| #chr | Position | Reference | Alteration | Allele Frequency Depth | IMPACT | SYMBOL | cDNA_position | CDS_position | Protein_position | Amino_acids | Codons | VARIANT_CLASS |
|------|----------|-----------|------------|-----------------------|--------|---------|--------------|--------------|----------------|------------|--------|---------------|
| chr1 | 40981007 CTG | C | 0.5 | 304 HIGH | EXO5 | 1866-1867 | 792-793 | 264-265 | SV/SX | tcTGG/tctg | deletion |
| chr1 | 47280746 GAT | G | 0.5 | 250 HIGH | CYP4B1 | 920-921 | 884-885 | 295 | D/X | gAT/g | deletion |
| chr1 | 54605318 T | TGG,TGGG 0.600,0.400 | 157 HIGH | CDCP2 | 2072-2073 | 1224-1225 | 408-409 | -/X | -/CC | insertion |
| chr1 | 120612002 CGG | C | 0.5 | 1450 HIGH | NOTCH2 | 237-238 | 17-18 | 6 | P/X | cCC/c | deletion |
| chr1 | 144923728 GT | G | 0.5 | 576 HIGH | PDE4DIP | 1020 | 729 | 243 | E/X | gaA/ga | deletion |
| chr1 | 156354347 TC | T | 1 | 296 HIGH | RHBG | 1303 | 1265 | 422 | S/X | tCc/tc | deletion |
| chr1 | 156565049 A | AAC | 1 | 474 HIGH | GPATCH4 | 1114-1115 | 1083-1084 | 361-362 | -/X | -/GT | insertion |
| chr1 | 247615261 GA | G | 0.5 | 435 HIGH | OR2B11 | 47 | 8 | F/X | tFc/tc | deletion |
| chr1 | 248801944 TCAAGCG | T | 0.5 | 453 HIGH | OR2T35 | 609-615 | 609-615 | 203-205 | CV/L | tgCGTGCTG/tg | deletion |
| chr2 | 96610395 C | CA | 0.5 | 517 HIGH | ANKR36C | 1555-1556 | 1470-1471 | 490-491 | -/X | -/T | insertion |
| chr2 | 96616501 C | CAA | 0.5 | 373 HIGH | ANKR36C | 1375-1376 | 1290-1291 | 430-431 | -/X | -/TT | insertion |
| chr2 | 96616505 AGC | A | 0.5 | 369 HIGH | ANKR36C | 1370-1371 | 1285-1286 | 429 | A/X | Gct/t | deletion |
| chr2 | 97818260 GGC | G | 0.5 | 272 HIGH | ANKR36 | 1427-1428 | 1183-1184 | 395 | A/X | Gct/t | deletion |
| chr2 | 97818264 G | GTT | 0.5 | 267 HIGH | ANKR36 | 1430-1431 | 1186-1187 | 396 | V/VX | gtt/gTtt | insertion |
| chr2 | 186603605 A | AG | 0.5 | 422 HIGH | FSIP2 | 251-252 | 251-252 | 84 | E/E | gag/gaGg | deletion |
| chr2 | 232458085 TGAGA | T | 0.5 | 557 HIGH | C2orf57 | 512-515 | 424-427 | 142-143 | ER/X | GAGAg/a | deletion |
| chr2 | 241621799 GC | G | 0.5 | 223 HIGH | AQP12B | 518 | 455 | 152 | S/X | acG/ac | deletion |
| chr3 | 44540791 TTC | T | 1 | 270 HIGH | ZNF852 | 1637-1638 | 1476-1477 | 492-493 | EK/EX | gaGaa/gaaa | deletion |
| chr3 | 56591278 T | TGGGGTAAGAG | 0.5 | 437 HIGH | CDC66 | 78-79 | 8-9 | 3 | L/LG* | ttg/tGGGTAAGAg/insertion |
| chr3 | 75714805 TG | TG | 0.5 | 1401 HIGH | FRG2C | 513 | 465 | 155 | G/X | ggg/gg | deletion |
| chr3 | 75786035 G | GA | 0.5 | 364 HIGH | ZNF717 | 3061-3062 | 2738-2739 | 913 | F/FX | ttc/ttTc | insertion |
| chr3 | 75787098 CCT | C | 0.5 | 789 HIGH | ZNF717 | 1997-1998 | 1674-1675 | 558-559 | TG/TX | acAgg/acgg | deletion |
| chr3 | 75787645 GAA | G | 0.5 | 721 HIGH | ZNF717 | 1450-1451 | 1127-1128 | 376 | F/X | tTt/t | deletion |
| chr3 | 75788150 A | AG | 0.5 | 828 HIGH | ZNF47 | 946-947 | 623-624 | 208 | T/TX | act/acTct | deletion |
| chr3 | 125725268 TAA | TA | 0.5 | 203 HIGH | SLCA1A3 | 1741-1744 | 1502-1505 | 501-502 | LL/X | tGTgTa/t | deletion |
