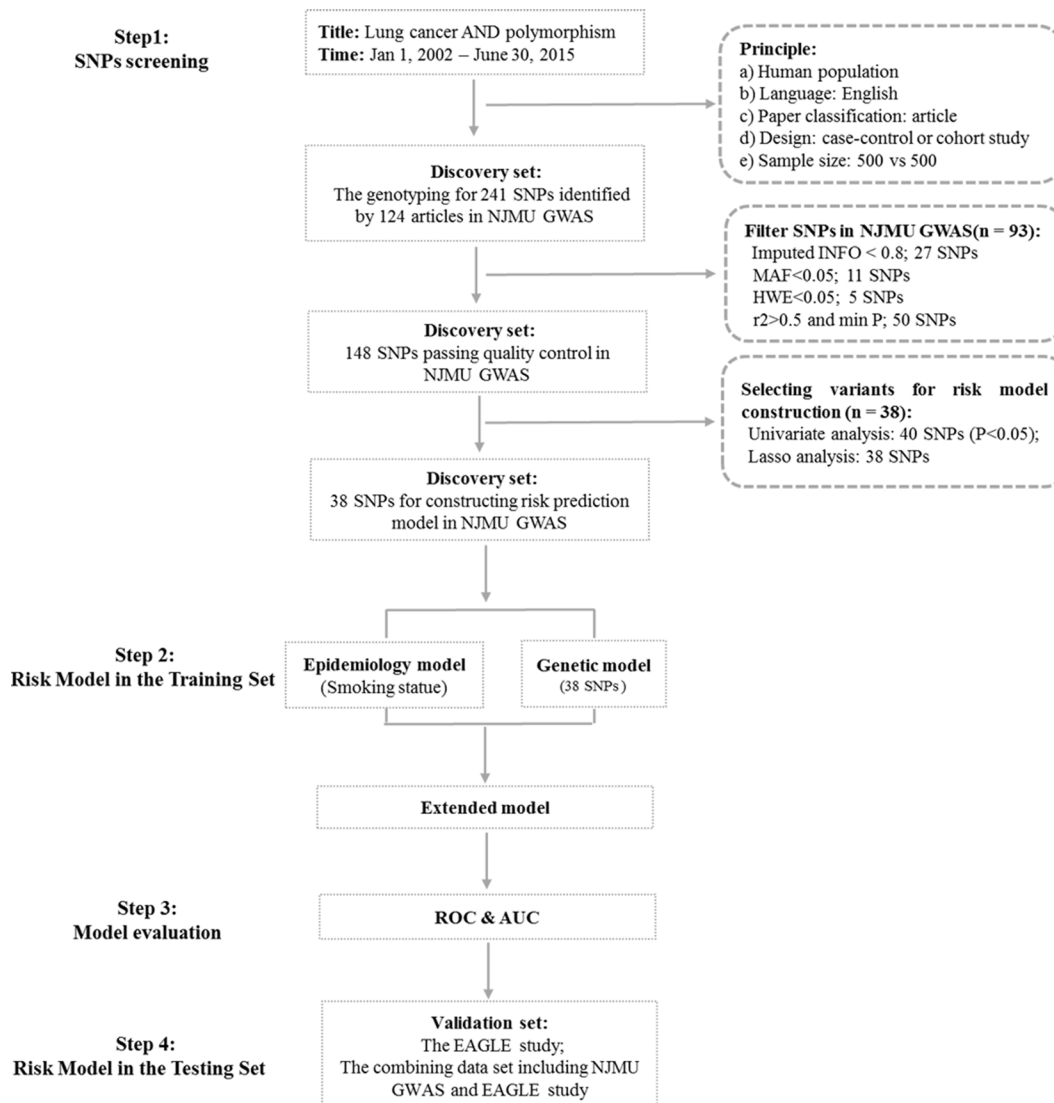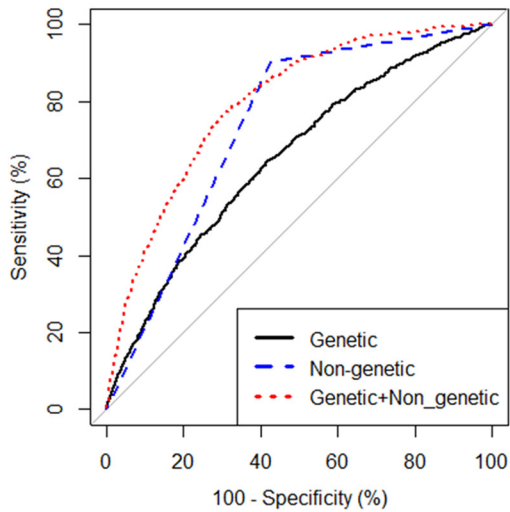# Risk assessment models for genetic risk predictors of lung cancer using two-stage replication for Asian and European populations

