Meta-analysis of exome array data identifies six novel genetic loci for lung function

Victoria E Jackson [1], Jeanne C Latourelle [2], Louise V Wain [1,3], Albert V. Smith [4,5], Megan L. Grove [6], Traci M Bartz [7], Maen Obeidat [8], Michael A Province [9], Wei Gao [10], Beenish Qaiser [11], David J Porteous [12], Patricia A Cassano [13,14], Tarunveer S. Ahluwalia [15,16], Niels Grarup [15], Jin Li [17], Elisabeth Altmaier [18], Jonathan Marten [19], Sarah E Harris [20,21], Ani Manichaikul [22], Tess D Pottinger [23,24], Ruifang Li-Gao [25], Allan Lind-Thomsen [26,27], Anubha Mahajan [28], Lies Lahousse [29,30], Medea Imboden [31,32], Alexander Teumer [33], Bram Prins [34], Leo-Pekka Lyytikäinen [35,36], Gudny Eiriksdottir [4], Nora Franceschini [37], Colleen M Sitlani [38], Jennifer A Brody [38], Yohan Bossé [39], Wim Timens [40,41], Aldi Kraja [9], Anu Loukola [11], Wenbo Tang [13,42], Yongmei Liu [43], Jette Bork-Jensen [15], Johanne M. Justesen [15], Allan Linneberg [44,45,46], Leslie A. Lange [47], Rajesh Rawal [18], Stefan Karrasch [48,49], Jennifer E Huffman [19], Blair H Smith [50], Gail Davies [20,51], Kristin M Burkart [23], Josyf C Mychaleckyj [22], Tobias N. Bonten [52,53], Stefan Enroth [26], Lars Lind [54], Guy G Brusselle [29,30,55], Ashish Kumar [31,32,28,56], Beate Stubbe [57], Understanding Society Scientific Group , Mika Kähönen [58,59], Annah B. Wyss [60], Bruce M Psaty [61,62], Susan R Heckbert [63], Ke Hao [64,65], Taina Rantanen [66], Stephen B Kritchevsky [67], Kurt Lohman [43], Tea Skaaby [44], Charlotta Pisinger [44], Torben Hansen [15], Holger Schulz [48,68], Ozren Polasek [69], Archie Campbell [12], John M Starr [20,70], Stephen S Rich [22], Dennis O. Mook-Kanamori [25,53], Åsa Johansson [26], Erik Ingelsson [71,72], André G Uitterlinden [73,30], Stefan Weiss [74,75], Olli T. Raitakari [76,77], Vilmundur Gudnason [4,5], Kari E. North [78], Sina A Gharib [79], Don D Sin [8,80], Kent D Taylor [81], George T O'Connor [82,83], Jaakko Kaprio [11,84,85], Tamara B Harris [86], Oluf Pedersen [15], Henrik Vestergaard [15,87], James G. Wilson [88], Konstantin Strauch [89,90], Caroline Hayward [19], Shona Kerr [19], Ian J Deary [20,51], R Graham Barr [23,91], Renée de Mutsert [25], Ulf Gyllensten [26], Andrew P Morris [92,28], M. Arfan Ikram [30,93,94], Nicole M Probst-Hensch [31,32], Sven Gläser [57,95], Eleftheria Zeggini [34], Terho Lehtimäki [35,36], David P Strachan [96], Josee Dupuis [10], Alanna C. Morrison [6], Ian P Hall [97], Martin D Tobin [1,3]*, Stephanie J London [60]*

1. Department of Health Sciences, University of Leicester, Leicester, UK
2. Department of Neurology, Boston University school of Medicine, Boston MA
3. National Institute for Health Research, Leicester Respiratory Biomedical Research Unit, Glenfield Hospital, Leicester, UK
4. Icelandic Heart Association, 201 Kopavogur, Iceland
5. University of Iceland, 101 Reykjavik Iceland
6. Human Genetics Center, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston. Houston TX 77030
7. Cardiovascular Health Research Unit, Departments of Medicine and Biostatistics, University of Washington, Seattle, WA, USA, 98101
8. The University of British Columbia Centre for Heart Lung Innovation, St Paul's Hospital, Vancouver, BC, Canada
9. Department of Genetics, Washington University School of Medicine, St. Louis, MO.
10. Department of Biostatistics, Boston University School of Public Health, Boston, MA, USA
11. Institute for Molecular Medicine Finland (FIMM), University of Helsinki, FI-00014, Helsinki, Finland
12. Centre for Genomic & Experimental Medicine, MRC Institute of Genetics & Molecular Medicine, University of Edinburgh, Edinburgh, EH4 2XU, UK
13. Division of Nutritional Sciences, Cornell University, Ithaca NY
14. Department of Healthcare Policy and Research, Division of Biostatistics and Epidemiology, Weill Cornell Medical College NY, NY
15. The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark
16. Steno Diabetes Center Copenhagen, Gentofte, Denmark
17. Department of Medicine, Division of Cardiovascular Medicine, Stanford University School of Medicine, Palo Alto, CA, USA

