Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture

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Supplementary Table 1 **Stage 1 meta-analyses results for markers that were selected for replication in stage 2.**

								FN-BMD		LS-BMD		
SNP	Locus	Position	Closest Gene	A1	A2	Freq1	Analysis	Beta	P	Beta	P	Known Locus/signal
rs2120461	1p36.23	8370309	*RERE*	t	c	0.68	Both sexes	0.048	**3.91E-08**	0.035	1.44E-04	no
rs7521902	1p36.12	22363311	*WNT4*	a	c	0.31	Secondary signal	-0.051	8.78E-08	-0.050	1.25E-06	yes
rs6426749	1p36.12	22584060	*ZBTB40*	c	g	0.17	Both sexes	0.108	**1.35E-23**	0.105	**2.35E-20**	yes
rs12137389	1p34.1	45710973	*TESK2*	t	c	0.02	Both sexes	-0.127	3.05E-06	-0.052	7.38E-02	no
rs17482952	1p31.3	68411973	*WLS*	a	g	0.93	Secondary signal	0.076	2.32E-07	0.063	7.19E-05	yes/no
rs12407028	1p31.3	68420304	*WLS*	t	c	0.61	Both sexes	0.048	**1.47E-08**	0.081	**6.86E-20**	yes
rs11809524	1p21.1	103232125	*COL11A1*	t	c	0.85	Both sexes	0.055	1.37E-06	0.047	1.06E-04	no
rs479336	1q24.3	170466196	*DNM3*	t	g	0.74	Both sexes	-0.050	1.06E-07	-0.024	1.34E-02	no
rs12120297	1q41	221617907	*SUSD4*	t	c	0.85	Both sexes	0.042	7.95E-04	0.065	3.05E-06	no
rs13413210	2p23.2	29426149	*ALK*	a	c	0.91	Males	-0.059	3.02E-02	-0.130	2.65E-06	no
rs7584262	2p21	42104053	*PKDCC*	t	c	0.23	Both sexes	0.053	1.44E-07	0.016	1.27E-01	no
rs4233949	2p16.2	54513211	*SPTBN1*	c	g	0.38	Both sexes	0.032	1.49E-04	0.062	**5.01E-12**	yes
rs730402	2p16.1	59948210	*BCL11A*	a	g	0.45	Males	0.070	2.62E-06	0.037	1.45E-02	no
rs17040773	2q13	112216506	*ANAPC1*	a	c	0.77	Both sexes	0.045	4.26E-06	0.005	6.14E-01	no
rs1878526	2q14.2	118755068	*INSIG2*	a	g	0.22	Females	0.013	2.77E-01	0.061	6.41E-07	no
rs1346004	2q24.3	166309292	*GALNT3*	a	g	0.49	Both sexes	-0.052	**1.79E-10**	-0.049	**1.29E-08**	yes
rs11675051	2q32.2	191154675	*NAB1*	a	g	0.32	Females	0.049	1.47E-06	0.019	8.15E-02	no
rs12995369	2q33.1	202535225	*ALS2CR7*	a	g	0.55	Both sexes	0.052	1.94E-07	0.031	4.71E-03	no
rs6436440	2q36.1	224413150	*AP1S3*	a	g	0.47	Females	0.046	1.17E-06	0.033	1.10E-03	no
rs2291296	3p24.2	25400886	*RARB*	a	g	0.17	Females	-0.007	5.88E-01	-0.061	3.76E-06	no
rs7427438	3p24.1	29369729	*RBMS3*	a	c	0.33	Females	-0.047	2.29E-06	-0.017	1.16E-01	no
rs430727	3p22.1	41103568	*CTNNB1*	t	c	0.47	Both sexes	-0.074	**9.73E-17**	-0.056	**2.87E-09**	yes
rs1026364	3q13.2	114852700	*KIAA2018*	t	g	0.36	Both sexes	0.041	2.01E-06	0.019	4.29E-02	no
rs344081	3q25.31	158038678	*LEKR1*	t	c	0.87	Males	0.112	6.83E-07	0.083	2.87E-04	no
rs3755955	4p16.3	984414	*IDUA*	a	g	0.16	Both sexes	-0.061	3.90E-07	-0.068	1.35E-07	no
rs6532023	4q22.1	88992873	*MEPE*	t	g	0.34	Both sexes	0.051	**2.55E-09**	0.061	**1.72E-11**	yes
rs1366594	5q14.3	88411817	*MEF2C*	a	c	0.53	Both sexes	0.092	**7.38E-29**	0.019	2.90E-02	yes
rs4957742	5q21.3	105200867	*EFNA5*	a	g	0.77	Both sexes	-0.044	4.74E-06	-0.028	7.56E-03	no
rs9466056	6p22.3	21492592	*CDKAL1*	a	g	0.38	Both sexes	-0.048	**1.80E-08**	-0.036	6.53E-05	no
rs11755164	6p21.1	44747162	*SUPT3H*	t	c	0.40	Both sexes	-0.012	2.26E-01	-0.052	3.52E-07	no
rs13204965	6q22.32	127208765	*RSPO3*	a	c	0.76	Females	0.069	2.90E-07	0.049	8.23E-04	yes
rs4869742	6q25.1	151949441	*C6orf97*	t	c	0.32	Both sexes	-0.068	**3.61E-14**	-0.087	**3.27E-20**	yes
rs7751941	6q25.1	151988351	*C6orf97*	a	g	0.21	Secondary signal	-0.048	5.34E-07	-0.077	**3.97E-14**	yes/yes
rs7788807	7p22.1_1	4734564	*FOXK1*	t	c	0.94	Females	0.043	3.34E-02	0.098	4.11E-06	no
rs2008425	7p22.1_2	5786972	*RNF216*	t	g	0.02	Females	-0.127	2.00E-03	-0.194	2.97E-06	no
rs10226308	7p14.1	37904947	*TXNDC3*	a	g	0.84	Secondary signal	-0.029	3.81E-03	-0.063	**3.36E-09**	yes/no

Supplementary Table 1 **Stage 1 meta-analyses results for markers that were selected for replication in stage 2.**

								FN-BMD		LS-BMD		
SNP	Locus	Position	Closest Gene	A1	A2	Freq1	Analysis	Beta	P	Beta	P	Known Locus/signal
rs6959212	7p14.1	38094851	*STARD3NL*	t	c	0.34	Both sexes	-0.030	6.36E-04	-0.077	**6.86E-17**	yes
rs2282930	7p12.2	50722173	*GRB10*	a	g	0.26	Females	-0.057	5.03E-07	-0.037	2.26E-03	no
rs4727338	7q21.3	95958611	*SLC25A13*	c	g	0.67	Both sexes	0.081	**2.99E-20**	0.074	**1.11E-15**	yes
rs13245690	7q31.31	120572300	*C7orf58*	a	g	0.65	Secondary signal	0.032	8.57E-05	0.052	**1.07E-09**	no
rs3801387	7q31.31	120762001	*WNT16*	a	g	0.74	Both sexes	-0.071	**4.23E-14**	-0.083	**1.35E-16**	no
rs7812088	7q36.1	150550762	*ABCF2*	a	g	0.12	Both sexes	0.061	1.22E-06	0.055	2.93E-05	no
rs1670346	7q36.3	157960022	*PTPRN2*	a	g	0.30	Both sexes	-0.042	2.81E-06	-0.020	3.49E-02	no
rs7017914	8q13.3	71753757	*XKR9*	a	g	0.49	Females	0.053	**4.70E-08**	0.010	3.52E-01	no
rs13272568	8q21.12	79197014	*PKIA*	a	c	0.44	Both sexes	-0.039	2.13E-06	-0.014	9.80E-02	no
rs2062377	8q24.12	120076601	*TNFRSF11B*	a	t	0.59	Both sexes	-0.063	**2.50E-14**	-0.081	**2.26E-20**	yes
rs4240467	9q33.2	123350111	*DAB2IP*	c	g	0.32	Males	-0.043	6.75E-03	-0.079	9.65E-07	no
rs7851693	9q34.11	132468648	*FUBP3*	c	g	0.63	Both sexes	0.047	**3.08E-08**	0.017	5.81E-02	no
rs3905706	10p11.23	28519948	*MPP7*	t	c	0.23	Both sexes	0.005	6.28E-01	0.063	**2.93E-09**	no
rs1373004	10q21.1	54097831	*MBL2*	t	g	0.12	Females	-0.065	6.32E-06	-0.089	**8.87E-09**	no
rs7071206	10q22.3_1	79071322	*KCNMA1*	t	c	0.76	Females	-0.020	8.68E-02	-0.087	**8.34E-13**	no
rs2784767	10q22.3_2	81884474	*PLAC9*	t	c	0.43	Females	0.052	4.80E-06	0.036	5.09E-03	no
rs7084921	10q24.2	101803792	*CPN1*	t	c	0.40	Females	0.045	3.13E-06	0.027	8.62E-03	no
rs11602954	11p15.5	192856	*BET1L*	a	g	0.23	Both sexes	0.034	1.06E-03	0.056	2.74E-07	no
rs7108738	11p15.2	15666660	*SOX6*	t	g	0.82	Both sexes	-0.093	**1.03E-17**	-0.047	4.51E-05	yes
rs10835187	11p14.1_1	27462253	*LIN7C*	t	c	0.54	Females	-0.028	3.70E-03	-0.052	4.14E-07	no
rs163879	11p14.1_2	30908250	*DCDC5*	t	c	0.66	Both sexes	-0.042	1.70E-06	-0.049	8.81E-08	yes
rs7932354	11p11.2	46678797	*ARHGAP1*	t	c	0.33	Both sexes	0.050	**2.29E-08**	0.041	1.23E-05	yes
rs600231	11q13.1	65017222	*SCYL1*	a	g	0.69	Females	-0.051	9.03E-07	-0.032	3.55E-03	no
rs3736228	11q13.2	67957871	*LRP5*	t	c	0.15	Both sexes	-0.054	1.79E-06	-0.081	**1.62E-11**	yes
rs2887571	12p13.33	1508432	*ERC1*	a	g	0.76	Both sexes	-0.037	1.06E-04	-0.052	2.20E-07	no
rs11048046	12p12.1	25496076	*IFLTD1*	a	g	0.08	Males	-0.148	3.59E-06	-0.055	8.30E-02	no
rs7953528	12p11.22	27908426	*KLHDC5*	a	t	0.18	Both sexes	0.058	5.75E-08	0.001	9.44E-01	no
rs12821008	12q13.12	47760872	*DHH*	t	c	0.40	Both sexes	0.032	1.89E-04	0.047	1.53E-07	no
rs2016266	12q13.13	52014222	*SP7*	a	g	0.69	Both sexes	-0.045	4.79E-07	-0.063	**1.53E-11**	yes
rs736825	12q13.13	52703843	*HOXC6*	c	g	0.56	Secondary signal	0.036	7.65E-06	0.054	**2.40E-10**	yes/no
rs1053051	12q23.3	105891355	*C12orf23*	t	c	0.51	Both sexes	-0.036	1.35E-05	-0.041	2.47E-06	no
rs9533090	13q14.11	41849449	*AKAP11*	t	c	0.48	Both sexes	-0.054	**9.84E-11**	-0.110	**1.02E-35**	yes
rs7326472	13q14.11	41877951	*AKAP11*	a	g	0.92	Secondary signal	-0.055	2.55E-03	-0.103	9.80E-08	yes/no
rs1286083	14q32.12	90512532	*RPS6KA5*	t	c	0.80	Both sexes	-0.059	**2.91E-08**	-0.074	**1.69E-11**	no
rs11623869	14q32.32	102953386	*MARK3*	t	g	0.34	Both sexes	-0.041	1.26E-06	-0.030	7.53E-04	yes
rs2118784	15q21.2	49238477	*CYP19A1*	a	c	0.29	Females	-0.050	1.41E-06	-0.038	5.26E-04	no

Supplementary Table 1 **Stage 1 meta-analyses results for markers that were selected for replication in stage 2.**

								FN-BMD		LS-BMD		
SNP	Locus	Position	Closest Gene	A1	A2	Freq1	Analysis	Beta	P	Beta	P	Known Locus/signal
rs9921222	16p13.3_1	315783	*AXIN1*	t	c	0.46	Both sexes	-0.043	2.46E-07	-0.049	**2.20E-08**	no
rs13336428	16p13.3_2	1472464	*C16orf38*	a	g	0.44	Both sexes	-0.043	2.87E-07	-0.036	5.94E-05	no
rs4985155	16p13.11	15036960	*NTAN1*	a	g	0.65	Both sexes	-0.031	3.53E-04	-0.045	8.71E-07	no
rs1564981	16q12.1	49543809	*CYLD*	a	g	0.50	Secondary signal	-0.025	1.05E-03	-0.045	6.24E-08	no
rs1566045	16q12.1	49579304	*SALL1*	t	c	0.80	Both sexes	-0.074	**4.95E-12**	-0.030	7.83E-03	no
rs10048146	16q24.1	85268161	*FOXL1*	a	g	0.80	Both sexes	0.056	1.28E-07	0.061	**2.95E-08**	yes
rs4790881	17p13.3	2015682	*SMG6*	a	c	0.67	Both sexes	0.051	**1.66E-08**	0.032	6.04E-04	no
rs4792909	17q21.31_1	39154350	*SOST*	t	g	0.37	Secondary signal	0.035	1.85E-05	0.044	5.14E-07	yes/yes
rs227584	17q21.31_1	39581073	*C17orf53*	a	c	0.67	Both sexes	-0.060	**3.44E-11**	-0.048	4.77E-07	yes
rs1864325	17q21.31_2	41333623	*MAPT*	t	c	0.22	Both sexes	-0.040	7.79E-05	-0.057	1.11E-07	yes
rs7226305	17q22	49464490	*KIF2B*	a	c	0.82	Both sexes	-0.017	1.29E-01	-0.058	1.33E-06	no
rs7217932	17q24.3	67460611	*SOX9*	a	g	0.46	Both sexes	0.045	**3.65E-08**	0.009	3.12E-01	no
rs4796995	18p11.21	13698574	*C18orf19*	a	g	0.61	Both sexes	0.040	3.18E-06	0.031	5.22E-04	no
rs884205	18q21.33	58205837	*TNFRSF11A*	a	c	0.25	Both sexes	-0.042	3.87E-05	-0.065	**4.85E-09**	yes
rs7257450	19p13.11	17349607	*PLVAP*	a	g	0.76	Females	0.014	2.78E-01	0.065	4.79E-06	no
rs10416218	19q13.11	38290967	*GPATCH1*	t	c	0.72	Both sexes	-0.042	5.73E-06	-0.056	**9.19E-09**	no
rs3790160	20p12.2	10587988	*JAG1*	t	c	0.50	Both sexes	0.043	1.32E-07	0.057	**5.36E-11**	yes
rs4817775	21q22.12	36406932	*CBR3*	a	c	0.58	Both sexes	0.023	6.24E-03	0.042	1.49E-06	no
rs4820539	22q11.23	21807970	*RTDR1*	a	g	0.44	Both sexes	0.038	4.86E-06	0.025	3.65E-03	no
rs5934507	Xp22.31	8877206	*FAM9B*	a	g	0.73	ChrX - men	-0.031	1.19E-02	-0.057	5.66E-06	no
rs5926033	Xp22.11	22594282	*DDX53*	t	c	0.71	ChrX - both sexes	0.037	4.13E-06	0.014	9.96E-02	no
rs5952638	Xp11.3	44579849	*DUSP21*	a	t	0.93	ChrX - both sexes	0.056	3.03E-04	0.069	2.29E-05	no
rs4492531	Xq13.3	74948856	*MAGEE2*	a	g	0.55	ChrX - both sexes	-0.066	1.98E-03	-0.094	2.40E-05	no
rs964181	Xq28	150792732	*MAGEA4*	t	c	0.41	ChrX - both sexes	0.036	4.72E-06	0.028	5.22E-04	no

The effect estimates (Beta) are expressed as standardized values per copy of the SNP allele (A1). Results are shown for the analysis from which the marker was selected for replication, shown in the Analysis column. Freq1 denotes allelic frequency of SNP allele A1, FN-BMD is BMD at the femoral neck and LS-BMD is BMD at lumbar spine. In the pooled analysis of both sexes were 32,961 subjects, 31,900 in the secondary signal analysis, 22,990 in the female only analysis and 9,9980 in males only. Subjects analysed for the X chromosome were 31,801. Wether a locus has previously been reported to associate with BMD, or a secondary signal at a known locus, is shown. Position is given according to NCBIbuild36.

Supplementary Table 2 **Secondary signals in BMD loci after conditional analysis**

									Second signal P value after conditioning (Discovery n=31,900)				Second signal P value after replication (Discovery + Replication n=56,123)			
									FNBMD		LSBMD		FNBMD		LSBMD	
Second signal SNP[a]	Locus	Closest Gene/Candidate	MAF	Conditioned SNP	Distance (bp)[b]	Genetic Distance (cM)	HapMap[c] r^2	A1[d]	Beta	P	Beta	P	Beta	P	Beta	P
rs17482952	1p31.3	*WLS*	0.07	rs12407028	8,331	0.01	0.062	a	0.08	2.32E-07	0.06	7.19E-05	0.08	**1.31E-11**	0.07	**1.69E-08**
rs7521902	1p36.12	*WNT4*	0.19	rs6426749	220,749	0.42	0.003	a	-0.05	8.78E-08	-0.05	1.25E-06	-0.04	**2.85E-09**	-0.05	**9.66E-11**
rs7751941	6q25.1	*C6orf97/ESR1*	0.23	rs4869742	38,910	0.11	0.008	a	-0.05	5.34E-07	-0.08	**3.97E-14**	-0.04	**1.59E-09**	-0.08	**1.99E-24**
rs10226308	7p14.1	*TXNDC3/SFRP4*	0.19	rs6959212	189,904	0.25	0.004	a	-0.03	3.81E-03	-0.06	**3.36E-09**	-0.02	1.53E-02	-0.06	**6.40E-13**
rs13245690	7q31.31	*C7orf58*	0.38	rs3801387	189,701	0.15	0.028	a	0.03	8.57E-05	0.05	**1.07E-09**	0.02	8.20E-04	0.05	**1.65E-11**
rs736825	12q13.13	*HOXC6*	0.35	rs2016266	689,621	NA	NA	c	0.04	7.65E-06	0.05	**2.40E-10**	0.04	**1.06E-09**	0.05	**7.68E-16**
rs7326472	13q14.11	*AKAP11/TNFSF11*	0.04	rs9533090	28,502	0.01	0.033	a	-0.05	2.55E-03	-0.10	9.80E-08	-0.05	5.07E-04	-0.07	2.61E-07
rs1564981	16q12.1	*CYLD*	0.47	rs1566045	35,495	0.10	0.009	a	-0.03	1.05E-03	-0.04	6.24E-08	-0.02	4.38E-05	-0.04	**1.95E-10**
rs4792909	17q21.31	*SOST*	0.35	rs227584	426,723	0.25	0.001	t	0.04	1.85E-05	0.04	5.14E-07	0.04	**1.95E-11**	0.04	**9.43E-10**

a Index marker representing the second signal in the originally associated locus after conditioning for the most significant SNP in the same region. **b** Distance of conditioned SNP from the index SNP. **c** HapMap CEU phase II release 22. **d** Coded allele of the second signal for which the Beta estimate is specified.

Supplementary Table 3 Gene x Gene interaction results.

TRAIT	SNP1	GENE1	SNP2	GENE2	Beta_interaction	se_interaction	I2	P_interaction
FNBMD	rs4869742	*C6orf97*	rs12821008	*DHH*	0.04	0.009	0	4.90E-05
FNBMD	rs11809524	*COL11A1*	rs9533090	*AKAP11*	0.04	0.011	20	2.18E-04
LSBMD	rs9466056	*CDKAL1*	rs2016266	*SP7*	0.02	0.007	8	2.23E-04
LSBMD	rs11675051	*NAB1*	rs2282930	*GRB10*	-0.03	0.009	0	5.98E-04
LSBMD	rs9921222	*AXIN1*	rs1864325	*MAPT*	0.03	0.009	37	7.58E-04
FNBMD	rs11675051	*NAB1*	rs3755955	*IDUA*	0.04	0.012	0	1.20E-03
FNBMD	rs2120461	*RERE*	rs2282930	*GRB10*	0.03	0.010	24	1.25E-03
LSBMD	rs7953528	*KLHDC5*	rs7257450	*PLVAP*	0.02	0.007	16	1.34E-03
LSBMD	rs7953528	*KLHDC5*	rs6532023	*MEPE*	0.02	0.007	0	1.34E-03

Nominally significant (P< 1.5x10-3) gene x gene interaction results for pair-wise tests of lead SNPs at 82 BMD loci with P<5x10-6 in Stage 1. Adjusting for 3321 tests, the P-value for significance is 1.5x10-5.

Supplementary Table 4A **Sex-combined meta-analysis results across stages for new loci associated with BMD at GWS level.**

						FNBMD								LSBMD							
						STAGE 1 (Up to 32,961)		STAGE 2 (Up to 50,933)				STAGE 1 + STAGE 2 (Up to 83,894)		STAGE 1 (Up to 31,800)		STAGE 2 (Up to 45,708)				STAGE 1 + STAGE 2 (Up to 77,508)	
SNP	**Locus**	**Closest Gene**	**A1a**	**A2**	**Freq1**	**Beta**	**P**	**Beta**	**P**	**I2**	**Q_{het} P**	**Beta**	**P**	**Beta**	**P**	**Beta**	**P**	**I2**	**Q_{het} P**	**Beta**	**P**
rs479336	1q24.3	*DNM3*	t	g	0.74	-0.05	1.06E-07	-0.04	**1.30E-08**	0	0.94	-0.04	**8.51E-15**	-0.02	0.01	-0.03	4.97E-04	0	0.84	-0.03	2.14E-05
rs7584262	2p21	*PKDCC*	t	c	0.23	0.05	1.44E-07	0.03	3.37E-04	0	0.75	0.04	**1.27E-09**	0.02	0.13	0.01	0.28	0	0.93	0.01	0.07
rs17040773	2q13	*ANAPC1*	a	c	0.76	0.05	4.26E-06	0.03	6.08E-05	21	0.14	0.04	**1.51E-09**	0.01	0.61	0.01	0.21	0	0.97	0.01	0.19
rs1878526	2q14.2	*INSIG2*	a	g	0.22	0.00	0.70	0.00	0.97	12	0.27	0.00	0.79	0.05	7.31E-06	0.04	3.38E-06	0	0.48	0.04	**1.22E-10**
rs1026364	3q13.2	*KIAA2018*	t	g	0.37	0.04	2.01E-06	0.03	2.51E-05	0	0.66	0.03	**4.08E-10**	0.02	0.04	0.02	7.26E-03	33	0.04	0.02	7.57E-04
rs344081	3q25.31	*LEKR1*	t	c	0.87	0.05	1.09E-04	0.03	2.50E-03	21	0.14	0.04	2.22E-06	0.06	2.76E-05	0.06	**3.54E-08**	0	0.77	0.06	**4.46E-12**
rs3755955	4p16.3	*IDUA*	a	g	0.16	-0.06	3.90E-07	-0.05	**6.14E-09**	6	0.37	-0.06	**1.46E-14**	-0.07	1.35E-07	-0.05	**5.52E-09**	20	0.16	-0.06	**5.24E-15**
rs11755164	6p21.1	*SUPT3H*	t	c	0.40	-0.01	0.23	-0.01	0.12	0	0.91	-0.01	0.05	-0.05	3.52E-07	-0.03	9.19E-06	0	0.82	-0.04	**5.60E-11**
rs9466056	6p22.3	*CDKAL1*	a	g	0.38	-0.05	**1.80E-08**	-0.03	1.55E-06	0	0.74	-0.04	**2.73E-13**	-0.04	6.53E-05	-0.03	1.11E-04	16	0.21	-0.03	**3.56E-08**
rs3801387	7q31.31	*WNT16*	a	g	0.74	-0.07	**4.23E-14**	-0.08	**2.00E-27**	12	0.27	-0.08	**5.02E-40**	-0.08	**1.35E-16**	-0.10	**1.50E-36**	17	0.19	-0.09	**3.17E-51**
rs13245690	7q31.31	*C7orf58*	a	g	0.65	0.03	8.57E-05	0.00	0.69	37	0.07	0.02	8.20E-04	0.05	**1.07E-09**	0.03	1.30E-03	18	0.24	0.05	**1.65E-11**
rs7812088	7q36.1	*ABCF2*	a	g	0.13	0.06	1.22E-06	0.04	4.41E-04	27	0.08	0.05	**7.28E-09**	0.06	2.93E-05	0.04	1.10E-03	50	0.002	0.04	2.24E-07
rs7017914*	8q13.3	*XKR9*	a	g	0.49	0.04	3.60E-07	0.02	0.02	10	0.35	0.03	2.29E-07	0.00	0.91	-0.01	0.11	5	0.78	-0.01	0.26
rs7851693	9q34.11	*FUBP3*	c	g	0.64	0.05	**3.08E-08**	0.05	**1.43E-15**	0	0.51	0.05	**3.37E-22**	0.02	0.06	0.04	6.71E-08	1	0.45	0.03	6.08E-08
rs3905706	10p11.23	*MPP7*	t	c	0.22	0.00	0.63	-0.02	1.67E-03	0	0.95	-0.01	0.03	0.06	**2.93E-09**	0.05	**6.68E-09**	0	0.49	0.05	**2.41E-16**
rs1373004	10q21.1	*MBL2*	t	g	0.13	-0.06	1.39E-05	-0.04	1.45E-04	19	0.18	-0.04	**1.45E-08**	-0.07	5.40E-08	-0.05	2.24E-06	26	0.10	-0.06	**1.56E-12**
rs7071206	10q22.3_1	*KCNMA1*	t	c	0.78	-0.01	0.29	0.01	0.26	1	0.45	0.00	0.81	-0.07	**1.54E-12**	-0.05	**6.24E-09**	28	0.07	-0.06	**5.02E-19**
rs7084921	10q24.2	*CPN1*	t	c	0.39	0.03	1.42E-04	0.03	1.55E-06	0	0.51	0.03	**9.03E-10**	0.02	0.01	0.03	1.92E-05	15	0.23	0.03	9.15E-07
rs10835187	11p14.1_1	*LIN7C*	t	c	0.55	-0.01	0.17	-0.01	0.08	0	0.91	-0.01	0.03	-0.04	3.04E-05	-0.02	2.36E-04	24	0.11	-0.03	**4.90E-08**
rs7953528	12p11.22	*KLHDC5*	a	t	0.18	0.06	5.75E-08	0.04	2.43E-06	0	0.54	0.05	**1.87E-12**	0.00	0.94	-0.02	0.05	0	0.94	-0.01	0.13
rs2887571	12p13.33	*ERC1*	a	g	0.76	-0.04	1.06E-04	-0.03	1.60E-05	25	0.10	-0.03	**6.49E-09**	-0.05	2.20E-07	-0.04	2.88E-06	0	0.52	-0.04	**5.59E-12**
rs12821008	12q13.12	*DHH*	t	c	0.39	0.03	1.89E-04	0.03	5.20E-04	0	0.72	0.03	3.34E-07	0.05	1.53E-07	0.05	**1.89E-09**	7	0.36	0.05	**1.17E-15**
rs1053051	12q23.3	*C12orf23*	t	c	0.52	-0.04	1.35E-05	-0.03	1.82E-05	13	0.27	-0.03	**9.60E-10**	-0.04	2.47E-06	-0.02	2.38E-03	0	0.86	-0.03	7.90E-08
rs1286083	14q32.12	*RPS6KA5*	t	c	0.81	-0.06	**2.91E-08**	-0.05	**9.32E-09**	0	0.50	-0.05	**2.02E-15**	-0.07	**1.69E-11**	-0.04	7.13E-06	25	0.10	-0.05	**1.75E-14**
rs4985155	16p13.11	*NTAN1*	a	g	0.67	-0.03	3.53E-04	-0.03	1.38E-07	4	0.41	-0.03	**1.74E-10**	-0.04	8.71E-07	-0.03	1.83E-04	0	0.66	-0.03	**2.15E-09**
rs9921222	16p13.3_1	*AXIN1*	t	c	0.48	-0.04	2.46E-07	-0.03	2.37E-06	43	0.01	-0.04	**5.18E-12**	-0.05	**2.20E-08**	-0.04	**8.29E-10**	28	0.07	-0.04	**1.00E-16**
rs13336428	16p13.3_2	*C16orf38*	a	g	0.43	-0.04	2.87E-07	-0.04	**1.08E-10**	0	0.79	-0.04	**1.49E-16**	-0.04	5.94E-05	-0.04	**5.75E-10**	0	0.65	-0.04	**1.66E-13**
rs1566045	16q12.1	*SALL1*	t	c	0.80	-0.07	**4.95E-12**	-0.06	**3.03E-12**	30	0.05	-0.06	**1.94E-22**	-0.03	7.83E-03	-0.01	0.55	25	0.11	-0.01	0.04
rs1564981	16q12.1	*CYLD*	a	g	0.50	-0.03	1.05E-03	-0.02	0.01	23	0.18	-0.02	4.38E-05	-0.04	6.24E-08	-0.03	5.37E-04	48	0.01	-0.04	**1.95E-10**
rs4790881	17p13.3	*SMG6*	a	c	0.69	0.05	**1.66E-08**	0.05	**1.18E-11**	12	0.28	0.05	**9.75E-19**	0.03	6.04E-04	0.04	1.65E-06	27	0.09	0.03	**3.38E-09**
rs7217932	17q24.3	*SOX9*	a	g	0.46	0.05	**3.65E-08**	0.03	2.69E-05	5	0.39	0.03	**1.92E-11**	0.01	0.31	0.01	0.15	0	0.69	0.01	0.08
rs4796995	18p11.21	*C18orf19*	a	g	0.63	0.04	3.18E-06	0.02	1.13E-03	39	0.01	0.03	**4.85E-08**	0.03	5.22E-04	0.01	0.11	14	0.24	0.02	6.65E-04
rs10416218	19q13.11	*GPATCH1*	t	c	0.73	-0.04	5.73E-06	-0.02	7.11E-04	0	0.69	-0.03	5.52E-08	-0.06	**9.19E-09**	-0.03	1.22E-04	0	0.96	-0.04	**6.64E-11**
rs5934507*	Xp22.31	*FAM9B*	a	g	0.73	-0.01	0.09	-0.01	0.16	34	0.25	-0.01	0.03	-0.02	6.81E-03	-0.01	0.34	37	0.08	-0.02	7.29E-03

P-values in bold reflect loci reaching GWS level. [a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele. The measure of heterogeneity (Cochran's Qhet P statistic and I2) was calculated in the Stage 2 samples. *These markers were GWS in the sex-stratified meta-analysis.

Supplementary Table 4B **Sex-combined meta-analysis results across stages for known loci associated with BMD at GWS level.**

						FNBMD								LSBMD							
						STAGE 1 (Up to 32,961)		STAGE 2 (Up to 50,933)				STAGE 1 + STAGE 2 (Up to 83,894)		STAGE 1 (Up to 31,800)		STAGE 2 (Up to 45,708)				STAGE 1 + STAGE 2 (Up to 77,508)	
SNP	Locus	Closest Gene	A1[a]	A2	Freq1	Beta	P	Beta	P	I^2	Q_{het} P	Beta	P	Beta	P	Beta	P	I^2	Q_{het} P	Beta	P
rs17482952	1p31.3	*WLS*	a	g	0.93	0.08	2.32E-07	0.08	1.23E-05	17	0.25	0.08	**1.31E-11**	0.06	7.19E-05	0.07	5.66E-05	8	0.36	0.07	**1.69E-08**
rs12407028	1p31.3	*WLS*	t	c	0.60	0.05	**1.47E-08**	0.05	**4.62E-16**	0	0.75	0.05	**3.44E-23**	0.08	**6.86E-20**	0.07	**1.12E-26**	27	0.09	0.08	**3.11E-45**
rs7521902	1p36.12	*WNT4*	a	c	0.31	-0.05	8.78E-08	-0.03	3.92E-03	0	0.45	-0.04	**2.85E-09**	-0.05	1.25E-06	-0.05	1.60E-05	42	0.03	-0.05	**9.66E-11**
rs6426749	1p36.12	*ZBTB40*	c	g	0.17	0.11	**1.35E-23**	0.11	**3.49E-35**	0	0.86	0.11	**7.39E-57**	0.11	**2.35E-20**	0.10	**3.66E-26**	0	0.80	0.10	**1.86E-44**
rs4233949	2p16.2	*SPTBN1*	c	g	0.38	0.03	1.49E-04	0.02	6.40E-03	0	0.56	0.02	5.91E-06	0.06	**5.01E-12**	0.04	**2.35E-08**	41	0.01	0.05	**2.25E-18**
rs1346004	2q24.3	*GALNT3*	a	g	0.50	-0.05	**1.79E-10**	-0.05	**1.16E-16**	30	0.06	-0.05	**1.08E-25**	-0.05	**1.29E-08**	-0.07	**1.50E-23**	6	0.37	-0.06	**3.87E-30**
rs430727	3p22.1	*CTNNB1*	t	c	0.48	-0.07	**9.73E-17**	-0.05	**3.43E-11**	12	0.28	-0.06	**4.41E-25**	-0.06	**2.87E-09**	-0.05	**9.58E-11**	27	0.10	-0.05	**1.54E-18**
rs6532023	4q22.1	*MEPE*	t	g	0.34	0.05	**2.55E-09**	0.06	**3.62E-18**	0	0.53	0.06	**4.95E-26**	0.06	**1.72E-11**	0.06	**7.32E-18**	3	0.41	0.06	**1.23E-27**
rs1366594	5q14.3	*MEF2C*	a	c	0.54	0.09	**7.38E-29**	0.08	**6.25E-34**	26	0.09	0.08	**4.47E-61**	0.02	0.03	0.01	0.14	0	0.53	0.01	0.01
rs13204965	6q22.32	*RSPO3*	a	c	0.76	0.05	1.49E-06	0.04	7.24E-07	0	0.82	0.04	**8.12E-12**	0.04	2.68E-04	0.04	3.90E-07	0	0.75	0.04	**3.61E-10**
rs7751941	6q25.1	*C6orf97*	a	g	0.21	-0.05	5.34E-07	-0.04	7.49E-04	0	0.84	-0.04	**1.59E-09**	-0.08	**3.97E-14**	-0.08	**8.27E-12**	32	0.10	-0.08	**1.99E-24**
rs4869742	6q25.1	*C6orf97*	t	c	0.31	-0.07	**3.61E-14**	-0.04	5.38E-07	16	0.21	-0.05	**4.15E-18**	-0.09	**3.27E-20**	-0.07	**5.05E-17**	14	0.24	-0.08	**3.95E-35**
rs10226308	7p14.1	*TXNDC3*	a	g	0.84	-0.03	3.81E-03	0.00	0.81	8	0.36	-0.02	0.02	-0.06	**3.36E-09**	-0.05	3.17E-05	28	0.13	-0.06	**6.40E-13**
rs6959212	7p14.1	*STARD3NL*	t	c	0.32	-0.03	6.36E-04	-0.05	**1.85E-11**	0	0.97	-0.04	**1.18E-13**	-0.08	**6.86E-17**	-0.07	**7.21E-23**	0	0.66	-0.07	**3.76E-38**
rs4727338	7q21.3	*SLC25A13*	c	g	0.67	0.08	**2.99E-20**	0.08	**2.61E-29**	26	0.09	0.08	**8.10E-48**	0.07	**1.11E-15**	0.07	**5.24E-21**	4	0.40	0.07	**2.13E-35**
rs2062377	8q24.12	*TNFRSF11B*	a	t	0.57	-0.06	**2.50E-14**	-0.05	**2.63E-12**	4	0.40	-0.06	**9.06E-25**	-0.08	**2.26E-20**	-0.07	**2.18E-20**	0	0.59	-0.08	**3.16E-39**
rs7932354	11p11.2	*ARHGAP1*	t	c	0.31	0.05	**2.29E-08**	0.05	**3.46E-11**	0	0.97	0.05	**5.12E-18**	0.04	1.23E-05	0.04	1.10E-07	0	0.60	0.04	**5.45E-12**
rs163879	11p14.1_2	*DCDC5*	t	c	0.68	-0.04	1.70E-06	-0.02	6.66E-04	34	0.03	-0.03	**2.06E-08**	-0.05	8.81E-08	-0.03	1.72E-05	0	0.58	-0.04	**2.19E-11**
rs7108738	11p15.2	*SOX6*	t	g	0.83	-0.09	**1.03E-17**	-0.07	**1.82E-17**	6	0.37	-0.08	**1.08E-32**	-0.05	4.51E-05	-0.03	3.93E-03	30	0.06	-0.03	2.14E-06
rs3736228	11q13.2	*LRP5*	t	c	0.16	-0.05	1.79E-06	-0.05	5.29E-06	0	0.80	-0.05	**4.83E-11**	-0.08	**1.62E-11**	-0.09	**1.30E-16**	0	0.85	-0.08	**2.08E-26**
rs736825	12q13.13	*HOXC6*	c	g	0.56	0.04	7.65E-06	0.04	2.76E-05	44	0.03	0.04	**1.06E-09**	0.05	**2.40E-10**	0.05	5.59E-07	41	0.04	0.05	**7.68E-16**
rs2016266	12q13.13	*SP7*	a	g	0.68	-0.04	4.79E-07	-0.03	4.48E-05	3	0.42	-0.03	**3.67E-10**	-0.06	**1.53E-11**	-0.05	**1.59E-10**	0	0.76	-0.05	**2.95E-20**
rs9533090[b]	13q14.11	*AKAP11*	t	c	0.49	-0.05	**9.84E-11**	-0.05	**1.04E-13**	27	0.09	-0.05	**4.94E-23**	-0.11	**1.02E-35**	-0.09	**1.92E-34**	**66.1**[b]	**2.73E-07**	-0.10	**4.82E-68**
rs11623869	14q32.32	*MARK3*	t	g	0.35	-0.04	1.26E-06	-0.04	**7.02E-11**	26	0.09	-0.04	**5.20E-16**	-0.03	7.53E-04	-0.04	**1.23E-08**	1	0.45	-0.04	**5.12E-11**
rs10048146	16q24.1	*FOXL1*	a	g	0.80	0.06	1.28E-07	0.05	**1.63E-08**	0	0.51	0.05	**1.00E-14**	0.06	**2.95E-08**	0.04	4.70E-05	0	0.93	0.05	**3.09E-11**
rs4792909	17q21.31_1	*SOST*	t	g	0.37	0.04	1.85E-05	0.05	8.74E-08	41	0.04	0.04	**1.95E-11**	0.04	5.14E-07	0.03	3.29E-04	23	0.18	0.04	**9.43E-10**
rs227584	17q21.31_1	*C17orf53*	a	c	0.70	-0.06	**3.44E-11**	-0.05	**1.18E-14**	9	0.32	-0.06	**2.56E-24**	-0.05	4.77E-07	-0.03	1.23E-04	13	0.27	-0.04	**9.92E-10**
rs1864325	17q21.31_2	*MAPT*	t	c	0.22	-0.04	7.79E-05	-0.02	0.06	10	0.31	-0.03	7.47E-05	-0.06	1.11E-07	-0.04	3.11E-05	14	0.25	-0.04	**4.89E-11**
rs884205	18q21.33	*TNFRSF11A*	a	c	0.27	-0.04	3.87E-05	-0.03	1.68E-06	0	0.70	-0.04	**3.18E-10**	-0.06	**4.85E-09**	-0.05	**2.61E-10**	0	0.71	-0.05	**1.58E-17**
rs3790160	20p12.2	*JAG1*	t	c	0.50	0.04	1.32E-07	0.03	2.44E-06	25	0.10	0.04	**3.61E-12**	0.06	**5.36E-11**	0.04	**3.84E-10**	21	0.15	0.05	**3.07E-19**

P-values in bold reflect loci reaching GWS level. [a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele. The measure of heterogeneity (Cochran's Qhet P statistic and I2) was calculated in the Stage 2 samples. [b]The SNP rs9533090 was the only GWS SNP with high degree of heterogeneity of effects (I2>50%). After applying random effects meta-analysis, this marker was still significant ($P=3.98\times10^{-13}$)

Supplementary Table 4C **Sex-combined meta-analysis results across stages for BMD loci not reaching GWS**

						FNBMD								LSBMD							
						STAGE 1 (Up to 32,961)		STAGE 2 (Up to 50,933)				STAGE 1 + STAGE 2 (Up to 83,894)		STAGE 1 (Up to 31,800)		STAGE 2 (Up to 45,708)				STAGE 1 + STAGE 2 (Up to 77,508)	
SNP	Locus	Closest Gene	A1[a]	A2	Freq1	Beta	P	Beta	P	I^2	Q_{het} P	Beta	P	Beta	P	Beta	P	I^2	Q_{het} P	Beta	P
rs11809524	1p21.1	*COL11A1*	t	c	0.85	0.06	1.37E-06	0.02	0.06	13	0.26	0.03	9.32E-06	0.05	1.06E-04	0.02	0.10	0	0.69	0.03	2.23E-04
rs12137389	1p34.1	*TESK2*	t	c	0.03	-0.13	3.05E-06	-0.01	0.69	31	0.05	-0.06	5.76E-04	-0.05	0.07	0.02	0.45	24	0.12	-0.01	0.52
rs2120461	1p36.23	*RERE*	t	c	0.67	0.05	3.91E-08	0.01	0.10	0	0.49	0.03	3.07E-06	0.04	1.44E-04	0.02	3.53E-03	21	0.15	0.03	*3.11E-06*
rs12120297	1q41	*SUSD4*	t	c	0.86	0.04	7.95E-04	-0.01	0.38	17	0.20	0.01	0.24	0.06	*3.05E-06*	0.01	0.45	0	0.53	0.03	1.19E-03
rs730402	2p16.1	*BCL11A*	a	g	0.45	0.03	9.01E-05	0.00	0.44	0	0.76	0.02	2.49E-03	0.02	0.04	0.001	0.88	0	0.57	0.01	0.16
rs13413210	2p23.2	*ALK*	a	c	0.91	-0.02	0.23	-0.01	0.58	0	0.69	-0.01	0.25	-0.05	3.86E-03	0.001	0.92	7	0.36	-0.02	0.10
rs11675051	2q32.2	*NAB1*	a	g	0.33	0.04	2.38E-06	0.01	0.07	23	0.12	0.02	1.02E-05	0.01	0.12	0.01	0.11	0	0.49	0.01	0.03
rs12995369	2q33.1	*ALS2CR7*	a	g	0.52	0.05	1.94E-07	0.01	0.24	6	0.37	0.02	8.40E-05	0.03	4.71E-03	0.001	0.84	14	0.24	0.01	0.09
rs6436440	2q36.1	*AP1S3*	a	g	0.47	0.03	2.46E-05	0.01	0.06	0	0.98	0.02	4.58E-05	0.03	6.44E-04	0.02	7.13E-03	0	0.70	0.02	2.41E-05
rs7427438	3p24.1	*RBMS3*	a	c	0.33	-0.04	2.99E-05	-0.01	0.13	34	0.04	-0.02	1.16E-04	-0.01	0.15	0.004	0.65	0	0.59	0.00	0.55
rs2291296	3p24.2	*RARB*	a	g	0.17	-0.004	0.74	-0.01	0.11	0	0.82	-0.01	0.15	-0.04	1.20E-04	-0.02	0.02	22	0.14	-0.03	3.01E-05
rs4957742	5q21.3	*EFNA5*	a	g	0.77	-0.04	4.74E-06	-0.01	0.45	0	0.55	-0.02	5.21E-04	-0.03	7.56E-03	-0.005	0.59	14	0.25	-0.01	0.03
rs2282930	7p12.2	*GRB10*	a	g	0.24	-0.04	8.09E-06	-0.02	0.01	0	0.71	-0.03	3.43E-06	-0.03	4.85E-03	-0.02	4.10E-03	0	0.84	-0.02	6.51E-05
rs7788807	7p22.1_1	*FOXK1*	t	c	0.94	0.02	0.17	0.00	0.96	0	0.89	0.01	0.41	0.06	1.74E-03	0.01	0.54	29	0.07	0.03	0.01
rs2008425	7p22.1_2	*RNF216*	t	g	0.02	-0.08	0.03	-0.05	0.06	20	0.15	-0.06	5.08E-03	-0.11	2.01E-03	-0.04	0.10	15	0.23	-0.06	1.86E-03
rs1670346	7q36.3	*PTPRN2*	a	g	0.29	-0.04	2.81E-06	0.00	0.78	0	0.60	-0.02	2.27E-03	-0.02	0.03	0.002	0.77	15	0.23	-0.01	0.28
rs13272568	8q21.12	*PKIA*	a	c	0.44	-0.04	2.13E-06	-0.02	9.76E-03	0	0.66	-0.03	6.08E-07	-0.01	0.10	-0.004	0.53	27	0.09	-0.01	0.13
rs4240467	9q33.2	*DAB2IP*	c	g	0.32	-0.0004	0.96	0.01	0.51	34	0.04	0.003	0.64	-0.01	0.56	-0.004	0.58	2	0.43	0.00	0.42
rs2784767	10q22.3_2	*PLAC9*	t	c	0.41	0.03	5.08E-04	0.00	0.60	19	0.17	0.01	0.02	0.02	0.07	-0.01	0.23	0	0.89	0.00	0.96
rs11602954	11p15.5	*BET1L*	a	g	0.24	0.03	1.06E-03	0.01	0.17	0	0.47	0.02	1.92E-03	0.06	*2.74E-07*	0.02	0.05	0	0.94	0.03	*2.25E-06*
rs600231	11q13.1	*SCYL1*	a	g	0.70	-0.04	1.19E-05	-0.02	0.01	0	0.74	-0.02	4.03E-06	-0.02	0.03	-0.005	0.53	0	0.94	-0.01	0.07
rs11048046	12p12.1	*IFLTD1*	a	g	0.09	-0.03	0.09	0.00	0.99	0	0.97	-0.01	0.25	-0.01	0.50	-0.001	0.98	0	0.73	-0.01	0.63
rs7326472	13q14.11	*AKAP11*	a	g	0.92	-0.05	2.55E-03	-0.04	0.06	30	0.12	-0.05	5.07E-04	-0.10	*9.80E-08*	-0.04	0.05	2	0.43	-0.07	*2.61E-07*
rs2118784	15q21.2	*CYP19A1*	a	c	0.28	-0.04	5.20E-05	0.00	0.55	17	0.20	-0.02	3.48E-03	-0.03	5.02E-03	-0.01	0.20	16	0.21	-0.02	6.72E-03
rs7226305	17q22	*KIF2B*	a	c	0.84	-0.02	0.13	0.00	0.71	0	0.75	-0.004	0.54	-0.06	*1.33E-06*	0.002	0.81	33	0.04	-0.02	6.66E-03
rs7257450	19p13.11	*PLVAP*	a	g	0.79	0.01	0.55	0.00	0.92	0	0.84	0.003	0.68	0.05	4.01E-05	-0.001	0.94	0	0.65	0.02	0.03
rs4817775	21q22.12	*CBR3*	a	c	0.59	0.02	6.24E-03	0.01	0.04	19	0.16	0.02	8.59E-04	0.04	*1.49E-06*	0.02	0.01	14	0.24	0.03	*8.94E-07*
rs4820539	22q11.23	*RTDR1*	a	g	0.42	0.04	4.86E-06	0.02	2.10E-03	1	0.45	0.03	1.65E-07	0.03	3.65E-03	0.02	1.63E-03	0	0.93	0.02	1.96E-05
rs5926033	Xp22.11	*DDX53*	t	c	0.71	0.04	4.13E-06	0.01	0.19	0	0.68	0.03	9.73E-06	0.01	0.10	0.01	0.35	0	0.49	0.01	0.06
rs5952638	Xp11.3	*DUSP21*	a	t	0.93	0.06	3.03E-04	0.01	0.72	12	0.35	0.04	2.74E-03	0.07	2.29E-05	-0.001	0.94	0	0.72	0.04	1.74E-03
rs4492531	Xq13.3	*MAGEE2*	a	g	0.55	-0.07	1.98E-03	0.01	0.59	0	0.92	-0.03	0.08	-0.09	2.40E-05	-0.02	0.39	4	0.41	-0.05	4.52E-04
rs964181	Xq28	*MAGEA4*	t	c	0.41	0.04	4.72E-06	-0.01	0.20	0	0.57	0.02	8.33E-03	0.03	5.22E-04	0.01	0.48	0	0.60	0.02	2.17E-03

P-values in italics reflect loci reaching sugestive significance level. [a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele. The measure of heterogeneity (Cochran's Qhet P statistic and I2) was calculated in the Stage 2 samples.

Supplementary Table 5A Gender-stratified meta-analysis results across stages for novel loci associated with BMD at GWS level.

						FNBMD													LSBMD										
						FEMALES						MALES							FEMALES						MALES					
						STAGE 1 (n=22,990)		STAGE 2 (n=39,060)		STAGE 1 + STAGE 2 (n=62,050)		STAGE 1 (n=9,971)		STAGE 2 (n=11,885)		STAGE 1 + STAGE 2 (n=21,856)		Gender Het[b]	STAGE 1 (n=22,177)		STAGE 2 (n=34,521)		STAGE 1 + STAGE 2 (n=56,698)		STAGE 1 (n=9,980)		STAGE 2 (n=11,214)		STAGE 1 + STAGE 2 (n=21,194)		Gender Het[b]
SNP	Locus	Closest Gene	A1[a]	A2	Freq1	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P
rs479336	1q24.3	*DNM3*	t	g	0.74	-0.05	8.17E-06	-0.03	2.73E-05	-0.04	**1.56E-09**	-0.06	9.51E-04	-0.06	2.94E-05	-0.06	1.02E-07	0.11	-0.03	0.01	-0.02	4.98E-03	-0.03	1.80E-04	-0.02	0.37	-0.03	0.03	-0.03	0.03	0.96
rs7584262	2p21	*PKDCC*	t	c	0.23	0.05	6.82E-05	0.03	3.42E-03	0.03	2.17E-06	0.07	1.06E-04	0.04	0.03	0.05	2.64E-05	0.21	0.01	0.25	0.02	0.11	0.01	0.05	0.02	0.20	-0.01	0.39	0.00	0.78	0.43
rs17040773	2q13	*ANAPC1*	a	c	0.77	0.04	3.96E-04	0.03	4.73E-04	0.04	7.58E-07	0.07	4.31E-04	0.03	0.04	0.05	1.14E-04	0.39	0.01	0.64	0.00	0.61	0.01	0.50	0.01	0.74	0.03	0.09	0.02	0.14	0.36
rs1878526	2q14.2	*INSIG2*	a	g	0.22	0.01	0.28	-0.01	0.42	0.00	0.99	-0.02	0.34	0.02	0.14	0.01	0.61	0.66	0.06	6.41E-07	0.04	6.13E-05	0.05	**5.44E-10**	0.02	0.28	0.04	0.02	0.03	0.01	0.27
rs1026364	3q13.2	*KIAA2018*	t	g	0.36	0.04	1.34E-04	0.03	1.10E-03	0.03	8.86E-07	0.04	8.57E-03	0.03	0.01	0.04	2.68E-04	0.55	0.02	0.12	0.02	0.05	0.02	0.01	0.02	0.17	0.02	0.08	0.02	0.03	0.59
rs344081	3q25.31	*LEKR1*	t	c	0.87	0.03	0.07	0.03	8.87E-03	0.03	1.52E-03	0.11	6.83E-07	0.03	0.11	0.07	6.62E-06	0.02	0.05	2.97E-03	0.06	1.24E-06	0.05	**1.49E-08**	0.08	2.87E-04	0.06	6.63E-03	0.07	8.69E-06	0.45
rs3755955	4p16.3	*IDUA*	a	g	0.16	-0.06	3.62E-05	-0.05	1.30E-06	-0.05	**2.22E-10**	-0.07	1.52E-03	-0.06	1.07E-03	-0.07	5.77E-06	0.46	-0.06	2.65E-05	-0.05	1.56E-06	-0.06	**2.22E-10**	-0.07	1.79E-03	-0.06	9.86E-04	-0.07	5.92E-06	0.50
rs11755164	6p21.1	*SUPT3H*	t	c	0.40	-0.02	0.13	-0.02	0.04	-0.02	0.01	-0.01	0.73	0.01	0.59	0.00	0.85	0.15	-0.05	1.09E-05	-0.04	2.47E-06	-0.04	**2.19E-10**	-0.06	5.21E-04	-0.01	0.55	-0.03	6.28E-03	0.28
rs9466056	6p22.3	*CDKAL1*	a	g	0.38	-0.04	9.17E-06	-0.04	3.86E-06	-0.04	**1.47E-10**	-0.06	2.48E-04	-0.02	0.10	-0.04	2.24E-04	0.91	-0.02	0.02	-0.03	7.87E-04	-0.03	4.50E-05	-0.06	2.55E-05	-0.03	0.06	-0.05	1.74E-05	0.12
rs3801387	7q31.31	*WNT16*	a	g	0.74	-0.07	**2.22E-11**	-0.08	**1.30E-23**	-0.08	**2.78E-33**	-0.06	1.33E-04	-0.07	1.66E-05	-0.06	**8.50E-09**	0.27	-0.10	**1.87E-16**	-0.11	**3.44E-36**	-0.11	**6.38E-51**	-0.05	2.12E-03	-0.06	4.87E-04	-0.05	3.41E-06	1.27E-04
rs7812088	7q36.1	*ABCF2*	a	g	0.12	0.06	8.92E-05	0.03	5.50E-03	0.04	3.86E-06	0.07	1.90E-03	0.05	0.03	0.06	1.92E-04	0.37	0.05	6.33E-04	0.04	1.28E-03	0.05	3.34E-06	0.06	0.01	0.02	0.43	0.04	0.02	0.68
rs7017914	8q13.3	*XKR9*	a	g	0.49	0.05	**4.70E-08**	0.02	7.11E-03	0.04	**1.94E-08**	0.02	0.16	0.00	0.85	0.01	0.38	0.03	0.01	0.35	-0.01	0.41	0.00	0.98	-0.02	0.21	-0.03	0.05	-0.02	0.02	0.06
rs7851693	9q34.11	*FUBP3*	c	g	0.63	0.05	1.02E-06	0.06	**8.04E-13**	0.05	**5.26E-18**	0.04	6.84E-03	0.05	3.27E-04	0.05	7.39E-06	0.58	0.02	0.02	0.04	2.11E-06	0.03	2.59E-07	0.00	0.88	0.04	9.42E-03	0.02	0.06	0.25
rs3905706	10p11.23	*MPP7*	t	c	0.23	0.01	0.58	-0.02	0.01	-0.01	0.11	0.00	0.96	-0.03	0.04	-0.02	0.13	0.63	0.07	**1.19E-08**	0.05	1.27E-06	0.05	**2.43E-13**	0.05	0.01	0.05	1.37E-03	0.05	4.91E-05	0.71
rs1373004	10q21.1	*MBL2*	t	g	0.12	-0.07	6.32E-06	-0.04	4.62E-04	-0.05	**3.01E-08**	-0.02	0.37	-0.03	0.11	-0.03	0.07	0.22	-0.09	**8.87E-09**	-0.06	3.58E-06	-0.07	**6.63E-13**	-0.03	0.18	-0.03	0.10	-0.03	0.03	0.06
rs7071206	10q22.3_1	*KCNMA1*	t	c	0.76	-0.02	0.09	0.01	0.52	0.00	0.59	0.01	0.41	0.02	0.26	0.02	0.17	0.14	-0.09	**8.34E-13**	-0.05	1.34E-07	-0.06	**1.64E-17**	-0.04	0.02	-0.04	0.01	-0.04	7.27E-04	0.12
rs7084921	10q24.2	*CPN1*	t	c	0.40	0.05	3.13E-06	0.03	2.13E-04	0.03	**7.16E-09**	0.00	0.82	0.04	2.46E-03	0.02	0.02	0.42	0.03	8.62E-03	0.03	2.90E-04	0.03	7.58E-06	0.02	0.25	0.03	0.03	0.02	0.02	0.75
rs10835187	11p14.1_1	*LIN7C*	t	c	0.54	-0.03	3.70E-03	-0.01	0.23	-0.02	6.41E-03	0.03	0.03	-0.02	0.13	0.00	0.77	0.10	-0.05	4.14E-07	-0.03	1.05E-03	-0.04	**1.23E-08**	0.01	0.74	-0.02	0.12	-0.01	0.35	0.03
rs7953528	12p11.22	*KLHDC5*	a	t	0.18	0.05	3.65E-05	0.03	4.54E-04	0.04	1.02E-07	0.08	8.17E-05	0.05	1.06E-03	0.06	4.29E-07	0.11	0.00	0.73	-0.02	0.13	-0.01	0.16	0.01	0.57	-0.02	0.16	-0.01	0.49	0.87
rs2887571	12p13.33	*ERC1*	a	g	0.76	-0.05	1.37E-05	-0.02	3.84E-03	-0.03	8.59E-07	-0.01	0.50	-0.06	1.48E-04	-0.04	9.81E-04	0.73	-0.05	5.60E-06	-0.04	6.13E-06	-0.05	**2.08E-10**	-0.05	1.96E-03	-0.03	0.09	-0.04	8.44E-04	0.64
rs12821008	12q13.12	*DHH*	t	c	0.40	0.03	1.87E-03	0.03	3.22E-03	0.03	1.94E-05	0.04	0.02	0.01	0.29	0.02	0.02	0.81	0.05	3.46E-06	0.04	2.47E-06	0.04	**4.53E-11**	0.04	8.86E-03	0.06	3.06E-05	0.05	1.36E-06	0.59
rs1053051	12q23.3	*C12orf23*	t	c	0.51	-0.04	3.11E-05	-0.03	4.55E-05	-0.04	**6.19E-09**	-0.02	0.11	-0.02	0.14	-0.02	0.03	0.36	-0.04	6.70E-05	-0.03	1.58E-03	-0.03	7.14E-07	-0.04	4.61E-03	-0.01	0.77	-0.03	0.02	0.71
rs1286083	14q32.12	*RPS6KA5*	t	c	0.80	-0.06	2.65E-06	-0.05	5.93E-08	-0.05	**8.93E-13**	-0.06	3.43E-03	-0.03	0.04	-0.04	4.85E-04	0.50	-0.07	**7.44E-09**	-0.05	9.43E-07	-0.06	**1.33E-13**	-0.07	1.44E-04	-0.01	0.69	-0.04	5.25E-03	0.13
rs4985155	16p13.11	*NTAN1*	a	g	0.65	-0.01	0.16	-0.03	4.29E-06	-0.03	5.56E-06	-0.07	1.79E-06	-0.04	9.32E-03	-0.05	2.96E-07	0.03	-0.03	1.16E-03	-0.03	1.16E-03	-0.03	5.35E-06	-0.06	4.76E-05	-0.03	0.08	-0.04	5.88E-05	0.28
rs9921222	16p13.3_1	*AXIN1*	t	c	0.46	-0.05	2.84E-06	-0.03	4.73E-05	-0.04	**1.08E-09**	-0.04	0.01	-0.03	0.02	-0.04	4.68E-04	1.00	-0.05	4.03E-06	-0.05	**7.94E-09**	-0.05	**1.37E-13**	-0.06	2.66E-04	-0.03	0.03	-0.04	3.62E-05	0.78
rs13336428	16p13.3_2	*C16orf38*	a	g	0.44	-0.05	2.56E-06	-0.04	**5.51E-09**	-0.04	**7.17E-14**	-0.04	0.02	-0.04	4.22E-03	-0.04	2.48E-04	0.57	-0.04	2.38E-05	-0.05	**7.82E-09**	-0.04	**1.03E-12**	-0.02	0.23	-0.03	0.02	-0.03	0.01	0.13
rs1566045	16q12.1	*SALL1*	t	c	0.80	-0.07	**2.01E-09**	-0.06	**5.05E-09**	-0.06	**8.89E-17**	-0.08	7.45E-05	-0.06	1.42E-04	-0.07	5.06E-08	0.55	-0.03	9.68E-03	-0.01	0.45	-0.02	0.03	-0.02	0.35	0.00	0.91	-0.01	0.61	0.49
rs4790881	17p13.3	*SMG6*	a	c	0.67	0.05	3.03E-06	0.05	**1.86E-11**	0.05	**2.54E-16**	0.05	1.27E-03	0.03	0.05	0.04	3.51E-04	0.32	0.04	8.79E-04	0.05	**2.72E-09**	0.05	**1.32E-11**	0.01	0.48	-0.01	0.45	0.00	0.93	3.56E-04
rs7217932	17q24.3	*SOX9*	a	g	0.46	0.04	4.30E-06	0.03	4.45E-05	0.03	**1.65E-09**	0.05	4.91E-04	0.02	0.23	0.03	1.25E-03	0.82	0.01	0.23	0.02	0.04	0.01	0.02	0.00	0.84	-0.01	0.57	0.00	0.78	0.14
rs4796995	18p11.21	*C18orf19*	a	g	0.61	0.04	1.09E-04	0.03	5.81E-04	0.03	3.30E-07	0.04	0.01	0.01	0.59	0.02	0.03	0.46	0.03	8.80E-03	0.01	0.18	0.02	7.27E-03	0.04	6.08E-03	0.01	0.43	0.03	0.01	0.49
rs10416218	19q13.11	*GPATCH1*	t	c	0.72	-0.05	1.23E-05	-0.03	9.88E-04	-0.03	1.55E-07	-0.03	0.10	-0.02	0.29	-0.02	0.06	0.31	-0.06	1.08E-06	-0.03	9.66E-04	-0.04	**2.68E-08**	-0.05	1.72E-03	-0.03	0.05	-0.04	3.75E-04	0.90
rs5934507	Xp22.31	*FAM9B*	a	g	0.73	0.00	0.75	0.00	0.98	0.00	0.84	-0.03	0.01	-0.08	8.26E-04	-0.04	1.64E-04	2.96E-03	0.00	0.75	0.01	0.48	0.01	0.46	-0.06	5.66E-06	-0.09	3.21E-04	-0.06	**1.18E-08**	**1.62E-08**

[a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele.[b]gender-specificity null hypothesis, i.e., βFEMALES = βMALES, estimated in the combined STAGE1 + STAGE 2 meta-analysis.

Supplementary Table 5B Gender-stratified meta-analysis results across stages for known loci associated with BMD at GWS level.

						FNBMD													LSBMD										
						FEMALES						MALES							FEMALES						MALES					
						STAGE 1 (n=22,990)		STAGE 2 (n=39,060)		STAGE 1 + STAGE 2 (n=62,050)		STAGE 1 (n=9,971)		STAGE 2 (n=11,885)		STAGE 1 + STAGE 2 (n=21,856)		Gender Het[b]	STAGE 1 (n=22,177)		STAGE 2 (n=34,521)		STAGE 1 + STAGE 2 (n=56,698)		STAGE 1 (n=9,980)		STAGE 2 (n=11,214)		STAGE 1 + STAGE 2 (n=21,194)		Gender Het[b]
SNP	Locus	Closest Gene	A1[a]	A2	Freq1	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P
rs12407028	1p31.3	*WLS*	t	c	0.61	0.06	**1.18E-08**	0.06	**1.77E-15**	0.06	**1.46E-22**	0.03	0.04	0.04	0.01	0.03	1.15E-03	0.04	0.08	**4.57E-16**	0.08	**2.19E-22**	0.08	**5.51E-37**	0.08	9.60E-08	0.07	5.19E-06	0.07	**2.81E-12**	0.60
rs6426749	1p36.12	*ZBTB40*	c	g	0.17	0.11	**1.88E-19**	0.11	**4.86E-27**	0.11	**7.83E-45**	0.09	1.64E-06	0.11	**1.26E-09**	0.10	**1.16E-14**	0.63	0.11	**7.58E-18**	0.10	**1.34E-20**	0.11	**1.08E-36**	0.09	2.26E-05	0.09	3.78E-07	0.09	**3.81E-11**	0.29
rs4233949	2p16.2	*SPTBN1*	c	g	0.38	0.03	4.49E-03	0.02	0.03	0.02	4.15E-04	0.04	4.67E-03	0.02	0.11	0.03	1.78E-03	0.39	0.06	**2.72E-09**	0.04	2.52E-06	0.05	**9.31E-14**	0.06	5.46E-05	0.05	1.47E-03	0.05	3.35E-07	0.74
rs1346004	2q24.3	*GALNT3*	a	g	0.49	-0.05	**1.35E-08**	-0.05	**3.89E-14**	-0.05	**3.31E-21**	-0.05	1.34E-03	-0.05	3.45E-04	-0.05	1.56E-06	0.54	-0.04	2.57E-05	-0.06	**2.84E-16**	-0.06	**1.17E-19**	-0.07	4.79E-06	-0.08	**3.89E-09**	-0.07	**1.04E-13**	0.10
rs430727	3p22.1	*CTNNB1*	t	c	0.47	-0.07	**7.29E-13**	-0.04	**3.29E-08**	-0.05	**1.39E-18**	-0.07	5.98E-06	-0.05	2.46E-04	-0.06	**6.85E-09**	0.56	-0.06	1.28E-07	-0.05	**6.40E-09**	-0.05	**4.53E-15**	-0.06	3.48E-05	-0.04	4.74E-03	-0.05	8.90E-07	0.88
rs6532023	4q22.1	*MEPE*	t	g	0.34	0.06	**2.04E-09**	0.06	**1.42E-13**	0.06	**1.22E-21**	0.03	0.07	0.06	4.78E-06	0.05	4.42E-06	0.40	0.07	**2.25E-11**	0.06	**1.48E-12**	0.06	**2.71E-22**	0.04	0.01	0.07	5.93E-07	0.06	9.85E-08	0.62
rs1366594	5q14.3	*MEF2C*	a	c	0.53	0.10	**6.48E-25**	0.08	**2.58E-26**	0.09	**7.85E-49**	0.08	**4.18E-08**	0.08	**1.78E-09**	0.08	**4.24E-16**	0.64	0.02	0.02	0.01	0.52	0.01	0.05	0.02	0.32	0.03	0.06	0.02	0.04	0.46
rs13204965	6q22.32	*RSPO3*	a	c	0.76	0.07	2.90E-07	0.05	4.43E-07	0.05	**1.90E-12**	0.02	0.21	0.02	0.35	0.02	0.12	0.04	0.05	8.23E-04	0.04	1.77E-05	0.04	5.38E-08	0.04	0.02	0.05	9.44E-03	0.05	5.73E-04	0.83
rs4869742	6q25.1	*C6orf97*	t	c	0.32	-0.07	**1.40E-11**	-0.03	9.59E-05	-0.05	**3.14E-13**	-0.06	1.48E-04	-0.06	1.53E-05	-0.06	**8.84E-09**	0.24	-0.09	**3.39E-15**	-0.06	**6.67E-11**	-0.07	**9.41E-24**	-0.09	8.95E-08	-0.09	**5.02E-09**	-0.09	**2.56E-15**	0.19
rs6959212	7p14.1	*STARD3NL*	t	c	0.34	-0.03	9.26E-03	-0.05	**1.09E-09**	-0.04	**1.30E-10**	-0.04	0.01	-0.04	3.31E-03	-0.04	9.15E-05	0.90	-0.08	**3.68E-13**	-0.08	**2.54E-20**	-0.08	**4.10E-32**	-0.07	4.23E-06	-0.05	2.20E-04	-0.06	**6.12E-09**	0.23
rs4727338	7q21.3	*SLC25A13*	c	g	0.67	0.08	**1.92E-15**	0.08	**6.04E-24**	0.08	**1.20E-37**	0.08	2.01E-07	0.07	3.73E-07	0.08	**3.33E-13**	0.73	0.07	**2.23E-10**	0.07	**1.00E-15**	0.07	**1.34E-24**	0.09	6.43E-08	0.07	1.18E-06	0.08	**4.67E-13**	0.48
rs2062377	8q24.12	*TNFRSF11B*	a	t	0.59	-0.06	**1.16E-09**	-0.05	**1.68E-09**	-0.05	**1.60E-17**	-0.07	8.34E-07	-0.06	3.26E-04	-0.06	**1.50E-09**	0.33	-0.08	**7.13E-16**	-0.07	**3.35E-15**	-0.07	**2.55E-29**	-0.07	9.83E-07	-0.08	8.65E-07	-0.08	**3.94E-12**	0.91
rs7932354	11p11.2	*ARHGAP1*	t	c	0.33	0.05	9.97E-07	0.04	2.77E-06	0.04	**1.60E-11**	0.05	3.41E-03	0.07	3.93E-07	0.06	**9.34E-09**	0.16	0.04	3.49E-04	0.04	1.09E-05	0.04	**1.34E-08**	0.04	8.59E-03	0.04	4.39E-03	0.04	1.09E-04	0.85
rs163879	11p14.1_2	*DCDC5*	t	c	0.66	-0.04	1.19E-04	-0.02	9.89E-03	-0.03	1.15E-05	-0.05	1.34E-03	-0.04	9.74E-03	-0.05	4.10E-05	0.15	-0.05	5.13E-07	-0.02	4.40E-03	-0.03	1.01E-07	-0.04	7.47E-03	-0.06	1.03E-04	-0.05	3.67E-06	0.18
rs7108738	11p15.2	*SOX6*	t	g	0.82	-0.09	**6.42E-14**	-0.07	**3.47E-14**	-0.08	**3.52E-26**	-0.08	2.55E-05	-0.07	9.09E-05	-0.07	**1.05E-08**	0.69	-0.05	1.20E-04	-0.02	0.03	-0.03	5.76E-05	-0.03	0.14	-0.03	0.05	-0.03	0.01	0.99
rs3736228	11q13.2	*LRP5*	t	c	0.15	-0.05	5.08E-04	-0.05	9.14E-05	-0.05	1.82E-07	-0.08	2.30E-04	-0.05	0.02	-0.06	2.06E-05	0.32	-0.08	**1.91E-08**	-0.10	**1.34E-15**	-0.09	**2.80E-22**	-0.10	5.51E-06	-0.06	0.01	-0.08	4.21E-07	0.53
rs2016266	12q13.13	*SP7*	a	g	0.69	-0.04	2.91E-05	-0.02	1.43E-03	-0.03	3.82E-07	-0.04	0.01	-0.04	7.19E-03	-0.04	2.39E-04	0.54	-0.07	**2.18E-10**	-0.05	**6.68E-09**	-0.06	**2.13E-17**	-0.04	5.72E-03	-0.04	5.36E-03	-0.04	9.14E-05	0.29
rs9533090	13q14.11	*AKAP11*	t	c	0.48	-0.06	**1.80E-10**	-0.05	**2.79E-13**	-0.06	**3.36E-22**	-0.03	0.03	-0.03	0.06	-0.03	3.61E-03	0.05	-0.12	**6.31E-31**	-0.10	**6.92E-33**	-0.11	**1.51E-61**	-0.09	**7.43E-09**	-0.08	7.96E-07	-0.09	**2.62E-14**	0.16
rs11623869	14q32.32	*MARK3*	t	g	0.34	-0.04	1.41E-05	-0.05	**1.70E-09**	-0.05	**1.27E-13**	-0.04	8.02E-03	-0.04	9.64E-03	-0.04	2.12E-04	0.59	-0.03	9.24E-03	-0.04	3.83E-07	-0.04	**2.30E-08**	-0.04	7.11E-03	-0.04	6.65E-03	-0.04	1.30E-04	0.74
rs10048146	16q24.1	*FOXL1*	a	g	0.80	0.05	5.29E-06	0.04	3.40E-05	0.05	**1.14E-09**	0.06	9.58E-04	0.07	4.50E-05	0.07	1.66E-07	0.15	0.07	1.55E-07	0.04	1.27E-04	0.05	**4.37E-10**	0.06	3.52E-03	0.03	0.13	0.04	2.10E-03	0.59
rs227584	17q21.31_1	*C17orf53*	a	c	0.67	-0.06	**3.31E-09**	-0.05	**1.35E-10**	-0.06	**3.15E-18**	-0.05	2.11E-03	-0.06	1.99E-05	-0.06	1.87E-07	0.86	-0.04	5.66E-05	-0.03	2.98E-03	-0.03	1.64E-06	-0.06	2.96E-04	-0.04	0.01	-0.05	1.63E-05	0.23
rs1864325	17q21.31_2	*MAPT*	t	c	0.22	-0.04	1.68E-03	-0.01	0.25	-0.02	4.60E-03	-0.05	4.55E-03	-0.03	0.06	-0.04	8.44E-04	0.14	-0.06	8.01E-06	-0.03	4.83E-04	-0.04	**3.96E-08**	-0.06	1.40E-03	-0.04	0.02	-0.05	9.06E-05	0.63
rs884205	18q21.33	*TNFRSF11A*	a	c	0.25	-0.05	2.57E-05	-0.04	9.47E-07	-0.04	**1.43E-10**	-0.03	0.13	-0.01	0.38	-0.02	0.10	0.06	-0.07	2.67E-07	-0.06	**9.12E-10**	-0.06	**1.66E-15**	-0.06	8.99E-04	-0.03	0.04	-0.04	1.63E-04	0.28
rs3790160	20p12.2	*JAG1*	t	c	0.50	0.04	2.58E-05	0.02	6.36E-04	0.03	1.31E-07	0.05	6.06E-04	0.05	2.90E-04	0.05	6.14E-07	0.09	0.06	**1.81E-08**	0.04	9.42E-07	0.05	**2.49E-13**	0.05	6.94E-04	0.06	3.49E-05	0.05	9.21E-08	0.45

[a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele. [b]gender-specificity null hypothesis, i.e., βFEMALES = βMALES, estimated in the combined STAGE1 + STAGE 2 meta-analysis.