Supplementary Materials
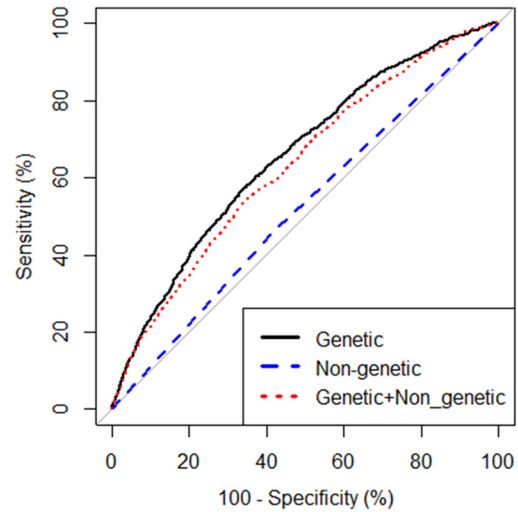

Supplementary Figure S1: The flow chart for genetic variants screening and risk prediction models construction.
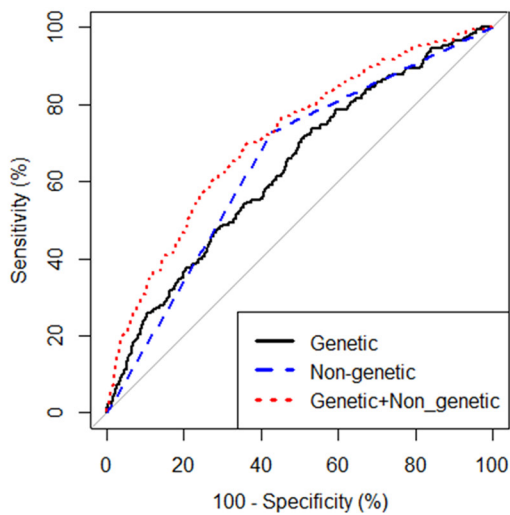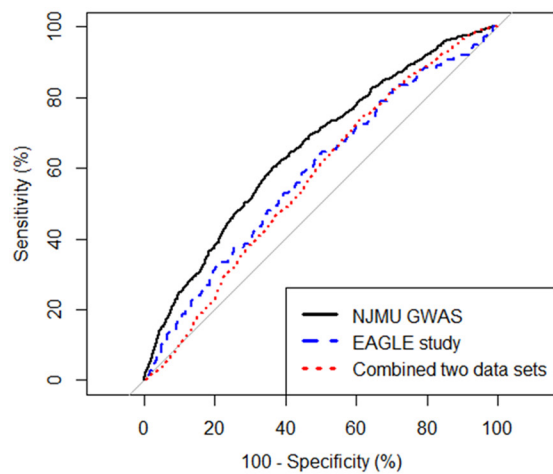
A The ROC curve for squamous carcinoma

B The ROC curve for adenocarcinoma

C The ROC curve for other types

D The epidemiologic ROC curve for non-smokers

Supplementary Figure S2: The area under curves (AUCs) for the different histology of lung cancer risk predicting models calculated by risk score method in discovery data set and the genetic model among the non-smokers in the two data sets. (**A**) For lung squamous carcinoma; (**B**) For lung adenocarcinoma; (**C**) For other histology of lung cancer; (**D**) For genetic model among the non-smokers in the two data sets.

Supplementary Table S1: Distribution of demographic characteristics for cases and controls included in the study

	NJMU GWAS		EAGLE study[a]		The two data sets	
	Case	**Control**	**Case**	**Control**	**Case**	**Control**
	2331 (%)	**3077 (%)**	**1937 (%)**	**1984 (%)**	**4268 (%)**	**5061 (%)**
Age						
< 60	1111 (47.66)	1429 (46.44)	423 (21.84)	502 (25.30)	1534 (35.94)	1931 (38.16)
60–70	799 (34.28)	1045 (33.96)	772 (39.86)	806 (40.63)	1571 (38.81)	1851 (36.57)
≥ 70	421 (18.06)	603 (19.60)	742 (38.30)	676 (34.07)	1163 (27.25)	1279 (25.27)
Sex						
Male	1711 (73.40)	2086 (67.79)	1532 (79.09)	1519 (76.56)	3243 (75.98)	3605 (71.23)
Female	620 (26.60)	991 (32.21)	405 (20.91)	465 (23.44)	1025 (24.02)	1456 (28.77)
Smoke status						
Never	838 (35.95)	1755 (57.04)	138 (7.12)	636 (32.06)	976 (22.87)	2391 (47.24)
Ever	1493 (64.05)	1322 (42.96)	1787 (92.26)	1343 (67.62)	3280 (76.85)	2665 (52.66)

[a]The smoking status has 12 and 5 missing data among the EAGLE study respectively.