Supplemental Data

Genome-wide Association and Follow-Up Replication Studies

Identified *ADAMTS18* and *TGFBR3* as Bone Mass

Candidate Genes in Different Ethnic Groups

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Figure S1. The LD Structure Covering *ADAMTS18* SNPs rs11859065, rs11864477, rs16945612 and rs11860781 in HapMap CEU Sample

R-squared (r^2) value was used to denote LD status. Color scheme is: $r^2 = 0$: white; $0 < r^2 < 1$: shades of grey; $r^2 = 1$: black.
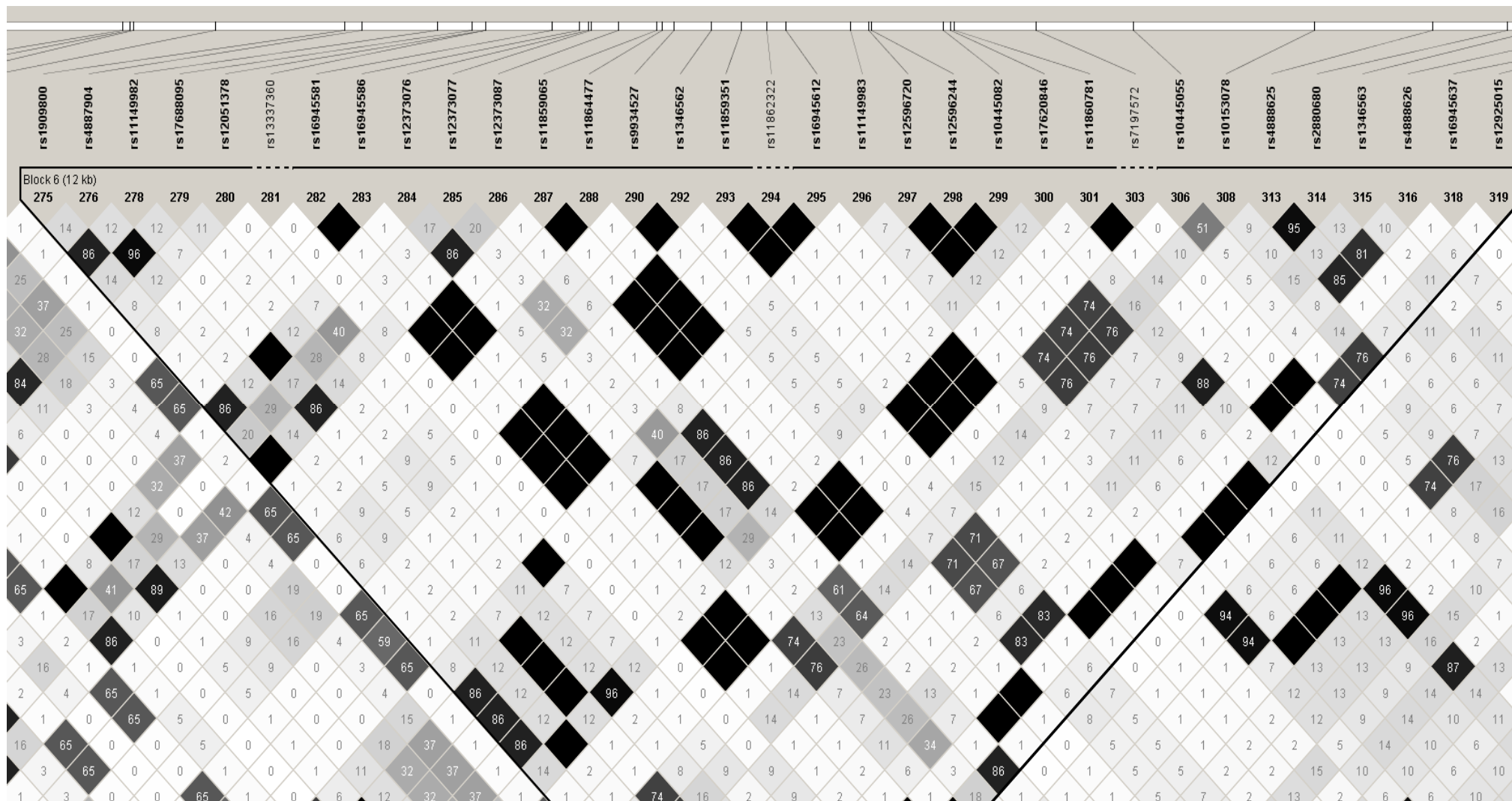
Figure S2. The LD Structure Covering *ADAMTS18* SNPs rs11859065, rs11864477, rs16945612 and rs11860781 in HapMap CHB Sample

