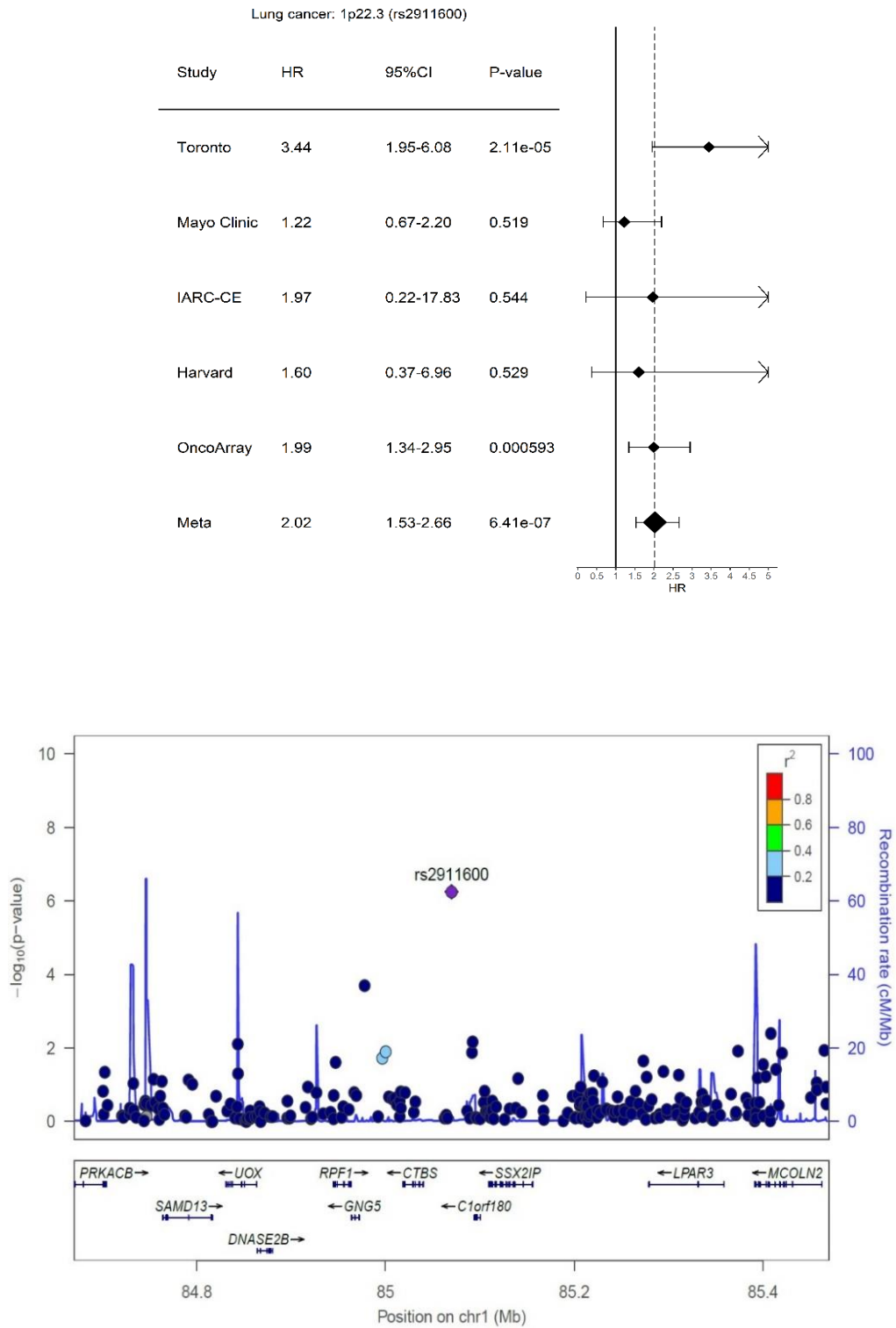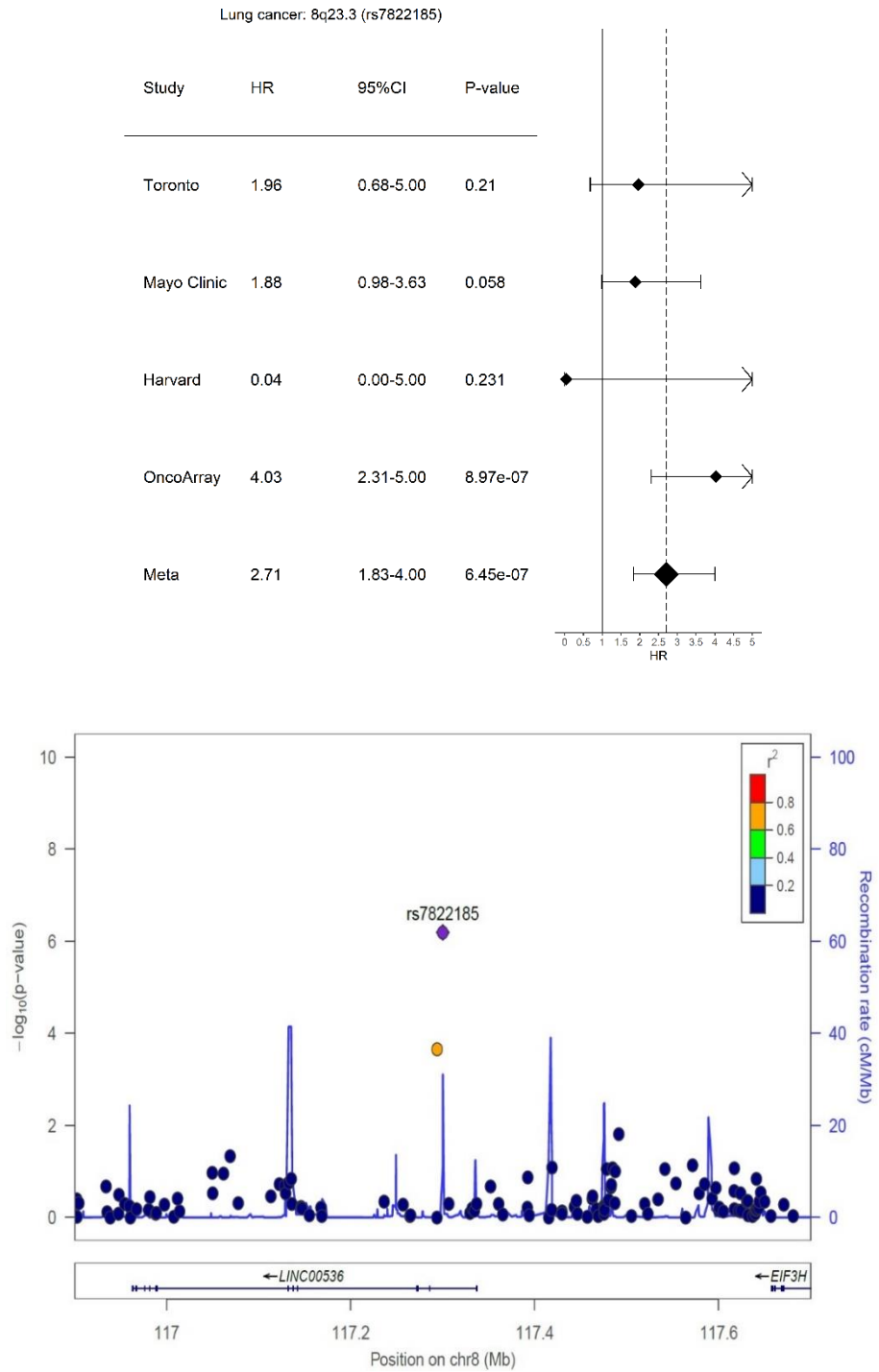**Supplementary Figure 3:** Top panel: forest plots for study-specific hazard ratios (HR) and 95% confidence intervals (CI) for A) 1p22.3- rs2911600 B) 8q23.3 - rs7822185 C) 9q31.3 - rs4978466 D) 10p14 - rs17143938 E) 4p14 - rs17603438 F) 5q11.2 - rs10041935 G) 7p21.3 - rs10247578 H) 10p15.3 - rs17158233 and I) 11q14.1 - rs17148028. Bottom panel: regional plots of association results and recombination rates. For each SNP, association results in the combined GWAS lung cancer cases, -log10P values (y-axis), are shown according to their corresponding chromosomal positions (x-axis) and genetic recombination rates from 1000 Genomes CEU samples. The most significant SNP genotyped labeled by its rsID is denoted by a purple circle. Center panel: Kaplan-Meier plot by genotype of the sentinel variant over 5-year time period.

