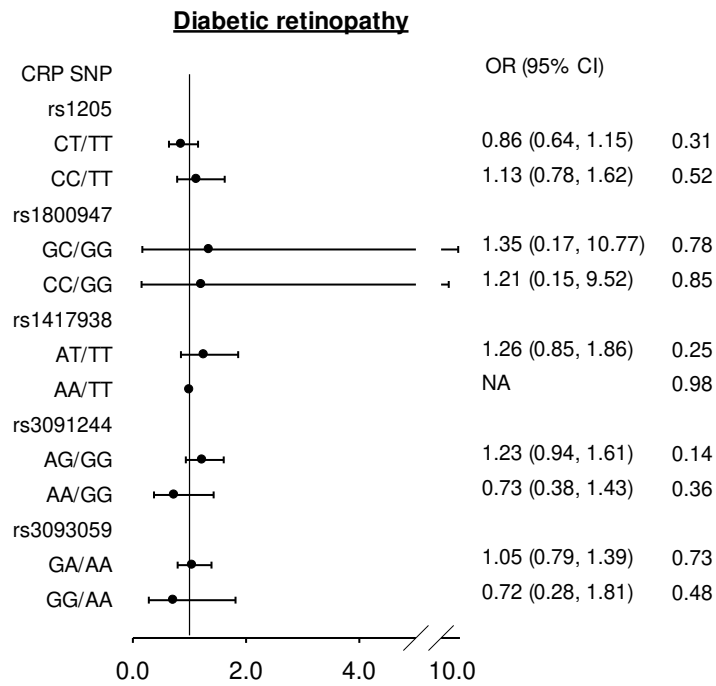


Supplemental Figure S1. Adjusted mean differences of log-transformed hsCRP in CRP SNPs



Supplemental Figure S2. The odds ratios of CRP SNPs with diabetic retinopathy

Supplemental Table S1. CRP SNPs list from Taiwan Biobank TWB v2.0

SNP	Function	Minor (major) allele	CHB MAF	Out study MAF
rs1205	UTR-3	C (T)	0.452	0.434
rs1800947	Coding region	G (C)	0.058	0.086
rs34672691	Coding region	G (A)	0.000	-
rs776402087	Coding region	Alleles T and C	-	-
rs377351051	Coding region	Alleles A and G	-	-
rs143101792	Coding region	C (G)	0.000	-
rs769624182	splice-3	Alleles C and G	-	-
rs1417938	Intron	A (T)	0.078	0.056
rs3091244	nearGene-5	G (T, A)	T=0.121, A=0.078	0.234
rs3093059	nearGene-5	G (A)	0.121	0.179
rs34188124	nearGene-5	C (T)	0.058	0.024

CHB: Han Chinese in Beijing; MAF: minor allele frequency.

MAF data was searched from <https://www.ncbi.nlm.nih.gov/variation/tools/1000genomes/>

Supplemental Table S2. Association of hsCRP with diabetic nephropathy in patients with type 2 diabetes

Variables	Diabetic nephropathy	
	Crude OR (95% CI)	Adjusted OR (95%CI)
per 1 unit increase in log-transformed hsCRP	1.17 (1.04, 1.32)*	1.15 (1.01, 1.32)*

OR: odds ratio; CI: Confidence interval; *: P<0.05.

Adjusted odds ratio: adjusting for sociodemographic characteristics, lifestyle behaviors and disease history.