Figure S3. The LD Structure Covering *ADAMTS18* SNPs rs11859065, rs11864477, rs16945612 and rs11860781 in HapMap YRI Sample
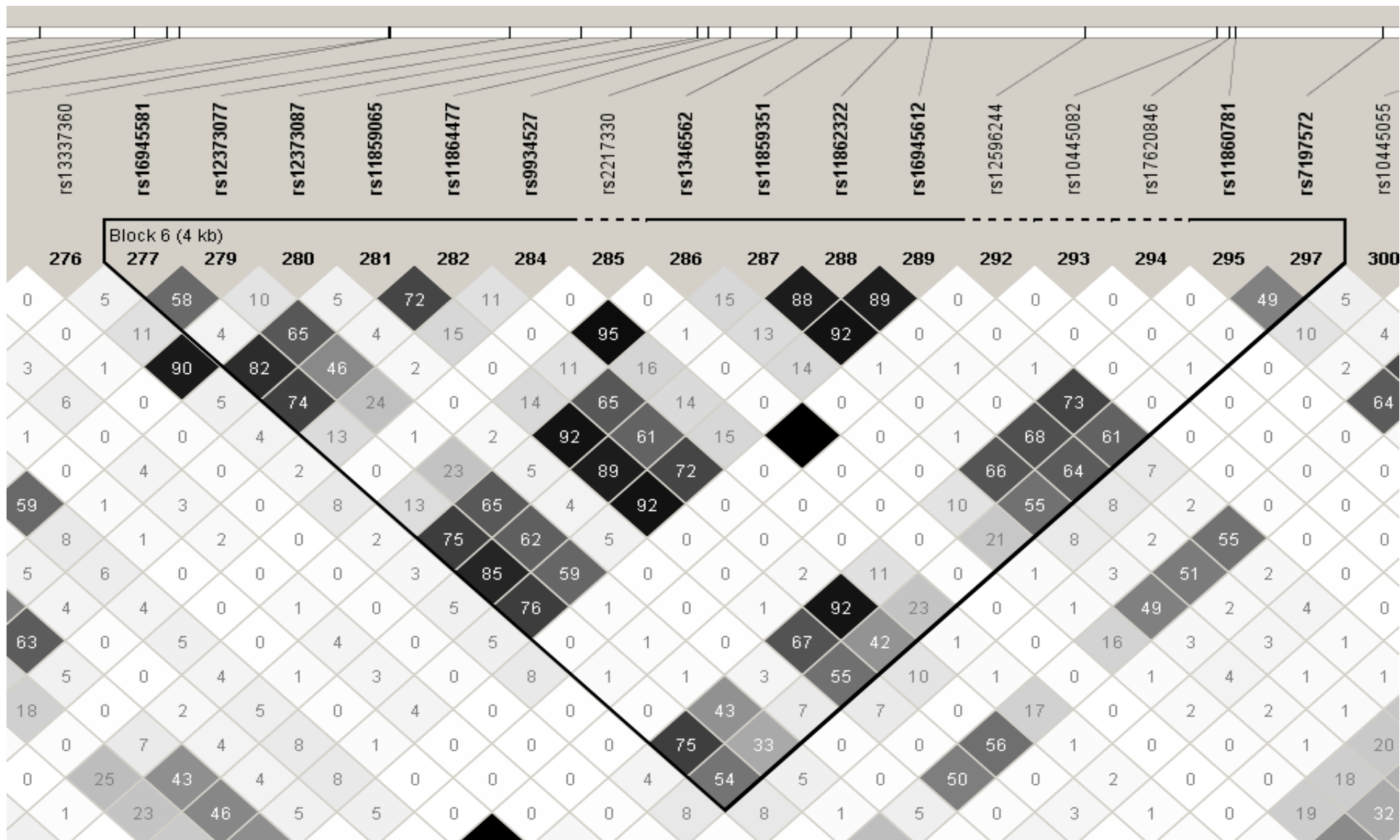
Figure S4. NCBI GEO Profiles Showing Differentially Expressed *ADAMTS18* in Normal Fracture and Non-union Fracture Subjects

Title: GDS368 / 42200_at / *ADAMTS18* / Homo sapiens
Summary: Identification of mechanisms leading to lack of skeletal repair in non-union fractures. Non-union fractures do not heal six months after injury and may cause advanced arthritis or loss of limb function. Normal and non-union callous bone samples examined.

