

Table 1 COPD genetic instrumental variants (IVs)

SNP	EA	OA	EAF	p-value	Beta	SE	Sample size	R ² (%)	F
rs3789044	A	G	0.230	1.86E-06	-0.106	0.022	193,638	0.012	22.76
rs192743950	A	G	0.054	2.60E-07	-0.222	0.043	193,638	0.014	26.55
rs1521046	C	T	0.437	3.53E-06	0.087	0.019	193,638	0.011	21.55
rs2138448	G	A	0.438	1.53E-06	-0.090	0.019	193,638	0.012	23.16
rs469195	T	C	0.160	1.59E-06	-0.122	0.026	193,638	0.012	22.96
rs190861688	A	C	0.010	2.51E-06	0.468	0.100	193,638	0.011	22.16
rs1379933	C	T	0.341	1.29E-06	-0.095	0.020	193,638	0.012	23.39
rs58875428	G	T	0.007	2.12E-06	0.535	0.113	193,638	0.012	22.48
rs172057	T	C	0.992	4.46E-06	-0.512	0.112	193,638	0.011	21.05
rs2637677	G	A	0.225	4.30E-06	0.102	0.022	193,638	0.011	21.09
rs62528367	A	G	0.083	8.60E-07	0.167	0.034	193,638	0.013	24.21
rs79907691	G	A	0.018	1.78E-06	0.341	0.071	193,638	0.012	22.85
rs113623975	G	A	0.101	2.17E-09	-0.187	0.031	193,638	0.018	35.77
rs56199726	C	T	0.058	2.25E-06	0.189	0.040	193,638	0.012	22.33
rs2818388	A	C	0.085	1.64E-07	0.175	0.033	193,638	0.014	27.45
rs144264580	T	C	0.035	4.52E-06	0.236	0.051	193,638	0.011	21.03
rs1925547	G	T	0.266	1.53E-06	0.101	0.021	193,638	0.012	23.13
rs2514168	A	G	0.179	4.74E-06	0.111	0.024	193,638	0.011	21.00
rs79926725	T	C	0.141	2.61E-06	-0.127	0.027	193,638	0.011	22.09
rs4762262	A	C	0.167	1.62E-07	0.131	0.025	193,638	0.014	27.50
rs79765478	C	T	0.139	2.07E-06	0.129	0.027	193,638	0.012	22.53
rs7313179	G	T	0.890	4.68E-06	0.137	0.030	193,638	0.011	20.92
rs117514908	G	C	0.036	3.08E-06	0.234	0.050	193,638	0.011	21.78
rs28929474	T	C	0.020	2.40E-10	0.440	0.070	193,638	0.021	40.14
rs8040868	C	T	0.379	5.84E-28	0.210	0.019	193,638	0.062	120.42
rs2199036	T	C	0.376	4.09E-06	0.088	0.019	193,638	0.011	21.32

rs74571623	C	G	0.015	9.70E-07	0.376	0.077	193,638	0.012	23.96
rs1801272	T	A	0.023	2.82E-07	-0.327	0.064	193,638	0.014	26.37
rs62232252	T	G	0.008	2.73E-06	0.507	0.108	193,638	0.011	21.99

Abbreviations: SNP, single-nucleotide polymorphism; EA, effect allele; OA, other allele; EAF, effect allele frequency; Beta, the regression coefficient based on COPD raising effect allele; SE, standard error; R^2 , the proportion of COPD variance explained by the selected genetic variants; F, F-statistics; COPD, chronic obstructive pulmonary disease.

Table 2 Association of COPD genetic instrumental variants (IVs) with respiratory TB GWAS

SNP	Exposure (COPD)			Outcome (respiratory TB)		
	Beta	SE	p-value	Beta	SE	p-value
rs113623975	-0.187	0.031	2.17E-09	-0.074	0.081	0.3650
rs117514908	0.234	0.050	3.08E-06	-0.031	0.133	0.8139
rs1379933	-0.095	0.020	1.29E-06	0.034	0.052	0.5136
rs144264580	0.236	0.051	4.52E-06	0.075	0.135	0.5807
rs1521046	0.087	0.019	3.53E-06	-0.022	0.049	0.6606
rs172057	-0.512	0.112	4.46E-06	0.711	0.293	0.0152
rs1801272	-0.327	0.064	2.82E-07	0.148	0.165	0.3691
rs190861688	0.468	0.100	2.51E-06	0.046	0.258	0.8590
rs1925547	0.101	0.021	1.53E-06	-0.038	0.056	0.4991
rs192743950	-0.222	0.043	2.60E-07	-0.006	0.113	0.9601
rs2138448	-0.090	0.019	1.53E-06	-0.020	0.049	0.6858
rs2199036	0.088	0.019	4.09E-06	-0.006	0.051	0.9110
rs2514168	0.111	0.024	4.74E-06	0.041	0.063	0.5142
rs2637677	0.102	0.022	4.30E-06	0.113	0.059	0.0545
rs2818388	0.175	0.033	1.64E-07	-0.083	0.087	0.3444
rs28929474	0.440	0.070	2.40E-10	0.116	0.179	0.5152
rs3789044	-0.106	0.022	1.86E-06	-0.150	0.058	0.0102
rs469195	-0.122	0.026	1.59E-06	-0.064	0.067	0.3446
rs4762262	0.131	0.025	1.62E-07	0.031	0.066	0.6439

