Supplementary Information

Contents

[Supplementary Methods 2](#_Toc526200272)

[Cohort descriptions and cohort-specific methods 2](#_Toc526200273)

[UK Biobank 6](#_Toc526200274)

[Derivation and quality control of FEV1 and FVC, COPD status, and smoking 6](#_Toc526200275)

[Sample-based genotyping quality control 7](#_Toc526200276)

[SNP-based Genotyping quality control 7](#_Toc526200277)

[Identification of individuals of European ancestry 7](#_Toc526200278)

[Selecting individuals for genome-wide association analysis 7](#_Toc526200279)

[Sensitivity analyses for smoking, sex, and COPD phenotypic misclassification 8](#_Toc526200280)

[Identification of cell types 9](#_Toc526200281)

[Fine-mapping 9](#_Toc526200282)

[Target gene identification 10](#_Toc526200283)

[DEPICT 10](#_Toc526200284)

[Methylation quantitative trait loci (mQTL) 10](#_Toc526200285)

[Drug repositioning using drug-gene expression signatures 10](#_Toc526200286)

[Supplementary Results 11](#_Toc526200287)

[Relationship of genome-wide significant variants to smoking 11](#_Toc526200288)

[Identification of sex-specific genetic effects 11](#_Toc526200289)

[COPD misclassification sensitivity analyses 11](#_Toc526200290)

[Functional consequences of fine-mapped variants 12](#_Toc526200291)

[Genetic correlation of COPD and related traits 12](#_Toc526200292)

[Identification of drug targets 12](#_Toc526200293)

[Supplementary Information for Select Candidate Target Genes 13](#_Toc526200294)

[Funding and acknowledgements 15](#_Toc526200295)

[References 21](#_Toc526200296)

# Supplementary Methods

## Cohort descriptions and cohort-specific methods

**ARIC**: Atherosclerosis Risk in Communities (ARIC)1,2 (NCT00005131), is a population based study of risk factors for atherosclerosis and its sequelae in adults from four U.S. centers. Subjects were aged 45-64 at recruitment in 1987-1989. Institutional Review Board (IRB) approval was obtained at all associated study centers and informed consent was obtained for all participants. ARIC spirometry measurements were performed with a Collins Survey II water-seal spirometer (Collins Medical, Inc.) and Pulmo-Screen II software (PDS Healthcare Products, Inc.). Genotyping was performed using the AffymetrixGeneChip SNP Array 6.0. The current analysis includes 7,224 Caucasian subjects with genotyping data, pulmonary function measures and complete covariate information. Imputation was performed using the 1000 Genomes3 Integrated Phase 1 v3 reference panel (March 2012) in IMPUTE24. Logistic regression was performed using FAST (<https://bitbucket.org/baderlab/fast/wiki/Home>) adjusting for age, sex, pack-years, current and ever smoking, and ancestry.

**Cardiovascular Health Study (CHS):** The Cardiovascular Health Study (CHS) is a population-based cohort study of risk factors for coronary heart disease and stroke in adults ≥65 years conducted across four centers5 (NCT00005133 and NCT00149435). IRB approval was obtained at participating centers and written informed consent was obtained for all participants. 5,201 predominantly European ancestry persons were recruited in 1989-1990 from random samples of Medicare eligibility lists. An additional predominantly African-American cohort of 687 persons was subsequently enrolled in 1992-1993 for a total sample of 5,888. European ancestry participants were excluded from the GWAS study sample due to the presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack. Genotyping was performed at the General Clinical Research Center’s Phenotyping/Genotyping Laboratory at Cedars-Sinai among CHS participants who consented to genetic testing and had DNA available using the Illumina 370CNV BeadChip system (for European ancestry participants, in 2007) or the Illumina HumanOmni1-Quad\_v1 BeadChip system (for African-American participants, in 2010). Additional genotypes were provided from the ITMAT-Broad-CARe (IBC) Illumina iSELECT chip (for European ancestry participants). Imputation was performed using 1000 Genomes3 Phase 1 v3 haplotypes and minimac4 (for European ancestry participants, 2012-11-16) or IMPUTE version 2.2.2 (for African-American participants). Logistic regression was performed in R, adjusting for age, sex, pack-years, current and ever smoking, CHS clinic (4 sites) and PCs 1-5.

**COPDGene:** Eligible subjects in COPDGene Study (NCT00608764, www.copdgene.org) were of non-Hispanic white (NHW) or African-American (AA) ancestry, aged 45-80 years old, with at least 10 pack-years of smoking and no diagnosed lung disease other than COPD or asthma6,7 21,22. IRB approval was obtained at all study centers, and all study participants provided written informed consent. Illumina (San Diego, CA) performed genotyping on the HumanOmniExpress array. Genotyping at the Z and S alleles was performed in all subjects. Subjects known or found to have severe alpha-1 antitrypsin deficiency were excluded. We performed imputation using MaCH8,9 10,11 and minimac4 4 (version 2012-10-09) and 1000 Genomes3 Phase I v3 European (EUR) and cosmopolitan reference panels, for whites and African-Americans, respectively. We removed variants with an r2 value of ≤ 0.3. We performed logistic regression on cases and controls defined based on pre-bronchodilator spirometry, adjusting for age, sex, pack-years, current smoking, and principal components of genetic ancestry, separately in non-Hispanic whites and African-Americans, using PLINK1.910 .

**Evaluation of COPD Longitudinally to Identify Predictive Surrogate End-points (ECLIPSE;** SCO104960, NCT00292552, www.eclipse-copd.com**):** Details of the ECLIPSE study and genome-wide association analysis have been described previously12. The ECLIPSE study was approved by the relevant ethics and review boards at the participating clinical centers. All participants provided written informed consent. Cases and controls were aged 40-75 with at least a 10 pack-year smoking history without other respiratory diseases. Genotyping was performed using the Illumina HumanHap 550 V3 (Illumina, San Diego, CA). Subjects and markers with a call rate of < 95% were excluded. Imputation was performed using MaCH8,9 and minimac4 (version 2012-10-09) and the 1000 Genomes3 Phase I v3 European (EUR) reference panel. Logistic regression was performed on cases and controls defined by pre-bronchodilator spirometry, adjusting for age, sex, pack-years, current smoking, and principal components of genetic ancestry using PLINK1.910.

**Expression Quantitative Trait Loci – Lung (eQTL)**: The lung eQTL study has been described previously13. Briefly, patients who underwent thoracic surgery were recruited at three academic sites: Laval University, University of British Columbia (UBC), and University of Groningen, henceforth referred to as Laval, UBC, and Groningen, respectively. Patients from Laval were those undergoing lung cancer surgery, the majority of the UBC patients had lung resection for small peripheral lung lesions with some samples derived from autopsy or at the time of lung transplantation. At Groningen, patients were recruited from those having surgery for various lung diseases, including patients that underwent therapeutic resection for lung tumors and lung transplantation. All patients provided written informed consent, and the study was approved by the ethics committees of the Institut universitaire de cardiologie et de pneumologie de Québec and the UBC-Providence Health Care Research Institute Ethics Board for Laval and UBC, respectively. The study protocol was consistent with the Research Code of the University Medical Center Groningen and Dutch national ethical and professional guidelines. Patients whose lung function could have been influenced by lung diseases other than COPD and lung cancer were excluded. This includes patients with severe alpha-1 antitrypsin deficiency (n=11), amyloidosis (n=1), bronchiectasis (n=3), bronchiolitis obliterans (n=2), bronchopulmonary dysplasia (n=2), cystic fibrosis (n=14), idiopathic pulmonary fibrosis (n=13), langerhans cell histiocytosis (n=1), lymphangioleiomyomatosis (n=1), primary pulmonary hypertension (n=4), sarcoidosis (n=3) and vascular malformation (n=1).

