**Supplementary Table S4. 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 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| rs16875983 | 8 | 108285287 | T | G | 0.25 | 1.22 (1.13-1.32) | 2.14 x 10-7 | *ANGPT1* |
| rs67687099 | 3 | 152747454 | D | R | 0.20 | 1.37 (1.22-1.55) | 3.25 x 10-7 | *HMGN2P13* |
| rs35026266 | 15 | 48769044 | T | C | 0.31 | 0.84 (0.79-0.91) | 2.52 x 10-6 | *FBN1* |
| rs10809667 | 9 | 1209532 | A | T | 0.23 | 1.20 (1.11-1.30) | 3.37 x 10-6 | *RPS27AP14* |
| rs56738713 | 5 | 29586419 | A | G | 0.08 | 1.37 (1.20-1.57) | 5.17 x 10-6 | *UBL5P1* |
| rs3924436 | 1 | 24908959 | A | G | 0.41 | 0.86 (0.81-0.92) | 5.42 x 10-6 | *NCMAP* |
| rs1687660 | 16 | 86416646 | C | G | 0.52 | 0.86 (0.81-0.92) | 6.11 x 10-6 | *LINC00917* |
| rs58435984 | 4 | 55127990 | T | C | 0.78 | 0.84 (0.77-0.90) | 8.58 x 10-6 | *PDGFRA* |
| rs141310268 | 18 | 45633672 | D | R | 0.14 | 0.80 (0.72-0.88) | 9.87 x 10-6 | *ZBTB7C* |
| rs817755 | 7 | 98202672 | A | C | 0.91 | 1.42 (1.21-1.65) | 1.00 x 10-5 | *NPTX2* |