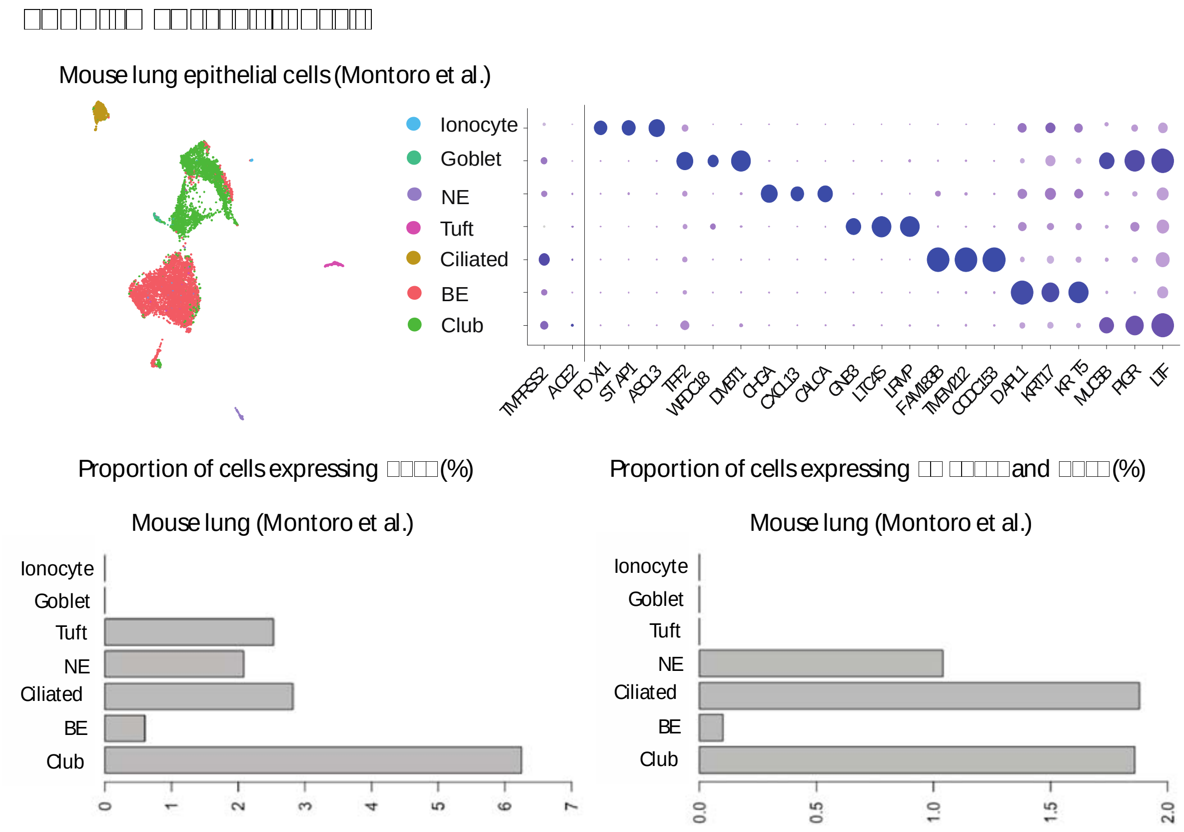
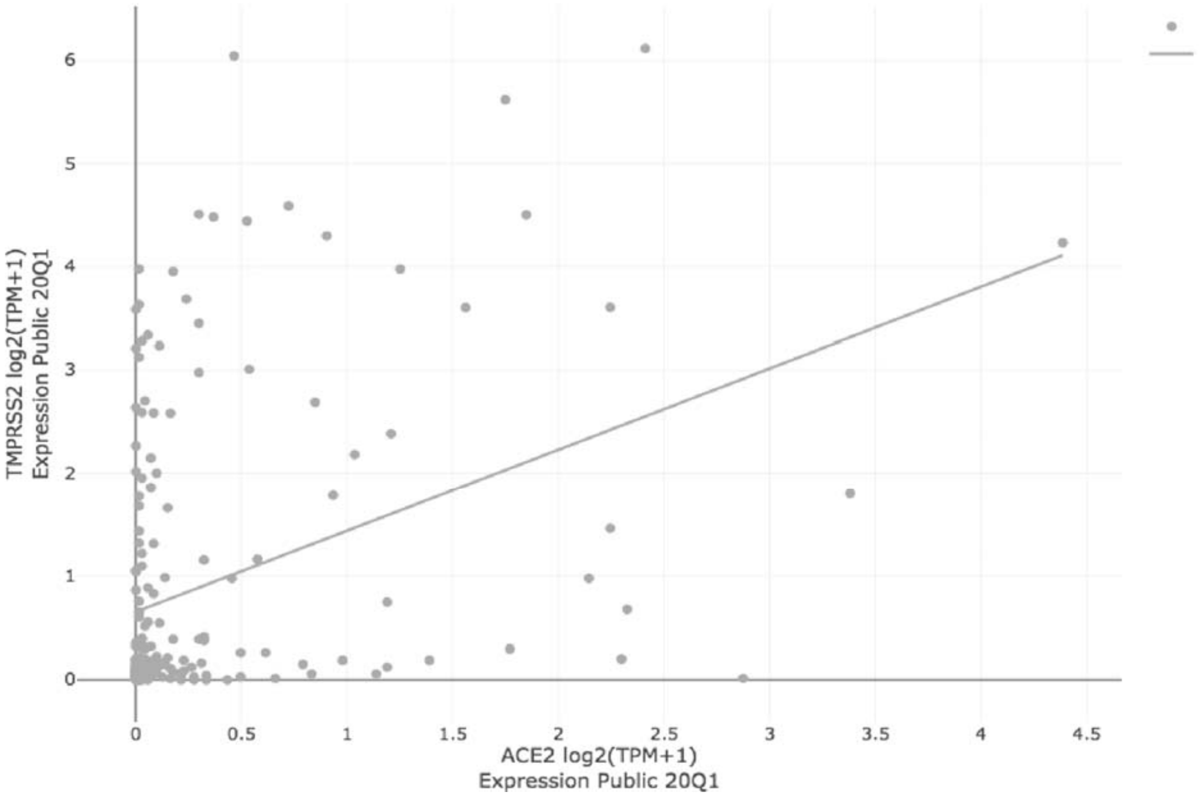


Supplementary Figure 1. Mouse lung epithelial cells distribution and the proportions of cells expressing *ACE2* and co-expressing of *TMPRSS2* and *ACE2* (%) from the Montoro study [6]. Each dataset was re-clustered and annotated by different cell types, for which distribution was shown in the Uniform Manifold Approximation and Projection (UMAP). A dot plot was generated showing the percentage of expression and average expression level for the most differentially expressed genes in each cell type as well as *ACE2* and *TMPRSS2*. The marker radius represents the percentage of expression and the color gradient represents the average expression level.

Supplementary Figure 2



Supplementary Figure 2. Comparison of *TMPRSS2* and *ACE2* gene expression levels in human lung cancer cell lines (n=206) from the depmap.org portal; Pearson's correlation = 0.363; p = 8.16 x 10^{-8} (linear regression).