Genotyping was carried out using the Illumina Human1M-Duo BeadChip. Standard genotyping quality controls were performed independently in the Laval, UBC and Groningen cohorts. Genotypes were then imputed with the Michigan Imputation Server14 using the Haplotype Reference Consortium version 1 (HRC.r1-1) data as reference set. Variants with an r2 value of ≤ 0.3 were removed from further analysis. Single-marker association tests were performed with PLINK v1.9010,11 adjusting for age, sex, smoking status, pack-years, ever smoking status, clinical center and genetic ancestry PC1 to PC10.

**Framingham Heart Study (FHS;** NCT00005121**):** Details on pulmonary function in the FHS have been previously published15,16. FHS was IRB-approved at the relevant institutions, and all participants provided written informed consent. We analyzed data from the most recent exam for each of the three generations of families participating in the FHS were analyzed. Genotypes were from the Affymetrix 500K array supplemented by the Affymetrix MIPS 50K. From a total number of 549,781 genotyped SNPs, 412,053 were used with MaCH8,9 for haplotype phasing, of which of 137,728 genotyped SNPs were removed by quality control. MaCH/minimac4,8,9 were used in this genotype imputation process to impute the FHS sample using the November 2010 release of the 1000 Genomes3 multi-ethnic panel. We used GEE implemented in the R package geepack with independent correlation matrix and clustering based on family, adjusted for sex, age, smoking status, pack years and genetic ancestry principal component 1 (to adjust for population stratification).

**KARE:** Details on the Korean Association Resource project (KARE) have been previously published17,18. KARE was initiated in 2007 to undertake genome-wide analyses among 10,038 participants in the rural-based Ansung and city-based Ansan South Korean cohorts. The study was approved at appropriate IRBs from participating institutions, and participants provided informed consent. KARE3 data were obtained from the third phenotype collection in 2008; lung function was collecting using the Vmax-2130 (Sensor Medics, Yorba Linda, CA, USA). Genotyping was performed using the Affymetrix Genome-Wide Human array 5.0 (Affymetrix, Inc., Santa Clara, CA, USA). We performed genotype imputation using IMPUTE2 and the 1000 Genomes3 Phase 3 cosmopolitan panel. Markers were converted to genotype from dosage with call rate ≥ 95%, minor allele frequency ≥ 1%, p for HWE ≥ 1.0x10-5, imputation quality score ≥ 0.9. Logistic regression, adjusting for age, sex, pack-years, principal components, current and ever smoking, was performed using PLINK19.

**LifeLines:** The LifeLines Cohort Study is a population-based cohort study established as a resource for research on complex interactions between environmental, phenotypic and genomic factors in the development of chronic diseases and healthy aging20–22. Between 2006 and 2013, inhabitants of the northern part of The Netherlands and their families were invited to participate, thereby contributing to a three-generation design. Participants visited one of the LifeLines research sites for pre-bronchodilator spirometry following ATS guidelines. All participants signed an informed consent form before they received an invitation for the physical examination. The LifeLines Cohort Study is conducted according to the principles of the Declaration of Helsinki and in accordance with research code University Medical Center Groningen (UMCG), The Netherlands. The LifeLines study is approved by the medical ethical committee of the UMCG. Blood samples for a subset of individuals were genotyped using the Illumina CytoSNP-12v2 array. Independent Caucasian-ancestry samples (n = 13,436) have been imputed using the 1000 Genomes3 phase1 v3 reference panels. Genotypes were pre-phased using SHAPEIT223 and aligned to the reference panels using Genotype Harmonizer (www.molgenis.org/systemsgenetics) in order to resolve strand issues. The samples were imputed using minimac4 (version 2012-10-09), yielding 28,681,763 SNPs. Associations between genomic dosages with moderate/severe COPD were assessed with logistic regression models adjusted for age, smoking status (never/ever), current smoking (no/yes), pack years smoked and sex. All analysis were performed in software package PLINK version 1.0719,24.

**Lovelace:** The Lovelace Smokers Cohort (LSC) has been actively enrolling smokers from the Albuquerque, NM metropolitan area since 2001 25. All participants provided written informed consent, and the study was approved by the relevant IRB. Enrollment was restricted to current and former smokers age 40 to 74 years old with a minimum of 10 pack-years of smoking and no personal history of lung cancer. A detailed questionnaire written in English was used to collect information on demographics; medical, cigarette smoking, and exposure history; socioeconomic status; diet; and quality of life. Pulmonary function testing was performed at each visit. All participants signed a consent form, and the Western Institutional Review Board approved this project. The GWAS discovery set was comprised of 1200 Caucasian (self-reported) smokers. The HumanOmni2.5-4v1-H BeadChip (Illumina, San Diego, CA) was used to genotype 2,450,000 SNPs in 1200 Caucasian smokers from the LSC. After quality assessment, 1163 subjects with 1,599,980 SNPs remained in the genetic association analysis. Logistic regression was performed using PLINK on white subjects, adjusting for age, sex, pack-years, current and ever smoking, and ancestry.

**Multi-Ethnic Study of Atherosclerosis (MESA)**: MESA is a longitudinal study of subclinical cardiovascular disease and risk factors that predict progression to clinically overt cardiovascular disease or progression of the subclinical disease26. Between 2000 and 2002, MESA recruited 6,814 men and women 45 to 84 years of age. Exclusion criteria were clinical cardiovascular disease, weight exceeding 136 kg (300 lb.), pregnancy, and impediment to long-term participation. The MESA Family Study recruited 1,595 African American and Hispanic participants, generally siblings of MESA participants, using the same inclusion and exclusion criteria as MESA except that clinical cardiovascular disease was permitted. The MESA Air Pollution Study recruited an additional 257 participants from Los Angeles and Riverside County, CA, and Rockland County, NY, using the same criteria as MESA, except that participants were ages 50 to 89 who lived in the area more than 50% of the year and had no plans to move in the next five years27. The MESA Lung Study performed spirometry following the 2005 ATS/ERS guidelines in a subset of the MESA and MESA Family Studies and all of the new recruits in the MESA Air Pollution Study28. All participants provided informed consent and the protocols of MESA were approved by the IRBs of collaborating institutions and the National Heart, Lung and Blood Institute.