Figure S5. NCBI GEO Profiles Showing Differentially Expressed *TGFBR3* in Normal Fracture and Non-union Fracture Subjects

Title: GDS367 / 1897_at / *TGFBR3* / Homo sapiens
Summary: Identification of mechanisms leading to lack of skeletal repair in non-union fractures. Non-union fractures do not heal six months after injury and may cause advanced arthritis or loss of limb function. Normal and non-union callous bone samples examined.
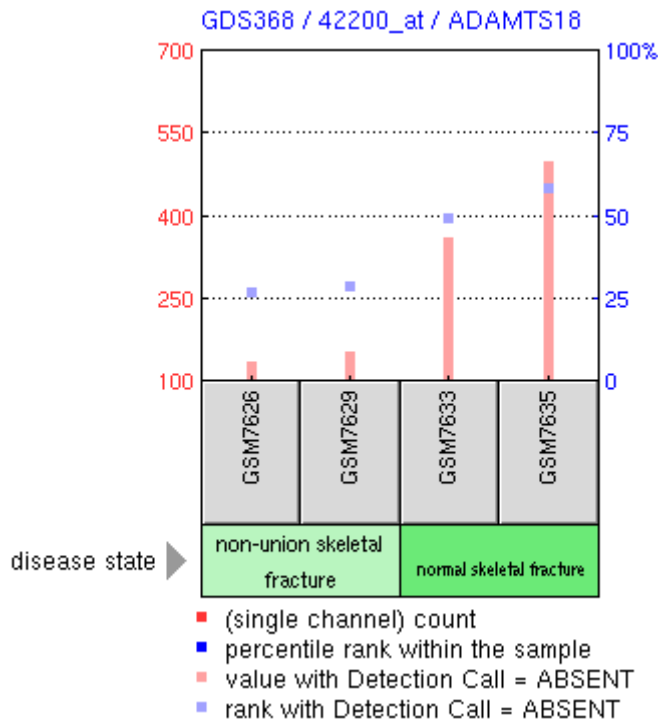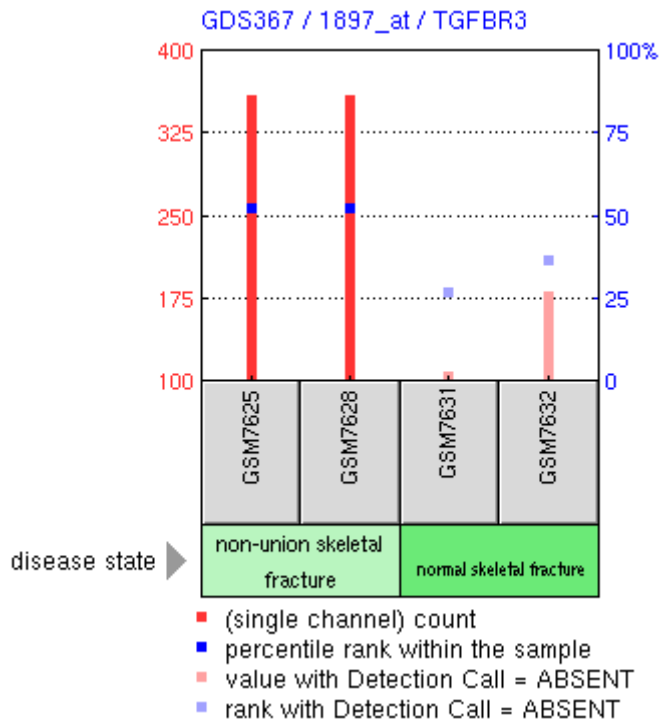
Table S1. Information of the Analyzed *ADAMTS18* SNPs and the p Values for Their Single-SNP and Sliding Window Association with Hip BMD in the Female Sample

