**Table s3.** Three gene-based Association Testing Results for genes associated with guttate psoriasis in the merged cohort

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SetID** | **N.Marker.All** | **N.Marker.Test** | **MAC** | **m** | **Method.bin** | **P.skat** | **P.skato** | **P.burden** |
| **DLGAP5** | 4 | 4 | 299 | 298 | QA | 2.03E-03 | 1.64E-04 | 8.26E-05 |
| **TXNIP** | 3 | 3 | 113 | 112 | QA | 1.88E-03 | 3.52E-04 | 1.69E-04 |
| **MED12L** | 5 | 5 | 119 | 118 | QA | 1.13E-03 | 3.14E-04 | 1.73E-04 |
| **MYO3A** | 11 | 11 | 421 | 415 | QA | 1.81E-02 | 9.85E-04 | 4.60E-04 |
| **ZNF416** | 3 | 3 | 10 | 10 | ER | 9.18E-03 | 1.21E-03 | 4.99E-04 |
| **AGL** | 6 | 6 | 96 | 96 | QA | 2.17E-03 | 1.36E-03 | 8.34E-04 |
| **CNOT4** | 3 | 3 | 25 | 25 | ER.A | 5.90E-03 | 2.05E-03 | 8.39E-04 |
| **TFPI** | 2 | 2 | 8 | 8 | ER | 3.80E-03 | 3.80E-03 | 8.82E-04 |
| **ZXDC** | 2 | 2 | 19 | 19 | ER | 4.00E-04 | 4.00E-04 | 9.18E-04 |
| **NCAM1** | 10 | 9 | 64 | 64 | QA | 6.24E-03 | 1.86E-03 | 9.56E-04 |
| **VSX1** | 3 | 3 | 16 | 16 | ER | 1.57E-02 | 4.25E-03 | 9.99E-04 |
| **C1orf168** | 5 | 4 | 87 | 87 | QA | 5.58E-04 | 6.44E-04 | 1.23E-03 |
| **TUBB1** | 4 | 4 | 82 | 82 | QA | 2.48E-02 | 2.68E-03 | 1.50E-03 |
| **FANCE** | 4 | 4 | 72 | 72 | QA | 5.23E-03 | 2.47E-03 | 1.51E-03 |
| **CHAF1A** | 4 | 4 | 33 | 33 | ER.A | 2.74E-02 | 3.72E-03 | 1.56E-03 |
| **PTTG1IP** | 2 | 2 | 6 | 6 | ER | 1.65E-03 | 1.65E-03 | 1.65E-03 |
| **TNFRSF18** | 6 | 6 | 160 | 159 | QA | 5.39E-03 | 3.03E-03 | 1.71E-03 |
| **ZNF154** | 2 | 2 | 41 | 41 | QA | 1.25E-03 | 1.56E-03 | 1.83E-03 |
| **PLEKHH1** | 2 | 2 | 12 | 11 | ER | 1.72E-03 | 2.56E-03 | 2.06E-03 |
| **KIAA0408** | 4 | 4 | 170 | 170 | QA | 5.36E-03 | 3.53E-03 | 2.08E-03 |
| **HIPK4** | 3 | 3 | 99 | 97 | QA | 2.11E-03 | 2.40E-03 | 2.31E-03 |
| **PXDN** | 5 | 5 | 330 | 321 | QA | 1.92E-02 | 4.30E-03 | 2.35E-03 |
| **RNF31** | 3 | 3 | 25 | 25 | ER.A | 9.05E-03 | 4.34E-03 | 2.51E-03 |
| **DIS3** | 5 | 5 | 67 | 67 | QA | 3.17E-02 | 4.47E-03 | 2.59E-03 |
| **PCDHGA7** | 3 | 3 | 151 | 151 | QA | 1.70E-02 | 3.80E-03 | 2.77E-03 |
| **KIAA1549L** | 4 | 4 | 46 | 46 | QA | 1.29E-02 | 5.01E-03 | 2.97E-03 |
| **CROT** | 3 | 3 | 106 | 106 | QA | 2.39E-02 | 5.00E-03 | 3.12E-03 |
