Supplementary Table 1. Other SNPs with strong association (P<1.0E-04) with spine bone size

SNP ID	Chr.	Position	Role	Gene	Allele[1]	MAF	β	P[2]	MAF	β[3]	P	β	P	P(F)	P(R)	Q	I
						Bone size — Initial Discovery			Bone size — Replication			Height — Chinese		Meta-analysis[4]			
rs2955948	11p13	34210736	intron	ABTB2	T/C	0.02	-1.13	9.40E-05	0.02	-0.57	0.4	-0.5	8.7E-02	8.5E-05	8.5E-05	4.4E-01	0.0
rs2141075	7q32.1	1.29E+08	intron	AHCYL2	C/T	0.25	-0.82	5.50E-05	0.24	-0.21	0.34	-0.56	8.3E-03	3.0E-04	8.9E-02	4.1E-02	76.1
rs4895102	3q13.11	1.06E+08	upstream	ALCAM	T/A	0.36	1.07	2.70E-05	0.36	-0.05	0.8	0.86	8.7E-04	1.8E-02	3.7E-01	5.0E-04	91.8
rs4144913	3q13.11	1.06E+08	upstream	ALCAM	G/C	0.38	1.08	2.80E-05	0.38	0	0.99	0.8	2.0E-03	1.2E-02	3.3E-01	7.0E-04	91.2
rs3947974	3q13.11	1.06E+08	upstream	ALCAM	C/A	0.39	1.03	7.00E-05	0.38	-0.05	0.79	0.76	3.6E-03	3.2E-02	3.8E-01	7.0E-04	91.2
rs2961359	3q13.11	1.06E+08	upstream	ALCAM	C/G	0.43	1.13	7.90E-05	0.43	0.2	0.29	0.64	2.8E-02	2.3E-03	1.7E-01	6.2E-03	86.7
rs1004944	3q13.11	1.06E+08	upstream	ALCAM	T/C	0.38	1.17	9.30E-05	0.38	-0.26	0.17	0.65	3.2E-02	3.3E-01	5.4E-01	1.0E-04	93.9
rs2961318	3q13.11	1.06E+08	upstream	ALCAM	C/T	0.43	1.11	9.80E-05	0.43	0.19	0.3	0.66	2.4E-02	2.7E-03	1.7E-01	6.9E-03	86.3
rs1074464	12p13.33	456668	intron	B4GALNT3	C/T	0.5	-0.85	2.90E-05	0.5	0.32	0.09	-0.4	5.5E-02	9.6E-02	6.5E-01	0.0E+00	94.3
rs7311655	12p13.33	456088	intron	B4GALNT3	G/T	0.49	-0.81	8.20E-05	0.49	0.27	0.16	-0.38	7.3E-02	9.4E-02	6.2E-01	1.0E-04	93.2
rs4727715	7q31.1	1.08E+08	downstream	IMMP2L	A/G	0.45	1.42	9.70E-05	0.45	0.06	0.73	0.7	6.3E-02	3.7E-02	3.0E-01	9.0E-04	91.0
rs1751779	9q21.11	71606733	upstream	PTAR1	C/T	0.08	-1.62	3.30E-05	0.08	0.12	0.74	-0.88	2.6E-02	1.1E-02	3.9E-01	9.0E-04	90.9
rs6799546	3p12.1	84021714	upstream	CADM2	G/T	0.49	1.08	3.70E-05	0.49	-0.24	0.2	0.4	5.7E-03	1.8E-01	5.3E-01	0.0E+00	94.1
rs6777459	3p12.1	84020038	upstream	CADM2	T/C	0.49	1.08	4.00E-05	0.48	-0.15	0.42	0.76	4.4E-03	8.4E-02	4.6E-01	1.0E-04	93.2
rs6777545	3p12.1	84020084	upstream	CADM2	A/G	0.49	1.07	4.20E-05	0.48	-0.19	0.3	0.75	5.1E-03	1.2E-01	5.0E-01	1.0E-04	93.6
