



**Bone & Joint
Research**

Supplementary Material

10.1302/2046-3758.122.BJR-2022-0206.R1

Table i. List of the top 50 significant single nucleotide polymorphisms (SNPs) identified by integrating forearm bone mineral density from discovery genome-wide association study and regulatory SNP annotation data.

SNP	SNP-related regulatory elements	element-gene pairs	eQTL	Beta	P _{GWAS}
rs7776725	TADs CIRs	ENSG00000234985 FAM3C PTPRZ1	N	0.186	1.21E-25
rs12531355	TADs	FAM3C PTPRZ1	N	0.184	7.73E-25
rs718766	TADs	FAM3C PTPRZ1	Y	0.181	1.62E-24
rs56364616	circRNAs TADs	FAM3C PTPRZ1	N	0.181	2.95E-24
rs7807953	circRNAs TADs	FAM3C PTPRZ1	N	0.179	3.91E-24
rs917727	circRNAs TADs	FAM3C PTPRZ1	Y	0.180	4.09E-24
rs12539772	circRNAs TADs	FAM3C PTPRZ1	N	0.179	4.36E-24
rs7808155	circRNAs TADs	FAM3C PTPRZ1	N	0.179	4.37E-24
rs917726	circRNAs TADs	FAM3C PTPRZ1	Y	0.179	5.16E-24
rs2254595	circRNAs TADs CIRs	FAM3C PTPRZ1	Y	0.135	1.26E-17
rs28476487	circRNAs		N	0.274	1.54E-17
rs6965592	circRNAs CIRs	FAM3C	N	0.274	1.64E-17
rs28624478	circRNAs		N	0.273	2.20E-17
rs4727924	TADs CIRs	ENSG00000234985 FAM3C PTPRZ1	N	0.133	2.41E-17
rs7793554	TADs CIRs	ENSG00000234985 FAM3C PTPRZ1	N	0.134	3.43E-17
rs7807894	TADs	FAM3C PTPRZ1	N	0.132	4.37E-17
rs6950995	circRNAs TFBRs	RNU6-517P	N	0.269	5.31E-17
rs10252157	circRNAs		N	0.268	5.49E-17
rs10251982	circRNAs		N	0.268	5.64E-17
rs7808138	circRNAs TFBRs	RNU6-517P	N	0.269	5.81E-17
rs7779605	circRNAs		N	0.268	6.21E-17
rs78521632	circRNAs		N	0.268	7.61E-17
rs28532880	circRNAs		N	0.266	1.06E-16
rs10260631	circRNAs		N	0.264	1.37E-16
rs10244109	circRNAs		N	0.264	1.54E-16
rs10260002	circRNAs		N	0.264	1.57E-16
rs77667920	circRNAs		N	0.263	1.61E-16
rs10226602	circRNAs		N	0.263	1.62E-16

rs10235191	circRNAs		N	0.263	1.85E-16
rs28695392	circRNAs		N	0.262	1.86E-16
rs10277559	circRNAs		N	0.262	2.33E-16
rs10264879	circRNAs		N	0.260	2.59E-16
rs10274123	circRNAs		N	0.260	2.71E-16
rs6951173	circRNAs		N	0.260	2.74E-16
rs78272488	circRNAs		N	0.261	3.02E-16
rs77634630	circRNAs		N	0.251	4.68E-16
rs10232353	circRNAs		N	0.258	4.80E-16
rs10225539	circRNAs		N	0.258	5.01E-16
rs28477952	circRNAs		N	0.258	5.70E-16
rs78065645	circRNAs		N	0.258	6.01E-16
rs61327650	circRNAs		N	0.257	6.24E-16
rs60326700	circRNAs		N	0.259	6.60E-16
rs73433957	circRNAs		N	0.257	7.46E-16
rs10230185	circRNAs		N	0.256	7.59E-16
rs59353128	circRNAs		N	0.256	9.25E-16
rs79162867	circRNAs		N	0.301	2.13E-15
rs10277676	circRNAs		N	0.241	4.86E-15
rs10215022	circRNAs		N	0.239	1.16E-14
rs76272871	circRNAs		N	0.231	1.37E-14
rs80183787	circRNAs		N	0.226	2.74E-14

CIRs, chromatin interactive regions; circRNAs, circular RNAs regions; eQTL, expression quantitative traits locus; GWAS, genome-wide association study; N, no; SNP, single nucleotide polymorphism; TADs, topologically associated domains; TFBRs, transcription factor binding regions; Y, yes.

