

RNA-sequencing across three matched tissues reveals shared
and tissue-specific gene expression and pathway signatures of COPD

Jarrett D. Morrow¹, Robert P. Chase¹, Margaret M. Parker¹, Kimberly Glass¹, Minseok Seo¹, Miguel Divo², Caroline A. Owen², Peter Castaldi¹, Dawn L. DeMeo^{1,2}, Edwin K. Silverman^{1,2}, Craig P. Hersh^{1,2}

1. Channing Division of Network Medicine, Brigham and Women's Hospital, Boston, MA, 02115

2. Division of Pulmonary and Critical Care Medicine, Brigham and Women's Hospital, Boston, MA, 02115

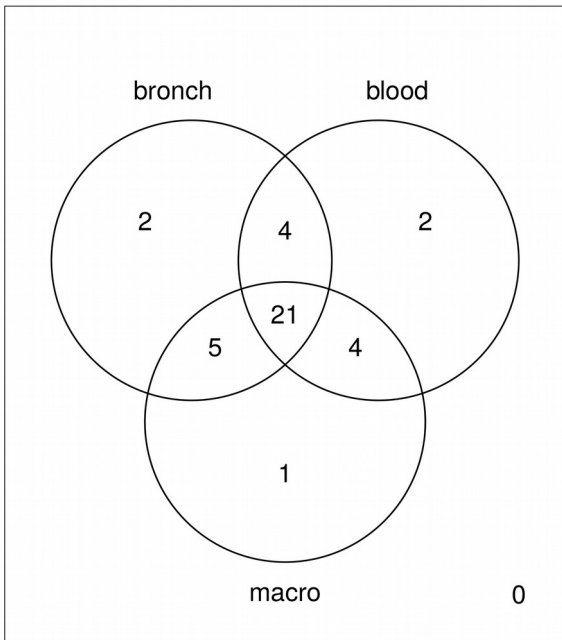


Figure S1. Summary of the RNA-seq data available across subjects and tissues (39 subjects, 94 total samples).

