

1 **Hepatobiliary phenotypes of adults with alpha-1 antitrypsin deficiency**

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10 **Abbreviations:**

AAT Alpha-1 antitrypsin

AATD Alpha-1 antitrypsin deficiency

CAP Controlled attenuation parameter

LSM Liver stiffness measurements

NAFLD Non-alcoholic fatty liver disease

NASH Non-alcoholic steatohepatitis

Pi Protease inhibitor

Pi*M Normal AAT allele

Pi*S Mutant *SERPINA1* allele variant termed ‘S’

Pi*Z Mutant *SERPINA1* allele variant termed ‘Z’

Pi*MZ AAT genotype with heterozygosity for the Pi*Z variant

Pi*SZ AAT genotype with compound heterozygosity for Pi*Z and Pi*S variant

Pi*ZZ AAT genotype with homozygosity for the Pi*Z variant

SERPINA1 AAT gene

TE Transient elastography (FibroScan®)

TM6SF2 Transmembrane 6 superfamily member 2

PNPLA3 Patatin-like phospholipase domain-containing protein 3

HSD17B13 17β-Hydroxysteroid dehydrogenase type 13 gene

11 **Word count:** 249 (Abstract) + 3393 (Manuscript)

12 **Figures:** 6

13 **Tables:** 2

14 **Supplementary material:** 704 words, 6 figures, 9 tables

1 **Significance of this study**

2 **What is already known about this subject?**

- 3 • Pi*Z and Pi*S are the most important genetic variants causing alpha1-antitrypsin deficiency (AATD).
4 • No reliable data on hepatobiliary phenotype exist for individuals with Pi*SS and Pi*SZ genotype, despite the
5 fact that both genotypes are seen in ~1:500 Caucasians
6 • The vast majority of AATD subjects remain undiagnosed during their lifetime and this fact complicates
7 AATD phenotyping.

8 **What are the new findings?**

- 9 • In a large community-based biobank as well as in a multinational cohort, subjects with Pi*SZ genotype were
10 markedly predisposed to liver fibrosis and seemed to be predisposed to primary liver cancer.
11 • Compared to the characteristic severe AATD genotype Pi*ZZ, Pi*SZ genotype causes intermediate
12 hepatobiliary phenotype, while Pi*SS does not seem to have major hepatobiliary consequences.

13 **How might it impact on clinical practice in the foreseeable future?**

- 14 • Our study defines the hepatic risks associated with the major AATD genotypes. These data, together with
15 the individual situation/susceptibility factors, should guide the counseling and management of AATD
16 individuals.
17 • The observed association with primary liver cancer should promote hepatologic surveillance of AATD
18 individuals and spur longitudinal studies characterizing the development of liver fibrosis and malignancy.
19

1 **ABSTRACT**

2 **Objective:** Alpha-1 antitrypsin deficiency (AATD) is a common, potentially lethal inborn disorder caused by
3 mutations in alpha-1 antitrypsin (AAT). Homozygosity for the 'Pi*Z' variant of AAT (Pi*ZZ genotype) causes lung
4 and liver disease, whereas a heterozygous 'Pi*Z' carriage (Pi*MZ genotype) predisposes to gallstones and liver
5 fibrosis. The clinical significance of the more common 'Pi*S' variant remains largely undefined and no robust data
6 exist on the prevalence of liver tumors in AATD.

7 **Design:** Baseline phenotypes of AATD individuals and non-carriers were analyzed in 482,380 participants in the UK
8 Biobank. 1104 participants of a multinational cohort (586 Pi*ZZ, 239 Pi*SZ, 279 non-carriers) underwent a
9 comprehensive clinical assessment. Associations were adjusted for age, sex, BMI, diabetes, and alcohol
10 consumption.

11 **Results:** Among UK Biobank participants, Pi*ZZ individuals displayed the highest liver enzyme values, the highest
12 occurrence of liver fibrosis/cirrhosis (aOR=21.7[8.8-53.7]) and primary liver cancer (aOR=44.5[10.8-183.6]).
13 Subjects with Pi*MZ genotype had slightly elevated liver enzymes and moderately increased odds ratio for liver
14 fibrosis/cirrhosis (aOR=1.7[1.2-2.2]) and cholelithiasis (aOR=1.3[1.2-1.4]). Individuals with homozygous Pi*S
15 mutation (Pi*SS genotype) harbored minimally elevated alanine aminotransferase values, but no other hepatobiliary
16 abnormalities. Pi*SZ participants displayed higher liver enzymes, more frequent liver fibrosis/cirrhosis
17 (aOR=3.1[1.1-8.2]) and primary liver cancer (aOR=6.6[1.6-26.9]). The higher fibrosis burden was confirmed in a
18 multinational cohort. Male sex, age \geq 50years, obesity, and the presence of diabetes were associated with significant
19 liver fibrosis.

20 **Conclusion:** Our study defines the hepatobiliary phenotype of individuals with the most relevant AATD genotypes
21 including their predisposition to liver tumors, thereby allowing evidence-based counseling and hepatological
22 monitoring.

23

24 **Keywords:** SERPINA1, Fibroscan, Pi*S, liver fibrosis, liver cirrhosis.