| **SIGLEC10** | 4 | 4 | 268 | 268 | QA | 3.56E-02 | 5.48E-03 | 3.15E-03 |
| **MAMDC2** | 5 | 5 | 152 | 152 | QA | 2.76E-02 | 5.76E-03 | 3.43E-03 |
| **YIPF1** | 3 | 3 | 46 | 46 | QA | 1.56E-02 | 4.79E-03 | 3.56E-03 |
| **SLC25A45** | 3 | 2 | 14 | 11 | ER | 6.41E-03 | 7.67E-03 | 3.56E-03 |
| **NOC4L** | 9 | 9 | 123 | 123 | QA | 1.59E-02 | 8.19E-03 | 4.42E-03 |
| **BTN3A1** | 2 | 2 | 135 | 133 | QA | 5.63E-03 | 6.38E-03 | 4.83E-03 |
| **SUN1** | 3 | 3 | 289 | 288 | QA | 2.45E-02 | 7.79E-03 | 4.89E-03 |
| **ATP5G3** | 2 | 2 | 142 | 141 | QA | 3.19E-03 | 3.56E-03 | 5.17E-03 |
| **CLIC3** | 2 | 2 | 44 | 44 | QA | 6.22E-03 | 6.48E-03 | 5.38E-03 |
| **MCF2L** | 6 | 6 | 179 | 179 | QA | 2.51E-02 | 7.39E-03 | 5.55E-03 |
| **NAA11** | 2 | 2 | 197 | 195 | QA | 2.17E-02 | 9.33E-03 | 5.77E-03 |
| **FOXP4** | 2 | 2 | 12 | 12 | ER | 4.63E-03 | 6.97E-03 | 5.86E-03 |
| **TRIB3** | 6 | 6 | 257 | 255 | QA | 1.36E-02 | 9.93E-03 | 5.88E-03 |
| **CCDC8** | 3 | 3 | 101 | 101 | QA | 4.70E-03 | 5.50E-03 | 5.94E-03 |
| **MFN2** | 2 | 2 | 3 | 3 | ER | 6.11E-03 | 6.11E-03 | 6.11E-03 |
| **PLSCR2** | 2 | 2 | 3 | 3 | ER | 6.11E-03 | 6.11E-03 | 6.11E-03 |
| **CLEC10A** | 4 | 4 | 294 | 151 | QA | 5.40E-03 | 5.59E-03 | 6.13E-03 |
| **SLC45A2** | 6 | 6 | 83 | 81 | QA | 2.04E-02 | 1.22E-02 | 6.72E-03 |
| **SNRNP48** | 2 | 2 | 78 | 78 | QA | 2.26E-03 | 3.63E-03 | 7.04E-03 |
| **SLC8A1** | 4 | 3 | 129 | 129 | QA | 1.19E-02 | 8.00E-03 | 7.33E-03 |
| **PGM3** | 3 | 3 | 245 | 245 | QA | 2.21E-02 | 1.20E-02 | 7.56E-03 |
| **TEX15** | 17 | 16 | 885 | 865 | UA | 3.61E-02 | 1.30E-02 | 7.85E-03 |
| **IZUMO1R** | 3 | 3 | 241 | 240 | QA | 1.28E-02 | 1.19E-02 | 7.93E-03 |
| **INCA1** | 3 | 3 | 120 | 120 | QA | 8.36E-03 | 9.64E-03 | 7.96E-03 |
| **RNF207** | 3 | 3 | 160 | 160 | QA | 4.64E-02 | 1.33E-02 | 8.08E-03 |
| **APOBR** | 2 | 2 | 34 | 34 | ER.A | 2.31E-02 | 1.39E-02 | 8.11E-03 |
| **GPR161** | 2 | 2 | 15 | 15 | ER | 7.42E-03 | 4.41E-03 | 8.30E-03 |
| **BAIAP3** | 2 | 2 | 34 | 34 | ER.A | 2.29E-02 | 1.37E-02 | 8.45E-03 |
| **FAM26E** | 2 | 2 | 212 | 211 | QA | 6.87E-03 | 7.74E-03 | 8.83E-03 |
| **TVP23A** | 2 | 2 | 210 | 206 | QA | 2.62E-02 | 1.02E-02 | 9.23E-03 |