Participants who consented to genetic analyses were genotyped in 2009 using the Affymetrix Human SNP array 6.0 29. The cleaned genotypic data was deposited with MESA phenotypic data into dbGaP as the MESA SHARe project (study accession phs000209); 8,224 consenting individuals (2,685 White, 2,588 non-Hispanic African-American, 2,174 Hispanic, 777 Chinese) were included, with 897,981 SNPs passing study specific quality control (QC). For GWAS, IMPUTE version 2.2.2 was used to perform imputation for the MESA SHARe participants using the cosmopolitan 1,000 Genomes3 Phase 1 v3 March 2012 reference set. Logistic regression was performed using SNPTEST v2.4.030, adjusting for age, sex, pack-years, current and ever smoking, and ancestry.

**National Emphysema Treatment Trial (NETT;** NCT00000606**,** [www.nhlbi.nih.gov/health/prof/lung/nett/](http://www.nhlbi.nih.gov/health/prof/lung/nett/)**) and Normative Aging Study (NAS)**: 31. NETT was a multicenter clinical trial to evaluate lung volume reduction surgery. All participants provided written informed consent, and the study was approved by the IRB at all participating institutions. Enrolled subjects had severe airflow obstruction by post-bronchodilator spirometry (FEV1 < 45% predicted) and evidence of emphysema on computed tomography (CT) chest imaging; exclusion criteria included, but not limited to, history of recurrent infections with significant sputum production or bronchiectasis. A subset of 382 self-reported white subjects without severe alpha-1 antitrypsin deficiency were enrolled in the NETT Genetics Ancillary Study. The Normative Aging Study is a longitudinal study of healthy men established in 1963 aged 21 to 80 years from the greater Boston area, free of known chronic medical conditions. The study was conducted by the Veterans Administration (VA) 32, and the local Institutional Review Board approved the study. Controls were of self-reported white ancestry and at least 10 pack-years of cigarette smoking with no evidence of airflow limitaiton on spirometry on their most recent visit. Genotyping for NETT-NAS was performed using the Illumina Quad 610 array (Illumina, San Diego, CA)33,34. Imputation was performed using MaCH8,9 and minimac4 (version 2012-10-09) and the 1000 Genomes Phase I v3 European (EUR) reference panel. Logistic regression was performed on cases and controls based on pre-bronchodilator spirometry, adjusting for age, sex, pack-years, current smoking, and principal components of ancestry using PLINK1.910,11.

**GenKOLS (Norway)**: The Norwegian GenKOLS (Genetics of Chronic Obstructive Lung Disease, GSK code RES11080)35 recruited subjects with > 2.5 pack years of smoking history from Bergen, Norway. Subjects with severe alpha-1 antitrypsin deficiency and other lung diseases (aside from asthma) were excluded. The Regional Committee for Medical Research Ethics (REK Vest), the Norwegian Data Inspectorate and the Norwegian Department of Health approved the case–control study. Written informed consent was obtained from all participants. Genotyping was performed using Illumina HumanHap 550 arrays (Illumina, San Diego, CA). Genotype imputation was performed using MaCH8,9 and minimac4 (version 2012-10-09) and the 1000 Genomes3 Phase I v3 European (EUR) reference panel. Logistic regression was performed on cases and controls defined by pre-bronchodilator spirometry, adjusting for age, sex, pack-years, current smoking, and principal components of genetic ancestry using PLINK1.910,11.

**The Rotterdam Study:** The Rotterdam Study is a prospective population-based cohort study founded in 1990 in a suburb of Rotterdam, the Netherlands36,37. The first cohort (RS-I) consists of 7,983 participants, aged 55 years and over. The second cohort (RS-II) was recruited in 2000 with the same inclusion criteria. The third cohort (RS-III) consists of 3,932 participants, aged 45 years and over and was recruited in 2006. The Rotterdam Study was approved by the institutional review board (Medical Ethics Committee) of the Erasmus Medical Center and by the review board of The Netherlands Ministry of Health, Welfare and Sports. All participants provided written informed consent. Spirometry was performed using the Master Screen® PFT Pro (CareFusion, San Diego, CA). A total of 6,291 subjects for RS I, 2,157 for RS II and 3,048 for RS III passed genotyping quality control. Regression coefficients and their standard errors were determined using the ProbABEL38 program according to an additive model, adjusting for age, sex, pack-years, smoking status, and ancestry.

**Subpopulations and intermediate outcome measures in COPD study (SPIROMICS;** NCT01969344**):** Participants of the NHLBI SPIROMICS study were 40-80 years of age at baseline with a smoking history ≥20 pack-years. Recruitment included non-smokers, smokers without COPD, mild-moderate COPD, and severe COPD39. All participants provided written informed consent and the Institutional Review Boards/Ethics Committees of all the cooperating institutions approved the study protocols. Genome-wide genotyping was performed using the Illumina OmniExpress HumanExome BeadChip using standard techniques in the first 571 subjects with COPD and 175 smoking controls. Imputation was performed against 1000 Genomes reference panels using Impute-v2.30 using a quality cutoff of 0.9, and association analysis performed using PLINK adjusting for age, sex, pack-years, smoking status, and ancestry.

**Studies with Custom Genotyping:**

**Boston Early-Onset COPD Study (BEOCOPD;** ClinicalTrials.gov: NCT01177618). BEOCOPD is an extended pedigree study constructed based on probands under 53 years of age with severe COPD (defined as pre-bronchodilator forced expiratory volume in one second (FEV1) < 40% predicted) and without severe alpha-1 antitrypsin deficiency40,41. IRB approval was obtained for the study, and all participants provided written informed consent.

**International COPD Genetics Network (ICGN):** ICGN recruited subjects (FEV1 < 60% predicted and FEV1/FVC < 90% predicted between ages 45-65) as probands and then enrolled available siblings and parents of the proband42,43. The study was IRB approved at all relevant institutions and participants provided written informed consent.

**Transcontinental COPD Genetics Study (TCGS) – Korea and Poland:** TCGS 44 and comprised of two case-control studies, based in Poland and in Korea. The study was approved by the appropriate IRBs, and all participants provided written informed consent. Both studies recruited individuals between 40 and 80 years of age, with at least 10 pack-years of cigarette smoking; where cases had severe COPD (FEV1 < 50% predicted) and controls had normal spirometry. Subjects with other lung diseases were excluded. TCGS-Poland enrolled white individuals, and TCGS-Korea enrolled Korean individuals.

**Genotyping in BECOPD, ICGN, and TCGS:**

We genotyped subjects using the Illumina HumanExome v1.2 array with custom content, including top results from prior genome-wide association studies, as previously described45. We performed single-variant association analysis adjusting for age, pack-years, sex, and current and ever smoking, together using a covariate additionally indicating study, via a logistic mixed model as implemented in GMMAT version 0.5 in R (version 3.2.0, <http://www.R-project.org/>)46 in whites in our family-based studies, and using standard logistic regressions in each of the two TCGS studies.

