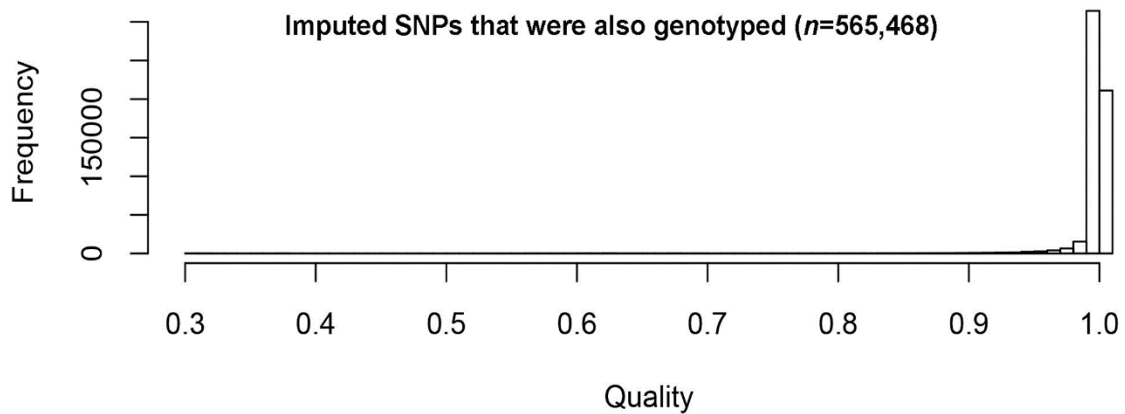
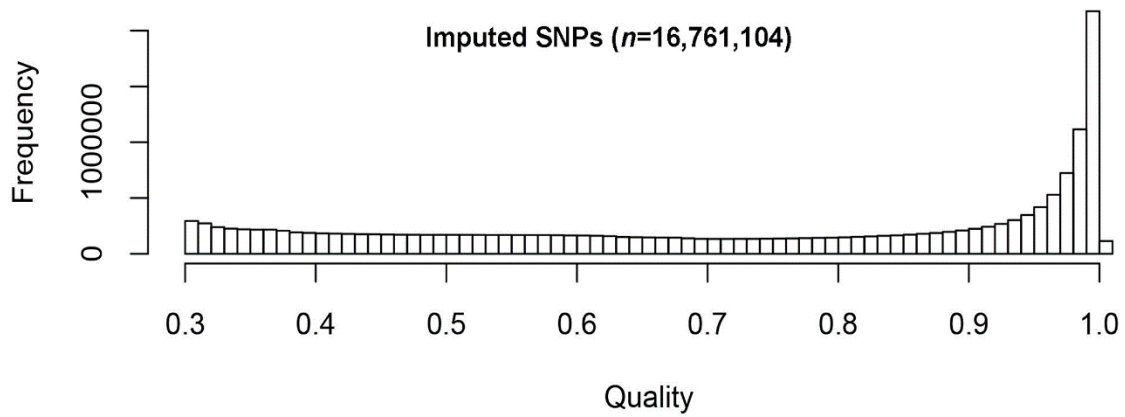


Supplementary Figure 1

Box and whiskers plots of the Consortium lung phenotype for 13 subgroups defined by combination of site and genotyping platform.

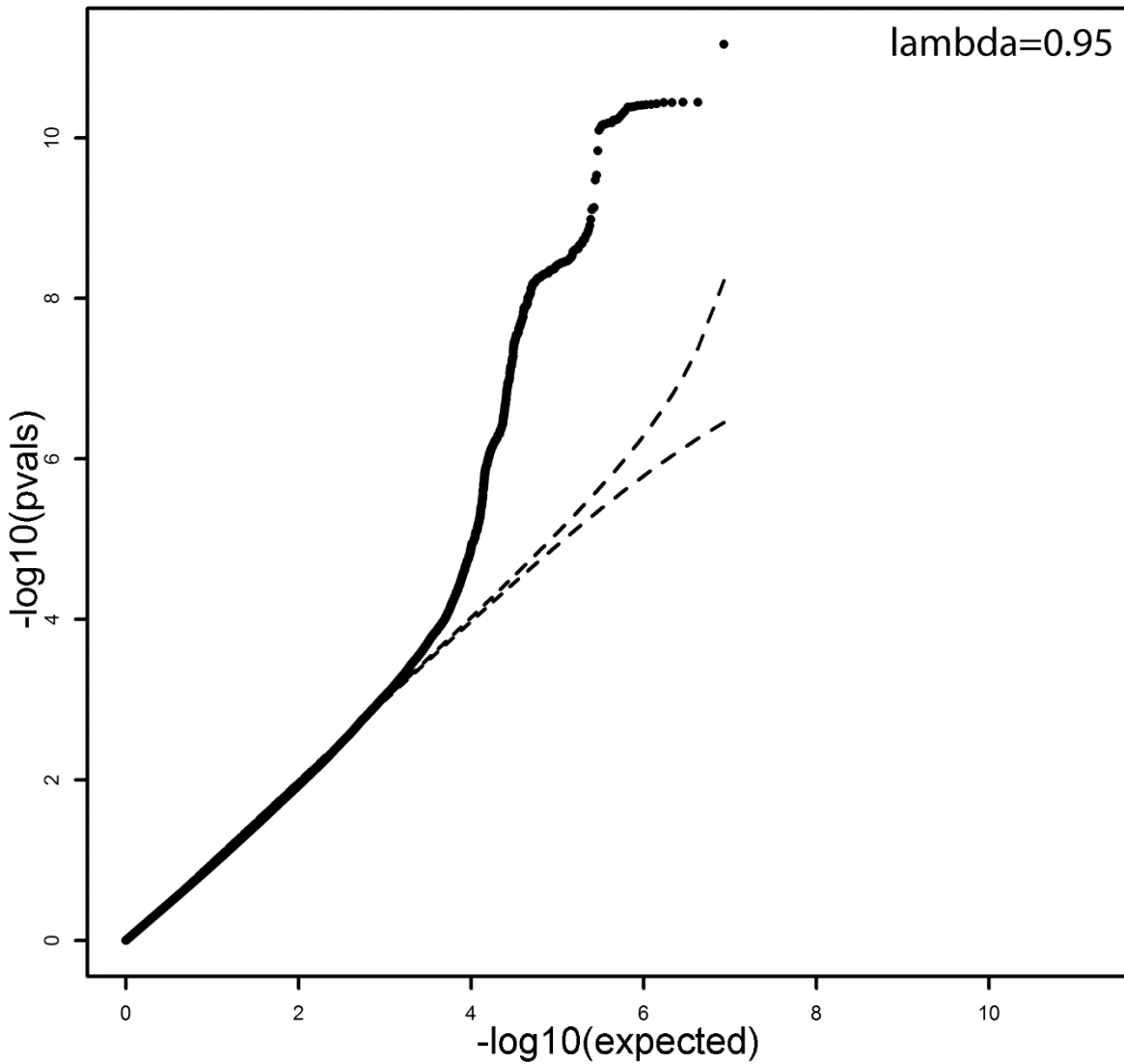
The borders of the box are the 1st and 3rd quartiles, and the band inside the box is the median. The interquartile range (IQR) is the 1st quartile subtracted from the 3rd quartile, and the whiskers are $\pm 1.5 \times \text{IQR}$. Values not included between the whiskers are plotted as outliers with dots. Note that the 13 subgroups had similar distributions of the Consortium lung disease phenotype.



