**Supplemental Table 1**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | Pos | dbSNP | Gene | Base conversion | Type | AA conversion | P Allele |
| 1 | 12776344 | rs3000859 | A<->W | AADACL3 | missense | M<->L | 0.002698 |
| 1 | 26627478 | rs2276712 | T<->Y | UBXN11 | synonymous | - | 0.008901 |
| 1 | 38423853 | rs9293 | G<->S | SF3A3 | 3'UTR | - | 0.019602 |
| 1 | 67852335 | rs4297265 | G<->R | IL12RB2 | synonymous | - | 0.020451 |
| 1 | 89886714 | rs6428538 | A<->R | LOC400759 | 3'UTR | - | 0.003993 |
| 1 | 160851826 | rs2274907 | A<->W | ITLN1 | missense | V<->D | 0.005733 |
| 1 | 207795320 | rs2296160 | A<->R | CR1 | missense | T<->A | 0.042188 |
| 1 | 207790088 | rs3811381 | C<->S | CR1 | missense | P<->R | 0.050000 |
| 1 | 207881557 | rs6683902 | A<->R | CR1L | missense | I<->V | 0.014589 |
| 2 | 3504687 | rs9950 | A<->R | ADI1 | synonymous | - | 0.00435 |
| 2 | 15674686 | rs13029846 | T<->Y | NAG | missense | I<->V | 0.034263 |
| 2 | 80801346 | rs17019360 | T<->Y | CTNNA2 | synonymous | - | 0.026793 |
| 2 | 86259443 | rs2276626 | C<->Y | POLR1A | synonymous | - | 0.042262 |
| 2 | 141032088 | rs1386356 | C<->Y | LRP1B | synonymous | - | 0.005313 |
| 2 | 152500449 | rs13013209 | C<->S | NEB | missense | L<->N | 0.006648 |
| 2 | 152527572 | rs7426114 | C<->Y | NEB | missense | V<->M | 2.43E-05 |
| 2 | 192160839 | rs17854823 | A<->W | MYO1B | synonymous | - | 0.004593 |
| 2 | 198508951 | rs10497806 | G<->R | RFTN2 | synonymous | - | 0.007441 |
| 2 | 231077112 | rs28930679 | G<->R | SP110 | missense | A<->V | 0.018189 |
| 3 | 42799765 | rs17238798 | G<->R | CCDC13 | missense | R<->W | 0.037768 |
| 3 | 50222926 | rs1046956 | T<->W | SEMA3F | missense | L<->M | 0.000558 |
| 3 | 52555957 | rs9853056 | T<->Y | STAB1 | synonymous | - | 0.046336 |
| 3 | 69299233 | rs4361282 | C<->S | FRMD4B | missense | E<->D | 0.00299 |
| 3 | 74413676 | rs6549590 | T<->Y | CNTN3 | synonymous | - | 0.021444 |
| 3 | 138033181 | rs9289556 | C<->Y | TXNDC6 | synonymous | - | 0.000178 |
| 3 | 156528401 | rs9812169 | G<->R | PA2G4P4 | 3'UTR | - | 0.039559 |
| 3 | 185990096 | rs2193587 | C<->Y | DGKG | missense | R<->L | 0.030012 |
| 4 | 946226 | rs11552301 | T<->Y | TMEM175 | synonymous | - | 0.033904 |
| 4 | 2951804 | rs2515960 | A<->R | NOP14 | missense | L<->S | 0.012208 |
| 4 | 2993980 | rs2515941 | T<->Y | GRK4 | synonymous | - | 0.000494 |
| 4 | 6302519 | rs1801212 | G<->A | WFS1 | missense | V<->I | 0.004176 |
| 4 | 6325086 | rs3796403 | G<->R | PPP2R2C | synonymous | - | 0.016073 |
| 4 | 20544184 | rs7690492 | C<->Y | SLIT2 | synonymous | - | 0.029482 |
| 4 | 76720885 | rs13119659 | T<->Y | USO1 | missense | S<->P | 0.001917 |
| 4 | 88535785 | rs116512524 | C<->Y | DSPP | synonymous | - | 0.026109 |
| 4 | 119736796 | rs2389688 | A<->M | SEC24D | synonymous | - | 0.008014 |
| 5 | 1244425 | rs4073918 | C<->Y | SLC6A18 | missense | P<->L | 0.000197 |
