| Gene | SNP | Location\_GRCh38 | Effect\_allele | Allele\_frq\_ECC | Allele\_frq\_CF | p\_bonferroni | Variant\_Type | Variant\_Effect |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ACAP3 | rs13306638 | chr1:1290851 | A | 0.199 | 0.089 | 7.89e-04 | downstream\_gene\_variant | - |
| rs2273275 | chr1:1290841 | A | 0.423 | 0.549 | 3.97e-02 | downstream\_gene\_variant | - |
| ADGRG1 | rs10852554 | chr16:57663620 | T | 0.395 | 0.565 | 3.49e-05 | 3\_prime\_UTR\_variant | - |
| rs74326170 | chr16:57657497 | A | 0.022 | 0.098 | 5.46e-05 | splice\_region\_variant&intron\_variant | - |
| rs2305308 | chr16:57656407 | G | 0.021 | 0.089 | 2.95e-04 | intron\_variant | - |
| rs117746167 | chr16:57656185 | A | 0.087 | 0.020 | 4.36e-03 | intron\_variant | - |
| CA6 | rs2274330 | chr1:8949411 | C | 0.111 | 0.286 | 2.44e-10 | synonymous\_variant | - |
| rs2274333 | chr1:8957145 | G | 0.514 | 0.337 | 6.85e-06 | missense\_variant | p.Ser90Gly |
| rs12082594 | chr1:8967768 | T | <0.001 | 0.033 | 3.59e-03 | synonymous\_variant | - |
| rs2274331 | chr1:8949488 | A | 0.083 | 0.167 | 2.29e-02 | intron\_variant | - |
| FFAR3 | rs150256974 | chr19:35358981 | G | 0.162 | 0.060 | 3.63e-04 | missense\_variant | p.Leu31Val |
| FFAR4 | rs41290218 | chr10:93587624 | A | 0.120 | 0.255 | 1.10e-05 | 3\_prime\_UTR\_variant | - |
| FZD6 | rs12549394 | chr8:103331379 | A | 0.117 | 0.018 | 1.20e-06 | missense\_variant | p.Ala664Glu |
| GABBR1 | rs29243 | chr6:29631325 | A | 0.029 | 0.087 | 2.42e-02 | upstream\_gene\_variant | - |
| GNAS | rs74934823 | chr20:58853892 | A | 0.003 | 0.049 | 5.55e-04 | missense\_variant | p.Arg147Lys |
| rs3730173 | chr20:58909879 | T | 0.027 | 0.099 | 5.86e-04 | intron\_variant | - |
| rs3730170 | chr20:58905365 | C | 0.038 | 0.108 | 7.33e-03 | downstream\_gene\_variant | - |
| rs8620 | chr20:58909186 | T | 0.019 | 0.072 | 1.81e-02 | synonymous\_variant | - |
| GNAT3 | . | chr7:80474462 | CATATAT | 0.005 | 0.059 | 7.79e-05 | intron\_variant | - |
| GPR107 | rs5900882 | chr9:130054119 | T | 0.037 | 0.137 | 2.65e-06 | intron\_variant | - |
| rs10615984 | chr9:130124897 | G | 0.045 | 0.141 | 2.50e-05 | intron\_variant | - |
| GPR161 | . | chr1:168136343 | AGG | 0.040 | 0.142 | 2.89e-06 | frameshift\_variant | p.Gly19fs |
| GPR87 | rs9819885 | chr3:151295108 | T | 0.056 | 0.145 | 6.68e-04 | synonymous\_variant | - |
| MED12L | . | chr3:151295224 | T | 0.079 | 0.020 | 2.61e-02 | intron\_variant | - |
| MIR5787 | . | chr3:50227258 | T | 0.070 | 0.011 | 5.01e-03 | upstream\_gene\_variant | - |
| MIR6825 | rs2289185 | chr3:127576916 | A | 0.236 | 0.094 | 1.60e-06 | upstream\_gene\_variant | - |
| OTOP1 | rs145781170 | chr4:4197180 | A | 0.112 | 0.018 | 3.90e-06 | missense\_variant | p.Leu552Phe |
| rs2980146 | chr4:4226737 | A | 0.006 | 0.056 | 8.23e-04 | missense\_variant | p.Ala43Val |
| PLCB2 | rs2229691 | chr15:40296801 | G | 0.579 | 0.379 | 1.04e-07 | synonymous\_variant | - |
| rs2305645 | chr15:40303364 | T | 0.151 | 0.295 | 1.20e-05 | splice\_region\_variant&intron\_variant | - |
| rs1869901 | chr15:40303426 | G | 0.228 | 0.382 | 4.55e-05 | intron\_variant | - |
