|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene**  **Table S1. Genes with significant (q-value <0.05) differences in pathogenic variant burden among Polish population (Thousand Polish Genomes database) compared with non-Finnish European (gnomAD)** | **Position** | **Allele** | **Variant ID** | **Allele frequency in Polish population** | **Allele frequency in gnomAD NFE** | **q-value** | **OR** | **IMPACT** | **Consequence** | **Clinical significance** |
| *APC* | chr5:112837834 | C>T | rs773020689 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *APC* | chr5:112838128 | G>A | rs776878597 | 0.00081 | 8.8e-05 | 0.021 | 21 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *APC* | chr5:112842318 | A>G | rs201375478 | 0.0016 | 0.00016 | 0.00038 | 23 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *APC* | chr5:112843372 | A>G | rs367676584 | 0.0012 | 1.5e-05 | 8.6e-05 | 190 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *APC* | chr5:112843452 | T>A | rs587781816 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ARSB* | chr5:78885603 | C>T | rs200040980 | 0.0024 | 0.00065 | 0.00064 | 8.6 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ARSB* | chr5:78969026 | C>T | rs1196325597 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Pathogenic/Likely pathogenic |
| *ARSB* | chr5:78985513 | C>T | rs72764913 | 0.026 | 0.03 | 2.3e-05 | 2 | MODIFIER | upstream gene variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108235718 | CA>C | rs587781831 | 0.00041 | 0 | 0.035 | N/A | HIGH | frameshift variant | Pathogenic/Likely pathogenic |
| *ATM* | chr11:108235814 | TATCTC>T | rs587780624 | 0.00041 | 0 | 0.035 | N/A | HIGH | frameshift variant | Pathogenic/Likely pathogenic |
| *ATM* | chr11:108282704 | G>A | rs56006345 | 0.00041 | 0 | 0.035 | N/A | LOW | splice polypyrimidine tract variant,splice region variant,  intron variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108293469 | C>T | rs35962982 | 0.0012 | 0.00035 | 0.025 | 7.9 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108304660 | G>C | rs3092828 | 0.0081 | 0.0054 | 3.2e-05 | 3.4 | LOW | splice polypyrimidine tract variant,intron variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108304736 | A>T | rs1801673 | 0.013 | 0.0073 | 5.3e-10 | 4.2 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108315883 | G>A | rs11212587 | 0.0028 | 0.0023 | 0.035 | 2.8 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108326110 | G>C | rs1800061 | 0.0016 | 0.00056 | 0.014 | 6.7 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108331877 | A>C | rs587779866 | 0.0012 | 2.9e-05 | 2E-04 | 95 | HIGH | splice acceptor variant | Pathogenic |
| *ATM* | chr11:108365744 | C>T | rs3092834 | 0.0012 | 0.00046 | 0.035 | 6.1 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *ATM* | chr11:108368115 | T>C | rs879796523 | 0.0032 | 0.001 | 0.00015 | 7.4 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *BRCA1* | chr17:43057062 | T>TG | rs80357906 | 0.0016 | 5.9e-05 | 2.6e-05 | 63 | HIGH | frameshift variant | Pathogenic |
| *BRCA1* | chr17:43067677 | C>A | rs80357087 | 0.0028 | 0.00038 | 5.1e-06 | 17 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *BRCA1* | chr17:43091826 | GTTTAC>G | rs80357609 | 0.00041 | 0 | 0.035 | N/A | HIGH | frameshift variant | Pathogenic |
| *CHEK2* | chr22:28725099 | A>G | rs17879961 | 0.028 | 0.0053 | 2.9e-44 | 12 | MODERATE | missense variant | Conflicting interpretations of pathogenicity|risk factor |
| *CHEK2* | chr22:28725240 | T>C | rs587781279 | 0.00041 | 0 | 0.035 | N/A | LOW | splice donor region variant,intron variant | Conflicting interpretations of pathogenicity |
| *CHEK2* | chr22:28725242 | C>T | rs121908698 | 0.0036 | 0.00018 | 1.6e-10 | 47 | HIGH | splice donor variant | Conflicting interpretations of pathogenicity |
| *CHEK2* | chr22:28725277 | C>T | rs368570187 | 0.0012 | 0.00019 | 0.0068 | 15 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *DICER1* | chr14:95099771 | C>CAA | rs1555368535 | 0.0028 | 0.039 | 2.3e-10 | 0.14 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *DICER1* | chr14:95105250 | C>G | rs1595371340 | 0.00081 | 0 | 0.0011 | N/A | LOW | splice polypyrimidine tract variant,splice region variant,intron variant | Conflicting interpretations of pathogenicity |