18. Research Unit of Molecular Epidemiology, Institute of Epidemiology II, Helmholtz Zentrum München, German Research Center for Environmental Health, 85764 Neuherberg, Germany
19. Medical Research Council Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh EH4 2XU, UK
20. Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh, Edinburgh, UK, EH8 9JZ
21. Centre for Genomic and Experimental Medicine, University of Edinburgh, Edinburgh, UK, EH4 2XU
22. Center for Public Health Genomics, Department of Public Health Sciences, University of Virginia, Charlottesville, VA
23. Department of Medicine, College of Physicians and Surgeons, Columbia University, New York, NY
24. Department of Preventive Medicine - Division of Health and Biomedical Informatics, Northwestern University - Feinberg School of Medicine, Chicago, IL
25. Department of Clinical Epidemiology, Leiden University Medical Center, Leiden, the Netherlands, 2333 ZA
26. Department of Immunology, Genetics, and Pathology, Biomedical Center, SciLifeLab Uppsala, Uppsala University, SE-75108 Uppsala, Sweden
27. Center for health and infectious disease research, Rigshospitalet, Copenhagen, Denmark
28. Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK
29. Respiratory Medicine, Ghent University Hospital, Ghent, Belgium, BE9000
30. Epidemiology, Erasmus Medical Center, Rotterdam, the Netherlands, 3000CA
31. Swiss Tropical and Public Health Institute, Basel, Switzerland
32. University of Basel, Switzerland
33. Institute for Community Medicine, University Medicine Greifswald, 17475 Greifswald, Germany
34. Human Genetics, Wellcome Trust Sanger Institute, Hinxton, UK, CB10 1SA
35. Department of Clinical Chemistry, Fimlab Laboratories, Tampere 33520, Finland
36. Department of Clinical Chemistry, Faculty of Medicine and Life Sciences, University of Tampere, Tampere 33014, Finland
37. Department of Epidemiology, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC 27514
38. Cardiovascular Health Research Unit, Department of Medicine, University of Washington, Seattle, WA, USA, 98101
39. Institut universitaire de cardiologie et de pneumologie de Québec, Department of Molecular Medicine, Laval University, Québec, Canada
40. University of Groningen, University Medical Center Groningen, Department of Pathology and Medical Biology, HPC-EA10, Groningen, The Netherlands, NL9713 GZ
41. University of Groningen, University Medical Center Groningen, Groningen Research Institute for Asthma and COPD
42. Boeringher Ingleheim, Danbury, CT,
43. Wake Forest School of Medicine, Winston-Salem, North Carolina, USA
44. Research Centre for Prevention and Health, Capital Region of Denmark, 2600 Copenhagen, Denmark
45. Department of Clinical Experimental Research, Rigshospitalet, 2600 Glostrup, Denmark
46. Department of Clinical Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark
47. Department of Medicine, Division of Bioinformatics and Personalized Medicine, University of Colorado Denver, Aurora, CO, USA
48. Institute of Epidemiology I, Helmholtz Zentrum München, German Research Center for Environmental Health, 85764 Neuherberg, Germany
49. Institute and Outpatient Clinic for Occupational, Social and Environmental Medicine, Ludwig-Maximilians-Universität, Munich, Germany.
50. Division of Population Health Sciences, Ninewells Hospital and Medical School, University of Dundee, Dundee, DD1 9SY, UK
51. Psychology, University of Edinburgh, Edinburgh, UK, EH8 9JZ
52. Department of Pulmonology, Leiden University Medical Center, Leiden, the Netherlands, 2333 ZA
53. Department of Public Health and Primary Care, Leiden University Medical Center, Leiden, the Netherlands, 2333 ZA
54. Department of Medical Sciences, Uppsala University Hospital, Uppsala, Sweden
55. Respiratory Medicine, Erasmus Medical Center, Rotterdam, the Netherlands, 3000CA
56. Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden
57. Internal Medicine B, University Medicine Greifswald, 17475 Greifswald, Germany

58. Department of Clinical Physiology, Tampere University Hospital, Tampere 33521, Finland
59. Department of Clinical Physiology, Faculty of Medicine and Life Sciences, University of Tampere, Tampere 33014, Finland
60. Epidemiology Branch, National Institute of Environmental Health Sciences, National Institute of Health, Dept of Health and Human Services, Research Triangle Park, NC, 27709, USA
61. Cardiovascular Health Research Unit, Departments of Epidemiology, Medicine and Health Services, University of Washington, Seattle, WA, 98101
62. Kaiser Permanente Washington Health Research Insititute
63. Cardiovascular Health Research Unit, Department of Epidemiology, University of Washington, Seattle, WA, 98101
64. Department of Genetics and Genomic Sciences , Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, New York, NY 10029-6574
65. Icahn Institute of Genomics and Multiscale Biology, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, New York, NY 10029-6574
66. Department of Health Sciences, University of Jyväskylä FI-40014 Jyväskylä, Finland
67. Sticht Center on Aging, Wake Forest School of Medicine, Winston-Salem, North Carolina
68. Comprehensive Pneumology Center Munich (CPC-M), Member of the German Center for Lung Research, Munich, Germany
69. Faculty of Medicine, University of Split, Split, Croatia
70. Alzheimer Scotland Research Centre, University of Edinburgh, Edinburgh, UK, EH8 9JZ
71. Department of Medical Sciences, Molecular Epidemiology and Science for Life Laboratory, Uppsala University, Uppsala, Sweden
72. Department of Medicine, Division of Cardiovascular Medicine, Stanford University School of Medicine, CA 94305, USA
73. Internal Medicine, Erasmus Medical Center, Rotterdam, the Netherlands, 3000CA
74. Interfaculty Institute for Genetics and Functional Genomics, University Medicine Greifswald, 17475 Greifswald, Germany
75. DZHK (German Centre for Cardiovascular Research), partner site: Greifswald, Greifswald, Germany.
76. Department of Clinical Physiology and Nuclear Medicine, Turku University Hospital, Turku 20521, Finland
77. Research Centre of Applied and Preventive Cardiovascular Medicine, University of Turku, Turku 20014, Finland
78. Department of Epidemiology and Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill, NC 27514
79. Computational Medicine Core, Center for Lung Biology, UW Medicine Sleep Center, Department of Medicine, University of Washington, Seattle, WA, 98109
80. Respiratory Division, Department of Medicine, University of British Columbia, Vancouver, BC, Canada
81. Institute for Translational Genomics and Population Sciences and Department of Pediatrics, Los Angeles Biomedical Research Institute at Harbor-UCLA Medical Center, Torrance, CA
82. Pulmonary Center, Department of Medicine, Boston University School of Medicine, Boston, MA 02118, USA
83. National Heart, Lung, and Blood Institute's and Boston University's Framingham Heart Study, Framingham, MA 01702, USA
84. Department of Public Health, University of Helsinki, FI-00014, Helsinki, Finland
85. Department of Health, National Institute for Health and Welfare, FI-00271 Helsinki, Finland
86. National Institute on Aging, National Institutes of Health, Bethesda, Maryland
87. Steno Diabetes Center Copenhagen, Gentofte, Denmark.
88. Department of Physiology and Biophysics, University of Mississippi Medical Center, Jackson, MS, USA
89. Institute of Genetic Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, 85764 Neuherberg, Germany
90. Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig-Maximilians-Universität, 81377 Munich, Germany
91. Department of Epidemiology, Mailman School of Public Health, Columbia University, New York, NY
92. Department of Biostatistics, University of Liverpool, Liverpool, UK
93. Radiology, Erasmus Medical Center, Rotterdam, the Netherlands, 3000CA
94. Neurology, Erasmus Medical Center, Rotterdam, the Netherlands, 3000CA
95. Vivantes Klinikum Spandau Berlin, Department of Internal Medicine - Pulmonary Diseases, 13585 Berlin
96. Population Health Research Institute, St George's, University of London, Cranmer Terrace, London SW17

0RE, UK
97. Division of Respiratory Medicine, University of Nottingham, Nottingham, UK

Abstract

Over 90 regions of the genome have been associated with lung function to date, many of which have also been implicated in chronic obstructive pulmonary disease (COPD). We carried out meta-analyses of exome array data and three lung function measures: forced expiratory volume in one second (FEV_1), forced vital capacity (FVC) and the ratio of FEV_1 to FVC (FEV_1/FVC). These analyses by the SpiroMeta and CHARGE consortia included 60,749 individuals of European ancestry from 23 studies, and 7,721 individuals of African Ancestry from 5 studies in the discovery stage, with follow-up in up to 111,556 independent individuals. We identified significant ($P<2{\cdot}8\times10^{-7}$) associations with six SNPs: a nonsynonymous variant in *RPAP1*, which is predicted to be damaging, three intronic SNPs (*SEC24C, CASC17* and *UQCC1*) and two intergenic SNPs near to *LY86* and *FGF10.* eQTL analyses found evidence for regulation of gene expression at three signals and implicated several genes including *TYRO3* and *PLAU*. Further interrogation of these loci could provide greater understanding of the determinants of lung function and pulmonary disease.

