Acellular Normal and Fibrotic Human Lung Matrices as a Culture System for *In Vitro* Investigation

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ONLINE SUPPLEMENTAL DATA

SUPPLEMENTAL METHODS:

Decellularization of Lung Matrices: Incubation times lasted, on average, 24 hours per step and involved instillation of solutions through both the pulmonary vasculature and the airways. In essence, lung samples were first agitated in sterile deionized, distilled water followed by incubation in 0.1% Triton X-100 to lyse cellular components. Samples were then washed 3 times with sterile PBS, followed by incubation with 2% sodium deoxycholate. Following three subsequent washes with sterile PBS, samples were incubated in 1M NaCl to lyse residual nuclei. After decanting NaCl, tissues were rinsed three times with sterile PBS and incubated with DNAse (30 μg/ml) in 1.3mM $MgSO_4$ and 2mM $CaCl_2$. The DNAse solution was decanted and tissues were washed three times with sterile PBS. This protocol was repeated three times. Resulting samples were then sterilized with a solution containing 0.18% peracetic acid and 4.8% ethanol for 20 minutes and then washed three times with sterile PBS and stored at 4°C. Effluent following each incubation step was collected and frozen at -80^{o}C until assayed by liquid chromatography-tandem mass spectrometry (see below).

Atomic Force Microscopy: Acellular tissue samples were dissected into strips of approximately 5 x 5 mm in length and width and 1000 μm in thickness, and were characterized using an MFP-3D-BIO atomic force microscope (AFM) (Asylum Research; Santa Barbara, CA). AFM nanoindentation tests were performed under fluid conditions (PBS, pH 7.4) using a 4.74 μm diameter spherical tipped-silicon nitride cantilever (Bruker, Camarillo, CA). Cantilever spring constants were measured prior to sample analysis using the thermal fluctuation method, with nominal values of 20-30 pN/nm (1). Two-dimensional force maps were taken in 30 x 30 μm grids, and force-indentation curves were individually analyzed using a Hertzian model for spherical tips, from which Young's modulus was obtained. The sample Poisson's ratio was assumed as 0.4 (2), and a power law of 1.5 was used to model tip geometry. All AFM measurements were made using a cantilever deflection set point of 100 nm and a rate of indentation of 22.86 μm/s.

<u>*Sample Preparation and Mass Spectrometry:*</u> Tissues were homogenized using a Bullet Blender (BB) in modified RIPA buffer (50mM Tris-HCl, pH 8.0, 50mM NaCl, 0.1% SDS, Roche complete protease inhibitor, Roche PhosStop phosphatase inhibitor) using 0.2mm Stainless Steel beads with a 1:1 tissue/bead ratio (w/w). The BB settings were: speed 8 for 3 minutes, speed 10 for3 minutes, speed 10 for 3 minutes. Samples were incubated on ice between homogenization steps. The tissue homogenate was centrifuged at low speed to remove cell debris and beads, then supernatant removed and centrifuged at 13.5K for 15 minutes. Protein quantitation was performed by Qubit fluorometry. 20μg of extracted protein was separated on a 4-12% Bis Tris NuPage gel (Invitrogen) in the MOPS buffer system. Each gel lane was excised into forty equally sized segments and each was processed by in-gel digestion using a ProGest robot (DigiLab). The in-gel digestion protocol was as follows; samples were washed with 25mM ammonium bicarbonate followed by acetonitrile, reduced with 10mM dithiothreitol at 60°C followed by alkylation with 50mM iodoacetamide at room temperature. Samples were digested with sequencing grade trypsin (Promega) at 37°C for 4h. Reactions were quenched with formic acid and the supernatant was analyzed directly without further processing. Each gel digest was analyzed by nanoLC-MS/MS with a NanoAcquity HPLC system (Waters) interfaced to a LTQ Orbitrap Velos (ThermoFisher). Peptides were loaded on a trapping column and eluted over a 75μm analytical column at 300nL/min; both columns were packed with Jupiter Proteo resin (Phenomenex). Data were acquired using Collision Induced Dissociated (CID), the mass spectrometer was operated in data-dependent mode, with MS performed in the Orbitrap at 60,000 FWHM resolution, MS/MS was performed in the Velos. Product ion data were searched against the combined forward and reverse SwissProt human protein database using the Mascot

search engine v2.3.02 (Matrix Science) via Mascot Daemon v2.3.2. Mascot search result files (DAT) were parsed to the Scaffold program (Proteome Software) for visualization and validation. Identified phosphorylation sites were manually validated.

Table E1. Mass spectrometry analysis of effluent following each of the listed decellularization steps. Proteins identified in the effluent are listed by order of abundance (highest to lowest) with number of unique peptides and peptide abundance (the amount of each peptide) listed in the corresponding columns. Matrisome-associated proteins are sparsely present in the effluent.

