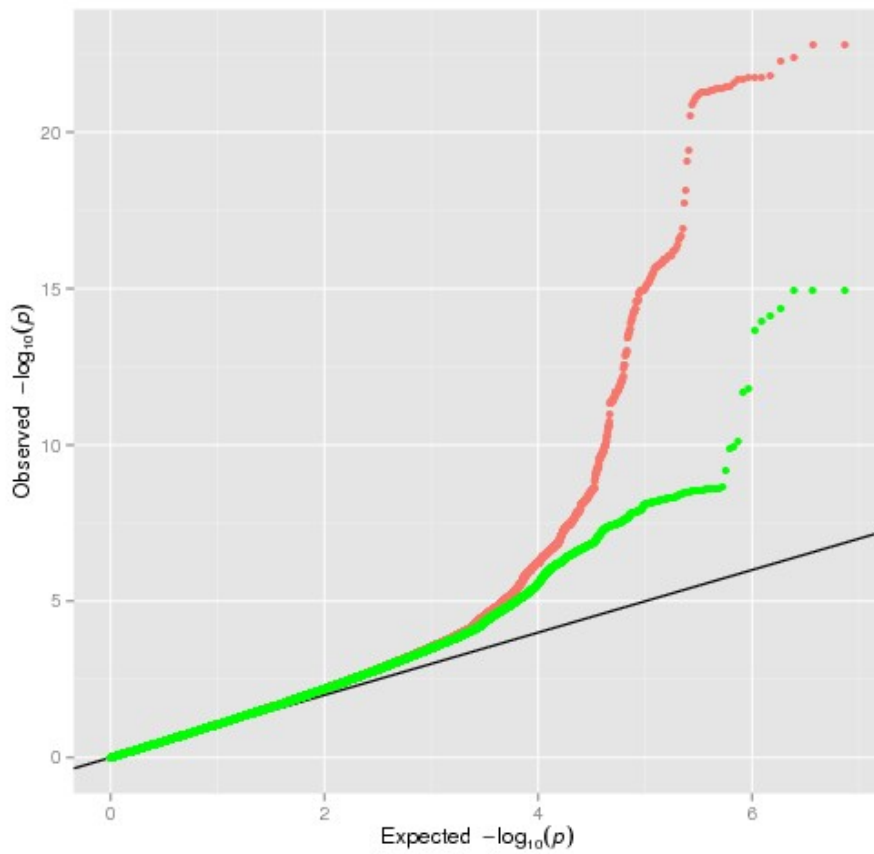


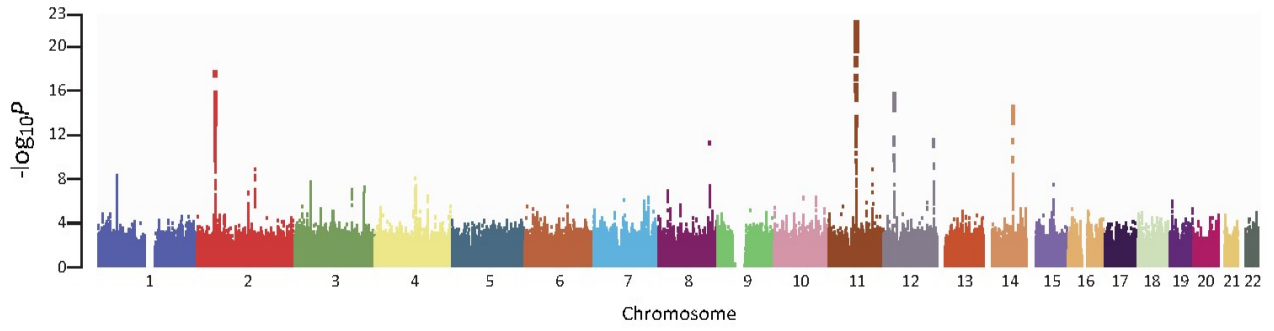
Supplementary Figures

Supplementary Figure 1. Quantile-quantile plots for the stage 1 meta-analysis.

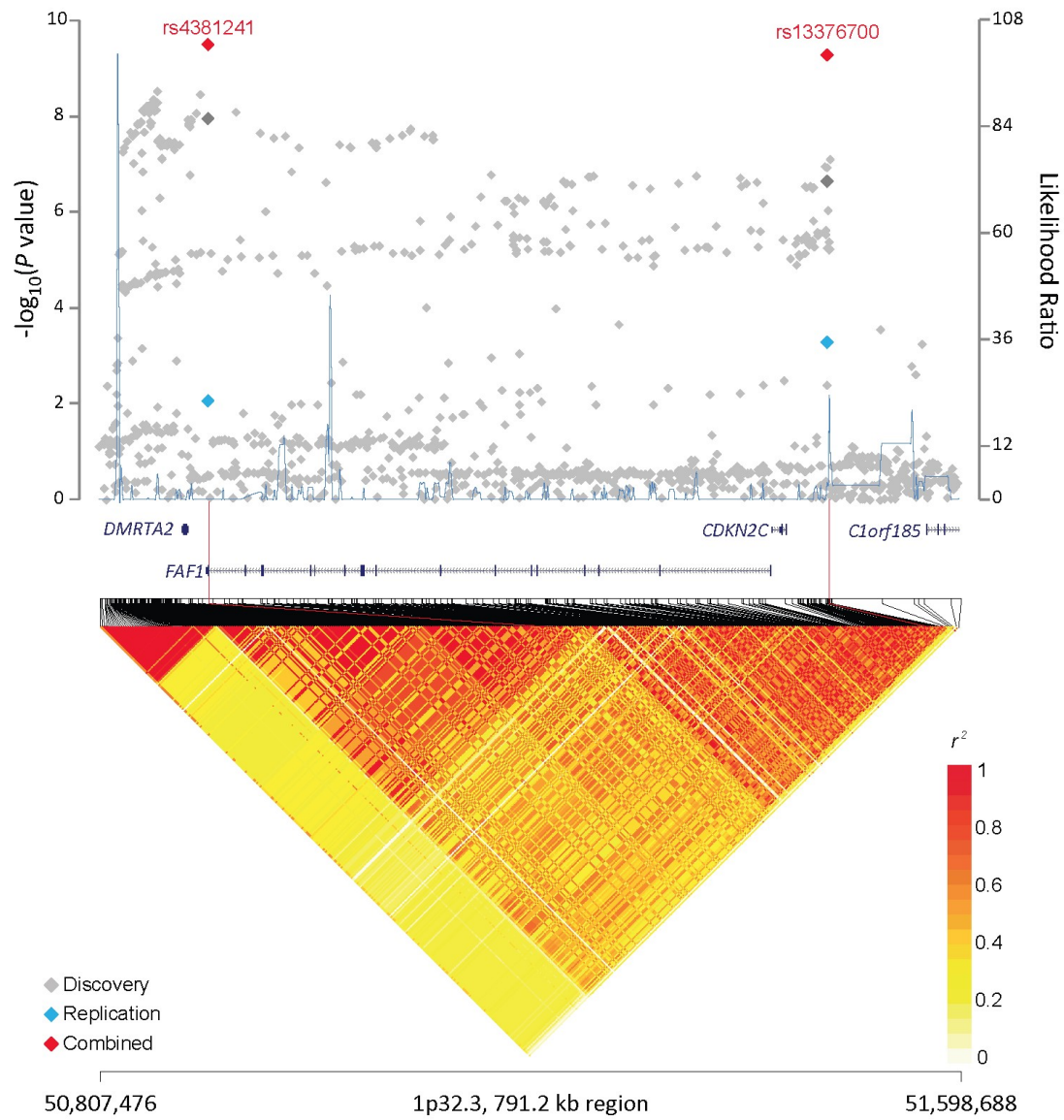


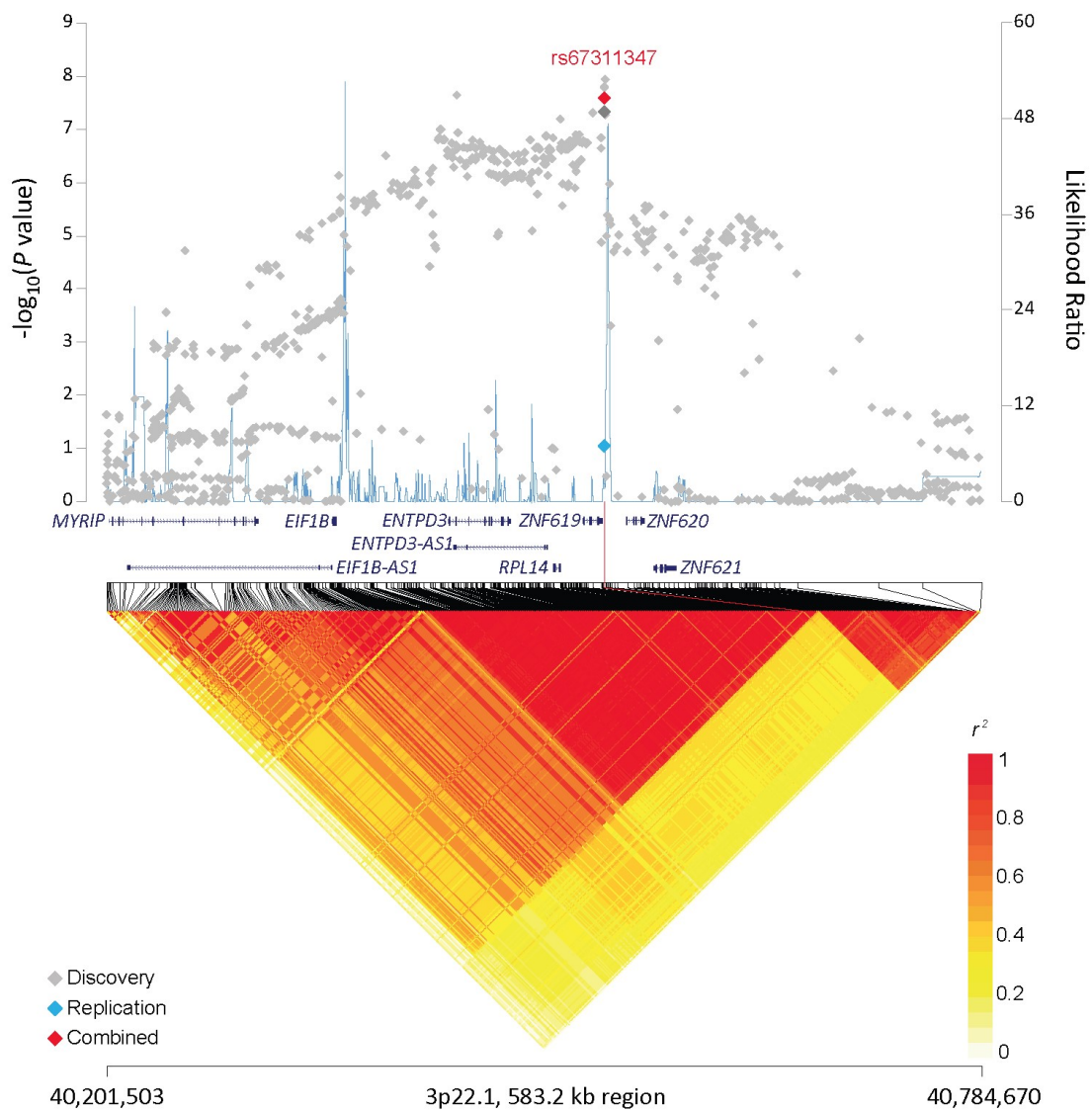
QQ plot after filtering out SNPs with $MAF < 0.01$. Red line includes all SNPs; green line excludes SNPs $\pm 500\text{kb}$ of previously identified locus.

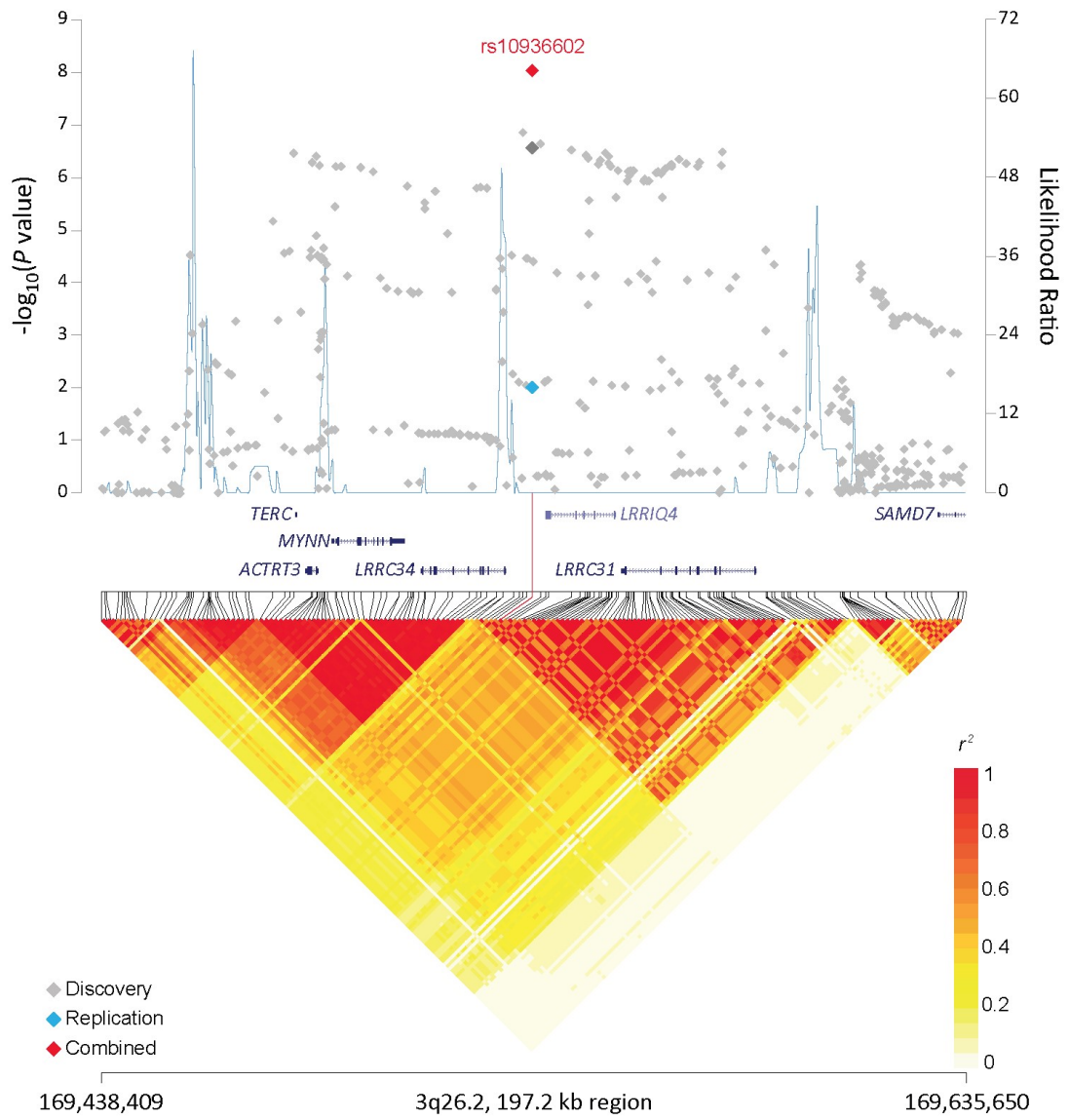
Supplementary Figure 2. Manhattan plot of GWAS association P-values.

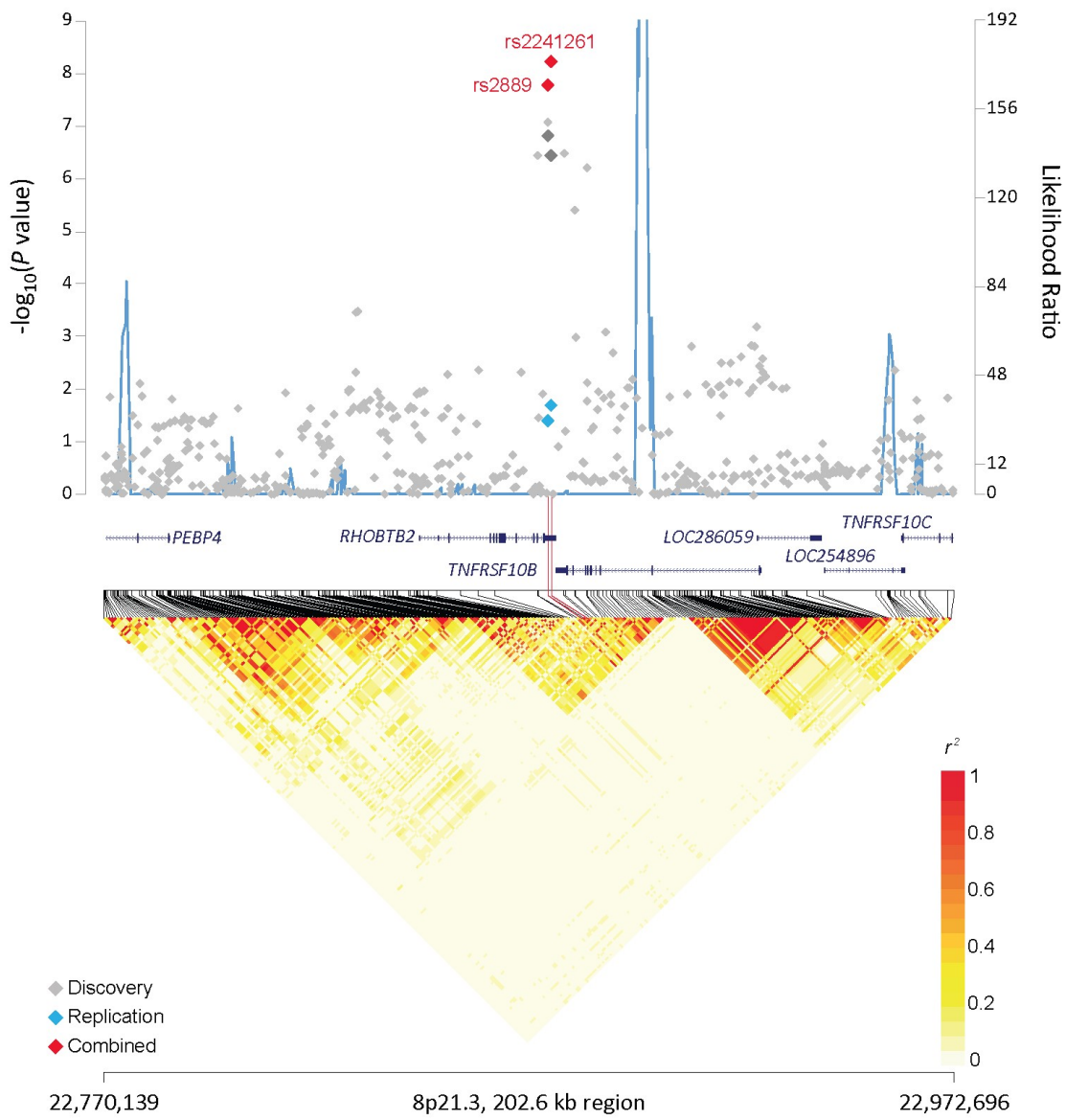


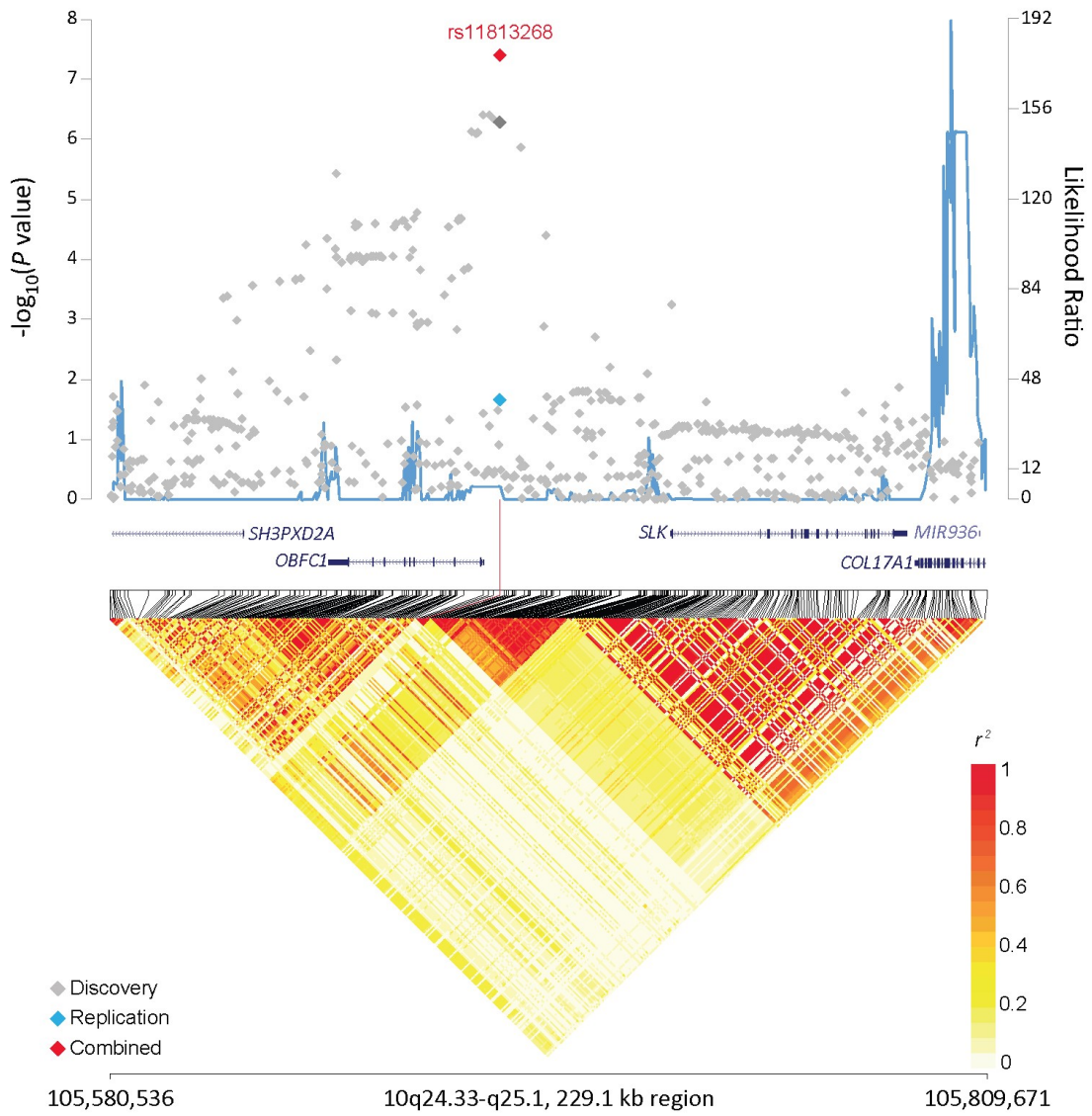
Supplementary Figure 3. Regional association LD plots

