**Table S2. SNPs sorted for present in 2/19 patients and in 2.5% or less of the genome 1000 dbase1.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| ID | Gene Symbol | AA Change | Allele  Freq | 1000  Genome Freq | n |
| chr1\_31896645\_G\_T | SERINC2 | GLY-TRP | 0.056 | 0.001 | 2 |
| chr2\_86716518\_G\_A | KDM3A | VAL-ILE | 0.053 | 0.001 | 2 |
| chr2\_112786034\_C\_T | MERTK | ARG-TRP | 0.053 | 0.001 | 2 |
| chr2\_163361158\_T\_A | KCNH7 | ASN-ILE | 0.056 | 0.001 | 2 |
| chr3\_124418847\_G\_A | KALRN | GLU-LYS | 0.053 | 0.001 | 2 |
| chr3\_148459552\_G\_T | AGTR1 | ALA-SER | 0.063 | 0.001 | 2 |
| chr3\_186395400\_G\_A | HRG | GLY-ARG | 0.053 | 0.001 | 2 |
| chr4\_126329821\_A\_G | FAT4 | TYR-CYS | 0.053 | 0.001 | 2 |
| chr5\_43656074\_C\_T | NNT | THR-MET | 0.053 | 0.001 | 2 |
| chr5\_55237432\_A\_C | IL6ST | ASP-GLU | 0.053 | 0.001 | 2 |
| chr5\_134345062\_A\_G | CATSPER3 | ASP-GLY | 0.053 | 0.001 | 2 |
| chr5\_138378394\_G\_A | SIL1 | THR-ILE | 0.053 | 0.001 | 2 |
| chr6\_106968250\_G\_T | AIM1 | SER-ILE | 0.053 | 0.001 | 2 |
| chr7\_102575018\_T\_A | LRRC17,FBXL13 | LEU-MET | 0.053 | 0.001 | 2 |
| chr8\_95201468\_G\_A | CDH17 | PRO-SER | 0.079 | 0.001 | 2 |
| chr10\_24817027\_G\_T | KIAA1217 | VAL-LEU | 0.059 | 0.001 | 2 |
| chr10\_45799452\_C\_T | OR13A1 | ARG-GLN | 0.094 | 0.001 | 2 |
| chr10\_50678884\_T\_G | ERCC6 | GLN-PRO | 0.053 | 0.001 | 2 |
| chr10\_50690906\_G\_A | ERCC6 | ARG-CYS | 0.063 | 0.001 | 2 |
| chr10\_121182694\_C\_T | GRK5 | ALA-VAL | 0.053 | 0.001 | 2 |
| chr11\_7063792\_G\_A | NLRP14 | VAL-MET | 0.053 | 0.001 | 2 |
| chr11\_57947505\_G\_C | OR9Q1 | VAL-LEU | 0.053 | 0.001 | 2 |
| chr12\_1943732\_G\_A | CACNA2D4,LRTM2 | VAL-ILE | 0.053 | 0.001 | 2 |
| chr12\_95456418\_C\_T | NR2C1 | GLY-SER | 0.053 | 0.001 | 2 |
| chr12\_112184086\_G\_A | ACAD10 | GLU-LYS | 0.053 | 0.001 | 2 |
| chr13\_45589616\_C\_G | KIAA1704 | PRO-ARG | 0.056 | 0.001 | 2 |
| chr13\_45913651\_G\_C | TPT1 | ALA-GLY | 0.105 | 0.001 | 4 |
| chr14\_23467755\_G\_A | C14orf93 | ARG-TRP | 0.053 | 0.001 | 2 |
| chr15\_86287031\_C\_A | AKAP13 | ASN-LYS | 0.118 | 0.001 | 4 |
| chr15\_89825056\_A\_G | FANCI | MET-VAL | 0.105 | 0.001 | 3 |
| chr17\_8052915\_C\_T | PER1 | VAL-ILE | 0.063 | 0.001 | 2 |
| chr17\_39728000\_C\_T | KRT9 | SER-ASN | 0.053 | 0.001 | 2 |
| chr19\_18119848\_G\_A | ARRDC2 | ARG-GLN | 0.053 | 0.001 | 2 |
| chr19\_19030611\_G\_A | DDX49 | GLY-SER | 0.059 | 0.001 | 2 |
| chr20\_60884852\_G\_A | LAMA5 | ALA-VAL | 0.053 | 0.001 | 2 |
| chr1\_32145693\_C\_T | COL16A1 | GLY-ARG | 0.056 | 0.002 | 2 |
| chr1\_147131553\_T\_C | ACP6 | ASP-GLY | 0.053 | 0.002 | 2 |
| chr1\_151140732\_G\_A | SCNM1,TNFAIP8L2 | GLU-LYS | 0.053 | 0.002 | 2 |
| chr1\_151143016\_T\_C | TMOD4 | MET-VAL | 0.053 | 0.002 | 2 |
| chr1\_151867657\_G\_C | THEM4 | SER-CYS | 0.088 | 0.002 | 3 |
| chr1\_182369105\_C\_T | TEDDM1 | MET-ILE | 0.053 | 0.002 | 2 |
| chr2\_68729939\_A\_G | APLF | TYR-CYS | 0.056 | 0.002 | 2 |
| chr2\_170350279\_A\_G | BBS5 | ASN-SER | 0.067 | 0.002 | 2 |
| chr2\_228173636\_A\_G | COL4A3 | GLN-ARG | 0.053 | 0.002 | 2 |
| chr3\_49935526\_T\_G | MST1R | GLN-PRO | 0.053 | 0.002 | 2 |
| chr3\_120495353\_C\_T | GTF2E1 | SER-PHE | 0.053 | 0.002 | 2 |
| chr4\_54218924\_C\_A | SCFD2 | GLY-VAL | 0.059 | 0.002 | 2 |
| chr4\_57829669\_G\_A | C4orf14 | PRO-SER | 0.053 | 0.002 | 2 |
| chr4\_126372555\_A\_G | FAT4 | ILE-VAL | 0.056 | 0.002 | 2 |
| chr4\_169060675\_C\_T | ANXA10 | ARG-CYS | 0.056 | 0.002 | 2 |
| chr6\_30520367\_C\_T | GNL1 | GLU-LYS | 0.053 | 0.002 | 2 |
| chr6\_44361309\_G\_A | CDC5L | none | 0.053 | 0.002 | 2 |
| chr6\_74440124\_G\_A | CD109 | ASP-ASN | 0.053 | 0.002 | 2 |
| chr7\_27196116\_C\_T | HOXA7 | GLY-ARG | 0.053 | 0.002 | 2 |
| chr7\_91700267\_T\_C | AKAP9 | SER-PRO | 0.053 | 0.002 | 2 |
| chr7\_117267812\_T\_G | CFTR | SER-ARG | 0.053 | 0.002 | 2 |
| chr8\_133899575\_G\_A | TG | GLY-ASP | 0.056 | 0.002 | 2 |
| chr9\_98011497\_G\_A | FANCC | SER-PHE | 0.053 | 0.002 | 2 |
| chr11\_65638718\_C\_T | EFEMP2 | GLY-SER | 0.053 | 0.002 | 2 |
| chr12\_15777273\_C\_T | EPS8 | ALA-THR | 0.053 | 0.002 | 2 |
| chr12\_51451867\_G\_A | LETMD1 | ARG-GLN | 0.053 | 0.002 | 2 |
| chr12\_64814251\_G\_A | XPOT | GLU-LYS | 0.056 | 0.002 | 2 |
| chr12\_129299435\_C\_T | SLC15A4 | GLY-SER | 0.053 | 0.002 | 2 |
| chr12\_132401539\_C\_T | ULK1 | ALA-VAL | 0.053 | 0.002 | 2 |
| chr14\_23532193\_T\_C | ACIN1 | GLN-ARG | 0.053 | 0.002 | 2 |
| chr15\_31197015\_T\_G | FAN1 | MET-ARG | 0.056 | 0.002 | 2 |
| chr16\_10788550\_C\_T | TEKT5 | VAL-ILE | 0.053 | 0.002 | 2 |
| chr17\_8413233\_G\_A | MYH10 | ALA-VAL | 0.053 | 0.002 | 2 |
| chr18\_9887582\_C\_A | TXNDC2 | PRO-HIS | 0.053 | 0.002 | 2 |
| chr19\_35633635\_C\_T | FXYD1 | ARG-CYS | 0.056 | 0.002 | 2 |
| chr20\_1961298\_T\_G | PDYN | MET-LEU | 0.053 | 0.002 | 2 |
| chr20\_16360240\_G\_A | KIF16B | ARG-TRP | 0.053 | 0.002 | 2 |
| chr20\_62597996\_T\_C | ZNF512B | ARG-GLY | 0.059 | 0.002 | 2 |
| chr22\_45312474\_C\_T | PHF21B | VAL-ILE | 0.056 | 0.002 | 2 |
| chr22\_45723898\_G\_A | FAM118A | ARG-GLN | 0.250 | 0.002 | 8 |
| chr1\_39763365\_G\_T | MACF1 | CYS-PHE | 0.053 | 0.003 | 2 |
| chr1\_114255975\_G\_T | PHTF1 | GLN-LYS | 0.079 | 0.003 | 2 |
| chr2\_70441562\_T\_C | TIA1 | GLN-ARG | 0.079 | 0.003 | 3 |
| chr2\_238275569\_T\_C | COL6A3 | LYS-ARG | 0.053 | 0.003 | 2 |
| chr5\_56778235\_A\_C | ACTBL2 | ASP-GLU | 0.053 | 0.003 | 2 |
| chr5\_112399751\_C\_G | MCC | GLY-ARG | 0.053 | 0.003 | 2 |
| chr5\_176813433\_C\_T | SLC34A1 | ALA-VAL | 0.053 | 0.003 | 2 |
| chr6\_32159931\_G\_C | GPSM3 | HIS-ASP | 0.067 | 0.003 | 2 |
| chr6\_71377781\_C\_A | SMAP1 | LEU-ILE | 0.053 | 0.003 | 2 |
| chr8\_17500162\_T\_A | PDGFRL | ILE-ASN | 0.053 | 0.003 | 2 |
| chr8\_145773779\_C\_T | ARHGAP39 | GLY-SER | 0.056 | 0.003 | 2 |
| chr9\_35042268\_A\_G | C9orf131 | GLU-GLY | 0.079 | 0.003 | 3 |
| chr10\_3162130\_A\_G | PFKP | GLU-GLY | 0.056 | 0.003 | 2 |
| chr10\_14816378\_G\_C | FAM107B | HIS-GLN | 0.053 | 0.003 | 2 |
| chr11\_55861523\_T\_C | OR8I2 | VAL-ALA | 0.053 | 0.003 | 2 |
| chr11\_56230010\_G\_T | OR5M9 | LEU-MET | 0.053 | 0.003 | 2 |
| chr12\_96181085\_G\_A | NTN4 | ARG-TRP | 0.053 | 0.003 | 2 |
| chr13\_31729776\_T\_G | HSPH1 | ASN-HIS | 0.053 | 0.003 | 2 |
| chr13\_31848718\_G\_A | B3GALTL | VAL-MET | 0.053 | 0.003 | 2 |
| chr14\_45606290\_C\_T | FANCM | THR-ILE | 0.056 | 0.003 | 2 |
| chr14\_105416323\_T\_C | AHNAK2 | LYS-ARG | 0.313 | 0.003 | 5 |
| chr19\_5455543\_G\_C | ZNRF4 | SER-THR | 0.053 | 0.003 | 2 |
| chr19\_13084333\_G\_A | DAND5 | ARG-HIS | 0.053 | 0.003 | 2 |
| chr19\_40424269\_C\_T | FCGBP | GLY-GLU | 0.059 | 0.003 | 2 |
| chr19\_52618471\_C\_T | ZNF616 | ARG-LYS | 0.053 | 0.003 | 2 |
| chr19\_56160797\_G\_A | CCDC106 | ALA-THR | 0.056 | 0.003 | 2 |
| chrX\_50658966\_G\_A | BMP15 | ALA-THR | 0.053 | 0.003 | 2 |
| chrX\_128884473\_G\_A | XPNPEP2 | VAL-ILE | 0.059 | 0.003 | 2 |
| chrX\_153594535\_G\_A | FLNA | THR-MET | 0.079 | 0.003 | 3 |
| chr1\_3683159\_A\_C | CCDC27 | ASN-HIS | 0.053 | 0.004 | 2 |
| chr1\_11733846\_C\_A | FBXO6 | GLN-LYS | 0.053 | 0.004 | 2 |
| chr1\_156255448\_A\_G | TMEM79 | ASP-GLY | 0.059 | 0.004 | 2 |
| chr1\_156911718\_C\_T | ARHGEF11 | MET-ILE | 0.053 | 0.004 | 2 |
| chr1\_157771966\_T\_C | FCRL1 | ILE-VAL | 0.053 | 0.004 | 2 |
| chr1\_236721780\_C\_T | HEATR1 | ARG-HIS | 0.053 | 0.004 | 2 |
| chr1\_238050081\_T\_C | ZP4 | SER-GLY | 0.053 | 0.004 | 2 |
| chr2\_73717921\_C\_G | ALMS1 | ASN-LYS | 0.079 | 0.004 | 2 |
| chr2\_144765026\_T\_C | GTDC1 | MET-VAL | 0.053 | 0.004 | 2 |
| chr2\_160994197\_C\_T | ITGB6 | GLY-ARG | 0.079 | 0.004 | 3 |
| chr2\_208988958\_T\_C | CRYGD | MET-VAL | 0.067 | 0.004 | 2 |
| chr2\_241808308\_C\_A | AGXT | THR-ASN | 0.133 | 0.004 | 4 |
| chr3\_119256020\_G\_A | CD80 | HIS-TYR | 0.053 | 0.004 | 2 |
| chr3\_127298917\_T\_C | TPRA1 | SER-GLY | 0.053 | 0.004 | 2 |
| chr3\_132403418\_C\_T | NPHP3 | ALA-THR | 0.056 | 0.004 | 2 |
| chr4\_147561147\_C\_A | POU4F2 | ASP-GLU | 0.053 | 0.004 | 2 |
| chr5\_102894730\_C\_T | NUDT12 | VAL-ILE | 0.053 | 0.004 | 2 |
| chr5\_112903383\_T\_G | YTHDC2 | ILE-MET | 0.056 | 0.004 | 2 |
| chr5\_150921969\_C\_T | FAT2 | ALA-THR | 0.056 | 0.004 | 2 |
| chr5\_150947751\_G\_A | FAT2 | PRO-SER | 0.056 | 0.004 | 2 |
| chr5\_151202476\_C\_T | GLRA1 | GLY-SER | 0.053 | 0.004 | 2 |
| chr5\_162868905\_A\_C | CCNG1 | ASN-HIS | 0.125 | 0.004 | 2 |
| chr6\_54219405\_G\_C | TINAG | LYS-ASN | 0.063 | 0.004 | 2 |
| chr6\_111587204\_A\_G | KIAA1919 | THR-ALA | 0.053 | 0.004 | 2 |
