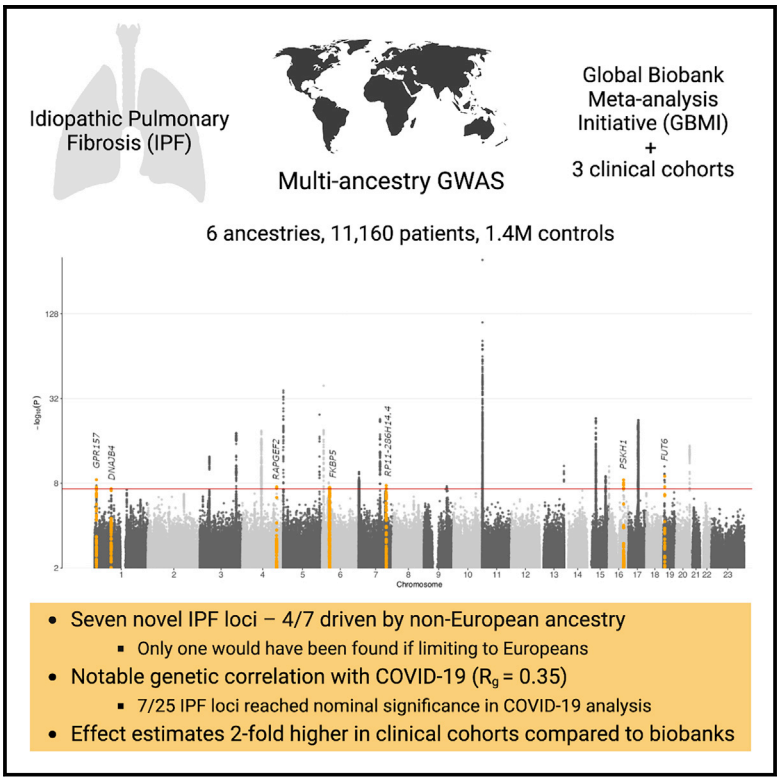
Cell Genomics

Article

Leveraging global multi-ancestry meta-analysis in the study of idiopathic pulmonary fibrosis genetics

Graphical abstract



Highlights

- IPF meta-analysis across 6 ancestries with 11,160 cases and 1.4 M controls
- Seven novel IPF loci—only one found if restricted to individuals of European ancestry
- Genetic overlap with severe COVID-19: $R_g \sim 0.35$, p = 0.001
- Two-fold higher effect size estimates in clinical cohorts compared with biobanks

Authors

Juulia J. Partanen, Paavo Häppölä, Wei Zhou, ..., Marjukka Myllärniemi, Mark J. Daly, Jukka T. Koskela

Correspondence

juulia.partanen@helsinki.fi (J.J.P.), jukka.koskela@helsinki.fi (J.T.K.)

In brief

Partanen et al. present a multi-ancestry IPF meta-analysis with 11,160 cases and 1.4 M controls. They identify seven novel genome-wide significant loci, only one of which would have been identified if the analysis had been limited to Europeans. They also report notable pleiotropy across IPF susceptibility and severe COVID-19 infection.

Partanen et al., 2022, Cell Genomics 2, 100181
October 12, 2022
https://doi.org/10.1016/j.xgen.2022.100181

CellPress

Cell Genomics

CellPress
OPEN ACCESS

Article

Leveraging global multi-ancestry meta-analysis in the study of idiopathic pulmonary fibrosis genetics

Juulia J. Partanen,[1,*] Paavo Häppölä,[1] Wei Zhou,[2,3,4] Arto A. Lehisto,[1] Mari Ainola,[5,6] Eva Sutinen,[5,6] Richard J. Allen,[7] Amy D. Stockwell,[8] Olivia C. Leavy,[7] Justin M. Oldham,[9] Beatriz Guillen-Guio,[7] Nancy J. Cox,[10,11] Jibril B. Hirbo,[10,11] David A. Schwartz,[12] Tasha E. Fingerlin,[13] Carlos Flores,[14,15,16,17] Imre Noth,[18] Brian L. Yaspan,[8] R. Gisli Jenkins,[19,20] Louise V. Wain,[7,21] Samuli Ripatti,[1,22] Matti Pirinen,[1,23,24] International IPF Genetics Consortium, Global Biobank Meta-Analysis Initiative (GBMI), Tarja Laitinen,[25] Riitta Kaarteenaho,[26,27] Marjukka Myllärniemi,[5,6] Mark J. Daly,[1,2,3,4] and Jukka T. Koskela[1,28,*]

[1]Institute for Molecular Medicine, Finland (FIMM), HiLIFE, University of Helsinki, Helsinki, Finland
[2]Analytic and Translational Genetics Unit, Department of Medicine, Massachusetts General Hospital, Boston, MA, USA
[3]Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, MA, USA
[4]Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, MA, USA
[5]Individualized Drug Therapy Research Program, Faculty of Medicine, University of Helsinki, Helsinki, Finland
[6]Department of Pulmonary Medicine, Heart and Lung Center, Helsinki University Hospital, Helsinki, Finland
[7]Department of Health Sciences, University of Leicester, Leicester, UK
[8]Human Genetics, Genentech, South San Francisco, CA, USA
[9]Division of Pulmonary, Critical Care and Sleep Medicine, Department of Internal Medicine, University of California, Davis, Sacramento, CA, USA
[10]Department of Medicine, Division of Genetic Medicine, Vanderbilt University Medical Center, Nashville, TN, USA
[11]Vanderbilt Genetic Institute, Vanderbilt University Medical Center, Nashville, TN, USA
[12]Department of Medicine, University of Colorado, Aurora, CO, USA
[13]Center for Genes, Environment and Health, National Jewish Health, Denver, CO, USA
[14]Research Unit, Hospital Universitario Ntra. Sra. de Candelaria, Santa Cruz de Tenerife, Spain
[15]CIBER de Enfermedades Respiratorias, Instituto de Salud Carlos III, Madrid, Spain
[16]Genomics Division, Instituto Tecnológico y de Energías Renovables (ITER), Santa Cruz de Tenerife, Spain
[17]Faculty of Health Sciences, University of Fernando Pessoa Canarias, Las Palmas de Gran Canaria, Spain
[18]Division of Pulmonary and Critical Care Medicine, Department of Medicine, University of Virginia, Charlottesville, VA, USA
[19]National Heart and Lung Institute, Imperial College London, London, UK
[20]Royal Brompton and Harefield Hospitals, Guy's and St Thomas' NHS Foundation Trust, London, UK
[21]National Institute for Health Research, Leicester Respiratory Biomedical Research Centre, Glenfield Hospital, Leicester, UK
[22]Faculty of Medicine, University of Helsinki, Helsinki, Finland
[23]Department of Public Health, University of Helsinki, Helsinki, Finland
[24]Department of Mathematics and Statistics, University of Helsinki, Helsinki, Finland
[25]Administration Center, Tampere University Hospital and University of Tampere, Tampere, Finland
[26]Research Unit of Internal Medicine, University of Oulu, Oulu, Finland
[27]Medical Research Center Oulu, Oulu University Hospital, Oulu, Finland
[28]Lead contact
*Correspondence: juulia.partanen@helsinki.fi (J.J.P.), jukka.koskela@helsinki.fi (J.T.K.)
https://doi.org/10.1016/j.xgen.2022.100181

SUMMARY

The research of rare and devastating orphan diseases, such as idiopathic pulmonary fibrosis (IPF) has been limited by the rarity of the disease itself. The prognosis is poor—the prevalence of IPF is only approximately four times the incidence, limiting the recruitment of patients to trials and studies of the underlying biology. Global biobanking efforts can dramatically alter the future of IPF research. We describe a large-scale meta-analysis of IPF, with 8,492 patients and 1,355,819 population controls from 13 biobanks around the globe. Finally, we combine this meta-analysis with the largest available meta-analysis of IPF, reaching 11,160 patients and 1,364,410 population controls. We identify seven novel genome-wide significant loci, only one of which would have been identified if the analysis had been limited to European ancestry individuals. We observe notable pleiotropy across IPF susceptibility and severe COVID-19 infection and note an unexplained sex-heterogeneity effect at the strongest IPF locus *MUC5B*.

INTRODUCTION

Idiopathic pulmonary fibrosis (IPF) is a chronic, progressive fibrotic disease of the lungs. It has no known etiology and pathogenesis, poor prognosis, and limited treatment options. The prevailing model of IPF pathogenesis suggests recurrent epithelial injury followed by aberrant repair and dysregulated interstitial matrix deposition with cell senescence playing an important role in promoting lung fibrosis.[1]

As IPF has, by definition, no identifiable cause, genome-wide approaches are especially attractive as they may provide insight into underlying causes, pathogenesis, and might potentially reveal novel therapeutic avenues. Genome-wide association studies (GWAS) of IPF have thus far reported at least 23 associated loci[2–11] highlighting genes involved in telomere maintenance,[12] cell adhesion, airway clearance, and innate immunity. These studies have mainly been restricted to common variants in individuals of European descent, and have identified few associations to functional variants. The most recent and largest meta-analysis concluded that IPF is highly polygenic with a significant number of associated variants remaining to be identified.[2] In addition, considerable genetic overlap between IPF and severe coronavirus disease 2019 (COVID-19) has been reported.[13–16]

To further explore the genetics of IPF susceptibility, we performed the first multi-ancestry study on the genetics of IPF in six populations, altogether comprising a 4-fold increase in the number of patients compared with the largest IPF study to date, via meta-analysis of the Global Biobank Meta-Analysis Initiative (GBMI) with the most recent published IPF study.[2] This allowed assessment of heterogeneity of effects over different ancestries, sex, and IPF diagnosis ascertainment between biobank and clinical cohort studies. With the increase in power, we were able to study population specific and rare variant effects. A notable fraction of the proposed loci have previously been associated with lung function. Fine-mapping in the Finnish population, making use of reduced allelic heterogeneity of a population isolate, identified a putative functional causal variant in the previously reported *KIF15* locus. We also describe significant pleiotropy between IPF and COVID-19, beyond what is known to date. Finally, we suggest possible sex-based heterogeneity at *MUC5B*, the strongest genetic risk factor for IPF.

RESULTS

Multi-ancestry meta-analysis reveals seven novel IPF loci

The GBMI IPF meta-analysis consisted of 8,492 cases and 1,355,819 controls representing 6 ancestries (Table 1). Out of 66.6 M variants included in analysis, 21.0 M were not present in the non-Finnish European (NFE) ancestry studies. While IPF prevalence and recruitment strategies varied greatly across contributing biobanks, the overall prevalence was 0.62% (Table S1). The GBMI IPF meta-analysis discovered 16 genome-wide significant loci, highlighting 2 potentially novel loci (Figure 1).

We then meta-analyzed the GBMI data with the largest IPF meta-analysis[2] to date, later referred to as the Allen et al. study, including 10.8 M variants and increasing the number of cases and controls to 11,160 and 1,364,410, respectively. Altogether the joint meta-analysis identified 25 independent IPF-associated loci (Figure 1; Data S1; Table S2). We report genome-wide significant results at 14/23 previously reported loci, with a further 7/23 showing consistent direction of effects at varying levels of significance (Table S3). The linkage disequilibrium (LD) score regression intercept[17] for the joint meta-analysis was not inflated (1.011) indicating independence of included studies. Quantile-quantile plots for meta-analyses are available in Figure S1.

Table 1. Ancestries in the GBMI IPF meta-analysis

Ancestry	Biobanks	N IPF patients	N controls	Frac cases (%)
NFE	BioVU, CCPM, ESTBB, HUNT, MGB, MGI, UCLA, UKBB	5,229	750,630	0.69
FIN	FinnGen	1,514	306,063	0.49
EAS	BBJ, CKB, UCLA	1,210	254,409	0.47
AMR	BioMe, UCLA	319	14,452	2.16
AFR	BioMe, UCLA	169	8,368	1.98
SAS	GNH	51	21,897	0.23
6*	13*	8,492*	1,355,819*	0.62*

AFR, African/African American; AMR, Latino/admixed American; EAS, East Asian; FIN, Finnish; NFE, non-Finnish European; SAS, South Asian. Biobanks: BioME, BioVU, Colorado Center for Personalized Medicine Biobank (CCPM), Michigan Genome Initiative (MGI), UCLA Precision Health Biobank (UCLA), and Mass General Brigham (MGB) in America, BioBank Japan (BBJ) and China Kadoorie Biobank (CKB) in East Asia, and Genes & Health (GNH), Estonian Biobank (ESTBB), FinnGen project, Trøndelag Health Study (HUNT), and UK Biobank (UKBB) in Europe. Frac cases, fraction of cases in total sample. *Refers to values for GBMI as a whole.

Beyond confirming nearly all of the previous signals, we identified seven potentially novel loci (Table 2; Figure 1). One locus was driven by rs539683219 at 16q22.1, an intronic *PSKH1* variant only found in the East Asian (EAS) population. Highlighting the importance of multi-ancestry analysis, four out of the seven novel loci were mostly driven by non-European ancestry, when assessed by highest minor allele frequency at population level within the meta-analysis. Minor allele frequency enrichment within the meta-analysis compared with NFEs was over 1.5-fold for these four index variants. Moreover, if only the European populations (including NFE and Finnish) were analyzed, only one of the seven loci reached genome-wide significance (Table S4).

