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Single nucleotide polymorphisms (SNPs) in Sulfatase modifying factor (*SUMF)-1* are associated with lung function and COPD

Linnea Jarenbäck[1], Sophia Frantz[2], Julie Weidner[1], Jaro Ankerst[1], Ulf Nihlén[1], Leif Bjermer[1], Per Wollmer[2], Ellen Tufvesson[1]*

[1]Dept. of Clinical Sciences Lund, Respiratory Medicine and Allergology, Lund University, Lund, Sweden

[2]Dept. of Translational Science, Clinical Physiology, Lund University, Skåne University Hospital, Malmö, Sweden

*Corresponding author: Ellen Tufvesson, Respiratory Medicine and Allergology, Dept. of Clinical Sciences Lund, Lund University, 221 84 Lund, Sweden

Tel: +46 222 7828

E-Mail: ellen.tufvesson@med.lu.se

Running title: SUMF-1 SNPs associate to COPD and advanced lung function

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Abstract

Single nucleotide polymorphisms (SNPs) in various genes have been shown to associate with chronic obstructive pulmonary disease (COPD), suggesting a role in disease pathogenesis. Sulfatase modifying factor (SUMF1) is a key modifier in connective tissue remodeling, and we have previously shown that several SNPs in *SUMF1* are associated with COPD. The aim of this study was to investigate the association between *SUMF1* SNPs and advanced lung function characteristics.

Never, former and current smokers with (n=154) or without (n=405) COPD were genotyped for 21 SNPs in *SUMF1* and performed spirometry, body plethysmography, diffusing capacity of carbon dioxide (D_{LCO}) and impulse oscillometry.

Four SNPs (rs793391, rs12634248, rs2819590 and rs304092) showed a significantly decreased odds ratio of having COPD when heterozygous for the variance allele, together with a lower forced expiratory volume in one second (FEV_1)/forced vital capacity (FVC) ratio and FEV_1 and an impaired peripheral resistance and reactance. Moreover, individuals homozygous for the variance allele of rs3864051 exhibited a strong association to COPD, a lower FEV_1/FVC, FEV_1 and D_{LCO}, and an impaired peripheral resistance and reactance. Other SNPs (rs4685744, rs2819562, rs2819561 and rs11915920) were instead associated with impaired lung volumes and exhibited a lower FVC, total lung capacity (TLC) and alveolar volume (V_A), if having the variance allele.

Several SNPs in the *SUMF1* gene are shown to be associated with COPD and impaired lung function. These genetic variants of *SUMF1* may cause a deficient sulfation balance in the extracellular matrix of the lung tissue and thereby contributing to the development of COPD.

Introduction

Chronic obstructive pulmonary disease (COPD) is mainly caused by long-term cigarette smoking[1], but multiple genetic factors may influence predisposition for lung damage and thereby the susceptibility for developing COPD [2]. Due to the heterogeneous nature of COPD, it is then most likely that COPD patients have different genetic patterns. The decreased lung function seen in COPD patients is mainly due to airway inflammation caused by oxidative stress, which subsequently leads to airways remodeling and tissue destruction [3-6]. Different gene polymorphisms related to these processes are important to investigate to better understand their role in disease development. The most well-known genetic factor associated with COPD is alpha-1 antitrypsin deficiency which is associated to polymorphism in the *SERPINA1*-gene [7]. In addition, mainly single nucleotide polymorphisms (SNPs) associated with inflammatory processes [8] and biological stress pathways [9] have been identified to be linked to COPD. Some polymorphisms related to connective tissue remodeling have also been identified, such as matrix metalloproteinase-7 (MMP-7) which is suggested to influence early development of COPD [10], and MMP-12 which was found to be associated with severe/very severe COPD [11].

In a previous study, we have found several SNPs in sulfatase modifying factor 1 (*SUMF1*) to be associated with COPD [12]. SUMF1 is the main regulator of all known sulfatases in the body [13], and modifies them into their active state. The role of the different sulfatases is then to remove sulphate from specific sulfated carbohydrate chains, and they thereby have an important role in the delicate balance of connective tissue remodeling. SUMF1 is well known for its implication in multiple sulfatase deficiency [14-18], but Arteaga-Solis *et al* [19] observed that *Sumf1*$^{-/-}$ mice exhibited an emphysema-like pattern in their lungs, due to post-natal alveolarization arrest. In our previous clinical study we showed that several SNPs in *SUMF1* were associated with COPD, of which rs793391 was the most significant. Twelve *SUMF1* SNPs were found to be significant by expression quantitative trait loci (eQTL) analysis, and certain splice variants of SUMF1 exhibited decreased expression levels in sputum cells from COPD patients compared to control subjects. In association with the *SUMF1* SNP rs11915920, which was a top hit in the eQTL analyses, we found decreased mRNA expression levels in sputum cells and lung fibroblasts in subjects with the variance allele, confirming the results of the lung tissue eQTL analysis [12]. A previous GWAS study has also identified SUMF1 to be associated with prominent emphysema but was not studied further [20].

The main objective of the present study was to investigate the association between *SUMF1* SNPs and advanced lung function characteristics. A secondary aim was to verify findings from our previous study in

a larger, well-defined cohort and to investigate if additional SNPs in *SUMF1* showed an association to lung function and COPD.

Material and Methods

Study population

A total of 598 patients were recruited from two sites within Skåne University Hospital, the Lung clinic in Lund and at Clinical Physiology in Malmö. In Lund, smokers and former smokers with or without COPD were recruited [21]. In the Malmö cohort, never-smokers without any reported lung disease or lower respiratory symptoms, smokers and former smokers with and without COPD and subjects with a self-reported diagnosis of chronic bronchitis/emphysema/COPD were included [22].

All subjects signed written informed consent and the Regional Ethical review Board in Lund approved the studies (431/2008 and 786/2003 + amendment 101/2015).

Lung function measurements

Spirometry (MasterScreen, Erich Jaeger GmbH, Würzburg, Germany), body plethysmography (MasterScreen Body, Erich Jaeger GmbH), diffusing capacity of carbon dioxide (D_{LCO}; MasterScreen Diffusion Jaeger) and impulse oscillometry (MasterScreen, Erich Jaeger GmbH, Würzburg, Germany) were performed after inhalation of β-agonist (Lund: Salbutamol 400mg, Handihaler using a spacer device; Malmö: Terbutalin, 1 mg, in Turbohaler). All measurements were performed according to manufactures protocols and according to European Respiratory Society/American Thoracic Society recommendations [23] when applicable. Reference values from Global lung initiative [24-26] were used to calculate percent of predicted normal (%pred).

Blood samples and SUMF1 genotyping

Whole blood was drawn from all subjects and stored in EDTA tubes at -80°C until analysis. DNA was extracted and genotyped for 21 SNPs in *SUMF1*: rs11915920, rs12634249, rs1356229, rs137852846, rs137852848, rs137852849, rs137852854, rs2322683, rs2633852, rs2819561, rs2819562, rs2819590, rs304092, rs308739, rs3864051, rs4685744, rs748169616, rs793391, rs794185, rs794187 and rs807785. This was analysed using Agena iplex genotyping at the Mutation Analysis Facility at Karolinska University Hospital (Huddinge, Sweden) using iPLEX® Gold chemistry and MassARRAY® mass spectrometry system [27] (Agena Bioscience, San Diego, CA, U.S.A.) as previously described [12].