| chr6\_121768751\_C\_T | GJA1 | ALA-VAL | 0.079 | 0.004 | 3 |
| chr7\_157931003\_C\_T | PTPRN2 | ARG-HIS | 0.056 | 0.004 | 2 |
| chr8\_17541943\_T\_G | MTUS1 | LYS-THR | 0.105 | 0.004 | 4 |
| chr8\_20112355\_A\_G | LZTS1 | LEU-PRO | 0.053 | 0.004 | 2 |
| chr9\_20990164\_G\_A | KIAA1797 | ALA-THR | 0.053 | 0.004 | 2 |
| chr9\_88938668\_G\_A | ZCCHC6 | THR-ILE | 0.079 | 0.004 | 3 |
| chr9\_125673614\_C\_G | ZBTB6 | MET-ILE | 0.056 | 0.004 | 2 |
| chr9\_134027138\_A\_G | NUP214 | ILE-VAL | 0.059 | 0.004 | 2 |
| chr11\_4869658\_G\_T | OR51S1 | PRO-THR | 0.053 | 0.004 | 2 |
| chr11\_67275063\_C\_T | CDK2AP2 | none | 0.053 | 0.004 | 2 |
| chr12\_40114781\_A\_G | C12orf40 | THR-ALA | 0.056 | 0.004 | 2 |
| chr14\_20876282\_G\_A | TEP1 | SER-PHE | 0.079 | 0.004 | 3 |
| chr14\_90767609\_C\_T | C14orf102 | VAL-MET | 0.053 | 0.004 | 2 |
| chr15\_62212298\_C\_T | VPS13C | ARG-HIS | 0.056 | 0.004 | 2 |
| chr15\_66621382\_G\_A | DIS3L | ARG-HIS | 0.053 | 0.004 | 2 |
| chr17\_28651840\_C\_T | TMIGD1 | VAL-ILE | 0.053 | 0.004 | 2 |
| chr17\_42849660\_G\_A | ADAM11 | ARG-GLN | 0.063 | 0.004 | 2 |
| chr19\_15905414\_A\_C | OR10H5 | LYS-GLN | 0.053 | 0.004 | 2 |
| chr19\_47280263\_T\_G | SLC1A5 | ILE-LEU | 0.053 | 0.004 | 2 |
| chr19\_48602951\_C\_A | PLA2G4C | VAL-PHE | 0.053 | 0.004 | 2 |
| chrX\_37663322\_G\_C | CYBB | GLY-ARG | 0.053 | 0.004 | 2 |
| chrX\_102962435\_T\_C | GLRA4 | ASP-GLY | 0.053 | 0.004 | 2 |
| chr1\_17588689\_T\_A | PADI3 | LEU-HIS | 0.083 | 0.005 | 3 |
| chr1\_23418803\_G\_C | LUZP1 | SER-CYS | 0.079 | 0.005 | 3 |
| chr1\_25291006\_G\_T | RUNX3 | none | 0.056 | 0.005 | 2 |
| chr1\_26526375\_G\_A | CATSPER4 | none | 0.053 | 0.005 | 2 |
| chr1\_57383357\_C\_T | C8A | PRO-SER | 0.053 | 0.005 | 2 |
| chr1\_86961291\_C\_G | CLCA1 | ASN-LYS | 0.053 | 0.005 | 2 |
| chr1\_92163646\_G\_A | TGFBR3 | PRO-SER | 0.056 | 0.005 | 2 |
| chr1\_109837853\_G\_A | MYBPHL | HIS-TYR | 0.088 | 0.005 | 3 |
| chr1\_205388384\_C\_G | LEMD1 | GLY-ALA | 0.053 | 0.005 | 2 |
| chr1\_214551420\_C\_T | PTPN14 | GLY-ASP | 0.053 | 0.005 | 2 |
| chr2\_55407644\_A\_T | C2orf63 | none | 0.056 | 0.005 | 2 |
| chr2\_160604372\_A\_G | 7-Mar | MET-VAL | 0.053 | 0.005 | 2 |
| chr2\_228388517\_T\_C | AGFG1 | VAL-ALA | 0.053 | 0.005 | 2 |
| chr3\_27387641\_C\_T | NEK10 | GLY-SER | 0.125 | 0.005 | 2 |
| chr3\_150398311\_C\_A | FAM194A | ARG-LEU | 0.053 | 0.005 | 2 |
| chr3\_193185128\_A\_G | ATP13A4 | VAL-ALA | 0.053 | 0.005 | 2 |
| chr4\_41686520\_C\_T | LIMCH1 | PRO-SER | 0.053 | 0.005 | 2 |
| chr4\_55127448\_G\_A | PDGFRA | GLY-ASP | 0.053 | 0.005 | 2 |
| chr4\_102751014\_G\_C | BANK1 | TRP-CYS | 0.094 | 0.005 | 2 |
| chr4\_102951333\_G\_A | BANK1 | ARG-GLN | 0.053 | 0.005 | 2 |
| chr5\_55272085\_G\_C | IL6ST | LEU-VAL | 0.053 | 0.005 | 2 |
| chr5\_102338739\_C\_G | PAM | SER-TRP | 0.071 | 0.005 | 2 |
| chr5\_110428060\_T\_C | WDR36 | LEU-PRO | 0.053 | 0.005 | 2 |
| chr5\_180030322\_C\_T | FLT4 | ARG-GLN | 0.100 | 0.005 | 3 |
| chr6\_51637536\_G\_T | PKHD1 | THR-LYS | 0.053 | 0.005 | 2 |
| chr6\_110763935\_T\_C | SLC22A16 | GLU-GLY | 0.053 | 0.005 | 2 |
| chr6\_111983038\_G\_C | FYN | ASP-GLU | 0.053 | 0.005 | 2 |
| chr8\_8185746\_T\_C | SGK223 | HIS-ARG | 0.088 | 0.005 | 2 |
| chr8\_22398155\_A\_G | PPP3CC | LYS-ARG | 0.053 | 0.005 | 2 |
| chr8\_82357149\_A\_G | PMP2 | ILE-THR | 0.056 | 0.005 | 2 |
| chr9\_80020874\_C\_A | VPS13A | HIS-ASN | 0.053 | 0.005 | 2 |
| chr9\_107266833\_G\_A | OR13F1 | CYS-TYR | 0.053 | 0.005 | 2 |
| chr10\_7765529\_A\_G | ITIH2 | GLN-ARG | 0.056 | 0.005 | 2 |
| chr10\_46121886\_C\_T | ANUBL1 | ARG-GLN | 0.056 | 0.005 | 2 |
| chr10\_51582911\_C\_T | NCOA4 | THR-ILE | 0.053 | 0.005 | 2 |
| chr10\_70760271\_T\_C | KIAA1279 | MET-THR | 0.079 | 0.005 | 2 |
| chr10\_135025208\_A\_G | KNDC1 | LYS-ARG | 0.059 | 0.005 | 2 |
| chr11\_28106253\_G\_A | KIF18A | PRO-SER | 0.056 | 0.005 | 2 |
| chr11\_130784886\_T\_C | SNX19 | SER-GLY | 0.053 | 0.005 | 2 |
| chr12\_48143315\_A\_G | RAPGEF3 | LEU-PRO | 0.079 | 0.005 | 3 |
| chr12\_48597051\_T\_G | OR10AD1 | THR-PRO | 0.053 | 0.005 | 2 |
| chr12\_58020582\_G\_A | B4GALNT1 | ALA-VAL | 0.079 | 0.005 | 3 |
| chr12\_124856830\_C\_T | NCOR2 | GLU-LYS | 0.079 | 0.005 | 2 |
| chr13\_47345630\_C\_T | ESD | GLY-ASP | 0.056 | 0.005 | 2 |
| chr14\_23282336\_G\_A | SLC7A7 | ALA-VAL | 0.053 | 0.005 | 2 |
| chr14\_23451345\_G\_A | JUB | PRO-LEU | 0.053 | 0.005 | 2 |
| chr14\_24572932\_G\_A | PCK2 | ARG-GLN | 0.053 | 0.005 | 2 |
| chr14\_95906095\_C\_A | C14orf49 | LYS-ASN | 0.053 | 0.005 | 2 |
| chr16\_2813096\_C\_G | SRRM2 | THR-ARG | 0.079 | 0.005 | 3 |
| chr16\_15808876\_C\_G | MYH11,NDE1 | GLU-ASP | 0.053 | 0.005 | 2 |
| chr16\_24950880\_C\_T | ARHGAP17 | ARG-GLN | 0.063 | 0.005 | 2 |
| chr16\_53504536\_A\_T | RBL2 | ARG-SER | 0.053 | 0.005 | 2 |
| chr16\_89350911\_G\_C | ANKRD11 | THR-SER | 0.053 | 0.005 | 2 |
| chr17\_8053916\_G\_A | PER1 | PRO-SER | 0.053 | 0.005 | 2 |
| chr17\_47784374\_G\_C | SLC35B1 | THR-SER | 0.053 | 0.005 | 2 |
| chr18\_67833306\_T\_C | RTTN | ILE-VAL | 0.056 | 0.005 | 2 |
| chr19\_17476933\_G\_T | PLVAP | PHE-LEU | 0.053 | 0.005 | 2 |
| chr19\_38202515\_G\_A | ZNF607 | SER-PHE | 0.368 | 0.005 | 11 |
| chr19\_48968015\_C\_T | KCNJ14 | ALA-VAL | 0.079 | 0.005 | 3 |
| chr19\_55144710\_A\_T | LILRB1 | GLN-LEU | 0.053 | 0.005 | 2 |
| chr21\_44190901\_T\_G | PDE9A | MET-ARG | 0.053 | 0.005 | 2 |
| chr22\_25158445\_G\_A | PIWIL3 | ARG-CYS | 0.053 | 0.005 | 2 |
| chr22\_37866063\_G\_A | MFNG | ARG-CYS | 0.056 | 0.005 | 2 |
| chrX\_107844666\_G\_T | COL4A5 | LYS-ASN | 0.053 | 0.005 | 2 |
| chr1\_115142870\_G\_A | DENND2C | SER-PHE | 0.053 | 0.006 | 2 |
| chr1\_248487701\_G\_A | OR2M7 | THR-ILE | 0.053 | 0.006 | 2 |
| chr2\_215617178\_C\_G | BARD1 | CYS-SER | 0.056 | 0.006 | 2 |
| chr2\_219678877\_C\_T | CYP27A1 | PRO-LEU | 0.053 | 0.006 | 2 |
| chr3\_46007825\_T\_C | FYCO1 | ASN-ASP | 0.079 | 0.006 | 3 |
| chr3\_123451932\_G\_A | MYLK | PRO-SER | 0.059 | 0.006 | 2 |
| chr4\_71024463\_G\_C | C4orf40 | GLY-ALA | 0.059 | 0.006 | 2 |
| chr5\_1254594\_C\_T | TERT | ALA-THR | 0.079 | 0.006 | 3 |
| chr5\_169028316\_C\_A | CCDC99 | ARG-SER | 0.053 | 0.006 | 2 |
| chr5\_171777393\_G\_A | SH3PXD2B | PRO-LEU | 0.063 | 0.006 | 2 |
| chr7\_92730745\_C\_T | SAMD9 | ALA-THR | 0.063 | 0.006 | 2 |
| chr7\_127015083\_G\_A | ZNF800 | PRO-SER | 0.059 | 0.006 | 2 |
| chr8\_17513484\_T\_C | MTUS1 | GLU-GLY | 0.053 | 0.006 | 2 |
| chr9\_35042296\_G\_A | C9orf131 | MET-ILE | 0.053 | 0.006 | 2 |
| chr9\_71998936\_C\_T | FAM189A2 | THR-ILE | 0.056 | 0.006 | 2 |
| chr10\_75258901\_C\_G | USP54 | GLY-ALA | 0.053 | 0.006 | 2 |
| chr11\_26587018\_C\_T | ANO3,MUC15 | ASP-ASN | 0.053 | 0.006 | 2 |
| chr11\_35226083\_C\_T | CD44 | THR-MET | 0.053 | 0.006 | 2 |
| chr12\_52885433\_G\_T | KRT6A | LEU-MET | 0.053 | 0.006 | 2 |
| chr12\_101018061\_C\_T | GAS2L3 | SER-LEU | 0.053 | 0.006 | 2 |
| chr17\_39521494\_G\_A | KRT33B | ALA-VAL | 0.053 | 0.006 | 2 |
| chr17\_79639684\_G\_A | CCDC137 | GLY-ARG | 0.083 | 0.006 | 2 |
| chr19\_53058429\_C\_T | ZNF808 | ARG-CYS | 0.053 | 0.006 | 2 |
| chr19\_55144711\_G\_C | LILRB1 | GLN-HIS | 0.053 | 0.006 | 2 |
| chr20\_33586968\_G\_A | MYH7B | ASP-ASN | 0.079 | 0.006 | 3 |
| chr22\_40364122\_G\_A | GRAP2 | ARG-GLN | 0.125 | 0.006 | 2 |
| chrX\_3248104\_C\_T | MXRA5 | ASP-ASN | 0.053 | 0.006 | 2 |
| chrX\_38020288\_G\_A | SRPX | PRO-SER | 0.056 | 0.006 | 2 |
| chr1\_8074334\_C\_T | ERRFI1 | ASP-ASN | 0.053 | 0.007 | 2 |
| chr1\_17660468\_C\_A | PADI4 | PRO-THR | 0.053 | 0.007 | 2 |
| chr1\_104162351\_A\_G | AMY2A | HIS-ARG | 0.053 | 0.007 | 2 |
| chr2\_183616913\_A\_C | DNAJC10 | MET-LEU | 0.056 | 0.007 | 2 |
| chr3\_169710614\_G\_C | SEC62 | GLU-ASP | 0.053 | 0.007 | 2 |
| chr4\_1165131\_C\_T | SPON2 | ALA-THR | 0.107 | 0.007 | 2 |
| chr4\_8235220\_C\_A | SH3TC1 | LEU-MET | 0.105 | 0.007 | 4 |
| chr4\_47954624\_C\_T | CNGA1 | ARG-GLN | 0.056 | 0.007 | 2 |
| chr4\_57797350\_C\_G | REST | PRO-ALA | 0.079 | 0.007 | 3 |
| chr4\_139144395\_T\_C | SLC7A11 | ILE-VAL | 0.053 | 0.007 | 2 |
| chr5\_32074462\_G\_A | PDZD2 | ALA-THR | 0.079 | 0.007 | 3 |
| chr5\_44809446\_g\_C | MRPS30 | GLU-GLN | 0.077 | 0.007 | 2 |
| chr5\_159686752\_C\_T | CCNJL | VAL-ILE | 0.053 | 0.007 | 2 |
| chr5\_176005481\_G\_A | CDHR2 | GLY-ARG | 0.079 | 0.007 | 3 |
| chr6\_29054914\_T\_A | OR2B3 | THR-SER | 0.079 | 0.007 | 3 |
| chr6\_38820493\_C\_A | DNAH8 | ASP-GLU | 0.053 | 0.007 | 2 |
