

Supplementary Figure Legends

Supplementary Figure 1: Chromatographic profile of QconCAT peptides

eQ1 & eQ2: Chromatogram of SRM transitions with corresponding peptide labeled with gene name in the QconCAT protein sequence below.

Supplementary Table 1: Global proteomics of Native and Decellularized Lungs

LC-MS/MS results of two native and two decellularized lungs. Each lung was processed into five fractions as outlined in Figure 1. Each fraction was run in analytical triplicate with the normalized values reported as peptide spectral matches, number of unique peptides, percent protein coverage, and total ion current. Protein level comparison are made between fractions using PSM results.

Supplementary Table 2: SRM parameters for QconCAT peptides

QconCAT peptides with gene name, retention time, Precursor ion, and corresponding transitions and optimized collision energy. Species specificity is included for each peptide. A note was included for those standard peptides that do not meet quality control criteria.

Supplementary Table 3: Absolute quantification of forty-nine cellular and ECM proteins in Native and Decellularized Lung

Quantitative analysis of lung tissue for both native and decellularized lungs. Total μg quantities for proteins are representative of the left lobe of a single lung, and normalized to the average dry weight of Native (58.1 μg s) and Decellularized (20.1 μg s)

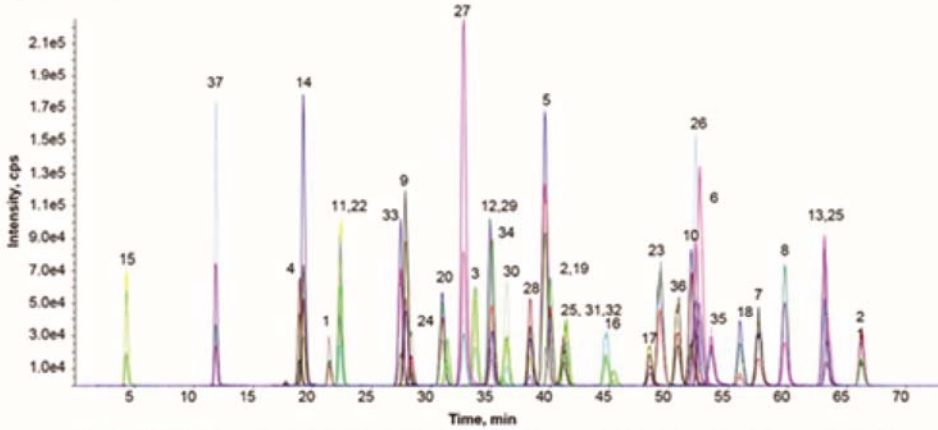
* Two different QconCAT peptides were used to quantify the protein.

[†] One of the two QconCAT peptides representing the protein of interest did not meet QC specs due to ion suppression.

‡ Standard Error of the Mean calculated with an n=6 for peptides (Biological duplicate, Technical Triplicate), with the exception of those with two QconCAT peptides, where n=12 (Biological duplicate, Technical duplicate for number of reporter peptides representing a single protein, Technical triplicate at the instrument level).