| chr3 | 130190720 AT | A | 1 | 283 HIGH | COL6A5 | 8264 | 7770 | 2590 | H/X | caT/ca | deletion |
| chr3 | 186460047 CAGTT | C | 0.5 | 520 HIGH | KNG1 | 2075-2078 | 1863-1866 | 621-622 | SV/SX | tcAGT/tc | deletion |
| chr4 | 3589719 CA | C | 0.5 | 416 HIGH | LINCO0955 | 374 | 88 | 30 | N/X | Aac/ac | deletion |
| chr4 | 5527115 A | AT | 0.5 | 147 HIGH | C4orf6 | 233-234 | 58-59 | 20 | I/I | att/aTt | insertion |
| chr4 | 47839998 C | CT | 0.5 | 193 HIGH | CORIN | 8-9 | 8-9 | 3 | Q/QX | cag/caAg | insertion |
| chr5 | 256483 CTT | C | 0.5 | 745 HIGH | SDHA | 2059-2060 | 1944-1945 | 648-649 | TL/TX | acTTtg/actg | deletion |
| chr5 | 77745853 C | CA | 1 | 101 HIGH | SCAMP1 | 886-887 | 729-730 | 243-244 | -/X | -/A | insertion |
| chr5 | 121488635 AT | A | 0.5 | 372 HIGH | ZNF47 | 1334 | 951 | 317 | N/X | aaT/aa | deletion |
| chr5 | 139931628 A | AGT | 1 | 214 HIGH | SRA1 | 1150-1151 | 328-329 | 110 | V/DX | gtg/gActg | deletion |
| chr5 | 139931629 C | CG | 1 | 216 HIGH | SRA1 | 1149-1150 | 327-328 | 109-110 | -/X | -/C | insertion |
| chr5 | 149378479 CT | C | 1 | 318 HIGH | TIGD6 | 1807 | 1032 | 344 | Q/X | caA/ca | deletion |
| chr5 | 175811094 C | CAT,CGT 0.500,0.500 | 432 HIGH | NOP16 | 806-807 | 583-584 | 195 | R/HX | cgt/cATgt | deletion |
| chr6 | 31324524 GCC | G | 1 | 784 HIGH | HLA-B | 311-312 | 282-283 | 94-95 | QA/HX | caGGca/caca | deletion |
| chr6 | 31324528 G | GTT | 1 | 762 HIGH | HLA-B | 308-309 | 279-280 | 93-94 | -/X | -/AA | insertion |
| chr6 | 32634301 TAG | T | 0.5 | 213 HIGH | HLA-DQB1 | 159-160 | 82-83 | 28 | L/X | Cta/a | deletion |
chr6    32634304 G    GAA  0.5  214 HIGH   HLA-DQB1   157-158   80-81   27  S/SX   tcc/tCTc   insertion
chr6    57398186 G    GA  0.5  702 HIGH   PRIM2    976-977   889-890   297  E/EX   gaa/gAa   insertion
chr6    138539183 A    AG  0.5  346 HIGH   PBOV1    444-445   349-350   117  L/PX   ctA/ctA   insertion
chr6    160560897 CTGTTAAGT C  0.5  302 HIGH   SLC22A1   1422-?    1275-?   425-?   deletion
chr7    31697913 C    CT  1  59 HIGH   CCDC129   3108-3109 3096-3097 1032-1033  -/X  -/T  insertion
chr7    36124231 G    GT  0.5  320 HIGH   PPP13004  382-383   233-234   78  S/SX   agt/agtT  insertion
chr7    72209527 CA     C  0.5  494 HIGH   TYW1B    1114   1015   339  */X  Tga/ga  deletion
chr7    76240785 CA     C  1  369 HIGH   POMZP3   1245   560   187  L/X   Ctg/cg  deletion
chr7    80290425 AAC A   0.5  471 HIGH   CD36    1013-1014 329-330   110  N/X   aA/c/a  deletion
chr7    101200669 A    AG  1  340 HIGH   COL26A1  1376-1377 1184-1185 395  E/EX   gag/gaGg  insertion
chr7    142919223 GT     G  0.5  308 HIGH   TAS2R40  95   53   18  V/X   gTc/gc  deletion
chr7    151945071 G    GT  0.5  1012 HIGH  KMT2C    2666-2667 2447-2448 816  Y/*  tac/tAc  insertion
chr8    75664694 CA     C  0.5  400 HIGH   RP11-758M4 306 248  83  H/X   cAc/cc  deletion
chr8    120202775 CG    C  1  409 HIGH   MAL2    167   65   22  R/X   cGg/cg  deletion
chr8    145106938 GCC G   1  818 HIGH   OPLAH    3581-3582 3499-3500 1167 G/X   GGC/c  deletion