Supplementary Figure 3A: Forest plot for study specific hazard ratio and regional plot (1p22.3-rs2911600)

Lung cancer: 1p22.3 (rs2911600)

Study	HR	95%CI	P-value
Toronto	3.44	1.95-6.08	2.11e-05
Mayo Clinic	1.22	0.67-2.20	0.519
IARC-CE	1.97	0.22-17.83	0.544
Harvard	1.60	0.37-6.96	0.529
OncoArray	1.99	1.34-2.95	0.000593
Meta	2.02	1.53-2.66	6.41e-07

Supplementary Figure 3B: Forest plot for study specific hazard ratio and regional plot (8q23.3 - rs7822185)

Lung cancer: 8q23.3 (rs7822185)

Study	HR	95%CI	P-value
Toronto	1.96	0.68-5.00	0.21
Mayo Clinic	1.88	0.98-3.63	0.058
Harvard	0.04	0.00-5.00	0.231
OncoArray	4.03	2.31-5.00	8.97e-07
Meta	2.71	1.83-4.00	6.45e-07

Supplementary Figure 3C: Forest plot for study specific hazard ratio and regional plot (9q31.3 - rs4978466)

Lung cancer: 9q31.3 (rs4978466)

Study	HR	95%CI	P-value
Mayo Clinic	0.88	0.72-1.06	0.182
IARC-CE	0.94	0.61-1.43	0.758
Harvard	0.57	0.37-0.86	0.007
MDACC	0.65	0.52-0.83	0.000384
OncoArray	0.76	0.64-0.90	0.001
Meta	0.76	0.69-0.85	4.78e-07
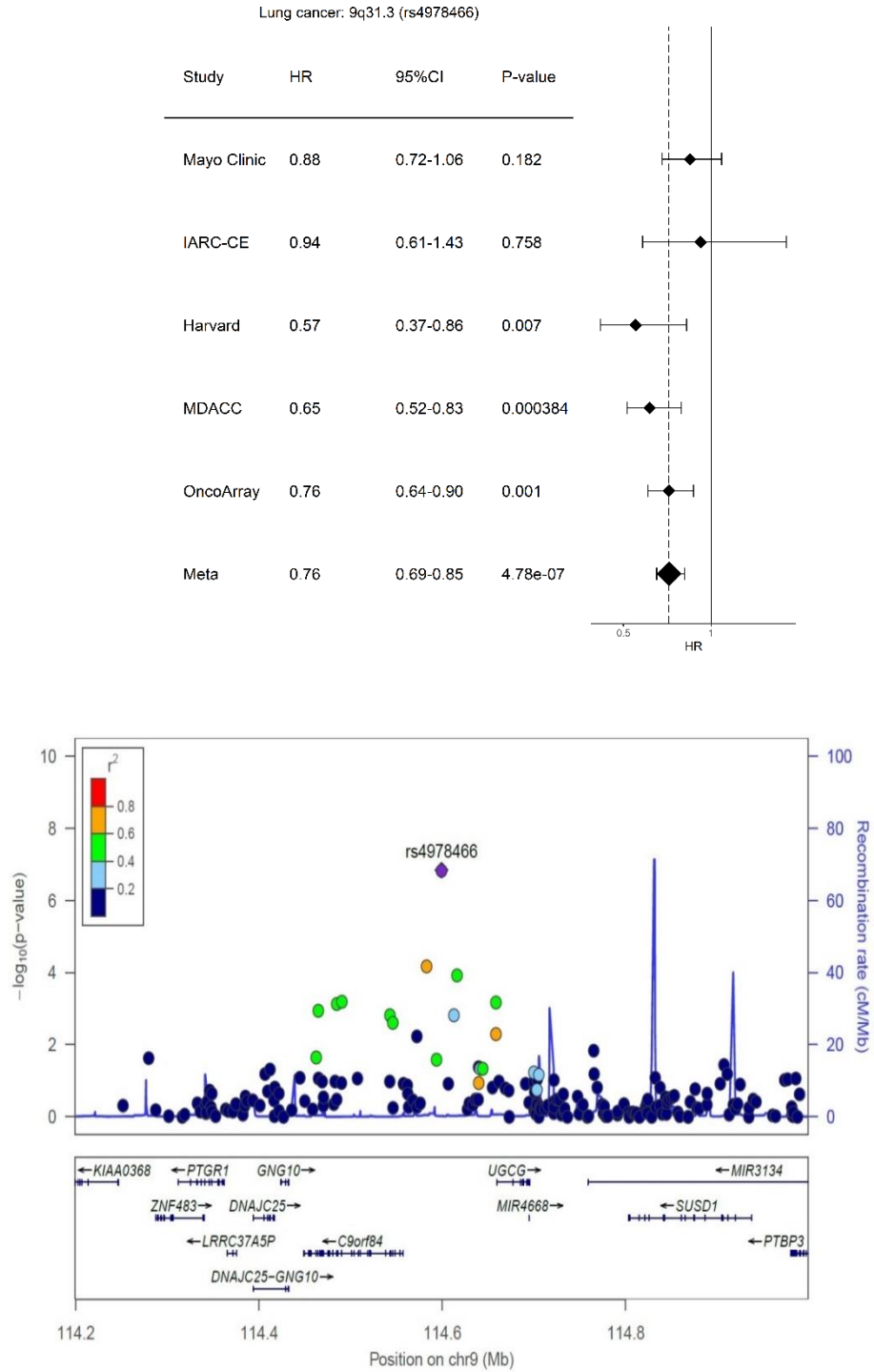
Supplementary Figure 3D: Forest plot for study specific hazard ratio and regional plot (10p14 - rs17143938)