Supplementary Figure 2

Histogram for distribution of quality scores from imputation.

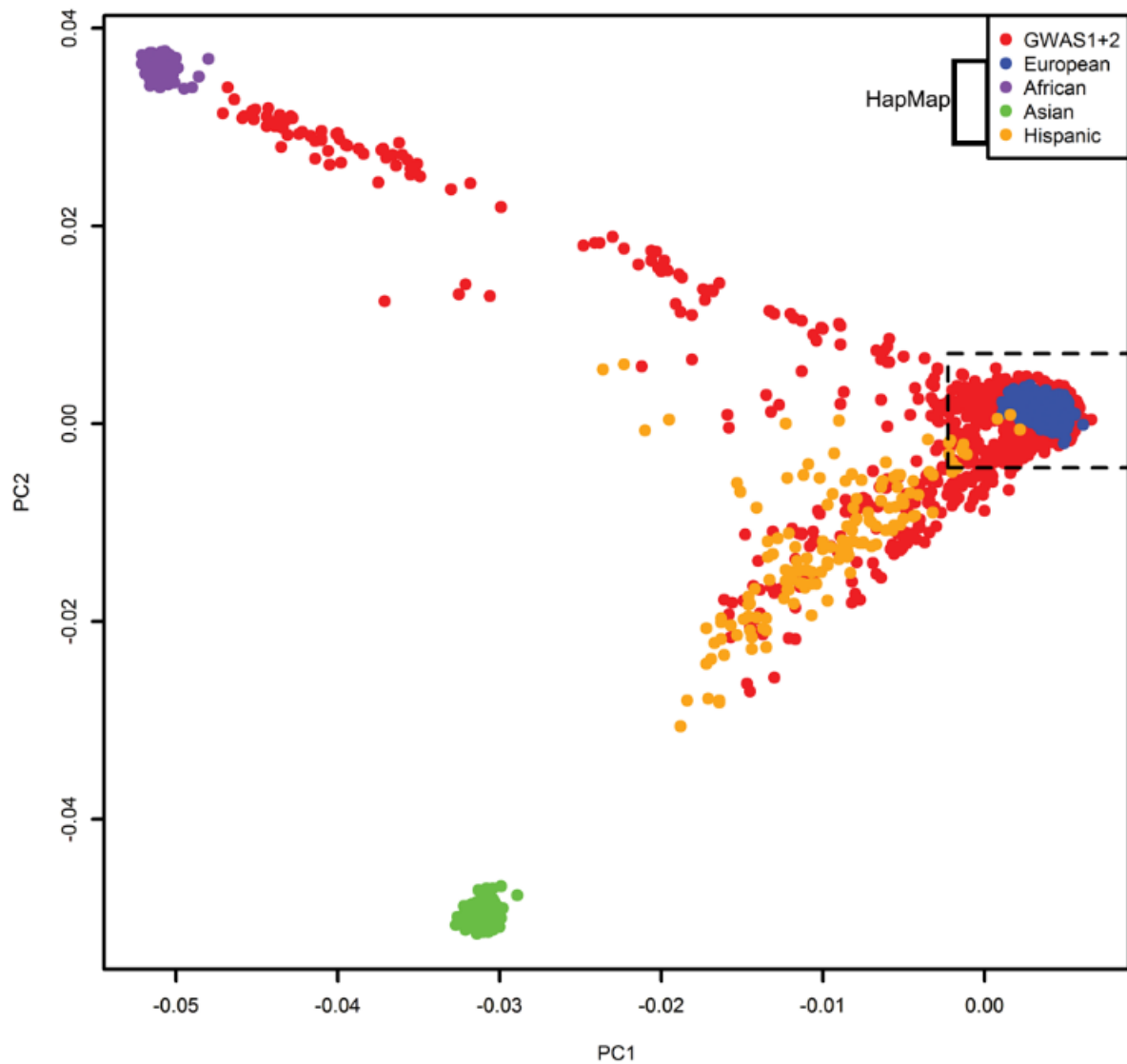
(Top) Histogram plot for the distribution of quality scores for SNPs imputed from genotyped SNPs on the 610 platform. The vast majority of imputed SNPs had quality scores near 1, indicating high quality. The other genotyping platforms had similar distributions of quality scores. Only ~50% of these imputed SNPs were used for analysis (8,520,458), as approximately half had minor allele frequencies < 0.005. **(Bottom)** Corresponding histogram plot for the subset of imputed SNPs that were also genotyped. As expected, those SNPs were imputed with even higher quality.