| chr6\_41903798\_C\_A | CCND3 | GLU-ASP | 0.059 | 0.007 | 2 |
| chr6\_90660954\_G\_C | BACH2 | LEU-VAL | 0.053 | 0.007 | 2 |
| chr6\_111583530\_G\_C | KIAA1919 | SER-THR | 0.053 | 0.007 | 2 |
| chr6\_160953642\_A\_G | LPA | LEU-PRO | 0.053 | 0.007 | 2 |
| chr7\_4002309\_C\_G | SDK1 | GLN-GLU | 0.053 | 0.007 | 2 |
| chr7\_7530225\_C\_A | COL28A1 | GLY-VAL | 0.059 | 0.007 | 2 |
| chr7\_12263971\_G\_A | TMEM106B | SER-ASN | 0.056 | 0.007 | 2 |
| chr7\_151810476\_A\_G | GALNT11 | GLU-GLY | 0.053 | 0.007 | 2 |
| chr9\_104335619\_T\_C | GRIN3A | ASN-SER | 0.053 | 0.007 | 2 |
| chr9\_125391012\_G\_C | OR1B1 | PRO-ARG | 0.053 | 0.007 | 2 |
| chr10\_105762909\_C\_G | SLK | ALA-GLY | 0.053 | 0.007 | 2 |
| chr10\_127693479\_A\_G | FANK1 | HIS-ARG | 0.053 | 0.007 | 2 |
| chr11\_124016058\_C\_T | VWA5A | ARG-CYS | 0.053 | 0.007 | 2 |
| chr12\_40740686\_A\_G | LRRK2 | ASN-ASP | 0.100 | 0.007 | 3 |
| chr12\_56532009\_C\_T | ESYT1 | ARG-CYS | 0.053 | 0.007 | 2 |
| chr13\_41515118\_C\_T | ELF1 | GLU-LYS | 0.053 | 0.007 | 2 |
| chr13\_94197611\_C\_T | GPC6 | LEU-PHE | 0.053 | 0.007 | 2 |
| chr14\_24683304\_C\_A | MDP1,NEDD8-MDP1 | ARG-MET | 0.053 | 0.007 | 2 |
| chr14\_30046511\_T\_C | PRKD1 | HIS-ARG | 0.053 | 0.007 | 2 |
| chr14\_68352672\_A\_G | RAD51B | TYR-CYS | 0.053 | 0.007 | 2 |
| chr14\_73421159\_A\_G | DCAF4 | SER-GLY | 0.053 | 0.007 | 2 |
| chr14\_94844947\_C\_T | SERPINA1 | GLU-LYS | 0.053 | 0.007 | 2 |
| chr16\_2296877\_C\_T | ECI1 | GLY-SER | 0.053 | 0.007 | 2 |
| chr16\_29891206\_C\_T | SEZ6L2 | ASP-ASN | 0.079 | 0.007 | 3 |
| chr16\_72170408\_C\_A | PMFBP1 | ARG-LEU | 0.053 | 0.007 | 2 |
| chr17\_6012979\_C\_T | WSCD1 | THR-ILE | 0.053 | 0.007 | 2 |
| chr17\_7669761\_G\_A | DNAH2 | GLU-LYS | 0.053 | 0.007 | 2 |
| chr17\_14248376\_A\_G | HS3ST3B1 | ILE-VAL | 0.083 | 0.007 | 3 |
| chr17\_37815304\_G\_C | STARD3 | GLY-ALA | 0.053 | 0.007 | 2 |
| chr17\_38450248\_G\_A | CDC6 | ASP-ASN | 0.053 | 0.007 | 2 |
| chr17\_39521142\_C\_T | KRT33B | ARG-HIS | 0.079 | 0.007 | 3 |
| chr17\_66366659\_C\_G | ARSG | ARG-GLY | 0.053 | 0.007 | 2 |
| chr17\_79205672\_G\_A | C17orf56 | ARG-TRP | 0.053 | 0.007 | 2 |
| chr19\_1008645\_C\_A | GRIN3B | ALA-GLU | 0.053 | 0.007 | 2 |
| chr19\_7708058\_C\_T | STXBP2 | THR-MET | 0.053 | 0.007 | 2 |
| chr19\_10132318\_T\_C | RDH8 | TYR-HIS | 0.053 | 0.007 | 2 |
| chr19\_21132072\_T\_C | ZNF85 | ILE-THR | 0.056 | 0.007 | 2 |
| chr19\_32845600\_G\_A | ZNF507 | ASP-ASN | 0.053 | 0.007 | 2 |
| chr19\_38652962\_C\_T | SIPA1L3 | PRO-LEU | 0.053 | 0.007 | 2 |
| chr19\_54744919\_T\_A | LILRA6 | ASP-VAL | 0.079 | 0.007 | 3 |
| chr19\_58452599\_T\_G | ZNF256 | LYS-THR | 0.053 | 0.007 | 2 |
| chrX\_107315933\_G\_A | VSIG1 | VAL-ILE | 0.053 | 0.007 | 2 |
| chr1\_1959699\_G\_A | GABRD | ARG-HIS | 0.059 | 0.008 | 2 |
| chr1\_154072601\_G\_A | NUP210L | PRO-LEU | 0.056 | 0.008 | 2 |
| chr2\_141773450\_T\_C | LRP1B | ILE-VAL | 0.053 | 0.008 | 2 |
| chr3\_44488293\_T\_C | ZNF445 | GLU-GLY | 0.053 | 0.008 | 2 |
| chr3\_167512569\_G\_A | SERPINI1 | ALA-THR | 0.079 | 0.008 | 3 |
| chr5\_36219710\_C\_T | NADKD1 | ARG-HIS | 0.056 | 0.008 | 2 |
| chr5\_139905844\_G\_A | ANKHD1-EIF4EBP3 | GLY-SER | 0.063 | 0.008 | 2 |
| chr5\_140530718\_G\_T | PCDHB6 | ALA-SER | 0.053 | 0.008 | 2 |
| chr6\_136882717\_G\_A | MAP3K5 | THR-ILE | 0.053 | 0.008 | 2 |
| chr7\_92085763\_C\_T | GATAD1 | ARG-TRP | 0.053 | 0.008 | 2 |
| chr8\_94747496\_A\_C | RBM12B | ASP-GLU | 0.056 | 0.008 | 2 |
| chr9\_103947810\_T\_G | LPPR1 | SER-ALA | 0.079 | 0.008 | 3 |
| chr9\_136913527\_G\_A | BRD3 | ALA-VAL | 0.059 | 0.008 | 2 |
| chr10\_95347041\_G\_A | O3FAR1 | ARG-HIS | 0.053 | 0.008 | 2 |
| chr10\_97096357\_C\_T | SORBS1 | GLY-GLU | 0.088 | 0.008 | 3 |
| chr11\_89896537\_A\_G | NAALAD2 | THR-ALA | 0.053 | 0.008 | 2 |
| chr11\_102401411\_A\_C | MMP7 | CYS-TRP | 0.056 | 0.008 | 2 |
| chr14\_20444393\_T\_C | OR4K15 | VAL-ALA | 0.053 | 0.008 | 2 |
| chr15\_40914831\_C\_G | CASC5 | THR-SER | 0.056 | 0.008 | 2 |
| chr16\_3293880\_A\_G | MEFV | ILE-THR | 0.053 | 0.008 | 2 |
| chr16\_4733253\_C\_T | MGRN1 | SER-LEU | 0.079 | 0.008 | 3 |
| chr16\_49669923\_G\_A | ZNF423 | ALA-VAL | 0.053 | 0.008 | 2 |
| chr17\_5338281\_G\_A | C1QBP | THR-MET | 0.105 | 0.008 | 4 |
| chr17\_74019453\_G\_A | EVPL | ARG-CYS | 0.053 | 0.008 | 2 |
| chr17\_77079575\_G\_A | ENGASE | ARG-GLN | 0.053 | 0.008 | 2 |
| chr17\_77082174\_C\_T | ENGASE | ARG-CYS | 0.053 | 0.008 | 2 |
| chr17\_78184601\_C\_T | SGSH | VAL-MET | 0.053 | 0.008 | 2 |
| chr21\_15873026\_T\_C | SAMSN1 | THR-ALA | 0.053 | 0.008 | 2 |
| chrX\_102004317\_A\_G | BHLHB9 | SER-GLY | 0.053 | 0.008 | 2 |
| chr1\_16332665\_C\_T | C1orf64 | LEU-PHE | 0.088 | 0.009 | 2 |
| chr1\_51868160\_C\_G | EPS15 | GLY-ALA | 0.053 | 0.009 | 2 |
| chr1\_82416040\_C\_T | LPHN2 | PRO-SER | 0.053 | 0.009 | 2 |
| chr1\_159890163\_T\_A | TAGLN2 | GLN-LEU | 0.079 | 0.009 | 2 |
| chr1\_220161969\_T\_C | EPRS | GLU-GLY | 0.056 | 0.009 | 2 |
| chr2\_108910751\_G\_A | SULT1C2 | ARG-GLN | 0.053 | 0.009 | 2 |
| chr2\_160604541\_G\_A | 7-Mar | SER-ASN | 0.088 | 0.009 | 3 |
| chr2\_182542998\_G\_T | NEUROD1 | PRO-HIS | 0.053 | 0.009 | 2 |
| chr3\_19575232\_C\_T | KCNH8 | PRO-SER | 0.053 | 0.009 | 2 |
| chr3\_46712490\_G\_A | ALS2CL | SER-PHE | 0.105 | 0.009 | 4 |
| chr4\_95376504\_A\_G | PDLIM5 | LYS-ARG | 0.053 | 0.009 | 2 |
| chr5\_38921864\_G\_A | OSMR | GLY-ASP | 0.053 | 0.009 | 2 |
| chr5\_133901939\_G\_T | PHF15 | GLY-VAL | 0.056 | 0.009 | 2 |
| chr6\_30862440\_A\_G | DDR1 | ASN-SER | 0.079 | 0.009 | 3 |
| chr6\_97599674\_G\_A | MMS22L | PRO-LEU | 0.053 | 0.009 | 2 |
| chr6\_152784621\_T\_C | SYNE1 | GLN-ARG | 0.056 | 0.009 | 2 |
| chr7\_1479642\_C\_A | MICALL2 | ALA-SER | 0.056 | 0.009 | 2 |
| chr7\_18067261\_G\_C | PRPS1L1 | ARG-GLY | 0.079 | 0.009 | 3 |
| chr7\_87537188\_A\_G | DBF4 | LYS-GLU | 0.063 | 0.009 | 2 |
| chr7\_89856433\_G\_A | STEAP2 | GLY-GLU | 0.053 | 0.009 | 2 |
| chr8\_100205255\_G\_A | VPS13B | ALA-THR | 0.056 | 0.009 | 2 |
| chr9\_140400464\_C\_T | PNPLA7 | GLU-LYS | 0.088 | 0.009 | 2 |
| chr11\_4903500\_G\_A | OR51T1 | ARG-HIS | 0.079 | 0.009 | 3 |
| chr11\_77090939\_C\_T | PAK1 | none | 0.056 | 0.009 | 2 |
| chr12\_46320944\_C\_T | SCAF11 | ARG-HIS | 0.053 | 0.009 | 2 |
| chr12\_52285090\_G\_A | ANKRD33 | GLY-GLU | 0.053 | 0.009 | 2 |
| chr12\_56630444\_G\_C | SLC39A5 | SER-THR | 0.056 | 0.009 | 2 |
| chr12\_57539082\_C\_T | LRP1 | ALA-VAL | 0.053 | 0.009 | 2 |
| chr12\_106729425\_G\_A | TCP11L2 | ASP-ASN | 0.063 | 0.009 | 2 |
| chr14\_39818076\_A\_G | CTAGE5 | ARG-GLY | 0.053 | 0.009 | 2 |
| chr14\_73733285\_G\_A | PAPLN | ALA-THR | 0.053 | 0.009 | 2 |
| chr16\_12145791\_G\_C | SNX29 | GLY-ALA | 0.053 | 0.009 | 2 |
| chr19\_8182174\_G\_A | FBN3 | none | 0.053 | 0.009 | 2 |
| chr19\_15350625\_C\_T | BRD4 | ARG-HIS | 0.056 | 0.009 | 2 |
| chr19\_41383849\_C\_G | CYP2A7 | SER-THR | 0.053 | 0.009 | 2 |
| chr20\_61391378\_A\_G | NTSR1 | TYR-CYS | 0.053 | 0.009 | 2 |
| chr1\_14105049\_C\_A | PRDM2 | ASP-GLU | 0.053 | 0.010 | 2 |
| chr1\_14107135\_C\_G | PRDM2 | PRO-ALA | 0.053 | 0.010 | 2 |
| chr1\_109810200\_G\_A | CELSR2 | ARG-LYS | 0.079 | 0.010 | 3 |
| chr1\_145583938\_C\_G | PIAS3 | SER-CYS | 0.053 | 0.010 | 2 |
| chr1\_155206167\_C\_T | GBA | GLU-LYS | 0.053 | 0.010 | 2 |
| chr1\_247875313\_G\_A | OR6F1 | LEU-PHE | 0.053 | 0.010 | 2 |
| chr2\_17947886\_G\_A | GEN1 | SER-ASN | 0.053 | 0.010 | 2 |
| chr2\_27438615\_G\_C | C2orf28 | ASP-HIS | 0.053 | 0.010 | 2 |
| chr2\_160690656\_G\_A | LY75,LY75-CD302 | PRO-LEU | 0.083 | 0.010 | 3 |
| chr2\_220251685\_T\_G | DNPEP | ASN-HIS | 0.079 | 0.010 | 3 |
| chr3\_32533246\_T\_C | CMTM6 | THR-ALA | 0.111 | 0.010 | 4 |
| chr3\_150384657\_G\_A | FAM194A | ARG-CYS | 0.079 | 0.010 | 3 |
| chr4\_100503136\_C\_G | MTTP | ARG-GLY | 0.053 | 0.010 | 2 |
| chr4\_106395144\_T\_C | PPA2 | THR-ALA | 0.083 | 0.010 | 2 |
| chr5\_23527559\_A\_G | PRDM9 | LYS-GLU | 0.053 | 0.010 | 2 |
| chr5\_34911914\_G\_C | RAD1 | THR-SER | 0.079 | 0.010 | 3 |
| chr5\_149360630\_C\_T | SLC26A2 | ARG-TRP | 0.118 | 0.010 | 3 |
| chr5\_150947162\_A\_G | FAT2 | VAL-ALA | 0.079 | 0.010 | 3 |
| chr5\_151771874\_C\_T | NMUR2 | GLU-LYS | 0.079 | 0.010 | 3 |
| chr5\_176409574\_G\_A | UIMC1 | ARG-TRP | 0.056 | 0.010 | 2 |
| chr6\_20109956\_A\_G | MBOAT1 | PHE-LEU | 0.053 | 0.010 | 2 |
| chr6\_45916999\_G\_T | CLIC5 | PRO-HIS | 0.079 | 0.010 | 3 |
| chr6\_106553096\_G\_A | PRDM1 | SER-ASN | 0.053 | 0.010 | 2 |
| chr6\_142400020\_G\_T | NMBR | PRO-HIS | 0.053 | 0.010 | 2 |