25

1 INTRODUCTION

2 AAT deficiency (AATD) is one of the most common, potentially lethal inborn disorders, with AATD-related lung
3 and liver disease being the major drivers of morbidity and mortality.[1] Mutations in the *SERPINA1* gene coding for
4 alpha-1 antitrypsin (AAT) lead to a ‘gain of function’ proteotoxic liver injury, whereas the lack of AAT in the
5 bloodstream facilitates the development of chronic obstructive pulmonary disease (COPD) and emphysema.[1]
6 The most common severe *SERPINA1* variant is termed ‘Pi*Z’ (rs28929474).[2, 3] The ‘Pi*S’ variant (rs17580) is
7 even more prevalent, but less detrimental.[1] The homozygous occurrence of ‘Pi*Z’ is found in 1:2000
8 Caucasians[2] and is termed ‘Pi*ZZ’, whilst heterozygous ‘Pi*Z’ carriage (termed ‘Pi*MZ’ genotype) is seen in 1:30
9 individuals of northern European descent. The strong predisposition of ‘Pi*ZZ’ individuals for lung disease is
10 supported by a large body of evidence and reflected in clinical management guidelines.[1] The susceptibility for liver
11 disease is less well documented.[3, 4] ‘Pi*ZZ’-related liver disease displays a biphasic pattern with the first peak in
12 early childhood as a neonatal cholestasis and second in the second half of adult life.[1, 5] Two cross-sectional studies
13 indicate that advanced liver fibrosis is ten to 20 times more common in ‘Pi*ZZ’ subjects compared to individuals
14 without a ‘Pi*Z’ mutation (non-carriers) and revealed that the non-invasive liver stiffness measurement (LSM) via
15 transient elastography (TE) constitute a useful surrogate of liver fibrosis.[4, 6] ‘Pi*MZ’ individuals seem to carry
16 moderately elevated odds for both lung and liver disease, and to be susceptible to gallstone disease.[1, 7]
17 Humans carrying both the ‘Pi*Z’ and the ‘Pi*S’ variant (termed ‘Pi*SZ’) are as frequent as 1:500 in certain
18 geographic regions,[8] while the occurrence of homozygous carriage of the ‘Pi*S’ variant (termed ‘Pi*SS’) might be
19 even higher.[9] Two studies demonstrated that ‘Pi*SZ’ individuals display a less severe lung phenotype than Pi*ZZ
20 subjects,[10, 11] whereas the extent of their liver disease was not systematically studied. Children with ‘Pi*SZ’
21 genotype develop a clinically relevant liver disease markedly less often than Pi*ZZ individuals[12, 13] Similar
22 findings have been reported in adults,[14] but multiple case reports have described “idiopathic” liver cirrhosis in
23 ‘Pi*SZ’ subjects.[15] Finally, while ‘Pi*SS’ genotype, is considered to confer minimal if any risks, little clinical data
24 are available to support this directly.[16]
25 Probably the greatest limitation when studying the AATD phenotype is the fact that the majority of AATD cases
26 remain undiagnosed and the proportion is even higher in individuals with less severe genotypes.[1] A Swedish birth
27 cohort-based study partially addressed this issue, but this study examined the individuals only up to 45 years of age,
28 i.e. before the peak of AATD-related adult liver disease and focused on Pi*ZZ individuals.[17] To provide unbiased
29 information about the hepatobiliary phenotype of individuals with major AATD genotypes, we used the UK biobank,
30 a community sample from the United Kingdom totaling nearly 500,000 individuals with available ‘Pi*Z’ and ‘Pi*S’
31 genotyping. To corroborate our findings, we prospectively recruited the largest, multi-national cohort of Pi*SZ
32 subjects without previously known chronic liver disease and compared their lung- and liver-related parameters to

- 1 those of Pi*ZZ participants, and non-carriers. The goal of our study was to provide data for evidence-based
- 2 management and counseling of these individuals.

1 **METHODS**

2 **Population-based UK biobank participants (Cohort 1)**

3 The 'UK biobank' (UKB) is a population-based cohort study conducted in the United Kingdom, which recruited
4 502,511 volunteers aged 37 to 73 years at baseline. All participants underwent an initial examination, which was the
5 basis for our study and gave informed consent for genotyping and data linkage to medical reports. Ongoing inpatient
6 hospital records beginning in 1996 were used to identify diagnoses according to ICD-10 codes (international
7 classification of diseases, 10th revision). Genotyping for both the Pi*Z (rs28929474) and Pi*S (rs17580) mutation of
8 *SERPINA1* was available in 487,503 subjects.

9 We excluded participants with viral hepatitis (ICD10: B16-B19: 713 MM, 20 MZ, 2 SZ) or risky alcohol
10 consumption (>60g alcohol/d for men, >40g alcohol/d for women: 3775 MM, 153 MZ, 9 SZ, 3 ZZ, 4 SS). We
11 compared *SERPINA1* variants to well-known genes, that modulate the risk of liver disease, i.e. *PNPLA3* p.I148M
12 (rs738409), *HSD17B13:T* (rs72613567), and *TM6SF2* p.E167K (rs5854926); homozygous carriers were compared
13 with non-carriers.

14 The presence of the following primary ICD10 codes was evaluated: Fibrosis and cirrhosis (K74.0-2+K74.6), primary
15 liver cancer (C22.0), cholelithiasis (K80), emphysema (J43.1+J43.2+J43.8+J43.9), and chronic bronchitis (J44). The
16 study has been approved by the UKB Access Committee (Project #47527). The presence of metabolic syndrome was
17 based on the IDF (International diabetes federation) definition, which consists of central obesity (defined as waist
18 circumference with ethnicity specific values) plus any two of the following four factors: (i) raised triglycerides \geq 150
19 mg/dL (1.7 mmol/L) or specific treatment for this lipid abnormality; (ii) reduced HDL cholesterol $<$ 40 mg/dL (1.03
20 mmol/L) in males or $<$ 50 mg/dL (1.29 mmol/L) in females or specific treatment for this lipid abnormality; (iii)
21 raised blood pressure systolic BP \geq 130 or diastolic BP \geq 85 mm Hg or treatment of previously diagnosed
22 hypertension; (iv) raised fasting plasma glucose (FPG) \geq 100 mg/dL (5.6 mmol/L), or previously diagnosed type 2
23 diabetes.

25 **Real life cohort without previously known liver disease (Cohort 2)**

26 *Study population*

27 1104 individuals were recruited as part of our global Alpha-1 Liver initiative, a multicenter registry effort for
28 AATD-related liver disease carrying out baseline assessment, that are shown herein, as well as a prospective follow-
29 up. The majority of non-carriers and Pi*ZZ participants was previously published.[6, 7] The inclusion criteria were
30 (i) age \geq 18 years, (ii) the ability to provide written informed consent, and (iii) no known pregnancy. To prevent an
31 enrichment with individuals with liver involvement, the following exclusion criteria were used: (i) the presence of

1 known liver disease or a liver co-morbidity identified in clinical and laboratory work-up, (ii) at least two independent
2 visits with elevated liver enzymes in medical records prior to baseline.