Supplementary Figure 3

Q-Q plot for the distribution of P values of imputed and genotyped SNPs using a random-effects model in the meta-analysis of the 13 GWAS1+2 subgroups for all individuals, with sex and principal components as covariates.

The genomic control value is $\lambda = 0.95$, so the distribution of P values is not over-inflated. The genomic control value from the meta-analysis of genotyped SNPs common to all platforms was similar ($\lambda = 0.94$; Q-Q plot not shown).

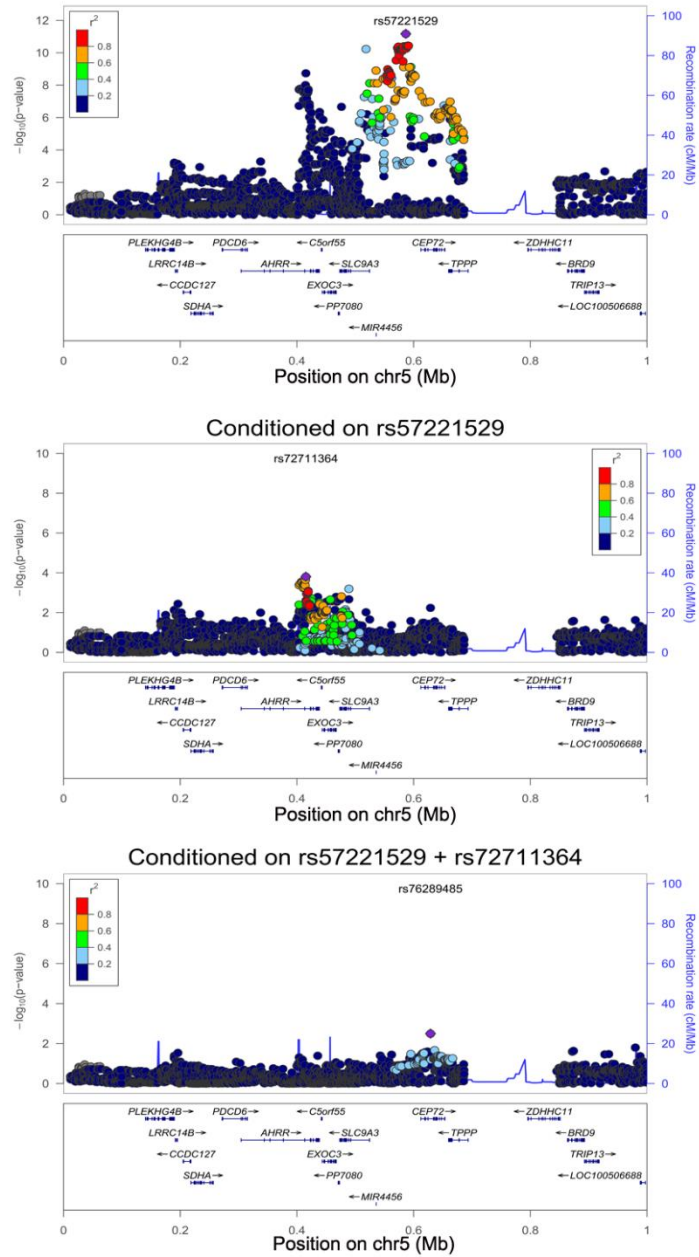


Supplementary Figure 4

Plot for the top two principal components from the joint analysis of GWAS1+2 individuals and HapMap3 individuals.

Individuals were judged to have European ancestry if principal components 1 and 2 fell within a mean \pm 6SD black rectangle formed using principal components from the HapMap3 European dataset.