chr8    145617534 TGGGGTGCT    0.5  340 HIGH   ADCK5   1301-?   1257-?   419-?   deletion
chr9    33797928 G    GCC  0.5  778 HIGH   PRSS3   473-474   473-474   158  R/SX   agg/agCCg  insertion
chr9    33797930 GAC G   0.5  806 HIGH   PRSS3   476-477   476-477   159  D/X   gAC/g  deletion
chr9    35812098 CACC GC C  0.5  565 HIGH   SPAG8   166-?   41-?   14-?   deletion
chr9    107367392 TGTTA T  0.5  679 HIGH   OR13C2   556-559   513-516  171-172 NN/X   aaTAc/aa  insertion
chr9    107367664 AGC A   0.5  429 HIGH   OR13C2   286-287   243-244  81-82  TL/TX   acGCta/acta deletion
chr9    125391770 C    CA  0.5  252 HIGH   OR1B1   82-83   44-45   15  L/FX   ttg/tTg  deletion
chr10   7605077 TC    T  1  196 HIGH   ITIH5   2876   2797   933  D/X   Gac/ac  deletion
chr10   27702256 G    GC  0.9  478 HIGH   PTCHD3   1041-1042 923-924  308  G/GX   ggc/gGc  deletion
chr10   89720856 AC    A  0.5  314 HIGH   PTEN    2365   1008  336  Y/X   taC/ta  deletion
chr10   96961793 GA    G  0.5  267 HIGH   C10orf129 370   245   82  E/X   gAa/ga  deletion
chr10   118383463 A    AG  1  204 HIGH   PNLIPRP2   83-84   57-58   19-20  -/X  -/G  insertion
chr11   1018215 G    GCA  0.5  645 HIGH   MUC6    4636-4637 4585-4586 1529  T/MX   act/aTgct  insertion
chr11   2320865 T    TG  0.5  366 HIGH   C11orf21  409-410   357-358  119-120  -/X  -/C  insertion
chr11   4592706 T    TAC  1  201 HIGH   C11orf40  600-601  200-201  -/X  -/GT  deletion
chr11   4680842 CAT C   0.5  368 HIGH   OR52I2   23-24   1-2   1  M/X   ATg/g  deletion
chr11   48387278 C    CACTGTCCTT  0.5  376 HIGH   OR4C5   739-740   739-740  247  R/HRRTVX  cgg/cACAGAAGinsertion
chr11   48387285 A    AGTCTTTAGT  0.5  376 HIGH   OR4C5   732-733   732-733  244-245  -/LXK  -/TACTAAAGAinsertion
chr11   48387683 GT    G  0.5  379 HIGH   OR4C5   334   334   112  T/X   Act/ct  deletion
chr11   48387917 AT   A  0.5  436 HIGH   OR4C5   100   100   34  I/X   Atc/tc  deletion
chr11   48387945 C    CCA  0.5  326 HIGH   OR4C5   72-73   72-73   24-25  -/X  -/Tg  insertion
chr11   56143255 T    TGA  0.5  449 HIGH   OR8U1   156-157   156-157  52-53  -/X  -/GA  insertion
chr11   56143259 AGT A   0.5  450 HIGH   OR8U1   161-162   161-162  54  S/X   aGT/a  deletion
chr11   56380546 CCAGA C  0.5  315 HIGH   OR5M1   429-432   429-432  143-144 CL/x   tgTCt/tg  deletion
chr11   59225129 GC    G  0.5  250 HIGH   OR4D6   720   697   233  R/X   CgG/gg  deletion
chr11   60165352 ATT A   1  334 HIGH   M5A4A14   258-259  167-168   56  I/X   aT/tA  deletion
chr11   67786064 A    AC  1  279 HIGH   ALDH3B1   346-347  230-231   77  N/NX   aac/aaC  insertion
chr11 76751541 CT C 1 1730 HIGH B3GN16 1085 947 316 L/X ctT/ct deletion
chr11 76751584 CT C 1 1884 HIGH B3GN16 1128 990 330 P/X ccT/cc deletion
chr11 76751603 CT C 1 1849 HIGH B3GN16 1147 1009 337 L/X Tg/tg deletion
chr11 94800902 G GC 1 1399 HIGH SRSF8 542-543 512-513 171 S/SX agc/agCc insertion
chr11 112832307 G GA 1 373 HIGH NCAM1 150-151 150-151 50-51 -/X -/A insertion
chr11 112832339 GC G 1 300 HIGH NCAM1 183 183 61 C/X tgC/tg deletion
chr11 118939939 T TC 0.5 257 HIGH VPS11 262-263 220-221 74 S/SX tcc/tccc insertion
