**Supplementary Table S7. Top 10 genes from MAGMA 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. Z Statistic: gene-based test statistic. P-value: obtained from *Z Statistic* under the assumption of a normally distributed model. FDR: false discovery rate (likelihood of gene association being a false positive result). Genes shown in bold were also identified with VEGAS2 (Table S6).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Chr | Start | Stop | nSNPs | Z Statistic | P-value | FDR | Bonferroni Adjusted P |
| ***ELP5*** | 17 | 7105372 | 7213259 | 123 | 4.71 | 1.23 x 10-6 | 0.009 | 0.023 |
| ***CLDN7*** | 17 | 7113222 | 7216863 | 124 | 4.69 | 1.39 x 10-6 | 0.009 | 0.026 |
| ***CTDNEP1*** | 17 | 7096906 | 7205259 | 114 | 4.67 | 1.50 x 10-6 | 0.009 | 0.028 |
| *TNFAIP8L3* | 15 | 51298798 | 51447473 | 212 | 4.59 | 2.26 x 10-6 | 0.009 | 0.042 |
| ***ACP2*** | 11 | 47210853 | 47320457 | 175 | 4.56 | 2.52 x 10-6 | 0.009 | 0.046 |
| ***GABARAP*** | 17 | 7093738 | 7195753 | 96 | 4.45 | 4.23 x 10-6 | 0.013 | 0.078 |
| ***PHF23*** | 17 | 7088347 | 7192825 | 104 | 4.36 | 6.59 x 10-6 | 0.017 | 0.121 |
| *DVL2* | 17 | 7078661 | 7187867 | 112 | 4.27 | 9.80 x 10-6 | 0.021 | 0.181 |
| *SLC2A4* | 17 | 7134986 | 7241367 | 155 | 4.22 | 1.21 x 10-5 | 0.021 | 0.223 |
| *ACADVL* | 17 | 7070444 | 7178586 | 104 | 4.22 | 1.22 x 10-5 | 0.021 | 0.224 |