| rs28395843 | chr15:40297763 | T | 0.005 | 0.047 | 3.57e-03 | downstream\_gene\_variant | - |
| rs9972418 | chr15:40291675 | T | 0.003 | 0.040 | 1.74e-02 | intron\_variant | - |
| RALB | rs4091515 | chr2:120285827 | G | 0.514 | 0.359 | 3.94e-04 | intron\_variant | - |
| RBP4 | rs11187539 | chr10:93587181 | A | 0.200 | 0.359 | 5.48e-06 | downstream\_gene\_variant | - |
| SCNN1A | rs57233912 | chr12:6348670 | A | 0.011 | 0.083 | 5.41e-06 | intron\_variant | - |
| rs11542844 | chr12:6355415 | T | 0.091 | 0.214 | 1.19e-05 | missense\_variant | p.Ala393Thr |
| rs72657545 | chr12:6348664 | T | 0.008 | 0.054 | 4.98e-03 | intron\_variant | - |
| SCNN1B | rs238547 | chr16:23348878 | T | 0.519 | 0.391 | 2.70e-02 | synonymous\_variant | - |
| SCNN1D | rs111819661 | chr1:1287578 | T | 0.175 | 0.020 | 1.30e-12 | missense\_variant | p.Arg461Cys |
| rs3753340 | chr1:1281678 | A | 0.221 | 0.074 | 6.71e-08 | intron\_variant | - |
| rs6690013 | chr1:1291377 | A | 0.264 | 0.147 | 3.66e-03 | missense\_variant | p.Gly726Ser |
| SCNN1G | rs5734 | chr16:23189440 | C | 0.438 | 0.270 | 1.77e-05 | synonymous\_variant | - |
| rs5735 | chr16:23189527 | C | 0.421 | 0.290 | 9.35e-03 | synonymous\_variant | - |
| TAS1R1 | rs10864628 | chr1:6575171 | A | 0.010 | 0.058 | 3.66e-03 | synonymous\_variant | - |
| TAS1R2 | rs72953138 | chr1:18857682 | A | 0.121 | 0.250 | 3.77e-05 | intron\_variant | - |
| TAS1R3 | rs112507608 | chr1:1334108 | A | 0.002 | 0.047 | 2.13e-04 | missense\_variant | p.Ala735Thr |
| TAS2R3 | rs2270009 | chr7:141764965 | C | 0.335 | 0.525 | 4.39e-07 | synonymous\_variant | - |
| TAS2R31 | rs192629609 | chr12:11030371 | C | 0.032 | 0.096 | 8.94e-03 | downstream\_gene\_variant | - |
| TAS2R4 | rs2234002 | chr7:141779000 | G | 0.303 | 0.529 | 7.61e-11 | synonymous\_variant | - |
| rs2234001 | chr7:141778774 | G | 0.309 | 0.486 | 3.54e-06 | synonymous\_variant | - |
| rs2233998 | chr7:141778508 | T | 0.361 | 0.534 | 1.53e-05 | synonymous\_variant | - |
| rs2233997 | chr7:141778505 | C | 0.069 | 0.013 | 1.62e-02 | missense\_variant | p.Tyr6Ser |
| TAS2R42 | . | chr12:11186007 | C | 0.099 | 0.222 | 2.75e-05 | missense\_variant | p.Pro311Ala |
| . | chr12:11186008 | A | 0.099 | 0.222 | 2.75e-05 | synonymous\_variant | - |
| . | chr12:11185949 | A | 0.098 | 0.217 | 4.52e-05 | downstream\_gene\_variant | - |
| . | chr12:11186175 | C | 0.106 | 0.227 | 7.06e-05 | missense\_variant | p.Trp255Gly |
| . | chr12:11185933 | C | 0.098 | 0.214 | 1.14e-04 | downstream\_gene\_variant | - |
| . | chr12:11186377 | T | 0.115 | 0.227 | 9.85e-04 | synonymous\_variant | - |
| TAS2R43 | rs200029065 | chr12:11091314 | G | 0.181 | 0.079 | 2.04e-03 | missense\_variant | p.Thr306Pro |
| TAS2R5 | rs2227264 | chr7:141790438 | G | 0.307 | 0.525 | 6.74e-10 | synonymous\_variant | - |
| rs2234012 | chr7:141790307 | A | 0.325 | 0.538 | 2.63e-09 | 5\_prime\_UTR\_variant | - |
| rs2234015 | chr7:141790999 | A | <0.001 | 0.027 | 3.26e-02 | missense\_variant | p.Arg213Gln |
| TAS2R8 | rs2537817 | chr12:10806059 | T | 0.028 | 0.126 | 3.70e-07 | synonymous\_variant | - |