

### Supplementary Table 1

Model	$\beta$	SE	L_CI	U_CI	P	$r^{2p}$
M1						$r^2=0.653$
AGE	-0.11	0.020	-0.15	-0.07	<b>1.09x10<sup>-8</sup></b>	0.025
GENDER	-1.28	0.035	-1.35	-1.21	<b>1.95x10<sup>-204</sup></b>	0.506
TIME DRAWN	-0.46	0.033	-0.52	-0.39	<b>3.22x10<sup>-40</sup></b>	0.125
TANNER STAGE	-0.25	0.015	-0.28	-0.22	<b>1.55x10<sup>-53</sup></b>	0.165
M1 + HEIGHT + WEIGHT						$r^2=0.666$
AGE	-0.10	0.019	-0.14	-0.07	<b>6.78x10<sup>-8</sup></b>	0.022
GENDER	-1.25	0.043	-1.33	-1.16	<b>1.41x10<sup>-145</sup></b>	0.394
TIME DRAWN	-0.45	0.033	-0.52	-0.39	<b>3.41x10<sup>-40</sup></b>	0.125
TANNER STAGE	-0.23	0.015	-0.26	-0.20	<b>6.88x10<sup>-47</sup></b>	0.145
HEIGHT	0.10	0.025	0.05	0.15	<b>4.28x10<sup>-5</sup></b>	0.013
WEIGHT	-0.16	0.024	-0.21	-0.12	<b>6.95x10<sup>-12</sup></b>	0.035
M2						$r^2=0.666$
AGE	-0.10	0.019	-0.14	-0.07	<b>6.61x10<sup>-8</sup></b>	0.022
GENDER	-1.31	0.063	-1.43	-1.18	<b>7.26x10<sup>-82</sup></b>	0.244
TIME DRAWN	-0.45	0.033	-0.51	-0.39	<b>5.85x10<sup>-40</sup></b>	0.125
TANNER STAGE	-0.23	0.016	-0.26	-0.20	<b>2.33x10<sup>-44</sup></b>	0.138
HEIGHT	0.12	0.030	0.06	0.18	<b>6.43x10<sup>-5</sup></b>	0.012
F-MASS	-0.11	0.020	-0.15	-0.07	<b>6.32x10<sup>-8</sup></b>	0.012
L-MASS	-0.16	0.039	-0.23	-0.08	<b>5.77x10<sup>-5</sup></b>	0.022

Table shows regression analyses of different covariates versus CTX in 1325 participants aged 15.5 (580 males, 745 females). M1= adjustment for average age, gender, tanner stage and whether the individual attended the clinic in the morning or afternoon. M1 + HEIGHT + WEIGHT = Model 1 in addition to height and weight; M2 = Model 1 in addition to total-body lean mass and fat mass. n= sample size; SE = standard error;  $\beta$  = SD change CTX per SD change in exposure (excluding categorical variables: gender, time drawn and tanner stage); L\_CI = lower 95% confidence estimate of  $\beta$ ; U\_CI = upper 95% confidence estimate of  $\beta$ ; P = strength of evidence against the null hypothesis of no association between the outcome and exposure variable;  $r^{2p}$  = partial proportion of the variance in the outcome explained by the exposure in the specified model.  $r^2$  = total proportion of variance in the CTX explained by the all exposures in the specified model