Statistical analysis

Baseline difference in demographic data and lung function between COPD and controls were analyzed using student's t-test or chi-square. Associations of SNPs to COPD were analyzed with multivariable logistic regression models including the SNP in an additive genetic model and were adjusted for confounding factors (age, sex and smoking status). Associations of SNPs to lung function parameters were done with multivariable linear regression, corrected for confounding factors (age, sex, height and smoking status). Figure 1-3 are presented as % of predicted when applicable to increase visualization, and data is analysed with one-way analyses of variance for overall comparison among the groups, followed by Bonferroni's multiple comparison test between separate groups.

Results

Subject characteristics

DNA from whole blood from a total of 559 subjects (405 controls and 154 COPD patients) were successfully genotyped and included in the final analysis (39 subjects were excluded due to other lung diseases, unsuccessful lung function performance or unsuccessful SNP analysis). Subjects were divided into two groups, COPD or healthy according to the Global Initiative for Obstructive pulmonary disease (GOLD) definition [28]. Subjects with COPD were significantly older and had more pack years of smoking compared to the control group (Table 1). Also, the COPD group consisted of a larger proportion of males and former smokers, and less never smokers and current smokers. As expected, all lung function variables were impaired in COPD compared to controls (Table 1).

Genotype frequencies

A total of 16 of the 21 analyzed SNPs had a variation among our study subjects, while five SNP genotypes (rs137852846, rs137852848, rs137852849, rs137852854 and rs748169616) were monomorphic, i.e. presenting as homozygous for the reference allele in all subjects, and therefore not included in the analyses.

Genotype frequencies for COPD and controls are presented separately in Table 2, and variant allele frequencies of all SNPs are presented in Supplementary Table 1.

Association to COPD

After adjusting for age, sex and smoking status, five of the SNPs were found to be significantly associated with COPD (Table 2). Four of them (rs793391, rs12634248, rs2819590 and rs304092) exhibited a significantly decreased odds ratio (OR) of having COPD if being heterozygous for the variance allele. Furthermore, when being homozygous for the variance allele for any of the aforementioned SNPs, a decreased OR of having COPD was not observed.

The rs3864051 displayed the most significant association with COPD, with 11 out of the 13 subjects that were homozygous for the variance allele had COPD. In addition, a tendency towards an increased risk of having COPD was also seen in subjects heterozygous for the variance allele of rs3864051.

Association with advanced lung function

When examining the different lung function parameters, as expected, the FEV_1/FVC ratio and also FEV_1 were similarly associated to the same SNPs as having COPD, showing a lower FEV_1/FVC ratio and a lower FEV_1 if being homozygous for the reference allele of rs793391 (Figure 1A and B), rs12634248, rs2819590 and rs304092 compared to being heterozygous for the variance allele (Table 3). Additionally, two other SNPs (rs794185 and rs794187) showed a similar association to FEV_1, with lower FEV_1 if being homozygous for the reference allele, but were not associated with having COPD. In conjunction with the association to COPD, lower FEV_1/FVC and FEV_1 were seen if subjects were homozygous for the variance allele of rs3864051 (Table 3 and Figure 2A and B).

In contrast, other SNPs were associated with FVC, showing a significantly lower FVC if the variance allele (both if being heterozygous or homozygous) for rs4685744, rs2819562, rs2819561 or rs11915920 (Table 3 and Figure 3A) was present, and a tendency of association also observed for rs2633852. In contrast, subjects heterozygous for the variance allele of rs794185 and rs794187 had a higher FVC if being heterozygous for the variance allele (Table 3) which followed the pattern of FEV_1 for these SNPs.

Besides being associated to FVC, the same SNPs (rs4685744, rs2819562, rs2819561, rs2633852 and rs11915920) were also significantly associated with total lung capacity (TLC), exhibiting a lower TLC if the variance allele was present, and most significant if being homozygous for the variance allele (Table 4 and Figure 3B). These SNPs also showed a similar association to residual volume (RV), but not significant, with

a lower RV if being homozygous for the variance allele. In addition, these SNPs show a higher D_{LCO}/V_A ratio if being homozygous for the variance allele, which is mostly due to a low V_A (Figure 3C and D), but also a higher D_{LCO}. Consistent with the association between rs3864051 and COPD, a lower D_{LCO} was observed if this SNP was homozygous for the variance allele (Figure 2C).

The resistance and reactance results were consistent with the findings of the SNPs associated to COPD and FEV_1 (Table 5). Total resistance (R5) (possibly here reflecting the peripheral airways as it is in concordance with R5-R20 which is a variable that is commonly taken to represent resistance of peripheral airways), is lower if being heterozygous for the variance allele of rs793391 (Figure 1C), rs12634248, rs2819590, rs304092, rs794185 and rs794187. A similar pattern was seen in airway reactance (X5 and AX), which was also less impaired if being heterozygous for the variance allele of these SNPs (Figure 1D). Consistent with its association to COPD and FEV_1, rs3864051 exhibited impaired resistance and reactance if being homozygous for the variance allele (Figure 2D).

There were no associations between rs1356229 or rs308739 and lung function (data not shown).

Discussion

In the present study, several SNPs in the *SUMF1* gene were shown to be associated with COPD and with impaired lung function. These SNPs appear in two blocks (see supplementary figure S1A) where one block was associated with COPD and airway obstruction, and the other block was associated with impaired lung volumes. One block (Block 2) included rs7933191, rs12634249, rs2819590 and rs304092, which were associated with having COPD, affecting FEV_1 and FEV_1/FVC, and airway resistance and reactance. This was also partly the case for rs794187 and rs794185. The other block (Block 1) included rs4685744, rs2819562, rs2819561, rs2633852 and rs11915920, and was associated with impaired FVC, TLC, RV and V_A. Furthermore, the most evident SNP associated with COPD was rs3864051, which also exhibited associations with impaired FEV_1, FEV_1/FVC, D_{LCO} and airway resistance and reactance.

Moreover, we here confirm in a separate, larger number of subjects our previous finding that SNP rs793391 was associated with COPD [12]. Furthermore, we determined additional SNPs in *SUMF1* (in Block 2) associated with COPD: rs12634248, rs2819590, rs304092. Similarly, these SNPs, together with rs794185 and rs794187, show associations to FEV_1, FEV_1/FVC, airway resistance and reactance, typical for an obstructive lung function profile. These SNPs showed weaker association to airway obstruction

when the subject was heterozygous for the variance allele, suggesting a protective role for having one variance allele over two reference alleles.