| **MVD** | 3 | 3 | 249 | 245 | QA | 2.90E-02 | 1.55E-02 | 9.36E-03 |
| **TIA1** | 2 | 2 | 14 | 14 | ER | 2.95E-02 | 2.95E-02 | 9.36E-03 |
| **FAT2** | 18 | 17 | 595 | 488 | QA | 4.58E-02 | 1.76E-02 | 9.60E-03 |
| **HIST1H3A** | 2 | 2 | 116 | 116 | QA | 2.34E-02 | 1.43E-02 | 9.72E-03 |
| **PNPLA1** | 4 | 4 | 59 | 59 | QA | 6.35E-03 | 7.49E-03 | 1.01E-02 |
| **TLR9** | 2 | 2 | 97 | 97 | QA | 1.17E-02 | 1.13E-02 | 1.04E-02 |
| **ITGB8** | 2 | 2 | 51 | 51 | QA | 5.22E-03 | 5.70E-03 | 1.06E-02 |
| **LNPEP** | 6 | 6 | 222 | 219 | QA | 3.12E-02 | 1.87E-02 | 1.09E-02 |
| **PGBD1** | 7 | 7 | 98 | 98 | QA | 2.34E-02 | 1.93E-02 | 1.15E-02 |
| **MTMR9** | 3 | 3 | 119 | 119 | QA | 1.21E-02 | 1.30E-02 | 1.17E-02 |
| **RFTN2** | 4 | 2 | 14 | 14 | ER | 3.54E-02 | 2.97E-02 | 1.17E-02 |
| **ERI3** | 2 | 2 | 37 | 37 | ER.A | 3.13E-02 | 1.99E-02 | 1.19E-02 |
| **CYB5R3** | 2 | 2 | 130 | 130 | QA | 1.61E-02 | 1.49E-02 | 1.21E-02 |
| **CD109** | 10 | 9 | 227 | 226 | QA | 8.33E-03 | 1.19E-02 | 1.23E-02 |
| **HNRNPH3** | 2 | 2 | 74 | 74 | QA | 3.67E-02 | 1.83E-02 | 1.23E-02 |
| **WFIKKN1** | 2 | 2 | 50 | 50 | QA | 1.38E-02 | 1.40E-02 | 1.24E-02 |
| **SLC2A11** | 7 | 7 | 429 | 183 | QA | 1.41E-02 | 1.43E-02 | 1.24E-02 |
| **FLOT2** | 2 | 2 | 13 | 13 | ER | 1.33E-02 | 7.46E-03 | 1.25E-02 |
| **GLYATL2** | 2 | 2 | 199 | 197 | QA | 1.54E-02 | 1.40E-02 | 1.26E-02 |
| **OR51G2** | 3 | 2 | 38 | 38 | ER.A | 2.22E-02 | 1.97E-02 | 1.26E-02 |
| **HOMER3** | 2 | 2 | 13 | 13 | ER | 6.09E-03 | 6.09E-03 | 1.27E-02 |
| **FAM160A2** | 6 | 5 | 159 | 158 | QA | 2.23E-02 | 2.04E-02 | 1.27E-02 |
| **ITPA** | 2 | 2 | 19 | 19 | ER | 1.43E-02 | 1.48E-02 | 1.30E-02 |
| **TMEM63C** | 5 | 5 | 231 | 229 | QA | 3.79E-02 | 1.88E-02 | 1.30E-02 |
| **CEP76** | 2 | 2 | 77 | 77 | QA | 5.47E-03 | 7.42E-03 | 1.31E-02 |
| **DDHD1** | 4 | 4 | 102 | 102 | QA | 4.63E-02 | 2.16E-02 | 1.32E-02 |
| **DNAJC17** | 3 | 3 | 124 | 124 | QA | 4.14E-02 | 2.03E-02 | 1.33E-02 |
| **GRM2** | 8 | 8 | 590 | 464 | QA | 1.93E-02 | 2.00E-02 | 1.37E-02 |
| **SLFN14** | 3 | 3 | 91 | 91 | QA | 7.12E-03 | 8.76E-03 | 1.38E-02 |
| **NUF2** | 2 | 2 | 22 | 22 | ER.A | 3.89E-02 | 2.19E-02 | 1.38E-02 |
| **HERPUD2** | 2 | 2 | 28 | 28 | ER.A | 1.19E-02 | 1.19E-02 | 1.40E-02 |