## UK Biobank

### Derivation and quality control of FEV1 and FVC, COPD status, and smoking

The UK Biobank is a resource with approximately 500,000 persons age 40-69 for whom extensive baseline questionnaire data, physiologic measures, and biologic specimens (urine and blood samples) have been obtained47. The UK Biobank participants provided informed consent. The UK Biobank’s Ethics and Governance Framework guides research ethics principles and polices, the adherence to which is overseen by the independent Ethics and Governance Council. Details of the derivation and quality control of spirometry, smoking, and case-control status were performed as described48. Briefly, of 502,682 individuals in UK Biobank, 445,754 individuals had at least two measures of FEV1 and FVC and spirometry metrics, age, sex, height, and smoking. We used blow quality metrics from the Vitalograph spirometer and compared pre-defined measurements with the blow curve time series. We considered blows as ‘acceptable’ if their blow quality metrics were blank, ACCEPT, BELOW6SEC ACCEPT, or BELOW6SEC. We assessed back-extrapolated volumes derived from blow curve time series measurements as previously described49 and excluded blows which their back-extrapolated volumes were greater than the larger of either 5% of FVC or 150 mL, leaving 776,927 blows from 387,277 participants. To confirm pre-defined FEV1 and FVC, we independently derived FEV1 and FVC from blow curve time series measurements. We further excluded blows which differences between pre-defined and newly derived FEV1 and FVC were greater than 5%. Following above exclusion, 776,318 blows from 387,052 participants remained in the analysis. Additionally, we assessed if individuals’ measures of FEV1 and FVC were reproducible, allowing differences between the highest measure and others to be up to 250 mL. We defined COPD using modified GOLD criteria (as stated previously) based on highest values of reproducible measures of FEV1 and FVC available in 324,299 individuals.

We assigned smoking status to individuals in UK Biobank based on their responses on questionnaires. Never-smokers were non-current smokers or smoked occasionally allowing up to 100 life-time cigarettes; ever-smokers were defined as either current, most days (current or all days in the past), or smoked occasionally with > 100 cigarettes. We defined pack-years as packs of cigarettes per day multiplied by years smoked. Pack-years was 0 for never smokers based on VariableID: 20116 smoking status. For ever smokers, we set pack-years to cigarettes per day (VariableID: 2887 in former smokers or VariableID: 3456 in current smokers) divided by 20 multiplied by duration of smoking (VariableID: 2897 minus VariableID: 2867 for former smokers and age at time of study minus VariableID: 3436 in current smokers).

### Sample-based genotyping quality control

Details on procedure, imputation, and quality control of genotyping in UK Biobank were published earlier50. Briefly, we excluded 968 individuals with outlying heterozygosity or missingness. We further excluded: 1) 378 samples with sex mismatch (reported and genetic sex) 2) 188 samples with >10 3rd degree relatives 3) 652 samples with putative sex chromosome aneuploidy. This left 486,367 samples with genotypes for further analysis.

### SNP-based Genotyping quality control

Besides the QC steps described in Bycroft et al.50, we filtered out: 1) variants with minor allele frequency lower than 1%; 2) variants with imputation quality lower than 0.5; 3) variants not included into the Haplotype Reference Consortium (HRC) imputation panel, as recommended by UK Biobank at the time of analysis. This left us with 7,810,596 variants.

### Identification of individuals of European ancestry

To identify individuals of European ancestry, we used K-means clustering on principal components (PCs) provided by UK Biobank. We performed K-means clustering using the first two PCs with number of clusters 3-8 in 486,367 samples passing sample-based quality control. Together with self-reported ethnicity data, we chose 6-cluster model as it reflects the expected broad ethnic groups. This left us 453,958 European individuals for further analysis (additional 45,865 putative European individuals in addition to 408,093 self-reported white British50).

### Selecting individuals for genome-wide association analysis

We intersected the individuals passing spirometry QC and sample-based genotyping QC and selected individuals with European ancestry as described above. This left us 321,057 individuals in total. To identify individuals who were outliers in phenotype distribution, we plotted the distribution for each measure (FEV1, FVC, and FEV1/FVC) adjusting for sex, age, age2, height, and smoking status (ever/never). We re-calculated phenotypic adjustment after excluding 10 European samples who were obvious outliers. As stated previously, we defined COPD using modified GOLD criteria for moderate to very severe airflow limitation51: FEV1 less than 80% of predicted value and FEV1/FVC less than 0.7. We excluded 59,358 individuals, who did not match the above criteria. To select completely unrelated individuals for genome-wide association analysis, we removed at least one individual from each related pair, giving preference to cases. Briefly, we created a graph from related pairs using genetic kinship information provided by UK Biobank. For each unconnected component, we removed control nodes (healthy individual), starting with the one with the highest degree. If all nodes were cases, we removed the one with the highest degree. We excluded additional 26,855 individuals based on kinship and further 34,035 individuals who had missing information on sex, ever smoking status, pack-years of smoking, and age. We also excluded subjects who had withdrawn consent (updated as of May 2018). After excluding individuals, we were left with 200,792 individuals for genome-wide association analysis of COPD.

## Sensitivity analyses for smoking, sex, and COPD phenotypic misclassification

To determine whether our results were driven by, or differed by, smoking status, we examined COPD-associated variants in relationship to ever-smoking status in UK Biobank. In addition, we separately examined these variants in ever- and never-smokers in UK Biobank. To test for sex-difference in genetic effects among our top variants, we performed a sex-stratified GWAS of COPD in UK Biobank and tested for differences between effects among males and females. For the latter we utilized the “difference test52,53”. In addition, we also included a variant-by-sex interaction term and tested this term. We defined significant effect differences by Bonferroni correction and further, we attempted to replicate all nominally significant variants (P for the difference test < 0.05) from our top SNPs in a meta-analysis of sex-stratified COPD association analyses in COPDGene NHW, COPDGene AA, ECLIPSE, and GenKOLS. We also investigated variants not our top variants but reaching genome-wide significance (P<5x10-8) only in one sex. We attempted to replicate these variants in the meta-analysis of COPD case-control cohorts as mentioned above. We used 5% Bonferroni corrected P value to determine significance in replication.

To simulate power for the difference test, we modified the power simulations in Winkler et al. 52 and made them applicable to a case-control dataset. We approximated the phenotypic variance attributable to the risk locus as in Peyrot et al.54:

where is the mean liability of case subjects and depends on the prevalence of COPD, is the risk allele frequency of variant , and is the relative risk, respectively. can be derived from and the direction of the effect .

The variance of a variant ( is defined as

Where is sample size in stratum .

Hence, we can derive the power of difference test as52

As denotes the cumulative standard normal distribution, is the q-th quantile of , is the alpha level of the test, and *f* = *n2/n1*.

We performed an array of analyses to ascertain if a pre-bronchodilator spirometry definition of COPD (as opposed post-bronchodilator spirometry) and the inclusion of subjects with self-reported asthma subsequently impacted both effect size estimates and P values of genetic association. First, in the COPDGene study, we examined the difference in COPD diagnosis using pre- and post-bronchodilator spirometry. Then, we stratified individuals by self-reported asthma and compared the percent of individuals in each stratum that were misclassified as having COPD based on a pre-bronchodilator spirometry definition of COPD. We also re-tested the association of COPD by excluding individuals in UK Biobank with self-reported asthma and the same control individuals as the primary analysis. Finally, in a subset of COPD case-control studies including COPDGene NHW and AA, ECLIPSE, and Norway/GenKOLS, we performed logistic regression (controlling for pack years, current smoking, sex, age, and PCs of genetic ancestry) and a meta-analysis to assess the relative COPD association effect sizes and P values of our top variants when using a pre- vs post-bronchodilator definition of COPD. For the comparison of effect sizes, we limited the variants being compared to those that were at least nominally significant (P < 0.05) in the meta-analysis of the COPD case-control studies.

