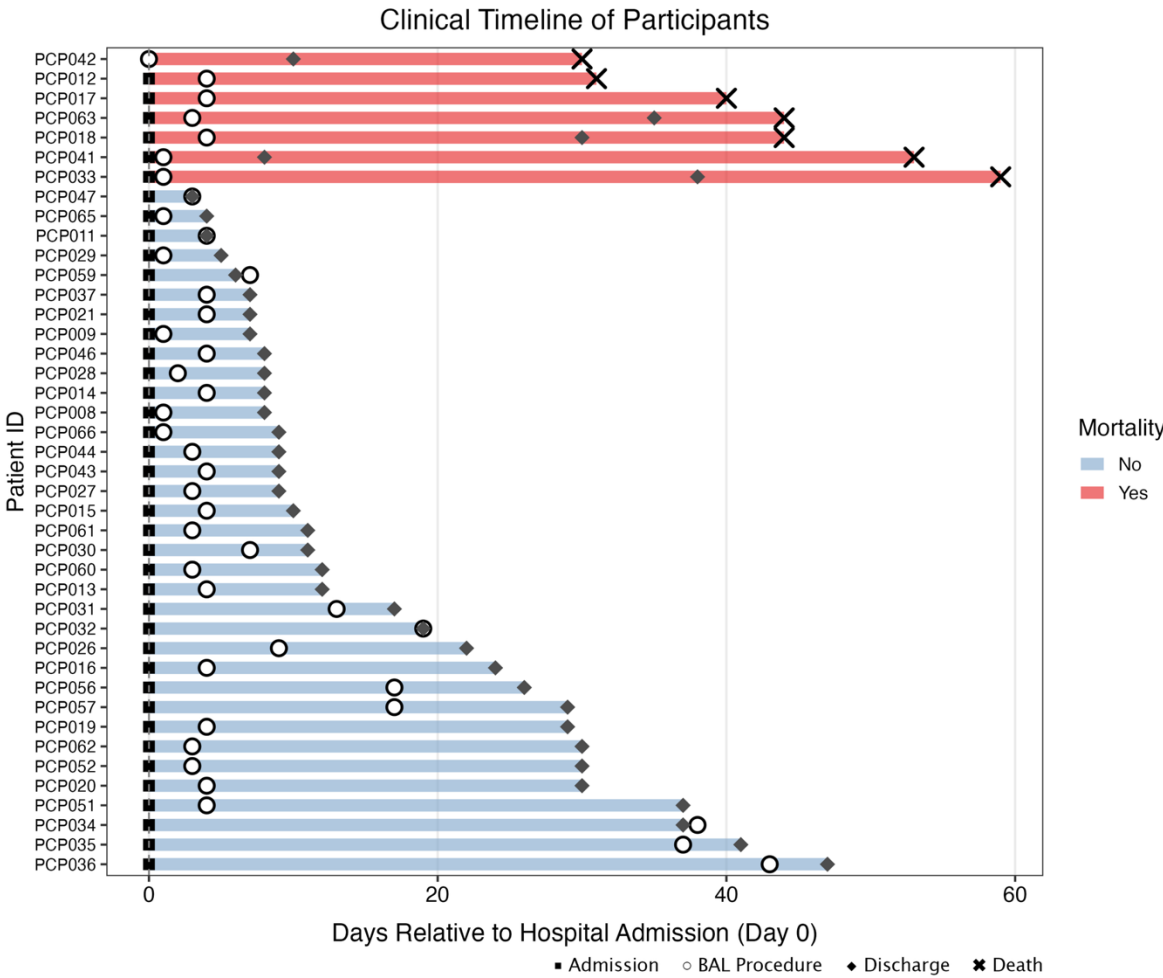