| 5 | 71756102 | rs7721922 | G<->R | ZNF366 | synonymous | - | 0.009085 |
| 5 | 79815658 | rs369998 | T<->Y | FAM151B | missense | I<->T | 0.029636 |
| 5 | 147480112 | rs2303065 | T<->Y | SPINK5 | synonymous | - | 0.015346 |
| 5 | 150578574 | rs3734038 | A<->R | CCDC69 | synonymous | - | 0.001269 |
| 5 | 150886882 | rs1105168 | G<->R | FAT2 | missense | P<->L | 0.032912 |
| 5 | 178540975 | rs1054480 | G<->R | ADAMTS2 | missense | P<->S | 0.000546 |
| 6 | 25426768 | rs9358856 | G<->R | LRRC16A | missense | V<->I | 0.034671 |
| 6 | 25726621 | rs9467583 | C<->Y | HIST1H2AA | synonymous | - | 0.024054 |
| 6 | 30530245 | rs114696540 | T<->Y | PRR3 | synonymous | - | 0.008095 |
| 6 | 35477025 | rs2064318 | C<->S | TULP1 | missense | L<->N | 0.007618 |
| 6 | 39034072 | rs6923761 | G<->R | GLP1R | missense | G<->S | 0.035366 |
| 6 | 46129345 | rs2235881 | G<->R | ENPP5 | synonymous | - | 0.001384 |
| 6 | 57512510 | rs4294007 | T<->K | PRIM2 | missense | H<->Q | 0.042098 |
| 6 | 62442604 | rs10484690 | A<->R | KHDRBS2 | synonymous | - | 0.002743 |
| 6 | 71238105 | rs2747701 | A<->R | FAM135A | missense | D<->G | 0.009383 |
| 6 | 150342232 | rs61730071 | G<->R | RAET1L | missense | T<->I | 0.02221 |
| 6 | 158870081 | rs705956 | A<->R | TULP4 | synonymous | - | 0.004232 |
| 6 | 158927651 | rs3828712 | A<->R | TULP4 | synonymous | - | 0.006225 |
| 7 | 10492168 | rs3801369 | A<->R | HSPA8P8 | 5'UTR | - | 0.000174 |
| 7 | 25194753 | rs12535348 | C<->Y | C7orf31 | missense | A<->T | 0.022123 |
| 7 | 100634640 | rs1791 | T<->K | MUC12 | missense | S<->A | 0.019801 |
| 7 | 100635661 | rs10953313 | T<->Y | MUC12 | missense | M<->T | 0.005014 |
| 7 | 100647819 | rs11766024 | C<->Y | MUC12 | missense | H<->Y | 0.013874 |
| 7 | 100647875 | rs11766048 | C<->M | MUC12 | synonymous | - | 0.023167 |
| 7 | 131195712 | rs12670788 | G<->R | PODXL | missense | S<->L | 0.001943 |
| 8 | 10467652 | rs4840501 | G<->S | RP1L1 | missense | A<->G | 0.002845 |
| 8 | 63659610 | rs1319275 | G<->R | NKAIN3 | synonymous | - | 0.003501 |
| 8 | 95541371 | rs957446 | T<->W | KIAA1429 | synonymous | - | 0.03552 |
| 8 | 108970367 | rs601558 | A<->R | RSPO2 | missense | L<->P | 0.015035 |
| 8 | 133637659 | rs2293979 | G<->R | LRRC6 | missense | T<->I | 0.015799 |
| 9 | 86284178 | rs1044175 | C<->M | UBQLN1 | synonymous | - | 0.007449 |
| 9 | 102595685 | rs10988904 | C<->Y | NR4A3 | synonymous | - | 0.025309 |
| 9 | 117552885 | rs3810936 | T<->Y | TNFSF15 | synonymous | - | 0.008689 |
| 9 | 125316179 | rs1341044 | T<->K | OR1N2 | missense | V<->G | 0.011678 |
| 10 | 47087680 | rs1048157 | C<->T | PPYR1 | synonymous | - | 0.023606 |
| 10 | 47087731 | rs1048158 | C<->Y | PPYR1 | synonymous | - | 0.039434 |
| 10 | 106907440 | rs41426648 | C<->Y | SORCS3 | synonymous | - | 0.016869 |
