Common and rare variants of *WNT16*, *DKK1* and *SOST* and their relationship with bone mineral density

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²Musculoskeletal Research Group, IMIM (Hospital del Mar Medical Research Institute), Centro de Investigación Biomédica en Red de Fragilidad y Envejecimiento Saludable (CIBERFES), ISCIII, Barcelona, Spain **Supplementary Table S1.** Variants that affect the binding of miRNA at least in 3 different miRNA databases (MiRNSP; miRNA-SNP; SNP Function Prediction; MicroSNiPer; miRdSNP; miRTarBase).

Gene	Variant	miRNA	Gain/loss	Log FC #	Adj. p-val [#]
	re171/3305	hsa-miR-541	Gain	*	Ns
WNT16	1517 143303	hsa-mir4263	Gain	*	Ns
	rs190011371	hsa-miR-383	Loss	-0.527	0.00408
	rs17883310	hsa-miR-1915-3p	Loss	1.58	0.00104
	rs17886183	hsa-miR-5583	Gain	*	Ns
SOST	rs75901553	hsa-miR-98-5p	Loss	*	Ns
		hsa-miR-3190	Gain	*	Ns
		hsa-miR-let-7a (and b.c.d.f.g)	Loss	-1.819	0.007

Gain: Minor allele creates a new binding site for the miRNA Loss: Minor allele abolish the binding site for the miRNA # Data from De Ugarte et al. (2015)¹. Data not shown in the publication. logFC: Logarithm (Osteoporotic/Non-osteoporotic)

* logFC < 0.5; Ns < 0.05

SNP	Gene	p value	NES	Tissue
WNT16	00110	praide	NL0	110000
rs17143281	FAM3C	1 30-11	0.65	Muscle - Skeletal
rs55710688	FAM3C	0.000020	0.00	Skin - Not Sun Exposed (Suprapubic)
10007 10000	17.000	0.000016	0.18	Skin - Sun Exposed (Lower leg)
	WNT16	0.000019	0.29	Adipose - Subcutaneous
	CPED1	0.000029	0.097	Artery - Tibial
rs2908004	EAM3C	0.000025	-0.15	Skin - Sun Exposed (Lower leg)
4 40005007	FAM3C	5.9e-8	0.22	Skin - Not Sun Exposed (Suprapubic)
rs142005327	17.000	9.5e-7	0.20	Skin - Sun Exposed (Lower leg)
		0.000032	0.13	Nerve - Tibial
	CPED1	0.000029	0.11	Artery - Tibial
	FAM3C	0.000050	-0.15	Skin - Sun Exposed (Lower leg)
rs2/0/466	CPED1	0.000058	0.094	Artery - Tibial
rs17143305	RP11-3L10.1	7.5e-14	0.87	Testis
	FAM3C	2.9e-29	-0.52	Skin - Sun Exposed (Lower leg)
		5.9e-26	-0.51	Skin - Not Sun Exposed (Suprapubic)
		2.7e-8	-0.21	Nerve - Tibial
		4.6e-8	-0.22	Thyroid
		7.8e-8	-0.27	Stomach
		8.8e-8	-0.34	Esophagus - Mucosa
		1.0e-7	-0.42	Adrenal Gland
		1.0e-7	-0.29	Muscle - Skeletal
		1.1e-7	-0.77	Brain - Spinal cord (cervical c-1)
		4.8e-7	-0.20	Adipose - Subcutaneous
		9.56-7	-0.31	Brain - Anterior cingulate cortex (BA24)
		0.0000028	-0.35	Adipage Viscoral (Omontum)
		0.0000031	-0.21	Reast Mammany Tissue
		0.0000032	-0.24	Artery - Tibial
		0.0000087	-0.18	Esophagus - Muscularis
		0.000022	-0.28	Brain - Frontal Cortex (BA9)
		0.000027	-0.30	Brain - Cortex
DKK1				
rs41281546	DKK1	8.6e-7	-0.29	Cells - Transformed fibroblasts
rs1569198	PRKG1-AS1	0.000047	0.16	Cells - Transformed fibroblasts
rs74711339	DKK1	1.3e-7	-0.35	Cells - Transformed fibroblasts
SOST				
rs1237278	SOST	8.9e-18	-0.26	Artery - Tibial
		3.6e-9	-0.61	Brain - Cortex
		5.4e-9	-0.27	Artery - Aorta
		1.1e-7	-0.43	Artery - Coronary
		0.000024	-0.28	Heart - Atrial Appendage
	MPP3	0.000013	0.22	Thyroid
	MPP2	0.000063	-0.17	Cells - Transformed fibroblasts
rs851058	SOST	3.4e-20	-0.28	Artery - Tibial
		1.1e-10	-0.29	Artery - Aorta
		1.2e-8	-0.47	Arrery - Coronary
	הספווס	4.2e-7	-0.35	Heart - Atrial Appendage
*******	DUSPS	0.000069	0.10	Cells - Transformed libroblasts
rs2023794	DUSPS	6.Ue-7	0.29	Cells - I ransformed fibroblasts
	IVIPP2	0.000022	0.46	Skin - Not Sun Exposed (Suprapuble)
		0.000048	0.50	Skin - Sun Exposed (Lower leg)

