**Supplementary Table S5. Most strongly associated marker in each region in the GWAS meta-analysis of all Asians aged <25 years.** EAF = effect allele frequency, OR = odds ratio.

| SNP | Chr | Pos | Effect allele | Other allele | EAF | OR (95%CI) | P-value | Nearest gene |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| rs72971923 | 18 | 69822333 | A | G | 0.15 | 0.32 (0.21-0.50) | 2.68 x 10-7 | *LOC101927537* |
| rs2069368 | 5 | 162870726 | C | G | 0.94 | 7.30 (3.28-16.26) | 1.14 x 10-6 | *CCNG1* |
| rs7905017 | 10 | 92868457 | A | G | 0.62 | 1.98 (1.50-2.62) | 1.63 x 10-6 | *LINC00502* |
| rs11079429 | 17 | 59472403 | A | G | 0.29 | 0.48 (0.35-0.65) | 2.23 x 10-6 | *BCAS3* |
| rs9957 | 5 | 179290154 | C | G | 0.74 | 1.92 (1.47-2.53) | 2.48 x 10-6 | *TBC1D9B* |
| rs17072824 | 18 | 62003510 | A | G | 0.10 | 0.35 (0.23-0.54) | 2.80 x 10-6 | *LINC01924* |
| rs779593 | 3 | 118029874 | T | C | 0.69 | 1.81 (1.41-2.32) | 2.95 x 10-6 | *LOC101926968* |
| rs143004236 | 7 | 135420794 | A | G | 0.05 | 0.13 (0.06-0.31) | 3.00 x 10-6 | *FAM180A* |
| rs11085245 | 19 | 18859757 | A | G | 0.83 | 0.45 (0.32-0.63) | 3.31 x 10-6 | *CRTC1* |
| rs12144639 | 1 | 213817311 | A | G | 0.22 | 0.53 (0.40-0.70) | 4.75 x 10-6 | *PROX1-AS1* |