3 All participants underwent clinical and laboratory work-up including standardized questionnaires with demographic
4 parameters, previously known chronic diseases and relevant comorbidities, as well as the evaluation of alcohol and
5 cigarette consumption. The need for augmentation therapy and long-term oxygen therapy and the COPD assessment
6 test (CAT) values constituted determinants of lung phenotype. AAT serum level was measured and genotyping was
7 conducted by the responsible national AAT reference laboratories, that performed PCR analysis and/or isoelectric
8 focusing as described.[6]

9 The Pi*SZ population consisted of 239 subjects from ten European countries (Germany, UK, Portugal, Spain, Italy,
10 Austria, Belgium, Ireland, Denmark, Poland) and the US (Supplementary table 1). Among the Pi*ZZ participants,
11 413 (70.5%) were from Germany. Non-carriers (n=279) were defined as individuals with normal serum AAT levels
12 (i.e. >110 mg/dL), in whom the presence of the 'Pi*Z' and 'Pi*S' variant was excluded as described.[6] 219 (78.5%)
13 of them were recruited in Germany, 60 (21.5%) in Austria.

14

15 **Statistical analysis**

16 All continuous variables were analyzed by unpaired, two-tailed t-tests or Mann-Whitney U test, and by a
17 multivariable model to account for confounders (age, sex, BMI, diabetes mellitus, and alcohol consumption) and
18 shown as mean (standard deviation) (normal distribution) or median [IQR] (non-normal distribution). Categorical
19 variables were displayed as relative (%) frequencies and analyzed using the Chi-square test. ORs were presented
20 with their corresponding 95% confidence intervals (CI). Multivariable logistic regression tested for independent
21 associations. Correlations were assessed by Spearman correlation coefficients, where appropriate. Differences were
22 considered to be statistically significant when $P < 0.05$. The data were analyzed using SPSS Statistics version 26
23 (IBM; Armonk, NY, USA) and Prism version 8 (GraphPad, LaJolla, CA, USA).

1 RESULTS

2 Lung- and liver-related parameters of AATD subjects in UK biobank (Cohort 1)

3 The 482 380 eligible UK Biobank participants comprised 138 Pi*ZZ (frequency 1:3496), 864 Pi*SZ (1:558), 1014
4 Pi*SS (1:476), and 17006 Pi*MZ individuals (1:28; Figure 1A). All subgroups displayed a similar age and sex
5 distribution as well as a comparable - mostly low or moderate - alcohol consumption. While diabetes mellitus was
6 infrequent, it was less common in Pi*ZZ subjects compared to non-carriers (5% vs. 2%, $p < 0.0001$; Table 1). As
7 expected, Pi*ZZ individuals showed a significantly lower FEV1/FVC ratio compared to all other genotypes despite
8 the lowest cigarette consumption (Table 1). The percentage of individuals with FEV1/FVC < 70% was the highest
9 among Pi*ZZ participants but was also significantly higher in Pi*SZ individuals compared to non-carriers.

10 Regarding liver-related blood parameters, mean ALT values were significantly higher in all analyzed AATD
11 genotypes compared to non-carriers (Table 1, Figure 2A). Pi*MZ and Pi*SZ subjects presented with higher AST
12 values than non-carriers, however, Pi*ZZ individuals had significantly higher AST values than any other assessed
13 AATD subgroup (Table 1, Figure 2B). Gamma-glutamyl transferase (GGT) values were comparable in non-carriers,
14 Pi*MZ, Pi*SS, and Pi*SZ individuals, while Pi*ZZ subjects significantly more often displayed elevated GGT levels.

15 Alkaline phosphatase (ALP) was significantly elevated in Pi*MZ and Pi*SZ participants when compared to non-
16 carriers, however, comparable to subjects without AATD mutation in Pi*ZZ, Pi*SS individuals (Table 1, Figure 2C).

17 The odds ratio of having elevated AST was the highest in Pi*ZZ individuals (adjusted OR=4.5[2.8-7.3], $p < 0.0001$;
18 Figure 3) and surpassed the odds seen in established genetic liver disease modifiers such as homozygous *PNPLA3* or
19 *TM6SF2* mutation (Figure 3; Supplementary tables 2-4). Pi*ZZ participants also had a moderately increased risk for
20 elevated ALT values (adjusted OR=2.1[1.2-3.6], $p < 0.0001$; Figure 3) with odds comparable to the ones seen in
21 subjects with a homozygous *PNPLA3* or *TM6SF2* mutation (Figure 3; Supplementary tables 2,3). Individuals with
22 Pi*MZ, Pi*SS, and Pi*SZ genotype had all significantly increased risk of presenting with elevated ALT values
23 (OR=1.2-1.5; Figure 3). To determine, whether AATD deficiency predisposes to elevated liver enzymes even in
24 metabolically inconspicuous individuals, we performed the liver enzyme analysis after exclusion of individuals with
25 the diagnosis non-alcoholic fatty liver disease (NAFLD; Supplementary figure 1) and after exclusion of individuals
26 with metabolic syndrome (Supplementary figure 2). Both analyses yielded largely identical results thereby
27 demonstrating an effect of AATD mutations even in metabolically inconspicuous individuals. In line with that, an
28 additional adjustment for PNPLA3 allele as the best-established genetic risk factor for metabolic liver disease, did
29 not change the results either (not shown).