SNP	Name	Position	Role	Allele[a]	MAF[b]	MAF[c]	P value[d]	P value[e]
1	rs2343047	75867997	3' UTR	C/A	0.434	0.356	0.811	0.851
2	rs17701900	75868793	3' UTR	C/T	0.137	0.186	0.490	0.830
3	rs7202055	75868813	3' UTR	T/C	0.192	0.200	0.452	0.854
4	rs17701924	75869296	3' UTR	A/C	0.204	0.186	0.923	0.355
5	rs17712821	75870261	3' UTR	G/T	0.135	0.183	0.671	0.355
6	rs12930139	75870453	3' UTR	A/G	0.135	0.183	0.699	0.355
7	rs17712826	75871382	3' UTR	T/C	0.177	0.200	0.431	0.355
8	rs17712844	75871485	3' UTR	C/G	0.135	0.183	0.613	0.355
9	rs12918088	75872617	3' UTR	T/C	0.135	0.175	0.553	0.028
10	rs16945428	75873761	3' UTR	T/C	0.109	0.161	0.158	0.028
11	rs889705	75874898	Exon23	G/C	0.153	0.183	0.914	0.493
12	rs889706	75875092	Exon23	C/T	0.158	0.183	0.520	0.393
13	rs1820253	75876072	Intron22	C/T	0.261	0.385	0.527	0.461
14	rs12925274	75878016	Intron22	G/T	0.109	0.167	0.138	0.461
15	rs4888617	75878059	Intron22	T/C	0.012	0.008	0.627	0.096
16	rs4887902	75879447	Intron22	C/A	0.010	0.018	0.524	0.180
17	rs17769706	75879810	Intron22	C/T	0.040	0.033	0.186	0.274
18	rs17769712	75880000	Intron22	G/A	0.109	0.169	0.136	0.534
19	rs11643318	75880258	Intron22	G/C	0.445	0.483	0.407	0.591
20	rs3743749	75880736	exon22	C/G	0.158	0.192	0.265	0.734
21	rs17769754	75885362	Intron17	T/A	0.122	0.167	0.244	0.905
22	rs1025315	75893430	Intron17	A/G	0.039	0.033	0.196	0.141
23	rs17769870	75893980	Intron17	T/C	0.113	0.158	0.123	0.083
24	rs8053462	75897582	Intron17	C/T	0.078	0.050	0.611	0.734
25	rs16945498	75902690	Intron17	T/G	0.013	0.000	0.208	0.555
26	rs2650911	75903148	Intron17	A/G	0.481	0.375	0.090	0.141
27	rs17770036	75903185	Intron17	C/T	0.253	0.150	0.075	0.577
28	rs965382	75903352	Intron17	C/T	0.217	0.225	0.744	0.171
29	rs1428842	75903575	Intron17	T/C	0.011	0.000	0.221	0.201
30	rs11640996	75903589	Intron17	G/C	0.237	0.150	0.053	0.202
31	rs2562122	75905043	Intron17	C/T	0.134	0.087	0.971	0.682
32	rs2562125	75907154	Intron17	C/T	0.493	0.397	0.029	0.156
33	rs9746086	75907584	Intron17	T/A	0.409	0.352	0.019	0.201
34	rs9746317	75912063	Intron15	A/G	0.138	0.167	0.661	0.682
35	rs274520	75912792	Intron14	A/G	0.075	0.042	0.680	0.156
36	rs8044883	75915465	Intron13	T/C	0.437	0.367	0.039	0.156
37	rs8059032	75915970	Intron13	A/G	0.440	0.367	0.049	0.156
38	rs8061205	75916480	Intron13	A/C	0.439	0.367	0.041	0.156
39	rs1428848	75919039	Intron12	T/C	0.421	0.367	0.053	0.505
40	rs891132	75919517	Intron12	C/G	0.359	0.225	0.002	0.505
41	rs6564427	75924089	Intron12	G/A	0.286	0.175	0.015	0.505
42	rs2650891	75924161	Intron12	C/A	0.495	0.300	0.007	0.505
43	rs11149981	75927639	Intron11	A/C	0.096	0.158	0.291	0.505
44	rs6564429	75930540	Intron11	A/G	0.126	0.075	0.885	0.544
45	rs8049128	75930624	Intron11	A/G	0.413	0.254	0.004	0.544