In contrast, the SNPs in the other block (Block 1) showed lower lung volumes (FVC, TLC, RV, V_A) when being heterozygous for the variance allele, and in most cases even more impairment if being homozygous for the variance allele. Two of these SNPs (rs11915920 and rs2819562) were included in a previous investigation using an eQTL analysis in lung tissue [12] and showed a very strong association between gene expression of SUMF1 in lung tissue and the genetic polymorphisms. Lower levels of *SUMF1* gene expression were seen in subjects having the variance allele, both if being heterozygous and even more prominent in those being homozygous for the variance allele. This might cause an impaired SUMF1 function, and thereby a dysfunctional down-stream sulfatase imbalance in the lungs [29], thus resulting in potential extracellular matrix issues. Our findings of lower lung volumes associated to *SUMF1* SNPs in this study are in conjunction with the finding of deficient alveolarization in *Sumf*$^{-/-}$ mice [19], which might be an explanation for the impaired lung function in these subjects.

Another SNP located between the two defined linkage blocks and strongly associated (OR: 14.22) with COPD when homozygote for the variance allele was rs3864051. It has been implicated in longevity [30], and the frequency of homozygosity for the variance allele is rare. In our study, it was found in only 13 out of 555 subjects, but 11 out of these subjects had COPD and only two were healthy. This could however be a significant risk factor for getting COPD, but since the frequency of being homozygote for this allele is low, more studies are needed to verify our findings.

Variant allele frequencies are similar in the population of the present study and the dbGaP database (see Supplementary Table 1), and most SNPs in the present study follow Hardy Weinberg equilibrium, except for rs3864051. Only 2.3 % of the study population were homozygous for the variance allele (TT), instead of the expected 6% (based on variant allele frequency of 0.24 in our population compared to 0.34 in the database, respectively). This could either be due to random error in included genotypes, or a bias in sampling due to COPD patients being less prone to participate in the study. The latter case would suggest even more COPD patients in the group of homozygous for the variance allele, which would strengthen the results of rs3864051 being highly associated with having COPD.

Most of the SNPs are in intron positions (Table 2), and only one SNP (rs2819590 in exon 1) is defined as giving rise to missense transcript and potentially affecting the SUMF1 protein directly. In addition, one SNP (2633852) is localized in exon 9 and suggested to be a synonymous, silent mutation in a coding

sequence (cds-syn). The role of the two aforementioned SNPs is not known, but they could be in undefined regulatory zones or act to regulate other genes. The associations between lung function and the SNPs in Block 2 could also be explained by the fact that they have a neighboring localization on the chromosome and are in a non-random association of alleles (as shown in the linkage disequilibrium (LD) plot in supplementary figure S1B) and thereby in block with rs2819590.

We have previously shown that the SNP rs793391 was associated with COPD in a selected study population of healthy current smokers and ex-smokers [12]. These findings were confirmed in the present study, but in a broader population including also many subjects that were never smokers. In a sub-analysis, we found that if the associations between the SNP and COPD were not adjusted for smoking status, the results were yet similar (p=0.012 and the same CI of the OR: 0.39-0.89). Hereby we showed that rs793391 was not only associated to COPD in smoking/ex-smoking subjects, but also in never smokers.

The association between certain SNPs and COPD may also be related to disease severity and progression. Certain SNPs located on chromosome 6 or the *HLA-DQB2* gene have been shown to be associated with susceptibility to early (mild/moderate) COPD [31], but only in comparison to never-smoking controls. The population investigated in the present study consists of mainly mild/moderate COPD, and our findings are therefore most representative for this group of patients.

Differences in lung function variables between the SNP genotypes could be read as clinically significant, which can easily be spotted when presenting the B-value, which for example for FEV_1 was over 120 ml for most SNPs (Table 3). This is within the recommended range of minimally clinical important difference [32] and suggest *SUMF1* genotypes to be a potential biomarker.

Over the past decade, the accessibility of whole-genome sequencing and the increased number of genome-wide association studies, have led to a substantial increase in the understanding of genetic variants that play a role in COPD susceptibility and COPD-related phenotypes [2]. Several variants are shown to be associated to COPD, emphysema and/or spirometric values, and specifically some genetic loci have been identified as being associated to D_{LCO} [33]. In the present study, two distinct blocks of SNPs were identified, and one block (Block 2) was associated to an obstructive phenotype, while the other block (Block 1) was associated with a phenotype with reduced lung volumes. We have previously shown that the SNPs in the latter block were highly significant in eQTL analysis of *SUMF1* and were associated with lower levels of *SUMF1* mRNA in sputum cells and lung fibroblasts. We therefore believe

that specific SNPs give rise to certain pathological effects, which may contribute to the heterogeneous nature of COPD.

In conclusion, we have found several SNPs in the *SUMF1* gene that are associated with COPD and with impaired lung function. These SNPs appear in two blocks, Block 2 is associated to COPD and airway obstruction, and Block 1 is associated to impaired lung volumes. We hereby confirm in a larger well-defined cohort, what we have previously shown in a smaller cohort, thus we are again proving that these SNPs may have a legitimate role in COPD pathogenesis. Additionally, we see again that the two linkage disequilibrium blocks appear to have different effects on aspects of the disease pathogenesis that we do not yet fully understand. Furthermore, a single SNP (rs3864051) is unconnected and strongly associated to COPD and impaired lung function. These genetic variants of *SUMF1* may cause a deficient sulfation balance in the extracellular matrix of the lung tissue and thereby contributing to the COPD disease.

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Figure legends

Figure 1. Lung function in COPD patients and controls divided by SNP rs793391 genotypes (as representative for Block 2). FEV_1 % of predicted (A), FEV_1/FVC (B), R5 (C) and AX (D) are divided according to the genotype of rs793391. * =p< 0.05. One-way analyses of variance were used for overall comparison among the groups (¬), followed by Bonferroni's multiple comparison test between separate groups (ⱶ). Genotypes are presented with the reference/reference genotype to the left. Data is presented as box-plots showing the median within the box of 25-75% percentile and whiskers of 5-95 percentile.

Figure 2. Lung function in COPD patients and controls divided by SNP rs11915920 genotypes (as representative for Block 1). FVC % of predicted (A), TLC % of predicted (B), V_A % of predicted (C) and D_{LCO}/V_A % of predicted (D) are divided according to the genotype of 11915920. * =p< 0.05. One way analyses of variance were used for overall comparison among the groups (¬), followed by Bonferroni's

multiple comparison test between separate groups (⊦). Genotypes are presented with the reference/reference genotype to the left. Data is presented as box-plots showing the median within the box of 25-75% percentile and whiskers of 5-95 percentile.

Figure 3. Lung function in COPD patients and controls divided by SNP rs3864051 genotypes. FEV_1 % of predicted (A), FEV_1/FVC (B), D_{LCO} % of predicted (C) and AX (D) are divided according to the genotype of rs3864051. *=p< 0.05, ***=p<0.001. One-way analyses of variance were used for overall comparison among the groups (¬), followed by Bonferroni's multiple comparison test between separate groups (⊦). Genotypes are presented with the reference/reference genotype to the left. Data is presented as box-plots showing the median within the box of 25-75% percentile and whiskers of 5-95 percentile.