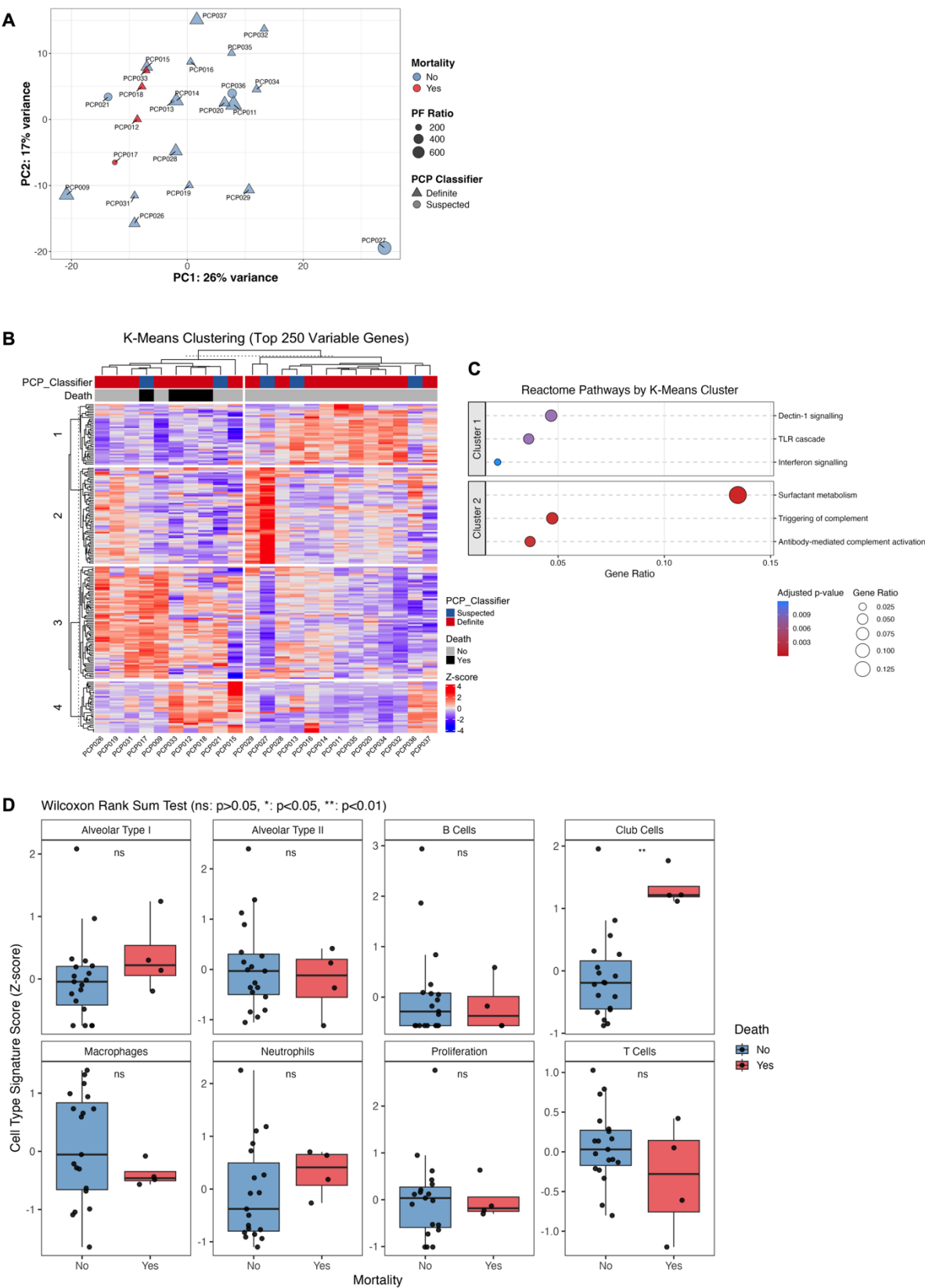