rs9855708	3p14.2	62595803	intron	CADPS	G/A	0.05	1.77	8.00E-05	0.05	-0.21	0.63	1.27	4.8E-03	1.8E-02	4.3E-01	1.4E-03	90.2
rs1915087	3q13.33	1.23E+08	3UTR	CD86	C/T	0.32	-0.78	7.90E-05	0.32	0.11	0.58	-0.29	1.5E-01	1.5E-02	4.5E-01	1.6E-03	90.0
rs6058847	20q11.21	30787796	intron	COMMD7	C/T	0.25	-0.91	6.10E-06	0.24	-0.1	0.67	-0.58	5.8E-03	2.6E-04	2.1E-01	6.2E-03	86.7
rs6058845	20q11.21	30787580	intron	COMMD7	T/G	0.24	-0.91	6.60E-06	0.23	0.02	0.94	-0.56	7.3E-03	8.9E-04	3.3E-01	2.2E-03	89.4
rs6057632	20q11.21	30783502	intron	COMMD7	A/G	0.24	-0.9	8.60E-06	0.23	0.02	0.95	-0.57	6.7E-03	1.0E-03	3.3E-01	2.5E-03	89.1
rs6058840	20q11.21	30782777	intron	COMMD7	T/A	0.24	-0.9	9.10E-06	0.23	0.02	0.93	-0.55	8.5E-03	1.1E-03	3.3E-01	2.4E-03	89.2
rs6057630	20q11.21	30782398	intron	COMMD7	A/G	0.24	-0.87	1.60E-05	0.23	0.06	0.8	-0.56	7.7E-03	2.1E-03	3.7E-01	2.2E-03	89.4
rs6057628	20q11.21	30772345	intron	COMMD7	C/T	0.24	-0.87	1.90E-05	0.23	0.03	0.91	-0.56	7.8E-03	1.9E-03	3.4E-01	3.1E-03	88.6
rs7167013	15q23	66615195	upstream	CORO2B	T/C	0.07	-2.37	8.20E-05	0.07	N/A	N/A	-0.53	3.9E-01	N/A	N/A	N/A	N/A
rs32121	5p15.2	11403359	intron	CTNND2	G/A	0.33	-0.8	9.10E-05	0.34	-0.06	0.77	-0.39	6.0E-02	2.6E-03	2.4E-01	1.1E-02	84.4
rs6601633	8p23.1	11842582	downstream	DEFB137	T/C	0.45	2.27	4.00E-05	0.45	-0.15	0.43	1.78	1.9E-03	5.6E-01	4.1E-01	0.0E+00	94.2
rs1125018	8p23.1	11844985	downstream	DEFB137	T/A	0.42	2.14	6.10E-05	0.42	-0.09	0.63	1.68	2.6E-03	3.7E-01	3.9E-01	1.0E-04	93.6
rs4840599	8p23.1	11842789	downstream	DEFB137	T/C	0.45	2.16	8.00E-05	0.45	-0.14	0.45	1.68	3.1E-03	5.6E-01	4.1E-01	1.0E-04	93.7
rs821589	1q42.2	2.3E+08	intron	DISC1	T/C	0.09	-1.02	3.50E-05	0.08	-0.07	0.85	-0.29	2.6E-01	4.7E-04	2.3E-01	2.5E-02	80.2
rs7963695	12p13.2	12587000	intron	DUSP16	A/C	0.09	0.99	7.20E-05	0.09	0.36	0.28	0.3	2.4E-01	1.3E-04	2.4E-02	1.2E-01	57.7
rs5764236	22q13.2	42446194	intron	EFCAB6	G/A	0.42	-1.3	2.70E-06	0.42	0.22	0.28	-0.81	4.8E-03	6.3E-02	4.8E-01	0.0E+00	95.0
rs174583	11q12.2	61366326	intron	FADS2	A/G	0.34	-0.77	8.10E-05	0.35	-0.36	0.07	-0.98	1.1E-06	4.2E-05	5.6E-03	1.4E-01	53.8
rs9301947	13q31.3	93714027	intron	GPC6	T/C	0.21	0.89	2.70E-05	0.21	0.04	0.86	0.74	7.1E-04	1.3E-03	2.7E-01	6.8E-03	86.4