| chr7\_100465824\_G\_A | TRIP6 | ARG-GLN | 0.088 | 0.010 | 3 |
| chr7\_127965924\_T\_G | RBM28 | MET-LEU | 0.053 | 0.010 | 2 |
| chr8\_41582031\_G\_T | ANK1 | ASN-LYS | 0.056 | 0.010 | 2 |
| chr9\_138439086\_T\_A | OBP2A | PHE-TYR | 0.053 | 0.010 | 2 |
| chr12\_52962167\_T\_C | KRT74 | SER-GLY | 0.056 | 0.010 | 2 |
| chr12\_132624434\_T\_C | DDX51 | GLN-ARG | 0.059 | 0.010 | 2 |
| chr13\_52971517\_C\_T | THSD1 | GLU-LYS | 0.079 | 0.010 | 3 |
| chr14\_23564437\_T\_C | ACIN1 | ASN-SER | 0.079 | 0.010 | 2 |
| chr14\_24040430\_C\_T | JPH4 | ALA-THR | 0.053 | 0.010 | 2 |
| chr14\_69341658\_G\_A | ACTN1 | PRO-LEU | 0.056 | 0.010 | 2 |
| chr14\_73961982\_C\_T | HEATR4 | GLY-GLU | 0.079 | 0.010 | 3 |
| chr14\_74036500\_C\_T | ACOT2 | ARG-TRP | 0.125 | 0.010 | 2 |
| chr15\_42434824\_C\_T | PLA2G4F | ARG-HIS | 0.079 | 0.010 | 3 |
| chr15\_43317071\_T\_C | UBR1 | ILE-VAL | 0.111 | 0.010 | 4 |
| chr16\_57283730\_G\_A | ARL2BP | GLU-LYS | 0.053 | 0.010 | 2 |
| chr16\_67434917\_C\_T | ZDHHC1 | ARG-GLN | 0.079 | 0.010 | 3 |
| chr16\_69143816\_G\_A | HAS3 | ARG-HIS | 0.079 | 0.010 | 3 |
| chr17\_33769039\_G\_A | SLFN13 | ARG-CYS | 0.053 | 0.010 | 2 |
| chr17\_74018597\_T\_C | EVPL | TYR-CYS | 0.071 | 0.010 | 2 |
| chr17\_76973249\_C\_T | LGALS3BP | VAL-MET | 0.053 | 0.010 | 2 |
| chr19\_41383115\_G\_A | CYP2A7 | ARG-TRP | 0.079 | 0.010 | 3 |
| chr19\_51582895\_G\_A | KLK14 | ARG-CYS | 0.077 | 0.010 | 2 |
| chr19\_52934741\_A\_C | ZNF534 | GLN-PRO | 0.056 | 0.010 | 2 |
| chr20\_7864284\_T\_C | HAO1 | LYS-GLU | 0.056 | 0.010 | 2 |
| chr20\_31607551\_G\_C | BPIFB2 | ASP-HIS | 0.056 | 0.010 | 2 |
| chr20\_62172244\_C\_G | SRMS | SER-THR | 0.088 | 0.010 | 3 |
| chrX\_46719498\_C\_T | RP2 | ARG-TRP | 0.056 | 0.010 | 2 |
| chrX\_103267974\_G\_A | H2BFWT | ARG-TRP | 0.067 | 0.010 | 2 |
| chr1\_19203725\_A\_G | ALDH4A1 | PHE-LEU | 0.111 | 0.011 | 3 |
| chr1\_67833643\_G\_A | IL12RB2 | GLY-ASP | 0.056 | 0.011 | 2 |
| chr1\_155175089\_C\_T | THBS3 | ARG-GLN | 0.053 | 0.011 | 2 |
| chr1\_207868022\_G\_T | CR1L | GLY-VAL | 0.143 | 0.011 | 2 |
| chr1\_212273606\_G\_A | DTL | SER-ASN | 0.053 | 0.011 | 2 |
| chr2\_24435599\_G\_A | ITSN2 | ARG-TRP | 0.079 | 0.011 | 3 |
| chr2\_120413984\_C\_G | PCDP1 | LEU-VAL | 0.053 | 0.011 | 2 |
| chr4\_57181629\_C\_T | KIAA1211 | PRO-LEU | 0.250 | 0.011 | 4 |
| chr4\_162697058\_C\_T | FSTL5 | GLY-GLU | 0.059 | 0.011 | 2 |
| chr5\_121786959\_G\_A | SNCAIP | ARG-HIS | 0.079 | 0.011 | 3 |
| chr6\_36839598\_C\_G | PPIL1 | CYS-SER | 0.053 | 0.011 | 2 |
| chr6\_155153307\_G\_A | SCAF8 | SER-ASN | 0.083 | 0.011 | 2 |
| chr7\_84727240\_A\_G | SEMA3D | SER-PRO | 0.053 | 0.011 | 2 |
| chr8\_6794366\_G\_T | DEFA4 | ALA-GLU | 0.053 | 0.011 | 2 |
| chr10\_95161268\_C\_T | MYOF | ASP-ASN | 0.053 | 0.011 | 2 |
| chr10\_101667814\_A\_G | DNMBP | MET-THR | 0.056 | 0.011 | 2 |
| chr10\_113926224\_A\_G | GPAM | ILE-THR | 0.053 | 0.011 | 2 |
| chr11\_376331\_T\_A | B4GALNT4 | PHE-TYR | 0.079 | 0.011 | 3 |
| chr11\_7507174\_C\_T | OLFML1 | PRO-LEU | 0.079 | 0.011 | 3 |
| chr11\_102584135\_G\_A | MMP8 | GLN-stop | 0.056 | 0.011 | 2 |
| chr12\_51208122\_C\_G | ATF1 | PRO-ALA | 0.079 | 0.011 | 3 |
| chr13\_24465537\_C\_T | C1QTNF9B-AS1 | GLY-GLU | 0.079 | 0.011 | 2 |
| chr15\_65158047\_G\_A | PLEKHO2 | ARG-GLN | 0.053 | 0.011 | 2 |
| chr16\_2003016\_G\_A | RPL3L | ALA-VAL | 0.053 | 0.011 | 2 |
| chr17\_78166326\_G\_A | CARD14 | GLU-LYS | 0.059 | 0.011 | 2 |
| chr18\_61323259\_A\_T | SERPINB3 | TRP-ARG | 0.056 | 0.011 | 2 |
| chr19\_58190130\_G\_A | ZSCAN4 | GLU-LYS | 0.053 | 0.011 | 2 |
| chr20\_31805464\_C\_A | BPIFA3 | ALA-GLU | 0.053 | 0.011 | 2 |
| chr1\_17668509\_G\_A | PADI4 | GLY-SER | 0.079 | 0.012 | 3 |
| chr1\_36937878\_C\_T | CSF3R | ASP-ASN | 0.053 | 0.012 | 2 |
| chr1\_52854961\_G\_A | ORC1 | ALA-VAL | 0.105 | 0.012 | 4 |
| chr1\_156146546\_C\_T | SEMA4A | PRO-SER | 0.053 | 0.012 | 2 |
| chr1\_161130701\_C\_T | USP21 | PRO-SER | 0.105 | 0.012 | 4 |
| chr1\_169484767\_A\_G | F5 | MET-THR | 0.083 | 0.012 | 2 |
| chr1\_180886140\_C\_T | KIAA1614 | ARG-CYS | 0.056 | 0.012 | 2 |
| chr1\_196918741\_G\_A | CFHR2 | CYS-TYR | 0.056 | 0.012 | 2 |
| chr1\_246805265\_A\_G | CNST | GLN-ARG | 0.063 | 0.012 | 2 |
| chr1\_248084440\_T\_G | OR2T8 | SER-ALA | 0.105 | 0.012 | 4 |
| chr2\_165947079\_C\_A | SCN3A | GLY-CYS | 0.053 | 0.012 | 2 |
| chr2\_185801103\_A\_C | ZNF804A | ASN-THR | 0.063 | 0.012 | 2 |
| chr3\_50513613\_C\_T | CACNA2D2 | ARG-GLN | 0.067 | 0.012 | 2 |
| chr3\_182583338\_T\_A | ATP11B | ILE-ASN | 0.079 | 0.012 | 3 |
| chr4\_8588986\_G\_A | GPR78 | ALA-THR | 0.083 | 0.012 | 3 |
| chr4\_107157623\_G\_A | TBCK | THR-MET | 0.079 | 0.012 | 3 |
| chr5\_141335594\_A\_G | PCDH12 | LEU-PRO | 0.053 | 0.012 | 2 |
| chr6\_31938120\_C\_T | DOM3Z | none | 0.053 | 0.012 | 2 |
| chr6\_51497503\_C\_A | PKHD1 | ARG-LEU | 0.053 | 0.012 | 2 |
| chr6\_56480500\_T\_C | DST | ILE-VAL | 0.083 | 0.012 | 3 |
| chr6\_56485023\_T\_C | DST | LYS-ARG | 0.056 | 0.012 | 2 |
| chr7\_99091172\_g\_A | ZNF394 | ARG-CYS | 0.053 | 0.012 | 2 |
| chr7\_105148593\_G\_A | PUS7 | HIS-TYR | 0.079 | 0.012 | 3 |
| chr8\_18080001\_G\_A | NAT1 | VAL-ILE | 0.053 | 0.012 | 2 |
| chr8\_18080196\_T\_G | NAT1 | SER-ALA | 0.056 | 0.012 | 2 |
| chr9\_15564100\_C\_T | C9orf93 | THR-ILE | 0.059 | 0.012 | 2 |
| chr10\_16932490\_G\_T | CUBN | LEU-ILE | 0.053 | 0.012 | 2 |
| chr10\_51465429\_C\_T | AGAP7 | ASP-ASN | 0.053 | 0.012 | 2 |
| chr11\_3690558\_G\_T | CHRNA10 | THR-ASN | 0.053 | 0.012 | 2 |
| chr11\_15243047\_G\_A | INSC | ASP-ASN | 0.083 | 0.012 | 2 |
| chr12\_38714242\_G\_A | ALG10B | GLU-LYS | 0.079 | 0.012 | 3 |
| chr12\_52758810\_C\_T | KRT85 | ASP-ASN | 0.053 | 0.012 | 2 |
| chr13\_24233219\_C\_T | TNFRSF19 | ALA-VAL | 0.053 | 0.012 | 2 |
| chr14\_20874411\_T\_C | TEP1 | HIS-ARG | 0.053 | 0.012 | 2 |
| chr14\_51372238\_T\_A | PYGL | ILE-LEU | 0.053 | 0.012 | 2 |
| chr14\_58605072\_C\_G | C14orf37 | GLU-ASP | 0.053 | 0.012 | 2 |
| chr14\_74759059\_G\_C | ABCD4 | THR-ARG | 0.053 | 0.012 | 2 |
| chr14\_78161131\_C\_T | ALKBH1 | MET-ILE | 0.053 | 0.012 | 2 |
| chr15\_31221493\_C\_T | FAN1 | PRO-SER | 0.053 | 0.012 | 2 |
| chr16\_16276345\_C\_T | ABCC6 | ARG-LYS | 0.053 | 0.012 | 2 |
| chr17\_8222870\_C\_T | ARHGEF15 | ARG-TRP | 0.056 | 0.012 | 2 |
| chr17\_11881356\_G\_A | ZNF18 | SER-LEU | 0.079 | 0.012 | 3 |
| chr18\_2890796\_G\_A | EMILIN2 | ARG-GLN | 0.105 | 0.012 | 4 |
| chr19\_35758745\_G\_C | LSR | GLU-GLN | 0.053 | 0.012 | 2 |
| chr19\_38573347\_T\_C | SIPA1L3 | MET-THR | 0.067 | 0.012 | 2 |
| chr19\_51563265\_G\_A | KLK13 | HIS-TYR | 0.053 | 0.012 | 2 |
| chr20\_54945309\_T\_C | AURKA | MET-VAL | 0.053 | 0.012 | 2 |
| chr21\_45542072\_T\_A | PWP2 | PHE-ILE | 0.053 | 0.012 | 2 |
| chr22\_45996298\_A\_G | FBLN1 | HIS-ARG | 0.083 | 0.012 | 3 |
| chr1\_1334475\_G\_C | CCNL2 | THR-SER | 0.083 | 0.013 | 2 |
| chr1\_17662705\_G\_C | PADI4 | ARG-THR | 0.053 | 0.013 | 2 |
| chr1\_40703244\_G\_A | RLF | GLY-ASP | 0.079 | 0.013 | 3 |
| chr1\_110302450\_C\_T | EPS8L3 | MET-ILE | 0.053 | 0.013 | 2 |
| chr1\_117753455\_A\_G | VTCN1 | LEU-PRO | 0.105 | 0.013 | 4 |
| chr1\_196967354\_G\_A | CFHR5 | ARG-HIS | 0.067 | 0.013 | 2 |
| chr1\_248263471\_G\_A | OR2L13 | ARG-HIS | 0.053 | 0.013 | 2 |
| chr1\_248308934\_C\_T | OR2M5 | ALA-VAL | 0.053 | 0.013 | 2 |
| chr2\_27308159\_G\_A | EMILIN1 | GLU-LYS | 0.053 | 0.013 | 2 |
| chr3\_49760431\_G\_C | GMPPB | HIS-ASP | 0.053 | 0.013 | 2 |
| chr3\_187447701\_C\_A | BCL6 | GLU-ASP | 0.053 | 0.013 | 2 |
| chr3\_197403844\_T\_C | KIAA0226 | ASN-SER | 0.053 | 0.013 | 2 |
| chr4\_113352075\_A\_G | ALPK1 | THR-ALA | 0.056 | 0.013 | 2 |
| chr4\_113352832\_C\_T | ALPK1 | SER-PHE | 0.053 | 0.013 | 2 |
| chr4\_126412154\_G\_A | FAT4 | ARG-LYS | 0.079 | 0.013 | 3 |
| chr5\_154307070\_G\_C | GEMIN5 | ARG-GLY | 0.056 | 0.013 | 2 |
| chr5\_176825069\_C\_T | SLC34A1 | HIS-TYR | 0.053 | 0.013 | 2 |
| chr6\_10964015\_G\_A | SYCP2L | none | 0.053 | 0.013 | 2 |
| chr6\_30610758\_G\_T | ATAT1 | GLY-VAL | 0.059 | 0.013 | 2 |
| chr6\_108197775\_G\_A | SEC63 | THR-ILE | 0.079 | 0.013 | 2 |
| chr6\_168297647\_A\_G | MLLT4 | ILE-VAL | 0.083 | 0.013 | 2 |
| chr7\_130023561\_G\_A | CPA1 | ALA-THR | 0.053 | 0.013 | 2 |
| chr10\_134996954\_G\_A | KNDC1 | ARG-GLN | 0.077 | 0.013 | 2 |
| chr11\_397063\_C\_A | PKP3 | PRO-THR | 0.063 | 0.013 | 2 |
| chr11\_6816792\_T\_C | OR6A2 | ILE-VAL | 0.053 | 0.013 | 2 |
| chr11\_86158235\_C\_T | ME3 | ALA-THR | 0.053 | 0.013 | 2 |
| chr12\_49087325\_T\_C | CCNT1 | THR-ALA | 0.056 | 0.013 | 2 |