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Serum albumin	293	224	163	166	4.23E-02	5.60E-02	3.84E-02	1.00E-01
Filamin-A	156	175	222	121	5.52E-03	1.07E-02	1.29E-02	1.80E-02
Plectin	82	47	116	30	1.53E-03	1.52E-03	3.55E-03	2.35E-03
Myosin-11	68	0	10	0	2.98E-03	0	7.17E-04	0
Actin, cytoplasmic 2	65	34	34	21	1.54E-02	1.40E-02	1.32E-02	2.09E-02
Vimentin	63	52	65	8	1.16E-02	1.66E-02	1.96E-02	6.19E-03
Talin-1	60	43	38	13	2.21E-03	2.75E-03	2.29E-03	2.01E-03
Actin, alpha cardiac muscle 1	55	21	22	0	1.30E-02	8.62E-03	8.52E-03	0
Serotransferrin	51	57	35	27	6.59E-03	1.28E-02	7.39E-03	1.46E-02
Spectrin alpha chain, brain	50	158	178	56	1.75E-03	9.56E-03	1.02E-02	8.20E-03
Alpha-enolase	43	26	16	6	9.10E-03	9.54E-03	5.54E-03	5.33E-03
Plastin-2	41	52	36	17	5.83E-03	1.28E-02	8.37E-03	1.01E-02
Phosphoglycerate kinase 1	40	10	16	22	8.85E-03	3.83E-03	5.78E-03	2.04E-02
Moesin	38	17	41	25	5.56E-03	4.31E-03	9.81E-03	1.54E-02
Early endosome antigen 1	37	10	58	0	2.27E-03	1.06E-03	5.82E-03	0
Myosin-9	36	5	36	11	1.58E-03	3.80E-04	2.58E-03	2.02E-03
Desmoplakin	36	42	70	26	1.08E-03	2.18E-03	3.43E-03	3.27E-03
Complement C3	36	10	27	12	1.92E-03	9.22E-04	2.35E-03	2.68E-03
Alpha-1-antitrypsin	36	13	9	7	7.62E-03	4.77E-03	3.11E-03	6.22E-03
Vinculin	35	56	35	48	2.81E-03	7.79E-03	4.59E-03	1.62E-02
Hemoglobin subunit beta	34	17	21	11	2.11E-02	1.83E-02	2.13E-02	2.87E-02
Heat shock cognate 71 kDa protein	34	7	9	8	4.77E-03	1.70E-03	2.06E-03	4.70E-03
Alcohol dehydrogenase 1B	32	12	15	2	7.96E-03	5.17E-03	6.10E-03	2.09E-03
Transgelin	30	18	13	8	1.30E-02	1.35E-02	9.19E-03	1.45E-02
Glutathione S-transferase P	30	20	21	6	1.30E-02	1.50E-02	1.49E-02	1.09E-02
Dihydropyrimidinase-related protein 2	27	25	19	0	4.33E-03	6.95E-03	4.98E-03	0
Haptoglobin	27	21	23	12	5.97E-03	8.05E-03	8.31E-03	1.11E-02
Selenium-binding protein 1	26	21	15	14	4.98E-03	6.96E-03	4.69E-03	1.12E-02
Triosephosphate isomerase	26	22	17	8	9.58E-03	1.41E-02	1.02E-02	1.24E-02
Retinal dehydrogenase 1	26	18	19	2	4.70E-03	5.64E-03	5.62E-03	1.52E-03
Alpha-actinin-4	26	19	39	14	2.46E-03	3.12E-03	6.04E-03	5.57E-03
Rab GDP dissociation inhibitor beta	25	0	10	3	4.88E-03	0	3.19E-03	2.46E-03
Leukotriene A-4 hydrolase	25	11	16	8	3.61E-03	2.75E-03	3.77E-03	4.84E-03
Heat shock 70 kDa protein 1A/1B	25	6	6	7	3.55E-03	1.48E-03	1.39E-03	4.18E-03
Junction plakoglobin	24	24	22	18	2.91E-03	5.05E-03	4.36E-03	9.17E-03
Heat shock protein HSP 90-alpha	24	6	16	7	2.81E-03	1.22E-03	3.06E-03	3.44E-03
Vitamin D-binding protein	24	15	15	6	4.51E-03	4.88E-03	4.60E-03	4.73E-03
Liver carboxylesterase 1	23	8	14	5	3.63E-03	2.19E-03	3.61E-03	3.31E-03
Heat shock protein HSP 90-beta	23	6	11	0	2.76E-03	1.25E-03	2.16E-03	0
Hemoglobin subunit delta	23	0	15	0	1.43E-02	0	1.52E-02	0
Filaggrin-2	22	21	12	13	8.83E-04	1.46E-03	7.87E-04	2.19E-03
Desmoglein-1	22	19	11	10	1.92E-03	2.87E-03	1.57E-03	3.66E-03
Transgelin-2	22	11	12	6	9.95E-03	8.62E-03	8.87E-03	1.14E-02
Alpha-actinin-1	22	0	32	0	2.13E-03	0	5.05E-03	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Peroxiredoxin-1	21	11	12	10	9.50E-03	8.62E-03	8.87E-03	1.90E-02
Hemoglobin subunit alpha	21	15	14	11	1.39E-02	1.72E-02	1.52E-02	3.06E-02
Tubulin alpha-1B chain	21	7	9	0	4.18E-03	2.41E-03	2.93E-03	0
Phosphoglucomutase-1	21	0	4	0	3.43E-03	0	1.07E-03	0
Hornerin	20	45	23	22	7.06E-04	2.75E-03	1.33E-03	3.26E-03
Plastin-3	20	10	14	0	2.80E-03	2.43E-03	3.21E-03	0
78 kDa glucose-regulated protein	20	10	10	5	2.76E-03	2.39E-03	2.26E-03	2.90E-03
Rab GDP dissociation inhibitor alpha	19	0	9	0	3.71E-03	0	2.87E-03	0
Ribonuclease inhibitor	19	9	9	0	3.78E-03	3.10E-03	2.93E-03	0
Protein disulfide-isomerase	19	8	11	6	3.32E-03	2.42E-03	3.14E-03	4.40E-03
Fibrinogen beta chain	19	9	8	2	3.38E-03	2.77E-03	2.32E-03	1.49E-03
Filamin-B	19	38	29	22	6.80E-04	2.36E-03	1.70E-03	3.30E-03
Tubulin beta-2C chain	18	0	0	0	3.58E-03	0	0	0
14-3-3 protein zeta/delta	18	12	13	3	6.40E-03	7.39E-03	7.55E-03	4.47E-03
14-3-3 protein gamma	18	7	9	0	6.40E-03	4.31E-03	5.23E-03	0
Profilin-1	18	9	6	3	1.19E-02	1.03E-02	6.51E-03	8.35E-03
Tubulin beta chain	18	4	3	0	3.58E-03	1.38E-03	9.76E-04	0
Protein DJ-1	17	4	4	3	8.46E-03	3.45E-03	3.25E-03	6.26E-03
14-3-3 protein beta/alpha	17	8	10	0	6.04E-03	4.93E-03	5.81E-03	0
Peptidyl-prolyl cis-trans isomerase A	16	17	12	9	8.85E-03	1.63E-02	1.08E-02	2.09E-02
Transaldolase	16	4	10	4	4.19E-03	1.82E-03	4.28E-03	4.40E-03
Radixin	16	21	15	0	2.31E-03	5.25E-03	3.54E-03	0
Phosphoglycerate mutase 1	16	0	0	0	5.49E-03	0	0	0
Gelsolin	16	23	11	19	1.85E-03	4.61E-03	2.08E-03	9.23E-03
L-lactate dehydrogenase A chain	16	3	3	0	4.30E-03	1.40E-03	1.32E-03	0
Chloride intracellular channel protein 1	16	0	0	0	5.90E-03	0	0	0
Keratinocyte proline-rich protein	15	14	10	16	2.33E-03	3.77E-03	2.54E-03	1.04E-02
Adenylyl cyclase-associated protein 1	15	5	5	0	2.87E-03	1.66E-03	1.56E-03	0
14-3-3 protein epsilon	15	10	11	3	5.15E-03	5.95E-03	6.17E-03	4.32E-03
F-actin-capping protein subunit beta	15	2	4	0	4.82E-03	1.11E-03	2.10E-03	0
Carbonyl reductase [NADPH] 1	15	0	0	0	4.98E-03	0	0	0
Annexin A2	15	18	33	13	3.83E-03	7.96E-03	1.38E-02	1.39E-02
Cathepsin D	15	8	10	0	3.32E-03	3.07E-03	3.61E-03	0
L-lactate dehydrogenase B chain	15	2	3	0	4.03E-03	9.32E-04	1.32E-03	0
Glyceraldehyde-3-phosphate dehydrogenase	15	17	13	5	4.15E-03	8.14E-03	5.87E-03	5.80E-03
Alpha-2-macroglobulin	15	8	16	14	9.16E-04	8.46E-04	1.60E-03	3.59E-03
Carbonic anhydrase 1	15	12	8	4	5.15E-03	7.14E-03	4.49E-03	5.76E-03
Fatty acid-binding protein, epidermal	14	9	11	5	9.29E-03	1.03E-02	1.19E-02	1.39E-02
Ras GTPase-activating-like protein IQGAP1	14	9	3	6	7.37E-04	8.21E-04	2.58E-04	1.33E-03
Protein disulfide-isomerase A3	14	3	7	9	2.44E-03	9.08E-04	2.00E-03	6.59E-03
Cytosol aminopeptidase	14	0	3	0	2.49E-03	0	8.71E-04	0
14-3-3 protein theta	14	0	0	0	4.98E-03	0	0	0
Ezrin	14	0	0	0	2.02E-03	0	0	0
Creatine kinase B-type	14	7	10	0	3.24E-03	2.81E-03	3.78E-03	0