Table ii. List of the top 50 significant single nucleotide polymorphisms (SNPs) identified by integrating femoral neck bone mineral density from discovery genome-wide association study and regulatory SNP annotation data.

SNP	SNP-related regulatory elements	element-gene pairs	eQTL	Beta	P _{GWAS}
rs6894139	lncRNAs		N	-0.077	1.43E-23
rs7725337	circRNAs lncRNAs		N	-0.066	9.05E-17
rs4916669	circRNAs lncRNAs		N	-0.065	1.34E-16
rs10069604	circRNAs lncRNAs		N	-0.065	1.46E-16
rs6452812	circRNAs		N	-0.065	1.81E-16
rs7714474	circRNAs		N	-0.065	2.17E-16
rs7728690	circRNAs		N	-0.065	2.18E-16
rs10070540	circRNAs		N	-0.065	2.24E-16
rs7721818	circRNAs		N	-0.064	2.92E-16
rs4020801	circRNAs		Y	-0.064	3.09E-16
rs13187246	circRNAs		N	-0.064	3.46E-16
rs6865194	CIRs	MEF2C-AS1	N	-0.064	3.79E-16
rs6965122	TFBRs	C7orf76	N	-0.065	1.08E-15
rs6452809	CIRs	MEF2C-AS1	N	-0.063	1.13E-15
rs4916744	CIRs	MEF2C-AS1	N	-0.063	1.18E-15
rs34636218	CIRs	MEF2C-AS1	N	-0.063	1.29E-15
rs4916738	lncRNAs		N	-0.063	1.41E-15
rs957629	lncRNAs		Y	-0.063	1.83E-15
rs6452808	CIRs	MEF2C-AS1	N	-0.063	1.99E-15
rs1485307	TFBRs	COLEC10	Y	0.062	2.49E-15
rs4916739	lncRNAs		N	-0.062	3.02E-15
rs4916745	CIRs	MEF2C-AS1	N	-0.062	3.06E-15
rs4916665	CIRs	MEF2C-AS1	N	-0.062	3.09E-15
rs2566752	circRNAs		Y	0.062	3.65E-15
rs7781370	TFBRs	C7orf76	N	-0.064	3.89E-15
rs13154117	lncRNAs		N	-0.062	4.29E-15
rs16931831	TADs	CALCB C11orf58 SOX6	N	0.080	4.41E-15
rs7798294	TFBRs	C7orf76	N	-0.063	4.51E-15
rs4383904	circRNAs		N	-0.063	4.60E-15
rs10040237	lncRNAs		N	-0.062	4.84E-15
rs4727338	circRNAs		N	-0.063	5.00E-15
rs12485899	TADs	ULK4	N	-0.060	5.94E-15
rs7632244	TADs	ULK4	N	-0.060	8.78E-15
rs10766280	TADs	CALCB C11orf58 SOX6	N	0.073	9.14E-15
rs4437116	TADs	ULK4	N	-0.059	1.12E-14
rs17280306	TADs	ULK4	N	-0.059	1.17E-14
rs7933516	TADs	CALCB C11orf58 SOX6	N	0.072	1.29E-14
rs417183	TADs	ULK4	Y	-0.059	1.31E-14
rs4757354	TADs	CALCB C11orf58 SOX6	N	0.072	1.40E-14
rs7609599	TADs	ULK4	N	-0.059	1.47E-14

rs4729260	circRNAs		N	-0.062	1.49E-14
rs35135108	TADs	ULK4	N	-0.059	1.58E-14
rs6762550	TADs	ULK4	N	-0.059	1.61E-14
rs2062377	TFBRs	COLEC10	Y	0.060	1.64E-14
rs378422	TADs	ULK4	Y	-0.059	1.66E-14
rs7621892	TADs	ULK4	N	-0.059	1.79E-14
rs10741684	TADs	CALCB C11orf58 SOX6	N	0.072	1.84E-14
rs34695788	TADs	ULK4	N	-0.059	2.28E-14
rs4974070	TADs	ULK4	N	-0.059	2.33E-14
rs11720396	TADs	ULK4	N	-0.059	2.62E-14

CIRs, chromatin interactive regions; circRNAs, circular RNAs regions; eQTL, expression quantitative traits locus; GWAS, genome-wide association study; N, no; SNP, single nucleotide polymorphism; TFBRs, transcription factor binding regions; TADs, topologically associated domains; Y, yes.