| chr12\_49994785\_G\_A | FAM186B | THR-MET | 0.105 | 0.013 | 4 |
| chr12\_108985976\_G\_A | TMEM119 | LEU-PHE | 0.059 | 0.013 | 2 |
| chr13\_95953517\_G\_T | ABCC4 | LEU-ILE | 0.056 | 0.013 | 2 |
| chr13\_103343308\_T\_C | METTL21C | ASN-SER | 0.053 | 0.013 | 2 |
| chr15\_31334362\_C\_T | TRPM1 | VAL-MET | 0.053 | 0.013 | 2 |
| chr16\_81232336\_T\_C | PKD1L2 | THR-ALA | 0.059 | 0.013 | 2 |
| chr17\_663472\_C\_A | GLOD4 | ALA-SER | 0.105 | 0.013 | 4 |
| chr17\_2227655\_G\_T | TSR1,SRR | HIS-GLN | 0.056 | 0.013 | 2 |
| chr17\_33679943\_C\_T | SLFN11 | SER-ASN | 0.053 | 0.013 | 2 |
| chr17\_73839326\_C\_T | UNC13D | ALA-THR | 0.056 | 0.013 | 2 |
| chr18\_51880889\_G\_A | STARD6 | ARG-stop | 0.083 | 0.013 | 2 |
| chr19\_42231159\_G\_A | CEACAM5 | GLY-ARG | 0.053 | 0.013 | 2 |
| chr19\_53611802\_T\_G | ZNF415 | ASN-THR | 0.056 | 0.013 | 2 |
| chr19\_55086249\_T\_C | LILRA2 | LEU-SER | 0.053 | 0.013 | 2 |
| chr19\_58118418\_C\_T | ZNF530 | HIS-TYR | 0.053 | 0.013 | 2 |
| chr21\_34997018\_C\_T | CRYZL1 | ALA-THR | 0.056 | 0.013 | 2 |
| chrX\_18972497\_C\_G | PHKA2 | GLU-GLN | 0.056 | 0.013 | 2 |
| chr1\_117568217\_G\_A | CD101 | VAL-ILE | 0.053 | 0.014 | 2 |
| chr1\_152277554\_G\_A | FLG | ARG-CYS | 0.079 | 0.014 | 3 |
| chr2\_167141109\_G\_T | SCN9A | PRO-THR | 0.100 | 0.014 | 3 |
| chr2\_210905194\_T\_C | C2orf67 | ASN-SER | 0.071 | 0.014 | 2 |
| chr3\_197432000\_C\_T | KIAA0226 | ARG-GLN | 0.053 | 0.014 | 2 |
| chr4\_2172456\_T\_C | POLN | SER-GLY | 0.053 | 0.014 | 2 |
| chr5\_86564564\_c\_T | RASA1 | ALA-VAL | 0.079 | 0.014 | 3 |
| chr5\_127873094\_G\_A | FBN2 | ALA-VAL | 0.107 | 0.014 | 3 |
| chr9\_21970916\_C\_T | CDKN2A | ALA-THR | 0.079 | 0.014 | 3 |
| chr9\_131107634\_G\_A | SLC27A4 | ARG-GLN | 0.059 | 0.014 | 2 |
| chr9\_138439792\_G\_A | OBP2A | ARG-HIS | 0.088 | 0.014 | 3 |
| chr10\_23295903\_T\_C | ARMC3 | SER-PRO | 0.053 | 0.014 | 2 |
| chr10\_127668854\_G\_C | FANK1 | ARG-SER | 0.053 | 0.014 | 2 |
| chr10\_134996950\_A\_G | KNDC1 | SER-GLY | 0.067 | 0.014 | 2 |
| chr11\_55111500\_T\_C | OR4A16 | ILE-THR | 0.059 | 0.014 | 2 |
| chr11\_86118683\_C\_A | CCDC81 | HIS-GLN | 0.083 | 0.014 | 3 |
| chr11\_86126337\_T\_G | CCDC81 | LEU-ARG | 0.079 | 0.014 | 3 |
| chr12\_26834858\_G\_A | ITPR2 | ALA-VAL | 0.079 | 0.014 | 3 |
| chr12\_48358203\_A\_G | TMEM106C | THR-ALA | 0.083 | 0.014 | 3 |
| chr12\_82752037\_T\_G | CCDC59 | ASN-THR | 0.053 | 0.014 | 2 |
| chr13\_73319236\_C\_T | BORA | SER-LEU | 0.056 | 0.014 | 2 |
| chr13\_96511868\_T\_A | UGGT2 | ASN-TYR | 0.067 | 0.014 | 2 |
| chr14\_68159269\_C\_T | RDH11 | GLU-LYS | 0.053 | 0.014 | 2 |
| chr15\_34159941\_T\_G | AVEN | GLU-ALA | 0.053 | 0.014 | 2 |
| chr15\_41688732\_C\_T | NDUFAF1 | GLU-LYS | 0.053 | 0.014 | 2 |
| chr18\_9944924\_a\_G | VAPA | ILE-VAL | 0.053 | 0.014 | 2 |
| chr19\_21476107\_T\_C | ZNF708 | HIS-ARG | 0.056 | 0.014 | 2 |
| chr19\_41847860\_G\_A | TGFB1 | THR-ILE | 0.079 | 0.014 | 3 |
| chr19\_55998317\_C\_A | NAT14 | ASP-GLU | 0.136 | 0.014 | 3 |
| chr20\_60902965\_G\_A | LAMA5 | ALA-VAL | 0.091 | 0.014 | 2 |
| chr22\_50318061\_G\_C | CRELD2 | GLU-GLN | 0.059 | 0.014 | 2 |
| chrX\_65418789\_G\_A | HEPH | ALA-THR | 0.053 | 0.014 | 2 |
| chr1\_19166829\_A\_G | TAS1R2 | ILE-THR | 0.056 | 0.015 | 2 |
| chr1\_94512565\_C\_T | ABCA4 | ARG-GLN | 0.079 | 0.015 | 3 |
| chr1\_152282910\_G\_C | FLG | ASP-GLU | 0.079 | 0.015 | 3 |
| chr2\_31593265\_T\_C | XDH | ILE-VAL | 0.132 | 0.015 | 5 |
| chr3\_155200133\_T\_C | PLCH1 | MET-VAL | 0.053 | 0.015 | 2 |
| chr3\_184070588\_C\_G | CLCN2 | GLU-ASP | 0.059 | 0.015 | 2 |
| chr3\_186461524\_C\_T | KNG1 | ARG-stop | 0.079 | 0.015 | 3 |
| chr4\_107847043\_C\_G | DKK2 | GLY-ARG | 0.053 | 0.015 | 2 |
| chr4\_178363496\_C\_A | AGA | VAL-LEU | 0.053 | 0.015 | 2 |
| chr5\_38406251\_C\_T | EGFLAM | ARG-CYS | 0.053 | 0.015 | 2 |
| chr5\_176004680\_A\_C | CDHR2 | MET-LEU | 0.079 | 0.015 | 3 |
| chr5\_176316455\_C\_T | HK3 | GLY-ARG | 0.056 | 0.015 | 2 |
| chr6\_7565727\_A\_T | DSP | ILE-PHE | 0.079 | 0.015 | 3 |
| chr7\_99454482\_G\_A | CYP3A43 | MET-ILE | 0.083 | 0.015 | 3 |
| chr7\_104752798\_G\_A | MLL5 | SER-ASN | 0.053 | 0.015 | 2 |
| chr8\_18730030\_C\_A | PSD3 | ARG-ILE | 0.053 | 0.015 | 2 |
| chr9\_20988423\_G\_A | KIAA1797 | ASP-ASN | 0.056 | 0.015 | 2 |
| chr10\_74881951\_G\_A | NUDT13 | GLY-ASP | 0.079 | 0.015 | 3 |
| chr10\_99003811\_G\_A | ARHGAP19 | HIS-TYR | 0.053 | 0.015 | 2 |
| chr10\_127705856\_T\_C | ADAM12 | ILE-VAL | 0.056 | 0.015 | 2 |
| chr11\_7060948\_C\_T | NLRP14 | SER-LEU | 0.053 | 0.015 | 2 |
| chr11\_7083610\_T\_A | NLRP14 | SER-THR | 0.053 | 0.015 | 2 |
| chr11\_48328121\_T\_C | OR4S1 | MET-THR | 0.053 | 0.015 | 2 |
| chr11\_72946279\_T\_C | P2RY2 | SER-PRO | 0.079 | 0.015 | 3 |
| chr11\_108143456\_C\_G | ATM | PRO-ARG | 0.071 | 0.015 | 2 |
| chr11\_115085467\_A\_C | CADM1 | ASP-GLU | 0.053 | 0.015 | 2 |
| chr12\_57578673\_G\_A | LRP1 | ASP-ASN | 0.079 | 0.015 | 3 |
| chr12\_108912178\_G\_A | FICD | none | 0.053 | 0.015 | 2 |
| chr12\_120313953\_C\_T | CIT | GLY-GLU | 0.079 | 0.015 | 3 |
| chr12\_122481879\_A\_C | BCL7A | ASN-THR | 0.079 | 0.015 | 3 |
| chr13\_24823928\_T\_C | SPATA13 | VAL-ALA | 0.083 | 0.015 | 3 |
| chr13\_31891743\_G\_A | B3GALTL | GLY-SER | 0.079 | 0.015 | 2 |
| chr14\_51206145\_A\_T | NIN | SER-THR | 0.053 | 0.015 | 2 |
| chr15\_34648647\_T\_A | C15orf55 | VAL-GLU | 0.111 | 0.015 | 3 |
| chr15\_40660043\_G\_T | DISP2 | GLY-VAL | 0.088 | 0.015 | 3 |
| chr16\_684579\_C\_T | C16orf13 | ALA-THR | 0.053 | 0.015 | 2 |
| chr17\_4535314\_G\_A | ALOX15 | THR-MET | 0.083 | 0.015 | 2 |
| chr17\_36483522\_G\_T | GPR179 | PRO-HIS | 0.083 | 0.015 | 2 |
| chr18\_28604374\_T\_C | DSC3 | ASN-SER | 0.059 | 0.015 | 2 |
| chr19\_372689\_G\_A | THEG | ARG-CYS | 0.053 | 0.015 | 2 |
| chr19\_8201121\_C\_T | FBN3 | ARG-GLN | 0.053 | 0.015 | 2 |
| chr19\_8203113\_C\_T | FBN3 | MET-ILE | 0.083 | 0.015 | 2 |
| chr19\_10463118\_G\_C | TYK2 | PRO-ALA | 0.053 | 0.015 | 2 |
| chr19\_19790178\_A\_G | ZNF101 | HIS-ARG | 0.079 | 0.015 | 3 |
| chr19\_55144100\_A\_G | LILRB1 | THR-ALA | 0.056 | 0.015 | 2 |
| chr19\_55144623\_C\_T | LILRB1 | THR-MET | 0.053 | 0.015 | 2 |
| chr19\_57868483\_G\_A | ZNF304 | ALA-THR | 0.079 | 0.015 | 3 |
| chr22\_37407109\_G\_C | TST | PRO-ALA | 0.053 | 0.015 | 2 |
| chr1\_21267993\_G\_C | EIF4G3 | PRO-ALA | 0.053 | 0.016 | 2 |
| chr1\_32842319\_T\_C | BSDC1 | ILE-VAL | 0.067 | 0.016 | 2 |
| chr1\_33836164\_G\_A | PHC2 | ALA-VAL | 0.083 | 0.016 | 2 |
| chr1\_35227162\_C\_T | GJB4 | ARG-CYS | 0.053 | 0.016 | 2 |
| chr1\_35250457\_C\_T | GJB3 | ARG-TRP | 0.079 | 0.016 | 3 |
| chr1\_52838992\_A\_G | ORC1 | MET-THR | 0.053 | 0.016 | 2 |
| chr1\_116937809\_A\_G | ATP1A1 | ILE-VAL | 0.053 | 0.016 | 2 |
| chr1\_117554216\_G\_A | CD101 | GLY-SER | 0.053 | 0.016 | 2 |
| chr1\_155290231\_T\_C | FDPS | VAL-ALA | 0.053 | 0.016 | 2 |
| chr1\_224482084\_C\_T | NVL | VAL-ILE | 0.105 | 0.016 | 3 |
| chr1\_240370702\_A\_G | FMN2 | THR-ALA | 0.053 | 0.016 | 2 |
| chr2\_103335646\_A\_G | MFSD9 | TRP-ARG | 0.056 | 0.016 | 2 |
| chr2\_108875267\_T\_C | SULT1C3 | TYR-HIS | 0.053 | 0.016 | 2 |
| chr2\_176829117\_G\_C | KIAA1715 | THR-SER | 0.053 | 0.016 | 2 |
| chr2\_189932764\_G\_A | COL5A2 | PRO-SER | 0.053 | 0.016 | 2 |
| chr2\_189940142\_T\_G | COL5A2 | MET-LEU | 0.056 | 0.016 | 2 |
| chr2\_204073414\_A\_G | NBEAL1 | THR-ALA | 0.079 | 0.016 | 3 |
| chr2\_216236712\_T\_C | FN1 | ILE-VAL | 0.053 | 0.016 | 2 |
| chr2\_220404484\_G\_C | CHPF | ALA-GLY | 0.056 | 0.016 | 2 |
| chr3\_52780205\_A\_G | NEK4 | PHE-LEU | 0.053 | 0.016 | 2 |
| chr3\_184070901\_C\_T | CLCN2 | ARG-GLN | 0.053 | 0.016 | 2 |
| chr4\_3526642\_T\_C | LRPAP1 | ASN-SER | 0.053 | 0.016 | 2 |
| chr4\_57215969\_C\_T | AASDH | ASP-ASN | 0.053 | 0.016 | 2 |
| chr4\_156832715\_A\_C | TDO2 | ASN-HIS | 0.056 | 0.016 | 2 |
| chr5\_78135241\_C\_T | ARSB | SER-ASN | 0.083 | 0.016 | 3 |
| chr6\_18139228\_C\_T | TPMT | ALA-THR | 0.053 | 0.016 | 2 |
| chr6\_30671588\_A\_T | MDC1 | VAL-GLU | 0.079 | 0.016 | 3 |
| chr6\_30671726\_G\_C | MDC1 | PRO-ARG | 0.079 | 0.016 | 3 |
| chr6\_30673625\_G\_A | MDC1 | SER-PHE | 0.079 | 0.016 | 3 |
| chr6\_30673662\_G\_C | MDC1 | PRO-ALA | 0.079 | 0.016 | 3 |
| chr6\_30681477\_G\_A | MDC1 | ARG-CYS | 0.088 | 0.016 | 3 |
| chr7\_66453476\_A\_G | SBDS | ILE-THR | 0.139 | 0.016 | 4 |
| chr7\_127224872\_G\_A | GCC1 | ALA-VAL | 0.079 | 0.016 | 3 |
| chr7\_135123060\_G\_C | CNOT4 | ALA-GLY | 0.053 | 0.016 | 2 |