Supplementary Table 2

LOCUS	RSID	POS	GENE	PMID	r <sup>2</sup>	EA	ALSPAC (n=3382)			YFS (n=1558)			GOOD (n=938)		
							$\beta^*$	SE	P	$\beta^*$	SE	P	$\beta^*$	SE	P
<b>8q24.12</b>	rs4355801	119993054	<i>TNFRSF11B</i>	19079262 & 18455228	0.90	A	-0.01	0.021	6.41x10 <sup>-1</sup>	-0.08	0.036	<b>3.47x10<sup>-2</sup></b>	0.08	0.043	7.17x10 <sup>-2</sup>
	rs7839059	120045723	<i>TNFRSF11B</i>	23437003	0.42	A	-0.04	0.022	9.58x10 <sup>-2</sup>	-0.13	0.042	<b>2.14x10<sup>-3</sup></b>	0.03	0.045	5.58x10 <sup>-1</sup>
	rs2062375	120046973	<i>TNFRSF11B</i>	20548944	0.97	C	-0.03	0.021	1.47x10 <sup>-1</sup>	-0.12	0.037	<b>7.79x10<sup>-4</sup></b>	0.06	0.043	1.48x10 <sup>-1</sup>
	<b>rs2062377</b> □	<b>120076601</b>	<b><i>TNFRSF11B</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>A</b>	-0.03	0.021	1.75x10 <sup>-1</sup>	-0.10	0.037	<b>9.00x10<sup>-3</sup></b>	0.06	0.043	1.77x10 <sup>-1</sup>
	rs6469792	120077552	<i>TNFRSF11B</i>	19079262	0.74	C	-0.04	0.021	<b>3.93x10<sup>-2</sup></b>	-0.10	0.036	<b>3.96x10<sup>-3</sup></b>	0.07	0.043	8.06x10 <sup>-2</sup>
	rs11995824	120081881	<i>TNFRSF11B</i>	19801982	0.79	G	-0.04	0.021	<b>4.53x10<sup>-2</sup></b>	-0.11	0.036	<b>2.16x10<sup>-3</sup></b>	0.04	0.043	3.07x10 <sup>-1</sup>
	rs6469804	120114010	<i>TNFRSF11B</i>	18445777 & 19079262	0.88	A	-0.03	0.021	2.41x10 <sup>-1</sup>	-0.09	0.037	<b>1.27x10<sup>-2</sup></b>	0.04	0.043	3.15x10 <sup>-1</sup>
	rs6993813	120121419	<i>TNFRSF11B</i>	18445777 & 19079262	0.69	C	-0.04	0.021	8.27x10 <sup>-2</sup>	-0.11	0.036	<b>3.09x10<sup>-3</sup></b>	0.04	0.043	3.89x10 <sup>-1</sup>
<b>13q14.11</b>	<b>rs9533090</b> □	<b>41849449</b>	<b><i>AKAP11</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>T</b>	0.00	0.021	8.23x10 <sup>-1</sup>	0.00	0.036	9.22x10 <sup>-1</sup>	0.03	0.045	5.16x10 <sup>-1</sup>
	rs9594738	41850145	<i>TNFSF11</i>	18445777 & 19079262	1.00	T	0.00	0.021	8.29x10 <sup>-1</sup>	0.00	0.036	9.10x10 <sup>-1</sup>	0.03	0.045	5.46x10 <sup>-1</sup>
	rs9533093	41859597	<i>TNFSF11</i>	19079262	0.23	T	0.04	0.024	8.60x10 <sup>-2</sup>	0.06	0.046	1.80x10 <sup>-1</sup>	0.06	0.055	2.66x10 <sup>-1</sup>
	rs9594759	41930593	<i>TNFSF11</i>	18445777 & 19079262	0.68	T	0.00	0.021	9.71x10 <sup>-1</sup>	-0.01	0.037	7.94x10 <sup>-1</sup>	0.02	0.045	6.06x10 <sup>-1</sup>
	rs1021188 □	42014133	<i>TNFSF11</i>	21124946 & 23437003	0.00	C	-0.08	0.027	<b>3.84x10<sup>-3</sup></b>	-0.02	0.056	6.75x10 <sup>-1</sup>	-0.06	0.060	2.93x10 <sup>-1</sup>
<b>18q21.33</b>	<b>rs884205</b> □	<b>58205837</b>	<b><i>TNFRSF11A</i></b>	<b>19801982   22504420</b>	<b>1.00</b>	<b>A</b>	-0.06	0.024	<b>7.22x10<sup>-3</sup></b>	-0.02	0.041	5.62x10 <sup>-1</sup>	-0.11	0.051	<b>2.75x10<sup>-2</sup></b>
	rs3018362	58233073	<i>TNFRSF11A</i>	19079262	0.68	A	-0.05	0.022	<b>1.62x10<sup>-2</sup></b>	-0.01	0.037	7.93x10 <sup>-1</sup>	-0.08	0.045	7.18x10 <sup>-2</sup>

