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SNPs identified by GWAS affect asthma risk through DNA methylation and expression of *cis*-genes in airway epithelium

Soyeon Kim^{1,2,6}, Erick Forno^{1,2,6}, Qi Yan^{1,2}, Yale Jiang^{1,3}, Rong Zhang⁴, Nadia Boutaoui^{1,2}, Edna Acosta-Pérez⁵, Glorisa Canino⁵, Wei Chen^{1,2,7} and Juan C. Celedón^{1,2,7}

Affiliations: ¹Division of Pediatric Pulmonary Medicine, UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA, USA. ²Dept of Pediatrics, School of Medicine, University of Pittsburgh, Pittsburgh, PA, USA. ³School of Medicine, Tsinghua University, Beijing, China. ⁴Dept of Statistics, University of Pittsburgh, Pittsburgh, PA, USA. ⁵Behavioral Sciences Research Institute, University of Puerto Rico, San Juan, Puerto Rico. ⁶Shared first authors. ⁷Shared senior authors.

Correspondence: Juan C. Celedón, Division of Pediatric Pulmonary Medicine, UPMC Children's Hospital of Pittsburgh, 4401 Penn Avenue, Pittsburgh, PA 15224, USA. E-mail: juan.celedon@chp.edu

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Many asthma-susceptibility SNPs are associated with expression of distant *cis*-genes in airway epithelium (AE) through DNA methylation. Over 40% of the genes whose expression in AE is associated with such SNPs are differentially expressed in atopic asthma. <http://bit.ly/2L1rnIk>

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To the Editor:

Over the past 12 years, many genome-wide association studies (GWAS) have been conducted to identify susceptibility variants for asthma [1–5]. The Trans-National Asthma Genetic Consortium (TAGC) recently conducted a large meta-analysis of GWAS [3], identifying 878 single nucleotide polymorphisms (SNPs) associated with asthma at 18 loci. The mechanisms underlying such associations are largely unknown but may include effects on gene expression that alter airway epithelial integrity and function.