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Tables

Table 1. Patient characteristics and lung function

	Controls (n=405)	**COPD** (n=154)	p-value
Sex, female/male, n (%)	239/166 (59/41%)	71/83 (46/54%)	**0.006**
Age, years	62 (8)	66 (6)	**<0.001**
Weight, kg	77 (16)	77 (15)	0.99
Height, cm	170 (9)	171 (9)	**0.025**
Smoking status, never/former/current smoker, n	76/145/184	5/92/57	**<0.001**
Pack years	22 (18)	36 (20)	**<0.001**
GOLD stage 1/2/3/4, n	n.a.	23/96/31/4	n.a.
Lung function			
FEV_1, L	2.85 (0.71)	1.87 (0.64)	**<0.001**
FEV_1, %pred	97 (13)	63 (17)	**<0.001**
FVC, L	3.40 (0.85)	3.19 (1.02)	**0.023**
FVC, %pred	91 (12)	83 (19)	**<0.001**
FEV_1/FVC	0.84 (0.06)	0.60 (0.17)	**<0.001**
RV, %pred	116 (21)	150 (45)	**<0.001**
TLC, %pred	102 (11)	106 (17)	**0.003**
D_{LCO}, %pred	93 (16)	66 (20)	**<0.001**
V_A, %pred	96 (16)	91 (13)	**<0.001**
D_{LCO}/V_A, %pred	97 (15)	72 (20)	**<0.001**
R5, kPa*s/L	0.31 (0.11)	0.41 (0.17)	**<0.001**
R20, kPa*s/L	0.24 (0.08)	0.28 (0.09)	**<0.001**
R5-R20, kPa*s/L	0.07 (0.05)	0.13 (0.10)	**<0.001**
X5, kPa*s/L	-0.09 (0.05)	-0.18 (0.13)	**<0.001**
AX, kPa*s/L	0.34 (0.39)	1.13 (1.33)	**<0.001**

Mean (SD). Categorical data were analyzed with Chi-Square test and numeric data with Student's t-test. %pred=% of predicted normal. FEV_1=forced expiratory volume in 1 second, FVC=forced volume capacity,

RV=residual volume, TLC=total lung capacity, D_{LCO}=diffusing lung capacity, V_A=alveolar volume, R5=resistance at 5Hz, R20=resistance at 20 Hz, X5=reactance at 5Hz and AX=reactance area.

Table 2. Genotype frequencies in healthy and COPD groups, respectively, and associations between different genotypes of *SUMF1* SNPs and COPD. Logistic regression between ref/ref and ref/var or var/var as indicated, and adjusted for age, sex and smoking status.

SNP	**ref/ref**			**ref/var var/var**			**p-value**	**OR**	**95%CI of OR**
		Healthy	COPD		Healthy	COPD			
rs1356229	CC	387 (96%)	149 (97%)	CT TT	16 (4%) 0 (0%)	5 (3%) 0 (0%)	0.74 -	1.20 -	0.42-3.45 -
rs308739	CC	348 (87%)	136 (88%)	TT AA	54 (13%) 0 (0%)	18 (12%) 0 (0%)	0.98 -	1.01 -	0.56-1.82 -
rs4685744	CC	109 (27%)	43 (28%)	CT TT	187 (46%) 107 (27%)	73 (47%) 38 (25%)	0.83 0.60	0.95 0.87	0.60-1.51 0.51-1.47
rs2819562	CC	87 (22%)	36 (23%)	CT TT	182 (45%) 133 (33%)	74 (48%) 44 (29%)	0.63 0.29	0.89 0.75	0.54-1.45 0.44-1.28
rs2819561	AA	87 (22%)	36 (23%)	AG GG	183 (46) 132 (33%)	74 (48%) 44 (29%)	0.61 0.29	0.88 0.75	0.54-1.44 0.44-1.29
rs2633852	AA	85 (21%)	36 (23%)	AG GG	181 (45%) 134 (34%)	74 (48%) 44 (29%)	0.61 0.26	0.88 0.73	0.54-1.44 0.43-1.26
rs11915920	CC	111 (28%)	43 (28%)	CT TT	186 (46%) 105 (26%)	75 (49%) 36 (23%)	0.99 0.55	1.00 0.85	0.63-1.58 0.50-1.45
rs807785	CC	33 (8%)	17 (11%)	CT TT	164 (41%) 206 (51%)	70 (45%) 67 (44%)	0.88 0.39	0.95 0.75	0.49-1.85 0.39-1.46
rs3864051	CC	228 (57%)	69 (45%)	CT TT	171 (43%) 2 (0.5%)	74 (48%) 11 (7%)	0.13 **0.001**	1.36 **14.22**	0.92-2.03 **3.04-66.49**
rs794187	CC	163 (41%)	68 (44%)	CT TT	190 (47%) 49 (12%)	70 (46%) 16 (10%)	0.37 0.46	0.83 0.78	0.55-1.25 0.41-1.50
rs794185	TT	114 (28%)	52 (34%)	TC CC	211 (52%) 78 (19%)	76 (49%) 26 (17%)	0.15 0.33	0.73 0.75	0.47-1.12 0.43-1.34
rs2322683	CC	53 (13%)	20 (13%)	CT TT	181 (45%) 169 (42%)	56 (37%) 77 (50%)	0.51 0.46	0.81 1.25	0.44-1.50 0.69-2.29
rs793391	TT	174 (43%)	81 (53%)	TG GG	185 (46%) 44 (11%)	54 (35%) 19 (12%)	**0.013** 0.70	**0.59** 0.88	**0.39-0.89** 0.48-1.64
rs12634249	CC	225 (56%)	96 (62%)	CA AA	157 (39%) 21 (5%)	46 (30%) 12 (8%)	**0.034** 0.56	**0.63** 1.26	**0.42-0.97** 0.58-2.73
rs2819590	CC	192 (48%)	91 (59%)	CT TT	175 (44%) 33 (8%)	47 (31%) 16 (10%)	**0.006** 0.97	**0.55** 1.01	**0.36-0.84** 0.52-1.98
rs304092	GG	191 (47%)	86 (56%)	GA AA	176 (44%) 35 (9%)	53 (34%) 15 (10%)	**0.031** 0.88	**0.63** 0.95	**0.42-0.96** 0.48-1.86

SNPs are sorted according to chromosome localization (chromosome localization is from GRCh38.p12). OR=Odds Ratio of having COPD depending on allele on different SNP in SUMF1. ref=reference allele, var=variance allele. Significant associations are depicted in bold.

Table 3. Associations between different genotypes of *SUMF1* SNPs and FEV_1, FVC and FEV_1/FVC in the total study population including both COPD and control subjects. Data is presented as p-values from linear regression between ref/ref and ref/var or var/var (using ref/ref as reference genotype) as indicated, and adjusted for age, sex, height and smoking status.

