



## Author Correction: Multi-ancestry genome-wide association analyses improve resolution of genes and pathways influencing lung function and chronic obstructive pulmonary disease risk

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In the version of the article initially published, the sample sizes in the main text and Supplementary Tables 1 and 2 were incorrect. In the abstract, the last paragraph of the Introduction, the first paragraph of the Results, the top box in Figure 1a and the Supplementary Information,

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# Corrections & amendments

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the total sample size has been corrected from 580,869 to 588,452 participants and the size of the European cohort from 468,062 to 475,645. Some of the effect sizes in Supplementary Table 14 (columns W, Z, AC, AF) had the wrong sign. There was also an error in Supplementary Table 3 where the sample size instead of the variant count was shown for EXCEED. The errors do not affect the conclusions of the study. Additionally, two acknowledgments for use of INTERVAL pQTL and Lung eQTL consortium data were omitted from the Supplementary Information. These errors have been corrected in the Supplementary Information and HTML and PDF versions of the article.

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