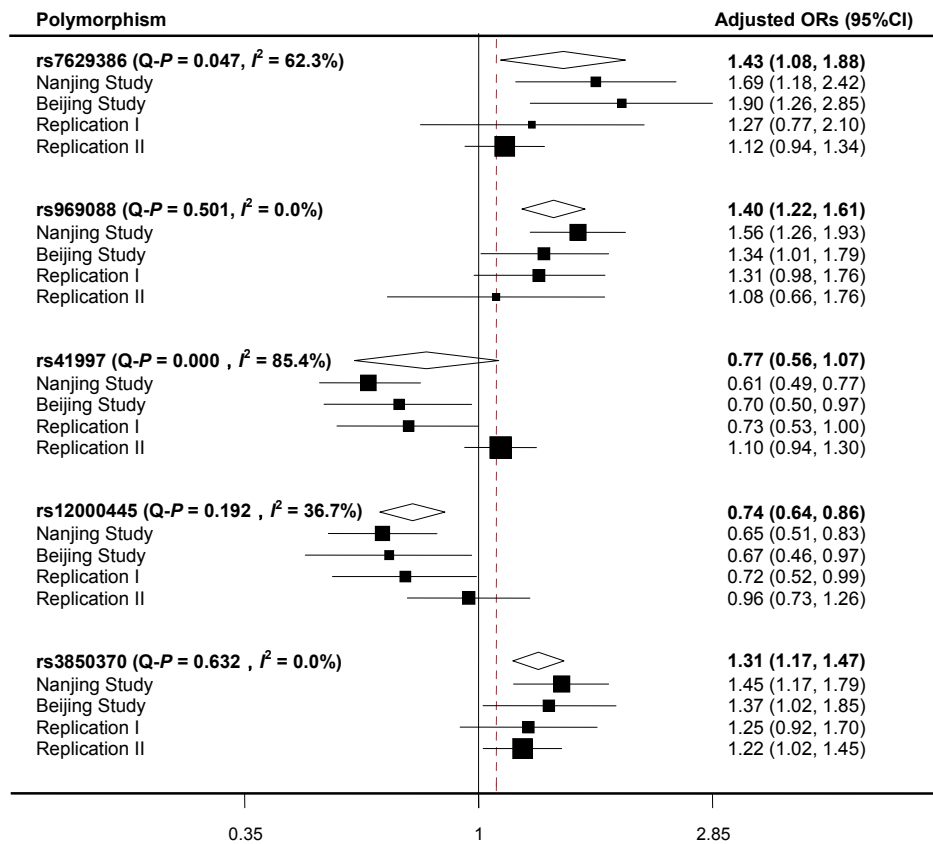Supplementary Table 1.Result for 33 selected SNPs in discovery studies
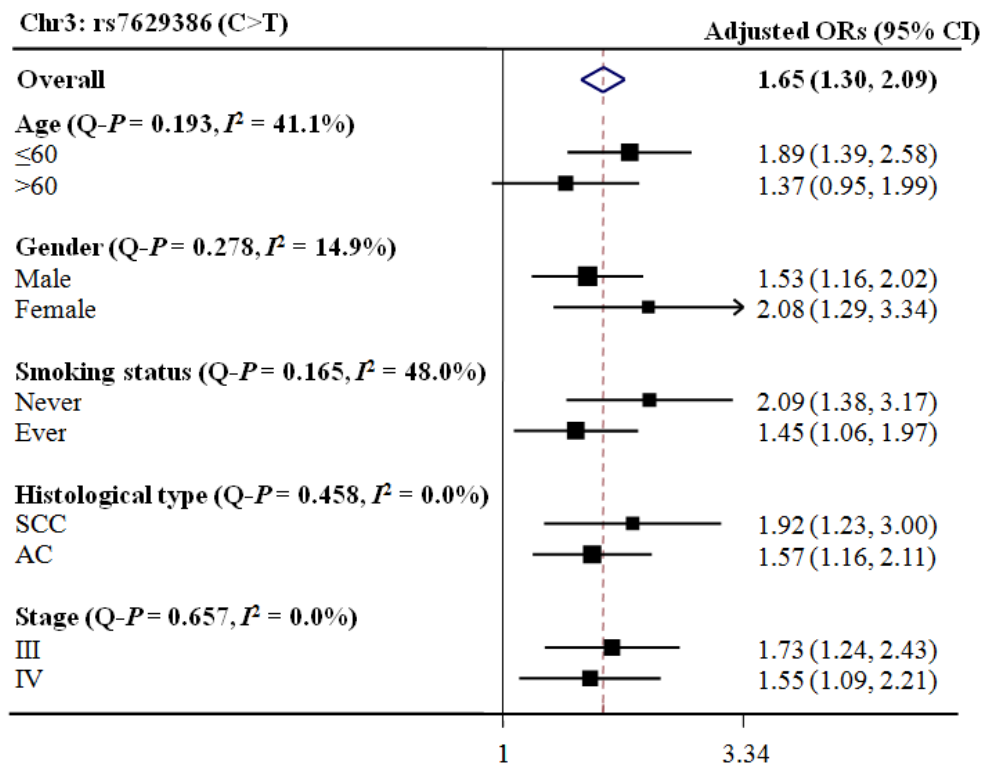
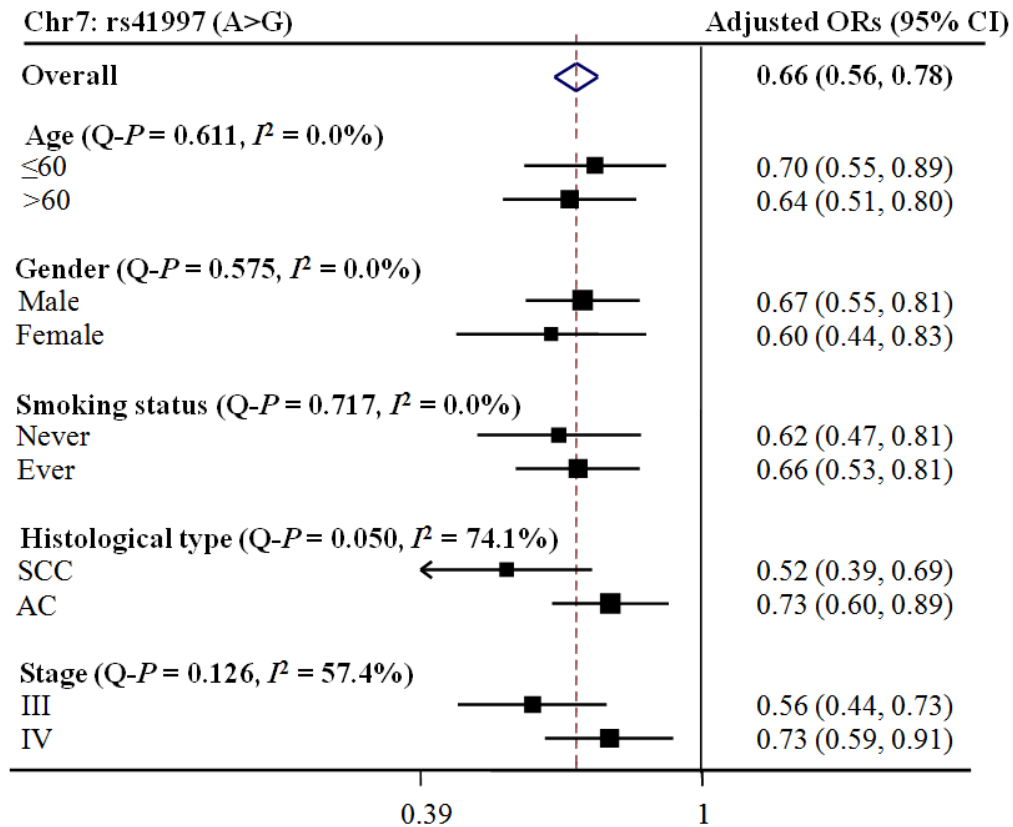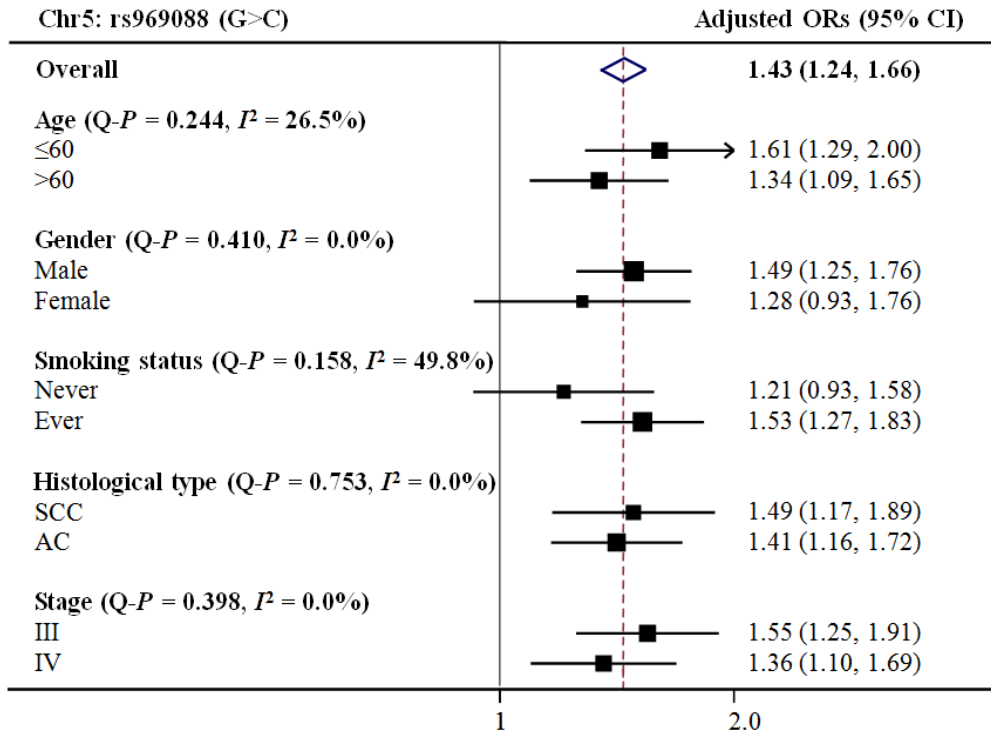| Chr.	SNP	Nanjing Study		Beijing Study		Meta Analysis		
		HR [a]	P [a]	HR [a]	P [a]	HR [b]	P [b]	Q-P [c]
1p13.1	rs12067801	1.85	2.24×10^{-3}	1.97	2.00×10^{-2}	1.89	3.03×10^{-5}	0.85
1p13.1	rs17035658	1.83	2.86×10^{-3}	1.86	3.18×10^{-2}	1.84	6.87×10^{-5}	0.95
2p25.2	rs17019595	1.79	6.51×10^{-4}	1.68	1.67×10^{-2}	1.75	1.25×10^{-5}	0.80
2q21.1	rs6430791	1.45	2.48×10^{-3}	1.51	1.17×10^{-2}	1.47	6.56×10^{-5}	0.85
2q21.1	rs6739473	1.45	2.49×10^{-3}	1.54	8.41×10^{-3}	1.48	4.89×10^{-5}	0.75
2q21.1	rs7573518	1.45	2.75×10^{-3}	1.51	1.17×10^{-2}	1.47	7.29×10^{-5}	0.84
2q21.1	rs7589111	1.47	1.59×10^{-3}	1.54	8.41×10^{-3}	1.50	3.06×10^{-5}	0.81
2q21.3	rs494905	1.87	5.68×10^{-5}	1.61	1.99×10^{-2}	1.77	1.41×10^{-6}	0.53
2q21.3	rs491200	1.53	5.33×10^{-4}	1.45	3.48×10^{-2}	1.50	2.92×10^{-5}	0.78
2q21.3	rs507968	1.50	6.30×10^{-4}	1.43	3.83×10^{-2}	1.48	3.53×10^{-5}	0.83
2q21.3	rs540053	1.53	5.87×10^{-4}	1.44	3.72×10^{-2}	1.50	3.39×10^{-5}	0.79
2q21.3	rs662438	1.51	7.30×10^{-4}	1.44	3.92×10^{-2}	1.49	4.46×10^{-5}	0.81
3p22.1	rs7629386	1.70	6.26×10^{-3}	1.91	3.76×10^{-3}	1.79	2.28×10^{-5}	0.67
5p14.1	rs2319809	1.57	8.51×10^{-5}	1.41	2.08×10^{-2}	1.51	3.73×10^{-6}	0.56