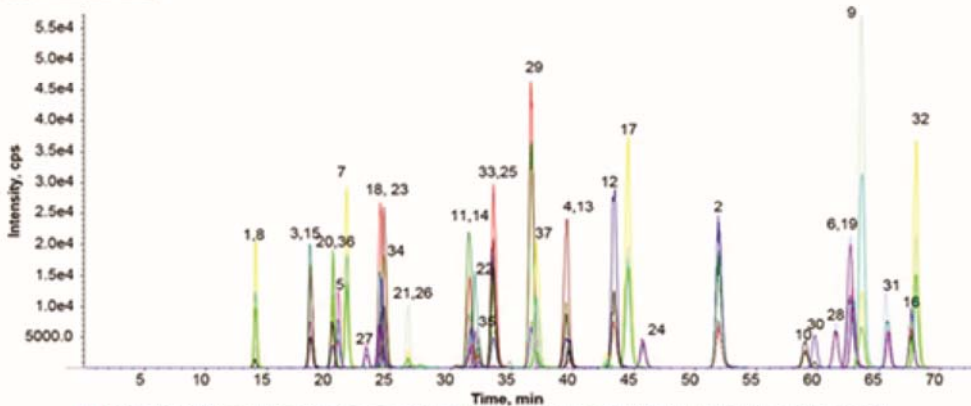
Supplemental Figure 1

eQ1: 43,900 Da



MKEGHHHHHGRQLAEEDLAQRDLYLENPEIKYALSNSIGPVRSGYEFADDRSTFDLLRLTAFGGFLKDDAWDLLRD
 PLEC TGM2 NID1 NID2 LAMA1 LAMA1 LAMA2
 1 2 3 4 5 6 7
 LADLAAYTALKISGVIGPYRLQLLEDLERAAQLDGLLEARALVEGGGILSRLSAEDLVLEGAGLRGFSGLDGAKGPAGPQ
 LAMA5 LAMB1 LAMB1 LAMB2 LAMB2 LAMC1 COL1A1 COL1A1
 8 9 10 11 12 13 14 15
 GPREMATQLAFMRILYHGYSLLYVQGNERSVSIgyLLVklQDLYSIVRVIVVITDGRlTLyTLLEGRGYILQEDGRlle
 COL2A1 COL4A1 COL4A2 COL18A1 COL14A1 COL7A1 FBN1 LAMA5
 16 17 18 19 20 21 22 23
 IVQAVSRGFVYKPDlKGYILQEDGRLEILEELVKYELGSGlAVLREAlVTDLPGRTPVLSAETFTGKGPSSGLLYNGQ
 FBN1 FBN1 TNXB HSPG2 TNXB TNC AGRN
 24 22 25 26 27 28 29
 KIALVITDGRNFVINVNRVAVVITDGRALEFVARLSQYLGTIAERDIDDELTlAKDLSSVQTLlTKYVVDTSKGRGRPGP
 COL6A1 COL6A2 COL6A2 COL6A3 COL6A5 MYH SPT ADH_Y
 30 31 32 33 34 35 36 37

eQ2: 47,942 Da



MKAGFAGDDAPRYLTVAAVFRtSGGAGlGSlRPTGLQYLNNANTFISpQRAAAITSDLESIGRFADLSEA
 ACTA1 TUBB DES LUM MGP POSTN VIM
 1 2 3 4 5 6 7
 ANRINQTYQQYGRASGIELFAIGVGRQGEALNlLETGYSRAGHIYVSGSAPSFPRYALlGYNAAYNRTSYTAVSLYS
 ANXA4 MATN ECM1 VTN MGP DCN
 8 9 10 11 12 13
 NPVrvGIVFTDGRSAyLARGVDEVTlVNIlTNRlQDLYSIVRGDSLAYGLRlDQPFtIlFRlSQNLlSRSLYSSSPGG
 MATN OGN ANXA2 COL18A1 SPP1 FBN5 PRELP VIM
 14 15 16 17 18 19 20 21
 AYVTRGInQQVWlGGRAgNTQGDfYIRDLlTVDSRYFESVLDRCsNNGlVAGFQSRNGAIHlFRDFPNlAFIRlDTV
 PRG2 EFEMP2 EMP1 DPT DPT POSTN PRELP EMILIN1
 22 23 24 25 26 27 28 29
 AGGLQGLRGLLVEPAANSYLLAERGLlGTlNNDNPEDDFTlRlQAlELEDlLRTGYYFDGI SRHLQlAlRVAVNDVHLLQ
 TG2 SUSD2 BGN FBN1 H2A LGALS3
 30 31 32 33 34 35
 YNHRGYSPTTtAERlSIVGSYVGNRGSEFELVDKlAAALEHHHHHHH
 ACTB ADH_Y
 36 37