Introduction

Lung function measures are important predictors of mortality and morbidity and form the basis for the diagnosis of chronic obstructive pulmonary disease (COPD), a leading cause of death globally.[1] Lung function is largely affected by environmental factors such as smoking and exposure to air pollution; however there is also a genetic component, with heritability estimates ranging between 39-66%.[2–5] A number of large-scale genome-wide association studies (GWAS) of lung function have successfully identified single nucleotide polymorphisms (SNPs) influencing lung function at over 90 independent loci.[6–13] Associations have also been identified in GWAS of COPD;[14–18] however the identification of disease associated SNPs has been restricted by limited sample sizes. Many signals first identified in powerful studies of quantitative lung function traits, have been found to be associated with risk of COPD, highlighting the potential clinical usefulness of comprehensive identification of lung function associated SNPs.[13]

Low frequency (minor allele frequency (MAF) 1-5%) and rare (MAF<1%) variants, have been largely underexplored by GWAS to date. Exome arrays have been designed to facilitate the investigation of these low frequency and rare variants, predominately within coding regions, in large sample sizes. Alongside a core content of rare coding SNPs, the exome array additionally includes common variation including tags for previously identified GWAS hits, ancestry informative SNPs, a grid of markers for estimating identity by descent and a random selection of synonymous SNPs.[19]

Results

We carried out a meta-analysis of exome array data and three lung function measures: forced expiratory volume in one second (FEV_1), forced vital capacity (FVC) and the ratio of FEV_1 to FVC (FEV_1/FVC). These analyses included 68,470 individuals from the SpiroMeta and CHARGE consortia in a discovery analysis, with follow-up in an independent sample of up to 111,556 individuals. All

studies are listed with their study-specific sample characteristics in Table 1, with full study descriptions, including details of spirometry and other measurements described in the Supplementary Note. The genotype calling procedures implemented by each study (Supplementary Table 1) and quality control of genotype data are described in the Supplementary Methods. We have undertaken both single variant analyses, and gene-based associations, which test for the joint effect of several rare variants in a gene (see methods for details).

Meta-analyses of single variant associations

We first evaluated single variant associations between FEV_1, FVC and FEV_1/FVC and the 179,215 SNPs which passed study level quality control and were polymorphic in both consortia. These analyses identified 34 SNPs in regions not previously associated with lung function, showing association with at least one trait at overall $P<10^{-5}$, and showing association with consistent direction and P<0·05 in both consortia (full results in Supplementary Table 2, quantile-quantile and Manhattan plots shown in Supplementary Figure 1). We followed up these SNP associations in a replication analysis comprising 3 studies with 111,556 individuals. Combining the results from the discovery and replication stages in a meta-analysis identified six SNPs in total that were independent to known signals and met the pre-defined significance threshold ($P<2{\cdot}8x10^{-7}$) overall in, or near to *FGF10*, *LY86*, *SEC24C*, *RPAP1, CASC17* and *UQCC1* (Table 2, Supplementary Figure 2). A SNP near to the *CASC17* signal (rs11654749, r^2=0·3 with rs1859962) has previously been associated with FEV_1 in a genome-wide analysis of gene-smoking interactions, although this association was not replicated at the time;[20] the present analysis provides the first evidence for independent replication of this signal. A seventh signal was also identified in *LCT* (Table 2, Supplementary Figure 2); whilst this locus has not previously been implicated in lung function, this SNP is known to vary in frequency across European populations,[21] and we cannot rule out that this association is not an artefact of population structure. Our discovery analysis furthermore identified associations ($P<10^{-5}$) in 25 regions previously associated with one or more of FEV_1, FVC and FEV_1/FVC (Supplementary Table 3).

Generally, the observed effect of the SNPs at the novel signals were similar in ever and never smokers; the exception was rs1448044 near *FGF10*, which showed a significant association with FVC only in ever smokers in our discovery analysis (ever smokers $P=1{\cdot}49x10^{-6}$; never smokers P=0·695, Supplementary Table 4 and Supplementary Figure 3). In the replication analysis, however, this association was observed in both ever and never smokers (ever smokers $P=3{\cdot}14x10^{-5}$; never smokers $P=1{\cdot}40x10^{-4}$, Supplementary Table 5). For rs1200345 (*RPAP1*) and rs1859962 (*CASC17*)), associations were most statistically significant in the analyses restricted to individuals of European Ancestry (Supplementary Table 4 and Supplementary Figure 3), as was the association with rs2322659 (*LCT*), giving further support that this association may be due to population stratification.

Meta-Analyses of gene-based associations

We undertook Weighted Sum Tests (WST)[22] and Sequence Kernel Association tests (SKAT)[23] to assess the joint effects of multiple low frequency variants within genes on lung function traits. In our discovery analyses of all 68,470 individuals, we tested up to 14,380 genes that had at least two variants with MAF<5% and met the inclusion criteria (exonic or loss of function [LOF], see methods for definitions) in both consortia. The SKAT analyses identified 16 genes associated (P<0·05 in both consortia and overall $P<10^{-4}$) with FEV_1, FVC or FEV_1/FVC (Supplementary Table 6), whilst the WST analyses identified 12 genes (Supplementary Table 7). There was one gene (*LY6G6D*) that was identified in both analyses. These genes were followed up in UK Biobank, with two genes, *GPR126* and *LTBP4,* showing evidence of replication in the exonic SKAT analysis ($P<3{\cdot}5x10^{-6}$); however conditional analyses in UK Biobank showed that both these associations were driven by single SNPs, that were identified in the single variant association analyses and have been previously reported in GWAS of these traits (Tables E6 & E7).

Functional characterization of novel loci

In order to gain further insight into the six loci identified in our analyses of single variant associations (excluding *LCT*), we employed functional annotation and assessed whether identified SNPs in these

regions were associated with gene expression levels. One of the identified novel SNPs was nonsynonymous, three intronic and two were intergenic. We found evidence that three of the SNPs may be involved in cis-acting regulation of the expression of several genes in multiple tissues (Supplementary Table 8).