Further replication of the novel loci was attempted in two individual European ancestry cohorts (case count 792 and 664), where six loci were polymorphic and imputed at high quality (minimum imputation $R^2 = 0.98$). Three of the six potentially novel findings replicated (at p value < 0.01 and with consistent direction of effects, Table S5).

Multiple novel variants associated with lung function and different organ manifestations

The Open Targets[18] resource was used to assess previous findings for the proposed novel loci (Table S6).

Three of the seven novel loci have previously been implicated with lung function parameters forced expiratory volume in 1 s (FEV1) and forced vital capacity (FVC). First, at 6p21.31, the

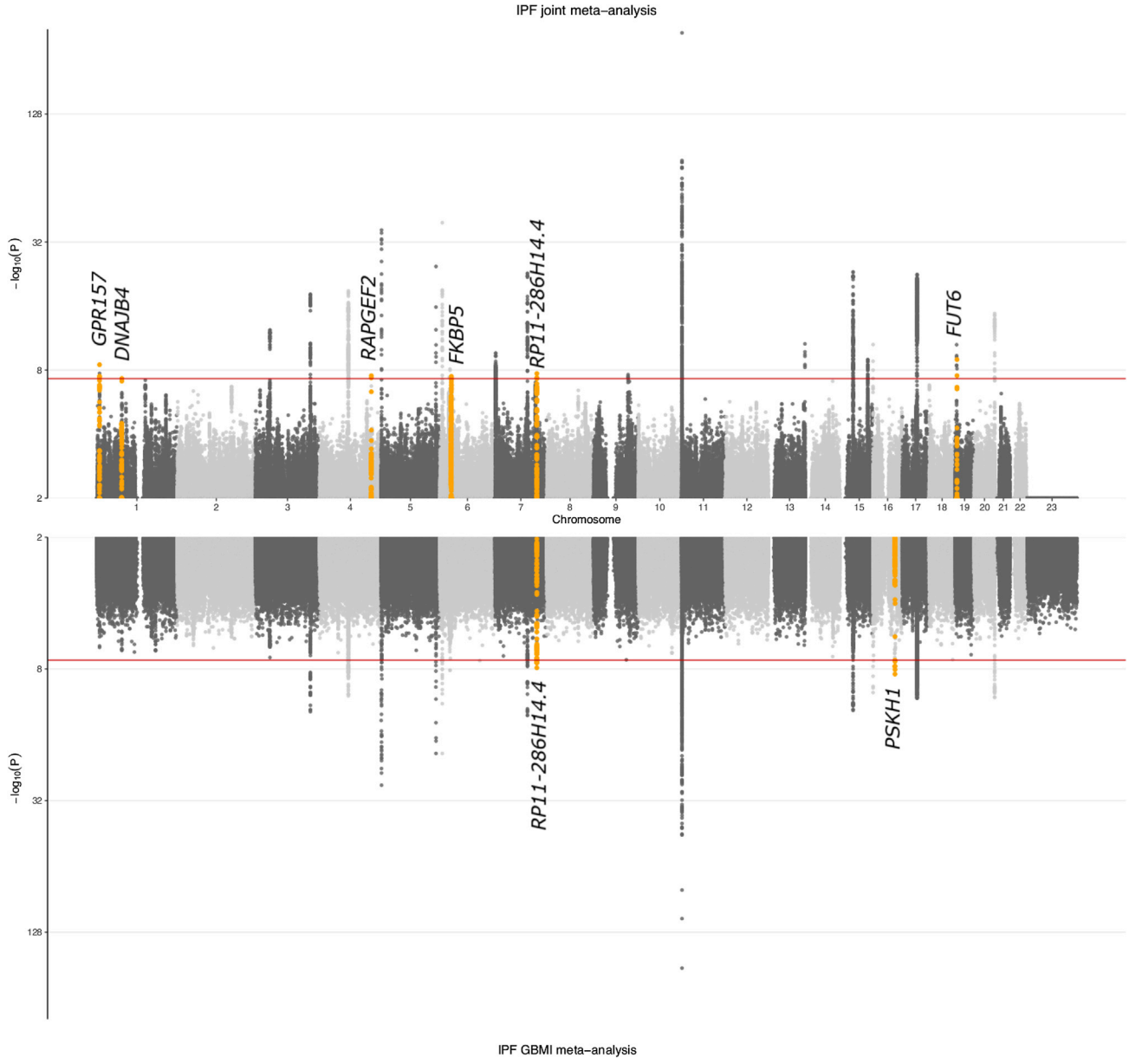


Figure 1. Genome-wide association results for IPF

Results from the joint meta-analysis are plotted in the top panel of the Miami plot and results from the GBMI meta-analysis in the bottom panel. Novel associations are highlighted in orange and annotated with the closest gene (index variant and variants in LD at $r^2 > 0.05$ are highlighted, except for the *PSKH1* signal for which variants within a 1 Mb window are highlighted due to missing LD information). Variants with p values ≤ 0.01 are plotted.

index variant rs9380529 in *FKBP5* was in the 95% credible set of a FVC signal.[19] The index variant for FVC (rs28435135, LD, $r^2 = 0.28$) had a negative beta coefficient, i.e., decreasing vital capacity, consistent with higher risk of IPF suggested in the present study. In addition, rs9380529 was in LD ($r^2 = 0.64$) with the lead variant (and included in the 95% credible set) for trunk and leg fat percentages in the UKB Neale v.2 analysis (http://www.nealelab.is/uk-biobank/). *FKBP5* encodes a FK506-binding protein that has been shown to modulate the mTOR signaling pathway[20] central in lung fibrinogenesis.[21]

Second, *GPR157* at 1p36.22 has been associated with FEV1/FVC ratio,[22] as the index variant rs7549256 from the current analysis was in LD ($r^2 = 0.55$) with the reported index variant (no data on credible set or effect available). rs7549256 was also in LD ($r^2 = 0.64$) with the index variant for insulin-like growth factor 1 levels.[23]

Third, no previous associations were found for the intergenic rs76537958 at 4q32.1, whereas variants in *RAPGEF2* (LD with rs76537958: $r^2 < 0.1$) have been associated with FVC in the UKB Neale v.2 analysis, as well as childhood and lifetime

Table 2. Novel associations from the GBMI and joint IPF meta-analyses

Variant	Rsid	Index variant gene	Most severe consequence	AF alt (%)	Max MAF pop	MAF enrichment vs NFE	OR [95% CI]	p value
1_9107187_C_A	rs7549256	*GPR157*	intron	64.16	EAS	1.5	0.91 [0.88–0.94]	3.29E−09
1_77998184_T_C	rs4130548	*DNAJB4*, *GIPC2*	intron	33.30	NFE	1	1.09 [1.06–1.13]	4.91E−08
4_159892716_A_T	rs76537958	*RAPGEF2*	intergenic	2.92	AFR	2.5	1.29 [1.18–1.42]	2.94E−08
6_35707919_A_G	rs9380529	*FKBP5*	intron	51.72	NFE	1	1.08 [1.05–1.12]	3.33E−08
7_129095384_G_A	rs34288126	*RP11-286H14.4*	noncoding transcript exon	12.70	FIN	1.1	1.13 [1.09–1.19]	1.50E−08
16_67895674_TG_T	rs539683219	*PSKH1*	intron	1.71	EAS	Inf	3.20 [2.17–4.70]	3.52E−09
19_5840608_C_T	rs708686	*FUT6*	upstream gene	31.47	AMR	1.6	1.11 [1.07–1.14]	1.08E−09

Sample size weighted mean imputation info score ≥0.80 for all variants, index variant gene and most severe consequence information from variant effect predictor (VEP), variant = chrom_pos_ref_alt (GRCh38); AF alt = within the meta-analysis sample size weighted GRCh38 alternate allele frequency; max MAF population = population with highest minor allele frequency (MAF), MAF enrichment is calculated as highest MAF divided by MAF in NFE. Effects are given for the alt allele. AFR, African/African American; AMR, Latino/admixed American; EAS, East Asian; FIN, Finnish; NFE, non-Finnish European; SAS, South Asian. Inf, polymorphic in only one population. p value threshold for genome-wide significance pval < 5E−8.

pneumonia.[24] In addition, *RAPGEF2* has been reported as a shared risk factor for both IPF and chronic obstructive pulmonary disease (COPD) in a network analysis.[25]

Regarding the four additional loci, rs4130548 at 1p31.1, has been implicated especially in body mass index, and was the index variant of the association signal.[26] At 19p13.3, rs708686 upstream of *FUT6* has been previously associated with carbohydrate antigen 19.9,[27] blood protein levels (FUT3),[28] and gallstones,[28,29] among others. *FUT6* affects fucosylation of mucins, including MUC5B, which may affect mucociliary clearance via changes in mucus viscoelasticity and pathogen binding.[30] No previously reported associations were found for the non-coding transcript exon variant rs34288126 at 7q32.1, or the EAS-specific intronic rs539683219 in *PSKH1* at 16q22.1. However, rs116906005, which is 190 kB downstream of the index variant in the *PSKH1* locus (LD with rs539683219: r^2 = 0.67 in EAS), has been previously associated with interstitial lung disease (ILD) in BioBank Japan.[31]

In contrast to other pulmonary diseases attributed to tobacco smoke exposure, such as COPD and lung cancer, no genome-wide significant association signal was seen in the *CHRNA3/5* locus (OR[95% CI] = 1.05[1.02–1.08], p = 0.0034 for rs16969968), a known nicotine dependence locus.[32]

Expression levels and profiles across tissues and cell types for the genes at the novel loci, obtained from GTEx[33,34] and IPF RNA sequencing studies,[35–37] are displayed[38] in Table S6, Figure S2, and Data S2. In summary, genes at five of the seven loci were expressed in the lung tissue (median TPM > 1, Table S6). Furthermore, genes at two loci (*GIPC2* and *FKBP5*) have been reported to be differentially expressed in IPF lung compared with controls[36] and, in addition to these, two more (*GPR157* and *RAPGEF2*) in end-stage IPF[37] (Table S6). Expression of the genes at the novel loci varied in level and tissue or cell-type specificity (Figure S2; Data S2). Of the genes differentially expressed in IPF, *FKBP5*, the gene with the highest expression level in lung, was expressed across different lung tissue cell types with highest expression levels among immune cells and fibroblasts, whereas *GIPC2* was almost exclusively expressed in ciliated and endothelial/lymphatic cells.

Fine-mapping in the Finnish population suggests missense variant in *KIF15* to be causal

To identify potential causal alleles within the identified loci, we performed fine-mapping of all identified loci in FinnGen, resulting in eight independent loci with suggested causal alleles (Table 3). None of the novel loci were successfully fine-mapped (i.e., had good quality credible sets with minimum LD between variants $r^2 \geq 0.25$).

Fine-mapping suggested deleterious coding causal variants at three loci. In addition to the previously reported coding variants in *TERT* and *SPDL1*,[4,6] fine-mapping identified a coding variant in *KIF15* (predicted missense, rs138043992, AF = 0.29%, OR[95% CI] = 1.71[1.39–2.10], posterior inclusion probability (PIP) = 0.24, ENSP00000324020.4:p.Arg501Leu), enriched 2.6-fold in the Finnish population compared with non-Finnish non-Estonian Europeans (NFEEs) (gnomAD v2.1.1), and predicted as probably damaging by Polyphen and deleterious by SIFT.[39,40]

When a known locus near *KANSL1/MAPT* was assessed, the signal was fine-mapped to *CRHR1* (intronic rs1568002709, AF = 11.7%, OR[95% CI] = 0.62[0.53–0.73], PIP = 0.003). There was, however, little resolution in the locus due to its exceptional LD structure[41] (Data S1).

Fine-mapping further suggested two independent signals at 11p15.5; the well-established *MUC5B* and an independent signal downstream of *MOB2*. Causality of the *MOB2* downstream variant (rs546531844, AF = 0.29%, 17 times enriched in Finns compared with NFEEs gnomAD v.2.1.1) was corroborated by two different fine-mapping methods. The "Sum of Single Effects" (SuSie) model[42] suggested two 95% credible sets at the 11p15.5 locus. One of the credible sets included the *MUC5B* upstream gene variant rs35705950 (PIP = 1) and the other included two variants: a *MOB2* downstream gene variant rs546531844 (PIP = 0.92) and a *MUC6* missense variant rs148815783 (PIP = 0.072). Another fine-mapping method, FINEMAP,[43,44] suggested four 95% credible sets (p = 0.55) at the locus. Three of the four credible sets consisted of one variant. Both the *MUC5B* upstream gene variant rs35705950 and the *MOB2* downstream gene variant rs546531844

Table 3. Fine-mapped good quality (minimum LD between variants $r^2 \geq 0.25$) credible sets in FinnGen

Locus	N variants in credible set	Credible set min LD (r^2)	Highest PIP variant	rsid	Gene for most severe consequence	Most severe consequence	PIP
3q26.2	35	0.91	3_169759718_A_G	rs12638862	*ACTRT3*	downstream gene	0.080
3p21.31	22	0.48	3_44801967_G_T	rs138043992	*KIF15*	missense	0.243
5p15.33	1	1.00	5_1272247_G_A	rs770066110	*TERT*	stop gained	1.000
5p15.33	1	1.00	5_1279370_T_C	rs776981958	*TERT*	missense	0.997
5q35.1	2	0.82	5_169588475_G_A	rs116483731	*SPDL1*	missense	0.875
11p15.5	1	1.00	11_1219991_G_T	rs35705950	*MUC5B*	upstream gene	1.000
11p15.5	2	0.34	11_1468491_G_A	rs546531844	*MOB2*	downstream gene	0.919
16p13.3	5	0.78	16_276685_G_A	rs184954013	*ARHGDIG*	intron	0.618
17q21.31	2,180	0.95	17_45753401_45753524del	rs1568002709	*CRHR1*	intron	0.003
20q13.33	17	0.51	20_63582806_G_A	rs73315845	*GMEB2*	downstream gene	0.077

Highest PIP variant = chrom_pos_ref_alt (GRCh38); PIP, posterior inclusion probability.

constructed their own one-variant credible sets (PIP = 1 and PIP = 0.96, respectively).