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Annexin A5	14	4	13	3	3.87E-03	1.92E-03	5.87E-03	3.48E-03
Fibrinogen gamma chain	14	5	7	7	2.68E-03	1.66E-03	2.19E-03	5.62E-03
Carbonic anhydrase 2	14	5	7	2	4.80E-03	2.97E-03	3.93E-03	2.88E-03
Clathrin heavy chain 1	13	0	2	0	6.74E-04	0	1.69E-04	0
Histone H4	13	6	5	0	1.18E-02	9.41E-03	7.39E-03	0
6-phosphogluconate dehydrogenase, decarboxylating	13	0	0	0	2.44E-03	0	0	0
Serpin B6	13	3	6	5	3.01E-03	1.20E-03	2.27E-03	4.86E-03
Leukocyte elastase inhibitor	13	9	10	0	3.01E-03	3.61E-03	3.78E-03	0
Peroxiredoxin-6	13	0	5	0	5.17E-03	0	3.25E-03	0
Transketolase	13	6	20	0	1.90E-03	1.52E-03	4.78E-03	0
Tryptophanyl-tRNA synthetase, cytoplasmic	13	0	13	0	2.44E-03	0	3.99E-03	0
Heat shock protein beta-1	13	2	6	0	5.62E-03	1.50E-03	4.24E-03	0
Lactotransferrin	13	32	36	12	1.66E-03	7.07E-03	7.51E-03	6.42E-03
LIM and cysteine-rich domains protein 1	12	0	0	0	2.91E-03	0	0	0
Microtubule-actin cross-linking factor 1, isoform 4	12	2	3	0	1.78E-04	5.15E-05	7.28E-05	0
Cytosolic non-specific dipeptidase	12	0	0	0	2.25E-03	0	0	0
Dihydropyrimidinase-related protein 3	12	13	5	0	1.93E-03	3.62E-03	1.31E-03	0
14-3-3 protein eta	12	0	0	0	4.26E-03	0	0	0
Elongation factor 1-alpha 1	12	5	6	0	2.39E-03	1.72E-03	1.95E-03	0
Phosphatidylethanolamine-binding protein 1	12	7	5	3	5.69E-03	5.75E-03	3.87E-03	5.97E-03
Tropomyosin alpha-1 chain	12	17	15	8	3.62E-03	8.88E-03	7.39E-03	1.01E-02
Bifunctional aminoacyl-tRNA synthetase	12	0	0	0	6.98E-04	0	0	0
Aldehyde dehydrogenase, mitochondrial	12	14	19	2	2.13E-03	4.31E-03	5.52E-03	1.49E-03
Prolow-density lipoprotein receptor-related protein 1	11	10	6	6	2.17E-04	3.41E-04	1.93E-04	4.96E-04
Rho GDP-dissociation inhibitor 1	11	0	2	0	4.76E-03	0	1.41E-03	0
4-trimethylaminobutyraldehyde dehydrogenase	11	5	6	0	2.03E-03	1.60E-03	1.81E-03	0
Malate dehydrogenase, cytoplasmic	11	8	9	2	3.04E-03	3.83E-03	4.07E-03	2.32E-03
Glutathione S-transferase Mu 3	11	3	2	0	4.05E-03	1.92E-03	1.20E-03	0
S-formylglutathione hydrolase	11	8	3	0	3.53E-03	4.45E-03	1.57E-03	0
Tropomyosin beta chain	11	21	16	4	3.32E-03	1.10E-02	7.89E-03	5.06E-03
Annexin A1	11	8	14	0	2.81E-03	3.54E-03	5.84E-03	0
Apolipoprotein A-I	11	0	0	0	3.53E-03	0	0	0
Ig gamma-1 chain C region	11	10	14	4	3.04E-03	4.79E-03	6.33E-03	4.64E-03
Isocitrate dehydrogenase [NADP] cytoplasmic	11	2	6	0	2.33E-03	7.34E-04	2.08E-03	0
Histone H2B type 1-K	11	3	4	0	7.82E-03	3.69E-03	4.65E-03	0
Skin-specific protein 32	10	10	5	10	3.83E-03	6.63E-03	3.13E-03	1.61E-02
Neuroblast differentiation-associated protein AHNAK	10	51	0	0	1.58E-04	1.40E-03	0	0
Alcohol dehydrogenase [NADP+]	10	7	7	0	2.69E-03	3.26E-03	3.08E-03	0
Gamma-enolase	10	0	0	0	2.12E-03	0	0	0
von Willebrand factor	10	0	0	0	3.22E-04	0	0	0

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Catalase	10	9	12	3	1.66E-03	2.59E-03	3.25E-03	2.09E-03
Fibrinogen alpha chain	10	4	6	0	1.05E-03	7.26E-04	1.03E-03	0
Ig kappa chain C region	10	8	13	0	8.29E-03	1.15E-02	1.76E-02	0
Basement membrane-specific heparan sulfate proteoglycan core protein	9	30	114	54	1.91E-04	1.10E-03	3.95E-03	4.81E-03
Histone H3.3	9	2	2	0	5.97E-03	2.30E-03	2.17E-03	0
Tropomyosin alpha-4 chain	9	17	19	0	3.09E-03	1.01E-02	1.07E-02	0
Transforming protein RhoA	9	0	0	0	4.07E-03	0	0	0
Fatty acid synthase	9	0	3	0	3.28E-04	0	1.79E-04	0
Malate dehydrogenase, mitochondrial	9	13	15	3	2.49E-03	6.23E-03	6.78E-03	3.48E-03
Peroxiredoxin-2	9	9	9	4	4.07E-03	7.05E-03	6.65E-03	7.59E-03
14-3-3 protein sigma	9	0	0	0	3.20E-03	0	0	0
Peroxiredoxin-5, mitochondrial	9	0	0	0	4.07E-03	0	0	0
Histone H2A type 1	9	4	0	0	6.40E-03	4.93E-03	0	0
Fructose-1,6-bisphosphatase 1	9	2	11	0	2.42E-03	9.32E-04	4.84E-03	0
Glucose-6-phosphate isomerase	9	7	9	0	1.42E-03	1.92E-03	2.32E-03	0
Ferritin heavy chain	9	8	5	9	4.26E-03	6.57E-03	3.87E-03	1.79E-02
Ferritin light chain	9	10	7	10	4.48E-03	8.62E-03	5.69E-03	2.09E-02
Serum amyloid P-component	9	6	11	5	3.58E-03	4.14E-03	7.16E-03	8.35E-03
Polymerase I and transcript release factor	8	8	0	0	1.85E-03	3.21E-03	0	0
Late cornified envelope protein 1C	8	8	0	0	6.63E-03	1.15E-02	0	0
Myosin light chain kinase, smooth muscle	8	0	0	0	3.77E-04	0	0	0
Nuclear mitotic apparatus protein 1	8	0	5	0	3.34E-04	0	3.42E-04	0
Spectrin beta chain, brain 1	8	50	33	3	2.89E-04	3.14E-03	1.95E-03	4.56E-04
Transitional endoplasmic reticulum ATPase	8	7	11	0	8.95E-04	1.36E-03	2.01E-03	0
Elongation factor 1-gamma	8	0	2	0	1.59E-03	0	6.51E-04	0
Cofilin-1	8	0	2	0	4.19E-03	0	1.71E-03	0
Desmin	8	15	15	0	1.47E-03	4.79E-03	4.52E-03	0
Calpain-2 catalytic subunit	8	0	3	0	9.95E-04	0	6.10E-04	0
Endoplasmin	8	2	3	0	8.65E-04	3.75E-04	5.30E-04	0
60 kDa heat shock protein, mitochondrial	8	5	6	0	1.31E-03	1.41E-03	1.60E-03	0
Cathepsin H	8	6	6	0	2.15E-03	2.80E-03	2.64E-03	0
Calpain-1 catalytic subunit	8	3	6	0	9.71E-04	6.31E-04	1.19E-03	0
Tropomyosin alpha-3 chain	8	12	13	0	2.41E-03	6.27E-03	6.41E-03	0
Hemopexin	8	2	4	2	1.53E-03	6.63E-04	1.25E-03	1.61E-03
Myoglobin	8	2	0	0	4.68E-03	2.03E-03	0	0
Ig alpha-1 chain C region	8	5	6	9	2.10E-03	2.27E-03	2.57E-03	9.89E-03
Alpha-1-antichymotrypsin	8	5	6	12	1.66E-03	1.80E-03	2.03E-03	1.04E-02
Coagulation factor XIII A chain	8	0	3	0	9.59E-04	0	5.88E-04	0
6-phosphogluconolactonase	8	0	0	0	2.84E-03	0	0	0
Proteasome activator complex subunit 2	7	0	0	0	2.58E-03	0	0	0
Ras-related protein Rab-1B	7	0	0	0	3.17E-03	0	0	0
Importin subunit beta-1	7	0	5	0	7.18E-04	0	8.38E-04	0
Lactoylglutathione lyase	7	6	2	0	3.32E-03	4.93E-03	1.55E-03	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Glutathione S-transferase omega-1	7	4	0	0	2.49E-03	2.46E-03	0	0
Ras-related protein Rab-1A	7	0	0	0	3.03E-03	0	0	0
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	7	0	0	0	1.88E-03	0	0	0
Eukaryotic initiation factor 4A-I	7	2	0	0	1.51E-03	7.50E-04	0	0
Macrophage-capping protein	7	5	6	3	1.83E-03	2.27E-03	2.57E-03	3.30E-03
Stress-induced-phosphoprotein 1	7	2	0	0	1.11E-03	5.47E-04	0	0
Protein-glutamine gamma-glutamyltransferase K	7	7	2	4	7.74E-04	1.34E-03	3.61E-04	1.86E-03
Aldose reductase	7	6	0	0	1.93E-03	2.87E-03	0	0
Elongation factor 2	7	2	6	0	7.33E-04	3.63E-04	1.03E-03	0
Alcohol dehydrogenase class-3	7	2	0	0	1.74E-03	8.62E-04	0	0
Calpain small subunit 1	7	3	2	0	2.49E-03	1.85E-03	1.16E-03	0
Ig gamma-2 chain C region	7	6	8	0	1.93E-03	2.87E-03	3.61E-03	0
Antithrombin-III	7	0	0	0	1.31E-03	0	0	0
Chloride intracellular channel protein 4	6	0	0	0	2.06E-03	0	0	0
Interleukin enhancer-binding factor 3	6	0	0	0	6.29E-04	0	0	0
Protein-glutamine gamma-glutamyltransferase E	6	3	3	4	7.75E-04	6.72E-04	6.34E-04	2.17E-03
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	6	0	0	0	1.61E-03	0	0	0
Ras-related protein Rab-11A	6	0	0	0	2.49E-03	0	0	0
Heterogeneous nuclear ribonucleoprotein K	6	3	4	0	1.17E-03	1.01E-03	1.28E-03	0
F-actin-capping protein subunit alpha-1	6	0	4	0	1.81E-03	0	1.97E-03	0
Lumican	6	6	0	4	1.57E-03	2.72E-03	0	4.40E-03
F-actin-capping protein subunit alpha-2	6	0	2	0	1.81E-03	0	9.86E-04	0
Heterogeneous nuclear ribonucleoprotein H	6	3	0	0	1.22E-03	1.06E-03	0	0
Flavin reductase	6	0	0	0	2.71E-03	0	0	0
Calreticulin	6	0	0	0	1.24E-03	0	0	0
Thymidine phosphorylase	6	0	0	0	1.19E-03	0	0	0
Protein S100-A9	6	3	6	0	4.59E-03	3.98E-03	7.51E-03	0
Myeloperoxidase	6	0	11	0	7.11E-04	0	2.13E-03	0
Napsin-A	6	0	3	0	1.33E-03	0	1.08E-03	0
WD repeat-containing protein 1	6	0	2	0	9.05E-04	0	4.93E-04	0
Glyoxylate reductase/hydroxypyruvate reductase	5	0	0	0	1.38E-03	0	0	0
EH domain-containing protein 2	5	2	0	0	8.16E-04	5.65E-04	0	0
Sialic acid synthase	5	0	0	0	1.24E-03	0	0	0
Serpin B12	5	6	4	3	1.08E-03	2.25E-03	1.41E-03	2.72E-03
Pulmonary surfactant-associated protein A2	5	8	6	12	1.91E-03	5.31E-03	3.75E-03	1.93E-02
Inorganic pyrophosphatase	5	0	0	0	1.51E-03	0	0	0
Protein disulfide-isomerase A6	5	2	6	6	1.04E-03	7.18E-04	2.03E-03	5.22E-03