30 Next, we assessed, whether the analyzed liver enzymes remain stable or fluctuate over time. To that end, we took
31 advantage of follow-up measurements that were available in a subset of UK Biobank individuals and correlated them
32 with baseline values. Plasma levels of GGT and ALP showed a strong correlation ($\rho = 0.7-0.85$; Supplementary

1 table 5), whereas the correlation between baseline and follow-up transaminases/bilirubin levels were somewhat
2 weaker (Supplementary table 5), which is in line with previous reports.[18]
3 In the least studied genotypes Pi*SS and Pi*SZ, male sex, age ≥ 50 years, and smoking were associated with higher
4 rates of decreased %FEV1/FVC (Figure 4). With regard to transaminases, the presence of BMI ≥ 30 kg/m² or diabetes
5 mellitus conferred an increased chance of displaying elevated values. Age ≥ 50 years was associated with increased
6 AST, but not ALT values (Figure 4).
7

1 **Table 1: Comparison of lung and liver phenotype in individuals with Pi*SS and Pi*SZ genotype compared to**
2 **Pi*ZZ, Pi*MZ, and non-carriers (Cohort 1).**
3

	Non-carriers (n=422 506)	MZ (n=17 006)	SS (n=1014)	SZ (n=864)	ZZ (n=138)
Characteristics					
Age, mean (SD), y	56.5 (8.1)	56.9 (8.1)	56.4 (8.2)	56.6 (7.8)	56.1 (8.0)
Women, No. (%)	229 360 (54)	9 289 (55)	545 (54)	474 (55)	65 (47)
BMI, mean (SD), kg/m ²	27.4 (4.8)	27.3 (4.7)	27.2 (4.6)	27.0 (4.6)	26.8 (4.7)
Alcohol, mean (SD), g/d	8.8 (10.1)	8.6 (9.9)	8.3 (9.8)	8.6 (9.8)	8.3 (8.3)
Risk factors					
BMI>30 kg/m ² , No. (%)	130 070 (31)	5 135 (30)	300 (30)	249 (29)	37 (27)
Diabetes mellitus, No. (%)	22 399 (5)	753 (4)	57 (6)	31 (4)	3 (2)
Lung status					
FEV1/VC, mean (SD), %	75.9 (7.3) ¹	75.9 (7.5) ²	76.0 (7.4) ³	75.7 (7.7) ⁴	71.5 (12.6) ^{1,2,3,4}
FEV1/VC<70%, No. (%)	59 476 (14) ^{5,6}	2 486 (15) ⁷	148 (15) ⁸	147 (17) ^{5,9}	44 (32) ^{6,7,8,9}
Cigarette consumption, mean (SD), py	23.2±18.7 ^{10,11}	23.1±18.9 ^{12,13}	25.7±19.9 ^{10,12,14}	22.5±18.6 ¹⁵	14.5±8.2 ^{11,13,14,15}
Liver status					
ALT, mean (SD), % of ULN	56.2 (32.7) ^{16,17,18,19}	58.8 (31.6) ¹⁶	59.3 (32.4) ¹⁷	59.9 (30.3) ¹⁸	62.5 (25.3) ¹⁹
ALT ≥ULN, No. (%)	26 914 (6.4) ^{20,21,22,23}	1 235 (7.2) ^{20,24}	90 (8.9) ²¹	76 (8.8) ²²	15 (10.9) ^{23,24}
AST, mean (SD), % of ULN	63.6 (26.0) ^{25,26,27}	65.2 (23.9) ^{25,28}	64.8 (24.5) ²⁹	66.0 (23.1) ^{26,30}	75.7 (21.8) ^{27,28,29,30}
AST ≥ULN, No. (%)	18 490 (4.4) ^{31,32}	847 (5.0) ^{31,33}	53 (5.2) ³⁴	46 (5.3) ³⁵	20 (14.5) ^{32,33,34,35}
GGT, mean (SD), % of ULN	73.3 (81.3)	75.6 (76.6)	77.1 (73.4)	76.4 (62.5)	83.1 (75.2)
GGT ≥ULN, No. (%)	68 510 (16.2) ^{36,37}	2 849 (16.8) ^{36,38}	185 (18.2)	157 (18.2)	30 (21.7) ^{37,38}
ALP, mean (SD), % of ULN	72.7 (24.7) ^{39,40}	75.3 (25.7) ^{39,41}	73.3 (24.4) ^{41,42}	76.3 (24.5) ^{40,42}	72.2 (21.4)
ALP ≥ULN, No. (%)	46 534 (11.0) ^{43,44}	2 305 (13.6) ⁴³	121 (11.9) ⁴⁵	134 (15.5) ^{44,45}	16 (11.6)
Bilirubin, mean (SD), mg/dl	0.53 (0.26)	0.54 (0.26)	0.54 (0.27)	0.54 (0.28)	0.56 (0.26)
Bilirubin ≥ULN, No. (%)	11 692 (2.8)	528 (3.1)	31 (3.1)	28 (3.2)	7 (5.1)

4 Quantitative measures are expressed as mean with standard deviation or relative frequency (%). All analyses were
5 adjusted for age, sex, BMI, presence of diabetes mellitus, and mean alcohol consumption.

6 Abbreviations: AATD, alpha-1 antitrypsin deficiency; ALT, alanine aminotransferase; ALP, alkaline phosphatase;
7 AST, aspartate aminotransferase; BMI, body mass index; GGT, gamma-glutamyl transferase; ULN, upper limit of
8 normal (sex-specific).

9 ¹p=6.0*10⁻¹²; ²p=2.5*10⁻¹¹; ³p=9.5*10⁻⁹; ⁴p=1.5*10⁻⁷; ⁵p=0.032; ⁶p=3.0*10⁻⁹; ⁷p=1.2*10⁻⁸; ⁸p=4.9*10⁻⁸; ⁹p=0.000006;
10 ¹⁰p=0.018; ¹¹p=0.017; ¹²p=0.021; ¹³p=0.022; ¹⁴p=0.009; ¹⁵p=0.044; ¹⁶p=7.9*10⁻³⁰; ¹⁷p=0.001; ¹⁸p=0.00007; ¹⁹p=0.006;
11 ²⁰p=6.5*10⁻⁹; ²¹p=0.0004; ²²p=0.001; ²³p=0.009; ²⁴p=0.046; ²⁵p=4.1*10⁻¹⁴; ²⁶p=0.004; ²⁷p=1.3*10⁻⁹; ²⁸p=5.1*10⁻⁹;