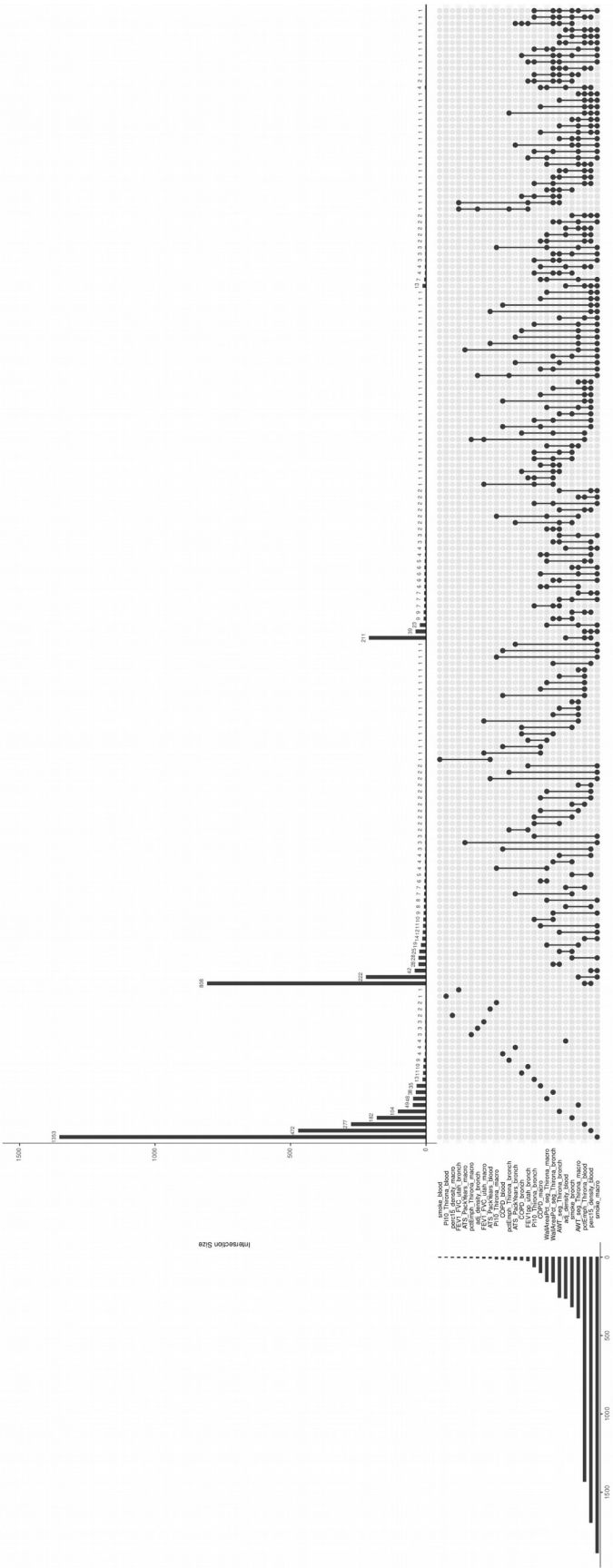


Figure S2. UpSet plot of the intersection of DESeq2 results for each of the three tissues and across the 11 phenotype variables. Each column provides a Venn diagram type intersection. Horizontal bars (Set Size) represent the number of differentially expressed genes. Single solid dots represent genes that do not intersect with any other set, and the solid dots connected by lines represent intersections. The vertical bars (Intersection Size) are proportional to the total number of genes for the solid dot(s) below them. For any given set (any row), the total number of differentially expressed genes may be determined by summing across all columns containing a solid dot.

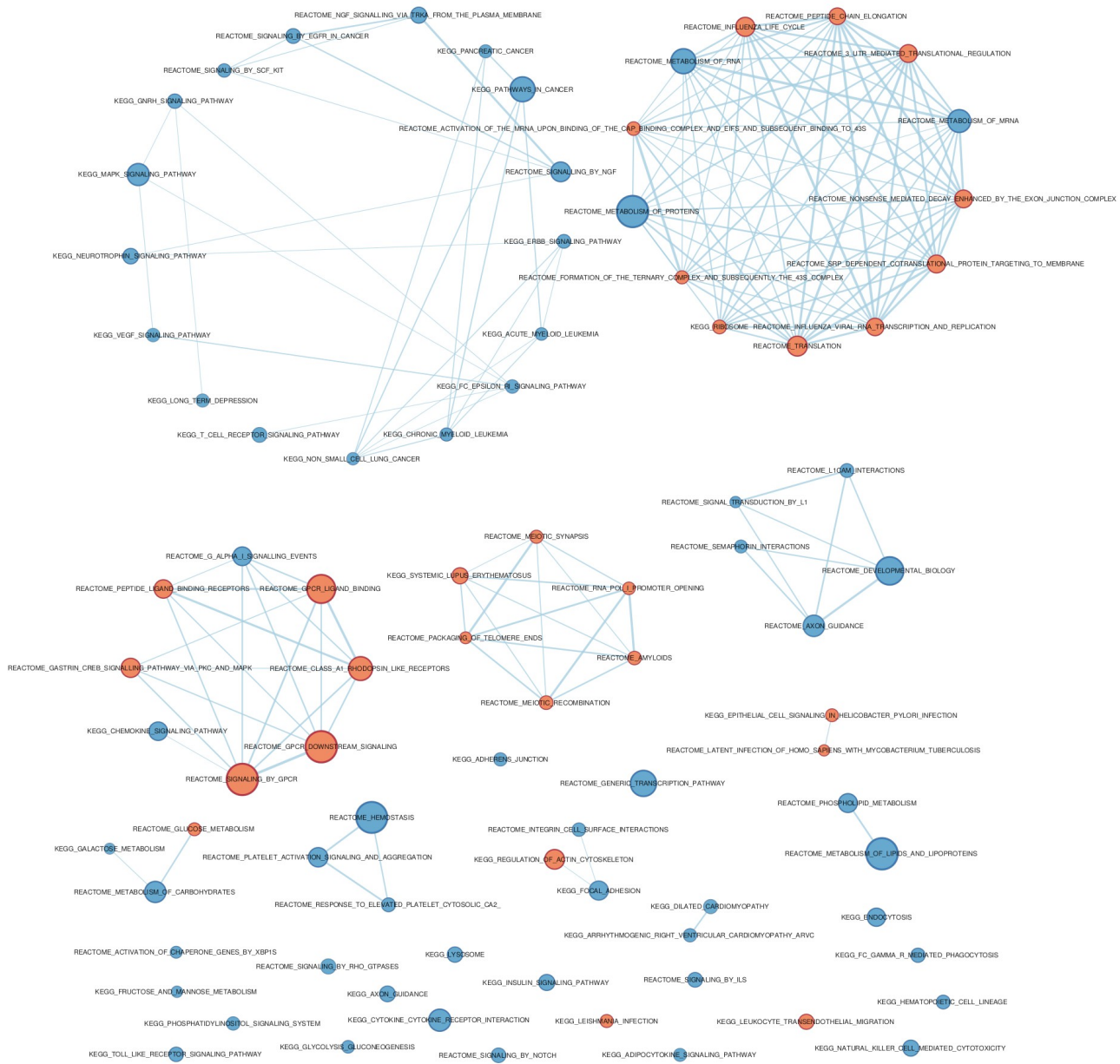


Figure S3. Overlapping pathways from blood and the bronchial epithelium in emphysema