After conditioning the REGENIE GWAS on the *MUC5B* variant rs35705950 the *MOB2* downstream gene variant rs546531844 association was no longer genome-wide significant and the effect size estimate was notably decreased (original beta = 1.35, original p = 1.33E–37, conditioned beta = 0.53, conditioned p = 1.41E−7). Imputation accuracy of the *MOB2* variant was not optimal (INFO = 0.85) and LD between the *MOB2* downstream variant and the *MUC5B* lead variant was low but not inexistent (r^2 = 0.072, D' = 0.766). Thus, the signal at *MOB2* remains to be confirmed.

Pleiotropy of effects across COVID-19 severity

As considerable genetic overlap between IPF and severe COVID-19 caused by SARS-CoV-2 infection has been reported,[13–16,45] we assessed the shared genetic background of IPF and severe COVID-19 using the largest sample sizes available for both traits: the joint IPF meta-analysis reported here and the most recent COVID-19 Host Genetics Initiative results (data release 6[46]). We discovered that, in addition to the four loci (*MUC5B*, *DPP9*, *KANSL1/CRHR1*, and *ZKSCAN1*)[13–16] previously associated with both IPF and COVID-19 hospitalization at a genome-wide level, three other genome-wide significant loci in the IPF meta-analysis passed the FDR-adjusted p value threshold of 0.05 in the COVID-19 scan (total 7/25, 28%; Figure 2; Table 4). As previously reported, the effect of *MUC5B* was reversed: the strong, established risk allele in IPF is clearly protective for severe COVID-19 (OR = 0.89, p = 1.2E−8). The *ATP11A* locus also demonstrated opposite effects for the two traits, while for the rest of the loci the direction of effects was shared. While genome-wide associations for both IPF and COVID-19 hospitalization have been reported separately in the 17q21.31 locus, we noted a shared signal at the locus with very high LD between the index variants (r^2 = 0.97).

Secondly, 6 of the 17 loci from the COVID-19 hospitalization scan passed the FDR-adjusted p value threshold of 0.05 in the IPF meta-analysis (35%, Table S7), suggesting further shared etiology at *CCHCR1*, *SLC22A31*, and *TAC4*.

Formal colocalization analysis was not possible as COVID-19 results have not been fine-mapped. Genetic correlation between the traits, determined by LDSC,[47] restricting to European samples for COVID-19 hospitalization and NFE samples for IPF, was 0.35 (95% CI 0.14–0.56, p = 0.001), somewhat higher compared with a previous estimate[14] and with less uncertainty.

Pleiotropy of the IPF signals beyond COVID-19 hospitalization was explored by colocalization analysis in FinnGen, pointing to shared signals between IPF and osteoporosis, cancers, and hypothyroidism (Table S8). At 16p13.3 an intronic *ARHGDIG* variant (rs184954013, AF in Finns = 2.5%, AF in NFE = 0.29%) colocalized with the osteoporotic fracture signal (causal posterior agreement [CLPA] = 0.74) and also with any form of osteoporosis (CLPA = 0.58). As we have reported prior to this study,[4] multiple malignancy-related colocalization signals were also detected (Table S8).

Sex-stratified analysis in biobanks suggests heterogenic effects at strongest IPF signal

Sex-stratified meta-analysis in the GBMI across six biobanks with results for both sexes identified a 1.6-fold larger effect for the strongest IPF-associated variant rs35705950 in the *MUC5B* locus in males (OR[95% CI] = 3.22[2.92–3.55], p = 1.0E−121) compared with females (OR[95% CI] = 2.04[1.82–2.29], p = 2.9E−34), Cochran's Q p value for heterogeneity = 3.4E−9. To investigate whether the difference in effects was due to confounding by case ascertainment differences across contributing biobanks, we assessed the effect of rs35705950 in each contributing biobank in males and females, noting a weaker effect in females across biobanks (Figure S3; Table S9). The result was, however, not replicated in four clinical cohorts in sex-stratified analysis or sex interaction analysis ($OR[95\%\ CI]_{males}$ = 4.81[4.37–5.30], $OR[95\%\ CI]_{females}$ = 4.75[4.13–5.45] [Tables S10 and S11], and results in subsets of the FinnGen study [Table S12]). The lifetime incidence of IPF in the longitudinal FinnGen register follow-up stratified by sex and carrying a *MUC5B* risk allele is illustrated in Figure S4. *MUC5B* carrier status did not have an effect on the number of IPF deaths or lung transplants among IPF cases in FinnGen (Table S13).

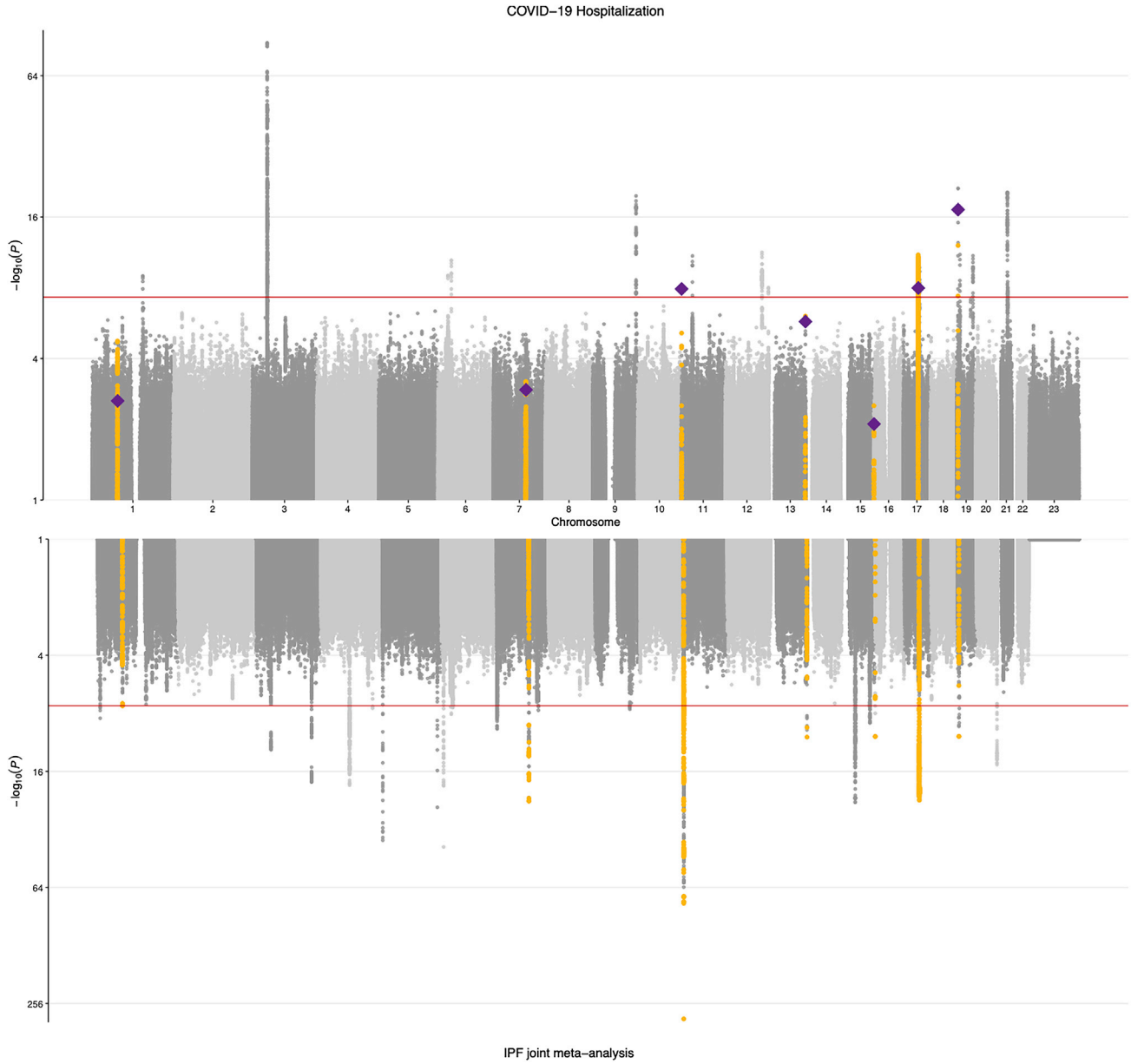


Figure 2. IPF meta-analysis and COVID-19 hospitalization results

COVID-19 hospitalization results are shown in the top panel and IPF joint meta-analysis results in the bottom panel. Genome-wide significant IPF signals that reached FDR-adjusted p value < 0.05 in COVID-19 hospitalization scan are highlighted in yellow. Index variants in the IPF scan are plotted as diamonds in the COVID-19 results. Variants with p values $\leq$ 0.1 are plotted.

The male-only meta-analysis identified two additional loci: 19q13.32 with index variant rs71338787 in *EML2* and Xq28 with index variant rs5945238 in *MPP1* (Table S14).

Heterogeneity assessment points to large effect of sample ascertainment

We observed heterogeneous effects across biobanks and ancestry at nearly half of the IPF genome-wide significant loci (11/25, 44%, FDR-adjusted Cochran's Q p value < 0.05, mean heterogeneity index I^2 = 0.62; Data S3; Table S2). Therefore, we explored whether there was a systematic difference between the effects observed in the latest IPF meta-analysis, involving carefully curated clinically defined IPF, and biobank defined IPF, generally obtained from ICD codes in electronic health records (EHR). Sample recruitment periods and time periods covered by the EHRs are available in Table S15. Limiting to samples of NFE descent and genome-wide significant loci in the meta-analysis, the effect size estimates were 2.1 times larger in the clinical cohort compared with the meta-analyzed biobank studies (Figure 3).

Table 4. COVID-19 pleiotropy

Variant	rsid	Index variant gene	Most severe consequence	OR [95% CI] IPF	OR [95% CI] COVID-19	p value IPF	p value COVID-19
1_77998184_T_C	rs4130548	*DNAJB4*, *GIPC2*	intron	1.09 [1.06–1.13]	1.04 [1.01–1.06]	4.91E−08	2.28E−03
7_100020983_G_A	rs6963345	*ZKSCAN1*	intron	1.16 [1.13–1.20]	1.04 [1.02–1.06]	1.27E−23	1.14E−03
11_1219991_G_T	rs35705950	*MUC5B*	upstream gene	2.76 [2.62–2.90]	0.89 [0.86–0.93]	<1E−300	1.22E−08
13_112881427_C_T	rs12585036	*ATP11A*	noncoding transcript exon	0.89 [0.86–0.92]	1.07 [1.04–1.09]	2.35E−11	1.80E−06
16_276685_G_A	rs184954013	*ARHGDIG*	intron	1.87 [1.55–2.25]	1.43 [1.1–1.86]	1.30E−13	7.83E−03
17_46126154_C_T	rs113120855	*KANSL1*	intron	0.80 [0.77–0.84]	0.92 [0.89–0.95]	8.92E−23	1.04E−08
19_4717660_A_G	rs12610495	*DPP9*	missense	1.12 [1.08–1.15]	1.11 [1.09–1.14]	2.95E−11	6.09E−18

Results for genome-wide significant index variants in joint IPF meta-analysis with FDR-adjusted p value < 0.05 in COVID-19 hospitalization scan (n = 7/25, 28%). Variant = chr_pos_ref_alt (GRCh38), effects are given for the alt allele.

Per each biobank, the median beta ratio ($\beta_{GBMI}/\beta_{Allen}$) varied from −0.04 to 0.62 (Figure S5).

To further study the effect of case ascertainment on effect size estimates, we divided the FinnGen study into three subsets based on diagnosis and original study cohort: a clinical IPF cohort (FinnishIPF,[48] n cases = 205), other IPF patients (n = 1,366), and non-IPF ILD patients (n = 1,624) and compared effect size estimates from these cohorts with those of the latest IPF meta-analysis. Again, effect size estimates were 0.9, 1.4, and 2.5 times larger in the latest IPF meta-analysis compared with the Finnish IPF, other IPF, and non-IPF ILD cohorts (Figure S6), providing further evidence that effect sizes in highly ascertained IPF patients are substantially higher compared with patients identified from biobanks. We further explored the effect of defining IPF cases based on the slightly more inclusive PheCode definition used by most biobanks compared with a more rigorous definition (International Classification of Diseases [ICD]-10 code J84.1) in FinnGen and noted that effect size estimates were somewhat attenuated in the PheCode-based IPF cases (0.87-fold, 95% CI 0.83–0.91; Figure S7).