rs9561522	13q31.3	93714245	intron	GPC6	T/C	0.21	0.89	3.30E-05	0.21	0.05	0.83	0.77	5.0E-04	1.4E-03	2.6E-01	7.5E-03	86.0
rs7909228	10q26.13	1.25E+08	upstream	HMX3	A/G	0.37	-1.25	8.60E-05	0.37	0.36	0.08	-1.28	9.0E-05	5.4E-01	5.9E-01	0.0E+00	94.5
rs2136768	7q31.31	1.18E+08	upstream	KCND2	G/C	0.44	0.99	1.30E-05	0.44	-0.08	0.69	0.26	2.7E-01	1.2E-02	4.0E-01	3.0E-04	92.4
rs1176712	7q31.31	1.18E+08	upstream	KCND2	C/T	0.44	0.97	1.50E-05	0.44	-0.07	0.71	0.23	3.1E-01	1.2E-02	3.9E-01	4.0E-04	92.1
rs1771631	8q22.1	95633516	intron	KIAA1429	C/T	0.23	1.58	5.50E-05	0.23	0.46	0.04	1.19	3.2E-03	1.4E-04	7.9E-02	1.3E-02	83.8
rs4822416	22q11.23	22146428	downstream	IGLL1	T/C	0.4	-1.11	6.70E-05	0.4	-0.21	0.27	-0.52	6.8E-02	1.5E-03	1.6E-01	7.6E-03	86.0
rs513069	11q24.1	1.22E+08	intron	LOC399995	T/C	0.32	-0.85	6.70E-05	0.32	-0.15	0.47	-0.36	9.4E-02	1.0E-03	1.6E-01	1.7E-02	82.6
rs512932	11q24.1	1.21E+08	intron	LOC399995	C/T	0.22	-0.9	9.90E-05	0.22	-0.15	0.52	-0.32	1.7E-01	1.4E-03	1.7E-01	2.0E-02	81.5
rs2025685	10p15.3	2321425	upstream	PFKP	G/A	0.47	0.82	3.80E-05	0.46	-0.12	0.51	0.54	7.9E-03	1.9E-02	4.6E-01	5.0E-04	91.7
rs1836868	16q21	62625490	upstream	CDH8	G/T	0.45	0.91	9.20E-05	0.46	-0.19	0.31	0.21	3.7E-01	9.2E-02	5.2E-01	2.0E-04	92.6
rs1083663	11p12	36890059	downstream	LRRC4C	A/G	0.31	0.84	8.50E-05	0.32	0.02	0.93	0.59	7.8E-03	5.6E-03	3.0E-01	5.1E-03	87.3
rs260140	13q21.32	66540918	intron	PCDH9	T/C	0.11	-2.46	4.30E-05	0.11	0.18	0.56	-1.81	2.6E-03	1.8E-01	4.1E-01	1.0E-04	93.9
rs6887891	5q11.2	50809847	upstream	PELO	T/A	0.36	-1.06	4.90E-05	0.37	0.1	0.61	-1.3	9.5E-07	4.1E-02	4.2E-01	4.0E-04	92.1
rs6610660	Xp11.4	41854099	upstream	CASK	G/A	0.05	-1.01	9.80E-05	0.05	-0.28	0.54	-0.69	8.0E-02	2.2E-04	3.6E-02	1.6E-01	48.6
rs1775814	11q14.2	86104990	upstream	PRSS23	C/T	0.17	1.13	6.20E-05	0.17	-0.35	0.16	0.56	5.3E-02	1.1E-01	6.1E-01	1.0E-04	93.6
rs413553	9p23	10078517	intron	PTPRD	T/C	0.44	1.31	3.00E-05	0.44	-0.38	0.05	1	1.9E-03	5.9E-01	6.0E-01	0.0E+00	95.3
rs7470838	9p23	9952381	intron	PTPRD	G/A	0.28	-0.79	8.70E-05	0.28	0.02	0.92	-0.38	6.9E-02	5.2E-03	3.4E-01	5.6E-03	87.0