Supplementary Table 5C Gender-stratified meta-analysis results across stages for BMD loci not reaching GWS level.

						FNBMD													LSBMD										
						FEMALES						MALES							FEMALES						MALES					
						STAGE 1 (n=22,990)		STAGE 2 (n=39,060)		STAGE 1 + STAGE 2 (n=62,050)		STAGE 1 (n=9,971)		STAGE 2 (n=11,885)		STAGE 1 + STAGE 2 (n=21,856)		Gender Het[b]	STAGE 1 (n=22,177)		STAGE 2 (n=34,521)		STAGE 1 + STAGE 2 (n=56,698)		STAGE 1 (n=9,980)		STAGE 2 (n=11,214)		STAGE 1 + STAGE 2 (n=21,194)		Gender Het[b]
SNP	Locus	Closest Gene	A1[a]	A2	Freq1	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	Beta	P	P
rs11809524	1p21.1	*COL11A1*	t	c	0.85	0.05	1.07E-04	0.02	0.06	0.03	1.20E-04	0.06	2.20E-03	0.01	0.67	0.03	0.02	0.90	0.05	1.25E-03	0.02	0.14	0.03	1.79E-03	0.06	3.98E-03	0.01	0.43	0.04	0.01	0.60
rs12137389	1p34.1	*TESK2*	t	c	0.02	-0.12	1.19E-04	-0.01	0.60	-0.06	3.36E-03	-0.13	5.67E-03	0.00	1.00	-0.07	0.04	0.75	-0.04	0.28	0.02	0.58	-0.01	0.77	-0.07	0.15	0.03	0.58	-0.03	0.48	0.65
rs2120461	1p36.23	*RERE*	t	c	0.68	0.04	9.40E-06	0.01	0.15	0.02	1.06E-04	0.06	1.21E-04	0.01	0.44	0.03	1.32E-03	0.39	0.04	1.61E-04	0.02	0.01	0.03	1.50E-05	0.03	0.06	0.02	0.14	0.03	0.02	0.84
rs12120297	1q41	*SUSD4*	t	c	0.85	0.05	2.59E-04	0.01	0.58	0.02	0.01	0.02	0.38	-0.05	4.64E-03	-0.03	0.08	5.06E-03	0.06	1.72E-04	0.01	0.19	0.03	1.38E-03	0.08	1.38E-03	-0.02	0.41	0.02	0.22	0.54
rs730402	2p16.1	*BCL11A*	a	g	0.45	0.02	0.07	-0.002	0.80	0.01	0.36	0.07	2.62E-06	0.03	0.05	0.05	4.29E-06	4.18E-04	0.01	0.25	-0.001	0.91	0.004	0.53	0.04	0.01	0.01	0.59	0.02	0.04	0.16
rs13413210	2p23.2	*ALK*	a	c	0.91	0.00	0.83	-0.01	0.44	-0.01	0.46	-0.06	0.03	0.01	0.74	-0.02	0.24	0.53	-0.01	0.59	-0.005	0.73	-0.01	0.55	-0.13	2.65E-06	0.02	0.43	-0.05	0.01	0.07
rs11675051	2q32.2	*NAB1*	a	g	0.32	0.05	1.47E-06	0.01	0.24	0.02	9.46E-05	0.02	0.28	0.02	0.11	0.02	0.06	0.74	0.02	0.08	0.01	0.26	0.01	0.05	0.001	0.95	0.02	0.25	0.01	0.39	0.78
rs12995369	2q33.1	*ALS2CR7*	a	g	0.55	0.05	4.56E-06	0.01	0.37	0.02	8.80E-04	0.06	1.26E-03	0.01	0.45	0.03	8.95E-03	0.55	0.02	0.05	-0.003	0.71	0.005	0.47	0.05	8.13E-03	0.02	0.23	0.03	9.05E-03	0.06
rs6436440	2q36.1	*AP1S3*	a	g	0.47	0.05	1.17E-06	0.02	0.01	0.03	5.58E-07	0.01	0.71	-0.01	0.47	-0.003	0.77	5.58E-03	0.03	1.10E-03	0.02	0.02	0.02	1.24E-04	0.02	0.11	0.02	0.27	0.02	0.06	0.69
rs7427438	3p24.1	*RBMS3*	a	c	0.33	-0.05	2.29E-06	-0.004	0.66	-0.02	6.70E-04	-0.01	0.67	-0.03	0.04	-0.02	0.07	0.82	-0.02	0.12	0.01	0.17	-0.0001	0.98	-0.01	0.73	-0.02	0.16	-0.01	0.21	0.30
rs2291296	3p24.2	*RARB*	a	g	0.17	-0.01	0.59	-0.01	0.13	-0.01	0.12	0.00	0.85	-0.01	0.63	-0.003	0.84	0.58	-0.06	3.76E-06	-0.02	0.03	-0.04	5.22E-06	-0.01	0.78	-0.02	0.40	-0.01	0.44	0.12
rs4957742	5q21.3	*EFNA5*	a	g	0.77	-0.05	1.27E-05	-0.01	0.21	-0.03	2.38E-04	-0.03	0.05	0.02	0.31	-0.01	0.51	0.23	-0.03	0.01	-0.01	0.51	-0.02	0.04	-0.03	0.15	0.000	0.99	-0.01	0.30	0.91
rs2282930	7p12.2	*GRB10*	a	g	0.26	-0.06	5.03E-07	-0.02	0.02	-0.03	1.08E-06	-0.01	0.45	-0.01	0.38	-0.01	0.25	0.14	-0.04	2.26E-03	-0.03	3.51E-03	-0.03	3.02E-05	-0.01	0.42	-0.01	0.48	-0.01	0.29	0.21
rs7788807	7p22.1_1	*FOXK1*	t	c	0.94	0.04	0.03	0.002	0.90	0.02	0.16	-0.03	0.28	-0.01	0.66	-0.02	0.29	0.10	0.10	4.11E-06	0.02	0.29	0.05	2.08E-04	-0.04	0.24	-0.02	0.44	-0.03	0.17	1.99E-03
rs2008425	7p22.1_2	*RNF216*	t	g	0.02	-0.13	2.00E-03	-0.06	0.02	-0.08	2.86E-04	0.01	0.80	0.01	0.82	0.01	0.74	0.03	-0.19	2.97E-06	-0.06	0.06	-0.10	2.14E-05	-0.05	0.38	0.01	0.86	-0.02	0.67	0.06
rs1670346	7q36.3	*PTPRN2*	a	g	0.30	-0.04	1.58E-05	0.00	0.53	-0.02	1.74E-03	-0.03	0.05	0.01	0.61	-0.01	0.37	0.43	-0.02	0.03	0.003	0.73	-0.01	0.27	-0.01	0.59	0.00	0.96	-0.004	0.69	0.81
rs13272568	8q21.12	*PKIA*	a	c	0.44	-0.04	4.34E-05	-0.02	0.03	-0.03	1.90E-05	-0.04	0.01	-0.02	0.21	-0.03	7.74E-03	0.88	-0.01	0.24	-0.01	0.31	-0.01	0.13	-0.01	0.34	0.01	0.54	-0.002	0.83	0.55
rs4240467	9q33.2	*DAB2IP*	c	g	0.32	0.02	0.14	0.01	0.56	0.01	0.16	-0.04	6.75E-03	0.004	0.77	-0.02	0.10	0.03	0.03	0.02	0.003	0.76	0.01	0.08	-0.08	9.65E-07	-0.03	0.10	-0.05	4.75E-06	1.36E-06
rs2784767	10q22.3_2	*PLAC9*	t	c	0.43	0.05	4.80E-06	0.003	0.67	0.02	4.34E-03	-0.01	0.42	0.002	0.86	-0.004	0.74	0.09	0.04	5.09E-03	-0.004	0.65	0.01	0.28	-0.01	0.67	-0.02	0.08	-0.02	0.10	0.05
rs11602954	11p15.5	*BET1L*	a	g	0.23	0.03	0.03	0.01	0.15	0.02	0.01	0.05	5.10E-03	0.003	0.85	0.03	0.04	0.59	0.05	6.74E-05	0.03	5.71E-03	0.04	4.24E-06	0.07	3.24E-04	-0.02	0.33	0.02	0.07	0.37
rs600231	11q13.1	*SCYL1*	a	g	0.69	-0.05	9.03E-07	-0.02	0.03	-0.03	1.98E-06	-0.01	0.49	-0.01	0.31	-0.01	0.22	0.18	-0.03	3.55E-03	-0.004	0.63	-0.01	0.03	0.001	0.97	-0.01	0.67	-0.003	0.77	0.38
rs11048046	12p12.1	*IFLTD1*	a	g	0.08	0.01	0.73	0.00	0.91	0.004	0.75	-0.15	3.59E-06	-0.01	0.85	-0.07	9.49E-04	2.21E-03	0.01	0.78	0.000	1.00	0.003	0.85	-0.05	0.08	-0.003	0.92	-0.03	0.20	0.23
rs2118784	15q21.2	*CYP19A1*	a	c	0.29	-0.05	1.41E-06	0.002	0.81	-0.02	6.15E-03	0.00	0.78	-0.02	0.10	-0.02	0.15	0.89	-0.04	5.26E-04	-0.01	0.35	-0.02	4.06E-03	-0.01	0.68	-0.01	0.34	-0.01	0.32	0.51
rs7226305	17q22	*KIF2B*	a	c	0.82	-0.02	0.16	0.01	0.59	-0.003	0.69	-0.02	0.39	-0.004	0.82	-0.01	0.47	0.67	-0.06	1.97E-05	0.01	0.56	-0.02	0.04	-0.05	0.01	-0.01	0.64	-0.03	0.05	0.54
rs7257450	19p13.11	*PLVAP*	a	g	0.76	0.01	0.28	0.00	0.63	0.01	0.32	-0.01	0.56	-0.01	0.59	-0.01	0.43	0.24	0.07	4.79E-06	0.00	0.89	0.02	0.02	0.02	0.37	0.004	0.79	0.01	0.45	0.55
rs4817775	21q22.12	*CBR3*	a	c	0.58	0.02	0.07	0.01	0.04	0.02	6.48E-03	0.04	0.02	0.01	0.51	0.02	0.04	0.68	0.04	1.45E-04	0.01	0.07	0.02	1.62E-04	0.05	9.98E-04	0.03	0.06	0.04	3.25E-04	0.26
rs4820539	22q11.23	*RTDR1*	a	g	0.44	0.04	1.18E-04	0.02	0.01	0.02	1.49E-05	0.04	8.38E-03	0.02	0.09	0.03	2.68E-03	0.68	0.02	0.06	0.02	8.80E-03	0.02	1.29E-03	0.04	0.02	0.02	0.08	0.03	4.78E-03	0.46
rs5926033	Xp22.11	*DDX53*	t	c	0.71	0.03	5.79E-03	0.02	0.17	0.02	3.21E-03	0.05	1.08E-04	0.005	0.85	0.04	4.20E-04	0.23	0.01	0.19	0.005	0.69	0.01	0.23	0.02	0.21	0.04	0.13	0.02	0.07	0.42
rs5952638	Xp11.3	*DUSP21*	a	t	0.93	0.05	0.01	0.01	0.77	0.03	0.05	0.06	9.82E-03	0.01	0.82	0.05	0.02	0.36	0.05	0.03	0.004	0.86	0.02	0.10	0.08	6.07E-04	-0.02	0.62	0.06	5.79E-03	0.16
rs4492531	Xq13.3	*MAGEE2*	a	g	0.55	-0.05	0.04	0.001	0.96	-0.02	0.19	-0.09	0.02	0.05	0.24	-0.03	0.25	0.76	-0.09	7.42E-04	-0.02	0.35	-0.05	4.09E-03	-0.11	3.35E-03	0.002	0.96	-0.06	0.02	0.71
rs964181	Xq28	*MAGEA4*	t	c	0.41	0.04	3.44E-04	-0.01	0.35	0.01	0.06	0.03	0.02	-0.02	0.37	0.02	0.13	0.83	0.02	0.03	0.00	0.71	0.01	0.08	0.03	0.01	0.02	0.35	0.03	9.21E-03	0.90

[a]Beta estimates (effect on each allele of the SNP on standardized BMD) and frequencies are reported for this allele. [b]gender-specificity null hypothesis, i.e., βFEMALES = βMALES, estimated in the combined STAGE1 + STAGE 2 meta-analysis.

Supplementary Table 6 Association of BMD loci with Any low-trauma fracture across stage categories

					STAGE 1 (In-silico 1) 5411 cases, 21909 controls		STAGE 2 (In-silico 2) 9187 cases, 45057 controls		STAGE 2 (De-novo genotyping) 16418 cases, 35478 controls		STAGE 2 (Insilico 2 + De-novo) 25605 cases, 80535 controls		COMBINED (STAGE 1 + STAGE 2) 31016 cases, 102444 controls			
SNP	Risk Allele	Locus	Closest Gene	Freq1	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)	P	I^2	Qhet P
rs6426749	G	1p36.12	*ZBTB40*	0.83	1.1 (1.03-1.16)	0.003	1.11 (1.06-1.17)	4.20E-05	1.03 (0.99-1.07)	0.141	1.06 (1.03-1.09)	2.36E-04	1.07 (1.04-1.1)	3.60E-06	24	0.07
rs7521902	A	1p36.12*	*WNT4*	0.27	1.08 (1.02-1.15)	0.012	1.12 (1.06-1.18)	1.50E-05	1.07 (1-1.13)	0.038	1.10 (1.06-1.14)	3.51E-06	1.09 (1.06-1.13)	1.40E-07	0	0.87
rs4233949	G	2p16.2	*SPTBN1*	0.63	1.05 (1-1.1)	0.052	1.08 (1.04-1.13)	3.00E-05	1.05 (1.02-1.09)	6.50E-04	1.07 (1.04-1.09)	1.39E-07	1.06 (1.04-1.08)	2.60E-08	6	0.36
rs430727	T	3p22.1	*CTNNB1*	0.47	1.07 (1.02-1.12)	0.003	1.04 (1.01-1.08)	0.026	1.06 (1.03-1.09)	2.90E-04	1.05 (1.03-1.08)	2.44E-05	1.06 (1.03-1.08)	2.90E-07	0	0.93
rs6532023	G	4q22.1	*MEPE*	0.67	1.07 (1.02-1.12)	0.006	1.03 (0.99-1.07)	0.12	1.08 (1.05-1.12)	5.20E-07	1.06 (1.04-1.09)	8.84E-07	1.06 (1.04-1.09)	1.70E-08	0	1.00
rs6959212	T	7p14.1	*STARD3NL*	0.33	1.06 (1.01-1.11)	0.021	1.02 (0.98-1.06)	0.276	1.05 (1.02-1.09)	0.001	1.04 (1.02-1.07)	1.02E-03	1.05 (1.02-1.07)	7.20E-05	2	0.43
rs4727338	G	7q21.3	*SLC25A13*	0.32	1.08 (1.03-1.13)	0.002	1.09 (1.05-1.14)	1.30E-05	1.06 (1.03-1.1)	1.10E-04	1.08 (1.05-1.1)	1.04E-08	1.08 (1.05-1.1)	5.90E-11	31	0.03
rs3801387	A	7q31.31	*WNT16*	0.74	1.01 (0.97-1.05)	0.666	1.07 (1.02-1.11)	0.004	1.09 (1.06-1.13)	2.30E-07	1.08 (1.05-1.11)	4.98E-09	1.06 (1.04-1.08)	2.70E-07	0	0.69
rs7851693	G	9q34.11	*FUBP3*	0.37	1.07 (1.03-1.12)	0.003	1.06 (1.02-1.1)	0.003	1.03 (1-1.06)	0.094	1.04 (1.01-1.06)	1.88E-03	1.05 (1.02-1.07)	3.50E-05	0	0.65
rs1373004	T	10q21.1	*MBL2/DKK1*	0.13	1.11 (1.04-1.19)	0.003	1.05 (1-1.12)	0.065	1.12 (1.07-1.17)	1.10E-06	1.09 (1.06-1.13)	7.19E-07	1.1 (1.06-1.13)	9.00E-09	0	0.64
rs163879	T	11p14.1	*DCDC5*	0.66	1.01 (0.96-1.06)	0.775	1.05 (1.01-1.1)	0.011	1.06 (1.03-1.1)	1.70E-04	1.06 (1.03-1.09)	6.40E-06	1.05 (1.03-1.07)	3.30E-05	28	0.05
rs3736228	T	11q13.2	*LRP5*	0.15	1.11 (1.04-1.19)	0.002	1.14 (1.08-1.2)	6.60E-07	1.05 (1-1.1)	0.051	1.09 (1.05-1.12)	2.06E-06	1.09 (1.06-1.13)	1.40E-08	0	0.78
rs1286083	T	14q32.12	*RPS6KA5*	0.81	1.07 (1.01-1.13)	0.024	1.08 (1.02-1.13)	0.004	1.04 (1-1.08)	0.05	1.05 (1.02-1.08)	9.76E-04	1.05 (1.03-1.08)	7.20E-05	34	0.01
rs4792909	G	17q21.31*	*SOST*	0.62	1.05 (1-1.11)	0.053	1.07 (1.03-1.12)	0.001	1.07 (1.02-1.13)	0.009	1.07 (1.04-1.11)	3.99E-05	1.07 (1.04-1.1)	6.90E-06	10	0.31
rs227584	A	17q21.31	*C17orf53*	0.67	1.05 (1-1.1)	0.076	1.06 (1.02-1.1)	0.007	1.04 (1.01-1.08)	0.01	1.05 (1.02-1.08)	2.17E-04	1.05 (1.03-1.07)	4.10E-05	0	0.49
rs4796995	G	18p11.21	*C18orf19*	0.39	1.15 (1.1-1.2)	3.50E-09	1.07 (1.03-1.11)	3.80E-04	1.06 (1.02-1.09)	3.90E-04	1.06 (1.04-1.09)	6.37E-07	1.08 (1.06-1.1)	8.80E-13	20	0.12

The odds ratios are per allele copy for any low-trauma fracture among cases as compared with controls across stages. Stage 1: Samples also used in the discovery of BMD-associated variants. Results of Stage 2 are here divided by In-silico replication and de-novo genotyped studies. The measures of heterogeneity (Cochran's Q statistic and I^2) was calculated in the combined data set across all stages.

Supplementary Table 7 Proportion of Fracture Risk explained by BMD.

				ANYFRACTURE (8594 cases, 23218 controls)						
				not FNBMD adjusted			FNBMD adjusted			Fracture risk
SNP	Risk Allele	Locus	Closest Gene	Effect	StdErr	P	Effect	StdErr	P	explained by BMD
rs4796995	G	18p11.21	*C18orf19*	0.08	0.02	8.77E-05	0.07	0.02	1.12E-03	0.15
rs4727338	G	7q21.3	*SLC25A13*	0.08	0.02	2.78E-04	0.05	0.02	1.46E-02	0.32
rs3801387	A	7q31.31	*WNT16*	0.08	0.02	3.17E-04	0.05	0.02	2.15E-02	0.35
rs227584	A	17q21.31_1	*C17orf53*	0.08	0.02	4.84E-04	0.06	0.02	9.78E-03	0.25
rs1373004	T	10q21.1	*MBL2*	0.11	0.03	5.09E-04	0.09	0.03	3.27E-03	0.14
rs163879	T	11p14.1_2	*DCDC5*	0.06	0.02	1.85E-03	0.06	0.02	5.29E-03	0.09
rs430727	T	3p22.1	*CTNNB1*	0.06	0.02	4.13E-03	0.05	0.02	2.63E-02	0.21
rs6532023	G	4q22.1	*MEPE*	0.05	0.02	1.27E-02	0.03	0.02	1.40E-01	0.40
rs4233949	G	2p16.2	*SPTBN1*	0.05	0.02	3.07E-02	0.04	0.02	5.60E-02	0.10
rs6959212	T	7p14.1	*STARD3NL*	0.04	0.02	4.68E-02	0.03	0.02	1.73E-01	0.30
rs3736228	T	11q13.2	*LRP5*	0.05	0.03	0.13	0.04	0.03	0.29	NS
rs7851693	G	9q34.11	*FUBP3*	0.03	0.02	0.17	0.01	0.02	0.56	NS
rs1286083	T	14q32.12	*RPS6KA5*	0.03	0.03	0.17	0.02	0.03	0.35	NS
rs6426749	G	1p36.12	*ZBTB40*	0.03	0.03	0.28	0.01	0.03	0.76	NS

Supplementary Table 8 **Results of meta-analysis for different types of fractures**

					ANYFRACTURE		NONVERTEBRAL FRACTURE		VERTEBRAL FRACTURE	
					31016 cases, 102444 controls		12941 cases, 41263 controls		3659 cases, 17,899 controls	
SNP	Locus	Closest Gene	Risk Allele	Freq	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)	P
rs6426749	1p36.12	*ZBTB40*	G	0.83	1.07 (1.04-1.1)	3.6E-06	1.09 (1.04-1.13)	1.8E-04	1.04 (0.97-1.12)	0.28
rs4233949	2p16.2	*SPTBN1*	G	0.63	1.06 (1.04-1.08)	2.6E-08	1.06 (1.02-1.09)	8.7E-04	1.02 (0.96-1.08)	0.50
rs430727	3p22.1	*CTNNB1*	T	0.47	1.06 (1.03-1.08)	2.9E-07	1.03 (1-1.07)	4.6E-02	1.07 (1.01-1.14)	0.02
rs6532023	4q22.1	*MEPE*	G	0.67	1.06 (1.04-1.09)	1.7E-08	1.07 (1.03-1.11)	2.4E-04	1.11 (1.04-1.18)	9.3E-04
rs6959212	7p14.1	*STARD3NL*	T	0.33	1.05 (1.03-1.08)	7.2E-05	1.07 (1.03-1.1)	3.4E-04	1.04 (0.98-1.1)	0.24
rs4727338	7q21.3	*SLC25A13*	G	0.32	1.08 (1.05-1.1)	5.9E-11	1.07 (1.04-1.11)	5.2E-05	1.08 (1.02-1.15)	0.01
rs3801387	7q31.31	*WNT16*	A	0.74	1.06 (1.04-1.08)	2.7E-07	1.1 (1.06-1.14)	2.4E-07	0.98 (0.93-1.05)	0.62
rs7851693	9q34.11	*FUBP3*	G	0.37	1.05 (1.02-1.07)	3.5E-05	1.05 (1.01-1.09)	4.8E-03	0.96 (0.91-1.02)	0.18
rs1373004	10q21.1	*MBL2*	T	0.13	1.1 (1.06-1.13)	9.0E-09	1.11 (1.05-1.17)	1.2E-04	1.05 (0.96-1.15)	0.29
rs163879	11p14.1	*DCDC5*	T	0.66	1.05 (1.03-1.07)	3.3E-05	1.05 (1.01-1.09)	6.3E-03	1.04 (0.98-1.11)	0.20
rs3736228	11q13.2	*LRP5*	T	0.15	1.09 (1.06-1.13)	1.4E-08	1.07 (1.02-1.13)	4.7E-03	1.02 (0.94-1.11)	0.61
rs1286083	14q32.12	*RPS6KA5*	T	0.81	1.05 (1.02-1.07)	7.2E-05	1.07 (1.03-1.12)	1.7E-03	0.99 (0.92-1.06)	0.74
rs227584	17q21.31	*C17orf53*	A	0.67	1.05 (1.03-1.07)	4.1E-05	1.04 (1.01-1.08)	2.1E-02	1.05 (0.99-1.12)	0.11
rs4796995	18p11.21	*C18orf19*	G	0.39	1.08 (1.06-1.1)	8.8E-13	1.08 (1.04-1.11)	1.5E-05	1.02 (0.97-1.08)	0.46

Supplementary Table 9 Weights for Allele Score Modeling

SNP	Allele1	Effect
rs6426749	G	2.75566397
rs1366594	C	2.10711923
rs3801387	A	1.99772615
rs4727338	G	1.98730776
rs17482952	G	1.95865719
rs7108738	T	1.73726641
rs6532023	G	1.54192161
rs736825	G	1.53931702
rs1566045	T	1.47159749
rs3755955	A	1.45336531
rs12407028	C	1.39606416
rs2062377	A	1.36741359
rs7851693	G	1.3622044
rs227584	A	1.35178601
rs1346004	A	1.34918141
rs10048146	G	1.33615843
rs9533090	T	1.27364809
rs1286083	T	1.25541591
rs6959212	T	1.19811477
rs3736228	T	1.18248718
rs7932354	C	1.15904581
rs430727	T	1.15123202
rs4790881	C	1.14341822
rs13336428	A	1.13299983
rs4792909	G	1.09653547
rs11623869	T	1.09132628
rs479336	T	1.08611708
rs13204965	C	1.08090789
rs7953528	T	1.07830329
rs7812088	G	0.98974698
rs17040773	C	0.91160906
rs4985155	A	0.89337688
rs4869742	T	0.88295849
rs7751941	A	0.86212171
rs884205	A	0.85691252
rs1026364	G	0.84128493
rs2887571	A	0.83347114
rs1053051	T	0.83347114
rs1373004	T	0.81784356
rs9466056	A	0.79961138
rs7584262	C	0.77617
rs3790160	C	0.73970564
rs7084921	C	0.73449644
rs2016266	A	0.6797999
rs12821008	C	0.66156772
rs9921222	T	0.65896312
rs1564981	A	0.65635852
rs10416218	T	0.65375393
rs344081	C	0.65375393
rs163879	T	0.65114933
rs7217932	G	0.64854473
rs7521902	A	0.64073094
rs3905706	T	0.61468497
rs4233949	G	0.53915165
rs4796995	G	0.47664131
rs1864325	T	0.44278154
rs7017914	G	0.43236316
rs10226308	G	0.2891103
rs10835187	T	0.28390111
rs11755164	T	0.20315859
rs13245690	G	0.1901356
rs7071206	C	0.14064826
rs1878526	A	0.06771953

Weights are based on the stage 2 meta-analysis effects sizes for FN-BMD and standarized using a mean centric calibration

Supplementary Table 10 Associated top SNPs from FN-BMD association analysis using 1000G imputed genotypes (Pooled analysis)

Targeted (Lead) SNPs (identified in HapMap Imputation)							Most significant SNPs (1000G Imputation)						
SNP rs#	Chr.	Position	Freq	Effect	SE	P-value	SNP rs#	Position	Freq	Effect	SE	P-value	$log10(P_{lead}/P_{1000G})$
rs1346004	2	166309292	0.51	-0.049	0.009	8.98E-08	rs28549203	166282329	0.31	-0.063	0.010	1.00E-09	-2.0
rs4727338	7	95958611	0.67	0.073	0.009	6.89E-15	rs4729260	95955854	0.68	0.079	0.010	1.40E-16	-1.7
rs7017914*	8	71753757	0.51	0.040	0.009	1.76E-05	rs3110251	72099528	0.52	-0.046	0.009	3.12E-07	-1.8
rs7932354	11	46678797	0.32	0.043	0.010	1.10E-05	rs12274785	46670855	0.70	-0.050	0.010	5.80E-07	-1.3
rs4796995	18	13698574	0.63	0.041	0.009	8.70E-06	rs12955116	13678383	0.33	-0.054	0.010	1.82E-07	-1.7

Loci with a more significant marker (defined as change in significance of more than one order of magnitud) identified in regional imputation using P values from targeted snps are updated from meta-analysis of same studies that contributed to 1000G regiontal imputation.

*This locus was selected in the gender-stratified meta-analysis

Supplementary Table 11 **Associated top SNPs from LS-BMD association analysis using 1000G imputed genotypes (Pooled analysis)**

Targeted (Lead) SNPs (identified in HapMap Imputation)							Most significant SNPs (1000G Imputation)						
SNP rs#	Chr.	Position	Freq	Effect	SE	P-value	SNP rs#	Position	Freq	Effect	SE	P-value	$\log10(P_{lead}/P_{1000G})$
rs1878526*	2	118755068	0.23	0.038	0.011	9.02E-04	chr2:118804639	118804639	0.08	0.100	0.022	3.41E-06	-2.4
rs3801387	7	120762001	0.74	-0.075	0.011	4.26E-12	rs3779381	120754026	0.76	-0.082	0.011	2.03E-13	-1.3
rs1373004*	10	54097831	0.12	-0.075	0.015	5.92E-07	rs7902708	54109734	0.12	-0.082	0.015	5.68E-08	-1.0
rs10835187*	11	27462253	0.55	-0.039	0.009	2.53E-05	rs12270727	26672194	0.06	0.214	0.036	2.80E-09	-4.0
rs3736228	11	67957871	0.15	-0.073	0.013	1.89E-08	rs2291467	67973332	0.25	-0.069	0.011	5.14E-10	-1.6
rs12821008	12	47760872	0.39	0.049	0.010	1.02E-06	rs3741619	47675743	0.36	0.058	0.011	5.38E-08	-1.3
rs2016266	12	52014222	0.69	-0.058	0.010	1.13E-08	rs894736	52704433	0.60	0.061	0.010	2.49E-10	-1.7
rs10416218	19	38290967	0.73	-0.047	0.011	9.61E-06	rs12977993	38272293	0.26	0.057	0.011	3.24E-07	-1.5

Loci with a more significant marker (defined as change in significance of more than one order of magnitud) identified in regional imputation using 1000Genomes.
P values from targeted snps are updated from meta-analysis of same studies that contributed to 1000G regiontal imputation.
*These loci were selected in the gender-stratified meta-analysis

Supplementary Table 12 Predicted functional SNPs (imputed from 1000 Genomes Project) in LD (r2 > 0.8) with targeted SNP in each locus

Targeted	FNBMD	LSBMD				Distance					FNBMD		LSBMD			
SNPs	P-values		Locus	Gene_Symbol	Functional SNP	(Kb)	r^2	D'	Allele	Freq	Effect	P-value	Effect	P-value	Type	Possible Functional Effects
rs12407028	7.89E-06	5.15E-12	1p31.3	*hsa-mir-1262*	rs2772297	4.37	1.00	1.00	t	0.40	-0.041	7.43E-06	-0.067	5.46E-12	INTRONIC	Promoter/regulatory region
rs4233949	1.96E-05	1.88E-12	2p16.2	*SPTBN1*	rs4305309	24.00	0.83	0.93	t	0.35	0.031	1.06E-03	0.069	1.64E-11	INTRONIC	Promoter/regulatory region
rs1026364	5.46E-05	1.22E-01	3q13.2	*KIAA2018*	rs9813630	7.4	0.91	1.00	a	0.66	-0.032	3.19E-04	-0.012	2.08E-01	SYNONYMOUS	Sense/synonymous; Splicing regulation
rs1026364	5.46E-05	1.22E-01	3q13.2	*KIAA2018*	rs9866806	9.9	0.91	1.00	c	0.35	0.035	1.69E-04	0.013	1.94E-01	NON_SYNONYMOUS	Missense (conservative); Splicing regulation
rs3755955	3.53E-07	9.29E-08	4p16.3	*IDUA*	rs3755955	0.00	1.00	1.00	a	0.16	-0.067	3.53E-07	-0.076	9.29E-08	NON_SYNONYMOUS	Missense (conservative)
rs3755955	3.53E-07	9.29E-08	4p16.3	*IDUA*	rs6815946	0.89	1.00	1.00	t	0.84	0.068	1.57E-07	0.079	1.74E-08	SYNONYMOUS_CODING	Sense/synonymous; Splicing regulation
rs3755955	3.53E-07	9.29E-08	4p16.3	*IDUA*	rs6848974	1.05	1.00	1.00	t	0.15	-0.061	1.25E-06	-0.063	3.77E-06	SPLICE_SITE	splicing site
rs3755955	3.53E-07	9.29E-08	4p16.3	*IDUA*	rs6831280	1.75	1.00	1.00	a	0.16	-0.069	1.18E-07	-0.079	1.88E-08	NON_SYNONYMOUS	Missense (conservative); Splicing regulation
rs4727338	6.89E-15	1.84E-12	7q21.3	*FLJ42280*	rs4729260	2.76	0.92	1.00	c	0.68	0.079	**1.40E-16**	0.079	**3.48E-14**	INTRONIC	Promoter/regulatory region
rs3801387	8.98E-11	4.26E-12	7q31.31	*WNT16*	rs3779381	7.98	0.87	1.00	a	0.76	-0.074	**2.77E-12**	-0.082	**2.03E-13**	INTRONIC	Promoter/regulatory region
rs7017914	1.76E-05	9.44E-01	8q13.3	*LACTB2*	rs13271442	6.0	0.97	1.00	t	0.49	0.043	**1.37E-06**	0.000	9.63E-01	WITHIN_NON_CODING_GENE	Promoter/regulatory region
rs7932354	1.10E-05	4.72E-05	11p11.2	*F2*	rs2070852	22.7	0.96	1.00	c	0.68	-0.044	6.23E-06	-0.044	1.89E-05	SPLICE_SITE	splicing site
rs3736228	2.38E-05	1.89E-08	11q13.2	*LRP5*	rs3736228	0.00	1.00	1.00	t	0.16	-0.052	2.38E-05	-0.073	1.89E-08	NON_SYNONYMOUS	Missense (conservative); Splicing regulation
rs2016266	1.26E-04	1.13E-08	12q13.13	*ESPL1*	rs1318648	57.41	0.93	1.00	a	0.65	-0.030	1.24E-03	-0.048	1.02E-06	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs2016266	1.26E-04	1.13E-08	12q13.13	*ESPL1*	rs1110720	45.63	0.96	1.00	a	0.65	-0.031	6.76E-04	-0.050	3.26E-07	SYNONYMOUS_CODING	Sense/synonymous; Splicing regulation
rs11623869	4.58E-08	7.13E-05	14q32.32	*MARK3*	rs2273699	39.84	0.96	1.00	a	0.64	0.049	2.08E-07	0.038	1.39E-04	SPLICE_SITE	splicing site
rs11623869	4.58E-08	7.13E-05	14q32.32	*CKB*	rs1803283	102.6	1.00	1.00	t	0.65	0.047	3.44E-07	0.034	4.91E-04	SYNONYMOUS	Sense/synonymous; Splicing regulation
rs4985155	1.60E-03	7.08E-06	16p13.11	*PDXDC1*	rs7200543	0.5	0.89	1.00	a	0.70	-0.029	2.43E-03	-0.046	6.37E-06	SYNONYMOUS	Sense/synonymous; Splicing regulation
rs4985155	1.60E-03	7.08E-06	16p13.11	*NTAN1*	rs1136001	2.52	0.89	1.00	t	0.29	0.029	2.42E-03	0.046	6.83E-06	3PRIME_UTR	Missense (conservative); Splicing regulation
rs227584	1.17E-09	5.88E-08	17q21.31_1	*C17orf53*	rs227584	0.00	1.00	1.00	a	0.69	-0.061	1.17E-09	-0.057	5.88E-08	NON_SYNONYMOUS	Missense (conservative); Splicing regulation
rs227584	1.17E-09	5.88E-08	17q21.31_1	*C17orf65/ASB16*	rs7212573	28.73	1.00	1.00	a	0.69	-0.060	2.20E-09	-0.056	1.08E-07	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs227584	1.17E-09	5.88E-08	17q21.31_1	*C17orf65/ASB16*	rs7212854	28.9	0.83	1.00	a	0.72	-0.056	4.84E-08	-0.052	1.86E-06	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs227584	1.17E-09	5.88E-08	17q21.31_1	*C17orf65/ASB16*	rs7217858	29.0	0.93	1.00	t	0.70	-0.057	1.45E-08	-0.054	4.67E-07	NON_SYNONYMOUS	Missense (conservative)
rs227584	1.17E-09	5.88E-08	17q21.31_1	*C17orf65/ASB16*	rs3826412	29.6	1.00	1.00	t	0.69	-0.059	3.18E-09	-0.056	1.05E-07	SPLICE_SITE	splicing site
rs1864325	3.26E-03	1.09E-04	17q21.31_2	*AC217771.1*	rs12373123	53.77	1.00	1.00	t	0.79	0.032	3.58E-03	0.044	1.68E-04	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs1864325	3.26E-03	1.09E-04	17q21.31_2	*AC217771.1*	rs12373139	53.71	1.00	1.00	a	0.21	-0.032	4.00E-03	-0.044	1.89E-04	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs1864325	3.26E-03	1.09E-04	17q21.31_2	*AC217771.1*	rs12373142	53.64	1.00	1.00	c	0.79	0.032	3.48E-03	0.044	1.62E-04	NON_SYNONYMOUS	Missense (non-conservative); Splicing regulatio
rs1864325	3.26E-03	1.09E-04	17q21.31_2	*MAPT*	rs10445337	89.61	1.00	1.00	t	0.79	0.031	4.24E-03	0.045	1.23E-04	NON_SYNONYMOUS	Missense (conservative)
rs10416218	6.10E-05	9.61E-06	19q13.11	*GPATCH1*	rs2287679	1.6	1.00	1.00	t	0.73	-0.041	4.56E-05	-0.048	5.99E-06	NON_SYNONYMOUS	Missense (conservative); Splicing regulation
rs10416218	6.10E-05	9.61E-06	19q13.11	*GPATCH1*	rs10416265	6.2	1.00	1.00	a	0.72	-0.040	1.02E-04	-0.044	4.23E-05	NON_SYNONYMOUS	Missense (conservative)

P values from targeted snps are updated from meta-analysis of same studies that contributed to 1000G regiontal imputation. Boldface represent loci where a more significant marker (defined as change in significance of more than one order of magnitud) identified in regional imputation using 1000Genomes using pooled analysis on the same trait.

Supplementary Table 13 Correlation between BMD at femoral neck and lumbar spine and gene expression in trans-iliacal bone biopsies

Locus	Gene	Probe	P value FN	r-FN	P value LS	r-LS
2p16.2	*PSME4*	212222_at	0.019	-0.255	6.30E-04	-0.365
10q21.1	*DKK1*	204602_at	1.30E-05	0.456	3.20E-04	0.383
17p13.3	*C17orf91*	214696_at	6.30E-04	-0.365	8.80E-04	-0.356
17q21.31_1	*SOST*	223869_at	4.80E-04	0.373	0.0069	0.292
17q21.31_1	*DUSP3*	201536_at	0.0051	-0.303	9.30E-04	-0.355

Transcripts with a P value < 0.001 at either the femoral neck (FN) or lumbar spine (LS) are shown, along with the respective Pearson correlation coefficient (r)

Supplementary Table 14 **Probable BMD-SNP cis eQTLs; Significant correlation between BMD associated SNP genotypes and gene expressions**

Locus	SNP	Allele[a]	Tissue (treatment)[b]	Gender	Gene	Probe	Effect[c]	P value	P adj[d]	Best SNP[e]	r2[f]	Best SNP Pvalue	P adj.[g]
1p36.12	rs6426749	G	Fibroblasts AE		*WNT4*	NM_030761	-	9.00E-09	na	rs7524102	1	2.70E-11	na
	rs6426749	G	Osteoblasts (pge2)		*WNT4*	NM_030761.3	-	2.60E-05	na	rs12742784	0.81	1.50E-05	na
	rs6426749	G	Osteoblasts (dex)		*WNT4*	NM_030761.3	-	5.30E-05	na	rs7524102	1	2.40E-05	na
	rs7521902	A	Adipose	females	*WNT4*	Contig30409_RC	-	1.20E-05	0.21	rs12042083	0.56	7.50E-06	0.12
2q13	rs17040773	C	Monocytes	mixed	*ANAPC1*	ILMN_1804812	+	3.60E-10	na	rs17040773	same SNP		na
	rs17040773	C	Adipose	mixed*	*ANAPC1*	NM_022662	+	1.90E-11	0.96	rs1548189	0.96	2.20E-13	0.0046
	rs17040773	C	Fibroblasts AE		*ANAPC1*	NM_022662	+	7.00E-06	na	rs1548189	0.96	2.40E-08	na
	rs17040773	C	Lymphoblasts AE	mixed	*ANAPC1*	NM_022662	+	1.50E-02	na	rs11689168	0.95	3.20E-07	na
2q32.2	rs11675051	G	Osteoblasts (bmp2)		*MFSD6*	NM_017694.2	-	5.40E-11	na	rs4638823	0.88	2.10E-11	na
	rs11675051	G	Osteoblasts (pge2)		*MFSD6*	NM_017694.2	-	7.70E-11	na	rs4597559	0.88	5.00E-11	na
	rs11675051	G	Osteoblasts (dex)		*MFSD6*	NM_017694.2	-	8.90E-11	na	rs4638823	0.88	2.90E-11	na
	rs11675051	G	Osteoblasts (pbs)		*MFSD6*	NM_017694.2	-	9.50E-10	na	rs17801596	0.78	8.60E-11	na
	rs11675051	G	Fibroblasts (eth)		*MFSD6*	NM_017694.3	-	9.20E-06	na	rs6756354	0.86	1.20E-06	na
	rs11675051	G	Fibroblasts (res)		*MFSD6*	NM_017694.3	-	3.30E-05	na	rs4343493	0.88	8.50E-07	na
	rs11675051	G	Fibroblasts (cho)		*MFSD6*	NM_017694.3	-	6.00E-05	na	rs4597559	0.88	1.40E-05	na
4q22.1	rs6532023	G	Adipose	mixed	*SPP1*	NM_000582	-	1.50E-05	0.48	rs1477603	0.66	2.80E-06	0.06
6q25.1	rs4869742	T	Monocytes	mixed	*C6orf97*	ILMN_1772588	+	8.00E-27	na	rs6900089	0.19	6.20E-29	na
8q13.3	rs7017914	G	Whole blood	mixed*	*LACTB2*	NM_016027	+	1.40E-20	0.31	rs13253842	0.87	9.60E-21	0.19
	rs7017914	G	Adipose	mixed	*LACTB2*	NM_016027	+	3.10E-05	0.36	rs6994814	0.77	4.00E-06	0.033
	rs7017914	G	Lymphoblasts	mixed	*LOC340435*	XM_291285.1	+	3.50E-15	na	rs2732090	0.97	1.50E-15	na
	rs7017914	G	Lymphoblasts AE	mixed	*XKR9*	NM_001011720	+	1.20E-21	na	rs7013657	1	1.10E-22	na
	rs7017914	G	Fibroblasts AE		*XKR9*	NM_001011720	+	6.90E-18	na	rs13252719	1	5.30E-18	na
11p11.2	rs7932354	C	Adipose	mixed*	*ARHGAP1*	NM_004308	+	1.70E-11	0.81	rs2070852	1	1.30E-11	0.45
	rs7932354	C	Adipose	females	*C11orf49*	Contig32649_RC	+	4.90E-05	0.5	rs6485690	0.81	1.30E-05	0.091
	rs7932354	C	Adipose	mixed	*LRP4*	AB011540	+	1.20E-06	0.42	rs1060573	0.5	9.60E-09	0.0019
11p14.1_1	rs10835187	T	Adipose	mixed*	*LIN7C*	NM_018362	-	2.80E-39	0.94	rs3763965	0.97	9.00E-43	5.10E-04
	rs10835187	T	Whole blood	mixed*	*LIN7C*	NM_018362	-	8.90E-16	0.78	rs3763965	0.97	2.60E-16	0.091
12q23.3	rs1053051	T	Adipose	mixed*	*C12orf23*	NM_152261	+	4.10E-13	na	rs1053051	same SNP		na
	rs1053051	T	Whole blood	mixed*	*C12orf23*	NM_152261	+	1.40E-08	0.79	rs7974499	0.79	7.40E-10	0.02
	rs1053051	T	Adipose	mixed	*MTERFD3*	NM_025198	+	1.00E-06	na	rs1053051	same SNP		na
14q32.32	rs11623869	T	Adipose	mixed*	*C14orf172*	NM_152307	+	1.30E-13	0.96	rs2273700	0.96	1.90E-14	0.064
	rs11623869	T	Whole blood	mixed*	*MARK3*	NM_002376	-	1.40E-26	0.62	rs3783402	0.96	4.00E-27	0.13
	rs11623869	T	Osteoblasts (bmp2)		*MARK3*	NM_002376.4	-	3.90E-04	na	rs879552	0.9	4.10E-05	na
16p13.11	rs4985155	A	Adipose	females	*KIAA2013*	NM_138346	+	6.90E-07	na	rs4985155	same SNP		na
	rs4985155	A	Adipose	mixed*	*NTAN1*	NM_173474	+	1.30E-10	0.92	rs4985148	0.82	9.50E-12	0.029
17q21.31_1	rs227584**	A	Monocytes	mixed	*C17orf53*	ILMN_1776490	+	5.30E-11	na	rs11079983	0.83	5.80E-14	na
	rs227584**	A	Monocytes	mixed	*C17orf65*	ILMN_1676731	+	5.00E-19	na	rs3826412	same SNP		na

Supplementary Table 14 **Probable BMD-SNP cis eQTLs; Significant correlation between BMD associated SNP genotypes and gene expressions**

Locus	SNP	Allele[a]	Tissue (treatment)[b]	Gender	Gene	Probe	Effect[c]	P value	P adj[d]	Best SNP[e]	r2[f]	Best SNP Pvalue	P adj.[g]
	rs227584	A	Adipose	mixed*	*C17orf65*	NM_178542	+	4.90E-18	0.29	rs721769	1	1.70E-18	0.089
	rs227584	A	Whole blood	mixed	*C17orf65*	NM_178542	+	4.70E-05	0.029	rs7089	0.93	3.90E-06	0.0021
	rs227584	A	Lymphoblasts	mixed	*C17orf65*	NM_178542.2	+	1.10E-04	na	rs7089	0.92	2.00E-05	na
	rs227584	A	Fibroblasts (eth)		*TMUB2*	NM_024107.2	+	4.00E-05	na	rs9910055	0.7	1.70E-06	na
	rs227584	A	Adipose	mixed	*TMUB2*	NM_177441	+	4.90E-05	na	rs227584	same SNP		na
	rs227584	A	Adipose	mixed*	*UBTF*	AF289595	+	9.00E-09	0.51	rs2071167	0.72	1.00E-10	0.0031
18q21.33	rs884205	A	Whole blood	females	*TNFRSF11A*	NM_003839	-	1.60E-06	na	rs884205	same SNP		na
	rs884205	A	Adipose	mixed	*TNFRSF11A*	NM_003839	-	1.70E-04	0.63	rs2957137	0.8	3.70E-05	0.082
19q13.11	rs10416218	T	Adipose	mixed	*RHPN2*	NM_033103	+	2.80E-04	0.11	rs9304844	0.95	4.00E-05	0.013

Results are shown for SNP eQTLs with P value < 5 x 10-5 (either for the BMD SNP or the most significantly associated, and highly correlated, SNP) that cannot be explained by other non-correlated SNPs. Transcripts that are located within +/- 500 kb of the top BMD SNPs were included in the analysis**. a** The allele that associates with lowered BMD; **b** The tissue (adipose, whole blood), cell type (monocytes) or cell lines (lymphoblasts, primary human fibroblasts, primary human osteblasts) analysed and their treatment: cholesterol (cho), resveratrol (res), ethanol (eth), bone morphogenetic protein BMP-2 (bmp2), dexamethasone (dex), prostaglandin E2 (pge2), and control PBS (pbs). Allelic expression analysis in lymphoblastoid cell lines is indicated by AE; **c** Direction of effect of the allele that associates with lowered BMD; **d** P-value of the BMD SNP after conditioning on the best SNP associated with the transcript; **e** SNP with the strongest association with the transcript in the region; **f** Correlation between the BMD SNP and best SNP associated with the transcript; **g** P-value of the best SNP after conditioning on the BMD SNP; ***** significant associated SNP correlation also observed for females and/or males for the transcript; ****** proxy, rs3826412[T], used for expression correlation analysis

Supplementary Table 15 **Non-BMD SNP cis eQTLs; Significant correlation between non-associated SNP genotypes and gene expressions**

Locus	SNP	Allele[a]	Tissue (treatment)[b]	Gender	Gene	Probe	Effect[c]	P value	P adj[d]	Best SNP[e]	r2[f]	Best SNP Pvalue	P adj.[g]
1p31.3	rs12407028	C	Whole Blood	mixed*	*WLS*	NM_024911	-	1.60E-07	1.60E-04	rs12065581	0.07	8.50E-51	4.90E-47
1p36.12	rs6426749	G	Osteoblasts (bmp2)		*WNT4*	NM_030761.3	-	1.50E-04	na	rs17837965	0	3.10E-05	na
	rs7521902	A	Osteoblasts (dex)		*ELA3B*	NM_007352.2	-	5.00E-05	na	rs16826658	0.51	3.50E-06	na
	rs7521902	A	Adipose	mixed*	*HSPC157*	NM_014179	-	1.70E-21	4.40E-04	rs3765351	0.22	1.70E-133	9.10E-104
	rs7521902	A	Whole Blood	mixed*	*HSPC157*	NM_014179	-	2.60E-15	0.01	rs3765351	0.22	9.10E-94	1.70E-75
2q24.3	rs1346004	A	Adipose	mixed*	*GALNT3*	NM_004482	-	1.40E-11	0.0016	rs11694833	0.03	1.10E-38	4.10E-29
	rs1346004	A	Adipose	mixed*	*TTC21B*	NM_024753	+	1.60E-05	0.84	rs9677856	0.19	2.40E-34	3.20E-29
2q32.2	rs11675051	G	Lymphoblasts AE	mixed	*TMEM194B*	NM_001142645	+	3.00E-10	na	rs10165399	0.43	5.70E-12	na
6p21.1	rs11755164	T	Adipose	mixed*	*SUPT3H*	NM_003599	+	4.60E-14	0.0082	rs2396373	0.27	1.20E-19	4.00E-08
	rs11755164	T	Whole Blood	mixed*	*SUPT3H*	NM_003599	+	2.50E-06	0.53	rs9349303	0.3	9.10E-17	1.40E-11
	rs4869742	T	Whole Blood	mixed*	*C6orf97*	NM_025059	+	2.80E-08	6.20E-05	rs852003	0.04	2.60E-15	6.20E-12
	rs7751941	A	Adipose	mixed*	*C6orf97*	NM_025059	+	1.00E-05	0.51	rs7776340	0.33	4.40E-13	1.40E-08
	rs7751941	A	Whole Blood	mixed*	*C6orf97*	NM_025059	+	1.50E-05	0.48	rs852003	0.24	2.60E-15	4.60E-11
7q31.31	rs3801387	A	Adipose	females	*WNT16*	NM_016087	-	9.00E-06	0.35	rs10231005	0.27	1.60E-10	5.20E-06
	rs13245690	G	Adipose	mixed*	*C7orf58*	NM_024913	-	4.00E-10	0.53	rs2222543	0.37	1.80E-27	9.50E-18
8q13.3	rs7017914**	G	Monocytes	mixed	*LACTB2*	ILMN_1660635	-	9.40E-28	na	rs13271014	0.1	3.80E-104	na
10q24.2	rs7084921**	T	Monocytes	mixed	*CWF19L1*	ILMN_1651886	-	8.80E-14	na	rs11597086	0.39	8.20E-50	na
	rs7084921	C	Adipose	mixed*	*CWF19L1*	NM_018294	-	1.90E-22	0.64	rs11597086	0.38	2.50E-68	1.40E-40
	rs7084921	C	Whole Blood	mixed	*CWF19L1*	NM_018294	-	2.90E-07	0.4	rs11597086	0.38	3.00E-22	5.10E-16
	rs7084921	C	Fibroblasts (cho)		*CWF19L1*	NM_018294.3	-	1.50E-05	na	rs4462272	0.65	3.30E-09	na
11p14.1_2	rs163879	T	Whole Blood	mixed	*DCDC5*	AB040926	+	1.80E-05	0.55	rs2122681	0.13	9.80E-19	2.10E-14
11q13.2	rs3736228	T	Adipose	mixed*	*SAPS3*	Contig52814_RC	+	7.30E-11	0.54	rs10896337	0.43	1.90E-32	1.40E-21
	rs3736228	T	Whole Blood	mixed	*SAPS3*	Contig52814_RC	+	2.40E-08	0.4	rs10896339	0.42	3.70E-25	9.80E-18
	rs3736228	T	Adipose	mixed	*SAPS3*	NM_018312	+	8.00E-07	0.12	rs10896347	0.47	1.90E-08	0.0022
12q13.12	rs12821008	C	Whole Blood	mixed*	*CCDC65*	NM_033124	-	3.10E-08	0.29	rs1054376	0.05	3.30E-91	4.60E-81
12q23.3	rs1053051	T	Whole Blood	mixed*	*AK055712*	Contig10844_RC	+	9.00E-06	0.045	rs10746071	0.78	1.30E-10	5.80E-07
	rs1053051	T	Adipose	mixed*	*AK055712*	Contig10844_RC	+	2.70E-13	0.2	rs10778515	0.6	3.20E-16	2.20E-04
13q14.11	rs9533090	T	Whole Blood	mixed*	*AKAP11*	NM_144490	+	7.30E-06	0.15	rs3783192	0.22	1.70E-19	4.20E-15
	rs9533090	T	Adipose	mixed	*AKAP11*	NM_144490	+	6.60E-07	0.15	rs7318683	0.18	1.40E-31	1.50E-25
	rs7326472	A	Adipose	mixed	*AKAP11*	NM_144490	+	1.50E-06	0.0075	rs7318683	0.06	1.40E-31	2.70E-27
14q32.32	rs11623869*;	G	Monocytes	mixed	*BAG5*	ILMN_2361695	-	2.70E-12	na	rs7148456	0.18	9.60E-24	na
	rs11623869*;	G	Monocytes	mixed	*MARK3*	ILMN_1704795	-	2.10E-08	na	rs975892	0.15	2.10E-38	na
	rs11623869	T	Whole Blood	mixed	*BAG5*	NM_004873	+	6.00E-06	0.23	rs752624	0.14	3.50E-17	1.20E-12
	rs11623869	T	Adipose	mixed*	*C14orf153*	NM_032374	+	2.10E-07	1.40E-02	rs2403197	0.19	3.50E-14	2.80E-09
	rs11623869	T	Whole Blood	mixed*	*KLC1*	NM_005552	-	3.90E-05	0.32	rs3212090	0.22	3.90E-22	3.20E-18
	rs11623869	T	Adipose	mixed*	*MARK3*	Contig43834_RC	-	2.10E-47	2.30E-07	rs4906319	0.15	1.90E-147	6.60E-89
	rs11623869	T	Whole Blood	mixed*	*MARK3*	Contig43834_RC	-	1.10E-68	2.60E-15	rs6575982	0.15	1.30E-147	7.60E-80
	rs11623869	T	Lymphoblasts AE	mixed	*BAG5*	NM_001015049	-	3.30E-06	na	rs942863	0.56	1.20E-08	na

Supplementary Table 15 **Non-BMD SNP cis eQTLs; Significant correlation between non-associated SNP genotypes and gene expressions**

Locus	SNP	Allele[a]	Tissue (treatment)[b]	Gender	Gene	Probe	Effect[c]	P value	P adj[d]	Best SNP[e]	r2[f]	Best SNP Pvalue	P adj.[g]
16p13.11	rs4985155	A	Adipose	females	*PDXDC1*	D87438	-	2.20E-05	0.48	rs1136001	0.78	5.20E-07	0.0072
16p13.3_1	rs9921222	T	Monocytes	mixed	*AXIN1*	ILMN_1766185	-	1.10E-14	na	rs1204042	0.07	5.40E-114	na
	rs9921222	T	Monocytes	mixed	*NME4*	ILMN_1800634	+	3.90E-23	na	rs763151	0.14	3.20E-204	na
	rs9921222	T	Monocytes	mixed	*TMEM8*	ILMN_1741371	-	7.90E-08	na	rs3830160	0.18	2.80E-80	na
	rs9921222	T	Adipose	mixed*	*AXIN1*	NM_181050	-	1.80E-06	0.12	rs214252	0.11	2.90E-22	3.80E-17
	rs9921222	T	Osteoblasts (dex)		*DECR2*	NM_020664.3	+	5.80E-06	na	rs1698231	0.1	1.60E-10	na
17p13.3	rs4790881	C	Whole Blood	mixed*	*SRR*	NM_021947	+	8.40E-09	0.37	rs17834563	0.06	4.60E-71	5.50E-61
17q21.31_1	rs4792909	G	Adipose	mixed*	*MPP3*	NM_001932	+	6.30E-15	0.92	rs17674998	0.14	4.20E-60	4.60E-42
19q13.11	rs10416218	T	Adipose	mixed*	*GPATCH1*	NM_018025	-	4.20E-19	0.16	rs7256470	0.66	1.60E-22	8.50E-05
	rs10416218	T	Adipose	mixed*	*WDR88*	NM_173479	-	1.40E-06	0.12	rs10423969	0.52	6.70E-16	6.80E-11
20p12.2	rs3790160	C	Whole Blood	mixed	*JAG1*	NM_000214	-	2.60E-05	0.073	rs6077861	0.22	3.50E-09	8.20E-06

Results are shown for SNP eQTLs with P value < 5 x 10-5 that can be be explained by other non-correlated and non-associated SNPs. Transcripts that are located within +/- 500 kb of the top BMD SNPs were included in the analysis. **a** The allele that associates with lowered BMD; **b** The tissue (adipose, whole blood), cell type (monocytes) or cell lines (lymphoblasts, primary human fibroblasts, primary human osteblasts) analysed and their treatment: cholesterol (cho), resveratrol (res), ethanol (eth), bone morphogenetic protein BMP-2 (bmp2), dexamethasone (dex), prostaglandin E2 (pge2), and control PBS (pbs). Allelic expression analysis in lymphoblastoid cell lines is indicated by AE; **c** Direction of effect of the allele that associates with lowered BMD; **d** P-value of the BMD SNP after conditioning on the best SNP associated with the transcript; **e** SNP with the strongest association with the transcript in the region; **f** Correlation between the BMD SNP and best SNP associated with the transcript; **g** P-value of the best SNP after conditioning on the BMD SNP; ***** significant associated SNP correlation also observed for females and/or males for the transcript; ****** proxy SNPs used for expression correlation analysis: rs12675271 for rs7017914, rs11190378 for rs7084921, and rs17679475 for rs11623869.

Supplementary Table 16. Candidate Genes selected by GRAIL

SNP	Grail SNP P-value	Candidate Gene
rs3736228	**2.80E-10**	***LRP5***
rs2062377	**3.17E-07**	***TNFRSF11B***
rs2016266	**3.55E-07**	***SP7***
rs11755164	**3.59E-07**	***RUNX2***
rs9533090	**4.14E-07**	***TNFSF11***
rs6426749	**8.04E-07**	***WNT4***
rs884205	**8.99E-07**	***TNFRSF11A***
rs2887571	**1.48E-05**	***WNT5B***
rs7217932	**2.04E-05**	***SOX9***
rs6532023	**2.17E-05**	***MEPE***
rs3801387	**3.66E-05**	***WNT16***
rs9921222	**4.04E-05**	***AXIN1***
rs1864325	**4.35E-05**	***WNT3***
rs6959212	**1.50E-04**	***SFRP4***
rs7953528	**3.27E-04**	***PTHLH***
rs430727	**3.57E-04**	***CTNNB1***
rs10048146	**8.76E-04**	***FOXL1***
rs7108738	**9.00E-03**	***SOX6***
rs12821008	0.02	*DHH*
rs13336428	0.02	*CLCN7*
rs9466056	0.02	*SOX4*
rs1366594	0.05	*MEF2C*
rs7017914	0.08	*LACTB2*
rs3790160	0.08	*JAG1*
rs3905706	0.12	*MPP7*
rs4869742	0.15	*C6orf97*
rs7932354	0.17	*DGKZ*
rs10416218	0.17	*GPATCH1*
rs479336	0.18	*DNM3*
rs3755955	0.22	*DGKQ*
rs12407028	0.22	*GPR177*
rs7851693	0.23	*FUBP3*
rs4233949	0.24	*SPTBN1*
rs7084921	0.26	*CHUK*
rs1566045	0.31	*CYLD*
rs17040773	0.42	*ANAPC1*
rs1026364	0.44	*NAT13*
rs1878526	0.46	*INSIG2*
rs13204965	0.49	*C6orf173*
rs11623869	0.50	*MARK3*
rs4727338	0.54	*SLC25A13*
rs4796995	0.60	*C18orf19*
rs10835187	0.61	*LIN7C*
rs163879	0.72	*DCDC1*
rs4790881	0.73	*MNT*
rs4985155	0.76	*PDXDC1*
rs1373004	0.76	*MBL2*
rs227584	0.78	*HDAC5*
rs7812088	0.83	*ABCF2*
rs1053051	0.85	*C12orf23*
rs344081	0.87	*TIPARP*
rs7071206	0.87	*KCNMA1*
rs1346004	0.89	*FAM130A2*
rs1286083	0.91	*RPS6KA5*
rs7584262	0.95	*LOC91461*

Boldface indicates significant relationships amongst loci (GRAIL P < 0.01)

Supplementary Table 17 Functional and biological evidence for genes underlying the GWAS loci

Locus	SNP	MAF	Candidate gene	Closest gene	eQTL	Knockout mouse with skeletal phenotype (MGI)	Monogenic syndrome with skeletal phenotype (OMIM)	LD functional variant(s) 1000 Genome Project	GRAIL Priority	Bone-active pathway	Score
1p31.3	rs12407028	0.39	*WLS*	YES		MGI:1915401				Wnt	3
1p36.12	rs6426749	0.17	*ZBTB40*	YES							1
1p36.12	rs7521902	0.31	*WNT4*	YES	NM_030761				YES	Wnt	4
1q24.3	**rs479336**	0.26	*DNM3*	YES							1
2p16.2	rs4233949	0.38	*SPTBN1*	YES				rs4305309			2
2p21	**rs7584262**	0.23	*PKDCC*	YES		MGI:2147077					2
2q13	**rs17040773**	0.23	*ANAPC1*	YES	ILMN_1804812						2
2q14.2	**rs1878526**	0.22	*INSIG2*	YES							1
2q24.3	rs1346004	0.49	*GALNT3*	YES		MGI:894695	MIM:211900				3
3p22.1	rs430727	0.47	*CTNNB1*	YES		MGI:88276			YES	Wnt	4
3q13.2	**rs1026364**	0.36	*KIAA2018*	YES				rs9813630			2
3q25.31	**rs344081**	0.13	*LEKR1*	YES							1
4p16.3	**rs3755955**	0.16	*IDUA*	YES		MGI:96418		rs6848974			3
4q22.1	rs6532023	0.34	*MEPE*	YES		MGI:2137384					2
4q22.1	rs6532023	0.34	*SPP1*		NM_000582	MGI:98389			YES	Endochondral Ossification	4
4q22.1	rs6532023	0.34	*IBSP*			MGI:96389					1
5q14.3	rs1366594	0.47	*MEF2C*	YES						Endochondral Ossification	2
6p21.1	**rs11755164**	0.40	*RUNX2*			MGI:99829			YES	Endochondral Ossification	3
6p22.3	**rs9466056**	0.38	*SOX4*								0
6q22.32	rs13204965	0.24	*RSPO3*	YES		MGI:1920030				Wnt	3
6q25.1	rs4869742	0.32	*ESR1*			MGI:1352467					1
7p14.1	rs10226308	0.16	*SFRP4*						YES	Wnt	2
7p14.1	rs6959212	0.34	*STARD3NL*	YES							1
7q21.3	rs4727338	0.33	*SLC25A13*	YES							1
7q31.31	**rs3801387**	0.26	*WNT16*	YES				rs3779381	YES	Wnt	4
7q36.1	**rs7812088**	0.12	*ABCF2*	YES							1
8q13.3	**rs7017914**	0.49	*LACTB2*		NM_016027			rs13271442			2
8q24.12	rs2062377	0.41	*TNFRSF11B*	YES		MGI:109587	MIM:602080		YES	OPG/RANK/RANKL	5
9q34.11	**rs7851693**	0.37	*FUBP3*	YES							1
10p11.23	**rs3905706**	0.23	*MPP7*	YES							1
10q21.1	**rs1373004**	0.12	*DKK1*			MGI:1329040				Wnt	2
10q22.3_1	**rs7071206**	0.24	*KCNMA1*	YES							1
10q24.2	**rs7084921**	0.40	*CPN1*	YES							1
11p11.2	rs7932354	0.33	*LRP4*		AB011540	MGI:2442252	MIM:604270				3
11p14.1_1	**rs10835187**	0.46	*LIN7C*	YES	NM_018362						2
11p14.1_2	rs163879	0.34	*DCDC5*	YES							1
11p15.2	rs7108738	0.18	*SOX6*	YES		MGI:98368			YES	Endochondral Ossification	4
11q13.2	rs3736228	0.15	*LRP5*	YES		MGI:1278315	MIM:259770,MIM:607634	rs3736228	YES	Wnt	6
12p11.22	**rs7953528**	0.18	*PTHLH*			MGI:97800	MIM:613382		YES	Endochondral Ossification	4
12p13.33	**rs2887571**	0.24	*WNT5B*						YES	Wnt	2
12q13.12	**rs12821008**	0.40	*DHH*	YES						Hedgehog	2
12q13.13	rs2016266	0.31	*SP7*	YES		MGI:2153568	MIM:613849		YES	MSC differentiation	5
12q13.13	rs736825	0.44	*HOXC6*	YES		MGI:96197				Wnt	3
12q23.3	**rs1053051**	0.49	*C12orf23*	YES	NM_152261						2
13q14.11	rs9533090	0.48	*TNFSF11*			MGI:1100089	MIM:259710		YES	OPG/RANK/RANKL	4
14q32.12	**rs1286083**	0.20	*RPS6KA5*	YES							1
14q32.32	rs11623869	0.34	*MARK3*	YES	NM_002376			rs2273699			3

Supplementary Table 17 Functional and biological evidence for genes underlying the GWAS loci

Locus	SNP	MAF	Candidate gene	Closest gene	eQTL	Knockout mouse with skeletal phenotype (MGI)	Monogenic syndrome with skeletal phenotype (OMIM)	LD functional variant(s) 1000 Genome Project	GRAIL Priority	Bone-active pathway	Score
16p13.11	**rs4985155**	0.35	*NTAN1*	YES	NM_173474			rs1136001			3
16p13.3_1	**rs9921222**	0.46	*AXIN1*	YES		MGI:1096327			YES	Wnt	4
16p13.3_2	**rs13336428**	0.44	*CLCN7*			MGI:1347048	MIM:611490				2
16q12.1	**rs1566045**	0.20	*CYLD*			MGI:1921506					1
16q24.1	rs10048146	0.20	*FOXL1*	YES		MGI:1347481			YES	TGF-beta	4
17p13.3	**rs4790881**	0.33	*SMG6*	YES							1
17q21.31_1	rs227584	0.33	*C17orf53*		ILMN_1776490			rs227584			2
17q21.31_1	rs4792909	0.37	*SOST*	YES		MGI:1921749	MIM:269500			Wnt	4
17q21.31_2	rs1864325	0.22	*WNT3*				MIM:273395		YES	Wnt	3
17q24.3	**rs7217932**	0.46	*SOX9*	YES		MGI:98371	MIM:608160		YES	Endochondral Ossification	5
18p11.21	**rs4796995**	0.39	*C18orf19*	YES							1
18q21.33	rs884205	0.25	*TNFRSF11A*	YES	NM_003839	MGI:1314891	MIM:602080		YES	OPG/RANK/RANKL	6
19q13.11	**rs10416218**	0.28	*GPATCH1*	YES				rs2287679			2
20p12.2	rs3790160	0.50	*JAG1*	YES							1
Xp22.31	**rs5934507**	0.27	*FAM9B*	YES							1

Aggregated evidence derived from human (OMIM) and mouse genetic (MGI) databases with that derived from our data (gene proximity to the associated variant, eQTL, LD with putative functional variants and pathway involvement). We prioritized 60 candidate genes likely to be underlying the GWAS signals coming from the 56 BMD loci together with a score on potential biological relevance. Of these 60 genes, 13 contained human mutations associated with monogenic skeletal syndromes while 27 genes had a knock-out mouse presenting with skeletal defects (11 genes had both). 10 of the 26 genes contained functional variants in LD with the GWAS SNP, 11 of the 14 genes contained eQTL transcripts, 18 genes annotated in the GRAIL analysis and 24 genes are members of a recognized biologic pathway relevant to bone biology.
Boldface indicates novel loci. eQTL and markers in LD with a putative functional variant are only shown for those related to the reported candidate gene in this table. For eQTLs the transcript associated with the given SNP is displayed. The score was generated by adding a point for each line of evidence (range 0-6).