| 11 | 309127 | rs1059091 | A<->R | IFITM2 | missense | I<->V | 0.029619 |
| 11 | 587425 | rs12800061 | C<->M | PHRF1 | synonymous | - | 0.041851 |
| 11 | 1264823 | rs4963031 | T<->Y | MUC5B | missense | L<->P | 0.030279 |
| 11 | 5602275 | rs1077126 | A<->R | OR52B6 | missense | T<->A | 0.003089 |
| 11 | 5602968 | rs10769086 | G<->A | OR52B6 | missense | V<->I | 0.017458 |
| 11 | 20673867 | rs2276433 | G<->R | SLC6A5 | synonymous | - | 0.004513 |
| 11 | 34969112 | rs11539202 | A<->R | PDHX | missense | T<->A | 0.036678 |
| 11 | 56954846 | rs716745 | C<->Y | LRRC55 | synonymous | - | 1.35E-06 |
| 11 | 65623519 | rs4621 | G<->R | CFL1 | synonymous | - | 3.07E-05 |
| 11 | 118110977 | rs2853006 | T<->C | MPZL3 | synonymous | - | 0.002559 |
| 11 | 123886865 | rs4084209 | T<->W | OR10G4 | missense | V<->E | 0.00238 |
| 12 | 7894056 | rs73056605 | G<->R | CLEC4C | missense | P<->S | 0.024036 |
| 12 | 10165469 | rs476474 | A<->G | CLEC12B | synonymous | - | 0.017565 |
| 12 | 52985293 | rs12824366 | A<->R | KRT72 | synonymous | - | 0.041837 |
| 12 | 80014907 | rs78187003 | A<->W | PAWR | synonymous | - | 0.01318 |
| 12 | 105568122 | rs935241 | G<->R | APPL2 | synonymous | - | 0.012698 |
| 12 | 105568176 | rs935240 | G<->R | APPL2 | synonymous | - | 0.008827 |
| 13 | 115030714 | rs7318644 | T<->Y | CDC16 | synonymous | - | 0.014577 |
| 14 | 21623290 | rs7145814 | T<->Y | OR5AU1 | missense | I<->V | 0.014611 |
| 14 | 50472405 | rs6572635 | G<->R | LOC283551 | missense | P<->L | 0.006316 |
| 14 | 74991855 | rs862031 | A<->R | LTBP2 | synonymous | - | 0.018711 |
| 14 | 75590822 | rs8017642 | G<->R | NEK9 | synonymous | - | 0.046575 |
| 14 | 91161862 | rs10146731 | C<->Y | TTC7B | synonymous | - | 0.003077 |
| 14 | 93943998 | rs61992606 | G<->R | KIAA1409 | synonymous | - | 0.028989 |
| 15 | 27772676 | rs140679 | C<->Y | GABRG3 | synonymous | - | 0.000798 |
| 15 | 72040774 | rs1872056 | C<->Y | THSD4 | synonymous | - | 0.025793 |
| 16 | 16162019 | rs35605 | T<->Y | ABCC1 | synonymous | - | 0.007582 |
| 16 | 72011181 | rs1559401 | G<->K | PKD1L3 | missense | H<->Q | 0.007922 |
| 16 | 81888152 | rs1143686 | A<->R | PLCG2 | synonymous | - | 0.017855 |
| 17 | 3632836 | rs1716 | G<->R | ITGAE | missense | R<->W | 0.001502 |
| 17 | 7217463 | rs11541855 | T<->Y | GPS2 | synonymous | - | 0.002318 |
| 17 | 18855611 | rs2076562 | T<->Y | SLC5A10 | synonymous | - | 0.048324 |
| 17 | 19812541 | rs203462 | T<->Y | AKAP10 | missense | I<->V | 0.0052 |
| 17 | 39406409 | rs2191379 | C<->M | KRTAP9-4 | missense | S<->Y | 0.004998 |
| 17 | 39406447 | rs3967754 | A<->R | KRTAP9-4 | 3'UTR | - | 0.005367 |
| 17 | 39620399 | rs12948056 | C<->Y | KRT32 | synonymous | - | 0.017485 |
| 17 | 62020348 | rs2058194 | T<->Y | SCN4A | missense | N<->D | 0.002847 |
| 17 | 64025331 | rs11652766 | A<->R | CCDC46 | synonymous | - | 0.005235 |