Table iii. List of the top 50 significant single nucleotide polymorphisms (SNPs) identified by integrating lumbar spine bone mineral density from genome-wide association study and regulatory SNP annotation data.

SNP	SNP-related regulatory elements	element-gene pairs	eQTL	Beta	P _{GWAS}
rs9533094	TADs	CCDC122 DCLK1	N	-0.083	2.80E-20
rs8001611	TADs	CCDC122 DCLK1	N	-0.083	3.21E-20
rs9533095	circRNAs TADs	CCDC122 DCLK1	N	-0.082	3.28E-20
rs9594738	TADs	CCDC122 TPTE2P5	N	-0.082	3.63E-20
rs2220189	TFBRs	COLEC10	Y	0.083	4.25E-20
rs9533090	TADs	CCDC122 TPTE2P5	N	-0.082	5.15E-20
rs2566752	circRNAs		Y	0.083	1.49E-19
rs2062377	TFBRs	COLEC10	Y	0.081	6.61E-19
rs1485307	TFBRs	COLEC10	Y	0.080	9.60E-19
rs7006553	CIRs	ENSG00000253603	N	0.078	9.99E-18
rs10955915	TFBRs	TNFRSF11B	N	0.077	1.21E-17
rs10505348	CIRs	TNFRSF11B	N	0.077	1.37E-17
rs72670452	circRNAs		N	0.085	5.82E-17
rs2033344	circRNAs		Y	0.085	6.24E-17
rs57748040	circRNAs		N	0.085	6.52E-17
rs2033345	circRNAs		Y	0.084	7.74E-17
rs17130567	circRNAs		N	0.084	9.72E-17
rs12568456	circRNAs		N	0.082	3.27E-16
rs7554551	circRNAs		N	0.074	1.29E-15
rs2026749	circRNAs		Y	-0.069	2.22E-14
rs17457561	TADs	CCDC122 DCLK1	N	-0.079	3.74E-14
rs61960926	circRNAs TADs	CCDC122 DCLK1	N	-0.079	3.98E-14
rs2566755	circRNAs		Y	0.082	4.01E-14
rs7807953	circRNAs TADs	FAM3C PTPRZ1	N	0.075	4.11E-14
rs12539772	circRNAs TADs	FAM3C PTPRZ1	N	0.075	5.80E-14
rs7808155	circRNAs TADs	FAM3C PTPRZ1	N	0.075	6.00E-14
rs1430742	circRNAs		Y	0.081	6.30E-14
rs6677666	circRNAs		N	0.073	9.44E-14
rs2291467	circRNAs		Y	-0.077	9.64E-14
rs917726	circRNAs TADs	FAM3C PTPRZ1	Y	0.074	1.19E-13
rs56364616	circRNAs TADs	FAM3C PTPRZ1	N	0.074	1.49E-13
rs2772300	circRNAs		Y	0.073	1.52E-13
rs917727	circRNAs TADs	FAM3C PTPRZ1	Y	0.074	1.52E-13
rs11228240	circRNAs		N	-0.075	1.58E-13
rs10896328	TADs	CHKA PPP6R3	N	-0.081	2.09E-13
rs718766	TADs	FAM3C PTPRZ1	Y	0.073	2.10E-13
rs1367447	circRNAs		Y	0.083	2.34E-13
rs12531355	TADs	FAM3C PTPRZ1	N	0.074	3.03E-13
rs67101048	circRNAs TADs	CHKA PPP6R3	N	-0.075	3.17E-13
rs7106339	TADs	CHKA PPP6R3	N	-0.075	3.26E-13
rs4084149	circRNAs TADs	CTTN PPP6R3	Y	-0.075	3.43E-13
rs55883802	circRNAs TADs	CHKA PPP6R3	N	-0.075	3.45E-13
rs7925275	circRNAs TADs	CTTN PPP6R3	N	-0.075	3.67E-13
rs1357651	TADs	AMPH ELMO1	Y	-0.068	3.75E-13

rs11228268	circRNAs TADs	CTTN PPP6R3	N	-0.075	3.83E-13
rs6591344	circRNAs		N	-0.075	3.92E-13
rs7101691	TADs	CHKA PPP6R3	N	-0.075	4.26E-13
rs66752716	circRNAs TADs	CHKA PPP6R3	N	-0.075	4.44E-13
rs55953412	circRNAs		N	-0.075	4.51E-13
rs11228262	circRNAs TADs	CHKA PPP6R3	N	-0.075	4.53E-13

CIRs, chromatin interactive regions; circRNAs, circular RNAs regions; eQTL, expression quantitative traits locus; GWAS, genome-wide association study; N, no; SNP, single nucleotide polymorphism; TADs, topologically associated domains; TFBRs, transcription factor binding regions; Y, yes.

