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

<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein expression</th>
<th>RNA profile</th>
<th>Human protein atlas</th>
<th>GTEx</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Nasopharynx</td>
<td>Bronchus</td>
<td>Lung macrophages</td>
<td>Lung pneumocytes</td>
</tr>
<tr>
<td>SMIM29(C6orf1)</td>
<td>High</td>
<td>Not detected</td>
<td>Medium</td>
<td>Medium</td>
</tr>
<tr>
<td>HMGA1</td>
<td>Medium</td>
<td>Low</td>
<td>Medium</td>
<td>Not detected</td>
</tr>
<tr>
<td>GIT2</td>
<td>High</td>
<td>Low</td>
<td>High</td>
<td>Low</td>
</tr>
<tr>
<td>TCHP</td>
<td>Medium</td>
<td>Medium</td>
<td>Low</td>
<td>Low</td>
</tr>
<tr>
<td>ARHGEF40</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>FAM13A</td>
<td>NA</td>
<td>Medium</td>
<td>Medium</td>
<td>Medium</td>
</tr>
<tr>
<td>TNXB</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>AGER</td>
<td>Not detected</td>
<td>Not detected</td>
<td>High</td>
<td>Medium</td>
</tr>
</tbody>
</table>

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.