46	rs6564430	75930688	Intron11	T/C	0.416	0.267	0.006	0.544
47	rs6564431	75930762	Intron11	T/C	0.391	0.258	0.005	0.345
48	rs1428836	75942716	Intron10	C/T	0.461	0.383	0.051	0.108
49	rs1428837	75943019	Intron10	T/A	0.023	0.010	0.567	0.090
50	rs10514416	75947951	Intron8	A/C	0.436	0.467	0.346	0.117
51	rs8044972	75957583	Intron4	T/C	0.233	0.158	0.255	2.90×10^{-5}
52	rs274540	75978552	Intron3	T/C	0.089	0.033	0.004	4.61×10^{-4}
53	rs17620748	75978837	Intron3	C/G	0.216	0.237	0.617	0.117
54	rs11859065	75985216	Intron3	A/G	0.118	0.104	1.28×10^{-6}	4.91×10^{-4}
55[f]	**rs11864477**	**75985270**	**Intron3**	**C/T**	**0.117**	**0.104**	**4.17×10^{-7}**	**2.90×10^{-5}**
56	rs16945612	75986473	Intron3	C/T	0.117	0.109	5.75×10^{-7}	4.61×10^{-4}
57	rs12596244	75987305	Intron3	G/A	0.172	0.217	0.043	4.12×10^{-4}
58	rs11860781	75988112	Intron3	T/A	0.120	0.104	2.03×10^{-6}	5.78×10^{-4}
59	rs4888626	75994422	Intron3	A/G	0.247	0.183	0.567	0.012
60	rs10781983	75998680	Intron3	G/A	0.412	0.275	0.010	0.073
61	rs8053681	76000669	Intron3	T/C	0.396	0.258	8.44×10^{-4}	0.082
62	rs11647255	76000954	Intron3	G/A	0.389	0.254	0.002	0.307
63	rs12446196	76002373	Intron3	T/A	0.156	0.233	0.039	0.312
64	rs17621104	76005589	Intron3	A/C	0.125	0.142	0.214	0.312
65	rs17621123	76006164	Intron3	G/A	0.233	0.208	0.090	0.080
66	rs8051254	76006457	Intron3	G/A	0.346	0.233	0.036	0.105
67	rs1428840	76006933	Intron3	C/T	0.318	0.299	0.029	0.089
68	rs11640978	76008941	Intron3	C/G	0.182	0.242	0.891	0.117
69	rs11149989	76008984	Intron3	A/G	0.328	0.208	0.013	0.080
70	rs17688488	76009622	Intron3	C/G	0.122	0.108	0.784	0.105
71	rs10781985	76009711	Intron3	G/A	0.326	0.212	0.007	0.089
72	rs10781986	76009728	Intron3	A/G	0.328	0.217	0.016	0.089
73	rs12934271	76011693	Intron3	G/A	0.327	0.217	0.009	0.063
74	rs12934409	76011737	Intron3	G/A	0.330	0.217	0.009	0.093
75	rs768503	76012089	Intron3	A/C	0.114	0.108	0.993	0.223
76	rs919376	76012822	Intron3	A/G	0.318	0.217	0.004	0.402
77	rs17688543	76013222	Intron3	C/T	0.201	0.242	0.656	0.784
78	rs1366548	76014290	Intron3	C/T	0.340	0.233	0.027	0.512
79	rs1366547	76019882	Intron3	T/G	0.497	0.408	0.030	0.264
80	rs1428849	76020099	Intron3	C/A	0.086	0.125	0.771	0.075
81	rs4888631	76027875	Promoter	C/G	0.364	0.242	0.010	0.012
82	rs1317683	76032948	Promoter	G/A	0.269	0.283	0.386	0.017

a. The former allele represents the minor allele of each locus.
b. Minor allele frequency calculated in our own white sample.
c. Minor allele frequency reported for whites in the public database such as HapMap or dbSNP.
d. P values for associations using single-SNP marker test.
e. P values for associations using size 5 haplotype sliding window test.
f. SNP–rs11864477 that is most significant for hip BMD is labeled in bold.