SNP	ref/ref	ref/var var/var	FEV_1	FVC	FEV_1/FVC
rs4685744	CC	CT TT	0.82 0.81	**0.030, B= -0.12** **0.037, B= -0.14**	0.093, B= 0.024 0.27
rs2819562	CC	CT TT	0.79 0.73	**0.048, B= -0.12** 0.057, B= -0.13	0.076, B= 0.027 0.074, B= 0.030
rs2819561	AA	AG GG	0.76 0.71	**0.050, B= -0.12** 0.060, B= -0.12	0.073, B= 0.0028 0.076, B= 0.029
rs2633852	AA	AG GG	0.72 0.67	0.062, B= -0.12 0.071, B= -0.12	0.075, B= 0.028 0.073, B= 0.030
rs11915920	CC	CT TT	0.98 0.84	**0.021, B= -0.13** **0.031, B= -0.14**	0.15 0.23
rs807785	CC	CT TT	0.87 0.41	0.64 0.87	0.61 0.16
rs3864051	CC	CT TT	0.48 **<0.001, B= -0.64**	0.14 0.31	0.67 **<0.001, B= -0.20**
rs794187	CC	CT TT	**0.028, B= 0.12** 0.72	0.062, B= 0.094 0.62	0.22 0.98
rs794185	TT	TC CC	**0.002, B= 0.18** **0.033, B= 0.16**	**0.004, B= 0.16** 0.057, B= 0.13	0.11 0.32
rs2322683	CC	CT TT	0.17 0.87	0.25 0.57	0.41 0.82
rs793391	TT	TG GG	**0.024, B= 0.12** 0.66	0.42 0.65	**0.039, B= 0.026** 0.79
rs12634249	CC	CA AA	**0.039, B= 0.11** 0.12	0.30 0.89	0.060, B= 0.024 0.077, B= -0.045
rs2819590	CC	CT TT	**0.010, B= 0.14** 0.76	0.36 0.74	**0.016, B= 0.030** 0.42
rs304092	GG	GA AA	**0.025, B= 0.12** 0.99	0.44 0.53	**0.037, B= 0.026** 0.39

B-value is the unstandardized beta-value, and is presented when $p<0.1$. Significant associations are depicted in bold, ref=reference allele, var=variance allele. ref=reference allele, var=variance allele. FEV_1=forced expiratory volume in 1 second, FVC=forced volume capacity.

Table 4. Associations between different genotypes of *SUMF1* SNPs and diffusion capacity and lung volumes in the total study population including both COPD and control subjects. Data is presented as p-values from linear regression between ref/ref and ref/var or var/var as indicated, and adjusted for age, sex, height and smoking status.

SNP	**ref/ref**	**ref/var var/var**	**D_{LCO}**	**V_A**	**D_{LCO}/V_A**	**RV**	**TLC**
rs4685744	CC	CT	0.26	0.23	0.080, B= 0.048	0.46	0.088, B= -0.14
		TT	0.14	**0.006, B= -0.22**	**0.001, B= 0.11**	0.068, B= -0,15	**0.009, B= -0.25**
rs2819562	CC	CT	0.12	0.41	**0.023, B= 0.067**	0.49	0.13
		TT	**0.041, B= 0.38**	0.083, B= -0.14	**<0.001, B= 0.11**	0.068, B= -0.15	**0.024, B= -0.22**
rs2819561	AA	AG	0.12	0.41	**0.023, B= 0.067**	0.47	0.12
		GG	**0.036, B= 0.39**	0.090, B= -0.14	**<0.001, B=0.11**	0.069, B= -0.15	**0.027, B= -0.21**
rs2633852	AA	AG	0.12	0.40	**0.022, B= 0.068**	0.41	0.11
		GG	**0.044, B= 0.38**	0.099, B= -0.14	**0.001, B= 0.11**	0.062, B= -0.15	**0.025, B= -0.22**
rs11915920	CC	CT	0.37	0.19	0.12	0.56	0.10, B= -0.14
		TT	0.11	**0.010, B= -0.21**	**<0.001, B= 0.11**	0.059, B= -0.15	**0.012, B= -0.24**
rs807785	CC	CT	0.91	0.38	0.75	0.26	0.062, B= -0.24
		TT	0.72	0.87	0.67	0.18	0.23
rs3864051	CC	CT	0.12	0.057, B= 0.11	0.70	0.56	0.063, B= 0.13
		TT	**0.029, B= -1,01**	0.49	0.080, B= -0.14	0.16	0.29
rs794187	CC	CT	0.15	**0.030, B= 0.13**	0.81	0.67	0.69
		TT	0.67	0.94	0.64	0.80	0.91
rs794185	TT	TC	0.091, B= 0.26	**0.001, B= 0.22**	0.86	0.32	0.36
		CC	0.14	0.29	0.33	0.37	0.76
rs2322683	CC	CT	0.96	0.061, B= 0.17	0.35	0.66	0.22
		TT	0.82	0.50	0.49	0.91	0.26
rs793391	TT	TG	0.34	0.064, B= 0.11	0.86	0.44	0.92
		GG	0.70	0.64	0.91	0.51	0.50
rs12634249	CC	CA	0.84	0.58	0.92	**0.022, B= -0.14**	0.29
		AA	0.18	0.73	0.25	0.27	0.81
rs2819590	CC	CT	0.32	0.078, B= 0.11	0.73	0.28	0.54
		TT	0.45	0.91	0.39	0.16	0.52
rs304092	GG	GA	0.43	0.095, B= 0.10	0.89	0.45	0.48
		AA	0.78	0.71	0.52	0.28	0.60

B-value is the unstandardized beta-value, and is shown when $p<0.1$. Significant associations are depicted in bold. ref=reference allele, var=variance allele. RV=residual volume, TLC=total lung capacity, D_{LCO}=diffusion lung capacity, V_A=alveolar volume.

Table 5. Associations between different genotypes of *SUMF1* SNPs and airway resistance and reactance measured by IOS in the total study population including both COPD and control subjects. Data is presented as p-values from linear regression between ref/ref and ref/var or var/var, adjusted for age, sex, height and smoking status.

SNP	**ref/ref**	**ref/var var/var**	**R5**	**R20**	**R5-R20**	**X5**	**AX**
rs4685744	CC	CT	0.56	0.35	0.82	0.83	0.72
		TT	0.32	0.46	0.44	0.64	0.95
rs2819562	CC	CT	0.32	0.41	0.28	0.52	0.21
		TT	0.69	0.82	0.80	0.95	0.61
rs2819561	AA	AG	0.31	0.41	0.27	0.50	0.20
		GG	0.67	0.85	0.74	0.94	0.63
rs2633852	AA	AG	0.27	0.33	0.26	0.48	0.19
		GG	0.83	0.99	0.86	0.97	0.55
rs11915920	CC	CT	0.61	0.36	0.89	0.70	0.85
		TT	0.33	0.52	0.39	0.65	0.92
rs807785	CC	CT	0.45	0.85	0.14	0.13	0.22
		TT	0.49	0.76	0.15	0.095, B= 0.022	0.26
rs3864051	CC	CT	0.29	0.45	0.39	0.21	0.36
		TT	**0.032, B= 0.079**	0.43	**0.003, B= 0.062**	**0.005, B= -0.067**	**0.009, B= 0.61**
rs794187	CC	CT	0.086, B= -0.020	0.72	**0.013, B= -0.017**	**0.018, B= 0.018**	**0.015, B= -0.18**
		TT	0.79	0.93	0.56	0.91	0.79
rs794185	TT	TC	**0.002, B= -0.039**	0.14	**<0.001, B= -0.026**	<0.001, B= 0.030	**<0.001, B= -0.30**
		CC	**0.030, B= -0.035**	0.39	**0.004, B= -0.026**	0.031, B=0.023	**0.020, B= -0.24**
rs2322683	CC	CT	0.21	0.33	0.27	0.11	0.11
		TT	0.62	0.89	0.48	0.89	0.81
rs793391	TT	TG	**0.014, B= -0.029**	0.16	**0.007, B= -0.018**	**0.012, B= 0.019**	**0.008, B= -0.20**
		GG	0.60	0.71	0.61	0.96	1.00
rs12634249	CC	CA	0.13	0.68	**0.029, B= -0.014**	**0.024, B= 0.017**	**0.028, B= -0.16**
		AA	0.39	0.87	0.30	0.59	0.48
rs2819590	CC	CT	**0.010, B= -0.030**	**0.048, B= -0.014**	**0.021, B= -0.015**	**0.025, B= 0.17**	**0.011, B= -0.19**
		TT	0.85	0.92	0.84	0.65	0.71
rs304092	GG	GA	**0.010, B= -0.030**	0.053, B= -0.014	**0.018, B= -0.016**	**0.029, 0.017**	0.022, B= -0.17
		AA	0.81	0.78	0.92	0.69	0.66

