

**Supplementary Table 2. Top ranked SNPs (*Pmeta* < 10-5) from the genome-wide meta-analysis on the sense of smell in Model 1** a

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***SNP*** | ***Chr.*** | ***Gene*** | ***Position*** | ***Score b*** | ***A1*** | ***A2*** | ***MAF*** | ***Direction c*** | ***I2 (%)*** | ***P for Cochran’s Q*** | ***Effect size d*** | ***s.e.*** | ***P*** |
| rs3751196 | 12 | *STAB2* | 102681632 | 5 | A | G | 0.06 | --- | 63.20 | 0.07 | -0.07 | 0.01 | 2.34E-07 |
| rs12229599 | 12 | *STAB2* | 102678505 | 7 | T | C | 0.04 | --- | 66.10 | 0.05 | -0.08 | 0.02 | 3.15E-07 |
| rs4111 | 3 | *ERC2* | 55929255 | 6 | A | C | 0.15 | +++ | 0.00 | 0.39 | 0.03 | 0.01 | 1.01E-06 |
| rs199443 | 17 | *NSF* | 42174733 | 1f | T | C | 0.20 | +++ | 0.00 | 0.60 | 0.03 | 0.01 | 4.01E-06 |
| rs17252438 | 13 | *PCDH9* | 66458613 | 7 | T | C | 0.05 | +++ | 19.60 | 0.29 | 0.05 | 0.01 | 4.15E-06 |
| rs2075650 | 19 | *TOMM40* | 50087459 | 1f | A | G | 0.13 | +++ | 0.00 | 0.68 | 0.04 | 0.01 | 4.24E-06 |
| rs2251885 | 9 | *PRG-3* | 102833365 | 6 | A | G | 0.37 | +++ | 0.00 | 0.83 | 0.02 | 0.01 | 4.85E-06 |
| rs649892 | 9 | *PRG-3* | 102834210 | 7 | T | G | 0.37 | --- | 0.00 | 0.82 | -0.02 | 0.01 | 5.02E-06 |
| rs4715057 | 6 | *C6orf1* | 48061760 | 5 | A | G | 0.02 | +++ | 39.10 | 0.19 | 0.11 | 0.02 | 5.75E-06 |
| rs9321099 | 6 | *C6orf1* | 128243832 | 5 | A | T | 0.09 | --- | 0.00 | 0.56 | -0.04 | 0.01 | 6.46E-06 |
| rs6052484 | 20 | *ADRA1D* | 4208610 | 7 | A | G | 0.26 | --- | 56.20 | 0.10 | -0.03 | 0.01 | 6.52E-06 |
| rs12291225 | 11 | *SPON1* | 14212760 | 7 | A | C | 0.25 | +++ | 0.00 | 0.72 | 0.03 | 0.01 | 6.92E-06 |
| rs2245691 | 9 | *PRG-3* | 102767101 | 6 | T | C | 0.32 | --- | 0.00 | 0.65 | -0.03 | 0.01 | 7.19E-06 |
| rs11174650 | 12 | *PPM1H* | 61466196 | 4 | T | C | 0.08 | --- | 39.60 | 0.19 | -0.04 | 0.01 | 8.13E-06 |
| rs2732614 | 17 | *KIAA1267*-*-LRRC37* | 41719986 | 1a | T | C | 0.20 | +++ | 0.00 | 0.78 | 0.03 | 0.01 | 8.34E-06 |
| rs16875528 | 4 | *DHX15* | 23917177 | 6 | T | C | 0.01 | +++ | 0.00 | 0.59 | 0.10 | 0.02 | 8.52E-06 |
| rs10005021 | 4 | *DHX15* | 23919610 | 7 | T | C | 0.01 | +++ | 0.00 | 0.60 | 0.11 | 0.02 | 8.78E-06 |
| rs520855 | 9 | *PRG-3* | 102778230 | 7 | A | G | 0.36 | +++ | 0.00 | 0.56 | 0.02 | 0.01 | 9.47E-06 |
| rs2243593 | 9 | *PRG-3* | 102785082 | 5 | A | G | 0.36 | --- | 0.00 | 0.56 | -0.02 | 0.01 | 9.50E-06 |

a Adjusted for age, gender, study center, cognitive function and the first two principal components.

b Score: the functional annotation score from the RegulomeDB; lower score indicates stronger evidence for a variant to be functional. Category 1 variants are defined as ‘likely to affect binding and linked to expression of a gene target’; categories 2 and 3 as ‘likely’ and ‘less likely to affect binding’, respectively; categories 4-6 as ‘minimal binding evidence’; and category 7 as ‘lack of evidence’ for an association. This is especially notable for category 1 as it is the only variable included in the model explicitly tied to eQTL status.

c The direction of effect in the order of the Atherosclerosis Risk in Communities study, the Health ABC Study and the Rush Religious Orders Study and Memory and Aging Project

d Effect size in ln(smell score+1) per allele change.

Chr.: Chromosome. MAF: minor allele frequency. s.e.: standard error.