| chr8\_95479680\_G\_C | RAD54B | LEU-VAL | 0.056 | 0.016 | 2 |
| chr9\_116224374\_G\_T | RGS3 | GLY-VAL | 0.053 | 0.016 | 2 |
| chr9\_134390870\_C\_A | POMT1 | ASP-GLU | 0.053 | 0.016 | 2 |
| chr10\_70987024\_G\_A | HKDC1 | ARG-GLN | 0.053 | 0.016 | 2 |
| chr10\_135010635\_G\_A | KNDC1 | CYS-TYR | 0.115 | 0.016 | 3 |
| chr11\_60906279\_G\_T | VPS37C | THR-ASN | 0.053 | 0.016 | 2 |
| chr11\_67200812\_C\_T | RPS6KB2 | PRO-LEU | 0.105 | 0.016 | 4 |
| chr14\_52509063\_G\_A | NID2 | PRO-SER | 0.056 | 0.016 | 2 |
| chr14\_90752754\_G\_A | C14orf102 | ARG-CYS | 0.053 | 0.016 | 2 |
| chr15\_31294702\_G\_T | TRPM1 | PRO-THR | 0.056 | 0.016 | 2 |
| chr15\_75012987\_G\_T | CYP1A1 | THR-ASN | 0.094 | 0.016 | 3 |
| chr17\_11543588\_G\_A | DNAH9 | none | 0.053 | 0.016 | 2 |
| chr17\_36552190\_A\_G | SOCS7 | LYS-ARG | 0.079 | 0.016 | 3 |
| chr17\_48594691\_G\_A | MYCBPAP | ARG-HIS | 0.053 | 0.016 | 2 |
| chr18\_19996805\_T\_C | CTAGE1 | ILE-VAL | 0.154 | 0.016 | 3 |
| chr18\_47363963\_T\_C | MYO5B | MET-VAL | 0.105 | 0.016 | 3 |
| chr18\_50683727\_T\_A | DCC | none | 0.053 | 0.016 | 2 |
| chr18\_56367823\_A\_G | MALT1 | ARG-GLY | 0.059 | 0.016 | 2 |
| chr19\_41220029\_G\_A | ADCK4 | ARG-CYS | 0.184 | 0.016 | 6 |
| chr19\_41235167\_G\_A | ITPKC | ARG-HIS | 0.053 | 0.016 | 2 |
| chr19\_48525466\_C\_T | ELSPBP1 | PRO-LEU | 0.053 | 0.016 | 2 |
| chr20\_60902402\_G\_A | LAMA5 | ARG-TRP | 0.125 | 0.016 | 4 |
| chr20\_62325833\_C\_A | RTEL1 | PRO-HIS | 0.053 | 0.016 | 2 |
| chr21\_43809092\_C\_T | TMPRSS3 | ALA-THR | 0.053 | 0.016 | 2 |
| chr22\_32550293\_C\_T | C22orf42 | ARG-HIS | 0.079 | 0.016 | 3 |
| chr22\_41574383\_A\_C | EP300 | GLN-PRO | 0.053 | 0.016 | 2 |
| chrX\_14929375\_G\_A | MOSPD2 | SER-ASN | 0.111 | 0.016 | 4 |
| chrX\_38147269\_G\_A | RPGR | THR-MET | 0.053 | 0.016 | 2 |
| chr1\_55050353\_G\_A | ACOT11 | ARG-HIS | 0.056 | 0.017 | 2 |
| chr1\_152282684\_G\_A | FLG | ARG-CYS | 0.079 | 0.017 | 3 |
| chr1\_155257818\_C\_T | HCN3 | PRO-LEU | 0.056 | 0.017 | 2 |
| chr1\_234565176\_C\_T | TARBP1 | VAL-MET | 0.079 | 0.017 | 3 |
| chr1\_234582720\_C\_T | TARBP1 | GLY-ARG | 0.056 | 0.017 | 2 |
| chr2\_98928757\_C\_T | VWA3B | THR-ILE | 0.053 | 0.017 | 2 |
| chr2\_202626437\_T\_C | ALS2 | ILE-VAL | 0.079 | 0.017 | 3 |
| chr4\_69795635\_A\_C | UGT2A3 | PHE-VAL | 0.053 | 0.017 | 2 |
| chr4\_121719544\_A\_T | PRDM5 | SER-THR | 0.056 | 0.017 | 2 |
| chr5\_135288632\_A\_G | LECT2 | ILE-THR | 0.053 | 0.017 | 2 |
| chr6\_88140811\_C\_A | C6orf165 | ALA-GLU | 0.056 | 0.017 | 2 |
| chr7\_30961790\_G\_A | AQP1 | GLY-ASP | 0.056 | 0.017 | 2 |
| chr7\_142655008\_G\_A | KEL | THR-MET | 0.053 | 0.017 | 2 |
| chr7\_148950895\_C\_T | ZNF212 | HIS-TYR | 0.077 | 0.017 | 2 |
| chr8\_65527669\_C\_T | CYP7B1 | ARG-HIS | 0.053 | 0.017 | 2 |
| chr8\_86021932\_T\_A | LRRCC1 | HIS-GLN | 0.107 | 0.017 | 3 |
| chr9\_123875921\_C\_G | CNTRL | LEU-VAL | 0.053 | 0.017 | 2 |
| chr9\_139297266\_C\_T | SDCCAG3 | VAL-ILE | 0.053 | 0.017 | 2 |
| chr10\_116702425\_A\_C | TRUB1 | GLU-ALA | 0.053 | 0.017 | 2 |
| chr11\_7324584\_G\_A | SYT9 | VAL-MET | 0.053 | 0.017 | 2 |
| chr11\_66358274\_A\_C | CCDC87 | LEU-ARG | 0.053 | 0.017 | 2 |
| chr11\_67809268\_C\_T | TCIRG1 | ARG-TRP | 0.056 | 0.017 | 2 |
| chr11\_108357137\_G\_A | KDELC2 | PRO-LEU | 0.079 | 0.017 | 3 |
| chr12\_113867073\_G\_C | SDSL | GLY-ALA | 0.053 | 0.017 | 2 |
| chr13\_86370571\_G\_A | SLITRK6 | LEU-PHE | 0.079 | 0.017 | 3 |
| chr14\_72169130\_T\_C | SIPA1L1 | ILE-THR | 0.053 | 0.017 | 2 |
| chr16\_10775857\_C\_G | TEKT5 | ASP-HIS | 0.059 | 0.017 | 2 |
| chr16\_27480797\_C\_T | GTF3C1 | ARG-HIS | 0.053 | 0.017 | 2 |
| chr16\_71220755\_A\_G | HYDIN | MET-THR | 0.079 | 0.017 | 3 |
| chr17\_36997503\_T\_C | C17orf98 | GLN-ARG | 0.053 | 0.017 | 2 |
| chr17\_74622774\_T\_C | ST6GALNAC1 | ILE-VAL | 0.053 | 0.017 | 2 |
| chr19\_11978828\_G\_T | ZNF439 | ARG-ILE | 0.053 | 0.017 | 2 |
| chr19\_17108094\_C\_T | CPAMD8 | VAL-ILE | 0.100 | 0.017 | 2 |
| chr19\_35510304\_C\_T | GRAMD1A | ARG-TRP | 0.059 | 0.017 | 2 |
| chr19\_55107854\_G\_T | LILRA1 | VAL-LEU | 0.053 | 0.017 | 2 |
| chr20\_7964476\_T\_C | TMX4 | TYR-CYS | 0.083 | 0.017 | 3 |
| chrX\_53654402\_T\_C | HUWE1 | ASN-SER | 0.053 | 0.017 | 2 |
| chr1\_12009911\_G\_A | PLOD1 | ALA-THR | 0.053 | 0.018 | 2 |
| chr1\_22852880\_G\_C | ZBTB40 | GLU-ASP | 0.053 | 0.018 | 2 |
| chr1\_25572984\_T\_G | C1orf63 | ARG-SER | 0.053 | 0.018 | 2 |
| chr1\_40775937\_G\_A | COL9A2 | THR-MET | 0.053 | 0.018 | 2 |
| chr1\_48825355\_G\_A | SPATA6 | ARG-TRP | 0.053 | 0.018 | 2 |
| chr1\_74648329\_G\_A | LRRIQ3 | HIS-TYR | 0.053 | 0.018 | 2 |
| chr1\_152281317\_G\_T | FLG | ASP-GLU | 0.079 | 0.018 | 3 |
| chr1\_152285181\_G\_T | FLG | HIS-GLN | 0.079 | 0.018 | 3 |
| chr1\_155640115\_C\_T | YY1AP1 | ASP-ASN | 0.083 | 0.018 | 3 |
| chr2\_15519924\_C\_T | NBAS | ARG-HIS | 0.105 | 0.018 | 4 |
| chr2\_48873925\_A\_G | GTF2A1L,STON1-GTF2A1L | TYR-CYS | 0.105 | 0.018 | 3 |
| chr2\_217543728\_G\_A | IGFBP5 | ARG-TRP | 0.053 | 0.018 | 2 |
| chr2\_220072431\_C\_A | ZFAND2B | PRO-HIS | 0.053 | 0.018 | 2 |
| chr2\_239161957\_C\_T | PER2 | VAL-ILE | 0.053 | 0.018 | 2 |
| chr3\_10276185\_C\_G | IRAK2 | LEU-VAL | 0.053 | 0.018 | 2 |
| chr4\_39448586\_C\_T | KLB | ALA-VAL | 0.107 | 0.018 | 2 |
| chr5\_94749787\_C\_T | FAM81B | GLN-stop | 0.053 | 0.018 | 2 |
| chr5\_126250812\_C\_T | 3-Mar | ARG-GLN | 0.059 | 0.018 | 2 |
| chr5\_137486640\_A\_T | BRD8 | CYS-SER | 0.053 | 0.018 | 2 |
| chr5\_159659262\_G\_A | FABP6 | MET-ILE | 0.053 | 0.018 | 2 |
| chr6\_29910660\_A\_G | HLA-A | GLN-ARG | 0.111 | 0.018 | 4 |
| chr6\_122773119\_T\_C | SERINC1 | SER-GLY | 0.079 | 0.018 | 3 |
| chr7\_123593764\_T\_C | SPAM1 | VAL-ALA | 0.059 | 0.018 | 2 |
| chr8\_81426196\_C\_A | ZBTB10 | ALA-GLU | 0.111 | 0.018 | 2 |
| chr8\_144557739\_G\_A | ZC3H3 | ARG-CYS | 0.083 | 0.018 | 2 |
| chr8\_145154222\_G\_A | SHARPIN | PRO-SER | 0.079 | 0.018 | 3 |
| chr9\_18928210\_G\_A | FAM154A | ALA-VAL | 0.053 | 0.018 | 2 |
| chr9\_18928441\_T\_C | FAM154A | LYS-ARG | 0.053 | 0.018 | 2 |
| chr9\_18928536\_G\_C | FAM154A | CYS-TRP | 0.053 | 0.018 | 2 |
| chr10\_82126600\_G\_A | DYDC2 | GLY-SER | 0.053 | 0.018 | 2 |
| chr10\_103988265\_G\_A | ELOVL3 | ASP-ASN | 0.053 | 0.018 | 2 |
| chr10\_118351414\_A\_G | PNLIPRP1 | ASN-ASP | 0.053 | 0.018 | 2 |
| chr11\_55033110\_A\_G | TRIM48 | GLU-GLY | 0.094 | 0.018 | 3 |
| chr11\_59807978\_G\_A | PLAC1L | GLY-SER | 0.053 | 0.018 | 2 |
| chr11\_71276655\_G\_A | KRTAP5-10 | GLY-ARG | 0.079 | 0.018 | 3 |
| chr12\_333193\_C\_T | SLC6A13 | VAL-ILE | 0.053 | 0.018 | 2 |
| chr12\_7985318\_C\_A | SLC2A14 | none | 0.079 | 0.018 | 2 |
| chr12\_64485153\_G\_A | SRGAP1 | VAL-ILE | 0.079 | 0.018 | 3 |
| chr12\_93139348\_A\_G | PLEKHG7 | ASP-GLY | 0.132 | 0.018 | 4 |
| chr14\_57947421\_G\_A | C14orf105 | GLN-stop | 0.053 | 0.018 | 2 |
| chr14\_92922782\_G\_A | SLC24A4 | SER-ASN | 0.053 | 0.018 | 2 |
| chr15\_86122875\_A\_C | AKAP13 | LYS-GLN | 0.079 | 0.018 | 3 |
| chr16\_3299468\_C\_T | MEFV | ARG-GLN | 0.132 | 0.018 | 5 |
| chr16\_30492823\_C\_T | ITGAL | ARG-TRP | 0.083 | 0.018 | 3 |
| chr16\_31473275\_A\_G | ARMC5 | ILE-VAL | 0.053 | 0.018 | 2 |
| chr16\_57732012\_G\_A | CCDC135 | ASP-ASN | 0.053 | 0.018 | 2 |
| chr16\_81209247\_C\_T | PKD1L2 | ARG-HIS | 0.053 | 0.018 | 2 |
| chr16\_90126993\_A\_G | PRDM7 | LEU-PRO | 0.105 | 0.018 | 4 |
| chr17\_15532147\_G\_A | TRIM16 | ARG-TRP | 0.053 | 0.018 | 2 |
| chr17\_38715186\_T\_C | CCR7 | MET-VAL | 0.053 | 0.018 | 2 |
| chr17\_59489707\_C\_T | C17orf82 | ALA-VAL | 0.111 | 0.018 | 4 |
| chr18\_25532304\_T\_C | CDH2 | ASN-SER | 0.105 | 0.018 | 4 |
| chr19\_4359191\_C\_T | MPND | PRO-LEU | 0.053 | 0.018 | 2 |
| chr19\_38229926\_G\_A | ZNF573 | ARG-TRP | 0.105 | 0.018 | 4 |
| chr19\_50251422\_C\_T | TSKS | GLU-LYS | 0.053 | 0.018 | 2 |
| chr22\_23915620\_C\_T | IGLL1 | GLY-SER | 0.079 | 0.018 | 3 |
| chrX\_31986607\_G\_A | DMD | ARG-TRP | 0.079 | 0.018 | 3 |
| chrX\_101970316\_A\_C | GPRASP2,ARMCX5-GPRASP2 | ARG-SER | 0.053 | 0.018 | 2 |
| chr1\_53569230\_T\_A | SLC1A7 | LYS-MET | 0.056 | 0.019 | 2 |
| chr1\_104117921\_G\_A | AMY2B | GLY-ARG | 0.105 | 0.019 | 4 |
| chr1\_186275564\_C\_T | PRG4 | THR-MET | 0.053 | 0.019 | 2 |
| chr1\_202710733\_C\_G | KDM5B | GLU-GLN | 0.053 | 0.019 | 2 |
| chr1\_207851554\_C\_T | CR1L | ARG-CYS | 0.143 | 0.019 | 2 |
| chr1\_248458718\_T\_C | OR2T12 | ARG-GLY | 0.079 | 0.019 | 3 |
| chr2\_21233999\_T\_C | APOB | ASN-SER | 0.053 | 0.019 | 2 |
| chr2\_223085955\_G\_T | PAX3 | THR-LYS | 0.053 | 0.019 | 2 |