Supplementary Table S2. GTEx eQTL data for all the SNVs found in the resequencing of *WNT16*, *DKK1* and *SOST*

NES: Normalized Effect Size

Supplementary Table S3. Minor allele frequency (MAF) from 1000 genomes project: total population (ALL), european population (EUR) and Iberian population in Spain (IBS) and the complete BARCOS cohort frequency.

SNP	Minor allele	ALL	EUR	IBS	BARCOS cohort
WNT16					
rs55710688	CCCA	0.252	0.233	0.276	0.257
rs2908004	А	0.510	0.443	0.416	0.445
rs142005327	СТ	0.257	0.254	0.29	0.28
rs113001389	А	0.004	0	0	0.0007
rs2707466	Т	0.503	0.440	0.407	0.463
rs190011371	С	0.001	0	0	0.002
DKK1					
rs1569198	А	0.682	0.507	0.477	0.468
rs74711339	G	0.019	0.043	0.033	0.057
SOST					
rs1237278	С	0.436	0.355	0.425	0.392
rs2023794	С	0.074	0.044	0.037	0.056
rs570754792	А	0.0004	0.002	0.005	0.001
rs17882143	Т	0.007	0.018	0.033	0.023
rs17883310	А	0.009	0.013	0.023	0.018

Supplementary Table S4. Effect size of the associated variants

SNP	Position		Effect size (β and OR)		
			LS-BMD	FN-BMD	
WNT16					
rs55710688	p.Met1? g.120965467_120965470dupCCCA	Fs 5'UP	0.018 (0.006, 0.031) 1.019 (1.006, 1.031)	0.009 (0.0001, 0.019) 1.01 (1.0001, 1.019)	
rs2908004	p.G72R/p.G82R	М	0.012 (0.0015, 0.023) 1.012 (1.001, 1.023)		
rs142005327	c.346+103_104dupCT c.316+103_104dupCT	I	0.018 (0.006, 0.03) 1.018 (1.006, 1.031)	0.011 (0.002, 0.02) 1.011 (1.002,1.02)	
rs2707466	p.T253I/p.T263I	М	0.014 (0.002, 0.026) 1.014 (1.002, 1.026)	0.01 (0.002, 0.019) 1.01 (1.002,1.019)	
rs3801387 [#]	c.603+2747A>G c.633+2747A>G	I	0.017 (0.005, 0.03) 1.017 (1.005, 1.03)	0.01 (0.0004, 0.019) 1.01 (1.0004, 1.019)	
DKK1					
rs1569198	c.548-43A>G	I		0.011 (0.003, 0.019) 1.011 (1.003,1.019)	
SOST					
rs17882143	p.Val10lle	М	<u>0.041 (0.003, 0.079)</u> <u>1.042 (1.003, 1.082)</u>		

Underline and Italics β and OR under dominant model

SNP genotyping previously in BARCOS (Estrada *et al.* (2012)²).