## Identification of cell types

Linkage equilibrium score regression (LDSC) requires specifically expressed gene sets to perform cell type-specific analysis55. For two human datasets56,57, we computed t-statistics for each cell type on gene expression data in Transcripts Per Kilobase Million (TPM) as described previously55. We constructed gene sets for each cell type using genes in the top 10% of sorted t-statistics55, and a control gene set (i.e., all genes available in a dataset). We annotated regions +/- 100-kb from each gene and computed LD scores as previously described55. For two mouse datasets58, we used pre-computed Wilcoxon or Welch P-values for each cell to select genes in the top 10%. We mapped gene identifiers from mouse to human using biomaRt59.

We tested for enrichment of lung cell type in sets of genome-wide significant variants using SNPsea60,61. Briefly, SNPsea performed three steps: identification of specifically expressed genes, assignment of gene in a locus, and significance testing. We first computed the Euclidean norm of gene expression values (TPM) in all cell types and divided expression values in each cell type using this value. The score was then converted to nonparametric percentiles. Second, we identified the most specifically expressed gene in a given locus by ranking the score. Finally, we then tested for significance using permutation using matched SNP sets.

## Fine-mapping

We used biomaRt59 to annotate variants in each credible set based on the Ensembl Variant Effect Predictor. We defined deleterious variants as those which resulted in non-synonymous, stop, or splice variants (terms: transcript\_ablation, splice\_acceptor\_variant, splice\_donor\_variant, stop\_gained, frameshift\_variant, stop\_lost, start\_lost, transcript\_amplification, inframe\_insertion, inframe\_deletion, missense\_variant, and protein\_altering\_variant). Variants were annotated using Haploreg v4.162 and SNPnexus63.

## Target gene identification

### DEPICT

DEPICT utilizes pairwise gene correlation data from ~77,000 microarrays to create data-driven “reconstituted” gene sets from a backbone of curated data from GO, KEGG, REACTOME, protein-protein interaction data, and murine phenotypic gene sets. These “reconstituted” gene sets are used to prioritize genes at each GWAS loci based on the similarity each gene’s “reconstituted” gene set membership to the gene set memberships of genes at other GWAS loci64.

### Methylation quantitative trait loci (mQTL)

Of all genome-wide significant loci, we searched for overlapping methylation quantitative trait loci (mQTL) using previously published data65. Briefly, lung tissues from 90 severe COPD cases (FEV1 < 50% predicted) and 36 control subjects undergoing lung transplantation, lung volume reduction surgery, or lung nodule resection66. All subjects were self-reported former smokers at least 1 month prior to the surgery. A cis-mQTL analysis was performed using the R/Bioconductor package Matrix eQTL (version 2.1.1)67. We tested associations of each CpG site and genetic variants within 500 kb upstream and downstream (from the CpG site) using a linear regression model adjusting for age, sex, smoking pack-years, two principal components of genetic ancestry, batch number, and principal components of methylation data as previous described65. To determine whether these signals co-localized (rather than being related due to linkage disequilibrium), we performed colocalization analysis between our genome-wide significant loci and mQTL using eCAVIAR68 (eQTL and GWAS CAusal Variants Identification in Associated Regions). We tested variants that were significant in both datasets, P < 0.0027 in GWAS (equivalent to Z score > 3, as recommended by the author68) and P < 3.2 x 10-6 in mQTL65. We estimated the posterior probability of a variant being shared in both GWAS and mQTL, using a cut-off of 0.1 as previous demonstrated68.

## Drug repositioning using drug-gene expression signatures

We used a gene-based association method that utilizes GWAS summary statistics and gene expression reference databases to produce a gene list for drug-gene expression similarity analysis69,70. In brief, we tested for associations of the genetic component of gene expression and COPD using gene expression data in a lung71. This method gave us a rank gene list of up-regulated and down-regulated genes. We used the Query, an application in clue.io72, to calculate connectivity score of our top 100 up-regulated and 100 down-regulated genes and drug-gene expression signatures. The connectivity score, ranging from -1 to 1, reflects the closeness between the expression profiles73. A negative connectivity score means that our down-regulated genes are at the top of the reference profile73. We included drug-gene expression signatures from 2,837 compounds in nine cell lines in the analysis72. To find candidate drugs for repositioning, we used negative connectivity score less than -90% as the threshold72, hypothesizing that a drug candidate need to produce an opposing or reverse expression signature induced by the disease.

# Supplementary Results

## Relationship of genome-wide significant variants to smoking

To assess the effect of smoking, we tested association of 82 genetic variants and smoking status (ever- and never- smokers) in the UK Biobank. Of the 82 identified loci, three were associated with cigarette smoking after Bonferroni correction (P < 0.05/82) including the strongest association at the known 15q25 locus, but also *IER3* (P = 9·2 x 10-5) at 6p21 and *SPPL2C* (P = 1·4 x 10-4) at 17q21. To test if smoking status could have confounded the association of these variants and COPD, we re-performed the analysis of COPD stratifying by smoking status in the UK Biobank. The lead variants at these latter two loci were highly significant for COPD in never-smokers (P = 6·7 x 10-13 and 2·8 x 10-5 at *IER3* and *SPPL2C* loci, respectively). Seventy-eight of 82 genetic loci were nominally significant in never-smokers (P < 0.05) with the exception of four loci including *TESK2*, *RBMS3*, *RIN3*, and *CHRNA3* (**Supplementary Table 14 and 15**).

## Identification of sex-specific genetic effects

Of 82 genetic variants associated with COPD, we did not find significant evidence of difference in effect sizes of COPD among males and females after adjusting for multiple testing (**Supplementary Table 16**). The strongest evidence for different effect size was at *TGFB2* locus (rs3009947, betamales=-0.06 and betafemales=-0.12, and P unadjusted =0.003). Twelfth of 82 COPD-associated variants were nominally significant for sex-difference (P<0.05); none of which was replicated in a meta-analysis of a subset of COPD case-control cohorts (**Supplementary Methods** and **Supplementary Table 16**). Similarly, using a test for sex interactions, we did not identify any significant variants after correcting for multiple testing (top unadjusted P = 0.003, **Supplementary Table 16**). Power calculations indicate that we were well-powered to detect effect size different of > 0.04 for an allele frequency of ~0.27; for details, see **Methods and Supplementary Figure 6**.

