**The details of meta polygenic risk score (metaPRS)**

**1. SNPs selection and generation of trait-specific PRS**

A total of 17 potential lung cancer-related traits were evaluated in this study, including (i) five smoking-related traits: smoking initiation (SI), smoking cessation (SC), cigarettes per day (CPD), age of initiation of regular smoking (AI), and nicotine metabolite ratio (NMR); (ii) four lung function-related traits: forced expired volume in 1-second (FEV1), forced vital capacity (FVC), peak expiratory flow (PEF), and FEV1/FVC; (iii) four chronic lung diseases: COPD, idiopathic pulmonary fibrosis (IPF), interstitial lung disease (ILD), and asthma; as well as (iv) BMI, height, family history of lung cancer (FHLC), and education, which had been widely included in previous lung cancer risk models.1,2 We derived the SNPs that showed genome-wide significance (*P*<5×10-8) from the largest available GWASs of these lung cancer-related traits in European ancestry from the GWAS Catalog.3 **Table S1** lists the details of the source literature for each PRS. To reduce redundancy and minimize the effects of linkage disequilibrium (LD), LD pruning was performed with r2>0.2 in a 1000-kb window for each trait. Imputed genotypes were transformed into PLINK hard calls, and then the trait-specific PRSs were constructed by combining the count of risk alleles (0, 1, or 2) for each individual, which was weighted by the effect size of the variants associated with the specific trait as previously reported.

Besides, a total of nine PRSs had been reported for overall lung cancer in previous studies.4 Here, we also evaluated the performance of these PRSs based on the UKB, and the optimal PRS was used for further construction of the meta polygenic risk score (metaPRS). Moreover, we also included 12 SNPs to construct a PRS for LUAD, seven SNPs to construct a PRS for LUSC, and two SNPs to construct a PRS for small cell lung carcinoma (SCLC) respectively, according to the largest GWASs of lung cancer in Europeans to date.5 Detailed information on the SNPs for each PRS is shown in **Table S2.**

**2 Generation of the metaPRS**

Each PRS was firstly standardized to zero mean and unit standard derivation (SD). Then, we conducted an elastic-net Cox regression using the R package ‘glmnet’ to access the associations between the 21 PRSs and lung cancer risk in the UKB, adjusting for age, sex, genotyping chip, and the top ten principal components of ancestry. Various models with different penalties were assessed using a 10-fold cross-validation method to determine the optimal model. The model that yielded the highest cross-validated area under the receiving-operating characteristic curve (AUC) was chosen as the final model, from which the adjusted coefficients for each PRS were obtained as weights. Finally, the metaPRS can be calculated via a weighted sum:

where β*j* is the coefficient from the penalized Cox regression model, and σj is the empirical SD of each PRS in the UKB.

**3. Code availability**

The code that generates the metaPRS is shown athttps://github.com/guanlian666/MetaPRS-and-lung-cancer (Stable 8+Supplementary Figure 1.R)

**4. Data availability**

The metaPRS data for the PLCO cohort is shown at https://github.com/guanlian666/MetaPRS-and-lung-cancer (PLCO\_metaPRS.Rdata).

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