**Supplementary Table S2. Most strongly associated marker in each region in the GWAS meta-analysis of all Europeans 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 |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| rs1620100 | 2 | 36179888 | T | C | 0.41 | 0.91 (0.87-0.94) | 1.14 x 10-6 | *MRPL50P1* |
| rs138222255 | 4 | 113801232 | A | T | 0.89 | 0.82 (0.76-0.89) | 2.52 x 10-6 | *ANK2* |
| rs73076614 | 12 | 22633729 | T | C | 0.95 | 1.24 (1.13-1.36) | 3.32 x 10-6 | *C2CD5* |
| rs10187347 | 2 | 227348324 | T | C | 0.47 | 0.91 (0.88-0.95) | 3.58 x 10-6 | *MIR5702* |
| rs11183146 | 12 | 46024937 | A | G | 0.54 | 0.84 (0.78-0.90) | 3.82 x 10-6 | *LINC00938* |
| rs4804959 | 19 | 31803331 | T | C | 0.61 | 1.12 (1.07-1.17) | 3.95 x 10-6 | *TSHZ3* |
| rs9393856 | 6 | 27767825 | T | G | 0.08 | 0.82 (0.75-0.89) | 4.37 x 10-6 | *TRNAQ10* |
| rs2184695 | 10 | 89890390 | A | C | 0.53 | 0.91 (0.87-0.95) | 4.66 x 10-6 | *MED6P1* |
| rs35587414 | 1 | 153174958 | T | C | 0.15 | 1.15 (1.08-1.23) | 4.84 x 10-6 | *LELP1* |
| rs5806282 | 13 | 102849565 | I | R | 0.75 | 1.12 (1.07-1.17) | 5.41 x 10-6 | *FGF14* |