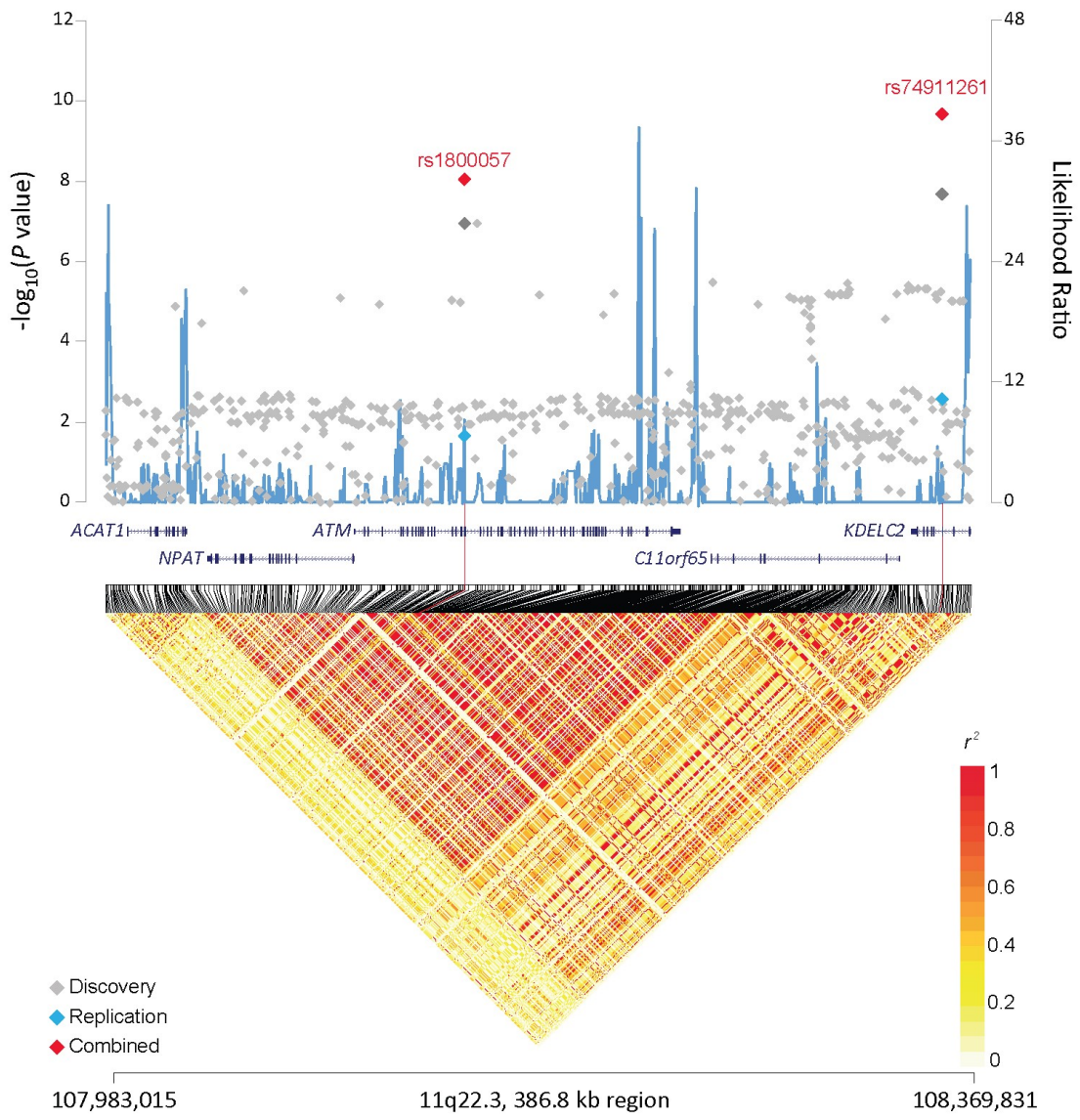


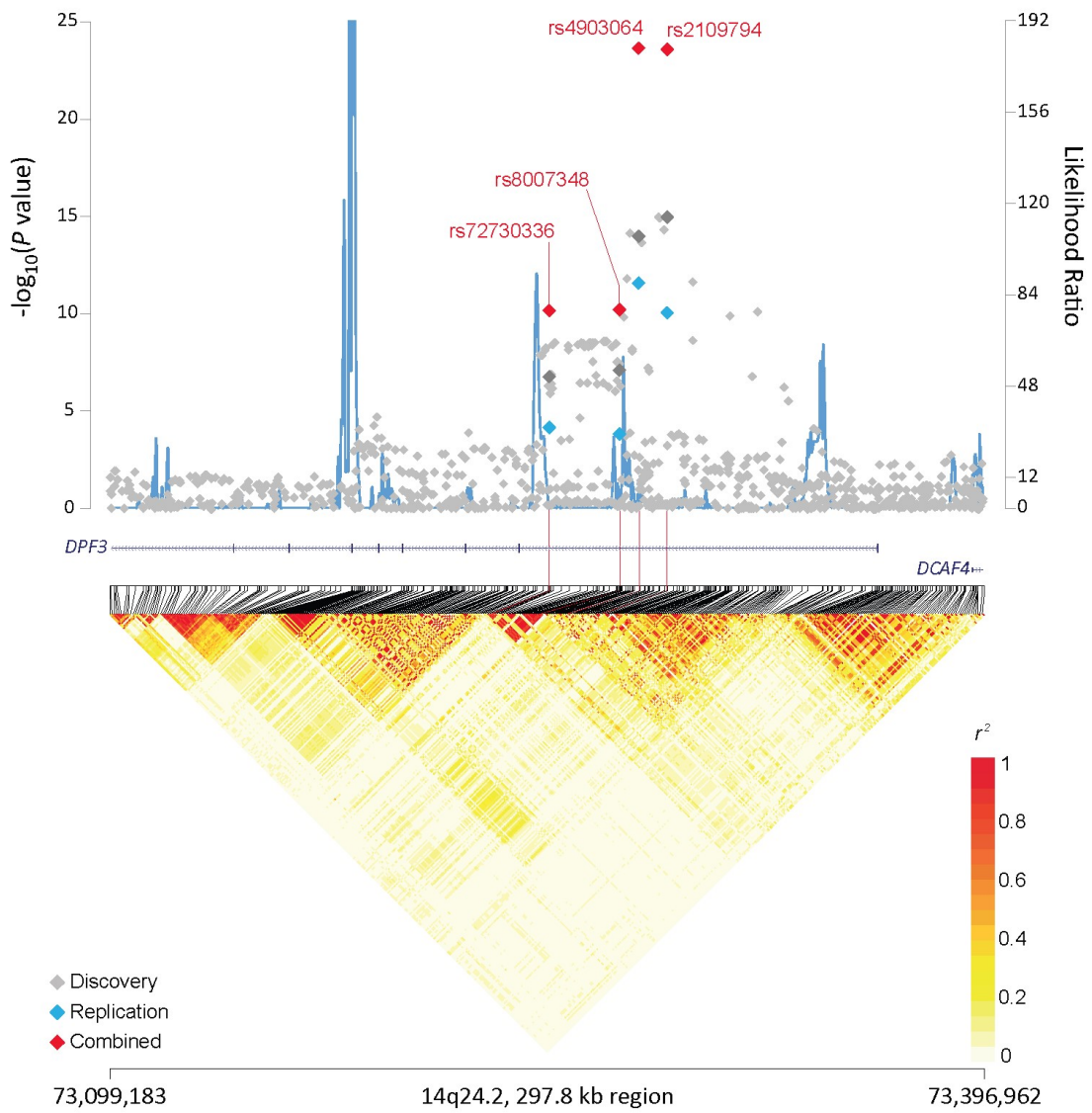










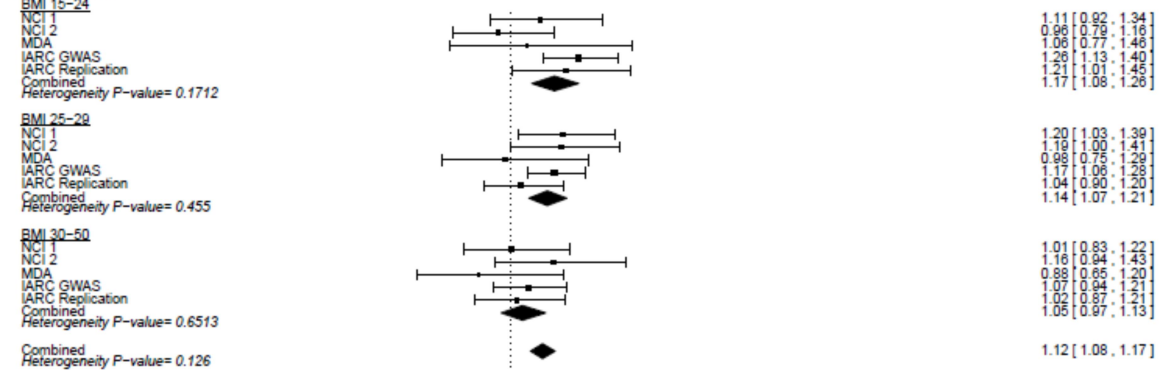


Supplementary Figure 4. SNP analyses stratified by sex, body mass index (BMI; <25, 25-29, 30+ kg/m²), smoking status (never, former, current), and history of diagnosed hypertension

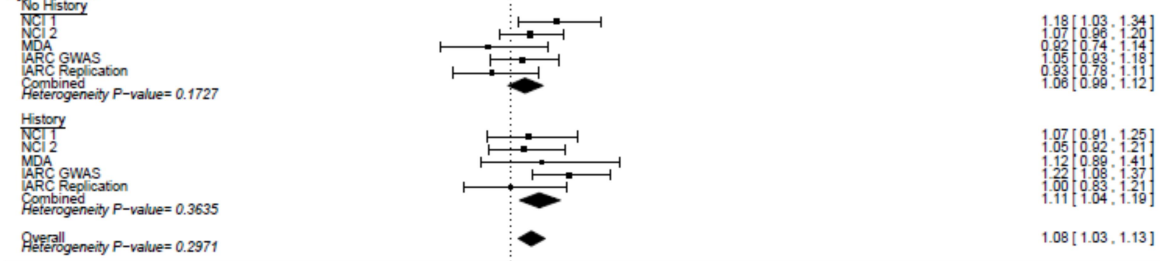
RSID	Position	Heterogeneity P-value				Notes
		BMI	Hypertension	Sex	Smoking	
rs4381241	chr1:50907438	0.1260	0.2971	0.9800	0.4365	
rs13376700	chr1:51477643	0.1441	0.8296	0.5867	0.7499	
rs6706003	chr2:46563392	0.7553	0.5484	0.4456	0.9480	
rs6755594	chr2:46589295	0.0072	0.5257	0.3656	0.4870	
rs72851889	chr2:144694129	0.4763	0.0759	0.9594	0.7222	
rs72855540	chr2:144990548	0.6065	0.1736	0.3559	0.7988	
rs67311347	chr3:40533243	0.9734	0.9460	0.2067	0.4066	
rs2203002	chr3:141796239	0.6793	0.3010	0.5532	0.8355	
rs10936602	chr3:169536637	0.0577	0.6883	0.0866	0.2242	
rs234043	chr3:172313367	0.4390	0.3124	0.9282	0.2813	
rs7697932	chr4:101005318	0.7494	0.0033	0.4040	0.0074	
rs17050872	chr4:131097748	0.5047	0.8624	0.4159	0.5546	
rs76912165	chr5:92965344	0.0322	0.8506	0.1022	0.5913	
rs1266819	chr6:52094946	0.8495	0.4585	0.0836	0.8467	
rs59294613	chr7:124554267	0.8329	0.3840	0.9974	0.0082	
rs73149977	chr7:134488864	0.8895	0.4190	0.6981	0.0130	
rs2889	chr8:22875909	0.2791	0.5079	0.2006	0.4373	
rs2241261	chr8:22876739	0.1427	0.4912	0.5391	0.6539	
rs7913447	chr10:73992040	0.7282	0.8890	0.8155	0.1781	
rs11813268	chr10:105682296	0.8877	0.6983	0.1433	0.2921	
rs7774900	chr11:95830733	0.5445	0.0733	0.8029	0.1773	
rs1800057	chr11:108143456	0.2800	0.6833	0.0614	0.8114	
rs74911261	chr11:108357137	0.2001	0.6537	0.1407	0.5375	
rs77736197	chr12:107623706	0.9695	0.4229	0.5077	0.0973	
rs72730336	chr14:73248661	0.2424	0.7131	0.0043	0.9807	Stronger effect in females; some heterogeneity observed among males
rs8007348	chr14:73272730	0.2646	0.7935	0.0026	0.9964	Stronger effect in females
rs4903064	chr14:73279420	0.2630	0.8311	<0.0001	0.1338	Stronger effect in females; some heterogeneity observed among females
rs2109794	chr14:73288855	0.2743	0.6162	<0.0001	0.2676	Stronger effect in females
rs11637556	chr15:66728951	0.2492	0.8158	0.9727	0.7230	
rs4804368	chr19:7190290	0.6837	0.1725	0.5010	0.0194	

rs4381241

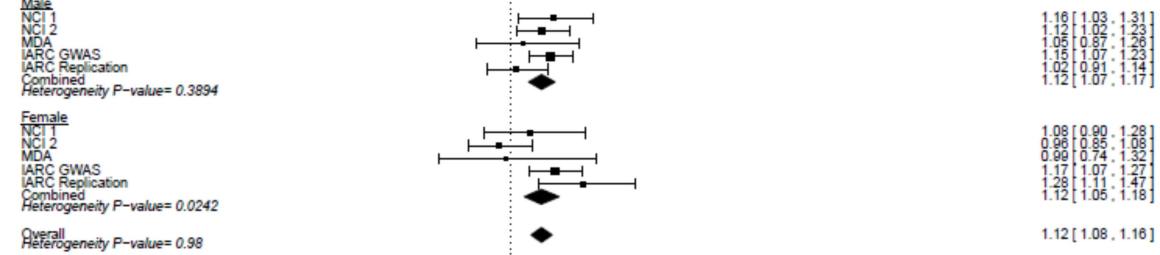
Body Mass Index



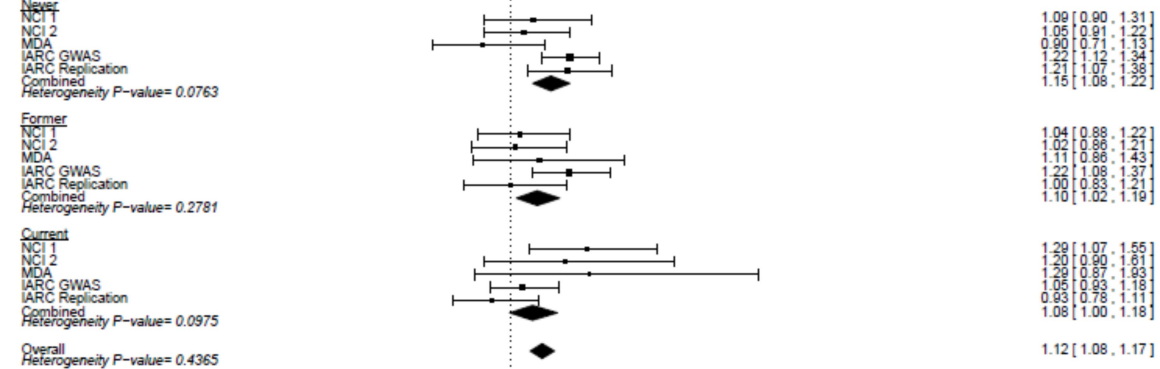
Hypertension



Sex



Smoking

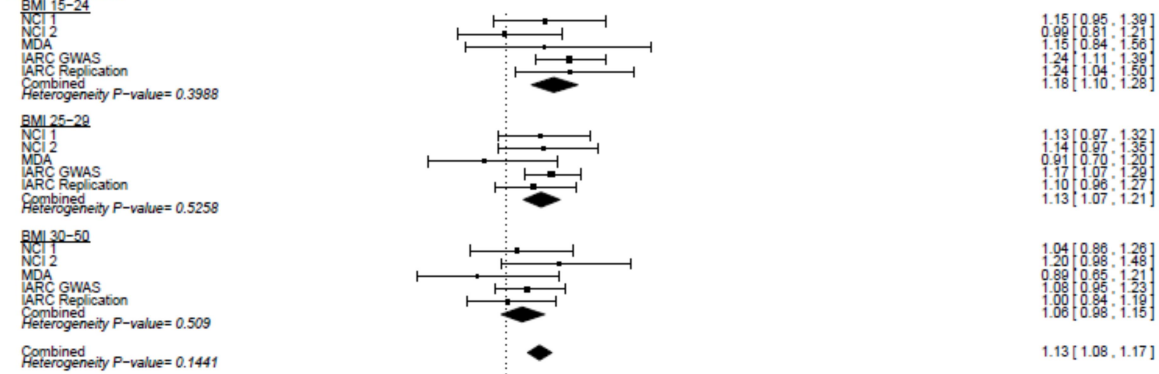


0.50 1.00 1.50 2.00

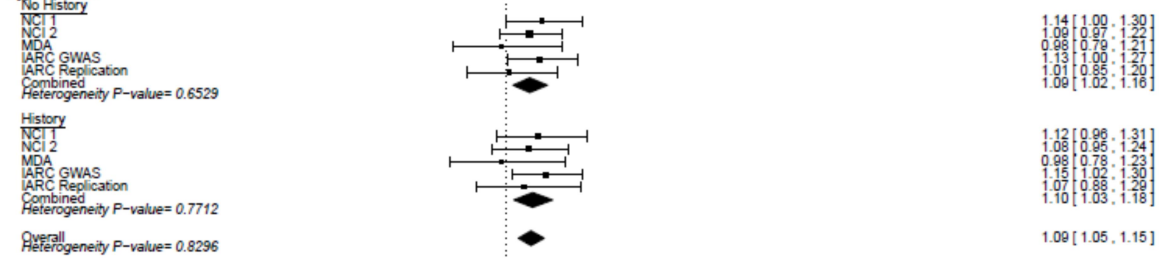
Odds Ratio

rs13376700

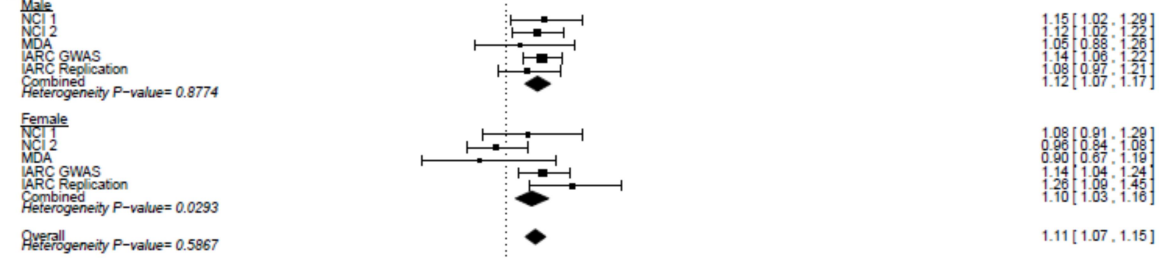
Body Mass Index



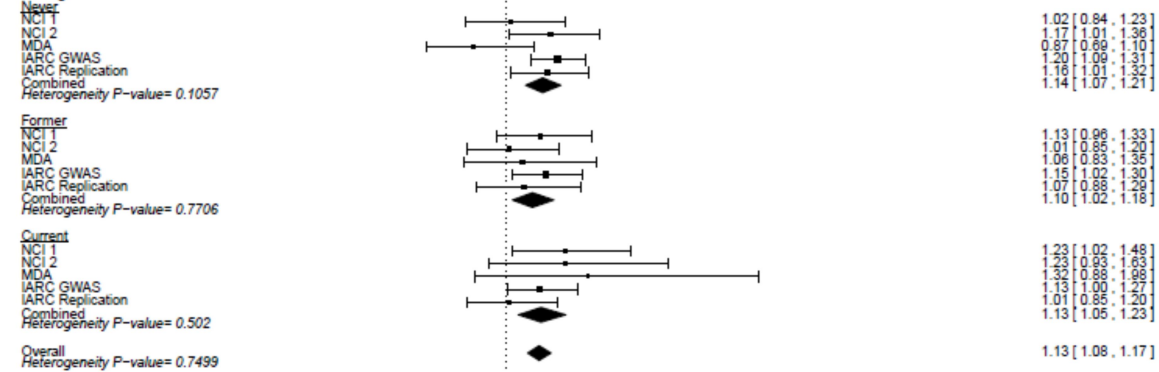
Hypertension



Sex



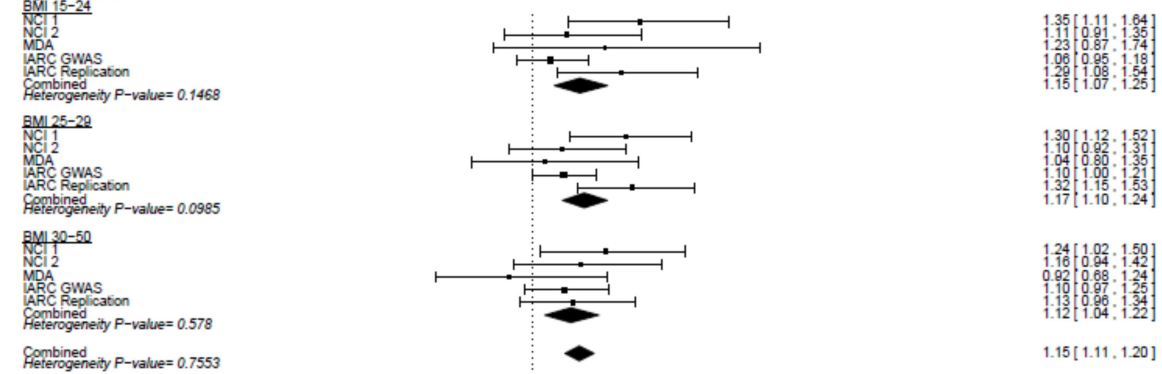
Smoking



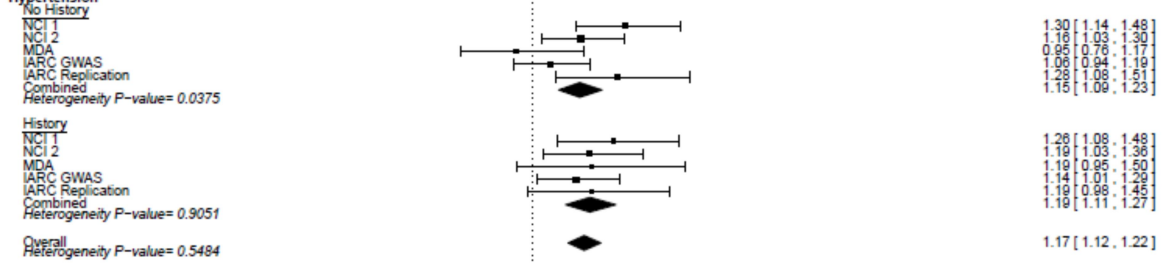
0.50 1.00 1.50 2.00
Odds Ratio

rs6706003

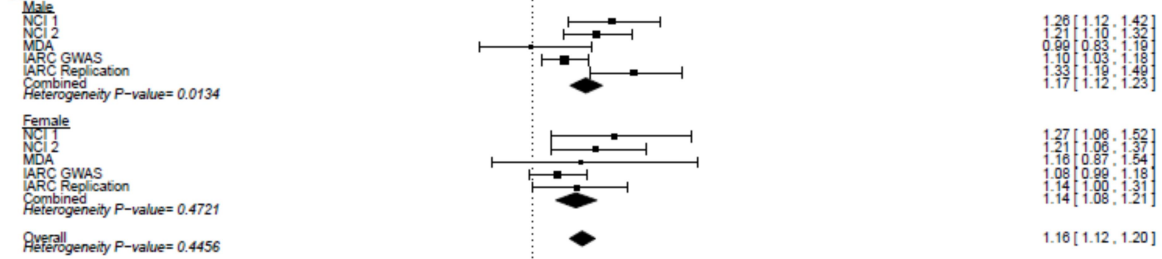
Body Mass Index



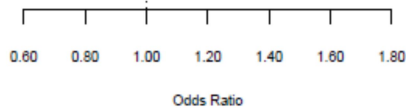
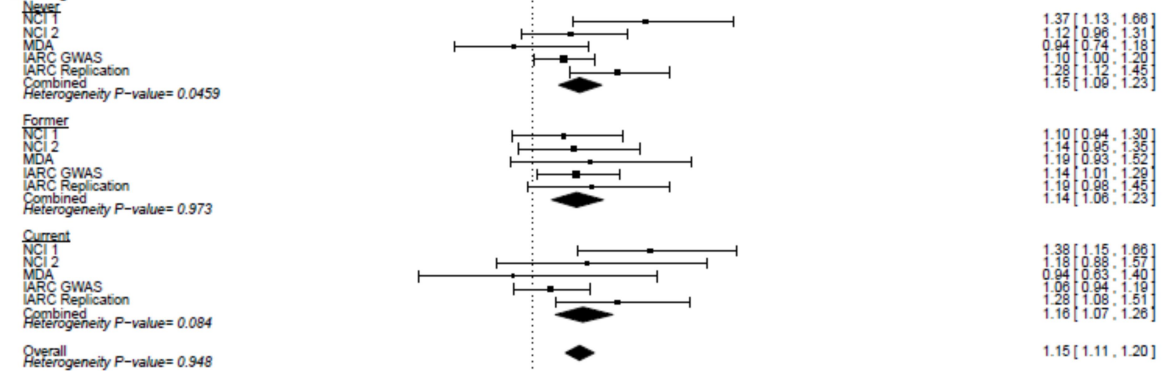
Hypertension