Lung cancer: 10p14 (rs17143938)

Study	HR	95%CI	P-value
Toronto	0.45	0.26-0.78	0.004
Mayo Clinic	0.73	0.47-1.14	0.162
IARC-CE	0.77	0.22-2.77	0.693
Harvard	0.58	0.27-1.24	0.158
OncoArray	0.56	0.42-0.75	0.000123
Meta	0.58	0.47-0.72	5.99e-07
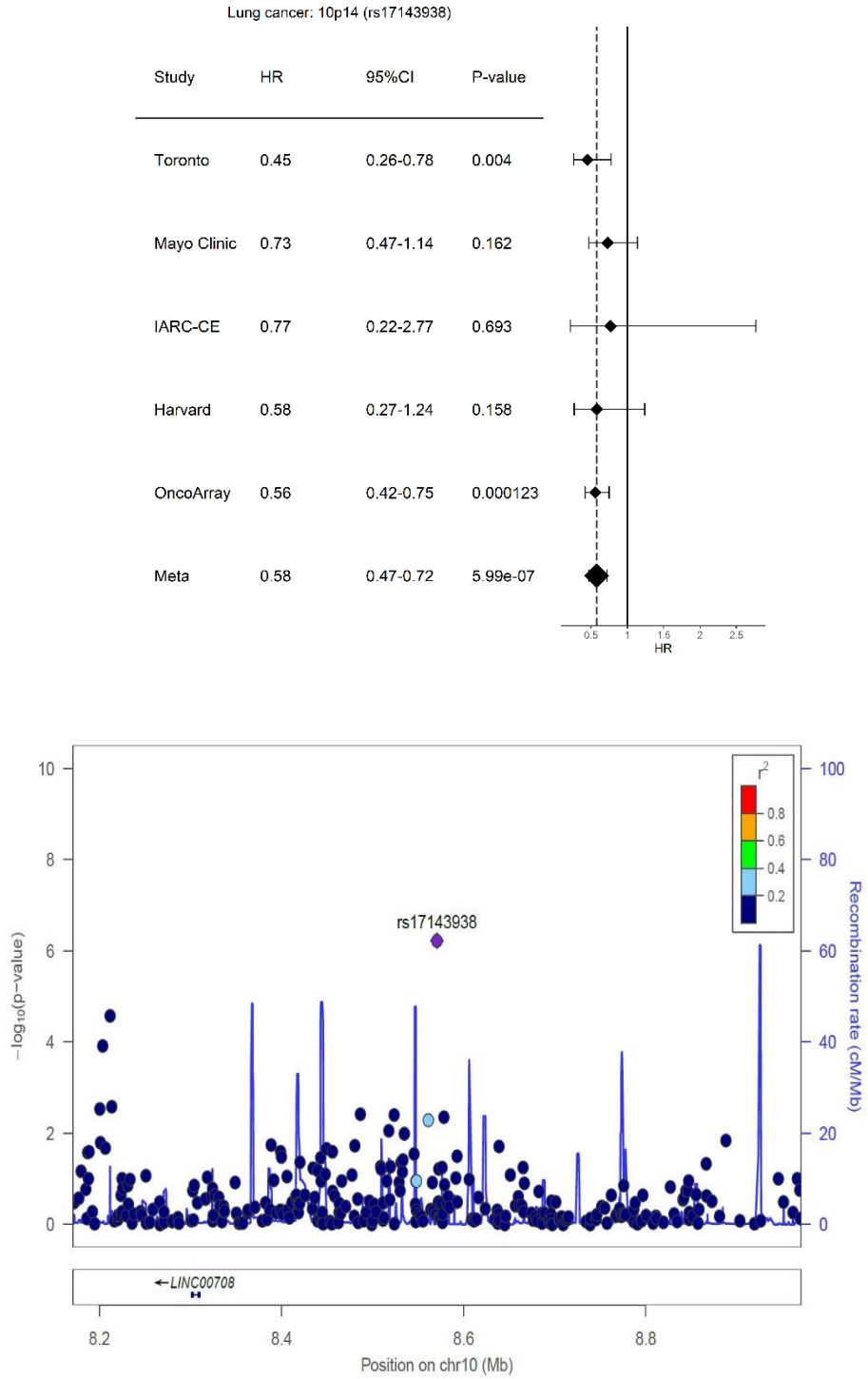
Supplementary Figure 3E: Forest plot for study specific hazard ratio and regional plot (4p14 - rs17603438)