| 17 | 65988049 | rs9891146 | T<->Y | C17orf58 | missense | I<->V | 0.018717 |
| 17 | 76497920 | rs690844 | C<->M | DNAH17 | missense | M<->I | 0.019226 |
| 18 | 6943264 | rs2016639 | G<->R | LAMA1 | synonymous | - | 0.018562 |
| 18 | 7017322 | rs539713 | A<->R | LAMA1 | synonymous | - | 0.000877 |
| 18 | 12718593 | rs2302768 | A<->R | PSMG2 | synonymous | - | 0.022489 |
| 18 | 56204991 | rs3809970 | C<->Y | ALPK2 | missense | G<->S | 0.01697 |
| 18 | 56246442 | rs12606191 | T<->Y | ALPK2 | synonymous | - | 0.013549 |
| 19 | 2339949 | rs3746285 | T<->Y | SPPL2B | synonymous | - | 0.034259 |
| 19 | 15839081 | rs2067083 | C<->Y | OR10H2 | synonymous | - | 0.03675 |
| 19 | 15852363 | rs11670007 | G<->R | OR10H3 | missense | R<->H | 0.012522 |
| 19 | 15852544 | rs11670326 | C<->Y | OR10H3 | synonymous | - | 0.024851 |
| 19 | 16060021 | rs16980821 | C<->Y | OR10H4 | synonymous | - | 0.035995 |
| 19 | 16060117 | rs16980994 | C<->M | OR10H4 | missense | N<->L | 0.022503 |
| 19 | 16275655 | rs6512087 | C<->Y | CIB3 | missense | G<->E | 0.008404 |
| 19 | 18305824 | rs2271881 | C<->Y | FKSG24 | synonymous | - | 0.006047 |
| 19 | 38377564 | rs7253969 | T<->Y | WDR87 | synonymous | - | 0.004006 |
| 19 | 52000624 | rs3752135 | T<->G | SIGLEC12 | missense | Y<->S | 0.000235 |
| 19 | 55237616 | rs2075731 | C<->Y | KIR3DL3 | synonymous | - | 0.030067 |
| 19 | 55241080 | rs11575928 | A<->R | KIR3DL3 | synonymous | - | 0.013214 |
| 19 | 55281315 | rs2304224 | G<->K | KIR2DL1 | missense | V<->F | 0.017632 |
| 19 | 55316329 | rs117677969 | A<->R | KIR2DL4 | missense | Y<->C | 1.65E-06 |
| 19 | 55331419 | rs78555555 | C<->Y | KIR3DL1 | missense | P<->S | 0.003087 |
| 19 | 55333246 | rs34481025 | C<->Y | KIR3DL1 | synonymous | - | 0.000305 |
| 19 | 55361942 | rs652188 | G<->K | KIR3DL2 | synonymous | - | 0.003759 |
| 20 | 1538266 | rs11697395 | G<->R | SIRPD | synonymous | - | 0.043938 |
| 20 | 19261623 | rs1569767 | G<->R | SLC24A3 | missense | V<->I | 0.002543 |
| 20 | 48491258 | rs542234 | T<->K | SLC9A8 | synonymous | - | 0.001828 |
| 20 | 56090807 | rs6025601 | A<->R | CTCFL | synonymous | - | 0.034362 |
| 21 | 31964916 | rs9305426 | A<->M | KRTAP6-3 | missense | Y<->S | 0.000223 |
| 21 | 43256252 | rs4920098 | C<->Y | PRDM15 | synonymous | - | 0.040135 |
| 21 | 46047633 | rs8127342 | A<->R | KRTAP10-9 | missense | Y<->C | 0.00604 |
| 21 | 46047710 | rs8131142 | T<->Y | KRTAP10-9 | synonymous | - | 0.011688 |
| 21 | 46122413 | rs113985571 | T<->Y | KRTAP10-13P | synonymous | - | 0.014262 |
| 22 | 37770630 | rs2071856 | G<->R | ELFN2 | synonymous | - | 0.000146 |

**Supplemental table 2**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | Pos | dbSNP | Gene | Base conversion | Type | AA Conversion | P  Genotype | P  Allele | P  Dominant | P  Recessive |
| 2 | 152527572 | rs7426114 | NEB | C<->Y | missense | V<->M | 0.005 | 0.004 | 0.001 | 0.468 |