Sex

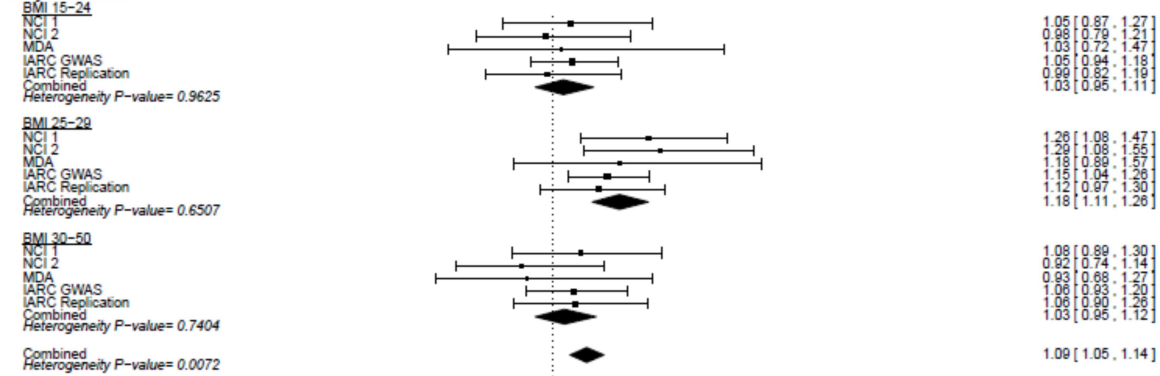


Smoking

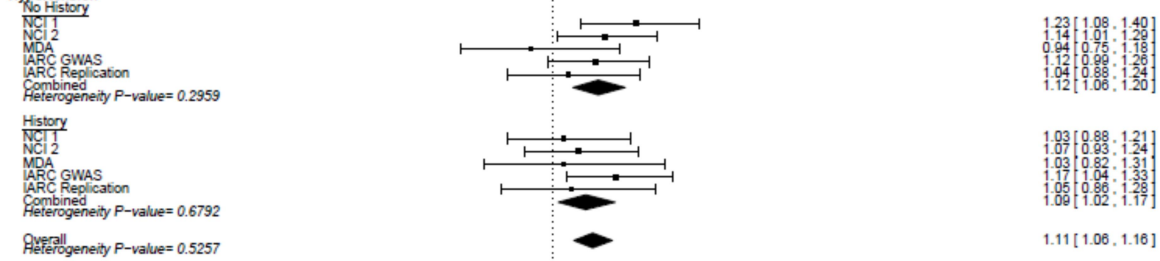


rs6755594

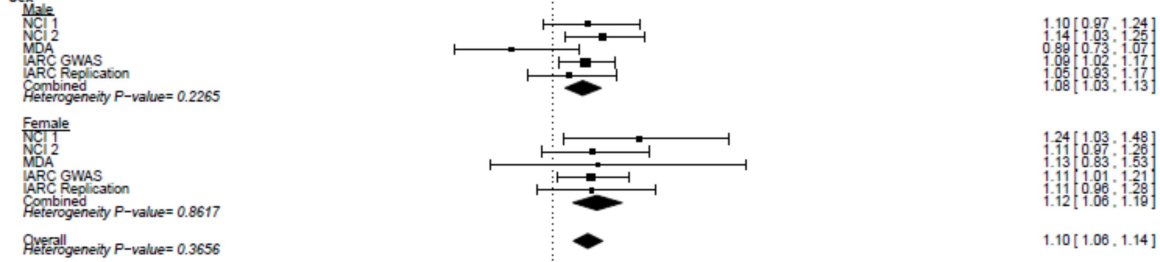
Body Mass Index



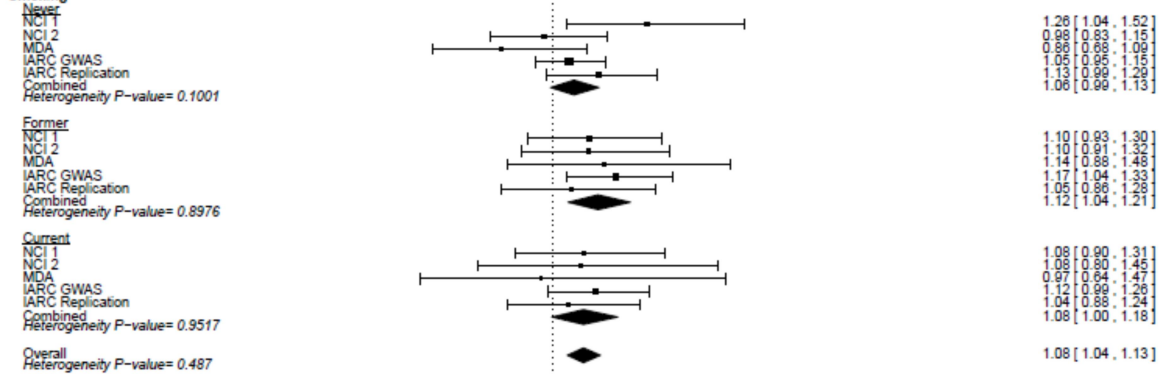
Hypertension



Sex



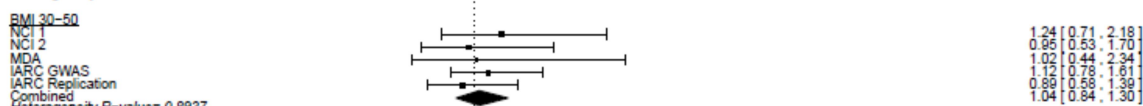
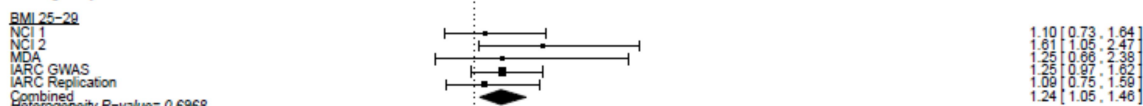
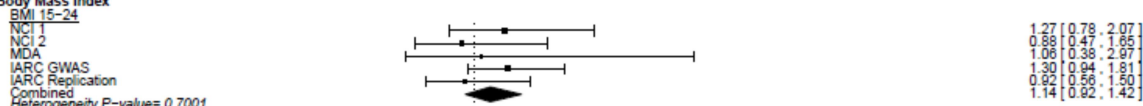
Smoking



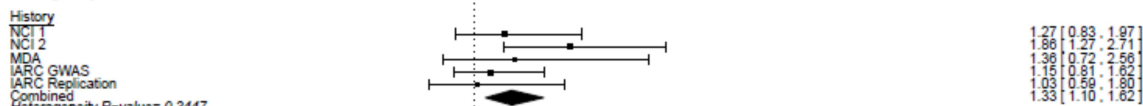
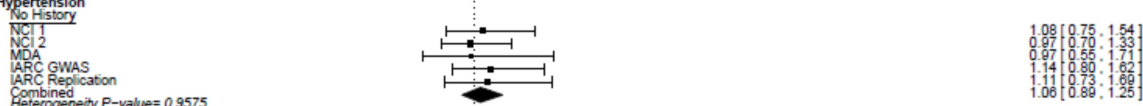
0.60 0.80 1.00 1.20 1.40 1.60
Odds Ratio

rs72851889

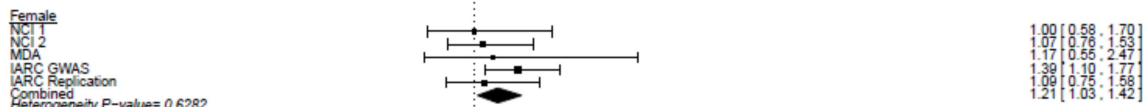
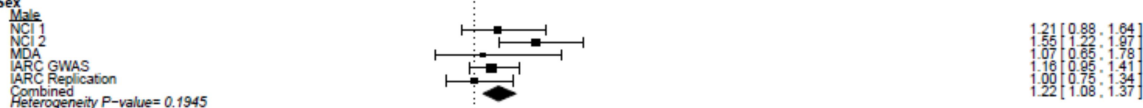
Body Mass Index



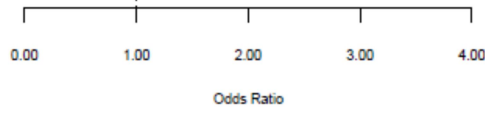
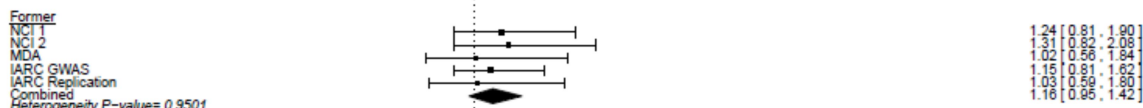
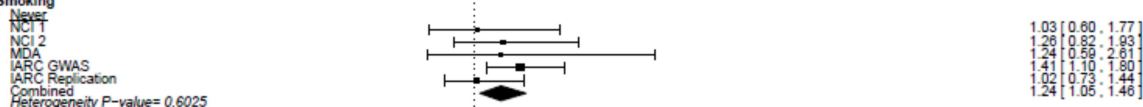
Hypertension



Sex

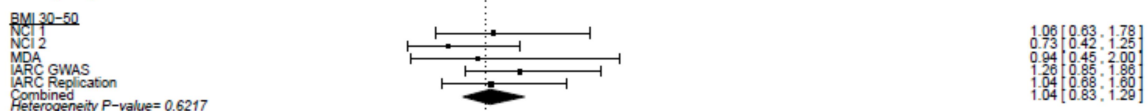
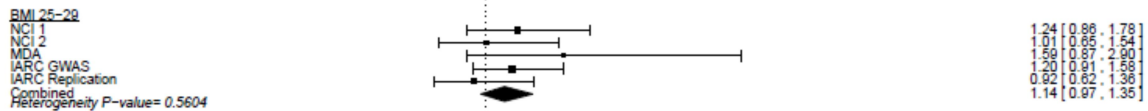
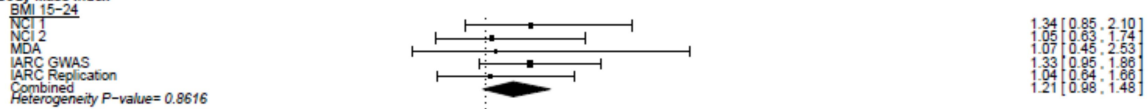


Smoking



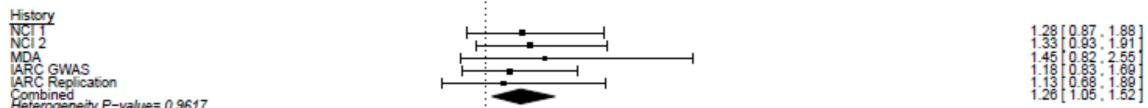
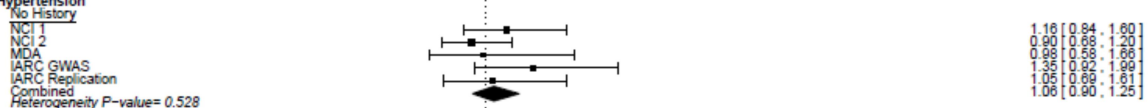
rs7285540

Body Mass Index



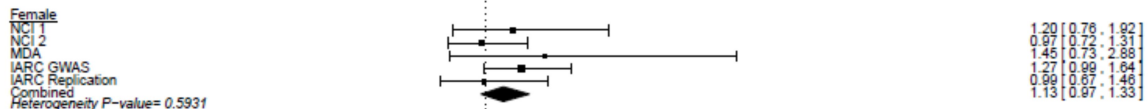
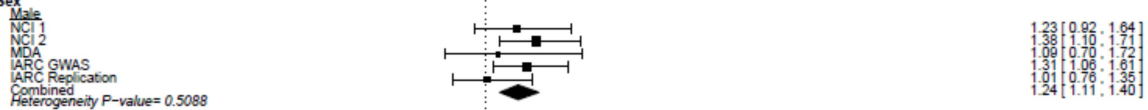
Combined
Heterogeneity P-value = 0.6065

Hypertension



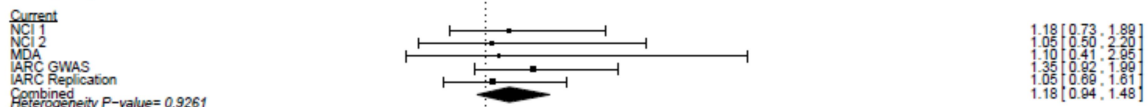
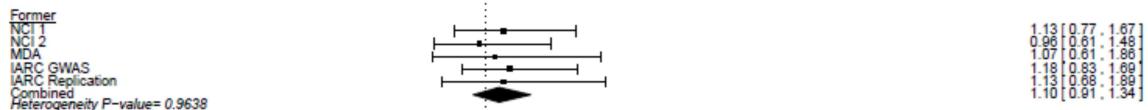
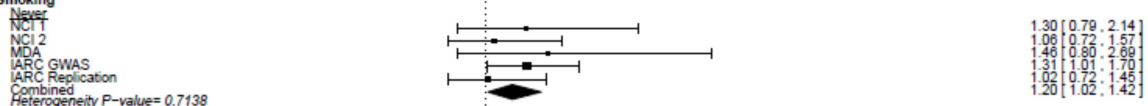
Overall
Heterogeneity P-value = 0.1736

Sex



Overall
Heterogeneity P-value = 0.3559

Smoking

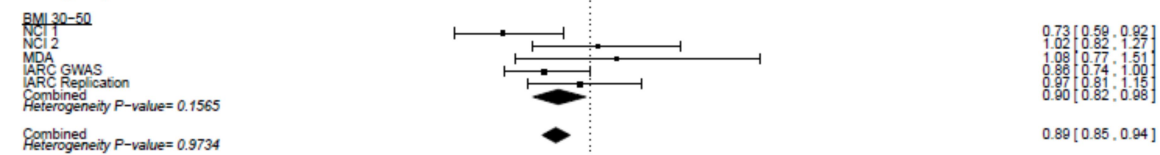
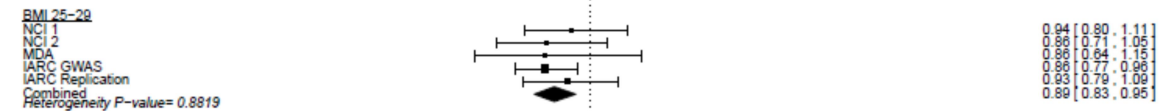
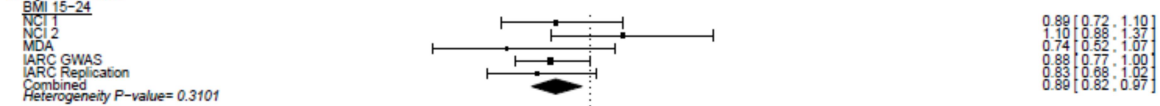


Overall
Heterogeneity P-value = 0.7988

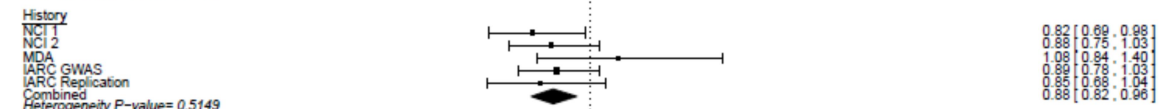
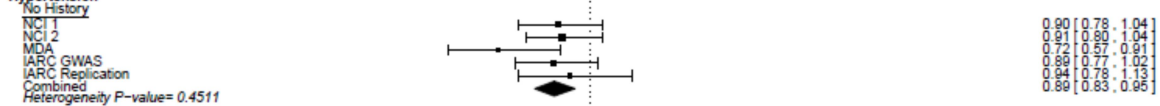


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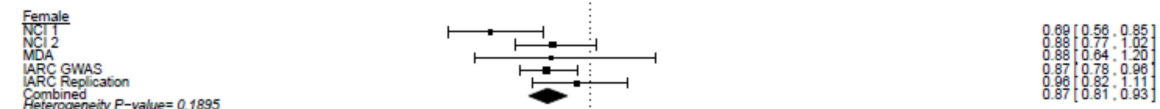
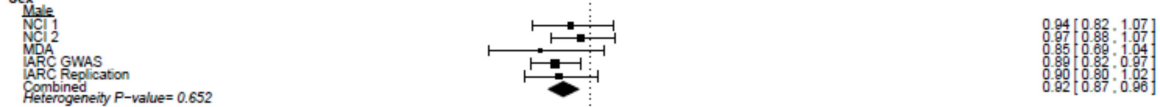
Body Mass Index



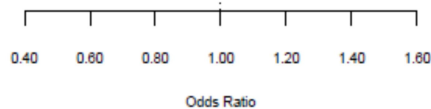
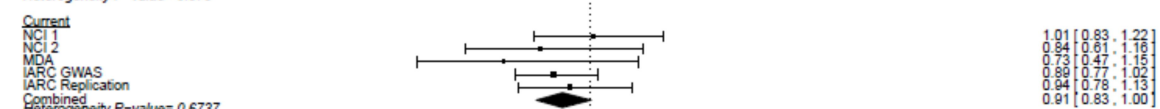
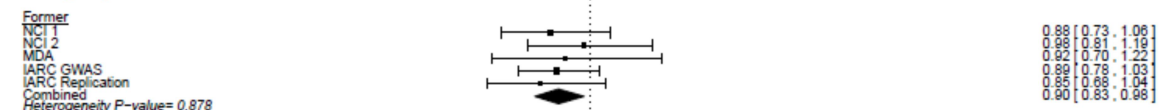
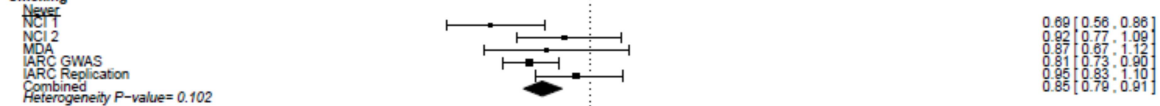
Hypertension



Sex

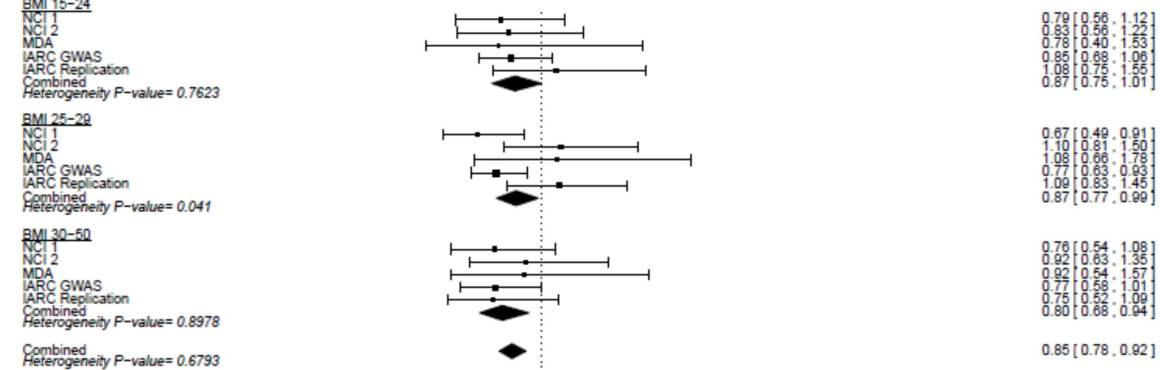


Smoking

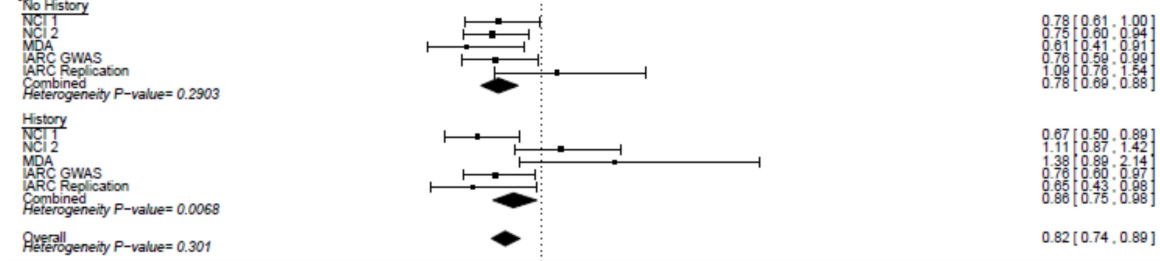


rs2203002

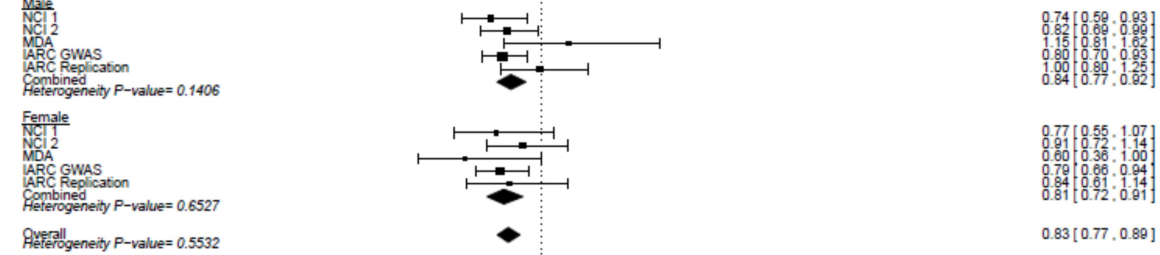
Body Mass Index



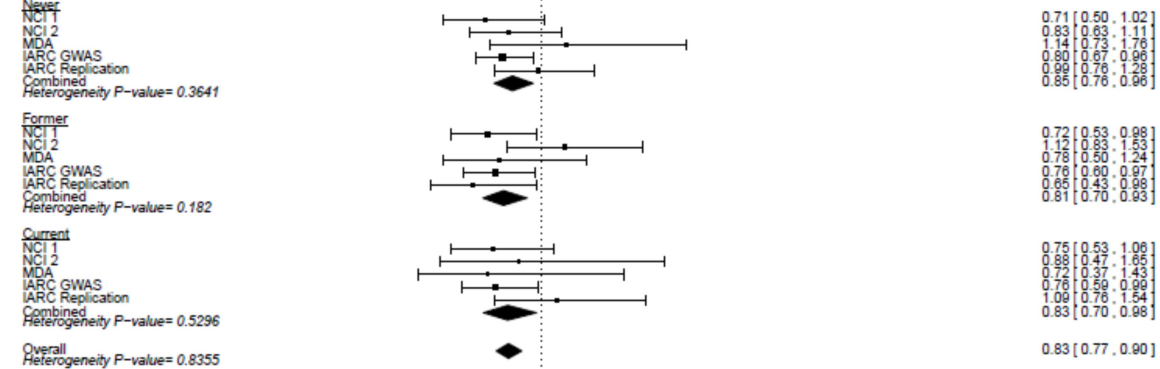
Hypertension



Sex

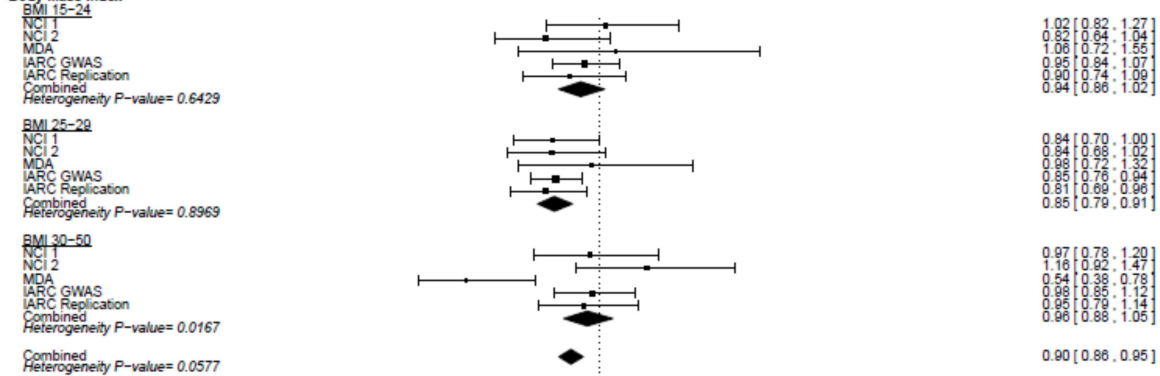


Smoking

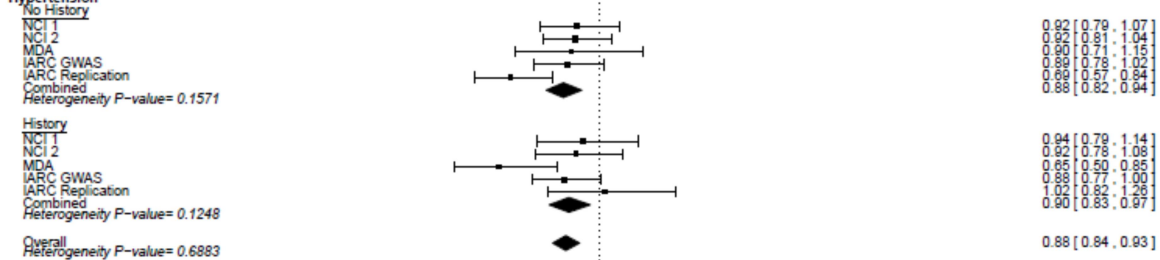


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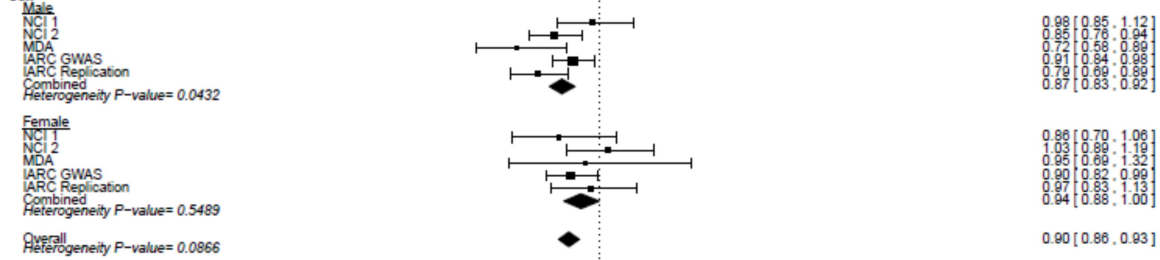
Body Mass Index



