Online Supplement

Similar Programmed Death Ligand 1 (PD-L1) expression profile in patients with mild COPD and lung cancer

Supplemental Figure 1. Correlation between total spatial PD-L1 expression levels and post-FEV1 (% predicted, **A**) and and CD68 expression levels (**B**) across all the study subjects. Results were shown as means \pm SEM. The statistical test used in these analyses was Pearson correlation considering a 95% confidence interval.

Supplemental Figure 2. Correlation between total spatial PD-L1 expression levels and post-FEV1 (% predicted) in vessels (A) and alveoli (B) across all the study subjects. In C and D, the correlation between spatial PD-L1 expression and post-FEV1 (% predicted) in bronchioles across COPD patients and controls, respectively. Results are shown as means ± SEM. The statistical tests used in these analyses was Spearman correlation test considering 95% confidence interval.

Supplemental Figure 3: Network of associations between top protein and genes and pathway analysis: In A and B, vessel- and bronchiole-specific RNA-protein association network (restricted to top 10 RNAs per protein, ranked by p-value). Red nodes=Up-regulated proteins in GOLD 1-2 compared to GOLD 3-4; Blue nodes= Associated RNAs; Red edges = positive association between the RNA and the protein; Blue edges = negative association between the RNA and the protein; Edge widths are proportional to the association effect sizes. In C, the top 30 (ranked by p-value) C7 (immunologic signature gene sets) macrophage-related pathways enriched in PD-L1 associated genes. The vertical dotted line indicates a FDR=0.05.

Supplemental Figure 4. PD-L1 mRNA expression in THP-1 cells after CSE exposure. THP-1 cells were treated with CSE at 10% for the indicated time, and the expression of PD-L1 was assessed by real-time PCR. PD-L1 mRNA expression is shown as fold change with respect to 0% CSE.

Supplemental Figure 1



Supplemental Figure 2



Supplemental Figure 3