5p14.1	rs969088	1.56	7.78×10^{-5}	1.36	4.06×10^{-2}	1.48	7.38×10^{-6}	0.45
7q31.31	rs1014268	0.63	2.60×10^{-5}	0.7	3.05×10^{-2}	0.65	5.52×10^{-6}	0.58
7q31.31	rs10953870	0.63	2.10×10^{-5}	0.68	1.58×10^{-2}	0.64	2.15×10^{-6}	0.70
7q31.31	rs17584024	0.62	2.13×10^{-5}	0.69	2.40×10^{-2}	0.64	3.70×10^{-6}	0.60
7q31.31	rs17584359	0.62	1.92×10^{-5}	0.71	3.18×10^{-2}	0.65	4.66×10^{-6}	0.51
7q31.31	rs20598	0.62	2.13×10^{-5}	0.67	1.45×10^{-2}	0.64	2.26×10^{-6}	0.71
7q31.31	rs2106595	0.63	1.78×10^{-5}	0.7	2.98×10^{-2}	0.65	3.59×10^{-6}	0.57
7q31.31	rs41988	0.62	2.13×10^{-5}	0.69	1.99×10^{-2}	0.64	3.08×10^{-6}	0.64
7q31.31	rs41997	0.61	1.61×10^{-5}	0.69	2.24×10^{-2}	0.64	2.84×10^{-6}	0.56
7q31.31	rs4727865	0.62	2.05×10^{-5}	0.69	2.37×10^{-2}	0.64	3.51×10^{-6}	0.59
7q31.31	rs6959273	0.64	3.92×10^{-5}	0.7	3.05×10^{-2}	0.66	7.84×10^{-6}	0.62
7q31.31	rs881802	0.62	1.36×10^{-5}	0.72	4.56×10^{-2}	0.65	4.94×10^{-6}	0.45
9p21.3	rs12000445	0.65	2.71×10^{-4}	0.66	2.58×10^{-2}	0.65	3.58×10^{-5}	0.92
9q33.1	rs1331614	1.39	9.26×10^{-4}	1.36	2.96×10^{-2}	1.38	7.53×10^{-5}	0.90
9q33.1	rs2109664	1.41	7.59×10^{-4}	1.39	2.17×10^{-2}	1.40	4.57×10^{-5}	0.93
9q33.1	rs4644327	1.42	6.53×10^{-4}	1.37	3.20×10^{-2}	1.40	5.68×10^{-5}	0.83
12p13.33	rs4980976	1.77	1.22×10^{-3}	1.72	2.59×10^{-2}	1.75	2.55×10^{-5}	0.91
13q32.1	rs9516673	1.46	8.93×10^{-4}	1.39	2.95×10^{-2}	1.43	5.77×10^{-5}	0.79
14q24.3	rs3850370	1.45	7.18×10^{-4}	1.38	3.64×10^{-2}	1.43	5.45×10^{-5}	0.80