B-value is the unstandardized beta-value and is shown when p<0.1. Significant associations are depicted in bold. ref=reference allele, var=variance allele. R5=resistance at 5Hz, R20=resistance at 20 Hz, X5=reactance at 5Hz and AX=reactance area.

Figure 1

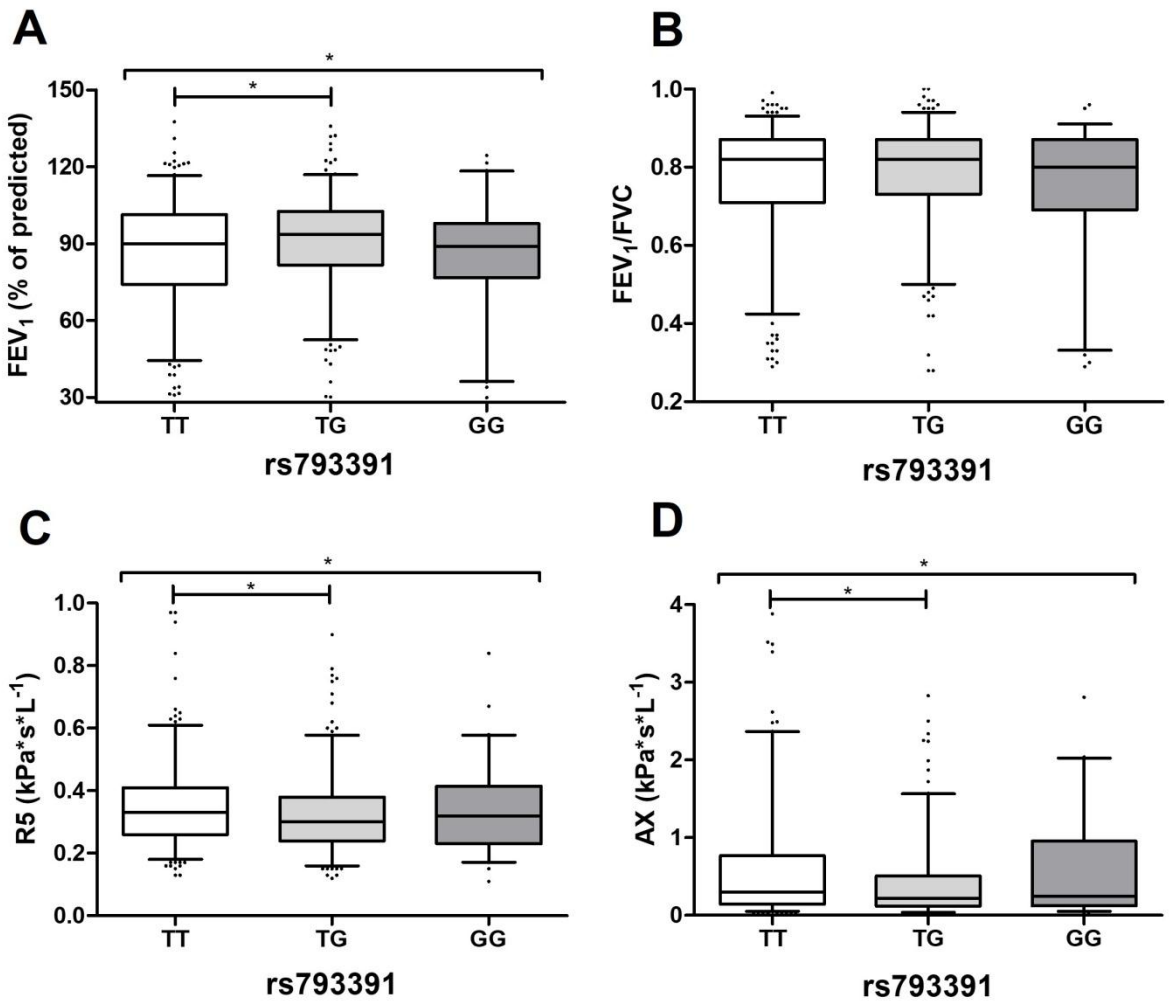

A
B
C
D
FEV1 (% of predicted)
FEV1/FVC
R5 (kPa*s*L-1)
AX (kPa*s*L-1)
TT
TG
GG
rs793391
*