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Septin-2	5	0	5	0	1.21E-03	0	1.98E-03	0
Neutral alpha-glucosidase AB	5	0	4	0	4.65E-04	0	6.08E-04	0
Heterogeneous nuclear ribonucleoprotein D0	5	3	0	0	1.31E-03	1.36E-03	0	0
Proteasome activator complex subunit 1	5	3	0	0	1.72E-03	1.78E-03	0	0
ADP-ribosylation factor 3	5	0	0	0	2.37E-03	0	0	0
Actin-related protein 2	5	0	0	0	1.11E-03	0	0	0
Proteasome subunit alpha type-6	5	5	4	0	1.84E-03	3.19E-03	2.41E-03	0
Heterogeneous nuclear ribonucleoprotein F	5	5	2	0	1.08E-03	1.87E-03	7.07E-04	0
Serpin B9	5	0	0	0	1.18E-03	0	0	0
Ubiquitin-like modifier-activating enzyme 1	5	0	6	3	4.22E-04	0	8.27E-04	1.06E-03
Protein-glutamine gamma-glutamyltransferase 2	5	0	5	0	6.46E-04	0	1.06E-03	0
Annexin A7	5	2	8	2	9.39E-04	6.51E-04	2.46E-03	1.58E-03
Nucleolin	5	5	3	4	6.46E-04	1.12E-03	6.34E-04	2.17E-03
Thioredoxin	5	4	2	4	4.15E-03	5.75E-03	2.71E-03	1.39E-02
Histone H1.4	5	0	0	0	2.26E-03	0	0	0
Ig lambda-2 chain C regions	5	3	6	2	4.52E-03	4.70E-03	8.87E-03	7.59E-03
Galectin-1	5	7	4	0	3.32E-03	8.05E-03	4.34E-03	0
Arginase-1	5	7	3	0	1.42E-03	3.45E-03	1.39E-03	0
Guanine nucleotide-binding protein G(i) subunit alpha-2	5	0	0	0	1.24E-03	0	0	0
Cystatin-B	5	4	3	0	4.52E-03	6.27E-03	4.44E-03	0
Alpha-1-acid glycoprotein 1	5	2	0	0	2.07E-03	1.44E-03	0	0
HLA class I histocompatibility antigen, A-2 alpha chain	5	0	0	2	1.21E-03	0	0	2.04E-03
Ceruloplasmin	5	2	0	3	4.08E-04	2.83E-04	0	1.03E-03
Protein diaphanous homolog 1	5	0	0	0	3.53E-04	0	0	0
Heterogeneous nuclear ribonucleoprotein Q	5	8	5	0	7.11E-04	1.97E-03	1.16E-03	0
Pyridoxal kinase	5	0	0	0	1.42E-03	0	0	0
Podocalyxin	5	4	2	0	8.43E-04	1.17E-03	5.51E-04	0
Synaptic vesicle membrane protein VAT-1 homolog	4	0	2	0	9.48E-04	0	7.75E-04	0
Gasdermin-A	4	4	0	0	8.12E-04	1.41E-03	0	0
Abhydrolase domain-containing protein 14B	4	0	0	0	1.81E-03	0	0	0
Fermitin family homolog 2	4	0	0	0	5.10E-04	0	0	0
Thioredoxin domain-containing protein 5	4	0	2	0	8.29E-04	0	6.78E-04	0
Advanced glycosylation end product-specific receptor	4	4	4	0	9.26E-04	1.60E-03	1.51E-03	0
Latent-transforming growth factor beta-binding protein 2	4	14	4	0	2.04E-04	1.24E-03	3.34E-04	0
Caldesmon	4	5	0	6	4.28E-04	9.27E-04	0	2.69E-03
Ras-related C3 botulinum toxin substrate 1	4	0	0	0	1.90E-03	0	0	0
GTP-binding nuclear protein Ran	4	0	0	0	1.66E-03	0	0	0
Ras-related protein Rap-1b	4	0	0	0	1.90E-03	0	0	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Ras-related protein Rab-14	4	0	0	0	1.66E-03	0	0	0
Cell division control protein 42 homolog	4	0	0	0	1.90E-03	0	0	0
Microfibril-associated glycoprotein 4	4	2	0	0	1.37E-03	1.19E-03	0	0
Rho GDP-dissociation inhibitor 2	4	3	2	0	1.73E-03	2.25E-03	1.41E-03	0
Seryl-tRNA synthetase, cytoplasmic	4	0	0	0	6.75E-04	0	0	0
Catenin beta-1	4	0	5	0	4.68E-04	0	9.57E-04	0
Endoplasmic reticulum resident protein 29	4	3	3	0	1.37E-03	1.78E-03	1.68E-03	0
Elongation factor 1-delta	4	0	0	0	1.28E-03	0	0	0
Serpin B3	4	0	0	0	8.85E-04	0	0	0
Polypyrimidine tract-binding protein 1	4	2	0	0	6.98E-04	6.05E-04	0	0
Proteasome subunit alpha type-4	4	3	2	0	1.37E-03	1.78E-03	1.12E-03	0
Proteasome subunit alpha type-2	4	0	0	0	1.53E-03	0	0	0
ATP synthase subunit alpha, mitochondrial	4	7	4	0	6.63E-04	2.01E-03	1.08E-03	0
Peptidyl-prolyl cis-trans isomerase B	4	4	7	0	1.66E-03	2.87E-03	4.74E-03	0
Fibulin-1	4	0	3	14	5.17E-04	0	6.34E-04	7.59E-03
cAMP-dependent protein kinase type II-alpha regulatory subunit	4	0	0	0	8.65E-04	0	0	0
Delta-aminolevulinic acid dehydratase	4	0	0	0	1.11E-03	0	0	0
X-ray repair cross-complementing protein 5	4	0	0	0	4.80E-04	0	0	0
X-ray repair cross-complementing protein 6	4	0	2	0	5.69E-04	0	4.65E-04	0
Annexin A3	4	0	5	0	1.11E-03	0	2.26E-03	0
Polyadenylate-binding protein 1	4	2	0	0	5.61E-04	4.86E-04	0	0
Glycogen phosphorylase, brain form	4	0	0	0	4.10E-04	0	0	0
Polyubiquitin-B	4	2	2	3	1.53E-03	1.33E-03	1.25E-03	4.82E-03
Annexin A4	4	0	8	0	1.11E-03	0	3.61E-03	0
Carbonic anhydrase 3	4	0	0	0	1.33E-03	0	0	0
Protein S100-A6	4	4	3	0	3.98E-03	6.90E-03	4.88E-03	0
ATP synthase subunit beta, mitochondrial	4	6	6	0	6.98E-04	1.82E-03	1.71E-03	0
Protein S100-A8	4	4	6	2	3.62E-03	6.27E-03	8.87E-03	7.59E-03
Superoxide dismutase [Mn], mitochondrial	4	5	4	3	1.59E-03	3.45E-03	2.60E-03	5.01E-03
Complement component C9	4	0	0	0	6.32E-04	0	0	0
Cystatin-A	4	4	2	0	3.62E-03	6.27E-03	2.96E-03	0
Complement factor B	4	0	0	0	4.63E-04	0	0	0
Purine nucleoside phosphorylase	4	3	3	0	1.24E-03	1.62E-03	1.52E-03	0
Superoxide dismutase [Cu-Zn]	4	3	0	5	2.49E-03	3.23E-03	0	1.30E-02
Glutamate dehydrogenase 1, mitochondrial	4	4	9	0	6.53E-04	1.13E-03	2.40E-03	0
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	4	0	0	0	1.33E-03	0	0	0
Heterogeneous nuclear ribonucleoprotein R	4	8	0	0	5.61E-04	1.94E-03	0	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Proteasome subunit alpha type-7	4	4	5	0	1.42E-03	2.46E-03	2.90E-03	0
Coronin-1C	3	6	6	0	5.63E-04	1.95E-03	1.84E-03	0
Aminopeptidase B	3	0	0	0	4.09E-04	0	0	0
Coronin-1B	3	0	0	0	5.53E-04	0	0	0
Aldose 1-epimerase	3	0	0	0	7.86E-04	0	0	0
Lipoma-preferred partner	3	0	0	0	4.52E-04	0	0	0
Thioredoxin reductase 1, cytoplasmic	3	0	0	0	4.20E-04	0	0	0
Poly(rC)-binding protein 1	3	0	2	0	8.07E-04	0	8.79E-04	0
Coactosin-like protein	3	0	0	0	1.87E-03	0	0	0
Bleomycin hydrolase	3	4	2	0	5.63E-04	1.30E-03	6.14E-04	0
Four and a half LIM domains protein 1	3	0	0	0	8.29E-04	0	0	0
Acid ceramidase	3	0	4	0	6.63E-04	0	1.45E-03	0
EGF-containing fibulin-like extracellular matrix protein 1	3	0	4	0	5.43E-04	0	1.18E-03	0
Desmocollin-1	3	5	4	2	2.99E-04	8.62E-04	6.51E-04	8.35E-04
Caveolin-1	3	0	0	0	1.49E-03	0	0	0
A-kinase anchor protein 12	3	22	0	0	1.56E-04	1.99E-03	0	0
Heterogeneous nuclear ribonucleoprotein U	3	2	2	0	3.28E-04	3.79E-04	3.57E-04	0
Mucin-5AC (Fragments)	3	0	0	0	5.66E-05	0	0	0
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	3	0	0	0	8.29E-04	0	0	0
Actin-related protein 3	3	0	0	0	6.35E-04	0	0	0
Destrin	3	0	0	0	1.57E-03	0	0	0
Myosin light polypeptide 6	3	8	6	0	1.76E-03	8.11E-03	5.74E-03	0
T-complex protein 1 subunit delta	3	0	0	0	5.15E-04	0	0	0
Hsc70-interacting protein	3	2	2	0	7.28E-04	8.41E-04	7.93E-04	0
Alpha-aminoadipic semialdehyde dehydrogenase	3	0	0	0	5.15E-04	0	0	0
Platelet-activating factor acetylhydrolase IB subunit alpha	3	0	0	0	6.35E-04	0	0	0
Aldo-keto reductase family 1 member C3	3	0	0	0	8.07E-04	0	0	0
V-type proton ATPase catalytic subunit A	3	0	0	0	4.39E-04	0	0	0
Protein S100-A11	3	3	3	2	2.49E-03	4.31E-03	4.07E-03	6.96E-03
Coronin-1A	3	6	3	0	5.85E-04	2.03E-03	9.57E-04	0
Proteasome subunit alpha type-5	3	0	2	0	1.15E-03	0	1.25E-03	0
Protein S100-A4	3	5	4	2	2.49E-03	7.18E-03	5.42E-03	6.96E-03
Proteasome subunit alpha type-3	3	2	2	0	1.07E-03	1.23E-03	1.16E-03	0
Zinc-alpha-2-glycoprotein	3	4	3	0	8.78E-04	2.03E-03	1.44E-03	0
Adenosylhomocysteinase	3	0	2	0	6.22E-04	0	6.78E-04	0
Small proline-rich protein 2E	3	4	0	3	3.73E-03	8.62E-03	0	1.57E-02
Mimecan	3	0	0	0	8.78E-04	0	0	0
Fatty acid-binding protein, adipocyte	3	2	3	0	1.99E-03	2.30E-03	3.25E-03	0
Farnesyl pyrophosphate synthase	3	0	0	0	6.22E-04	0	0	0
Translationally-controlled tumor protein	3	0	0	0	1.49E-03	0	0	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Protein disulfide-isomerase A4	3	0	3	0	4.09E-04	0	6.68E-04	0
Prolactin-inducible protein	3	2	2	2	1.76E-03	2.03E-03	1.91E-03	4.91E-03
Clusterin	3	0	0	3	5.74E-04	0	0	2.41E-03
Putative heterogeneous nuclear ribonucleoprotein A1-like 3	3	7	2	0	8.78E-04	3.55E-03	9.57E-04	0
Complement C4-A	3	0	3	0	1.55E-04	0	2.53E-04	0
Histone H1.0	3	2	4	0	1.42E-03	1.64E-03	3.10E-03	0
Fatty acid-binding protein, heart	3	2	0	0	1.99E-03	2.30E-03	0	0
Fructose-bisphosphate aldolase A	3	11	30	0	7.65E-04	4.86E-03	1.25E-02	0
Angiotensinogen	3	0	0	0	5.63E-04	0	0	0
Adenylate kinase isoenzyme 1	3	0	0	0	1.36E-03	0	0	0
NADH-cytochrome b5 reductase 3	3	0	0	0	8.78E-04	0	0	0
N-acetyl-D-glucosamine kinase	2	0	0	0	5.38E-04	0	0	0
Fibulin-5	2	0	0	3	3.98E-04	0	0	2.51E-03
Methionine adenosyltransferase 2 subunit beta	2	0	0	0	5.24E-04	0	0	0
Alpha-parvin	2	0	0	0	4.74E-04	0	0	0
Protein S100-A14	2	0	0	0	1.66E-03	0	0	0
Mucin-5B	2	3	0	0	3.34E-05	8.68E-05	0	0
Ester hydrolase C11orf54	2	2	0	0	5.69E-04	9.85E-04	0	0
Testis-expressed sequence 15 protein	2	0	0	0	6.32E-05	0	0	0
Acetyl-CoA acetyltransferase, cytosolic	2	2	0	0	4.85E-04	8.41E-04	0	0
Tubulin polymerization-promoting protein family member 3	2	0	0	0	1.05E-03	0	0	0
3-hydroxybutyrate dehydrogenase type 2	2	0	0	0	7.37E-04	0	0	0
Endoplasmic reticulum resident protein 44	2	0	3	0	4.23E-04	0	1.04E-03	0
Cell division control protein 6 homolog	2	0	0	0	3.16E-04	0	0	0
ERO1-like protein alpha	2	0	0	0	3.69E-04	0	0	0
BTB/POZ domain-containing protein KCTD12	2	2	0	0	5.53E-04	9.58E-04	0	0
EF-hand domain-containing protein D2	2	0	0	0	7.37E-04	0	0	0
Protein POF1B	2	2	2	0	2.88E-04	5.00E-04	4.71E-04	0
Programmed cell death 6-interacting protein	2	0	0	0	2.07E-04	0	0	0
Late cornified envelope protein 1D	2	0	0	0	1.81E-03	0	0	0
Hsp90 co-chaperone Cdc37	2	0	0	0	4.52E-04	0	0	0
Zyxin	2	0	0	0	3.26E-04	0	0	0
Serine/threonine-protein phosphatase 2A activator	2	0	0	0	4.85E-04	0	0	0
Inter-alpha-trypsin inhibitor heavy chain H4	2	0	0	0	1.93E-04	0	0	0
Calcyphosin	2	2	0	0	9.48E-04	1.64E-03	0	0
Plakophilin-1	2	4	7	2	2.40E-04	8.31E-04	1.37E-03	1.01E-03
Kinesin heavy chain isoform 5A	2	0	0	0	1.70E-04	0	0	0
1,4-alpha-glucan-branching enzyme	2	0	0	0	2.49E-04	0	0	0