SNP rs1200345 in *RPAP1* is a nonysynomous variant, predicted to be deleterious by both SIFT (deleterious) and Polyphen (possibly damaging) (Supplementary Table 9); *RPAP1* is ubiquitously expressed, with high levels of protein detected in the lung (Supplementary Table 10). SNP rs1200345 or proxies (r^2>0·8) were also found to be amongst the most strongly associated SNPs with expression levels of *RPAP1* in several tissues including lung, and with a further six genes in lung tissue (Supplementary Table 8) including *TYRO3,* one of the TAM family of receptor tyrosine kinases. *TYRO3* regulates several processes including cell survival, migration and differentiation and is highly expressed in lung macrophages (Supplementary Table 10). Evidence for associations with gene expression was found at two more of the novel signals (sentinel SNPs rs3849969 and rs6088813), implicating a further 16 genes. Of note, in blood eQTL databases, a proxy of a SNP in complete linkage disequilibrium (r^2=1) with rs3849969 (rs3812637) was an eQTL for plasminogen activator, urokinase (*PLAU*).

Discussion

We undertook an analysis of 68,470 individuals from 23 studies with data from the exome array and three lung function traits, following up the most significant single SNP and gene-based associations in an independent sample of up to 111,556 individuals. The combined analyses of our discovery and replication single variant associations identified six SNPs meeting the pre-defined significance threshold ($P<2{\cdot}8\times10^{-7}$). The replication stage results for these six SNPs also meet Bonferroni corrected significance for independent replication ($P<1{\cdot}47\times10^{-3}$, corrected for 34 SNPs being tested).

One of these SNPs is in a region that has previously been implicated in lung function (near *KCJN2/SOX9*),[20] whilst the remaining five SNPs, although all common, have not previously been identified in other GWAS of lung function. In a recent 1000 Genomes imputed analysis of lung function (which includes some of the studies contributing to the present discovery analysis), all of these SNPs showed at least suggestive association ($2{\cdot}97 \times 10^{-3} > P > 1{\cdot}28 \times 10^{-5}$) with one or more lung function trait, but none reached the required threshold ($P < 5 \times 10^{-6}$) to be taken forward for replication in that analysis.[12]

We further identified a seventh association ($P < 2{\cdot}8 \times 10^{-7}$) with rs2322659 in *LCT*. Given SNPs in this region are known to vary in frequency across European populations, we cannot dismiss the possibility that this association may be confounded by population stratification; hence we do not report this signal as a novel lung function locus. We undertook a look-up of associations in our discovery meta-analyses of 7 loci (including LCT) that were identified as showing differences in allele frequency between individuals from different regions in the UK,[24] and subsequently across European populations.[25] Aside from the association between the *LCT* locus and FVC, no significant associations were observed between SNPs at these loci and any lung function trait, in either the analyses restricted to EA individuals, or in the analysis of EA and AA individuals combined (Supplementary Table 11); this suggests population structure was generally accounted for adequately in our analyses.

One of the novel signals was with a nonsynonymous SNPs: rs1200345 in *RPAP1*, which is predicted to be deleterious. This SNP and proxies with $r^2 > 0{\cdot}8$ were also associated with expression in lung tissue of seven genes, including *RPAP1* and the TAM receptor *TYRO3*. TAM receptors play a role in the inhibition of Toll-like receptors (TLRs)-mediated innate immune response by initiating the transcription of cytokine signalling genes (SOCS-1 and 3) which limit cytokine overproduction and inflammation.[26,27] It has been shown that influenza viruses H5N1 and H7N9 can cause downregulation of Tyro3, resulting in an increased inflammatory cytokine response.[27]

Three further signals were with intronic SNPs in *SEC24C*, *CASC17*, and *UQCC1*. Two of these intronic SNPs have previously been implicated in GWAS of other traits: rs1859962 in *CASC17* with prostate cancer[28] and rs6088813 in *UQCC1* with height.[29] The *CASC17* locus, near *KCNJ2/SOX9* has also previously been implicated in lung function, showing significant association with FEV_1 in a genome-wide analysis of gene-smoking interactions, however this association was not formally replicated.[20] Whilst the individuals utilised in the discovery stage of this analysis overlap with those included in this previous interaction analysis, the replication stage of the present study provides the first evidence of replication for this signal in independent cohorts. In the present analysis, there was no evidence that the results differed by smoking status.

SNPs rs6088813 in *UQCC1* and rs3849969 in *SEC24C* were identified as eQTLs for multiple genes. Notably, a SNP in complete linkage disequilibrium with rs3849969 (rs3812637, r^2=1) is associated with expression of *PLAU* in blood. The plasminogen activator, urokinase (PLAU) plays a role in fibrinolysis and immunity, and with its receptor (PLAUR) is involved in degradation of the extra cellular matrix, cell migration, cell adhesion and cell proliferation.[30] A study of preterm infants with respiratory distress syndrome, a condition characterised by intra-alveolar fibrin deposition, found *PLAU* and its inhibitor *SERPINE1* to be expressed in the alveolar epithelium, and an increased ratio of *SERPINE1* to *PLAU* was associated with severity of disease.[31] Studies in mice have also shown that increased expression of *PLAU* may be protective against lung injury, by reducing fibrosis.[32] *PLAU* has also been found to be upregulated in lung epithelial cells subjected to cyclic strain[33] and in patients with COPD and lung cancer, PLAU was found to be expressed in alveolar macrophages and epithelial cells.[30]

The final two signals were with common intergenic SNPs close to *LY86* and *FGF10*. *LY86* (lymphocyte antigen 86) interacts with the Toll-like receptor signalling pathway, when bound with RP105 to form a heterodimer. [34] The sentinel SNP rs1294421 has previously been associated with waist-hip ratio,[35] and an intronic SNP within *LY86* (rs7440529, LD with rs1294421: r^2=0·005) has previously been implicated in asthma in two studies of individuals of Han Chinese ancestry. [36,37] FGF10 is a member

of the fibroblast growth factor family of proteins, involved in a number of biological processes, including embryonic development, cell growth, morphogenesis, tissue repair, tumor growth and invasion. Specifically, the FGF10 signalling pathway plays an essential role in lung development and lung epithelial renewal.[38] A study in mice demonstrated that a deficiency in *FGF10* resulted in a fatal disruption of branching morphogenesis during lung development.[39]

Our discovery analyses included individuals of both European and African ancestry. Two of the identified six novel signals showed inconsistent effects in the African and European ancestry individuals. For these SNPs, the associations in African Ancestry individuals were not statistically significant, and we report associations from the analysis restricted to European ancestry individuals only. For the remaining four SNPs similar effects were observed in both the European and African ancestry individuals (Supplementary Figure 3). We also examined the effects of the novel SNPs in ever smokers and never smokers separately and found these to be broadly similar, with the exception of rs1448044 in *FGF10,* which in the discovery analysis showed significant association with FVC in ever smokers, whilst showing no association in never smokers (P=0·695). In our replication stage analyses, similar effects were seen in both ever and never smokers for this SNP however, and the combined analysis of discovery and replication stages for this SNP, including both ever and never smokers, met the exome chip-wide significance level overall ($P=4{\cdot}22 \times 10^{-9}$). We also considered whether this signal could be driven by smoking behaviour in our discovery stage as our primary analyses in SpiroMeta did not adjust for smoking quantity. We undertook a look-up of this SNP in the publicly available results of a GWAS of several smoking behaviour traits;[40] there was only weak evidence that this SNP was associated with ever versus never smoking (P=0·039), and no evidence for association with amount smoked (cigarettes per day, P=0·10).