Supplemental Figure 1



Supplemental Figure 1. Clinical timelines of study participants. Swimmer plot detailing the temporal clinical course of the 42 participants enrolled in the study. The x-axis represents the number of days relative to hospital admission (Day 0). Each horizontal bar represents an individual patient, with blue indicating survival and red indicating death within the follow-up period. Markers denote the timing of specific clinical events: hospital admission (black squares), the diagnostic bronchoalveolar lavage (BAL) procedure (white circles), death (black crosses), and hospital discharge (black diamonds).

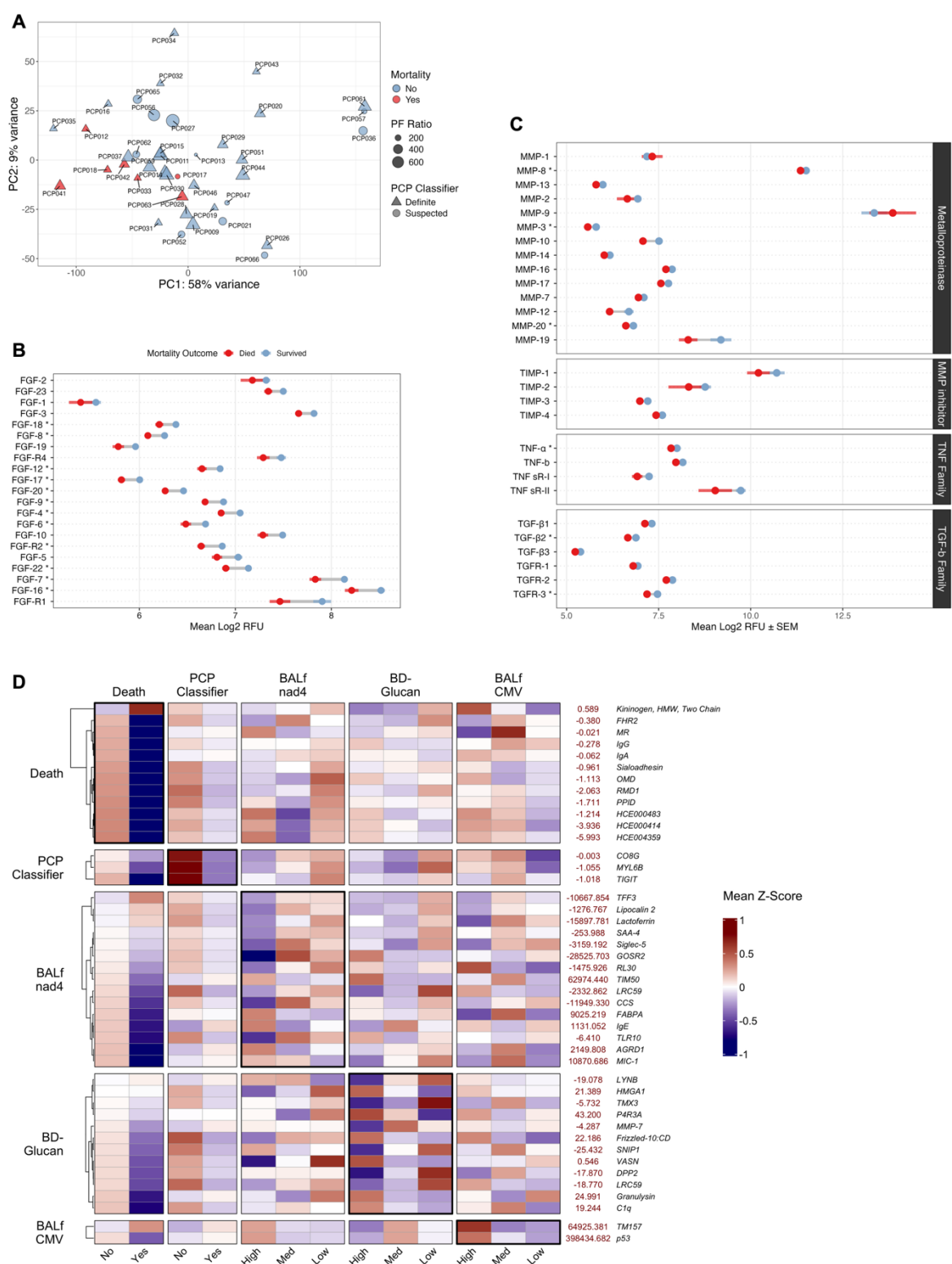
Supplemental Figure 2



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Supplemental Figure 2. Unsupervised clustering and cell type deconvolution of the alveolar microenvironment. **(A)** Principal component analysis of the global BAL fluid transcriptome from 24 participants, plotted by mortality (blue = survived, red = died) and PCP classifier (triangle: definite; circle: suspected). Point size is scaled to the patient's PaO₂/FiO₂ (P/F) ratio. **(B)** K-means clustering heatmap of the top 250 most variable genes (Z-score transformed). **(C)** Reactome pathway enrichment for the gene clusters identified in **B**, highlighting pathways significantly associated with Clusters 3 and 4. **(D)** Estimated relative abundance (Z-score) of specific structural and immune cell populations in BALf, derived from bulk RNA-Seq cell type deconvolution. Statistical significance for **D** was evaluated using the Wilcoxon rank-sum test (ns: non-significant; * p≤0.05; ** p≤0.01).

