

Supplementary Table 1. Data source informations and instrument selection process

	Lipid levels			DM	BMI
	LDL	HDL	TG		
Reference		1		2	3
Population		Korean		East Asians	East Asians
Study design		GWAS for MR		Meta-analysis of GWAS	Meta-analysis of GWAS
Data source		Korean Genome and Epidemiology Study (KoGES)		23 GWAS	21 GWAS
Sample size		35,000		433,540	134,548
Instrument inclusions & exclusions					
Number of SNPs with $p < 5.0 \times 10^{-8}$ (a)	20	29	20	171	12
SNPs in LD ($R^2 > 0.25$) (b)	0	0	0	0	0
SNPs with direct influence on PD (c)	0	1	0	1	0
Proxy SNPs unidentifiable (d)	9	7	3	58	1
Pallindromic SNPs or ambiguous strand information (e)	0	2	0	23	3
Final number of SNP {a-(b+c+d+e)}	11	19	17	89	8

LDL, low-density lipoprotein cholesterol; HDL, high-density lipoprotein cholesterol; TG, triglyceride; DM, diabetes mellitus; BMI, body mass index; GWAS, genome-wide association study; MR, Mendelian randomization; SNPs, single nucleotide polymorphisms; LD, linkage disequilibrium; PD, Parkinson's disease.

REFERENCES

1. Lee SH, Lee JY, Kim GH, Jung KJ, Lee S, Kim HC, et al. Two-sample Mendelian randomization study of lipid levels and ischemic heart disease. *Korean Circ J* 2020;50:940-948.
2. Spracklen CN, Horikoshi M, Kim YJ, Lin K, Bragg F, Moon S, et al. Identification of type 2 diabetes loci in 433,540 East Asian individuals. *Nature* 2020;582:240-245.
3. Wen W, Zheng W, Okada Y, Takeuchi F, Tabara Y, Hwang JY, et al. Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. *Hum Mol Genet* 2014;23:5492-5504.