Table showing association of previously reported RANK (*TNFRSF11A*), RANKL (*TNFSF11*) and OPG (*TNFRSF11B*) variants with cortical thickness in ALSPAC (n=3382), GOOD (n=938) and Young Finns (n=1558). (POS) = position in the genome based on hg18; (GENE) = closest gene; (PMID) = accession number of the publication in Pubmed which described the association with BMD; (r<sup>2</sup>) = the pairwise LD estimate in CEU populations between the SNP in bold and all other SNPs in that locus; (EA) = effect allele; ( $\beta^*$ ) = effect size; (SE) = standard error of  $\beta^*$ ; (P) = P-value; (PMID) = accession number of the publication in Pubmed which described the association with BMD. \*Effect estimates expressed as adjusted SD per copy of the effect allele (EA). Note: rs9533090 □ is found upstream of *TNFSF11*, but is closest to *AKAP11*. □ - denotes the variants which were used to generate allele scores (i.e. independent signals).

Supplementary Table 3

LOCUS	RSID	POS	GENE	PMID	r <sup>2</sup>	EA	ALSPAC (n=3382)			YFS (n=1558)			GOOD (n=938)		
							$\beta^*$	SE	P	$\beta^*$	SE	P	$\beta^*$	SE	P
<b>8q24.12</b>	rs4355801	119993054	<i>TNFRSF11B</i>	19079262 & 18455228	0.90	A	-0.05	0.018	<b>2.74x10<sup>-3</sup></b>	-0.13	0.036	<b>2.89x10<sup>-4</sup></b>	-0.12	0.044	<b>5.11x10<sup>-3</sup></b>
	rs7839059	120045723	<i>TNFRSF11B</i>	23437003	0.42	A	-0.07	0.019	<b>1.04x10<sup>-4</sup></b>	-0.14	0.041	<b>4.88x10<sup>-4</sup></b>	-0.17	0.046	<b>2.07x10<sup>-4</sup></b>
	rs2062375	120046973	<i>TNFRSF11B</i>	20548944	0.97	C	-0.07	0.018	<b>2.97x10<sup>-4</sup></b>	-0.16	0.036	<b>1.16x10<sup>-5</sup></b>	-0.14	0.044	<b>2.21x10<sup>-3</sup></b>
	<b>rs2062377</b> □	<b>120076601</b>	<b><i>TNFRSF11B</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>A</b>	-0.06	0.018	<b>1.27x10<sup>-3</sup></b>	-0.16	0.037	<b>2.17x10<sup>-5</sup></b>	-0.11	0.044	<b>1.14x10<sup>-2</sup></b>
	rs6469792	120077552	<i>TNFRSF11B</i>	19079262	0.74	C	-0.05	0.018	<b>5.92x10<sup>-3</sup></b>	-0.14	0.036	<b>1.45x10<sup>-4</sup></b>	-0.10	0.044	<b>1.81x10<sup>-2</sup></b>
	rs11995824	120081881	<i>TNFRSF11B</i>	19801982	0.79	G	-0.05	0.018	<b>2.66x10<sup>-3</sup></b>	-0.14	0.036	<b>7.79x10<sup>-5</sup></b>	-0.14	0.045	<b>1.39x10<sup>-3</sup></b>
	rs6469804	120114010	<i>TNFRSF11B</i>	18445777 & 19079262	0.88	A	-0.05	0.018	<b>3.25x10<sup>-3</sup></b>	-0.15	0.037	<b>2.68x10<sup>-5</sup></b>	-0.12	0.044	<b>8.67x10<sup>-3</sup></b>
	rs6993813	120121419	<i>TNFRSF11B</i>	18445777 & 19079262	0.69	C	-0.05	0.018	<b>5.38x10<sup>-3</sup></b>	-0.15	0.036	<b>5.40x10<sup>-5</sup></b>	-0.14	0.044	<b>1.30x10<sup>-3</sup></b>
<b>13q14.11</b>	<b>rs9533090</b> □	<b>41849449</b>	<b><i>AKAP11</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>T</b>	-0.02	0.018	2.09x10 <sup>-1</sup>	-0.11	0.035	<b>1.48x10<sup>-3</sup></b>	0.01	0.046	8.98x10 <sup>-1</sup>
	rs9594738	41850145	<i>TNFSF11</i>	18445777 & 19079262	1.00	T	-0.02	0.018	2.09x10 <sup>-1</sup>	-0.11	0.035	<b>1.47x10<sup>-3</sup></b>	-0.01	0.046	9.01x10 <sup>-1</sup>
	rs9533093	41859597	<i>TNFSF11</i>	19079262	0.23	T	-0.01	0.021	7.59x10 <sup>-1</sup>	-0.04	0.046	3.56x10 <sup>-1</sup>	-0.01	0.055	8.66x10 <sup>-1</sup>
	rs9594759	41930593	<i>TNFSF11</i>	18445777 & 19079262	0.68	T	-0.01	0.018	6.20x10 <sup>-1</sup>	0.01	0.037	8.67x10 <sup>-1</sup>	0.04	0.046	3.79x10 <sup>-1</sup>
	rs1021188 □	42014133	<i>TNFSF11</i>	21124946 & 23437003	0.00	C	-0.12	0.024	<b>1.97x10<sup>-7</sup></b>	-0.16	0.056	<b>3.10x10<sup>-3</sup></b>	-0.30	0.063	<b>1.65x10<sup>-6</sup></b>
<b>18q21.33</b>	<b>rs884205</b> □	<b>58205837</b>	<b><i>TNFRSF11A</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>A</b>	-0.09	0.021	<b>3.05x10<sup>-5</sup></b>	0.02	0.040	5.95x10 <sup>-1</sup>	-0.04	0.051	4.90x10 <sup>-1</sup>
	rs3018362	58233073	<i>TNFRSF11A</i>	19079262	0.68	A	-0.07	0.019	<b>1.93x10<sup>-4</sup></b>	-0.02	0.036	5.35x10 <sup>-1</sup>	-0.06	0.046	2.07x10 <sup>-1</sup>