## COPD misclassification sensitivity analyses

In 10,720 persons with both pre-bronchodilator and post-bronchodilator spirometry available in the COPDGene study, we defined ground truth for COPD status using post-bronchodilator spirometry. Using a pre-bronchodilator definition of COPD resulted in 113 out of 4,289 individuals (2.6%) without COPD being incorrectly assigned as a COPD cases and 18 out of 3,694 individuals (0.49%) with COPD being incorrectly assigned as controls (**Supplementary Table 17**). A self-reported doctor diagnosis of asthma had no significant impact on either the overall misclassification of individuals as being controls, COPD cases, or neither (16.6% without asthma and 18.3% with asthma, χ squared p value = 0.17); or specifically on the misclassification of individuals without COPD as having COPD (1.5% without asthma and 1.7% with asthma, χ squared p value = 0.77) when using pre-bronchodilator instead of post-bronchodilator spirometry.

When comparing the relative effect size of our top 164 variants for a pre- versus post-bronchodilator definition of COPD in the subset of our COPD case-control cohorts (COPDGene, ECLIPSE, GenKOLS), 49 variants were at least nominally significant for association with COPD in the meta-analysis (**Supplemental Table 18**). For these 49 variants, the odds ratio obtained when using a pre- versus post-bronchodilator definition of COPD was very similar with Pearson correlation coefficient of 0.92 (p value < 1e-10). Generally, the post-bronchodilator COPD definition yielded larger effect sizes; however, the 95% confidence intervals for all estimates crossed the line of identity (**Supplemental Figure 7**).

We performed additional GWAS by excluding 6,717 self-reported asthma from 21,081 COPD cases in the UK Biobank. While the decreased sample size resulted in less significant associations, we observed highly concordant estimates of effect size between the analysis including and excluding asthma (**Supplementary Figure 8**). One outlier was the variant rs2070600 in *AGER*, which demonstrated a higher OR after excluding individuals with asthma. Association statistics for all genome-wide significant loci are shown in **Supplementary Tables 19 and 20**.

To estimate the effect of asthma inclusion in the overlapping loci analysis, we re-ran gwas-pw using statistics from GWAS of COPD including individuals with asthma. The analysis including asthmatic individuals identified 24 shared genome segments between COPD and asthma (posterior probability of shared association > 0.7). All segments identified in the analysis excluding asthmatics were also identified in this analysis, with the exception of the segment in chr12 (near *STAT6*) (posterior probability of 0.81 excluding asthma, 0.29 including asthma). Results of all loci (with and without exclusion of asthma cases) are shown in **Supplementary Table 21**.

In addition to individual loci effect, we re-estimated the genetic correlation between COPD and asthma using asthma-excluded statistics of COPD. The genetic correlation decreased but remained highly significant, from 0.42 (s.e.=0.04, p=3.1x10-26) to 0.26 (s.e.=0.05, p=4.2x10-8).

## Functional consequences of fine-mapped variants

We explored functional consequence of variants with high posterior probability of association (PPA) from the fine-mapping analysis. We used various non-coding variation scoring systems to suggest variants’ functional status. An intronic variant at *NPNT* (rs34712979) appeared to reside in regulatory regions for several cell types, including enhancers for fetal lung (**Supplementary Table 6**), and was predicted to be functional: CADD phred score =15.18 (among 15% most deleterious substitutions), FATHMM non-coding score=0.98 (predicted deleterious if >0.5), DeepSEA functional significance score=0.004 (a range of 0-1; lower scores mean higher likelihood of functional significance of the variant), FunSeq2 non-coding score=0.96 (a range of 0-1; higer scores mean more likely to be functional), ReMM score=0.95 (higher scores indicate more likely to be deleterious variants).

## Genetic correlation of COPD and related traits

To gain further insight of genetic contribution of COPD and other traits, we estimated genetic correlation among traits using linkage disequilibrium score regression (LDSC) in LD hub74,75 (**Supplementary Table 22**). We again identified correlations between COPD and lung function (FEV1 and FEV1/FVC), asthma, height, and additionally identified correlation of COPD and lung cancer (rg=0.18, P=0.003). However, we were not able to identify significant correlations with common COPD comorbidities, including bone mineral density, major depressive disorder, coronary artery disease, or type 2 diabetes mellitus.We found suggestive (P < 0.05) genetic correlation between COPD and hand grip, angina, weight, schizophrenia, and gastroesophageal reflux disease (**Supplementary Table 22**).

## Identification of drug targets

The recent development of richer datasets of drug-induced gene expression signatures72 and a statistical framework that utilizes genome-wide associations69 allow us to utilize genome-wide data for drug repositioning. This approach considers the similarity between disease and drug-induced gene expression signatures in an opposing pattern (i.e., use drug to reverse diseased gene expression signature). We approximated COPD gene expression patterns by calculating transcriptome-wide associations in lung tissue from genetic predictors76. We calculated standardized connectivity scores72 from drug-gene expression profiles across 2,837 compounds in nine cell lines including A594 and A555. We identified seven compounds with an opposing connectivity score >= 90%: leu-enkephalin (an opioid receptor agonist), huperizine-a (an acetylcholinesterase inhibitor), periplocymarin (an apoptosis stimulant), PAC-1 (a caspase activator), TER-14687 (an inhibitor of translocation of PKCq in T cells), vincristine (a tubulin inhibitor), and terreic-acid (a Bruton's tyrosine kinase (BTK) inhibitor).

# Supplementary Information for Select Candidate Target Genes

\* empirical pattern of gene expression in tissues from Human Protein Atlas77 (broad=expressed in multiple tissues, exclusive=expressed exclusively in lung, none=rarely expressed in lung).