| *DICER1* | chr14:95115562 | G>A | rs2275182 | 0.2 | 0.2 | 5.4e-44 | 2.3 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *DICER1* | chr14:95133439 | T>C | rs117358479 | 0.0069 | 0.0032 | 2E-06 | 4.9 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *GPD1L* | chr3:32140231 | A>G | rs72552293 | 0.015 | 0.0028 | 2.6e-23 | 12 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *INSR* | chr19:7125507 | C>T | rs1799816 | 0.0081 | 0.0071 | 0.00086 | 2.6 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *INSR* | chr19:7142970 | C>G | rs78433961 | 0.002 | 0.00068 | 0.0048 | 6.9 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *INSR* | chr19:7152840 | G>T | rs142391704 | 0.00081 | 0.00019 | 0.048 | 9.7 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *INSR* | chr19:7184640 | G>GGAGA | rs3835070 | 0.023 | 0.021 | 5.8e-08 | 2.5 | LOW | splice polypyrimidine tract variant,splice region variant,intron variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160038797 | T>C | rs116418256 | 0.0081 | 0.008 | 0.0036 | 2.3 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160039359 | G>A | rs192835895 | 0.012 | 0.0028 | 8.7e-18 | 9.9 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160039373 | GACACACAC>G | rs56656397 | 0.14 | 0.16 | 4.3e-22 | 2 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160039373 | GAC>G | rs56656397 | 0.13 | 0.14 | 1.5e-27 | 2.2 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160039373 | GACACAC>G | rs56656397 | 0.06 | 0.081 | 2.6e-07 | 1.7 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160041721 | C>T | rs3795339 | 0.0012 | 0.00037 | 0.027 | 7.6 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160042003 | T>C | rs145947380 | 0.0032 | 0.00063 | 8.7e-06 | 12 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *KCNJ10* | chr1:160042480 | C>T | rs115466046 | 0.015 | 0.017 | 0.0016 | 2 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *MYH9* | chr22:36292033 | G>A | rs727503286 | 0.00081 | 7.3e-05 | 0.016 | 25 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *PALB2* | chr16:23635002 | T>C | rs515726072 | 0.0016 | 0.00018 | 0.00049 | 21 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *PALB2* | chr16:23637964 | A>T | rs774949203 | 0.00041 | 0 | 0.035 | N/A | LOW | splice polypyrimidine tract variant,intron variant | Conflicting interpretations of pathogenicity |
| *PALB2* | chr16:23641145 | G>A | rs377085677 | 0.00081 | 8.8e-05 | 0.021 | 21 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *PALB2* | chr16:23641315 | C>G | rs138200248 | 0.019 | 0.0073 | 2.2e-18 | 5.9 | MODIFIER | upstream gene variant | Conflicting interpretations of pathogenicity |
| *PLCB1* | chr20:8132322 | C>T | rs532302075 | 0.021 | 0.0098 | 3.7e-17 | 4.8 | MODIFIER | 5 prime UTR variant | Conflicting interpretations of pathogenicity |
| *PLCB1* | chr20:8739374 | G>C | rs768572485 | 0.00081 | 4.4e-05 | 0.0084 | 42 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *PLCB1* | chr20:8788453 | T>C | rs75820839 | 0.00081 | 1E-04 | 0.025 | 18 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *POT1* | chr7:124851922 | T>C | rs573222502 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *PTEN* | chr10:87958028 | T>C | rs1060503839 | 0.00041 | 0 | 0.035 | N/A | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *PTEN* | chr10:87965754 | G>A | rs576872432 | 0.0012 | 5.9e-05 | 0.00064 | 47 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *PTEN* | chr10:87966971 | C>T | rs180953647 | 0.027 | 0.0043 | 3.9e-47 | 14 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43106469 | G>A | rs377767388 | 0.0016 | 7.4e-05 | 4.3e-05 | 51 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43111500 | C>T | rs377130948 | 0.0041 | 0.00024 | 4.4e-11 | 40 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43114546 | C>T | rs148935214 | 0.0045 | 0.00076 | 3.7e-08 | 13 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43114671 | G>A | rs1799939 | 0.2 | 0.18 | 