1 ²⁹p=7.4*10⁻⁸; ³⁰p=2.5*10⁻⁷; ³¹p=0.00004; ³²p=1.5*10⁻⁹; ³³p=7.4*10⁻⁸; ³⁴p=0.00001; ³⁵p=0.00001; ³⁶p=0.004;
2 ³⁷p=0.013; ³⁸p=0.028; ³⁹p=4.4*10⁻⁴⁴; ⁴⁰p=0.000003; ⁴¹p=0.019; ⁴²p=0.003; ⁴³p=1.0*10⁻²⁴; ⁴⁴p=0.00001; ⁴⁵p=0.015.
3 SI conversion factors: To convert ALT, AST, GGT, and ALP to μ kat/L, multiply values by 0.0167; to convert
4 Bilirubin to μ mol/L, multiply values by 17.104.
5
6

7 **Lung- and liver-related diagnoses of AATD subjects in UK biobank (Cohort 1)**

8 With regard to lung-related ICD codes, the diagnosis of COPD and emphysema was >20x enriched in Pi*ZZ
9 participants compared to non-carriers. It was not more common in Pi*SS and Pi*SZ subjects, while the much more
10 frequent Pi*MZ individuals displayed a moderately increased odds ratio for emphysema (adjusted OR=1.6[1.3-1.9],
11 p<0.0001; Supplementary table 6; Figure 5). Consistently with a previous publication,[19] gallstone disease was
12 enriched in Pi*MZ carriers vs. non-carriers (adjusted OR=1.3[1.2-1.4], p<0.0001), but in none of the other AATD
13 genotypes. The diagnosis liver fibrosis/cirrhosis was nearly 20x more common in Pi*ZZ individuals compared to
14 non-carriers (adjusted OR=21.7[8.8-53.7], p<0.0001), but also markedly enriched in Pi*SZ subjects (adjusted
15 OR=3.1[1.1-8.2], p=0.027) and moderately in Pi*MZ participants (1.7[1.2-2.2]; p=0.001; Supplementary table 6;
16 Figure 5). Both Pi*SZ and Pi*ZZ individuals harbored a numerically higher risk of liver fibrosis/cirrhosis than any
17 of the previously described genetic liver disease modifiers (Figure 6A; Supplementary tables 2-4, 6). Similarly, both
18 Pi*SZ and Pi*ZZ subjects, but none of the other AATD genotypes, possessed a markedly increased risk for the
19 diagnosis of primary liver cancer. Again, the risk of Pi*ZZ individuals for primary liver cancer surpassed the odds
20 seen in individuals with other genetic modifiers, while Pi*SZ was comparable to known risk factors *TM6SF2* and
21 *PNPLA3* (Figure 6, Supplementary tables 2-4, 6).

22 A sensitivity analysis revealed that in the Pi*SZ and Pi*MZ populations, the ‘fibrosis/cirrhosis’ phenotype is
23 markedly enriched in males, obese individuals, and subjects \geq 50 years old (Supplementary figure 3).
24

25 **Lung and liver phenotype in a multinational AATD cohort (Cohort 2)**

26 Our multinational cohort consisted of 586 Pi*ZZ subjects, 239 Pi*SZ individuals, and 279 non-carriers, all without
27 previously known or co-existing liver disease (Table 2; Figure 1B). Pi*SZ subjects were underrepresented when
28 compared to the community-based UK Biobank cohort. All three subgroups showed similar rates of diabetes mellitus
29 and alcohol consumption, while differences in other demographic factors were seen (Table 2). When only
30 participants without augmentation therapy were considered, Pi*SZ individuals showed intermediate AAT serum
31 levels (63.8 \pm 19.8 mg/dl vs. 139.5 \pm 25.1 mg/dl in non-carriers vs. 28.3 \pm 16.0 mg/dl in Pi*ZZ, all p<0.0001, Table 2;
32 Supplementary figure 4A). The cut-off AAT level of 99.5 mg/dL differentiated well between Pi*SZ individuals and
33 non-carriers (sensitivity 97.9%, specificity 98.4%, Table 2; Supplementary figure 4A). Pi*SZ individuals had an
34 intermediate lung phenotype as reflected by their CAT scores and need for long-term oxygen treatment, i.e.the

1 levels/frequencies were higher than in non-carriers, but significantly lower/less frequent compared to Pi*ZZ
2 individuals (Table 2). With regard to liver enzymes, Pi*SZ individuals had lower AST and ALT than Pi*ZZ subjects,
3 while GGT was higher in Pi*SZ subjects than non-carriers. Mean ALP levels were the highest in Pi*SZ individuals
4 (Supplementary figure 4C-F, Supplementary table 7), whereas GLDH and bilirubin levels did not show obvious
5 differences among the subgroups (Supplementary table 7).

6 In TE, Pi*SZ individuals had intermediate LSM values, i.e. LSMs were higher than in non-carriers (5.2 ± 2.5 kPa vs.
7 4.6 ± 1.6 kPa, $p=0.002$), but lower than in Pi*ZZ subjects (5.2 ± 2.5 kPa vs. 6.6 ± 5.2 kPa; $p=0.022$, Table 2;
8 Supplementary figure 4B) and similar results were seen when only non-obese individuals were assessed
9 (Supplementary table 8). In the entire cohort, thirteen percent of Pi*SZ individuals showed LSM values ≥ 7.1 kPa
10 suggesting liver fibrosis stage of at least 2 on a 0-4 scale[20] compared to 5% of non-carriers (adjusted OR=2.6 [1.1-
11 6.1], $p=0.024$; Table 2) and 24% of Pi*ZZ subjects (adjusted OR=0.5 [0.2-0.8], $p=0.013$; Table 2). Pi*SZ individuals
12 with LSM ≥ 7.1 kPa had significantly higher BMI values and were more frequently diabetic (Supplementary table 9).
13 *Vice versa*, diabetic individuals more frequently displayed elevated AST and ALT values than subjects without
14 diabetes (Supplementary figure 5).