Primers	Sequence (5'→3')	Tm	Mg²+ (mM)	Elongation time (s)
WNT16-Frag1a-F	GGTAGCTCCAGTAAGAGATTC	00	0	45
WNT16-Frag1a-R	CAGATTACCGTGTCTTTGGGT	62	2	15
WNT16-Frag1b-F	CGGAGCCGCTCTCCACCA	<u></u>	0	45
WNT16-Frag1b-R	ATTAGGTCACTCGTCTAAGGG	62	2	15
WNT16-Frag2-F	ACTTTCAACTGAGGCTGGGG	<u></u>	0	45
WNT16-Frag2-R	CTGGAACTGGGGAGTCAGG	02	2	15
WNT16-Frag3-F	CTTCCTTTCTAAATATGTACTCG	59	2	15
WNT16-Frag3-R	AGGGCTGCCAGTGTTTGGTT	50	2	15
WNT16-Frag4-F1	TGGGACAAAAACCAAAGGACG	62	2	15
WNT16-Frag4-R1	TGACCACATGGGTGTTGTAAC	02	2	15
WNT16-Frag4-F2	AGGATGATCTGCTCTATGTTAAT	62	2	15
WNT16-Frag4-R2	CCCACCATTATTGAGTCCTGT	02	2	10
DKK1-Frag1-F	GCGCTGATCACAGTCCTTATC	63	2	15
DKK1-Frag1-R	TGCTATAACGCTCGCTGGTA	00	2	10
DKK1-Frag2-F	GCAGTGGGCAGTAACAGGT	62	25	35
DKK1-Frag2-R	TGTATTGAATCATTGAGGGACA	02	2.0	
DKK1-Frag3-F	GAGGAAGTTTGGCTTGTGTTT	62	2	15
DKK1-Frag3-R	CGAAGGAGAAGACAGTAGGAAA	02	2	10
DKK1-Frag4a-F	GAACCACCTTGTCTTCAAAAATG	63	15	20
DKK1-Frag4a-R	TCCAAGAGATCCTTGCGTTC	00		20
DKK1-Frag4b-F	AGGTGCTGCACTGCCTATTT	63	1.5	20
DKK1-Frag4b-R	CCGTATCCTCATTCCAATCAA			
SOST_Frag0a_F	CCGAGTTGGGCAGATCACC	62	1.5	15
SOST_Frag0a_R	TTAATGCAGACGGTCCAGCC			
SOST_Frag0b_F	ACGCGTTCCAGGGATGAATC	62	1.5	15
SOST_Frag0b_R	GGCCAAGGCAGCATTTTCTC			
SOST_Frag1_F	GCTAGAGGAGAAGTCTTGG	62	2	10
SOST_Frag1_R	CCATTCTTCCCCACCTCC	-		-
SOST_Frag2a_F	AGATGTTCAGGGGCAAAAGC	63	2	30
SOST_Frag2a_R	GGAAGTCGGGCCCACTAG	00	-	00
SOST_Frag2b_F	GTCACCGAGCTGGTGTGCT	62	2	20
SOST_Frag2b_R	CTCAGGGCCTGGAAGGTCT	03	2	30
SOST_Frag3a_F	CTCAAGGACTTCGGGACCGA	60	2	15
SOST_Frag3a_R	AAATGAGGGTGGAGGTGG	02	2	15
SOST_Frag3b_F	AGTCCTGGCTCTGCCACTAA	60	2	15
SOST_Frag3b_R	GGACACATTTCTGCCTAGAAAA	00	2	15
SOST_Frag3c_F	GGGGGAAAAACTACAAGTGC	62	2	15
SOST_Frag3c_R	TCCTTTCCAAACCCAGACC	02	2	10
ECR5_F	TCCTTGCCACGGGCCACCAGCTTT	62	2	5
ECR5 R	CCCCCTCATGGCTGGTCTCATTTG	52	~	5

Supplementary Table S5. PCR condicitons. Sequence of the primers $(5' \rightarrow 3')$, annealing temperature (°C), amount of magnesium (mM) and elongation time at 72°C (seconds).

WNT16

rs4727920; g.120965562A>G; c.65+28A>G (WNT16a) / g.120965562A>G (WNT16b); example of one HBM woman carrying the variant.