Through the use of the exome array, we aimed to identify associations with low frequency and rare functional variants, thereby potentially uncovering some of the missing heritability of lung function. However, whilst our discovery analyses identified single SNP associations with 23 low frequency variants (Supplementary Table 2), we did not replicate any of these findings. Eleven of these 23 SNPs

we were unable to follow-up in our replication studies, due to them either being not genotyped, or monomorphic. Overall, our lack of convincing associations with rare variants is likely due to limited statistical power for identifying single variant associations, particularly if those variants exhibit only modest effects.[41] We additionally employed SKAT and WST gene-based tests to investigate the joint effects of low frequency and rare variants within genes, on lung function traits. These analyses identified associations with a number of genes that did not appear to be driven by single SNPs. Replication of these signals proved difficult however, as again many SNPs included within the discovery stage of these analyses were not genotyped, or were monomorphic in the replication studies. This often meant a disparity in the gene unit being tested in our discovery and replication samples; hence the interpretation of these results was not straightforward. In the end, we were able to replicate only findings with common SNPs. This finding is in line with several other studies of complex traits and exome array data that have been unable to report robust associations with low frequency variants[42–44] and it is clear that future studies, will require increasingly larger sample sizes in order to fully evaluate the effect of variants across the allele frequency spectrum. The identification of common SNPs remains important however, as such findings have the potential to highlight drug targets,[45] and these variants collectively could have utility in risk prediction.

This study has identified six common SNPs, independent to signals previously implicated in lung function. Further interrogation of these loci could lead to greater understanding of lung function and lung disease, and could provide novel targets for therapeutic interventions.

Methods

Study Design, cohorts and genotyping

The SpiroMeta analysis included 23,751 individuals of European ancestry (EA) from 11 studies, and the CHARGE analysis comprised 36,998 EA individuals and a further 7,721 individuals of African ancestry (AA) from 12 studies. Follow-up analyses were conducted in an independent sample of up to 111,556 individuals from UK Biobank, the UK Household Longitudinal Study (UKHLS) and the Netherlands Epidemiology of Obesity (NEO) Study (Figure 1). All studies (excluding UK Biobank) were genotyped using either the Illumina Human Exome BeadChip v1or the Illumina Infinium HumanCoreExome-12 v1·0 BeadChip. UK Biobank samples were genotyped using the Affymetrix Axiom UK BiLEVE or UK Biobank arrays.

Statistical analyses

Consortium level analyses: Within the SpiroMeta Consortium, each study contributing to the discovery analyses calculated single-variant score statistics, along with covariance matrices describing correlations between variants, using RAREMETALWORKER[46] or rvtests.[47] For each trait, these summary statistics were generated separately in ever and never smokers, with adjustment for sex, age, age^2 and height, and with each trait being inverse normally transformed prior to association testing. For studies with unrelated individuals, further adjustments were made for the first 10 ancestry principal components, whilst studies with related individuals utilised linear mixed models to account for familial relationships and underlying population structure.

Within the CHARGE Consortium, each study generated equivalent summary statistics using the R package SeqMeta.[48] For each trait, summary statistics were generated in ever and never smokers separately, and in all individuals combined. The untransformed traits were used for all analyses, adjusted for smoking status and pack-years, age, age^2, sex, height, height^2, centre/cohort. Models for FVC were additionally adjusted for weight. Linear regression models, with adjustment for

principal components of ancestry were used for studies with unrelated individuals, and linear mixed models were used for family-based studies.

Within each consortium we used the score statistics and variance-covariance matrices generated by each study to construct both single variant and gene-based tests using either RAREMETAL[46] (SpiroMeta) or SeqMeta[48] (CHARGE). For single variant associations, score statistics were combined in fixed effects meta-analyses. Two gene-based tests were constructed: first, the Weighted Sum Test (WST) using Madsen Browning weightings,[22] and secondly, the Sequence Kernel Association Test (SKAT).[23] We performed the SKAT and WST tests using two subsets of SNPs: 1) including all SNPs with an overall consortium-wide MAF<5% that were annotated as splicing, stopgain, stoploss, or frameshift (loss of function [LOF] analysis), and 2) including all SNPs meeting the LOF analysis criteria in addition to all other nonsynonymous variants with consortium wide MAF<5% (exonic analysis). Variants were annotated to genes using dbNSFP v2·6[49] on the basis of the GRCh37/hg19 database.

For both single variant and gene-based associations, consortium-level results were generated for ever smokers and never smokers separately, and in all individuals combined. Within the CHARGE Consortium, results were combined separately for the EA and AA studies and also in a trans-ethnic analysis of both ancestries.

Combined Meta-Analysis: The single variant association results from the SpiroMeta and CHARGE consortia were combined as follows: The genomic inflation statistic (λ) was calculated for SNPs with consortium-wide MAF>1%; where λ had a value greater than one, genomic control adjustment was applied to the consortium level P-values. The consortium-level results were then combined using sample size weighted z-score meta-analysis. The λ was again calculated for the meta-analysis results and genomic control applied, as appropriate. Since we were interested in identifying low frequency and rare variants, we applied no MAF or minor allele count (MAC) filter. We identified SNPs of interest as those with an overall $P<10^{-5}$ and a consistent direction of effect and P<0·05 observed in both consortia. Where we identified a SNP within 1Mb of a previously identified lung function SNP,

we deemed the SNP to represent an independent signal if it had $r^2<0{\cdot}2$ with the known SNP, and if it retained a $P<10^{-5}$, when conditional analyses were carried out with the known SNP, or a genotyped proxy, using data from the SpiroMeta Consortium, or UK Biobank. Our primary meta-analysis included all individuals; we additionally carried out analyses in smoking subgroups (ever and never smokers), and in the subgroup of individuals of European ancestry only.

For genes which contained at least 2 polymorphic SNPs in both consortia, we combined the results of the consortium level gene based tests using either z-score meta-analysis (WST) or Fisher's Method for combining P-values (SKAT). We identified genes of interest as those with $P<0{\cdot}05$ observed in both consortia and an overall $P<10^{-4}$. As in the analyses of single variant associations, our primary meta-analyses included all individuals, with secondary analyses undertaken in smoking and ancestry specific subgroups.

Replication Analyses: All SNP and gene-based associations were followed up for the trait with which they showed the most statistically significant association only. For associations identified through the smoking subgroup analyses, we followed up associations in the appropriate smoking strata; however no ancestry stratified follow-up was undertaken as replication studies included only a sufficient number of individuals of European Ancestry.

