**Table S3: SNP associations for serum TSH levels in eMERGE study African Americans.** Tests of association using linear regression, adjusted for age, sex, principal component (PC) 1, and BMI were performed. Tests of association at p<1x10-04 are listed. Gene listed is the gene in closest proximity to the SNP. Coded allele frequency (CAF) is for the allele frequency in eMERGE African Americans in the serum TSH study (n=351).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **CHR** | **SNP** | **GENE** | **GENE REGION** | **CODED ALLELE** | **CAF** | **BETA (SE)** | **P VALUE** |
| 13 | rs1409005 | *POU4F1-AS1* | downstream-POU4F1 | T | 0.20 | 0.25 (0.05) | 5.02E-07 |
| 1 | rs2378497 | *DUSP10* | upstream | G | 0.08 | 0.33 (0.07) | 3.53E-06 |
| 20 | rs6062344 | *TCEA2* | intronic | T | 0.40 | 0.18 (0.04) | 4.06E-06 |
| 16 | rs270421 | *WWOX* | downstream | C | 0.28 | 0.19 (0.04) | 7.75E-06 |
| 7 | rs2299116 | *CREB5* | intronic | A | 0.17 | 0.25 (0.06) | 8.16E-06 |
| 2 | rs6728613 | *MYT1L* | intronic | A | 0.24 | 0.20 (0.04) | 1.14E-05 |
| 10 | rs6585018 | *PDCD4* | near-5' | G | 0.17 | -0.22 (0.05) | 1.17E-05 |
| 14 | rs1013757 | - | downstream-TTC6, | A | 0.32 | -0.19 (0.04) | 1.33E-05 |
| 2 | rs4073401 | *MYT1L* | intronic | T | 0.24 | 0.19 (0.04) | 1.33E-05 |
| 14 | rs12883861 | - | downstream-LOC728755 | G | 0.20 | 0.21 (0.05) | 1.63E-05 |
| 7 | rs9784959 | *ABCA13* | intronic | A | 0.30 | -0.18 (0.04) | 1.82E-05 |
| 16 | rs270422 | *WWOX* | downstream | A | 0.29 | 0.18 (0.04) | 2.17E-05 |
| 12 | rs261875 | *BICD1* | intronic | C | 0.32 | 0.18 (0.04) | 2.24E-05 |
| 7 | rs274614 | *GRM3* | intronic | G | 0.30 | -0.18 (0.04) | 2.36E-05 |
| 3 | rs11711934 | *DNAH1* | intronic | C | 0.31 | -0.17 (0.04) | 2.45E-05 |
| 2 | rs12621889 | *KIAA1715* | intronic | T | 0.06 | 0.36 (0.08) | 2.68E-05 |
| 2 | rs12464144 | *KIAA1715* | intronic | A | 0.06 | 0.36 (0.08) | 2.68E-05 |
| 18 | rs10163845 | *NETO1* | near-5' | A | 0.28 | -0.18 (0.04) | 2.74E-05 |
| 19 | rs12610504 | *ZNF536* | downstream | G | 0.19 | 0.20 (0.05) | 3.07E-05 |
| 13 | rs1274744 | - | intergenic | C | 0.42 | -0.17 (0.04) | 3.21E-05 |
| 5 | rs10060607 | *SLC36A3* | intronic | A | 0.30 | 0.18 (0.04) | 3.28E-05 |
| 18 | rs1824304 | *FAM59A* | intronic | C | 0.37 | 0.17 (0.04) | 3.32E-05 |
| 2 | rs841452 | *HS6ST1* | upstream | C | 0.37 | 0.17 (0.04) | 3.52E-05 |
| 7 | rs11977108 | *ABCA13* | intronic | A | 0.17 | -0.21 (0.05) | 3.70E-05 |