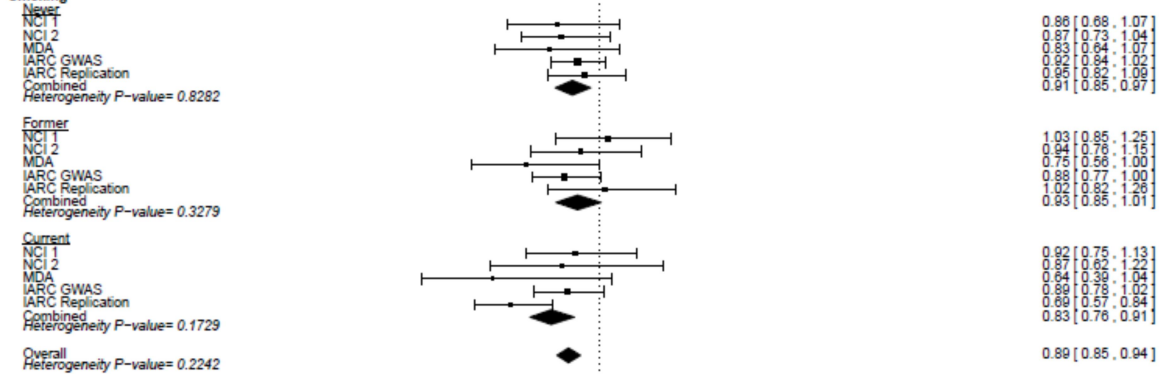
Hypertension



Sex

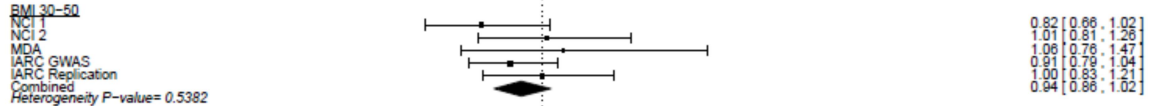
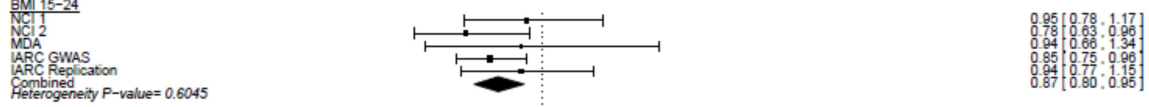


Smoking

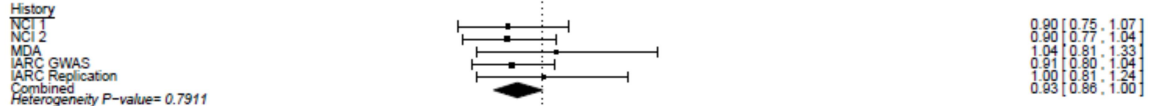
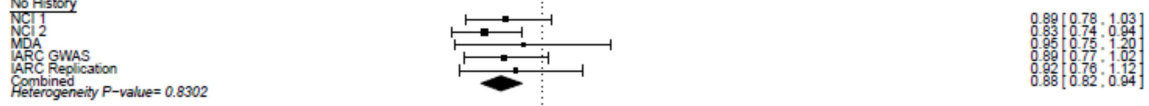


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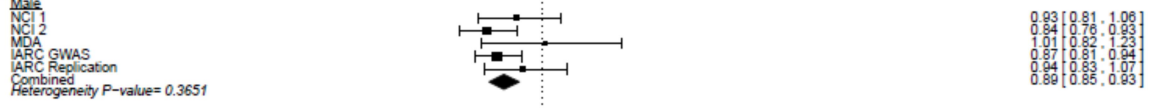
Body Mass Index



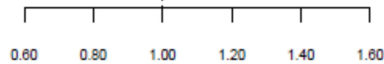
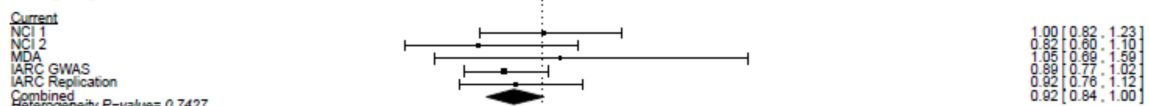
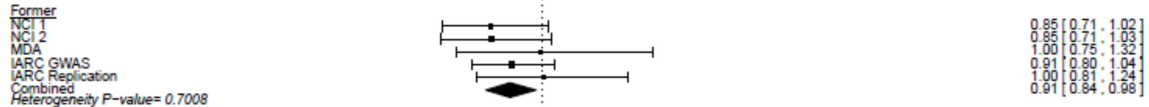
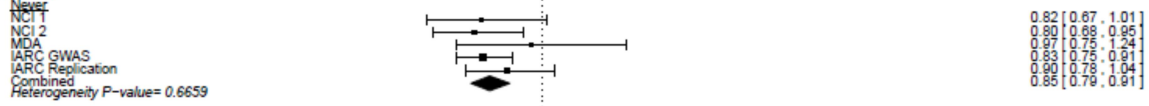
Hypertension



Sex



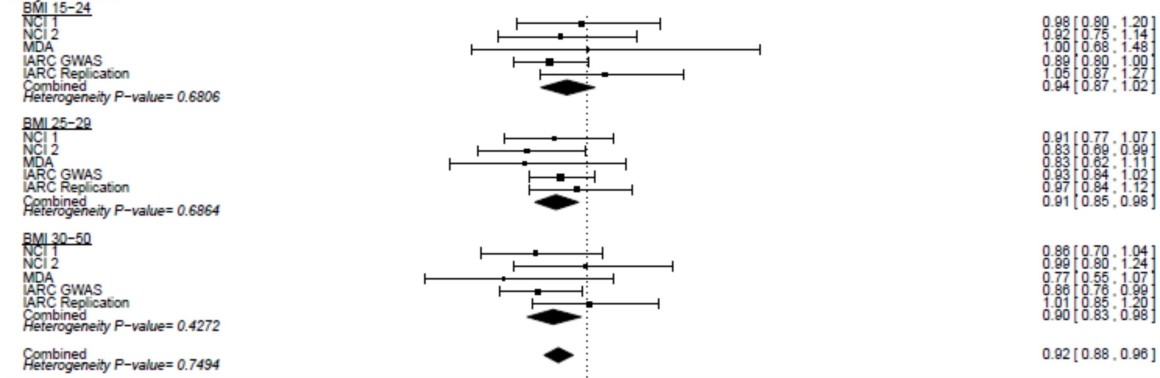
Smoking



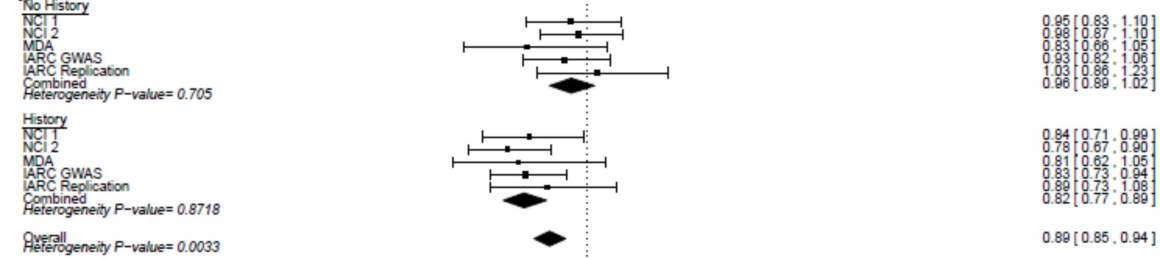
Odds Ratio

rs7697932

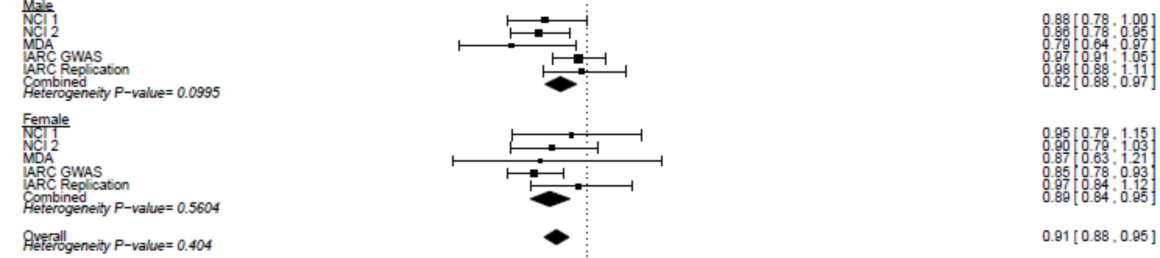
Body Mass Index



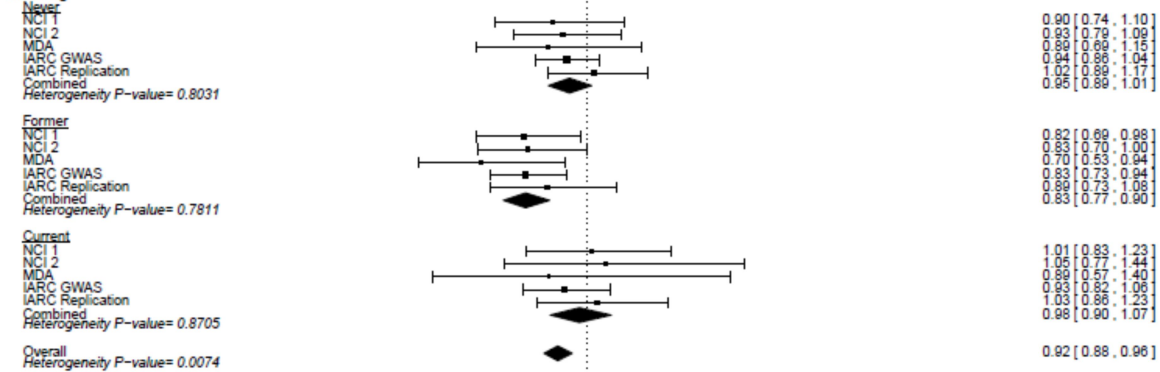
Hypertension



Sex



Smoking

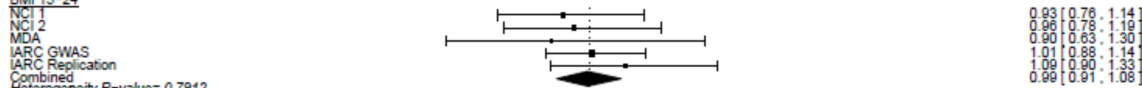


0.40 0.60 0.80 1.00 1.20 1.40 1.60
Odds Ratio

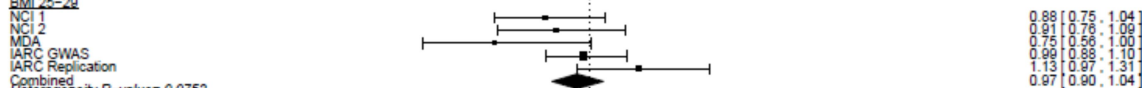
rs17050872

Body Mass Index

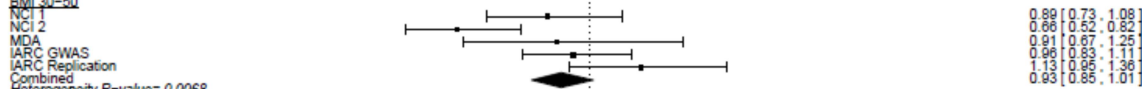
BMI 15-24



BMI 25-29



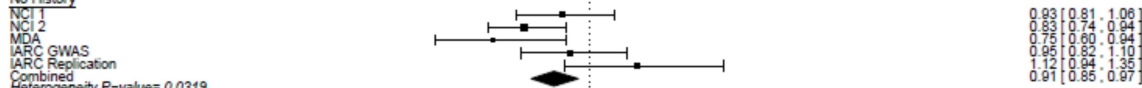
BMI 30-50



Combined Heterogeneity P-value = 0.5047

Hypertension

No History



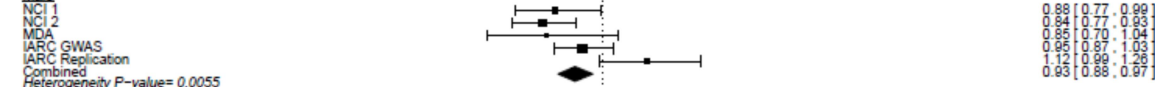
History



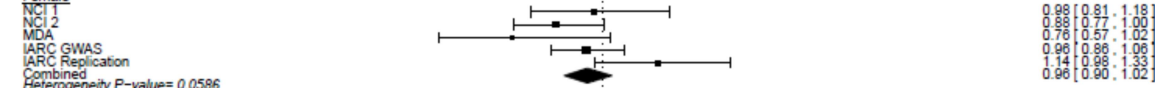
Overall Heterogeneity P-value = 0.8624

Sex

Male



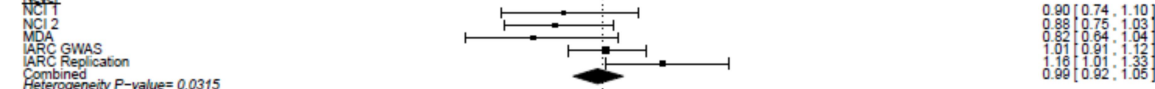
Female



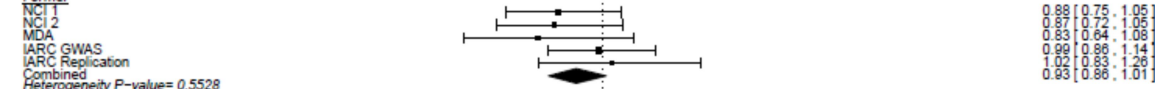
Overall Heterogeneity P-value = 0.4159

Smoking

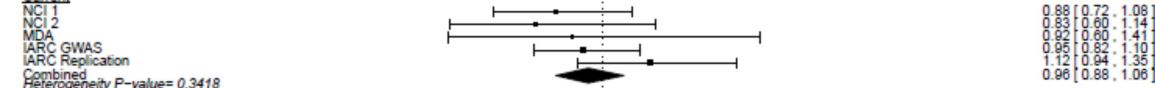
Never



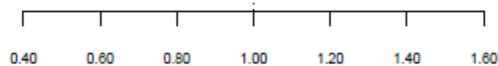
Former



Current



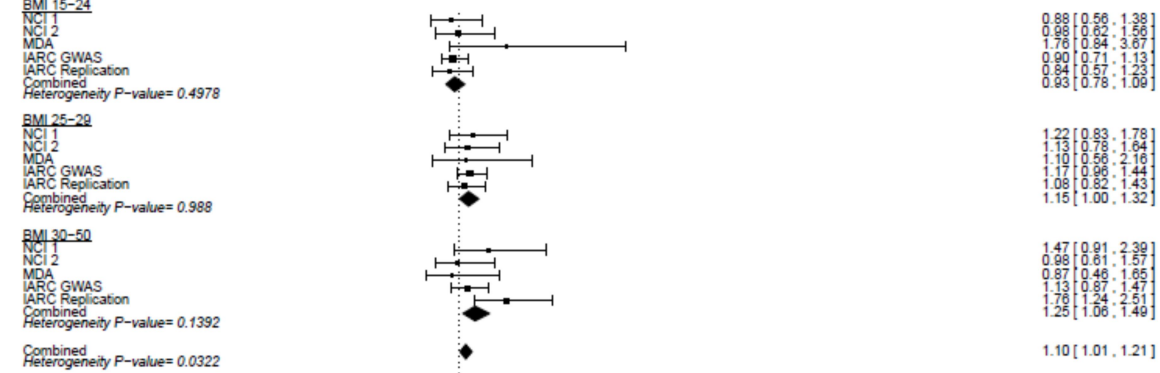
Overall Heterogeneity P-value = 0.5546



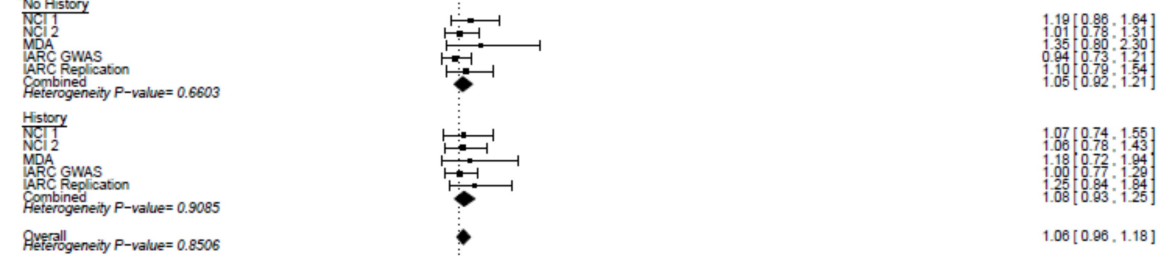
Odds Ratio

rs76912165

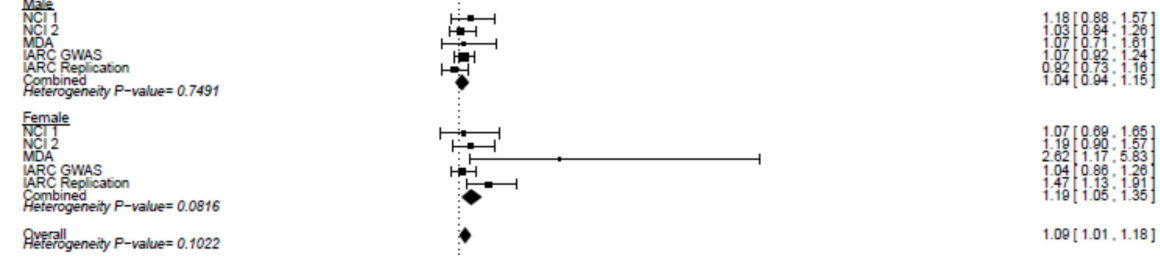
Body Mass Index



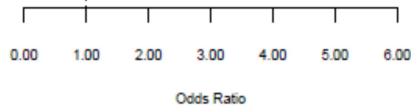
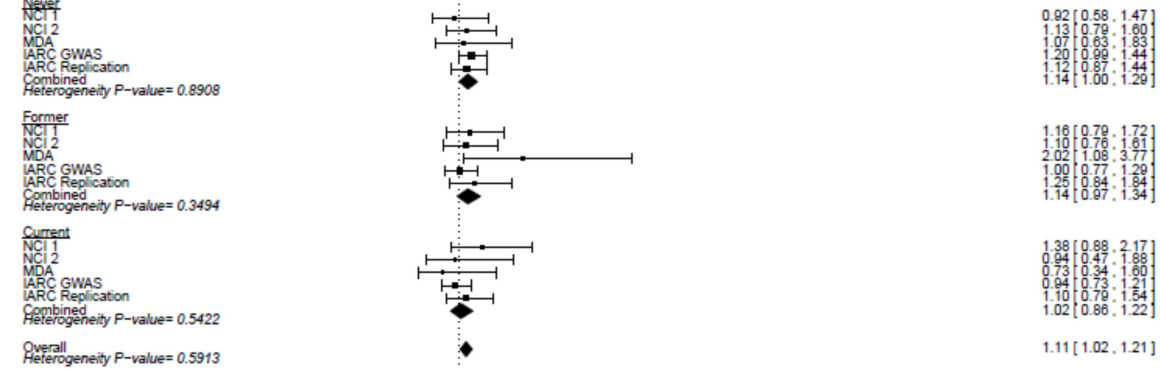
Hypertension



Sex

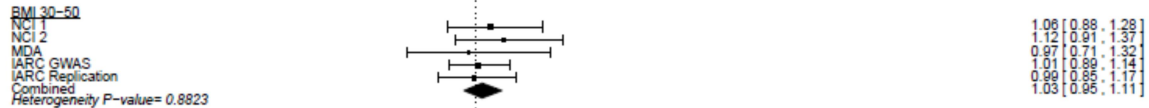
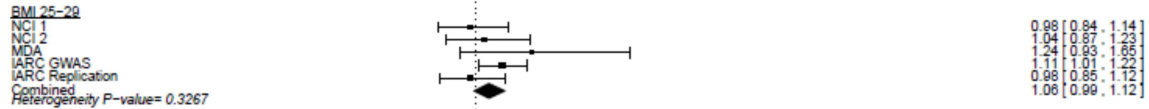
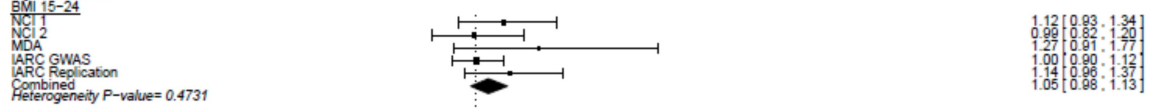