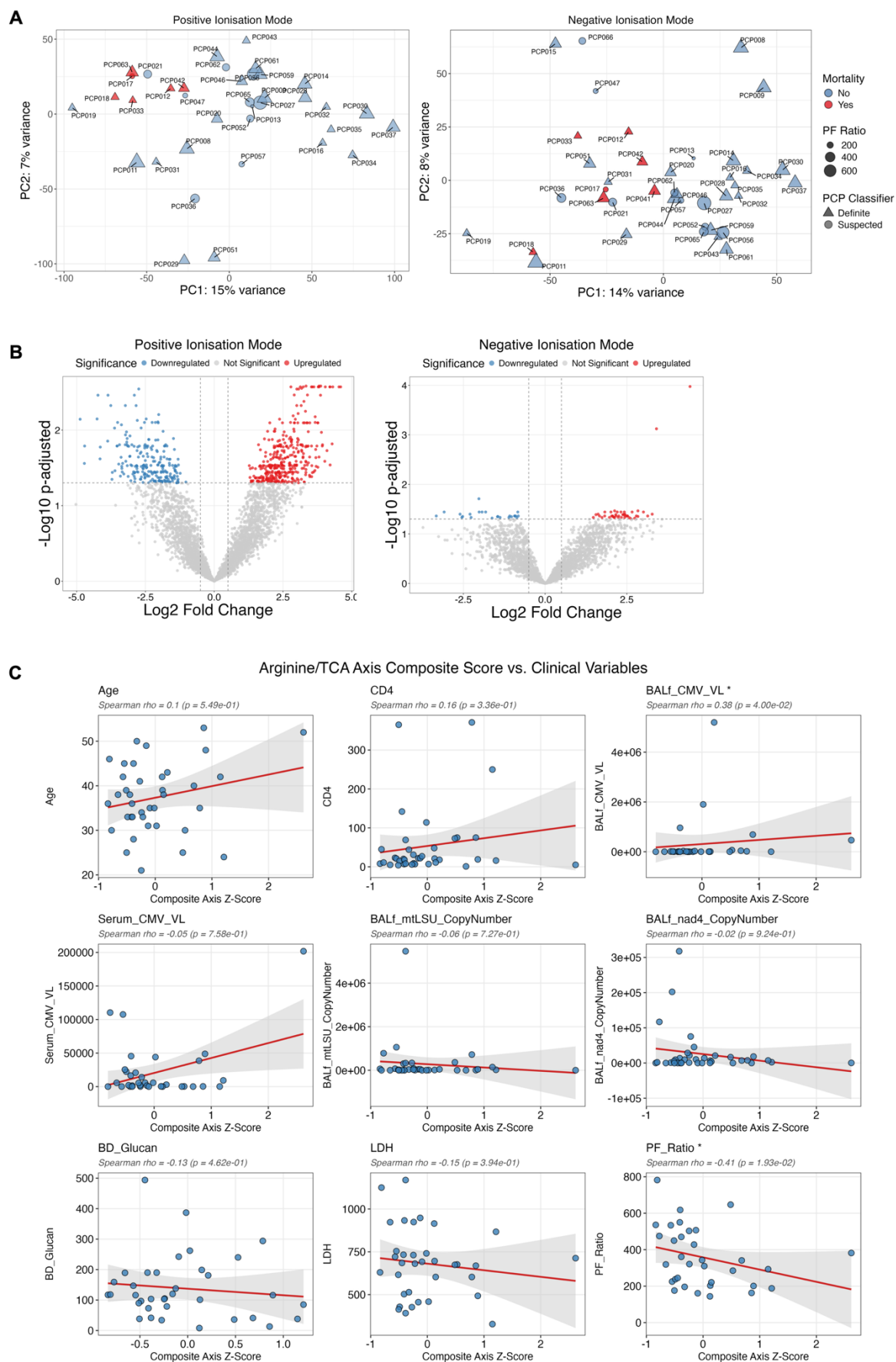
Supplemental Figure 3



Supplemental Figure 3. Proteomic markers of alveolar repair and predictive multi-trait Lasso regression. (A) Principal component analysis of the global BAL fluid proteome, with point size scaled

