

Table S1. Genome-wide significant total body bone mineral density variants. Lumbar spine, Pelvis, Trunk and Femoral Ward.

BMD of the Spine											
7	rs4727924	121031879	q31.31	C	T	1.63x10 ⁻⁰⁸	FAM3C/WNT16 intronic	BMD, Fracture risk	UK BioBanK, GEFOS	5.56x10 ⁻¹⁶⁰ , 4.39x10 ⁻¹⁰	194,39, 335,587
7	rs2536172	120997560	q31.31	A	T	5.75x10 ⁻⁰⁸	FAM3C/WNT16 intronic	Fractured /broken bones	UK BioBanK	2.09x10 ⁻¹⁸⁰	194,398
BMD of the Pelvis											
7	rs1839588	37979888	p14.1	C	T	2.00x10 ⁻⁰⁸	SFRP4/ intronic	BMD	UK BioBanK	2.70x10 ⁻²⁴	194,398
BMD of the Trunk											
7	rs4727924	121031879	q31.31	C	T	1.63x10 ⁻⁰⁸	FAM3C/WNT16 intronic	BMD, Fracture risk	UK BioBanK,GE FOS	5.56x10 ⁻¹⁶⁰ , 4.39x10 ⁻¹⁰	194,39, 335,587
7	rs2536172	120997560	q31.31	A	T	5.75x10 ⁻⁰⁸	FAM3C/WNT16 intronic	Fractured /broken bones	UK BioBanK	2.09x10 ⁻¹⁸⁰	194,398
4	rs1050715238	95757373	q22.3	A	G	4.77x10 ⁻⁰⁸	BMPR1B/ Intronic	No Data	N/A	N/A	N/A
11	rs371319602	96953896	q21	A	C	6.00x10 ⁻⁰⁸	intergenic	No Data	N/A	N/A	N/A
BMD of the Femoral Ward											
2	rs62150773	109035597	q12.3	G	C	1.72x10 ⁻⁰⁸	intergenic variant	No Data	N/A	N/A	N/A

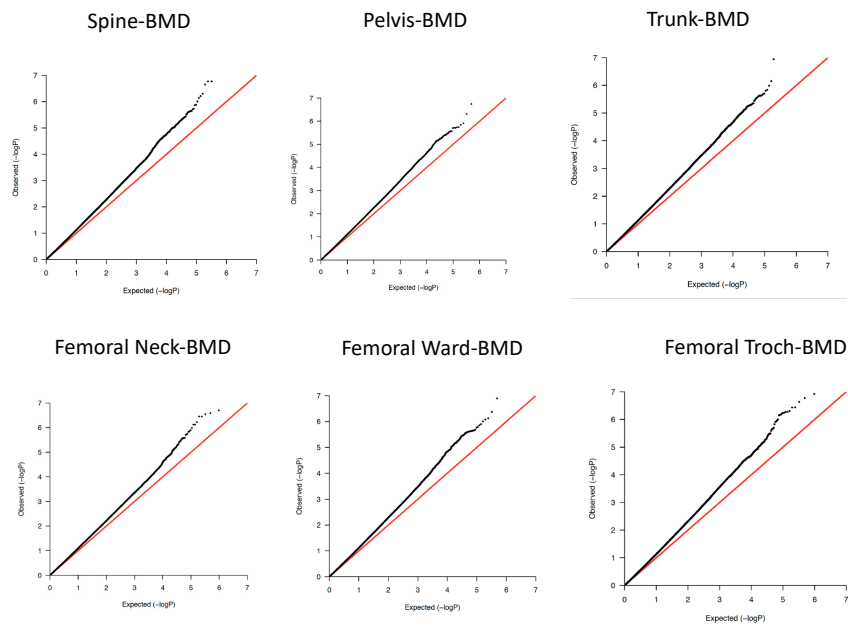


Figure S1. quantile-quantile plots (QQ-plots) for Spine, Pelvis, Trunk, Femoral (neck, ward, troch) BMD.

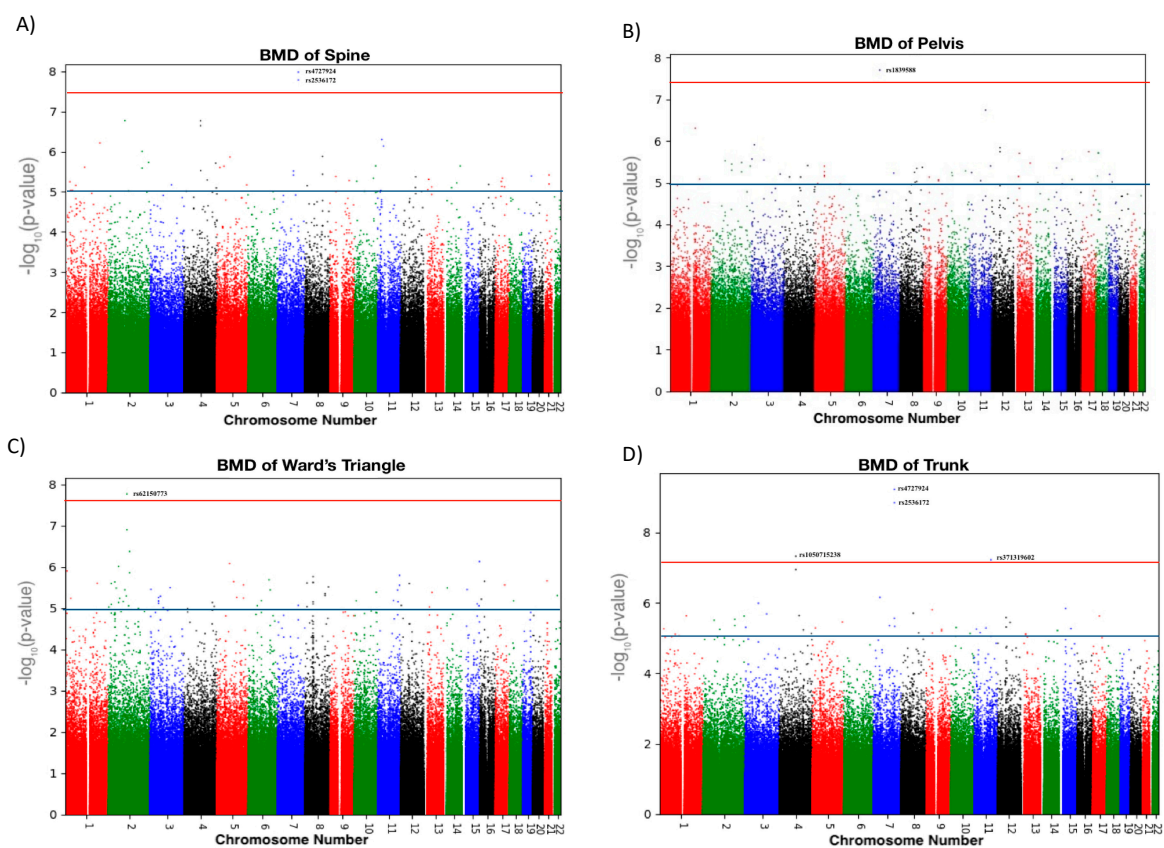


Figure S2. Manhattan plots representing genome-wide association results for Spine, Pelvis, Ward's triangle and trunk bone mineral density (BMD) of 3000 participants. The P values ($-\log_{10}$) are plotted against their respective positions on each chromosome. Results are shown for all variants with significance level $P \leq 10^{-8}$.