Smoking

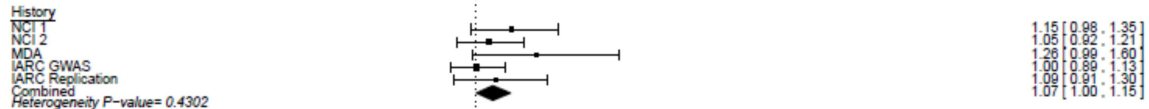
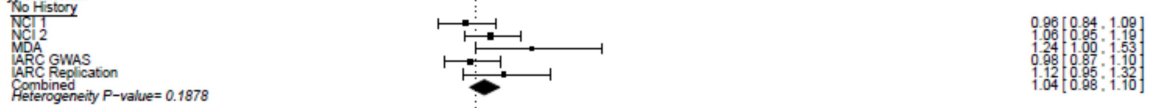


rs1266819

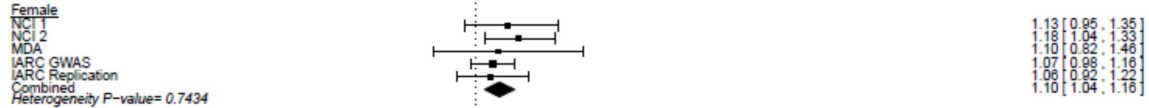
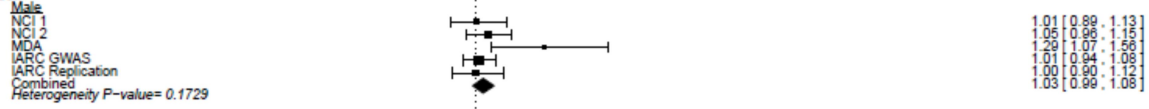
Body Mass Index



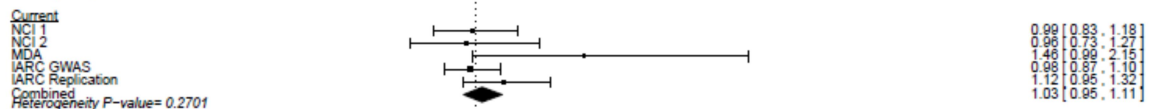
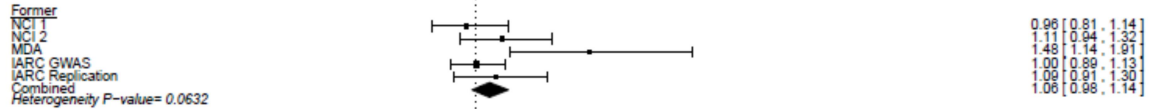
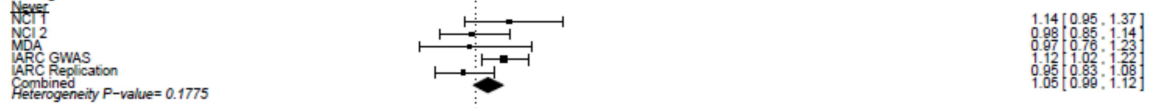
Hypertension



Sex

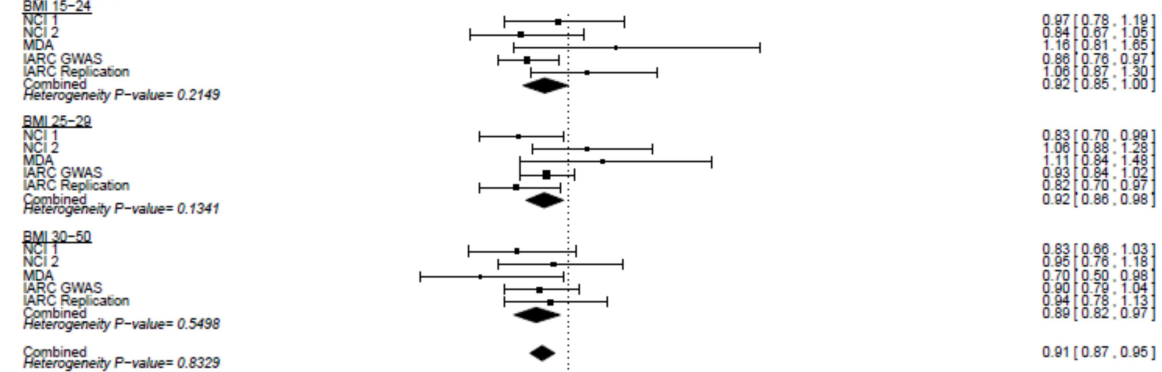


Smoking

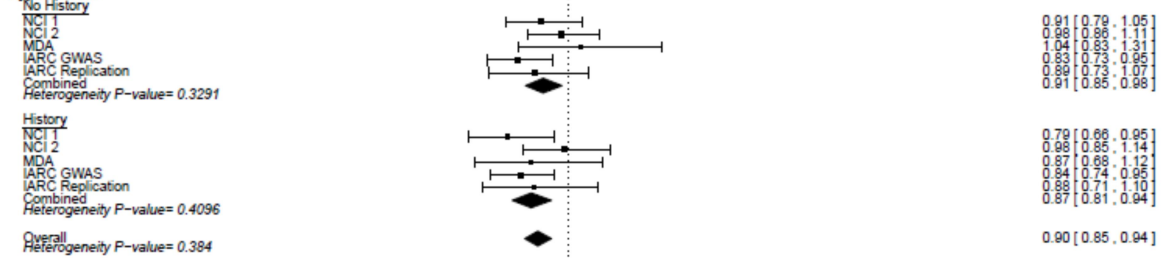


rs59294613

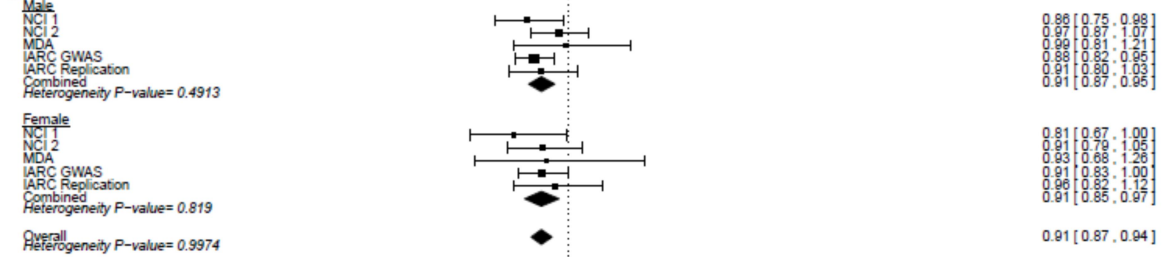
Body Mass Index



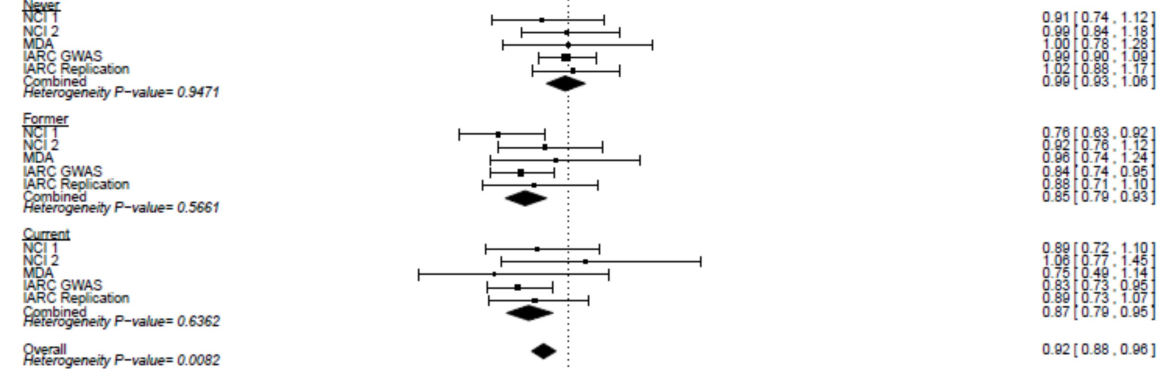
Hypertension



Sex



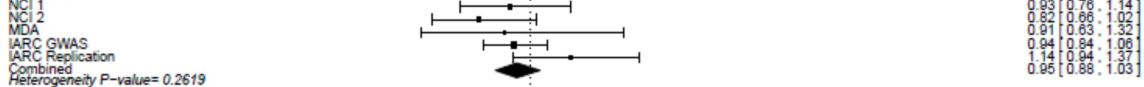
Smoking



rs73149977

Body Mass Index

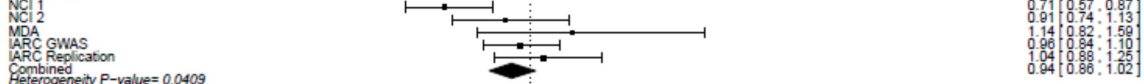
BMI 15-24



BMI 25-29



BMI 30-50

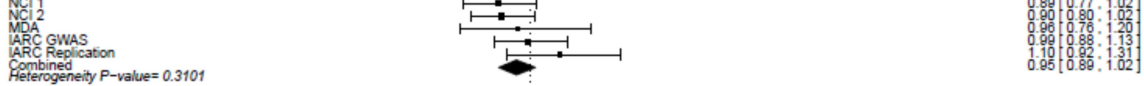


Combined
Heterogeneity P-value= 0.8895

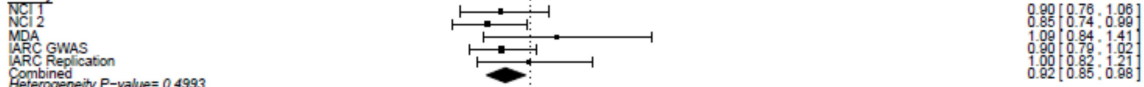
0.94 [0.90, 0.98]

Hypertension

No History



History

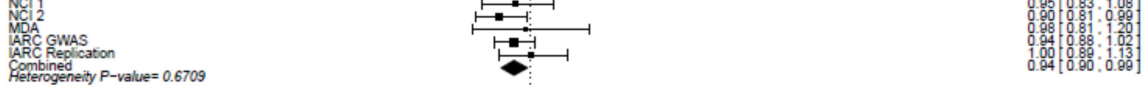


Overall
Heterogeneity P-value= 0.419

0.94 [0.89, 0.98]

Sex

Male



Female

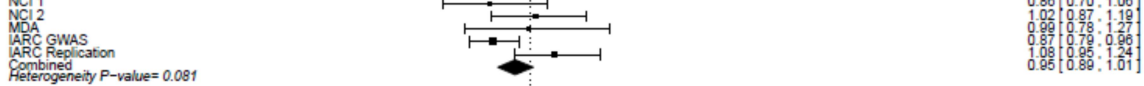


Overall
Heterogeneity P-value= 0.6981

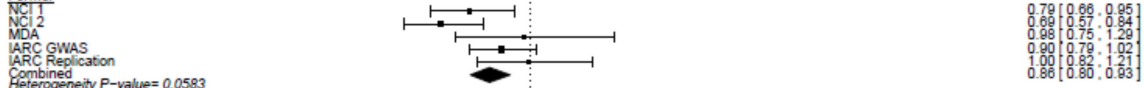
0.94 [0.90, 0.97]

Smoking

Never



Former



Current



Overall
Heterogeneity P-value= 0.013

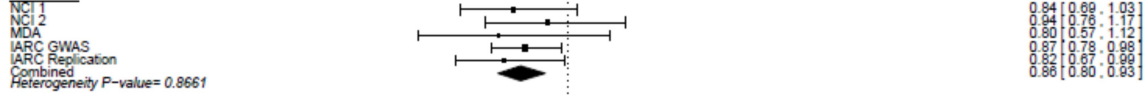
0.94 [0.90, 0.98]



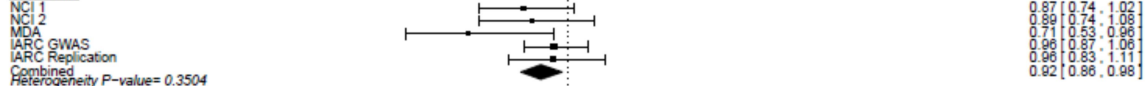
rs2889

Body Mass Index

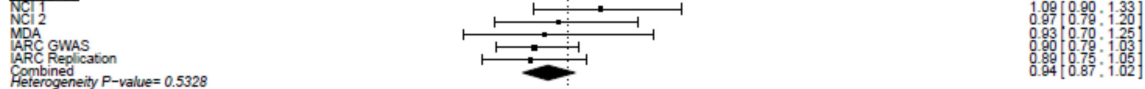
BMI 15-24



BMI 25-29



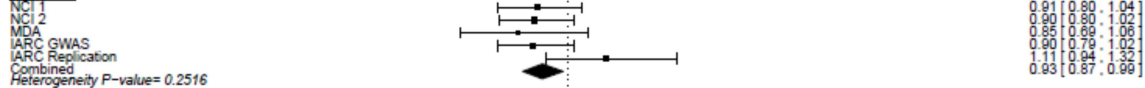
BMI 30-50



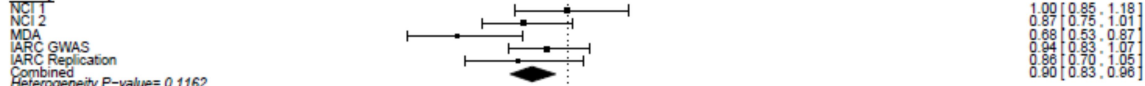
Combined Heterogeneity P-value= 0.2791

Hypertension

No History



History



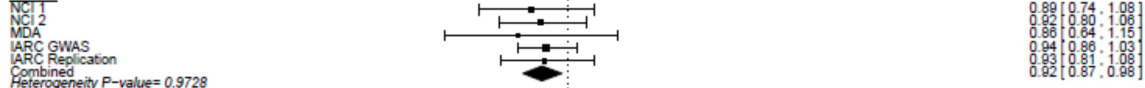
Overall Heterogeneity P-value= 0.5079

Sex

Male



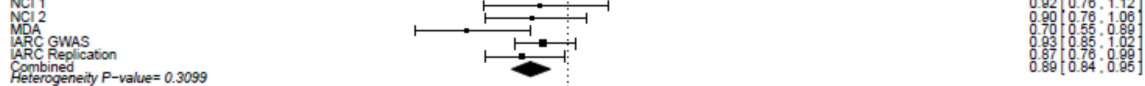
Female



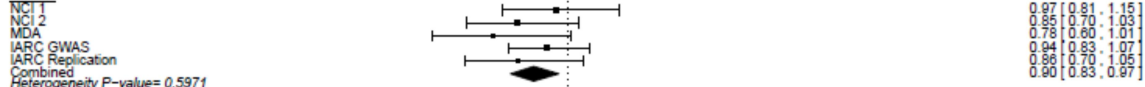
Overall Heterogeneity P-value= 0.2006

Smoking

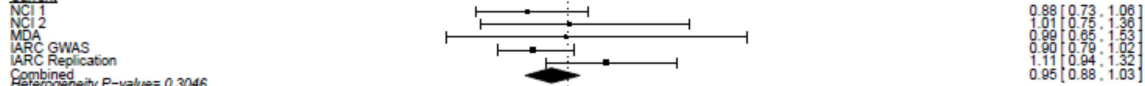
Never



Former



Current

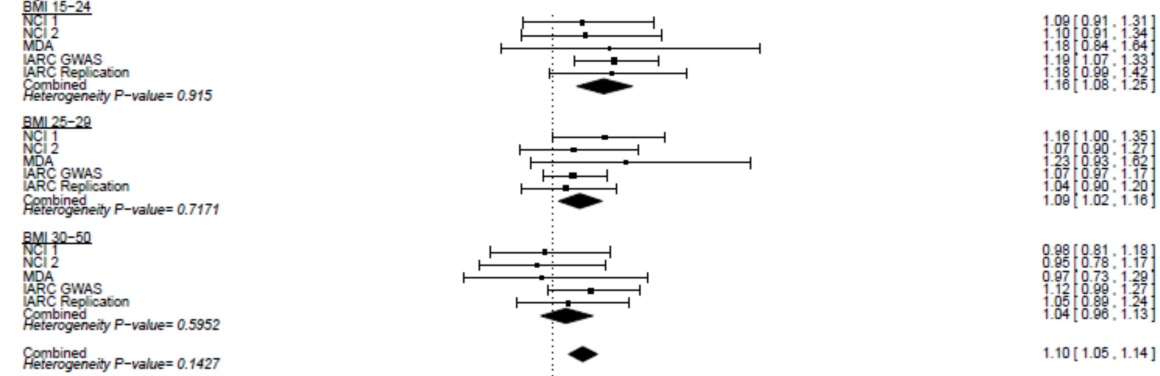


Overall Heterogeneity P-value= 0.4373

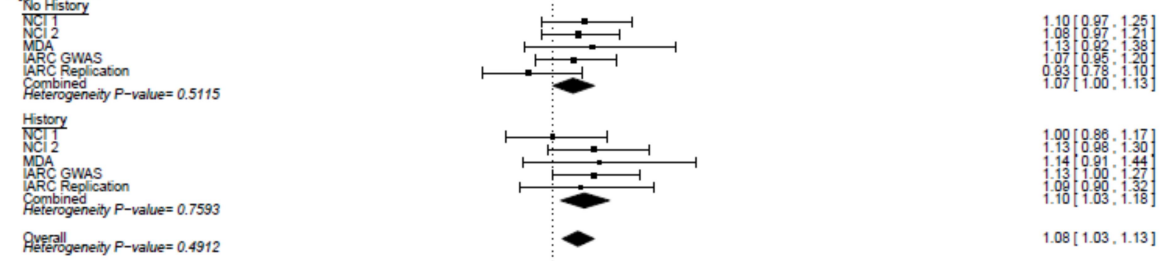


rs2241261

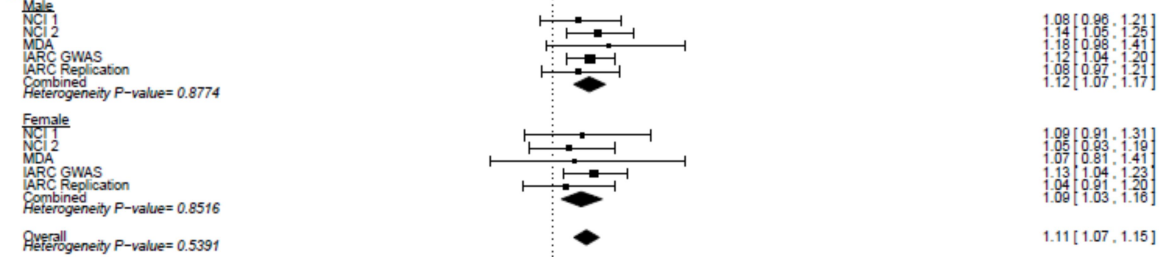
Body Mass Index



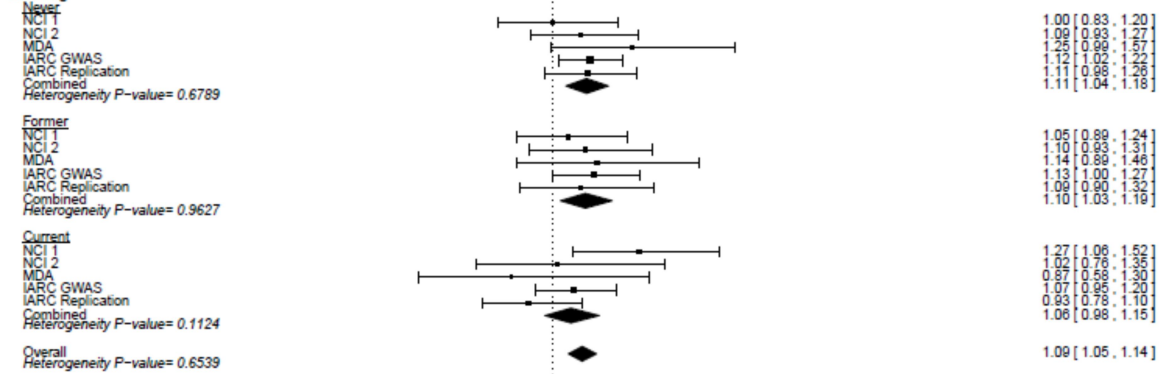
Hypertension



Sex



Smoking



rs7913447

Body Mass Index

BMI 15-24

NCI 1		0.92 [0.76, 1.12]
NCI 2		1.07 [0.86, 1.31]
MDA		0.80 [0.56, 1.14]
IARC GWAS		0.93 [0.83, 1.04]
IARC Replication		0.88 [0.73, 1.06]
Combined		0.93 [0.86, 1.01]
Heterogeneity P-value= 0.6151		

BMI 25-29

NCI 1		0.92 [0.79, 1.08]
NCI 2		0.79 [0.66, 0.95]
MDA		0.75 [0.56, 1.01]
IARC GWAS		0.95 [0.86, 1.06]
IARC Replication		0.97 [0.84, 1.12]
Combined		0.93 [0.87, 0.99]
Heterogeneity P-value= 0.1704		

BMI 30-50

NCI 1		0.84 [0.69, 1.03]
NCI 2		0.84 [0.68, 1.04]
MDA		0.97 [0.71, 1.32]
IARC GWAS		0.89 [0.78, 1.02]
IARC Replication		0.95 [0.80, 1.13]
Combined		0.89 [0.82, 0.97]
Heterogeneity P-value= 0.8341		

Combined		0.92 [0.88, 0.96]
Heterogeneity P-value= 0.7282		

Hypertension

No History

NCI 1		0.88 [0.76, 0.98]
NCI 2		0.95 [0.81, 1.05]
MDA		0.81 [0.65, 1.02]
IARC GWAS		0.97 [0.85, 1.10]
IARC Replication		1.04 [0.87, 1.23]
Combined		0.92 [0.87, 0.98]
Heterogeneity P-value= 0.3192		

History

NCI 1		0.99 [0.94, 1.17]
NCI 2		0.90 [0.78, 1.04]
MDA		0.81 [0.64, 1.03]
IARC GWAS		0.86 [0.76, 0.97]
IARC Replication		1.07 [0.89, 1.30]
Combined		0.92 [0.85, 0.99]
Heterogeneity P-value= 0.2306		

Overall		0.92 [0.88, 0.97]
Heterogeneity P-value= 0.889		

Sex

Male

NCI 1		0.94 [0.83, 1.06]
NCI 2		0.91 [0.82, 1.00]
MDA		0.84 [0.69, 1.02]
IARC GWAS		0.87 [0.77, 1.01]
IARC Replication		0.92 [0.82, 1.02]
Combined		0.92 [0.88, 0.97]
Heterogeneity P-value= 0.837		

Female

NCI 1		0.88 [0.73, 1.07]
NCI 2		0.91 [0.80, 1.04]
MDA		0.74 [0.55, 1.00]
IARC GWAS		0.95 [0.87, 1.04]
IARC Replication		0.95 [0.85, 1.13]
Combined		0.93 [0.88, 0.99]
Heterogeneity P-value= 0.5173		

Overall		0.93 [0.89, 0.96]
Heterogeneity P-value= 0.8155		

Smoking

Never

NCI 1		0.79 [0.64, 0.95]
NCI 2		0.87 [0.75, 1.02]
MDA		0.74 [0.58, 0.94]
IARC GWAS		0.99 [0.90, 1.09]
IARC Replication		0.87 [0.77, 0.99]
Combined		0.90 [0.85, 0.96]
Heterogeneity P-value= 0.068		

Former

NCI 1		0.95 [0.90, 1.13]
NCI 2		0.95 [0.72, 1.04]
MDA		0.83 [0.64, 1.07]
IARC GWAS		0.86 [0.76, 0.97]
IARC Replication		1.07 [0.89, 1.30]
Combined		0.91 [0.84, 0.98]
Heterogeneity P-value= 0.3175		