Figure 2

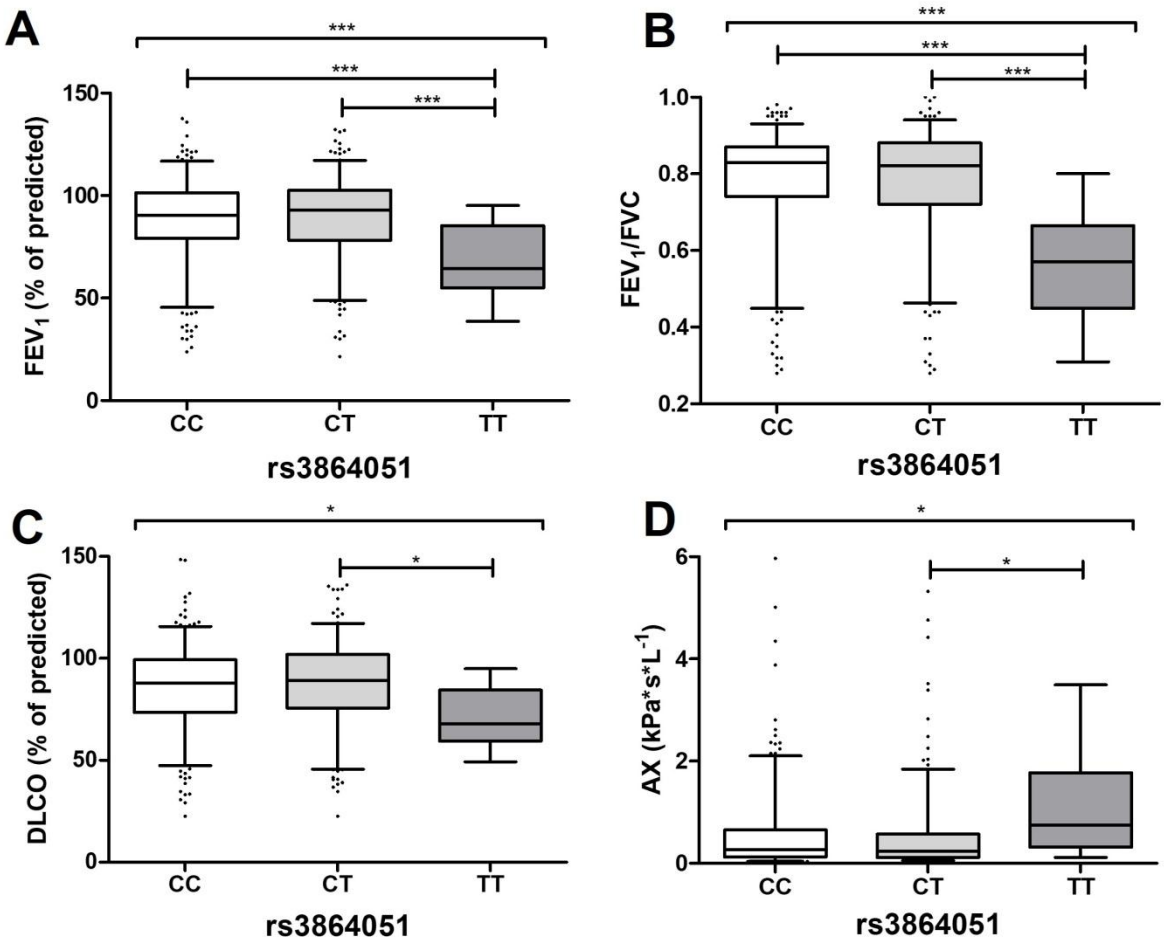
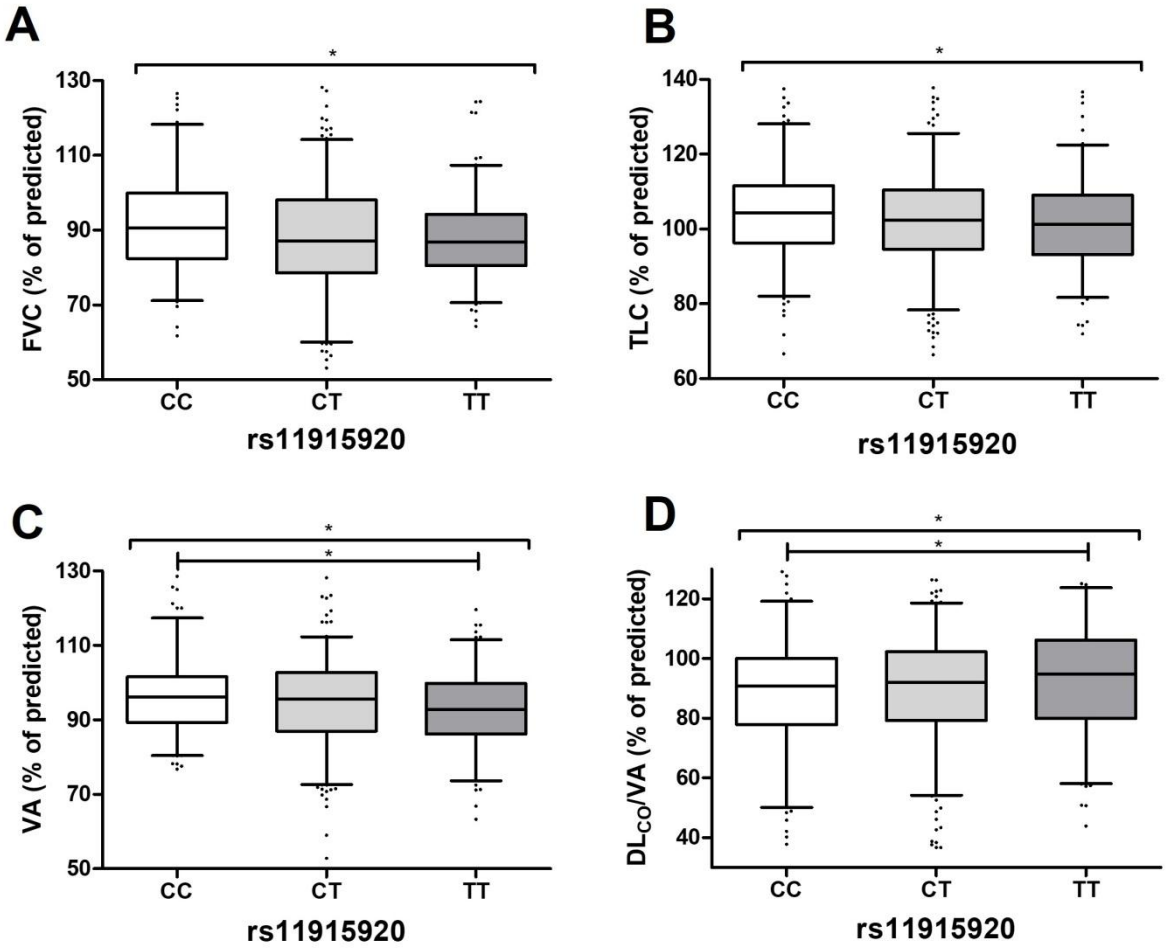

A
***
***
***
150
100
50
0
FEV1 (% of predicted)
CC
CT
TT
rs3864051
B
***
***
***
1.0
0.8
0.6
0.4
0.2
FEV1/FVC
CC
CT
TT
rs3864051
C
*
*
150
100
50
0
DLCO (% of predicted)
CC
CT
TT
rs3864051
D
*
*
6
4
2
0
AX (kPa*s*L-1)
CC
CT
TT
rs3864051

Figure 3


A
FVC (% of predicted)
130
110
90
70
50
CC
CT
TT
rs11915920
*
B
TLC (% of predicted)
140
120
100
80
60
CC
CT
TT
rs11915920
*
C
VA (% of predicted)
130
110
90
70
50
CC
CT
TT
rs11915920
*
*
D
DLCO/VA (% of predicted)
120
100
80
60
40
CC
CT
TT
rs11915920
*
*