The large effect of case ascertainment on effect size estimates was corroborated by meta-regression results, where case ascertainment explained most of the observed heterogeneity (mean R^2 = 55.8%), while ancestry, by comparison, explained very little (mean R^2 = 6.2%). After adjusting for ancestry, all 11 loci with heterogeneous effects expressed evidence of remaining heterogeneity. To study the effect of case ascertainment, we compared the effect estimates of two clinical cohorts, the latest IPF meta-analysis and the FinnishIPF subcohort of FinnGen, to the estimates of the 13 GBMI biobanks (excluding the clinical subcohort from FinnGen). Having divided FinnGen into 2 subcohorts, 10 of the 25 loci expressed evidence of heterogeneity. However, after accounting for case ascertainment status (whether the studies were based on clinical cohorts or not), only 4 of these 10 loci expressed evidence of remaining heterogeneity.

DISCUSSION

We conducted the first multi-ancestry meta-analysis of IPF increasing the number of cases over 4-fold compared with the latest IPF meta-analysis. Incorporating 11,160 patients from 6 ancestries allowed us to identify 7 novel loci associated with IPF susceptibility. Three of the identified loci, *GPR157*, *FKBP5*, and *RAPGEF2* have been previously associated with lung function measurements. Furthermore, *FKBP5* affects the mTOR signaling pathway,[20] central in lung fibrinogenesis,[21] and another novel locus, *FUT6*, affects mucin fucosylation potentially influencing mucociliary clearance.[30] Genes at two of the novel loci (*GIPC2*, *FKBP5*) have been reported to be differentially expressed in IPF lung compared with controls.[36]

Highlighting the importance of multi-ancestry analysis, one of the novel loci (*PSKH1*) was only polymorphic in the EAS population and three additional index variants were enriched within the meta-analysis at least 1.5-fold in a non-European population compared with NFEs. Moreover, only one of the loci would have reached genome-wide significance had the analysis been restricted to European populations. The power boost of the multi-ancestry meta-analysis comes from an increase in both sample size and sample diversity, allowing identification of loci whose index variants are more frequent in other ancestries than European. In addition to boosting power, increasing the ancestral diversity of IPF genetic association studies allows analyzing a broader set of genetic variation, as nearly a third of the variants in GBMI were not present in the GBMI NFE studies. It also enables cross-validating new findings across biobanks and increases representation of understudied populations.

Fine-mapping in the Finnish population, enriched for deleterious low-frequency coding variants,[49] suggested a predicted missense variant causal at the *KIF15* locus. In future studies, after further increases in samples sourced from diverse ancestries, fine-mapping in multiple populations should be undertaken. Cross-ancestry fine-mapping, however, still has notable challenges to be resolved.[50]

COVID-19 severity and IPF share a notable proportion of their genetic background, as genetic correlation was estimated to be substantial ($R_g \sim 0.35$), higher than previous estimates.[14] Of the 25 IPF index variants, seven reached the FDR-adjusted nominal p value in the COVID-19 hospitalization scan (out of which three were genome-wide significant: *CRHR1*, in addition to the previously reported *MUC5B* and *DPP9*). Effects at these loci were mostly in the same direction for the two traits, but variants in *MUC5B* and *ATP11A* showed opposite directions of effects. The strongest IPF risk locus *MUC5B* confers protection from

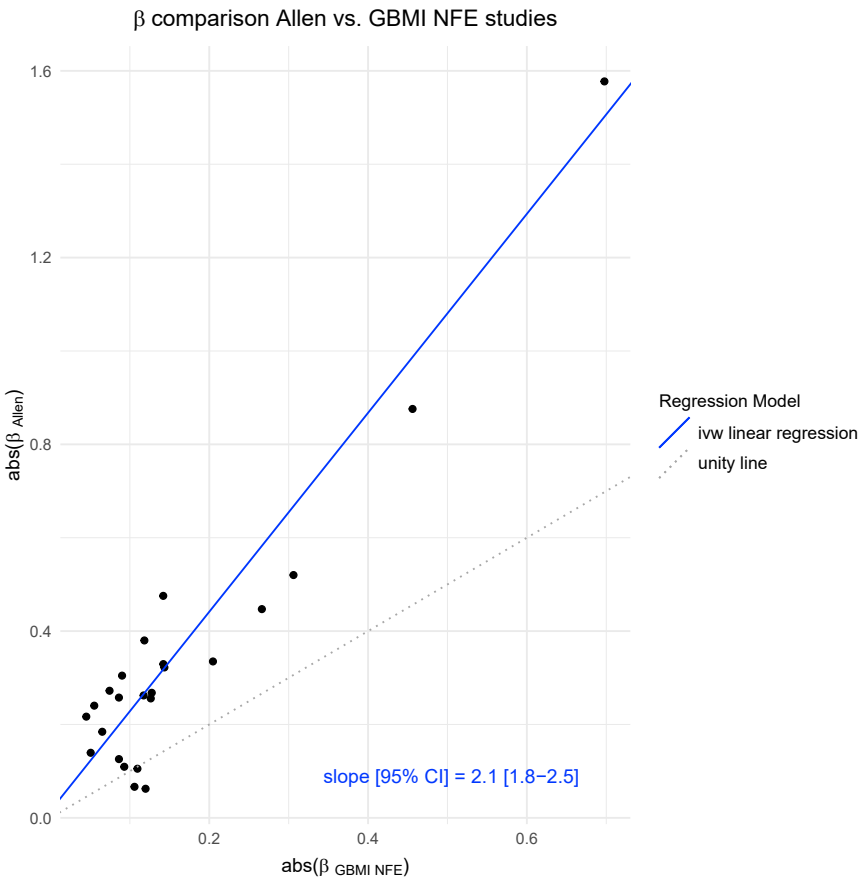


Figure 3. Effect size estimate comparison latest IPF meta-analysis versus GBMI

Scatter plot of absolute value of latest IPF meta-analysis beta against absolute value of meta-analyzed GBMI NFE beta with inverse variance weighted linear regression line (weights from Allen et al. study) and accompanying slope estimate. The analysis was performed within the non-Finnish European ancestry and variants included were genome-wide significant in the joint IPF meta-analysis.

severe COVID-19 and has been associated with survival in IPF patients.[51] Histologically, acute exacerbations of IPF present with diffuse alveolar damage, which is also present in severe COVID-19.[52]

Interestingly, we observed a sex-stratified effect in GBMI at *MUC5B*, the strongest common genetic risk factor for IPF, where the effect was 1.6 times larger in males compared with females. This result should, however, be considered with caution as it was not replicated in four clinical cohorts and may arise from confounding factors, such as ascertainment and age distribution differences in the sexes. These confounders should be investigated in future studies before the observed difference is inferred to represent a biological difference between the sexes. Yet, patient gender bias has been suggested to cause overdiagnosis of IPF in males and underdiagnosis in females,[53] which would attenuate effect estimates in males and increase them in females. With relevance to misexpression of MUC5B in IPF, rs35705950 has been suggested to introduce a *de novo* binding site for HOXA9,[54] a transcription factor differentially expressed by sex in whole blood[55] and transcriptionally regulated by sex hormones.[56,57] Also, FOXA2, a transcription factor binding 32 bp downstream of rs35705950 in the enhancer region 3 kB upstream of *MUC5B*, has a strong effect on MUC5B expression[54] and has been shown essential for sexual dimorphism in liver cancer.[58]

The meta-analysis with contributing biobanks featuring a wide variety of sampling strategies enabled studying between study heterogeneity, which revealed that case ascertainment has a large effect on IPF effect size estimates. Nearly a half of the genome-wide significant IPF loci expressed evidence of heterogeneity, which was mainly due to differences in case ascertainment—whether the patients were recruited from a hospital's pulmonary clinic or identified from health registries. Effect size estimates were more than 2-fold for clinical IPF cohorts compared with patients recruited from biobanks, in part due to the marginally more inclusive PheCode-based case definition used in the biobanks. For GWAS, however, the substantially larger number of patients available from biobanks benefits discovery even given the attenuated effect size estimates.

We present the first multi-ancestry meta-analysis of IPF to date with an over 4-fold increase in cases compared with the latest IPF meta-analysis. We discover multiple novel loci, the vast majority of which are driven by non-European populations and many of which have been linked to lung traits. We confirm and further describe the notable overlap of genetic determinants of IPF and severe COVID-19, calling for functional research. We describe a possible sex-dependent effect at the strongest IPF risk factor, the *MUC5B* locus, and demonstrate a 2-fold difference in effect size estimates derived from clinical cohorts as opposed to biobanks. To conclude, leveraging global multi-ancestry analysis further elucidates the genetic background of IPF by both revealing novel loci and providing increased resolution into previously identified ones.

Limitations of the study

Limitations of the study include between study heterogeneity, pointing to differing ascertainment between studies. However, this has limited impact on our novel findings, as only one of the novel loci showed evidence of heterogeneity (*DNAJB4*/*GIPC2*). Second, and with relevance to the former, the PheCode-based IPF case definition including other interstitial idiopathic

pneumonias increased the risk of misclassification in biobanks and contributed to the observed heterogeneity. In addition, as recruitment of participants spanned over two decades, changes in diagnostic practices for IPF may introduce chronological bias. Third, even though samples representing four non-European ancestries were included, the sample was still dominated by participants of European ancestry. Furthermore, fine-mapping was successful for only a minority of the loci. Finally, the novel findings of this study require future functional studies to elucidate their possible biological effects.

CONSORTIA

GBMI authors

Wei Zhou, Masahiro Kanai, Kuan-Han H. Wu, Humaira Rasheed, Kristin Tsuo, Jibril B Hirbo, Ying Wang, Arjun Bhattacharya, Huiling Zhao, Shinichi Namba, Ida Surakka, Brooke N. Wolford, Valeria Lo Faro, Esteban A. Lopera-Maya, Kristi Läll, Marie-Julie Favé, Sinéad B. Chapman, Juha Karjalainen, Mitja Kurki, Maasha Mutaamba, Juulia J. Partanen, Ben M. Brumpton, Sameer Chavan, Tzu-Ting Chen, Michelle Daya, Yi Ding, Yen-Chen A. Feng, Christopher R. Gignoux, Sarah E. Graham, Whitney E. Hornsby, Nathan Ingold, Ruth Johnson, Triin Laisk, Kuang Lin, Jun Lv, Iona Y. Millwood, Priit Palta, Anita Pandit, Michael H. Preuss, Unnur Thorsteinsdottir, Jasmina Uzunovic, Matthew Zawistowski, Xue Zhong, Archie Campbell, Kristy Crooks, Geertruida H. de Bock, Nicholas J. Douville, Sarah Finer, Lars G. Fritsche, Christopher J. Griffiths, Yu Guo, Karen A. Hunt, Takahiro Konuma, Riccardo E. Marioni, Jansonius Nomdo, Snehal Patil, Nicholas Rafaels, Anne Richmond, Jonathan A. Shortt, Peter Straub, Ran Tao, Brett Vanderwerff, Kathleen C. Barnes, Marike Boezen, Zhengming Chen, Chia-Yen Chen, Judy Cho, George Davey Smith, Hilary K. Finucane, Lude Franke, Eric R. Gamazon, Andrea Ganna, Tom R. Gaunt, Tian Ge, Hailiang Huang Jennifer Huffman Jukka T. Koskela, Clara Lajonchere, Matthew H. Law, Liming Li, Cecilia M. Lindgren, Ruth J.F. Loos, Stuart MacGregor, Koichi Matsuda, Catherine M. Olsen, David J. Porteous, Jordan A. Shavit, Harold Snieder, Richard C. Trembath, Judith M. Vonk, David Whiteman, Stephen J. Wicks, Cisca Wijmenga, John Wright, Jie Zheng, Xiang Zhou, Philip Awadalla, Michael Boehnke, Nancy J. Cox, Daniel H. Geschwind, Caroline Hayward, Kristian Hveem, Eimear E. Kenny, Yen-Feng Lin, Reedik Mägi, Hilary C. Martin, Sarah E. Medland, Yukinori Okada, Aarno V. Palotie, Bogdan Pasaniuc, Serena Sanna, Jordan W. Smoller, Kari Stefansson, David A. van Heel, Robin G. Walters, Sebastian Zöllner, BioBank Japan, BioMe, BioVU, Canadian Partnership for Tomorrow's Health/Ontario Health Study, China Kadoorie Biobank Collaborative Group, Colorado Center for Personalized Medicine, deCODE Genetics, Estonian Biobank, FinnGen, Generation Scotland, Genes & Health, LifeLines, Mass General Brigham Biobank, Michigan Genomics Initiative, QIMR Berghofer Biobank, Taiwan Biobank, The HUNT Study, UCLA ATLAS Community Health Initiative, UK Biobank, Alicia R. Martin, Cristen J. Willer, Mark J. Daly, and Benjamin M. Neale

Author affiliations are available in the supplemental information section.

International IPF Genetics Consortium

Richard J. Allen, Helen L. Booth, William A. Fahy, Ian P. Hall, Simon P. Hart, Mike R. Hill, Nik Hirani, Richard B. Hubbard, R. Gisli Jenkins, Toby M. Maher, Robin J. McAnulty, Ann B. Millar, Philip L. Molyneaux, Vidya Navaratnam, Eunice Oballa, Helen Parfrey, Gauri Saini, Ian Sayers, Martin D. Tobin, Louise V. Wain Moira K. B. Whyte, Ayodeji Adegunsoye, Carlos Flores, Naftali Kaminski, Shwu-Fan Ma, Imre Noth, Justin M. Oldham, Mary E. Strek, Yingze Zhang, Tasha Fingerlin, David A. Schwartz, Beatriz Guillen-Guio, Maria Molina-Molina, Margaret Neighbors Xuting Sheng, Amy Stockwell, and Brian L. Yaspan.