15 The simultaneously assessed CAP as a surrogate of hepatic steatosis did not show major differences between Pi*SZ
16 and non-carriers, nor between Pi*SZ individuals and Pi*ZZ subjects (Table 2). On the other hand, increased liver
17 enzyme levels were seen primarily in Pi*SZ individuals with liver steatosis (as revealed by an analysis of a subgroup
18 with CAP ≥ 248 dB/m) that displayed higher AST, GGT, and ALP levels than “steatotic” non-carriers (Supplementary
19 figure 6).

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1 **Table 2: Characteristics of Pi*SZ individuals in comparison to Pi*ZZ subjects and non-carriers in a multi-**
 2 **center registry cohort (Cohort 2).**
 3

	Non-carriers (n= 279)	Pi*SZ (n= 239)	Pi*ZZ (n= 586)	<i>P value</i> <i>Pi*SZ vs.</i> <i>non-</i> <i>carriers</i> <i>(uni-</i> <i>variable)</i>	<i>P value</i> <i>Pi*SZ vs.</i> <i>non-</i> <i>carriers</i> <i>(multi-</i> <i>variable)</i>	<i>P value</i> <i>Pi*SZ vs.</i> <i>Pi*ZZ</i> <i>(uni-</i> <i>variable)</i>	<i>P value</i> <i>Pi*SZ</i> <i>vs.</i> <i>Pi*ZZ</i> <i>(multi-</i> <i>variable)</i>
Characteristics							
Age, mean (SD), y	52.4 (14.6)	50.4 (16.1)	54.2 (13.2)	0.142		0.002	
Women, No. (%)	137 (49.1)	135 (56.5)	271 (46.2)	0.094		0.008	
BMI, mean (SD), kg/m ²	25.6 (4.5)	26.6 (5.5)	25.0 (4.4)	0.022		<0.0001	
Alcohol, mean (SD), g/d	7.4 (9.7)	7.3 (11.9)	5.6 (9.6)	0.958		0.086	
AAT serum level [#] , mean (SD), mg/dL	139.5 (25.1)	63.8 (19.8)	28.3 (16.0)	<0.0001	<0.0001	<0.0001	<0.0001
Risk factors							
BMI ≥30 kg/m ² , No. (%)	35 (12.9)	51 (23.1)	61 (10.5)	0.003		<0.0001	
Diabetes mellitus, No. (%)	13 (5.0)	7 (3.5)	20 (4.2)	0.426		0.654	
Relevant alcohol intake ⁺ , No. (%)	32 (11.5)	30 (17.5)	48 (8.2)	0.070		<0.0001	
Lung status							
CAT score, mean (SD), points	7.0 (6.0)	14.1 (9.2)	16.5 (8.1)	<0.0001	<0.0001	0.022	0.004
Cigarette consumption, mean (SD), py	8.3 (16.5)	11.0 (17.1)	9.9 (13.4)	0.147	0.232	0.501	0.434
Long-term oxygen treatment, No. (%)	1 (0.4)	12 (6.5)	109 (22.6)	<0.0001	0.003	<0.0001	<0.0001
Liver status							
Liver stiffness [°] , mean (SD), kPa	4.6 (1.6)	5.2 (2.5)	6.6 (5.2)	0.001	0.002	<0.0001	0.022
Liver stiffness ≥7.1 kPa [°] , No. (%)	15 (5.4)	24 (12.6)	140 (23.9)	0.006	0.024	0.001	0.013
Liver stiffness ≥10.0 kPa (%) [°] , No. (%)	3 (1.1)	7 (3.7)	76 (13.0)	0.057	0.199	<0.0001	0.006
CAP [°] , mean (SD), dB/m	249.5 (58.1)	259.6 (60.7)	264.6 (57.0)	0.122	0.056	0.401	0.132
CAP ≥248 dB/m (%) [°] , No. (%)	136 (51.9)	67 (57.3)	288 (60.8)	0.334	0.234	0.489	0.296
CAP ≥280 dB/m (%) [°] , No. (%)	79 (30.2)	46 (39.3)	173 (36.5)	0.080	0.009	0.572	0.422

4 Quantitative measures are expressed as mean with standard deviation or relative frequency (%). All multivariable
 5 analyses were adjusted for age, sex, BMI, presence of diabetes mellitus, and mean alcohol consumption. The cut-offs
 6 for non-invasive liver parameters were chosen according to etiology-unspecific recommendations: Liver stiffness
 7 ≥7.1 kPa indicating significant liver fibrosis (fibrosis stage ≥2 on a 0-4 scale) and ≥10 kPa showing advanced
 8 fibrosis (fibrosis stage ≥3). Controlled-attenuation parameter (CAP) ≥248 dB/m suggesting the presence of steatosis
 9 grade ≥1, and CAP ≥280 dB/m indicating the presence of steatosis grade 3.

10 ⁺ Alcohol intake >12 g/d for women, >24 g/d for men (individuals with alcohol consumption >40 g/d females or >60
 11 g/d males had been excluded *a priori*).

12 [#] AAT serum levels of individuals, who did not receive AAT augmentation therapy, are shown.

13 [°] Liver stiffness and CAP only available in 190 Pi*SZ individuals.

1 Abbreviations: BMI, body mass index; AAT, alpha-1 antitrypsin; CAT, chronic obstructive pulmonary disease
2 assessment test; CAP, controlled attenuation parameter.
3 SI conversion factors: To convert AAT to $\mu\text{mol/L}$, multiply values by 0.184.
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6 **DISCUSSION**

7 We analysed the hepatobiliary phenotype of individuals with the most common AATD genotypes using UK Biobank
8 as a unique, openly available resource with deep genetic, physical, and health data.[21] Although it does not
9 constitute an entirely representative population sample since it mainly comprises of individuals of British descent
10 from higher income classes and contains only a few Black, Indian, Pakistani, and Chinese participants,[21] it
11 represents the best available approximation of such a cohort in that it recruited and systematically genotyped
12 participants independently on their known *SERPINA1* genotype. This approach is crucial since the vast majority of
13 AATD individuals remain undetected and were therefore not considered in previous studies. The AAT genotyping
14 used in our study was extracted from the UK Biobank Axiom™ array and the results remained unknown to the study
15 subjects. The frequencies of analysed genotypes agreed well with their published occurrence in Caucasian
16 population[8] – an observation that further validates our approach.