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Receptor expression-enhancing protein 5	2	0	0	0	9.48E-04	0	0	0
Cytochrome c	2	2	3	0	1.66E-03	2.87E-03	4.07E-03	0
Dermcidin	2	3	4	5	1.81E-03	4.70E-03	5.91E-03	1.90E-02
Peptidyl-prolyl cis-trans isomerase FKBP1A	2	3	0	0	1.66E-03	4.31E-03	0	0
Epididymal secretory protein E1	2	0	0	0	1.17E-03	0	0	0
40S ribosomal protein S3a	2	0	0	0	6.63E-04	0	0	0
Neutrophil defensin 1	2	2	2	2	1.99E-03	3.45E-03	3.25E-03	8.35E-03
Puromycin-sensitive aminopeptidase	2	0	0	0	1.93E-04	0	0	0
Adenosine kinase	2	0	0	0	4.85E-04	0	0	0
Prolargin	2	3	0	0	4.52E-04	1.18E-03	0	0
Annexin A11	2	0	9	0	3.69E-04	0	2.71E-03	0
T-complex protein 1 subunit theta	2	0	0	0	3.32E-04	0	0	0
Sulfotransferase 1A1	2	0	0	0	5.85E-04	0	0	0
Proteasome subunit beta type-3	2	2	2	0	8.65E-04	1.50E-03	1.41E-03	0
Alanyl-tRNA synthetase, cytoplasmic	2	0	0	0	1.86E-04	0	0	0
Prolyl endopeptidase	2	0	0	0	2.46E-04	0	0	0
Glycogenin-1	2	0	0	0	5.10E-04	0	0	0
Adapter molecule crk	2	0	0	0	5.85E-04	0	0	0
3,2-trans-enoyl-CoA isomerase, mitochondrial	2	2	2	0	6.03E-04	1.05E-03	9.86E-04	0
Caspase-14	2	3	0	2	7.11E-04	1.85E-03	0	2.98E-03
S-adenosylmethionine synthase isoform type-2	2	0	0	0	4.52E-04	0	0	0
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2	0	0	0	3.06E-04	0	0	0
Thioredoxin-dependent peroxide reductase, mitochondrial	2	4	3	0	7.11E-04	2.46E-03	1.74E-03	0
Inositol monophosphatase 1	2	0	0	0	6.63E-04	0	0	0
Proteasome subunit beta type-5	2	0	0	0	7.11E-04	0	0	0
Proteasome subunit beta type-6	2	2	0	0	7.96E-04	1.38E-03	0	0
40S ribosomal protein S3	2	0	0	0	7.37E-04	0	0	0
Inter-alpha-trypsin inhibitor heavy chain H2	2	0	0	0	1.88E-04	0	0	0
Aspartate aminotransferase, cytoplasmic	2	0	0	0	4.33E-04	0	0	0
Mucin-1	2	2	2	3	1.63E-04	2.83E-04	2.67E-04	1.03E-03
Nucleoside diphosphate kinase A	2	0	2	0	1.17E-03	0	1.91E-03	0
Heterogeneous nuclear ribonucleoprotein L	2	0	0	0	3.11E-04	0	0	0
Macrophage migration inhibitory factor	2	0	0	0	1.66E-03	0	0	0
Xaa-Pro dipeptidase	2	4	0	0	3.62E-04	1.25E-03	0	0
Uteroglobin	2	0	0	0	1.99E-03	0	0	0
cAMP-dependent protein kinase type I-alpha regulatory subunit	2	0	0	0	4.63E-04	0	0	0
60 kDa SS-A/Ro ribonucleoprotein	2	4	0	0	3.26E-04	1.13E-03	0	0

