**Table S9**.Sensitivity analysis comparing genome-wide significant SNPs associated with bone mineral density measured at four skeletal sites.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | **MODEL0 (n = 9416 \ 9385\*)** | **MODEL 1a (n = 9416 \ 9385\*)** | **MODEL1b CEU (n = 7508 \ 7476\*)** |
| **TRAIT** | **RSID** | **LOCUS** | **POS** | **GENE** | **EA** | ***β*** | **SE** | ***P*** | **I2** | **PHET** | ***β*** | **SE** | ***P*** | **I2** | **PHET** | ***β*** | **SE** | ***P*** | **I2** | **PHET** |
| **TBLH-BMD** | rs3765350 | 1p36.12 | 22319903 | *WNT4* | A | 0.1073 | 0.0174 | **7.04E-10** | 0 | 9.32E-01 | 0.11 | 0.0174 | **2.85E-10** | 0 | 1.00E+00 | 0.1159 | 0.0197 | **4.07E-09** | 0 | 6.43E-01 |
|  | rs6726821 | 2q24.3 | 166286360 | *GALNT3* | T | 0.0909 | 0.0145 | **3.95E-10** | 0 | 8.11E-01 | 0.0916 | 0.0146 | **3.22E-10** | 0 | 9.73E-01 | 0.0889 | 0.0165 | 6.86E-08 | 0 | 7.64E-01 |
|  | rs7776725 | 7q31.31 | 120820357 | *FAM3C\*\** | C | 0.1593 | 0.0174 | **5.67E-20** | 54.7 | 1.38E-01 | 0.1613 | 0.0174 | **2.28E-20** | 57.9 | 1.24E-01 | 0.1582 | 0.0199 | **1.73E-15** | 64.7 | 9.24E-02 |
|  | rs7466269 | 9q34.11 | 132453905 | *FUBP3* | A | 0.0843 | 0.0153 | **3.26E-08** | 0 | 4.74E-01 | 0.0812 | 0.0153 | 1.09E-07 | 0 | 5.16E-01 | 0.0756 | 0.0173 | 1.18E-05 | 42 | 1.89E-01 |
|  | rs4420311 | 12p11.22 | 27875457 | *KLHDC5\*\** | G | 0.085 | 0.0155 | **4.44E-08** | 0 | 7.03E-01 | 0.0843 | 0.0156 | 6.08E-08 | 0 | 6.34E-01 | 0.0872 | 0.0173 | 4.30E-07 | 0 | 4.01E-01 |
|  | rs17536328 | 13q14.11 | 42041029 | *TNFSF11* | T | 0.0864 | 0.015 | **7.58E-09** | 0 | 5.94E-01 | 0.0874 | 0.015 | **5.34E-09** | 0 | 5.94E-01 | 0.0866 | 0.0169 | 3.07E-07 | 0 | 5.64E-01 |
|  | rs754388 | 14q32.12 | 92185163 | *RIN3* | C | 0.1195 | 0.0201 | **2.96E-09** | 36 | 2.11E-01 | 0.1255 | 0.0202 | **5.02E-10** | 21.2 | 2.60E-01 | 0.1219 | 0.0223 | **4.83E-08** | 17.6 | 2.71E-01 |
| **LL-BMD** | rs3765350 | 1p36.12 | 22319903 | *WNT4* | A | 0.0972 | 0.0175 | **2.89E-08** | 0 | 7.12E-01 | 0.0991 | 0.0175 | **1.59E-08** | 0 | 7.12E-01 | 0.1071 | 0.0198 | **6.43E-08** | 0 | 8.71E-01 |
|  | rs2908004 | 7q31.31 | 120757005 | *WNT16\*\** | A | 0.0999 | 0.015 | **3.01E-11** | 0 | 6.19E-01 | 0.0992 | 0.0151 | **4.49E-11** | 0 | 4.66E-01 | 0.1039 | 0.0172 | **1.45E-09** | 42 | 1.89E-01 |
|  | rs7466269 | 9q34.11 | 132453905 | *FUBP3* | A | 0.0869 | 0.0153 | **1.51E-08** | 0 | 4.57E-01 | 0.0833 | 0.0154 | 6.08E-08 | 0 | 4.77E-01 | 0.0793 | 0.0173 | 4.76E-06 | 34 | 2.18E-01 |
|  | rs4420311 | 12p11.22 | 27875457 | *KLHDC5\*\** | G | 0.0864 | 0.0156 | **3.21E-08** | 0 | 9.75E-01 | 0.0861 | 0.0157 | **3.80E-08** | 0 | 8.75E-01 | 0.0921 | 0.0173 | 1.07E-07 | 0 | 4.63E-01 |
|  | rs754388 | 14q32.12 | 92185163 | *RIN3* | C | 0.13 | 0.0203 | **1.40E-10** | 0 | 5.26E-01 | 0.1348 | 0.0203 | **3.14E-11** | 0 | 5.75E-01 | 0.1351 | 0.0224 | **1.75E-09** | 0 | 4.89E-01 |
| **UL-BMD** | rs2235529 | 1p36.12 | 22323074 | *WNT4* | C | 0.117 | 0.0205 | **1.21E-08** | 0 | 3.22E-01 | 0.1181 | 0.0205 | **8.73E-09** | 0 | 3.46E-01 | 0.1173 | 0.0229 | 2.99E-07 | 14.7 | 2.79E-01 |
|  | rs6726821 | 2q24.3 | 166286360 | *GALNT3* | T | 0.0828 | 0.0145 | **1.13E-08** | 0 | 7.07E-01 | 0.0818 | 0.0145 | **1.69E-08** | 0 | 7.07E-01 | 0.0789 | 0.0164 | 1.60E-06 | 0 | 8.50E-01 |