17 An important limitation of our study is the difficulty to reliably identify all individuals with non-alcoholic fatty liver
18 disease (NAFLD) and non-alcoholic steatohepatitis (NASH) since these disorders were not systematically assessed
19 in the UK Biobank baseline visits and since they remain underdiagnosed in the clinical routine. To offset this
20 limitation, we repeated the analyses after excluding individuals with the ICD code NAFLD as well as with presence
21 of metabolic syndrome and demonstrated that the differences persist even after these actions. Moreover, liver
22 transaminase levels significantly fluctuated over time and therefore, a single measurement is not sufficient to
23 comprehensively evaluate a liver phenotype of AATD individuals. Notably, the limited usefulness of single ALT
24 measurements for evaluation of AATD individuals was reported previously.[22]

25 In UK biobank cohort, the Pi*ZZ participants suffered a >20 times higher risk of liver fibrosis and cirrhosis as well
26 as ~45 times higher risk of primary liver cancer. The former finding is in line with previous reports demonstrating
27 that signs of advanced fibrosis are nine to 20-fold more common in Pi*ZZ individuals compared to people without
28 AAT mutations as well as the observation that Pi*ZZ individuals are 20 times more likely to require liver
29 transplantation than the general population.[6, 23] The odds of Pi*ZZ subjects to develop advanced liver
30 fibrosis/cirrhosis are substantially higher than the ones reported for other established genetic conditions such as
31 mutations in *PNPLA3*, *TM6SF2*, or *HSD17B13* gene.[23, 24] While the predisposition to liver fibrosis is now
32 supported by a solid body of evidence, reports on liver cancer in Pi*ZZ individuals are very limited[1] and further
33 analyses are needed. Pi*ZZ participants had the highest AST/ALT values, but their ALP levels were similar to the

1 ones seen in non-carriers and they did not present with an increased risk of cholelithiasis. Since gallstones constitute
2 mainly of lipids such as cholesterol, the alterations in lipid metabolism that were observed in Pi*ZZ individuals (i.e.
3 lower serum levels of triglycerides, very low-density lipoproteins and low-density lipoproteins compared to controls)
4 and indicated an impaired hepatic secretion of lipids might play a role.[6] Collectively, our data revealing a marked
5 susceptibility of Pi*ZZ individuals to end-stage liver disease should prompt their thorough hepatological monitoring.
6 The availability of genetic information allowed us to systematically study AATD genotypes, that are not assessed in
7 clinical routine such as Pi*MZ and Pi*SS. With regard to Pi*MZ, our data confirmed previous findings of a mild
8 increase in transaminases as well as a moderately increased risk of liver fibrosis/cirrhosis and cholelithiasis.[7, 19,
9 24] On the other hand, the increased occurrence of emphysema was seen in some, but not all population-based
10 studies.[1] With regard to Pi*SS genotype, our data are novel and support the current opinion that these individuals
11 display no or only minimal predisposition to lung and liver disease. It provides an important guidance for physicians
12 and a relief for the carriers of this genotype.

13
14 A focus of our work was on the Pi*SZ phenotype, that is underrepresented in clinical routine compared to Pi*ZZ
15 subjects. This might be due to their less conspicuous AAT serum levels as well as their less pronounced disease
16 phenotype.[10, 11, 25] Consistently with published data, the Pi*SZ individuals available in the UK Biobank
17 displayed no or only minimal lung phenotype,[10, 11] while our multi-center cohort was skewed towards more lung-
18 diseased individuals, likely due to the fact that it often prompted the diagnosis of AATD. Although Pi*SZ
19 individuals display normal or only minimally elevated transaminases, both analyzed cohorts revealed a marked
20 predisposition to liver fibrosis. The UK biobank cohort also suggested an increased susceptibility to primary liver
21 cancer that was not assessed in the second cohort. The more pronounced association with liver fibrosis compared to
22 lung emphysema might be attributable to the fact that the liver phenotype constitutes a “gain-of-function” toxicity
23 while lung injury seems to arise due to a loss-of-function situation. Accordingly, the intermediate AAT serum levels
24 seen in Pi*SZ individuals might be sufficient to protect the lung from proteolytic damage, while misfolding and
25 polymerization of AAT may generate biologically relevant proteotoxic stress in the liver. The identified hetero-
26 polymerization between Pi*S and Pi*Z [26] might be responsible for the greater liver fibrosis burden than that of the
27 Pi*MZ state despite the absence of any Pi*SS signal (suggesting no clinically significant challenge with S AAT
28 misfolding alone). While Pi*SZ subjects display clear predisposition to liver fibrosis and primary liver cancer, their
29 susceptibility is markedly lower than the one seen in Pi*ZZ individuals, which is consistent with the observed lower
30 levels of intracellular polymers and a less pronounced lung phenotype.[10, 11]

31 In addition to the characterization of the hepatobiliary phenotype of AATD individuals, we demonstrated that male
32 sex, obesity, diabetes, and higher age are associated with increased risk of liver fibrosis/cirrhosis as well as primary

1 liver cancer. Notably, the same factors were implicated in liver fibrosis development in Pi*MZ and Pi*ZZ
2 individuals.[4, 6, 7, 27] Among them, obesity and diabetes are potentially modifiable and their effects as drivers of
3 non-alcoholic fatty liver disease extends beyond AATD.[28, 29] They are associated with increased oxidative stress
4 and lipolysis and may aggravate the endoplasmic reticulum stress occurring in AATD.[30, 31] Male sex is another
5 parameter linked to AATD since the production of AAT is stimulated by testosterone and males therefore produce
6 higher amounts of the potentially toxic protein.[32]

7 In conclusion, our data characterize the hepatobiliary phenotype of individuals with major AATD genotypes with a
8 focus on Pi*SZ and should help in patient management and counselling. While Pi*ZZ individuals need a closer
9 monitoring, the surveillance of Pi*MZ and Pi*SZ subjects needs to be adjusted to the overall clinical context that
10 includes the presence of hepatic co-morbidities/metabolic risk factors, other genetic factors as well as the
11 presence/absence of baseline liver fibrosis. The association with primary liver cancer should spur hepatological
12 surveillance of both Pi*ZZ and Pi*SZ individuals. However, further studies are warranted to determine, whether a
13 screening is needed for all Pi*SZ/Pi*ZZ individuals or only those with advanced liver fibrosis. Longitudinal
14 assessment is needed to define the rate of disease development and tumor occurrence in the individuals with different
15 AATD genotypes.