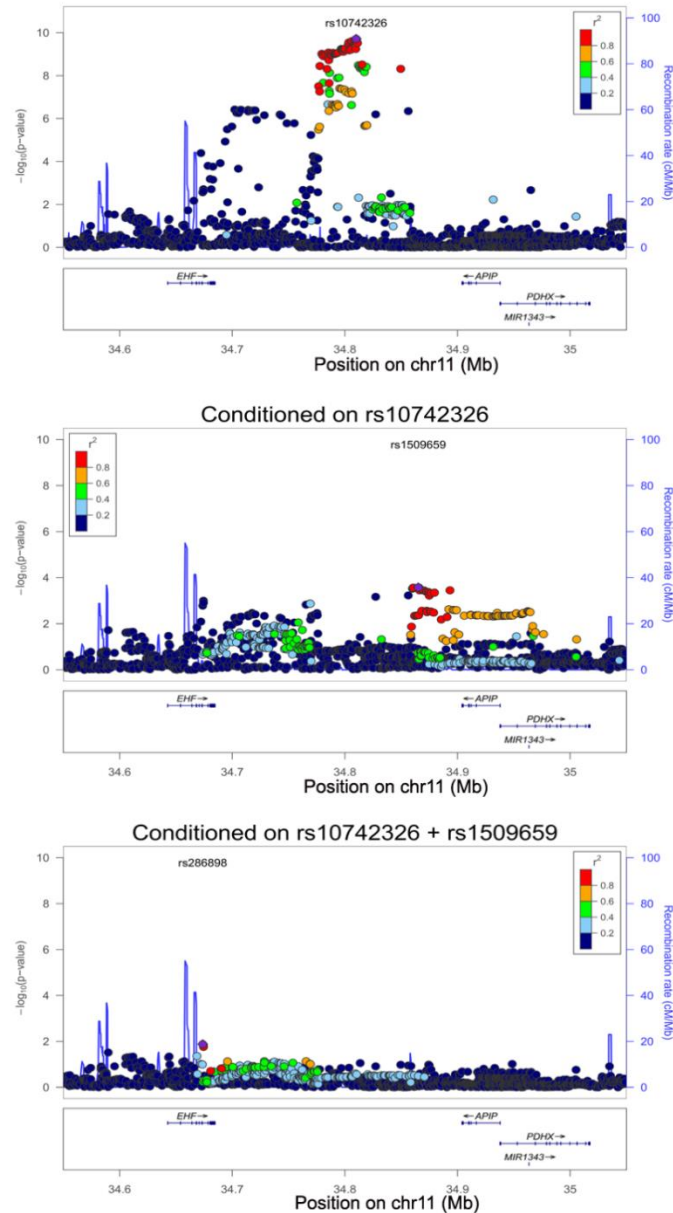
a



Supplementary Figure 5 (and next page)

Conditional analysis of the associations on chr5p15.3 (a) and 11p12-p13 (b).

b



Supplementary Figure 5 (continued)

Conditional analysis of the associations on chr5p15.3 (a) and 11p12-p13 (b).

GEC software (<http://statgenpro.psychiatry.hku.hk/gec/>) was used to calculate the number of independent tests in each region. (a) The middle plot of this panel shows that after conditioning on the most significant SNP (rs57221529) at chr5p15.3 there are SNPs (near *AHRR*) that meet a regional Bonferroni significance threshold. (b) The middle plot of this panel shows that after conditioning on the most significant SNP (rs10742326) at chr11p12-p13 that there are SNPs (near/over *APIP*) that meet a regional Bonferroni significance threshold. (a,b) The bottom plots show that after conditioning on both SNPs (from the top and middle plots), that neither region has any significant association.

Supplementary Table 1. Associations for highest ranked SNP in each significant region by GWAS1 and/or GWAS2 for all patients and p.Phe508del homozygotes