| **PCDHA10** | 2 | 2 | 95 | 95 | QA | 1.96E-02 | 1.98E-02 | 1.42E-02 |
| **CHRNG** | 5 | 5 | 61 | 61 | QA | 4.85E-02 | 2.14E-02 | 1.43E-02 |
| **RFX5** | 2 | 2 | 39 | 39 | ER.A | 4.69E-02 | 1.96E-02 | 1.44E-02 |
| **LIMD1** | 2 | 2 | 42 | 42 | QA | 3.02E-02 | 1.81E-02 | 1.45E-02 |
| **COQ7** | 3 | 2 | 79 | 79 | QA | 8.45E-03 | 9.08E-03 | 1.46E-02 |
| **COG5** | 4 | 4 | 26 | 26 | ER.A | 2.69E-02 | 2.58E-02 | 1.46E-02 |
| **ZNF485** | 2 | 2 | 84 | 84 | QA | 3.04E-02 | 1.72E-02 | 1.48E-02 |
| **MOCOS** | 4 | 4 | 106 | 106 | QA | 1.36E-02 | 1.49E-02 | 1.49E-02 |
| **ETFB** | 3 | 3 | 202 | 201 | QA | 1.72E-02 | 1.88E-02 | 1.57E-02 |
| **ITGB5** | 3 | 3 | 123 | 122 | QA | 2.74E-03 | 3.79E-03 | 1.59E-02 |
| **RERE** | 3 | 2 | 82 | 82 | QA | 4.45E-02 | 2.11E-02 | 1.63E-02 |
| **ITPR1** | 6 | 6 | 38 | 38 | ER.A | 1.82E-02 | 2.21E-02 | 1.66E-02 |
| **DDIAS** | 4 | 4 | 196 | 195 | QA | 3.81E-02 | 2.55E-02 | 1.66E-02 |
| **NALCN** | 2 | 2 | 8 | 8 | ER | 1.01E-02 | 1.01E-02 | 1.67E-02 |
| **HTRA2** | 2 | 2 | 4 | 4 | ER | 2.63E-02 | 2.63E-02 | 1.69E-02 |
| **ZNF563** | 2 | 2 | 4 | 4 | ER | 2.63E-02 | 2.63E-02 | 1.69E-02 |
| **TGM1** | 7 | 7 | 286 | 284 | QA | 3.90E-02 | 2.80E-02 | 1.69E-02 |
| **CYP26C1** | 4 | 3 | 192 | 192 | QA | 4.49E-02 | 2.67E-02 | 1.73E-02 |
| **DENND4B** | 3 | 3 | 66 | 66 | QA | 1.73E-02 | 2.16E-02 | 1.74E-02 |
| **DAB2IP** | 2 | 2 | 202 | 201 | QA | 7.23E-03 | 7.68E-03 | 1.75E-02 |
| **SH3PXD2A** | 11 | 9 | 3501 | 3190 | UA | 2.54E-02 | 2.46E-02 | 1.76E-02 |
| **CFAP65** | 11 | 11 | 528 | 519 | UA | 1.70E-02 | 1.81E-02 | 1.81E-02 |
| **PPP2R4** | 2 | 2 | 28 | 28 | ER.A | 2.95E-02 | 2.18E-02 | 1.86E-02 |
| **AAK1** | 5 | 5 | 129 | 128 | QA | 3.06E-02 | 2.37E-02 | 1.86E-02 |
| **ATL2** | 3 | 3 | 4160 | 3712 | UA | 2.42E-02 | 2.37E-02 | 1.86E-02 |
| **IGSF9** | 3 | 3 | 32 | 32 | ER.A | 1.11E-02 | 1.35E-02 | 1.89E-02 |
| **BLK** | 3 | 3 | 27 | 27 | ER.A | 1.15E-02 | 1.80E-02 | 1.89E-02 |
| **FAM65C** | 6 | 6 | 139 | 137 | QA | 6.96E-03 | 1.02E-02 | 1.95E-02 |
| **NCR3** | 3 | 2 | 324 | 323 | QA | 1.99E-02 | 2.56E-02 | 1.96E-02 |
| **CHRD** | 4 | 3 | 120 | 120 | QA | 4.14E-02 | 2.42E-02 | 1.97E-02 |
| **ZNF343** | 6 | 6 | 192 | 188 | QA | 4.46E-02 | 3.06E-02 | 2.03E-02 |