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
40S ribosomal protein SA	2	2	0	0	6.03E-04	1.05E-03	0	0
Annexin A6 OS=Homo sapiens	2	0	2	0	2.62E-04	0	4.28E-04	0
Pulmonary surfactant-associated protein B	2	0	0	0	4.74E-04	0	0	0
Cathepsin B	2	0	0	0	5.24E-04	0	0	0
Creatine kinase M-type	2	2	0	0	4.63E-04	8.02E-04	0	0
Lupus La protein	2	2	0	0	4.23E-04	7.34E-04	0	0
Fructose-bisphosphate aldolase B	2	0	3	0	5.10E-04	0	1.25E-03	0
Histidine-rich glycoprotein	2	0	0	0	3.32E-04	0	0	0
Transthyretin	2	0	0	0	1.24E-03	0	0	0
Retinol-binding protein 4	2	0	0	0	8.65E-04	0	0	0
Kininogen-1	2	0	0	0	2.76E-04	0	0	0
Argininosuccinate synthase	2	2	0	0	4.23E-04	7.34E-04	0	0
3'(2'),5'-bisphosphate nucleotidase 1	2	0	0	0	6.03E-04	0	0	0
Serum deprivation-response protein	2	0	0	0	4.23E-04	0	0	0
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	2	3	2	0	6.42E-04	1.67E-03	1.05E-03	0
Acyl-protein thioesterase 1	2	0	0	0	7.96E-04	0	0	0
Aflatoxin B1 aldehyde reductase member 2	2	0	0	0	4.98E-04	0	0	0
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	2	0	0	0	2.19E-04	0	0	0
Actin-related protein 2/3 complex subunit 3	2	0	0	0	9.48E-04	0	0	0
Actin-related protein 2/3 complex subunit 2	2	0	0	0	5.85E-04	0	0	0
Late cornified envelope protein 2B	2	3	0	0	1.81E-03	4.70E-03	0	0
Zinc finger protein 734	2	0	0	0	3.06E-04	0	0	0
EMILIN-1	0	0	0	7	0	0	0	2.73E-03
Proliferation-associated protein 2G4	0	3	3	0	0	1.18E-03	1.11E-03	0
Coiled-coil domain-containing protein 19, mitochondrial	0	2	0	0	0	5.23E-04	0	0
Prenylcysteine oxidase 1	0	0	2	0	0	0	5.71E-04	0
Ribosome-binding protein 1	0	0	0	2	0	0	0	5.49E-04
Calmodulin-like protein 5	0	3	8	0	0	3.23E-03	8.13E-03	0
Septin-11	0	2	3	0	0	7.04E-04	9.96E-04	0
Aconitate hydratase, mitochondrial	0	0	2	0	0	0	3.83E-04	0
Collagen alpha-1(XII) chain	0	0	2	0	0	0	9.77E-05	0
Leucine-rich repeat-containing protein 15	0	0	19	0	0	0	4.83E-03	0
Target of Nesh-SH3	0	3	0	0	0	4.35E-04	0	0
Membrane primary amine oxidase	0	0	5	2	0	0	9.57E-04	9.82E-04
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0	2	3	0	0	1.01E-03	1.44E-03	0
2,4-dienoyl-CoA reductase, mitochondrial	0	2	5	0	0	9.58E-04	2.26E-03	0
Laminin subunit alpha-4	0	6	6	0	0	5.10E-04	4.81E-04	0
Transforming growth factor-beta-induced protein ig-h3	0	0	3	0	0	0	6.51E-04	0