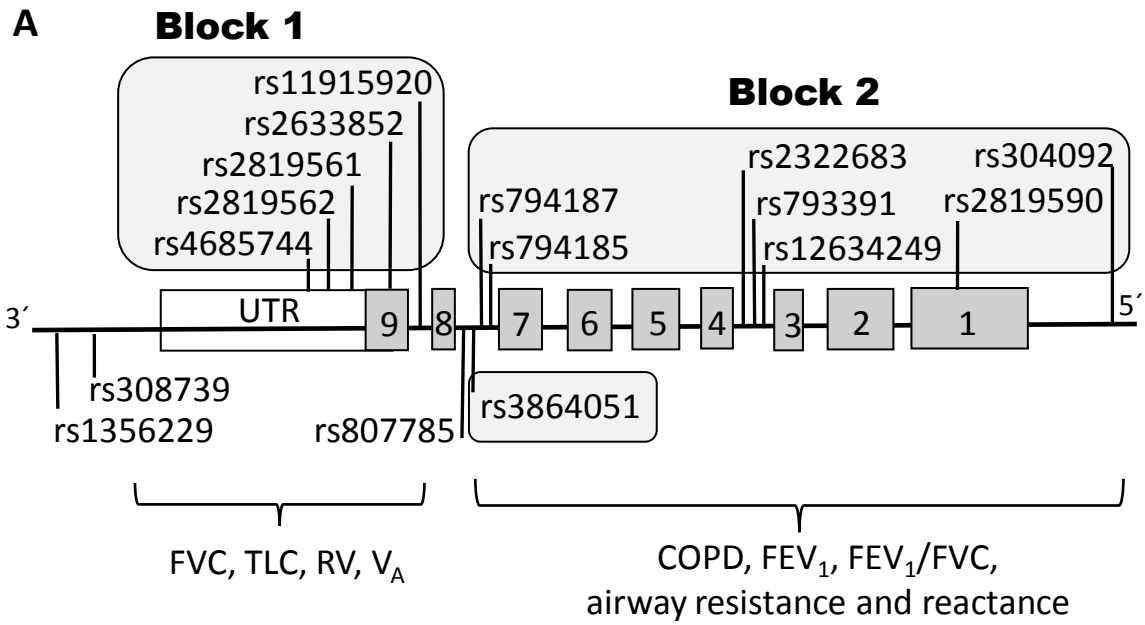
Supplementary Table

Supp Table 1. SNPs chromosomal localization and variant allele frequency (VAF) within all subjects and according to database (dbGaP VAF).

SNP	Chromosome localization	ref/ref		ref/var var/var		VAF		dbGaP VAF
rs1356229	3:4087317 intron	CC	536 (96.2%)	CT TT	21 (3.8%) 0 (0.0%)	C T	0.98 0.02	0.97 0.03
rs308739	3:4334346 intron	CC	484 (87.1%)	CA AA	72 (12.9%) 0 (0.0%)	C A	0.94 0.06	0.94 0.06
rs4685744	3:4361853 intron/utr3	CC	152 (27.3%)	CT TT	260 (46.7%) 145 (26.0%)	C T	0.51 0.49	0.50 0.50
rs2819562	3:4361930 intron/utr3	CC	123 (22.1%)	CT TT	256 (46.0%) 177 (31.8%)	C T	0.45 0.55	0.45 0.55
rs2819561	3:4362083 intron/utr3	AA	123 (22.1%)	AG GG	257 (46.2%) 176 (31.7%)	A G	0.45 0.55	0.45 0.55
rs2633852	3:4362153 intron/cds-syn	AA	121 (21.8%)	AG GG	255 (46.0%) 178 (32.1%)	A G	0.45 0.55	0.42 0.58
rs11915920	3:4368850 intron/utr3	CC	154 (27.7%)	CT TT	261 (46.9%) 141 (25.4%)	C T	0,51 0.49	0.50 0.50
rs807785	3:4379029 intron	CC	50 (9.0%)	CT TT	234 (42.0%) 273 (49.0%)	C T	0.30 0.70	0.30 0.70
rs3864051	3:4390432 Intron	CC	297 (53.5%)	CT TT	245 (44.1%) 13 (2.3%)	C T	0.76 0.24	0.67 0.34
rs794187	3:4394488 Intron	CC	231 (41.5%)	CT TT	260 (46.8%) 65 (11.7%)	C T	0.65 0.35	0.66 0.34
rs794185	3:4395674 Intron	TT	166 (29.8%)	TC CC	287 (51.5%) 104 (18.7%)	T C	0.56 0.44	0.58 0.42
rs2322683	3:4426914 intron	CC	73 (13.1%)	CT TT	237 (42.6%) 246 (44.2%)	C T	0.34 0.66	0.33 0.67
rs793391	3:4427508 intron	TT	255 (45.8%)	TG GG	239 (42.9%) 63 (11.3%)	T G	0.67 0.33	0.70 0.30
rs12634249	3:4444619 intron	CC	321 (57.6%)	CA AA	203 (36.4%) 33 (5.9%)	C A	0.76 0.24	0.77 0.23
rs2819590	3:4467058 missense	CC	283 (51.1%)	CT TT	222 (40.1%) 49 (8.8%)	C T	0.71 0.29	0.71 0.29
rs304092	3:4477309 unknown	GG	277 (49.8%)	GA AA	229 (41.2) 50 (9.0%)	G A	0.70 0.30	0.71 0.29

SNPs are sorted according to chromosome localization (chromosome localization is from GRCh38.p12). dbGaPVAF is from ALFA Allele Frequency project (ethnical origin: European), release version: 20201027095038

Figure S1



B

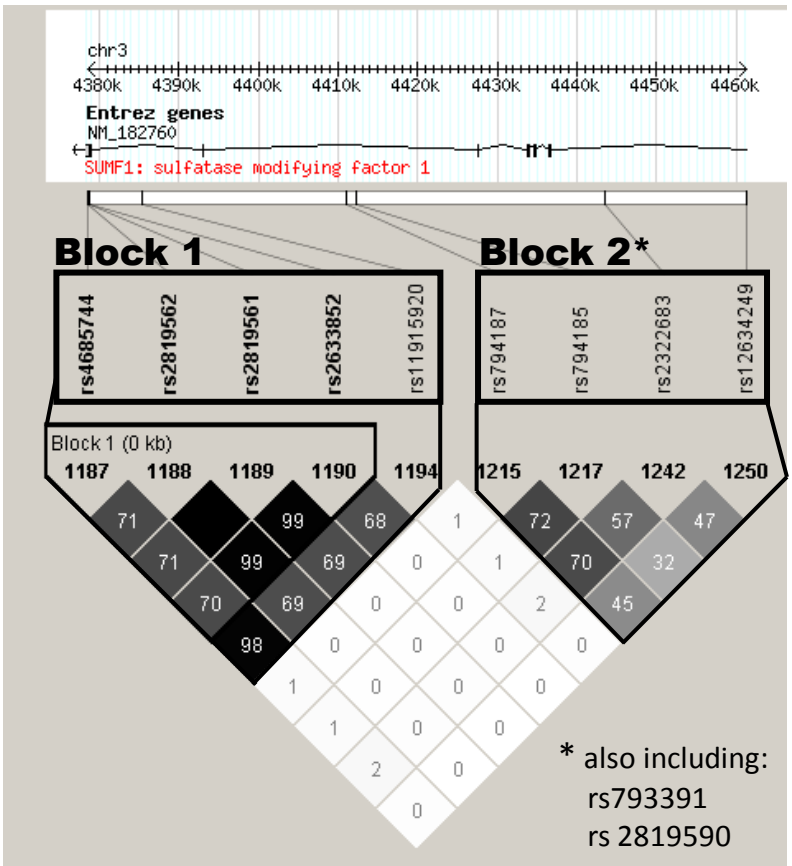


Figure S1 The analysed SNPs are shown in relation to exon localization (A) and appear in two blocks as shown in the linkage disequilibrium (LD) plot graphed from Haplowiev (B) where one block (Block 2) was associated with COPD and airway obstruction, and the other block (Block 1) was associated with impaired lung volumes. FEV_1=forced expiratory volume in 1 second, FVC=forced volume capacity, RV=residual volume, TLC=total lung capacity, V_A=alveolar volume and UTR=untranslated region.