| **KCNIP4** | 2 | 2 | 19 | 19 | ER | 3.46E-02 | 2.41E-02 | 2.05E-02 |
| **NFAT5** | 5 | 5 | 255 | 254 | QA | 2.92E-02 | 3.05E-02 | 2.05E-02 |
| **SLC27A5** | 3 | 2 | 42 | 42 | QA | 1.76E-02 | 2.10E-02 | 2.12E-02 |
| **OR10J3** | 2 | 2 | 167 | 167 | QA | 2.33E-02 | 2.36E-02 | 2.12E-02 |
| **STIL** | 4 | 4 | 108 | 108 | QA | 5.31E-03 | 9.04E-03 | 2.13E-02 |
| **CLEC16A** | 3 | 3 | 14 | 14 | ER | 3.37E-02 | 2.03E-02 | 2.14E-02 |
| **KIF1A** | 2 | 2 | 97 | 97 | QA | 9.19E-03 | 1.40E-02 | 2.15E-02 |
| **AXIN1** | 2 | 2 | 4 | 4 | ER | 2.16E-02 | 2.16E-02 | 2.16E-02 |
| **SYCE1** | 2 | 2 | 4 | 4 | ER | 2.16E-02 | 2.16E-02 | 2.16E-02 |
| **CCDC14** | 3 | 3 | 205 | 205 | QA | 8.24E-03 | 1.24E-02 | 2.19E-02 |
| **CABP5** | 2 | 2 | 9 | 9 | ER | 1.92E-02 | 2.72E-02 | 2.24E-02 |
| **PINK1** | 4 | 4 | 14 | 14 | ER | 2.94E-03 | 7.30E-03 | 2.26E-02 |
| **LY6K** | 2 | 2 | 25 | 25 | ER.A | 4.83E-02 | 2.78E-02 | 2.26E-02 |
| **COCH** | 2 | 2 | 25 | 25 | ER.A | 3.78E-02 | 3.23E-02 | 2.27E-02 |
| **OR8B4** | 2 | 2 | 161 | 160 | QA | 3.43E-02 | 2.62E-02 | 2.28E-02 |
| **STPG2** | 2 | 2 | 16 | 16 | ER | 4.98E-02 | 2.42E-02 | 2.42E-02 |
| **GATM** | 2 | 2 | 16 | 16 | ER | 4.29E-02 | 3.68E-02 | 2.42E-02 |
| **PRDM5** | 3 | 3 | 181 | 181 | QA | 2.41E-02 | 2.59E-02 | 2.43E-02 |
| **COL6A2** | 12 | 11 | 262 | 260 | QA | 2.84E-02 | 3.45E-02 | 2.46E-02 |
| **NARS** | 3 | 3 | 181 | 179 | QA | 3.08E-02 | 3.58E-02 | 2.52E-02 |
| **CLTCL1** | 10 | 10 | 169 | 153 | QA | 3.49E-02 | 3.75E-02 | 2.54E-02 |
| **MEGF8** | 7 | 6 | 157 | 157 | QA | 6.15E-03 | 1.10E-02 | 2.58E-02 |
| **TIMMDC1** | 3 | 3 | 178 | 104 | QA | 2.52E-02 | 2.71E-02 | 2.59E-02 |
| **DTHD1** | 4 | 4 | 159 | 137 | QA | 3.23E-02 | 3.55E-02 | 2.62E-02 |
| **CEP72** | 8 | 8 | 570 | 363 | QA | 1.14E-02 | 1.59E-02 | 2.63E-02 |
| **DPPA2** | 2 | 2 | 2 | 2 | ER | 2.65E-02 | 2.65E-02 | 2.65E-02 |
| **HEPACAM** | 2 | 2 | 2 | 2 | ER | 2.65E-02 | 2.65E-02 | 2.65E-02 |
| **WNT9B** | 2 | 2 | 2 | 2 | ER | 2.65E-02 | 2.65E-02 | 2.65E-02 |
| **OR2H1** | 6 | 5 | 191 | 191 | QA | 3.83E-02 | 4.05E-02 | 2.69E-02 |
| **CDK5RAP2** | 5 | 4 | 6 | 6 | ER | 1.98E-03 | 3.98E-03 | 2.73E-02 |
| **TJP1** | 3 | 3 | 50 | 50 | QA | 4.38E-02 | 3.19E-02 | 2.80E-02 |