Table showing association of previously reported RANK (*TNFRSF11A*), RANKL (*TNFSF11*) and OPG (*TNFRSF11B*) variants with cortical BMD in ALSPAC (n=3382), GOOD (n=938) and Young Finns (n=1558). (POS) = position in the genome based on hg18; (GENE) = closest gene; (PMID) = accession number of the publication in Pubmed which described the association with BMD; (r<sup>2</sup>) = the pairwise LD estimate in CEU populations between the SNP in bold and all other SNPs in that locus; (EA) = effect allele; ( $\beta^*$ ) = effect size; (SE) = standard error of  $\beta^*$ ; (P) = P-value; (PMID) = accession number of the publication in Pubmed which described the association with BMD. \*Effect estimates expressed as adjusted SD per copy of the effect allele (EA). Note: rs9533090 □ is found upstream of *TNFSF11*, but is closest to *AKAP11*. □ - denotes the variants which were used to generate allele scores (i.e. independent signals).

Supplementary Table 4

LOCUS	RSID	POS	GENE	PMID	r <sup>2</sup>	EA	ALSPAC (n=3382)			YFS (n=1558)			GOOD (n=938)		
							β*	SE	P	β*	SE	P	β*	SE	P
8q24.12	rs4355801	119993054	<i>TNFRSF11B</i>	19079262 & 18455228	0.90	A	0.03	0.016	6.18x10 <sup>-2</sup>	0.12	0.036	<b>1.08x10<sup>-3</sup></b>	0.02	0.035	6.70x10 <sup>-1</sup>
	rs7839059	120045723	<i>TNFRSF11B</i>	23437003	0.42	A	0.02	0.017	1.94x10 <sup>-1</sup>	0.05	0.041	2.44x10 <sup>-1</sup>	0.03	0.037	3.58x10 <sup>-1</sup>
	rs2062375	120046973	<i>TNFRSF11B</i>	20548944	0.97	C	0.03	0.016	6.34x10 <sup>-2</sup>	0.08	0.036	<b>1.96x10<sup>-2</sup></b>	-0.01	0.035	8.37x10 <sup>-1</sup>
	<b>rs2062377</b> □	<b>120076601</b>	<b><i>TNFRSF11B</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>A</b>	0.02	0.016	2.74x10 <sup>-1</sup>	0.09	0.037	<b>1.46x10<sup>-2</sup></b>	-0.01	0.035	8.34x10 <sup>-1</sup>
	rs6469792	120077552	<i>TNFRSF11B</i>	19079262	0.74	C	0.01	0.016	5.88x10 <sup>-1</sup>	0.08	0.036	<b>1.90x10<sup>-2</sup></b>	0.01	0.035	8.47x10 <sup>-1</sup>
	rs11995824	120081881	<i>TNFRSF11B</i>	19801982	0.79	G	0.01	0.016	5.34x10 <sup>-1</sup>	0.08	0.036	<b>2.22x10<sup>-2</sup></b>	0.01	0.036	6.77x10 <sup>-1</sup>
	rs6469804	120114010	<i>TNFRSF11B</i>	18445777 & 19079262	0.88	A	0.02	0.016	3.03x10 <sup>-1</sup>	0.09	0.037	<b>9.92x10<sup>-3</sup></b>	0.00	0.035	9.38x10 <sup>-1</sup>