Author affiliations are available in the supplemental information section.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE
- RESOURCE AVAILABILITY
  - Lead contact
  - Materials availability
  - Data and code availability
- EXPERIMENTAL MODEL AND SUBJECT DETAILS
- METHOD DETAILS
  - Phenotype definition and quality control
  - Meta-analysis
  - Fine-mapping
  - Phenome-wide lookup
  - LD score regression intercept and genetic correlation
  - Colocalization
  - Sex-stratified and sex interaction analyses
  - Heterogeneity evaluation
- QUANTIFICATION AND STATISTICAL ANALYSIS

SUPPLEMENTAL INFORMATION

Supplemental information can be found online at https://doi.org/10.1016/j.xgen.2022.100181.

ACKNOWLEDGMENTS

We would like to thank Jaakko Kaprio, Juha Partanen, Sami Kilpinen, and Clara Benoit-Pilven from the University of Helsinki for providing insight on sections of the manuscript. This research used the SPECTRE High Performance Computing Facility at the University of Leicester.

This work was supported by the Doctoral Programme in Population Health, University of Helsinki (to J.J.P.); and The Finnish Medical Foundation (to J.J.P.); NHLBI (to J.O.); Wellcome Trust (221680/Z/20/Z to B.G.-G.); NHLBI (to D.A.S.), DoD (to D.A.S.); Spanish Ministry of Science and Innovation and Instituto de Salud Carlos III, co-financed by the European Regional Development Fund (ERDF) "A Way of Making Europe" from the European Union (EU) (RTC-2017-6471-1 and PI20/00876 to C.F.); Cabildo Insular de Tenerife (CGIEU0000219140 to C.F.); NIH (to I.N.), Medical Research Council – project grant (to R.G.J.); NIHR Research Professorship (to R.G.J.); GSK/Asthma + Lung UK Chair in Respiratory Research (C17-1) (to L.V.W.); Research Foundation of the Pulmonary Diseases HES (to R.K.); Jalmari and Rauha Ahokas Foundation (to R.K.); the Research Foundation of North Finland, Oulu, Finland, and a state subsidy of Oulu University Hospital (to R.K.); HUS State Research Funding (to M.M.); Academy of Finland (to J.T.K.). R.J.A. is an Action for

Pulmonary Fibrosis Mike Bray Research Fellow. The work of the contributing biobanks for GBMI was supported by numerous grants from governmental and charitable bodies (see below). The research was partially supported by the National Institute for Health Research (NIHR) Leicester Biomedical Research Center; the views expressed are those of the author(s) and not necessarily those of the National Health Service (NHS), the NIHR, or the Department of Health. The Genotype-Tissue Expression (GTEx) Project was supported by the Common Fund of the Office of the Director of the National Institutes of Health, and by NCI, NHGRI, NHLBI, NIDA, NIMH, and NINDS. The Graphical abstract was created with BioRender.com.

BioBank Japan Project: The BioBank Japan Project was supported by the Tailor-Made Medical Treatment program of the Ministry of Education, Culture, Sports, Science, and Technology (MEXT), the Japan Agency for Medical Research and Development (AMED). S.N. was supported by Takeda Science Foundation. Y.O. was supported by JSPS KAKENHI (19H01021 and 20K21834), and AMED (JP21km0405211, JP21ek0109413, JP21ek0410075, JP21gm4010006, and JP21km0405217), JST Moonshot R&D (JPMJMS2021 and JPMJMS2024), Takeda Science Foundation, and Bioinformatics Initiative of Osaka University Graduate School of Medicine, Osaka University.

BioMe - The Mount Sinai BioMe Biobank: The Mount Sinai BioMe Biobank has been supported by The Andrea and Charles Bronfman Philanthropies and in part by Federal funds from the NHLBI and NHGRI (U01HG00638001, U01HG007417, and X01HL134588). We thank all participants in the Mount Sinai Biobank. We also thank all our recruiters who have assisted and continue to assist in data collection and management and are grateful for the computational resources and staff expertise provided by Scientific Computing at the Icahn School of Medicine at Mount Sinai.

BioVU: The BioVU projects at Vanderbilt University Medical Center are supported by numerous sources: institutional funding, private agencies, and federal grants. These include the NIH-funded Shared Instrumentation Grant nos. S10OD017985 and S10RR025141; CTSA grants UL1TR002243, UL1TR000445, and UL1RR024975 from the National Center for Advancing Translational Sciences. Its contents are solely the responsibility of the authors and do not necessarily represent official views of the National Center for Advancing Translational Sciences or the National Institutes of Health. Genomic data are also supported by investigator-led projects that include U01HG004798, R01NS032830, RC2GM092618, P50GM115305, U01HG006378, U19HL065962, R01HD074711; and additional funding sources listed at https://victr.vumc.org/biovu-funding/.

Colorado Center for Personalized Medicine (CCPM): CCPM would like to thank Richard Zane, Steve Hess, Sarah White, Emily Hearst, Emily Roberts, and the entire Health Data Compass team. CCPM was developed with support from UCHealth, Children's Hospital Colorado, CU Medicine, CU Department of Medicine, and CU School of Medicine.

China Kadoorie Biobank collaborative group: The China Kadoorie Biobank collaborative group would like to thank the International Steering Committee: Junshi Chen, Zhengming Chen (PI), Robert Clarke, Rory Collins, Yu Guo, Liming Li (PI), Jun Lv, Richard Peto, Robin Walters, and Chen Wang. The China Kadoorie Biobank collaborative group would also like to thank the International Co-ordinating Centre, Oxford: Daniel Avery, Fiona Bragg, Derrick Bennett, Ruth Boxall, Ka Hung Chan, Yumei Chang, Yiping Chen, Zhengming Chen, Johnathan Clarke, Robert Clarke, Huaidong Du, Zammy Fairhurst-Hunter, Hannah Fry, Simon Gilbert, Alex Hacker, Parisa Hariri, Mike Hill, Michael Holmes, Pek Kei Im, Andri Iona, Maria Kakkoura, Christiana Kartsonaki, Rene Kerosi, Kuang Lin, Mohsen Mazidi, Iona Millwood, Qunhua Nie, Alfred Pozarickij, Paul Ryder, Sam Sansome, Dan Schmidt, Paul Sherliker, Rajani Sohoni, Becky Stevens, Iain Turnbull, Robin Walters, Lin Wang, Neil Wright, Ling Yang, Xiaoming Yang, and Pang Yao; and the National Co-ordinating Centre, Beijing: Yu Guo, Xiao Han, Can Hou, Chun Li, Chao Liu, Jun Lv, Pei Pei, and Canqing Yu. Regional coordinating centers would like to thank Guangxi Provincial CDC: Naying Chen, Duo Liu, and Zhenzhu Tang; Liuzhou CDC: Ningyu Chen, Qilian Jiang, Jian Lan, Mingqiang Li, Yun Liu, Fanwen Meng, Jinhuai Meng, Rong Pan, Yulu Qin, Ping Wang, Sisi Wang, Liuping Wei, and Liyuan Zhou; Gansu Provincial CDC: Caixia Dong, Pengfei Ge, Xiaolan Ren; Maiji CDC: Zhongxiao Li, Enke Mao, Tao Wang, Hui Zhang, and Xi Zhang; Hainan Provincial CDC: Jinyan Chen, Ximin Hu, and Xiaohuan Wang; Meilan CDC: Zhendong Guo, Huimei Li, Yilei Li, Min Weng, and Shukuan Wu; Heilongjiang Provincial CDC: Shichun Yan, Mingyuan Zou, and Xue Zhou; Nangang CDC: Ziyan Guo, Quan Kang, Yanjie Li, Bo Yu, and Qinai Xu; Henan Provincial CDC: Liang Chang, Lei Fan, Shixian Feng, Ding Zhang, and Gang Zhou; Huixian CDC: Yulian Gao, Tianyou He, Pan He, Chen Hu, Huarong Sun, and Xukui Zhang; Hunan Provincial CDC: Biyun Chen, Zhongxi Fu, Yuelong Huang, Huilin Liu, Qiaohua Xu, and Li Yin; Liuyang CDC: Huajun Long, Xin Xu, Hao Zhang, and Libo Zhang; Jiangsu Provincial CDC: Jian Su, Ran Tao, Ming Wu, Jie Yang, Jinyi Zhou, and Yonglin Zhou; Suzhou CDC: Yihe Hu, Yujie Hua, Jianrong Jin Fang Liu, Jingchao Liu, Yan Lu, Liangcai Ma, Aiyu Tang, and Jun Zhang; Qingdao CDC: Liang Cheng, Ranran Du, Ruqin Gao, Feifei Li, Shanpeng Li, Yongmei Liu, Feng Ning, Zengchang Pang, Xiaohui Sun, Xiaocao Tian, Shaojie Wang, Yaoming Zhai, and Hua Zhang; Licang CDC: Wei Hou, Silu Lv, and Junzheng Wang; Sichuan Provincial CDC: Xiaofang Chen, Xianping Wu, Ningmei Zhang, and Weiwei Zhou; Pengzhou CDC: Xiaofang Chen, Jianguo Li, Jiaqiu Liu, Guojin Luo, Qiang Sun, and Xunfu Zhong; Zhejiang Provincial CDC: Weiwei Gong, Ruying Hu, Hao Wang, Meng Wan, and Min Yu; and Tongxiang CDC: Lingli Chen, Qijun Gu, Dongxia Pan, Chunmei Wang, Kaixu Xie, and Xiaoyi Zhang. China Kadoorie Biobank gratefully acknowledges the participants, project staff, and the China National Centre for Disease Control and Prevention (CDC) and its regional offices. China's National Health Insurance provides electronic linkage to all hospital treatment. Funding sources: baseline survey and first re-survey—Kadoorie Charitable Foundation, Hong Kong; long-term follow-up—UK Wellcome Trust (212946/Z/18/Z, 202922/Z/16/Z, 104085/Z/14/Z, 088158/Z/09/Z), National Natural Science Foundation of China (91843302), National Key Research and Development Program of China (2016YFC 0900500, 0900501, 0900504, 1303904); DNA extraction and genotyping – GlaxoSmithKline, UK Medical Research Council (MC-PC-13049, MC-PC-14135); core funding for the project to the Clinical Trial Service Unit and Epidemiological Studies Unit at Oxford University—British Heart Foundation (CH/1996001/9454), UK Medical Research Council (MC-UU-00017/1, MC-UU-12026/2, MC_U137686851), Cancer Research UK (C16077/A29186, C500/A16896).

Estonian Biobank: Estonian Biobank research was supported by the European Union through Horizon 2020 research and innovation program under grant no. 810645 and through the European Regional Development Fund project no. MOBEC008, by the Estonian Research Council grant PUT (PRG1291, PRG687, and PRG184) and by the European Union through the European Regional Development Fund project no. MOBERA21 (ERA-CVD project DETECT ARRHYTHMIAS, GA no JTC2018-009), project no. 2014-2020.4.01.15-0012, and project no. 2014-2020.4.01.16-0125. Estonian Biobank would like to acknowledge Dr. Tõnu Esko, Dr. Lili Milani, Dr. Reedik Mägi, Dr. Mari Nelis, and Dr. Andres Metspalu, all from the Institute of Genomics, University of Tartu, Tartu, Estonia.

FinnGen: The FinnGen project is funded by two grants from Business Finland (HUS 4685/31/2016 and UH 4386/31/2016) and the following industry partners: AbbVie Inc., AstraZeneca UK Ltd, Biogen MA Inc., Bristol Myers Squibb (and Celgene Corporation & Celgene International II Sàrl), Genentech Inc., Merck Sharp & Dohme Corp, Pfizer Inc., GlaxoSmithKline Intellectual Property Development Ltd, Sanofi US Services Inc., Maze Therapeutics Inc., Janssen Biotech Inc., and Novartis AG. Following biobanks are acknowledged for delivering biobank samples to FinnGen: Auria Biobank (www.auria.fi/biopankki), THL Biobank (www.thl.fi/biobank), Helsinki Biobank (www.helsinginbiopankki.fi), Biobank Borealis of Northern Finland (https://www.ppshp.fi/Tutkimus-ja-opetus/Biopankki/Pages/Biobank-Borealis-briefly-in-English.aspx), Finnish Clinical Biobank Tampere (www.tays.fi/en-US/Research_and_development/Finnish_Clinical_Biobank_Tampere), Biobank of Eastern Finland (www.ita-suomenbiopankki.fi/en), Central Finland Biobank (www.ksshp.fi/fi-FI/Potilaalle/Biopankki), Finnish Red Cross Blood Service Biobank (www.veripalvelu.fi/verenluovutus/biopankkitoiminta) and Terveystalo Biobank (www.terveystalo.com/fi/Yritystietoa/Terveystalo-Biopankki/Biopankki/). All Finnish Biobanks are members of BBMRI.fi infrastructure (www.bbmri.fi). Finnish Biobank Cooperative-FINBB (https://finbb.fi/) is the coordinator of BBMRI-ERIC operations in Finland. The Finnish biobank data can be accessed through the Fingenious services (https://site.fingenious.fi/en/) managed by FINBB.