| **PSME4** | 4 | 3 | 202 | 200 | QA | 2.35E-02 | 3.16E-02 | 2.82E-02 |
| **TXNDC15** | 3 | 3 | 161 | 159 | QA | 4.36E-02 | 4.41E-02 | 2.82E-02 |
| **STARD6** | 5 | 5 | 204 | 203 | QA | 3.18E-02 | 3.95E-02 | 2.85E-02 |
| **ARHGAP19** | 2 | 2 | 9 | 9 | ER | 2.69E-02 | 2.69E-02 | 2.87E-02 |
| **ACTBL2** | 2 | 2 | 101 | 101 | QA | 3.89E-02 | 4.05E-02 | 2.87E-02 |
| **PPP6R1** | 6 | 4 | 110 | 110 | QA | 4.29E-02 | 4.47E-02 | 2.95E-02 |
| **NRXN3** | 2 | 2 | 90 | 90 | QA | 1.88E-02 | 2.01E-02 | 2.97E-02 |
| **PRSS48** | 2 | 2 | 92 | 91 | QA | 4.02E-02 | 3.21E-02 | 3.00E-02 |
| **FCMR** | 2 | 2 | 33 | 32 | ER.A | 4.03E-02 | 4.13E-02 | 3.04E-02 |
| **CERK** | 7 | 7 | 196 | 192 | QA | 3.21E-02 | 4.18E-02 | 3.08E-02 |
| **GFM2** | 3 | 3 | 4 | 4 | ER | 1.22E-02 | 1.22E-02 | 3.10E-02 |
| **MASP2** | 3 | 3 | 4 | 4 | ER | 1.22E-02 | 1.22E-02 | 3.10E-02 |
| **RIPK1** | 2 | 2 | 125 | 125 | QA | 2.45E-02 | 2.89E-02 | 3.12E-02 |
| **PARP1** | 3 | 3 | 50 | 50 | QA | 6.07E-03 | 8.30E-03 | 3.16E-02 |
| **FAM171A1** | 2 | 2 | 57 | 57 | QA | 1.49E-02 | 1.67E-02 | 3.21E-02 |
| **OR10J1** | 2 | 2 | 137 | 136 | QA | 4.87E-02 | 3.39E-02 | 3.25E-02 |
| **GPR21** | 3 | 3 | 5 | 5 | ER | 1.87E-02 | 1.87E-02 | 3.32E-02 |
| **ZNF569** | 2 | 2 | 84 | 83 | QA | 2.53E-02 | 3.09E-02 | 3.33E-02 |
| **C17orf47** | 2 | 2 | 61 | 61 | QA | 4.71E-02 | 3.69E-02 | 3.39E-02 |
| **RNF145** | 2 | 2 | 33 | 33 | ER.A | 1.30E-02 | 1.92E-02 | 3.40E-02 |
| **ARHGAP18** | 2 | 2 | 7 | 7 | ER | 4.25E-02 | 4.10E-02 | 3.46E-02 |
| **ADAMTS16** | 2 | 2 | 27 | 27 | ER.A | 1.45E-02 | 1.53E-02 | 3.47E-02 |
| **CCBE1** | 3 | 2 | 21 | 21 | ER.A | 3.35E-02 | 3.65E-02 | 3.47E-02 |
| **ADGRG7** | 5 | 5 | 175 | 174 | QA | 4.59E-02 | 4.02E-02 | 3.48E-02 |
| **ANKEF1** | 6 | 6 | 450 | 223 | QA | 4.24E-02 | 3.97E-02 | 3.50E-02 |
| **KMT2D** | 12 | 12 | 444 | 433 | QA | 3.88E-02 | 4.67E-02 | 3.55E-02 |
| **CAMK4** | 2 | 2 | 166 | 166 | QA | 4.39E-02 | 3.76E-02 | 3.56E-02 |
| **LGALS3BP** | 5 | 5 | 344 | 193 | QA | 2.04E-02 | 2.16E-02 | 3.58E-02 |
| **SEMA4A** | 2 | 2 | 31 | 30 | ER.A | 1.40E-02 | 1.72E-02 | 3.61E-02 |
| **MBD6** | 2 | 2 | 42 | 42 | QA | 4.32E-02 | 3.94E-02 | 3.70E-02 |
| **C7orf62** | 2 | 2 | 197 | 196 | QA | 3.01E-02 | 3.21E-02 | 3.71E-02 |