	rs6993813	120121419	<i>TNFRSF11B</i>	18445777 & 19079262	0.69	C	0.01	0.016	5.01x10 <sup>-1</sup>	0.09	0.036	<b>1.20x10<sup>-2</sup></b>	0.02	0.035	6.58x10 <sup>-1</sup>
13q14.11	<b>rs9533090</b> □	<b>41849449</b>	<b><i>AKAP11</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>T</b>	-0.02	0.016	3.36x10 <sup>-1</sup>	0.08	0.036	<b>1.71x10<sup>-2</sup></b>	0.00	0.037	9.42x10 <sup>-1</sup>
	rs9594738	41850145	<i>TNFSF11</i>	18445777 & 19079262	1.00	T	-0.02	0.016	3.37x10 <sup>-1</sup>	0.08	0.035	<b>1.95x10<sup>-2</sup></b>	0.01	0.037	8.46x10 <sup>-1</sup>
	rs9533093	41859597	<i>TNFSF11</i>	19079262	0.23	T	-0.02	0.018	2.60x10 <sup>-1</sup>	0.07	0.046	1.31x10 <sup>-1</sup>	-0.01	0.044	8.67x10 <sup>-1</sup>
	rs9594759	41930593	<i>TNFSF11</i>	18445777 & 19079262	0.68	T	-0.01	0.016	5.20x10 <sup>-1</sup>	0.03	0.036	3.75x10 <sup>-1</sup>	-0.04	0.037	3.06x10 <sup>-1</sup>
	rs1021188 □	42014133	<i>TNFSF11</i>	21124946 & 23437003	0.00	C	0.05	0.020	<b>9.21x10<sup>-3</sup></b>	0.04	0.056	5.27x10 <sup>-1</sup>	0.06	0.050	2.08x10 <sup>-1</sup>
18q21.33	<b>rs884205</b> □	<b>58205837</b>	<b><i>TNFRSF11A</i></b>	<b>19801982 &amp; 22504420</b>	<b>1.00</b>	<b>A</b>	0.05	0.018	<b>7.03x10<sup>-3</sup></b>	0.04	0.040	3.26x10 <sup>-1</sup>	0.02	0.041	6.53x10 <sup>-1</sup>
	rs3018362	58233073	<i>TNFRSF11A</i>	19079262	0.68	A	0.04	0.017	<b>2.91x10<sup>-2</sup></b>	0.02	0.036	6.15x10 <sup>-1</sup>	0.05	0.037	1.83x10 <sup>-1</sup>

Table showing association of previously reported RANK (*TNFRSF11A*), RANKL (*TNFSF11*) and OPG (*TNFRSF11B*) variants with Periosteal Circumference in ALSPAC (n=3382), GOOD (n=938) and Young Finns (n=1558). (POS) = position in the genome based on hg18; (GENE) = closest gene; (PMID) = accession number of the publication in Pubmed which described the association with BMD; (r<sup>2</sup>) = the pairwise LD estimate in CEU populations between the SNP in bold and all other SNPs in that locus; (EA) = effect allele; (β\*) = effect size; (SE) = standard error of β\*; (P) = P-value; (PMID) = accession number of the publication in Pubmed which described the association with BMD. \*Effect estimates expressed as adjusted SD per copy of the effect allele (EA). Note: rs9533090 □ is found upstream of *TNFSF11*, but is closest to *AKAP11*. □ - denotes the variants which were used to generate allele scores (i.e. independent signals).