[a] Adjusted for age, gender, histology, stage and smoking status in additive genetic model.
[b] Results from the meta analysis
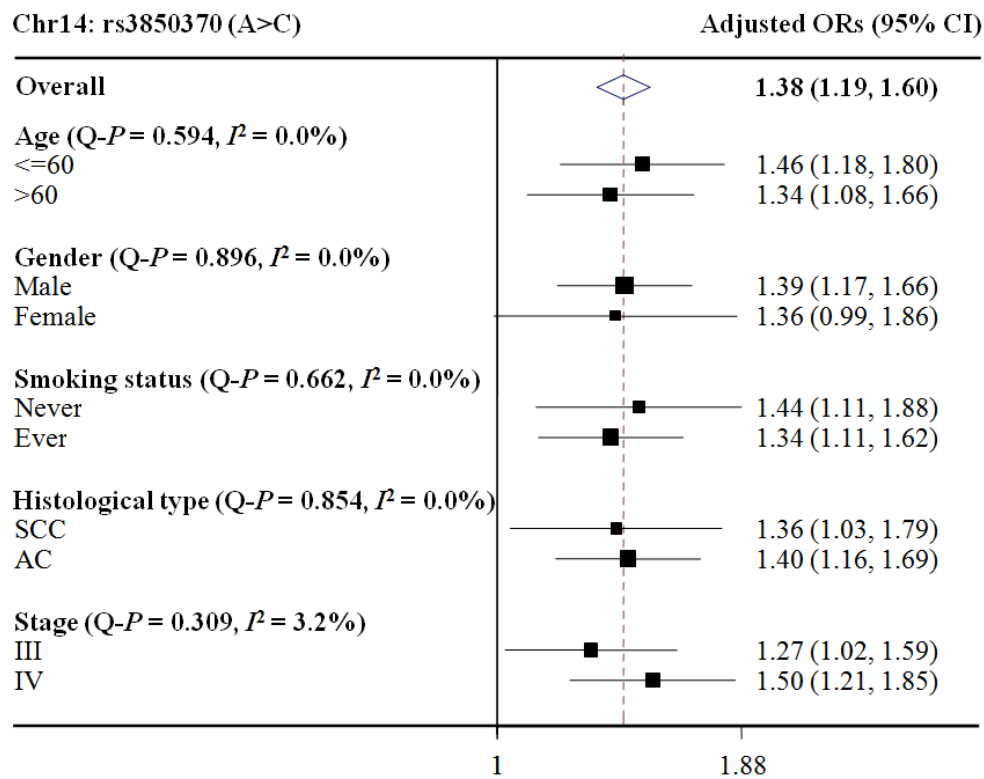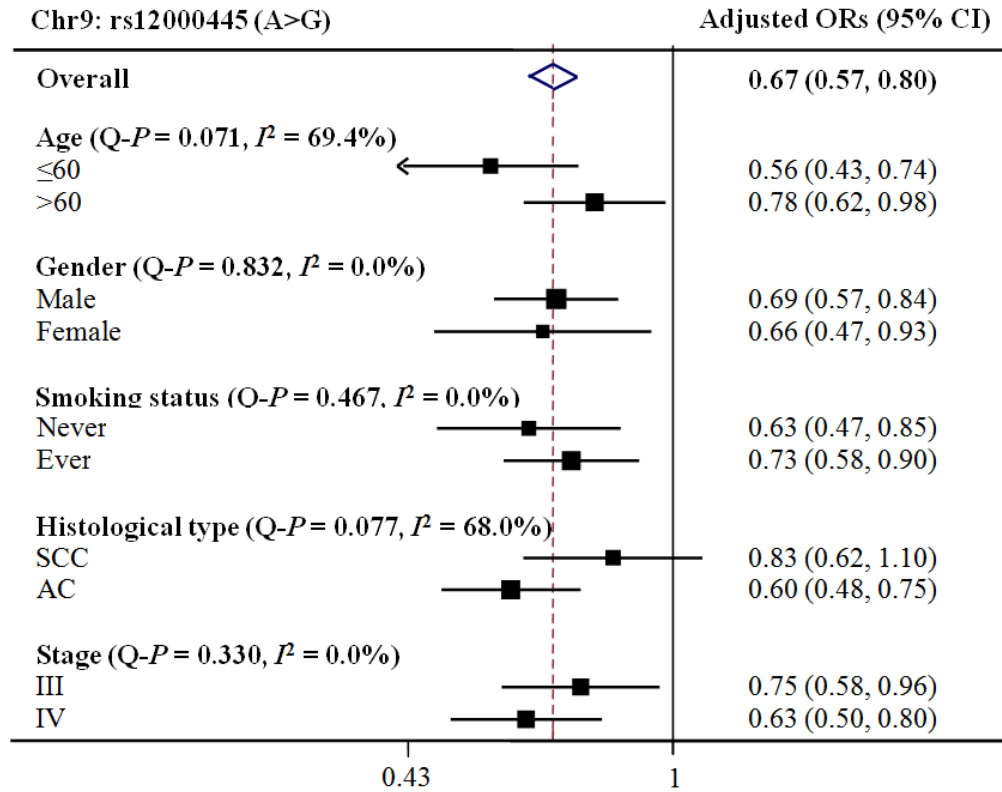[c] P value for Cochrane Q statistics test

