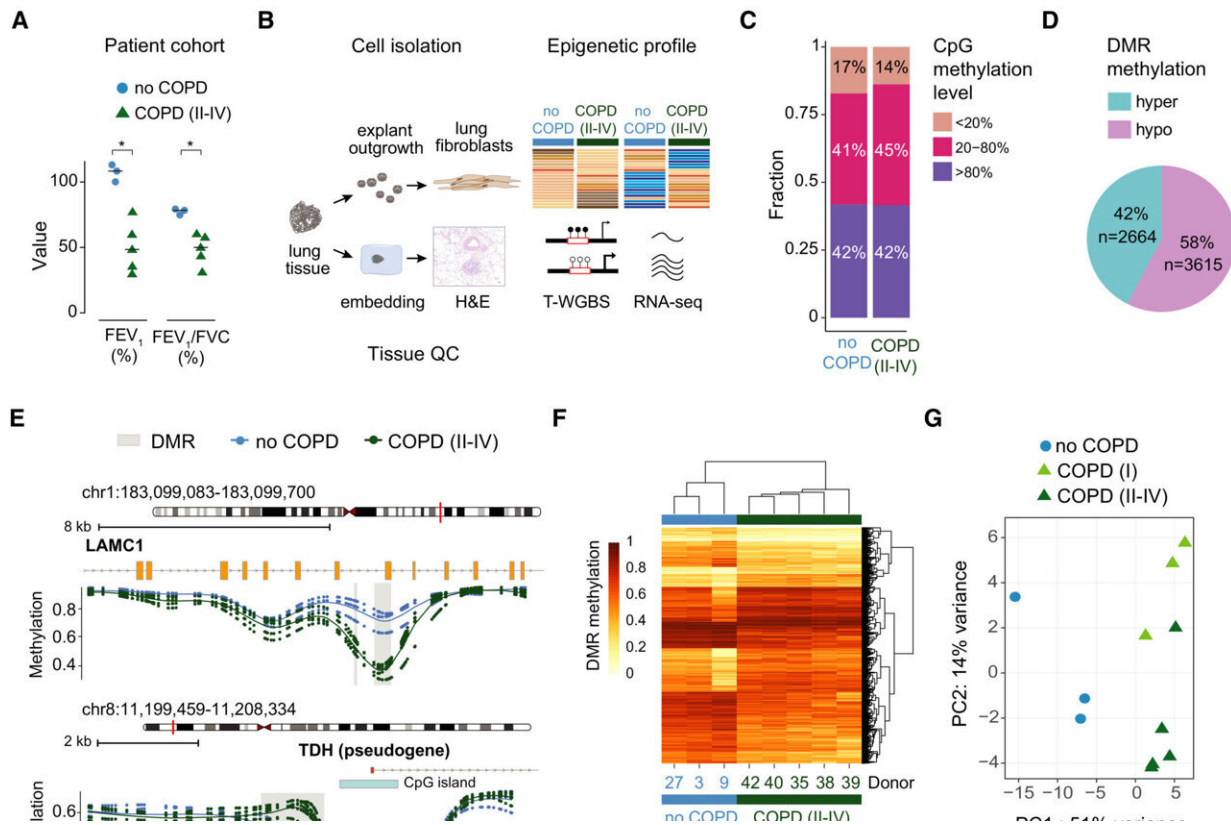


Epigenetic profiling identifies potential COPD treatment targets

May 24 2023



Genome-wide DNA methylation changes occur early in human lung fibroblasts during COPD and progress with disease development. A. Lung function data of COPD (II-IV) and no COPD (ex-smoker controls) donors used in this study. The lung function between the two groups is significantly different. B. Schematic diagram illustrating the experimental approach used for epigenetic (T-WGBS) and transcriptomic (RNA-seq) profiling of purified primary parenchymal lung fibroblasts. C–I. T-WGBS data of primary fibroblasts from no COPD and COPD (II–IV) patients were analyzed at single CpGs level (C) and on DMRs

(D–I). C. Genome wide CpG methylation statistics. Bar plot showing the fraction of high (> 80%), moderate (20–80%), and low (

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