| 3 | rs4678798 | *ARPP21* | intronic | A | 0.14 | 0.24 (0.06) | 3.71E-05 |
| 4 | rs6851816 | *MLF1IP* | intronic | T | 0.50 | 0.16 (0.04) | 3.83E-05 |
| 22 | rs133201 | *LRP5L* | 5'-untranslated region | A | 0.09 | 0.27 (0.06) | 4.04E-05 |
| 12 | rs2593996 | *BICD1* | intronic | C | 0.50 | -0.16 (0.04) | 4.09E-05 |
| 19 | rs1054713 | *KLK1* | cds-synon | T | 0.26 | 0.19 (0.05) | 4.16E-05 |
| 19 | rs12609319 | *ZNF536* | downstream | T | 0.19 | 0.20 (0.05) | 4.23E-05 |
| 3 | rs1918092 | - | downstream-*ARL8B*, downstream-*EDEM1* | C | 0.09 | 0.30 (0.07) | 4.90E-05 |
| 12 | rs2303478 | *ASCL4* | downstream | A | 0.28 | 0.18 (0.04) | 5.11E-05 |
| 1 | rs3738605 | *SZRD1* | 3'-untranslated region | A | 0.12 | 0.24 (0.06) | 5.12E-05 |
| 19 | rs2659099 | *MGC45922* | near-5' | T | 0.29 | 0.18 (0.04) | 5.13E-05 |
| 3 | rs4955261 | *CMTM8* | upstream | G | 0.39 | 0.16 (0.04) | 5.19E-05 |
| 13 | rs4772145 | *DOCK9* | downstream | T | 0.43 | 0.15 (0.04) | 5.23E-05 |
| 2 | rs13403407 | *C2orf43* | intronic | C | 0.47 | -0.16 (0.04) | 5.31E-05 |
| 3 | rs1513476 | *ARPP21* | intronic | C | 0.14 | 0.22 (0.05) | 5.46E-05 |
| 2 | rs17032566 | *CAMKMT* | intronic | T | 0.07 | -0.30 (0.07) | 5.52E-05 |
| 17 | rs1105813 | *DNAH2* | intronic | T | 0.43 | 0.16 (0.04) | 5.61E-05 |
| 12 | rs1563333 | *DYNLL1* | intronic | A | 0.22 | -0.19 (0.05) | 5.64E-05 |
| 10 | rs1907356 | *C10orf11* | intronic | T | 0.16 | -0.21 (0.05) | 5.71E-05 |
| 10 | rs11001788 | *C10orf11* | intronic | A | 0.16 | -0.21 (0.05) | 5.71E-05 |
| 2 | rs12470895 | *LOC729164* | ncRNA | T | 0.20 | 0.21 (0.05) | 5.86E-05 |
| 3 | rs646929 | *CACNA2D3* | intronic | C | 0.08 | 0.30 (0.07) | 5.96E-05 |
| 3 | rs2335640 | *DNAH1* | intronic | C | 0.30 | -0.17 (0.04) | 5.98E-05 |
| 12 | rs3742049 | *COQ5* | missense | T | 0.25 | 0.18 (0.04) | 6.08E-05 |
| 3 | rs17052068 | *DNAH1* | intronic | T | 0.30 | -0.16 (0.04) | 6.46E-05 |
| 1 | rs2819757 | *RYR2* | intronic | C | 0.18 | 0.22 (0.05) | 6.49E-05 |
| 2 | rs10804139 | *PARD3B* | upstream | A | 0.38 | -0.16 (0.04) | 6.54E-05 |
| 18 | rs736218 | *FAM59A* | intronic | C | 0.38 | 0.16 (0.04) | 6.66E-05 |
| 9 | rs10989120 | *MSANTD3-TMEFF1* | intronic | A | 0.39 | -0.19 (0.05) | 7.05E-05 |
| 12 | rs10744020 | *C12orf36* | downstream | C | 0.23 | 0.16 (0.04) | 7.05E-05 |
| 19 | rs2659103 | *KLK1* | intronic | T | 0.25 | 0.19 (0.05) | 7.29E-05 |
| 1 | rs10918914 | *XCL2* | downstream | G | 0.17 | 0.22 (0.05) | 7.39E-05 |