16

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1 **Authorship statement:**

- 2 Study concept and design: M.F., C.V.S., P.S.
- 3 Acquisition of data: M.F., C.V.S., V.P., K.H., M.P., M.C.R., F.B., P.E., K.T., M.M., B.B., V.W., J.C.W., J.V., F.N.,
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5 N.T.G., V.C., W.J.G., C.T., A.M.T., N.G.M, P.S.
- 6 Analysis and interpretation of data: M.F., C.V.S., P.S.
- 7 Drafting of the manuscript: M.F., C.V.S., P.S.
- 8 Critical revision of the manuscript for important intellectual content: all authors
- 9 Figures and tables: M.F., C.V.S., P.S.
- 10 Statistical analysis: M.F., C.V.S.
- 11 Obtained funding: C.V.S., K.H., P.E., M.M., D.A.L., C.T., A.M.T., P.S.
- 12 Study supervision: M.F., C.V.S., P.S.
- 13 All authors had full access to all of the data and approved the final version of this manuscript. All authors take
14 responsibility for the integrity of the data and the accuracy of the data analysis.
- 15

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14

15

1 **FIGURE LEGENDS**

2

3 **Figure 1: Overview of analyzed cohorts.**

4 A) Cohort 1: Population-based study analyzing UK Biobank participants aged 37 to 73 years at baseline. B) Cohort
5 2: Prospectively recruited individuals available in a multinational, cross-sectional Alpha-1 Liver initiative.

6

7 **Figure 2: Liver related parameters in individuals heterozygous for the Pi*Z variant (Pi*MZ), homozygous for
8 the Pi*S variant (Pi*SS), heterozygous for both Pi*S and Pi*Z (Pi*SZ), and homozygous for the Pi*Z variant
9 (Pi*ZZ) compared to non-carriers (Cohort 1).**

10 422 506 non-carriers, 17 006 Pi*MZ subjects, 1014 Pi*SS individuals, 864 Pi*SZ subjects, and 138 Pi*ZZ
11 individuals underwent laboratory analysis. P values were adjusted for age, sex, BMI, alcohol consumption, and
12 presence of diabetes mellitus. Scatter plots of serum level of alanine aminotransferase (ALT; A), aspartate
13 aminotransferase (AST; B), and alkaline phosphatase (ALP; C), all normalized to the sex-specific upper limit of
14 normal (ULN).

15

16 **Figure 3: Risk of Pi*SS and Pi*SZ subjects to show elevated AST or ALT compared to heterozygous (Pi*MZ)
17 and homozygous (Pi*ZZ) Pi*Z carriers as well as homozygous carriers of PNPLA3 p.I148M (rs738409),
18 HSD17B13:T (rs72613567), and TM6SF2 p.E167K (rs5854926) (Cohort 1).**

19 Adjusted odds ratios (aOR) with their corresponding 95% confidence intervals (CI) are shown for aspartate
20 aminotransferase (AST; A) and alanine aminotransferase (ALT; B). The risk to display levels higher than the
21 corresponding sex-dependent upper limit of normal (ULN) was compared to the respective non-carriers. Odds ratios
22 were adjusted for age, sex, BMI, alcohol consumption, and diabetes mellitus.

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24 **Figure 4: Rate of Pi*SS and Pi*SZ subjects with decreased Tiffenau Index, elevated AST, or elevated ALT in
25 different subpopulations (Cohort 1).**

26 Relative frequencies (%) are shown and visualized by a color coding (right panel). Decreased Tiffenau-index is
27 defined as FEV1/VC <70%. Smokers are defined as “ever-smokers” and non-smokers are defined as “never-
28 smokers”. Abbreviations: ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index
29 (kg/m²); DM, diabetes mellitus; FEV1, forced expiratory volume in 1 second; VC, vital capacity.

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1 **Figure 5: Odds ratios of ICD10 diagnoses in individuals heterozygous or homozygous for the Pi*Z variant**
2 **(Pi*MZ/Pi*ZZ), homozygous for Pi*S variant (Pi*SS) and heterozygous for Pi*S and Pi*Z (Pi*SZ) (Cohort**
3 **1).**

4 Adjusted odds ratios (aOR) with their corresponding 95% confidence intervals (CI) are shown for Pi*MZ, Pi*SS,
5 Pi*SZ, and Pi*ZZ subjects compared to non-carriers. Odds ratios were adjusted for age, sex, BMI, alcohol
6 consumption, and diabetes mellitus. If in one group no cases are available, the corresponding aOR was set as 1[1;1].

7
8 **Figure 6: Odds ratios of ICD10 diagnoses in individuals heterozygous (or homozygous for Pi*Z**
9 **(Pi*MZ/Pi*ZZ), heterozygous for Pi*S and Pi*Z (Pi*SZ) or homozygous for displayed genetic liver fibrosis**
10 **modifiers.**

11 Genetic liver fibrosis modifiers include *PNPLA3* p.I148M (rs738409), *HSD17B13*:T (rs72613567), and *TM6SF2*
12 p.E167K (rs5854926)). Adjusted odds ratios (aOR) with their 95% confidence intervals (CI) compared to the
13 corresponding non-carriers. Odds ratios were adjusted for age, sex, BMI, alcohol consumption, and diabetes mellitus.

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