**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).