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 ran 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 (58.1µgs) and Decellularized (20.1µgs)

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

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

[Ŧ] 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