rs56199726	0.189	0.040	2.25E-06	0.048	0.106	0.6488
rs58875428	0.535	0.113	2.12E-06	1.202	0.325	0.0002
rs62232252	0.507	0.108	2.73E-06	-0.018	0.282	0.9493
rs62528367	0.167	0.034	8.60E-07	0.027	0.089	0.7659
rs7313179	0.137	0.030	4.68E-06	0.180	0.079	0.0235
rs74571623	0.376	0.077	9.70E-07	-0.001	0.196	0.9947
rs79765478	0.129	0.027	2.07E-06	0.037	0.071	0.6060
rs79907691	0.341	0.071	1.78E-06	0.199	0.188	0.2911
rs79926725	-0.127	0.027	2.61E-06	0.041	0.071	0.5659
rs8040868	0.210	0.019	5.84E-28	0.091	0.050	0.0706

Abbreviations: SNP, single-nucleotide polymorphism; Beta, the regression coefficient based on COPD or respiratory TB raising effect allele; SE, standard error; COPD, chronic obstructive pulmonary disease. GWAS: genome wide association study.

Table 3 Respiratory TB genetic instrumental variants (IVs)

SNP	EA	OA	EAF	p-value	Beta	SE	Sample size	R ² (%)	F
rs31343	G	A	0.103	4.17E-06	0.379	0.082	218,448	0.010	21.21
rs33915496	G	A	0.381	4.09E-06	0.237	0.051	218,448	0.010	21.24
rs116751036	G	A	0.064	1.40E-06	0.516	0.107	218,448	0.011	23.30
rs10278079	G	A	0.258	4.11E-06	-0.260	0.056	218,448	0.010	21.22
rs79200236	G	A	0.102	1.30E-06	0.401	0.083	218,448	0.011	23.43
rs72756942	A	T	0.188	2.77E-06	-0.297	0.063	218,448	0.010	21.93
rs117949649	T	C	0.051	3.16E-06	0.540	0.116	218,448	0.010	21.73
rs145571464	A	T	0.043	3.14E-06	0.592	0.127	218,448	0.010	21.71
rs1954228	A	T	0.002	4.74E-06	3.359	0.734	218,448	0.010	20.94
rs11078587	A	T	0.524	1.09E-06	0.240	0.049	218,448	0.011	23.78

Abbreviations: SNP, single-nucleotide polymorphism; EA, effect allele; OA, other allele; EAF, effect allele frequency; Beta, the regression coefficient based on respiratory TB raising effect allele; SE, standard error; R², the proportion of respiratory TB variance explained by the selected genetic variants; F, F-statistics; TB, tuberculosis.

Table 4 Association of respiratory TB genetic instrumental variants (IVs) with COPD GWAS

SNP	Exposure (respiratory TB)			Outcome (COPD)		
	Beta	SE	p-value	Beta	SE	p-value
rs10278079	-0.260	0.056	4.11E-06	-0.013	0.021	0.5482
rs11078587	0.240	0.049	1.09E-06	0.035	0.019	0.0576
rs116751036	0.516	0.107	1.40E-06	-0.028	0.039	0.4742
rs117949649	0.540	0.116	3.16E-06	-0.041	0.043	0.3385
rs145571464	0.592	0.127	3.14E-06	0.037	0.046	0.4214
rs1954228	3.359	0.734	4.74E-06	0.115	0.232	0.6219
rs31343	0.379	0.082	4.17E-06	0.048	0.031	0.1135
rs33915496	0.237	0.051	4.09E-06	-0.001	0.020	0.9489
rs72756942	-0.297	0.063	2.77E-06	0.032	0.024	0.1736
rs79200236	0.401	0.083	1.30E-06	-0.029	0.031	0.3419

Abbreviations: SNP, single-nucleotide polymorphism; Beta, the regression coefficient based on COPD or respiratory TB raising effect allele; SE, standard error; COPD, chronic obstructive pulmonary disease. GWAS: genome wide association study; TB, tuberculosis.