**Supplemental Table 1.** The role of potential population structure in the associations of the *APOE* ε2 and ε4 alleles with FEV1, FVC and FEV1/FVC in the genotyped LLFS participants.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Trait | Effect  allele | N | Men & Women, Model 1 | | | Men & Women, Model 2 | | |
| Beta | SE | P-value | Beta | SE | P-value |
| FEV1 | ε2 | 3,251 | -15.75 | 22.53 | .484 | -14.03 | 22.53 | .533 |
|  | ε4 | 3,342 | -2.79 | 21.78 | .898 | -3.65 | 21.78 | .867 |
| FVC | ε2 | 3,251 | -24.27 | 26.94 | .368 | -21.96 | 26.94 | .415 |
|  | ε4 | 3,342 | 15.83 | 25.94 | .542 | 15.24 | 25.94 | .557 |
| FEV1/FVC | ε2 | 3,251 | 0.09 | 0.32 | .785 | 0.08 | 0.32 | .808 |
|  | ε4 | 3,342 | -0.72 | 0.30 | .018\* | -0.73 | 0.30 | .016\* |

The ε3/ε3 genotype was considered as the reference.

Model 1: basic adjustments (age, sex, family groups, and field center) only.

Model 2: basic adjustments + first five principal components.

The models were fitted for the sample of men and women combined with no stratification by lung disease status. We excluded individuals with missing information on principal components to match the sample sizes in models 1 and 2. Because of this exclusion, the results in this table for model 1 are slightly different from those in Table 2.

\* denotes significant result (*p-value* < 0.05).