Genes and Health: Genes & Health is/has recently been core-funded by Wellcome (WT102627, WT210561), the Medical Research Council (UK) (M009017),

Higher Education Funding Council for England Catalyst, Barts Charity (845/1796), Health Data Research UK (for London substantive site), and research delivery support from the NHS National Institute for Health Research Clinical Research Network (North Thames). Genes & Health is/has recently been funded by Alnylam Pharmaceuticals, Genomics PLC; and a Life Sciences Industry Consortium of Bristol-Myers Squibb Company, GlaxoSmithKline Research and Development Limited, Maze Therapeutics Inc., Merck Sharp & Dohme LLC, Novo Nordisk A/S, Pfizer Inc., Takeda Development Centre Americas Inc. We thank Social Action for Health, Centre of The Cell, members of our Community Advisory Group, and staff who have recruited and collected data from volunteers. We thank the NIHR National Biosample Centre (UK Biocentre), the Social Genetic & Developmental Psychiatry Centre (King's College London), Wellcome Sanger Institute, and Broad Institute for sample processing, genotyping, sequencing, and variant annotation. We thank Barts Health NHS Trust, NHS Clinical Commissioning Groups (City and Hackney, Waltham Forest, Tower Hamlets, Newham, Redbridge, Havering, Barking, and Dagenham), East London NHS Foundation Trust, Bradford Teaching Hospitals NHS Foundation Trust, Public Health England (especially David Wyllie), Discovery Data Service/Endeavour Health Charitable Trust (especially David Stables)—for GDPR-compliant data sharing backed by individual written informed consent. Most of all, we thank all of the volunteers participating in Genes & Health. We would like to acknowledge the Genes & Health Research Team (in alphabetical order by surname): Shaheen Akhtar, Mohammad Anwar, Elena Arciero, Samina Ashraf, Gerome Breen, Raymond Chung, Charles J. Curtis, Maharun Chowdhury, Grainne Colligan, Panos Deloukas, Ceri Durham, Sarah Finer, Chris Griffiths, Qin Qin Huang, Matt Hurles, Karen A. Hunt, Shapna Hussain, Kamrul Islam, Ahsan Khan, Amara Khan, Cath Lavery, Sang Hyuck Lee, Robin Lerner, Daniel MacArthur, Bev MacLaughlin, Hilary Martin, Dan Mason, Shefa Miah, Bill Newman, Nishat Safa, Farah Tahmasebi, Richard C. Trembath, Bhavi Trivedi, David A. van Heel, and John Wright.

The HUNT Study: A special thanks to all the HUNT participants for donating their time, samples, and information to help others. The Trøndelag Health Study (HUNT) is a collaboration between HUNT Research Centre (Faculty of Medicine and Health Sciences, NTNU, Norwegian University of Science and Technology), Trøndelag County Council, Central Norway Regional Health Authority, and the Norwegian Institute of Public Health. The genotyping in HUNT was financed by the National Institutes of Health; University of Michigan; the Research Council of Norway; the Liaison Committee for Education, Research and Innovation in Central Norway; and the Joint Research Committee between St Olavs hospital and the Faculty of Medicine and Health Sciences, NTNU. The genetic investigations of the HUNT Study is a collaboration between researchers from the K.G. Jebsen Center for Genetic Epidemiology, NTNU and the University of Michigan Medical School and the University of Michigan School of Public Health. The K.G. Jebsen Center for Genetic Epidemiology is financed by Stiftelsen Kristian Gerhard Jebsen; Faculty of Medicine and Health Sciences, NTNU, Norway. We want to thank clinicians and other employees at Nord-Trøndelag Hospital Trust for their support and for contributing to data collection in this research project. We also acknowledge HUNT-MI Leadership: Kristian Hveem, Cristen Willer, Oddgeir Lingaas Holmen, Mike Boehnke, Goncalo Abecasis, Bjorn Olav Åsvold, and Ben Brumpton; Scientific Advisory Committee: Ele Zeggini, Mark Daly, and Bjørn Pasternak; HUNT Research Centre: Jørn Søberg Fenstad, Anne Jorunn Vikdal, and Marit Næss; HUNT Cloud: Oddgeir Lingaas Holmen, Sandor Zeestraten, and Tom Erik Røberg; data applications and registry linkages: Maiken E. Gabrielsen and Anne Heidi Skogholt; low-pass whole sequencing genome bioinformatics and statistical analysis: He Zhang, Hyun Min Kang, and Jin Chen; array genotyping: Sten Even Erlandsen and Vidar Beisvåg; GWAS bioinformatics, QC, imputation, and statistical analysis: Wei Zhou, Jonas Nielsen, Lars Fritsche, Hyun Min Kang, Oddgeir Holmen, Ben Brumpton, and Laurent Thomas; CNV calling: Ellen Schmidt and Ryan Mills; and statistical methods development for analyzing HUNT data: Wei Zhou and Shawn Lee. The K.G. Jebsen Centre for Genetic Epidemiology is financed by Stiftelsen Kristian Gerhard Jebsen. The genotyping in HUNT was financed by the National Institutes of Health; University of Michigan; the Research Council of Norway; Stiftelsen Kristian Gerhard Jebsen; the Liaison Committee for Education, Research and Innovation in Central Norway; and the Joint Research Committee between St Olav's hospital and the Faculty of Medicine and Health Sciences, NTNU.

Mass General Brigham (MGB) Biobank: Samples, genomic data, and health information were obtained from the Mass General Brigham (MGB) Biobank, a biorepository of consented patients' samples at Mass General Brigham (parent organization of Massachusetts General Hospital and Brigham and Women's Hospital). We are grateful to all of the participants and clinical and research teams who made this work possible. Support for genotyping was provided through MGB Personalized Medicine. We would like to acknowledge MGB Biobank Leadership: Elizabeth W. Karlson, MD; Shawn N. Murphy, MD, PhD; Susan A Slaugenhaupt, PhD; Jordan W. Smoller, MD, ScD; and Scott T. Weiss, MD, MSc.

Michigan Genomics Initiative: The authors acknowledge the Michigan Genomics Initiative participants, Precision Health at the University of Michigan, the University of Michigan Medical School Central Biorepository, and the University of Michigan Advanced Genomics Core for providing data and specimen storage, management, processing, and distribution services, and the Center for Statistical Genetics in the Department of Biostatistics at the School of Public Health for genotype data curation, imputation, and management in support of the research reported in this publication.

UCLA ATLAS Community Health Initiative (UCLA): We gratefully acknowledge the resources provided by the Institute for Precision Health (IPH) and participating UCLA ATLAS Community Health Initiative patients. The UCLA ATLAS Community Health Initiative in collaboration with UCLA ATLAS Precision Health Biobank, is a program of IPH, which directs and supports the biobanking and genotyping of biospecimen samples from participating UCLA patients in collaboration with the David Geffen School of Medicine, UCLA CTSI, and UCLA Health. Members of the UCLA ATLAS Community Health Initiative include Ruth Johnson, Yi Ding, Vidhya Venkateswaran, Arjun Bhattacharya, Alec Chiu, Tommer Schwarz, Malika Freund, Lingyu Zhan, Kathryn S. Burch, Christa Caggiano, Brian Hill, Nadav Rakocz, Brunilda Balliu, Jae Hoon Sul, Noah Zaitlen, Valerie A. Arboleda, Eran Halperin, Sriram Sankararaman, Manish J. Butte, Clara Lajonchere, Daniel H. Geschwind, and Bogdan Pasaniuc, on behalf of the UCLA Precision Health Data Discovery Repository Working Group and UCLA Precision Health ATLAS Working Group.

UK BioBank: Access to data from the UK BioBank was obtained through application no. 31063. Principal investigators: Ben Neale, Claire Churchhouse. Project overview: "Methodological extensions to estimate genetic heritability and shared risk factors for phenotypes of the UK Biobank." Website for Pan-UKBB results can be found here: https://pan.ukbb.broadinstitute.org/

Other G.D.S., T.R.G., and J.Z. are supported by a grant from the Medical Research Council for the Integrative Epidemiology Unit at the University of Bristol MC_UU_00011/1 & 4. J.Z. is supported by the Academy of Medical Sciences (AMS) Springboard Award, the Wellcome Trust, the Government Department of Business, Energy and Industrial Strategy (BEIS), the British Heart Foundation and Diabetes UK (SBF006\1117). J.Z. is funded by the Vice-Chancellor Fellowship from the University of Bristol. W.Z. was supported by the National Human Genome Research Institute of the National Institutes of Health under award no. T32HG010464.

ICDA: The authors would like to acknowledge the organizing committee of the International Common Disease Alliance for intellectual contributions on the set up of the GBMI as a nascent activity to the larger effort. We also thank them for the use of their slack platform. Website for ICDA can be found here: https://www.icda.bio/

The Hail Team and Data Management at the Stanley Center for Psychiatric Research: Hail is an open-source Python library that simplifies genomic data analysis in the cloud. It provides powerful, easy-to-use data science tools that can be used to interrogate biobank-scale genomic data and was used in the analysis of the data for this paper. We would especially like to thank Daniel King from the Hail team and Sam Bryant from the Stanley Center Data Management team for helping with the Google bucket set up and data sharing. The website for Hail can be found here: https://hail.is/.

AUTHOR CONTRIBUTIONS

Study design, J.J.P., P.H., W.Z., M.J.D., and J.T.K.; data collection/contribution, W.Z., J.M.O., N.J.C., J.B.H., D.A.S., T.E.F., C.F., I.N., B.L.Y., R.G.J., L.V.W., International IPF Genetics Consortium, GBMI, R.K., and M.M.; data analysis, J.J.P., P.H., W.Z., A.A.L., R.J.A., A.D.S., O.C.L., B.G.-G., and

J.T.K.; writing, J.J.P., P.H., and J.T.K.; revision, J.J.P., P.H., M.A., R.K., M.J.D., and J.T.K. All authors provided critical input to interpretation of the data and have approved the final version of the manuscript.

DECLARATION OF INTERESTS

A.S. and B.L.Y. are full-time employees of Genentech with stock and stock options in Roche. D.A.S. is the founder and chief scientific officer of Eleven P15, a company focused on the early diagnosis and treatment of IPF. T.E.F. is a consultant to Eleven P15. R.G.J. has received research funding from Astra Zeneca, Biogen, Galecto, GlaxoSmithKline, RedX, and Pliant; consulting fees from Bristol Myers Squibb, Daewoong, Veracyte, Resolution Therapeutics, RedX, and Pliant; payment for lectures, presentations, speakers bureaus, manuscript writing or educational events from Chiesi, Roche, PatientMPower, and AstraZeneca; payment for Participation on a Data Safety Monitoring Board or Advisory Board from Boehringer Ingelheim, Galapagos, and Vicore, had a Leadership or fiduciary role in other board, society, committee or advocacy group (unpaid) in NuMedii and Action for Pulmonary Fibrosis; and is a trustee for Action for Pulmonary Fibrosis. L.V.W. has received research funding from GSK and Orion Pharma and consultancy for Galapagos. M.J.D. is a founder of Maze Therapeutics. J.T.K. and M.J.D. are members of the Pfizer Finland FinnGen Advisory Board.

INCLUSION AND DIVERSITY

We worked to ensure ethnic or other types of diversity in the recruitment of human subjects. The author list of this paper includes contributors from the location where the research was conducted who participated in the data collection, design, analysis, and/or interpretation of the work.

Received: January 25, 2022
Revised: May 24, 2022
Accepted: September 7, 2022
Published: October 12, 2022