| 4 | 119736796 | rs2389688 | SEC24D | A<->M | synonymous | - | 0.062 | 0.013 | 0.031 | 0.083 |
| 5 | 1244425 | rs4073918 | SLC6A18 | C<->Y | missense | P<->L | 0.021 | 0.002 | 0.025 | 0.010 |
| 5 | 71756102 | rs7721922 | ZNF366 | G<->R | synonymous | - | 0.006 | 0.700 | 0.057 | 0.032 |
| 5 | 79815658 | rs369998 | FAM151B | T<->Y | missense | I<->T | 0.043 | 0.037 | 0.014 | 0.918 |
| 5 | 150578574 | rs3734038 | CCDC69 | A<->R | synonymous | - | 0.017 | 0.037 | 0.009 | 0.440 |
| 5 | 150886882 | rs1105168 | FAT2 | G<->R | missense | P<->L | 0.136 | 0.042 | 0.048 | 0.281 |
| 6 | 30530245 | rs114696540 | PRR3 | T<->Y | synonymous | - | 0.045 | 0.196 | 0.641 | 0.013 |
| 7 | 10492168 | rs3801369 | HSPA8P8 | A<->R | 5'UTR | - | 0.070 | 0.198 | 0.048 | 0.021 |
| 11 | 56954846 | rs716745 | LRRC55 | C<->Y | synonymous | - | 0.050 | 0.009 | 0.030 | 0.428 |
| 12 | 80014907 | rs78187003 | PAWR | A<->W | synonymous | - | 0.089 | 0.045 | 0.286 | 0.028 |
| 17 | 39620399 | rs12948056 | KRT32 | C<->Y | synonymous | - | 0.058 | 0.126 | 0.028 | 0.020 |
| 18 | 56204991 | rs3809970 | ALPK2 | C<->Y | missense | G<->S | 0.050 | 0.120 | 0.031 | 0.016 |
| 19 | 52000624 | rs3752135 | SIGLEC12 | T<->G | missense | Y<->S | 0.126 | 0.028 | 0.118 | 0.605 |
| 19 | 55281315 | rs2304224 | KIR2DL1 | G<->K | missense | V<->F | 0.093 | 0.021 | 0.057 | 0.093 |

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| CHR | Pos | dbSNP | Gene | Base conversion | Type | AA Conversion | P Genotype | P  Allele | P Dominant | P  Recessive |
| 1 | 89886714 | rs6428538 | LOC400759 | A<->R | 3'UTR | - | 0.048 | 0.058 | 0.048 | 1.000 |
| 1 | 207795320 | rs2296160 | CR1 | A<->R | missense | T<->A | 0.202 | 0.018 | 0.074 | 0.378 |
| 2 | 231077112 | rs28930679 | SP110 | G<->R | missense | A<->V | 0.033 | 0.166 | 0.027 | 0.453 |
| 4 | 946226 | rs11552301 | TMEM175 | T<->Y | synonymous | - | 0.029 | 0.962 | 0.246 | 0.025 |
| 4 | 2993980 | rs2515941 | GRK4 | T<->Y | synonymous | - | 0.045 | 0.767 | 0.178 | 0.135 |
| 5 | 1244425 | rs4073918 | SLC6A18 | C<->Y | missense | P<->L | 0.035 | 0.210 | 0.044 | 0.369 |
| 7 | 131195712 | rs12670788 | PODXL | G<->R | missense | S<->L | 0.006 | 0.137 | 0.837 | 0.114 |
| 10 | 106907440 | rs41426648 | SORCS3 | C<->Y | synonymous | - | 0.008 | 0.254 | 0.009 | 0.003 |
| 18 | 6943264 | rs2016639 | LAMA1 | G<->R | synonymous | - | 0.039 | 0.034 | 0.076 | 0.265 |
| 18 | 56246442 | rs12606191 | ALPK2 | T<->Y | synonymous | - | 0.028 | 0.010 | 0.099 | 0.604 |
| 19 | 15852363 | rs11670007 | OR10H3 | G<->R | missense | R<->H | 0.138 | 0.179 | 0.071 | 0.047 |
| 20 | 56090807 | rs6025601 | CTCFL | A<->R | synonymous | - | 0.064 | 0.017 | 0.073 | 0.509 |

**Supplemental table 3**

**Supplemental table 4. Haplotype analysis of the CR1 gene**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Label | F case | F control | ChiSq | Prob > ChiSq | ChiSq-All | Prob > ChiSq-All |
| AC | 0.08 | 0.12 | 0.754481 | 0.385061 | 9.436495 | 0.024017 |
