

# **Proteomic analysis reveals key proteins in extracellular vesicles cargo associated with idiopathic pulmonary fibrosis in vitro**

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*Supplementary Figures*

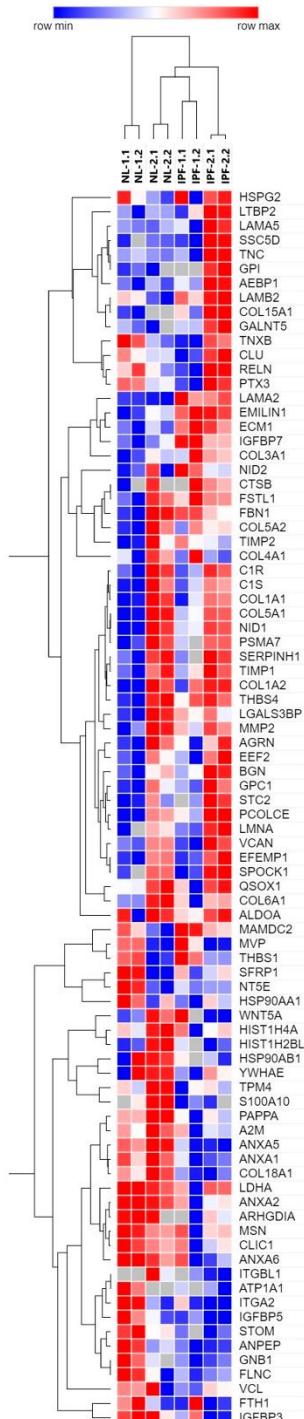


Figure S1: Heat map showing differentially expressed proteins in EVs cargo isolate from cell lines bearing both IPF and healthy phenotype. Protein intensities were log2 transformed and Z-scored to be normalized between groups. Up-regulated and down-regulated proteins are depicted in red and blue colors, respectively. IPF, idiopathic pulmonary fibrosis; NL, normal lung.

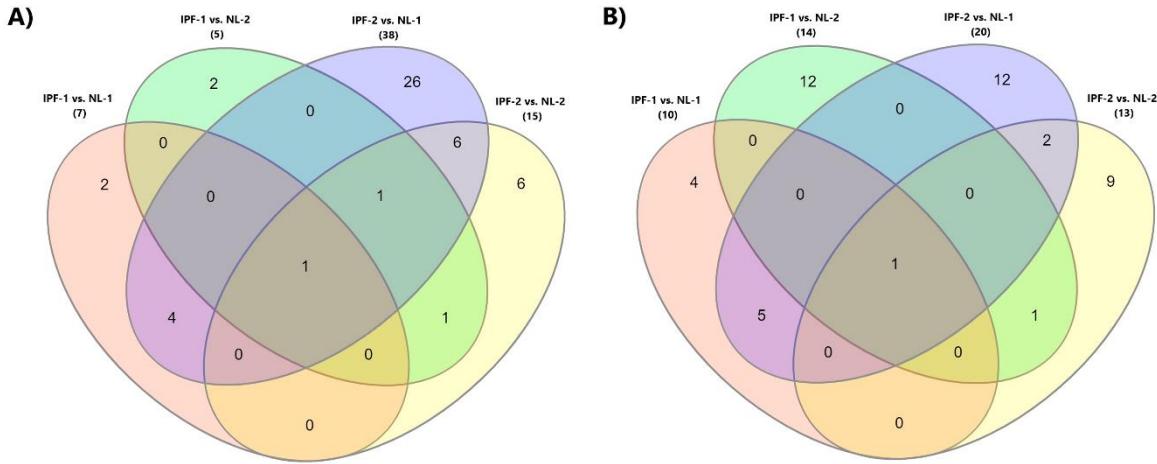


Figure S2: Distribution of differentially expressed proteins. (A) Venn diagram showing the distribution of up-regulated proteins in the comparison groups. (B) Venn diagram showing the distribution of down-regulated proteins in the comparison groups. IPF, idiopathic pulmonary fibrosis; NL, normal lung.

#### Supplementary Tables

Figure S1: Heat map showing differentially expressed proteins in EVs cargo isolated from cell lines bearing both IPF and healthy phenotype.

Figure S2: Distribution of differentially expressed proteins.

Table S1: Proteins identified by proteomic analysis using LFQ intensity value  $\neq 0$  in at least one biological replicate.

Table S2: Proteins identified by proteomic analysis using LFQ intensity value  $\neq 0$  and MS/MS (spectral) count  $\geq 2$  in at least one biological replicate.

Table S3: Proteins identified in a single EVs group.

Table S4: Proteins identified as differentially expressed (fold change  $\geq 1$  or  $\leq -1$  and  $p < 0.05$ ) in IPF-1 vs. NL-1 comparison.

Table S5: Proteins identified as differentially expressed (fold change  $\geq 1$  or  $\leq -1$  and  $p < 0.05$ ) in IPF-1 vs. NL-2 comparison.

Table S6: Proteins identified as differentially expressed (fold change  $\geq 1$  or  $\leq -1$  and  $p < 0.05$ ) in IPF-2 vs. NL-1 comparison.

Table S7: Proteins identified as differentially expressed (fold change  $\geq 1$  or  $\leq -1$  and  $p < 0.05$ ) in IPF-2 vs. NL-2 comparison.

Table S8: Proteins identified as differentially expressed (fold change  $\geq 1$  or  $\leq -1$  and  $p < 0.05$ ) in two or more comparisons.

Table S9: GO enrichment (biological process) for up-regulated proteins in the pairwise comparisons using GeneCodis.

Table S10: GO enrichment (biological process) for down-regulated proteins in the pairwise comparisons GeneCodis.

Table S11: GO enrichment (molecular function) for up-regulated proteins in the pairwise comparisons using GeneCodis.

Table S12: GO enrichment (molecular function) for down-regulated proteins in the pairwise comparisons using GeneCodis.

Table S13: GO enrichment (cellular component) for up-regulated proteins in the pairwise comparisons using GeneCodis.

Table S14: GO enrichment (cellular component) for down-regulated proteins in the pairwise comparisons using GeneCodis

Table S15: Enrichment pathways (KEGG) for up-regulated proteins in the pairwise comparisons using GeneCodis.

Table S16: Enrichment pathways (KEGG) for down-regulated proteins in the pairwise comparisons using GeneCodis.