chr12 4753565 T TC 0.5 172 HIGH AKAP3 2627-2628 2102-2103 701 G/GX gga/ggGa insertion
chr12 4753569 GA G 0.5 172 HIGH AKAP3 2623 2098 700 S/X Tct/ct deletion
chr12 12630675 GCACGC G 0.5 533 HIGH DUSP16 1717-1721 1085-1089 362-363 SV/X aGCGTG/a deletion
chr12 12630681 TGGGC T 0.5 517 HIGH DUSP16 1712-1715 1080-1083 360-361 VP/X gtGCCC/gt deletion
chr12 48596875 CA CA 0.5 316 HIGH OR10AD1 295-296 200-201 67 L/LX ctg/ctTg insertion
chr12 51740407 CATAAA C 1 166 HIGH CEL1 53-56 12-15 4-5 L/YX ctTAT/TCT deletion
chr12 51740415 A AAG 1 166 HIGH CEL1 48-49 7-8 3 V/AX gtc/gCTtc deletion
chr12 51740416 C CG 1 164 HIGH CEL1 47-48 6-7 2-3 -/X -/C insertion
chr12 85638645 GA G 0.5 160 HIGH LRRQ1 5157 5096 1699 E/X gaA/ga deletion
chr13 25671097 A AT 0.5 645 HIGH PABPC3 798-799 761-762 254 K/NX aag/taTg insertion
chr13 25671272 AG A 0.5 591 HIGH PABPC3 974 937 313 A/X Gcc/gc deletion
chr13 20470852 CT C 1 439 HIGH OR4Q2 532 532 178 F/X Ttt/tt deletion
chr14 20528448 TCATAGATTTT C 0.5 387 HIGH OR4L1 246-264 246-264 82-88 IIDDLLT/X atCAgATGTTT/G deletion
chr14 20666175 C CA 0.5 482 HIGH OR11G2 681-682 681-682 227-2228 -/X -/A insertion
chr14 22955249 CA C 0.5 248 HIGH TRAJ52 35 36 12 T/X acA/ac deletion
chr14 22972783 AC A 1 380 HIGH TRAJ37 50 52 18 P/X Cca/ca deletion
chr14 22974150 TC T 1 392 HIGH TRAJ36 56 58 20 P/X Ccc/cc deletion
chr14 75537321 T TA 1 406 HIGH ZC2HC1C 534-535 45-46 15-16 -/X -/A insertion
chr14 92040589 TC T 1 314 HIGH AL133373.1 794 367 123 E/X Gag/ag deletion
chr15 106329449 ATG A 1 232 HIGH IGHJ6 18-19 18-19 6-7 YM/YX taCATg/tatg deletion
chr15 106329453 A ACC 1 228 HIGH IGHJ6 15-16 15-16 5-6 -/X -/GG insertion
chr15 30665280 TCA T 0.5 192 HIGH CHRFAM7A 681-682 227-228 76 L/X cTG/c deletion
chr15 44089414 A AAG 0.5 217 HIGH SERINC4 1007-1008 772-773 258 M/TX atg/aCTtg deletion
chr15 72105928 AC A 1 363 HIGH NR2E3 1138 deletion
chr15 102029685 G GCC 1 212 HIGH PCSK6 187-188 187-188 63 P/RX ccc/cGGc deletion
chr15 2059621 GC G 1 976 HIGH ZNF598 140 125 42 G/X gGc/gc deletion
chr15 2979977 G GA 0.5 331 HIGH FLYWCH1 634-635 291-292 97-98 -/X -/A insertion
chr16 70896015 GA G 0.5 425 HIGH HYDIN 11863 11712 3904 I/X atT/at insertion
chr16 81161473 G GTACTGCCAg 0.5 202 HIGH PKD1L2 4297-4298 4186-4187 1396 T/SFPOAWQYX acc/aGCTTCCC insertion
chr16 81242148 GGT G 0.9 249 HIGH PKD1L2 706-707 706-707 236 N/X AAc/c deletion
chr16 88599695 GGA G 1 481 HIGH ZFPM1 1652-1653 1330-1331 444 E/X GAg/g deletion
chr16 88599700 CT C 1 453 HIGH ZFPM1 1657 1335 445 P/X ccT/cc deletion
chr16 88780634 AGGTGTA A 1 366 HIGH CTU2 1165-? 1097-? 366-? deletion
chr17 3594276 TG T 1 209 HIGH P2RX5 732 333 111 P/X ccC/cc deletion
chr17 16843037 CAG C 0.5 319 HIGH TNFRSF13B 717-718 704-705 235 P/X cCT/c deletion
Impact: high, the variant is assumed to have high (disruptive) impact in the protein, probably causing protein truncation, loss of function or triggering nonsense mediated decay; moderate, a non-disruptive variant that might change protein effectiveness. (https://asia.ensembl.org/Help/Glossary?id=535, accessed March 2019)