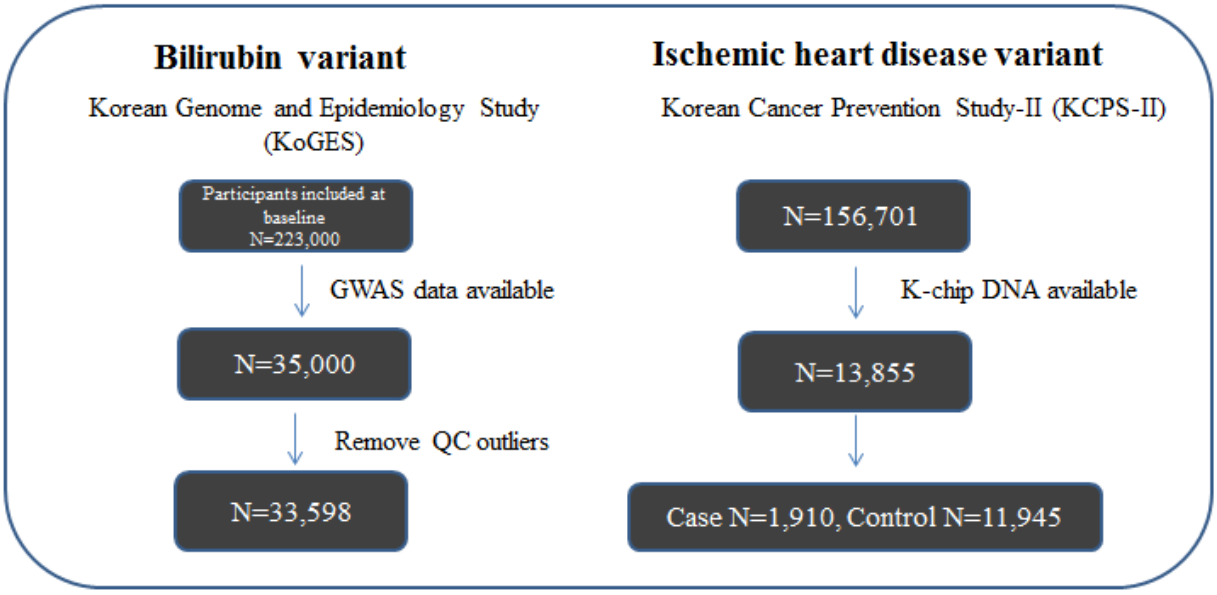
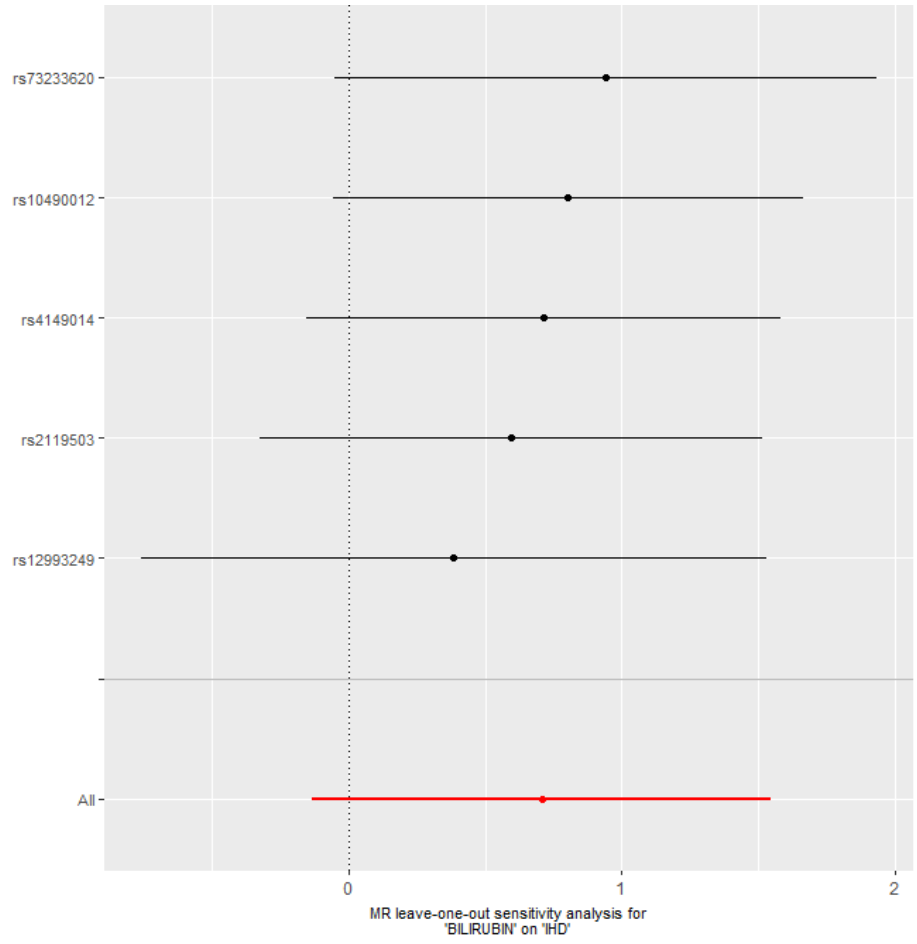
Supplementary Material 1. Flow chart of study population in two-sample Mendelian Randomization