Supplementary Figure 1. Forest plot represent the effect of the five identified marker SNPs on NSCLC overall survival among different subgroups in all subjects. I^2 and P values are from heterogeneity tests.

| Polymorphism		Adjusted ORs (95%CI)
rs7629386 (Q-P = 0.047, I^2 = 62.3%)		**1.43 (1.08, 1.88)**
Nanjing Study		1.69 (1.18, 2.42)
Beijing Study		1.90 (1.26, 2.85)
Replication I		1.27 (0.77, 2.10)
Replication II		1.12 (0.94, 1.34)
rs969088 (Q-P = 0.501, I^2 = 0.0%)		**1.40 (1.22, 1.61)**
Nanjing Study		1.56 (1.26, 1.93)
Beijing Study		1.34 (1.01, 1.79)
Replication I		1.31 (0.98, 1.76)
Replication II		1.08 (0.66, 1.76)
rs41997 (Q-P = 0.000 , I^2 = 85.4%)		**0.77 (0.56, 1.07)**
Nanjing Study		0.61 (0.49, 0.77)
Beijing Study		0.70 (0.50, 0.97)
Replication I		0.73 (0.53, 1.00)
Replication II		1.10 (0.94, 1.30)
rs12000445 (Q-P = 0.192 , I^2 = 36.7%)		**0.74 (0.64, 0.86)**
Nanjing Study		0.65 (0.51, 0.83)
Beijing Study		0.67 (0.46, 0.97)
Replication I		0.72 (0.52, 0.99)
Replication II		0.96 (0.73, 1.26)
rs3850370 (Q-P = 0.632 , I^2 = 0.0%)		**1.31 (1.17, 1.47)**
Nanjing Study		1.45 (1.17, 1.79)
Beijing Study		1.37 (1.02, 1.85)
Replication I		1.25 (0.92, 1.70)
Replication II		1.22 (1.02, 1.45)

0.35   1   2.85

Supplementary Figure 2. Forest plots represent the effect of the five identified marker SNPs (rs7629386 at 3p22.1, rs969088 at 5p14.1, rs41997 at 7q31.31, rs12000445 at 9p21.3 and rs3850370 at 14q24.3) on NSCLC overall survival among different subgroups in all Chinese. I^2 and P values are from heterogeneity tests; SCC: squamous cell carcinoma; AC: adenocarcinoma.

Chr3: rs7629386 (C>T)	Adjusted ORs (95% CI)
Overall	1.65 (1.30, 2.09)
Age (Q-P = 0.193, I^2 = 41.1%)	
≤60	1.89 (1.39, 2.58)
>60	1.37 (0.95, 1.99)
Gender (Q-P = 0.278, I^2 = 14.9%)	
Male	1.53 (1.16, 2.02)
Female	2.08 (1.29, 3.34)
Smoking status (Q-P = 0.165, I^2 = 48.0%)	
Never	2.09 (1.38, 3.17)
Ever	1.45 (1.06, 1.97)
Histological type (Q-P = 0.458, I^2 = 0.0%)	
SCC	1.92 (1.23, 3.00)
AC	1.57 (1.16, 2.11)
Stage (Q-P = 0.657, I^2 = 0.0%)	
III	1.73 (1.24, 2.43)
IV	1.55 (1.09, 2.21)

1   3.34

Chr5: rs969088 (G>C) — Adjusted ORs (95% CI)

	Adjusted ORs (95% CI)
Overall	**1.43 (1.24, 1.66)**
Age (Q-P = 0.244, I^2 = 26.5%)	
≤60	1.61 (1.29, 2.00)
>60	1.34 (1.09, 1.65)
Gender (Q-P = 0.410, I^2 = 0.0%)	
Male	1.49 (1.25, 1.76)
Female	1.28 (0.93, 1.76)
Smoking status (Q-P = 0.158, I^2 = 49.8%)	
Never	1.21 (0.93, 1.58)
Ever	1.53 (1.27, 1.83)
Histological type (Q-P = 0.753, I^2 = 0.0%)	
SCC	1.49 (1.17, 1.89)
AC	1.41 (1.16, 1.72)
Stage (Q-P = 0.398, I^2 = 0.0%)	
III	1.55 (1.25, 1.91)
IV	1.36 (1.10, 1.69)

(axis: 1   2.0)

Chr7: rs41997 (A>G) — Adjusted ORs (95% CI)

	Adjusted ORs (95% CI)
Overall	**0.66 (0.56, 0.78)**
Age (Q-P = 0.611, I^2 = 0.0%)	
≤60	0.70 (0.55, 0.89)
>60	0.64 (0.51, 0.80)
Gender (Q-P = 0.575, I^2 = 0.0%)	
Male	0.67 (0.55, 0.81)
Female	0.60 (0.44, 0.83)
Smoking status (Q-P = 0.717, I^2 = 0.0%)	
Never	0.62 (0.47, 0.81)
Ever	0.66 (0.53, 0.81)
Histological type (Q-P = 0.050, I^2 = 74.1%)	
SCC	0.52 (0.39, 0.69)
AC	0.73 (0.60, 0.89)
Stage (Q-P = 0.126, I^2 = 57.4%)	
III	0.56 (0.44, 0.73)
IV	0.73 (0.59, 0.91)