Lung Adenocarcinoma: 4p14 (rs17603438)

Study	HR	95%CI	P-value
Toronto	0.40	0.23-0.67	0.000593
Mayo Clinic	0.50	0.32-0.81	0.0042
IARC-CE	3.19	0.22-5	0.393
Harvard	0.59	0.18-1.91	0.375
OncoArray	0.55	0.34-0.89	0.0147
Meta	0.50	0.38-0.66	6.92e-07
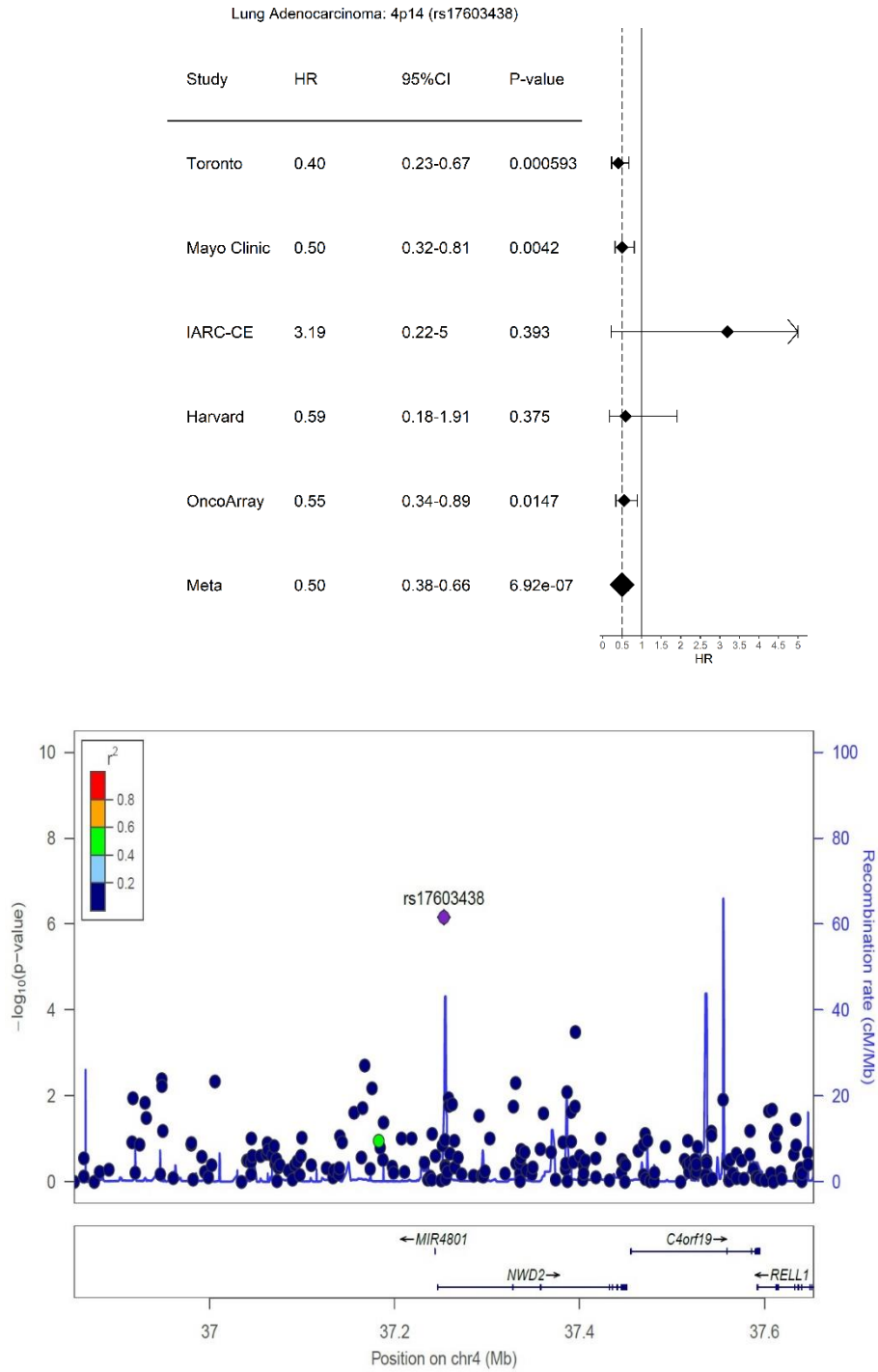
Supplementary Figure 3F: Forest plot for study specific hazard ratio and regional plot (5q11.2 - rs10041935)