Table S2. Information of the Analyzed *TGFBR3* SNPs and the p Values for Their

Single-SNP and Sliding Window Association with Spine BMD in the Total Sample

SNP	Name	Position	Role	Allele[a]	MAF[b]	MAF[c]	*P* value[d]	*P* value[e]
1	rs1555890	91933474	Intron17	G/A	0.106	0.125	0.192	0.160
2	rs1555889	91933529	Intron17	A/G	0.111	0.125	0.224	0.460
3	rs1555887	91933545	Intron17	C/T	0.264	0.208	0.748	0.322
4	rs3754014	91944008	Intron15	T/A	0.227	0.200	0.424	0.438
5	rs6660484	91945196	Intron15	G/A	0.437	0.460	0.846	0.749
6	rs3767569	91945959	Intron15	A/G	0.163	0.142	0.389	0.713
7	rs17512269	91949650	Intron14	T/C	0.218	0.258	0.816	0.239
8	rs10782997	91949982	Intron14	A/T	0.446	0.483	0.404	0.471
9	rs1805113	91950526	exon14	T/C	0.445	0.492	0.510	0.418
10	rs11165313	91952036	Intron13	G/C	0.095	0.267	0.136	0.418
11	rs10157635	91960481	Intron8	T/C	0.059	0.017	0.009	0.627
12	rs1542703	91961359	Intron8	G/C	0.280	0.200	0.259	0.206
13	rs17131541	91964397	Intron8	T/G	0.057	0.017	0.011	0.154
14	rs10874909	91964971	Intron8	G/A	0.057	0.017	0.008	0.154
15	rs11466581	91968641	Intron6	A/G	0.436	0.500	0.918	0.217
16	rs6677523	91975055	Intron5	G/A	0.112	0.167	0.640	0.217
17	rs2087299	91976391	Intron5	T/C	0.443	0.483	0.858	0.498
18	rs17131544	91977675	Intron5	C/T	0.112	0.167	0.653	0.498
19	rs4658112	91981254	Intron5	T/C	0.328	0.317	0.606	0.148
20	rs12403389	91981352	Intron5	C/G	0.335	0.358	0.251	9.63×10^{-6}
21[f]	**rs17131547**	**91983608**	**Intron5**	**A/G**	**0.013**	**0.021**	**3.91×10^{-4}**	**3.47×10^{-8}**
22	rs17573483	91990833	Intron5	A/G	0.161	0.183	0.701	0.281
23	rs7526590	91994042	Intron5	T/A	0.180	0.167	0.133	0.063
24	rs284174	91994196	Intron5	G/T	0.418	0.392	0.089	0.055
25	rs12133753	91994677	Intron5	T/C	0.181	0.167	0.222	0.029
26	rs284175	91994863	Intron5	G/A	0.421	0.392	0.171	0.662
27	rs284180	92000436	Intron4	C/A	0.428	0.400	0.271	0.645
28	rs17131554	92000796	Intron4	G/A	0.142	0.127	0.551	0.063
29	rs1473488	92014334	Intron4	C/T	0.470	0.483	0.052	0.225
30	rs12751910	92015895	Intron4	A/G	0.316	0.283	0.956	0.501
31	rs17443164	92018636	Intron4	G/C	0.316	0.288	0.906	0.891
32	rs12756024	92021028	Intron4	A/C	0.467	0.483	0.060	0.891
33	rs284142	92029214	Intron4	C/T	0.356	0.342	0.388	0.891
34	rs1192529	92029248	Intron4	A/G	0.355	0.333	0.352	0.429
35	rs1192528	92029668	Intron4	G/C	0.354	0.333	0.393	0.429
36	rs284164	92041655	Intron3	A/G	0.104	0.092	0.724	0.429
37	rs284160	92042658	Intron3	A/G	0.107	0.093	0.716	0.429
38	rs10493859	92046232	Intron3	T/G	0.324	0.267	0.884	0.802
39	rs284148	92050431	Intron3	A/G	0.105	0.085	0.815	0.802
40	rs10493858	92060525	Intron3	C/G	0.221	0.325	0.249	0.802
41	rs901913	92065750	Intron3	A/C	0.106	0.092	0.722	0.802
42	rs2810884	92066921	Intron3	A/G	0.326	0.267	0.872	0.802
43	rs12726500	92068810	Intron3	C/A	0.348	0.305	0.431	0.420
44	rs2489186	92069643	Intron3	A/G	0.104	0.092	0.740	0.420

45	rs11590254	92089161	Intron3	T/A	0.312	0.300	0.193	0.852
46	rs2799524	92089900	Intron3	T/C	0.098	0.092	0.581	0.857
47	rs2634030	92090479	Intron3	G/A	0.097	0.100	0.617	0.755
48	rs17516329	92092369	Intron3	T/A	0.310	0.100	0.151	0.533
49	rs2634028	92093441	Intron3	A/C	0.090	0.092	0.866	0.174
50	rs11576557	92096397	Intron3	T/C	0.122	0.127	0.444	0.460
51	rs1805110	92099633	exon3	T/C	0.098	0.012	0.613	0.379
52	rs2489189	92104324	Intron2	T/A	0.069	0.092	0.984	0.566
53	rs12569180	92105007	Intron2	C/G	0.309	0.308	0.069	0.471
54	rs10493856	92107337	Intron2	G/A	0.406	0.442	0.041	0.361
55	rs9661103	92108494	Intron2	T/C	0.316	0.308	0.119	0.685

a–e has the same meaning as Appendix Table 1.
f. SNP–rs17131547 that is most significant for spine BMD is labeled in bold.