(axis: 0.39   1)

Chr9: rs12000445 (A>G)   Adjusted ORs (95% CI)

Overall	0.67 (0.57, 0.80)
Age (Q-P = 0.071, I^2 = 69.4%)	
≤60	0.56 (0.43, 0.74)
>60	0.78 (0.62, 0.98)
Gender (Q-P = 0.832, I^2 = 0.0%)	
Male	0.69 (0.57, 0.84)
Female	0.66 (0.47, 0.93)
Smoking status (Q-P = 0.467, I^2 = 0.0%)	
Never	0.63 (0.47, 0.85)
Ever	0.73 (0.58, 0.90)
Histological type (Q-P = 0.077, I^2 = 68.0%)	
SCC	0.83 (0.62, 1.10)
AC	0.60 (0.48, 0.75)
Stage (Q-P = 0.330, I^2 = 0.0%)	
III	0.75 (0.58, 0.96)
IV	0.63 (0.50, 0.80)

0.43   1

Chr14: rs3850370 (A>C)   Adjusted ORs (95% CI)

Overall	1.38 (1.19, 1.60)
Age (Q-P = 0.594, I^2 = 0.0%)	
<=60	1.46 (1.18, 1.80)
>60	1.34 (1.08, 1.66)
Gender (Q-P = 0.896, I^2 = 0.0%)	
Male	1.39 (1.17, 1.66)
Female	1.36 (0.99, 1.86)
Smoking status (Q-P = 0.662, I^2 = 0.0%)	
Never	1.44 (1.11, 1.88)
Ever	1.34 (1.11, 1.62)
Histological type (Q-P = 0.854, I^2 = 0.0%)	
SCC	1.36 (1.03, 1.79)
AC	1.40 (1.16, 1.69)
Stage (Q-P = 0.309, I^2 = 3.2%)	
III	1.27 (1.02, 1.59)
IV	1.50 (1.21, 1.85)

1   1.88

5

Supplementary Figure 3. Kaplan-Meier plots of survival for NSCLC by rs7629386. (A) Nanjing discovery set ; (B) Beijing discovery set ; (C) Replication I ; (D) Replication II.