Reference Coordinates	280 280 390 310 320 320 320 320 320 320 320 320 320 32
Translate Trace Hajority	T G G G T T T T G T T T A T T T T T G G A G A
WWT16_Frag1A_SC.seq(1>403) wWT16_HBM_Frag1A_3a.ab1(1>159)	→ tgggttttgtttattttggagaacaaacatttttcaatgg
rs201022838	3° a 120969332C>A \circ c 66-289C>A (W/NT16a) / c -15C>A (W/NT16b) example
of the only HBM	A woman carrying the variant
Reference Coordinates	400 410 420 430 440
Translate Trace	AGGAGCGGCTGGGCTGGGGGGGCCCATGCGGGGGGGGGG
WNT16_FRAG1B_SC.seq(1>647)	A C C A C C C C C T C C C C C C C C C C
♥ WIIU_DM_FIGGD_U. DD(U	
rs17143291:	g.120969825C>A: p.Thr90Thr (WNT16a) / p.Thr100Thr (WNT16b); example
of one I BM wo	man carrying the variant
Reference Coordinates	
♥ Translate ♥ Trace Najority	
wmTl6_LBM_Frag2_le.abl(118>535	Mannahan Man
re1/7/06013	$P_{\rm c} = 1200600200 \text{ T} = 216 \text{ (580-T} (WNIT16-)) = 246 \text{ (580-T} (WNIT16-))$
13147430312	2, 9.1209099290>1, 0.310+300>1 (WWW110a)/ 0.340+300>1 (WW1110b),
Translate Trace Najority	сселсал стсстссассееттсстесалаталаеталатаетестасетест
WHT15_Frag2_SC.seq(1>573) ···· ♥WHT15_HEM_Frag2_Sa.abl(1>430)	
rs140239870 example of one	D; g.120970018A>G; c.316+147A>G (WNT16a)/ c.346+147A>G (WNT16b); LBM woman carrying the variant.
Peference Coordinates Translate Trace	490
Majoricy WNT16_Frag2_SC.seq(1>573) ···→ ▼WNT16_LBH_Frag2_3g.abl(1>535) →	n c c t t t a g t g c a c g g g g a t t g a g a g c t a c a a a g g c c a g a c c t g g g a g c a g g t g c g a g
	how have have have have have have here have have here have have here here here here here here here he
rs113001389	9: g.120970045C>A; c.316+174C>A (WNT16a)/ c.346+174C>A (WNT16b);
example of the	only LBM woman carrying the variant.
Reference Coordinates	
Translate Trace Majority	6 6 A T T 6 A 6 A 6 C T A C A A A 6 6 C C A 6 A C C T 6 6 6 6 A 6 C A 6 6 T 6 C 6 A 6 C T 6 6 A 6 6
UNT16_Frag2_SC.seq(1>573) WNT16_HBM_Frag2_4g.ab1(8>529)	→ ggattgagagctacaaaggccagacctggggagcaggtgcgagcctggagg
rs190011371	1; g.120979568G>C; g.120979568G>C (WNT16a) /c.*169G>C (WNT16b);
example of the	only LBM woman carrying the variant.
Reference Coordinates	
Majority Secuencia consenso Exon 4(II).	$\frac{1}{8}$
▼zscore_bajo_exon4(ii)_r_7a.abl	L(1>600) ←

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Supplementary Figure S1. Examples of DNA sequence chromatograms from various individuals, each containing one of the *WNT16* rare variants described in this paper. In all cases, the variants are in heterozigosis and are signaled by arrows.

DKK1

rs540255939; g.54074079C>A; c.-116C>A; example of the only LBM woman carrying the variant.

