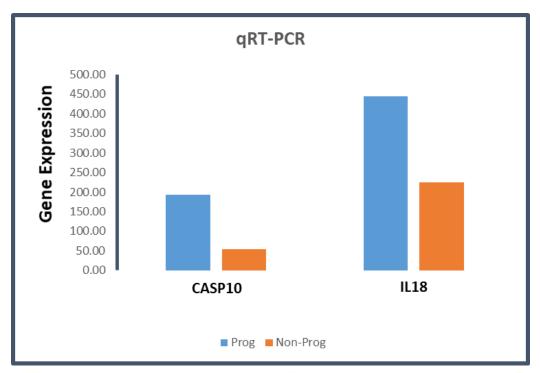


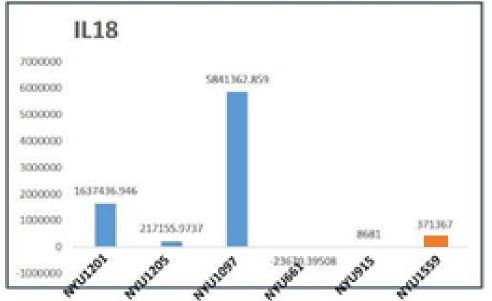
Performance in training set





	Log2 FC	SE (log2)	Lower confidence limit (log2)	Upper confidence limit (log2)	Linear FC	Lower confidence limit (linear)	Upper confidence limit (linear)	p
NEFL-mRNA	1.67	0.292	1.1	2.25	3.19	2.14	4.74	7.60E-05
IL18-mRNA	0.948	0.168	0.619	1.28	1.93	1.54	2.42	7.60E-05
CASP10-mRNA	1.53	0.271	0.999	2.06	2.89	2	4.17	7.60E-05
IFNA7-mRNA	1.54	0.276	0.998	2.08	2.9	2	4.22	7.94E-05
GAGE1-mRNA	1.41	0.261	0.894	1.92	2.65	1.86	3.78	0.000135
CT45A1-mRNA	1.78	0.333	1.13	2.43	3.44	2.18	5.4	0.000135
PMCH-mRNA	1.87	0.35	1.18	2.55	3.65	2.27	5.87	0.000135
COL3A1-mRNA	1.5	0.281	0.945	2.05	2.82	1.93	4.13	0.000135
ABL1-mRNA	-0.677	0.137	-0.947	-0.408	0.625	0.519	0.754	0.000754
FC, fold change								





Progressors

Non Progressors