Table iv. List of the top 50 significant single nucleotide polymorphisms (SNPs) from replication genome-wide association study dataset (analyzed by rSNPBase analysis).

SNP	SNP-related regulatory elements	element-gene pairs	eQTL	P _{GWAS}
rs193001539	circRNAs,CIRs	MTHFS	N	8.79E-33
rs148733427	circRNAs		N	5.21E-32
rs190012265	circRNAs,TADs	ATXN2, ALDH2, SH2B3, ENSG00000257452, TCHP, MYO1H, SART3, ACAD10	N	5.32E-32
rs567400816	TFBRs	ENSG00000259479	N	1.73E-31
rs143270695	CIRs	ENSG00000270458	N	2.63E-31
rs140630159	TADs	SOS2	N	3.11E-31
rs139787135	circRNAs,TADs	ASS1, LAMC3, RAPGEF1	N	5.05E-31
rs140275387	circRNAs		N	7.95E-31
rs75359995	circRNAs,CIRs	L2HGDH, ATL1, ATP5S	N	9.48E-31
rs563804550	circRNAs,CIRs,lncRNAs	SYNCRIP	N	2.42E-30
rs544911771	TADs	STARD9, ENSG00000259536	N	2.53E-30
rs148031129	circRNAs,CIRs	HSPA4	N	3.22E-30
rs114280518	circRNAs		N	4.44E-30
rs150185395	circRNAs		N	9.52E-30
rs111304240	circRNAs		N	9.65E-30
rs111674570	circRNAs		N	1.00E-29
rs528492209	circRNAs		N	1.00E-29
rs573309789	circRNAs		N	1.09E-29
rs112954732	circRNAs		N	1.09E-29
rs148806100	circRNAs,CIRs	VCPKMT	N	1.12E-29
rs113769894	circRNAs		N	1.12E-29
rs148856758	circRNAs		N	1.33E-29
rs564162248	circRNAs		N	1.34E-29
rs564895997	circRNAs		N	1.34E-29
rs543788091	circRNAs		N	1.47E-29
rs113031788	circRNAs		N	1.48E-29
rs533228897	circRNAs		N	1.48E-29
rs113480545	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	1.57E-29

rs112708852	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	1.67E-29
rs556791626	CIRs	ENSG00000253940	N	1.75E-29
rs113922671	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	1.78E-29
rs528702153	circRNAs		N	1.91E-29
rs147022702	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.09E-29
rs113804302	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.11E-29
rs113545620	circRNAs		N	2.28E-29
rs112428487	circRNAs		N	2.48E-29
rs566304266	circRNAs		N	2.61E-29
rs113387374	circRNAs,TADs,CIRs	TNKS2-AS1, BTAF1, HTR7, IDE, HELLS	N	2.61E-29
rs113923595	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.68E-29
rs112612696	circRNAs,TADs,CIRs	FGFBP3, BTAF1, HTR7, IDE, HELLS	N	2.68E-29
rs113264437	TADs	BTAF1, HTR7, IDE, HELLS	N	2.69E-29
rs113481475	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.70E-29
rs113786188	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.70E-29
rs112165562	circRNAs,TADs	BTAF1, HTR7, IDE, HELLS	N	2.82E-29
rs76294407	circRNAs		N	1.58E-28
rs561772537	circRNAs,TFBRs	ENSG00000238853	N	3.43E-28
rs183968453	circRNAs		N	6.31E-28
rs112005839	circRNAs		N	7.40E-28
rs115441706	circRNAs		N	8.12E-28
rs148872136	circRNAs		N	1.15E-27

CIRs, chromatin interactive regions; circRNAs, circular RNAs regions; eQTL, expression quantitative traits locus; GWAS, genome-wide association study; N, no; SNP, single nucleotide polymorphism; TADs, topologically associated domains; TFBRs, transcription factor binding regions; Y, yes.