| GC | 0.69 | 0.79 | 2.907783 | 0.088153 |
| GG | 0.21 | 0.08 | 9.262686 | 0.002339 |

**Supplemental table 5.** GO analysis

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Function | Process | Component | GeneCards Super-pathway |
| NEB | Actin binding  Protein binding  Structural constituent of muscle | Muscle filament sliding  Muscle organ development  Regulation of actin filament length  Somatic muscle development | Z disc  Actin cytoskeleton  Cytosol | Striated Muscle Contraction |
| GRK4 | ATP binding  G-protein coupled receptor kinase activity  Rhodopsin kinase activity | G-protein couples receptor internalization  Receptor internalization  Regulation/Termination of G-protein coupled receptor protein signaling pathway  Signal transduction | Cell cortex  Cytosol  Dendrite  Neuronal cell body | Calcium Regulation in the Cardiac Cell  Endocytosis |
| SLC6A18 | neurotransmitter: sodium symporter activity | Amino acid transport  Ion transport  Transmembrane transport | Integral to plasma membrane  Plasma membrane | Amino acid and oligopeptide SLC transporters  SLC-mediated transmembrane transport  Amine compound SLC transporters |
| LRRC55 |  | Ion transport | Integral to membrane  Plasma membrane |  |
| SIGLEC12 |  | Cell adhesion | Integral to membrane |  |
| ELFN2 | Phosphatase binding  Protein phosphatase inhibitor activity | Negative regulation of phosphatase activity | Integral to membrane |  |
| CR1 | Complement component C3b binding/receptor activity  Complement component C4b binding/receptor activity | Complement activation, classical pathway  Innate immune response  Negative regulation of complement Activation, alternative/classical pathway  Negative/positive regulation of serine-type endopeptidase activity  Regulation of complement activation | Cell surface  Integral to plasma membrane  Plasma membrane | Immune respone  Immune system |
| OR10H3 | G-Protein coupled receptor activity  Olfactory receptor activity |  | Integral to membrane  Plasma membrane | Signaling by GPCR  Olfactory transduction |

|  |  |  |
| --- | --- | --- |
| Trait | dbSNP | Reference |
| Cortical vBMD | rs1021188, rs271170, rs7839059, rs6909279 | ([31](#_ENREF_31)) |
| Trabecular vBMD | rs9287237 |
| Cortical vBMD | rs17638544 |
| Femoral neck BMD, Calcaneal quantitative ultrasound parameters, index of cortical instability of the femoral neck | rs2908004, rs2707466 | ([34](#_ENREF_34)) |
| Femoral neck, total hip, lumbar spine and whole body BMD, Femoral shaft cross-sectional area | rs2306029, rs6485702 | [48](#_ENREF_48) |
| CBT, forearm BMD, forearm fracture, tibial cortical thickness | rs2707466 | ([36](#_ENREF_36)) |
| Forearm fracture | rs7776725 |
| Tibial cortical thickness | rs9525638 |
