**Supplementary Table S6. Top 10 genes from VEGAS2 gene-based association test with ±50kb buffers for all Europeans.** Start and stop positions listed include ±50kb buffers. nSNPs: number of variants included in gene region. Test Statistic: gene-based χ2 test statistic to *nSNPs* degrees of freedom. P-value: obtained from Test Statistic and adjusting for LD between variants. FDR: false discovery rate (likelihood of gene association being a false positive result). Top SNP: variant within gene locus with strongest association signal from previous SNP-based association test. Genes shown in bold were also identified with MAGMA (Table S7).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Chr | Start | Stop | nSNPs | Test Statistic | P-value | FDR | Top SNP |
| ***ACP2*** | 11 | 47210852 | 47320457 | 175 | 1680.63 | 1.00 x 10-5 | 0.097 | rs3758670 |
| *MADD* | 11 | 47240926 | 47401582 | 271 | 2472.89 | 1.10 x 10-5 | 0.097 | rs2697920 |
| *NR1H3* | 11 | 47219850 | 47340584 | 191 | 1929.38 | 1.20 x 10-5 | 0.097 | rs3758670 |
| *DDB2* | 11 | 47186492 | 47310769 | 193 | 1638.98 | 2.00 x 10-5 | 0.097 | rs3758670 |
| ***CLDN7*** | 17 | 7113221 | 7216512 | 123 | 980.06 | 2.00 x 10-5 | 0.097 | rs222836 |
| ***CTDNEP1*** | 17 | 7096905 | 7205259 | 114 | 1013.67 | 2.90 x 10-5 | 0.111 | rs222836 |
| ***ELP5*** | 17 | 7105371 | 7213259 | 123 | 1012.32 | 3.20 x 10-5 | 0.111 | rs222836 |
| ***GABARAP*** | 17 | 7093737 | 7195753 | 96 | 952.50 | 4.10 x 10-5 | 0.118 | rs222836 |
| *TYR* | 11 | 88861039 | 89078927 | 402 | 3017.77 | 4.40 x 10-5 | 0.118 | rs12808354 |
| ***PHF23*** | 17 | 7088346 | 7192825 | 104 | 903.47 | 7.90 x 10-5 | 0.174 | rs222836 |