C

D

7
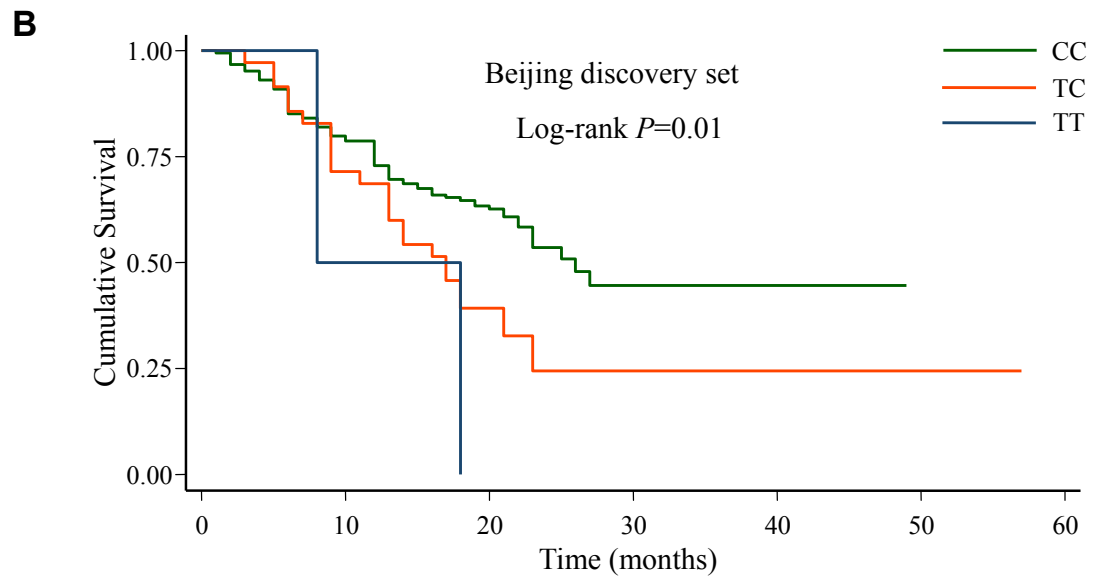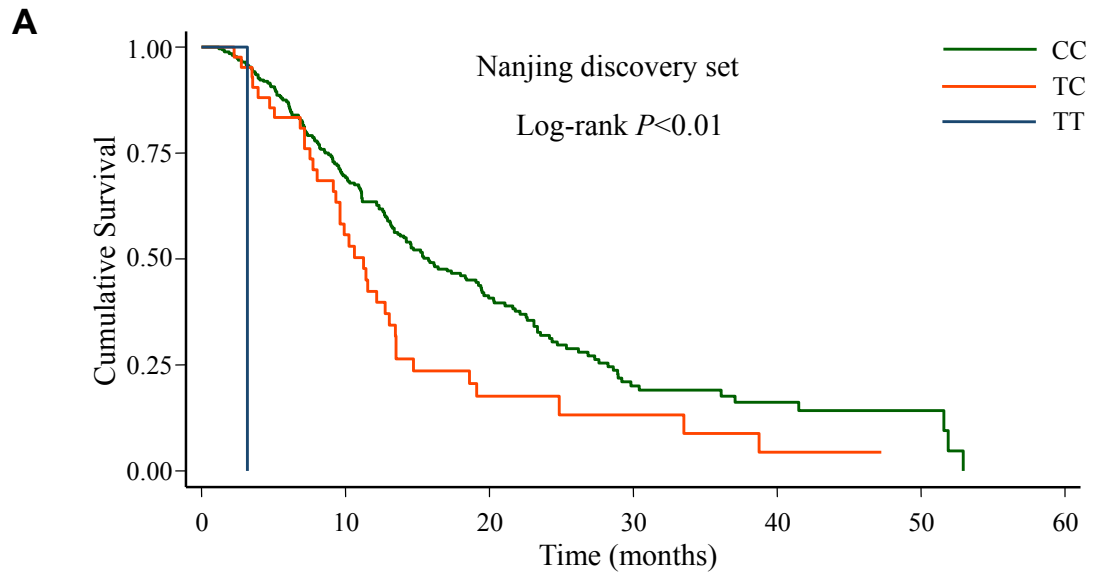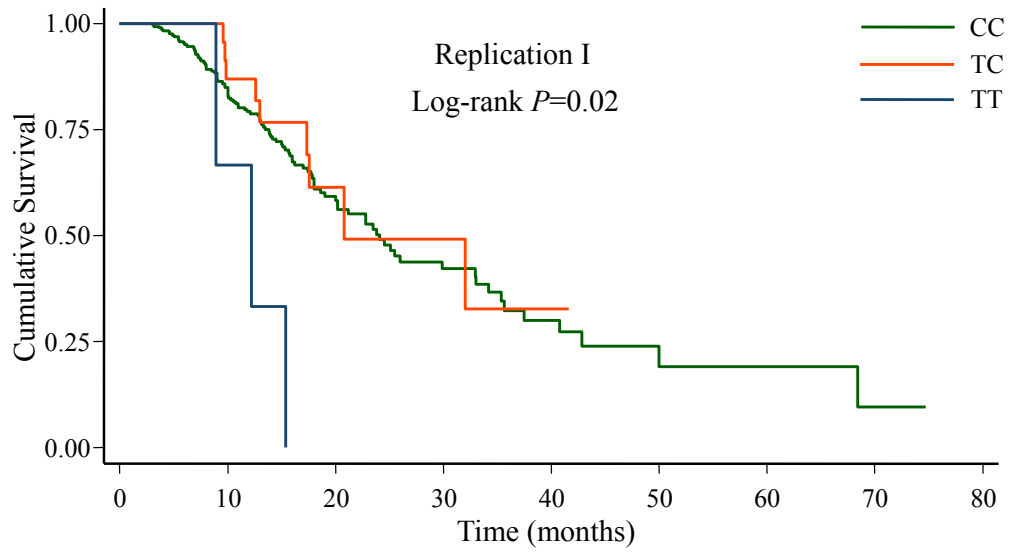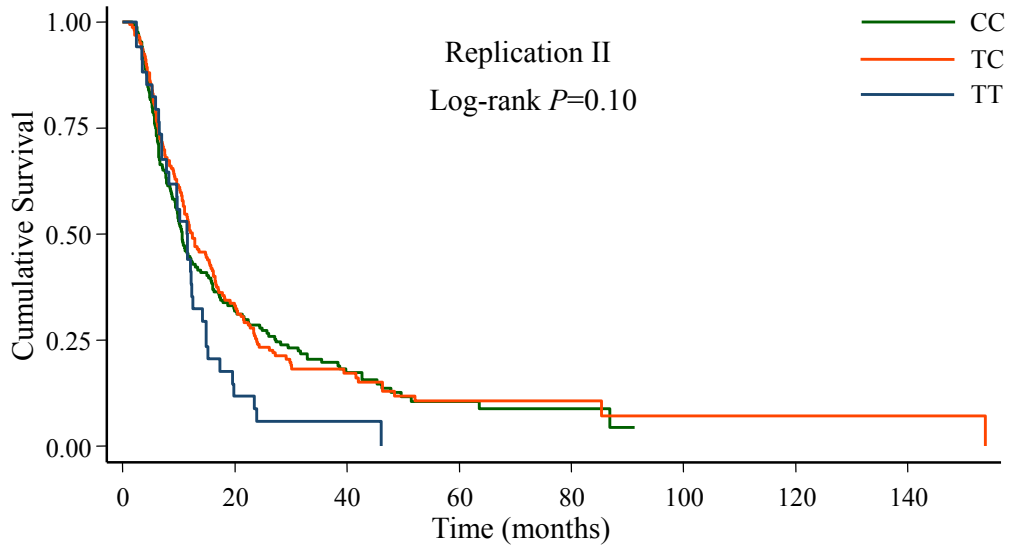
Supplementary Figure 4. Kaplan-Meier plots of