| Gene | SNP | Location\_GRCh38 | Effect\_allele | p\_bonferroni | Variant\_Type | Variant\_Effect |
| --- | --- | --- | --- | --- | --- | --- |
| ACAP3 | rs13306638 | chr1:1290851 | A | 5.30e-04 | downstream\_gene\_variant | - |
| ADGRG1 | rs74326170 | chr16:57657497 | A | 3.52e-04 | splice\_region\_variant&intron\_variant | - |
| rs2305308 | chr16:57656407 | G | 1.04e-03 | intron\_variant | - |
| rs117746167 | chr16:57656185 | A | 1.83e-03 | intron\_variant | - |
| CA6 | rs2274330 | chr1:8949411 | C | 5.29e-10 | synonymous\_variant | - |
| rs2274333 | chr1:8957145 | G | 2.58e-06 | missense\_variant | p.Ser90Gly |
| rs2274331 | chr1:8949488 | A | 3.72e-03 | intron\_variant | - |
| FFAR3 | rs150256974 | chr19:35358981 | G | 3.58e-05 | missense\_variant | p.Leu31Val |
| FFAR4 | rs41290218 | chr10:93587624 | A | 2.01e-05 | 3\_prime\_UTR\_variant | - |
| FZD6 | rs12549394 | chr8:103331379 | A | 9.02e-06 | missense\_variant | p.Ala664Glu |
| GABBR1 | rs29243 | chr6:29631325 | A | 1.68e-02 | upstream\_gene\_variant | - |
| GNAS | rs3730170 | chr20:58905365 | C | 8.44e-04 | downstream\_gene\_variant | - |
| rs3730173 | chr20:58909879 | T | 3.20e-03 | intron\_variant | - |
| rs74934823 | chr20:58853892 | A | 3.81e-02 | missense\_variant | p.Arg147Lys |
| rs8620 | chr20:58909186 | T | 4.43e-02 | synonymous\_variant | - |
| GNAT3 | rs799936 | chr7:80462665 | A | 1.44e-03 | intron\_variant | - |
| GPR107 | rs10615984 | chr9:130124897 | G | 9.02e-06 | intron\_variant | - |
| GPR87 | rs9819885 | chr3:151295108 | T | 7.00e-04 | synonymous\_variant | - |
| MED12L | chr3\_151295224 | chr3:151295224 | T | 9.90e-03 | intron\_variant | - |
| MIR6825 | rs2289185 | chr3:127576916 | A | 4.15e-08 | upstream\_gene\_variant | - |
| OTOP1 | rs145781170 | chr4:4197180 | A | 8.75e-05 | missense\_variant | p.Leu552Phe |
| PLCB2 | rs2229691 | chr15:40296801 | G | 4.31e-08 | synonymous\_variant | - |
| rs2305645 | chr15:40303364 | T | 9.98e-07 | splice\_region\_variant&intron\_variant | - |
| rs936212 | chr15:40289342 | C | 1.05e-02 | missense\_variant | p.Glu1095Gly |
| RBP4 | rs11187539 | chr10:93587181 | A | 2.23e-06 | downstream\_gene\_variant | - |
| SCNN1A | rs11542844 | chr12:6355415 | T | 3.83e-05 | missense\_variant | p.Ala393Thr |
| rs57233912 | chr12:6348670 | A | 1.31e-04 | intron\_variant | - |
| rs72657545 | chr12:6348664 | T | 8.67e-03 | intron\_variant | - |
| SCNN1B | rs250563 | chr16:23367958 | T | 4.51e-02 | splice\_region\_variant&synonymous\_variant | p.Phe293Phe |
| SCNN1D | rs111819661 | chr1:1287578 | T | 3.29e-09 | missense\_variant | p.Arg461Cys |
| rs3753340 | chr1:1281678 | A | 5.12e-09 | intron\_variant | - |
| rs6690013 | chr1:1291377 | A | 5.84e-04 | missense\_variant | p.Gly726Ser |
| rs609805 | chr1:1291509 | A | 9.89e-03 | missense\_variant | p.Gly770Arg |
| rs2273276 | chr1:1290912 | A | 3.10e-02 | synonymous\_variant | - |
| SCNN1G | rs5734 | chr16:23189440 | C | 1.99e-05 | synonymous\_variant | - |
| rs5735 | chr16:23189527 | C | 8.77e-04 | synonymous\_variant | - |
| TAS1R2 | rs72953138 | chr1:18857682 | A | 9.27e-06 | intron\_variant | - |
| TAS2R31 | rs192629609 | chr12:11030371 | C | 4.39e-03 | downstream\_gene\_variant | - |
| TAS2R40 | rs10260248 | chr7:143222638 | A | 2.18e-02 | missense\_variant | p.Ser187Tyr |
| TAS2R42 | chr12\_11186007 | chr12:11186007 | C | 3.98e-05 | missense\_variant | p.Pro311Ala |
| chr12\_11186008 | chr12:11186008 | A | 3.98e-05 | synonymous\_variant | - |
| chr12\_11185949 | chr12:11185949 | A | 1.20e-04 | downstream\_gene\_variant | - |
| chr12\_11186175 | chr12:11186175 | C | 1.91e-04 | missense\_variant | p.Trp255Gly |
| chr12\_11186377 | chr12:11186377 | T | 7.58e-04 | synonymous\_variant | - |
| TAS2R43 | rs200029065 | chr12:11091314 | G | 1.04e-03 | missense\_variant | p.Thr306Pro |