| chr4\_3148570\_G\_A | HTT | VAL-ILE | 0.079 | 0.019 | 3 |
| chr4\_146077132\_C\_T | OTUD4 | ALA-THR | 0.053 | 0.019 | 2 |
| chr5\_102338811\_A\_G | PAM | ASP-GLY | 0.118 | 0.019 | 4 |
| chr5\_102537285\_A\_G | PPIP5K2 | SER-GLY | 0.079 | 0.019 | 3 |
| chr7\_94540527\_G\_A | PPP1R9A | ASP-ASN | 0.132 | 0.019 | 5 |
| chr7\_134849209\_C\_T | TMEM140 | PRO-SER | 0.132 | 0.019 | 4 |
| chr8\_10466089\_G\_C | RP1L1 | ALA-GLY | 0.053 | 0.019 | 2 |
| chr8\_10466161\_C\_T | RP1L1 | GLY-ASP | 0.053 | 0.019 | 2 |
| chr11\_1298430\_C\_A | TOLLIP | ALA-SER | 0.071 | 0.019 | 2 |
| chr11\_7083620\_T\_C | NLRP14 | LEU-SER | 0.053 | 0.019 | 2 |
| chr11\_7694002\_G\_A | CYB5R2 | PRO-SER | 0.053 | 0.019 | 2 |
| chr11\_45937306\_C\_T | PEX16 | VAL-MET | 0.079 | 0.019 | 3 |
| chr11\_60197299\_G\_A | MS4A5 | GLY-GLU | 0.091 | 0.019 | 2 |
| chr11\_64599139\_C\_T | CDC42BPG | ALA-THR | 0.059 | 0.019 | 2 |
| chr11\_68174189\_G\_A | LRP5 | VAL-MET | 0.056 | 0.019 | 2 |
| chr14\_88452945\_G\_A | GALC | none | 0.053 | 0.019 | 2 |
| chr19\_17108136\_G\_A | CPAMD8 | ARG-TRP | 0.143 | 0.019 | 3 |
| chr19\_31039669\_C\_T | ZNF536 | ALA-VAL | 0.105 | 0.019 | 4 |
| chr20\_32266134\_C\_T | E2F1 | GLY-SER | 0.079 | 0.019 | 3 |
| chr21\_45820196\_C\_T | TRPM2 | ARG-CYS | 0.053 | 0.019 | 2 |
| chr1\_29320013\_G\_A | EPB41 | VAL-ILE | 0.053 | 0.020 | 2 |
| chr1\_82456585\_G\_A | LPHN2 | ARG-LYS | 0.079 | 0.020 | 3 |
| chr1\_152191696\_G\_C | HRNR | SER-ARG | 0.079 | 0.020 | 3 |
| chr1\_152193605\_C\_T | HRNR | GLY-ASP | 0.079 | 0.020 | 3 |
| chr1\_152281691\_G\_A | FLG | ARG-TRP | 0.079 | 0.020 | 3 |
| chr1\_152281745\_G\_T | FLG | GLN-LYS | 0.079 | 0.020 | 3 |
| chr1\_152282794\_G\_A | FLG | THR-ILE | 0.079 | 0.020 | 3 |
| chr1\_160011512\_G\_A | KCNJ10 | ARG-CYS | 0.079 | 0.020 | 3 |
| chr1\_217804767\_A\_G | SPATA17 | ASN-SER | 0.105 | 0.020 | 4 |
| chr1\_248309159\_C\_A | OR2M5 | ALA-ASP | 0.053 | 0.020 | 2 |
| chr2\_110959026\_G\_T | NPHP1 | PRO-THR | 0.091 | 0.020 | 2 |
| chr2\_215813331\_C\_T | ABCA12 | ASP-ASN | 0.056 | 0.020 | 2 |
| chr3\_193031875\_C\_T | ATP13A5 | ALA-THR | 0.053 | 0.020 | 2 |
| chr4\_3137674\_G\_A | HTT | GLY-ARG | 0.056 | 0.020 | 2 |
| chr5\_118480316\_G\_A | DMXL1 | SER-ASN | 0.105 | 0.020 | 4 |
| chr6\_73904557\_C\_T | KCNQ5 | PRO-LEU | 0.079 | 0.020 | 3 |
| chr6\_131179302\_C\_G | EPB41L2 | GLU-GLN | 0.053 | 0.020 | 2 |
| chr6\_143929450\_G\_A | PHACTR2 | ASP-ASN | 0.053 | 0.020 | 2 |
| chr6\_159398803\_C\_T | RSPH3 | GLU-LYS | 0.053 | 0.020 | 2 |
| chr6\_159401898\_C\_T | RSPH3 | ARG-GLN | 0.053 | 0.020 | 2 |
| chr7\_92132493\_T\_C | PEX1 | ILE-MET | 0.059 | 0.020 | 2 |
| chr9\_105767349\_g\_T | CYLC2 | ASP-TYR | 0.071 | 0.020 | 2 |
| chr10\_129690837\_G\_T | CLRN3 | PRO-GLN | 0.056 | 0.020 | 2 |
| chr12\_52960884\_C\_T | KRT74 | ALA-THR | 0.077 | 0.020 | 2 |
| chr14\_21109745\_C\_G | OR6S1 | VAL-LEU | 0.053 | 0.020 | 2 |
| chr15\_93557954\_G\_C | CHD2 | GLY-ALA | 0.053 | 0.020 | 2 |
| chr15\_98512431\_C\_T | ARRDC4 | THR-MET | 0.079 | 0.020 | 3 |
| chr15\_99762041\_C\_T | TTC23 | ARG-HIS | 0.079 | 0.020 | 3 |
| chr16\_15870032\_A\_G | MYH11 | none | 0.053 | 0.020 | 2 |
| chr16\_27373980\_C\_T | IL4R | SER-LEU | 0.053 | 0.020 | 2 |
| chr19\_7584483\_A\_C | ZNF358 | LYS-GLN | 0.053 | 0.020 | 2 |
| chr19\_14578707\_G\_A | PKN1 | ARG-GLN | 0.063 | 0.020 | 2 |
| chr19\_20044932\_G\_A | ZNF93 | VAL-ILE | 0.056 | 0.020 | 2 |
| chr19\_41356246\_C\_T | CYP2A6 | SER-ASN | 0.053 | 0.020 | 2 |
| chr19\_44932521\_C\_T | ZNF229 | ARG-GLN | 0.079 | 0.020 | 3 |
| chr19\_55525818\_C\_T | GP6 | GLY-SER | 0.079 | 0.020 | 3 |
| chr19\_57326970\_T\_C | PEG3,ZIM2 | ASN-SER | 0.053 | 0.020 | 2 |
| chr20\_60768573\_C\_T | GTPBP5 | ARG-TRP | 0.053 | 0.020 | 2 |
| chr21\_38563639\_C\_T | TTC3 | PRO-SER | 0.077 | 0.020 | 2 |
| chr22\_43218397\_T\_C | ARFGAP3 | SER-GLY | 0.053 | 0.020 | 2 |
| chrX\_23723711\_C\_G | ACOT9 | GLU-GLN | 0.059 | 0.020 | 2 |
| chrX\_38268220\_A\_G | OTC | GLN-ARG | 0.053 | 0.020 | 2 |
| chr1\_63872032\_T\_C | ALG6 | TYR-HIS | 0.079 | 0.021 | 3 |
| chr1\_152193162\_C\_T | HRNR | GLY-SER | 0.079 | 0.021 | 3 |
| chr2\_27167617\_G\_A | DPYSL5 | ALA-THR | 0.158 | 0.021 | 6 |
| chr2\_79313990\_C\_T | REG1B | ARG-HIS | 0.053 | 0.021 | 2 |
| chr2\_102968212\_A\_G | IL1RL1 | GLN-ARG | 0.316 | 0.021 | 10 |
| chr2\_162904013\_T\_C | DPP4 | none | 0.071 | 0.021 | 2 |
| chr3\_38167095\_A\_G | ACAA1 | VAL-ALA | 0.053 | 0.021 | 2 |
| chr3\_74334560\_C\_T | CNTN3 | ARG-GLN | 0.053 | 0.021 | 2 |
| chr3\_186572089\_T\_C | ADIPOQ | TYR-HIS | 0.053 | 0.021 | 2 |
| chr4\_5016883\_G\_A | CYTL1 | ARG-CYS | 0.053 | 0.021 | 2 |
| chr4\_38987965\_C\_T | TMEM156 | VAL-ILE | 0.083 | 0.021 | 3 |
| chr4\_75248505\_G\_T | EREG | CYS-PHE | 0.053 | 0.021 | 2 |
| chr4\_96091414\_C\_T | UNC5C | ALA-THR | 0.053 | 0.021 | 2 |
| chr5\_35705844\_A\_C | SPEF2 | LYS-GLN | 0.125 | 0.021 | 2 |
| chr5\_101834469\_G\_A | SLCO6A1 | ALA-VAL | 0.079 | 0.021 | 3 |
| chr5\_150666946\_C\_T | SLC36A3 | ARG-HIS | 0.079 | 0.021 | 3 |
| chr6\_33260215\_C\_T | RGL2 | GLY-GLU | 0.053 | 0.021 | 2 |
| chr7\_151949735\_T\_C | MLL3 | ILE-MET | 0.059 | 0.021 | 2 |
| chr8\_10464604\_T\_C | RP1L1 | HIS-ARG | 0.132 | 0.021 | 5 |
| chr8\_17739639\_C\_A | FGL1 | ARG-LEU | 0.053 | 0.021 | 2 |
| chr8\_17743051\_A\_T | FGL1 | PHE-ILE | 0.053 | 0.021 | 2 |
| chr8\_32611970\_G\_T | NRG1 | VAL-LEU | 0.053 | 0.021 | 2 |
| chr8\_130789767\_G\_A | GSDMC | PRO-SER | 0.053 | 0.021 | 2 |
| chr8\_144804299\_T\_C | MAPK15 | SER-PRO | 0.053 | 0.021 | 2 |
| chr8\_144808926\_C\_T | FAM83H | GLY-GLU | 0.056 | 0.021 | 2 |
| chr9\_137642654\_G\_A | COL5A1 | GLY-SER | 0.083 | 0.021 | 2 |
| chr10\_7774358\_C\_G | ITIH2 | LEU-VAL | 0.111 | 0.021 | 4 |
| chr10\_123996970\_G\_A | TACC2 | GLY-ARG | 0.053 | 0.021 | 2 |
| chr10\_129907610\_G\_A | MKI67 | ARG-TRP | 0.053 | 0.021 | 2 |
| chr11\_5878836\_T\_A | OR52E8 | ILE-PHE | 0.053 | 0.021 | 2 |
| chr12\_1137217\_A\_G | ERC1 | SER-GLY | 0.053 | 0.021 | 2 |
| chr12\_7288432\_A\_G | CLSTN3 | SER-GLY | 0.053 | 0.021 | 2 |
| chr12\_39735348\_C\_A | KIF21A | GLY-VAL | 0.053 | 0.021 | 2 |
| chr12\_52841174\_C\_T | KRT6B | GLY-SER | 0.056 | 0.021 | 2 |
| chr12\_69744014\_C\_A | LYZ | THR-ASN | 0.105 | 0.021 | 4 |
| chr12\_93181768\_C\_A | EEA1 | ALA-SER | 0.056 | 0.021 | 2 |
| chr15\_31295151\_T\_G | TRPM1 | ASN-THR | 0.053 | 0.021 | 2 |
| chr16\_16276292\_T\_C | ABCC6 | ILE-VAL | 0.053 | 0.021 | 2 |
| chr16\_81916912\_A\_G | PLCG2 | HIS-ARG | 0.053 | 0.021 | 2 |
| chr16\_89927151\_C\_T | SPIRE2 | SER-LEU | 0.067 | 0.021 | 2 |
| chr17\_1540027\_C\_T | SCARF1 | ALA-THR | 0.067 | 0.021 | 2 |
| chr17\_37792090\_G\_A | PPP1R1B | ARG-HIS | 0.056 | 0.021 | 2 |
| chr17\_40263400\_C\_T | DHX58 | ARG-GLN | 0.056 | 0.021 | 2 |
| chr19\_18376518\_T\_A | KIAA1683 | GLN-LEU | 0.079 | 0.021 | 3 |
| chr19\_18897440\_T\_C | COMP | ASN-ASP | 0.053 | 0.021 | 2 |
| chr19\_35232987\_A\_C | ZNF181 | ARG-SER | 0.125 | 0.021 | 3 |
| chr19\_38782485\_G\_C | SPINT2 | VAL-LEU | 0.056 | 0.021 | 2 |
| chr19\_54783693\_C\_T | LILRB2 | ARG-HIS | 0.053 | 0.021 | 2 |
| chr20\_5843952\_G\_A | C20orf196 | ARG-GLN | 0.105 | 0.021 | 4 |
| chr1\_39340558\_G\_A | GJA9 | PRO-SER | 0.053 | 0.022 | 2 |
| chr1\_161132821\_C\_A | USP21 | PRO-THR | 0.105 | 0.022 | 3 |
| chr1\_183099560\_G\_A | LAMC1 | ARG-GLN | 0.053 | 0.022 | 2 |
| chr1\_206224635\_G\_C | AVPR1B | LYS-ASN | 0.083 | 0.022 | 3 |
| chr2\_165578602\_C\_T | COBLL1 | VAL-MET | 0.132 | 0.022 | 4 |
| chr2\_209179939\_A\_G | PIKFYVE | MET-VAL | 0.053 | 0.022 | 2 |
| chr2\_239237388\_G\_A | TRAF3IP1 | ARG-GLN | 0.053 | 0.022 | 2 |
| chr3\_15686693\_G\_C | BTD | ASP-HIS | 0.053 | 0.022 | 2 |
| chr3\_48623124\_G\_A | COL7A1 | PRO-LEU | 0.079 | 0.022 | 3 |
| chr4\_5755516\_T\_A | EVC | PHE-LEU | 0.059 | 0.022 | 2 |
| chr4\_123171659\_T\_A | KIAA1109 | ASP-GLU | 0.053 | 0.022 | 2 |
| chr4\_123179900\_C\_T | KIAA1109 | ARG-TRP | 0.105 | 0.022 | 4 |
| chr5\_5182286\_C\_T | ADAMTS16 | PRO-SER | 0.059 | 0.022 | 2 |
| chr5\_70858268\_A\_G | BDP1 | ASN-SER | 0.083 | 0.022 | 3 |
| chr5\_140558628\_T\_C | PCDHB8 | VAL-ALA | 0.079 | 0.022 | 3 |
| chr6\_32487242\_G\_A | HLA-DRB5 | THR-ILE | 0.133 | 0.022 | 3 |
| chr6\_44270870\_C\_T | AARS2 | VAL-MET | 0.079 | 0.022 | 3 |
| chr6\_74497102\_G\_A | CD109 | GLY-GLU | 0.079 | 0.022 | 2 |
| chr6\_149903597\_A\_G | C6orf72 | LYS-GLU | 0.056 | 0.022 | 2 |
| chr7\_72985148\_C\_T | TBL2 | VAL-ILE | 0.053 | 0.022 | 2 |
| chr7\_73279659\_G\_A | WBSCR28 | GLY-SER | 0.053 | 0.022 | 2 |