|  |  |  |  |
| --- | --- | --- | --- |
| Locus (SNP) | Genes | Expression\* | Evidence |
| 1p13.3 | *DENND2D* | Broad | DENN domain containing 2D predominantly expresses in lymph node and appendix77. It is involved in Rab guanyl-nucleotide exchange factor activity78. |
|  | *CEPT1* | Broad | Choline/ethanolamine phosphotransferase 1 encodes an enzyme which functions in the synthesis of choline- or ethanolamine- containing phospholipids79. |
|  | *DRAM2* | Broad | DNA damage regulated autophagy modulator 2 encodes the protein that binds microtubule-associated protein 1 light chain 3 and is required for autophagy80. It is also associated with non-ST elevation myocardial infarction81 and retinal dystrophy82. |
|  | *CHIA* | Exclusive | Chitinase, acidic encodes a protein that degrades chitin79. Its expression is specific to lung77,83. Genetic variants in or around this gene were associated with baseline FEV1 and rate of FEV1 decline84, asthma85–88, acid mammalian chitinase activity87,89, and IgE86 although there were also some null results90. The protein is involved in T helper-2 (Th2)-mediated diseases and protects pulmonary epithelial cells from growth factor withdrawal- and Fas ligand-induced apoptosis91. It was induced via a Th2-specific, interleukin-13 (IL-13)-mediated pathway in epithelial cells and macrophages in an aeroallergen asthma model92, and ADAM17/EGFR-dependent pathway93. |
|  | *OVGP1* | Broad | Oviductal glycoprotein 1 encodes an epithelial glycoprotein. It is secreted from non-ciliated oviductal epithelial cells and associates with ovulated oocytes, blastomeres, and spermatozoan acrosomal regions79. |
|  | *WDR77* | Broad | WD repeat domain 77 encodes an androgen receptor coactivator79. It may be involved in the early stages of prostate cancer79. |
|  | *ATP5F1* (*ATP5PB*) | Broad | ATP synthase peripheral stalk-membrane subunit b encodes a subunit of mitochondrial ATP synthase79. Its hypomethylation was involved in drug resistance in chronic myeloid leukemia94. |
|  | *FAM212B* (*INKA2*) | Broad | Inka box actin regulator 2 is broadly expressed in multiple tissues including lung79. |
|  | *PROK1* | None | Prokineticin 1 induces proliferation, migration, and fenestration in capillary endothelial cells derived from endocrine glands79. It is induced by hypoxia, and often is complementary to the expression of vascular endothelial growth factor (VEGF)79. It was involved in angiogenesis in cystic fibrosis95. |
|  | *KCNC4* | Broad | Potassium voltage-gated channel subfamily C member 4 encodes a protein that generates atypical voltage-dependent transient current that may be important for neuronal excitability79. It was related to subacute hypoxia in pulmonary arterial smooth muscle cells96. |
| 3p14.3 | *ABHD6* | Broad | Abhydrolase domain containing 6 is involved in the control of macrophage activation and inflammation97. |
|  | *ARF4* | Broad | ADP ribosylation factor 4 encodes a protein that stimulates the ADP-ribosyltransferase activity of cholera toxin and plays a role in vesicular trafficking and as an activator of phospholipase D79. It is involved in Golgi stress and susceptibility to pathogens98. |
|  | *IL17RD* | Broad | Interleukin 17 receptor D encodes a membrane protein belonging to the interleukin-17 receptor (IL-17R) protein family79. The gene product affects fibroblast growth factor signaling, inhibiting or stimulating growth through MAPK/ERK signaling79. It also interacts with TNF receptor 2 (TNFR2) to activate NF-κB99. |
|  | *ARHGEF3* | Broad | Rho guanine nucleotide exchange factor 3 encodes a protein that activates RHOA and RHOB, which have a role in bone cell biology79. Its gene product also regulates a SPARC protein that participates in the assembly and turnover of the extracellular matrix100. It also has a role in iron uptake101. Genetic variants in or around this gene were associated with bone mineral density79. |
| 7p21.1 | *ITGB8* | Broad | Integrin subunit beta 8 is a member of the integrin beta chain family and encodes a single-pass type I membrane protein that binds to an alpha subunit to form an integrin complex79. The complexes mediate cell-cell and cell-extracellular matrix interactions and this complex plays a role in human airway epithelial proliferation79 and repair102. Its expression was increased in COPD103–105. It is involved in dendritic cell trafficking, and airway inflammation and fibrosis processes104. It mediates epithelial homeostasis through an MMP-dependent pathway106 and TGF-B103,107. It is also regulated by SP3, AP-1, and the p38 pathway108. |
|  | *ABCB5* | None | ATP binding cassette subfamily B member 5 belongs to the ATP-binding cassette (ABC) transporter superfamily of integral membrane proteins109. |
|  | *TMEM196* | None | Transmembrane protein 196 is a novel functional tumor suppressor and is associated with lung cancer110. |
| 11p15.2 | *BTBD10* | Broad | The gene product of BTB domain containing 10 is an Akt activator111. This gene was associated with neurologic diseases112. |
|  | *PARVA* | Broad | Parvin alpha encodes a member of the parvin family of actin-binding proteins79. The encoded protein is part of the integrin-linked kinase signaling complex and plays a role in cell adhesion, motility and survival79. |
|  | *MICALCL* | Broad | MICAL C-terminal like gene product is predominantly expressed in skin, testis, and lung77. |
| 15q25.2 | *ADAMTSL3* | Broad | ADAMTS like 3 encodes a gene product that plays a role in cell-matrix interactions or in assembly of specific extracellular matrices113. It was associated with schizophrenia114 and cardiac disorders in tetrasomy115. |
|  | *BNC1* | None | Basonuclin 1 encodes a zinc finger protein that is present in the basal cell layer of the epidermis and in hair follicles, and in the germ cells of testis and ovary79,116. Its gene product modulates epithelial plasticity and TGF-β1-induced loss of epithelial cell integrity117. It is a Pol I and Pol II transcription factor that is associated with epithelial expansion and proliferation118,119. |
|  | *BTBD1* | Broad | BTB domain containing 1 encodes a protein that binds topoisomerase I. It is a transcription factor120 in the human histone deacetylase family121. Its gene product is involved in mesenchymal122 and muscle cell differentiation123. |

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**COPDGene® Investigators – Core Units**

*Administrative Center*: James D. Crapo, MD (PI); Edwin K. Silverman, MD, PhD (PI); Barry J. Make, MD; Elizabeth A. Regan, MD, PhD

*Genetic Analysis Center*: Terri Beaty, PhD; Ferdouse Begum, PhD; Peter J. Castaldi, MD, MSc; Michael Cho, MD; Dawn L. DeMeo, MD, MPH; Adel R. Boueiz, MD; Marilyn G. Foreman, MD, MS; Eitan Halper-Stromberg; Lystra P. Hayden, MD, MMSc; Craig P. Hersh, MD, MPH; Jacqueline Hetmanski, MS, MPH; Brian D. Hobbs, MD; John E. Hokanson, MPH, PhD; Nan Laird, PhD; Christoph Lange, PhD; Sharon M. Lutz, PhD; Merry-Lynn McDonald, PhD; Margaret M. Parker, PhD; Dandi Qiao, PhD; Elizabeth A. Regan, MD, PhD; Edwin K. Silverman, MD, PhD; Emily S. Wan, MD; Sungho Won, Ph.D.; Phuwanat Sakornsakolpat, M.D.; Dmitry Prokopenko, Ph.D.

*Imaging Center*: Mustafa Al Qaisi, MD; Harvey O. Coxson, PhD; Teresa Gray; MeiLan K. Han, MD, MS; Eric A. Hoffman, PhD; Stephen Humphries, PhD; Francine L. Jacobson, MD, MPH; Philip F. Judy, PhD; Ella A. Kazerooni, MD; Alex Kluiber; David A. Lynch, MB; John D. Newell, Jr., MD; Elizabeth A. Regan, MD, PhD; James C. Ross, PhD; Raul San Jose Estepar, PhD; Joyce Schroeder, MD; Jered Sieren; Douglas Stinson; Berend C. Stoel, PhD; Juerg Tschirren, PhD; Edwin Van Beek, MD, PhD; Bram van Ginneken, PhD; Eva van Rikxoort, PhD; George Washko, MD; Carla G. Wilson, MS;

*PFT QA Center, Salt Lake City, UT*: Robert Jensen, PhD

*Data Coordinating Center and Biostatistics*, *National Jewish Health, Denver, CO*: Douglas Everett, PhD; Jim Crooks, PhD; Camille Moore, PhD; Matt Strand, PhD; Carla G. Wilson, MS

*Epidemiology Core*, *University of Colorado Anschutz Medical Campus, Aurora, CO*: John E. Hokanson, MPH, PhD; John Hughes, PhD; Gregory Kinney, MPH, PhD; Sharon M. Lutz, PhD; Katherine Pratte, MSPH; Kendra A. Young, PhD

*Mortality Adjudication Core:* Surya Bhatt, MD; Jessica Bon, MD; MeiLan K. Han, MD, MS; Barry Make, MD; Carlos Martinez, MD, MS; Susan Murray, ScD; Elizabeth Regan, MD; Xavier Soler, MD; Carla G. Wilson, MS

*Biomarker Core*: Russell P. Bowler, MD, PhD; Katerina Kechris, PhD; Farnoush Banaei-Kashani, Ph.D. **COPDGene® Investigators – Clinical Centers**

*Ann Arbor VA:* Jeffrey L. Curtis, MD; Carlos H. Martinez, MD, MPH; Perry G. Pernicano, MD.