Gene	Analysis	Effects	Id	Base pair	Minor allele	Minor allele frequency	Coefficient	<i>P</i> value	<i>P</i> value, Europeans	<i>P</i> value, Males	<i>P</i> value, Females
<i>MUC4/MUC20</i> (chr3)	GWAS1&2	Random	rs863582	195,478,694	G	0.33	0.11	1.39×10^{-07}	7.03×10^{-10}	6.84×10^{-07}	2.98×10^{-05}
		Fixed	rs3103933 *	195,485,440	A	0.37	0.12	3.27×10^{-11}	8.11×10^{-11}	1.52×10^{-07}	1.77×10^{-05}
	p.Phe508del/p.Phe508del	Random	rs2688482	195,529,118	T	0.31	0.12	7.22×10^{-08}	3.40×10^{-07}	0.007	6.09×10^{-06}
		Fixed	rs2688482	195,529,118	T	0.31	0.12	7.22×10^{-08}	3.40×10^{-07}	0.001	6.09×10^{-06}
	GWAS2	Random	rs863582	195,478,694	G	0.33	0.11	0.001	7.36×10^{-04}	1.02×10^{-04}	0.015
		Fixed	rs3103933	195,485,440	A	0.37	0.12	1.28×10^{-06}	1.28×10^{-05}	1.27×10^{-04}	0.001
	p.Phe508del/p.Phe508del	Random	rs2688482	195,529,118	T	0.31	0.12	7.64×10^{-05}	3.70×10^{-04}	0.043	8.22×10^{-04}
		Fixed	rs2688482	195,529,118	T	0.31	0.12	7.64×10^{-05}	3.70×10^{-04}	0.015	8.22×10^{-04}
	GWAS1	Random	rs78151003	195,489,534	G	0.45	0.12	4.10×10^{-06}	7.48×10^{-07}	0.012	3.25×10^{-04}
		Fixed	rs78151003	195,489,534	G	0.45	0.12	4.10×10^{-06}	7.48×10^{-07}	0.003	3.25×10^{-04}
	p.Phe508del/p.Phe508del	Random	rs9871110	195,625,326	A	0.47	0.09	1.18×10^{-04}	8.26×10^{-05}	0.003	0.012
		Fixed	3:195522714:GGGA	195,522,714	R	0.26	0.14	6.90×10^{-05}	2.90×10^{-05}	0.023	4.21×10^{-04}
<i>SLC9A3</i> (chr5)	GWAS1&2	Random	rs57221529 *	586,624	G	0.19	-0.16	6.81×10^{-12}	1.00×10^{-11}	1.66×10^{-06}	8.51×10^{-07}
		Fixed	5:584767:G_GGT	584,767	I	0.18	-0.16	4.62×10^{-12}	4.19×10^{-12}	7.58×10^{-07}	1.87×10^{-06}
	p.Phe508del/p.Phe508del	Random	rs56302516	518,434	T	0.24	-0.17	4.16×10^{-09}	5.78×10^{-08}	2.57×10^{-05}	0.049
		Fixed	rs56302516	518,434	T	0.24	-0.17	4.16×10^{-09}	8.49×10^{-10}	2.57×10^{-05}	0.049
	GWAS2	Random	rs57221529	586,624	G	0.19	-0.16	5.33×10^{-07}	2.11×10^{-07}	2.05×10^{-05}	4.42×10^{-04}
		Fixed	5:584767:G_GGT	584,767	I	0.18	-0.16	3.77×10^{-09}	2.20×10^{-09}	9.75×10^{-06}	1.10×10^{-04}
	p.Phe508del/p.Phe508del	Random	rs7726839	618,586	G	0.23	-0.17	1.83×10^{-07}	2.51×10^{-08}	3.01×10^{-05}	0.002
		Fixed	rs55726539	526,807	A	0.26	-0.26	8.69×10^{-06}	9.44×10^{-09}	1.81×10^{-05}	1.57×10^{-10}
	GWAS1	Random	rs56302516	518,434	T	0.24	-0.17	3.89×10^{-07}	5.40×10^{-07}	2.40×10^{-04}	5.03×10^{-04}
		Fixed	rs182219748	443,344	C	0.37	-0.12	1.80×10^{-07}	2.62×10^{-07}	1.12×10^{-04}	5.87×10^{-04}
	p.Phe508del/p.Phe508del	Random	rs4271701	513,785	A	0.39	-0.15	1.12×10^{-05}	1.14×10^{-05}	0.003	0.014
		Fixed	rs4271701	513,785	A	0.39	-0.15	1.12×10^{-05}	1.14×10^{-05}	0.003	0.001
<i>HLA-DRA</i> (chr6)	GWAS1&2	Random	rs140348826	32,434,135	A	0.33	-0.10	6.29×10^{-07}	5.93×10^{-05}	0.011	2.24×10^{-05}
		Fixed	rs117230773 *	32,433,741	A	0.36	-0.13	1.71×10^{-09}	7.18×10^{-09}	1.06×10^{-04}	5.66×10^{-06}
	p.Phe508del/p.Phe508del	Random	rs643889	32,575,918	T	0.33	-0.10	4.96×10^{-05}	1.11×10^{-04}	0.124	0.006
		Fixed	rs117230773	32,433,741	A	0.36	-0.13	3.56×10^{-06}	7.00×10^{-06}	0.034	3.17×10^{-05}
	GWAS2	Random	rs114742324	32,657,351	C	0.31	-0.10	3.87×10^{-04}	8.26×10^{-04}	0.012	0.192
		Fixed	rs114742324	32,657,351	C	0.31	-0.10	3.87×10^{-04}	8.26×10^{-04}	3.90×10^{-04}	0.104
	p.Phe508del/p.Phe508del	Random	rs116476006	32,375,431	C	0.09	-0.16	0.003	0.010	0.087	0.012
		Fixed	rs116476006	32,375,431	C	0.09	-0.16	0.003	0.010	0.087	0.012
	GWAS1	Random	rs117230773	32,433,741	A	0.36	-0.13	2.02×10^{-09}	1.81×10^{-08}	1.02×10^{-04}	8.66×10^{-06}
		Fixed	rs117230773	32,433,741	A	0.36	-0.13	2.02×10^{-09}	1.81×10^{-08}	1.02×10^{-04}	8.66×10^{-06}
	p.Phe508del/p.Phe508del	Random	rs117230773	32,433,741	A	0.36	-0.13	5.41×10^{-07}	1.05×10^{-06}	0.013	1.92×10^{-05}
		Fixed	rs114656294	32,433,276	G	0.50	0.15	2.60×10^{-07}	8.29×10^{-07}	0.002	3.05×10^{-05}
<i>APIP/EHF</i> (chr11)	GWAS1&2	Random	rs7112043	34,789,386	T	0.41	0.09	3.74×10^{-09}	6.06×10^{-09}	3.31×10^{-06}	0.003
		Fixed	rs546131	34,851,760	G	0.36	-0.09	3.46×10^{-09}	7.03×10^{-09}	1.37×10^{-05}	2.03×10^{-04}
	p.Phe508del/p.Phe508del	Random	rs10742326 *	34,810,010	A	0.42	0.12	1.92×10^{-10}	1.64×10^{-08}	2.21×10^{-07}	1.71×10^{-05}
		Fixed	rs7929679	34,805,849	G	0.50	0.11	1.91×10^{-10}	1.32×10^{-09}	1.49×10^{-07}	1.39×10^{-05}
	GWAS2	Random	11:34797572:GTTAT	34,797,572	D	0.42	0.07	7.14×10^{-04}	0.002	0.003	0.067
		Fixed	11:34797572:GTTAT	34,797,572	D	0.42	0.07	7.14×10^{-04}	0.002	0.003	0.039