1.1e-56 | 2.6 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43118460 | A>T | rs77724903 | 0.011 | 0.0018 | 3E-20 | 14 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43124887 | C>T | rs17158558 | 0.024 | 0.016 | 6.5e-14 | 3.5 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43126647 | A>G | rs201740483 | 0.0081 | 0.00084 | 9E-18 | 22 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *RET* | chr10:43129699 | A>G | rs775114955 | 0.0012 | 4E-04 | 0.032 | 7 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *SEC23B* | chr20:18524971 | C>T | rs201418257 | 0.00081 | 0 | 0.0011 | N/A | HIGH | stop gained | Pathogenic |
| *SEC23B* | chr20:18525868 | C>T | rs146917730 | 0.022 | 0.016 | 1.7e-11 | 3.2 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *SERPINA1* | chr14:94388565 | A>G | rs11558258 | 0.051 | 0.039 | 7.1e-22 | 3 | MODIFIER | 5 prime UTR variant | Conflicting interpretations of pathogenicity |
| *SLC26A4* | chr7:107674187 | A>C | CM033462 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Likely pathogenic |
| *SLC26A4* | chr7:107683277 | G>A | rs727505080 | 0.00081 | 0.00016 | 0.037 | 11 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *SLC26A4* | chr7:107683349 | AT>A | COSV105848651 | 0.00041 | 0 | 0.035 | N/A | HIGH | frameshift variant | Likely pathogenic |
| *SLC26A4* | chr7:107689054 | T>C | rs111033212 | 0.0028 | 0.0011 | 0.0014 | 5.9 | MODERATE | missense variant,splice region variant | Likely pathogenic |
| *SLC26A4* | chr7:107690220 | A>C | rs28939086 | 0.0016 | 0.00032 | 0.0029 | 11 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *SLC26A4* | chr7:107694718 | T>G | rs397516418 | 0.00041 | 0 | 0.035 | N/A | HIGH | splice donor variant | Pathogenic/Likely pathogenic |
| *SLC26A4* | chr7:107698071 | C>T | rs765197819 | 0.00041 | 0 | 0.035 | N/A | MODERATE | missense variant | Likely pathogenic |
| *SLC26A4* | chr7:107715796 | C>T | rs17154362 | 0.0061 | 9E-04 | 1.3e-11 | 16 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *SMAD3* | chr15:67138026 | C>A | rs958007552 | 0.00081 | 1E-04 | 0.025 | 18 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *SMAD3* | chr15:67191325 | A>G | rs191679355 | 0.00081 | 1E-04 | 0.025 | 18 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *STK11* | chr19:1206797 | C>CT | rs927999961 | 0.0012 | 0.00022 | 0.009 | 13 | MODIFIER | 5 prime UTR variant | Conflicting interpretations of pathogenicity |
| *STK11* | chr19:1219421 | C>T | rs863224669 | 0.00081 | 3E-05 | 0.0054 | 63 | LOW | splice region variant,intron variant | Conflicting interpretations of pathogenicity |
| *STK11* | chr19:1221319 | C>A | rs377208033 | 0.00081 | 1.5e-05 | 0.003 | 130 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *STK11* | chr19:1226556 | C>T | rs200078204 | 0.0016 | 0.00087 | 0.037 | 4.3 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *STK11* | chr19:1226655 | C>T | rs587782259 | 0.0041 | 0.00038 | 1.5e-09 | 24 | MODIFIER | 3 prime UTR variant | Conflicting interpretations of pathogenicity |
| *TERT* | chr5:1278812 | C>T | rs146768484 | 0.0089 | 0.00094 | 3E-19 | 22 | LOW | splice polypyrimidine tract variant,intron variant | Conflicting interpretations of pathogenicity |
| *TERT* | chr5:1293652 | G>A | rs34094720 | 0.0057 | 0.0049 | 0.0053 | 2.7 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *TOE1* | chr1:45340381 | G>A | rs3219466 | 0.039 | 0.034 | 1.2e-13 | 2.6 | MODIFIER | intron variant | Conflicting interpretations of pathogenicity |
| *WRN* | chr8:31058542 | A>G | rs34477820 | 0.01 | 0.0054 | 5.8e-08 | 4.3 | MODERATE | missense variant,splice region variant | Conflicting interpretations of pathogenicity |
| *WRN* | chr8:31064438 | G>C | rs145764920 | 0.0061 | 0.0027 | 5.5e-06 | 5.2 | LOW | splice donor region variant,intron variant | Conflicting interpretations of pathogenicity |
| *WRN* | chr8:31081176 | G>T | rs4987238 | 0.0045 | 0.0018 | 5.7e-05 | 5.7 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |
| *WRN* | chr8:31141445 | G>A | rs140768346 | 0.0045 | 0.0025 | 0.00074 | 4.1 | MODERATE | missense variant | Conflicting interpretations of pathogenicity |