Single variant associations in UK Biobank were tested in ever smokers and never smokers separately using the score test as implemented in SNPTEST v2·5b4.[50] Traits were adjusted for age, age^2, height, sex, ten principal components and pack-years (ever smokers only), and inverse normally transformed. For UKHLS, analyses were undertaken analogously to the SpiroMeta discovery studies using RAREMETALWORKER, while for NEO, analyses were undertaken in the same way as was done in the CHARGE discovery studies using SeqMeta. The single variant results from all replication studies were combined using sample size weighted Z-score meta-analysis. Subsequently we combined the results from the discovery and replication stage analyses and we report SNPs with

overall exome-wide significance of $P<2{\cdot}8x10^{-7}$ (Bonferroni corrected for the original 179,215 SNPs tested).

We followed up genes of interest ($P<10^{-4}$) using data from UK Biobank only. Summary statistics for UK Biobank were generated using RAREMETALWORKER, with gene-based tests then constructed using RAREMETAL. Finally, we combined the results from the discovery analysis with the replication results in an overall combined meta-analysis using either z-score meta-analysis (WST) or Fisher's Method (SKAT). We declared genes with overall $P<3{\cdot}5x10^{-6}$ (Bonferroni corrected for 14,380 genes tested) in our combined meta-analysis to be statistically significant. For these statistically significant genes, we carried out additional analyses using the UK Biobank data in which we conditioned on the most significantly associated individual SNP within that gene, to determine whether this was a true gene-based signal, or whether the association could be ascribed to the single SNP (if the conditional P<0·01, then association was deemed to not be driven by the single SNP).

Characterization of findings

In order to gain further insight into the loci identified in our analyses of single variant associations, we assessed whether these regions were associated with gene expression levels in various tissues (FDR of 5%, or q-value<0·05), by querying a publically available blood eQTL database [51] and the GTEx project [52] for the sentinel SNPs, or any proxy ($r^2>0{\cdot}8$). We further assessed SNPs of interest (and proxies) within a lung eQTL resource based on non-tumour lung tissues of 1,111 individuals.[53–55] Descriptions of these resources and further details of the look-ups are provided in the Supplementary Methods. Moreover, all sentinel SNPs and proxies with $r^2>0.8$ were annotated using ENSEMBL's Variant Effect Predictor (VEP);[56] potentially deleterious coding variants were identified as those annotated as 'deleterious' by SIFT[57] or 'probably damaging' or 'possibly damaging' by PolyPhen-2.[58] For all genes implicated through the expression data or functional annotation, we searched for evidence of protein expression in the respiratory system by querying the Human Protein Atlas.[59]

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Author Contributions

Ordered Alphabetically:

ABW, AGE, AL, BMP, BS, CH, CP, DOMK, DPS, EZ, GGB, HS, IPH, JBJ, JK, KMB, LL, MAI, MAP, MDT, MK, NG, NMPH, OP, OTR, RdM, RGB, SBK, SG, SJL, SSR, TA, TBH, TH, TL, TR, TS, UG contributed to study concept and designs. AC, AJ, A.Manichaikul, BHS, BMP, BS, CP, DJP, DPS, EI, GGB, GTOC, IJD, JBJ, JGW, JK, JMS, KS, LAL, LL, LL, MAP, MI, MK, NG, NMPH, OP, OTR, PAC, RdM, RGB, RR, SBK, SE, SEH, SG, SK, SK, TA, TBH, TDP, TL, TNB, TR, UG, WT, WT contributed to phenotype data acquisition and quality control. AGE, AJ, AK, AK, ALT, ALT, A.Manichaikul, APM, AT, BMP, BP, CH, DOMK, EI, GD, HV, IJD, JAB, JCM, JGW, JL, KDT, KEN, KL, L-PL, LAL, LL, MAP, MI, MLG, NMPH, OP, RGB, RLG, RR, SBK, SE, SEH, SRH, SSR, SW, TBH, TDP, TH, TL, YL contributed to genotype data acquisition and quality control. DDS, KH, WT, YB contribute to eQTL data acquisition and quality control. ABW, ACM, AK, AK, ALT, A.Mahajan, A.Manichaikul, APM, AT, BP, BQ, CH, CMS, EA, HV, IPH, JAB, JCL, JD, JEH, JL, JM, JMJ, KL, L-PL, LL, LVW, MDT, MI, MO, NF, NMPH, OP, PAC, RLG, SE, SEH, SJL, SW, TDP, TH, TMB, VEJ, WG, WT, YL contributed to data analysis. All authors contributed to writing and/or critical review of the manuscript.

The 'Understanding Society Scientific Group' include the following: Understanding Society Scientific Group: Michaela Benzeval, Jonathan Burton, Nicholas Buck, Annette Jäckle, Meena Kumari, Heather Laurie, Peter Lynn, Stephen Pudney, Birgitta Rabe, Shamit Saggar, Noah Uhrig, Dieter Wolke.

Competing Interests

JK Consulted for Pfizer on nicotine dependence in 2012-2014. WT received fees to the Institution, all outside the submitted work, from Pfizer, GSK, Chiesi, Roche Diagnostics / Ventana, Biotest, Merck Sharp Dohme, Novartis, Lilly Oncology, Boehringer Ingelheim, grants from Dutch Asthma Fund. BMP serves on the DSMB of a clinical trial funded by the manufacturer (Zoll LifeCor) and on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson.

Correspondance:

Martin D Tobin, Department of Health Sciences, College of Medicine, Biological Sciences and Psychology, University of Leicester, Centre for Medicine, University Road, Leicester, LE1 7RH, UK;

Stephanie J London, Epidemiology Branch, National Institute of Environmental Health Sciences, National Institute of Health, Dept of Health and Human Services, Research Triangle Park, NC, 27709, USA