	GWAS2	Random	11:34783993:TC_T	34,783,993	D	0.40	0.08	0.003	0.024	0.022	0.006
	p.Phe508del/p.Phe508del	Fixed	11:34783993:TC_T	34,783,993	D	0.40	0.08	0.003	0.016	0.022	0.005
	GWAS1	Random	rs523246	34,845,011	G	0.28	-0.13	6.05×10^{-09}	8.71×10^{-08}	3.76×10^{-04}	2.97×10^{-04}
	All	Fixed	rs508062	34,843,820	C	0.28	-0.13	6.01×10^{-09}	7.71×10^{-09}	3.67×10^{-04}	1.89×10^{-06}
	GWAS1	Random	rs11032874	34,806,607	G	0.50	0.15	2.32×10^{-10}	8.64×10^{-10}	6.75×10^{-04}	5.91×10^{-05}
	p.Phe508del/p.Phe508del	Fixed	rs11032874	34,806,607	G	0.50	0.15	2.32×10^{-10}	7.18×10^{-10}	1.12×10^{-06}	5.91×10^{-05}
	GWAS1&2	Random	rs5952223 *	115,386,565	T	0.28	0.08	1.83×10^{-09}	1.25×10^{-09}	3.64×10^{-04}	2.84×10^{-05}
	All	Fixed	rs7879546	115,348,275	C	0.48	0.07	1.11×10^{-09}	4.55×10^{-10}	5.49×10^{-06}	1.02×10^{-05}
	GWAS1&2	Random	rs5952123	115,418,444	C	0.36	0.10	6.64×10^{-08}	1.44×10^{-07}	2.79×10^{-04}	0.006
	p.Phe508del/p.Phe508del	Fixed	rs5952223	115,386,565	T	0.28	0.08	3.30×10^{-08}	4.63×10^{-08}	9.49×10^{-06}	8.02×10^{-04}
	GWAS2	Random	rs5952120	115,401,529	C	0.27	0.09	2.29×10^{-06}	5.17×10^{-06}	1.86×10^{-05}	0.054
	All	Fixed	rs5952218	115,382,260	T	0.23	0.10	1.86×10^{-06}	1.32×10^{-06}	5.26×10^{-05}	0.027
	GWAS2	Random	rs5952123	115,418,444	C	0.36	0.10	1.65×10^{-05}	3.51×10^{-05}	0.003	0.159
	p.Phe508del/p.Phe508del	Fixed	rs145287377	115,387,123	C	0.21	0.14	2.48×10^{-06}	2.64×10^{-06}	2.00×10^{-05}	0.110
	GWAS1	Random	rs5952140	115,464,983	C	0.49	-0.08	1.51×10^{-06}	6.61×10^{-07}	7.21×10^{-04}	5.47×10^{-05}
	All	Fixed	rs12559259	115,348,321	G	0.45	0.10	1.66×10^{-07}	4.36×10^{-08}	0.004	8.03×10^{-08}
	GWAS1	Random	rs5952140	115,464,983	C	0.49	-0.08	9.40×10^{-07}	1.52×10^{-06}	2.03×10^{-04}	3.52×10^{-04}
	p.Phe508del/p.Phe508del	Fixed	rs12559259	115,348,321	G	0.45	0.10	2.23×10^{-07}	2.81×10^{-07}	0.001	1.38×10^{-05}

*Asterisks indicate SNPs of maximum significance between random- and fixed-effects meta-analysis and between all CFTR genotypes and p.Phe508del homozygotes P-values are derived from a meta-analysis using inverse variance-based weighting.

Supplementary Table 2. Replication-based analysis

Chr	SNP	<i>P</i> value, North American ^a	<i>P</i> value, French ^a
3	rs3103933	3.6×10^{-8}	8.7×10^{-5}
5	rs57221529	2.7×10^{-10}	0.003
6	rs116003090	4.1×10^{-8}	0.054 ^b
11	rs10742326	9.3×10^{-9}	0.003
X	rs5952223	9.8×10^{-7}	1.8×10^{-4}

^aMeta-analysis *P* values based on a fixed effects model, for the 11 North American and two French subgroups. ^b*P* values ranged from 0.030 to 0.054 for the six imputed SNPs that exceeded genome-wide significance in the meta-analysis.

Supplementary Table 3. eQTLs in lung, whole blood, LCLs and monocytes

A. GTEx: eQTLs for top-ranked GWAS SNP at each locus^a

Chr	SNP	transcript	Lung eQTL <i>P</i> value	Blood eQTL <i>P</i> value
3	rs3103933	<i>MUC20</i>	0.001	3.6 x 10 ⁻⁴
		<i>AC0695133</i>	0.005	0.001
		<i>SDHAP2</i>	0.012	0.018
		<i>MUC4</i>	0.498	N/A
5	rs57221529	<i>EXOC3</i>	0.017	0.002
		<i>CTD-2228K2.7</i>	0.022	0.042
		<i>SLC9A3</i>	0.179	0.054
		<i>TPPP</i>	0.236	0.017
6	rs116003090	<i>HLA-DRB1</i>	2.4 x 10 ⁻⁸	8.1 x 10 ⁻¹⁰
		<i>HLA-DRB5</i>	0.005	0.043
		<i>HLA-DRA</i>	0.040	0.29
		<i>BTNL2</i>	0.026	0.49
11	rs10742326	<i>APIP</i>	2.7 x 10 ⁻⁶	0.02
		<i>EHF</i>	0.19	0.07
X			N/A	N/A