survival for NSCLC by rs3850370. (A) Nanjing discovery set ; (B) Beijing discovery set ; (C) Replication I ; (D) Replication II.
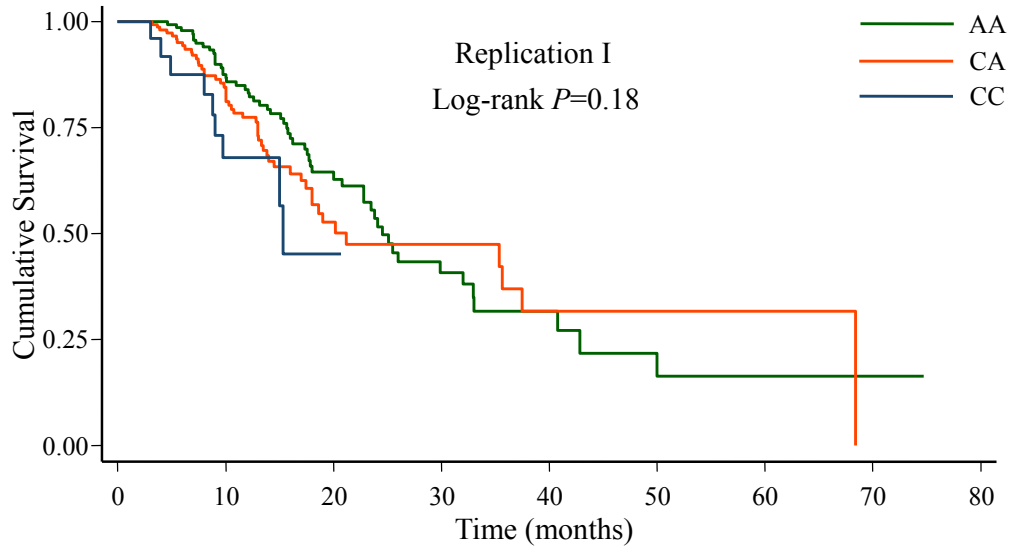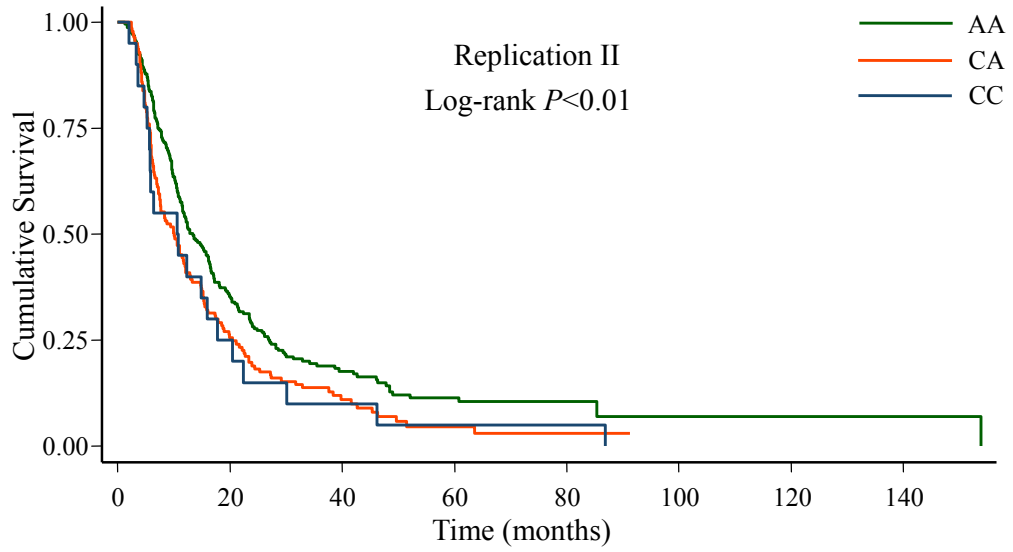
C

