**Supplementary Table S3** Candidate causal variants selected for validation study from the discovery stage of previous GWAS studya.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SNP | Chr. | Positionb | Allelec | MAF | OR | *P*d |
| rs1889268 | chr9 | 101767961 | T/C | 0.33 | 1.27 | 2.73E-04 |
| rs10819587 | chr9 | 101781301 | A/G | 0.21 | 1.30 | 4.79E-04 |
| rs73503719 | chr9 | 101768847 | A/G | 0.43 | 1.22 | 1.33E-03 |
| rs7031588 | chr9 | 101822302 | C/T | 0.42 | 1.22 | 1.57E-03 |
| rs1413298 | chr9 | 101823373 | A/G | 0.40 | 1.20 | 3.20E-03 |

GWAS, Genome-wide association study; MAF, minor allele frequencey; OR, odds ratio; SNP, single nucleotide polymorphism.

a GWAS stage I in Han Chinese (1,172 controls/1,044 cases); genotyping using Illumina HumanOmniZhongHua-8 BeadChip.

b Position is GRCh37.

c Minor allele/major allele.

d *P* value of association analysis using logistic regression adjusted for age and first three principal components of population stratification.