B. GTEx: Top-ranked eQTL at each locus^b

Chr	SNP	<i>r</i> ² ‡	transcript	Lung eQTL <i>P</i> value	Blood eQTL <i>P</i> value
3	rs2550262	0.67	<i>MUC20</i>	0.001	1.3 x 10 ⁻⁴
			<i>AC0695133</i>	0.006	2.9 x 10 ⁻⁴
			<i>SDHAP2</i>	0.008	0.020
			<i>TNK</i>	0.11	0.036
			<i>MUC4</i>	0.41	N/A
5	rs72703080	0.62	<i>CTD-2228K2.7</i>	6.4 x 10 ⁻⁴	0.002
			<i>SLC9A3</i>	0.012	0.013
			<i>EXOC3</i>	0.023	0.011
			<i>TPPP</i>	0.589	0.032
6	rs146014754	0.79	<i>DRB1</i>	1.7 x 10 ⁻⁹	3.7 x 10 ⁻¹¹
			<i>DRB5</i>	6.0 x 10 ⁻⁵	7.9 x 10 ⁻⁴
			<i>DRA</i>	0.032	0.39
			<i>BTNL2</i>	0.031	0.60
11	rs72920721	0.91	<i>APIP</i>	5.4 x 10 ⁻⁷	0.006
			<i>EHF</i>	0.14	0.055
X				N/A	N/A

C. Other eQTL Databases: Top-ranked eQTL at each locus^c

Chr	SNP	<i>r</i> ² ‡	transcript	UChicago SCAN LCL eQTL <i>P</i> value	UNC seeQTL LCL or monocyte Q value
3	rs844518	0.63	<i>MUC20</i>	N/A	0.016
6	rs9268853	0.96	<i>HLA-DRB1</i>	5.0 x 10 ⁻⁷	0.003
			<i>HLA-DRB5</i>	5.0 x 10 ⁻⁷	5.2 x 10 ⁻²⁴
			<i>HLA-DRA</i>	N/A	2.1 x 10 ⁻⁴
11	rs1588355	0.66	<i>APIP</i>	N/A	6.5 x 10 ⁻⁴

eQTL *P* values from association testing in a linear regression model.

^a eQTLs and genes with nominal *P* value < 0.05 in either lung and/or whole blood; data for two other genes (*MUC4* and *EHF*) are also shown, given biological plausibility for role in lung disease. N/A= not available. *P* values < 0.002 meet Bonferroni criteria (<http://statgenpro.psychiatry.hku.hk/gec/>) for significance at $\alpha = 0.05$.

^b Top-ranked regional eQTL *P* values (with ‡ *r*² > 0.6 with top-ranked GWAS SNPs from 3A, above).

^c *P* values < 10⁻⁵ considered "significant" in the SCAN database, while seeQTL reports *Q* values for all cis-associations.

Supplementary Table 4. Association in GWAS1+2 for previously reported variants in candidate genes

Gene/locus	Chr	Variant rs#	Aliases	Previously reported phenotype(s)	Previously reported association <i>P</i> value	Previously reported number of subjects	<i>P</i> value, GWAS1+2 all (<i>n</i> = 6,365)	<i>P</i> value, GWAS1+2 p.Phe508del/p.Phe508del (<i>n</i> = 4,139)
8.1AH	6	rs909253	+252 A>G	FEV ₁ % pred	<0.04	404 ^{a,1}	0.88	0.69
		rs1800629	-308 G>A				0.53	0.08
		rs1061581	1267 A>G				NA	NA
		rs1800625	-429 T>C				0.1076	0.3918
A1AT	14	rs17580	S allele	FEV ₁ % pred	0.043	157 ² 215 ³ 79 ⁴	0.34	0.36
		rs28929474	Z allele				0.76	0.83
ABCC1	16	rs504348	4741 C>G	Age at which FEV ₁ <60%	<0.05	203 ⁵	0.64	0.97
ACE	17	none	indel	Age at which FEV ₁ <50%	0.03	261 ⁶	Not tested	Not tested
ADBR2	5	rs1042713	Arg16Gly	FEV ₁ % pred	<0.05	126 ⁷	0.42	0.63
				FVC	<0.05			
				Flows at lower lung volumes	<0.01			
				Longitudinal FEV ₁	<0.01			
AGER	6	rs1800625	-429T>C	FEV ₁	0.02	967 ^{a,8}	0.11	0.39
				CF-specific percentile z-score	0.03			
				KNORMA	0.03			
CEACAM3	19	rs6508999 to rs10414823		Disease severity	0.0469 ^b	37 nuclear families ⁹	0.20 ^c 0.19 ^d	0.51 ^c 0.51 ^d
CEACAM6	19	rs1549960 to rs11548735		Disease severity	0.0106 ^b	37 nuclear families ⁹	0.31 ^c 0.22 ^d	0.23 ^c 0.19 ^d
EDNRA	4	rs5335	6672 G>C	Longitudinal FEV ₁	0.002	1,577 ¹⁰	0.13	0.19
GCLC	6	none	(GAG) _n	FEV ₁ % pred	0.097	440 ¹¹	Not tested	Not tested
					0.001 (mild) 0.533 (severe)			
GSTM1	1	none	GSTM1*0/ GSTM1*0	FEV ₁ % pred	0.16	53 ¹² 194 ¹³ 60 ¹⁴	Not tested	Not tested
				Chrispin-Norman score	0.02			
				Shwachman score	0.04			
GSTM3	1	rs1799735	GSTM3*A GSTM3*B	FEV ₁	0.01	146 ¹⁵	NA	NA
				FVC	0.002			
HFE	6	rs1800562 and/or rs1799945	C282Y and/or H63D	FEV ₁ % pred	0.03	82 ¹⁶	0.29	0.20
				FVC% pred	0.02			
				Annual change in FEV ₁ % pred	0.003			
				Annual change in FVC% pred	0.001			
HMOX1	22	rs2071749	11354 A>G	FEV ₁ % pred	0.01	755 ^{a,17}	0.12	0.15
		rs7817	57460 C>T	Cross-sectional measures of lung function	0.004	320 ¹⁸		
IFRD1	7			Longitudinal measures of lung function	0.016			

