**Title:** The proteomic response is linked to regional lung volumes in ventilator-induced lung injury

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**Supplementary Figure 1 – Regional variation in lung volumes:** Regional sVt andsEEV were compared among 10 lung regions at baseline (T0) in the animals treated with saline (A and B) or acid (C and D). Values are Mean (SD). \**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001, compared with R4. n = 7 per group. sVt: specific tidal volume; sEEV: specific end-expiratory volume.

**Supplementary Figure 2 – Regional variation in protein expression:** Heat map (A) of proteomic profiling shows the baseline protein (n = 1943) expression of 10 lung regions (n = 7 per subgroup) in the Saline/FB (control) group. Red indicates high expression of protein, and green indicates relatively low expression of the protein. Protein expression was grouped using principal component analysis and clustered based on the regional difference (B).

**Supplementary Figure 3 – Protein abundance rank from proteomics:** The graph shows the number of identified proteins (x-axis) versus their label-free quantification (LFQ) intensity values (y-axis).

**Supplementary Figure 4 - Protein interaction network generated using STRING software:** Protein–protein interaction regulatory network was established using the differentially expressed proteins identified in the Acid/MV group. Two major protein clusters are shown in the dotted rectangles. CCC: complement and coagulation cascades; MRC: mitochondrial respiratory chain**.**

**Supplementary Figure 5 – Correlation of the differentially expressed proteins belonging to the same pathway:** The correlation matrices show the correlations amongst the three groups of proteins: overlapping CCC proteins (A), unique CCC proteins (B) and MRC proteins (C). The colour in the cell corresponds to the correlation coefficients on the x-axis. CCC: complement and coagulation cascades; MRC: mitochondrial respiratory chain**.** *p* < 0.001 for all correlations.