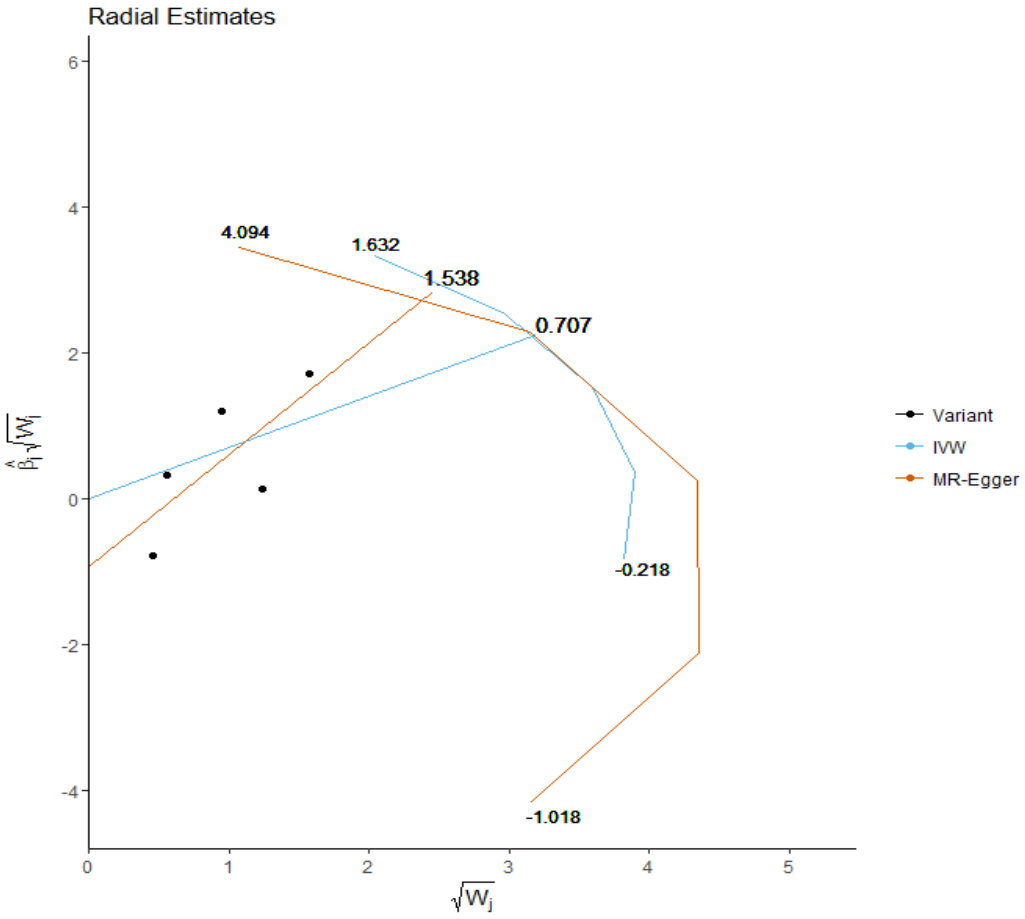


*KNIH: Korea National Institute of Health

Supplementary Material 2. Leave-one-out analysis



Supplementary Material 3. Radial plot showing no significant outliers



Supplementary Material 4. Association of ischemic heart disease in bilirubin genetic variants based on two-sample Mendelian randomization using SNPs from previously identified from European ancestry

				Reported GWAS Studies		Current study on 2-sample Mendelian randomization analysis (IVW)	
SNP	Genes	Chr	MAF	*p*-value	Reference	Beta (*SE*)	*p*-value
rs6742078	*UGT1A1*	2	0.32	5E-324	(1)		
rs887829	*UGT1A1*	2	0.32	5E-324	(1),(2)		
rs11891311	*UGT1A1*	2	0.35	1E-235	(1),(2)	0.49 (0.28)	0.0809
rs4149056	*SLCO1B1*	12	0.15	7E-13	(1)		
rs2117032	*SLCO1B3*	12	0.46	3E-14	(2)		

(1) Johnson AD, Kavousi M, Smith AV et al: Genome-wide association meta-analysis for total serum bilirubin levels. Hum Mol Genet 2009; 18: 2700–2710.
(2) Sanna S, Busonero F, Maschio A et al: Common variants in the SLCO1B3 locus are associated with bilirubin levels and unconjugated hyperbilirubinemia. Hum Mol Genet 2009; 18: 2711–2718
Abbreviation, GWAS; genome-wide association study. Chr: chromosome, MAF; minor allele frequency, SE; standard error, IVW: inverse variance weighted

Supplementary Material 5. Ethnic differences in allele frequencies of *SLCO1B1* and *SLCO1B3* based on 1000 Genomes reference

	rs4149014		**rs73233620**	
Population	Ref Allele	Alt Allele	Ref Allele	Alt Allele
African	0.940	0.060	0.775	0.225
East Asian	0.667	0.333	0.822	0.178
Europe	0.981	0.019	0.975	0.025
South Asian	0.96	0.04	0.97	0.03
American	0.97	0.03	0.95	0.05

Ref : reference, Alt : alternative