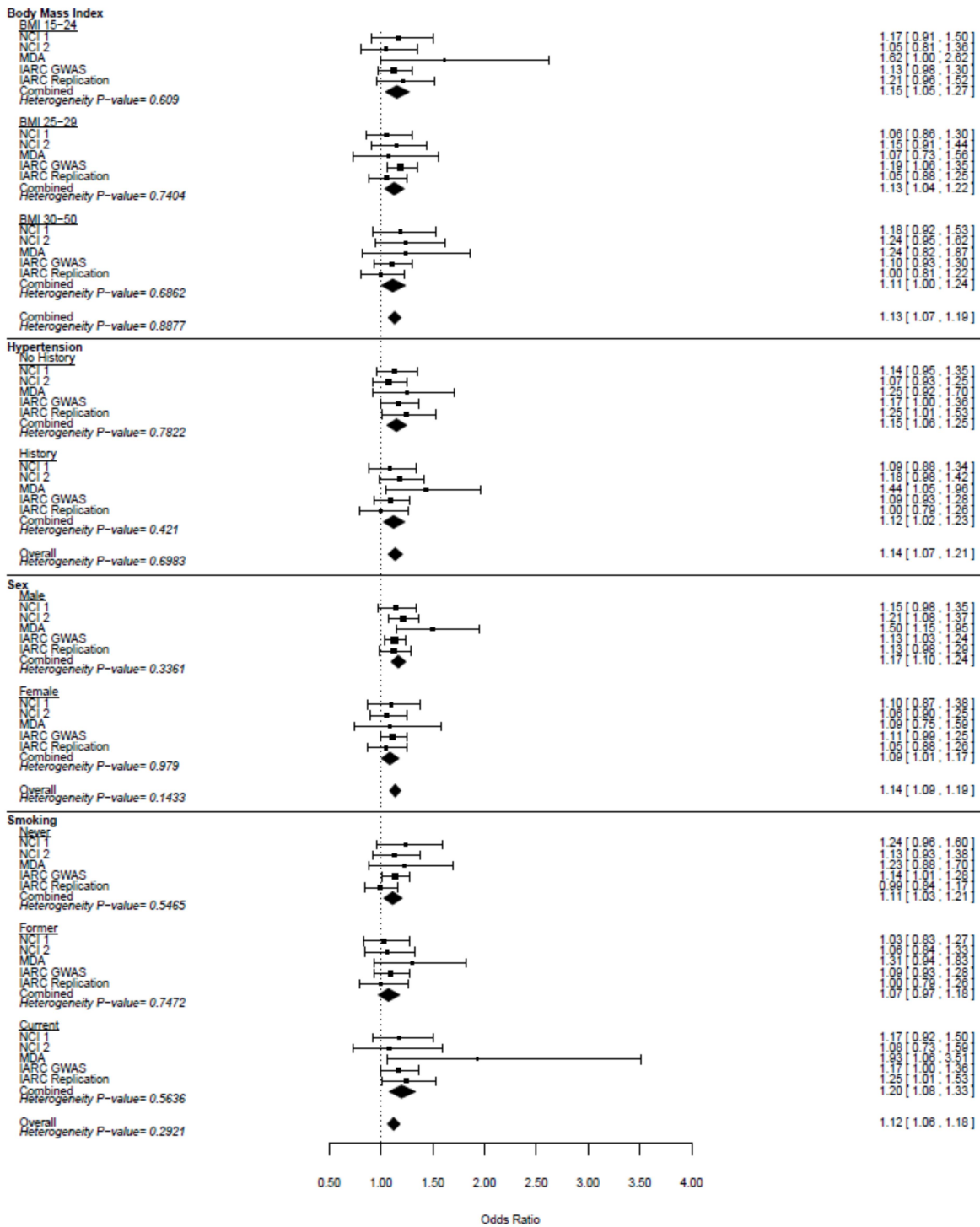
Current

NCI 1		0.97 [0.81, 1.17]
NCI 2		0.96 [0.71, 1.29]
MDA		1.09 [0.70, 1.65]
IARC GWAS		0.97 [0.85, 1.10]
IARC Replication		1.04 [0.87, 1.23]
Combined		0.99 [0.91, 1.08]
Heterogeneity P-value= 0.9614		

Overall		0.92 [0.89, 0.96]
Heterogeneity P-value= 0.1781		

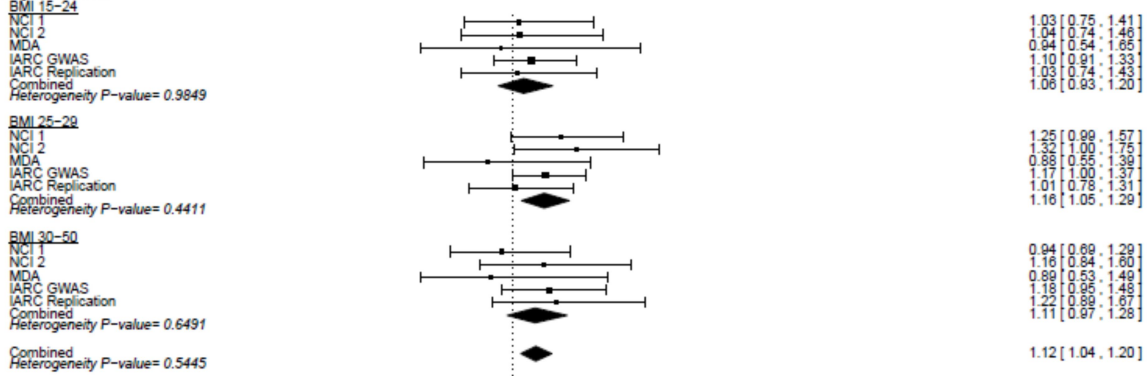


rs11813268

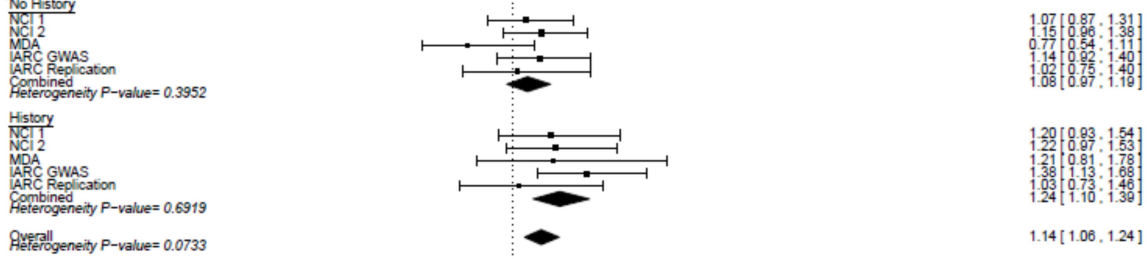


rs7774900

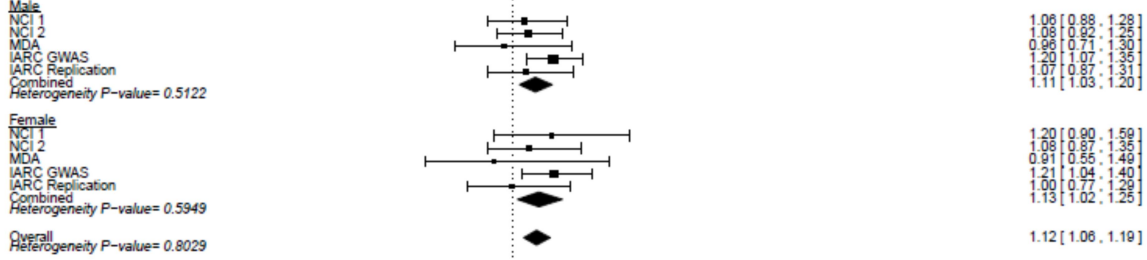
Body Mass Index



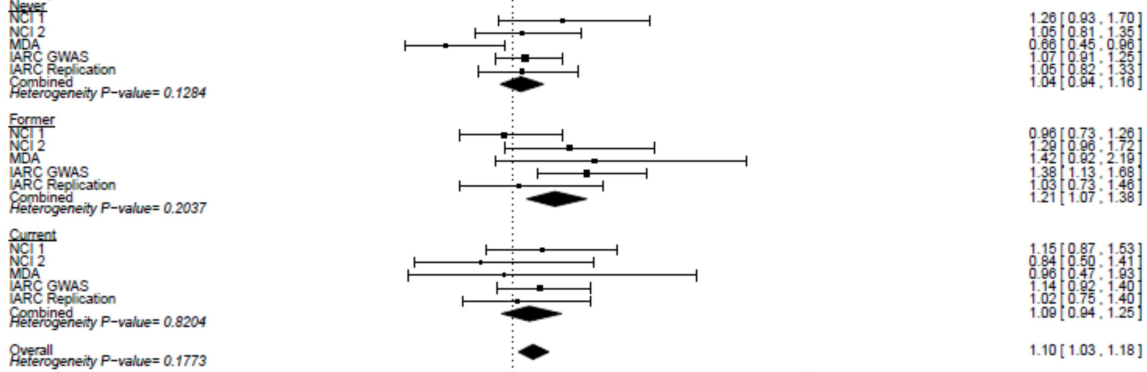
Hypertension



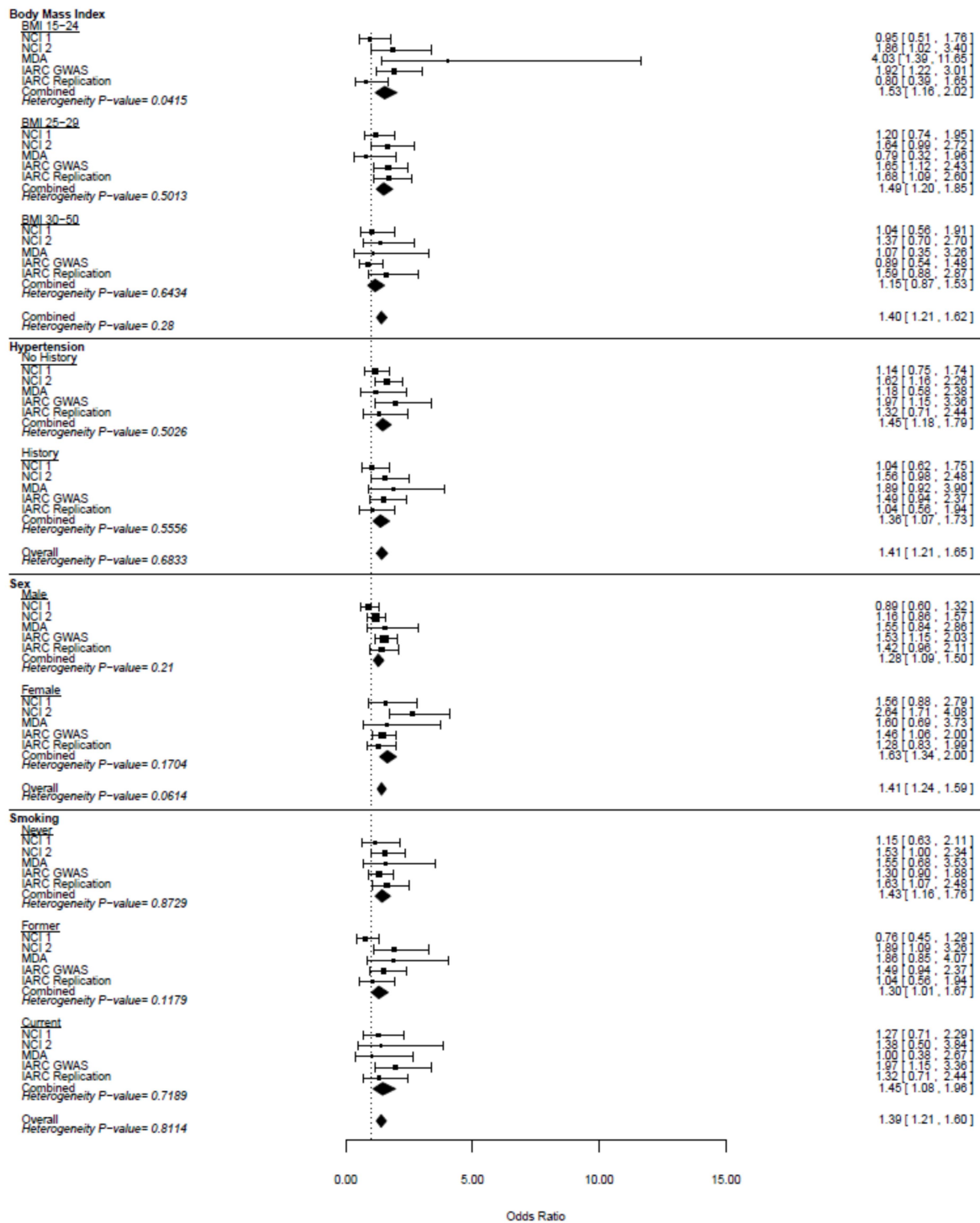
Sex



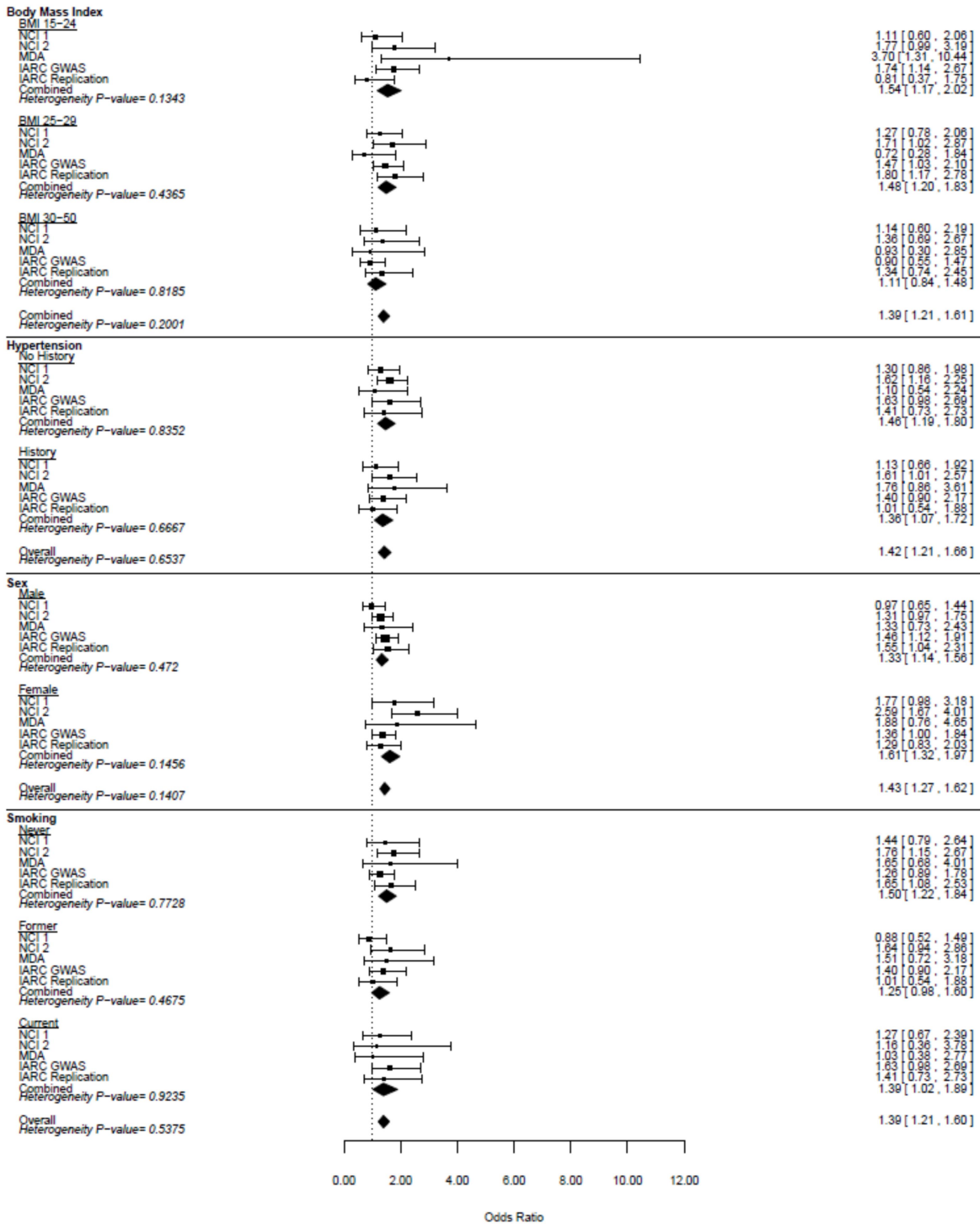
Smoking



rs1800057

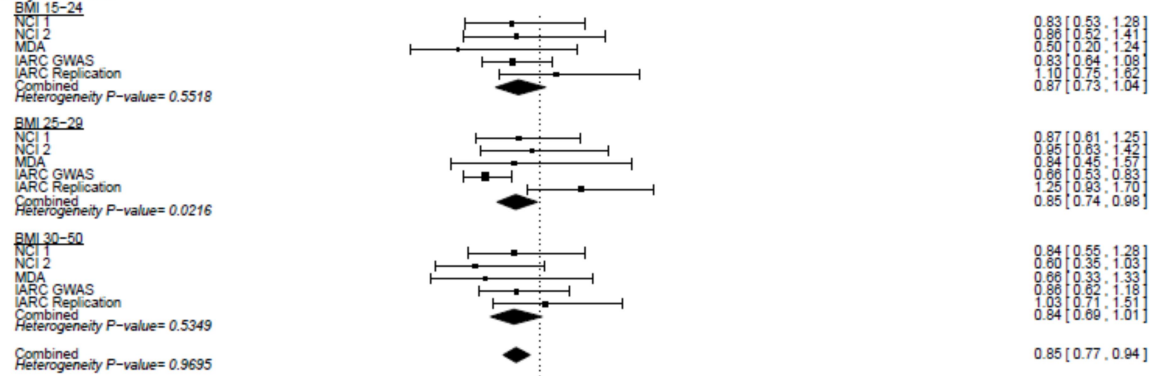


rs74911261

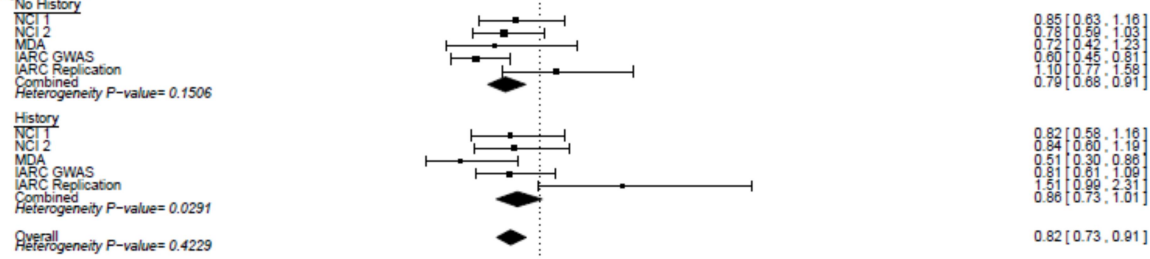


rs77736197

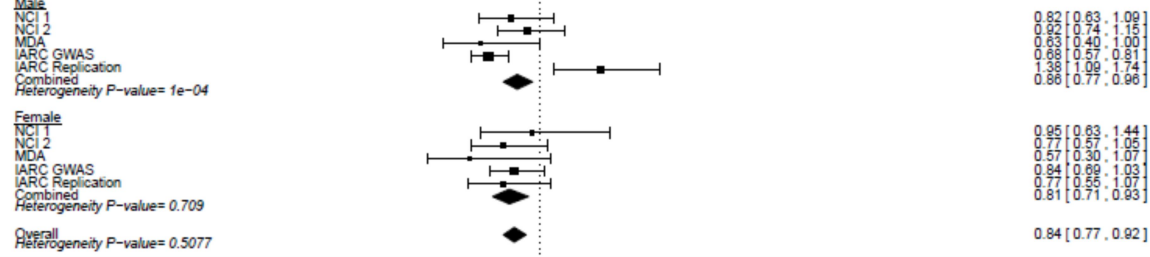
Body Mass Index



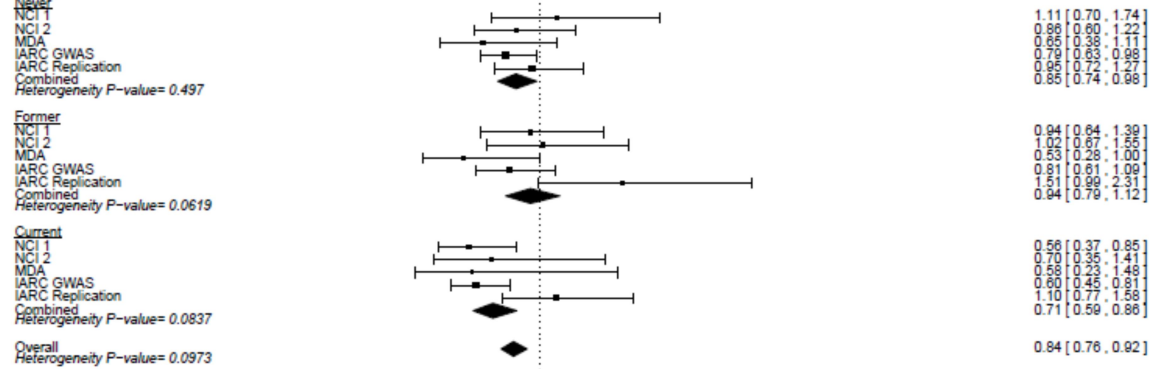
Hypertension



Sex

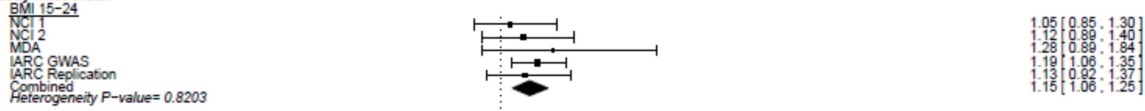


Smoking

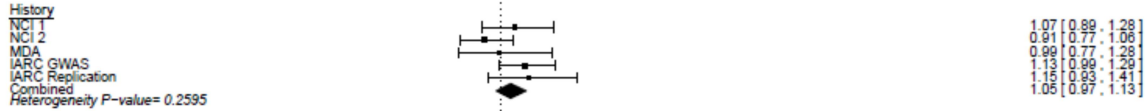
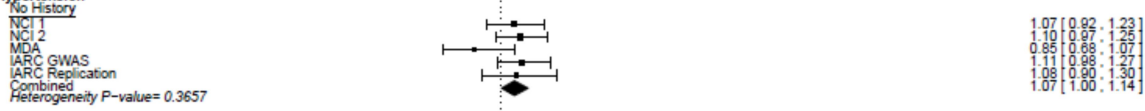


rs72730336

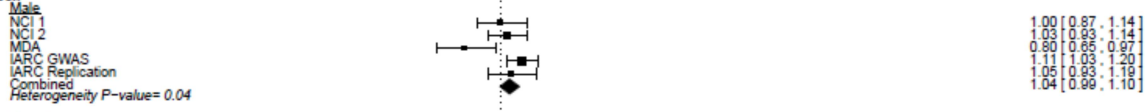
Body Mass Index



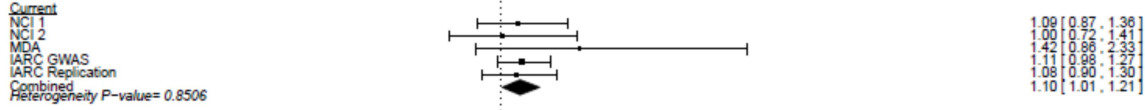
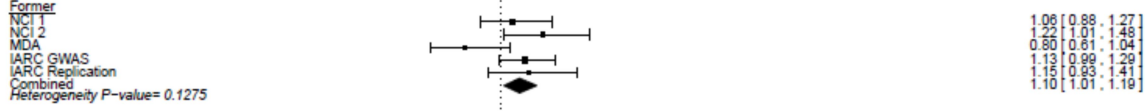
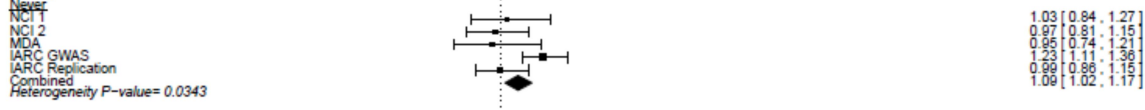
Hypertension