rs1891203	1q42.13	2.27E+08	upstream	RAB4A	G/T	0.21	-1.35	5.70E-05	0.21	-0.23	0.32	-0.58	9.2E-02	1.9E-03	1.7E-01	5.8E-03	86.9
rs1779818	8q22.1	95406477	downstream	RAD54B	C/T	0.05	1.65	6.20E-05	0.04	0.74	0.11	1.16	6.6E-03	4.8E-05	8.0E-03	1.4E-01	55.1
rs2014429	11p13	31897611	upstream	RCN1	A/G	0.29	0.83	3.60E-05	0.3	-0.01	0.98	0.66	1.2E-03		3.2E-01	3.6E-03	88.2
rs6484545	11p13	31912507	upstream	RCN1	A/T	0.22	0.79	9.90E-05	0.22	-0.1	0.66	0.71	5.8E-04	7.9E-03	4.3E-01	3.8E-03	88.0
rs2827909	21q21.2	23442973	intron	RPL13A	A/C	0.15	0.85	9.10E-05	0.15	0.02	0.94	0.64	4.6E-03	2.2E-03	2.8E-01	1.4E-02	83.3
rs706922	6q21	1.14E+08	upstream	MARCKS	G/A	0.1	-2.39	9.90E-05	0.1	0.02	0.96	-0.97	1.2E-01	8.5E-02	3.5E-01	5.0E-04	91.9
rs1696074	16p13.12	12815810	downstream	SNORA27	A/G	0.03	-0.97	3.60E-05	0.03	-0.86	0.14	-0.71	2.7E-03	1.1E-05	1.1E-05	8.6E-01	0.0
rs4012246	3q27.3	1.88E+08	intron	ST6GAL1	C/T	0.43	-0.86	5.60E-05	0.43	-0.07	0.72	-0.45	3.8E-02	2.8E-03	2.4E-01	6.1E-03	86.7
rs1189992	2q22.1	1.38E+08	intron	THSD7B	C/T	0.08	2.78	9.90E-05	0.08	-0.21	0.55	1.57	2.8E-02	2.4E-01	4.1E-01	2.0E-04	93.0
rs1162906	14q32.11	90220389	intron	TTC7B	T/C	0.15	1.27	9.50E-05	0.15	0.48	0.07	1.06	1.3E-01	1.0E-04	3.0E-02	6.0E-02	71.7
rs1699957	Xq25	1.29E+08	upstream	UTP14A	A/T	0.02	0.8	1.10E-05	0.02	0.26	0.69	0.37	4.9E-02	1.4E-05	1.4E-05	4.3E-01	0.0
rs926598	Xq25	1.29E+08	upstream	UTP14A	C/G	0.02	0.78	1.60E-05	0.02	0.18	0.8	0.4	9.2E-02	6.2E-05	6.2E-05	3.9E-01	0.0
rs636493	20q13.12	44543741	intron	ZNF840	G/A	0.17	2.1	8.80E-05	0.16	-0.26	0.31	0.81	1.2E-01	4.3E-01	4.6E-01	1.0E-04	93.7

1. The first allele represents the minor allele of each SNP.

2. P values after correction of population stratification: EIGENSTRAT was employed to calculate the principal components and the ten default main eigenvectors were used as covariate to adjust BS.

3. The direction of effect indicated by β is calculated for minor allele.

4. Meta-analysis for initial discovery and replication studies for bone size was performed with the command "--meta-analysis" in PLINK. P(F): Fixed-effects meta-analysis P-value; P(R):Random-effects meta-analysis P-value; Q: P-value for Cochrane's Q statistic; I: I2 heterogeneity index.