## Supplementary Text 1. TOPMed WGSA annotation filters used to define functional variants.

Variants with any matches to the filters below were considered functional variants.

**For SNPs and indels**

ref\_hg19=ref\_hg38 = Y

unique\_variant = Y

VEP\_refseq\_Consequence = transcript\_ablation

VEP\_refseq\_Consequence = splice\_acceptor\_variant

VEP\_refseq\_Consequence = splice\_donor\_variant

VEP\_refseq\_Consequence = stop\_gained

VEP\_refseq\_Consequence = frameshift\_variant

VEP\_refseq\_Consequence = stop\_lost

VEP\_refseq\_Consequence = start\_lost

VEP\_refseq\_Consequence = transcript\_amplification

CADD\_phred > 20

fathmm-MKL\_non-coding\_pred = D

fathmm-MKL\_coding\_pred = D

fathmm-XF\_pred = D

clinvar\_clnsig = Pathogenic

clinvar\_clnsig = Likely\_pathogenic

**Available to SNPs only**

M-CAP\_pred = D

REVEL\_score > 0.5

MutPred\_score > 0.8

SIFT4G\_pred = D

## Supplementary Text 2. Description of UK Biobank and replication analysis

The UK Biobank study is a prospective study with approximately 500,000 participants living in the UK (Bycroft et al. 2018; Sudlow et al. 2015) . All people aged 40 to 69 years who registered in the National Health Service and lived within 25 miles from a study center were invited to participate in 2006-2010. Data were collected using a computer-assisted interview and self-completed questionnaires, and anthropometric assessments were performed. Genome-wide genotyping was performed using the UK Biobank Axiom array from Affymetrix (Bycroft et al. 2018). Imputation was performed using the Haplotype Reference Consortium (HRC) panel as the first choice, and the merged UK10K and 1000 Genomes phase 3 reference panels were used for SNPs not in the HRC panel (Huang et al. 2015). Details on genotyping, imputation, and quality control (QC) of genotype markers for UK Biobank genetic data are described in (Bycroft *et al.* 2018). Quality control spirometry data was undertaken as described in (Shrine *et al.* 2019). We performed a GWAS using a subset of unrelated individuals (N = 627) in the UK Biobank participants who self-identified as black, had lung function measures available and an asthma status according to International Classification of Diseases (ICD) code 493 and/or self-reported doctor diagnosis of asthma. We excluded subjects who had a mismatch between self-reported and genetic sex as determined by chromosomal make-up, sex chromosome configurations that were not XX or XY, or had non-normal heterozygosity and missing rates according to measures provided by the UK Biobank team. At the genotype level, variants with minor allele frequency (MAF) < 0.01 or imputation INFO score measure < 0.3 were excluded. Association tests were conducted using PLINK 2.0 (Chang *et al.* 2015; Purcell and Chang. 2013) with FEV1 as outcome while adjusting for age, sex, height, and five ancestry PCs.

LITERATURE CITED

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