REFERENCES

1. Lederer, D.J., and Martinez, F.J. (2018). Idiopathic pulmonary fibrosis. N. Engl. J. Med. *378*, 1811–1823.
2. Allen, R.J., Guillen-Guio, B., Oldham, J.M., Ma, S.-F., Dressen, A., Paynton, M.L., Kraven, L.M., Obeidat, M., Li, X., Ng, M., et al. (2020). Genome-wide association study of susceptibility to idiopathic pulmonary fibrosis. Am. J. Respir. Crit. Care Med. *201*, 564–574.
3. Seibold, M.A., Wise, A.L., Speer, M.C., Steele, M.P., Brown, K.K., Loyd, J.E., Fingerlin, T.E., Zhang, W., Gudmundsson, G., Groshong, S.D., et al. (2011). A common MUC5B promoter polymorphism and pulmonary fibrosis. N. Engl. J. Med. *364*, 1503–1512.
4. Koskela, J.T., Häppölä, P., Liu, A., Partanen, J., Genovese, G., Artomov, M., Myllymäki, M.N.M., Kanai, M., Zhou, W., Karjalainen, J.M., et al. (2021). Genetic variant in SPDL1 reveals novel mechanism linking pulmonary fibrosis risk and cancer protection. Preprint at bioRxiv. https://doi.org/10.1101/2021.05.07.21255988.
5. Ishigaki, K., Akiyama, M., Kanai, M., Takahashi, A., Kawakami, E., Sugishita, H., Sakaue, S., Matoba, N., Low, S.-K., Okada, Y., et al. (2020). Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nat. Genet. *52*, 669–679.
6. Dhindsa, R.S., Mattsson, J., Nag, A., Wang, Q., Wain, L.V., Allen, R., Wigmore, E.M., Ibanez, K., Vitsios, D., Deevi, S.V.V., et al. (2021). Identification of a missense variant in SPDL1 associated with idiopathic pulmonary fibrosis. Commun. Biol. *4*, 392.
7. Mushiroda, T., Wattanapokayakit, S., Takahashi, A., Nukiwa, T., Kudoh, S., Ogura, T., Taniguchi, H., Kubo, M., Kamatani, N., and Nakamura, Y.; Pirfenidone Clinical Study Group (2008). A genome-wide association study identifies an association of a common variant in TERT with susceptibility to idiopathic pulmonary fibrosis. J. Med. Genet. *45*, 654–656.
8. Noth, I., Zhang, Y., Ma, S.-F., Flores, C., Barber, M., Huang, Y., Broderick, S.M., Wade, M.S., Hysi, P., Scuirba, J., et al. (2013). Genetic variants associated with idiopathic pulmonary fibrosis susceptibility and mortality: a genome-wide association study. Lancet Respir. Med. *1*, 309–317.
9. Fingerlin, T.E., Murphy, E., Zhang, W., Peljto, A.L., Brown, K.K., Steele, M.P., Loyd, J.E., Cosgrove, G.P., Lynch, D., Groshong, S., et al. (2013). Genome-wide association study identifies multiple susceptibility loci for pulmonary fibrosis. Nat. Genet. *45*, 613–620.
10. Allen, R.J., Porte, J., Braybrooke, R., Flores, C., Fingerlin, T.E., Oldham, J.M., Guillen-Guio, B., Ma, S.-F., Okamoto, T., John, A.E., et al. (2017). Genetic variants associated with susceptibility to idiopathic pulmonary fibrosis in people of European ancestry: a genome-wide association study. Lancet Respir. Med. *5*, 869–880.
11. Fingerlin, T.E., Zhang, W., Yang, I.V., Ainsworth, H.C., Russell, P.H., Blumhagen, R.Z., Schwarz, M.I., Brown, K.K., Steele, M.P., Loyd, J.E., et al. (2016). Genome-wide imputation study identifies novel HLA locus for pulmonary fibrosis and potential role for auto-immunity in fibrotic idiopathic interstitial pneumonia. BMC Genet. *17*, 74.
12. Duckworth, A., Gibbons, M.A., Allen, R.J., Almond, H., Beaumont, R.N., Wood, A.R., Lunnon, K., Lindsay, M.A., Wain, L.V., Tyrrell, J., and Scotton, C.J. (2021). Telomere length and risk of idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease: a mendelian randomisation study. Lancet Respir. Med. *9*, 285–294.
13. COVID-19 Host Genetics Initiative (2021). Mapping the human genetic architecture of COVID-19. Nature.
14. Fadista, J., Kraven, L.M., Karjalainen, J., Andrews, S.J., Geller, F., COVID-19 Host Genetics Initiative, Baillie, J.K., Wain, L.V., Jenkins, R.G., and Feenstra, B. (2021). Shared genetic etiology between idiopathic pulmonary fibrosis and COVID-19 severity. EBioMedicine *65*, 103277.
15. COVID-19 Host Genetics Initiative; and Ganna, A. (2021). Mapping the human genetic architecture of COVID-19: an update. Preprint at medRxiv. https://doi.org/10.1101/2021.11.08.21265944.
16. Allen, R.J., Guillen-Guio, B., Croot, E., Kraven, L.M., Moss, S., Stewart, I., Gisli Jenkins, R., and Wain, L.V. Genetic overlap between idiopathic pulmonary fibrosis and COVID−19.
17. Bulik-Sullivan, B.K., Loh, P.-R., Finucane, H.K., Ripke, S., Yang, J., Schizophrenia Working Group of the Psychiatric Genomics Consortium; Patterson, N., Daly, M.J., Price, A.L., and Neale, B.M. (2015). LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nat. Genet. *47*, 291–295.
18. Ghoussaini, M., Mountjoy, E., Carmona, M., Peat, G., Schmidt, E.M., Hercules, A., Fumis, L., Miranda, A., Carvalho-Silva, D., Buniello, A., et al. (2021). Open Targets Genetics: systematic identification of trait-associated genes using large-scale genetics and functional genomics. Nucleic Acids Res. *49*, D1311–D1320.
19. Shrine, N., Guyatt, A.L., Erzurumluoglu, A.M., Jackson, V.E., Hobbs, B.D., Melbourne, C.A., Batini, C., Fawcett, K.A., Song, K., Sakornsakolpat, P., et al. (2019). New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nat. Genet. *51*, 481–493.
20. Hausch, F., Kozany, C., Theodoropoulou, M., and Fabian, A.-K. (2013). FKBPs and the Akt/mTOR pathway. Cell Cycle *12*, 2366–2370.
21. Woodcock, H.V., Eley, J.D., Guillotin, D., Platé, M., Nanthakumar, C.B., Martufi, M., Peace, S., Joberty, G., Poeckel, D., Good, R.B., et al. (2019). The mTORC1/4E-BP1 axis represents a critical signaling node during fibrogenesis. Nat. Commun. *10*, 6.
22. Kichaev, G., Bhatia, G., Loh, P.-R., Gazal, S., Burch, K., Freund, M.K., Schoech, A., Pasaniuc, B., and Price, A.L. (2019). Leveraging polygenic functional enrichment to improve GWAS power. Am. J. Hum. Genet. *104*, 65–75.
23. Sinnott-Armstrong, N., Naqvi, S., Rivas, M., and Pritchard, J.K. (2021). GWAS of three molecular traits highlights core genes and pathways alongside a highly polygenic background. Elife *10*, e58615.

24. Hayden, L.P., Cho, M.H., McDonald, M.-L.N., Crapo, J.D., Beaty, T.H., Silverman, E.K., and Hersh, C.P.; COPDGene Investigators * (2017). Susceptibility to childhood pneumonia: a genome-wide analysis. Am. J. Respir. Cell Mol. Biol. *56*, 20–28.

25. Halu, A., Liu, S., Baek, S.H., Hobbs, B.D., Hunninghake, G.M., Cho, M.H., Silverman, E.K., and Sharma, A. (2019). Exploring the cross-phenotype network region of disease modules reveals concordant and discordant pathways between chronic obstructive pulmonary disease and idiopathic pulmonary fibrosis. Hum. Mol. Genet. *28*, 2352–2364.

26. Locke, A.E., Kahali, B., Berndt, S.I., Justice, A.E., Pers, T.H., Day, F.R., Powell, C., Vedantam, S., Buchkovich, M.L., Yang, J., et al. (2015). Genetic studies of body mass index yield new insights for obesity biology. Nature *518*, 197–206.

27. Olafsson, S., Alexandersson, K.F., Gizurarson, J.G.K., Hauksdottir, K., Gunnarsson, O., Olafsson, K., Gudmundsson, J., Stacey, S.N., Sveinbjornsson, G., Saemundsdottir, J., et al. (2020). Common and rare sequence variants influencing tumor biomarkers in blood. Cancer Epidemiol. Biomarkers Prev. *29*, 225–235.

28. Emilsson, V., Ilkov, M., Lamb, J.R., Finkel, N., Gudmundsson, E.F., Pitts, R., Hoover, H., Gudmundsdottir, V., Horman, S.R., Aspelund, T., et al. (2018). Co-regulatory networks of human serum proteins link genetics to disease. Science *361*, 769–773.

29. Ferkingstad, E., Oddsson, A., Gretarsdottir, S., Benonisdottir, S., Thorleifsson, G., Deaton, A.M., Jonsson, S., Stefansson, O.A., Norddahl, G.L., Zink, F., et al. (2018). Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nat. Commun. *9*, 5101.

30. Janssen, W.J., Stefanski, A.L., Bochner, B.S., and Evans, C.M. (2016). Control of lung defence by mucins and macrophages: ancient defence mechanisms with modern functions. Eur. Respir. J. *48*, 1201–1214.

31. Sakaue, S., Kanai, M., Tanigawa, Y., Karjalainen, J., Kurki, M., Koshiba, S., Narita, A., Konuma, T., Yamamoto, K., Akiyama, M., et al. (2021). A cross-population atlas of genetic associations for 220 human phenotypes. Nat. Genet. *53*, 1415–1424.

32. Bierut, L.J., Madden, P.A.F., Breslau, N., Johnson, E.O., Hatsukami, D., Pomerleau, O.F., Swan, G.E., Rutter, J., Bertelsen, S., Fox, L., et al. (2007). Novel genes identified in a high density genome wide association study for nicotine dependence. Hum. Mol. Genet. *16*, 24–35.

33. GTEx Consortium (2020). The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science *369*, 1318–1330.

34. Eraslan, G., Drokhlyansky, E., Anand, S., Subramanian, A., Fiskin, E., Slyper, M., Wang, J., Van Wittenberghe, N., Rouhana, J.M., Waldman, J., et al. (2021). Single-nucleus cross-tissue molecular reference maps to decipher disease gene function. Preprint at bioRxiv. https://doi.org/10.1101/2021.07.19.452954.

35. Reyfman, P.A., Walter, J.M., Joshi, N., Anekalla, K.R., McQuattie-Pimentel, A.C., Chiu, S., Fernandez, R., Akbarpour, M., Chen, C.-I., Ren, Z., et al. (2019). Single-cell transcriptomic analysis of human lung provides insights into the pathobiology of pulmonary fibrosis. Am. J. Respir. Crit. Care Med. *199*, 1517–1536.

36. Yang, I.V., Coldren, C.D., Leach, S.M., Seibold, M.A., Murphy, E., Lin, J., Rosen, R., Neidermyer, A.J., McKean, D.F., Groshong, S.D., et al. (2013). Expression of cilium-associated genes defines novel molecular subtypes of idiopathic pulmonary fibrosis. Thorax *68*, 1114–1121.

37. Sivakumar, P., Thompson, J.R., Ammar, R., Porteous, M., McCoubrey, C., Cantu, E., 3rd, Ravi, K., Zhang, Y., Luo, Y., Streltsov, D., et al. (2019). RNA sequencing of transplant-stage idiopathic pulmonary fibrosis lung reveals unique pathway regulation. ERJ Open Res. *5*, 00117–02019.

38. Speir, M.L., Bhaduri, A., Markov, N.S., Moreno, P., Nowakowski, T.J., Papatheodorou, I., Pollen, A.A., Raney, B.J., Seninge, L., Kent, W.J., and Haeussler, M. (2021). UCSC cell browser: visualize your single-cell data. Bioinformatics *37*, 4578–4580.

39. Adzhubei, I.A., Schmidt, S., Peshkin, L., Ramensky, V.E., Gerasimova, A., Bork, P., Kondrashov, A.S., and Sunyaev, S.R. (2010). A method and server for predicting damaging missense mutations. Nat. Methods *7*, 248–249.

40. Ng, P.C., and Henikoff, S. (2003). SIFT: predicting amino acid changes that affect protein function. Nucleic Acids Res. *31*, 3812–3814.

41. Zody, M.C., Jiang, Z., Fung, H.-C., Antonacci, F., Hillier, L.W., Cardone, M.F., Graves, T.A., Kidd, J.M., Cheng, Z., Abouelleil, A., et al. (2008). Evolutionary toggling of the MAPT 17q21.31 inversion region. Nat. Genet. *40*, 1076–1083.

42. Wang, G., Sarkar, A., Carbonetto, P., and Stephens, M. (2020). A simple new approach to variable selection in regression, with application to genetic fine mapping. J. Roy. Stat. Soc. B *82*, 1273–1300.

43. Benner, C., Spencer, C.C.A., Havulinna, A.S., Salomaa, V., Ripatti, S., and Pirinen, M. (2016). FINEMAP: efficient variable selection using summary data from genome-wide association studies. Bioinformatics *32*, 1493–1501.

44. Benner, C. (2019). FINEMAP : A Statistical Method for Identifying Causal Genetic Variants (Helsingin Yliopisto).

45. Wang, L., Balmat, T.J., Antonia, A.L., Constantine, F.J., Henao, R., Burke, T.W., Ingham, A., McClain, M.T., Tsalik, E.L., Ko, E.R., et al. (2021). An atlas connecting shared genetic architecture of human diseases and molecular phenotypes provides insight into COVID-19 susceptibility. Genome Med. *13*, 83.

46. COVID-19 Host Genetics Initiative (2022). A first update on mapping the human genetic architecture of COVID-19. Nature *608*, E1–E10.

47. Bulik-Sullivan, B., Finucane, H.K., Anttila, V., Gusev, A., Day, F.R., Loh, P.-R., Perry, J.R.B., Patterson, N., Robinson, E.B., , et al.; ReproGen Consortium; Psychiatric Genomics Consortium; Genetic Consortium for Anorexia Nervosa of the Wellcome Trust Case Control Consortium 3; and Duncan, L.ReproGen Consortium (2015). An atlas of genetic correlations across human diseases and traits. Nat. Genet. *47*, 1236–1241.

48. Kaunisto, J., Salomaa, E.-R., Hodgson, U., Kaarteenaho, R., Kankaanranta, H., Koli, K., Vahlberg, T., and Myllärniemi, M. (2019). Demographics and survival of patients with idiopathic pulmonary fibrosis in the FinnishIPF registry. ERJ Open Res. *5*, 00170–02018.

49. Lim, E.T., Würtz, P., Havulinna, A.S., Palta, P., Tukiainen, T., Rehnström, K., Esko, T., Mägi, R., Inouye, M., Lappalainen, T., et al. (2014). Distribution and medical impact of loss-of-function variants in the Finnish founder population. PLoS Genet. *10*, e1004494.

50. Kanai, M., Ulirsch, J.C., Karjalainen, J., Kurki, M., Karczewski, K.J., Fauman, E., Wang, Q.S., Jacobs, H., Aguet, F., Ardlie, K.G., et al. Insights from complex trait fine-mapping across diverse populations.

