

**eTable 6.** Genetic correlations and genetic overlap between the five trait pairs were estimated by HDL<sup>a</sup>

Trait pair	Genetic correlation	se	<i>P</i> .HDL	<i>P</i> .HDL(adjusted)
AST-COPD	0.7834	0.0576	$4.22 \times 10^{-42}$	$4.22 \times 10^{-41}$
AST-IPF	0.3248	0.0889	$2.59 \times 10^{-04}$	$4.32 \times 10^{-04}$
AST-LC	0.1538	0.0463	$8.86 \times 10^{-04}$	$1.27 \times 10^{-03}$
AST-SNO	0.1561	0.0207	$4.37 \times 10^{-14}$	$1.46 \times 10^{-13}$
COPD-IPF	0.6094	0.1474	$3.54 \times 10^{-05}$	$7.08 \times 10^{-05}$
COPD-LC	0.7097	0.0930	$2.35 \times 10^{-14}$	$1.18 \times 10^{-13}$
COPD-SNO	0.1633	0.0271	$1.58 \times 10^{-09}$	$3.95 \times 10^{-09}$
IPF-LC	0.1083	0.1725	$5.30 \times 10^{-01}$	$5.30 \times 10^{-1}$
IPF-SNO	0.2379	0.0948	$1.21 \times 10^{-02}$	$1.51 \times 10^{-02}$
LC-SNO	0.1250	0.0516	$1.55 \times 10^{-02}$	$1.72 \times 10^{-02}$

Abbreviations: HDL, high-definition likelihood method; rg, genetic correlation; se, standard error; AST, Asthma; COPD, Chronic obstructive pulmonary disease; IPF, Idiopathic Pulmonary Fibrosis; LC, Lung Cancer; SNO, Snoring.

<sup>a</sup> HDL was used to estimate the genetic correlation between two traits. A false discovery rate (FDR) was used to correct all *P*.value. The significance threshold was set at *P*.adjusted<0.05. HDL described nearly identical results to LDSC except that IPF and LC suggested no genetic association in HDL.