to the patient's PaO₂/FiO₂ (P/F) ratio. **(B-C)** Dumbbell plots displaying the mean log₂ RFU (± SEM) of **(B)** Fibroblast Growth Factor (FGF) family members and **(C)** extracellular matrix regulators, including metalloproteinases and the TNF/TGF-β families, comparing survivors (blue) to non-survivors (red). **(D)** Heatmap of predictive hub proteins identified via cross-validated multi-trait Lasso regression. Continuous clinical traits were binned into statistical tertiles (High, Med, Low) to visualise dose-dependent trajectories. Colour intensity represents the mean row-scaled Z-score of the extracted proteins.

Supplemental Figure 4



Supplemental Figure 4. Metabolomic quality control and clinical correlation analysis. (A)

Principal component analysis of polar metabolites detected in positive and negative ionisation modes.

Point size is scaled to the patient's $\text{PaO}_2/\text{FiO}_2$ (P/F) ratio. **(B)** Volcano plots demonstrating

differentially abundant metabolic features following Benjamini-Hochberg FDR correction. Red

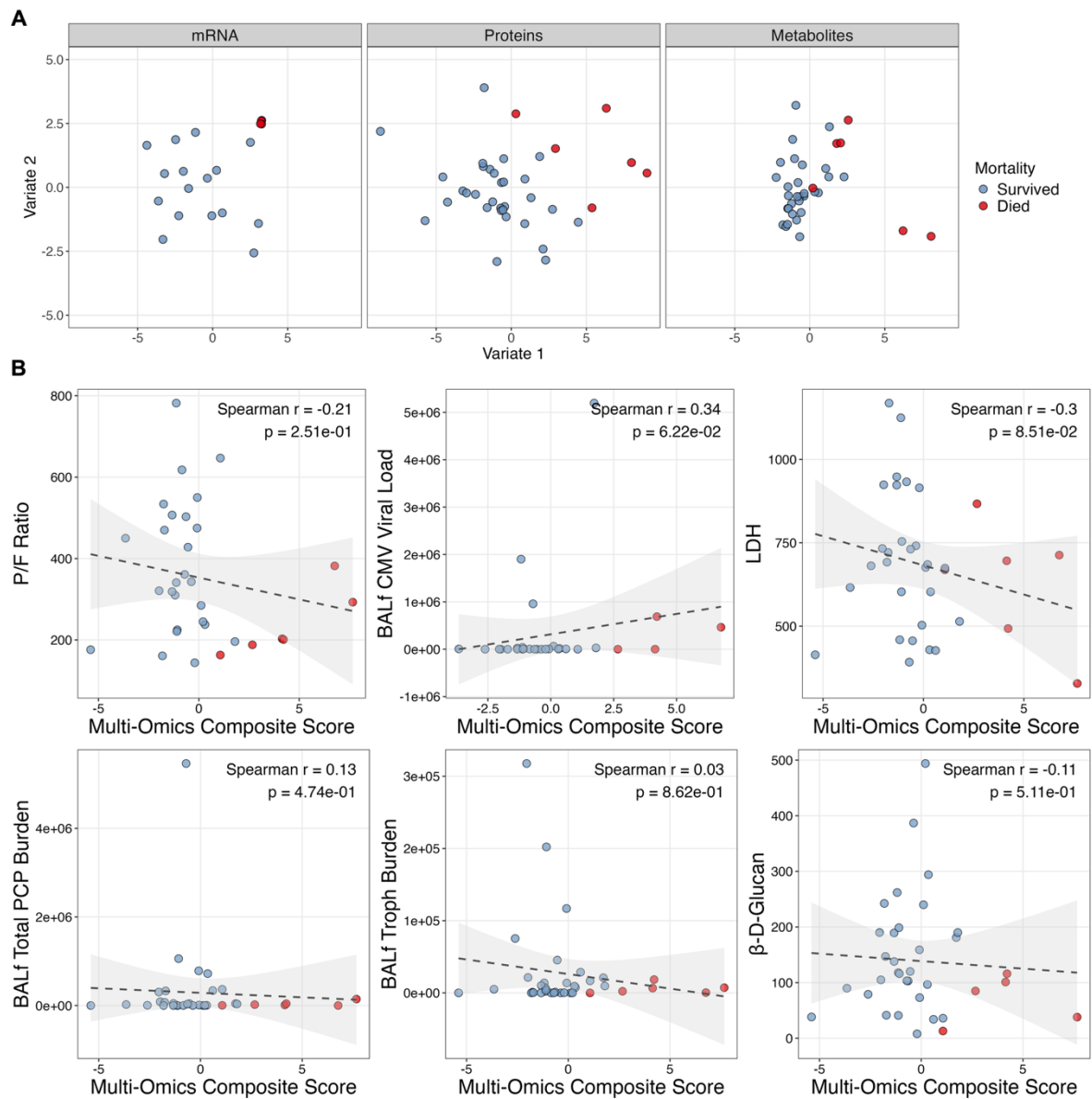
indicates significantly upregulated features; blue indicates significantly downregulated features. **(C)**