Supplementary Table 18A: Study design

Stage 1: GWAS BMD Discovery

	Study							Sample QC				
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity (es)	Call rate	Other exclusions	Total sample size with GWA and BMD and/or fracture data available	Short Study Description	References
1	AFOS	Amish Family Osteoporosis Study	Cohort/ Founder population	Population-based	United States of America	Lancaster County, Pennsylvania	Old Order Amish (European Ancestry)	> 98%	1) missing covariate data; 2) genotype data not imputed at time of analysis.	918	The AFOS study was designed to identify genetic determinants of osteoporosis in the Old Order Amish (OOA) population from Lancaster County, PA USA. The OOA populatio is a closed, Caucasian founder population made up of large families and the OOA population lives a relatively homogenous lifestyle.	[PMID:14969401] {Streeten, 2004 Reduced incidence of hip fracture in the Old Order Amish}; [PMID:16939402] {Streeten, 2006 Quantitative trait loci for BMD identified by autosome-wide linkage scan to chromosomes 7q and 21q in men from the Amish Family Osteoporosis Study}
2	AOGC	Anglo-Australasian Osteoporosis Genetics Consortium	Extreme truncate selection	Population-based, clinical-based	Australia, New Zealand, United Kingdom	Brisbane, Sydney, Dubbo, Perth, Melbourne, Geelong, Hobart, Sheffield, Kiel, Paris, Berlin, Aberdeen, Hereford	North-western European	> 98%	1) missing DNA; 2) gender mismatch with typed X-linked markers; 3) excess autosomal heterozygosity 4) duplicates and/or 1st or 2nd degree relatives 5) ethnic outliers 6) missing body weight and height.	1,955	A consortium of investigators who have collected unrelated individuals with extreme BMD phenotypes (z scores +1.5 to +4; or -1.5 to -4) as a powerful strategy for gene discovery in quantitative traits.	[PMID: 18021006] {Sims, 2008 Genetic analyses in a sample of individuals with high or low BMD shows association with multiple Wnt pathway genes}; [PMID: 21533022] {Duncan, 2011 Genome-wide association study using extreme truncate selection identifies novel genes affecting bone mineral density and fracture risk}
3	CHS	Cardiovascular Health Study	Cohort	Population-based	United States of America	Sacramento, Pittsburgh	European American	> 95%	1) presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack; 2) missing DNA; 3) non-Caucasian ethnicity; 4) gender mismatch; 5) discordance with prior genotyping.	3,291	A population-based cohort study of risk factors for coronary heart disease and stroke in adults ≥65 years conducted across four field centers. The original predominantly Caucasian cohort was recruited in 1989-1990 from random samples of the Medicare eligibility lists. genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai using the Illumina 370CNV BeadChip system on 3980 CHS participants who were free of CVD at baseline, consented to genetic testing, and had DNA available for genotyping.	[PMID: 20031568] {Fried, 2009 Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium: Design of prospective meta-analyses of genome-wide association studies from 5 cohorts}
4	DeCODE	DeCODE Genetics Study	Cross-sectional	Population-based, clinical-based	Iceland	NA	North-western European	≥91%	1) missing BMD measurement; 2) missing body weight and height.	7,605	The study includes 40,000 individuals taking part in various disease projects	[PMID: 18445777] {Styrkarsdottir, 2008 Multiple genetic loci for bone mineral density and fractures}; [PMID: 19079262] {Styrkarsdottir, 2009 Multiple genetic loci for bone mineral density and fractures}
5	ERF	Erasmus Rucphen Family	Cohort	Family-based isolate	The Netherlands	Rucphen	North-western European	> 95%	1) gender mismatch; 2) ethnic outliers; 3) Missing phenotype data; 4) high IBS; 5) excess heterozygosity.	1,602	A family-based cohort study that is embedded in the Genetic Research in Isolated Populations (GRIP) program in the South West of the Netherlands. The aim of this program was to identify genetic risk factors in the development of complex disorders.For the ERF study, 22 families that had at least five children baptized in the community church between 1850-1900 were identified with the help of genealogical records. All living descendants of these couples and their spouses were invited to take part in the study. Data collection started in June 2002 and was finished in February 2005	[PMID: 15054401] {Aulchenko, 2004 Linkage disequilibrium in young genetically isolated Dutch population}

Supplementary Table 18A: Study design

Stage 1: GWAS BMD Discovery

	Study							Sample QC				
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity (es)	Call rate	Other exclusions	Total sample size with GWA and BMD and/or fracture data available	Short Study Description	References
6	**EPICNOR**	Europen Prospective Investigation into Cancer, Norfolk study	Cohort	Population-based	United Kingdom	Norfolk	European	≥ 97.7%	1) missing DNA; 2) Missing body weight and height; 3) gender mismatch with typed X-linked markers; 4) heterozygosity <23% or >30%; 5) >5.0% discordance in SNP pairs with r2= 1 in HapMap; 6) ethnic outliers; 7) related individuals and duplicates.	249	A random sample of 1,511 men and women in the top decade of age in the 25,000 participant EPIC-Norfolk prospective study were recruited into a bone fragility study with DXA measurements. GWA data were available for 249 participants with BMD measurements who had been entered into a GWAS investigation of obesity.	[PMID: 12753873] {Kaptoge, 2003 Effects of gender, anthropometric variables, and aging on the evolution of hip strength in men and women aged over 65}; [PMID: 10466767] {Day, 1999 EPIC-Norfolk: study design and characteristics of the cohort. European Prospective Investigation of Cancer}; [PMID: 19079261] {Willer, 2009 Six new loci associated with body mass index highlight a neuronal influence on body weight regulation};
7	**FHS**	Framingham Heart Study	Cohort	Population-based, family-based	United States of America	Framingham	European American	≥ 97%	1. autosomal heterozygosity <0.26 or > 0.30; 2. ethnic outliers (using Eigenstrata).	3,886	The Framingham Osteoporosis Study is an ancillary study of the parent, Framingham Study. The Framingham Study is a family-based, multigenerational cohort study initiated originally to study the risk factors for cardiovascular disease	[PMID: 14819398] {Dawber, 1951 Epidemiological approaches to heart disease: the Framingham Study}; [PMID: 474565] {Kannel, 1979 An investigation of coronary heart disease in families. The Framingham offspring study} [PMID: 17372189] {Splansky, 2007 The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination}
8	**GOOD**	Gothenburg Osteoporosis and Obesity Determinants Study	Cohort	Population-based	Sweden	Gothenburg	Northern European	≥ 97.5%	1) excess autosomal heterozygosity > 0.336~FDR>0.1%; 2) duplicates and/or 1st or 2nd degree relatives using IBS probabilities >97% from PLINK; 3) ethnic outliers using IBS distances > 3SD from PLINK.	938	A study intiated to determine both environmental and genetic factors involved in the regulation of bone and fat mass.	[PMID: 16007330] Lorentzon, M. et al Free testosterone is a positive whereas free estradiol is a negative predictor of cortical bone size in young Swedish men-The GOOD Study. J Bone Miner Res 20, 1334-1341 (2005).
9	**HABC**	Health Aging and Body Composition	Cohort	Population-based	United States of America	Pittsburgh, PA; Memphis, TN	European American	≥ 97%	1) missing DNA; 2) 1st or 2nd degree relatives; 3) missing body weight and height; 4) ethnic outliers.	1,649	A population-based, propsective cohort study of well-functioning, unrelated men and women aged 70 and older. It was initiated to assess changes in body composition.	[PMID: 12028178] {Visser, 2002 Leg muscle mass and composition in relation to lower extremity performance in men and women aged 70 to 79: the health, aging and body composition study}; [PMID: 16043679] {Strotmeyer, 2005 Nontraumatic fracture risk with diabetes mellitus and impaired fasting glucose in older white and black adults: the health, aging, and body composition study}; [PMID:] {Strotmeyer, 2004 Diabetes is associated independently of body composition with BMD and bone volume in older white and black men and women: The Health, Aging, and Body Composition Study}
10	**HKOS**	Hong Kong Osteoporosis Study	Case-control	Population-based, clinical-based	China	Hong Kong	Southern Chinese of Han origin	≥ 95%	1) missing DNA; 2) gender mismatch with typed X-linked markers; 3) autosomal heterozygosity ≤ 27% or ≥ 31%; 4) being related or identical to other individuals in the sample.	800	A sample of 800 unrelated subjects with extreme BMD phenotype (Z-score ≤ −1.28 or ≥ +1.0 at either lumbar spine or femoral neck) were selected from a growing database of Hong Kong Southern Chinese (more than 7,000 volunteers)	[PMID:20096396] {Kung, 2010 Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies};

Supplementary Table 18A: Study design

Stage 1: GWAS BMD Discovery

	Study							Sample QC				
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity (es)	Call rate	Other exclusions	Total sample size with GWA and BMD and/or fracture data available	Short Study Description	References
11	**Indiana**	Indiana Genetics of Bone Fragility Study	Cross-sectional	Population-based, family-based, clinical-based	United States of America	Indianapolis, IN	European American	> 98%	1) history of chronic disease, taking medications known to affect bone mass or metabolism, weight >136 kg; 2) irregular menses or a history of pregnancy or lactation within three months prior to enrollment; 3) familial relationships that could not be unambiguously determined (n=14); 4) Three pairs of sisters (n=6 samples) were removed from further analysis due to evidence of substantial admixture with other populations.	1,487	A study designed to identify genetic factors underlying peak bone mineral density variation in normal premenopausal women as a risk factor for osteoporotic fracture. The GWAS sample consists primarily of white sibling pairs and sibships, with subjects aged 20-40 years, with similar samples of men and African-American subjects collected as well.	[PMID: 20164292] {Koller, 2010 Genome-wide association study of bone mineral density in premenopausal European-American women and replication in African-American women}
12	**ORCADES**	The Orkney Complex Disease Study	Cohort	Population-based, family-based	United Kingdom	Orkney	North-western European	≥ 95%	1) Gender mismatch; 2) Ethnic outliers using IBS distances >3SD from PLINK; 3) Missing weight or height; 4) Excess autosomal heterozygosity.	427	The ORCADES study is an ongoing family-based genetic epidemiology collection in the isolated Scottish archipelago of Orkney	[PMID:20418889] {Liu, 2010 Meta-analysis and imputation refines the assotiation of 15q25 with smoking quantity}; [PMID:20010834] {Repapi, 2010 Genome-wide association study identifies five loci associated with lung function}; [PMID:19060911] {Aulchenko, 2009 Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts};
13	**RS-I**	Rotterdam Study-I	Cohort	Population-based	The Netherlands	Rotterdam	North-western European	≥ 97.5%	1) missing DNA; 2) gender mismatch with typed X-linked markers; 3) excess autosomal heterozygosity > 0.336~FDR>0.1%; 4) duplicates and/or 1st or 2nd degree relatives using IBS probabilities >97% from PLINK; 5) ethnic outliers using IBS distances > 3SD from PLINK; 6) missing body weight and height.	5,746	A prospective population-based cohort study of chronic disabling conditions in Dutch elderly individuals aged 55 years and over. The RS-III cohort included individuals aged 45 years and over.	[PMID:19700477] {Estrada, 2009 GRIMP: a web- and grid-based tool for high-speed analysis of large-scale genome-wide association using imputed data}; [PMID:19728115] {Hofman, 2009 The Rotterdam Study: 2010 objectives and design update}; [PMID:1833235] {Hofman, 1991 Determinants of disease and disability in the elderly: the Rotterdam Elderly Study};
14	**RS-II**	Rotterdam Study-III	Cohort	Population-based	The Netherlands	Rotterdam	North-western European	≥ 97.5%		2,157		
15	**RS-III**	Rotterdam Study-III	Cohort	Population-based	The Netherlands	Rotterdam	North-western European	≥ 97.5%		1,212		
16	**TUK-1**	TwinsUK	Cohort	Population-based, family-based	United Kingdom	NA	North-western European	≥ 95%	1) autosomal heterozygosity <0.33 or > 0.37; 2) ethnic outliers (using STRUCTURE); 3) missing BMD or weight measurements.	1,511	TwinsUK is a population-based registry of British Twins representative of the general British population.	[PMID: 19841454] {Richards, 2009 Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture}; [PMID: 18455228] {Richards, 2008 Bone mineral density, osteoporosis, and osteoporotic fractures: a genome-wide association study}
17	**TUK-23**	TwinsUK	Cohort	Population-based, family-based	United Kingdom	NA	North-western European	≥ 95%		2,801		

Supplementary Table 18B: Study-specific descriptive statistics

Stage 1: GWAS BMD Discovery

				Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
1 AFOS	Age (yrs)	Questionnaire	443	51.3	15.5	51.5	20.2	95.1	475	52.2	14.6	53.7	18.6	92.7
	BMI (kg/m²)	Calculated	443	26.4	3.7	26.1	18.3	43.6	475	28.4	5.6	27.8	16.7	49.3
	Weight (kg)	Measured	443	77.9	12.2	76.8	50.9	125.4	475	72.2	14.5	71.1	37.8	120.4
	Height (cm)	Measured	443	171.5	6.4	172.1	154.2	193.5	475	159.5	5.9	160.0	137.6	175.5
	LS-BMD (g/cm2)	Hologic 4500	443	1.0	0.1	1.0	0.6	1.4	475	0.9	0.2	0.9	0.4	1.4
	FN-BMD (g/cm2)	Hologic 4500	443	0.9	0.1	0.8	0.5	1.3	475	0.8	0.1	0.8	0.4	1.4
2 AOGC	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,051	70.4	8.3	71.0	48.0	86.0
high BMD group	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,044	30.1	5.5	29.4	16.2	48.3
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,047	77.5	14.7	76.0	44.0	134.7
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,044	160.5	6.2	160.2	139.1	180.0
	LS-BMD (g/cm2)	Both Lunar and Hologic	0	NA	NA	NA	NA	NA	618	1.3	0.2	1.2	0.8	2.1
	FN-BMD (g/cm2)	Both Lunar and Hologic	0	NA	NA	NA	NA	NA	1,021	0.9	0.1	0.9	0.6	1.8
AOGC	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	900	68.7	8.8	68.0	50.0	86.0
low BMD group	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	893	24.3	4.8	23.4	14.8	48.5
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	894	61.5	13.7	59.3	34.5	136.0
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	893	158.8	7.3	159.0	127.5	188.0
	LS-BMD (g/cm2)	Both Lunar and Hologic	0	NA	NA	NA	NA	NA	552	0.9	0.2	0.9	0.5	1.5
	FN-BMD (g/cm2)	Both Lunar and Hologic	0	NA	NA	NA	NA	NA	865	0.6	0.1	0.6	0.3	1.0
3 CHS	Age (yrs)	Questionnaire	340	77.0	4.8	76.0	70.0	93.0	568	76.3	4.2	75.0	69.0	93.0
	BMI (kg/m²)	Measured	340	26.3	3.8	26.1	11.1	41.4	568	26.0	5.1	25.8	7.5	44.6
	Weight (kg)	Measured	340	78.5	12.2	78.1	34.1	116.8	568	65.8	13.7	64.9	22.3	116.4
	Height (cm)	Measured	340	173	6.4	172	152	193	568	159	6.0	159	142	183
	LS-BMD (g/cm2)	Whole Body Scan	340	1.1	0.2	1.1	0.6	2.6	568	0.9	0.2	0.9	0.4	3.3
	FN-BMD (g/cm2)	Measured	340	0.8	0.1	0.8	0.4	1.4	568	0.6	0.1	0.6	0.3	1.1
4 DeCODE	Age (yrs)	NationalRegistry	1,136	66.1	14.2	69.2	20.1	96.1	6,469	59.7	13.8	59.9	20.0	97.8
	BMI (kg/m²)	Calculated	1,136	26.7	4.1	26.5	13.9	42.5	6,461	26.3	4.8	25.6	13.5	59.7
	Weight (kg)	Measured	1,136	83.4	14.4	83.0	38.4	129.5	6,461	71.1	13.4	69.7	30.0	129.3
	Height (cm)	Measured	1,136	176.5	6.7	176.0	148.5	196.0	6,469	164.4	6.2	164.5	116.5	188.0
	LS-BMD (g/cm2)	Hologic	1,135	1.0	0.2	1.0	0.5	1.7	6,461	0.9	0.2	0.9	0.4	1.8
	FN-BMD (g/cm2)	Hologic	1,115	0.8	0.1	0.9	0.4	1.3	6,279	0.7	0.1	0.6	0.2	1.4
5 ERF	Age (yrs)	Questionnaire	1,419	50.6	14.9	50.9	17.6	88.6	1,815	50.6	15.9	50.7	16.7	95.7
	BMI (kg/m²)	Measured	1,223	27.1	3.9	26.8	15.9	42.4	1,517	26.4	4.7	25.7	15.5	45.6
	Weight (kg)	Measured	1,232	83.3	14.0	81.8	41.9	154.7	1,532	69.4	13.6	67.4	42.1	161.0
	Height (cm)	Measured	1,232	174.8	7.2	174.7	152.2	196.5	1,533	161.8	6.5	161.6	141.0	182.8
	LS-BMD (g/cm2)	GE-lunar DPX-L	1,215	1.2	0.2	1.2	0.6	1.8	1,504	1.1	0.2	1.1	0.6	1.8
	FN-BMD (g/cm2)	GE-lunar DPX-L	1,207	1.0	0.1	1.0	0.5	1.7	1,512	0.9	0.1	0.9	0.5	1.3
6 EPIC Norfolk	Age (yrs)	Questionnaire	109	72.3	3.2	71.8	67.4	78.4	111	72.4	3.0	72.8	67.5	78.7
	BMI (kg/m²)	Measured	109	28.1	4.0	28.1	19.0	39.3	111	29.6	4.5	29.5	18.4	41.0
	Weight (kg)	Measured	109	82.7	12.9	82.8	56.4	128.5	111	74.9	12.5	74.4	46.8	104.0
	Height (cm)	Measured	109	171.5	5.3	171.7	154.9	188.9	111	159.0	5.7	159.1	144.9	177.2
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	Hologic QDR 1000W	109	0.8	0.1	0.8	0.5	1.3	111	0.7	0.1	0.7	0.5	1.0
7 FHS	Age (yrs)	Questionnaire	1,548	64.5	10.9	64.0	35.0	92.0	2,081	64.9	11.5	65.0	29.0	96.0
	BMI (kg/m²)	Measured	1,540	28.4	4.4	27.9	17.1	53.4	2,060	27.3	5.5	26.4	15.4	58.2
	Weight (kg)	Measured	1,544	86.0	14.9	84.4	46.3	170.1	2,066	69.8	15.0	67.6	36.3	158.8
	Height (cm)	Measured	1,540	174	7	174	152	200	2,060	160	7	160	138	183

Supplementary Table 18B: Study-specific descriptive statistics

Stage 1: GWAS BMD Discovery

			Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
	LS-BMD (g/cm2)	GE-lunar DPX-L	1,492	1.3	0.2	1.3	0.7	2.4	2,008	1.1	0.2	1.1	0.5	2.0
	FN-BMD (g/cm2)	GE-lunar DPX-L	1,531	1.0	0.1	1.0	0.5	1.7	2,043	0.8	0.2	0.8	0.1	1.4
8 GOOD	Age (yrs)	Questionnaire	938	18.9	0.6	18.8	18.0	20.1	0	NA	NA	NA	NA	NA
	BMI (kg/m²)	Measured	938	22.4	3.2	21.9	16.1	41.6	0	NA	NA	NA	NA	NA
	Weight (kg)	Measured	938	73.9	11.6	72.0	51.3	127.0	0	NA	NA	NA	NA	NA
	Height (cm)	Measured	938	182	7.0	182	161	203	0	NA	NA	NA	NA	NA
	LS-BMD (g/cm2)	GE_Lunar_Prodigy	938	1.2	0.2	1.2	0.8	1.7	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	GE_Lunar_Prodigy	938	1.2	0.2	1.2	0.8	1.8	0	NA	NA	NA	NA	NA
9 HABC	Age (yrs)	Questionnaire	879	73.9	2.9	74.0	69.0	80.0	784	73.6	2.8	73.0	69.0	80.0
	BMI (kg/m²)	Measured	879	27.1	3.7	26.7	17.6	44.2	784	26.1	4.5	25.6	15.6	44.7
	Weight (kg)	Measured	879	81.6	12.4	80.0	52.2	134.5	784	66.4	12.1	65.1	40.8	123.0
	Height (cm)	Measured	879	173.6	6.4	173.4	151.1	194.8	784	159.4	5.8	159.6	141.6	175.6
	LS-BMD (g/cm2)	Hologic QDR 4500	871	1.1	0.2	1.1	0.6	2.4	778	0.9	0.2	0.9	0.6	1.7
	FN-BMD (g/cm2)	Hologic QDR 4500	869	0.8	0.1	0.8	0.4	1.3	776	0.7	0.1	0.7	0.3	1.1
10 HKOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	800	48.9	15.6	50.0	20.0	84.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	800	22.7	3.9	22.0	15.0	40.5
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	800	54.7	10.2	53.2	33.5	93.5
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	800	155	6.7	156	127	175
	LS-BMD (g/cm2)	Hologic- Delphi W	0	NA	NA	NA	NA	NA	800	0.9	0.2	0.9	0.3	1.6
	FN-BMD (g/cm2)	Hologic- Delphi W	0	NA	NA	NA	NA	NA	800	0.7	0.2	0.7	0.3	1.9
11 Indiana	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,481	33.1	7.2	33.3	20.0	50.7
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,476	25.6	5.9	24.1	15.7	57.3
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,476	70.0	16.6	66.0	41.2	166.0
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,476	165.5	6.1	165.3	146.8	192.3
	LS-BMD (g/cm2)	GE_Lunar_Prodigy	0	NA	NA	NA	NA	NA	1,479	1.3	0.1	1.3	0.9	1.8
	FN-BMD (g/cm2)	GE_Lunar_Prodigy	0	NA	NA	NA	NA	NA	1,479	1.0	0.1	1.0	0.6	1.6
12 ORCADES	Age (yrs)	Questionnaire	194	57.7	13.5	58.9	24.5	86.8	233	58.8	13.0	61.0	23.6	81.7
	BMI (kg/m²)	Measured	194	27.8	4.4	27.2	16.8	47.7	233	27.7	5.2	26.5	18.5	47.2
	Weight (kg)	Measured	194	84.8	14.3	83.3	42.0	147.5	233	71.5	13.7	69.3	43.0	115.4
	Height (cm)	Measured	194	174.7	6.6	175.2	157.9	198.6	233	160.7	6.2	160.9	139.5	181.0
	LS-BMD (g/cm2)	Hologic QDR 4500	194	1.1	0.2	1.1	0.7	1.6	233	1.0	0.2	1.0	0.6	1.4
	FN-BMD (g/cm2)	Hologic QDR 4500	192	0.8	0.1	0.8	0.6	1.3	229	0.8	0.1	0.7	0.5	1.0
13 RS-I	Age (yrs)	Questionnaire	2,427	68.1	8.2	67.1	55.0	97.8	3,547	70.3	9.6	69.4	55.0	99.2
	BMI (kg/m²)	Measured	2,372	25.7	3.0	25.6	14.2	38.2	3,372	26.7	4.1	26.3	15.4	59.5
	Weight (kg)	Measured	2,375	78.6	10.7	77.8	41.0	122.3	3,383	69.6	11.3	68.7	40.1	146.5
	Height (cm)	Measured	2,372	174.8	6.8	174.6	151.0	198.0	3,375	161.3	6.6	161.5	101.0	191.5
	LS-BMD (g/cm2)	GE-lunar DPX-L	2,116	1.2	0.2	1.2	0.5	2.0	2,798	1.0	0.2	1.0	0.5	1.7
	FN-BMD (g/cm2)	GE-lunar DPX-L	2,106	0.9	0.1	0.9	0.4	1.4	2,799	0.8	0.1	0.8	0.4	1.5
14 RS-II	Age (yrs)	Questionnaire	785	63.7	6.8	61.5	55.1	89.3	902	63.8	7.4	61.4	55.1	92.3
	BMI (kg/m²)	Measured	785	26.9	3.3	26.8	16.8	40.5	902	27.4	4.4	26.8	16.7	45.5
	Weight (kg)	Measured	785	83.5	11.4	82.5	54.0	126.8	902	72.8	12.5	71.2	44.1	125.3
	Height (cm)	Measured	785	176.0	6.5	175.9	156.8	203.0	902	162.9	6.2	163.0	141.5	189.6
	LS-BMD (g/cm2)	GE-lunar DPX-L	781	1.2	0.2	1.2	0.7	1.9	898	1.1	0.2	1.1	0.5	2.0
	FN-BMD (g/cm2)	GE-lunar DPX-L	779	1.0	0.1	1.0	0.6	1.6	888	0.9	0.1	0.9	0.5	1.4
15 RS-III	Age (yrs)	Questionnaire	528	56.1	5.5	56.3	45.9	84.2	683	56.1	5.4	56.6	45.8	87.9
	BMI (kg/m²)	Measured	525	28.0	4.0	27.3	19.5	46.7	683	27.6	5.0	26.7	14.0	48.2
	Weight (kg)	Measured	525	89.7	14.1	87.7	60.8	149.9	683	75.2	14.3	73.1	35.0	137.6

Supplementary Table 18B: Study-specific descriptive statistics

Stage 1: GWAS BMD Discovery

			Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
	Height (cm)	Measured	525	178.8	6.7	178.6	160.5	197.5	683	165.0	6.2	164.8	146.5	184.5
	LS-BMD (g/cm2)	GE-lunar DPX-L	437	1.2	0.2	1.2	0.8	1.8	583	1.2	0.2	1.2	0.7	1.9
	FN-BMD (g/cm2)	GE-lunar DPX-L	511	1.0	0.1	1.0	0.6	1.5	666	0.9	0.1	0.9	0.6	1.5
16 TUK-1	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,523	49.8	13.1	51.2	16.6	80.9
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,523	25.2	4.8	24.2	17.4	40.1
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,523	67.5	12.7	65.2	35.1	128.3
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,523	162.1	6.3	162.0	148.0	177.0
	LS-BMD (g/cm2)	Hologic QDR 4500W	0	NA	NA	NA	NA	NA	1,517	1.0	0.2	1.0	0.6	1.8
	FN-BMD (g/cm2)	Hologic QDR 4500W	0	NA	NA	NA	NA	NA	1,487	0.8	0.1	0.8	0.3	1.3
17 TUK-23	Age (yrs)	Questionnaire	373	49.8	14.6	50.1	18.3	81.4	2,439	50.0	13.8	51.8	16.2	82.1
	BMI (kg/m²)	Measured	365	25.8	3.3	25.7	19.1	35.2	2,359	25.4	4.7	24.6	17.7	41.4
	Weight (kg)	Measured	373	80.4	11.8	79.8	40.5	122.7	2,439	67.6	13.0	65.5	40.0	166.0
	Height (cm)	Measured	365	175.1	7.1	175.0	161.0	191.0	2,359	162.2	6.3	162.0	149.0	177.0
	LS-BMD (g/cm2)	Hologic QDR 4500W	371	1.0	0.2	1.0	0.6	1.5	2,427	1.0	0.1	1.0	0.5	1.6
	FN-BMD (g/cm2)	Hologic QDR 4500W	368	0.9	0.1	0.9	0.5	1.3	2,404	0.8	0.1	0.8	0.4	3.6

Supplementary Table 18C: Study descriptives fracture

Stage 1: GWAS BMD Discovery

Study	Trait	Assessment method	Men		Women	
			Fracture N	Non-fracture N	Fracture N	Non-fracture N
1 AFOS	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
2 AOGC	All fractures	Interview with questionnaire	NA	NA	431	1,224
	Non-vertebral fractures	Radiographic	NA	NA	294	1,224
	Vertebral fractures	NA	NA	NA	NA	NA
3 CHS	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
4 DeCODE	All fractures	Medical records, radiograhic documentation, questionnaire	532	6,890	1,453	7,673
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
5 ERF	All fractures	Interview	594	721	470	1,141
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
6 EPICNOR	All fractures	Medical records	143	1,478	228	1,703
	Non-vertebral fractures	Medical records	119	1,502	203	1,728
	Vertebral fractures	NA	NA	NA	NA	NA
7 FHS	All fractures	Self-report and medical records	583	1,351	937	1,431
	Non-vertebral fractures	Medical records	401	1,153	738	1,352
	Vertebral fractures	Radiographic	48	1,506	77	2,013
8 GOOD	All fractures	Radiographic doc	304	687	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
9 HABC	All fractures	Radiographic	109	769	199	584
	Non-vertebral fractures	Radiographic	88	790	165	618
	Vertebral fractures	NA	NA	NA	NA	NA

Supplementary Table 18C: Study descriptives fracture

Stage 1: GWAS BMD Discovery

Study	Trait	Assessment method	Men		Women	
			Fracture N	Non-fracture N	Fracture N	Non-fracture N
10 HKOS	All fractures	Medical records, Radiographic and Questionnaire	NA	NA	79	627
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
11 Indiana	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
12 ORCADES	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
13 RS-I	All fractures	Medical records	227	2,151	753	2,615
	Non-vertebral fractures	Medical records	174	2,201	622	2,761
	Vertebral fractures	Medical records and Radiographic	128	1,184	201	1,470
14 RS-II	All fractures	Medical records	41	941	88	1,080
	Non-vertebral fractures	Medical records	33	951	71	1,102
	Vertebral fractures	Medical records and Radiographic	9	975	22	1,151
15 RS-III	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
16 TUK-1	All fractures	Medical records, Radiographic and Questionnaire	NA	NA	332	1,337
	Non-vertebral fractures	Medical records and Radiographic	NA	NA	48	1,621
	Vertebral fractures	NA	NA	NA	NA	NA
17 TUK-23	All fractures	Medical records, Radiographic and Questionnaire	52	406	475	2,416
	Non-vertebral fractures	Medical records and Radiographic	1	457	72	2,819
	Vertebral fractures	NA	NA	NA	NA	NA

Supplementary Table 18D: Genotyping/Imputation

Stage 1: GWAS BMD Discovery

Cohort	Genotyping						Imputation			Association analyses					
	Platform	Genotype calling algorithm	Inclusion criteria			SNPs that met QC criteria	Imputation software	Inclusion criteria		Analyses software	No. analyzed SNPs	Men	Women	λ LSBMD	λ FNBMD
			MAF	Call rate*	p for HWE			MAF	Imputation quality*						
1 AFOS	Affymetrix / 500K or 6.0	Birdseed	≥ 1%	≥ 95.0%	$> 10^{-6}$	338,598	MACH	≥1%	MACH R2 ≥ 0.3	MMAP (J. O'Connell)	2,543,013	443	475	1.06	1.07
2 AOGC	Illumina Infinium II 370CNVQuad (n=1882); HumHap300 (n=140), 370CNVDuo (n=4) and 610Quad (n=10)	BeadStudio	≥ 1%	≥ 98%	$> 10^{-7}$	289,499	MACH	≥ 1%	MACH R2 ≥ 0.3	MACH2DAT	2,543,887	0	1,955	1.01	1.02
3 CHS	Illumina 370CNV	BeadStudio	> 1%	≥97%	$> 10^{-5}$	306,655	BimBam	≥1%	$(O/E)\sigma^2$ ratio ≥ 0.3	R	2,335,99	347	563	1.03	0.98
4 DeCODE	Illumina HH300 and 370CNV	BeadStudio	> 1%	> 96%	$> 10^{-6}$	281,410	IMPUTE	≥1%	Prop_info >0.4	SNPTEST	2,454,808	1,136	6,469	1.00	1.00
5 EPICNOR	Afffymetrix 500K	BRLMM	≥ 1%	≥ 90%	$> 10^{-6}$	397,438	IMPUTE	≥1%	Prop_info >0.4	SNPTEST	2,313,843	109	111	-	1.00
6 ERF	Ilumina 318K, 370K, Afymetrix 250K	Beadstudio, BRLMM	> 1%	> 98%	$> 10^{-6}$	487,573	MACH	≥1%	MACH R2 ≥ 0.3	ProbABEL	2,543,887	887	1,178	1.07	1.02
7 FHS	Affymetrix 500K Dual GeneChip + 50K gene-centered MIP set	BRLMM	≥ 1%	≥ 97%	$\geq 10^{-6}$	378,163	MACH	≥1%	$(O/E)\sigma^2$ ratio ≥ 0.3	Kinship R-Package	2,471,285	1,554	2,090	1.03	1.02
8 GOOD	Illumina / HumanHap 610 Quad	Beadstudio Genecall	≥ 1%	≥ 98%	$> 10^{-6}$	521,160	MACH	≥1%	MACH R2 ≥ 0.3	MACH2QTL via GRIMP	2,543,887	938	0	0.99	1.01
9 HABC	Illumina/ Human 1M-Duo	Beadstudio	≥1%	≥97%	$> 10^{-6}$	914,263	MACH	≥1%	MACH R2 ≥ 0.3	SNPTEST	2,543,887	871	778	1.00	1.01
10 HKOS	Illumina / Human610-Quad	Illumina's GenomeStudio	≥ 1%	≥ 95%	$> 10^{-4}$	488,853	IMPUTE	≥1%	Prop_info >0.4	SNPTEST	2,329,916	0	778	1.00	1.01
11 Indiana	Illumina 610Quadv1_B	Beadstudio v3.2.32	≥ 1%	≥ 95%	$> 10^{-4}$	553,331	IMPUTE	≥1%	Prop_info >0.4	Merlin	2,626,037	0	1,487	1.01	0.99
12 ORCADES	Illumina / HumanHap 300K V.2	Beadstudio Genecall	≥ 1%	≥ 98.0%	$> 10^{-6}$	306,207	MACH	≥1%	MACH R2 ≥ 0.3	R, GenABEL, ProbABEL	2,543,887	194	233	1.00	1.01
13 RS-I	Illumina / HumanHap 550K V.3 /HumanHap 550 V.3 DUO;	Beadstudio Genecall	≥ 1%	≥ 97.5%	$> 10^{-6}$	512,349	MACH	≥1%	MACH R2 ≥ 0.3	MACH2QTL via GRIMP	2,543,887	2,378	3,368	1.07	1.05
14 RS-II	Illumina / HumanHap 550K V.3 /HumanHap 550 V.3 DUO;	Beadstudio Genecall	≥ 1%	≥ 97.5%	$> 10^{-6}$	466,389	MACH	≥1%	MACH R2 ≥ 0.3	MACH2QTL via GRIMP	2,543,887	982	1,168	1.01	1.00
15 RS-III	Illumina / HumanHap610	Beadstudio Genecall	≥ 1%	≥ 97.5%	$> 10^{-6}$	514,073	MACH	≥1%	MACH R2 ≥ 0.3	MACH2QTL via GRIMP	2,543,887	517	695	1.00	1.00
16 TUK-1	Illumina HumanHap 300 & 550. Illumina HumanCNV370 Duo	Beadstudio Genecall	≥ 1%	≥ 95%	$> 10^{-6}$	313,575	IMPUTE	≥1%	Prop_info >0.4	GenABEL	2,561,701	0	1,511	1.01	1.01
17 TUK-23	Illumina 610k	Beadstudio Genecall	≥ 1%	≥ 95%	$> 10^{-6}$	545,026	IMPUTE	≥1%	Prop_info >0.4	GenABEL	2,561,701	375	2,426	0.99	1.08

Supplementary Table 19A: Study design

Stage 2: In-silico Replication BMD Loci and Fracture association

	Study						Sample QC				
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Call rate	Other exclusions	Total sample size with available GWA and BMD and/or fracture data	Short Study Description	References
1	**AGES**	Age, Gene/Environment Susceptibility Reykjavik Study	Cohort	Population-based	Iceland	Reykjavik	Northern European	>97%	1) mismatch with genotypes from other experiments; 2) missing height and weight.	3,185	The Age Gene/Environment Susceptibility-Reykjavik Study originally comprised a random sample of 30,795 men and women born in 1907-1935 and living in Reykjavik in 1967. A total of 19,381 people attended, resulting in a 71% recruitment rate. The study sample was divided into six groups by birth year and birth date within month. One group was designated for longitudinal follow up and was examined in all stages; another was designated as a control group and was not included in examinations until 1991. Other groups were invited to participate in specific stages of the study. Between 2002 and 2006, the AGES-Reykjavik study re-examined 5,764 survivors of the original cohort who had participated before in the Reykjavik Study.	[PMID: 17351290] [Harris, 2007 Age, Gene/Environment Susceptibility-Reykjavik Study: multidisciplinary applied phenomics}
2	**DeCODE insilico rep**	DeCODE Genetics Study (replication set)	Case-control	Population-based, clinical-based	Iceland	NA	North-western European	≥ 98%	1) missing body weight and height; 2) missing age at fracture; 3) missing ever/never fracture information.	2,878	The study includes 40,000 individuals taking part in various disease projects	[PMID: 18445777] {Styrkarsdottir, 2008 Multiple genetic loci for bone mineral density and fractures}; [PMID: 19079262] {Styrkarsdottir, 2009 Multiple genetic loci for bone mineral density and fractures}
3	**PROSPER/ PHASE**	The PROpective Study of Pravastatin in the Elderly at Risk	Cohort, randomized-controled trial	Clinical-based	The Netherlands/ United Kingdom /Ireland	Leiden/ Glasgow/ Cork	European	≥ 97.5%	1) missing DNA; 2) gender mismatch with typed X-linked markers; 3) excess autosomal heterozygosity > 0.336~FDR>0.1%; 4) duplicates and/or 1st or 2nd degree relatives using IBS probabilities >97% from PLINK; 5) ethnic outliers using IBS distances > 3SD from PLINK; 6) Missing body weight and height.	5,242	A randomized controlled clinical trial to test the effect of pravastatin on cardiovascular outcomes in the elderly at risk.	[PMID: 12457784] {Shepherd, 2002 Pravastatin in elderly individuals at risk of vascular disease (PROSPER): a randomised controlled trial}
4	**WGHS**	Women's Genome Health Study	Cohort	Population-based	North America, primarily US	NA	European	≥ 98%	Self-reported European ancestry confirmed by idenity-by-state analysis using ancestry informative SNPS in PLINK.	22,330	A population-based cohort derived from the approximately 72% of women who provided a blood sample in the Women's Health Study, a trial of aspirin and vitamin E in prevention of cardiovascular disease and cancer among middle-aged, female health care professionals. The WGHS now has over 15 years of follow-up for incident clinical events, including bone fracture.	[PMID: 18070814] {Ridker, 2008 Women's Genome Health Study Working Group. Rationale, design, and methodology of the Women's Genome Health Study: a genome-wide association study of more than 25,000 initially healthy american women}
5	**WHI GeCHIP - Hip Fracture GWAS**	Women's Health Initiative Genetic Components of HIP Fracture (GeCHIP) Consortium - Hip Fracture	Case-control	Population-based	United States	Multi-center (n=40)	Caucasian	> 95%	1) low call rate (<= 95%) 2) low agreement rate with duplicate sample (both samples dropped) 3) duplicate sample 4) identical twins and 1st degree relatives (sample w/ lower call rate dropped) 5) chomosomal abnormalities (excessive CNV) 6) Missing body weight and height	4,656	Hip fracture portion of GeCHIP. This is a case control sample from the Women's Health Initiative. All hip fractures in the WHI Clinical Trial (CT) and Observational Study (OS) through Aug2007 were selected and matched to controls. In the OS, controls were matched on on age (+/-1yr), race/ethnicity (exact), enrollment date (+/- 365 days) and current HT use at baseline (exact). For the CT age (+/-1yr), race/ethnicity (exact), earliest randomization date (+/- 365 days), HT use (active vs. placebo, or if not enrolled current HT use at baseline; exact) and CaD use (active vs. placebo vs. not enrolled; exact). Controls were excluded if they self-reported a prior history of postmenopausal fracture (age >= 55 years)	[PMID: 9492970] {1998, Design of the Women's Health Initiative clinical trial and observational study. The Women's Health Initiative Study Group}

Supplementary Table 19A: Study design

Stage 2: In-silico Replication BMD Loci and Fracture association

	Study						Sample QC				
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Call rate	Other exclusions	Total sample size with available GWA and BMD and/or fracture data	Short Study Description	References
6	YFS	CV risk in Young Finns Study	Cohort	Population-based	Finland	Multicentre	North-western European	> 95%	1) missing DNA; 2) Missing body weight.	1,586	One of the largest follow-up studies into cardiovascular risk from childhood to adulthood. The main aim of the Young Finns Study is to determine the contribution made by childhood lifestyle, biological and psychological measures to the risk of cardiovascular diseases in adulthood.	[PMID: 18263651] {Raitakari, 2008 Cohort profile: the cardiovascular risk in Young Finns Study}

Supplementary Table 19B: Study-specific descriptive statistics

Stage 2: In-silico Replication BMD Loci and Fracture association

				Men						Women					
Study	Trait	Assessment method	N	mean	sd	median	min	max	N	mean	sd	median	min	max
1 AGES	Age (yrs)	Questionnaire	1,351	76.5	5.3	76.0	67.0	94.0	1,865	76.3	5.6	76.0	66.0	95.0
	BMI (kg/m²)	Measured	1,351	27.0	3.8	26.7	15.9	40.6	1,865	27.2	4.9	26.8	14.8	48.5
	Weight (kg)	Measured	1,351	83.2	13.3	81.6	42.0	144.7	1,865	70.5	13.3	69.3	37.2	128.3
	Height (cm)	Measured	1,351	175.4	6.2	175.2	153.1	196.4	1,865	160.9	5.8	160.9	139.3	182.6
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
2 DeCODE insilico	Age (yrs)	NationalRegistry	832	54.8	16.3	54.6	20.3	89.0	2,046	57.1	14.3	56.8	20.0	91.7
	BMI (kg/m²)	Calculated	831	26.4	3.7	26.1	16.6	42.0	2,045	25.9	4.5	25.2	16.2	47.2
	Weight (kg)	Measured	831	84.1	13.4	82.7	46.6	129.3	2,045	70.2	12.9	68.1	34.5	124.2
	Height (cm)	Measured	831	178.5	6.5	178.5	155.0	203.0	2,045	164.7	6.0	165.0	133.0	185.0
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
3 PROSPER/PHASE	Age (yrs)	Questionnaire	2,524	75.0	3.3	74.5	70.2	83.3	2,718	75.7	3.4	75.4	69.4	83.4
	BMI (kg/m²)	Measured	2,524	26.6	3.6	26.3	15.2	45.1	2,718	27.1	4.7	26.7	15.6	50.1
	Weight (kg)	Measured	2,524	78.7	11.9	78.0	40.0	127.0	2,718	68.3	12.7	67.0	35.5	138.0
	Height (cm)	Measured	2,524	172.1	6.7	172.0	143.0	198.0	2,718	158.8	6.6	159.0	135.0	180.0
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
4 WGHS	Age (yrs)	Questionnaire	NA	NA	NA	NA	NA	NA	22,330	54.1	7.1	52.0	38.0	89.0
	BMI (kg/m²)	Questionnaire	NA	NA	NA	NA	NA	NA	22,330	25.9	5.0	24.9	14.2	59.6
	Weight (kg)	Questionnaire	NA	NA	NA	NA	NA	NA	22,330	70.0	14.2	68.0	38.6	175.1
	Height (cm)	Questionnaire	NA	NA	NA	NA	NA	NA	22,330	164	6.0	165	13	201
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WHI GeCHIP - Hip Fracture 5 GWAS	Age (yrs)	Questionnaire	NA	NA	NA	NA	NA	NA	4,656	69.0	6.5	70.0	50.0	79.0
	BMI (kg/m²)	Measured	NA	NA	NA	NA	NA	NA	4,655	27.0	5.5	26.0	13.4	69.4
	Weight (kg)	Measured	NA	NA	NA	NA	NA	NA	4,656	70.5	14.9	68.1	37.5	171.5
	Height (cm)	Measured	NA	NA	NA	NA	NA	NA	4,656	161.6	6.5	161.5	116.0	183.4
	LS-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
6 YFS	Age (yrs)	Questionnaire	185	37.5	5.0	37.0	27.0	46.0	238	37.6	5.2	37.0	27.0	46.0
	BMI (kg/m²)	Measured	180	26.4	4.1	26.1	17.9	41.2	228	25.5	5.2	24.2	16.6	58.8
	Weight (kg)	Measured	180	85.7	15.2	84.0	54.0	136.0	228	70.5	15.2	66.0	47.0	166.0
	Height (cm)	Measured	180	179.9	6.5	180.0	164.0	197.0	228	166.3	5.6	166.0	151.0	184.0
	LS-BMD (g/cm2)	Prodigy	185	1.2	0.2	1.2	0.8	1.7	238	1.2	0.2	1.2	0.8	1.6
	FN-BMD (g/cm2)	Prodigy	185	1.0	0.2	1.0	0.7	1.9	238	1.0	0.1	1.0	0.6	1.4

Supplementary Table 19C: Study descriptives fracture

Stage 2: In-silico Replication BMD Loci and Fracture association

	Study	Trait	Assessment method	Men		Women	
				Fracture N	Non-fracture N	Fracture N	Non-fracture N
1	**AGES**	All fractures	Medical and radiographic records	448	892	1,011	834
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA
2	**DeCODE insilico**	All fractures	Medical records, radiograhic documentation, questionnaire	532	6,980	1,878	7,864
		Non-vertebral fractures	Medical records, questionnaire	276	418	1,785	3,736
		Vertebral fractures	NA	NA	NA	NA	NA
3	**PROSPER/PHASE**	All fractures	Medical records	117	2,407	309	2,409
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA
4	**WGHS**	All fractures	Questionnaire	NA	NA	1,795	20,535
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA
	WHI GeCHIP - Hip Fracture			NA	NA	2,166	2,490
5	**GWAS**	All fractures	Medical records				
		Non-vertebral fractures	Medical records	NA	NA	2,166	2,490
		Vertebral fractures	NA	NA	NA	NA	NA
6	**YFS**	All fractures	Medical records	96	603	106	781
		Non-vertebral fractures	Medical records	NA	NA	NA	NA
		Vertebral fractures	Medical records and Radiographic	NA	NA	NA	NA

Supplementary Table 19D: Genotyping/Imputation

Stage 2: In-silico Replication BMD Loci and Fracture association

	Cohort	Genotyping						Imputation			Association analyses			
		Platform	Genotype calling algorithm	Inclusion criteria			SNPs meeting QC criteria	Imputation software	Inclusion criteria		Analyses software	No. analyzed SNPs	Men	Women
				MAF	Call rate*	P for HWE			MAF	Imputation quality*				
1	**AGES**	Illumina Hu370CNV	BEadstudio Genecall	≥ 1%	>97%	$> 10^{-6}$	329,804	MACH	≥1%	MACH R2 ≥ 0.3	ProbABEL	82	1,340	1,845
2	**DeCODE insilico**	Illumina HH300 and 370CNV	BeadStudio	> 1%	> 96%	$> 10^{-6}$	281,410	IMPUTE	≥1%	MACH R2 ≥ 0.3	SNPTEST	82	1,136	6,469
3	**PROSPER/PHASE**	Illumina Beadchip 660K-quad	Beadstudio Genecall	≥ 1%	≥ 97.5%	$> 10^{-6}$	557,192	MACH	≥1%	MACH R2 ≥ 0.3	PLINK	82	2,524	2,718
4	**WGHS**	Illumina/HumanHap300 Duo Plus	Beadstudio v3.3	> 1%	≥ 98%	$> 10^{-6}$	339,596	MACH	≥1%	MACH R2 ≥ 0.3	ProbAbel	82	0	22,330
5	**WHI GeCHIP - Hip Fracture GWAS**	Illumina HumanHap 550K, Illumina HumanHap 610K	Beadstudio Gencall	> 0.5%	> 95%	$> 10^{-6}$	499,982	MACH	≥1%	MACH R2 ≥ 0.3	R	82	0	4,656
6	**YFS**	Illumina Custom BeadChip Human670K	Illumina	> 1%	> 95%	$> 10^{-6}$	546,677	MACH	≥1%	MACH R2 ≥ 0.3	ProbABEL	82	1,123	1,319

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Study								
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
1	**AOGC-GOS**	Anglo-Australasian Osteoporosis Genetics Consortium - Geelong Osteoporosis Study	Population cohort, and case/control for fracture cases	Population based, clinical-based	Australia	Geelong	Caucasian (North-west European)	2,922	Population-based BMD cohort (from electoral rolls) and case-control for fracture cases; all drawn from Geelong general population of men and women	[PMID: 19707703] {Henry, 2010 Bone mineral density reference ranges for Australian men: Geelong Osteoporosis Study}; [PMID: 11090233] {Henry, 2000 Prevalence of osteoporosis in Australian women: Geelong Osteoporosis Study}
2	**AOGC-SHEFFIELD**	Anglo-Australasian Osteoporosis Genetics Consortium - Sheffield	Cohort	Population-based	UK	Sheffield	Caucasian (North-west European)	4,014	Large population-based cohort of community-dwelling elderly women aged ≥ 75 years	[PMID: 17042717] {McCloskey, 2007 Clodronate reduces the incidence of fractures in community-dwelling elderly women unselected for osteoporosis: results of a double-blind, placebo-controlled randomized study}
3	**APOSS**	Aberdeen Prospective Osteoporosis Screening Study	Cohort	Population-based	UK	Aberdeen	North-western European	3,268	APOSS is a longitudinal population-based study of osteoporotic fracture risk assessment in Caucasian women aged 45-54 years of age at baseline.	[PMID: 16355284] {Macdonald, 2006 Large-scale population-based study shows no evidence of association between common polymorphism of the VDR gene and BMD in British women}
4	**AROS**	Aarhus Osteoporosis Study	Case-control	Clinical-based	Denmark	Aarhus	Northern European	801	Case-control study	[PMID: 20508921] {Harsløf, 2010 Genotypes and haplotypes of the estrogen receptor genes, but not the retinoblastoma-interacting zinc finger protein 1 gene are associated with osteoporosis}
5	**AUSTRIOS-A**	Austrios A "Young cohort"	Cohort	Population-based	Austria	Graz	Central European	805	Men and women with and without osteoporosis	[PMID: 16299058] {Gugatschka, 2002 Molecularly-defined lactose malabsorption, milk consumption and anthropometric differences in adult males}; [PMID: 14753735] {Obermayer-Pietsch, 2004 Genetic predisposition for adult lactose intolerance and relation to diet, bone density, and bone fractures}
6	**AUSTRIOS-B**	Austrios B "old cohort"	Cohort	Clinical-based	Austria	Graz	Central European	2,064	95 nursing homes in Austria, patients had to be relatively healthy	[PMID: 16735485] {Dobnig, 2006 Type 2 diabetes mellitus in nursing home patients: effects on bone turnover, bone mass and fracture risk}
7	**BARCOS**	Barcelona Cohorte Osteoporosis	Cohort	Population-based	Spain	Barcelona	Mediterranean European	1,453	The Barcelona is a cohort study of unrelated women aged 44 years and over that were recruited from the Menopausal Unit of the Hospital del Mar, Barcelona. All of the participants were consecutive, unselected, postmenopausal women who had presented to the outpatient clinic for a baseline visit due to menopause.	[PMID: 17878995] {Bustamante, 2007 Promoter 2 -1025 T/C polymorphism in the RUNX2 gene is associated with femoral neck bmd in Spanish postmenopausal women}; [PMID: 17984249] {Bustamante, 2007 Polymorphisms in the interleukin-6 receptor gene are associated with bone mineral density and body mass index in Spanish postmenopausal women}

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Study								
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
8	**CABRIO-C**	Cantabria-Camargo	Cross-sectional	Community-based	Spain	Santander	Caucasian (Spanish)	1,450	Community-based study designed to evaluate the prevalence of metabolic bone diseases in postmenopausal women and men older than 50 attended at a primary care center in Northern Spain.	[PMID: 20594548] {Olmos, 2010 Bone turnover markers in Spanish adult men The Camargo Cohort Study}; [PMID: 19737549] {Martinez, 2009 Bone turnover markers in Spanish postmenopausal women: the Camargo cohort study}
9	**CABRIO-CC**	Cantabria Osteoporosis Case-control	Case-control, cross-sectional	Clinic-based plus volunteers	Spain	Santander	Caucasian (Spanish)	2,321	Clinic-based study of control individuals and patients with osteoporosis living in Cantabria, a region in Northern Spain	[PMID: 17118999] {Riancho, 2007 Identification of an aromatase haplotype that is associated with gene expression and postmenopausal osteoporosis}; [PMID: 17218734] {Zarrabeitia, 2007 Adiposity, estradiol, and genetic variants of steroid-metabolizing enzymes as determinants of bone mineral density}
10	**CAIFOS**	Calcium Intake Fracture Outcome Study	Cohort, randomized-controled trial	Population-based	Australia	Perth	Caucasian	1,347	Randomized-controled trial and cohort study	[PMID: 16636212] {Prince, 2006 Effects of calcium supplementation on clinical fracture and bone structure: results of a 5-year, double-blind, placebo-controlled trial in elderly women}
11	**Calex-family**	Calex-family study	Cohort	Population-based, fami	Finland	Jyväskylä and its surrondings	North European	647	The Calex-family study is a family-based study to study Fractures in Puberty - Causes and Implications in Old Age	[PMID: 19171028] {Cheng, 2009 Trait-specific tracking and determinants of body composition: a 7-year follow-up study of pubertal growth in girls}; [PMID: 19481189] {Cheng, 2009 Low volumetric BMD is linked to upper-limb fracture in pubertal girls and persists into adulthood: a seven-year cohort study}; [PMID: 20200961] {Wang, 2010 Familial resemblance and diversity in bone mass and strength in the population are established during the first year of postnatal life}
12	**CaMos**	Canadian Multicentre Osteoporosis Study	Cohort	Population-based	Canada	Vancouver, Calgary, Saskatoon, Hamilton, Toronto, Kingston, Québec City, Halifax, St John's	North-western European	2,321	The CaMos Study is a population-based, randomly selected, prospective cohort study from 9 Canadian cities followed for 14 years for osteoporosis-related traits and outcomes.	[PMID: 11199195] {Tenenhouse, 2000 Estimation of the prevalence of low bone density in Canadian women and men using a population-specific DXA reference standard: the Canadian Multicentre Osteoporosis Study (CaMos)}; [PMID: 17129177] {Richards, 2007 Changes to osteoporosis prevalence according to method of risk assessment} [PMID: 17242321] {Richards, 2007 Effect of selective serotonin reuptake inhibitors on the risk of fracture}

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

Study									
Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
13 DECODErep	DeCODE Genetics Study	Cross-sectional	Iceland	NA	NA	North-western European	3,138	The study includes 40,000 individuals taking part in various disease projects	[PMID: 18445777] {Styrkarsdottir, 2008 Multiple genetic loci for bone mineral density and fractures}; [PMID: 19079262] {Styrkarsdottir, 2009 Multiple genetic loci for bone mineral density and fractures}
14 DOES	Dubbo Osteoporosis Epidemiology Study	Cohort	Population-based, family-based	Australia	Sydney (Dubbo)	Mainly Caucasian	1,457	A cohort study of approximately 2/3rds of the men and women in Dubbo, aged 60 years or older from 1989 every 2 years to the present. Data collected include BMD, life style, medical assessment, medication use and a wide range of health conditions and outcomes. It has been extended recently to include any person older than 20 years	[PMID: 19190316] {Bliuc, 2009 Mortality risk associated with low-trauma osteoporotic fracture and subsequent fracture in men and women}; [PMID: 19419321] {Frost, 2009 Timing of repeat BMD measurements: development of an absolute risk-based prognostic model}
15 DOPS	Danish Osteoporosis Prevention Study	Cohort	Population-based	Denmark	Aarhus, Odense, Cope	Northern European	1,716	Population-based study of perimenopausal women. The women were followed for 10 years. App. 35% were treated with HRT	[PMID: 10340280] {Mosekilde, 1999 The Danish Osteoporosis Prevention Study (DOPS): project design and inclusion of 2000 normal perimenopausal women}
16 EDOS	Edinburgh Osteoporosis Study	Cross-sectional	Clinical-based	UK	Edinburgh and Lothian	British (white caucasian)	2,020	Clinical referral population of patients assessed for evaluation of osteoporosis	None
17 EPICNOR	Europen Prospective Investigation into Cancer, Norfolk study	Cohort	Population-based	UK	Norfolk	European	1,399	A random sample of 1,511 men and women in the top decade of age in the 25,000 participant EPIC-Norfolk prospective study were recruited into a bone fragility study with DXA measurements. GWA data were available for 249 participants with BMD measurements who had been entered into a GWAS investigation of obesity.	[PMID: 12753873] {Kaptoge, 2003 Effects of gender, anthropometric variables, and aging on the evolution of hip strength in men and women aged over 65}; [PMID: 10466767] {Day, 1999 EPIC-Norfolk: study design and characteristics of the cohort. European Prospective Investigation of Cancer}; [PMID: 19079261] {Willer, 2009 Six new loci associated with body mass index highlight a neuronal influence on body weight regulation};

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

Study									
Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
18 EPOLOS	Early risk identification and effective prevention of osteoporosis based bone fractures in Polish population.	Cross-sectional	Population-based	Poland	Warsaw, Lodz, Poznan, Krakow, Wroclaw, Bydgoszcz	Central European	715	The EPOLOS Study is a population-based, cross-sectional study of unrelated men and women aged 19-81 years, initiated to identify early risk and effective prevention of osteoporosis based bone fractures in Polish population.	[PMID: 20502405] {Skowrońska-Jóźwiak, 2010 Comparison of selected methods for fracture risk assessment in postmenopausal women: analysis of the Łódź population in the EPOLOS study}; [PMID: 20502404] {Skowrońska-Jóźwiak, 2010 Effect of sex, age, and anthropometric parameters on the size and shape of vertebrae in densitometric morphometry: results of the EPOLOS study}; [PMID: 19396748] {Skowrońska-Jóźwiak, 2009 Identification of vertebral deformities in the Polish population by morphometric X-ray absorptiometry - results of the EPOLOS study}
19 EPOS	European Prospective Osteoporosis Study	Cohort	Population-based	Europe	18 centres across 13 countries in Europe	European	2,092	EPOS was an extension of the European Vertebral Osteoporosis Study (EVOS) study and aimed to quantify incidence of vertebral and non-vertebral fractures. EVOS had recruited some 17,342 men and women aged over 50 years from 36 centres in 19 European countries. Each centre had recruited a random sample of up to 300 men and 300 women from population registers stratified into six 5-year age bands: 50-54, 70-74 and 75+. A total of 7,273 participants from 31 EVOS centres took part in the EPOS follow up study.	[PMID: 8797123] {O'Neill, 1996 The prevalence of vertebral deformity in european men and women: the European Vertebral Osteoporosis Study}; [PMID: 10824241] {Ismail, 2000 Validity of self-report of fractures: results from a prospective study in men and women across Europe. EPOS Study Group. European Prospective Osteoporosis Study Group}; [PMID: 11918229] {EPOS study group, 2002 Incidence of vertebral fracture in europe: results from the European Prospective Osteoporosis Study (EPOS)}
20 FLOS	FLORENCE study	Cohort	Population-based	Italy	Florence	Southern European	1,000	The FLOS Study is a population-based cohort study of unrelated men and women aged 50 years and over, collected to perform genetic studies in osteoporosis.	[PMID: 11344237] {Masi, 2001 Polymorphism of the aromatase gene in postmenopausal Italian women: distribution and correlation with bone mass and fracture risk}
21 Geos	Quebec sample	Cohort	Population-based	Canada	Quebec	North-western European	2,379	Population-based sample collected for the sudy of bone mineral variation. Only women from 18 to 84 years	[PMID: 19821770] {Elfassihi, 2010 Association with replication between estrogen-related receptor gamma (ESRRgamma) polymorphisms and bone phenotypes in women of European ancestry}

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

Study									
Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
22 GEVUR	Institute of Biochemistry and Genetics Ufa Scientific Centre RAS	Case-control	Population-based, clinical-based	Russia	Ufa	Russians, Tatars	999	The GEVUR Study is case-control and population-based, prospective cohort study of unrelated women aged 50 years and over, men with osteoporotic fractures and helthy men	[PMID: 15657606] {Laan, 2005 X-chromosome as a marker for population history: linkage disequilibrium and haplotype study in Eurasian populations}; [PMID: 16465065] {Kutuev, 2006 From East to West: patterns of genetic diversity of populations living in four Eurasian regions}; [PMID:18619040] {Selezneva, 2008 Association of polymorphisms and haplotypes in the 5' region of COLIA1 gene with the risk of osteoporotic fractures in Russian women from Volga-Ural region}
23 GROS	GENETIC ANALYSIS OF OSTEOPOROSIS IN GREECE	Cohort, case-control	Population-based, clinical-based	GREECE	ATHENS	GREEK	606	The GROS study is a population-based, prospective cohort study of unrelated Greek men and women aged 43 years and over who visited the Department of Orthopaedic Surgery, University Hospital of Thessalia, Larissa, Greece.	None
24 HCS	Hertfordshire Cohort Study	Cohort	Population-based	UK	Hertfordshire county	Caucasian	2,927	The Hertfordshire Cohort Study is a population-based cohort study of men and women born between 1931 and 1939 in the county of Hertfordshire, UK. It was initiated to evaluate interactions between the genome, the intrauterine and early postnatal development, and adult diet and lifestyle in the aetiology of chronic disorders in later life.	[PMID: 15964908] {Syddall, 2005 Cohort Profile: The Hertfordshire Cohort Study}
25 HK	Chinese Community Elderly Men and Women Cohorts	Cohort	Population-based	Hong Kong, China	Hong Kong, China	Chinese	3,872	Two thousand Chinese men and women living in the community, aged 65 years and above, were recruited by posting public advertisements at community centers for the elderly and housing estates in Hong Kong since 2001.	[PMID: 20949110;] {Styrkarsdottir, 2010 European bone mineral density loci are also associated with BMD in East-Asian populations}; [PMID: 19766747] {Tang, 2010 Sex-specific effect of Pirin gene on bone mineral density in a cohort of 4000 Chinese}
26 KorAMC	Korean osteoporosis study at Asan Medical Center	Cross-sectional	Clinical-based	Korea	Seoul	East Asian, Korean	1,397	KorAMC study is a hospital registered, cross-sectional study of postmenopausal Korean women.	[PMID: 17620055] {Koh, 2007 Association of FLT3 polymorphisms with low BMD and risk of osteoporotic fracture in postmenopausal women}
27 LASA	Longitudinal Aging Study Amsterdam	Cohort	Population-based	The Netherlands	Amsterdam, Zwolle, Oss and surroundings	North-western European	956	LASA is an ongoing multidisciplinary cohort study on predictors and consequences of changes in physical, cognitive, emotional and social functioning in older persons.	[PMID: 11927198] {Deeg, 2002 Attrition in the Longitudinal Aging Study Amsterdam: The effect of differential inclusion in side studies}
28 ManMc	Manitoba McGill Fracture Study	Cross-Sectional	Population-based	Canada	Winnipeg	Caucasian (97%)	1,105	The Manitoba-McGill Fracture Study is a population based sample of women experiencing a validated clinical hip or forearm fracture requiring orthopedic intervention.	[PMID: 21124974] {Ladouceur, 2010 An Efficient Paradigm for Genetic Epidemiology Cohort Creation}

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

Study									
Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
29 MrOS Sweden	MrOS Sweden	Cohort	Population-based	Sweden	Gothenburg, Uppsala and Malmö	Northern European	2,922	The Osteoporotic Fractures in Men (MrOS) study is a multicenter, prospective study including 3,014 elderly men in Sweden, Hong Kong (~2,000), and the United States (~6,000). The MrOS Sweden cohort consist of three sub-cohorts from three different Swedish cities (n=1,005 in Malmö, n=1,010 in Göteborg, and n=999 in Uppsala). Study subjects (men aged 69–80 years) were randomly identified using national population registers, contacted and asked to participate. To be eligible for the study, the subjects had to be able to walk without assistance, provide self-reported data, and sign an informed consent; there were no other exclusion criteria. The study was approved by the ethics committees at the Universities of Gothenburg, Lund, and Uppsala. Informed consent was obtained from all study participants.	[PMID: 16598372] {Mellström, 2006 Free testosterone is an independent predictor of BMD and prevalent fractures in elderly men: MrOS Sweden}
30 NOSOS	North of Scotland Osteoporosis Study	Cohort	Population-based	UK	Aberdeen, Dingwall	North-western European	1,293	NOSOS is a population-based osteoporosis screening programme of postmenopausal females aged 60-82 years of age at baseline.	[PMID: 18633668] {Mavroeidi, 2009 Physical activity and dietary calcium interactions in bone mass in Scottish postmenopausal women}; [PMID: 20966103] {Judson, 2010 The Functional ACTN3 577X Variant Increases the Risk of Falling in Older Females: Results From Two Large Independent Cohort Studies}
31 OAS	Odense Androgen Study	Cohort	Population-based	Denmark	Odense	Scandinavians	600	Population-based study on Danish men aged 60-74 years. Follow-up on incident clinical fractures (from inclusion until dec 2010)	Clinicaltrials.gov identifier: NCT00155961
32 OSTEOS	Osteoporosis: SNPs To Environment Study	Cross-sectional	Population-based	Greece	Athens	Mediterranean	629	OSTEOS is a cross-sectional study of unrelated women, aimed to assess genetic and enrironmental factors, especially nutrition, and their possible interactions on BMD	[PMID: 21115334] {Stathopoulou, 2010 The role of vitamin D receptor gene polymorphisms in the bone mineral density of Greek postmenopausal women with low calcium intake}; [PMID: 20630166] {Stathopoulou, 2010 Low-density lipoprotein receptor-related protein 5 polymorphisms associate with bone mineral density in Greek postmenopausal women. An interaction with calcium intake}
33 PERF	Prospective Epidemiological Risk Factor	Randomized-controled trial	Clinical-based	Denmark	Copenhagen	North-western European	3,973	The Prospective Epidemiological Risk Factor (PERF) Study is based on subjects who were screened for or enrolled into RCT to identify genetic and other risk factors of diseases in the elderly	[PMID: 17109061] {Bagger, 2006 Links between cardiovascular disease and osteoporosis in postmenopausal women: serum lipids or atherosclerosis per se?}

Supplementary Table 20A: Study design

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Study								
	Short name	Full name	Study design	Study base	Country of origin	City/region of origin	Ethnicity	Total sample size with DNA and BMD and/or fracture data available	Short Study Description	References
34	**SLO-PREVAL**	Prevalence of osteoporosis in Slovenia	Cross-sectional	Population-based	Slovenia	Ljubljana	Central European	716	SLO-PREVAL study is a cross-sectional study where premenopausal women aged between 35-50 years and postmenopausal women and men aged over 50 years were included to perform genotype-phenotype association studies.	[PMID:12213850] {Arko, 2002 Sequence variations in the osteoprotegerin gene promoter in patients with postmenopausal osteoporosis}; [PMID:18502820] {Mencej, 2008 Tumour necrosis factor superfamily member 11 gene promoter polymorphisms modulate promoter activity and influence bone mineral density in postmenopausal women with osteoporosis}; [PMID:19781675] {Trošt 2010 A microarray based identification of osteoporosis-related genes in primary culture of human osteoblasts}
35	**UFO-1**	The Umeå Fracture and Osteoporosis Study	Nested case-cohort	Population-based	Sweden	Umeå	Caucasians	4,317	The UFO study is a nested case-control study investigating associations between genes, lifestyle and osteoporotic fractures. The study is based on the prosepctive and populationbased Northern Sweden Health and Disease Study cohort, initiated to assess risk factors for diabetes and cardiovascular disesase.	[PMID: 20464545] {Englund, 2010 Physical activity in middle-aged women and hip fracture risk: the UFO study}; [PMID:14660243] {Hallmans, 2003 Cardiovascular disease and diabetes in the Northern Sweden Health and Disease Study Cohort - evaluation of risk factors and their interactions}
	UFO-2		Cohort					2,022		
36	**WHI GeCHIP - BMD**	Women's Health Initiative Genetic Components of HIP Fracture (GeCHIP) Consortium - BMD	Quasi-case-control.	Population-based	United States	Multi-center (n=3)	Caucasian	3,923	BMD portion of GeCHIP. This is a subsample of the Women's Health Initiative BMD cohort (n=11,488) . Measurements were made at 3 of 40 US clinical centers (Pittsburgh PA, Birmingham AL, and Tucson/Phoenix AZ). Women (n=4000) were selected from the WHI BMD cohort with the best/worst hip-Z-score (baseline) and best/worst physical functioning score (last available RAND36).	[PMID: 14519707] {Cauley, 2003 Effects of estrogen plus progestin on risk of fracture and bone mineral density: the Women's Health Initiative randomized trial}