| Forearm BMD | rs2908004, rs2536189, rs1554634, rs10274324 |
| FN-BMD, LS-BMD | rs10226308, rs10835187, rs13245690, rs1564981, rs17482952, rs2062377, rs227584 | [50](#_ENREF_50) |
| FN-BMD, LS-BMD, Anyfracture, nonvertebral fracture | rs3736228 |
| LS-BMD | rs3779381 |
| FN-BMD, LS-BMD | rs4792909, rs4796995, rs5934507 |
| FN-BMD, LS-BMD, Anyfracture, nonvertebral fracture | rs6426749 |
| FN-BMD, LS-BMD, Anyfracture, nonvertebral fracture, vertebral fracture | rs6532023 |
| FN-BMD, LS-BMD | rs7326472, rs736825, rs7521902, rs7751941, rs884205, rs9533090 |
| PCA of 17 osteoporosis-related phenotypes | rs10148694, rs12665525, rs4447275, rs4773155, rs6911565, rs6919366, rs7158720, rs9351097, rs9362320, rs9362321, rs9362322 | ([33](#_ENREF_33)) |
| BMD (postmenopausal woman, age 55-85 years) | rs1054627, rs1152620, rs13204965, rs13336428, rs1863196, rs4667492, rs6710518, rs7550034, rs9466056 | [51](#_ENREF_51) |
| BMDc, aBMD | rs1038304, rs2010281, rs3018362, rs4355801 | [46](#_ENREF_46) |
| Hip fracture | rs10514713 | ([39](#_ENREF_39)) |
| BR and CT | rs7430431 |

**Supplemental table 6.** Candidate SNPs

**Supplemental table 7.** Candidate gene

|  |  |
| --- | --- |
| Gene | Associated phenotype/s |
| ADAMTS18 | BMD |
| ARHGAP1 | BMD |
| CATK | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| CLCN7 | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| COL1A1 | Low BMD, fractures, spine and hip BMD |
| COL1A2 | Low BMD, fractures |
| CRHR1 | spine BMD |
| CRTAP | Low BMD, fractures |
| CTNNB1 | femoral neck BMD |
| CYP17 | Osteoporosis |
| DCDC1 | lumbar spineBMD |
| DCDC5 | lumbar spineBMD |
| ESR1 | Osteoporosis, tall stature, BMD |
| F2 | BMD |
| FAM3C | ultrasound properties of bone |
| FLJ42280 | spine and hip BMD |
| FOXC2 | spine BMD |
| FOXL1 | spine BMD |
| GPR177 | bone mass |
| HDAC5 | BMD |
| IBSP | BMD |
| ITGA1 | BMD |
| LEPRE | Low BMD, fractures |
| LRP4 | femoral neckBMD |
| LRP5 | High bone mass, torus palatinus, Low bone mass, fractures, BMD, bone mass |
| LRP5a |  |
| MARK3 | hip BMD |
| MEF2C | BMD |
| MEPE | spineBMD |
| MHC | BMDand fracture |
| OPN | BMD |
| OSTM1 | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| PPIB | Low BMD, fractures |
| RANK | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| RANKL | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| SFRP4 | ultrasound properties of bone |
| SOST | High bone mass, bone overgrowth,nerve compression syndromes,hip BMD |
| SOX6 | BMD |
| SP7 | BMD |
| SPP1 | BMD |
| SPTBN1 | spine BMD |
| STARD3NL | BMD |
| TCIRG1 | High bone mass, fractures, bone marrow,failure, blindness, osteoarthritis,osteomyelitis |
| TGFB1 | low BMD |
| TGFB3 | genetic susceptibility to osteoporosis |
| TNFRS11A | BMD |
| TNFRS11B | BMD, fracture |
| TNFSF11 | BMD |
| VDR | genetic susceptibility to osteoporosis |
| ZBTB40 | hip and spine BMD |