Lung Adenocarcinoma: 5q11.2 (rs10041935)

Study	HR	95%CI	P-value
Toronto	1.07	0.74-1.55	0.7
Mayo Clinic	0.74	0.57-0.96	0.023
IARC-CE	0.97	0.54-1.74	0.918
Harvard	0.64	0.39-1.07	0.089
MDACC	0.59	0.46-0.76	4.76e-05
OncoArray	0.73	0.58-0.91	0.005
Meta	0.73	0.65-0.83	6.84e-07
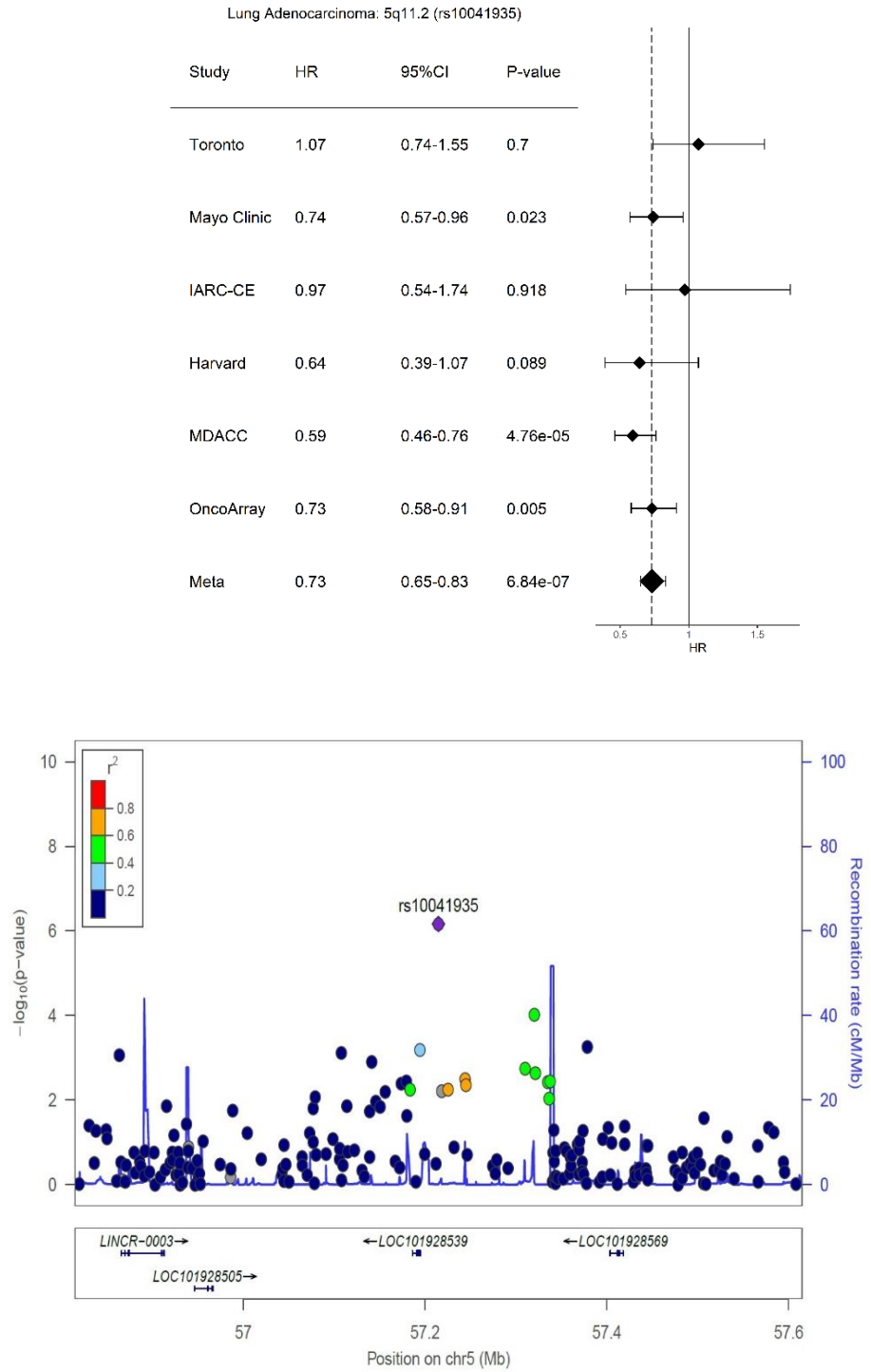
Supplementary Figure 3G: Forest plot for study specific hazard ratio and regional plot (7p21.3 - rs10247578)

Lung Adenocarcinoma: 7p21.3 (rs10247578)