Identified Proteins	Number of Peptides				Peptide abundance			
	Triton X	Deoxycholate	NaCl	DNAse	Triton X	Deoxycholate	NaCl	DNAse
Phosphoglucomutase-like protein 5	0	0	2	0	0	0	5.25E-04	0
Periostin	0	0	3	0	0	0	5.25E-04	0
Latent-transforming growth factor beta-binding protein 1	0	0	0	10	0	0	0	2.23E-03
Major vault protein	0	0	7	2	0	0	1.15E-03	8.44E-04
Filamin-C	0	0	0	37	0	0	0	5.31E-03
Collagen alpha-1(XIV) chain	0	0	9	0	0	0	7.55E-04	0
Lamin-B2	0	9	4	4	0	2.28E-03	9.57E-04	2.46E-03
2-oxoglutarate dehydrogenase, mitochondrial	0	0	2	0	0	0	2.80E-04	0
Neutrophil gelatinase-associated lipocalin	0	4	0	0	0	3.00E-03	0	0
60S ribosomal protein L11	0	2	0	0	0	1.72E-03	0	0
Small nuclear ribonucleoprotein Sm D3	0	2	2	0	0	2.46E-03	2.32E-03	0
Calmodulin	0	3	0	0	0	3.04E-03	0	0
Lysozyme C	0	2	6	0	0	2.03E-03	5.74E-03	0
10 kDa heat shock protein, mitochondrial	0	2	0	0	0	3.14E-03	0	0
Cadherin-13	0	0	0	2	0	0	0	1.07E-03
Adenylate kinase 2, mitochondrial	0	2	0	0	0	1.33E-03	0	0
Heterogeneous nuclear ribonucleoprotein A3	0	4	0	0	0	1.72E-03	0	0
Peroxisomal multifunctional enzyme type 2	0	0	3	0	0	0	6.10E-04	0
Basal cell adhesion molecule	0	0	3	3	0	0	7.28E-04	1.87E-03
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0	0	3	0	0	0	6.97E-04	0
Nestin	0	6	3	0	0	5.85E-04	2.76E-04	0
Glutathione synthetase	0	0	2	0	0	0	6.26E-04	0
Galectin-7	0	3	6	0	0	3.45E-03	6.51E-03	0
Histidine ammonia-lyase	0	2	0	0	0	4.72E-04	0	0
Trifunctional enzyme subunit alpha, mitochondrial	0	0	10	0	0	0	1.96E-03	0
Collagen alpha-1(XVIII) chain	0	2	5	0	0	1.94E-04	4.57E-04	0
Collagen alpha-1(XV) chain	0	0	2	0	0	0	2.29E-04	0
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	0	4	3	0	0	1.41E-03	9.96E-04	0
Fibrillin-1	0	0	0	69	0	0	0	9.23E-03
Long-chain-fatty-acid--CoA ligase 1	0	0	2	0	0	0	4.17E-04	0
Carbamoyl-phosphate synthase [ammonia], mitochondrial	0	5	2	0	0	5.23E-04	1.97E-04	0
HLA class I histocompatibility antigen, B-13 alpha chain	0	0	2	0	0	0	8.13E-04	0
60S ribosomal protein L12	0	0	2	0	0	0	1.81E-03	0
Calmodulin-like protein 3	0	0	2	0	0	0	1.91E-03	0
Myosin regulatory light polypeptide 9	0	2	0	0	0	1.72E-03	0	0
Myeloblastin	0	0	2	0	0	0	1.16E-03	0

Identified Proteins	**Number of Peptides**				**Peptide abundance**			
	Triton X	**Deoxycholate**	**NaCl**	**DNAse**	**Triton X**	**Deoxycholate**	**NaCl**	**DNAse**
Heterogeneous nuclear ribonucleoproteins A2/B1	0	8	0	0	0	3.73E-03	0	0
Non-specific lipid-transfer protein	0	2	0	0	0	5.85E-04	0	0
Tenascin-X	0	2	16	6	0	7.43E-05	5.61E-04	5.40E-04
Biglycan	0	6	4	0	0	2.46E-03	1.55E-03	0
Voltage-dependent anion-selective channel protein 1	0	0	2	0	0	0	1.05E-03	0
Lamin-B1	0	6	2	0	0	1.57E-03	4.93E-04	0
Tryptase beta-2	0	2	5	0	0	1.11E-03	2.62E-03	0
NADPH--cytochrome P450 reductase	0	0	2	0	0	0	4.22E-04	0
Aggrecan core protein	0	3	3	2	0	2.07E-04	1.95E-04	3.34E-04
CD44 antigen	0	0	2	0	0	0	3.97E-04	0
Pyruvate kinase isozymes M1/M2	0	4	7	0	0	1.19E-03	1.96E-03	0
Nidogen-1	0	0	0	14	0	0	0	4.30E-03
Glucosidase 2 subunit beta	0	2	2	0	0	5.85E-04	5.51E-04	0
Versican core protein	0	2	3	0	0	9.25E-05	1.31E-04	0
Nucleoprotein TPR	0	0	3	0	0	0	1.83E-04	0
Collagen alpha-3(VI) chain	0	7	58	43	0	3.51E-04	2.74E-03	5.22E-03
Laminin subunit gamma-1	0	13	11	21	0	1.26E-03	1.01E-03	4.93E-03
Lysosomal alpha-glucosidase	0	3	0	0	0	4.93E-04	0	0
Fructose-bisphosphate aldolase C	0	0	7	0	0	0	2.92E-03	0
Dihydrolipoyl dehydrogenase, mitochondrial	0	6	4	0	0	1.92E-03	1.20E-03	0
Dihydropteridine reductase	0	3	0	0	0	1.99E-03	0	0
Collagen alpha-2(IV) chain	0	0	0	6	0	0	0	1.49E-03
Complement decay-accelerating factor	0	0	0	2	0	0	0	2.04E-03
Laminin subunit beta-1	0	3	4	0	0	2.61E-04	3.29E-04	0
Decorin	0	4	9	0	0	1.72E-03	3.66E-03	0
Trypsin-1	0	0	2	2	0	0	1.20E-03	3.09E-03
Acyl-CoA-binding protein	0	2	0	0	0	3.45E-03	0	0
Epoxide hydrolase 1	0	0	2	0	0	0	6.14E-04	0
60S acidic ribosomal protein P0	0	2	0	0	0	1.01E-03	0	0
Alpha-1B-glycoprotein	0	0	0	2	0	0	0	1.55E-03
Fibronectin	0	0	10	20	0	0	6.18E-04	3.18E-03
Beta-2-glycoprotein 1	0	0	2	0	0	0	8.56E-04	0
Prelamin-A/C	0	27	46	6	0	6.29E-03	1.01E-02	3.39E-03
Ig gamma-3 chain C region	0	0	8	0	0	0	3.17E-03	0
Aspartate aminotransferase, mitochondrial	0	9	10	0	0	3.23E-03	3.39E-03	0
Peptidoglycan recognition protein 1	0	0	0	3	0	0	0	5.69E-03
Citrate synthase, mitochondrial	0	0	3	0	0	0	9.38E-04	0
Protein CutA	0	0	0	2	0	0	0	4.40E-03
Periplakin	0	2	4	0	0	1.68E-04	3.17E-04	0
Laminin subunit alpha-5	0	0	0	5	0	0	0	5.22E-04
Agrin	0	37	74	15	0	2.97E-03	5.60E-03	2.91E-03
Putative high mobility group protein B1-like 1	0	2	0	0	0	1.44E-03	0	0