		rs3807213	47556 G>T	FEV ₁ % pred (adjusted) Longitudinal measures of lung function	No Association 0.080	1,978 ¹	0.95	0.45
		rs6968084	38923 C>T	Cross-sectional measures of lung function	0.082		0.81	0.84
<i>IL1b</i>	2	rs1143634 rs1143639		Longitudinal FEV ₁	0.120 0.057	808 ^{a,19} 126 families ^{a,19}	0.33 0.34	0.23 0.23
<i>IL8</i>	4	rs2227306 rs2227307 rs2227543 rs4073	+781C>T +396T>G -251 A>T	Longitudinal FEV ₁	0.19 0.04 0.06 0.07	737/385 ^{a,20} 727/385 ^{a,20} 732/385 ^{a,20} 733/385 ^{a,20}	0.06 0.11 0.06 0.06	0.29 0.23 0.28 0.12
<i>MBL2</i>	10	rs1800450 rs1800451	X1 – B (A>G) X1 – C (A>G)	FEV ₁ % FVC%	0.003 0.03	149 ²¹ 164 ²² 179 ²³ 298 ²⁴ 47 ²⁵ 135 ²⁶ 254 ²⁷ 105 ²⁸	0.79 0.95	0.34 0.66
<i>NOS1</i>		none	(GT) ₁₈₋₃₆	Longitudinal FEV ₁	0.025	59 ²⁹ 40 ³⁰	Not tested	Not tested
<i>NOS3</i>	7	rs1799983	894 G>T	FEV ₁	0.08 (in females)	70 ³¹	0.88	0.84
<i>PPP2R1A</i>	19	rs2162779	c.*465T>A	Functional residual capacity	0.0033	95 ³²	0.91	0.92
<i>PPP2R4</i>	9	rs3118625	c.-185A>C	FEV ₁ Lung clearance index	0.0048 0.0059	95 ³²	1.00	0.61
<i>SERPINA3</i>	14	rs4934	T-15A	FEV ₁ % pred	0.04	157 ³³	0.45	0.53
<i>SFTPA1</i>	10	none	6A ³ & 6A ³ /1A ¹ haplotype	FEV ₁ % pred	0.01	135 ²⁶	Not tested	Not tested
<i>SFTPA2</i>	10	none	1A ¹ & 6A ³ /1A ¹ haplotype	FEV ₁ % pred	0.009 0.13	135 ²⁶	Not tested	Not tested
<i>SLC6A14</i>	23	rs5905283 rs3788766		Longitudinal FEV ₁	0.004 0.0002	815 ^{a,34}	0.23 0.54	0.59 0.34
<i>SLC9A3</i>	5	rs4957061 rs17563161	521096 C>T	Longitudinal FEV ₁ KNoRMA	0.05 1.5 x 10 ⁻⁶	752 ^{a,35} 815 ^{a,34}	5.69 x 10 ⁻⁶ 1.17 x 10 ⁻⁴	7.93 x 10 ⁻⁶ 3.58 x 10 ⁻³
<i>SNAP23</i>	15	rs9302112	c.267-9T>C	FEF ₅₀ Functional residual capacity Volume of trapped gas	0.0088 0.011 0.0043	95 ^{a,32}	0.20	0.61
<i>TGFB1</i>	19	rs1800470 rs1800469	codon 10 C29T C-509T	Age at which FEV ₁ <50% Age at which FVC <70% Impairment of lung function (FEV ₁)	<0.02 <0.005 0.006	171 ³⁶ 808 ^{a,37} 261 ⁶ 808 ^{a,37} 498 ^{a,37} 329 ^{a,38} 105 ²⁸ 472 ^{a,39}	0.78 0.47	0.47 0.54

<i>TNFA</i>	6	rs1800629	G-308A +691G ins/del	Mean FEV ₁ % pred	0.02 0.008	53 ¹² 180 ⁴⁰	0.53	0.08
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Variants previously reported in candidate gene studies (as of May/June 2014) as associating with some aspect of pulmonary function in CF patients (Phenotype Tested) are listed here with their rs#, other names of the variants (aliases), the reported p-values, the number of subjects tested to achieve that p-value and the publication reporting the association. The right-hand columns give the meta-analysis *P* value calculated using inverse variance-based weighting for those variants in this study, both for all subjects enrolled and for p.Phe508del homozygotes. The current study evaluated single nucleotide polymorphism only, so other types of variants, such as insertions or deletions (indels) or variable number of repeats were not tested. ^aThese cohorts are not independent of the current study. ^b*P* value reflects the association of the haplotype to the lung disease. ^c*P* value reflects the association of the first SNP in the previously reported haplotype range to the GWAS1+2 phenotype. ^d*P* value reflects the association of the last SNP in the previously reported haplotype range to the GWAS1+2 phenotype.

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