| Gene | SNP | Location\_GRCh38 | Effect\_allele | p\_bonferroni | Variant\_Type | Variant\_Effect |
| --- | --- | --- | --- | --- | --- | --- |
| ADGRG1 | rs74326170 | chr16:57657497 | A | 2.43e-04 | splice\_region\_variant&intron\_variant | - |
| rs2305308 | chr16:57656407 | G | 1.23e-02 | intron\_variant | - |
| rs10852554 | chr16:57663620 | T | 1.36e-02 | 3\_prime\_UTR\_variant | - |
| CA6 | rs2274330 | chr1:8949411 | C | 5.31e-08 | synonymous\_variant | - |
| rs2274333 | chr1:8957145 | G | 7.88e-03 | missense\_variant | p.Ser90Gly |
| FFAR3 | rs150256974 | chr19:35358981 | G | 3.65e-02 | missense\_variant | p.Leu31Val |
| FFAR4 | rs41290218 | chr10:93587624 | A | 6.53e-04 | 3\_prime\_UTR\_variant | - |
| FZD6 | rs12549394 | chr8:103331379 | A | 2.26e-03 | missense\_variant | p.Ala664Glu |
| GNAS | rs3730170 | chr20:58905365 | C | 3.61e-03 | downstream\_gene\_variant | - |
| GNAT3 | . | chr7:80474462 | CATATAT | 3.17e-02 | intron\_variant | - |
| GPR107 | rs5900882 | chr9:130054119 | T | 2.62e-05 | intron\_variant | - |
| rs10615984 | chr9:130124897 | G | 5.14e-04 | intron\_variant | - |
| GPR161 | . | chr1:168136343 | AGG | 2.43e-04 | frameshift\_variant | p.Gly19fs |
| MIR6825 | rs2289185 | chr3:127576916 | A | 1.27e-05 | upstream\_gene\_variant | - |
| OTOP1 | rs145781170 | chr4:4197180 | A | 6.32e-03 | missense\_variant | p.Leu552Phe |
| PLCB2 | rs2229691 | chr15:40296801 | G | 6.16e-04 | synonymous\_variant | - |
| rs2305645 | chr15:40303364 | T | 9.60e-04 | splice\_region\_variant&intron\_variant | - |
| rs1869901 | chr15:40303426 | G | 2.96e-03 | intron\_variant | - |
| RALB | rs4091515 | chr2:120285827 | G | 4.59e-04 | intron\_variant | - |
| RBP4 | rs11187539 | chr10:93587181 | A | 2.37e-05 | downstream\_gene\_variant | - |
| SCNN1A | rs57233912 | chr12:6348670 | A | 9.86e-05 | intron\_variant | - |
| rs11542844 | chr12:6355415 | T | 3.56e-03 | missense\_variant | p.Ala393Thr |
| rs72657545 | chr12:6348664 | T | 8.67e-03 | intron\_variant | - |
| SCNN1B | rs250563 | chr16:23367958 | T | 3.96e-02 | splice\_region\_variant&synonymous\_variant | p.Phe293Phe |
| SCNN1D | rs111819661 | chr1:1287578 | T | 5.29e-06 | missense\_variant | p.Arg461Cys |
| rs3753340 | chr1:1281678 | A | 2.85e-05 | intron\_variant | - |
| SCNN1G | rs5734 | chr16:23189440 | C | 1.58e-02 | synonymous\_variant | - |
| TAS1R1 | rs10864628 | chr1:6575171 | A | 4.39e-02 | synonymous\_variant | - |
| TAS1R2 | rs72953138 | chr1:18857682 | A | 8.64e-04 | intron\_variant | - |
| TAS2R3 | rs2270009 | chr7:141764965 | C | 3.45e-05 | synonymous\_variant | - |
| TAS2R4 | rs2234002 | chr7:141779000 | G | 9.44e-07 | synonymous\_variant | - |
| rs2234001 | chr7:141778774 | G | 5.50e-04 | synonymous\_variant | - |
| rs2233998 | chr7:141778508 | T | 6.79e-04 | synonymous\_variant | - |
| TAS2R42 | . | chr12:11186007 | C | 9.43e-04 | missense\_variant | p.Pro311Ala |
| . | chr12:11186008 | A | 9.43e-04 | synonymous\_variant | - |
| . | chr12:11185949 | A | 2.67e-03 | downstream\_gene\_variant | - |
| . | chr12:11186175 | C | 3.32e-03 | missense\_variant | p.Trp255Gly |
| . | chr12:11185933 | C | 7.76e-03 | downstream\_gene\_variant | - |
| . | chr12:11186377 | T | 2.27e-02 | synonymous\_variant | - |
| TAS2R43 | rs200029065 | chr12:11091314 | G | 8.44e-03 | missense\_variant | p.Thr306Pro |
| TAS2R5 | rs2234012 | chr7:141790307 | A | 2.34e-06 | 5\_prime\_UTR\_variant | - |
| rs2227264 | chr7:141790438 | G | 2.38e-06 | synonymous\_variant | - |
| TAS2R8 | rs2537817 | chr12:10806059 | T | 2.25e-04 | synonymous\_variant | - |