Sex

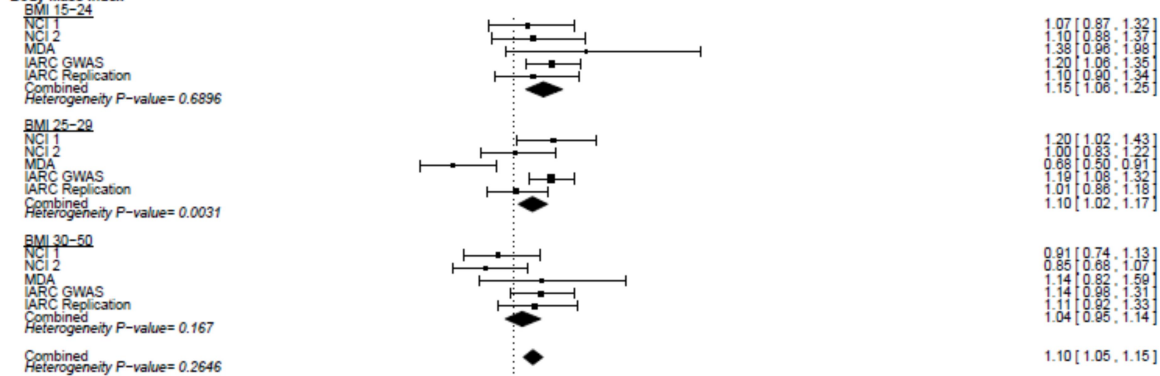


Smoking

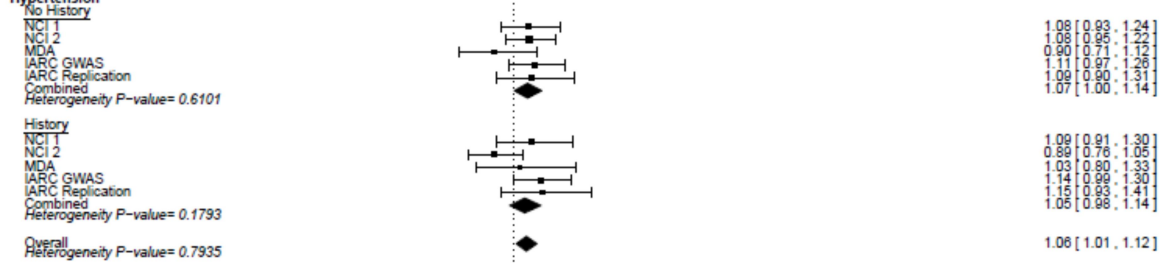


rs8007348

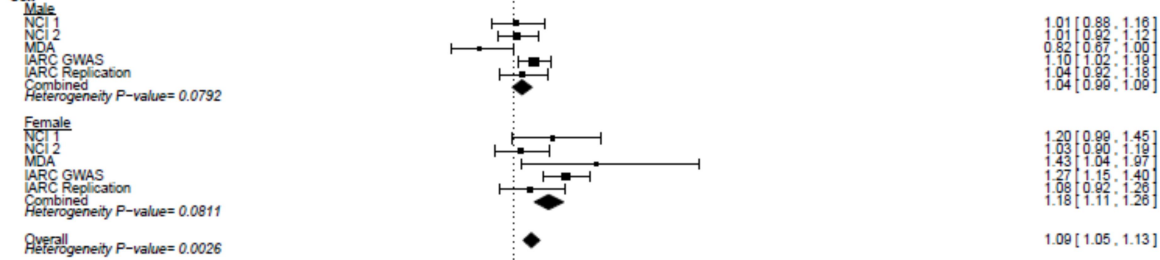
Body Mass Index



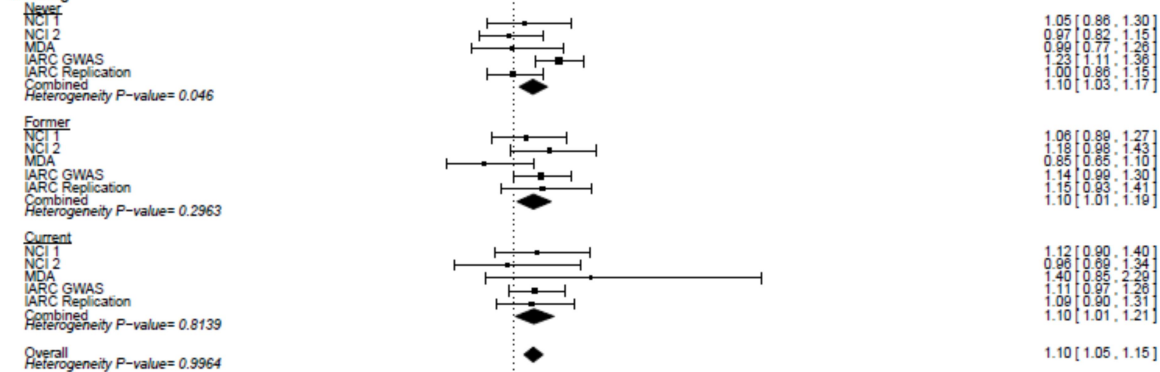
Hypertension



Sex

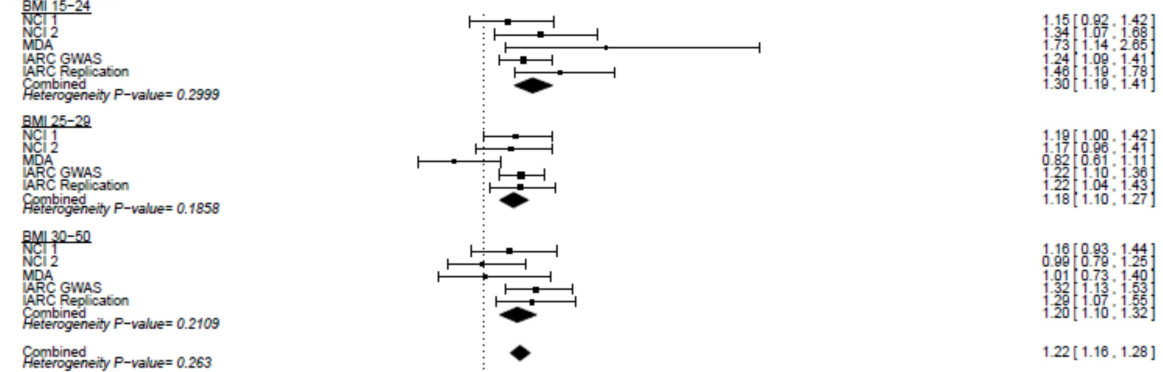


Smoking

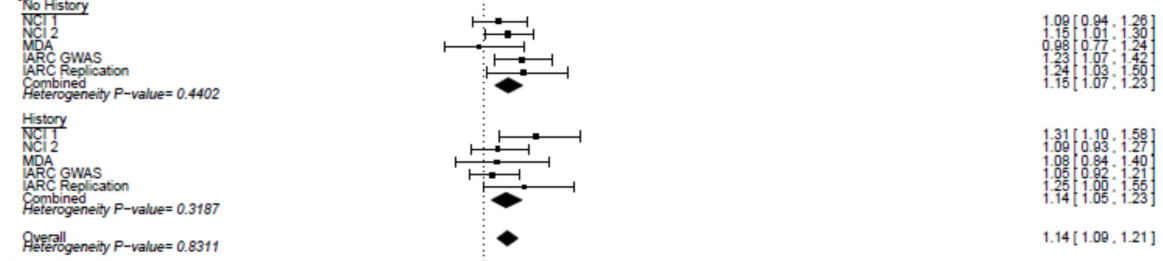


rs4903064

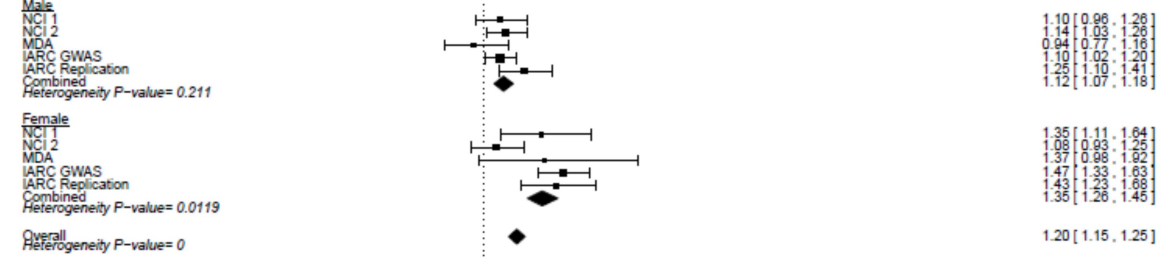
Body Mass Index



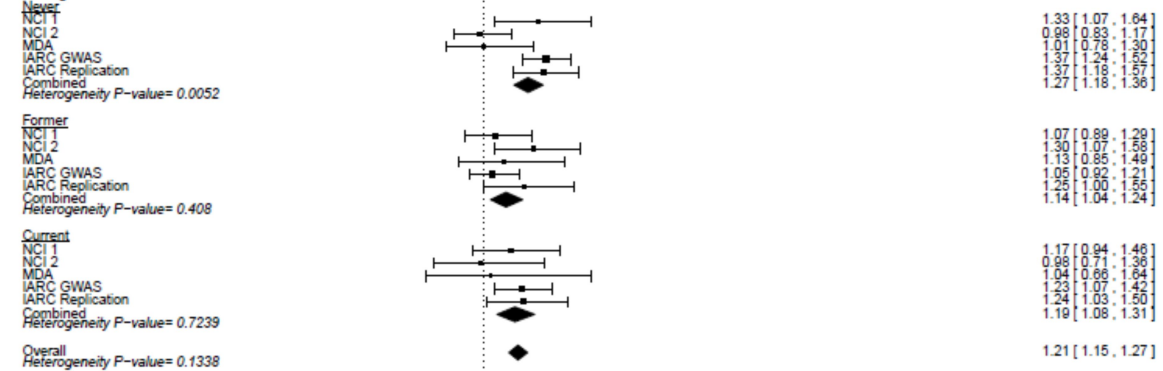
Hypertension



Sex

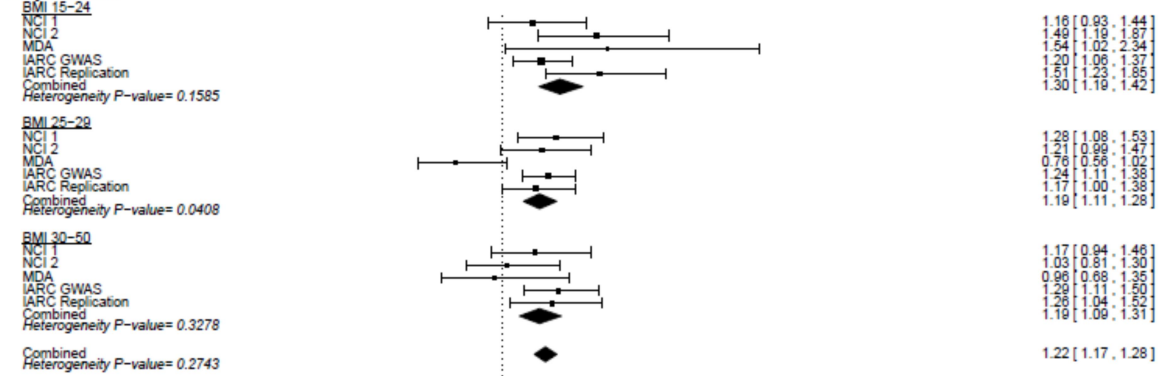


Smoking

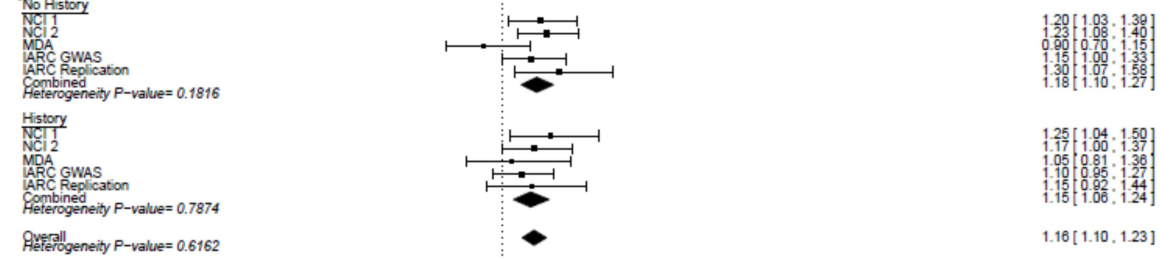


rs2109794

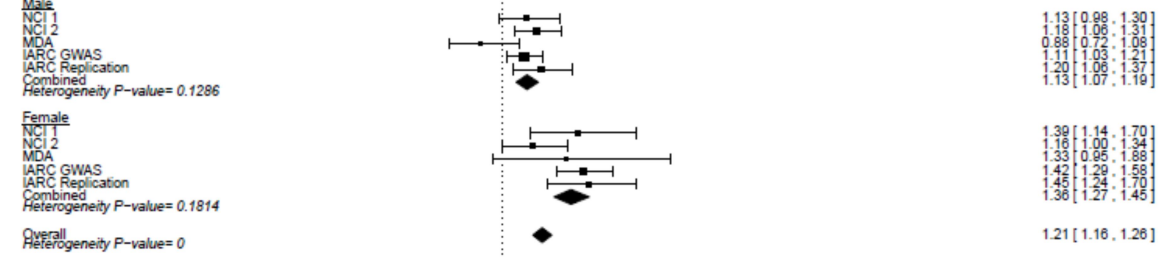
Body Mass Index



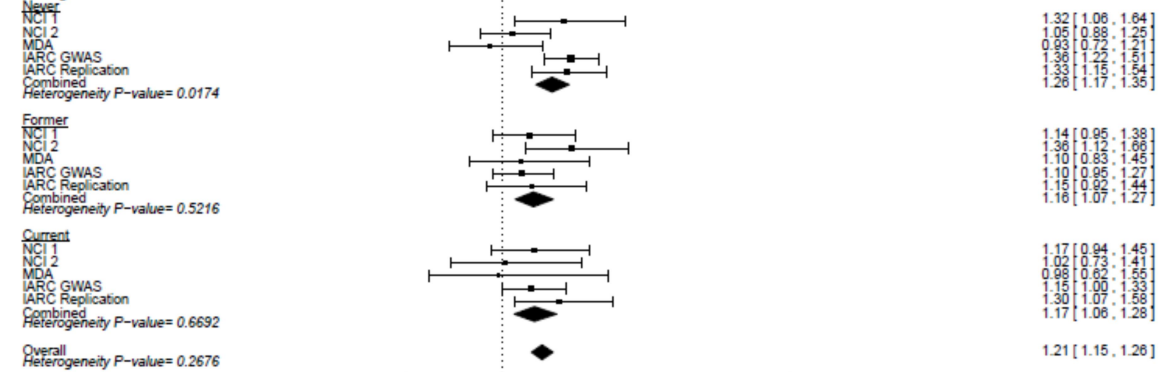
Hypertension



Sex



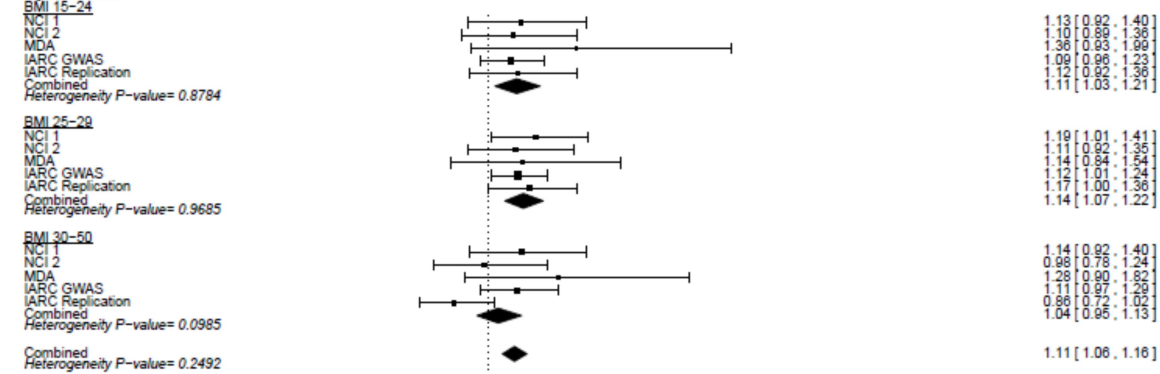
Smoking



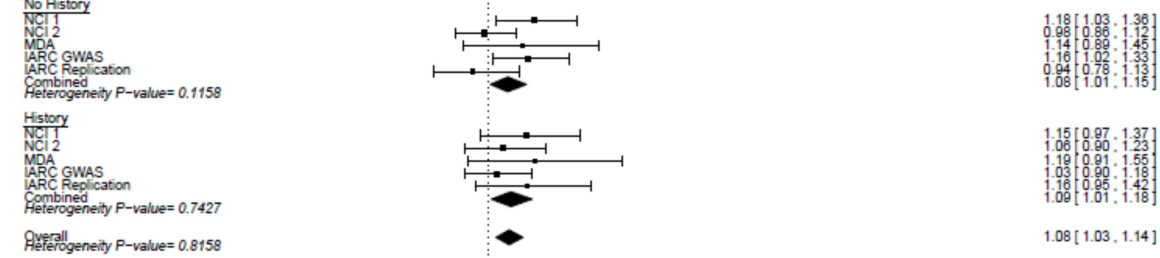
Odds Ratio

rs11637556

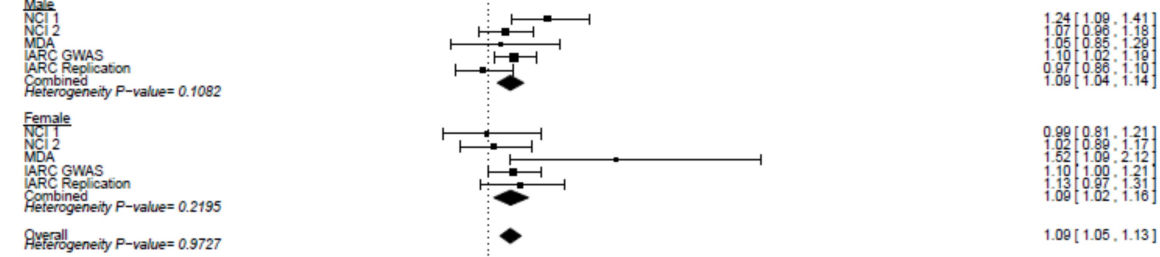
Body Mass Index



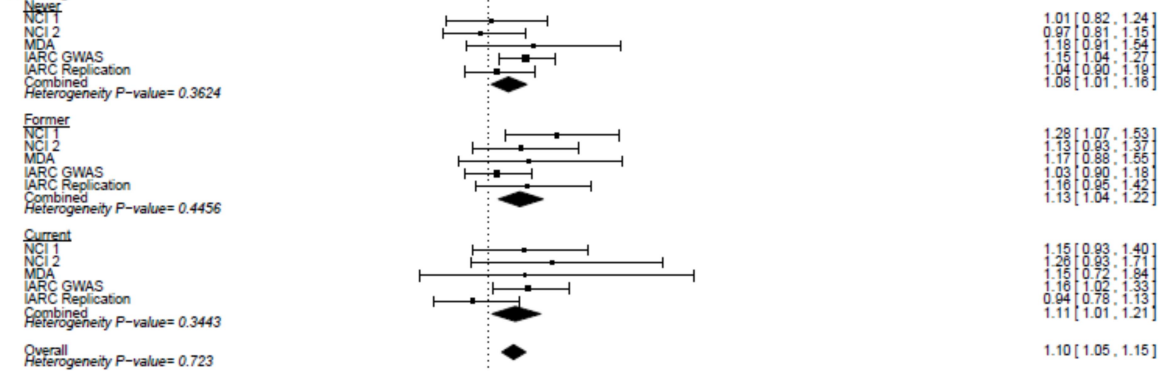
Hypertension



Sex



Smoking



rs4804368

Body Mass Index

BMI 15-24

NCI 1		1.00 [0.83 , 1.21]
NCI 2		1.05 [0.86 , 1.29]
MDA		0.71 [0.50 , 1.01]
IARC GWAS		0.95 [0.85 , 1.06]
IARC Replication		0.95 [0.79 , 1.15]
Combined		0.95 [0.89 , 1.04]
Heterogeneity P-value= 0.4388		

BMI 25-29

NCI 1		0.94 [0.80 , 1.11]
NCI 2		1.00 [0.84 , 1.19]
MDA		0.84 [0.63 , 1.10]
IARC GWAS		0.92 [0.84 , 1.02]
IARC Replication		0.95 [0.82 , 1.10]
Combined		0.94 [0.89 , 1.00]
Heterogeneity P-value= 0.8541		

BMI 30-60

NCI 1		0.99 [0.81 , 1.20]
NCI 2		0.91 [0.74 , 1.12]
MDA		0.80 [0.59 , 1.09]
IARC GWAS		0.87 [0.77 , 0.99]
IARC Replication		0.98 [0.83 , 1.17]
Combined		0.92 [0.84 , 0.99]
Heterogeneity P-value= 0.6653		

Combined		0.94 [0.90 , 0.98]
Heterogeneity P-value= 0.6837		

Hypertension

No History

NCI 1		0.92 [0.81 , 1.05]
NCI 2		0.90 [0.80 , 1.01]
MDA		0.79 [0.63 , 0.98]
IARC GWAS		0.89 [0.79 , 1.00]
IARC Replication		0.91 [0.77 , 1.09]
Combined		0.89 [0.84 , 0.95]
Heterogeneity P-value= 0.8024		

History

NCI 1		1.05 [0.89 , 1.24]
NCI 2		0.98 [0.85 , 1.13]
MDA		0.76 [0.60 , 0.97]
IARC GWAS		0.93 [0.82 , 1.05]
IARC Replication		0.97 [0.86 , 1.08]
Combined		0.95 [0.89 , 1.02]
Heterogeneity P-value= 0.2994		

Overall		0.92 [0.88 , 0.96]
Heterogeneity P-value= 0.1725		

Sex

Male

NCI 1		0.95 [0.84 , 1.08]
NCI 2		0.91 [0.83 , 0.99]
MDA		0.78 [0.64 , 0.94]
IARC GWAS		0.88 [0.82 , 0.94]
IARC Replication		1.05 [0.94 , 1.18]
Combined		0.91 [0.87 , 0.95]
Heterogeneity P-value= 0.0362		

Female

NCI 1		1.05 [0.87 , 1.26]
NCI 2		0.91 [0.80 , 1.03]
MDA		0.79 [0.59 , 1.06]
IARC GWAS		0.97 [0.89 , 1.06]
IARC Replication		0.87 [0.75 , 1.00]
Combined		0.94 [0.89 , 0.99]
Heterogeneity P-value= 0.3433		

Overall		0.92 [0.89 , 0.95]
Heterogeneity P-value= 0.501		

Smoking

Never

NCI 1		0.99 [0.82 , 1.20]
NCI 2		0.87 [0.75 , 1.02]
MDA		0.77 [0.60 , 0.98]
IARC GWAS		0.94 [0.86 , 1.03]
IARC Replication		0.98 [0.86 , 1.12]
Combined		0.93 [0.88 , 0.99]
Heterogeneity P-value= 0.3931		