51. Dudbridge, F., Allen, R.J., Sheehan, N.A., Schmidt, A.F., Lee, J.C., Jenkins, R.G., Wain, L.V., Hingorani, A.D., and Patel, R.S. (2019). Adjustment for index event bias in genome-wide association studies of subsequent events. Nat. Commun. *10*, 1561.

52. Schaller, T., Hirschbühl, K., Burkhardt, K., Braun, G., Trepel, M., Märkl, B., and Claus, R. (2020). Postmortem examination of patients with COVID-19. JAMA *323*, 2518–2520.

53. Assayag, D., Morisset, J., Johannson, K.A., Wells, A.U., and Walsh, S.L.F. (2020). Patient gender bias on the diagnosis of idiopathic pulmonary fibrosis. Thorax *75*, 407–412.

54. Helling, B.A., Gerber, A.N., Kadiyala, V., Sasse, S.K., Pedersen, B.S., Sparks, L., Nakano, Y., Okamoto, T., Evans, C.M., Yang, I.V., and Schwartz, D.A. (2017). Regulation of MUC5B expression in idiopathic pulmonary fibrosis. Am. J. Respir. Cell Mol. Biol. *57*, 91–99.

55. Oliva, M., Muñoz-Aguirre, M., Kim-Hellmuth, S., Wucher, V., Gewirtz, A.D.H., Cotter, D.J., Parsana, P., Kasela, S., Balliu, B., Viñuela, A., et al. (2020). The impact of sex on gene expression across human tissues. Science *369*, eaba3066.

56. Huang, L., Pu, Y., Hepps, D., Danielpour, D., and Prins, G.S. (2007). Posterior Hox gene expression and differential androgen regulation in the developing and adult rat prostate lobes. Endocrinology *148*, 1235–1245.

57. Ma, L., Benson, G.V., Lim, H., Dey, S.K., and Maas, R.L. (1998). Abdominal B(AbdB)HoxaGenes: regulation in adult uterus by estrogen and progesterone and repression in müllerian duct by the synthetic estrogen diethylstilbestrol (DES). Dev. Biol. *197*, 141–154.

58. Li, Z., Tuteja, G., Schug, J., and Kaestner, K.H. (2012). Foxa1 and Foxa2 are essential for sexual dimorphism in liver cancer. Cell *148*, 72–83.

59. Global Biobank Meta-analysis Initiative; and Zhou, W. (2021). Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases. Preprint at bioRxiv. https://doi.org/10.1101/2021.11.19.21266436.

60. Zou, Y., Carbonetto, P., Wang, G., and Stephens, M. (2022). Fine-mapping from summary data with the "sum of Single effects" model. PLoS Genet. *18*, e1010299.

61. Mbatchou, J., Barnard, L., Backman, J., Marcketta, A., Kosmicki, J.A., Ziyatdinov, A., Benner, C., O'Dushlaine, C., Barber, M., Boutkov, B., et al. (2021). Computationally efficient whole-genome regression for quantitative and binary traits. Nat. Genet. *53*, 1097–1103.

62. Firth's Bias-Reduced Logistic Regression [R package logistf version 1.24] (2020).

63. Machiela, M.J., and Chanock, S.J. (2015). LDlink: a web-based application for exploring population-specific haplotype structure and linking correlated alleles of possible functional variants. Bioinformatics *31*, 3555–3557.

64. Chang, C.C., Chow, C.C., Tellier, L.C., Vattikuti, S., Purcell, S.M., and Lee, J.J. (2015). Second-generation PLINK: rising to the challenge of larger and richer datasets. GigaScience *4*, 7.

65. Thompson, S.G., and Higgins, J.P.T. (2002). How should meta-regression analyses be undertaken and interpreted? Stat. Med. *21*, 1559–1573.

66. Balduzzi, S., Rücker, G., and Schwarzer, G. (2019). How to perform a meta-analysis with R: a practical tutorial. Evid. Base Ment. Health *22*, 153–160.

STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited data		
Global Biobank Meta-Analysis Initiative (GBMI) genome-wide meta-analysis results	GBMI	https://www.globalbiobankmeta.org/resources
Allen et al. genome-wide meta-analysis results	Allen et al. (2020)	https://github.com/genomicsITER/PFgenetics
Software and algorithms		
UCSC liftOver		https://genome.ucsc.edu/cgi-bin/hgLiftOver
REGENIE	Mbatchou J. et al. (2021)	https://doi.org/10.1038/s41588-021-00870-7
LD score regression	Bulik-Sullivan B. K. et al. (2015)	https://github.com/bulik/ldsc/
PLINK 2.0	Chang et al. (2015)	https://www.cog-genomics.org/plink/2.0/
R statistical programming		https://www.r-project.org/
Other		
GBMI custom scripts used for quality control, meta-analysis and summary		https://github.com/globalbiobankmeta
FinnGen fine-mapping pipeline		https://github.com/FINNGEN/finemapping-pipeline
Project code	This paper	https://doi.org/10.5281/zenodo.6993906

RESOURCE AVAILABILITY

Lead contact

Further information and requests should be directed to and will be fulfilled by the lead contact, Jukka Koskela (jukka.koskela@helsinki.fi).

Materials availability

This study did not generate new materials.

Data and code availability

Full joint meta-analysis summary statistics and GBMI meta-analysis results are available for downloading at https://www.globalbiobankmeta.org/resources and can be browsed at the PheWeb Browser http://results.globalbiobankmeta.org. Custom scripts used for quality control, meta-analysis and summary of the GBMI results are available at https://github.com/globalbiobankmeta. FinnGen fine-mapping pipeline scripts are available at https://github.com/FINNGEN/finemapping-pipeline. Original code generated within this project has been deposited at Zenodo and is publicly available at https://doi.org/10.5281/zenodo.6993906. Any additional information is available from the lead contact upon request.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

13 biobanks in Europe, Asia, and USA encompassing 6 ancestries contributed to the Global Biobank Meta-Analysis Initiative (GBMI) IPF meta-analysis, totaling 8,492 cases and 1,355,819 controls (Table 1, Table S1). Sample ancestry was determined by individual biobanks and successful determination was ensured by comparing projected principal components, calculated by each biobank for their samples based on marker loadings standardized for all GBMI biobanks, to the 1000 Genomes Project and the Human Genome Diversity Project (HGDP). Sample recruitment strategies differed between the biobanks (Table S1). The three clinical IPF cohorts of the latest IPF meta-analysis (Chicago, Colorado and UK), totaling 2,668 cases and 8,591 controls, all of European ancestry, are described elsewhere.[2] The two cohorts used for replication (UUS and Genentech) were also used for replication in the latest IPF meta-analysis and are described elsewhere.[2] There was sample overlap of 3,366 controls between the GBMI meta-analysis (UKBB) and the three clinical IPF cohorts (UK cohort) of the latest IPF meta-analysis, but there was no IPF case overlap. All analyses were limited to adults (age $\geq$18).

METHOD DETAILS

Phenotype definition and quality control

The GBMI phenotypic and genotypic quality control are described elsewhere.[59] Analysis was performed in most biobanks for PheCode 502, constructed from health data available from each biobank (Table S16, phenotype definitions used in each biobank are in Table S15). IPF cases for the PheCode 502 were determined using the following International Classification of Diseases (ICD)-codes: ICD-9: 515, 515.0, ICD-10: J84.1, J84.10, J84.17, J84.8, J84.89. In the latest IPF meta-analysis, case definition was based on American Thoracic Society and European Respiratory Society guidelines, and quality control steps are described elsewhere.[2]

Meta-analysis

For GBMI, GWASs stratified by ancestry and sex were conducted in each biobank after standard sample-level and variant-level quality control. Thereafter, inverse-variance weighted fixed-effect meta-analyses were performed for all biobanks across all ancestries, all biobanks by each ancestry, and all biobanks by sex, detailed description elsewhere.[59] Meta-analysis of the GBMI meta-analysis and the latest IPF meta-analysis, referred to as the joint meta-analysis, was likewise performed using the inverse-variance weighted fixed effects model in R (version 4.1). Prior to meta-analysis, the summary statistics of the latest IPF meta-analysis were lifted over from GRCh37 to GRCh38 using UCSC liftOver (https://genome.ucsc.edu/cgi-bin/hgLiftOver). Liftover results were verified by comparing the results to LiftOver results from Picard: of the 10,790,934 variants lifted over by UCSC liftOver 10,777,976 (99.9%) overlapped with LiftOver results from Picard, indicating high concordance in the results of the two methods.

All variants are reported based on the human genome reference sequence GRCh38. Only variants that were genome-wide significant in the joint meta-analysis were considered in downstream analyses. Genome-wide significant loci were determined by taking a 1 Mb region around each genome-wide significant variant and merging overlapping regions. The HLA region on chromosome 6 (GRCh38 chr6:28,510,120-33,480,577) was considered as one locus. Loci which did not include a previously reported IPF associated variant irrespective of the variant's p value in the meta-analysis were considered novel.

Fine-mapping

Fine-mapping was performed for the IPF GWAS in FinnGen release 7 using the "Sum of Single Effects" (SuSie) model[42,60] and FINEMAP[43,44] for corroborative analyses. Fine-mapping regions were defined by taking a 3 Mb window around each index variant in the joint IPF meta-analysis and merging overlapping regions. 95% credible sets (encompassing at least 95% of the probability of including the causal variant) were analyzed and the probability of variant causality was evaluated using the posterior inclusion probability (PIP). Conditional analysis in FinnGen was performed using REGENIE[61] with dosages of the variant conditioned on as covariates alongside other covariates (age, sex, ten first principal components, and batch). Individual causal signals were explored in FinnGen using logistic regression with Firth correction implemented in the "logistf" R package.[62]

Phenome-wide lookup

To assess the shared effects of potentially novel loci, we considered associations with phenotypes in the Open Targets Genetics (OTG) obtained from the GWAS catalog. Linkage disequilibrium (LD) between variants was assessed using the LD pair tool[63] (https://ldlink.nci.nih.gov/), restricting to the 1000 Genomes Project non-Finnish European sub-populations for variants polymorphic in non-Finnish Europeans and source population otherwise.

LD score regression intercept and genetic correlation

The LD score regression v.1.0.1 intercept[17] was used to quantify the contribution of confounding biases to the IPF meta-analysis results. As this method depends on matching the LD structure of the analysis sample to a reference panel, the analysis was restricted to the NFE samples. LD score regression[47] was also used to estimate the genetic correlation between IPF and COVID-19 hospitalization using samples of NFE and European ancestry for IPF and COVID-19, respectively. Pre-calculated LD scores from the 1000 Genomes European reference population were obtained online (https://data.broadinstitute.org/alkesgroup/LDSCORE/) and the analysis was conducted using the standard program settings for variant filtering (removal of non-HapMap3 SNPs, minor allele frequency of <1%, or allele mismatch with reference).

Colocalization

Colocalization analysis was performed in FinnGen release 7. Colocalization analysis was based on assessing agreement of the fine-mapped credible sets across two traits. Agreement was measured by causal posterior agreement (CLPA), calculated as the sum of minimum PIP between the two traits per variant in overlapping credible sets.

Sex-stratified and sex interaction analyses

We performed sex-stratified analysis in six biobanks in the GBMI. In FinnGen sex-stratified analyses were conducted in release 5 with 378 and 110524 female, and 650 and 86462 male IPF cases and controls, respectively. In addition, we performed sex-stratified and sex interaction analyses in four clinical cohorts (Colorado, UK, UUS, and Genentech) using the PLINK 2.0 software[64] (https://www.cog-genomics.org/plink/2.0/). The analyses were not performed in the Chicago study for rs35705950 as the imputation quality

(imputation R^2) was less than 0.5. In the sex-stratified analysis the effect of the *MUC5B* variant rs35705950 on IPF case status was tested in males and females separately using logistic regression adjusting for the ten first principal components. The rs35705950-by-sex interaction analysis was performed using the following logistic regression model:

$$\text{logit}(P(\text{Phenotype}_i)) = \beta_0 + \beta_1 \text{rs35705950}_i + \beta_2 \text{Sex}_i + \beta_3 \text{rs35705950}_i * \text{Sex}_i + \beta_4 \text{PC}_{1i} + ... + \beta_{14} \text{PC}_{10i} + \varepsilon_i$$

where

Phenotype$_i$ is IPF status for individual *i*, *rs35705950* is the dosage for rs35705950 (additive effect), *Sex* is binary coded, *rs35705950*Sex* is the interaction term and *PC*$_1$ to *PC*$_{10}$ are the first ten standardised principal components.

The results from the four clinical cohorts were meta-analyzed using inverse-variance weighted fixed effect meta-analysis, implemented using the R package "metagen" (https://www.rdocumentation.org/packages/meta/versions/4.9-6/topics/metagen).

Heterogeneity evaluation

Heterogeneity of effect sizes across studies and between sexes was evaluated at each variant using Cochran's Q p value and heterogeneity index. To study the contribution of different sample recruitment strategies on heterogeneity, effect size estimates of selected studies for genome-wide significant IPF loci were compared and an inverse-variance weighted linear regression line was fitted. To evaluate the extent to which sample recruitment and ancestry contributed to heterogeneity, we used meta-regression[65] using the "meta" R package.[66]

QUANTIFICATION AND STATISTICAL ANALYSIS

Sample sizes and sample age and sex characteristics are available in Tables 1 and S1. All meta-analyses were performed using the inverse-variance weighted fixed effects model in R. The p value threshold for genome-wide significance was $P < 5E\text{-}8$. The p value for heterogeneity was calculated based on Cochran's heterogeneity statistic.