Spearman rank correlation analysis between the composite Arginine/TCA axis Z-score and

continuous clinical variables. A significant inverse correlation is observed between the composite

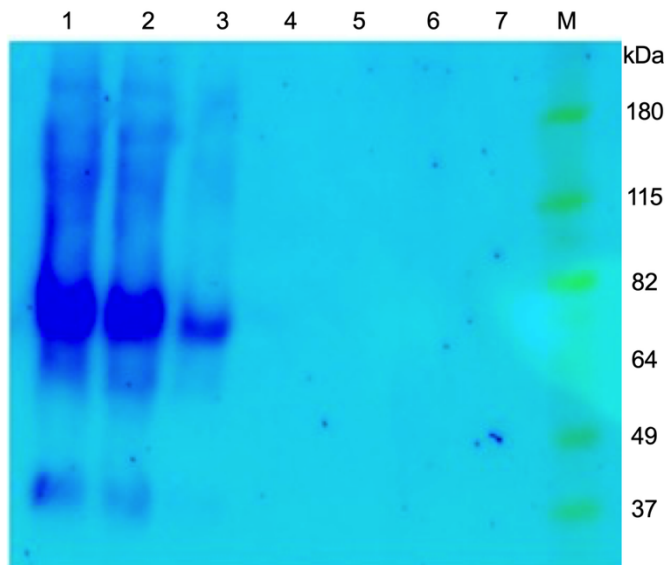
metabolic score and the P/F ratio.

Supplemental Figure 5



Supplemental Figure 5. Multi-omics class separation and clinical correlations. (A) DIABLO sample projection scatter plots of latent variates (Component 1 vs Component 2) demonstrating class separation between survivors (blue) and non-survivors (red) across the mRNA, protein, and metabolite blocks. **(B)** Spearman rank correlation analysis evaluating the relationship between the two-omics composite severity score and continuous clinical variables (P/F ratio, BALf CMV viral load, LDH, BALf total PCP burden, BALf troph burden, and 1,3- β -D-Glucan). The dashed lines represent linear trends, with grey shading indicating the 95% confidence interval.

Supplemental Figure 6



1 - *P. murina* antigen (5µg)
 2 - *P. murina* antigen (10µg)
 3 - *P. murina* antigen (20µg)
 4 - Rag2^{-/-}Il2rγ^{-/-} lung homogenate (5µg)
 5 - C57BL/6 lung homogenate (5µg)
 6 - Rag2^{-/-}Il2rγ^{-/-} lung homogenate (25µg)
 7 - C57BL/6 lung homogenate (25µg)
 M - Marker

Supplemental Figure 6. Western blot analysis of commercial IVIG against *Pneumocystis murina* antigens. Sonicated *P. murina* protein antigen (Lanes 1-3: 5 µg, 10 µg, and 20 µg, respectively) and uninfected murine lung tissue homogenates were resolved by SDS-PAGE and probed with pooled human IVIG (Octagam 10%, Lot no: M451c8541). Uninfected controls include lung homogenates from immunodeficient Rag2^{-/-}Il2rγ^{-/-} mice (Lane 4: 5 µg; Lane 6: 25 µg) and immunocompetent C57BL/6 mice (Lane 5: 5 µg; Lane 7: 25 µg). M: Molecular weight marker (kDa).