Study	HR	95%CI	P-value
Toronto	1.61	1.16-2.25	0.005
Mayo Clinic	1.52	1.21-1.93	0.000407
IARC-CE	0.68	0.29-1.57	0.364
Harvard	0.93	0.55-1.59	0.791
MDACC	1.49	1.16-1.91	0.002
OncoArray	1.27	1.03-1.55	0.023
Meta	1.38	1.23-1.55	7.69e-08
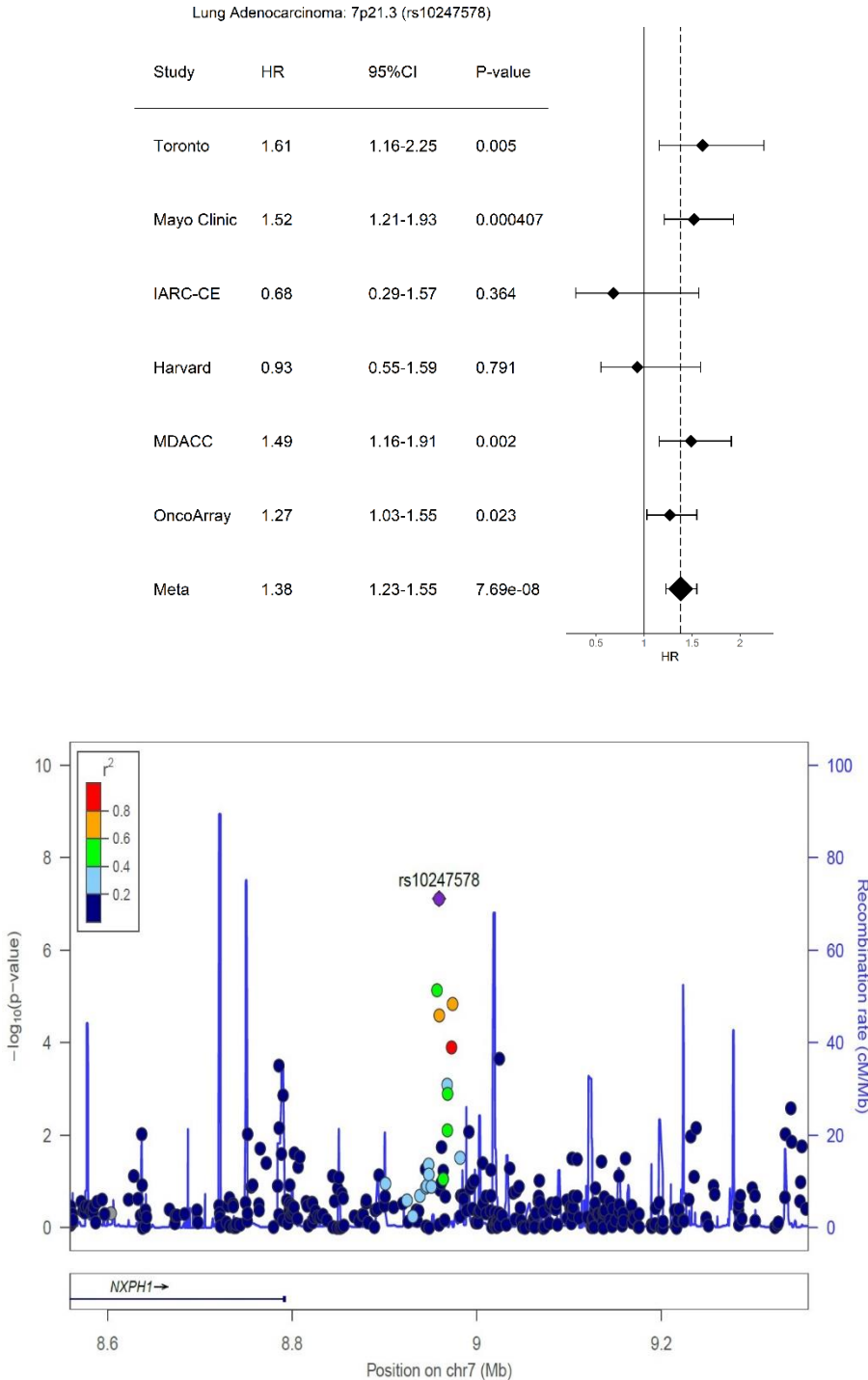
Supplementary Figure 3H: Forest plot for study specific hazard ratio and regional plot (10p15.3 - rs17158233)

Lung Adenocarcinoma: 10p15.3 (rs17158233)