*Baylor College of Medicine, Houston, TX*: Nicola Hanania, MD, MS; Philip Alapat, MD; Mustafa Atik, MD; Venkata Bandi, MD; Aladin Boriek, PhD; Kalpatha Guntupalli, MD; Elizabeth Guy, MD; Arun Nachiappan, MD; Amit Parulekar, MD;

*Brigham and Women’s Hospital, Boston, MA*: Dawn L. DeMeo, MD, MPH; Craig Hersh, MD, MPH; Francine L. Jacobson, MD, MPH; George Washko, MD

*Columbia University, New York, NY*: R. Graham Barr, MD, DrPH; John Austin, MD; Belinda D’Souza, MD; Gregory D.N. Pearson, MD; Anna Rozenshtein, MD, MPH, FACR; Byron Thomashow, MD

*Duke University Medical Center, Durham, NC*: Neil MacIntyre, Jr., MD; H. Page McAdams, MD; Lacey Washington, MD

*HealthPartners Research Institute, Minneapolis, MN*: Charlene McEvoy, MD, MPH; Joseph Tashjian, MD

*Johns Hopkins University, Baltimore, MD*: Robert Wise, MD; Robert Brown, MD; Nadia N. Hansel, MD, MPH; Karen Horton, MD; Allison Lambert, MD, MHS; Nirupama Putcha, MD, MHS

*Los Angeles Biomedical Research Institute at Harbor UCLA Medical Center, Torrance, CA*: Richard Casaburi, PhD, MD; Alessandra Adami, PhD; Matthew Budoff, MD; Hans Fischer, MD; Janos Porszasz, MD, PhD; Harry Rossiter, PhD; William Stringer, MD

*Michael E. DeBakey VAMC, Houston*, *TX*: Amir Sharafkhaneh, MD, PhD; Charlie Lan, DO

*Minneapolis VA:* Christine Wendt, MD; Brian Bell, MD

*Morehouse School of Medicine, Atlanta, GA*: Marilyn G. Foreman, MD, MS; Eugene Berkowitz, MD, PhD; Gloria Westney, MD, MS.

*National Jewish Health, Denver, CO*: Russell Bowler, MD, PhD; David A. Lynch, MB

*Reliant Medical Group, Worcester, MA*: Richard Rosiello, MD; David Pace, MD

*Temple University, Philadelphia, PA:* Gerard Criner, MD; David Ciccolella, MD; Francis Cordova, MD; Chandra Dass, MD; Gilbert D’Alonzo, DO; Parag Desai, MD; Michael Jacobs, PharmD; Steven Kelsen, MD, PhD; Victor Kim, MD; A. James Mamary, MD; Nathaniel Marchetti, DO; Aditi Satti, MD; Kartik Shenoy, MD; Robert M. Steiner, MD; Alex Swift, MD; Irene Swift, MD; Maria Elena Vega-Sanchez, MD

*University of Alabama, Birmingham, AL:* Mark Dransfield, MD; William Bailey, MD; Surya Bhatt, MD; Anand Iyer, MD; Hrudaya Nath, MD; J. Michael Wells, MD

*University of California, San Diego, CA*: Joe Ramsdell, MD; Paul Friedman, MD; Xavier Soler, MD, PhD; Andrew Yen, MD

*University of Iowa, Iowa City, IA*: Alejandro P. Comellas, MD; Karin F. Hoth, PhD; John Newell, Jr., MD; Brad Thompson, MD

*University of Michigan, Ann Arbor, MI*: MeiLan K. Han, MD, MS; Ella Kazerooni, MD; Carlos H. Martinez, MD, MPH

*University of Minnesota, Minneapolis, MN*: Joanne Billings, MD; Abbie Begnaud, MD; Tadashi Allen, MD

*University of Pittsburgh, Pittsburgh, PA*: Frank Sciurba, MD; Jessica Bon, MD; Divay Chandra, MD, MSc; Carl Fuhrman, MD; Joel Weissfeld, MD, MPH

*University of Texas Health Science Center at San Antonio, San Antonio, TX*: Antonio Anzueto, MD; Sandra Adams, MD; Diego Maselli-Caceres, MD; Mario E. Ruiz, MD

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**ECLIPSE Investigators** — *Bulgaria:* Y. Ivanov, Pleven; K. Kostov, Sofia. *Canada:* J. Bourbeau, Montreal; M. Fitzgerald, Vancouver, BC; P. Hernandez, Halifax, NS; K. Killian, Hamilton, ON; R. Levy, Vancouver, BC; F. Maltais, Montreal; D. O'Donnell, Kingston, ON. *Czech Republic:* J. Krepelka, Prague. *Denmark:* J. Vestbo, Hvidovre. *The Netherlands:* E. Wouters, Horn-Maastricht. *New Zealand:* D. Quinn, Wellington. *Norway:* P. Bakke, Bergen. *Slovenia:* M. Kosnik, Golnik. *Spain:* A. Agusti, J. Sauleda, P. de Mallorca. *Ukraine:* Y. Feschenko, V. Gavrisyuk, L. Yashina, Kiev; N. Monogarova, Donetsk. *United Kingdom:* P. Calverley, Liverpool; D. Lomas, Cambridge; W. MacNee, Edinburgh; D. Singh, Manchester; J. Wedzicha, London. *United States:* A. Anzueto, San Antonio, TX; S. Braman, Providence, RI; R. Casaburi, Torrance CA; B. Celli, Boston; G. Giessel, Richmond, VA; M. Gotfried, Phoenix, AZ; G. Greenwald, Rancho Mirage, CA; N. Hanania, Houston; D. Mahler, Lebanon, NH; B. Make, Denver; S. Rennard, Omaha, NE; C. Rochester, New Haven, CT; P. Scanlon, Rochester, MN; D. Schuller, Omaha, NE; F. Sciurba, Pittsburgh; A. Sharafkhaneh, Houston; T. Siler, St. Charles, MO; E. Silverman, Boston; A. Wanner, Miami; R. Wise, Baltimore; R. ZuWallack, Hartford, CT.

**ECLIPSE Steering Committee**: H. Coxson (Canada), C. Crim (GlaxoSmithKline, USA), L. Edwards (GlaxoSmithKline, USA), D. Lomas (UK), W. MacNee (UK), E. Silverman (USA), R. Tal Singer (Co-chair, GlaxoSmithKline, USA), J. Vestbo (Co-chair, Denmark), J. Yates (GlaxoSmithKline, USA).

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