Supplementary Table 20B: Study-specific descriptive statistics

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men						Women					
Study	Trait	Assessment method	N	mean	sd	median	min	max	N	mean	sd	median	min	max
1 AOGC-GOS	Age (yrs)	Questionnaire	1,322	59.3	17.9	60.4	20.0	94.0	1,600	54.3	19.6	54.1	20.3	95.5
	BMI (kg/m²)	Calculated	1,319	27.2	4.3	26.8	17.1	49.7	1,598	26.7	5.3	25.7	15.9	53.8
	Weight (kg)	Measured	1,319	82.8	14.4	81.5	41.8	154.7	1,598	68.8	14.4	66.6	35.3	138.9
	Height (cm)	Measured	1,321	174.2	7.2	174.3	153.6	201.0	1,598	160.5	7.0	160.9	132.3	186.0
	LS-BMD (g/cm2)	Lunar	1,310	1.3	0.2	1.2	0.6	2.1	1,598	1.1	0.2	1.1	0.6	1.9
	FN-BMD (g/cm2)	Lunar	1,255	1.0	0.2	1.0	0.5	1.5	1,575	0.9	0.2	0.9	0.5	1.4
2 AOGC-SHEFFIELD	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	3,979	80.1	4.0	79.0	74.3	100.0
	BMI (kg/m²)	Calculated	0	NA	NA	NA	NA	NA	3,971	26.8	4.4	26.3	15.1	47.1
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	4,008	65.1	11.3	64.3	35.8	116.3
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	3,971	155.9	6.0	155.7	134.3	178.0
	LS-BMD (g/cm2)	Hologic QDR4500A	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	Hologic QDR4500A	0	NA	NA	NA	NA	NA	4,001	0.6	0.1	0.6	0.3	1.0
3 APOSS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	3,268	48.5	2.4	48.1	44.2	56.3
	BMI (kg/m²)	Calculated	0	NA	NA	NA	NA	NA	3,261	25.4	4.4	24.5	15.2	56.9
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	3,264	66.0	12.0	63.5	40.0	146.0
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	3,264	161.3	5.9	161.0	136.0	185.0
	LS-BMD (g/cm2)	Norland	0	NA	NA	NA	NA	NA	3,264	1.1	0.2	1.0	0.6	2.0
	FN-BMD (g/cm2)	Norland	0	NA	NA	NA	NA	NA	3,263	0.9	0.1	0.9	0.5	1.4
4 AROS	Age (yrs)	Social security	176	54.3	15.7	55.0	19.0	85.0	621	61.8	12.9	65.0	20.0	87.0
	BMI (kg/m²)	Calculated	143	25.2	3.7	24.7	17.4	36.5	547	24.4	4.1	23.9	15.7	51.2
	Weight (kg)	Measured	145	78.1	12.4	76.2	54.5	119.0	551	63.8	11.0	62.8	38.6	118.4
	Height (cm)	Measured	144	176.2	7.4	176.0	158.0	203.0	548	161.7	6.7	162.0	143.0	194.0
	LS-BMD (g/cm2)	Hologic and Norland	173	0.9	0.2	0.9	0.5	1.4	603	0.8	0.2	0.8	0.5	1.5
	FN-BMD (g/cm2)	Hologic and Norland	173	0.7	0.1	0.7	0.5	1.2	600	0.7	0.1	0.6	0.3	1.1
5 AUSTRIOS-A	Age (yrs)	Questionnaire	271	56.6	12.0	58.0	22.0	77.0	534	47.1	15.8	45.5	18.0	85.0
	BMI (kg/m²)	Calculated	268	26.7	3.6	26.0	18.9	37.8	496	23.7	3.9	22.8	16.0	39.0
	Weight (kg)	Measured	268	83.4	12.1	82.0	58.0	125.0	496	63.9	10.6	62.0	36.0	106.0
	Height (cm)	Measured	268	176.7	6.6	177.0	160.0	197.0	496	164.2	6.3	164.0	148.0	183.0
	LS-BMD (g/cm2)	Hologic	262	1.0	0.2	1.0	0.7	1.5	522	0.9	0.1	0.9	0.5	1.7
	FN-BMD (g/cm2)	Hologic	265	0.8	0.1	0.8	0.6	1.2	522	0.7	0.1	0.7	0.3	1.2
6 AUSTRIOS-B	Age (yrs)	Questionnaire	327	84.3	5.7	85.0	69.0	101.0	1,737	83.9	6.2	85.0	68.0	103.0
	BMI (kg/m²)	Calculated	311	25.1	4.0	24.7	15.0	37.3	1,637	25.7	4.8	25.2	13.8	46.1
	Weight (kg)	Measured	314	68.2	12.5	67.0	39.0	113.0	1,648	60.4	12.2	60.0	31.0	111.0
	Height (cm)	Measured	312	164.9	8.2	166.0	140.0	185.0	1,645	153.3	7.4	154.0	125.0	198.0
	LS-BMD (g/cm2)	NA	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
7 BARCOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,451	65.5	9.1	65.0	35.0	100.0
	BMI (kg/m²)	Calculated	0	NA	NA	NA	NA	NA	1,441	26.4	4.1	26.0	17.3	52.3
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,443	65.0	10.5	64.0	41.0	134.0
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,442	156.8	6.3	156.0	135.0	180.0
	LS-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,443	0.9	0.1	0.8	0.5	1.4
	FN-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,351	0.7	0.1	0.7	0.4	1.2
8 CABRIO-C	Age (yrs)	Questionnaire	543	63.9	8.5	63.0	50.0	92.0	907	62.0	9.8	59.0	42.0	94.0
	BMI (kg/m²)	Calculated	543	28.7	3.2	28.5	18.8	41.0	887	28.3	4.7	27.6	17.7	47.1
	Weight (kg)	Measured	543	81.5	11.0	80.0	44.5	118.4	887	68.7	12.0	67.0	42.0	119.0
	Height (cm)	Measured	543	168.2	6.1	168.0	150.0	189.0	889	155.9	6.0	156.0	138.0	188.0
	LS-BMD (g/cm2)	Hologic	535	1.0	0.2	1.0	0.6	1.7	896	0.9	0.1	0.9	0.6	1.4
	FN-BMD (g/cm2)	Hologic	529	0.8	0.1	0.8	0.4	1.2	897	0.7	0.1	0.7	0.4	1.1
9 CABRIO-CC	Age (yrs)	Questionnaire	538	73.3	11.9	74.0	39.0	100.0	1,771	74.5	12.3	75.0	43.0	104.0

Supplementary Table 20B: Study-specific descriptive statistics

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
	BMI (kg/m²)	Calculated	326	28.1	3.5	27.9	17.1	41.8	991	27.1	4.2	26.8	16.0	45.8
	Weight (kg)	Measured	326	78.1	11.4	78.0	46.0	137.0	995	65.0	10.4	64.0	36.0	110.0
	Height (cm)	Measured	326	166.7	6.8	167.0	145.0	192.0	992	154.7	6.1	155.0	138.0	178.0
	LS-BMD (g/cm2)	Hologic	279	1.0	0.1	1.0	0.5	1.4	923	0.8	0.2	0.8	0.5	1.4
	FN-BMD (g/cm2)	Hologic	280	0.8	0.1	0.8	0.5	1.3	926	0.7	0.1	0.7	0.4	1.1
10 CAIFOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,347	80.2	2.7	80.0	75.0	87.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,135	27.2	4.7	26.8	15.7	48.2
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,135	67.6	12.1	65.9	39.6	114.4
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,137	157.5	6.0	158.0	115.0	178.0
	LS-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,082	1.0	0.2	0.9	0.5	1.7
	FN-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,043	0.7	0.1	0.7	0.4	1.1
11 CALEX	Age (yrs)	Questionnaire	190	55.2	15.1	52.3	19.9	87.3	457	46.0	19.0	47.4	18.0	91.7
	BMI (kg/m²)	Measured	190	26.3	3.3	26.1	18.3	37.0	457	25.3	4.5	24.6	16.0	47.2
	Weight (kg)	Measured	190	81.4	10.7	80.8	56.8	108.6	457	68.1	12.3	66.5	46.1	127.0
	Height (cm)	Measured	190	175.9	6.5	176.0	154.0	194.0	457	164.2	6.2	164.0	148.0	180.0
	LS-BMD (g/cm2)	Lunar	189	1.2	0.2	1.2	0.8	1.9	451	1.2	0.2	1.2	0.7	1.8
	FN-BMD (g/cm2)	Lunar	189	1.0	0.2	1.0	0.7	1.5	450	1.0	0.1	1.0	0.6	1.5
12 CAMOS	Age (yrs)	Questionnaire	705	65.4	16.6	69.0	18.0	95.0	1,616	67.3	14.9	70.0	18.0	99.0
	BMI (kg/m²)	Measured	701	26.9	3.8	26.6	18.0	40.6	1,600	26.9	5.2	26.2	16.5	64.3
	Weight (kg)	Measured	701	81.7	13.4	80.7	47.7	126.5	1,601	69.4	13.7	67.4	38.2	158.5
	Height (cm)	Measured	701	174.1	7.1	174.0	151.0	198.0	1,600	160.6	6.4	160.0	141.0	182.9
	LS-BMD (g/cm2)	Hologic or Lunar	705	1.0	0.2	1.0	0.6	1.6	1,603	1.0	0.2	1.0	0.5	1.6
	FN-BMD (g/cm2)	Hologic or Lunar	704	0.8	0.1	0.8	0.5	1.4	1,599	0.7	0.1	0.7	0.4	1.3
13 DECODErep	Age (yrs)	National registry	910	55.5	16.3	55.6	20.3	89.0	2,228	57.5	14.3	57.7	20.0	97.0
	BMI (kg/m²)	Measured	910	26.4	3.7	26.2	16.6	42.0	2,228	25.9	4.5	25.3	14.8	47.2
	Weight (kg)	Measured	910	84.3	13.5	83.0	46.6	129.3	2,228	70.1	12.7	68.5	34.5	124.2
	Height (cm)	Measured	910	178.5	6.5	178.5	155.0	203.0	2,228	164.7	5.9	165.0	133.0	185.0
	LS-BMD (g/cm2)	Hologic	779	1.0	0.2	1.0	0.6	1.6	1,877	1.0	0.2	1.0	0.5	1.6
	FN-BMD (g/cm2)	Hologic	763	0.8	0.2	0.8	0.4	1.3	1,857	0.8	0.1	0.7	0.4	1.2
14 DOES	Age (yrs)	Questionnaire	569	75.6	5.5	75.0	61.0	90.0	888	76.2	6.3	76.0	60.0	99.0
	BMI (kg/m²)	Measured	569	26.7	4.0	26.3	17.7	44.4	888	26.1	5.0	25.8	14.3	56.0
	Weight (kg)	Measured	569	78.4	13.2	77.0	43.0	128.0	888	65.2	13.1	65.0	33.0	128.0
	Height (cm)	Measured	569	171.3	6.3	171.0	154.0	196.0	888	157.8	6.1	158.0	139.0	186.0
	LS-BMD (g/cm2)	Lunar DPX and Prodigy	567	1.3	0.2	1.3	0.7	2.1	883	1.0	0.2	1.0	0.4	1.8
	FN-BMD (g/cm2)	Lunar DPX and Prodigy	557	0.9	0.2	0.9	0.4	1.5	872	0.7	0.1	0.7	0.4	1.1
15 DOPS	Age (yrs)	Social security	0	NA	NA	NA	NA	NA	1,716	50.6	2.8	50.5	43.7	59.0
	BMI (kg/m²)	Calculated	0	NA	NA	NA	NA	NA	1,715	25.0	4.3	24.2	12.8	48.3
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,715	67.7	11.8	65.6	34.0	135.5
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,715	164.5	6.0	164.5	147.0	189.0
	LS-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,710	1.0	0.1	1.0	0.6	1.6
	FN-BMD (g/cm2)	Hologic	0	NA	NA	NA	NA	NA	1,702	0.8	0.1	0.8	0.5	1.3
16 EDOS	Age (yrs)	Questionnaire	370	62.4	13.6	62.4	18.3	93.1	1,645	66.2	12.4	67.6	20.5	94.3
	BMI (kg/m²)	Measured	354	26.4	5.3	26.0	14.9	51.6	1,603	26.0	5.1	25.1	14.9	52.5
	Weight (kg)	Measured	354	77.3	17.2	76.0	40.6	144.8	1,603	65.1	13.7	63.2	40.0	128.9
	Height (cm)	Measured	357	170.6	8.8	171.0	100.8	200.0	1,631	158.0	7.1	158.0	128.5	190.0
	LS-BMD (g/cm2)	Hologic	353	0.9	0.2	0.8	0.4	1.6	1,613	0.8	0.2	0.8	0.4	1.5
	FN-BMD (g/cm2)	Hologic	309	0.7	0.1	0.7	0.3	1.2	1,453	0.6	0.1	0.6	0.3	1.2
17 EPIC Norfolk	Age (yrs)	Questionnaire	680	72.5	3.1	72.1	66.9	79.3	719	72.4	3.2	72.3	60.0	85.0
	BMI (kg/m²)	Measured	680	26.8	3.3	26.7	17.5	39.2	710	26.8	4.3	26.4	17.8	45.7

Supplementary Table 20B: Study-specific descriptive statistics

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
	Weight (kg)	Measured	680	79.6	10.9	78.8	48.0	128.5	710	67.9	11.3	66.8	43.0	105.5
	Height (cm)	Measured	680	172.3	6.3	172.0	153.0	196.0	714	159.1	5.9	159.0	139.0	178.0
	LS-BMD (g/cm2)	NA	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	Hologic QDR 1000W	674	0.8	0.1	0.8	0.5	1.5	698	0.7	0.1	0.7	0.3	1.1
18 EPOLOS	Age (yrs)	Questionnaire	317	50.4	16.5	50.9	19.8	80.9	398	55.5	15.6	58.5	20.0	81.6
	BMI (kg/m²)	Measured	317	26.6	4.0	26.3	17.1	39.4	397	26.7	4.9	26.4	16.4	40.9
	Weight (kg)	Measured	317	80.0	12.7	80.0	48.0	120.0	397	68.0	12.3	67.0	40.0	109.0
	Height (cm)	Measured	317	173.3	7.4	173.0	151.0	190.0	398	159.6	6.4	160.0	128.0	176.0
	LS-BMD (g/cm2)	Lunar DPX	297	1.1	0.2	1.0	0.5	2.1	367	1.0	0.2	1.0	0.5	1.7
	FN-BMD (g/cm2)	Lunar DPX	298	0.9	0.2	0.9	0.4	1.6	366	0.8	0.1	0.8	0.4	1.2
19 EPOS	Age (yrs)	Questionnaire	719	62.9	8.2	62.5	43.9	90.4	1,373	63.4	8.8	62.6	40.5	95.0
	BMI (kg/m²)	Measured	661	27.6	3.7	27.4	18.2	41.4	1,176	27.5	4.7	27.0	16.8	52.9
	Weight (kg)	Measured	661	78.7	11.5	78.7	47.0	120.0	1,177	68.1	11.5	67.0	41.3	115.0
	Height (cm)	Measured	661	168.9	7.3	169.0	145.0	188.0	1,179	157.4	6.9	157.0	136.0	186.0
	LS-BMD (g/cm2)	Hologic (7 centres) /Lunar (5 centres) /Sopha (1 centre) /Norland (2 centres)	238	1.0	0.2	1.0	0.6	1.6	482	0.9	0.2	0.9	0.5	1.6
	FN-BMD (g/cm2)	Hologic (7 centres) /Lunar	513	0.8	0.1	0.8	0.4	1.4	926	0.7	0.1	0.7	0.3	1.3
20 FLOS	Age (yrs)	Questionnaire	161	53.9	14.7	56.0	20.0	78.0	839	60.9	12.0	62.0	19.0	89.0
	BMI (kg/m²)	Measured	161	26.2	3.6	26.0	18.5	54.1	839	24.1	3.5	23.9	15.0	44.2
	Weight (kg)	Measured	161	80.8	13.6	80.0	60.0	185.0	839	61.8	9.3	60.3	37.0	116.0
	Height (cm)	Measured	161	175.6	7.0	176.0	156.0	192.0	839	160.0	6.7	160.0	138.0	181.0
	LS-BMD (g/cm2)	Hologic	158	1.0	0.1	1.0	0.7	1.6	835	0.9	0.2	0.9	0.4	1.6
	FN-BMD (g/cm2)	Hologic	139	0.8	0.2	0.8	0.3	1.1	781	0.7	0.2	0.7	0.3	1.3
21 GEOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	2,379	53.8	9.6	54.0	18.0	84.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	2,372	25.8	4.6	25.0	15.2	46.7
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	2,374	65.0	11.9	63.0	40.2	118.8
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	2,377	158.6	6.0	159.0	130.0	184.0
	LS-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	2,377	1.1	0.2	1.1	0.6	1.8
	FN-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	2,376	0.9	0.1	0.9	0.4	1.4
22 GEVUR	Age (yrs)	Questionnaire	134	59.2	12.9	59.0	19.0	83.0	839	62.2	8.2	61.0	40.0	85.0
	BMI (kg/m²)	Measured	96	26.2	4.9	25.2	15.4	40.6	830	27.8	4.9	27.3	14.2	45.2
	Weight (kg)	Measured	96	76.2	14.0	76.0	49.0	120.0	830	70.6	13.2	70.0	40.0	128.0
	Height (cm)	Measured	97	170.8	7.5	170.0	156.0	192.0	833	159.3	6.3	159.0	134.0	185.0
	LS-BMD (g/cm2)	Hologic	105	0.9	0.2	0.9	0.4	1.4	194	0.9	0.2	0.9	0.5	1.4
	FN-BMD (g/cm2)	Hologic	99	0.9	0.2	0.8	0.3	1.2	373	0.8	0.2	0.8	0.3	1.3
23 GROS	Age (yrs)	Questionnaire	83	70.2	12.8	72.0	43.0	90.0	523	69.1	11.7	70.0	43.0	95.0
	BMI (kg/m²)	Measured	83	26.3	3.9	26.0	17.3	37.9	521	27.5	4.7	27.0	16.4	45.8
	Weight (kg)	Measured	83	71.5	12.3	71.0	40.0	120.0	521	71.7	10.9	69.0	40.0	112.0
	Height (cm)	Measured	83	164.8	10.4	167.0	121.0	182.0	523	161.8	7.3	162.0	146.0	182.0
	LS-BMD (g/cm2)	Varius (Lunar, Hologic)	21	0.9	0.2	0.9	0.5	1.5	272	0.8	0.2	0.8	0.5	1.5
	FN-BMD (g/cm2)	Varius (Lunar, Hologic)	6	0.8	0.2	0.9	0.5	1.0	55	0.8	0.1	0.8	0.5	1.2
24 HCS	Age (yrs)	Questionnaire	1,571	65.7	2.9	65.8	59.2	72.6	1,356	66.7	2.7	66.5	60.9	73.1
	BMI (kg/m²)	Measured	1,562	27.1	3.7	26.8	16.1	49.2	1,354	27.5	4.8	27.0	15.2	48.1
	Weight (kg)	Measured	1,563	82.4	12.6	81.0	45.5	144.5	1,354	71.2	13.2	70.0	40.0	135.5
	Height (cm)	Measured	1,564	174.1	6.5	174.3	149.6	195.6	1,354	160.9	5.9	160.8	140.9	180.8
	LS-BMD (g/cm2)	Hologic	495	1.1	0.2	1.1	0.7	1.6	440	0.9	0.2	0.9	0.4	1.4
	FN-BMD (g/cm2)	Hologic	493	0.9	0.1	0.8	0.5	1.3	440	0.7	0.1	0.7	0.5	1.1

Supplementary Table 20B: Study-specific descriptive statistics

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men						Women					
Study	**Trait**	**Assessment method**	**N**	**mean**	**sd**	**median**	**min**	**max**	**N**	**mean**	**sd**	**median**	**min**	**max**
25 HK	Age (yrs)	Questionnaire	1,888	72.4	5.0	72.0	65.0	92.0	1,984	72.6	5.4	72.0	65.0	98.0
	BMI (kg/m²)	Measured	1,888	23.5	3.1	23.5	13.1	36.3	1,984	23.9	3.5	23.7	12.7	40.3
	Weight (kg)	Measured	1,888	62.4	9.4	62.4	35.9	103.1	1,984	54.5	8.5	54.2	28.8	89.0
	Height (cm)	Measured	1,888	163.1	5.8	163.1	141.9	187.2	1,984	150.9	5.3	150.8	133.7	170.3
	LS-BMD (g/cm2)	Hologic	1,853	0.9	0.2	0.9	0.4	1.6	1,934	0.8	0.1	0.7	0.3	1.3
	FN-BMD (g/cm2)	Hologic	1,884	0.7	0.1	0.7	0.4	1.1	1,977	0.6	0.1	0.6	0.3	1.0
26 KorAMC	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,397	59.5	7.4	59.0	45.0	87.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,397	23.4	2.8	23.3	14.4	35.5
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,397	56.2	7.2	56.0	27.0	86.0
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,397	155.0	5.3	155.0	121.0	171.0
	LS-BMD (g/cm2)	Hologic, QDR4500A, ExpertXL, ProdigyAdvance	0	NA	NA	NA	NA	NA	1,387	0.9	0.2	0.9	0.4	1.5
	FN-BMD (g/cm2)	Hologic, QDR4500A, Expe	0	NA	NA	NA	NA	NA	1,387	0.7	0.1	0.7	0.3	1.1
27 LASA	Age (yrs)	Questionnaire	464	72.4	6.5	72.2	61.9	85.6	485	72.6	6.6	72.1	61.8	85.3
	BMI (kg/m²)	Measured	438	25.8	3.2	25.9	17.4	39.1	441	27.8	4.5	27.4	16.9	45.8
	Weight (kg)	Measured	440	77.9	11.3	77.0	47.0	119.0	449	71.6	12.0	70.5	42.0	120.5
	Height (cm)	Measured	438	173.4	6.7	173.4	156.4	195.3	442	160.5	6.3	160.4	141.9	177.6
	LS-BMD (g/cm2)	Hologic QDR 2000	253	1.0	0.2	1.0	0.5	1.8	262	0.9	0.2	0.9	0.6	1.4
	FN-BMD (g/cm2)	Hologic QDR 2000	252	0.7	0.1	0.7	0.3	1.1	251	0.7	0.1	0.6	0.4	1.0
28 MANMC	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,105	56.4	8.6	57.0	27.0	86.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	LS-BMD (g/cm2)	NA	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	NA	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
29 MrOS Sweden	Age (yrs)	Questionnaire	2,922	75.4	3.2	75.4	69.9	81.0	0	NA	NA	NA	NA	NA
	BMI (kg/m²)	Measured	2,922	26.4	3.5	26.2	13.3	44.6	0	NA	NA	NA	NA	NA
	Weight (kg)	Measured	2,922	80.7	12.1	79.9	37.0	138.3	0	NA	NA	NA	NA	NA
	Height (cm)	Measured	2,922	174.8	6.5	174.6	145.2	199.4	0	NA	NA	NA	NA	NA
	LS-BMD (g/cm2)	Hologic (Gothenburg), Lunar (Uppsala and Malmö)	2,893	1.2	0.2	1.1	0.6	2.0	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	Hologic (Gothenburg), Lur	2,814	0.9	0.1	0.8	0.4	1.4	0	NA	NA	NA	NA	NA
30 NOSOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	1,268	69.7	5.5	69.3	60.2	82.2
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	1,291	27.0	4.6	26.6	16.2	55.2
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	1,291	67.8	12.3	66.5	40.0	132.5
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	1,293	158.4	6.0	158.0	131.0	177.0
	LS-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	1,278	1.1	0.2	1.1	0.5	1.8
	FN-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	1,243	0.8	0.1	0.8	0.4	1.3
31 OAS	Age (yrs)	Questionnaire	600	68.1	4.2	68.0	60.0	76.0	0	NA	NA	NA	NA	NA
	BMI (kg/m²)	Measured	593	27.6	4.0	27.2	15.7	54.3	0	NA	NA	NA	NA	NA
	Weight (kg)	Measured	593	83.7	12.5	82.5	48.0	137.9	0	NA	NA	NA	NA	NA
	Height (cm)	Measured	593	174.3	6.7	174.3	128.4	191.8	0	NA	NA	NA	NA	NA
	LS-BMD (g/cm2)	Hologic	589	1.0	0.2	1.0	0.6	1.6	0	NA	NA	NA	NA	NA
	FN-BMD (g/cm2)	Hologic	584	0.8	0.1	0.8	0.5	1.2	0	NA	NA	NA	NA	NA
32 OSTEOS	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	626	60.5	10.4	60.0	35.0	90.0
	BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	627	27.4	5.0	26.3	17.4	46.7
	Weight (kg)	Measured	0	NA	NA	NA	NA	NA	627	66.8	11.7	65.0	42.0	119.5
	Height (cm)	Measured	0	NA	NA	NA	NA	NA	628	156.2	7.0	156.0	130.0	176.0

Supplementary Table 20B: Study-specific descriptive statistics

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

				Men						Women					
	Study	Trait	Assessment method	N	mean	sd	median	min	max	N	mean	sd	median	min	max
		LS-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	599	1.0	0.2	1.0	0.4	1.6
		FN-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	342	0.8	0.1	0.8	0.5	1.1
33	PERF	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	3,927	64.1	7.9	64.9	45.2	80.8
		BMI (kg/m²)	Measured	0	NA	NA	NA	NA	NA	3,973	25.2	3.4	24.9	14.9	43.8
		Weight (kg)	Measured	0	NA	NA	NA	NA	NA	3,973	66.1	9.7	65.2	36.1	116.6
		Height (cm)	Measured	0	NA	NA	NA	NA	NA	3,973	161.8	6.0	162.0	134.3	190.0
		LS-BMD (g/cm2)	Lunar, Hologic	0	NA	NA	NA	NA	NA	3,927	0.9	0.2	0.9	0.4	1.5
		FN-BMD (g/cm2)	Lunar, Hologic	0	NA	NA	NA	NA	NA	3,915	0.7	0.1	0.7	0.3	1.1
34	SLOPREVAL	Age (yrs)	Questionnaire	123	67.9	6.5	66.0	55.0	89.0	593	62.1	10.6	62.0	38.0	93.0
		BMI (kg/m²)	Measured	123	27.7	3.9	27.4	19.6	43.4	593	26.9	4.5	26.0	18.9	44.9
		Weight (kg)	Measured	123	81.6	12.6	80.0	55.0	130.0	593	69.1	12.2	67.0	45.0	115.0
		Height (cm)	Measured	123	171.7	6.3	171.0	159.0	192.0	593	160.4	6.3	160.0	137.0	181.0
		LS-BMD (g/cm2)	Hologic	123	1.0	0.2	1.0	0.7	1.5	588	0.9	0.2	0.8	0.4	1.5
		FN-BMD (g/cm2)	Hologic	96	0.8	0.2	0.8	0.5	1.3	566	0.7	0.1	0.7	0.3	1.2
35	UFO-1	Age (yrs)	Questionnaire	1,011	54.2	7.7	59.7	29.5	71.5	3,306	58.6	7.6	59.9	29.6	76.9
		BMI (kg/m²)	Measured	997	26.4	3.6	25.9	17.3	55.8	3,175	25.5	4.2	24.8	10.1	62.5
		Weight (kg)	Measured	998	82.4	12.7	81.0	40.0	163.2	3,187	68.0	11.6	66.0	25.0	164.0
		Height (cm)	Measured	997	176.6	6.3	176.0	152.0	197.0	3,200	163.4	5.9	163.0	122.0	191.0
		LS-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	385	1.0	0.2	0.9	0.4	1.6
		FN-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	415	0.8	0.1	0.8	0.5	1.2
	UFO-2	Age (yrs)	Questionnaire	421	48.2	10.3	50.0	24.0	70.0	1,601	53.3	10.2	54.0	19.0	80.0
		BMI (kg/m²)	Measured	421	25.9	3.2	25.5	18.7	41.6	1,601	25.3	4.3	24.6	14.3	46.6
		Weight (kg)	Measured	421	82.1	11.4	81.0	51.0	129.0	1,601	68.1	12.1	66.0	36.0	127.0
		Height (cm)	Measured	421	177.9	6.1	178.0	152.0	198.0	1,601	164.0	6.1	164.0	130.0	190.0
		LS-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
		FN-BMD (g/cm2)	Lunar	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
36	WHI GeCHIP - BMD	Age (yrs)	Questionnaire	0	NA	NA	NA	NA	NA	3,929	64.5	7.1	65.0	50.0	79.0
		BMI (kg/m²)	measured	0	NA	NA	NA	NA	NA	3,908	27.7	6.0	26.5	14.3	67.9
		Weight (kg)	measured	0	NA	NA	NA	NA	NA	3,923	72.4	16.5	69.4	36.0	176.5
		Height (cm)	measured	0	NA	NA	NA	NA	NA	3,910	1.6	0.1	1.6	1.0	1.9
		LS-BMD (g/cm2)	Hologic QDR 2000, 2000+, or 4500W	0	NA	NA	NA	NA	NA	3,761	1.0	0.2	1.0	0.5	1.8
		FN-BMD (g/cm2)	Hologic QDR 2000, 2000+	0	NA	NA	NA	NA	NA	3,929	0.7	0.1	0.7	0.4	1.3

Supplementary 20C: Study descriptives fracture

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

				Men		Women
	Study	Trait	Assessment method	Fracture N	Non-fracture N	Fracture N	Non-fracture N
1	AOGC-GOS	All fractures	Questionnaire, radiography	335	670	239	1,093
		Non-vertebral fractures	Questionnaire, radiography	74	670	167	1,093
		Vertebral fractures	NA	NA	NA	NA	NA
2	AOGC-SHEFFIELD	All fractures	Questionnaire, radiography lateral morphometry	NA	NA	1,373	2,013
		Non-vertebral fractures	Questionnaire, radiography	NA	NA	955	2,027
		Vertebral fractures	Radiography lateral morphometry	NA	NA	565	3,411
3	APOSS	All fractures	Self-reported	NA	NA	560	2,275
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA
4	AROS	All fractures	Radiographic	64	38	271	92
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	Radiographic	64	38	271	92
5	AUSTRIOS-A	All fractures	Medical records, radiograhic	118	125	116	378
		Non-vertebral fractures	Medical records, radiograhic	118	123	105	389
		Vertebral fractures	NA	NA	NA	NA	NA
6	AUSTRIOS-B	All fractures	Medical records, radiograhic	144	183	816	921
		Non-vertebral fractures	Medical records, radiograhic	32	295	273	1,464
		Vertebral fractures	Radiographic	128	199	675	1,062
7	BARCOS	All fractures	Medical records, radiograhic documentation	NA	NA	179	1,258
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA
8	CABRIO-C	All fractures	Patient-referred, medical records	131	412	210	697
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	Radiographic documentation	68	438	127	747
9	CABRIO-CC	All fractures	Patient-referred, medical records	176	364	946	829
		Non-vertebral fractures	Patient-referred, medical records	133	378	658	925
		Vertebral fractures	Radiographic documentation	25	30	195	324
10	CAIFOS	All fractures	Self-reported	NA	NA	749	598
		Non-vertebral fractures	Self-reported	NA	NA	179	1,168
		Vertebral fractures	Radiographic	NA	NA	428	600

Supplementary 20C: Study descriptives fracture

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men		Women	
Study	Trait	Assessment method	Fracture N	Non-fracture N	Fracture N	Non-fracture N
11 CALEX	All fractures	Questionnaire, medical records, radiograhic documentation	41	110	72	301
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
12 CAMOS	All fractures	Medical records, radiograhic documentation	98	559	312	1,226
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
13 DECODErep	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
14 DOES	All fractures	X-ray reports	141	373	405	462
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
15 DOPS	All fractures	Radiographic	NA	NA	425	1,291
	Non-vertebral fractures	Radiographic	NA	NA	239	1,477
	Vertebral fractures	Radiographic	NA	NA	108	1,605
16 EDOS	All fractures	Medical records, radiograhic documentation	286	38	1,270	159
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
17 EPICNOR	All fractures	Medical records	78	602	157	562
	Non-vertebral fractures	Medical records	77	603	150	569
	Vertebral fractures	NA	NA	NA	NA	NA
18 EPOLOS	All fractures	Self -reports (fractures data from questionnaire filled in by physician)	109	208	139	259
	Non-vertebral fractures	Self -reports (fractures data from questionnaire filled in by physician)	109	208	139	259
	Vertebral fractures	NA	NA	NA	NA	NA
19 EPOS	All fractures	Self-report, questionnaire, medical records, radiograhic documentation	214	505	517	856

Supplementary 20C: Study descriptives fracture

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men		Women	
Study	**Trait**	**Assessment method**	**Fracture N**	**Non-fracture N**	**Fracture N**	**Non-fracture N**
	Non-vertebral fractures	Self-report, questionnaire, medical records, radiograhic documentation	124	595	403	970
	Vertebral fractures	Radiographic documentation	112	607	201	1,172
20 FLOS	All fractures	Medical records, radiograhic documentation	83	78	118	721
	Non-vertebral fractures	Medical records, radiograhic documentation	83	78	72	767
	Vertebral fractures	Radiographic documentation	5	156	68	771
21 GEOS	All fractures	Self-report	NA	NA	110	1,799
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
22 GEVUR	All fractures	Medical records, radiograhic documentation	61	99	346	493
	Non-vertebral fractures	Medical records, radiograhic documentation	52	108	324	515
	Vertebral fractures	NA	NA	NA	NA	NA
23 GROS	All fractures	Medical records, radiograhic documentation	54	26	340	125
	Non-vertebral fractures	Medical records, radiograhic documentation	49	31	313	154
	Vertebral fractures	Radiographic documentation	5	75	28	435
24 HCS	All fractures	Self-report	103	1,399	253	1,036
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
25 HK	All fractures	Medical records, radiograhic documentation	316	1,572	478	1,506
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
26 KorAMC	All fractures	Self-report and radiographic	NA	NA	171	1,226
	Non-vertebral fractures	Self-report and radiographic	NA	NA	101	1,193
	Vertebral fractures	NA	NA	NA	NA	NA
27 LASA	All fractures	Self-report, GP questionnaire	150	314	176	309
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	Radiographic documentation (Genant)	117	137	121	132

Supplementary 20C: Study descriptives fracture

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

			Men		Women	
Study	**Trait**	**Assessment method**	**Fracture N**	**Non-fracture N**	**Fracture N**	**Non-fracture N**
28 MANMC	All fractures	Medical records, Surgical Report, ICD-9 Codes	NA	NA	848	0
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
29 MrOS Sweden	All fractures	Questionnaire, radiographic documentation	1255	1,651	NA	NA
	Non-vertebral fractures	Radiographic documentation	157	2,765	NA	NA
	Vertebral fractures	Radiographic documentation	309	2,613	NA	NA
30 NOSOS	All fractures	Self-report	NA	NA	385	843
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
31 OAS	All fractures	Incident clinical fractures+ baseline vertebral fractures	97	503	NA	NA
	Non-vertebral fractures	Incident clinical fractures	24	576	NA	NA
	Vertebral fractures	Radiographic documentation	77	523	NA	NA
32 OSTEOS	All fractures	NA	NA	NA	NA	NA
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
33 PERF	All fractures	Medical records, radiograhic documentation	NA	NA	1,051	2,405
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
34 SLOPREVAL	All fractures	Medical records	14	56	77	116
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA
35 UFO-1	All fractures	Medical records, radiograhic documentation	493	518	1,691	1,615
	Non-vertebral fractures	Medical records, radiograhic documentation	493	518	1,691	1,615
	Vertebral fractures	NA	NA	NA	NA	NA
UFO-2	All fractures	Medical records, radiograhic documentation	10	411	181	1,420
	Non-vertebral fractures	NA	NA	NA	NA	NA
	Vertebral fractures	NA	NA	NA	NA	NA

Supplementary 20C: Study descriptives fracture

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Study	Trait	Assessment method	Men		Women	
				Fracture N	Non-fracture N	Fracture N	Non-fracture N
36	WHI GeCHIP - BMD	All fractures	NA	NA	NA	NA	NA
		Non-vertebral fractures	NA	NA	NA	NA	NA
		Vertebral fractures	NA	NA	NA	NA	NA

Supplementary Table 20D: De-novo Genotyping QC

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Cohort	Genotyping							
		Genotyping Center	Genotyped SNPs	Sample Call rate	Samples meeting QC criteria	MAF	SNP Call rate	P for HWE	SNPs that met QC criteria
1	AOGC-GOS	AOGC	74	80%	2635	> 1%	>90%	$> 10^{-6}$	72
2	AOGC-SHEFFIELD	AOGC	74	80%	3817	> 1%	>90%	$> 10^{-6}$	71
3	APOSS	KBIO	82	80%	3066	> 1%	>90%	$> 10^{-6}$	82
4	AROS	KBIO	96	80%	789	> 1%	>90%	$> 10^{-6}$	96
5	AUSTRIOS-A	KBIO	82	80%	638	> 1%	>90%	$> 10^{-6}$	49
6	AUSTRIOS-B	KBIO	82	80%	834	> 1%	>90%	$> 10^{-6}$	49
7	BARCOS	KBIO	96	80%	1422	> 1%	>90%	$> 10^{-6}$	96
8	CABRIO-C	KBIO	96	80%	1361	≥ 1%	>90%	$> 10^{-6}$	96
9	CABRIO-CC	KBIO	82	80%	2178	> 1%	>90%	$> 10^{-6}$	82
10	CAIFOS	KBIO	96	80%	1321	> 1%	>90%	$> 10^{-6}$	96
11	CALEX	KBIO	82	80%	645	> 1%	>90%	$> 10^{-6}$	82
12	CAMOS	KBIO	96	80%	2342	> 1%	>90%	$> 10^{-6}$	96
13	DECODErep	DECODE	95	80%	2620	> 1%	>90%	$> 10^{-6}$	95
14	DOES	DECODE	95	80%	1347	> 1%	>90%	$> 10^{-6}$	90
15	DOPS	KBIO	96	80%	1670	> 1%	>90%	$> 10^{-6}$	96
16	EDOS	KBIO	96	80%	1996	> 1%	>90%	$> 10^{-6}$	96
17	EPICNOR	KBIO	82	80%	1377	≥ 1%	>90%	$> 10^{-6}$	82
18	EPOLOS	KBIO	82	80%	688	> 1%	>90%	$> 10^{-6}$	81
19	EPOS	KBIO	82	80%	2003	≥ 1%	>90%	$> 10^{-6}$	82
20	FLOS	KBIO	96	80%	726	> 1%	>90%	$> 10^{-6}$	96
21	GEOS	KBIO	82	80%	2232	> 1%	>90%	$> 10^{-6}$	87

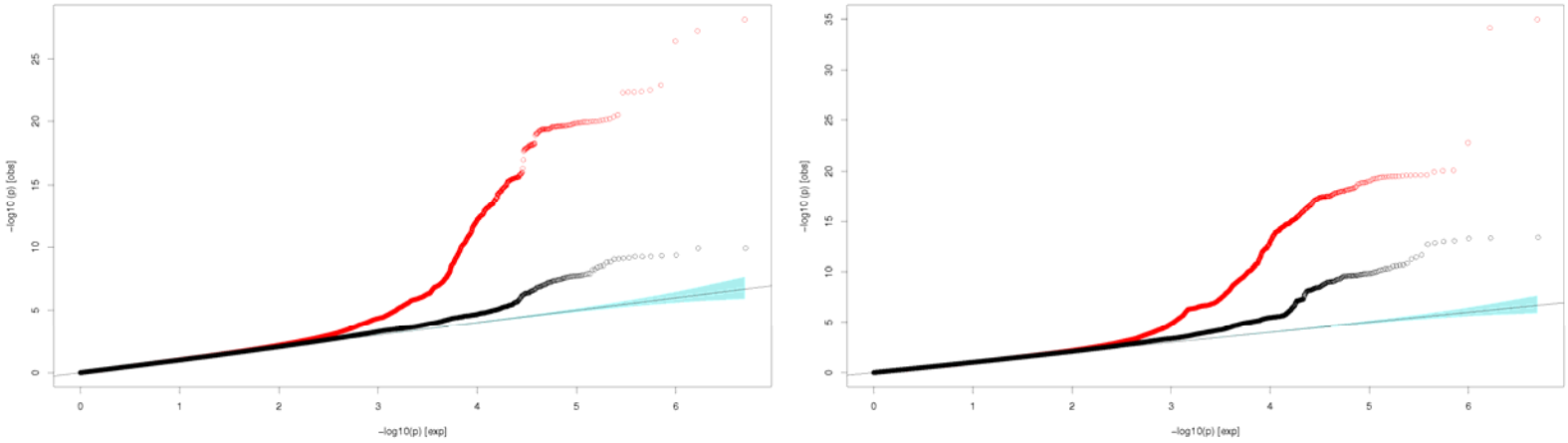
Supplementary Table 20D: De-novo Genotyping QC

Stage 2: De-novo genotyping Replication BMD Loci and Fracture association

	Cohort	Genotyping							
		Genotyping Center	Genotyped SNPs	Sample Call rate	Samples meeting QC criteria	MAF	SNP Call rate	P for HWE	SNPs that met QC criteria
22	**GEVUR**	KBIO	96	80%	756	> 1%	>90%	$> 10^{-6}$	96
23	**GROS**	KBIO	96	80%	459	> 1%	>90%	$> 10^{-6}$	96
24	**HCS**	KBIO	82	80%	2824	> 1%	>90%	$> 10^{-6}$	82
25	**HK**	DECODE	95	80%	3772	> 1%	>90%	$> 10^{-6}$	94
26	**KorAMC**	DECODE	95	80%	1390	> 1%	>90%	$> 10^{-6}$	95
27	**LASA**	KBIO	82	80%	891	> 1%	>90%	$> 10^{-6}$	82
28	**MANMC**	KBIO	82	80%	1007	> 1%	>90%	$> 10^{-6}$	82
29	**MrOS Sweden**	KBIO	96	80%	2477	> 1%	>90%	$> 10^{-6}$	87
30	**NOSOS**	KBIO	82	80%	1191	> 1%	>90%	$> 10^{-6}$	82
31	**OAS**	KBIO	96	80%	581	> 1%	>90%	$> 10^{-6}$	96
32	**OSTEOS**	KBIO	0	Failed	Failed	Failed	Failed	Failed	Failed
33	**PERF**	DECODE	95	80%	3346	> 1%	>90%	$> 10^{-6}$	95
34	**SLO-PREVAL**	KBIO	96	80%	677	> 1%	>90%	$> 10^{-6}$	93
35	**UFO**	KBIO	82	80%	5921	> 1%	>90%	$> 10^{-6}$	82
36	**WHI GeCHIP - BMD**	WHI	67	98%	3923	>0.5%	>98%	$> 10^{-6}$	67

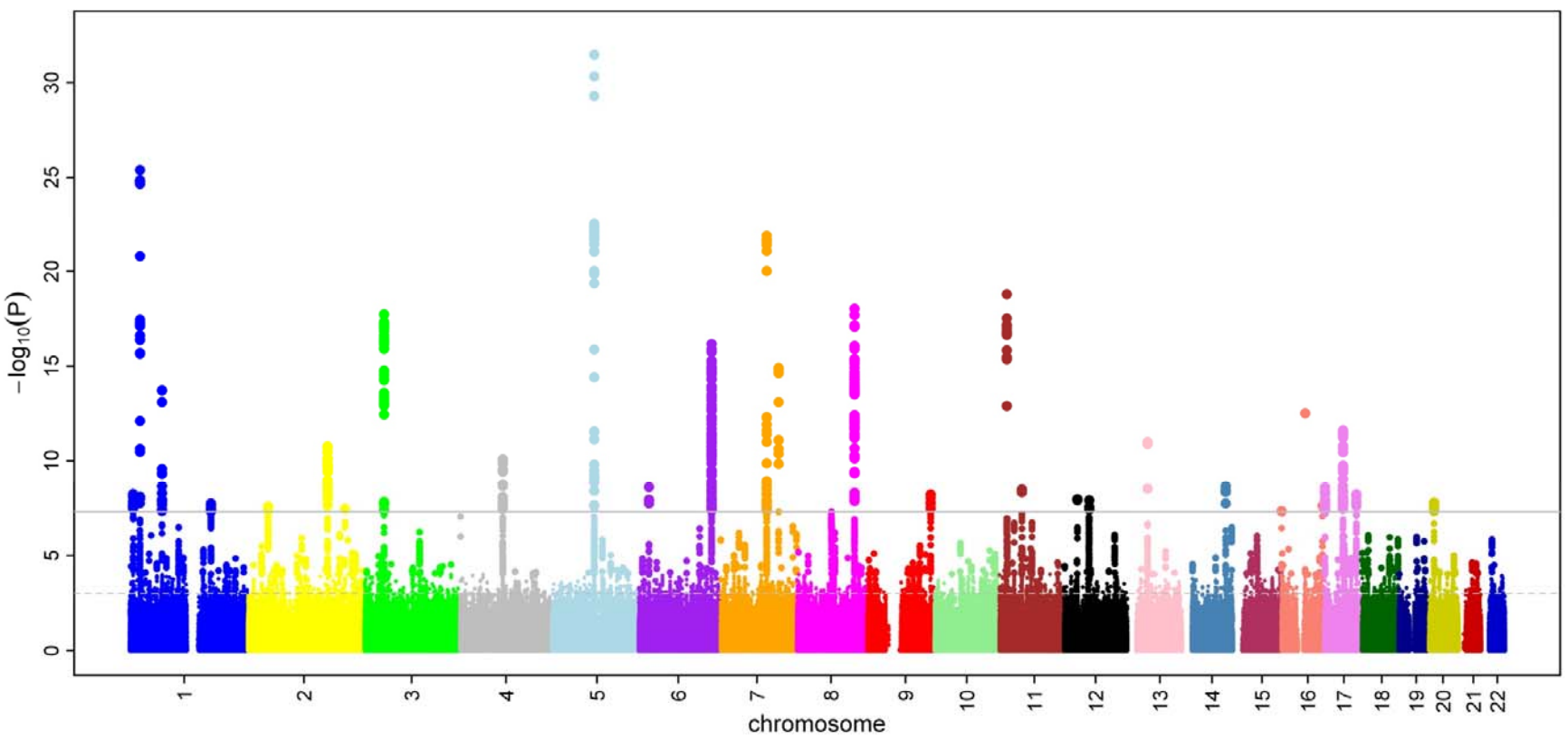
Supplementary Figures

Supplementary Figure 1. Quantile-quantile (Q-Q) plots. A) femoral neck BMD. B) and lumbar spine BMD. The plots compare additive model statistics to those expected under the null distribution using fixed-effects for all analyzed HapMap CEU imputed SNPs passing quality control criteria in the studies (red dots) and after adjustment for 82 SNPs selected for replication(black dots).

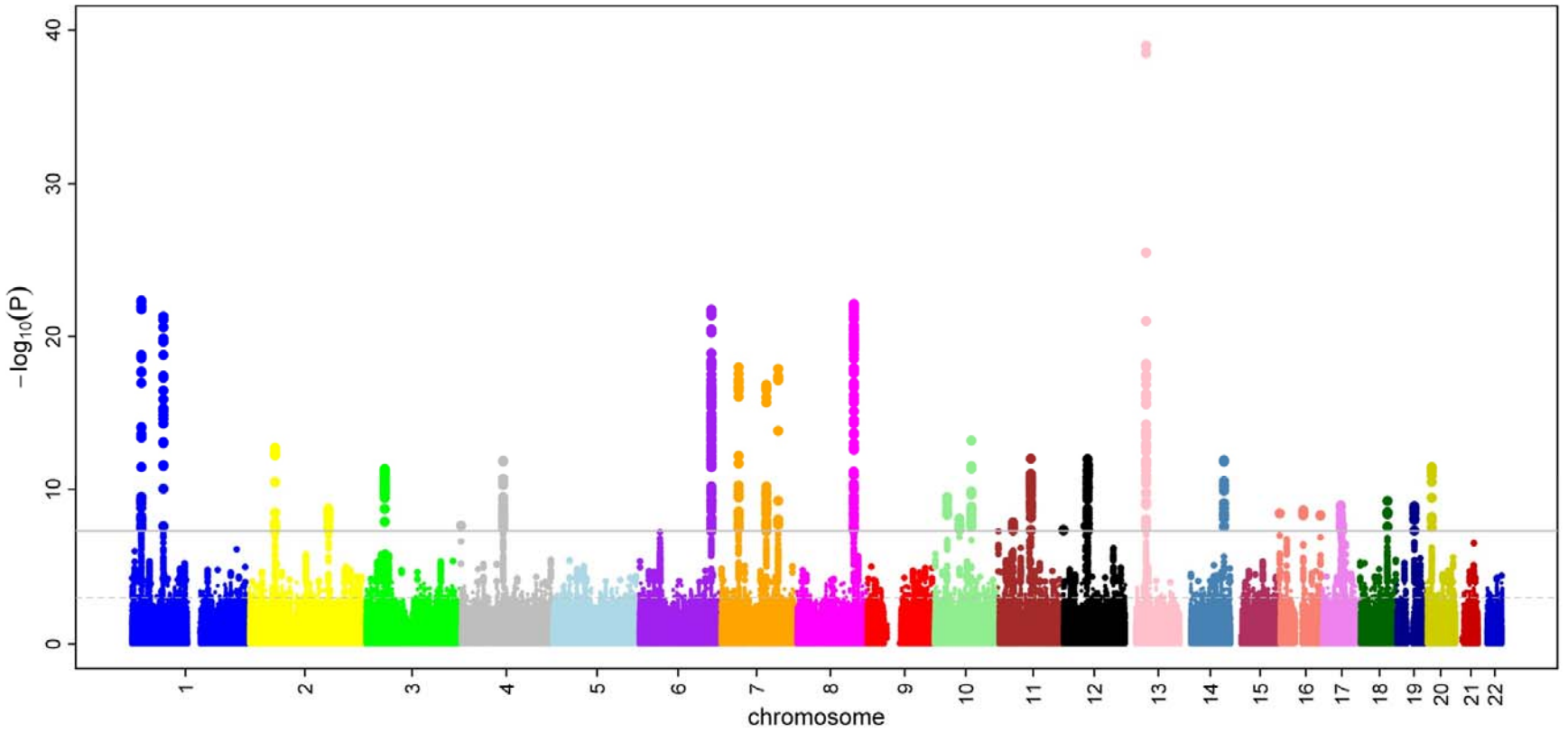


Supplementary Figure 2. Manhattan plots. Plots display loci associated at genome-wide significant level with femoral neck BMD (a) and lumbar spine BMD and (b) for all SNPs analyzed using fixed-effects.

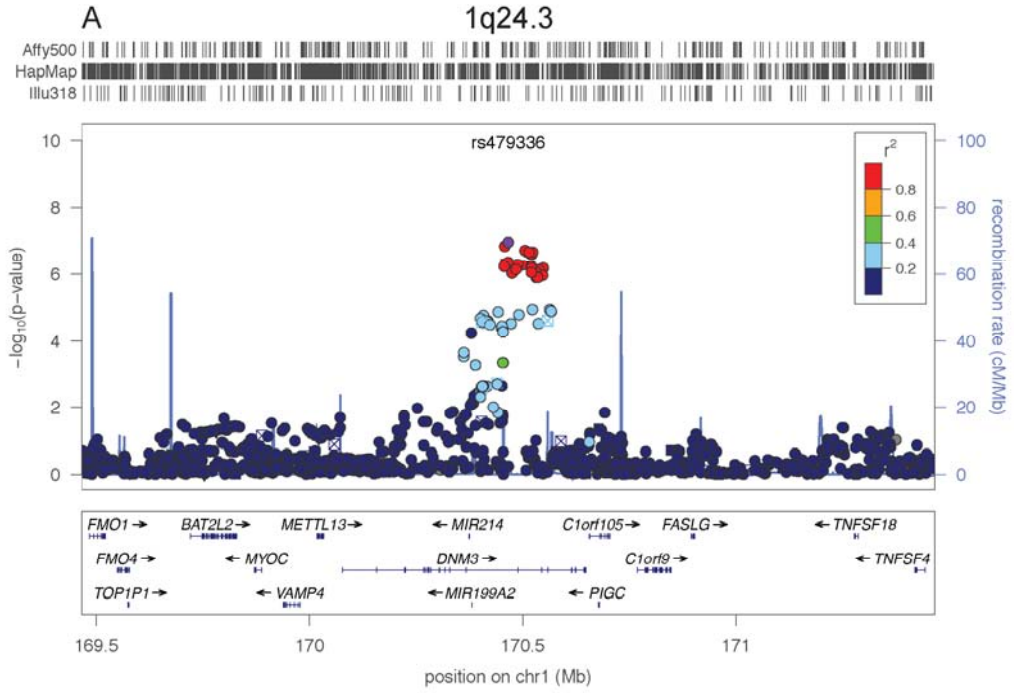
A

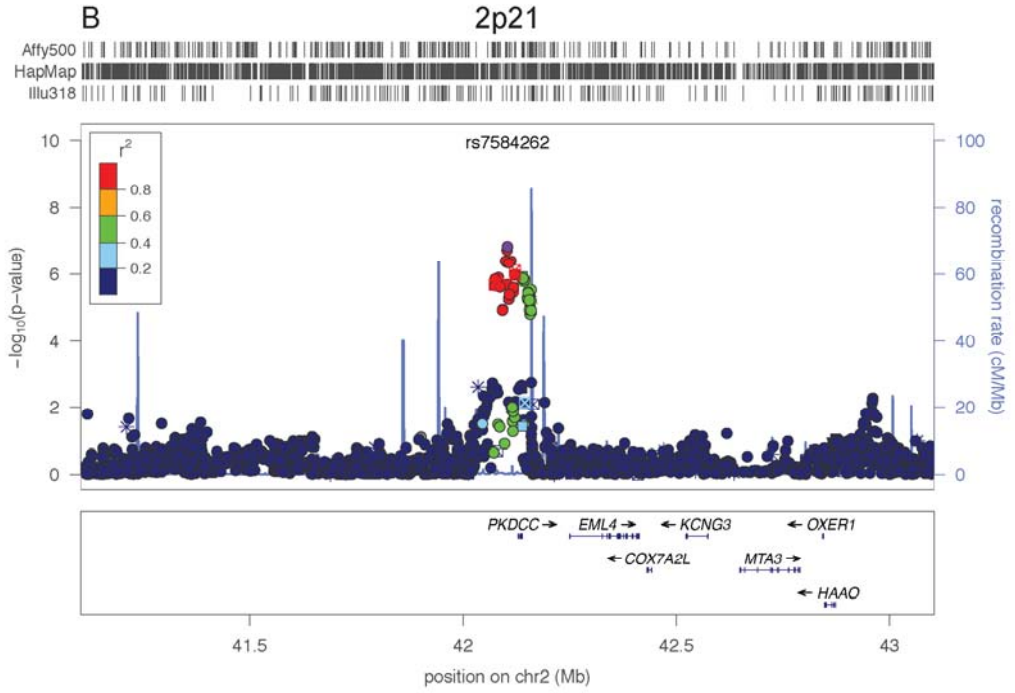


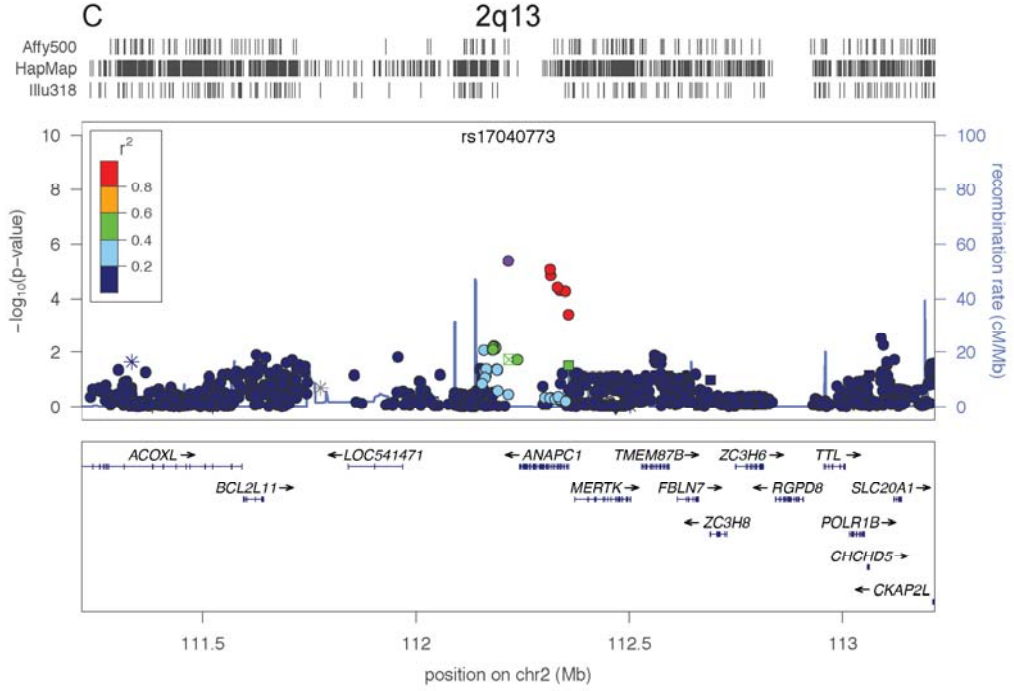
B

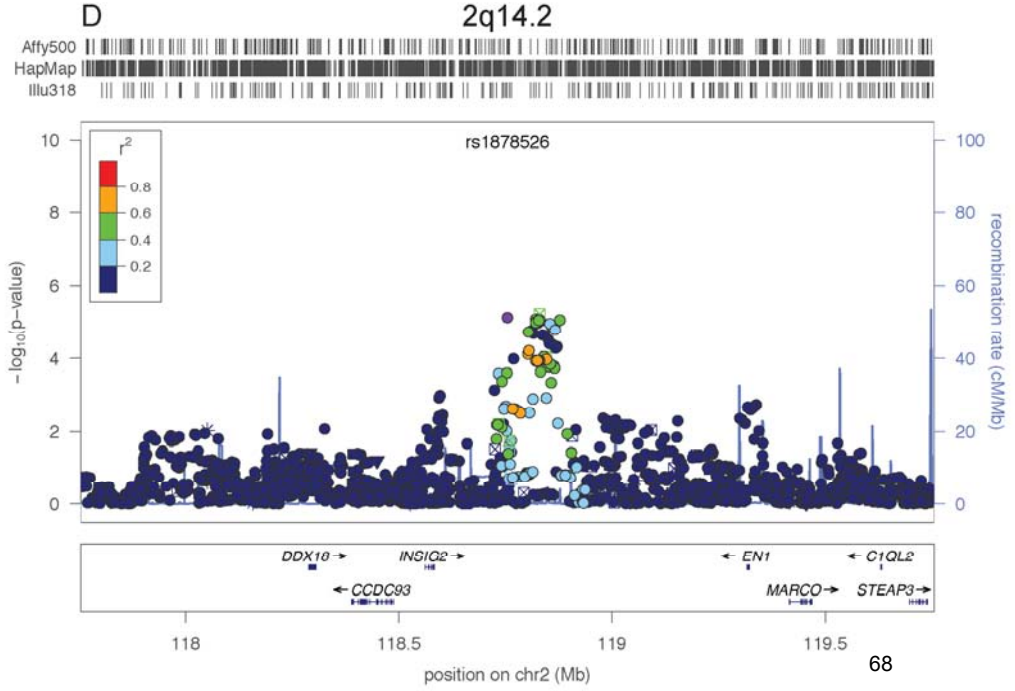

−log10(P)
0
10
20
30
40
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
chromosome

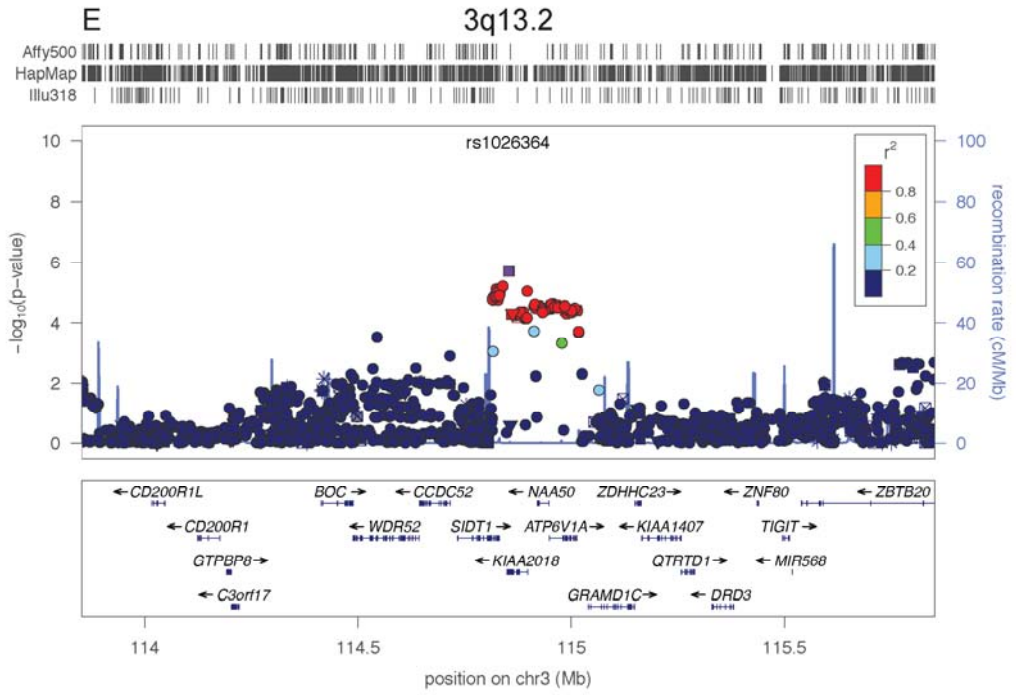
Supplementary Figure 3. Regional plots. Regional association plot for each of the 32 novel (A. 1q24.3, B. 2p21, C. 2q13, D. 2q14.2, E. 3q13.2, F. 3q25.31, G. 4p16.3, H. 6p21.1, I. 6p22.3, J. 7q31.31, K. 7q36.1, L. 8q13.3, M. 9q34.11, N. 10p11.23, O. 10q21.1, P. 10q22.3_1, Q. 10q24.2, R. 11p14.1_1, S. 12p11.22, T. 12p13.33, U. 12q13.12, V. 12q23.3, W. 14q32.12, X. 16p13.11, Y. 16p13.3_1, Z. 16p13.3_2, AA. 16q12.1, AB. 17p13.3, AC. 17q24.3, AD. 18p11.21, AE. 19q13.11, AF. Xp22.31) and 24 previously reported loci (BA. 1p31.3, BB. 1p36.12, BC. 2p16.2, BD. 2q24.3, BE. 3p22.1, BF. 4q22.1, BG. 5q14.3, BH. 6q22.32, BI. 6q25.1, BJ. 7p14.1, BK. 7q21.3, BL. 8q24.12, BM. 11p11.2, BN. 11p14.1_2, BO. 11p15.2, BP. 11q13.2, BQ. 12q13.13, BR. 13q14.11, BS. 14q32.32, BT. 16q24.1, BU. 17q21.31_1, BV. 17q21.31_2, BW. 18q21.33, BX. 20p12. 2). SNPs are plotted by position in a 1Mb window against association with BMD (–log10 P). Plot highlighting the most significant SNP in the stage 1 BMD meta-analysis. Blue peaks indicate recombination rates. The SNPs surrounding the most significant SNP are color coded to reflect their LD with this SNP (from pairwise r^2 values from the HapMap CEU). Genes, exons and the direction of transcription from the UCSC genome browser are noted.