Figure 1: Study Design

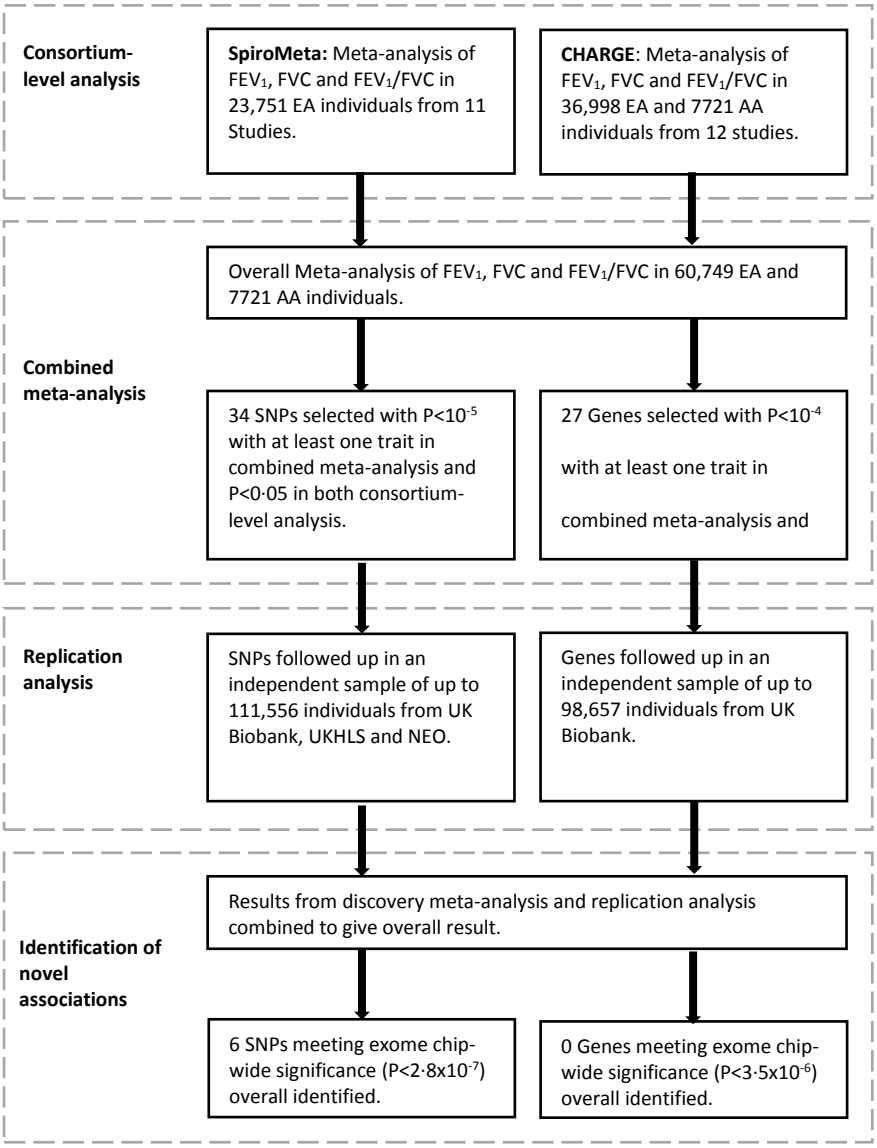

Table 1: Sample characteristics of 11 SpiroMeta and 12 CHARGE studies contributing to the discovery analyses and 3 studies contributing to the replication analyses.

Discovery Studies							
SpiroMeta Studies	**Total Sample**	**n (%) Male**	**Ever Smokers, n (%)**	**Age, mean (SD)**	**FEV_1, litres. mean (SD)**	**FVC, litres. mean (SD)**	**FEV_1/FVC, mean (SD)**
1958 British Birth Cohort (B58C)	5270	2961 (56·2%)	2866 (53·3%)	44·00 (0·00)	3·35 (0·79)	4·29 (1·03)	0·788 (0·09)
Generation Scotland (GS:SFHS)	8164	3413 (41·8%)	3806 (46·6%)	51·59 (13·33)	2·78 (0·87)	3·91 (1·01)	0·710 (0·12)
Cooperative Health Research in the Region of Augsburg (KORA F4)	1447	701 (48·5%)	900 (62·2%)	54·82 (9·66)	3·24 (0·85)	4·20 (1·04)	0·771 (0·07)
CROATIA-Korcula cohort (KORCULA)	791	296 (36·8%)	418 (52·0%)	55·56 (13·69)	2·72 (0·83)	3·29 (0·95)	0·829 (0·10)
Lothian Birth Cohort 1936 (LBC1936)	974	501 (50·6%)	554 (55·9%)	69·55 (0·84)	2·38 (0·67)	3·04 (0·87)	0·787 (0·10)
Study of Health in Pomerania (SHIP)	1681	831 (49·4%)	955 (56·8%)	52·25 (13·43)	3·29 (0·88)	3·88 (1·03)	0·848 (0·07)
Northern Swedish Population Health Study (NSPHS)	880	407 (46·3%)	122 (13·9%)	49·13 (19·96)	2·93 (0·90)	3·53 (1·06)	0·831 (0·09)
Prospective Investigation of the Vasculature in Uppsala Seniors (Pivus)	836	413 (49·4%)	426 (51·0%)	70·20 (0·17)	2·44 (0·68)	3·20 (0·87)	0·76 (0·10)
Swiss study on Air Pollution and Lung Disease in adults (SAPALDIA)	2707	1379 (50·9%)	1399 (51·7%)	40·86 (10·92)	3·65 (0·83)	4·62 (1·04)	0·794 (0·07)
The Cardiovascular Risk in Young Finns Study (YFS)	434	198 (47·3%)	186 (44·4%)	38·88 (5·07)	3·73 (0·75)	4·68 (0·99)	0·800 (0·06)
Finnish Twin Cohort (FTC)	214	0 (0%)	0 (0%)	68·73 (3·31)	2·18 (0·47)	2·79 (0·58)	0·786 (0·08)
Total	**23,398**						
CHARGE Studies (European Ancestry)	**Total Sample**	**n (%) Male**	**Ever Smokers, n (%)**	**Age, mean (SD)**	**FEV_1, litres. mean (SD)**	**FVC, litres. mean (SD)**	**FEV_1/FVC, mean (SD)**
AGES-Reykjavik study (AGES)	1566	649 (41·4%)	900 (57·5%)	76·1 (5·62)	2·13 (0·70)	2·87 (0·86)	0·744 (0·09)
Atherosclerosis Risk in Communities Study (ARIC)	10,680	5015 (47·0%)	631 (59·1%)	54·3 (5·70)	2·94 (0·77)	3·98 (0·98)	0·738 (0·07)
Cardiovascular Health Study (CHS)	3967	1737 (43·8%)	2089 (52·7%)	72·8 (5·55)	2·11 (0·66)	3·00 (0·86)	0·702 (0·10)
NHLBI Family Heart Study (FAMHS)	1651	718 (43·5%)	698 (42·3)	53·5 (12·60)	2·91 (0·853)	3·89 (1·05)	0·746 (0·08)
Framingham Heart Study (FHS)	7113	3241 (45·5%)	3780 (53·1)	50·7 (14·12)	3·10 (0·925)	4·09 (1·12)	0·755 (0·08)
Health Aging and Body Composition Study (HABC)	1457	786 (53·2%)	831 (56·5%)	73·7 (2·83)	2·31 (0·66)	3·11 (0·81)	0·741 (0·08)