| **EML4** | 2 | 2 | 48 | 48 | QA | 4.97E-02 | 4.09E-02 | 3.71E-02 |
| **ASCC2** | 4 | 4 | 16 | 8 | ER | 1.80E-02 | 1.80E-02 | 3.79E-02 |
| **CCDC151** | 3 | 3 | 10 | 10 | ER | 1.80E-02 | 1.98E-02 | 3.82E-02 |
| **KCTD16** | 3 | 2 | 22 | 22 | ER.A | 2.03E-02 | 2.65E-02 | 3.85E-02 |
| **CRELD1** | 3 | 3 | 34 | 34 | ER.A | 1.87E-02 | 2.87E-02 | 3.92E-02 |
| **TRPM6** | 5 | 4 | 29 | 29 | ER.A | 4.82E-02 | 4.26E-02 | 3.92E-02 |
| **SEL1L** | 3 | 3 | 72 | 72 | QA | 2.38E-02 | 2.82E-02 | 3.94E-02 |
| **HERC6** | 5 | 5 | 146 | 139 | QA | 1.55E-02 | 2.41E-02 | 3.98E-02 |
| **PIF1** | 5 | 5 | 192 | 191 | QA | 7.90E-03 | 1.44E-02 | 4.04E-02 |
| **PIEZO2** | 3 | 3 | 51 | 41 | QA | 2.71E-02 | 4.14E-02 | 4.19E-02 |
| **LCORL** | 2 | 2 | 37 | 37 | ER.A | 2.38E-02 | 2.43E-02 | 4.22E-02 |
| **SLC2A13** | 3 | 3 | 119 | 119 | QA | 3.92E-03 | 6.47E-03 | 4.27E-02 |
| **PCDHA7** | 4 | 4 | 59 | 59 | QA | 2.41E-02 | 3.83E-02 | 4.27E-02 |
| **STK31** | 7 | 7 | 547 | 432 | QA | 9.72E-04 | 1.79E-03 | 4.30E-02 |
| **SCIN** | 5 | 5 | 44 | 33 | QA | 3.00E-02 | 4.55E-02 | 4.32E-02 |
| **GAL3ST1** | 2 | 2 | 55 | 55 | QA | 3.71E-02 | 4.72E-02 | 4.33E-02 |
| **ADTRP** | 2 | 2 | 41 | 41 | QA | 3.97E-02 | 4.86E-02 | 4.34E-02 |
| **ANK3** | 9 | 9 | 239 | 236 | QA | 1.12E-02 | 1.79E-02 | 4.38E-02 |
| **MURC** | 2 | 2 | 7 | 7 | ER | 1.85E-02 | 1.85E-02 | 4.42E-02 |
| **RABGGTA** | 2 | 2 | 7 | 7 | ER | 1.85E-02 | 1.85E-02 | 4.42E-02 |
| **FOXJ3** | 2 | 2 | 24 | 24 | ER.A | 1.68E-02 | 1.86E-02 | 4.44E-02 |
| **TMEM14B** | 2 | 2 | 10 | 10 | ER | 4.84E-02 | 4.84E-02 | 4.44E-02 |
| **GRM1** | 2 | 2 | 7 | 7 | ER | 4.45E-02 | 4.45E-02 | 4.49E-02 |
| **TONSL** | 3 | 3 | 189 | 185 | QA | 6.81E-03 | 7.93E-03 | 4.55E-02 |
| **STIM1** | 2 | 2 | 13 | 13 | ER | 2.66E-02 | 2.66E-02 | 4.55E-02 |
| **CNTN1** | 2 | 2 | 31 | 31 | ER.A | 3.74E-02 | 4.79E-02 | 4.56E-02 |
| **SEC24D** | 2 | 2 | 10 | 10 | ER | 2.41E-02 | 2.41E-02 | 4.62E-02 |
| **GJB4** | 5 | 4 | 166 | 166 | QA | 4.53E-02 | 4.91E-02 | 4.67E-02 |
| **CECR2** | 6 | 6 | 128 | 128 | QA | 2.57E-02 | 3.31E-02 | 4.94E-02 |

N.Marker.All: number of SNPs in the gene; N.Marker.Test: number of SNPs used for the test; MAC: minor allele count; M: number of individuals with minor alleles.