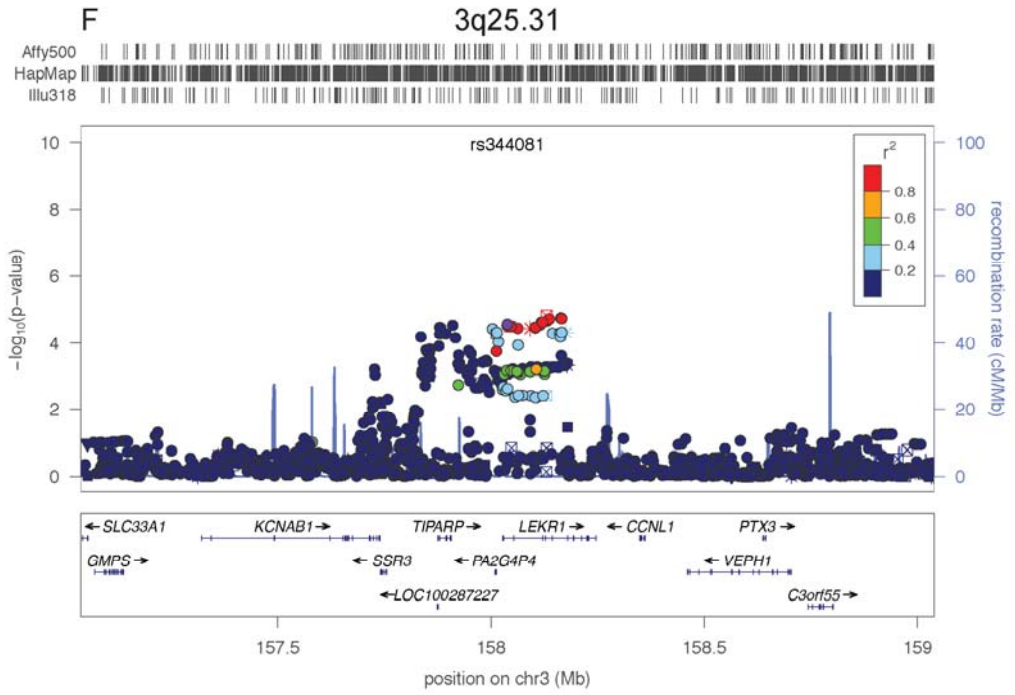

A
1q24.3
Affy500
HapMap
Illu318
rs479336
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
FMO1
BAT2L2
METTL13
MIR214
C1orf105
FASLG
TNFSF18
FMO4
MYOC
DNM3
C1orf9
TNFSF4
TOP1P1
VAMP4
MIR199A2
PIGC
169.5
170
170.5
171
position on chr1 (Mb)

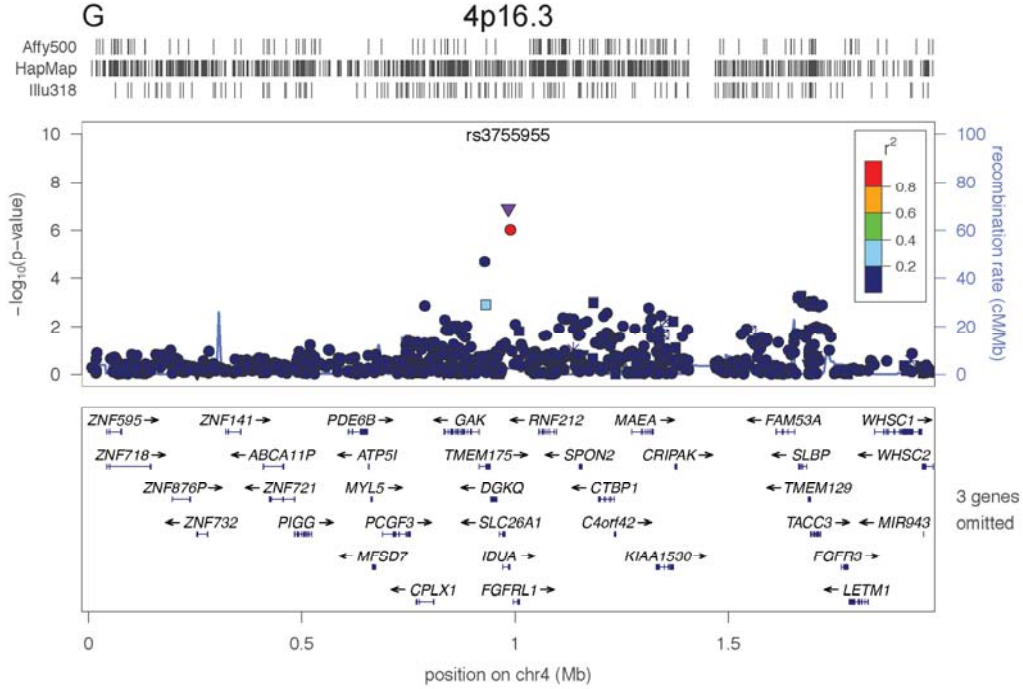

B
2p21
Affy500
HapMap
Illu318
rs7584262
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
PKDCC
EML4
KCNG3
OXER1
COX7A2L
MTA3
HAAO
41.5
42
42.5
43
position on chr2 (Mb)

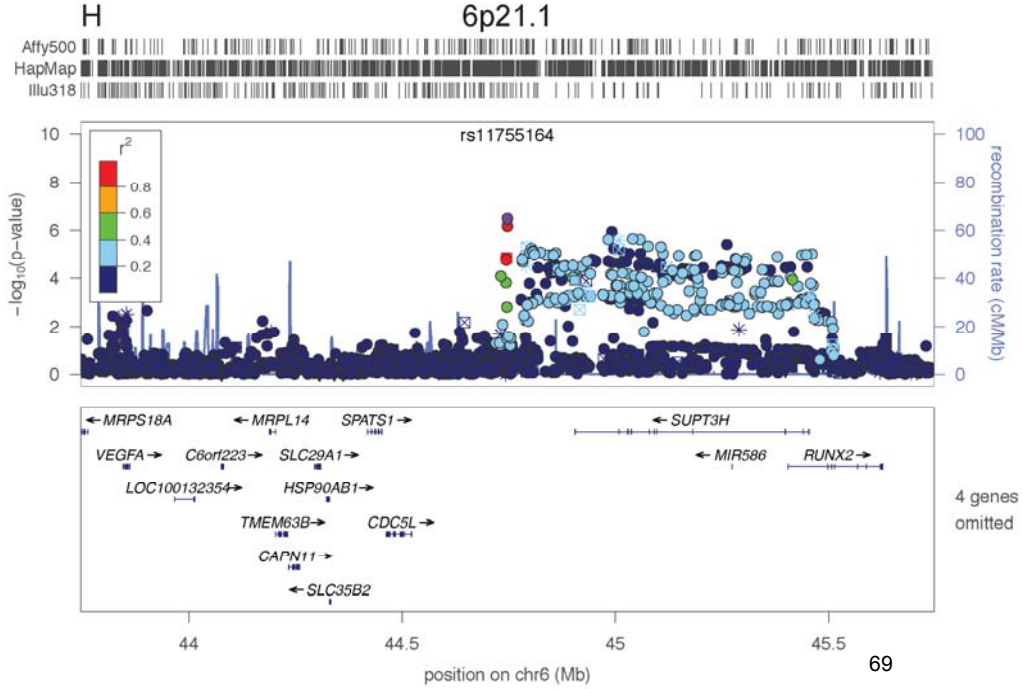

C
2q13
Affy500
HapMap
Illu318
rs17040773
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ACOXL
LOC541471
ANAPC1
TMEM87B
ZC3H6
TTL
BCL2L11
MERTK
FBLN7
RGPD8
SLC20A1
ZC3H8
POLR1B
CHCHD5
CKAP2L
111.5
112
112.5
113
position on chr2 (Mb)

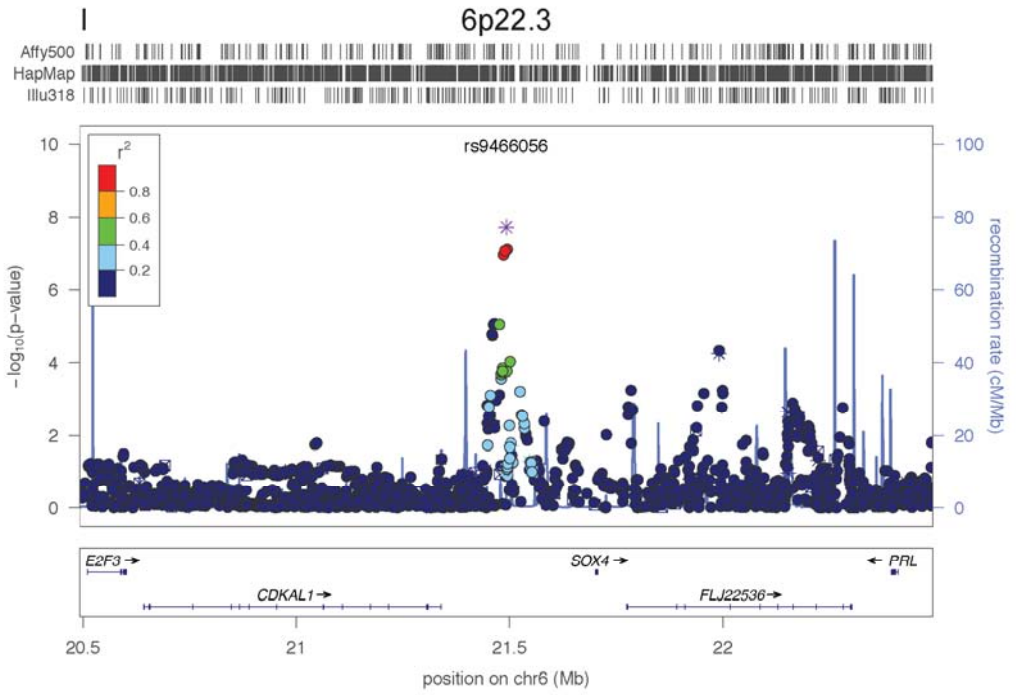

D
2q14.2
Affy500
HapMap
Illu318
rs1878526
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
DDX18
INSIG2
EN1
C1QL2
CCDC93
MARCO
STEAP3
118
118.5
119
119.5
position on chr2 (Mb)

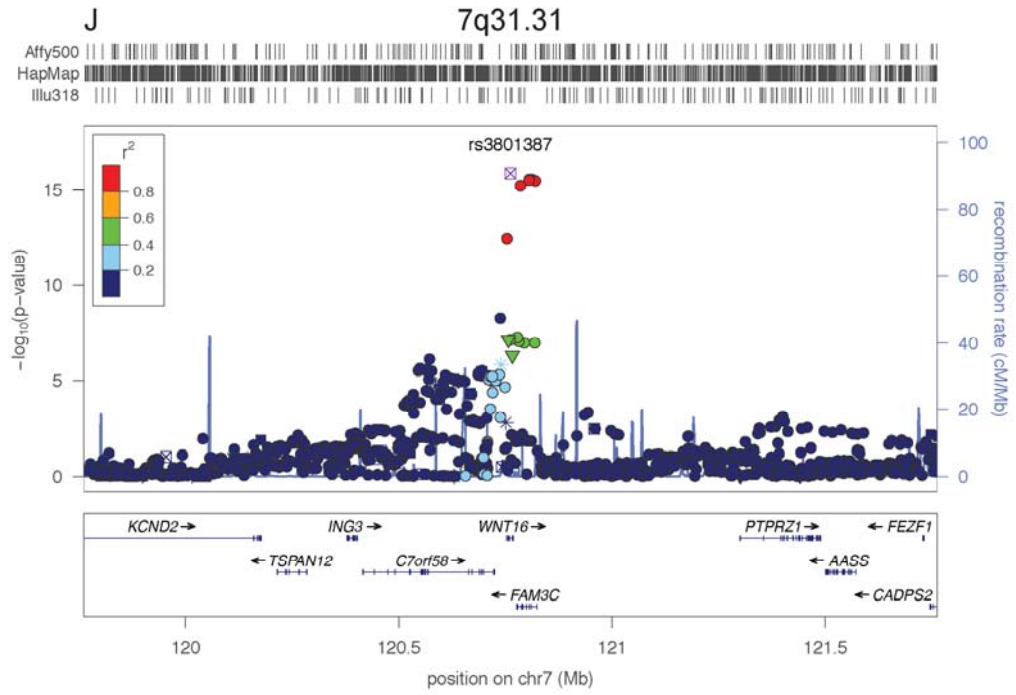

E
3q13.2
Affy500
HapMap
Illu318
rs1026364
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
CD200R1L
BOC
CCDC52
NAA50
ZDHHC23
ZNF80
ZBTB20
CD200R1
WDR52
SIDT1
ATP6V1A
KIAA1407
TIGIT
GTPBP8
KIAA2018
QTRTD1
MIR568
C3orf17
GRAMD1C
DRD3
114
114.5
115
115.5
position on chr3 (Mb)

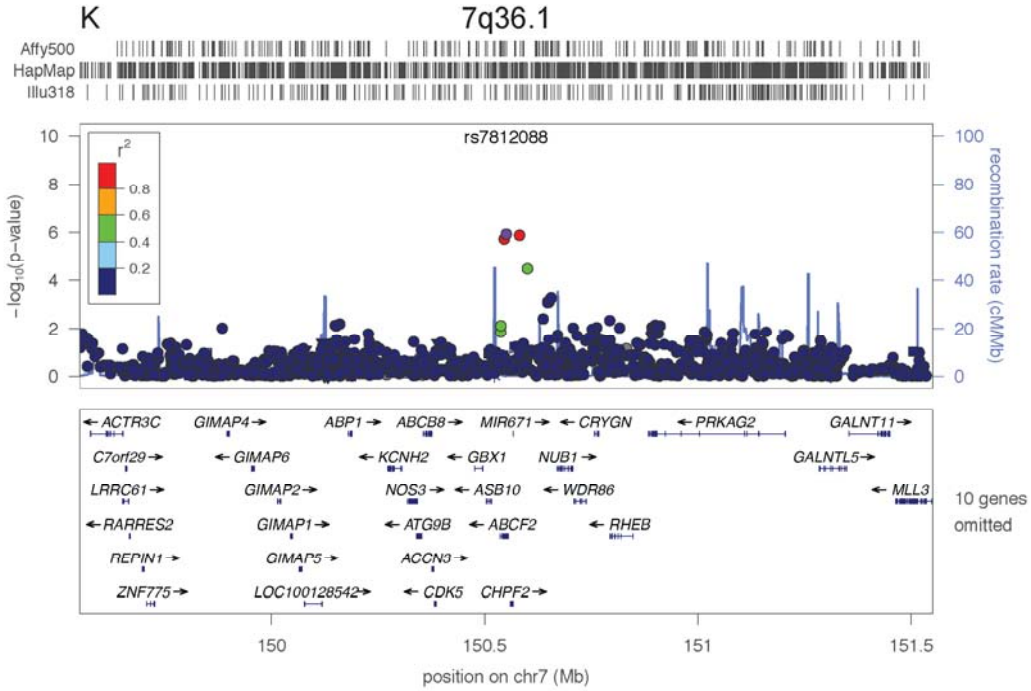

F
3q25.31
Affy500
HapMap
Illu318
rs344081
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
SLC33A1
KCNAB1
TIPARP
LEKR1
CCNL1
PTX3
GMPS
SSR3
PA2G4P4
VEPH1
LOC100287227
C3orf55
157.5
158
158.5
159
position on chr3 (Mb)

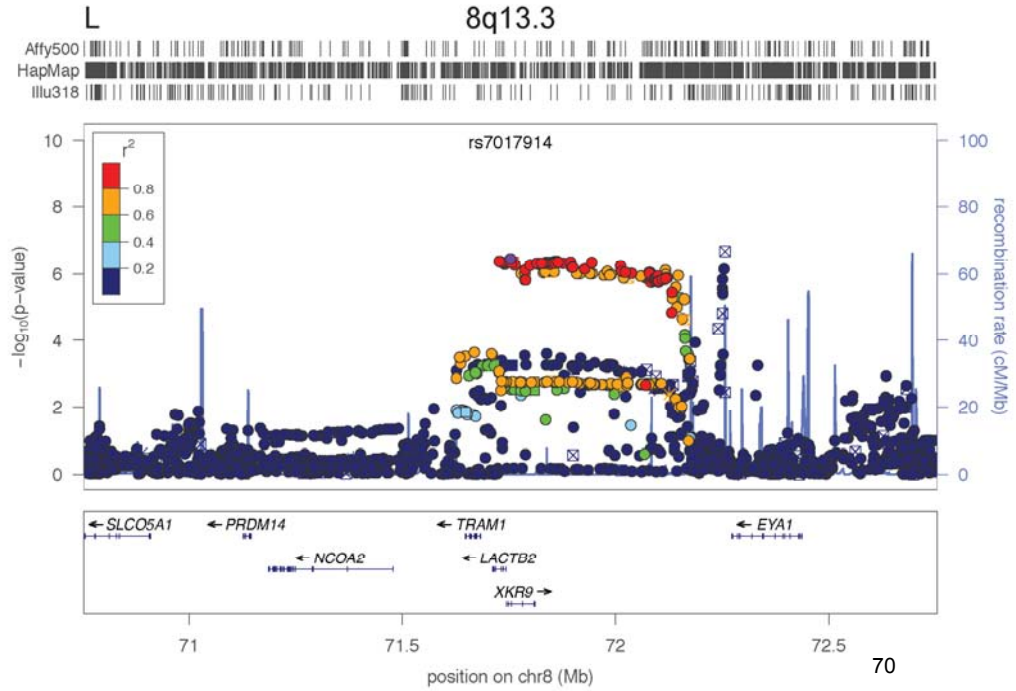

G
4p16.3
Affy500
HapMap
Illu318
rs3755955
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ZNF595
ZNF141
PDE6B
GAK
RNF212
MAEA
FAM53A
WHSC1
ZNF718
ABCA11P
ATP5I
TMEM175
SPON2
CRIPAK
SLBP
WHSC2
ZNF876P
ZNF721
MYL5
DGKQ
CTBP1
TMEM129
ZNF732
PIGG
PCGF3
SLC26A1
C4orf42
TACC3
MIR943
MFSD7
IDUA
KIAA1530
FGFR3
CPLX1
FGFRL1
LETM1
3 genes
omitted
0
0.5
1
1.5
position on chr4 (Mb)

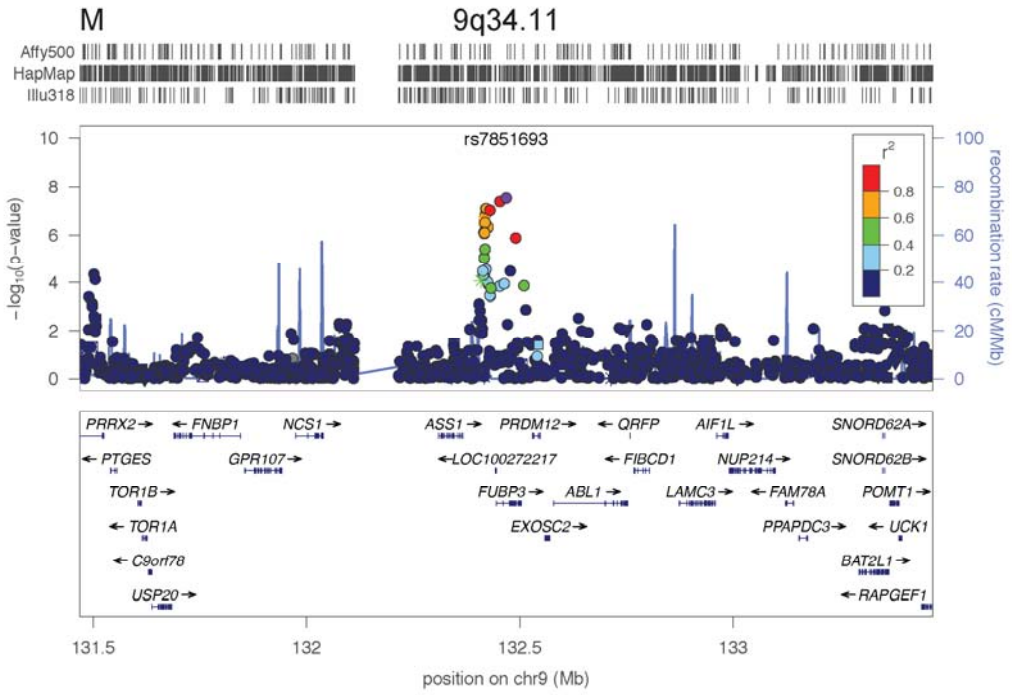

H
6p21.1
Affy500
HapMap
Illu318
rs11755164
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
MRPS18A
MRPL14
SPATS1
SUPT3H
VEGFA
C6orf223
SLC29A1
MIR586
RUNX2
LOC100132354
HSP90AB1
TMEM63B
CDC5L
CAPN11
SLC35B2
4 genes
omitted
44
44.5
45
45.5
position on chr6 (Mb)

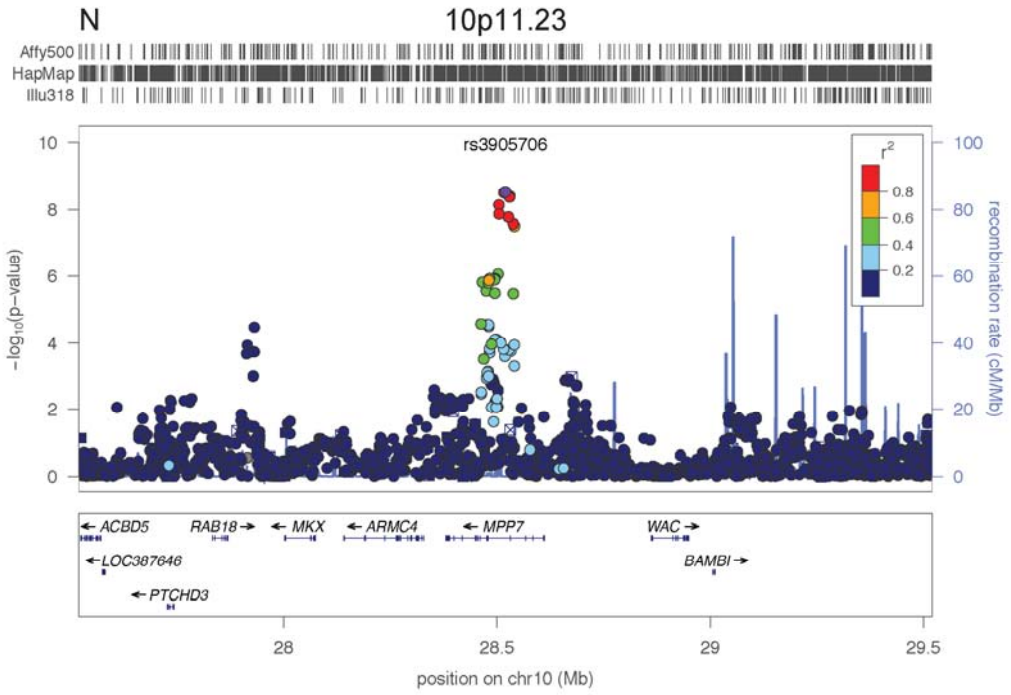

I
6p22.3
Affy500
HapMap
Illu318
rs9466056
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
E2F3
SOX4
PRL
CDKAL1
FLJ22536
20.5
21
21.5
22
position on chr6 (Mb)

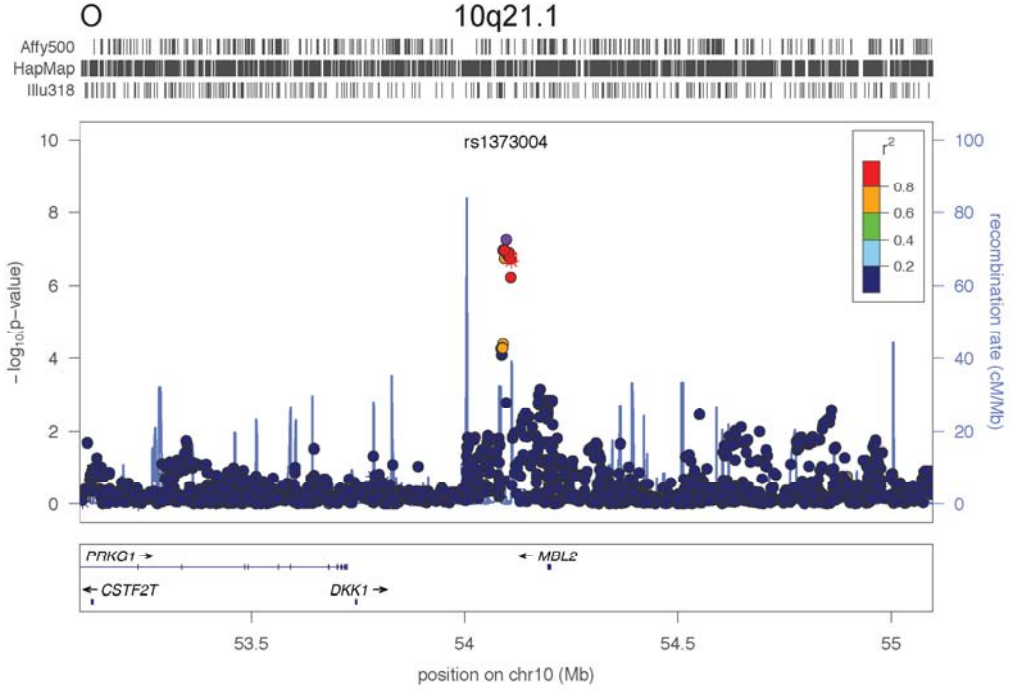

J
7q31.31
Affy500
HapMap
Illu318
rs3801387
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
KCND2
ING3
WNT16
PTPRZ1
FEZF1
TSPAN12
C7orf58
AASS
FAM3C
CADPS2
120
120.5
121
121.5
position on chr7 (Mb)

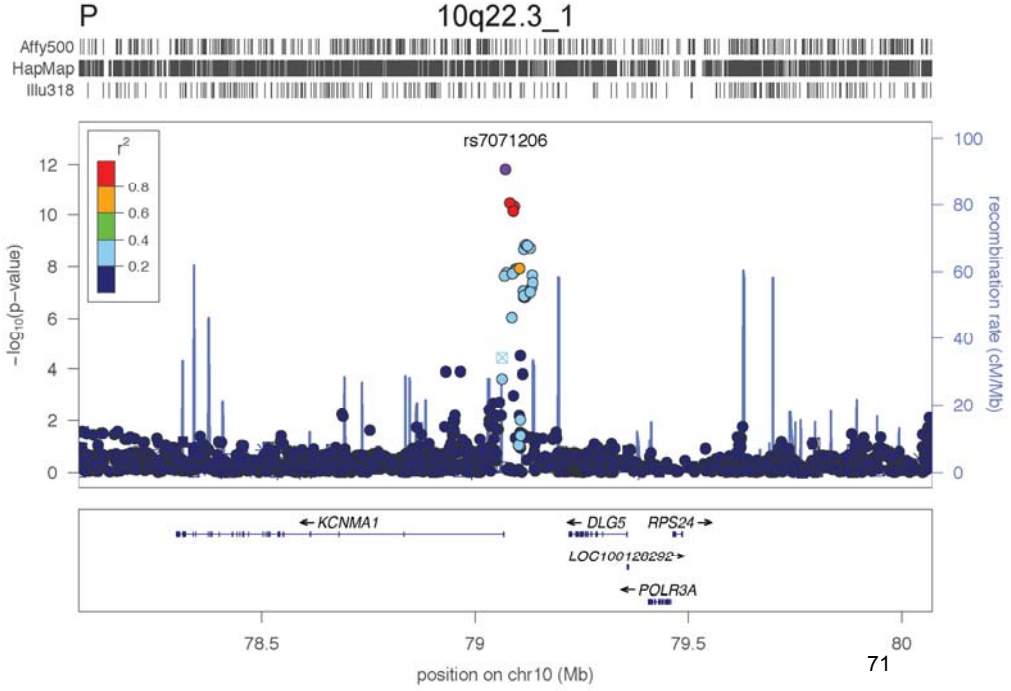

K
7q36.1
Affy500
HapMap
Illu318
rs7812088
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ACTR3C
GIMAP4
ABP1
ABCB8
MIR671
CRYGN
PRKAG2
GALNT11
C7orf29
GIMAP6
KCNH2
GBX1
NUB1
GALNTL5
LRRC61
GIMAP2
NOS3
ASB10
WDR86
MLL3
RARRES2
GIMAP1
ATG9B
ABCF2
RHEB
REPIN1
GIMAP5
ACCN3
ZNF775
LOC100128542
CDK5
CHPF2
10 genes
omitted
150
150.5
151
151.5
position on chr7 (Mb)

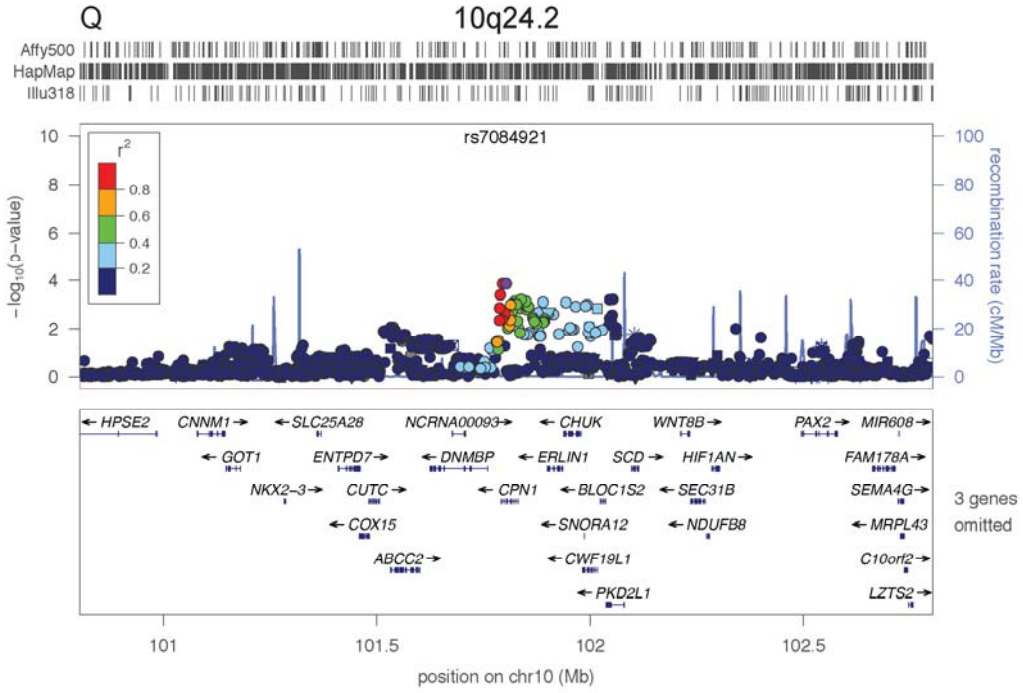

L
8q13.3
Affy500
HapMap
Illu318
rs7017914
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
SLCO5A1
PRDM14
TRAM1
EYA1
NCOA2
LACTB2
XKR9
71
71.5
72
72.5
position on chr8 (Mb)

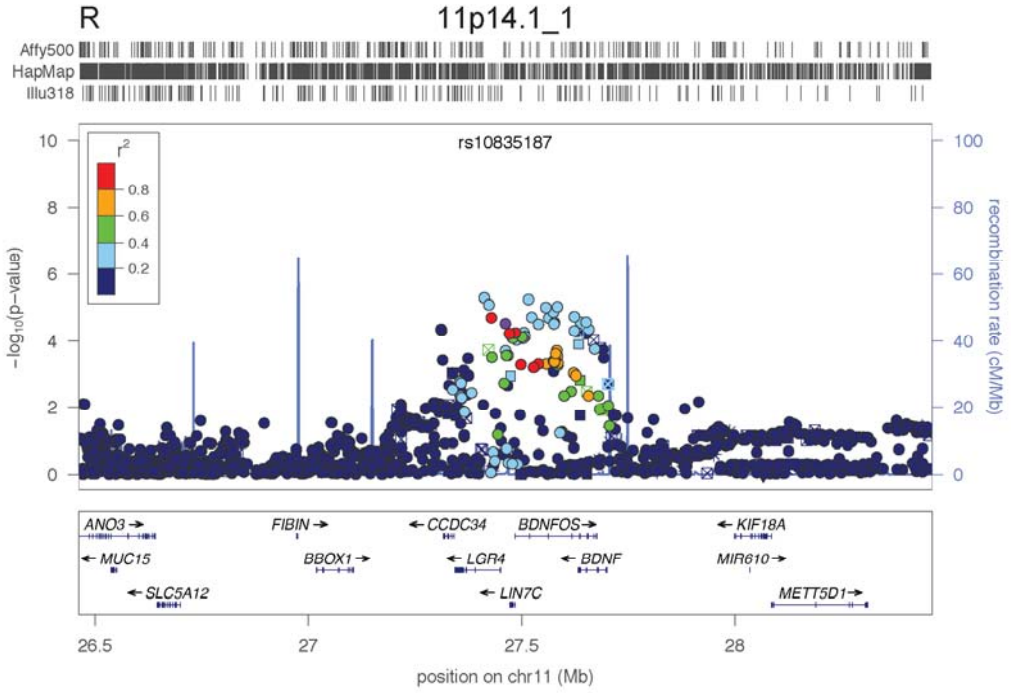

M
9q34.11
Affy500
HapMap
Illu318
rs7851693
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
PRRX2 FNBP1 NCS1 ASS1 PRDM12 QRFP AIF1L SNORD62A
PTGES GPR107 LOC100272217 FIBCD1 NUP214 SNORD62B
TOR1B FUBP3 ABL1 LAMC3 FAM78A POMT1
TOR1A EXOSC2 PPAPDC3 UCK1
C9orf78 BAT2L1
USP20 RAPGEF1
131.5
132
132.5
133
position on chr9 (Mb)

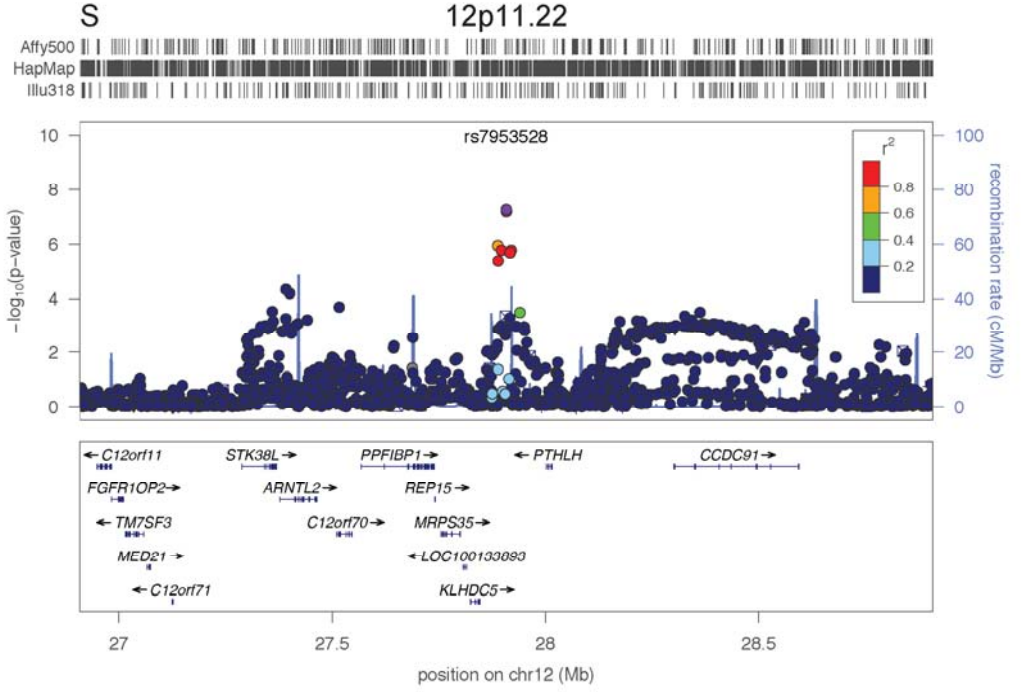

N
10p11.23
Affy500
HapMap
Illu318
rs3905706
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ACBD5 RAB18 MKX ARMC4 MPP7 WAC
LOC387646 BAMBI
PTCHD3
28
28.5
29
29.5
position on chr10 (Mb)

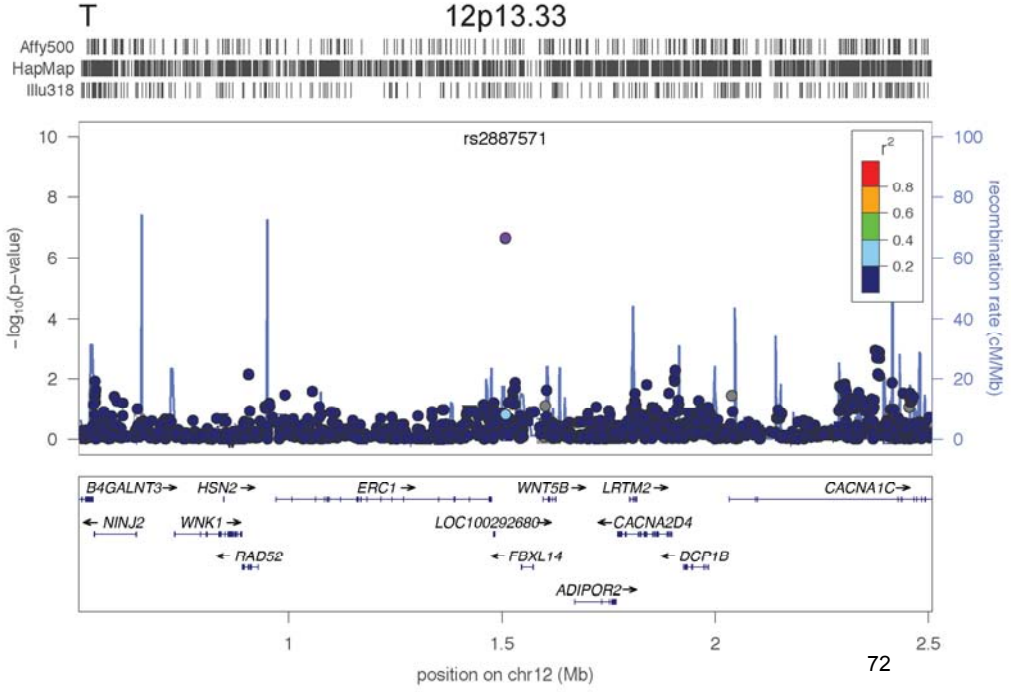

O
10q21.1
Affy500
HapMap
Illu318
rs1373004
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
PRKG1 MBL2
CSTF2T DKK1
53.5
54
54.5
55
position on chr10 (Mb)

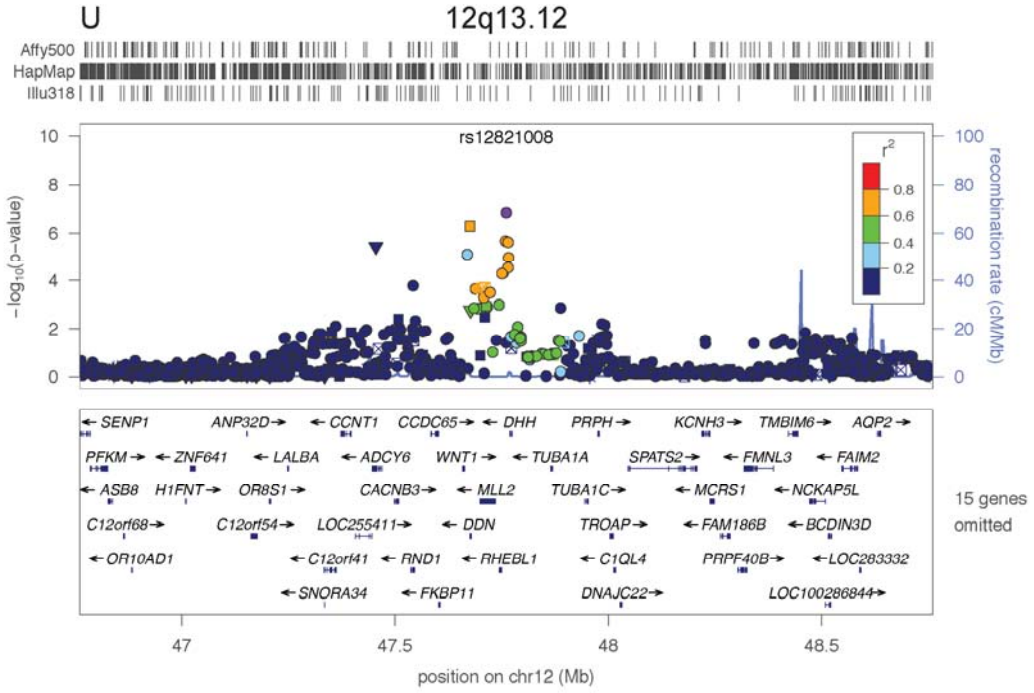

P
10q22.3_1
Affy500
HapMap
Illu318
rs7071206
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
KCNMA1 DLG5 RPS24
LOC100126292
POLR3A
78.5
79
79.5
80
position on chr10 (Mb)

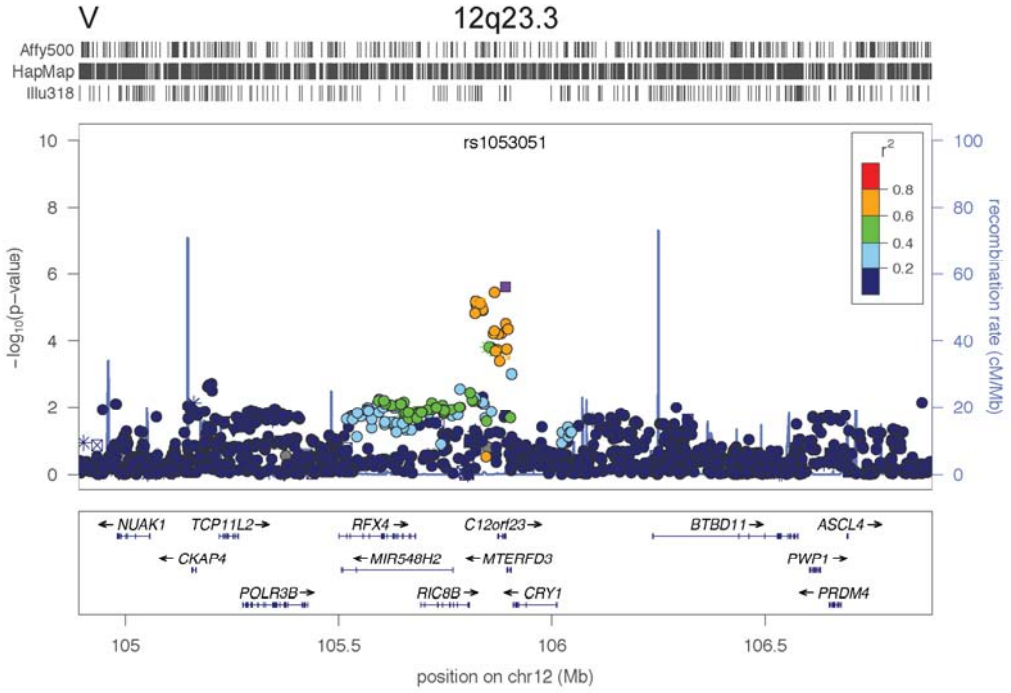

Q
10q24.2
Affy500
HapMap
Illu318
rs7084921
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
HPSE2
CNNM1
SLC25A28
NCRNA00093
CHUK
WNT8B
PAX2
MIR608
GOT1
ENTPD7
DNMBP
ERLIN1
SCD
HIF1AN
FAM178A
NKX2−3
CUTC
CPN1
BLOC1S2
SEC31B
SEMA4G
COX15
SNORA12
NDUFB8
MRPL43
ABCC2
CWF19L1
C10orf2
PKD2L1
LZTS2
3 genes
omitted
101
101.5
102
102.5
position on chr10 (Mb)

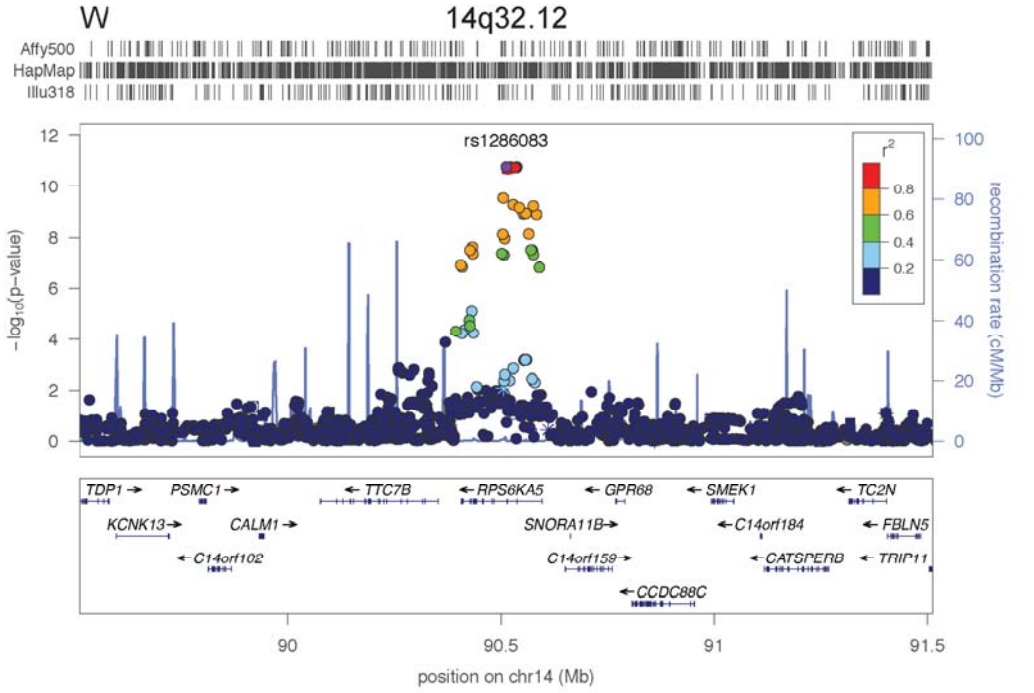

R
11p14.1_1
Affy500
HapMap
Illu318
rs10835187
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ANO3
FIBIN
CCDC34
BDNFOS
KIF18A
MUC15
BBOX1
LGR4
BDNF
MIR610
SLC5A12
LIN7C
METT5D1
26.5
27
27.5
28
position on chr11 (Mb)

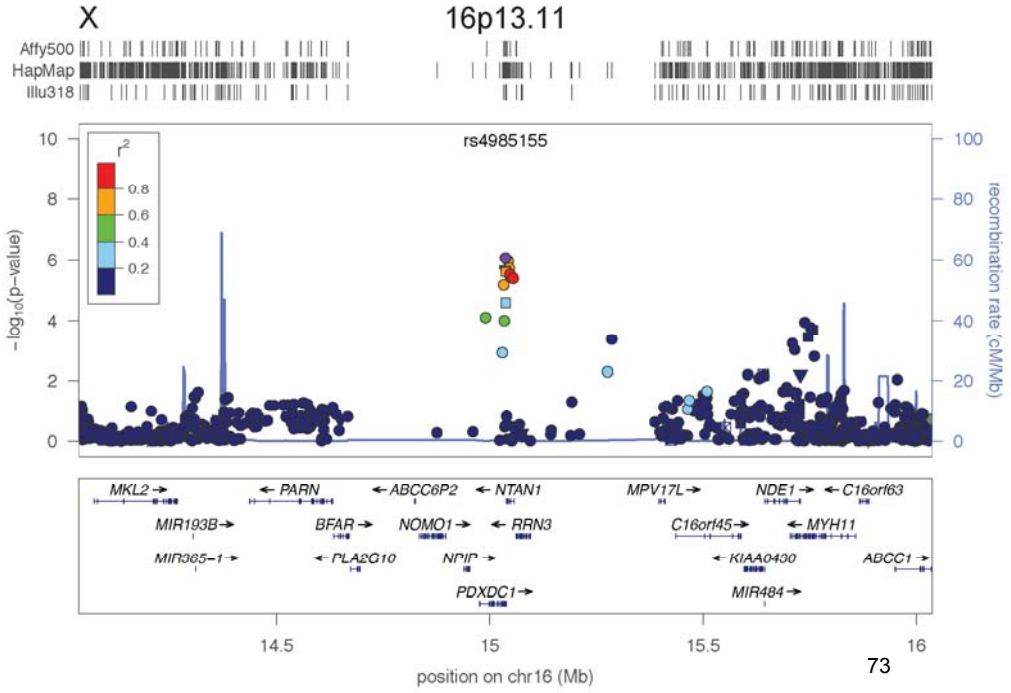

S
12p11.22
Affy500
HapMap
Illu318
rs7953528
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
C12orf11
STK38L
PPFIBP1
PTHLH
CCDC91
FGFR1OP2
ARNTL2
REP15
TM7SF3
C12orf70
MRPS35
MED21
LOC100133893
C12orf71
KLHDC5
27
27.5
28
28.5
position on chr12 (Mb)

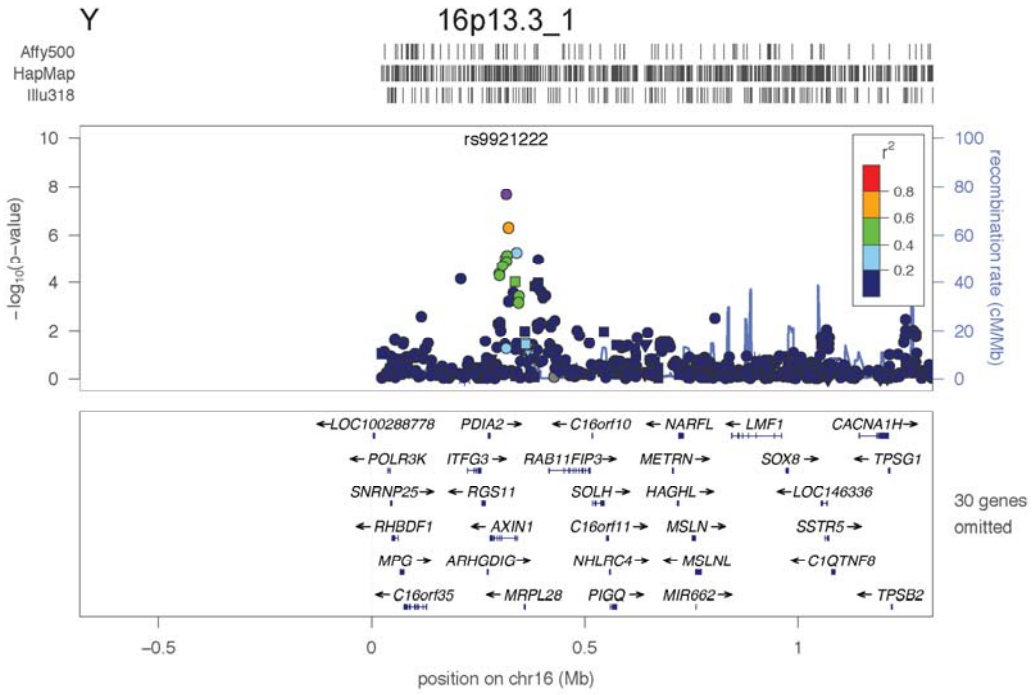

T
12p13.33
Affy500
HapMap
Illu318
rs2887571
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
B4GALNT3
HSN2
ERC1
WNT5B
LRTM2
CACNA1C
NINJ2
WNK1
LOC100292680
CACNA2D4
RAD52
FBXL14
DCP1B
ADIPOR2
1
1.5
2
2.5
position on chr12 (Mb)

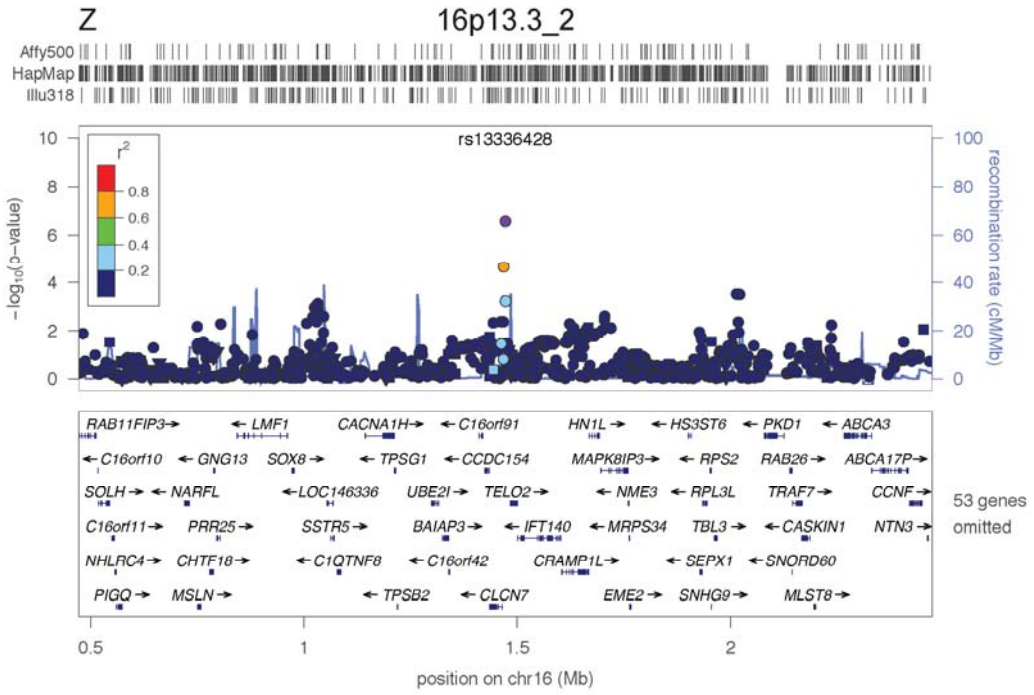

U
12q13.12
Affy500
HapMap
Illu318
rs12821008
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
SENP1 ANP32D CCNT1 CCDC65 DHH PRPH KCNH3 TMBIM6 AQP2
PFKM ZNF641 LALBA ADCY6 WNT1 TUBA1A SPATS2 FMNL3 FAIM2
ASB8 H1FNT OR8S1 CACNB3 MLL2 TUBA1C MCRS1 NCKAP5L
C12orf68 C12orf54 LOC255411 DDN TROAP FAM186B BCDIN3D
OR10AD1 C12orf41 RND1 RHEBL1 C1QL4 PRPF40B LOC283332
SNORA34 FKBP11 DNAJC22 LOC100286844
15 genes omitted
position on chr12 (Mb)

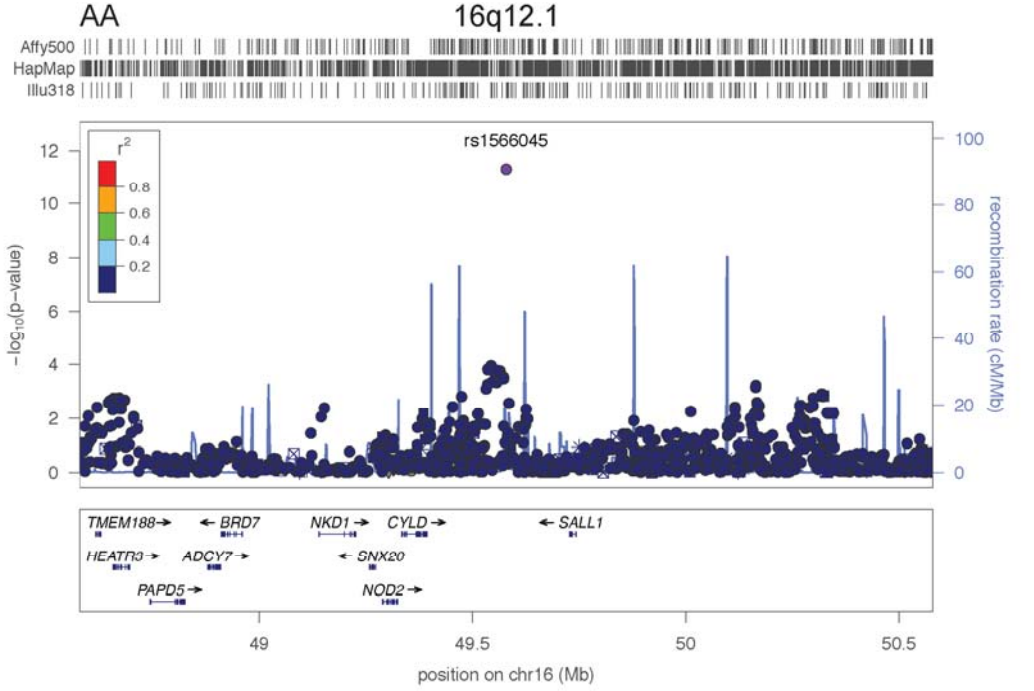

V
12q23.3
Affy500
HapMap
Illu318
rs1053051
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
NUAK1 TCP11L2 RFX4 C12orf23 BTBD11 ASCL4
CKAP4 MIR548H2 MTERFD3 PWP1
POLR3B RIC8B CRY1 PRDM4
position on chr12 (Mb)

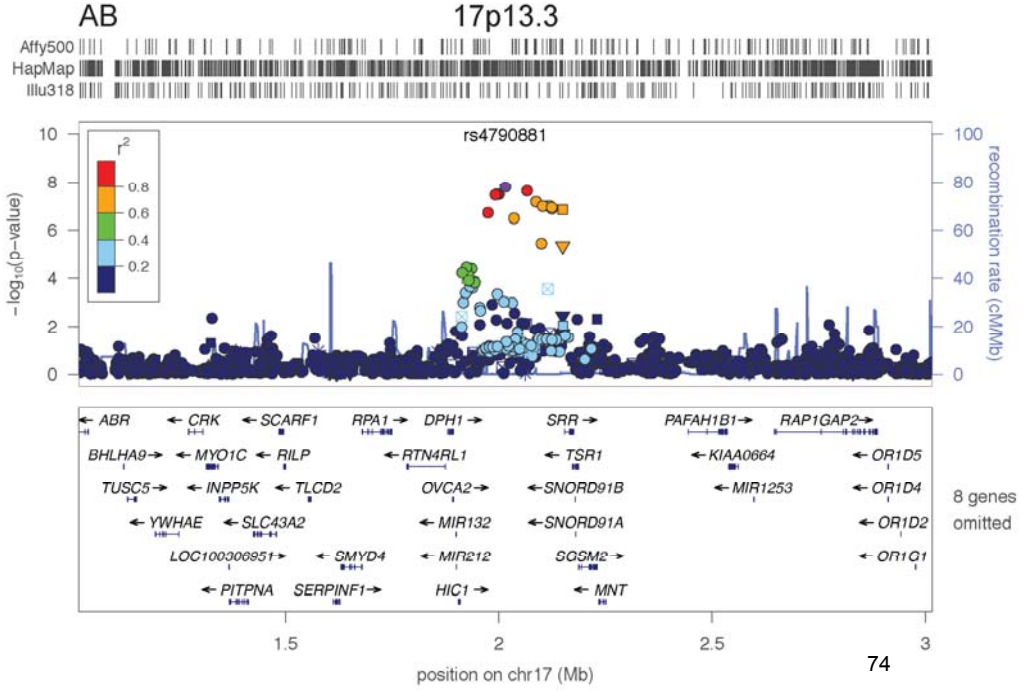

W
14q32.12
Affy500
HapMap
Illu318
rs1286083
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
TDP1 PSMC1 TTC7B RPS6KA5 GPR68 SMEK1 TC2N
KCNK13 CALM1 SNORA11B C14orf184 FBLN5
C14orf102 C14orf159 CATSPERB TRIP11
CCDC88C
position on chr14 (Mb)

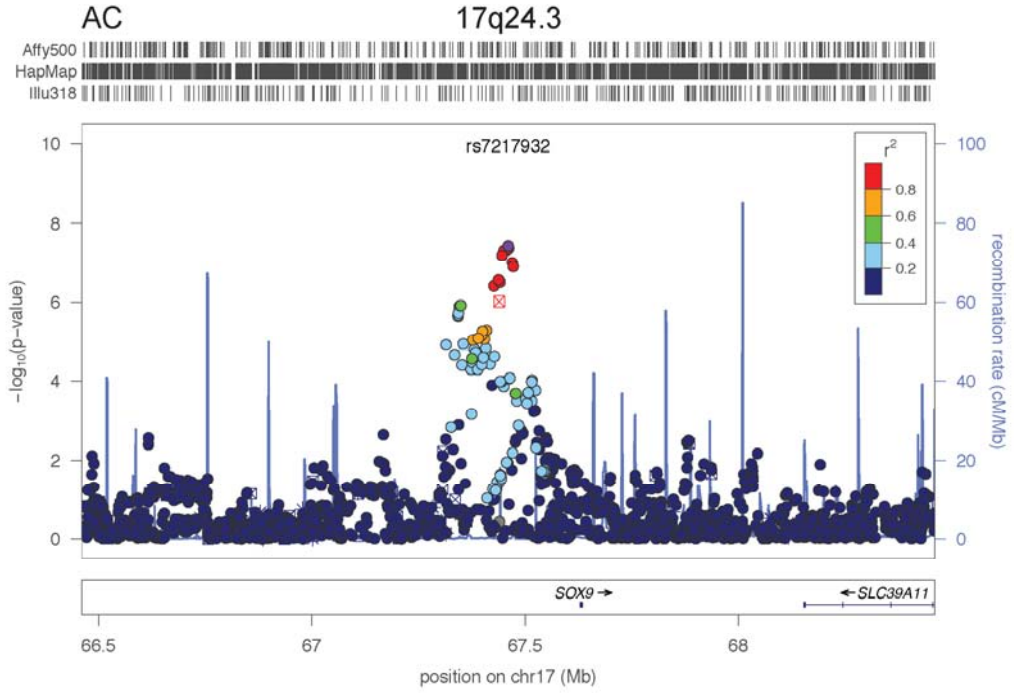

X
16p13.11
Affy500
HapMap
Illu318
rs4985155
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
MKL2 PARN ABCC6P2 NTAN1 MPV17L NDE1 C16orf63
MIR193B BFAR NOMO1 RRN3 C16orf45 MYH11
MIR365-1 PLA2G10 NPIP KIAA0430 ABCC1
PDXDC1 MIR484
position on chr16 (Mb)

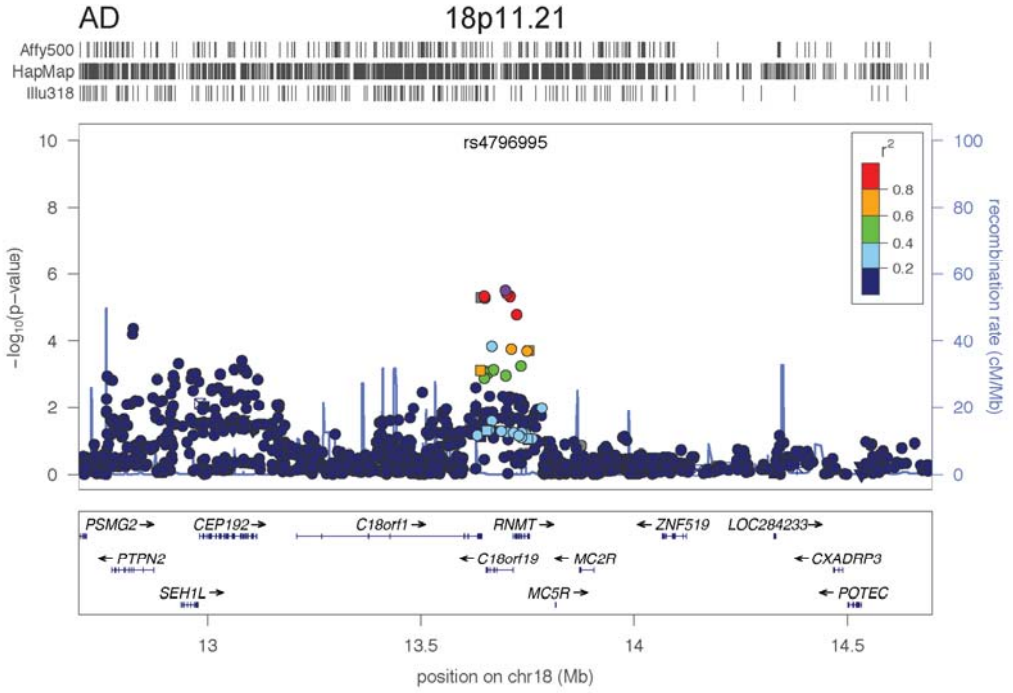

Y
16p13.3_1
Affy500
HapMap
Illu318
rs9921222
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
LOC100288778 PDIA2 C16orf10 NARFL LMF1 CACNA1H
POLR3K ITFG3 RAB11FIP3 METRN SOX8 TPSG1
SNRNP25 RGS11 SOLH HAGHL LOC146336
RHBDF1 AXIN1 C16orf11 MSLN SSTR5
MPG ARHGDIG NHLRC4 MSLNL C1QTNF8
C16orf35 MRPL28 PIGQ MIR662 TPSB2
30 genes omitted
position on chr16 (Mb)

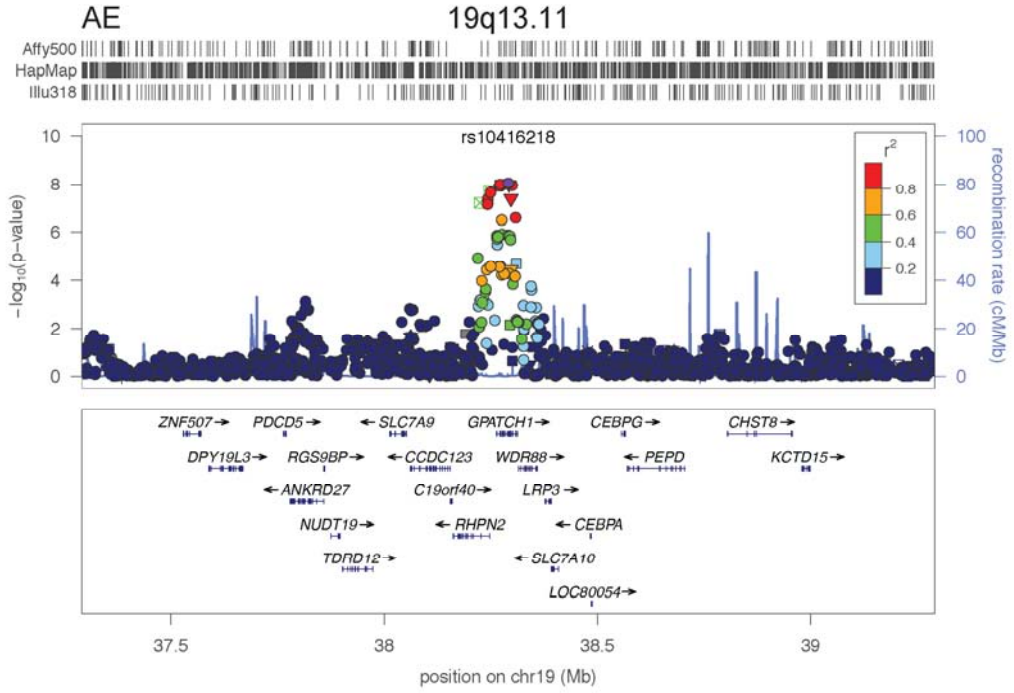

Z
16p13.3_2
Affy500
HapMap
Illu318
rs13336428
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
RAB11FIP3 LMF1 CACNA1H C16orf91 HN1L HS3ST6 PKD1 ABCA3
C16orf10 GNG13 SOX8 TPSG1 CCDC154 MAPK8IP3 RPS2 RAB26 ABCA17P
SOLH NARFL LOC146336 UBE2I TELO2 NME3 RPL3L TRAF7 CCNF
C16orf11 PRR25 SSTR5 BAIAP3 IFT140 MRPS34 TBL3 CASKIN1 NTN3
NHLRC4 CHTF18 C1QTNF8 C16orf42 CRAMP1L SEPX1 SNORD60
PIGQ MSLN TPSB2 CLCN7 EME2 SNHG9 MLST8
53 genes omitted
position on chr16 (Mb)

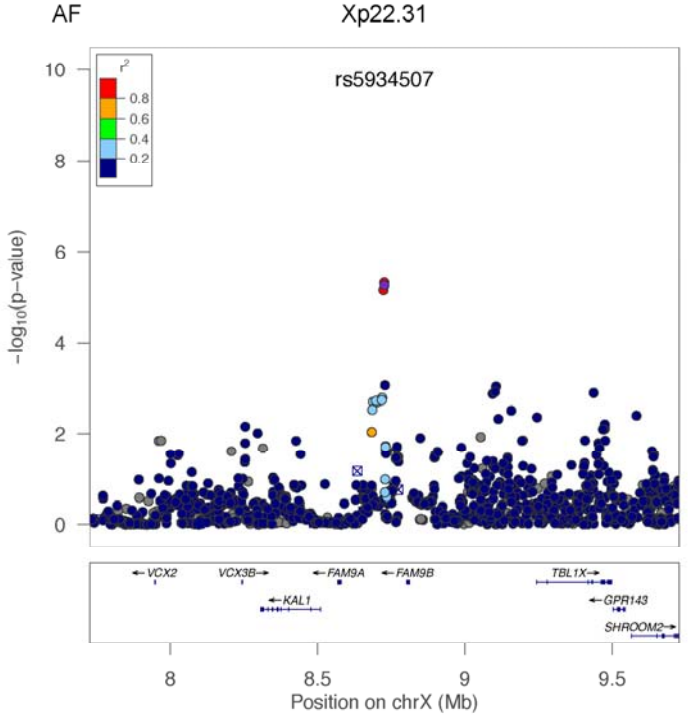

AA
16q12.1
Affy500
HapMap
Illu318
rs1566045
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
TMEM188 BRD7 NKD1 CYLD SALL1
HEATR3 ADCY7 SNX20
PAPD5 NOD2
position on chr16 (Mb)

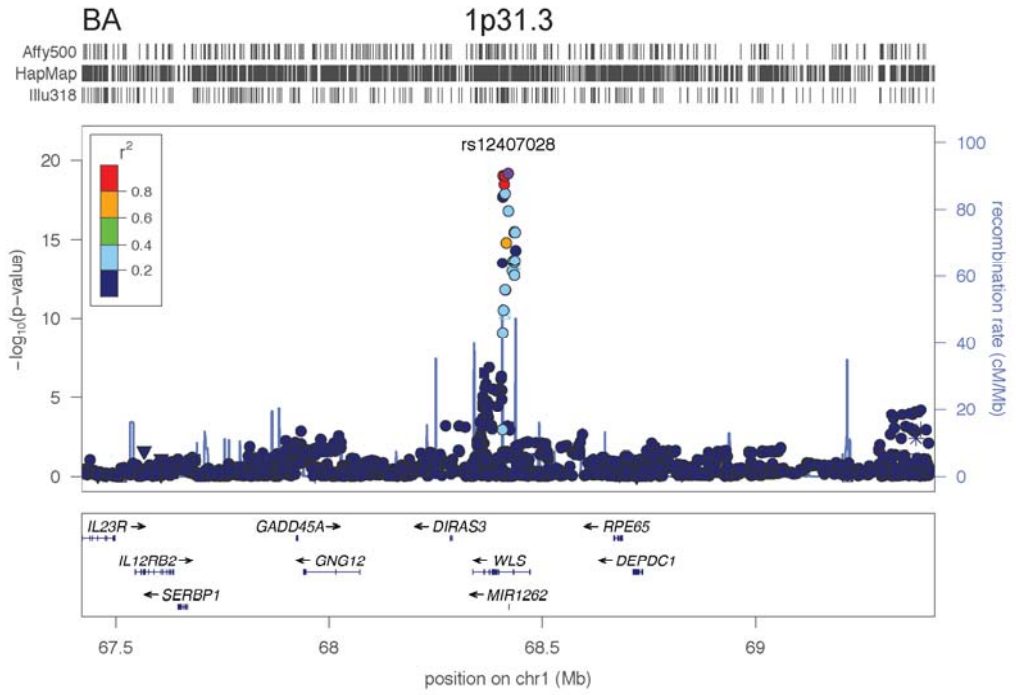

AB
17p13.3
Affy500
HapMap
Illu318
rs4790881
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ABR CRK SCARF1 RPA1 DPH1 SRR PAFAH1B1 RAP1GAP2
BHLHA9 MYO1C RILP RTN4RL1 TSR1 KIAA0664 OR1D5
TUSC5 INPP5K TLCD2 OVCA2 SNORD91B MIR1253 OR1D4
YWHAE SLC43A2 MIR132 SNORD91A OR1D2
LOC100506851 SMYD4 MIR212 SGSM2 OR1G1
PITPNA SERPINF1 HIC1 MNT
8 genes omitted
position on chr17 (Mb)

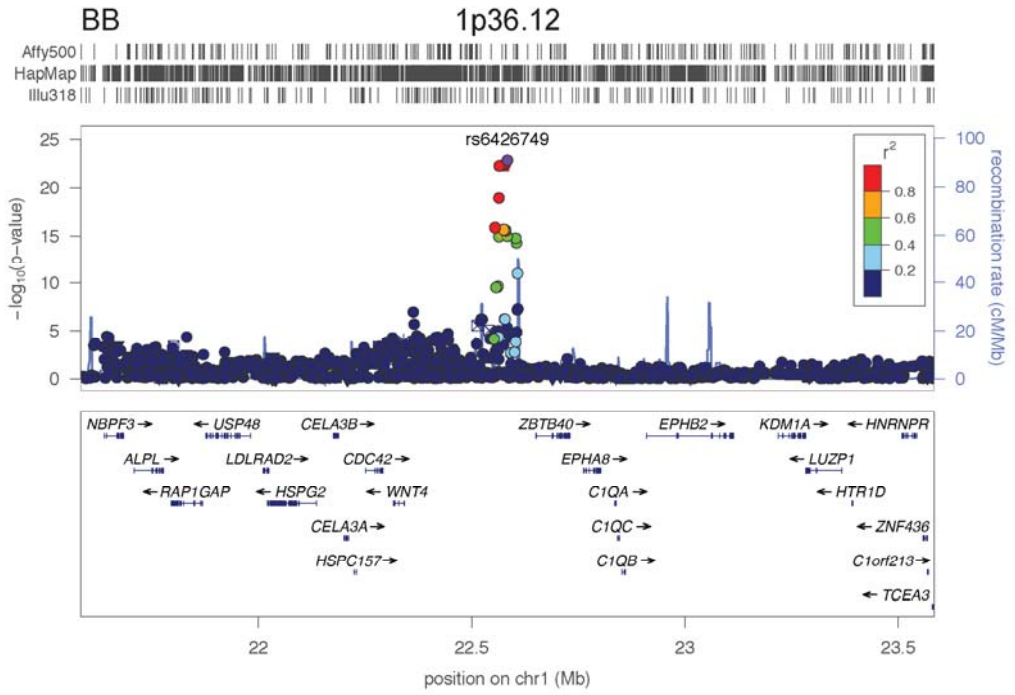

AC
17q24.3
Affy500
HapMap
Illu318
rs7217932
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
SOX9
SLC39A11
66.5
67
67.5
68
position on chr17 (Mb)