Health2006 Study	2714	1217 (44·8%)	1577 (58·1%)	49·4 (13·04)	3·13 (0·82)	3·99 (0·99)	0·784 (0·07)
Health2008 Study	687	297 (43·2%)	384 (55·9%)	46·7 (8·22)	3·27 (0·79)	4·13 (0·97)	0·791 (0·06)
Inter99 Study (without pack-years)	1115	549 (49·2%)	1115 (100%)	47·2 (7·76)	3·26 (0·71)	4·12 (0·92)	0·796 (0·07)
Inter99 Study (with pack-years)	4179	2027 (48·5%)	2307 (55·2%)	45·8 (7·95)	3·21 (0·76)	4·10 (0·97)	0·788 (0·08)
Multi-Ethnic Study of Atherosclerosis (MESA)	1323	654 (49·4%)	751 (56·8%)	66·0 (9·8)	2·57 (0·76)	3·51 (0·10)	0·733 (0·08)
The Rotterdam Study (RS)	546	299 (54·8%)	382 (70·0%)	79·4 (5·00)	2·27 (0·68)	3·03 (0·86)	0·750 (0·08)
Total	**36,998**						
CHARGE Studies (African Ancestry)	**Total Sample**	**n (%) Male**	**Ever Smokers, n (%)**	**Age, mean (SD)**	**FEV_1, litres. mean (SD)**	**FVC, litres. mean (SD)**	**FEV_1/FVC, mean (SD)**
Atherosclerosis Risk in Communities Study (ARIC)	3180	1183 (37·2%)	1680 (59·1%)	53·6 (5·83)	2·48 (0·65)	3·25 (0·82)	0·765 (0·08)
Cardiovascular Health Study (CHS)	624	232 (37·2%)	340 (54·4%)	73·2 (5·49)	1·76 (0·58)	2·48 (0·80)	0·717 (0·11)
Health Aging and Body Composition Study (HABC)	943	433 (45·9%)	543 (57·6%)	73·4 (2·90)	1·96 (0·57)	2·61 (0·71)	0·749 (0·09)
Jackson Heart Study (JHS)	2143	793 (36·8%)	688 (31·9%)	52·8 (12·6)	2·43 (0·72)	3·02 (0·86)	0·807 (0·09)
Multi-Ethnic Study of Atherosclerosis (MESA)	861	404 (46·9%)	467 (54·2%)	65·6 (9·6)	2·19 (0·66)	2·92 (0·86)	0·756 (0·09)
Total	**7721**						
Replication Studies							
Study Name	**Total Sample**	**n (%) Male**	**Ever Smokers, n (%)**	**Age, mean(SD)**	**FEV_1, litres. mean (SD)**	**FVC, litres. mean (SD)**	**FEV_1/FVC, mean (SD)**
UK Biobank	98,657	45,166 (45·8%)	56,404 (57·2%)	56·7 (7·92)	2·75 (0·80)	3·67 (0·98)	0·75 (0·07)
UK Household Longitudinal Study (UKHLS)	7443	3293 (44·2%)	4509 (60·5%)	53·10 (15·94)	2·89 (0·90)	3·83 (1·08)	0·753 (0·09)
Netherlands Epidemiology of Obesity study (NEO)	5456	2672 (48·0%)	3674 (66·0%)	55·9 (5·9)	3·26 (0·80)	4·26 (1·02)	0·77 (0·07)
Total	**111,556**						

Table 2: Novel loci associated with lung function traits.

Results are shown for variant in novel loci associated ($P<2{\cdot}7\times10^{-7}$) with lung function traits in a two stage meta-analysis consisting of up to 68,470 individuals from the SpiroMeta and CHARGE Consortia in the discovery analyses, with follow-up in up to 111,556 individuals from UK Biobank, UKHLS and NEO. For each SNP, the result for the trait-smoking-ancestry combination which resulted in the most statistically significant association is given. The results for these SNPs and all three traits are shown in Supplementary Table 12. Beta values from SpiroMeta ($\boldsymbol{\beta_{Sp}}$) reflect effect-size estimates on an inverse-normal transformed scale after adjustments for age, age^2, sex, height and ancestry principal components, and stratified by ever smoking status (Analysis of All individuals only). Beta values from CHARGE ($\boldsymbol{\beta_{CH}}$) reflect effect-size estimates on an untransformed scale (litres for FEV_1 and FVC; ratio for FEV_1/FVC). Samples sizes (**N**), Z-statistics (**Z**) and two-sided P-values (**P**) are given for the combined discovery analysis and the replication analysis. Two-sided P-values are also given for the full two-stage combined analyses (discovery + replication).

								Consortium Results		**Combined Discovery Meta-Analysis**			**Replication**			**Two-stage Combined**
SNP	**Chr:Pos**	**(Nearest) Gene(s)**	**Trait**	**Smoking**	**Ancestry**	**Effect / other allele**	**Effect Allele Frequency (Discovery)**	β_{CH}	β_{Sp}	N_{disc}	Z_{disc}	P_{disc}	N_{rep}	Z_{rep}	P_{rep}	P_{meta}
rs2322659	2:136555659	LCT (nonsynonymous)	FVC	All Individuals	EA Only	T/C	23·5%	27·34	0·032	55,591	5·597	$2{\cdot}18\times10^{-8}$	12,899	2·286	0·0223	$1{\cdot}70\times10^{-9}$
rs1448044	5:44296986	*FGF10*(dist=8111), *NNT*(dist=591,318)	FVC	Ever Smokers	EA+AA	A/G	35·6%	18·63	0·057	30,966	4·813	$1{\cdot}49\times10^{-6}$	64,400	4·805	$1{\cdot}55\times10^{-6}$	$2{\cdot}22\times10^{-11}$
rs1294421	6:6743149	*LY86*(dist=87,933), *RREB1*(dist=364,681)	FEV_1/FVC	All Individuals	EA+AA	T/G	36·8%	-0·222	-0·038	68,099	-5·479	$4{\cdot}27\times10^{-8}$	111,556	-8·171	$3{\cdot}06\times10^{-16}$	$9{\cdot}74\times10^{-23}$
rs3849969	10: 75525999	*SEC24C* (intronic)	FEV1	All Individuals	EA+AA	T/C	29·4%	13·10	0·036	68,116	4·767	$1{\cdot}87\times10^{-6}$	111,556	5·042	$4{\cdot}60\times10^{-7}$	$4{\cdot}99\times10^{-12}$
rs1200345	15: 41819716	*RPAP1* (nonsynonymous)	FEV1/FVC	All Individuals	EA only	C/T	48·8%	-0·217	-0·025	60,381	-4·586	$4{\cdot}51\times10^{-6}$	111,556	-5·725	$1{\cdot}03\times10^{-8}$	$2{\cdot}33\times10^{-13}$
rs1859962	17: 69108753	*CASC17* (intronic)	FEV_1	All Individuals	EA only	G/T	48·2%	15·39	0·026	60,395	4·876	$1{\cdot}08\times10^{-6}$	111,554	4·612	$3{\cdot}99\times10^{-6}$	$4{\cdot}10\times10^{-11}$
rs6088813	20: 33975181	*UQCC1* (intronic)	FVC	All Individuals	EA+AA	C/A	36·7%	-16·16	-0·023	68,115	-4·634	$3{\cdot}58\times10^{-6}$	111,556	-7·688	$1{\cdot}50\times10^{-14}$	$4{\cdot}90\times10^{-19}$