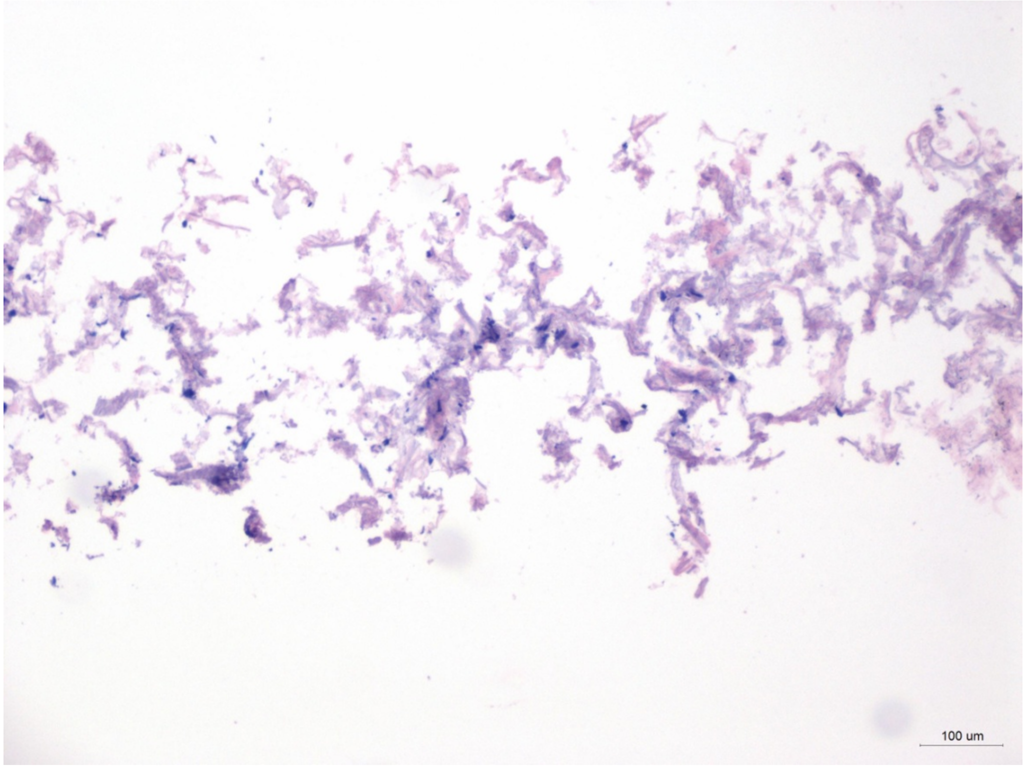
Table E2. Relative abundance of matrisome-associated proteins in decellularized lung matrix (DLM) compared to paired native lung (LUNG). By mass spectrometry. In general, DLM was highly enriched for most structural proteins. Very few proteins were lower in abundance following decellularization.

Identified Proteins	**Fold Change (DLM/LUNG)**
Microfibrillar-associated protein 2	18.99
Metalloproteinase inhibitor 3	17.29
Asporin	16.16
Microfibrillar-associated protein 5	15.42
Collagen alpha-1(VII) chain	14.68
Collagen alpha-6(VI) chain	9.93
Dermatopontin	8.94
Collagen alpha-1(VI) chain	7.31
Fibrillin-1	7.07
Collagen alpha-2(VI) chain	5.84
Nephronectin	5.52
Laminin subunit alpha-5	5.32
Collagen alpha-2(IV) chain	4.95
Transforming growth factor-beta-induced protein ig-h3	4.57
Mimecan	4.21
Collagen alpha-1(IV) chain	3.80
Fibulin-5	3.56
EGF-containing fibulin-like extracellular matrix protein 1	3.55
Laminin subunit beta-2	3.53
Protein AMBP	2.82
Collagen alpha-3(VI) chain	2.52
Fibrinogen beta chain	2.48
Fibromodulin	2.29
Nidogen-1	2.12
Laminin subunit gamma-1	2.04
Collagen alpha-1(III) chain	1.98
EMILIN-1	1.97
Microfibril-associated glycoprotein 4	1.96
Fibulin-2	1.76
Tenascin	1.72
Vitronectin	1.65
Fibrinogen gamma chain	1.52
Fibrinogen alpha chain	1.50
Nidogen-2	1.39
Collagen alpha-2(I) chain	1.37
Aggrecan core protein	1.37
Collagen alpha-1(XII) chain	1.32
Decorin	1.30
Periostin	1.29
Laminin subunit alpha-4	1.12

Annexin A7	1.09
Basement membrane-specific heparan sulfate proteoglycan core protein	1.08
Laminin subunit beta-1	0.98
Versican core protein	0.90
Collagen alpha-1(I) chain	0.88
Fibronectin	0.78
Hyaluronan and proteoglycan link protein 1	0.77
Deleted in malignant brain tumors 1 protein	0.61
Annexin A6	0.60
Biglycan	0.57
Annexin A2	0.55
Prolargin	0.53
Fibulin-1	0.53
Collagen alpha-1(XIV) chain	0.51
Annexin A11	0.47
Alpha-1-antichymotrypsin	0.45
Annexin A4	0.40
Latent-transforming growth factor beta-binding protein 4	0.39
Collagen alpha-1(XVIII) chain	0.38
Matrix metalloproteinase-9	0.33
Annexin A5	0.31
Thrombospondin-1	0.30
Inter-alpha-trypsin inhibitor heavy chain H4	0.29
Neutrophil elastase	0.27
Leukocyte elastase inhibitor	0.26
Tenascin-X	0.23
Lumican	0.22
Alpha-1-antitrypsin	0.22
Collagen alpha-1(XV) chain	0.16
Laminin subunit alpha-2	0.15
Annexin A1	0.08
Agrin	0.07
Inter-alpha-trypsin inhibitor heavy chain H2	0.04
Latent-transforming growth factor beta-binding protein 2	0.03
Elastin	-
Matrix metalloproteinase-23	-
Matrix Gla protein	-
EGF-containing fibulin-like extracellular matrix protein 2	-
Collagen alpha-1(VIII) chain	-
Plasminogen	-
Fibrillin-2	-
Collagen alpha-1(X) chain	-
Laminin subunit beta-3	-

Laminin subunit gamma-2	-
Extracellular matrix protein 1	-
Laminin subunit alpha-3	-
Latent-transforming growth factor beta-binding protein 1	-
Tubulointerstitial nephritis antigen-like	-
Collagen alpha-5(VI) chain	-
Disintegrin and metalloproteinase domain-containing protein 10	0.00
Metalloproteinase inhibitor 1	0.00
Collagen alpha-1(II) chain	0.00
Annexin A3	0.00
Inter-alpha-trypsin inhibitor heavy chain H1	0.00
Cartilage matrix protein	0.00
Serpin H1	0.00
SPARC-like protein 1	0.00
Chondroitin sulfate proteoglycan 4	0.00

Figure E1.



SUPPLEMENTAL FIGURE LEGEND

Figure E1. H&E stained vertical section of an acellular lung matrix slice 48 hours after fibroblast seeding. Hematoxylin-stained nuclei can be seen in the center portion of the slice, indicating the fibroblasts migrated through the matrix. 10x magnification.

REFERENCES

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