Cumulative Survival

Replication I
Log-rank *P*=0.18

AA
CA
CC

1.00
0.75
0.50
0.25
0.00

0   10   20   30   40   50   60   70   80
Time (months)

D

Cumulative Survival

Replication II
Log-rank *P*<0.01

AA
CA
CC

1.00
0.75
0.50
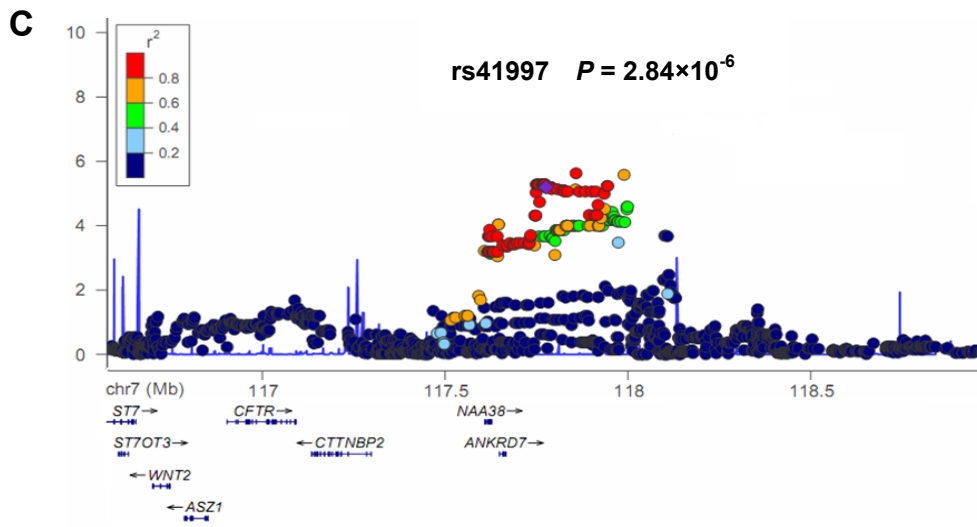0.25
0.00

0   20   40   60   80   100   120   140
Time (months)
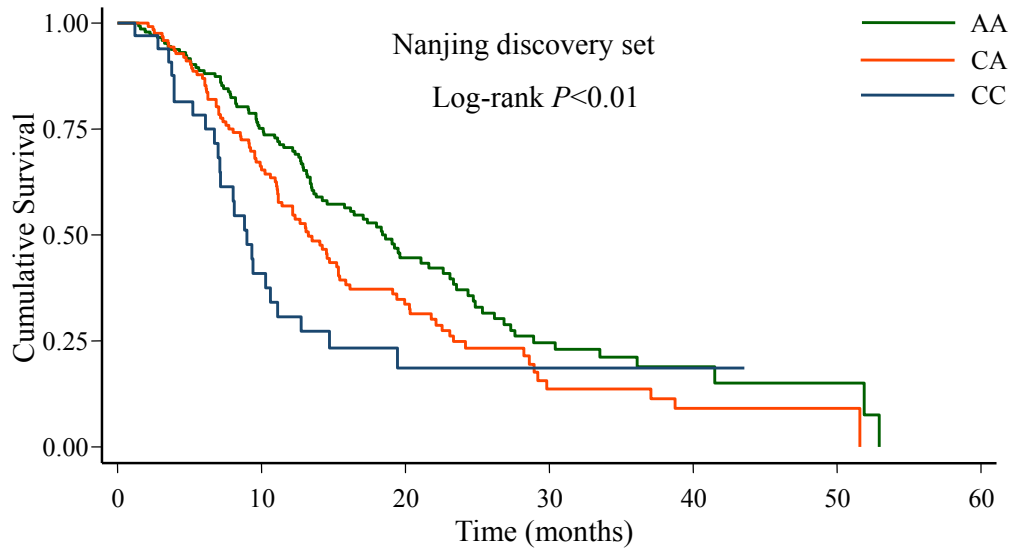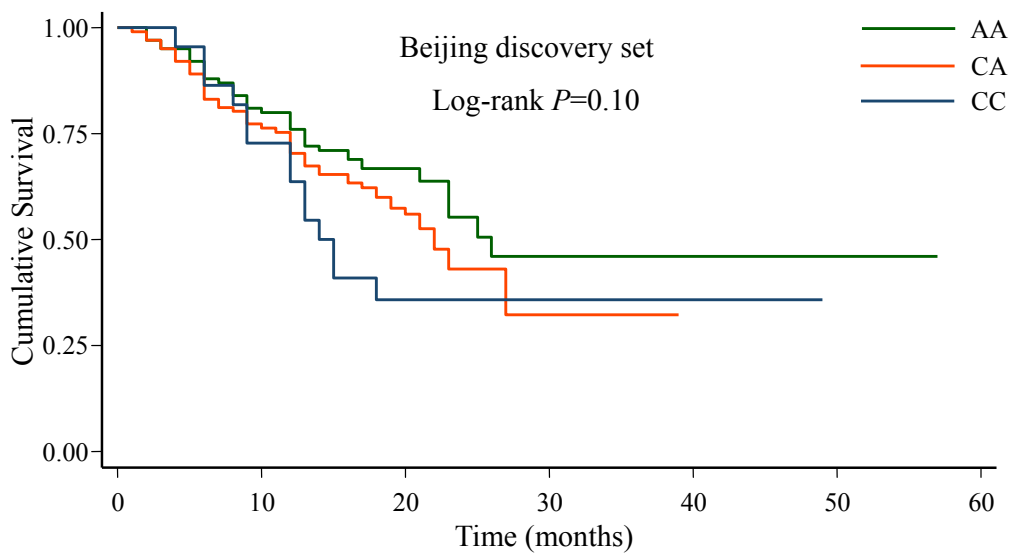
Supplementary Figure 5. Regional plots of ra1878022 and rs10937823 in our GWA scan. Results ($-\log_{10} P$) are shown in the region flanking 1200 kb on either side of the marker SNPs. The marker SNPs were shown in purple diamond and the R^2 values of the rest of the SNPs are indicated by different colors.
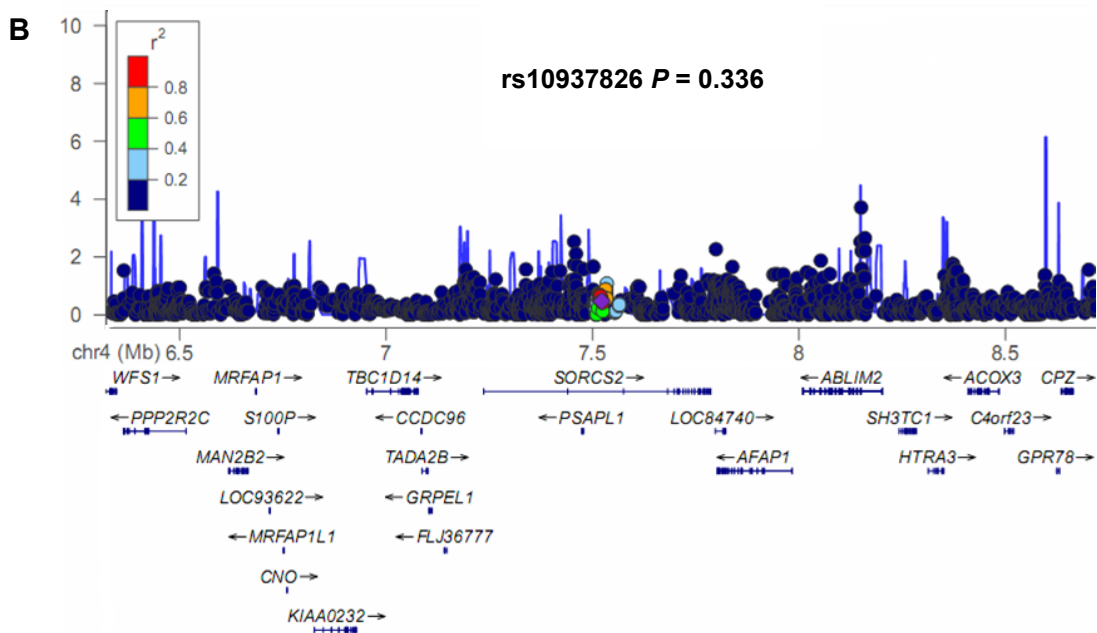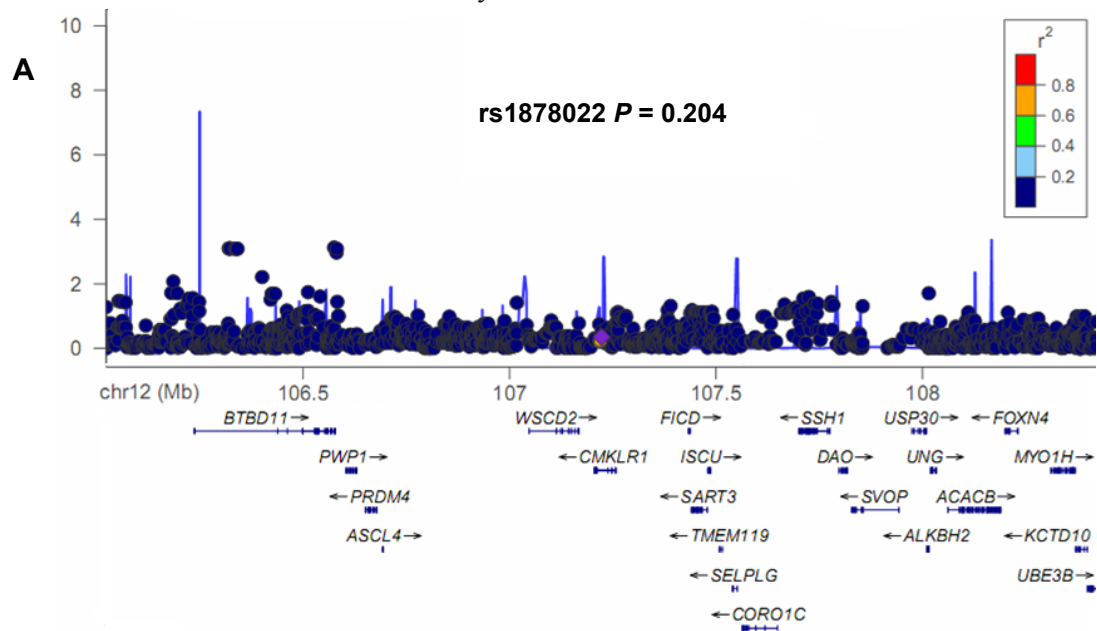
Supplementary Figure 6. Regional plot of the five identified marker SNPs in 535 Han Chinese with GWAS scan. Results ($-\log_{10} P$) are shown in the region flanking 1200 kb on either side of the marker SNPs (1000 kb around rs2109664). The marker SNPs were shown in purple diamond and the R^2 values of the rest of the SNPs are indicated by different colors. (A) Chr3: rs7629386 (C>T); (B) Chr5: rs969088 (G>C); (C) Chr7: rs41997 (A>G); (D) Chr9: rs12000445 (A>G); (E) Chr14: rs3850370 (A>C).

C rs41997 $P = 2.84×10^{-6}$

D rs12000445 $P = 3.58×10^{-6}$

E