| chr9\_21217166\_T\_C | IFNA16 | ILE-VAL | 0.053 | 0.022 | 2 |
| chr10\_7772035\_A\_G | ITIH2 | ASN-SER | 0.105 | 0.022 | 4 |
| chr11\_408174\_G\_T | SIGIRR | SER-TYR | 0.079 | 0.022 | 2 |
| chr11\_419706\_T\_C | ANO9 | THR-ALA | 0.079 | 0.022 | 2 |
| chr11\_7507182\_A\_G | OLFML1 | THR-ALA | 0.105 | 0.022 | 4 |
| chr11\_57947163\_G\_A | OR9Q1 | ALA-THR | 0.079 | 0.022 | 3 |
| chr11\_59224765\_A\_C | OR4D6 | ASP-ALA | 0.053 | 0.022 | 2 |
| chr11\_64813685\_G\_C | NAALADL1 | LEU-VAL | 0.079 | 0.022 | 3 |
| chr12\_18841115\_G\_A | PLCZ1 | SER-LEU | 0.105 | 0.022 | 4 |
| chr14\_64604595\_G\_A | SYNE2 | GLU-LYS | 0.053 | 0.022 | 2 |
| chr15\_51350287\_T\_G | TNFAIP8L3 | ASN-HIS | 0.139 | 0.022 | 4 |
| chr16\_1272275\_C\_T | TPSG1 | ARG-HIS | 0.077 | 0.022 | 2 |
| chr16\_3299586\_G\_A | MEFV | PRO-SER | 0.132 | 0.022 | 5 |
| chr16\_4920335\_A\_G | UBN1 | TYR-CYS | 0.053 | 0.022 | 2 |
| chr16\_19548030\_T\_A | CCP110 | PHE-ILE | 0.056 | 0.022 | 2 |
| chr16\_49671177\_T\_C | ZNF423 | ASN-SER | 0.053 | 0.022 | 2 |
| chr18\_43204739\_C\_T | SLC14A2 | THR-ILE | 0.079 | 0.022 | 3 |
| chr19\_2936535\_G\_A | ZNF77 | GLN-stop | 0.158 | 0.022 | 6 |
| chr19\_10426597\_T\_C | FDX1L | ARG-GLY | 0.100 | 0.022 | 3 |
| chr19\_17108052\_C\_T | CPAMD8 | VAL-MET | 0.063 | 0.022 | 2 |
| chr19\_19745479\_C\_T | GMIP | ASP-ASN | 0.067 | 0.022 | 2 |
| chr19\_42213670\_G\_A | CEACAM5 | ALA-THR | 0.079 | 0.022 | 3 |
| chr19\_52034506\_C\_T | SIGLEC6 | ARG-GLN | 0.053 | 0.022 | 2 |
| chr19\_52520372\_C\_T | ZNF614 | GLY-GLU | 0.125 | 0.022 | 4 |
| chr20\_24964558\_T\_C | C20orf3 | ILE-VAL | 0.079 | 0.022 | 3 |
| chr20\_25282967\_C\_T | ABHD12 | ALA-THR | 0.053 | 0.022 | 2 |
| chr22\_44031042\_T\_C | EFCAB6 | THR-ALA | 0.053 | 0.022 | 2 |
| chrX\_16847765\_A\_G | TXLNG | ILE-VAL | 0.079 | 0.022 | 3 |
| chrX\_92964617\_G\_A | FAM133A | GLU-LYS | 0.059 | 0.022 | 2 |
| chrX\_152721728\_T\_C | HAUS7 | THR-ALA | 0.079 | 0.022 | 3 |
| chr1\_16354394\_C\_T | CLCNKA | ALA-VAL | 0.118 | 0.023 | 4 |
| chr1\_158624528\_G\_T | SPTA1 | ALA-ASP | 0.105 | 0.023 | 4 |
| chr1\_180905263\_C\_T | KIAA1614 | ARG-TRP | 0.053 | 0.023 | 2 |
| chr1\_221053574\_a\_C | HLX | GLN-HIS | 0.133 | 0.023 | 3 |
| chr1\_241767708\_C\_T | OPN3 | VAL-ILE | 0.053 | 0.023 | 2 |
| chr2\_98809432\_T\_C | VWA3B | ILE-THR | 0.105 | 0.023 | 4 |
| chr2\_182780874\_C\_T | SSFA2 | PRO-LEU | 0.053 | 0.023 | 2 |
| chr3\_172835392\_A\_T | SPATA16 | SER-THR | 0.079 | 0.023 | 3 |
| chr5\_115338958\_G\_T | AQPEP | VAL-PHE | 0.077 | 0.023 | 2 |
| chr5\_132561468\_C\_A | FSTL4 | GLU-ASP | 0.132 | 0.023 | 5 |
| chr5\_149003626\_G\_A | ARHGEF37 | ALA-THR | 0.079 | 0.023 | 3 |
| chr6\_29142347\_A\_T | OR2J2 | LYS-MET | 0.079 | 0.023 | 3 |
| chr7\_7278447\_T\_A | C1GALT1 | ILE-ASN | 0.063 | 0.023 | 2 |
| chr7\_37923923\_T\_C | TXNDC3 | ILE-THR | 0.091 | 0.023 | 2 |
| chr9\_215296\_A\_G | DOCK8,C9orf66 | VAL-ALA | 0.063 | 0.023 | 2 |
| chr9\_19290794\_A\_C | DENND4C | ILE-LEU | 0.083 | 0.023 | 3 |
| chr9\_33385241\_C\_A | AQP7 | GLY-VAL | 0.053 | 0.023 | 2 |
| chr9\_136522274\_C\_T | DBH | ARG-CYS | 0.053 | 0.023 | 2 |
| chr10\_25312895\_C\_A | THNSL1 | ALA-GLU | 0.083 | 0.023 | 3 |
| chr10\_85956268\_C\_A | CDHR1 | HIS-GLN | 0.053 | 0.023 | 2 |
| chr11\_430339\_C\_G | ANO9 | VAL-LEU | 0.056 | 0.023 | 2 |
| chr12\_13366504\_G\_A | EMP1 | SER-ASN | 0.105 | 0.023 | 4 |
| chr12\_52760957\_C\_T | KRT85 | ARG-HIS | 0.053 | 0.023 | 2 |
| chr12\_91366649\_G\_C | EPYC | SER-CYS | 0.056 | 0.023 | 2 |
| chr17\_47284735\_T\_C | GNGT2 | GLN-ARG | 0.053 | 0.023 | 2 |
| chr17\_74162548\_C\_T | RNF157 | GLY-ARG | 0.053 | 0.023 | 2 |
| chr18\_74580780\_C\_T | ZNF236 | SER-LEU | 0.105 | 0.023 | 4 |
| chr19\_7992976\_T\_C | TIMM44 | ILE-VAL | 0.056 | 0.023 | 2 |
| chr19\_8197958\_C\_T | FBN3 | VAL-ILE | 0.118 | 0.023 | 3 |
| chr19\_43763144\_C\_T | PSG9 | GLY-ARG | 0.079 | 0.023 | 2 |
| chr20\_17602571\_A\_G | RRBP1 | CYS-ARG | 0.105 | 0.023 | 3 |
| chr21\_45945648\_G\_C | TSPEAR | HIS-GLN | 0.079 | 0.023 | 3 |
| chr22\_42526763\_C\_T | CYP2D6 | VAL-MET | 0.063 | 0.023 | 2 |
| chrX\_49113312\_G\_A | FOXP3 | none | 0.079 | 0.023 | 3 |
| chr1\_33944993\_A\_G | ZSCAN20 | LYS-ARG | 0.053 | 0.024 | 2 |
| chr1\_43232504\_C\_A | LEPRE1 | ALA-SER | 0.063 | 0.024 | 2 |
| chr1\_43675499\_C\_T | WDR65 | SER-LEU | 0.079 | 0.024 | 3 |
| chr1\_43804340\_G\_A | MPL | VAL-MET | 0.053 | 0.024 | 2 |
| chr1\_110019439\_A\_G | SYPL2 | GLU-GLY | 0.053 | 0.024 | 2 |
| chr1\_201079344\_G\_C | CACNA1S | ALA-GLY | 0.053 | 0.024 | 2 |
| chr2\_241622034\_G\_C | AQP12B | THR-SER | 0.125 | 0.024 | 4 |
| chr3\_105264176\_G\_T | ALCAM | MET-ILE | 0.053 | 0.024 | 2 |
| chr4\_4322670\_C\_T | ZBTB49 | ALA-VAL | 0.111 | 0.024 | 4 |
| chr5\_102537298\_C\_T | PPIP5K2 | THR-MET | 0.056 | 0.024 | 2 |
| chr5\_122364538\_T\_C | PPIC | LYS-ARG | 0.083 | 0.024 | 3 |
| chr5\_171777495\_G\_T | SH3PXD2B | PRO-GLN | 0.056 | 0.024 | 2 |
| chr6\_26093141\_G\_A | HFE | CYS-TYR | 0.105 | 0.024 | 4 |
| chr6\_108214694\_C\_T | SEC63 | VAL-ILE | 0.053 | 0.024 | 2 |
| chr7\_2289586\_G\_A | NUDT1 | VAL-MET | 0.053 | 0.024 | 2 |
| chr9\_91616843\_G\_A | S1PR3 | ARG-GLN | 0.053 | 0.024 | 2 |
| chr9\_95396712\_G\_A | IPPK | LEU-PHE | 0.053 | 0.024 | 2 |
| chr9\_120475602\_C\_T | TLR4 | THR-ILE | 0.059 | 0.024 | 2 |
| chr10\_124358498\_T\_G | DMBT1 | ILE-MET | 0.167 | 0.024 | 2 |
| chr11\_60703882\_G\_A | TMEM132A | VAL-MET | 0.053 | 0.024 | 2 |
| chr11\_62397114\_T\_C | GANAB | MET-VAL | 0.105 | 0.024 | 3 |
| chr12\_53453433\_G\_A | TENC1 | ALA-THR | 0.056 | 0.024 | 2 |
| chr13\_38211105\_T\_C | TRPC4 | ILE-VAL | 0.105 | 0.024 | 4 |
| chr14\_20837033\_T\_C | TEP1 | HIS-ARG | 0.158 | 0.024 | 6 |
| chr14\_20846950\_C\_T | TEP1 | ARG-GLN | 0.105 | 0.024 | 4 |
| chr14\_64604592\_C\_G | SYNE2 | PRO-ALA | 0.053 | 0.024 | 2 |
| chr16\_816977\_G\_A | MSLN | GLY-GLU | 0.105 | 0.024 | 4 |
| chr16\_15818842\_A\_G | MYH11,NDE1 | VAL-ALA | 0.053 | 0.024 | 2 |
| chr17\_2202323\_T\_C | SMG6 | ASN-SER | 0.056 | 0.024 | 2 |
| chr17\_11511480\_G\_A | DNAH9 | ARG-HIS | 0.071 | 0.024 | 2 |
| chr17\_39525750\_C\_T | KRT33B | GLU-LYS | 0.053 | 0.024 | 2 |
| chr18\_13681962\_A\_T | C18orf19 | TYR-ASN | 0.079 | 0.024 | 3 |
| chr19\_38876202\_C\_T | GGN | SER-ASN | 0.053 | 0.024 | 2 |
| chr19\_45297479\_C\_T | CBLC | PRO-SER | 0.053 | 0.024 | 2 |
| chr20\_57244396\_G\_A | STX16 | ARG-GLN | 0.056 | 0.024 | 2 |
| chr22\_50722167\_T\_C | PLXNB2 | THR-ALA | 0.059 | 0.024 | 2 |
| chrX\_83141579\_A\_G | CYLC1 | HIS-ARG | 0.053 | 0.024 | 2 |
| chrX\_151123384\_G\_A | GABRE | PRO-LEU | 0.059 | 0.024 | 2 |
| chr1\_881918\_G\_A | NOC2L | SER-LEU | 0.083 | 0.025 | 3 |
| chr1\_45800156\_C\_T | MUTYH | VAL-MET | 0.105 | 0.025 | 3 |
| chr1\_186281400\_C\_T | TPR,PRG4 | THR-MET | 0.053 | 0.025 | 2 |
| chr2\_69177269\_C\_A | GKN2 | ASP-TYR | 0.083 | 0.025 | 2 |
| chr2\_102968211\_C\_A | IL1RL1 | GLN-LYS | 0.316 | 0.025 | 10 |
| chr2\_160604514\_C\_T | 7-Mar | THR-MET | 0.088 | 0.025 | 3 |
| chr2\_240982275\_A\_G | PRR21 | ILE-THR | 0.079 | 0.025 | 3 |
| chr4\_1843324\_C\_T | LETM1 | ARG-HIS | 0.132 | 0.025 | 5 |
| chr6\_28121278\_A\_G | ZNF192 | GLN-ARG | 0.053 | 0.025 | 2 |
| chr8\_23002090\_C\_T | TNFRSF10D | ARG-HIS | 0.083 | 0.025 | 3 |
| chr9\_116191205\_A\_C | C9orf43 | ASN-THR | 0.083 | 0.025 | 3 |
| chr10\_54531242\_G\_A | MBL2 | ARG-CYS | 0.132 | 0.025 | 4 |
| chr10\_97143826\_T\_C | SORBS1 | TYR-CYS | 0.132 | 0.025 | 4 |
| chr11\_4598956\_c\_T | C11orf40 | TRP-stop | 0.056 | 0.025 | 2 |
| chr11\_130332457\_T\_C | ADAMTS15 | TYR-HIS | 0.079 | 0.025 | 2 |
| chr12\_31256517\_C\_T | DDX11 | ALA-VAL | 0.088 | 0.025 | 3 |
| chr12\_52841179\_T\_C | KRT6B | TYR-CYS | 0.088 | 0.025 | 3 |
| chr12\_121712301\_C\_T | CAMKK2 | SER-ASN | 0.056 | 0.025 | 2 |
| chr14\_22038562\_T\_C | OR10G3 | TYR-CYS | 0.079 | 0.025 | 3 |
| chr15\_41046883\_C\_A | FAM82A2 | GLN-HIS | 0.056 | 0.025 | 2 |
| chr16\_31470886\_T\_A | ARMC5 | PHE-TYR | 0.115 | 0.025 | 3 |
| chr17\_5271763\_G\_C | RABEP1 | MET-ILE | 0.132 | 0.025 | 4 |
| chr17\_18653188\_G\_T | FBXW10 | ARG-LEU | 0.056 | 0.025 | 2 |
| chr17\_67017930\_T\_C | ABCA9 | ASN-SER | 0.083 | 0.025 | 3 |
| chr17\_73517536\_G\_A | TSEN54 | VAL-MET | 0.053 | 0.025 | 2 |
| chrX\_153689893\_G\_A | PLXNA3 | ARG-GLN | 0.053 | 0.025 | 2 |

1 Gene ID, symbols, amino acid changes, patient and Genome 200 allele frequency are given starting from SNPS that are found in 2 or in **n** number of patients (n).