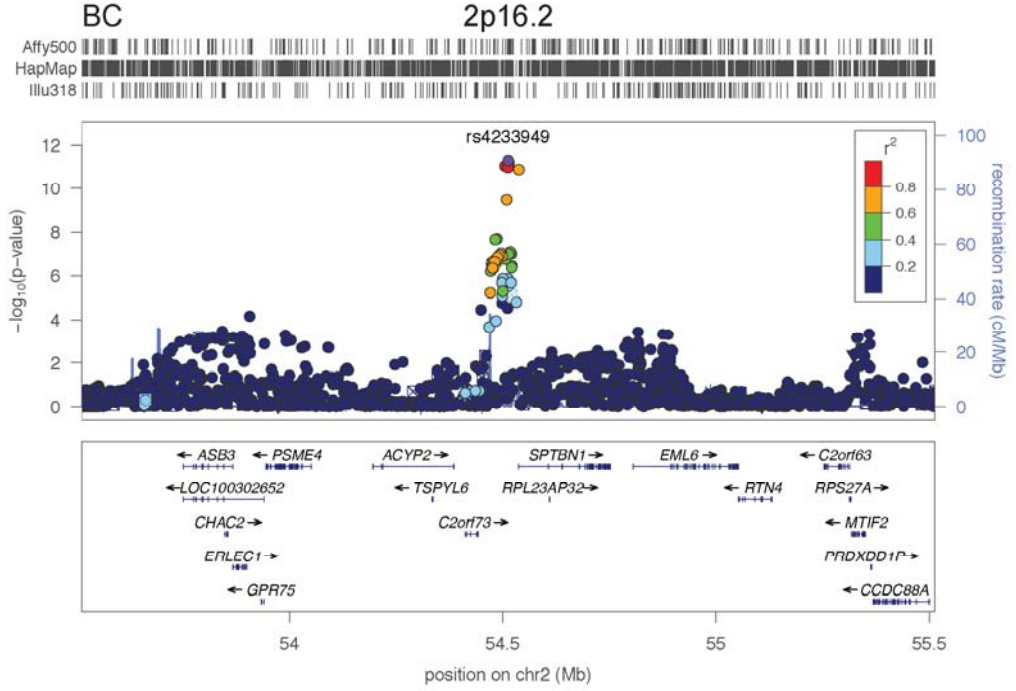

AD
18p11.21
Affy500
HapMap
Illu318
rs4796995
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
PSMG2
CEP192
C18orf1
RNMT
ZNF519
LOC284233
PTPN2
C18orf19
MC2R
CXADRP3
SEH1L
MC5R
POTEC
13
13.5
14
14.5
position on chr18 (Mb)

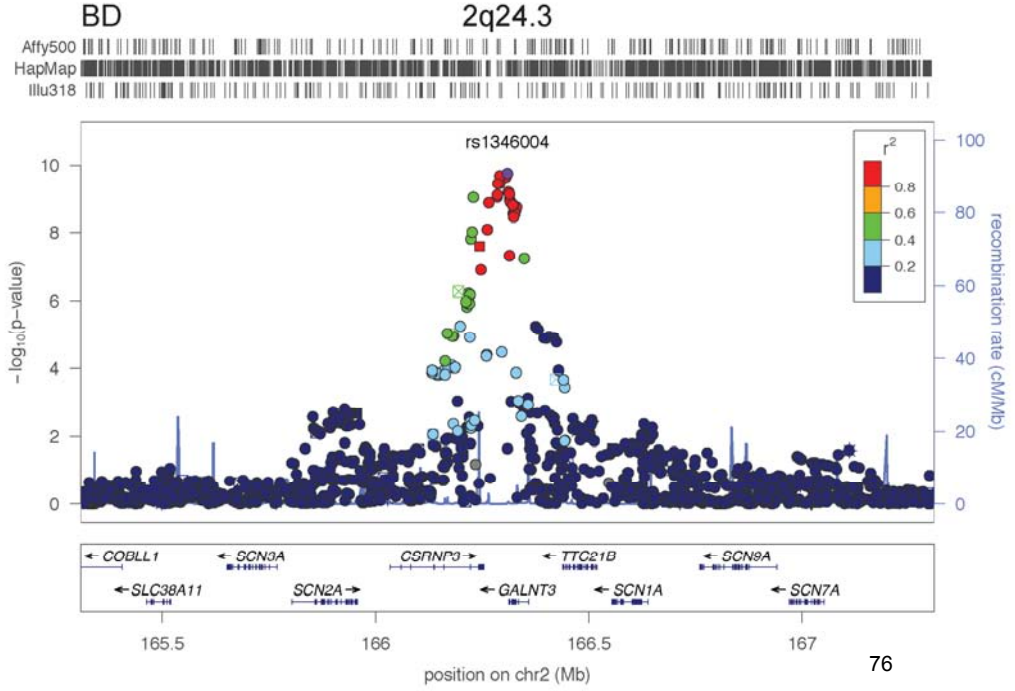

AE
19q13.11
Affy500
HapMap
Illu318
rs10416218
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ZNF507
PDCD5
SLC7A9
GPATCH1
CEBPG
CHST8
DPY19L3
RGS9BP
CCDC123
WDR88
PEPD
KCTD15
ANKRD27
C19orf40
LRP3
NUDT19
RHPN2
CEBPA
TDRD12
SLC7A10
LOC80054
37.5
38
38.5
39
position on chr19 (Mb)

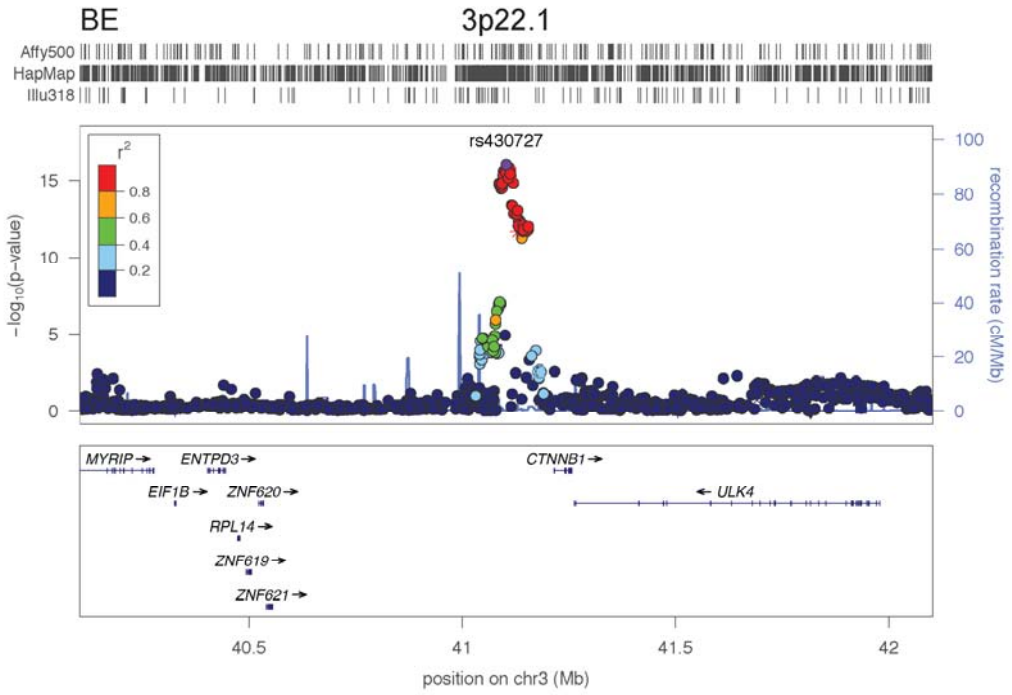

AF
Xp22.31
rs5934507
r²
0.8
0.6
0.4
0.2
−log10(p−value)
VCX2
VCX3B
FAM9A
FAM9B
TBL1X
KAL1
GPR143
SHROOM2
8
8.5
9
9.5
Position on chrX (Mb)

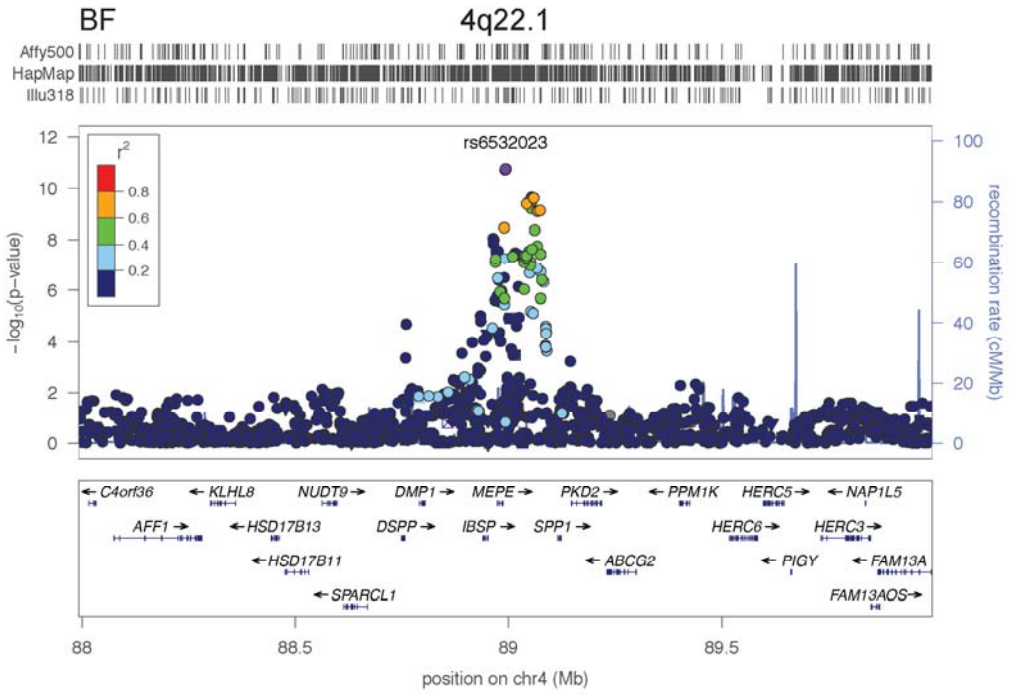

BA
1p31.3
Affy500
HapMap
Illu318
rs12407028
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
IL23R
GADD45A
DIRAS3
RPE65
IL12RB2
GNG12
WLS
DEPDC1
SERBP1
MIR1262
67.5
68
68.5
69
position on chr1 (Mb)

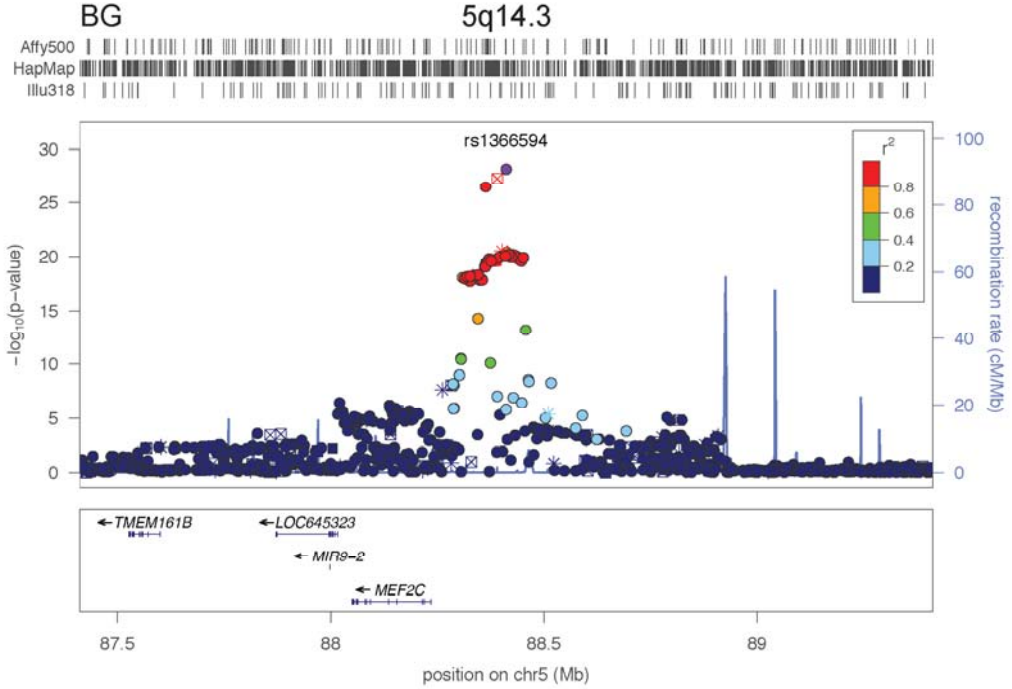

BB
1p36.12
Affy500
HapMap
Illu318
rs6426749
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
NBPF3
USP48
CELA3B
ZBTB40
EPHB2
KDM1A
HNRNPR
ALPL
LDLRAD2
CDC42
EPHA8
LUZP1
RAP1GAP
HSPG2
WNT4
C1QA
HTR1D
CELA3A
C1QC
ZNF436
HSPC157
C1QB
C1orf213
TCEA3
22
22.5
23
23.5
position on chr1 (Mb)

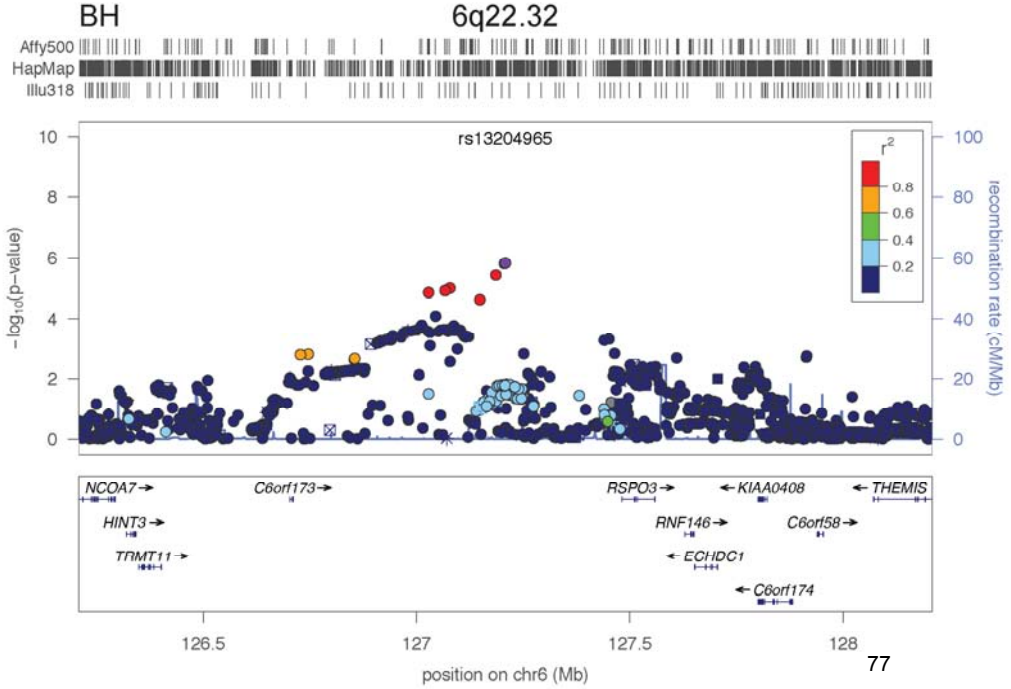

BC
2p16.2
Affy500
HapMap
Illu318
rs4233949
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ASB3
PSME4
ACYP2
SPTBN1
EML6
C2orf63
LOC100302652
TSPYL6
RPL23AP32
RTN4
RPS27A
CHAC2
C2orf73
MTIF2
ERLEC1
GPR75
CCDC88A
54
54.5
55
55.5
position on chr2 (Mb)

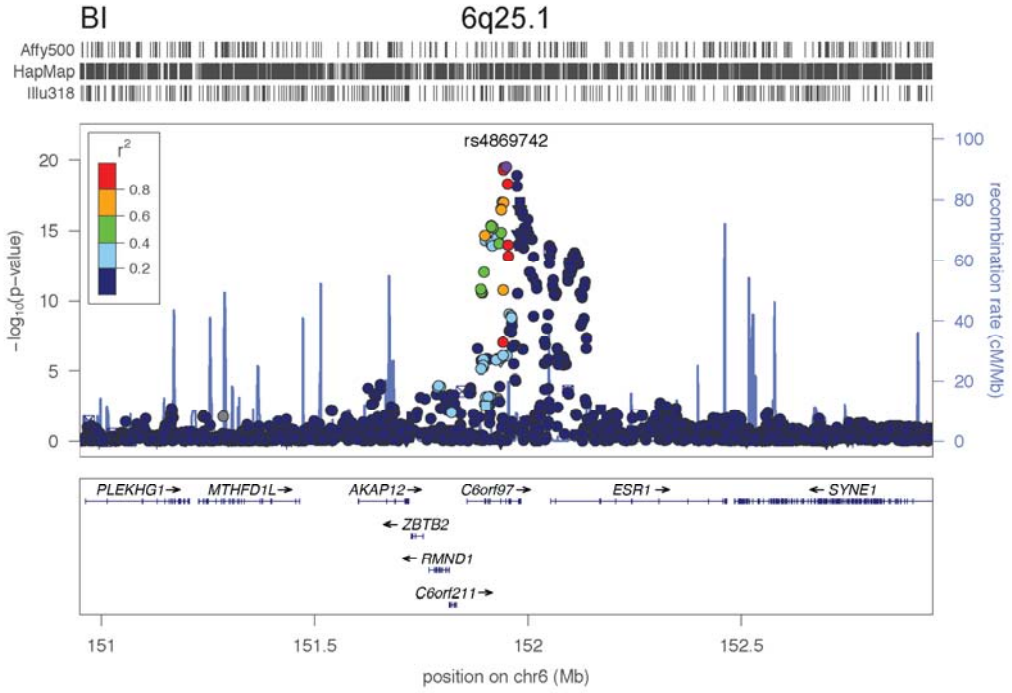

BD
2q24.3
Affy500
HapMap
Illu318
rs1346004
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
COBLL1
SCN3A
TTC21B
SCN9A
SLC38A11
SCN2A
GALNT3
SCN1A
SCN7A
165.5
166
166.5
167
position on chr2 (Mb)

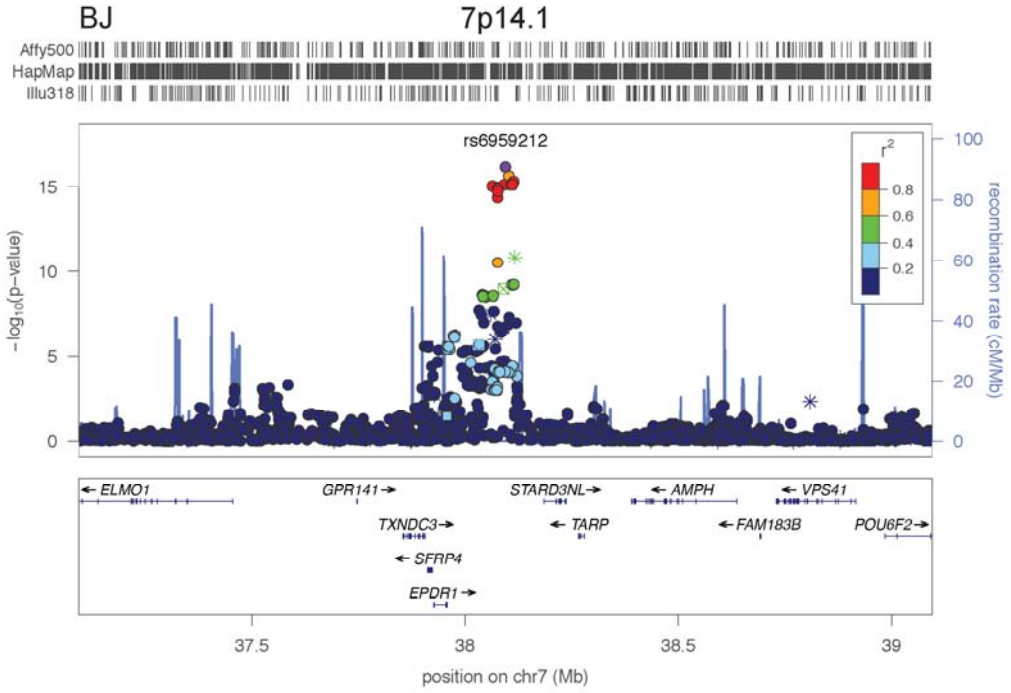

BE
3p22.1
Affy500
HapMap
Illu318
rs430727
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
MYRIP
ENTPD3
CTNNB1
EIF1B
ZNF620
ULK4
RPL14
ZNF619
ZNF621
40.5
41
41.5
42
position on chr3 (Mb)

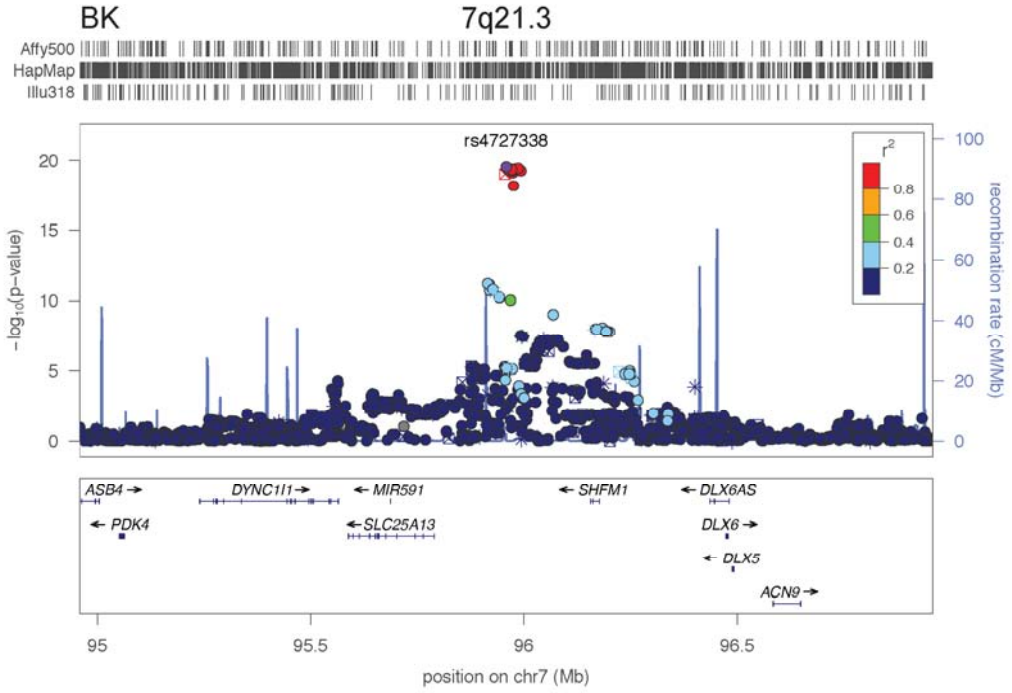

BF
4q22.1
Affy500
HapMap
Illu318
rs6532023
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
C4orf36
KLHL8
NUDT9
DMP1
MEPE
PKD2
PPM1K
HERC5
NAP1L5
AFF1
HSD17B13
DSPP
IBSP
SPP1
HERC6
HERC3
HSD17B11
ABCG2
PIGY
FAM13A
SPARCL1
FAM13AOS
88
88.5
89
89.5
position on chr4 (Mb)

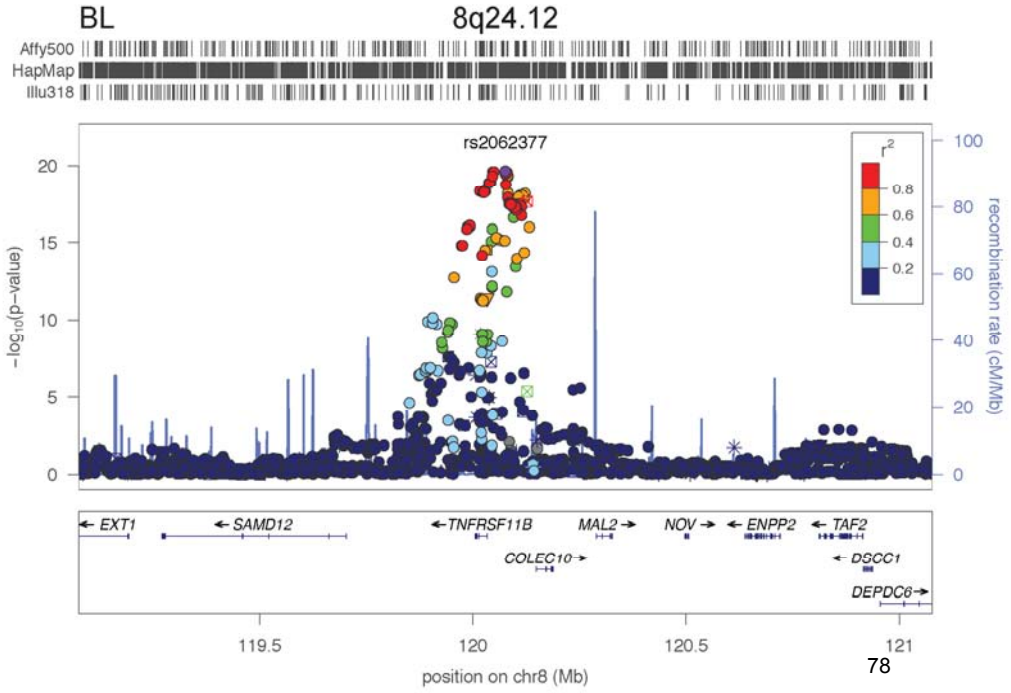

BG
5q14.3
Affy500
HapMap
Illu318
rs1366594
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
TMEM161B
LOC645323
MEF2C
87.5
88
88.5
89
position on chr5 (Mb)

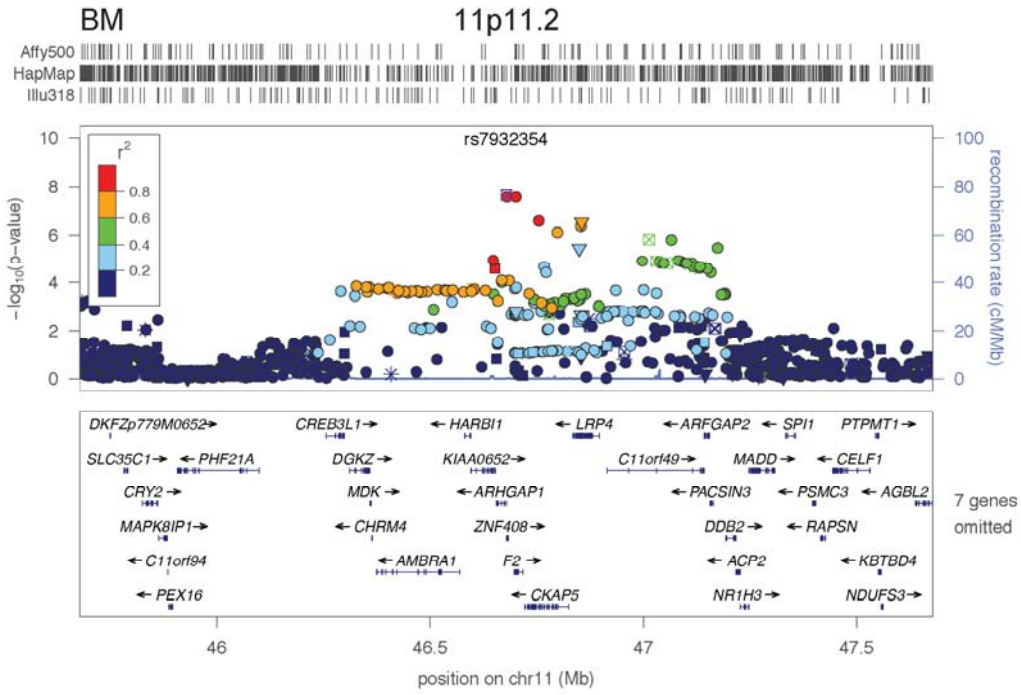

BH
6q22.32
Affy500
HapMap
Illu318
rs13204965
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
NCOA7
C6orf173
RSPO3
KIAA0408
THEMIS
HINT3
RNF146
C6orf58
ECHDC1
C6orf174
126.5
127
127.5
128
position on chr6 (Mb)

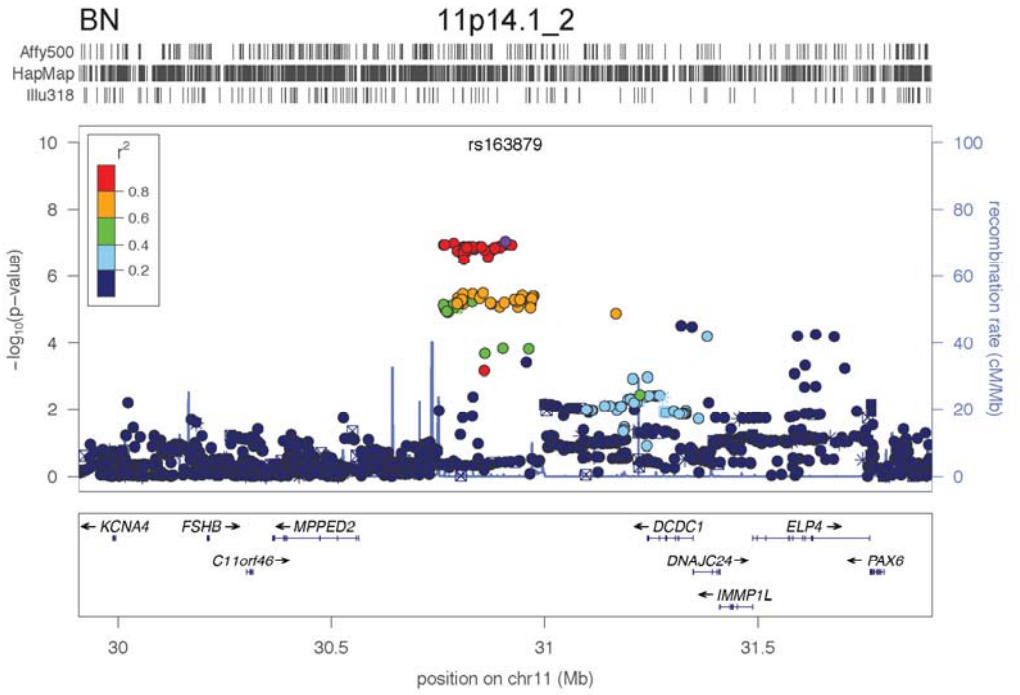

BI
6q25.1
Affy500
HapMap
Illu318
rs4869742
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
PLEKHG1
MTHFD1L
AKAP12
C6orf97
ESR1
SYNE1
ZBTB2
RMND1
C6orf211
151
151.5
152
152.5
position on chr6 (Mb)

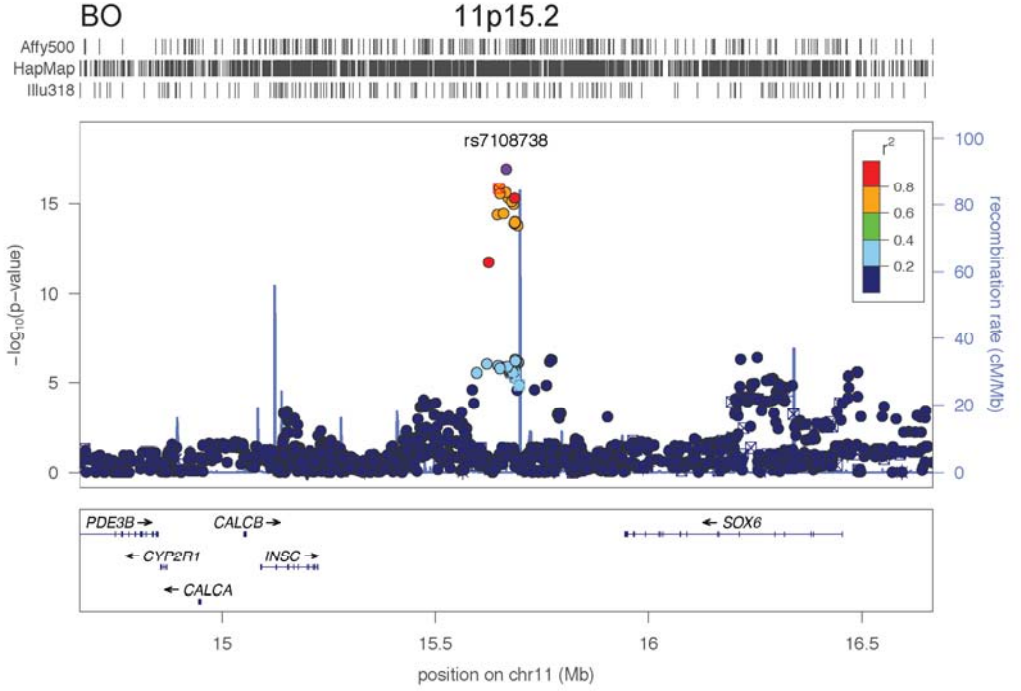

BJ
7p14.1
Affy500
HapMap
Illu318
rs6959212
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ELMO1
GPR141
STARD3NL
AMPH
VPS41
TXNDC3
TARP
FAM183B
POU6F2
SFRP4
EPDR1
37.5
38
38.5
39
position on chr7 (Mb)

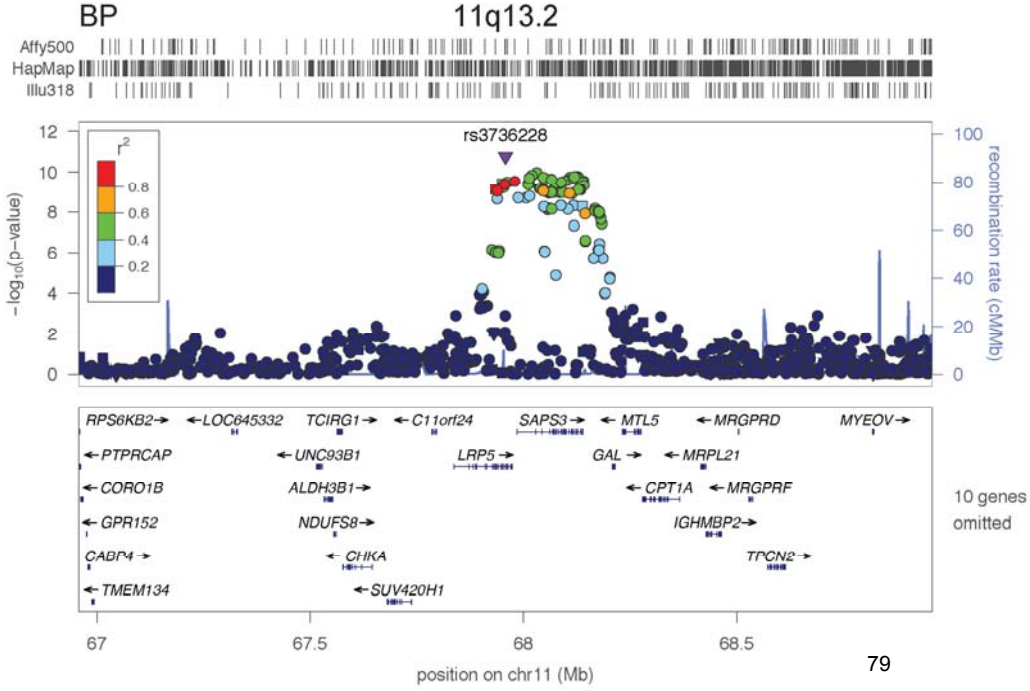

BK
7q21.3
Affy500
HapMap
Illu318
rs4727338
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
ASB4
DYNC1I1
MIR591
SHFM1
DLX6AS
PDK4
SLC25A13
DLX6
DLX5
ACN9
95
95.5
96
96.5
position on chr7 (Mb)

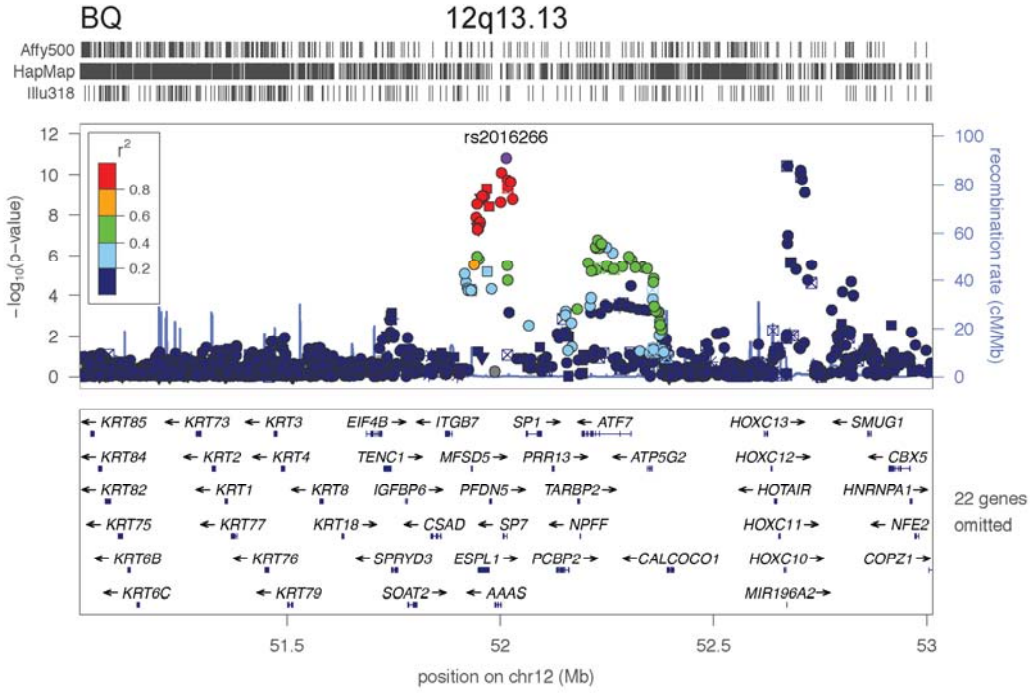

BL
8q24.12
Affy500
HapMap
Illu318
rs2062377
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
EXT1
SAMD12
TNFRSF11B
MAL2
NOV
ENPP2
TAF2
COLEC10
DSCC1
DEPDC6
119.5
120
120.5
121
position on chr8 (Mb)

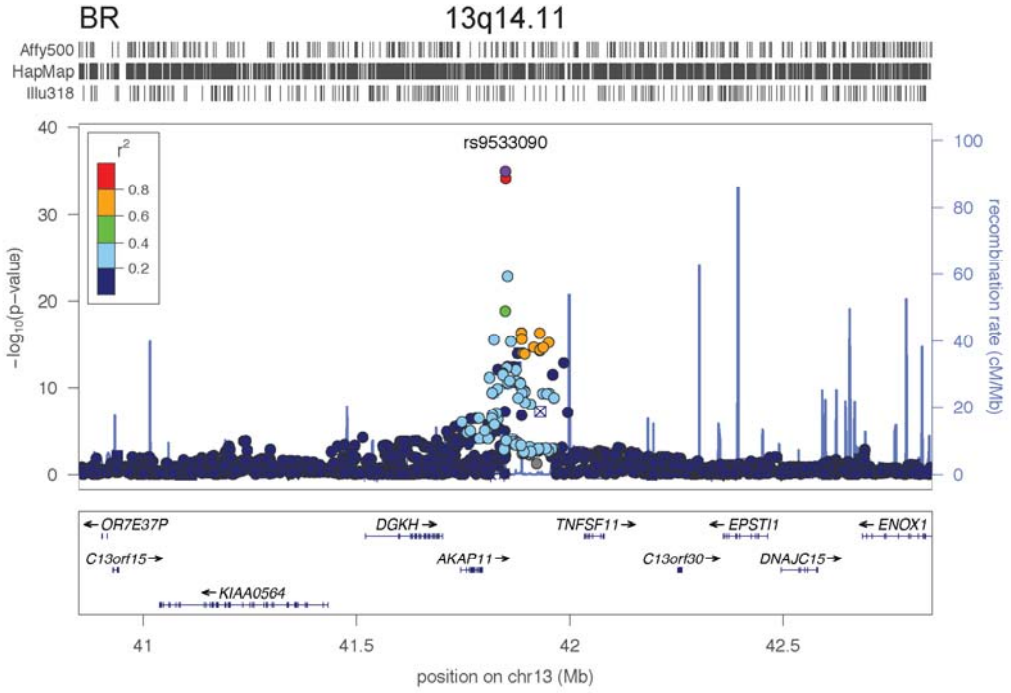

BM
11p11.2
Affy500
HapMap
Illu318
rs7932354
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
DKFZp779M0652
CREB3L1
HARBI1
LRP4
ARFGAP2
SPI1
PTPMT1
SLC35C1
PHF21A
DGKZ
KIAA0652
C11orf49
MADD
CELF1
CRY2
MDK
ARHGAP1
PACSIN3
PSMC3
AGBL2
MAPK8IP1
CHRM4
ZNF408
DDB2
RAPSN
C11orf94
AMBRA1
F2
ACP2
KBTBD4
PEX16
CKAP5
NR1H3
NDUFS3
7 genes omitted
position on chr11 (Mb)

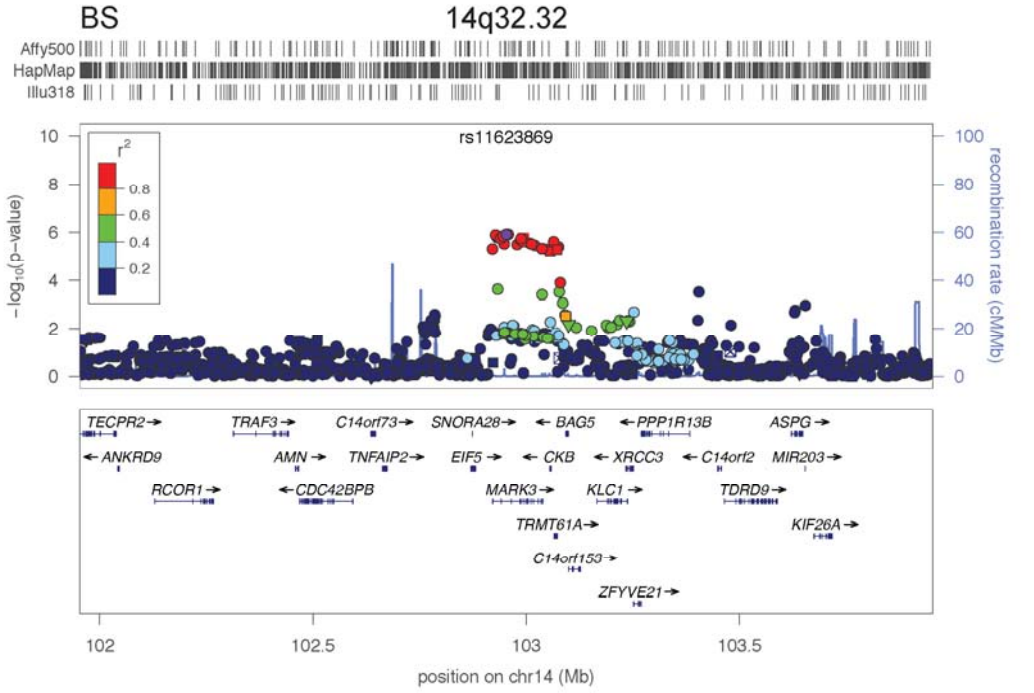

BN
11p14.1_2
Affy500
HapMap
Illu318
rs163879
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
KCNA4
FSHB
MPPED2
DCDC1
ELP4
C11orf46
DNAJC24
PAX6
IMMP1L
position on chr11 (Mb)

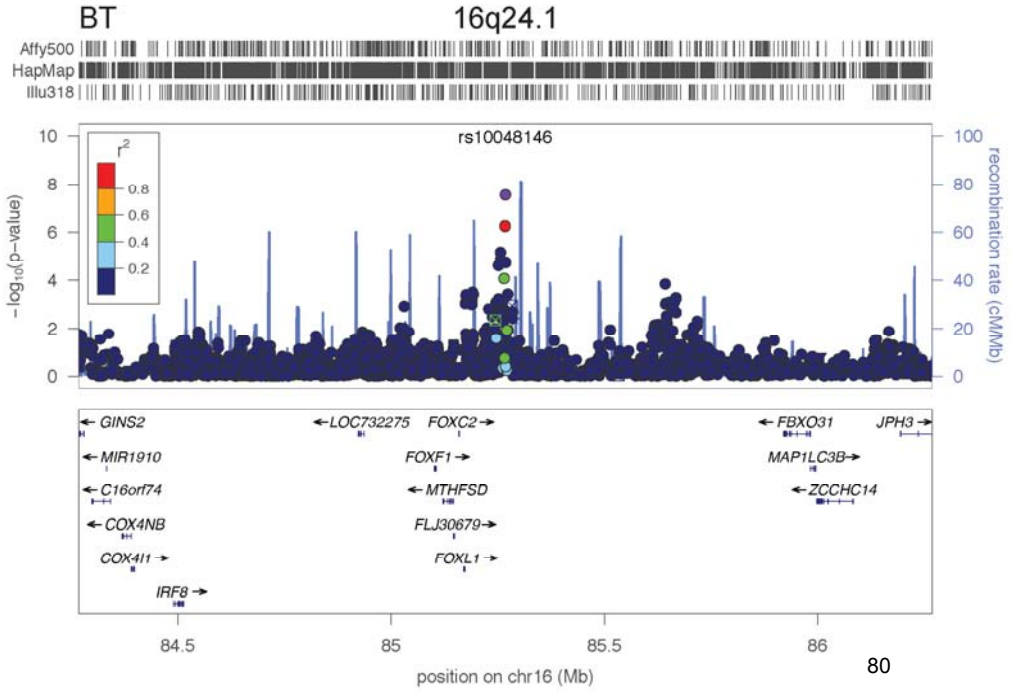

BO
11p15.2
Affy500
HapMap
Illu318
rs7108738
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
PDE3B
CALCB
SOX6
CYP2R1
INSC
CALCA
position on chr11 (Mb)

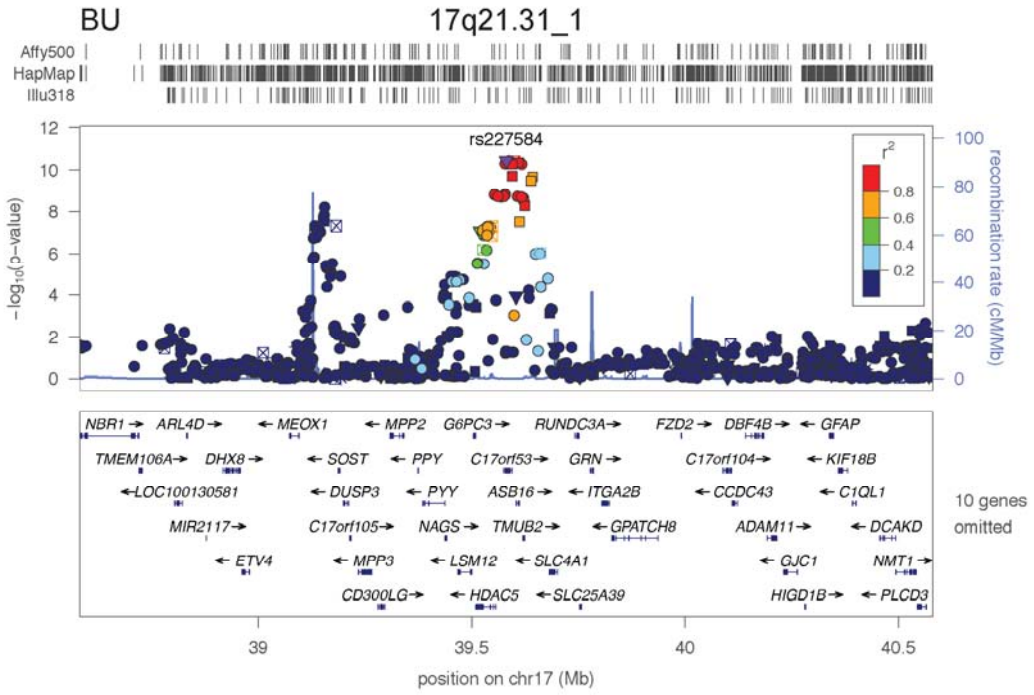

BP
11q13.2
Affy500
HapMap
Illu318
rs3736228
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
RPS6KB2
LOC645332
TCIRG1
C11orf24
SAPS3
MTL5
MRGPRD
MYEOV
PTPRCAP
UNC93B1
LRP5
GAL
MRPL21
CORO1B
ALDH3B1
CPT1A
MRGPRF
GPR152
NDUFS8
IGHMBP2
CHKA
TMEM134
SUV420H1
10 genes omitted
position on chr11 (Mb)

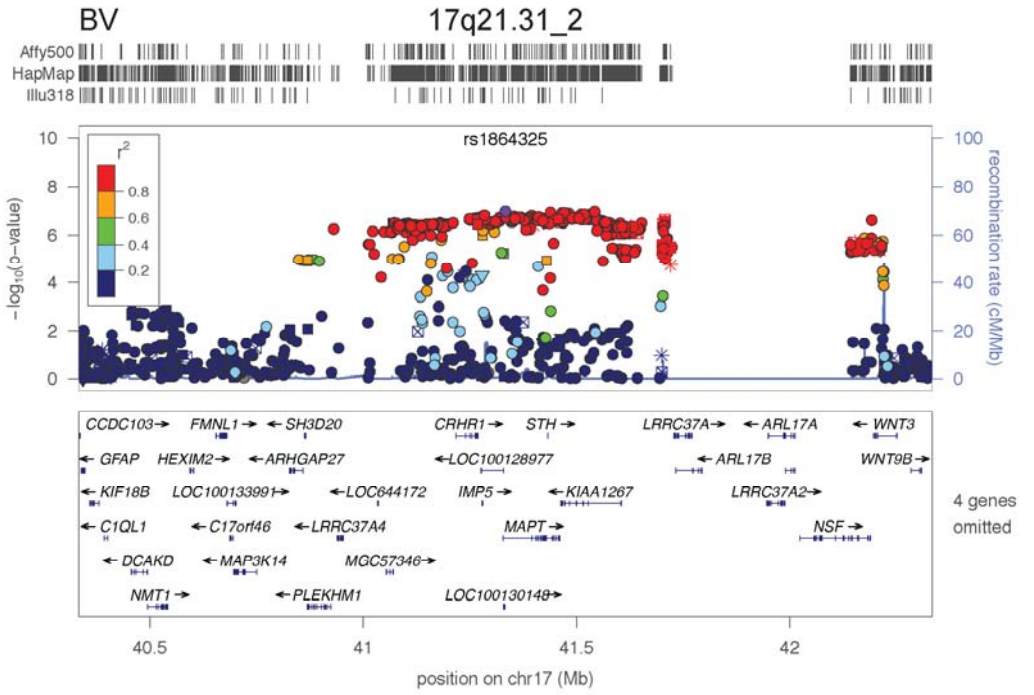

BQ
12q13.13
Affy500
HapMap
Illu318
rs2016266
r²
0.8
0.6
0.4
0.2
−log10(p−value)
recombination rate (cM/Mb)
KRT85 KRT73 KRT3 EIF4B ITGB7 SP1 ATF7 HOXC13 SMUG1
KRT84 KRT2 KRT4 TENC1 MFSD5 PRR13 ATP5G2 HOXC12 CBX5
KRT82 KRT1 KRT8 IGFBP6 PFDN5 TARBP2 HOTAIR HNRNPA1
KRT75 KRT77 KRT18 CSAD SP7 NPFF HOXC11 NFE2
KRT6B KRT76 SPRYD3 ESPL1 PCBP2 CALCOCO1 HOXC10 COPZ1
KRT6C KRT79 SOAT2 AAAS MIR196A2
22 genes omitted
position on chr12 (Mb)

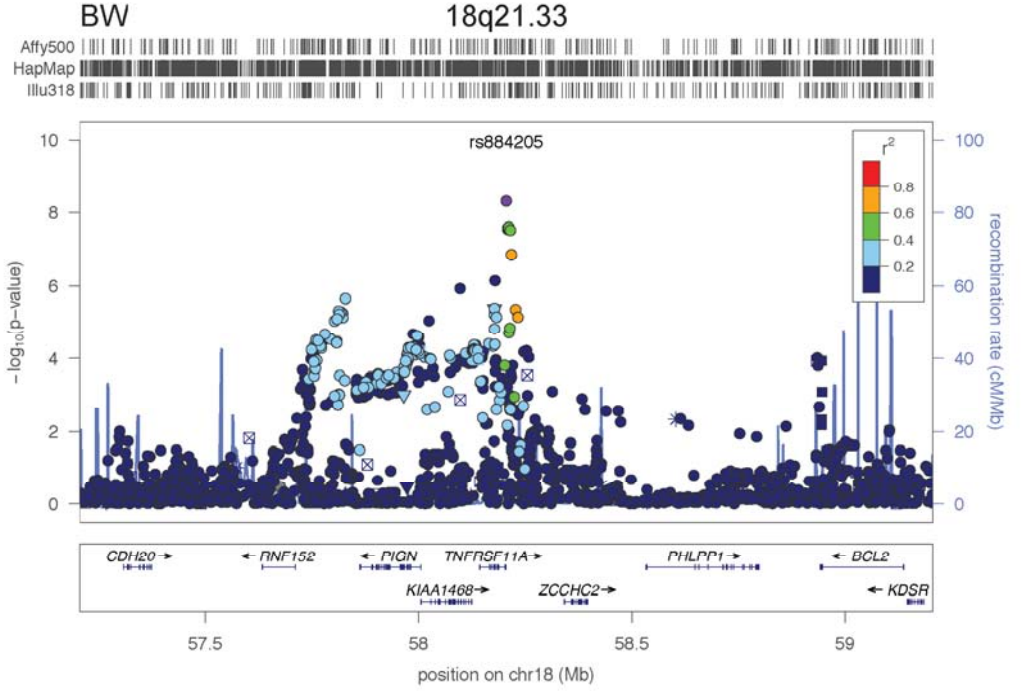

BR
13q14.11
Affy500
HapMap
Illu318
rs9533090
r²
−log10(p−value)
recombination rate (cM/Mb)
OR7E37P DGKH TNFSF11 EPSTI1 ENOX1
C13orf15 AKAP11 C13orf30 DNAJC15
KIAA0564
position on chr13 (Mb)

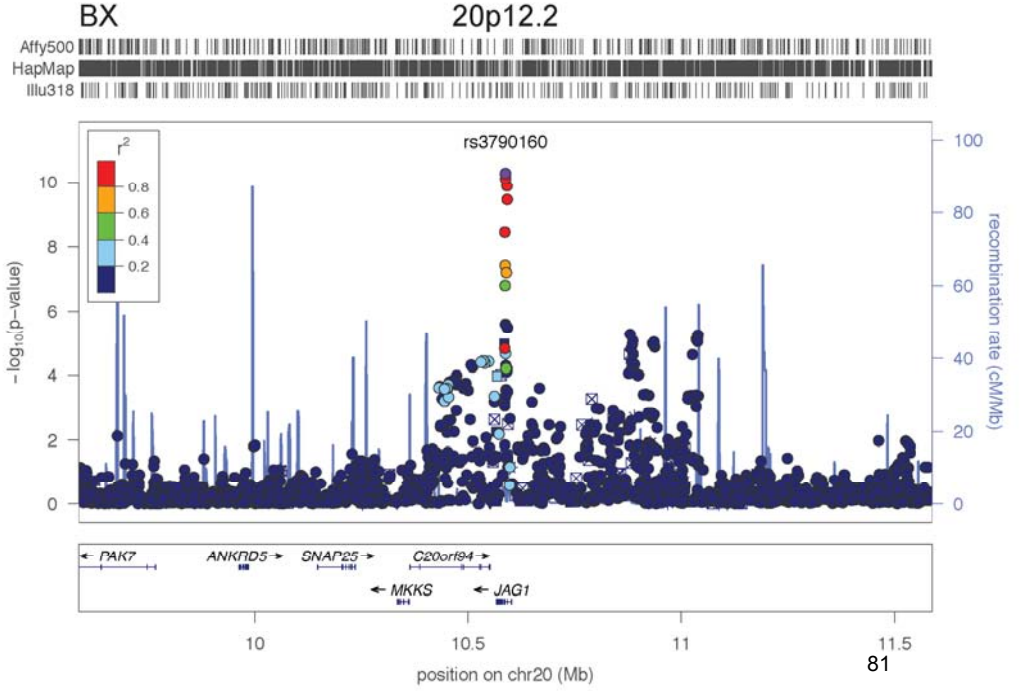

BS
14q32.32
Affy500
HapMap
Illu318
rs11623869
r²
−log10(p−value)
recombination rate (cM/Mb)
TECPR2 TRAF3 C14orf73 SNORA28 BAG5 PPP1R13B ASPG
ANKRD9 AMN TNFAIP2 EIF5 CKB XRCC3 C14orf2 MIR203
RCOR1 CDC42BPB MARK3 KLC1 TDRD9
TRMT61A KIF26A
C14orf153
ZFYVE21
position on chr14 (Mb)


BT
16q24.1
Affy500
HapMap
Illu318
rs10048146
r²
−log10(p−value)
recombination rate (cM/Mb)
GINS2 LOC732275 FOXC2 FBXO31 JPH3
MIR1910 FOXF1 MAP1LC3B
C16orf74 MTHFSD ZCCHC14
COX4NB FLJ30679
COX4I1 FOXL1
IRF8
position on chr16 (Mb)

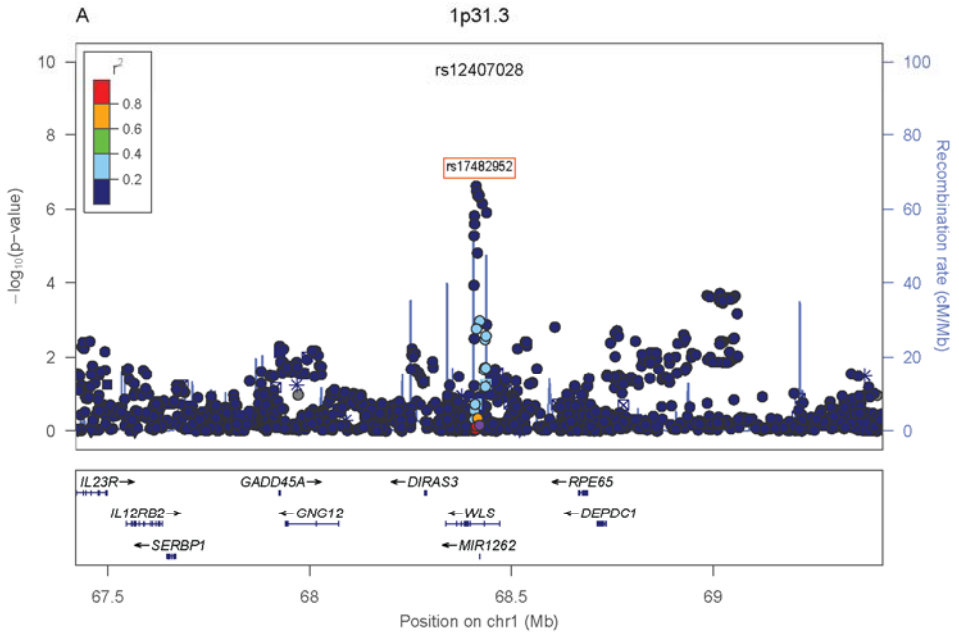

BU
17q21.31_1
Affy500
HapMap
Illu318
rs227584
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
NBR1→ ARL4D→ ←MEOX1 ←MPP2 G6PC3→ RUNDC3A→ FZD2→ DBF4B→ ←GFAP
TMEM106A→ DHX8→ ←SOST ←PPY C17orf53→ GRN→ C17orf104→ ←KIF18B
←LOC100130581 ←DUSP3 ←PYY ASB16→ ←ITGA2B ←CCDC43 ←C1QL1
MIR2117→ C17orf105→ NAGS→ TMUB2→ ←GPATCH8 ADAM11→ ←DCAKD
←ETV4 ←MPP3 ←LSM12 ←SLC4A1 ←GJC1 NMT1→
CD300LG→ ←HDAC5 ←SLC25A39 HIGD1B→ ←PLCD3
10 genes omitted
position on chr17 (Mb)

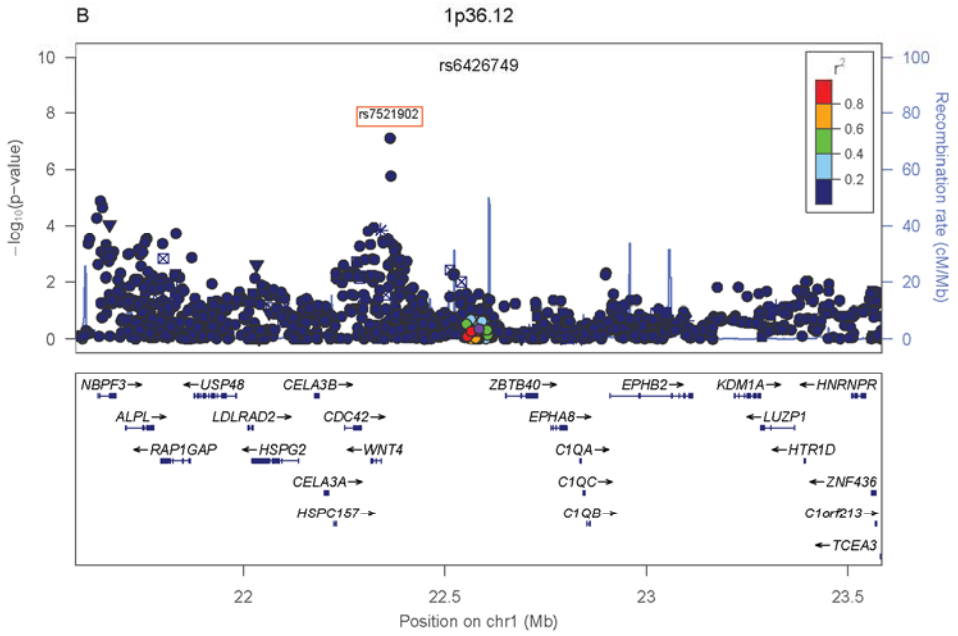

BV
17q21.31_2
Affy500
HapMap
Illu318
rs1864325
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
CCDC103→ FMNL1→ ←SH3D20 CRHR1→ STH→ LRRC37A→ ←ARL17A ←WNT3
←GFAP HEXIM2→ ←ARHGAP27 ←LOC100128977 ←ARL17B WNT9B→
←KIF18B LOC100133991→ ←LOC644172 IMP5→ ←KIAA1267 LRRC37A2→
←C1QL1 ←C17orf46 ←LRRC37A4 MAPT→ NSF→
←DCAKD ←MAP3K14 MGC57346→
NMT1→ ←PLEKHM1 LOC100130148→
4 genes omitted
position on chr17 (Mb)

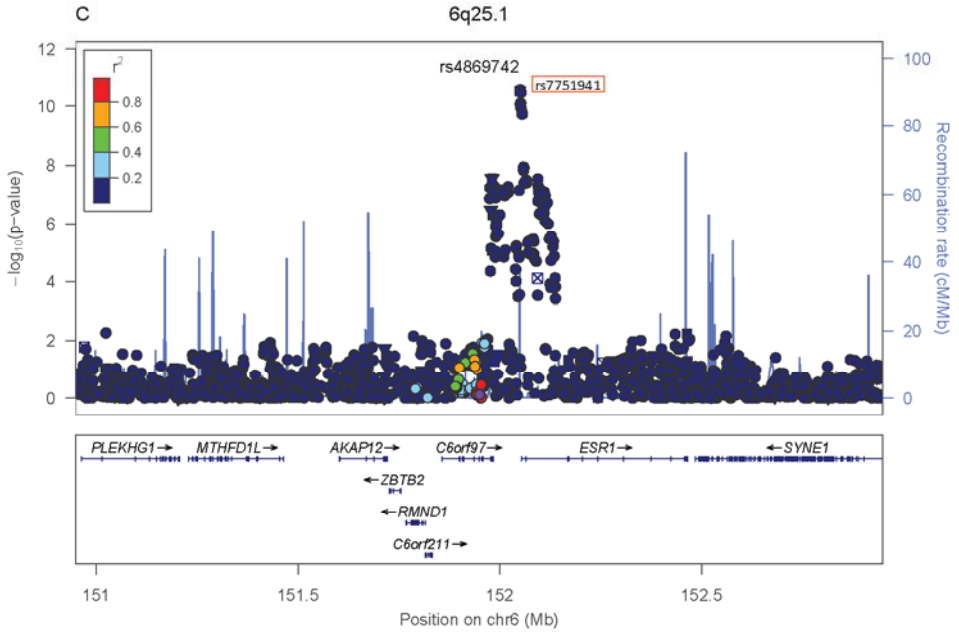

BW
18q21.33
Affy500
HapMap
Illu318
rs884205
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
CDH20→ ←RNF152 ←PIGN TNFRSF11A→ PHLPP1→ ←BCL2
KIAA1468→ ZCCHC2→ ←KDSR
position on chr18 (Mb)

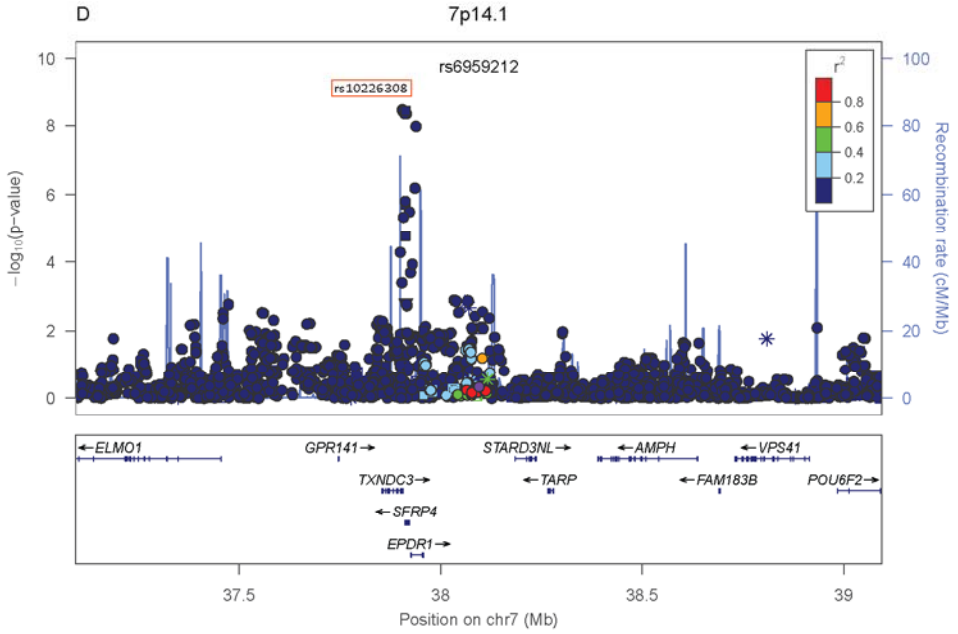

BX
20p12.2
Affy500
HapMap
Illu318
rs3790160
r^2
0.8
0.6
0.4
0.2
$-\log_{10}$(p-value)
recombination rate (cM/Mb)
←PAK7 ANKRD5→ SNAP25→ C20orf94→
←MKKS ←JAG1
position on chr20 (Mb)

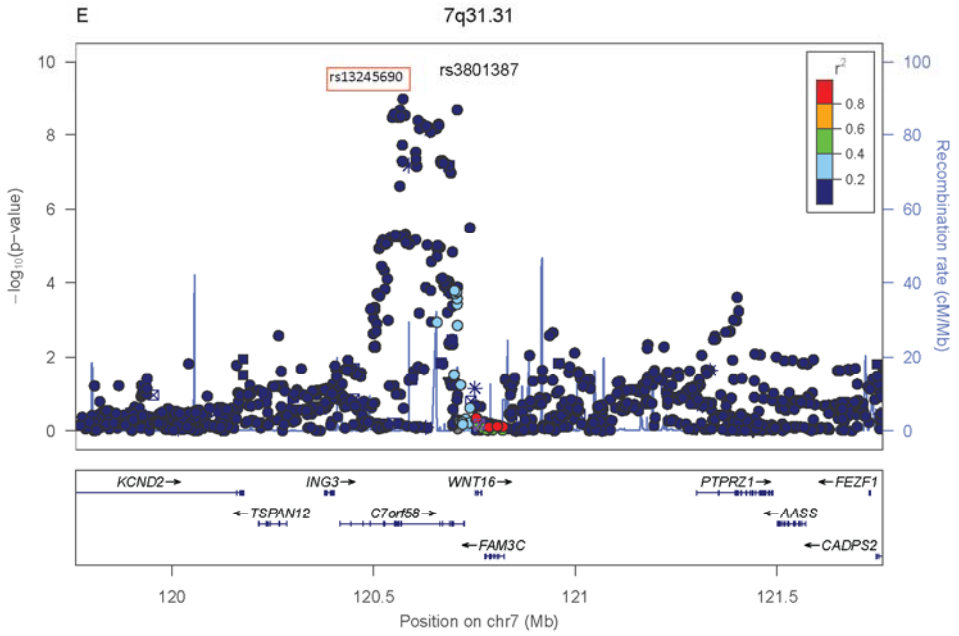
Supplementary Figure 4. Regional plots. Regional association plot for each of the 9 secondary signals after conditioning for the index SNP. The secondary signal is highlighted with a red box. A. 1p31.3, B. 1p36.12, C. 6q25.1, D. 7p14.1, E. 7q31.31, F. 12q13.13, G. 13q14.11, H. 16q12.1, I. 17q21.31.