|  | rs1262476 | 6q22.32 | 127028689 | *CENPW\*\** | G | 0.1036 | 0.0175 | **2.93E-09** | 72.3 | 5.76E-02 | 0.1022 | 0.0175 | **4.67E-09** | 59.1 | 1.18E-01 | 0.1045 | 0.0191 | **4.17E-08** | 64.6 | 9.30E-02 |
|  | rs798943 | 7q31.31 | 120546135 | *CPED1\*\** | G | 0.1949 | 0.0152 | **1.47E-37** | 0 | 5.57E-01 | 0.1931 | 0.0152 | **6.44E-37** | 0 | 6.48E-01 | 0.2016 | 0.0171 | **3.05E-32** | 43.8 | 1.82E-01 |
|  | rs9525638 | 13q14.11 | 42026577 | *TNFSF11* | C | 0.0889 | 0.0149 | **2.47E-09** | 0 | 7.13E-01 | 0.0894 | 0.0149 | **2.04E-09** | 0 | 7.38E-01 | 0.0949 | 0.0169 | **1.92E-08** | 0 | 9.35E-01 |
| **SK-BMD** | rs3920498 | 1p36.12 | 22365474 | *WNT4* | G | 0.1337 | 0.0189 | **1.56E-12** | 0 | 5.01E-01 | 0.1371 | 0.0194 | **1.57E-12** | 0 | 4.31E-01 | 0.139 | 0.0215 | **1.01E-10** | 0 | 4.15E-01 |
|  | rs2130604 | 6q22.32 | 126862254 | *CENPW* | T | 0.1123 | 0.0169 | **3.33E-11** | 0 | 7.48E-01 | 0.1109 | 0.0174 | **1.85E-10** | 0 | 8.42E-01 | 0.1291 | 0.0195 | **3.59E-11** | 27.8 | 2.39E-01 |
|  | rs3012465 | 6q23.2 | 133392629 | *EYA4* | G | 0.1267 | 0.0152 | **8.29E-17** | 0 | 8.96E-01 | 0.1284 | 0.0152 | **3.59E-17** | 0 | 9.74E-01 | 0.1215 | 0.0172 | **1.61E-12** | 0 | 5.48E-01 |
|  | rs13223036 | 7q31.31 | 120534544 | *CPED1\*\** | T | 0.1687 | 0.0152 | **1.53E-28** | 0 | 9.22E-01 | 0.169 | 0.0152 | **1.51E-28** | 0 | 8.20E-01 | 0.1652 | 0.017 | **3.24E-22** | 0 | 5.39E-01 |
|  | rs2450083 | 8q24.12 | 120132723 | *COLEC10\*\** | T | 0.1019 | 0.0152 | **2.13E-11** | 0 | 8.20E-01 | 0.1025 | 0.0152 | **1.75E-11** | 0 | 7.95E-01 | 0.0959 | 0.0172 | **2.50E-08** | 0 | 3.47E-01 |
|  | rs10835187 | 11p14.1 | 27462253 | *LIN7C\*\** | C | 0.1271 | 0.0149 | **1.63E-17** | 41.1 | 1.93E-01 | 0.1272 | 0.0149 | **1.67E-17** | 46.5 | 1.72E-01 | 0.1245 | 0.017 | **2.76E-13** | 73.7 | 5.11E-02 |
|  | rs12272917 | 11q13.2 | 68019946 | *PPP6R3\*\** | T | 0.1088 | 0.0169 | **1.34E-10** | 53 | 1.45E-01 | 0.1094 | 0.017 | **1.15E-10** | 62.4 | 1.03E-01 | 0.1213 | 0.019 | **1.89E-10** | 0.9 | 3.15E-01 |
|  | rs884205 | 18q21.33 | 58205837 | *TNFRSF11A* | C | 0.1037 | 0.0184 | **1.84E-08** | 0 | 4.15E-01 | 0.1007 | 0.0184 | **4.73E-08** | 0 | 3.72E-01 | 0.1033 | 0.02 | 2.29E-07 | 37.5 | 2.06E-01 |

(TBLH-BMD) = total-body less head BMD, (LL-BMD) = lower limb BMD, (UL-BMD) = upper limb BMD, (SK-BMD) = skull BMD. (MODEL 0) = GWAS meta-analysis performed on age-, gender-, weight- or height-adjusted BMD, (MODEL 1a) = GWAS meta-analysis performed on age-, gender-, weight- and height-adjusted BMD, (MODEL 1b) = GWAS meta-analysis performed on age-, gender-, weight- and height-adjusted BMD measurements in individuals of European ancestry. (GENE) = closest gene, (POS) = position in the genome based on hg18, (EAF) = effect allele frequency, (*β*) = estimates of effect size expressed as adjusted SD per copy of the effect allele (EA), (SE) = standard error of *β*, (*P*) = pvalue, (I2) = Cochran’s Q statistic evaluating heterogeneity, (*P*HET) = evidence of heterogeneity and \*Sample sizes used for SK-BMD genome-wide meta-analysis. \*\*Please note that *PTHLH* is also located at the 12p11.22 locus containing *KLHDC5, RSPO3* is also located at the 6q.22.32 locus containing *CENPW, FAM3C and CPED1* are also located at the 7q.31.31 locus containing *WNT16*, *TNFRSF11B* is also located at the 8q.24.12 locus containing *COLEC10, LGR4* is also located at the 11p14.1 locus containing *LIN7C* and *LRP5* is also located at the 11q13.2 locus containing *PPP6R3.*