Study	HR	95%CI	P-value
Toronto	4.15	1.19-14.45	0.025
Mayo Clinic	1.33	0.21-8.36	0.762
IARC-CE	4.51	0.87-23.30	0.072
Harvard	11.64	1.59-84.95	0.016
OncoArray	3.47	1.82-6.62	0.000156
Meta	3.68	2.23-6.09	3.66e-07
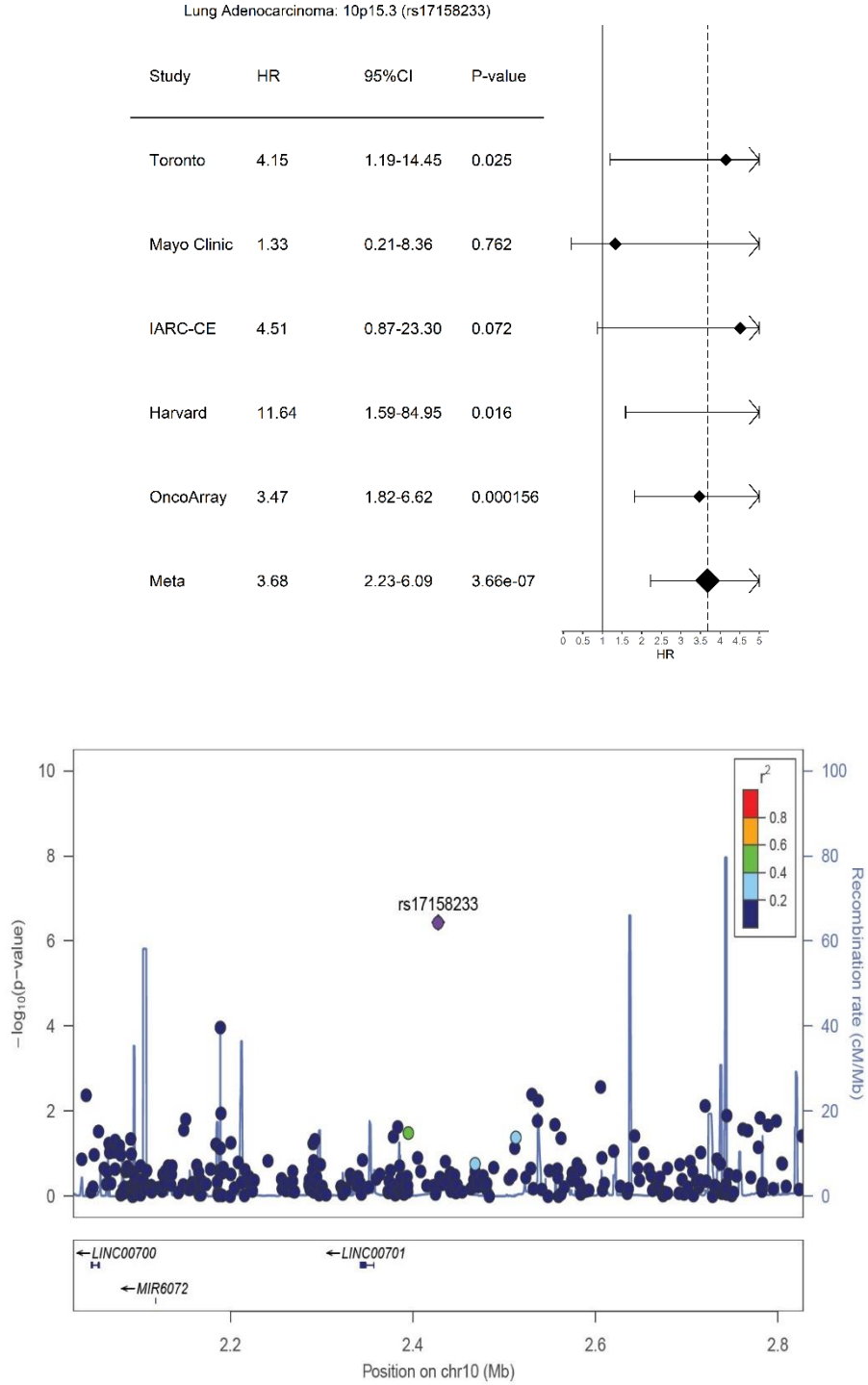
Supplementary Figure 3I: Forest plot for study specific hazard ratio, Kaplan-Meier plot and regional plot (11q14.1 - rs17148028)

Lung Adenocarcinoma: 11q14.1 (rs17148028)

Study	HR	95%CI	P-value
Mayo Clinic	0.51	0.26-1.00	0.051
IARC-CE	0.43	0.13-1.37	0.152
Harvard	0.57	0.22-1.53	0.266
OncoArray	0.46	0.32-0.66	2.02e-05
Meta	0.48	0.36-0.64	5.66e-07