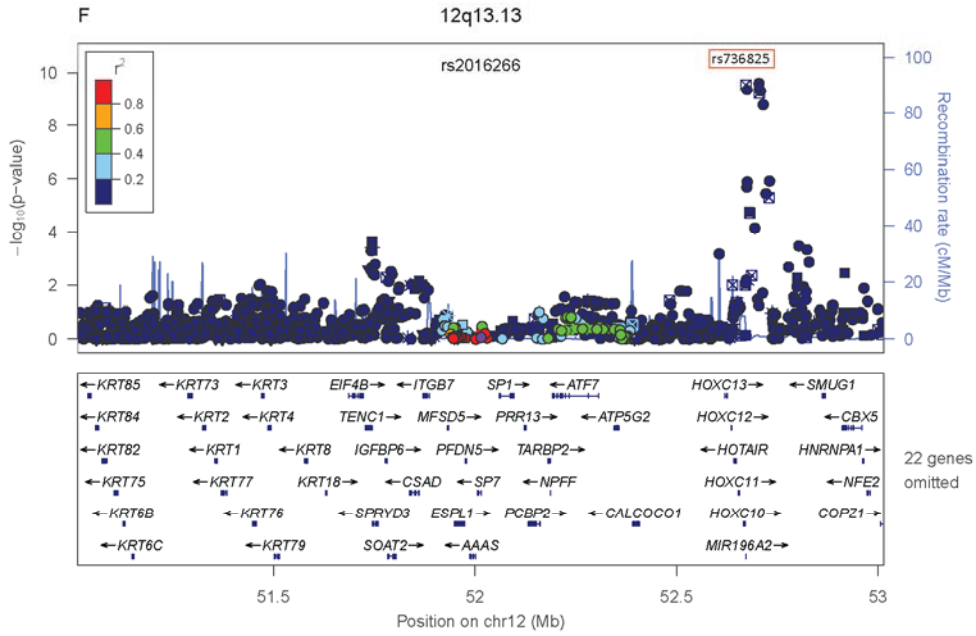

A
1p31.3
rs12407028
rs17482952
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
IL23R
GADD45A
DIRAS3
RPE65
IL12RB2
GNG12
WLS
DEPDC1
SERBP1
MIR1262
67.5
68
68.5
69
Position on chr1 (Mb)

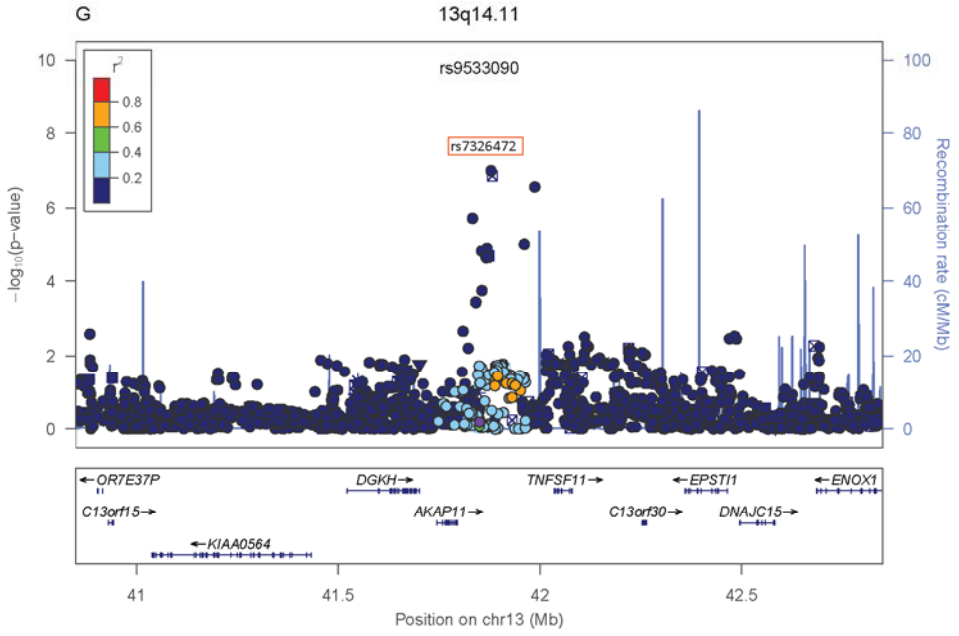

B
1p36.12
rs6426749
rs7521902
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
NBPF3
USP48
CELA3B
ZBTB40
EPHB2
KDM1A
HNRNPR
ALPL
LDLRAD2
CDC42
EPHA8
LUZP1
RAP1GAP
HSPG2
WNT4
C1QA
HTR1D
CELA3A
C1QC
ZNF436
HSPC157
C1QB
C1orf213
TCEA3
22
22.5
23
23.5
Position on chr1 (Mb)

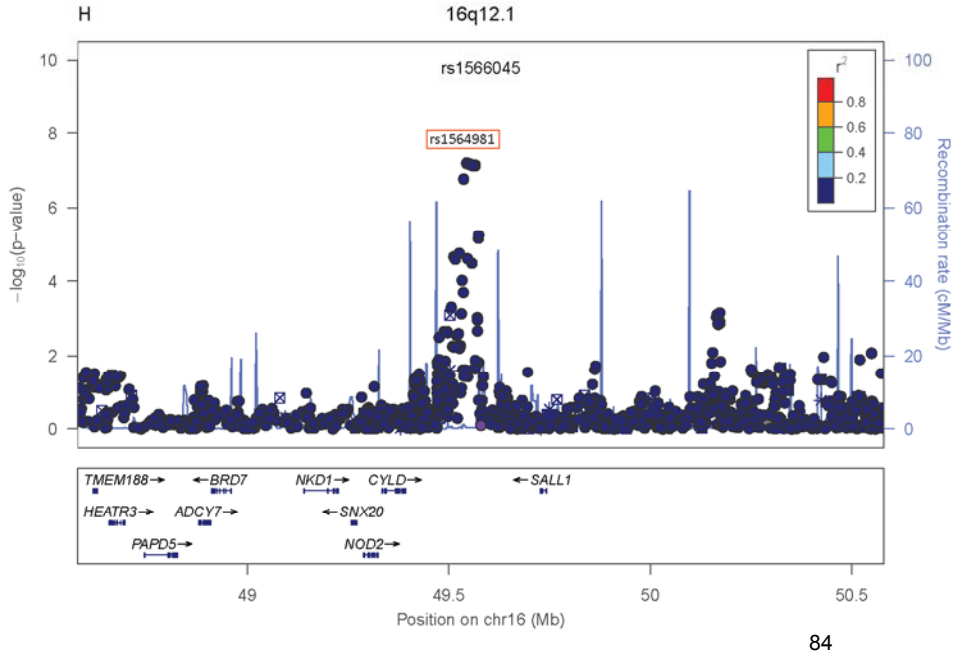

C
6q25.1
rs4869742
rs7751941
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
PLEKHG1
MTHFD1L
AKAP12
C6orf97
ESR1
SYNE1
ZBTB2
RMND1
C6orf211
151
151.5
152
152.5
Position on chr6 (Mb)

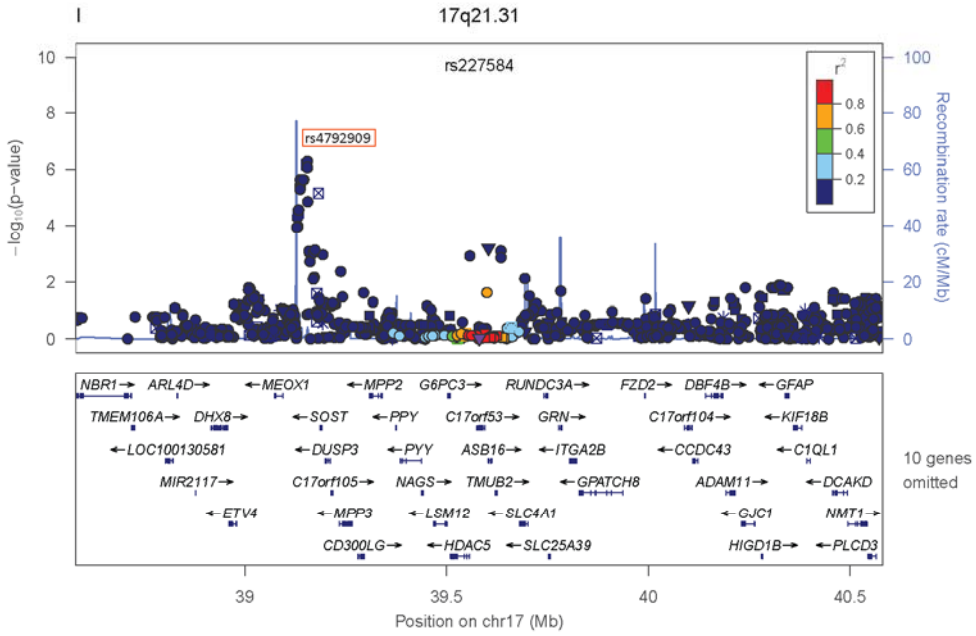

D
7p14.1
rs6959212
rs10226308
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
ELMO1
GPR141
STARD3NL
AMPH
VPS41
TXNDC3
TARP
FAM183B
POU6F2
SFRP4
EPDR1
37.5
38
38.5
39
Position on chr7 (Mb)


E
7q31.31
rs13245690
rs3801387
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
KCND2→
ING3→
WNT16→
PTPRZ1→
FEZF1
TSPAN12
C7orf58→
AASS
FAM3C
CADPS2
Position on chr7 (Mb)

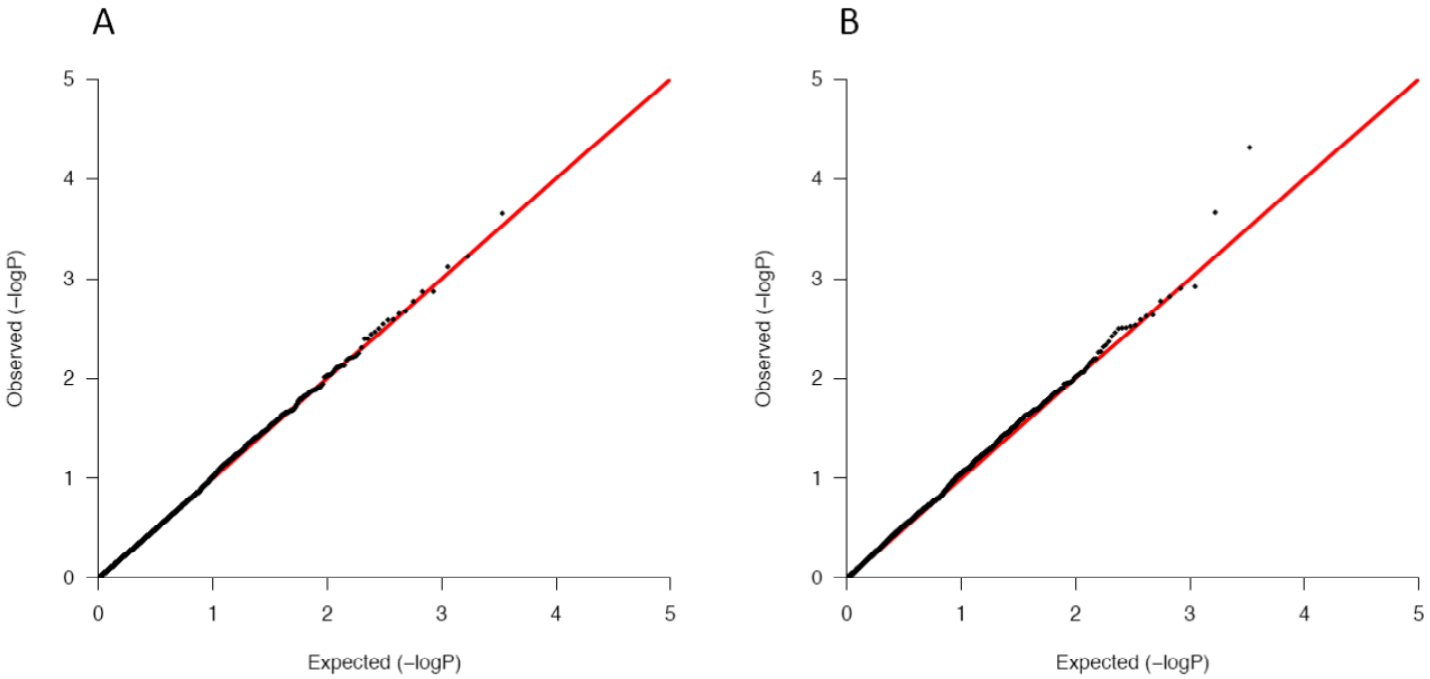

F
12q13.13
rs2016266
rs736825
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
KRT85 KRT73 KRT3 EIF4B ITGB7 SP1 ATF7 HOXC13 SMUG1
KRT84 KRT2 KRT4 TENC1 MFSD5 PRR13 ATP5G2 HOXC12 CBX5
KRT82 KRT1 KRT8 IGFBP6 PFDN5 TARBP2 HOTAIR HNRNPA1
KRT75 KRT77 KRT18 CSAD SP7 NPFF HOXC11 NFE2
KRT6B KRT76 SPRYD3 ESPL1 PCBP2 CALCOCO1 HOXC10 COPZ1
KRT6C KRT79 SOAT2 AAAS MIR196A2
22 genes omitted
Position on chr12 (Mb)


G
13q14.11
rs9533090
rs7326472
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
OR7E37P
DGKH→
TNFSF11→
EPSTI1
ENOX1
C13orf15→
AKAP11→
C13orf30→
DNAJC15→
KIAA0564
Position on chr13 (Mb)


H
16q12.1
rs1566045
rs1564981
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
TMEM188→
BRD7
NKD1→
CYLD→
SALL1
HEATR3→
ADCY7→
SNX20
PAPD5→
NOD2→
Position on chr16 (Mb)

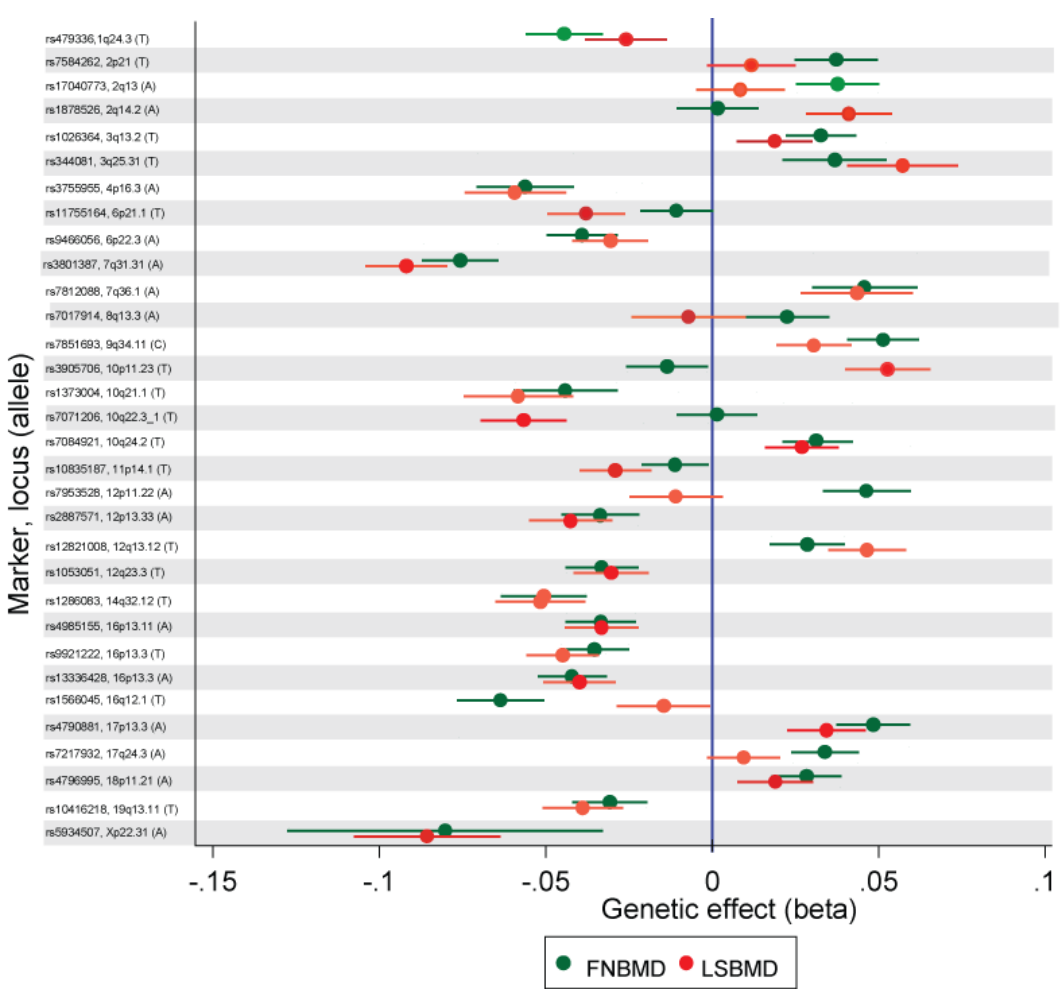

I
17q21.31
rs227584
rs4792909
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
NBR1 ARL4D MEOX1 MPP2 G6PC3 RUNDC3A FZD2 DBF4B GFAP
TMEM106A DHX8 SOST PPY C17orf53 GRN C17orf104 KIF18B
LOC100130581 DUSP3 PYY ASB16 ITGA2B CCDC43 C1QL1
MIR2117 C17orf105 NAGS TMUB2 GPATCH8 ADAM11 DCAKD
ETV4 MPP3 LSM12 SLC4A1 GJC1 NMT1
CD300LG HDAC5 SLC25A39 HIGD1B PLCD3
10 genes omitted
Position on chr17 (Mb)

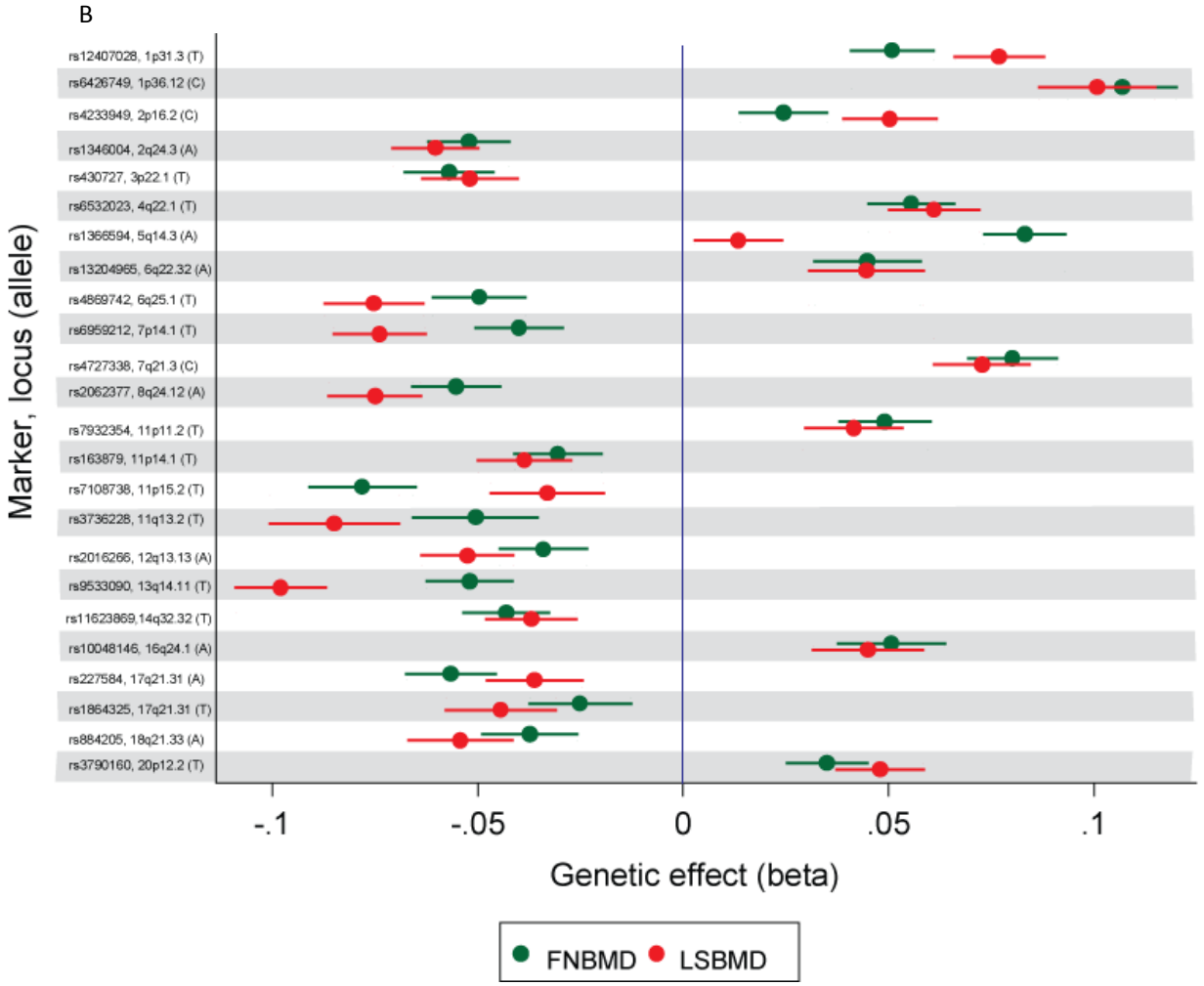
Supplementary Figure 5. QQ plots for gene-gene interaction results on 3311 SNP-SNP pairs. A) Results for FN-BMD. B) Results for LS-BMD



Supplementary Figure 6. *Summary genetic effect estimates for the significant BMD associations.* Genetic effect estimates for the 56 loci reaching GWS in the overall meta-analysis (17 discovery and 34 replication studies; n=50,933) are shown for FNBMD (green circles) and LSBMD (red circles). Significant genetic associations are shown separately for the 32 loci that were novel (A) and the 24 loci reported previously (B).

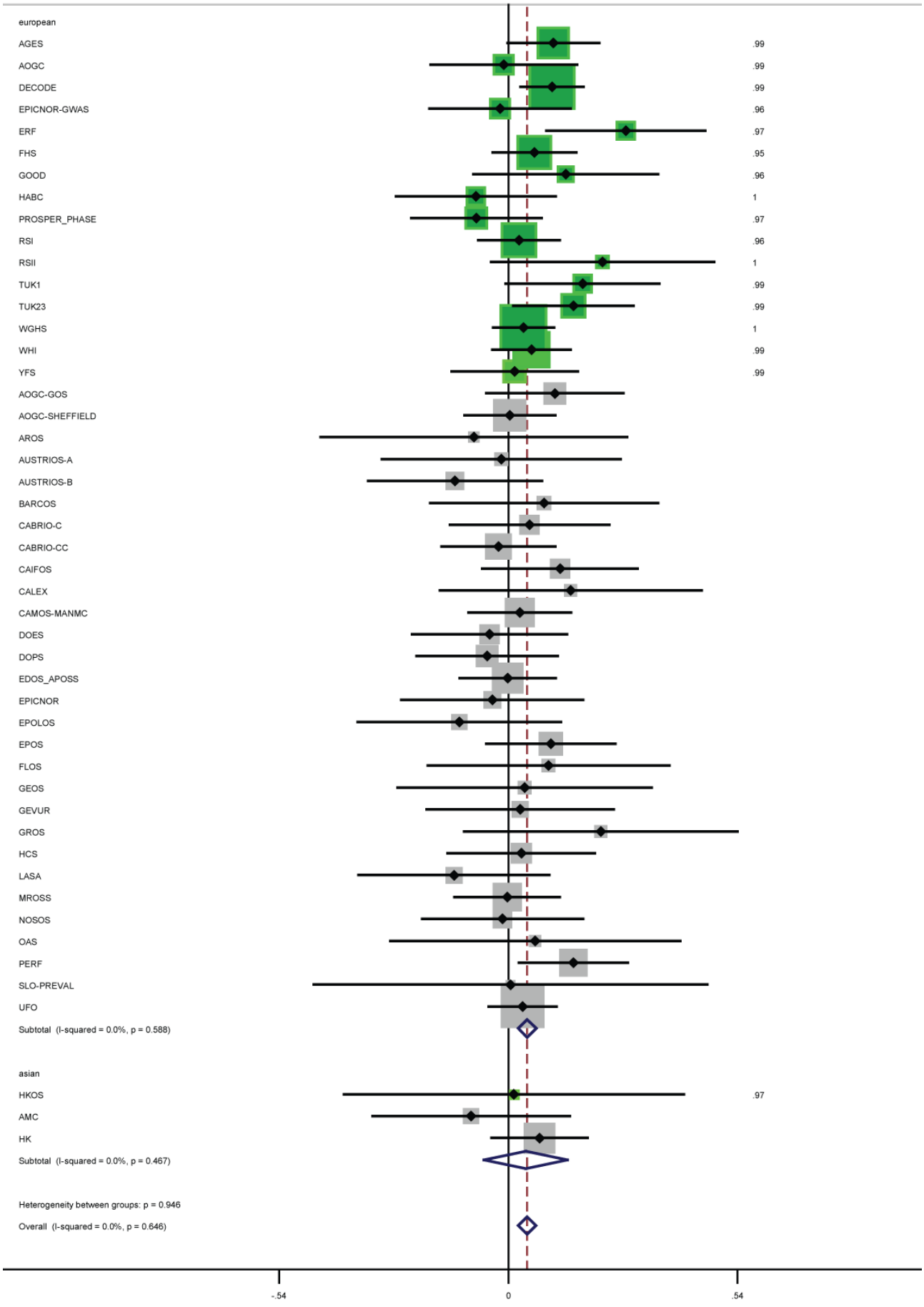
A



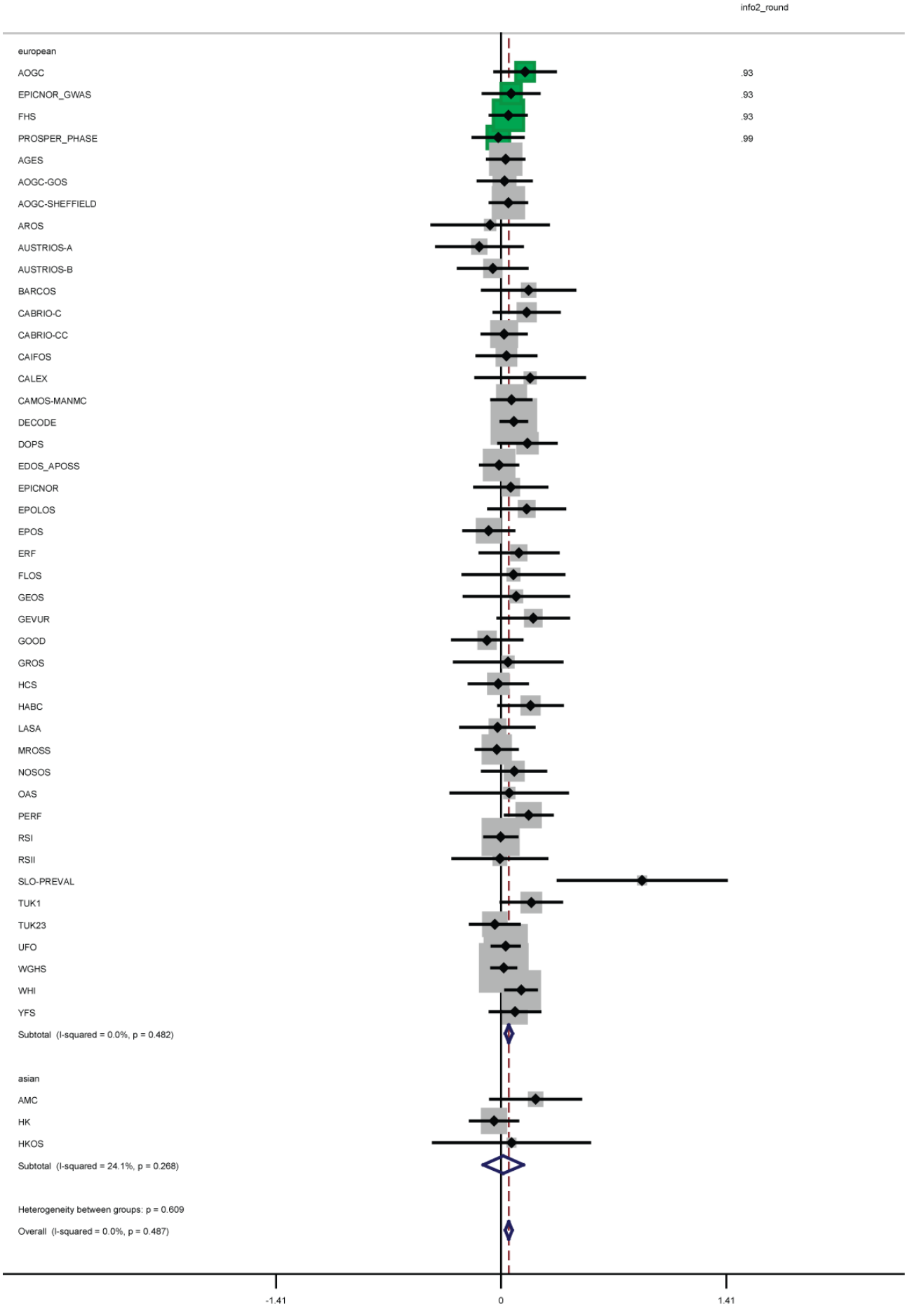

B
rs12407028, 1p31.3 (T)
rs6426749, 1p36.12 (C)
rs4233949, 2p16.2 (C)
rs1346004, 2q24.3 (A)
rs430727, 3p22.1 (T)
rs6532023, 4q22.1 (T)
rs1366594, 5q14.3 (A)
rs13204965, 6q22.32 (A)
rs4869742, 6q25.1 (T)
rs6959212, 7p14.1 (T)
rs4727338, 7q21.3 (C)
rs2062377, 8q24.12 (A)
rs7932354, 11p11.2 (T)
rs163879, 11p14.1 (T)
rs7108738, 11p15.2 (T)
rs3736228, 11q13.2 (T)
rs2016266, 12q13.13 (A)
rs9533090, 13q14.11 (T)
rs11623869,14q32.32 (T)
rs10048146, 16q24.1 (A)
rs227584, 17q21.31 (A)
rs1864325, 17q21.31 (T)
rs884205, 18q21.33 (A)
rs3790160, 20p12.2 (T)
Marker, locus (allele)
-.1
-.05
0
.05
.1
Genetic effect (beta)
FNBMD
LSBMD

Supplementary Figure 7. Forest plots for each one of the BMD loci associated with fracture risk (rs7851693, rs227584, rs163879, rs6959212, rs430727, rs1286083, rs4233949, rs6532023, rs3801387, rs4792909, rs6426749, rs4727338, rs3736228, rs7521902, rs1373004, rs4796995) and those loci that are part of the OPG/RANK/RANKL pathway (rs2062377, rs884205, rs9533090). Studies are grouped by ethnic group. Imputed markers are colored in green. The imputation quality score is displayed for imputed markers at the right column.

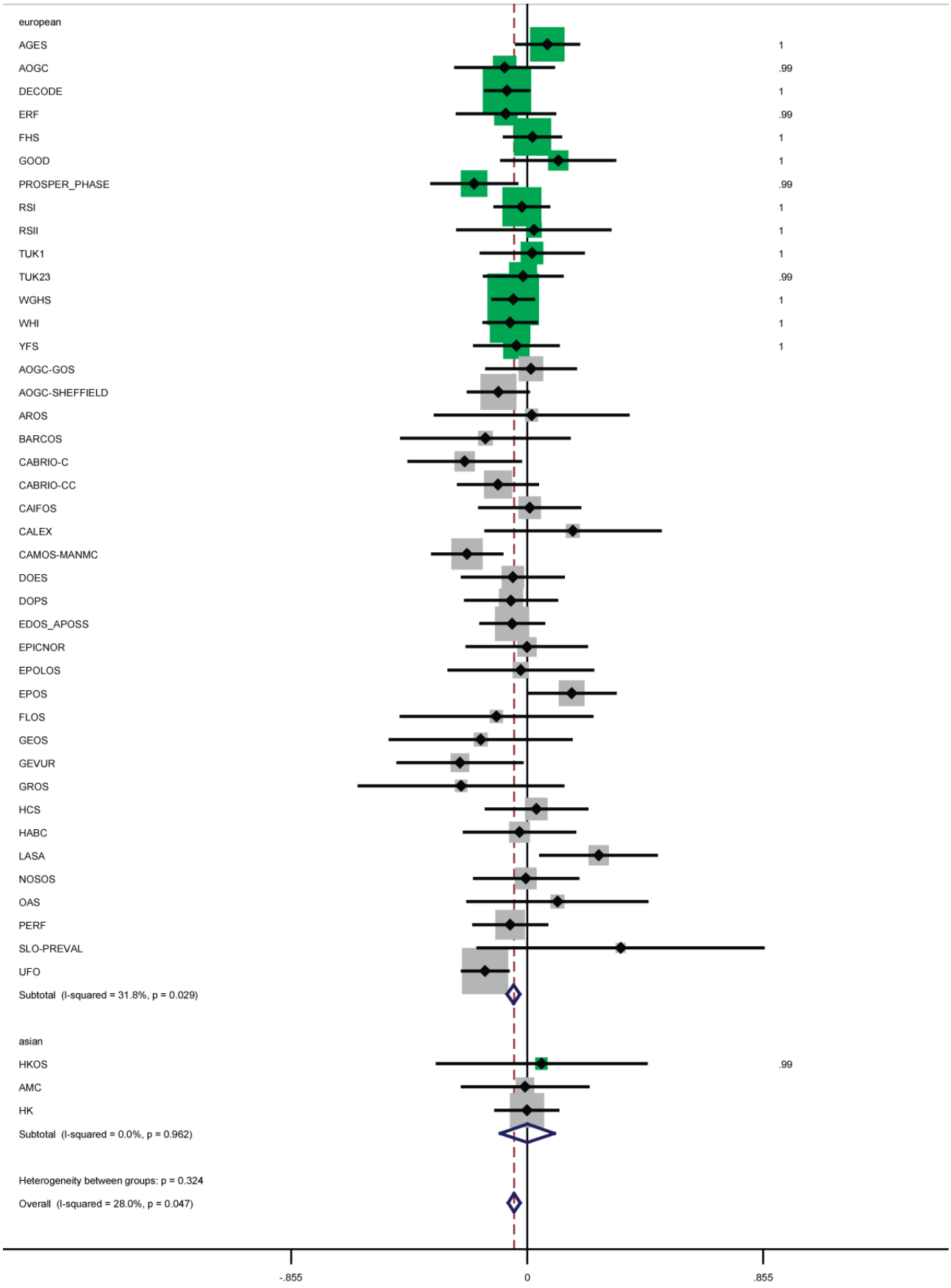
rs7851693


european
AGES
AOGC
DECODE
EPICNOR-GWAS
ERF
FHS
GOOD
HABC
PROSPER_PHASE
RSI
RSII
TUK1
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 0.0%, p = 0.588)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.467)
Heterogeneity between groups: p = 0.946
Overall (I-squared = 0.0%, p = 0.646)
.99
.99
.99
.96
.97
.95
.96
1
.97
.96
1
.99
.99
1
.99
.99
.97
-.54
0
.54

rs227584


info2_round
european
AOGC
EPICNOR_GWAS
FHS
PROSPER_PHASE
AGES
AOGC-GOS
AOGC-SHEFFIELD
AROS
AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DECODE
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
ERF
FLOS
GEOS
GEVUR
GOOD
GROS
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
RSI
RSII
SLO-PREVAL
TUK1
TUK23
UFO
WGHS
WHI
YFS
Subtotal (I-squared = 0.0%, p = 0.482)
asian
AMC
HK
HKOS
Subtotal (I-squared = 24.1%, p = 0.268)
Heterogeneity between groups: p = 0.609
Overall (I-squared = 0.0%, p = 0.487)
.93
.93
.93
.99
-1.41
0
1.41

rs163879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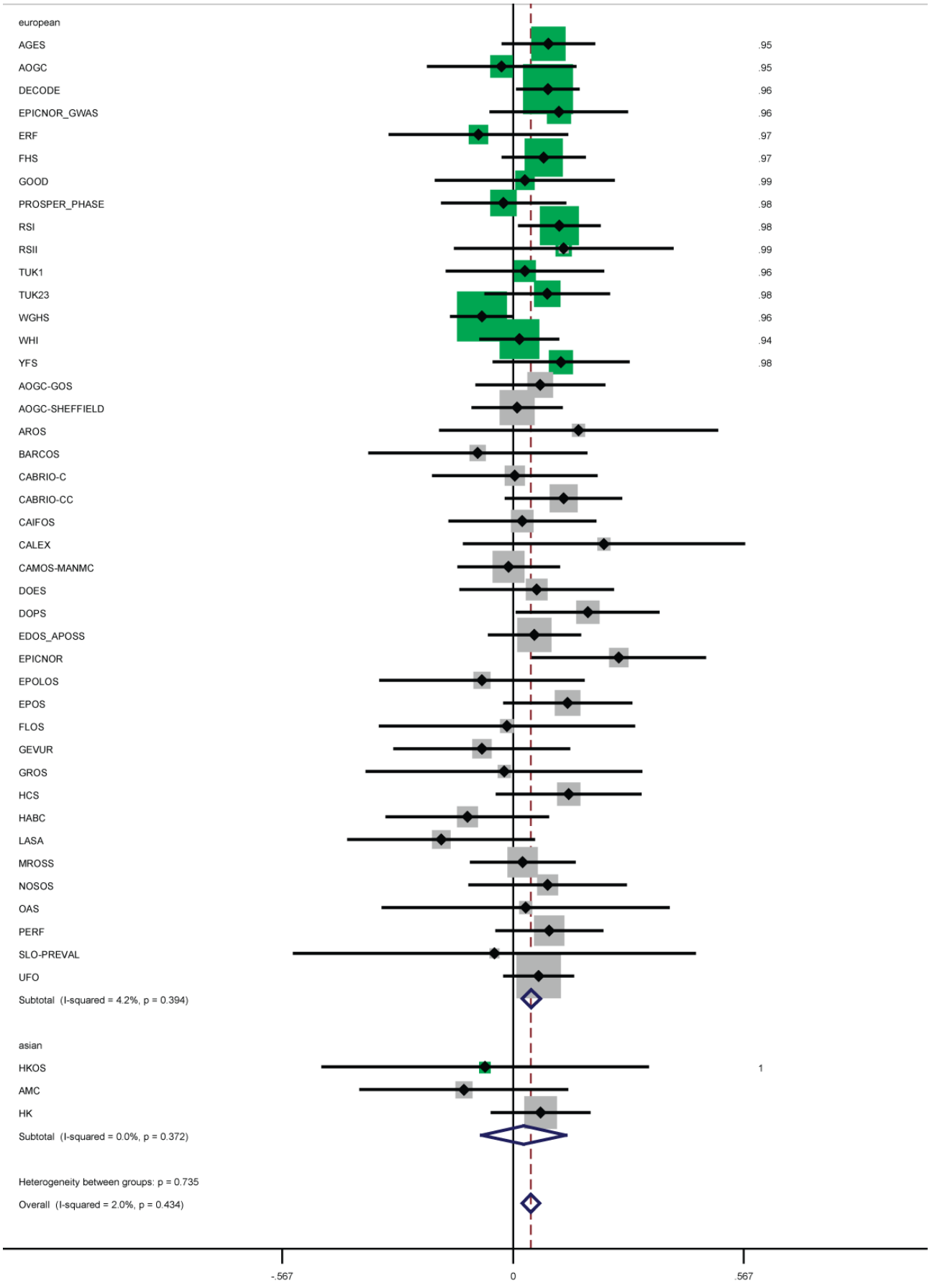
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
HABC
LASA
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 31.8%, p = 0.029)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.962)
Heterogeneity between groups: p = 0.324
Overall (I-squared = 28.0%, p = 0.047)
1
.99
1
.99
1
1
.99
1
1
1
.99
1
1
1
.99
-.855
0
.855

rs6959212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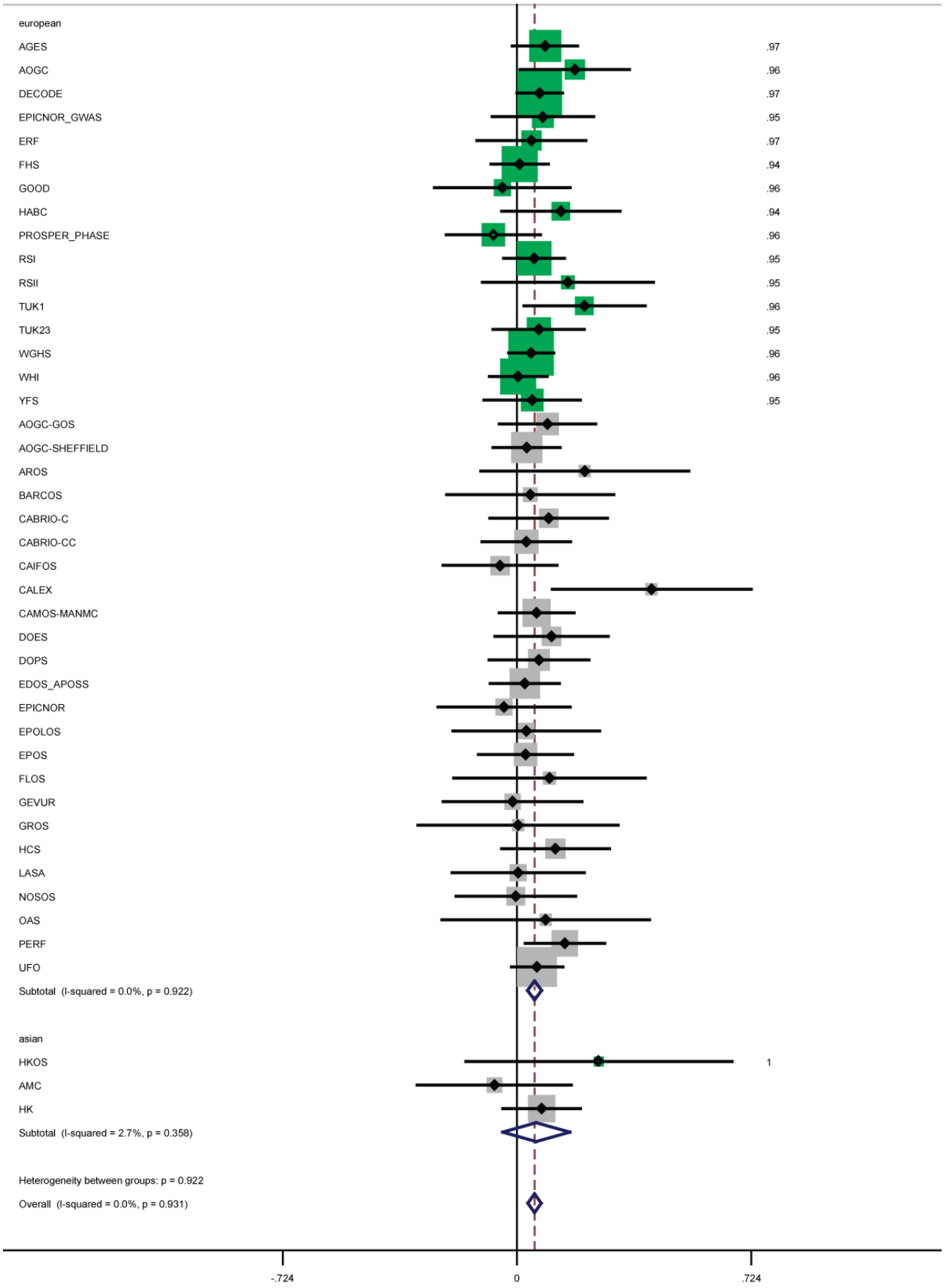
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEVUR
GROS
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 4.2%, p = 0.394)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.372)
Heterogeneity between groups: p = 0.735
Overall (I-squared = 2.0%, p = 0.434)
.95
.95
.96
.96
.97
.97
.99
.98
.98
.99
.96
.98
.96
.94
.98
1
-.567
0
.567

rs430727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ERF
FHS
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HABC
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RSI
RSII
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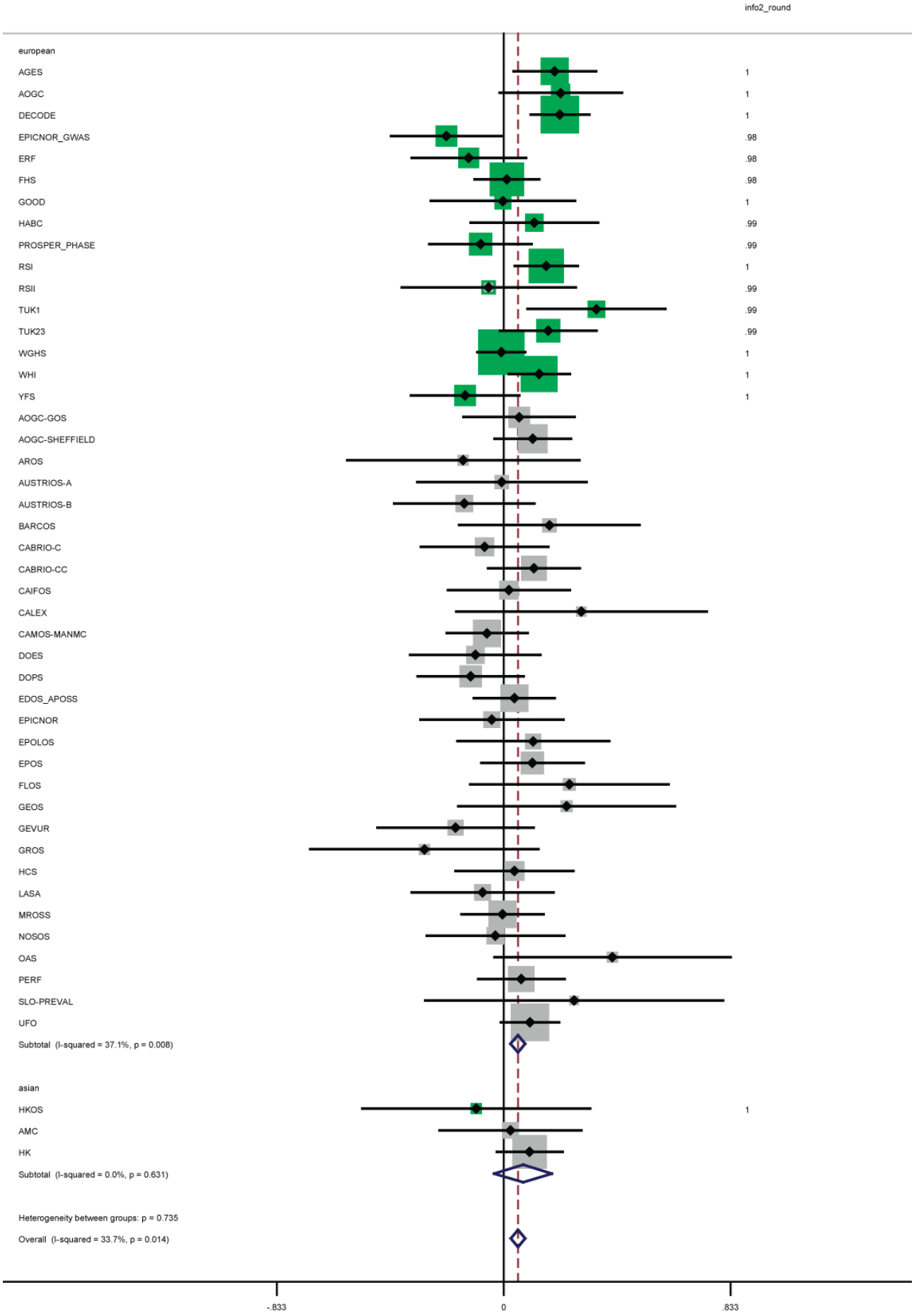
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEVUR
GROS
HCS
LASA
NOSOS
OAS
PERF
UFO
Subtotal (I-squared = 0.0%, p = 0.922)
asian
HKOS
AMC
HK
Subtotal (I-squared = 2.7%, p = 0.358)
Heterogeneity between groups: p = 0.922
Overall (I-squared = 0.0%, p = 0.931)
.97
.96
.97
.95
.97
.94
.96
.94
.96
.95
.95
.96
.95
.96
.96
.95
1
-.724
0
.724

rs1286083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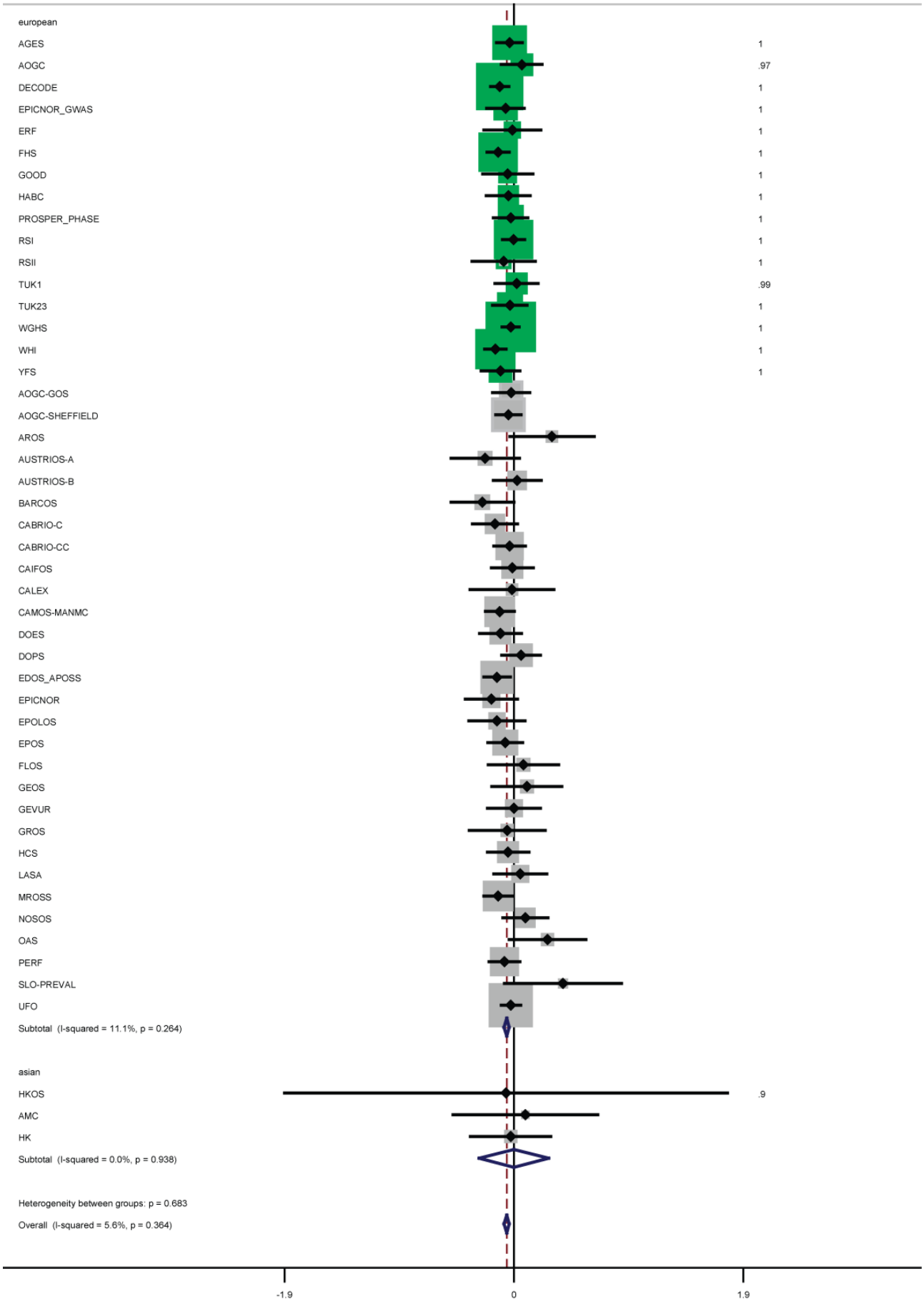
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 37.1%, p = 0.008)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.631)
Heterogeneity between groups: p = 0.735
Overall (I-squared = 33.7%, p = 0.014)
1
1
1
.98
.98
.98
1
.99
.99
1
.99
.99
.99
1
1
1
1
-.833
0
.833

rs4233949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HABC
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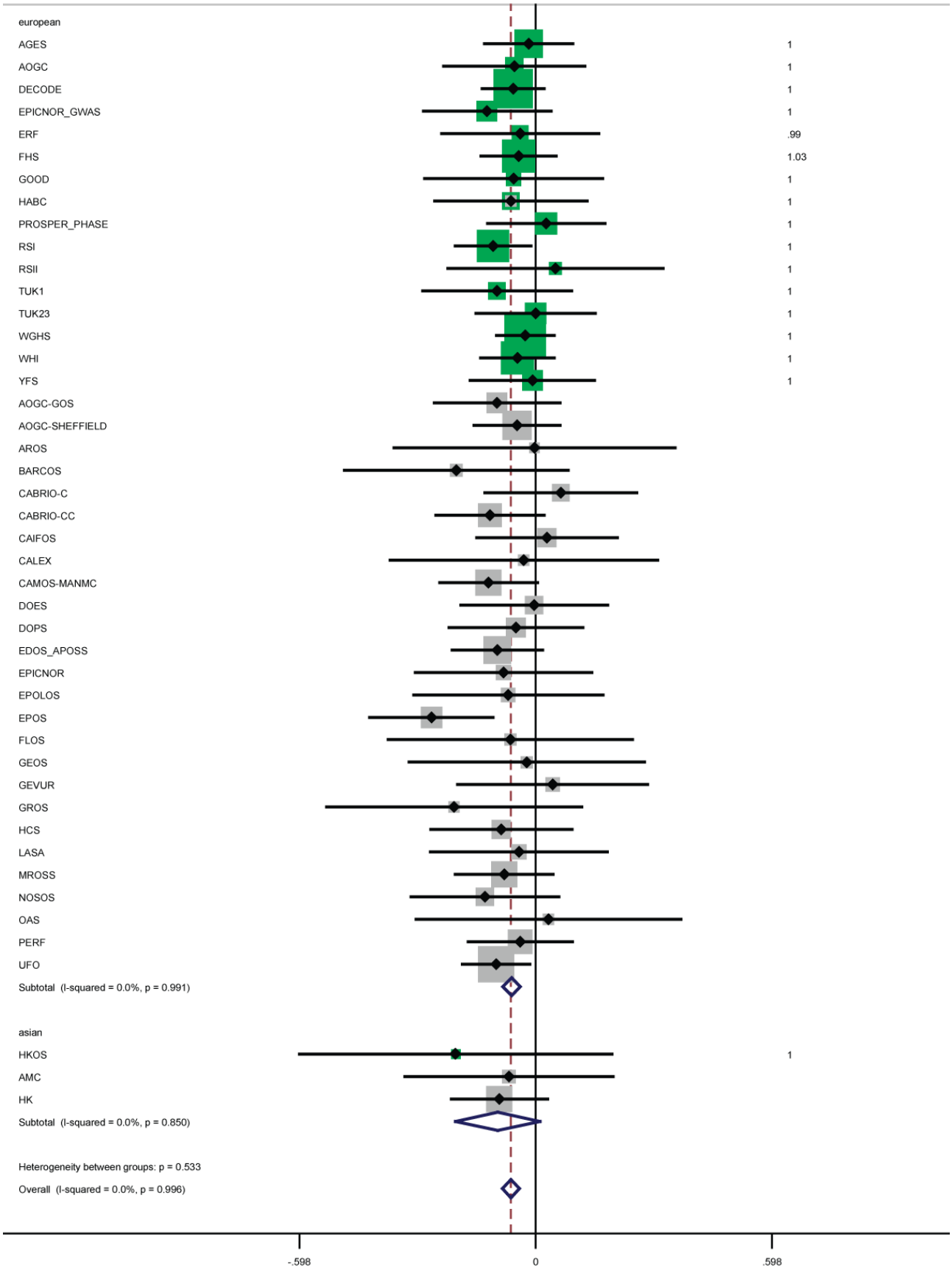
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 11.1%, p = 0.264)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.938)
Heterogeneity between groups: p = 0.683
Overall (I-squared = 5.6%, p = 0.364)
1
.97
1
1
1
1
1
1
1
1
1
.99
1
1
1
1
.9
-1.9
0
1.9

rs6532023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HABC
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RSI
RSII
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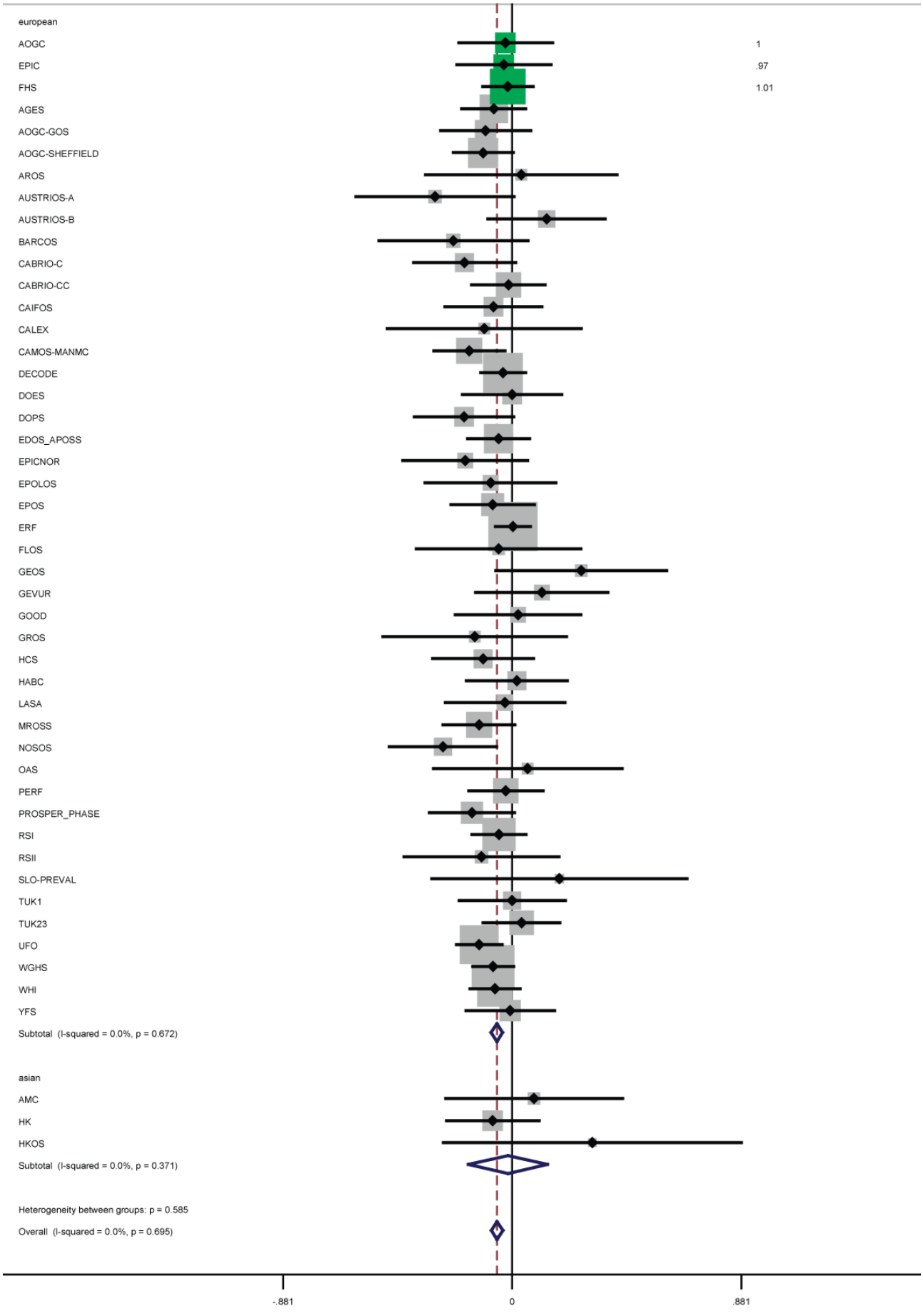
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
UFO
Subtotal (I-squared = 0.0%, p = 0.991)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.850)
Heterogeneity between groups: p = 0.533
Overall (I-squared = 0.0%, p = 0.996)
1
1
1
1
.99
1.03
1
1
1
1
1
1
1
1
1
1
-.598
0
.598

rs3801387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FHS
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AOGC-SHEFFIELD
AROS
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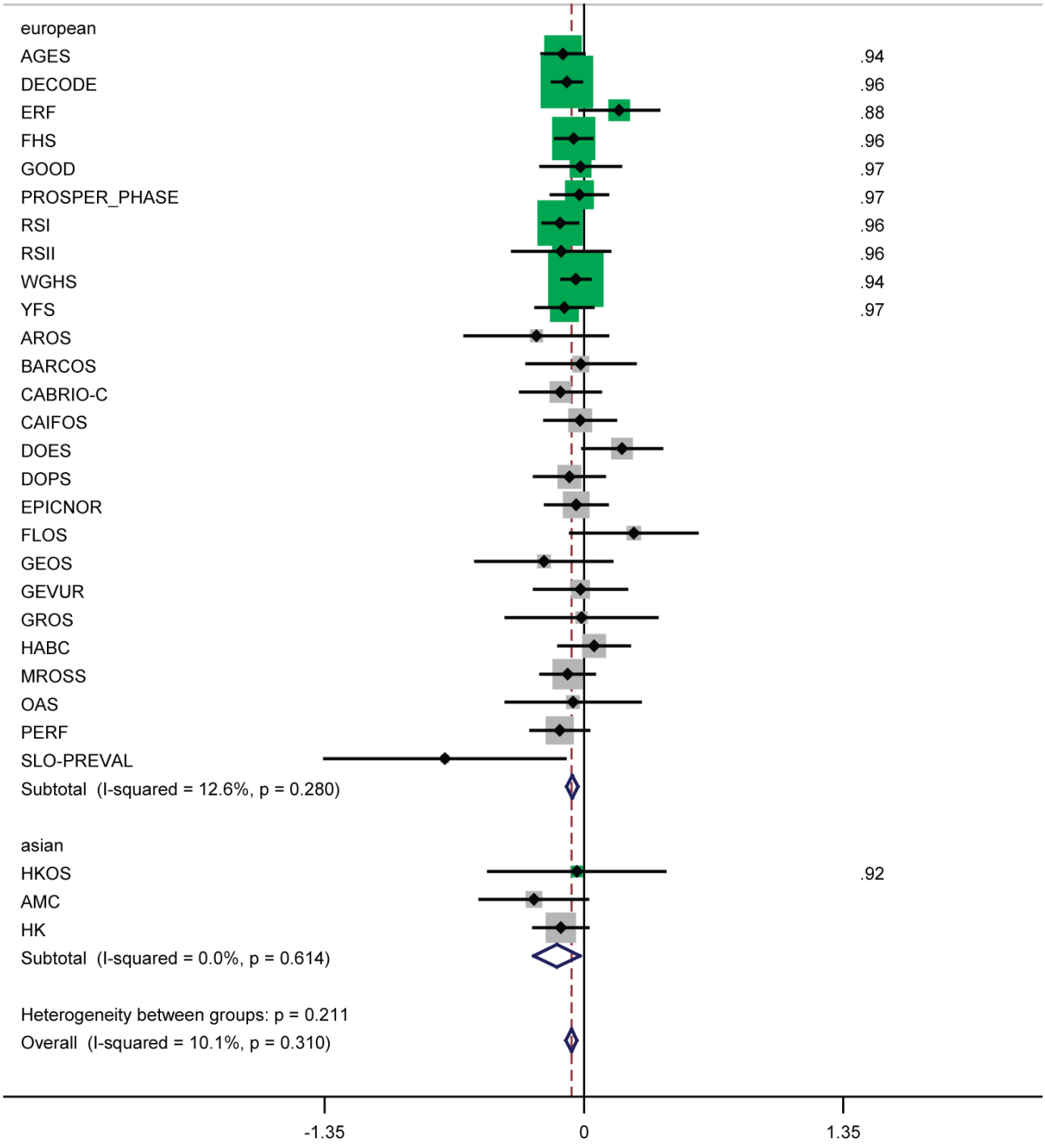
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DECODE
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
ERF
FLOS
GEOS
GEVUR
GOOD
GROS
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
PROSPER_PHASE
RSI
RSII
SLO-PREVAL
TUK1
TUK23
UFO
WGHS
WHI
YFS
Subtotal (I-squared = 0.0%, p = 0.672)
asian
AMC
HK
HKOS
Subtotal (I-squared = 0.0%, p = 0.371)
Heterogeneity between groups: p = 0.585
Overall (I-squared = 0.0%, p = 0.695)
1
.97
1.01
-.881
0
.881

rs4792909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RSII
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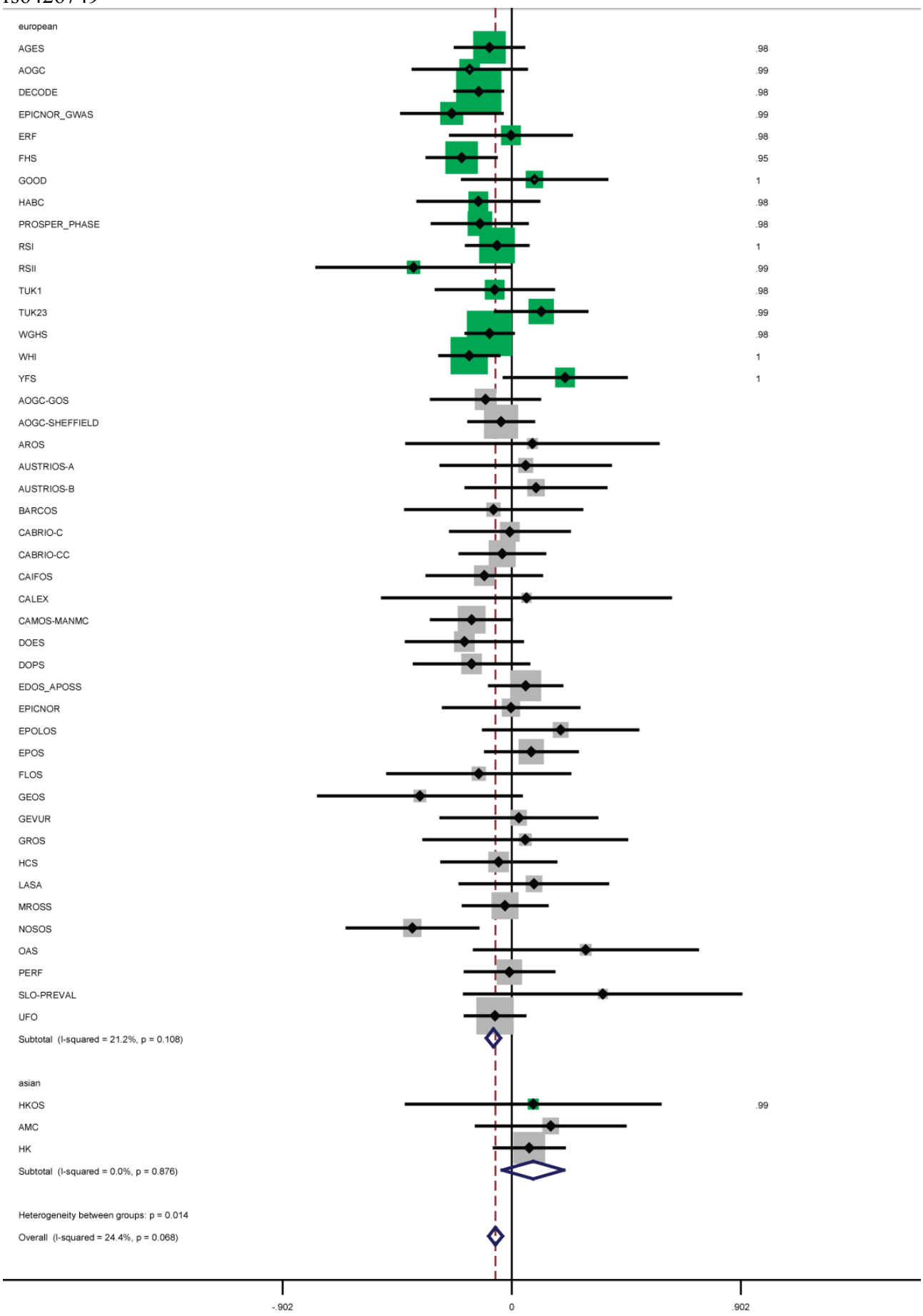
BARCOS
CABRIO-C
CAIFOS
DOES
DOPS
EPICNOR
FLOS
GEOS
GEVUR
GROS
HABC
MROSS
OAS
PERF
SLO-PREVAL
Subtotal (I-squared = 12.6%, p = 0.280)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.614)
Heterogeneity between groups: p = 0.211
Overall (I-squared = 10.1%, p = 0.310)
.94
.96
.88
.96
.97
.97
.96
.96
.94
.97
.92
-1.35
0
1.35

