

Supplementary Table 2. Protein and mRNA expression profiles of implicated genes from single association analyses

Gene	Protein expression				RNA profile			
	Human protein atlas				Human protein atlas		GTEx	
	Nasopharynx	Bronchus	Lung macrophages	Lung pneumocytes	TPM	Category	RPKM	Category
<i>SMIM29(C6orf1)</i>	High	Not detected	Medium	Medium	21.2	Medium	14.8	Medium
<i>HMGA1</i>	Medium	Low	Medium	Not detected	25.9	Medium	27.1	Medium
<i>GIT2</i>	High	Low	High	Low	25	Medium	8.5	Low
<i>TCHP</i>	Medium	Medium	Low	Low	11	Medium	5.8	Low
<i>ARHGEF40</i>	NA	NA	NA	NA	10.2	Medium	15.2	Medium
<i>FAM13A</i>	NA	Medium	Medium	Medium	17.8	Medium	3.4	Low
<i>TNXB</i>	NA	NA	NA	NA	16.4	Medium	20.3	Medium
<i>AGER</i>	Not detected	Not detected	High	Medium	889.2	Medium	424.4	High

Implicated genes were those located at or close to the position of the candidate top 9 single nucleotide polymorphisms. Protein expression are qualitative antibody based protein profiles in the human lung from the Human Protein Atlas. RNA expression is quantitative data estimating the transcript abundance of each protein-coding gene by RNA-seq from the Human Protein Atlas and GTEx.

GTEx, genotype-tissue expression; TPM, transcript per million; RPKM, reads per kilobase gene model and million mapped reads; *SMIM29*, small integral membrane protein 29; *HMGA1*, high mobility group AT-hook 1; *GIT2*, G protein-coupled receptor kinase interacting ArfGAP 2; *TCHP*, trichoplein keratin filament binding protein; *ARHGEF40*, rho guanine nucleotide exchange factor 40; NA, not available; *FAM13A*, family with sequence similarity 13 member A; *TNXB*, tenascin XB; *AGER*, advanced glycosylation end-product specific receptor.