| 12 | rs261878 | *BICD1* | intronic | C | 0.32 | -0.16 (0.04) | 7.42E-05 |
| 15 | rs12914266 | *SQRDL* | intronic | A | 0.29 | 0.17 (0.04) | 7.58E-05 |
| 7 | rs6965055 | *C7orf10* | intronic | G | 0.39 | -0.16 (0.04) | 7.65E-05 |
| 7 | rs7808606 | *C7orf10* | intronic | C | 0.39 | -0.15 (0.04) | 7.66E-05 |
| 14 | rs17322359 | *PRKD1* | upstream | T | 0.10 | 0.25 (0.06) | 7.74E-05 |
| 5 | rs11949641 | *MSX2* | downstream | A | 0.23 | 0.18 (0.05) | 7.89E-05 |
| 1 | rs12120382 | *CHRM3* | upstream | C | 0.09 | 0.29 (0.07) | 7.96E-05 |
| 2 | rs6731363 | *LOC729164* | ncRNA | A | 0.20 | 0.20 (0.05) | 7.99E-05 |
| 4 | rs13144021 | *NR3C2* | upstream | G | 0.14 | 0.23 (0.06) | 8.00E-05 |
| 18 | rs877128 | *MC2R* | intronic | A | 0.25 | 0.18 (0.04) | 8.10E-05 |
| 10 | rs7923004 | *BBIP1* | intronic | C | 0.18 | -0.20 (0.05) | 8.19E-05 |
| 8 | rs6999969 | *XKR6* | intronic | C | 0.42 | -0.16 (0.04) | 8.33E-05 |
| 11 | rs1027388 | *LRRC4C* | intronic | A | 0.28 | -0.17 (0.04) | 8.36E-05 |
| 1 | rs17011253 | - | upstream-DUSP10 | C | 0.09 | 0.27 (0.07) | 8.38E-05 |
| 10 | rs942077 | *RBM20* | missense | G | 0.48 | -0.15 (0.04) | 8.47E-05 |
| 4 | rs4370216 | INTERGENIC |  | C | 0.46 | -0.15 (0.04) | 8.55E-05 |
| 4 | rs2333727 | *HSFY2* | upstream | C | 0.46 | -0.15 (0.04) | 8.55E-05 |
| 7 | rs1029357 | *SAMD9L* | 3'-untranslated region | G | 0.46 | 0.15 (0.04) | 8.57E-05 |
| 9 | rs1332598 | *MSANTD3-TMEFF1* | intronic | A | 0.23 | -0.19 (0.05) | 8.69E-05 |
| 5 | rs6864667 | *SLC12A7* | intronic | G | 0.47 | 0.15 (0.04) | 8.98E-05 |
| 12 | rs4411338 | *CCND2* | upstream | C | 0.29 | 0.16 (0.04) | 9.05E-05 |
| 19 | rs171953 | *KLK1* | downstream | G | 0.48 | -0.15 (0.04) | 9.07E-05 |
| 19 | GA035020 | *SSC5D* | intronic | T | 0.25 | 0.19 (0.05) | 9.11E-05 |
| 15 | rs2040578 | *SV2B* | intronic | G | 0.29 | 0.17 (0.04) | 9.13E-05 |
| 17 | rs1106826 | *DNAH2* | intronic | A | 0.32 | 0.17 (0.04) | 9.23E-05 |
| 20 | rs6090040 | *TCEA2* | intronic | C | 0.47 | 0.15 (0.04) | 9.35E-05 |
| 20 | rs4408777 | *RGS19* | intronic | G | 0.33 | 0.16 (0.04) | 9.39E-05 |
| 16 | rs2521676 | - | intergenic | G | 0.39 | 0.16 (0.04) | 9.73E-05 |
| 1 | rs16845412 | - | intergenic | G | 0.10 | 0.27 (0.07) | 9.76E-05 |
| 4 | rs10518306 | *LOC285419* | intronic | A | 0.06 | 0.35 (0.09) | 9.78E-05 |
| 8 | rs10098991 | - | intergenic | C | 0.44 | 0.16 (0.04) | 9.86E-05 |
| 16 | rs8059691 | *EMC8* | intronic | G | 0.11 | 0.23 (0.06) | 9.90E-05 |