Reference Coordinates	250 260 270 280 290
Translate Trace Majority	N G C T C T G T G C T C C T G C A G T C A G G A C T C T G G A C C G C A G G G G G C T C C C G G G G G C T C C G G G G
DKK1_Ex1_SC.seq(1>811) \rightarrow \forall DKK1_LBM_Ex1_4h.ab1(30>783) \rightarrow	A G C T C T G C T G C A G T C A G G A C T C T G G G A C C G C A G G G G G C T C C C G G
	b = 0.000 = 0.000000 b = 0.0000000000000
	<u>x </u>
rs149268042:	g.54074798G>T: p.Arg120Leu; example of the only HBM woman carrying
the variant.	, , , , , , , , , , , , , , , , , , ,
Reference Coordinates	220
P Translate ♥ Trace G T (Majority DFW1 Even2 SC eser(1) 500) → C T (T C G C C T G C A G G A A G C G C C G A A A A C G C T G C A T G C G T C A C G C T A T G T G C T C C C C G G G A
w dkk1_hbm_ex2_4e.ab1(1>564) →	
D T	
c 406+195G>A	$a = \frac{1}{2}$, a 54075040G>A: example of the only HBM woman carrying the variant
Reference Coordinates	
▶ Translate ▼ Trace A Hajority	T C T T C A T T G C A A G T G T T T A A T C G G G A A G A A G A G A G A G A G T T G G G A G G T C T C T G R
$DKK1_Exon2_SC.seq(1>600) \rightarrow A$ $\forall dkk1_hba_ex2_5g.ab1(18>563) \leftarrow$	T C T T C A T T G C A A G T G T T T A A T C G G G A G A A G A G A G A G A G A G T T G G G A G G T C T C T G
rs200054686;	g.54076944deIT; c.*377deIT, example of the only LBM woman carrying the
variant.	
(1>897)	
hatter the A	MAN MANAMINA MANAMANA MANAMANA MANAMANA MANAMANA
20 25 30	35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115
rs953208416;	g.54077319C>1; c.*752C>1, example of the only HBM woman carrying the
variant.	1120 1140 1150 1150 1170
Translate Trace	ататт бат са б ст стабаатаа ст ттааа бааа б
Majority DKK1_Ex5_SC.seq(1>917) →	n A T A T T G A T C A G C T C T A G A A T A A C T T T A A A G A A G A C G T G T T C T G C A T T G A T .
♥DKK1_HBM_EX4(11)_3D.aD1(1>866) →	
rs79759877; g	54077322G>A; c.*755G>A; example of the only HBM woman carrying the
variant.	
Reference Coordinates	
Najority	
▼dkk1_hbn_ex5_3a.ab1(15>858) ←	
	Mary Mary Mary Mary Mary Mary Mary Mary
rs549135224	g.54077585G>A; example of one HBM woman carrying the variant
Reference Coordinates	
Translate Trace Najority	атааттт 6 са 6 тат стт 6 а 6 та ста ст 6 са т6 са а 6 са 6 а ст 6 т ст 6 а 1
DKK1_Ex5_SC.seq(1>917) → ▼dkk1_hbm_ex5_7e.ab1(3>541) ←	a ta a t t t g c a g t a t c t t g a g t a c t a c t g c a t g c a a a g c a g a c t t g t t c t a a t

Supplementary Figure S2. Examples of DNA sequence chromatograms from

various individuals, each containing one of the *DKK1* rare variants described in this paper. In all cases, the variants are in heterozigosis and are signaled by arrows. In the case of rs20054686, which is a heterozygous deletion, the whole chromatogram to the right of it is affected.

SOST rs18426919	6; g.41838340G>A; example of one HBM woman carrying the variant.
Reference Coordinates Translate Consensus FragOA1_SC.seq(1>661)	210
▼sost_0al_hbm_r_6f.ab1(1>423) ◆	Martin
rs79715828	; g.41838130G>A ; example of the only HBM woman carrying the variant.
Reference Coordinates Translate Trace Najority	400
Frag0A1_SC.seq(l>661) ▼sost_0al_hbm_r_lf.ab1(l>434)	
rs74252774	; g.41838012G>T; example of the only HBM woman carrying the variant.
▶ Translate ▶ Consensus Frag0Al_SC. seq(1>661)	C A A A T A A G G A A A G G A A A G G A A A G G A A A T C A C G T C C A G T C C T G A G A C T T G C C A T C A A A T A A G G A A A G G A A A G G A A A G G A A A T C A C G T C C A G T C C T G A G A C T T G C C A T C A A A T A A G G A A A G G A A A G G A A A G G A A A T C A C G T C C A G T C C T G A G A C T T G C C A T
♥ 505t_041_bba_t_4d.ab1(1>424) ♥	hummannannan
rs56786595	6; g.41837786C>T; example of one HBM woman carrying the variant.
Translate Trace Najority	са в 6 в 6 6 с в 6 т с 6 т с т 6 6 т с т 6 6 т с в 6 в 6 6 6 6 т т в в с в 6 т с с в 6 в т т с с в 6 в 6 с в в в 6 6 6 с в в в 6 с в в 6 с в в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в 6 с в
Frag0&2_SC.seq(1>713) ♥ sost_hba_frag0b_r_lf.ab1(3>704)	
rs61105240	; g.41837720C>T; example of the only HBM woman carrying the variant.
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Supplementary Figure S3. Examples of DNA sequence chromatograms from various individuals, each containing one of the *SOST* rare variants described in this paper. In all cases, the variants are in heterozigosis and are signaled by arrows. In the case of rs17885979, which is a heterozygous deletion, the whole chromatogram to the right of it is affected.



Supplementary Figure S4. Boxplots for the nominally significant associated SNPs rs55710688, rs2908004, rs142005327, rs2707466, rs17882143, rs1569198 with LS-BMD or FN-BMD.

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