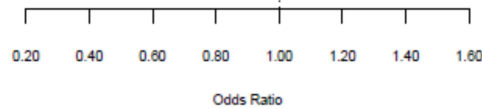
Former

NCI 1		1.20 [1.01 , 1.42]
NCI 2		1.08 [0.90 , 1.29]
MDA		0.87 [0.69 , 1.11]
IARC GWAS		0.93 [0.82 , 1.05]
IARC Replication		0.97 [0.86 , 1.08]
Combined		1.00 [0.93 , 1.08]
Heterogeneity P-value= 0.1025		

Current

NCI 1		0.73 [0.61 , 0.88]
NCI 2		1.04 [0.78 , 1.39]
MDA		0.53 [0.34 , 0.84]
IARC GWAS		0.89 [0.79 , 1.00]
IARC Replication		0.91 [0.77 , 1.09]
Combined		0.86 [0.79 , 0.93]
Heterogeneity P-value= 0.048		

Overall		0.93 [0.90 , 0.97]
Heterogeneity P-value= 0.0194		



rs714024

Body Mass Index

BMI 15-24

NCI 1	1.10 [0.90, 1.33]
NCI 2	0.94 [0.76, 1.15]
MDA	0.95 [0.68, 1.33]
IARC GWAS	1.05 [0.94, 1.18]
IARC Replication	0.97 [0.91, 1.17]
Combined	1.02 [0.95, 1.10]
Heterogeneity P-value= 0.7481	

BMI 25-28

NCI 1	1.18 [1.00, 1.38]
NCI 2	1.25 [1.02, 1.46]
MDA	1.23 [0.92, 1.64]
IARC GWAS	0.97 [0.88, 1.07]
IARC Replication	1.05 [0.91, 1.22]
Combined	1.06 [1.00, 1.14]
Heterogeneity P-value= 0.0796	

BMI 30-39

NCI 1	0.99 [0.82, 1.20]
NCI 2	1.31 [1.06, 1.63]
MDA	0.97 [0.71, 1.33]
IARC GWAS	1.17 [1.02, 1.34]
IARC Replication	0.94 [0.80, 1.11]
Combined	1.06 [1.00, 1.17]
Heterogeneity P-value= 0.0768	

Combined
Heterogeneity P-value= 0.5997

Hypertension

No History

NCI 1	1.04 [0.91, 1.19]
NCI 2	1.10 [0.98, 1.24]
MDA	1.13 [0.90, 1.41]
IARC GWAS	1.06 [0.95, 1.22]
IARC Replication	0.98 [0.82, 1.16]
Combined	1.07 [1.00, 1.14]
Heterogeneity P-value= 0.8036	

History

NCI 1	1.18 [1.01, 1.39]
NCI 2	1.07 [0.92, 1.23]
MDA	1.08 [0.85, 1.37]
IARC GWAS	1.03 [0.91, 1.17]
IARC Replication	1.13 [0.94, 1.37]
Combined	1.06 [1.01, 1.17]
Heterogeneity P-value= 0.7231	

Overall
Heterogeneity P-value= 0.6901

Sex

Male

NCI 1	1.16 [1.02, 1.30]
NCI 2	1.10 [1.00, 1.21]
MDA	1.11 [0.91, 1.34]
IARC GWAS	1.04 [0.97, 1.13]
IARC Replication	1.06 [0.91, 1.18]
Combined	1.06 [1.03, 1.13]
Heterogeneity P-value= 0.6862	

Female

NCI 1	1.00 [0.83, 1.20]
NCI 2	1.15 [1.01, 1.32]
MDA	1.12 [0.83, 1.51]
IARC GWAS	1.07 [0.98, 1.17]
IARC Replication	0.91 [0.79, 1.04]
Combined	1.05 [0.99, 1.11]
Heterogeneity P-value= 0.1327	

Overall
Heterogeneity P-value= 0.4444

Smoking

Never

NCI 1	1.17 [0.96, 1.41]
NCI 2	1.11 [0.95, 1.31]
MDA	1.06 [0.83, 1.35]
IARC GWAS	1.04 [0.94, 1.14]
IARC Replication	0.99 [0.87, 1.13]
Combined	1.05 [0.99, 1.12]
Heterogeneity P-value= 0.6224	

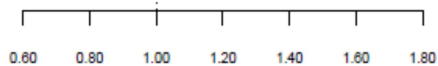
Former

NCI 1	1.09 [0.92, 1.29]
NCI 2	1.26 [1.05, 1.51]
MDA	1.21 [0.93, 1.59]
IARC GWAS	1.03 [0.91, 1.17]
IARC Replication	1.13 [0.94, 1.37]
Combined	1.11 [1.03, 1.20]
Heterogeneity P-value= 0.4496	

Current

NCI 1	1.04 [0.87, 1.25]
NCI 2	0.88 [0.66, 1.19]
MDA	0.82 [0.61, 1.09]
IARC GWAS	1.08 [0.95, 1.22]
IARC Replication	0.98 [0.82, 1.16]
Combined	1.02 [0.94, 1.11]
Heterogeneity P-value= 0.7134	

Overall
Heterogeneity P-value= 0.331



Odds Ratio

Supplementary Tables.

Supplementary Table 1. Description of the studies participating in the RCC GWAS meta-analysis.

Study Name (Abbreviation)	Design; Location	Study Population	Genotyped Samples		Samples Used in Final Analysis		Genotyping Array	
			Cases	Controls	Cases	Controls	Cases	Controls
NEW SAMPLES			5,722	7,439	5,198	7,331		
IARC-2 scan								
The European Prospective Investigation into Cancer and Nutrition (EPIC)	Prospective cohort 10 European countries	Adults aged 35-74 enrolled between 1992 and 2000 (n=521,468) Incident cancers identified through health insurance records, cancer and pathology registries and active follow-up (subjects and next of skin) Genomic DNA extracted from buffy coat	127	138	127	138	Omni 5	Omni 5
CeRePP	Case series France	Pathologically confirmed RCC recruited through the CeRePP network. Controls recruited from a systematic urologic screening program, which includes men or women who had no history or symptoms of kidney diseases and with a normal morphologic status of kidneys at ultrasonographic examination. Genomic DNA extracted from blood and saliva samples.	411	429	402	422	Omni 5	Omni 5
Umea	Prospective cohort Sweden	Population-based cohort, recruiting since 1985; resident from the Västerbotten county in northern Sweden. Incident cases identified through linkage to national death and cancer registries. Genomic DNA extracted from blood.	306	312	297	301	Omni 5	Omni 5
Karolinska	2 Prospective cohorts Sweden	COSM: Cohort of Swedish Men (45,306 men enrolled in 1997) and SMC: Swedish Mammography Cohort (61,433 women enrolled between 1987 and 1990), in central Sweden. Incident cases identified through linkage to national death and cancer registries. Genomic DNA extracted from saliva.	131	298	131	295	Omni 5	Omni 5
Consortium For the Investigation of Renal Malignancies/ Melbourne Collaborative Cohort Study (ConFIRM/MCCS)	Case-control and cohort studies; Australia	Incident cases diagnosed in Victoria and Queensland in the period 2011-2014 and aged 18-74 years (ConFIRM), and from within the MCCS when fresh blood collected; Controls selected from healthy participants in the MCCS cohort; Genomic DNA extracted from whole blood (ConFIRM) and buffy coat (MCCS).	188	398	184	396	Omni 5	Omni 5
The IARC K2 study	Case-control study 4 central/eastern Europe countries	Multicentric study conducted in 2007-2013 in Russia, Czech Republic, Romania, and Serbia. Hospital or population-based controls depending on recruiting centers.	1,675	1,458	1,640	1,388	Omni 5	Omni 5/ Omni Express
IARC-2 Scan Total			2,838	3,033	2,781	2,940		
NCI-2 Scan:								
Agricultural Health Study (AHS)	Prospective cohort; USA (Iowa, North Carolina)	Private and commercial pesticide applicators and spouses of private applicators, enrolled between 1993 and 1997 (n = 89,655). Incident cancers identified through linkage with state cancer registries. Germline DNA extracted from buccal cell samples.	78	-	7	-	Omni Express	-
Alpha-Tocopherol, Beta-Carotene Cancer Prevention Study (ATBC)	Prospective cohort / randomized trial; Finland	Male smokers aged 50-69 at entry, enrolled between 1985 and 1988 (n = 29,133). Incident cancers identified through linkage to Finnish Cancer Registry. Germline DNA extracted from whole blood samples.	41	221*	39	221*	Omni Express	Omni 2.5

BioVU	Hospital biorepository; USA (Nashville)	Renal cancer patients treated at Vanderbilt University Medical Center between 2006 and 2012. Controls selected from among patients admitted for non-cancer condition, frequency matched by age and sex.	714	222	629	207	Omni Express	Omni Express
American Cancer Society Cancer Prevention Study II Nutrition Cohort (CPS-II)	Prospective cohort; USA	Men and women aged 50-74 at entry, enrolled between 1992 and 1993 (n = 184,194). Incident cancers identified from biannual follow-up questionnaires or linkage with state cancer registries. Germline DNA extracted from blood and buccal cell samples.	85	212*	70	212*	Omni Express	Omni 2.5
Dana-Farber/Harvard Cancer Center (DFHCC)	Case series; USA (Boston)	Patients with localized renal cancer treated at DFHCC between 2002 and 2010. Genomic DNA extracted from blood samples.	234	-	206	-	Omni Express	-
Health Professionals Follow-up Study (HPFS)	Prospective cohort; USA	Men in selected health professions, enrolled in 1986 (n = 51,529). Incident cancers identified from follow-up questionnaires and subsequent medical record review. Germline DNA extracted from blood samples.	50	85*	38	85*	Omni Express	Omni Express
Nurses' Health Study (NHS)	Prospective cohort; USA	Female registered nurses aged 30-55, enrolled in 1976 (n = 121,700). Incident cancers identified by mailed follow-up questionnaire and subsequent medical record review. Germline DNA extracted from blood samples.	66	434*	57	434*	Omni Express	Omni Express
Physicians Health Study (PHS)	Prospective cohort / randomized trial; USA	Male physicians aged 50+ enrolled between 1982 and 1984 (n = 22,071). Incident cancers identified by mailed follow-up questionnaire. Germline DNA extracted from blood samples.	27	-	21	-	Omni Express	-
Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial (PLCO)	Prospective cohort / cancer screening trial; USA	Men and women aged 55-74 at entry, enrolled between 1993 and 2001 (n = 155,000). Incident cancers identified from annual questionnaires, with confirmation through medical records. Germline DNA extracted from buffy coat and buccal cell samples.	118	3,003*	93	3,003*	Omni Express	Omni 2.5
Van Andel Research Institute (VARI)	Case series; USA	Renal cancer patients treated at the Spectrum Health Hospital in Grand Rapids, MI, and in hospitals affiliated with the Cooperative Human Tissue Network (CHTN). Germline DNA extracted from adjacent normal kidney tissue.	1,050	-	920	-	Omni Express	-
Vitamins and Lifestyle Study (VITAL)	Prospective cohort; USA (Washington State)	Men and women aged 50-76, enrolled between 2000 and 2002. Incident cancers identified by linkage to the western Washington SEER cancer registry. Germline DNA extracted from buccal cell samples.	112	-	91	-	Omni Express	-
Women's Health Initiative (WHI)	Prospective cohort / randomized trial; USA	Women aged 50-79, enrolled between 1993 and 1998. Incident cancers were identified by mailed follow-up questionnaires, and verified by medical records. Genomic DNA extracted from buffy coat samples.	300	229*	239	229*	Omni Express	Omni Express
Women's Health Study (WHS)	Prospective cohort / randomized trial; USA	Female health professionals aged 45 years or older, enrolled in 1993. Incident cancers identified by mailed follow-up questionnaire. Genomic DNA extracted from blood samples.	9	-	7	-	Omni Express	-
NCI-2 Scan Total			2,884	4,406	2,417	4,391		

PREVIOUSLY AVAILABLE SAMPLES	6,031	13,436	5,585	13,075
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IARC-1 scan

The European Prospective Investigation into Cancer and Nutrition (EPIC) [additional to above]	Prospective cohort 10 European countries	Adults aged 35-74 enrolled between 1992 and 2000 (n=521,468). Incident cancers identified through health insurance records, cancer and pathology registries and active follow-up (subjects and next of kin). Genomic DNA extracted from buffy coat	319	434	275	414	610Q	550K
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The Nord-Trøndelag Health (HUNT2) and Tromsø Studies (Tromsø IV)	2 Prospective cohorts Norway	HUNT2: Adults aged 20+ enrolled between 1995 and 1997 (N=65,285) Tromsø IV: Adults aged 25+ enrolled between 1994-1995 (N=27,158) Cases identified through Norwegian Cancer Registries Genomic DNA extracted from buffy coat	145	433	133	388	610Q	317K
The NCI/IARC study in central Europe (CE)	Case-control study 4 European countries	Hospital based study conducted between 1999-2003 (except Poland) 2004-2007 (Poland). Controls matched to lung cancer and included in previous GWAS of lung cancer Genomic DNA extracted from buffy coat and RBC	1,152	2,179	1,096	2,058	317K	317K
Arsenic Health Risk Assessment and Molecular Epidemiology study in Central Europe (ASHRAM)	Case-control study Slovakia and Hungary	Cases recruited in 6 counties between 2002-2004 Controls matched to lung cancer and included in previous GWAS of lung cancer Genomic DNA extracted from whole blood	89	425	84	399	610Q	317K
CeRePP [additional to above]	Case series France	Pathologically confirmed RCC involved in PROGENE-CeRePP cohort French controls originally participated in a hospital based case-control study of UADT cancer Genomic DNA extracted from blood	79	166	58	146	610Q	317K
The Leeds cohort	Case series UK	RCC from the Leeds cohort recruited between 1998-2007 Genomic DNA extracted from blood	363	-	348	-	610Q	-
SEARCH Kidney cancer study (SEARCH)	Case series UK	Population based case series including all patients with a kidney cancer aged 70- and diagnosed between 2002-2006 Genomic DNA extracted from blood	187	-	181	-	610Q	-
WTCCC	Controls UK	Dataset generated by the Wellcome Trust Sanger Institute in collaboration with the 1958 Birth cohort Genomic DNA extracted from blood	-	1,438	-	1,361	-	550K
Moscow	Case-control study Moscow	Incident cases were recruited between 2007-2009. Hospital based controls were match and recruited during same period Genomic DNA extracted from blood	305	323	263	305	610Q	610Q
IARC -I Scan Total			2,639	5,398	2,438	5,071		
<u>NCI-I Scan:</u>								
Alpha-Tocopherol, Beta-Carotene Cancer Prevention Study (ATBC)	See above	See above	177	1,288*	163	1,288*	660W	610K
American Cancer Society Cancer Prevention Study II Nutrition Cohort (CPS-II)	See above	See above	226	730*	202	730*	660W	610K
Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial (PLCO)	See above	See above	330	845*	284	845*	660W	550/610K
National Cancer Institute U.S. Kidney Cancer Study (USKC)	Case-control; USA (Chicago, Detroit)	Cases: 1,227 men and women aged 20-79 at diagnoses, identified from Chicago hospital records and Metropolitan Detroit Cancer Surveillance System between 2003 and 2007. Controls: 1,235 men and women recruited from state Department of Motor Vehicle records (ages 30-64) and Medicare beneficiary records (ages 65+), frequency matched to cases on age, race, sex, region. Genomic DNA extracted from blood and buccal cell samples.	720	595	662	561	610K	610K
NCI-I Scan Total:			1,453	3,458	1,311	3,424		

<u>MD Anderson Scan:</u>	Case-control; USA (Texas)	Cases: 894 Caucasian men and women treated for renal cancer at the University of Texas MD Anderson Cancer Center. Controls:556 Caucasian men and women identified through random-digit dialing. Genomic DNA extracted from blood samples.	894	556	893	556	660W	660W
<u>UK Scan:</u>	Case series; UK	Cases: adult renal cancer patients identified from UK clinical oncology centers and the Institute of Cancer Research and Royal Marsden NHS Hospitals Trust. Controls: previously genotyped samples from the Wellcome Trust Case Control Consortium 2 1958 birth cohort and UK Blood Service Control Group (WTCC controls included in the IARC-1 scan were excluded). Genomic DNA extracted from blood samples.	1,045	4,024*	944	4,024*	Omni Express	Hap 1.2M Duo

*Previously scanned controls

Supplementary Table 2. Meta-analysis results for previously reported RCC GWAS loci

SNP	Locus	Previously Reported GWAS				Current Meta-Analysis				
		Study	OR	(95% CI)	<i>P</i>	OR	(95% CI)	<i>P</i>	<i>P</i> _{Heterogeneity}	MAF
rs3845536	1q24.1	Henrion et al. ¹	1.21	(1.13-1.30)	2.3 x 10 ⁻⁸	1.05	(1.01-1.09)	0.0062	3.0 x 10 ⁻⁵	0.36
rs7579899	2p21	Purdue et al. ²	1.15	(1.10-1.21)	2.3 x 10 ⁻⁹	1.15	(1.11-1.20)	5.3 x 10 ⁻¹⁵	0.31	0.49
rs11894252	2p21	Purdue et al. ²	1.14	(1.09-1.20)	1.8 x 10 ⁻⁸	1.16	(1.12-1.20)	2.7 x 10 ⁻¹⁵	0.28	0.49
rs12105918	2q22.3	Henrion et al. ³	1.29	(1.18-1.41)	1.8 x 10 ⁻⁸	1.25	(1.16-1.34)	3.9 x 10 ⁻⁹	0.14	0.06
rs35252396*	8q24	Gudmundsson et al. ⁴	1.27	(1.18-1.37)	5.4 x 10 ⁻¹¹	1.13	(1.10-1.18)	2.8 x 10 ⁻¹²	0.17	0.44
rs7105934	11q13	Purdue et al. ²	0.69	(0.62-0.76)	7.8 x 10 ⁻¹⁴	0.70	(0.65-0.75)	4.9 x 10 ⁻²²	0.20	0.08
rs718314	12p11.23	Wu et al. ⁵	1.19	(1.13-1.26)	8.9 x 10 ⁻¹⁰	1.18	(1.14-1.23)	2.2 x 10 ⁻¹⁶	0.45	0.26
rs1049380	12p11.23	Wu et al. ⁵	1.18	(1.12-1.25)	6.1 x 10 ⁻⁹	1.15	(1.11-1.19)	2.0 x 10 ⁻¹²	0.02	0.44
rs4765623	12q24	Purdue et al. ²	1.15	(1.09-1.20)	2.6 x 10 ⁻⁸	1.14	(1.10-1.18)	2.8 x 10 ⁻¹²	0.22	0.34

ORs computed for minor allele vs. common allele.

*Current meta-analysis based on rs64070588, in complete LD with rs35252396.

Supplementary Table 3. Description of the studies included in replication stage.

Study Name (Abbreviation)	Design; Location	Study Population	Genotyped Samples	
			Cases	Controls
IARC Replication	Case-control and cohort studies; Europe and Australia	The sample set was composed of additional cases and controls selected from the following studies described in Supp table 1: IARC K2, CE, Umea, and ConFIRM/MCCS	1,674	4,222
Mayo Clinic (Mayo)	Case-control; USA	Cases: Caucasian men and women treated for RCC at Mayo. Controls: patients admitted to General Medicine Clinics at Mayo	909	1,479
MD Anderson (MDA)	Case-control; Houston, USA	Cases: Caucasian men and women treated for renal cancer at MDA. Controls: Caucasian men and women identified through random-digit dialing. (additional samples to these described in Supp table 1).	599	600

Supplementary Table 4. Technical validation of top SNPs; concordance rates between genome-wide-scanned or imputed SNPs and Taqman genotyping.

SNP	IARC-1/2		NCI-2	
	% concordance	Pearson correlation coefficient (r^2)	% concordance	Pearson correlation coefficient (r^2)
rs10936602 ^a	99.6	0.995	100.00	1.000
rs11637556 ^b	99.8	0.998	100.00	0.999
rs11813268 ^b	97.8	0.958	99.82	0.994
rs1266819 ^b	99.7	0.997	99.82	0.996
rs13376700 ^b	99.7	0.997	99.46	0.985
rs17050872 ^a	98.3	0.979	100.00	1.000
rs1800057 ^b	98.8	0.824	98.89	0.817
rs2109794 ^b	99.3	0.990	99.81	0.989
rs2203002 ^a	99.3	0.971	99.05	0.878
rs2241261 ^a	99.6	0.995		
rs234043 ^a	99.2	0.990	99.82	0.996
rs2889 ^a	99.1	0.990	99.64	0.991
rs4381241 ^a	99.7	0.997	99.82	0.991
rs4662750 ^a	97.0	0.967	97.90	0.909
rs4804368 ^a	99.8	0.997	99.82	0.993
rs4903064 ^a	98.9	0.985	99.05	0.948
rs59294613 ^b	99.9	0.999	100.00	1.000
rs6706003 ^b	98.1	0.980	98.23	0.944
rs67311347 ^b	98.9	0.985	98.68	0.863
rs6755594 ^b	98.1	0.979	99.26	0.967
rs714024 ^b	98.8	0.986	98.64	0.926
rs72730336 ^b	99.8	0.997	99.82	0.991
rs72851889 ^b	97.0	0.781	96.29	0.591
rs72855540 ^b	99.1	0.933	98.85	0.825
rs73149977 ^a	99.4	0.992	99.82	0.992
rs74911261 ^a	99.3	0.905	99.63	0.899
rs76912165 ^b	96.6	0.851	96.61	0.491
rs7697932 ^b	99.1	0.990	98.57	0.906
rs77736197 ^a	99.7	0.985	99.25	0.895
rs77774900 ^a	99.0	0.970	99.42	0.906
rs7913447 ^b	98.3	0.980	98.85	0.941
rs8007348 ^b	99.8	0.997	100.00	1.000

^aImputed or genotyped across scans; ^bimputed across all scans.

Supplementary Table 5. Associations with 13-SNP RCC polygenic risk score (PRS): overall, and by histology, age at onset and stage

Analysis	OR	95% CI	P
All RCC			
Across PRS deciles			
1	1.00		
2	1.34	(1.16-1.54)	3.60E-05
3	1.41	(1.23-1.62)	8.30E-07
4	1.56	(1.36-1.79)	1.00E-10
5	1.71	(1.50-1.96)	1.98E-15
6	1.93	(1.69-2.20)	8.40E-23
7	1.93	(1.69-2.20)	7.20E-23
8	2.11	(1.85-2.40)	1.20E-29
9	2.52	(2.22-2.86)	8.40E-46
10	3.24	(2.86-3.67)	1.20E-76
Continuous (per PRS unit increase)	2.85	(2.62-3.11)	2.30E-125
By histology (per PRS unit increase)			
Clear cell RCC vs. controls	3.24	(2.91-3.62)	3.40E-100
Papillary RCC vs. controls	1.83	(1.44-2.32)	5.30E-07
Chromophobe RCC vs. controls	2.34	(1.58-3.46)	2.40E-05
By RCC age at onset (per PRS unit increase)			
<60 vs. 60+	1.01	(0.88-1.15)	9.10E-01
By stage (per PRS unit increase)			
2 vs. 1	0.92	(0.63-1.36)	6.90E-01
3 vs. 1	1.24	(0.91-1.70)	1.80E-01
4 vs. 1	1.36	(0.97-1.93)	8.00E-02

Supplementary Note

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AHS

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Supplementary References

1. Henrion, M.Y. *et al.* Common variation at 1q24.1 (ALDH9A1) is a potential risk factor for renal cancer. *PLoS One* **10**, e0122589 (2015).
2. Purdue, M.P. *et al.* Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. *Nat Genet* **43**, 60-5 (2011).
3. Henrion, M. *et al.* Common variation at 2q22.3 (ZEB2) influences the risk of renal cancer. *Hum Mol Genet* **22**, 825-31 (2013).
4. Gudmundsson, J. *et al.* A common variant at 8q24.21 is associated with renal cell cancer. *Nat Commun* **4**, 2776 (2013).
5. Wu, X. *et al.* A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. *Hum Mol Genet* **21**, 456-62 (2012).