rs6426749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GOOD
HABC
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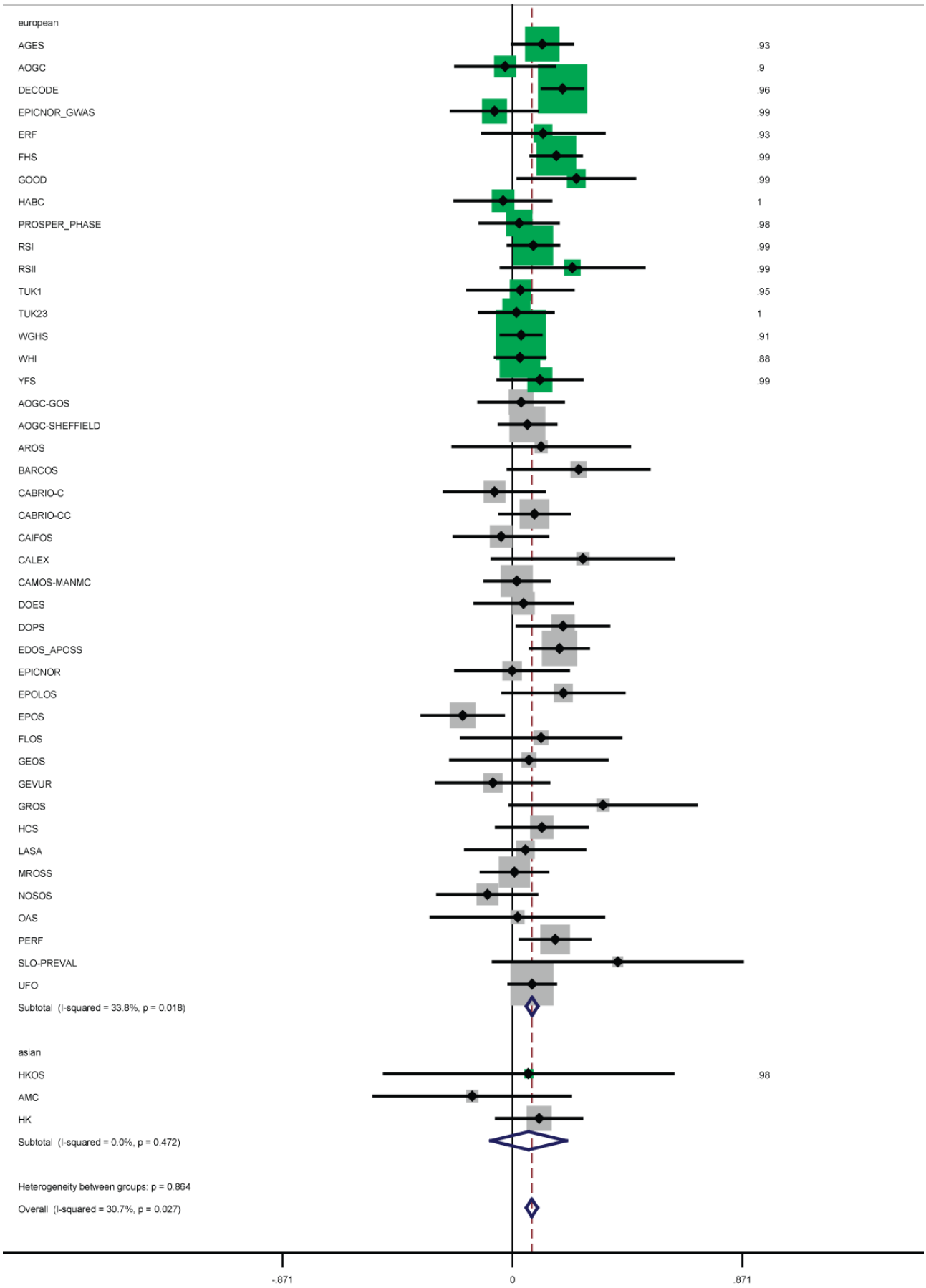
RSII
TUK1
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 21.2%, p = 0.108)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.876)
Heterogeneity between groups: p = 0.014
Overall (I-squared = 24.4%, p = 0.068)
.98
.99
.98
.99
.98
.95
1
.98
.98
1
.99
.98
.99
.98
1
1
.99
-.902
0
.902

rs4727338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AGES
.93
AOGC
.9
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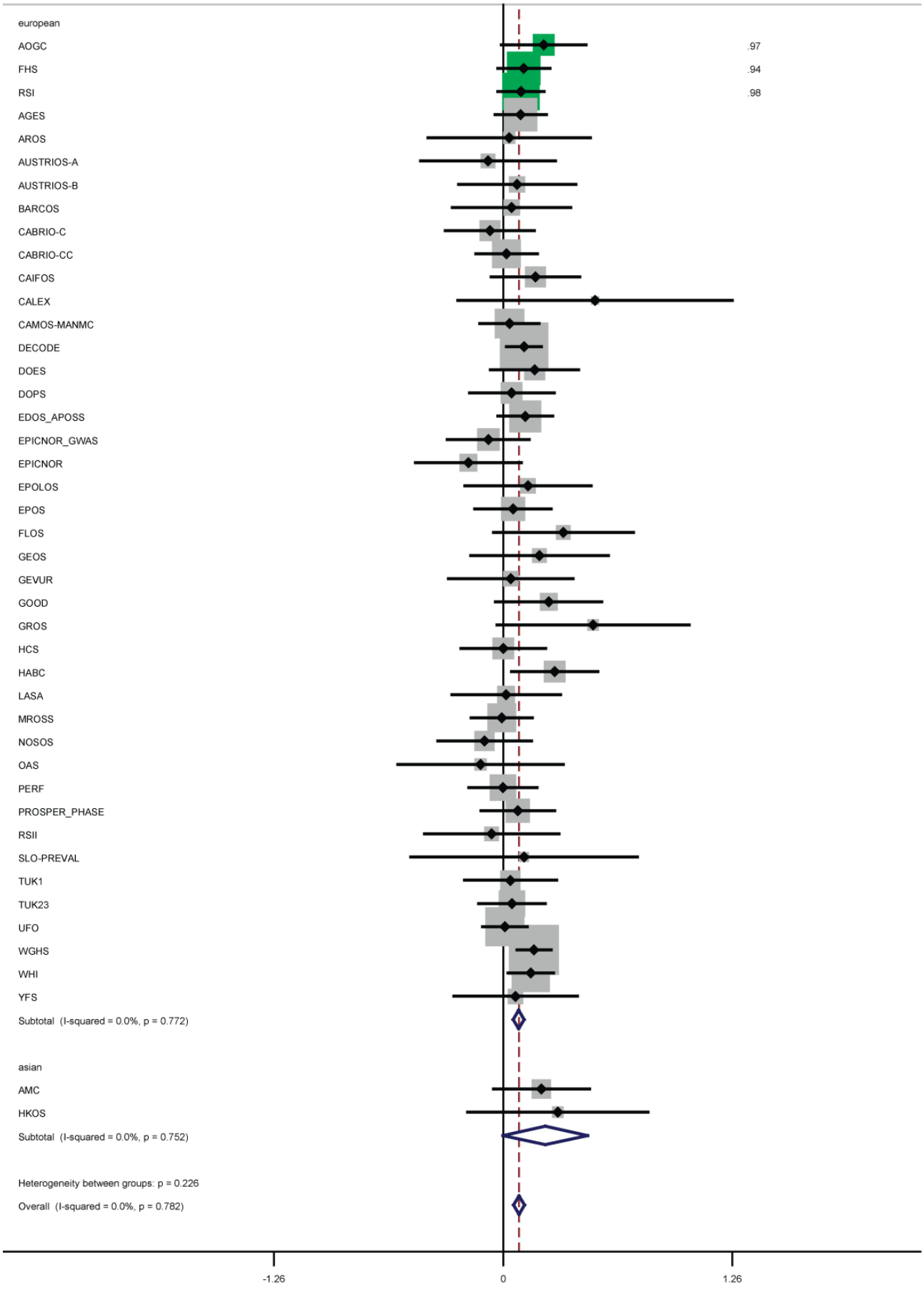
.96
EPICNOR_GWAS
.99
ERF
.93
FHS
.99
GOOD
.99
HABC
1
PROSPER_PHASE
.98
RSI
.99
RSII
.99
TUK1
.95
TUK23
1
WGHS
.91
WHI
.88
YFS
.99
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 33.8%, p = 0.018)
asian
HKOS
.98
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.472)
Heterogeneity between groups: p = 0.864
Overall (I-squared = 30.7%, p = 0.027)
-.871
0
.871

rs3736228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GEOS
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GOOD
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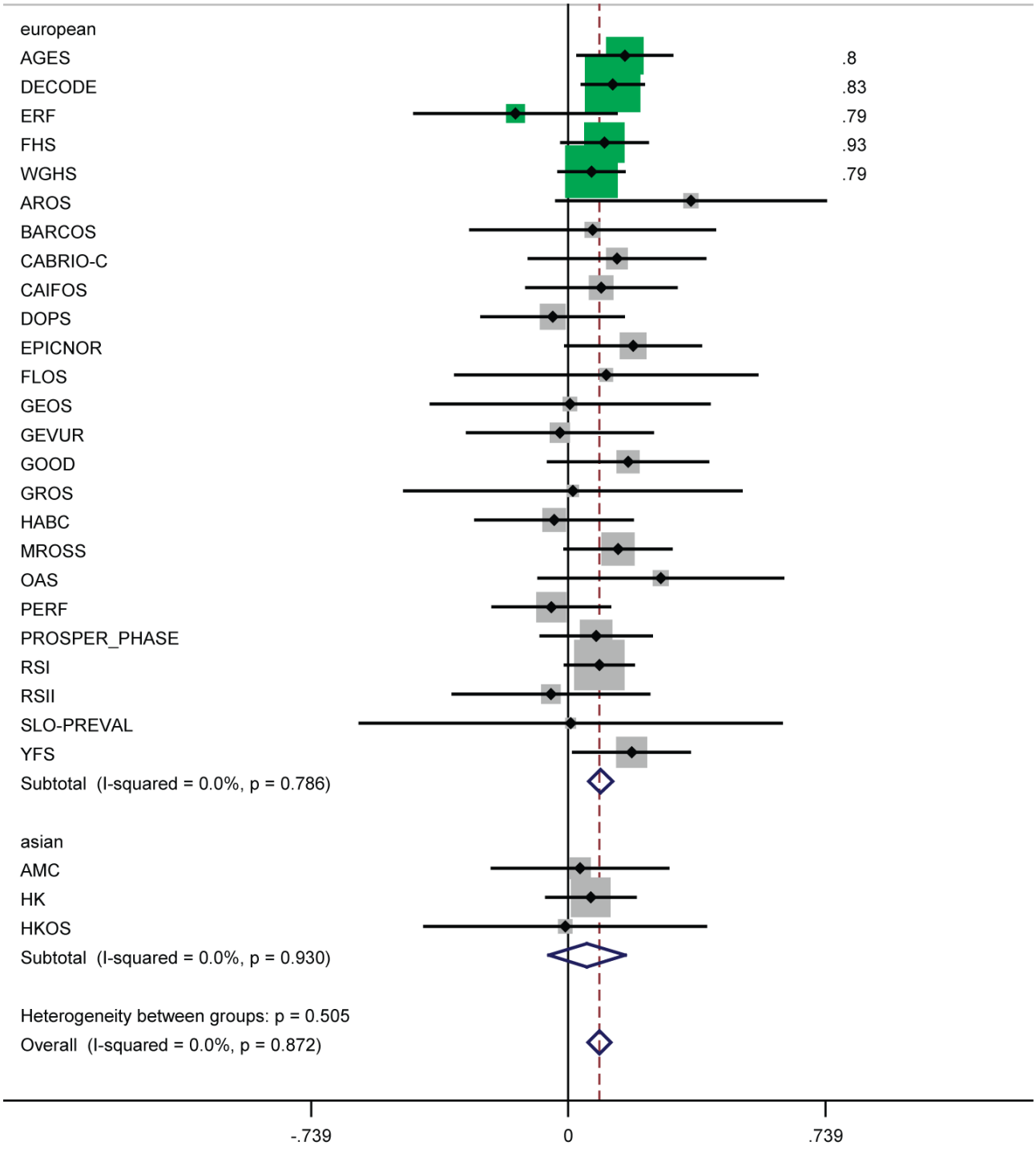
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
PROSPER_PHASE
RSII
SLO-PREVAL
TUK1
TUK23
UFO
WGHS
WHI
YFS
Subtotal (I-squared = 0.0%, p = 0.772)
asian
AMC
HKOS
Subtotal (I-squared = 0.0%, p = 0.752)
Heterogeneity between groups: p = 0.226
Overall (I-squared = 0.0%, p = 0.782)
.97
.94
.98
-1.26
0
1.26

rs7521902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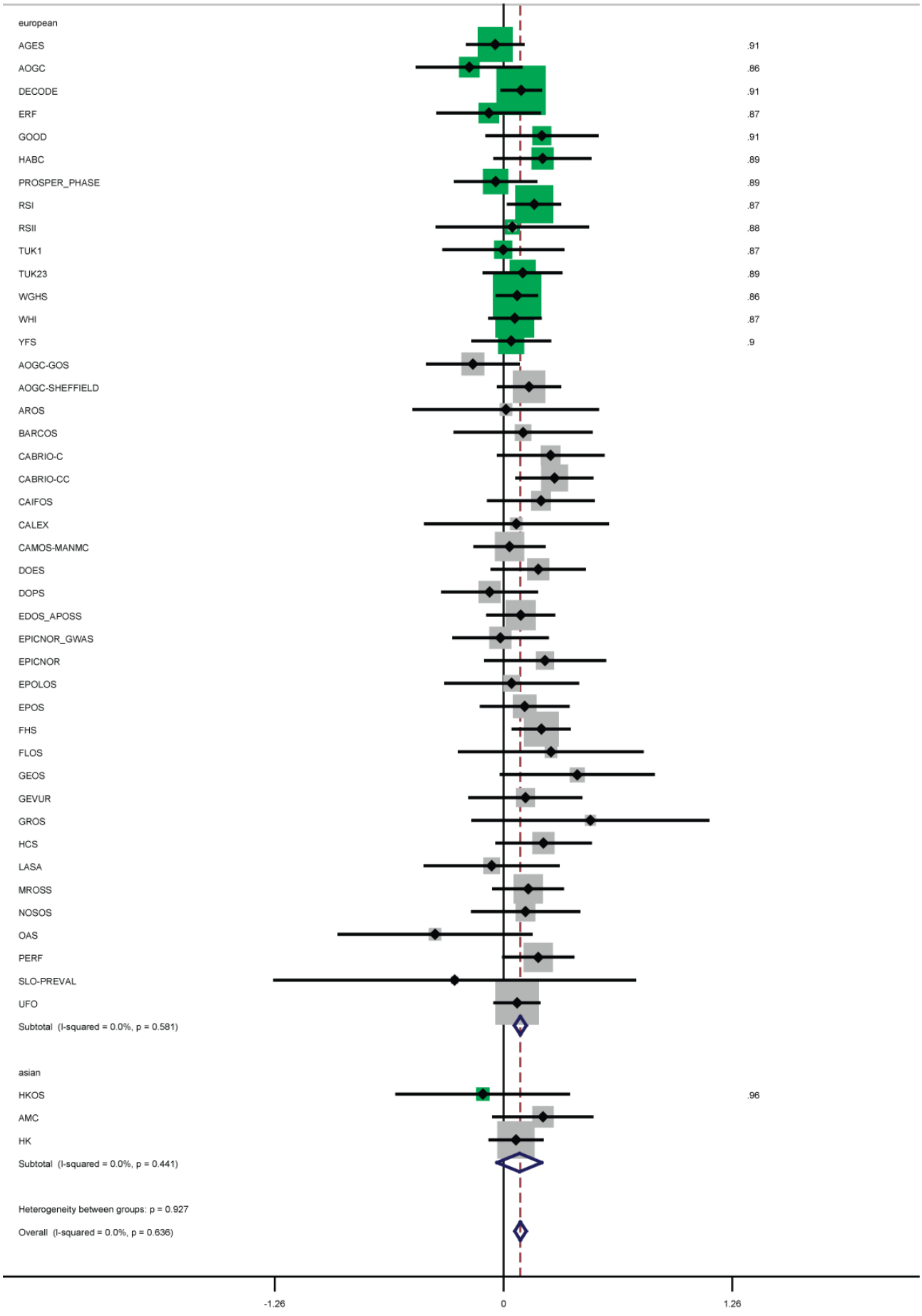
FLOS
GEOS
GEVUR
GOOD
GROS
HABC
MROSS
OAS
PERF
PROSPER_PHASE
RSI
RSII
SLO-PREVAL
YFS
Subtotal (I-squared = 0.0%, p = 0.786)
asian
AMC
HK
HKOS
Subtotal (I-squared = 0.0%, p = 0.930)
Heterogeneity between groups: p = 0.505
Overall (I-squared = 0.0%, p = 0.872)
.8
.83
.79
.93
.79
-.739
0
.739

rs1373004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AOGC-SHEFFIELD
AROS
BARCOS
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CABRIO-CC
CAIFOS
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DOES
DOPS
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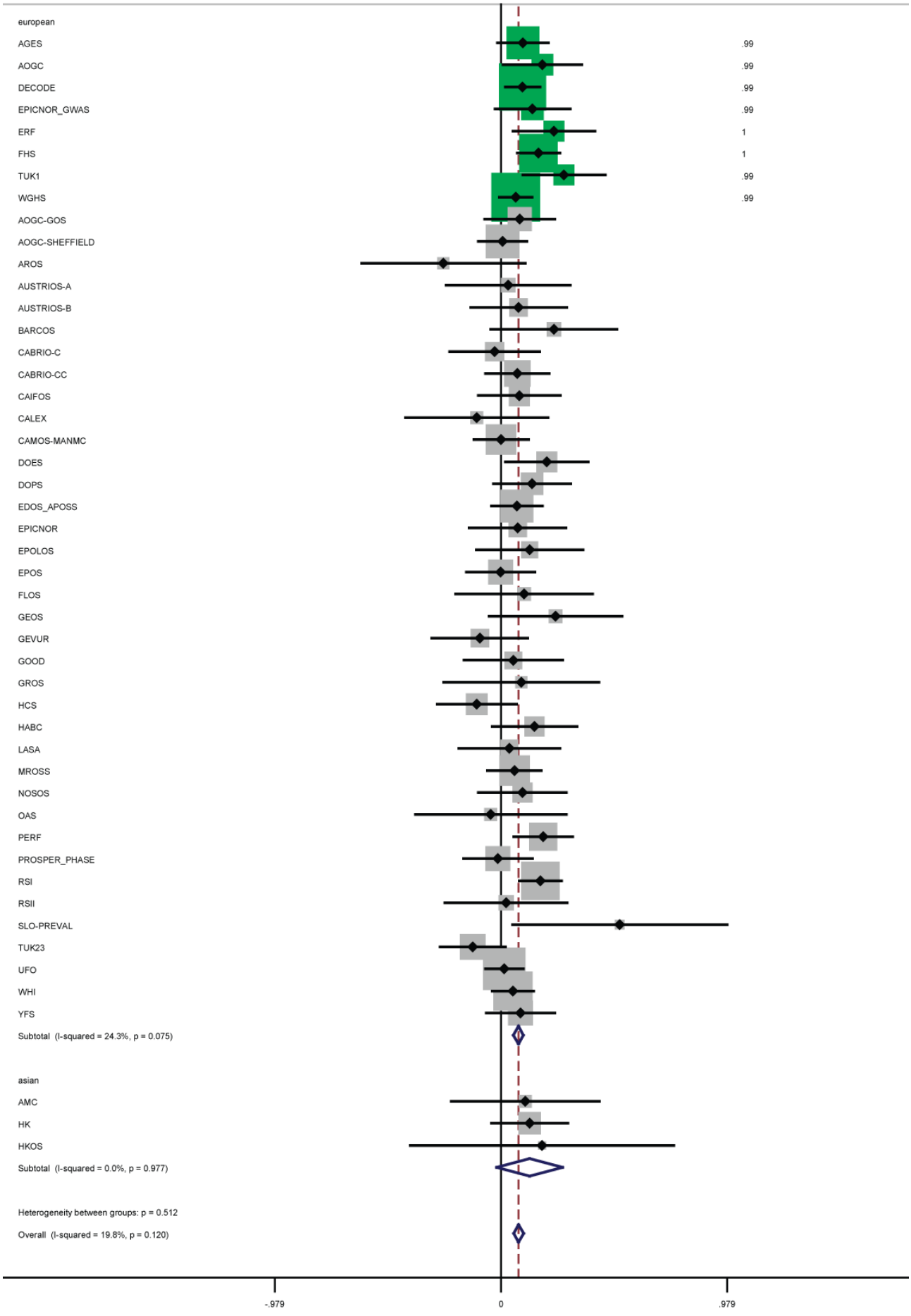
EPOLOS
EPOS
FHS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 0.0%, p = 0.581)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.441)
Heterogeneity between groups: p = 0.927
Overall (I-squared = 0.0%, p = 0.636)
.91
.86
.91
.87
.91
.89
.89
.87
.88
.87
.89
.86
.87
.9
.96
-1.26
0
1.26

rs4796995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AOGC-SHEFFIELD
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BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
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DOES
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EPICNOR
EPOLOS
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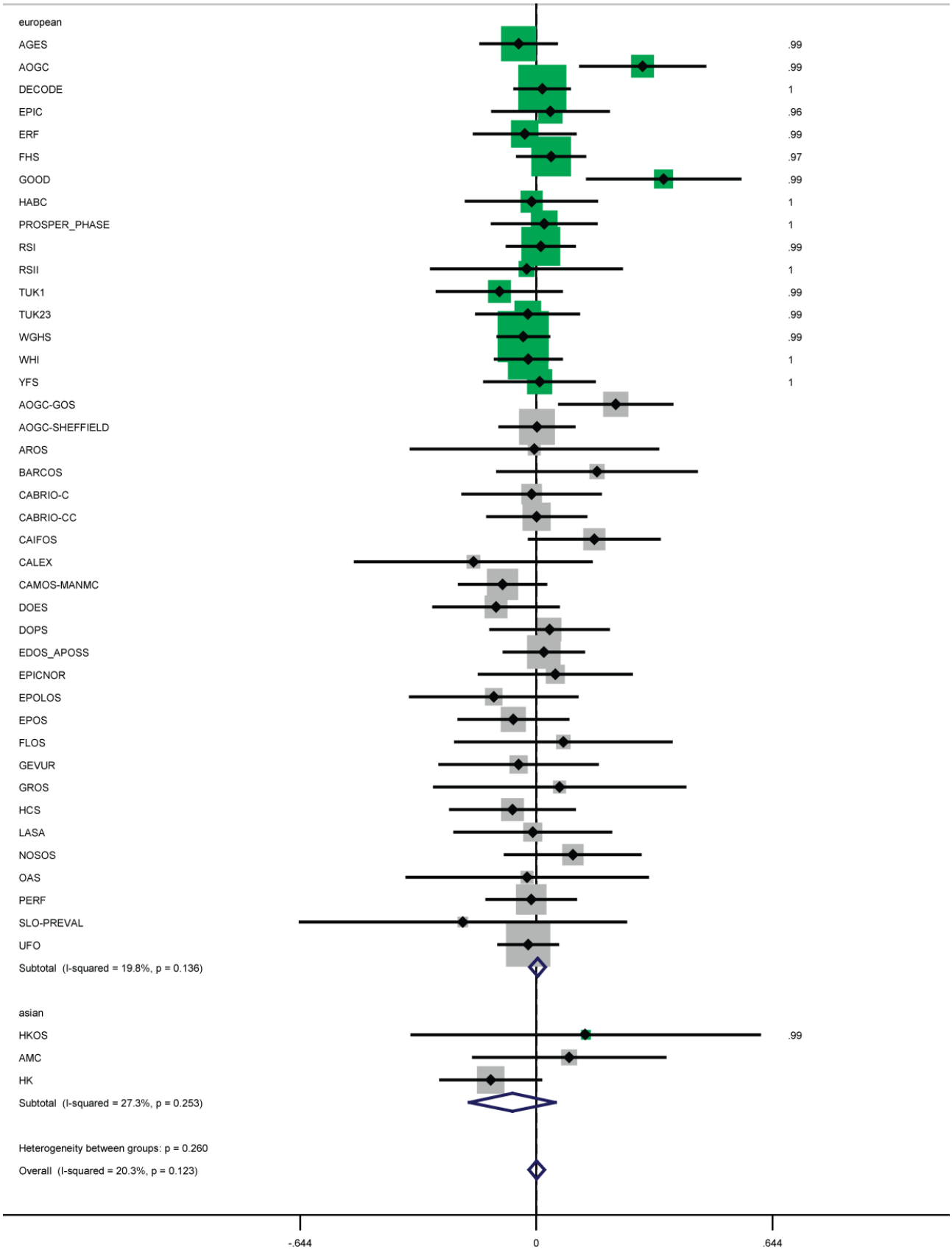
FLOS
GEOS
GEVUR
GOOD
GROS
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
PROSPER_PHASE
RSI
RSII
SLO-PREVAL
TUK23
UFO
WHI
YFS
Subtotal (I-squared = 24.3%, p = 0.075)
asian
AMC
HK
HKOS
Subtotal (I-squared = 0.0%, p = 0.977)
Heterogeneity between groups: p = 0.512
Overall (I-squared = 19.8%, p = 0.120)
.99
.99
.99
.99
1
1
.99
.99
-.979
0
.979

rs2062377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WGHS
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YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
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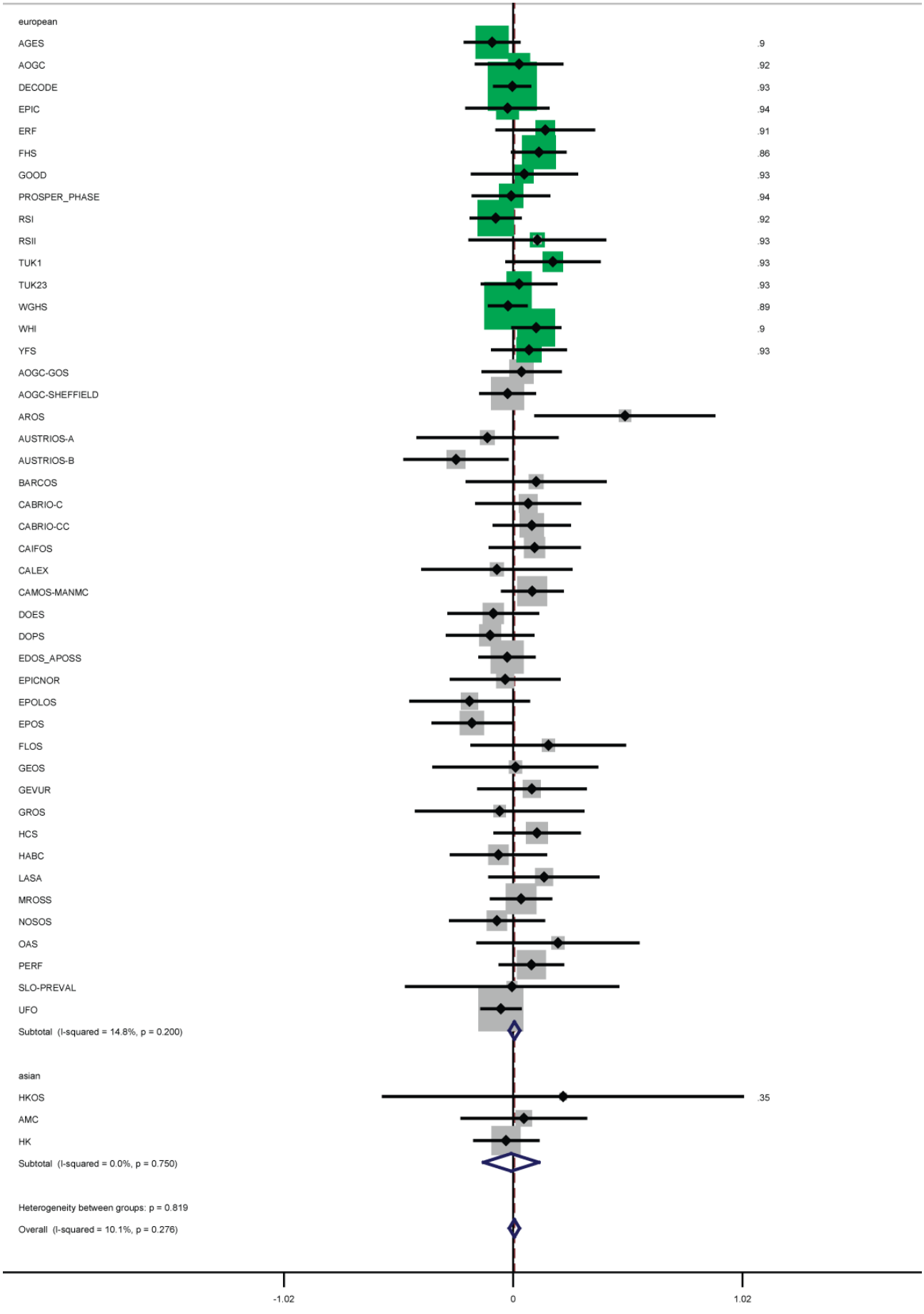
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEVUR
GROS
HCS
LASA
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 19.8%, p = 0.136)
asian
HKOS
AMC
HK
Subtotal (I-squared = 27.3%, p = 0.253)
Heterogeneity between groups: p = 0.260
Overall (I-squared = 20.3%, p = 0.123)
.99
.99
1
.96
.99
.97
.99
1
1
.99
1
.99
.99
.99
1
1
.99
-.644
0
.644

rs884205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RSII
TUK1
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WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
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AUSTRIOS-A
AUSTRIOS-B
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
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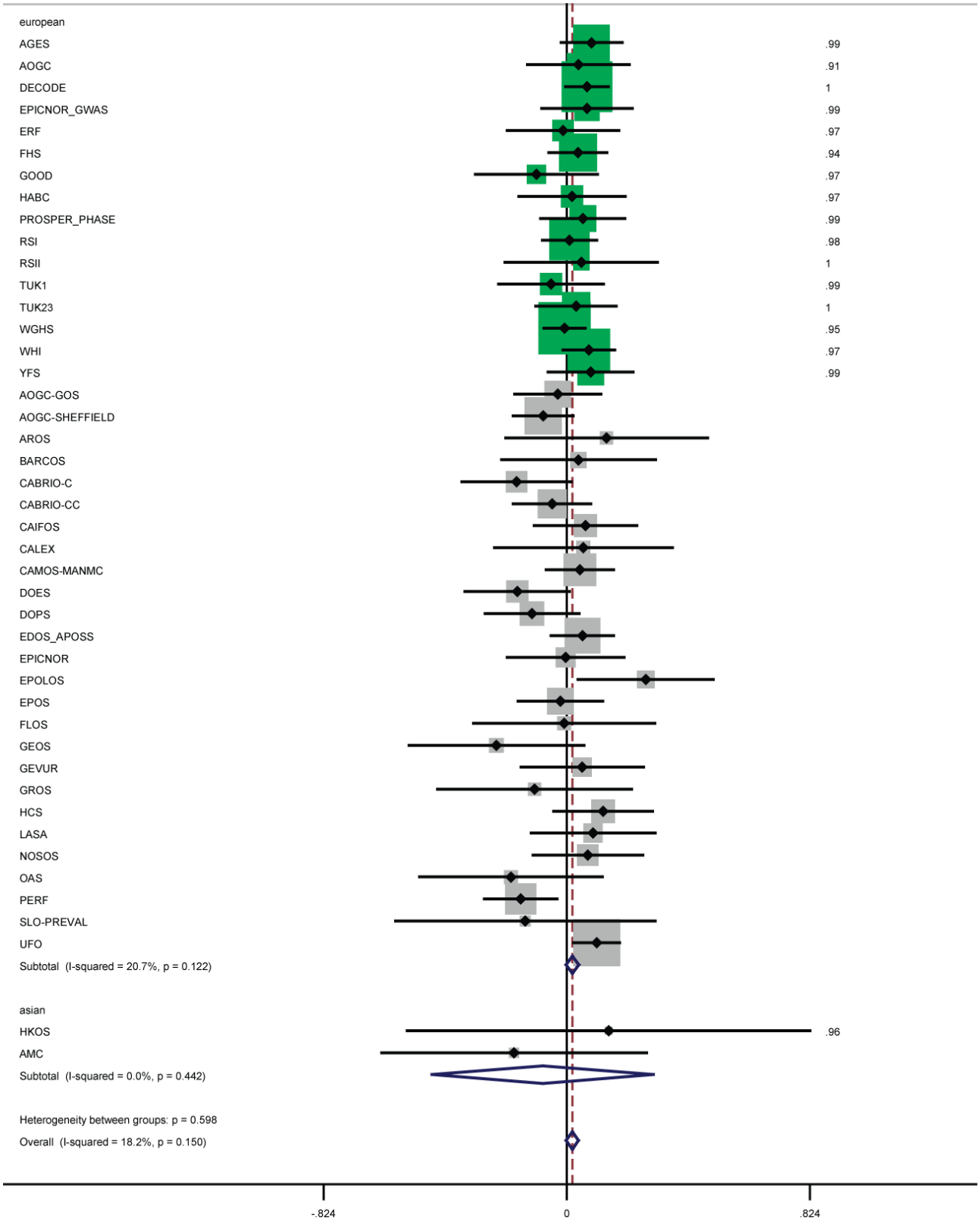
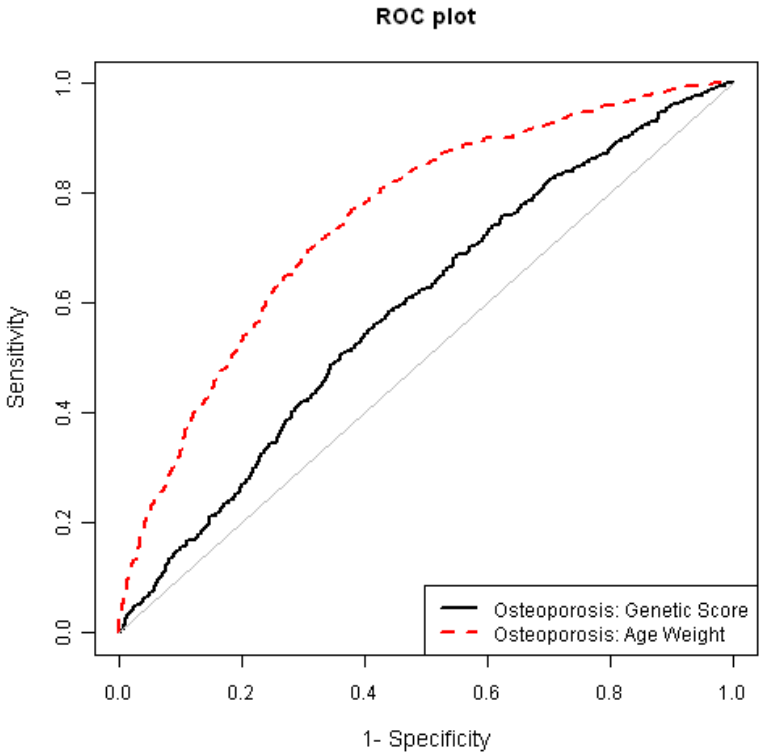
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
HABC
LASA
MROSS
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 14.8%, p = 0.200)
asian
HKOS
AMC
HK
Subtotal (I-squared = 0.0%, p = 0.750)
Heterogeneity between groups: p = 0.819
Overall (I-squared = 10.1%, p = 0.276)
.9
.92
.93
.94
.91
.86
.93
.94
.92
.93
.93
.93
.89
.9
.93
.35
-1.02
0
1.02

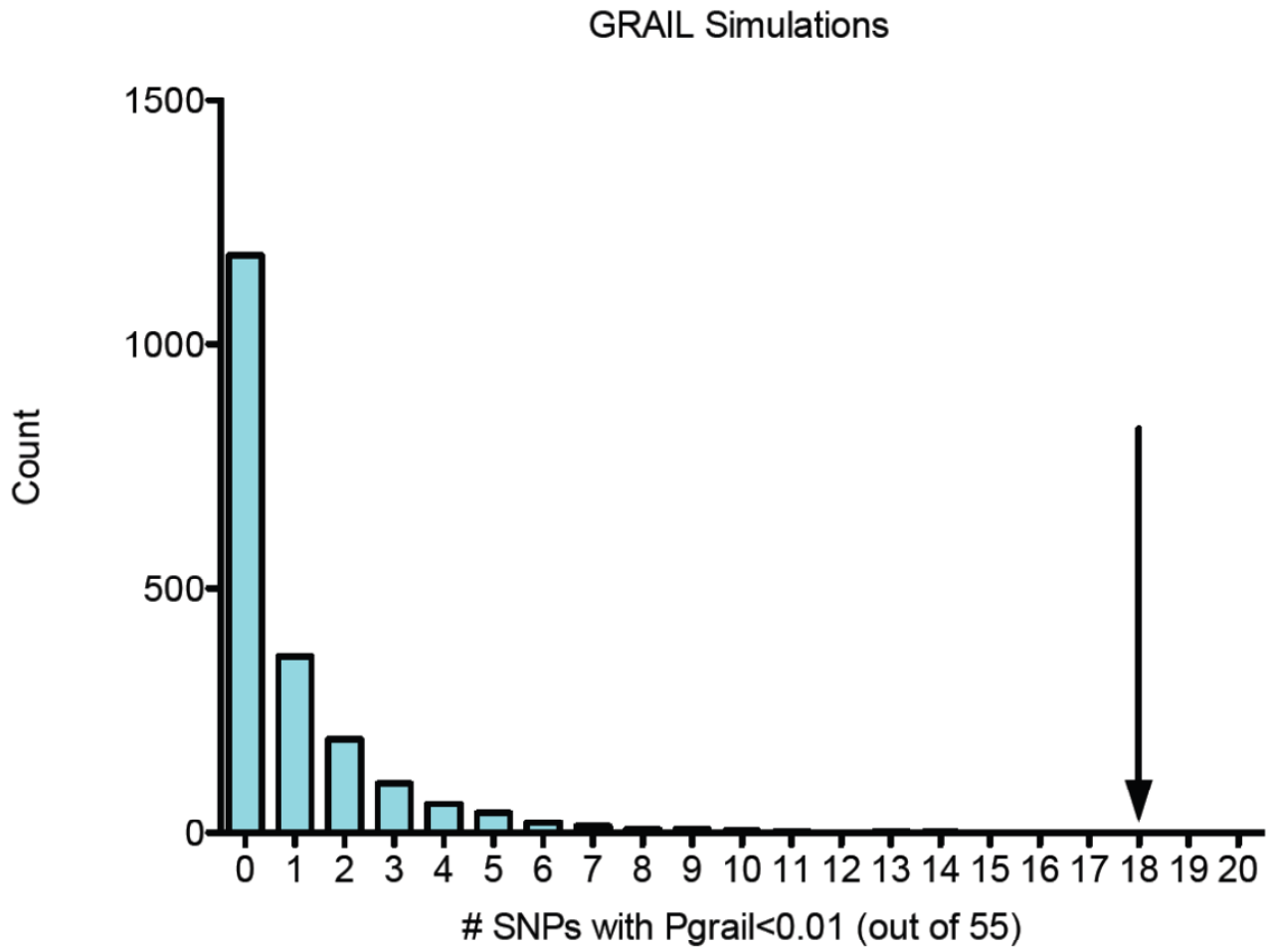
rs9533090

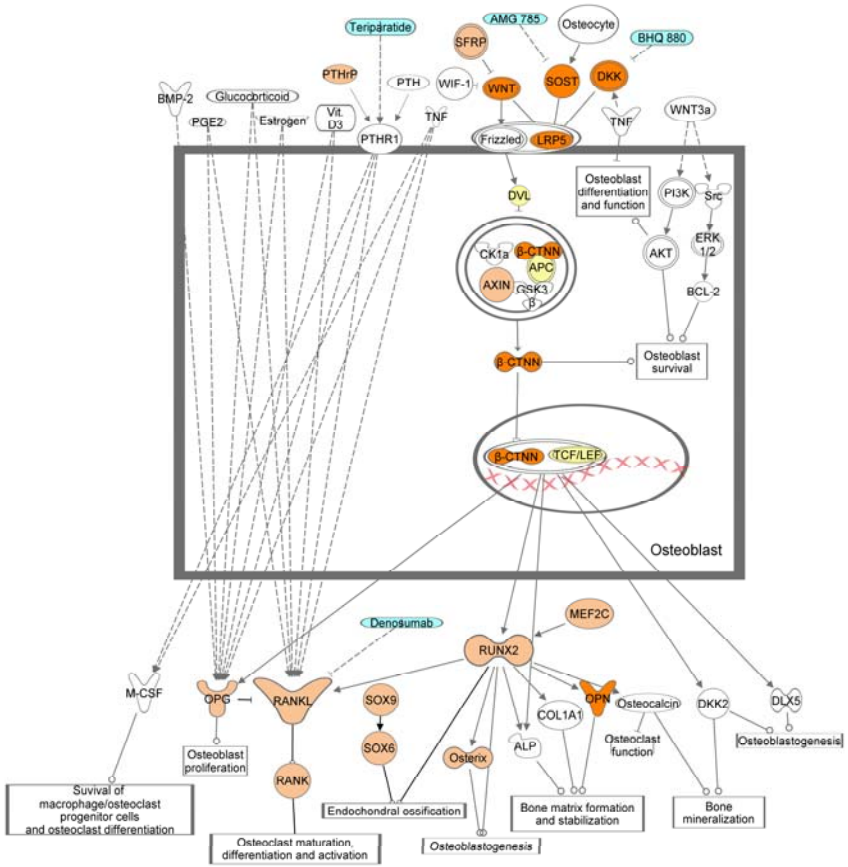

european
AGES
AOGC
DECODE
EPICNOR_GWAS
ERF
FHS
GOOD
HABC
PROSPER_PHASE
RSI
RSII
TUK1
TUK23
WGHS
WHI
YFS
AOGC-GOS
AOGC-SHEFFIELD
AROS
BARCOS
CABRIO-C
CABRIO-CC
CAIFOS
CALEX
CAMOS-MANMC
DOES
DOPS
EDOS_APOSS
EPICNOR
EPOLOS
EPOS
FLOS
GEOS
GEVUR
GROS
HCS
LASA
NOSOS
OAS
PERF
SLO-PREVAL
UFO
Subtotal (I-squared = 20.7%, p = 0.122)
asian
HKOS
AMC
Subtotal (I-squared = 0.0%, p = 0.442)
Heterogeneity between groups: p = 0.598
Overall (I-squared = 18.2%, p = 0.150)
.99
.91
1
.99
.97
.94
.97
.97
.99
.98
1
.99
1
.95
.97
.99
.96
-.824
0
.824

Supplementary Figure 8. The area under the Receiver-operator characteristics (ROC) curves (AUC) of two different models predicting the risk of osteoporosis (T-score ≤ -2.5) in the 2,836 genotyped women of the PERF study. Model 1, represented by the solid black line, includes only the genetic score (AUC = 0.59 [0.56- 0.61]). Model 2, represented by the dashed red line, includes age, weight, (AUC= 0.75 [0.73 -0.77]).



Supplementary Figure 9. Two thousand sets of 55 randomly selected SNPs evaluated in GRAIL. Black arrow points to the number of significant loci identified by GRAIL using the 55 GWS BMD loci. None of the 2,000 sets had more than 15 SNPs with P<0.01





Supplementary Figure 10. Graphic representation of the different pathways critical to bone biology including osteoblastic differentiation; Wnt-mediated osteoblastic activation and function; RANK-mediated osteoclastic activation and endochondral ossification. The figure is derived from an image generated by Ingenuity Pathway Analysis (IPA) software version 2011 (Ingenuity Systems). The osteoblast is the main bone-forming cell. Genes identified by SNPs associated with BMD at genome-wide significant levels are coloured pink, genes identified by markers associated with fracture risk are coloured orange, genes identified by markers associated with BMD at P<0.0001 are coloured in yellow and current pharmacological compounds used or under development (Phase II trials) for the treatment of osteoporosis are coloured aquamarine.

SUPPLEMENTARY NOTE

1. DE-NOVO GENOTYPING (STAGE 2)

1.1. De novo genotyping

A total of 62,203 samples from 34 studies with either BMD and/or fracture information was de-novo genotyped in four main genotyping centers (KBioSciences, AOGC, deCODE and WHI) (Supplementary Methods Table 3D).

1.1.1. KBioSciences

The majority of the studies opted for whole genome amplification (WGA) before genotyping. WGA was done by K-Biosciences (http://www.kbioscience.co.uk/lab%20services/wga/wga.html) and samples were stored in freezers for genotyping. We evaluated the genotype concordance between raw DNA genotypes and amplified DNA genotypes in a panel of 82 SNPs within 96 samples. The genotype accuracy before and after amplification was 99.971%. DNA from the OSTEOS study could not be amplified with enough quality and was therefore excluded from all analyzes. All SNPs genotyped by K-Biosciences (www.kbioscience.co.uk) used a competitive allele specific PCR (KASPar) assay. A Y-chromosome specific assay was evaluated in all samples. Sample mismatches between the gender specific assay and the reported gender in the questionnaire were removed from analysis.

1.1.2. AOGC

AOGC samples from the Geelong Osteoporosis Study cohort and the Sheffield cohort were directly genotyped at the University of Queensland Diamantina Institute. Two genotyping platforms were used: Applied Biosystems OpenArray (for 72 SNPs) and KBioSciences technology for the remaining 10 SNPs for which a taqman probe could not be designed. Positive and negative controls were used on each plate. Nine SNPs failed QC (rs10048146, rs7017914, rs9466056, rs3736228, rs3755955, rs4240467, rs12995369, rs17040773,rs1053051; 2 using the KBioSciences platform and 7 using OpenArray).

1.1.3. deCODE

GENOMOS samples from the PERF (Denmark), DOES (Australia), AMC (South Korea) and the Hong Kong elderly cohorts were directly genotyped for replication at the deCODE Genetics, along with additional deCODE study samples (Iceland). The genotyping was performed on the Centaurus (Nanogen) platform[1]. The quality of each Cenaturus SNP assay was evaluated by genotyping each assay in the CEU HapMap samples and comparing the results with the HapMap data. Assays with mismatches >1% were not used and positive and negative controls were present on all genotyping plates in order to ensure correct genotyping. Functional assays meeting all quality criteria could not be made for the markers rs4727338, rs4869742, rs6959212, rs430727, rs1286083, rs6532023, rs4790881, rs12995369 and rs4792909 and these proxy SNPs, rs7781370, rs4870044, rs1403987, rs87938, rs1286077, rs1471403, rs11657636, rs11690020 and rs7220711 were genotyped instead, respectively. For the SNP rs11048046 a functional assay could not be made nor was there a known proxy SNP available. Nine hundred samples from the chip-typed deCODE discovery cohort were also directly genotyped for comparison with the imputed genotypes. The median of the correlation between genotyped and imputed genotypes was 0.97.

1.1.4. WHI

A custom Illumina (Illumina, Inc., San Diego, CA, USA) iSELECT genotyping array was designed to analyze 3,923 samples. From the 82 main BMD SNPs the following 15 rsIDs could not be included in the array given design restrictions: rs4240467, rs12821008, rs4233949, rs7851693, rs3736228, rs7953528, rs1566045, rs2062377, rs6426749, rs7932354, rs4869742, rs4727338, rs430727, rs11048046, rs7427438.

1.2. Quality Control

Genotyped calls from K-Biosciences, AOGC and deCODE were centrally controlled for: Sample call rate > 80%, SNP call rate > 90%, HWE P > $1x10^{-4}$, MAF > 1%. The following QC filters were applied for samples genotyped by WHI: Sample call rate > 98%, SNP call rate > 98%, HWE P > $1x10^{-6}$, MAF > 0.5%.

2. ADDITIONAL ANALYSES

2.1. Secondary signals

To evaluate the presence of multiple association signals in one locus, each stage 1 study repeated the primary GWA analysis using models additionally adjusted for the top 82 lead SNPs associated with BMD at P < $5x10^{-6}$ with the objective of identifying additional signals in the discovered loci. The effect estimates for each association were calculated using inverse variance fixed-effects meta-analysis. Assuming that approximately 3,000 Mbp in the human genome are usually "genotypable" we tested ~ 5.5% of ~ 1 million tests. Hence the threshold we used for selecting secondary signals for replication was set to 9×10^{-7}.

2.2.Gene x Gene interaction

Each individual study extracted genotype imputation dosages for each of the top 82 lead SNPs to investigate potential gene-gene interaction. An R-script was provided to each individual study and was run using the extracted dosages. The allele coding was such that the BMD increasing allele (based on the Stage 1 meta-analysis) was always the dosage increasing allele. For the additive dosage and pair-wise interaction analyses ($Y=b_0+b_1.A+b_2.B+b_3.AB+e$; test of H0: $b_3 = 0$), the dosages were regressed against residuals of sex-standardized Z-scores of FN-BMD and LS-BMD, adjusted for appropriate covariates as with the primary GWA study. For each pair, a linear regression analysis including the two SNPs and their interaction term was performed. Interaction terms were deemed significant at levels of $1.5x10^{-5}$ accounting for (82*81)/2 =3321 interaction tests.

2.3. Fine Mapping using 1000 Genomes Project data

We imputed SNPs within the 2 Mb genomic region (1 Mb upstream and 1 Mb downstream) of top SNP from each of the 82 loci using the CEU or CHB/JPT as appropriate reference panels of the 1000 Genome Project that was released in June 2010. The imputation was performed using either MACH or IMPUTE in samples from 9 discovery cohorts including, AOGC (women only), DECODE, FHS, GOOD (men only), HEALTHABC, HKOS (women only), INDIANA (women only), ORCADES, RSI, RSII and RSIII. The total sample is 21,699 men and women for FN-BMD and 20,835 men and women for LS-BMD. A total of 495,634 SNPs with variance ratio > 0.3 in at least one study was imputed and used for this analysis. SNP-phenotype association was performed in each study and a fixed-effected inverse-variance meta-analysis was performed to estimate association p-values. We excluded SNPs only available in 4 or less studies. SNPs with higher heterogeneity ($I^2 > 50$) were also excluded. We defined "stronger evidence of association" as a P-value difference of more than one order of magnitude to avoid drawing conclusions from random variation in the test statistics. Physical-based SNP annotation by categorizing according to their position relative to genes (intronic, exonic, UTR, promoter, flanking, inter-genic, etc.) was done using the Human GRCh37 reference genome and Ensembl transcripts. Pair-wise Linkage Disequilibrium (LD) was estimated using haplotype information from 1000 Genome Project European reference panel. Functional predictions of gene or SNPs have been shown to provide supportive evidence of GWAS findings and can be used to prioritize the GWAS top hits for further studies[2]. We predicted the potential functional effects on following types of SNPs: the premature translation termination (nonsense); the exonic SNPs that cause an amino acid change in conservative genomic region across multiple species (non-conservative non-synonymous)[3]; the exonic SNPs that affect protein function based on sequence homology and the physical properties of amino acids (non-conservative non-synonymous)[4]; the splicing sites that lead to a protein domain being abolished.[5]; synonymous SNPs located at exonic splicing enhancer motifs[6,7] and the exonic splicing silencer motifs[8]; the transcription factor binding sites at promoter regions[9-11];the 3-UTR post-transcriptional regulatory region[12]; and miRNA sites[13].

2.4.Gene expression

Expression profiles at 55 of the 56 GWS loci were analysed within several eQTL datasets. We chose to omit the 17q21.31_2 locus because of the known rearrangements at this locus (inversion, duplications, and deletions) with resulting variable number of many of the genes at this locus.

The first eQTL dataset, published by Reppe and colleagues[14], tested the relationship between gene expressions in trans-iliacal bone biopsies and BMD in 84 unrelated postmenopausal women. Transcripts that located within +/- 500kb of the candidate SNPs at the GWS loci were queried in a dataset of eQTLs that correlated with adjusted BMD with a p-value below 0.1 in the published dataset, 163 uniquely mapping transcripts in total for FN- and LS-BMD. Affymetrix HG U133 2.0 plus array was used for expression analysis, as previously described[14].

The second eQTL dataset used expression data from multiple publicly available and in-house datasets to carry out cis-association analysis: **a**) CEU lymphoblastoid cell lines (n=60) for expression QTL association[15] using Illumina Sentrix Human-6 Expression BeadChip version 1 and Genotypes from HapMap project, **b**) allelic expression cis-associations using llumina Human1M-duo BeadChip for lymphoblastoid cell lines (n=53)[16] and for fibroblasts, Illumina HumanRef-8 v3.0 for expression traits and Illumina HapMap 1M Duo chip for genotypes (Pastinen, unpublished data), and **c**) RNAseq CEU eQTLs, where expression values were taken from RNA sequencing data (Illumina GA2) and genotypes from HapMap project[17] (lymphoblastoid cell lines, n=60); **d**) primary human fibroblasts (n=64) treated with cholesterol, resveratrol, and ethanol (Pastinen, unpublished data), and primary human osteoblasts (HOb) (n=104) treated with bone morphogenetic protein BMP-2, dexamethasone, prostaglandin E2, and control PBS using Illumina HumRef-8v2 BeadChips for expression traits and Illumina HapMap 550k Duo chip for genotypes[18]. Cis-regulatory effects were tested using SNPs mapping the candidate SNP +/- 500kb. For the fibroblast and osteoblast samples, due to limited genotype information, we imputed the genotypes (MACH 1.0) for HapMap SNPs to provide a larger density of SNPs to test. Cis-associations for most datasets were carried out using a linear regression model implemented in the PLINK software package. Association analysis for the HOb datasets was carried out using MACH2QTL, using the genotype imputation data. For the RNAseq CEU eQTL analysis, Spearman-rank correlation was used as implemented in the R (version 2.12.1) software package. Variance r^2 is given for all eQTL datasets except for the RNAseq CEU analysis, where the rho value was calculated.

The third eQTL dataset at deCODE Genetics utilizes expression data from adipose tissue and whole blood from 603 and Icelandic individuals, respectively[19]. Genotyping was performed using Infinium HumanHap300 and 370CNV BeadChips (Illumina) and genotypes imputed into HapMap 2.5m SNPs using IMPUTE. Expression analysis was performed using an Agilent microarry of 23,700 transcripts. The correlation between the SNPs and expression of genes at the 56 GWS loci (located within +/- 500kb from the candidate SNP) was tested by linear regression analysis of normalized expression level (age, sex, BMI and weight adjusted, and for differential cell count in case of whole blood) on SNP genotypes as previously described[20].

The fourth eQTL dataset is derived from circulating monocytes in 1,490 unrelated individuals, published by Zeller and colleagues[21] (publicly available at genecanvas.ecgene.net). All associations between SNPs and expressions with a p-value$<5 \times 10^{-5}$ were available for querying, using data analysed as described[21], of expression traits measured on Illumina Human HT-12 expression BeadChip (12,808 detectable expression traits) and SNPs genotyped on an

Affymetrix 6.0 array. Expression of genes located within +/- 500kb from the candidate GWS SNPs at the 56 loci were queried for association in the dataset. Proxy SNPs were used for 42 SNPs that are not present on the Affymetrix 6.0 array (r2>0.7), no proxy was available for the 4 SNPs, rs5934507 (chrX), rs13336428 (16p13.3_2), rs1566045 (16q12.1) and rs3755955 (4p16.3) and these loci therefore not represented in this dataset. Study-wise threshold of significance correcting of the number of expressions tested was set at $P< 5 x10^{-5}$.

2.5. Literature-based annotation with GRAIL

The Gene Relationships Across Implicated Loci (GRAIL)[22] software was used to investigate relationships between 55 autosomal loci identified from the combined results. Briefly, GRAIL evaluates connectivity and relationships between identified loci, by systematically mining Pubmed abstracts for shared text amongst possible genes at associated loci. Genes from independently identified loci that have increased sharing of text in the scientific literature are more likely to be functionally related and therefore more likely to be truly involved in disease pathogenesis[22]. As no information about the phenotype is used, the relatedness of genes at associated loci is not biased with respect to the phenotype. We conducted GRAIL analysis using the December 2006 Pubmed data set (avoiding potential bias from investigation of candidate genes stimulated by GWAS), the HG18 build of the human genome, and the 55 autosomal BMD loci with a p-value $<5 \times 10^{-8}$.

To confirm the significance of these findings, we followed a previously described strategy.[22] We applied GRAIL to 2000 random matched SNP sets; each set consisted of 55 SNPs randomly selected from a previously published[23] set of 56,988 HapMap SNPs after LD pruning. We selected SNPs in LD with at least one gene, and so that in aggregate the total number of genes implicated was 224 +/-11 genes. These SNP sets matched the 55 SNPs associated with BMD in terms of total gene content, since those genes implicated 224 genes in aggregate. Then we individually tested each SNP test through GRAIL, noting with each run what proportion of SNPs demonstrated connectivity with p_{text} scores ≤ 0.01.

2.6. Allele Risk Modeling

To estimate the cumulative effect of the genetic variants, we constructed genetic susceptibility scores that summed the weighted number of 55 autosomal and 8 secondary BMD-decreasing alleles, where the weights were derived from the beta-coefficients of the relationship between BMD and the BMD-decreasing allele. The "osteoporosis" outcome, was defined as having a FN-BMD T-score < -2.5. We used the NHANES[24] (female) mean and SD (mean 0.849, SD 0.109) to estimate T-scores from the raw FN-BMD (T = (ZFNBMD-0.849)/0.109). For the fracture risk modeling, first we used the 16 SNPs also associated with fracture risk were used to construct the genetic susceptibility scores and then compared the results by including the rest of the non-significantly associated SNPs. For this analysis, the weights were derived from the beta-coefficients of the relationship between fracture risk and the risk-increasing allele.

Models were estimated using the Prospective Epidemiological Risk Factor (PERF) study. This study is composed of postmenopausal women, in the age rage 55-86 years, taking part in a prospective epidemiological study and in various clinical trials for osteoporosis at the Center for Clinical and Basic Research, Copenhagen. Baseline DEXA- measurement (Hologic QDR2000) at the hip (total hip) and lumbar spine (L2-L4) was used. Osteoporotic fractures included low trauma fractures from medical records and radiographic documentation. (Supplementary Methods Table 3A, 3B, 3C). A subset of 2,836 women with both FN-BMD and fracture information were used for this analysis.

The PERF study was genotyped in Stage 2, had relatively large numbers of women with fracture ascertainment, and was not included in the discovery set. Furthermore, effect estimates of a meta-analysis excluding PERF in the Stage 2 replication samples were used to weight BMD-decreasing alleles. Weights were transformed to have a mean=1 by dividing each effect by the median of the FN-BMD effects. Weights for each of the 63 SNPs are available in the Supplementary Tables.

We performed profile scoring for each individual of the PERF study as implemented in PLINK, where:

$Score_i = \Sigma_{j=1 \text{ to } m} b_j x_{ij}$, where

m= number of SNPs

b_j =effect of allele at locus j

x_{ij}=number of reference alleles of individual i at locus j

The resulting genetic scores were divided in quintiles and the mean FN-BMD, osteoporosis risk and fracture risk estimates were computed per each quintile of weighted allele score. The performance of the osteoporosis and fracture prediction properties of the genetic score was quantified using the area under the receptor-operator characteristics (ROC) curves implemented in the software PredictABEL[25]. For this analysis the continuous weighted genotypic risk score was used in a regression model. Finally, the measure of variance explained (adjusted r^2) was estimated from a linear regression model incorporating the quantitative score as the predictor and the age- and weight adjusted standardized FN-BMD residuals as outcome.

3. URLS

METAL: http://www.sph.umich.edu/csg/abecasis/Metal/

KbioSicences: http://www.kbioscience.co.uk/

PLINK: http://pngu.mgh.harvard.edu/purcell/plink/

GenABEL suite: http://www.genabel.org/

HapMap: http://www.hapmap.org/

LocusZoom: http://csg.sph.umich.edu/locuszoom/

1000 Genomes: http://www.1000genomes.org/

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5. COHORT-SPECIFIC CONTRIBUTIONS

Type of Contribution	Cohort	Name	Overseeing (PI)	Genotyping	Phenotyping	Data analysis
GWAS	AFOS	Alan R Shuldiner	X			
GWAS	AFOS	Braxton D Mitchell	X			
GWAS	AFOS	Elizabeth A Streeten	X		X	
GWAS	AFOS	Laura M Yerges-Armstrong				X
GWAS	AOGC	Dana Willner				X
GWAS	AOGC	David M Evans				X
GWAS	AOGC	Elaine M Dennison			X	
GWAS	AOGC	Emma L Duncan		X	X	X
GWAS	AOGC	Eugene McCloskey	X		X	
GWAS	AOGC	Geoffrey C Nicholson	X		X	
GWAS	AOGC	Graeme Jones	X		X	
GWAS	AOGC	Graeme R Clark		X		
GWAS	AOGC	Ian R Reid	X		X	
GWAS	AOGC	John A Eisman	X		X	X
GWAS	AOGC	John P Kemp				X
GWAS	AOGC	Matthew A Brown	X	X	X	X
GWAS	AOGC	Patrick Danoy		X		
GWAS	AOGC	Paul J Leo				X
GWAS	AOGC	Philip N Sambrook	X		X	
GWAS	AOGC	Richard Eastell	X		X	
GWAS	CHS	Bruce M Psaty	X			
GWAS	CHS	Guo Li				X
GWAS	CHS	Jerome I Rotter		X		X
GWAS	CHS	John Robbins			X	
GWAS	CHS, HealthABC	Jane A Cauley	X		X	
GWAS	deCODE	Gudmar Thorleifsson				X
GWAS	deCODE	Gunnar Sigurdsson			X	
GWAS	deCODE	Hrefna Johannsdottir		X		
GWAS	deCODE	Kari Stefansson	X			
GWAS	deCODE	Stefan Th. Palsson		X		
GWAS	deCODE	Thorvaldur Ingvarsson			X	
GWAS	deCODE	Unnur Styrkarsdottir	X	X	X	X
GWAS	deCODE	Unnur Thorsteinsdottir	X			
GWAS	EPIC-Norfolk	Alireza Moayyeri			X	X
GWAS	EPIC-Norfolk	Kay-Tee Khaw	X			
GWAS	EPIC-Norfolk	Nick J Wareham	X	X		
GWAS	EPIC-Norfolk	Robert Luben		X	X	X
GWAS	EPIC-Norfolk,EPOS	Jonathan Reeve	X		X	
GWAS	EPIC-Norfolk,EPOS	Stephen K Kaptoge			X	X
GWAS	ERF	Ben A Oostra			X	
GWAS	ERF	Cornelia M van Duijn	X		X	
GWAS	ERF	M. Carola Zillikens	X		X	
GWAS	ERF	Najaf Amin				X
GWAS	ERF	Yurii S Aulchenko		X		
GWAS	Fram	Ching-Ti Liu				X
GWAS	Fram	David Karasik				X
GWAS	Fram	Douglas P. Kiel	X		X	X
GWAS	Fram	Kannabiran Nandakumar				X
GWAS	Fram	L. Adrienne Cupples	X	X		
GWAS	Fram	Yanhua Zhou				X
GWAS	Fram	Yi-Hsiang Hsu				X
GWAS	GOOD, MrOS Sweden	Claes Ohlsson	X	X	X	
GWAS	GOOD	Joel Eriksson				X
GWAS	GOOD	Liesbeth Vandenput		X		X
GWAS	GOOD	Mattias Lorentzon	X	X	X	
GWAS	Health ABC	Candace M. Kammerer				X
GWAS	Health ABC	Frances A. Tylavsky	X			
GWAS	Health ABC	Ryan L. Minster				X
GWAS	Health ABC	Steven R. Cummings	X			
GWAS	Health ABC	Yongmei Liu		X	X	
GWAS	Health ABC,AGES	Tamara B. Harris	X			
GWAS	HKOS	Annie Wai Chee Kung	X		X	
GWAS	HKOS	Pak Chung Sham	X			X
GWAS	HKOS	Su-Mei Xiao		X	X	X
GWAS	INDIANA	Daniel L Koller				X
GWAS	INDIANA	Michael J Econs	X		X	

5. COHORT-SPECIFIC CONTRIBUTIONS

Type of Contribution	Cohort	Name	Overseeing (PI)	Genotyping	Phenotyping	Data analysis
GWAS	INDIANA	Munro Peacock	X		X	
GWAS	ORCADES	James F Wilson	X		X	
GWAS	ORCADES,EDOS	Omar ME Albagha			X	X
GWAS	ORCADES,EDOS	Stuart H Ralston	X		X	
GWAS	RS-I, RS-II & RS-III	Albert Hofman	X		X	
GWAS	RS-I, RS-II & RS-III	Andre G. Uitterlinden	X	X	X	
GWAS	RS-I, RS-II & RS-III	Carolina Medina-Gómez		X		
GWAS	RS-I, RS-II & RS-III	Fernando Rivadeneira	X	X	X	X
GWAS	RS-I, RS-II & RS-III	Huibert A.P. Pols	X		X	
GWAS	RS-I, RS-II & RS-III	Joyce B.J. van Meurs		X	X	
GWAS	RS-I, RS-II & RS-III	Karol Estrada		X		X
GWAS	RS-I, RS-II & RS-III	Ling Oei		X		X
GWAS	RS-I, RS-II & RS-III	Lizbeth Herrera		X		
GWAS	RS-I, RS-II & RS-III	Martha Castano-Betancourt			X	
GWAS	TUK1, TUK23	Frances MK Williams			X	
GWAS	TUK1, TUK23	Hou-Feng Zheng				X
GWAS	TUK1, TUK23	J Brent Richards	X			X
GWAS	TUK1, TUK23	Rui Li				X
GWAS	TUK1, TUK23	Scott G Wilson			X	
GWAS	TUK1, TUK23	Timothy D Spector	X	X	X	
Meta-analytical center	IOANNINA	Evangelia E Ntzani				X
Meta-analytical center	IOANNINA	Evangelos Evangelou				X
Meta-analytical center	IOANNINA	John P.A. Ioannidis	X			X
GxG	GXG Analytical support	Andrew R Wood				X
INSILICO	AGES Reykjavik study	Albert V Smith				X
INSILICO	AGES Reykjavik study	Kristin Siggeirsdottir			X	
INSILICO	AGES Reykjavik study	Melissa Garcia				X
INSILICO	AGES Reykjavik study	Thor Aspelund			X	X
INSILICO	AGES Reykjavik study	Vilmundur Gudnason	X		X	
INSILICO	PROSPER/PHASE study	Brendan M. Buckley	X			
INSILICO	PROSPER/PHASE study	Ian Ford	X			
INSILICO	PROSPER/PHASE study	J Wouter Jukema	X			
INSILICO	PROSPER/PHASE study	P Eline Slagboom	X			
INSILICO	PROSPER/PHASE study	Stella Trompet		X		X
INSILICO	WGHS	Daniel I. Chasman	X	X	X	X
INSILICO	WGHS	Lynda M. Rose			X	X
INSILICO	WGHS	Paul M Ridker	X		X	
INSILICO	WHI	Aaron K Aragaki		X	X	X
INSILICO	WHI	Andrea Z Lacroix		X	X	X
INSILICO	WHI	Charles Kooperberg		X	X	X
INSILICO	WHI	David J Duggan		X		
INSILICO	WHI	Rebecca D Jackson	X	X	X	X
INSILICO	Young Finns Study	Jorma Viikari	X		X	
INSILICO	Young Finns Study	Marika Laaksonen			X	
INSILICO	Young Finns Study	Mika Kähönen	X		X	
INSILICO	Young Finns Study	Olli Raitakari	X		X	X
INSILICO	Young Finns Study	Terho Lehtimäki	X	X		X
INSILICO	Young Finns Study	Ville Aalto				X
De novo	APOSS, NOSOS	David M. Reid			X	
De novo	APOSS, NOSOS	Lynne J Hocking				X
De novo	AROS, DOPS	Bente Lomholt Langdahl	X			
De novo	AROS, DOPS	Lise Bjerre Husted			X	
De novo	AUSTRIOSA, AUSTRIOSB	Barbara Obermayer-Pietsch		X	X	X
De novo	AUSTRIOSA, AUSTRIOSB	Olivia Trummer		X		
De novo	BARCOS	Natàlia Garcia-Giralt			X	
De novo	BARCOS	Roser Urreizti	X			
De novo	BARCOS	Susana Balcells	X			
De novo	BARCOS	Xavier Nogues	X		X	
De novo	Cabrio-C, Cabrio-CC	Jesús González-Macías	X			
De novo	Cabrio-C, Cabrio-CC	José M. Olmos	X		X	
De novo	Cabrio-C, Cabrio-CC	José A. Riancho	X		X	
De novo	Cabrio-C, Cabrio-CC	María T. Zarrabeitia	X			
De novo	AOGC,CAIFOS	Richard L Prince	X	X	X	
De novo	CAIFOS	Joshua R Lewis		X		
De novo	CAIFOS	Kun Zhu			X	
De novo	Calex-family	Markku Alen	X			

5. COHORT-SPECIFIC CONTRIBUTIONS

Type of Contribution	Cohort	Name	Overseeing (PI)	Genotyping	Phenotyping	Data analysis
De novo	Calex-family	Sulin Cheng		X		X
De novo	CaMos	David Goltzman	X			
De novo	CaMos	Millan S. Patel				X
De novo	DOES	Jacqueline R Center			X	X
De novo	DOES	Tuan V Nguyen				X
De novo	EDOS	Nerea Alonso			X	
De novo	EPOLOS	Marcin Kruk			X	
De novo	EPOLOS	Roman S Lorenc	X			
De novo	EPOS	Serena Scollen		X		
De novo	FLOS	Laura Masi	X		X	
De novo	FLOS	Maria Luisa Brandi	X		X	
De novo	GEOS	François Rousseau	X		X	
De novo	GEOS	Sylvie Giroux		X	X	
De novo	GEVUR	Elza Khusnutdinova		X		
De novo	GEVUR	Rita Khusainova		X		
De novo	GROS	Panagoula Kollia	X			
De novo	GROS	Theodora Koromila			X	X
De novo	GROS	Zoe Dailiana			X	
De novo	HCS	Cyrus Cooper	X			
De novo	HCS	Karen A. Jameson			X	
De novo	HK	Jean Woo			X	
De novo	HK	Nelson L.S. Tang	X			
De novo	HK	Ping C. Leung			X	
De novo	KorAMC	Ghi Su Kim			X	
De novo	KorAMC	Jung-Min Koh	X		X	
De novo	KorAMC	Seung Hun Lee			X	
De novo	LASA	Natasja M. van Schoor			X	
De novo	LASA	Paul Lips	X			
De novo	ManMC	William D. Leslie	X			
De novo	MrOS Sweden	Dan Mellström	X		X	
De novo	MrOS Sweden	Magnus Karlsson	X		X	
De novo	MrOS Sweden	Östen Ljunggren	X		X	
De novo	OAS	Morten Frost	X		X	
De novo	OAS	Wim van Hul	X		X	
De novo	OSTEOS	George Dedoussis	X			
De novo	PERF	Claus Christiansen	X		X	
De novo	SLO-PREVAL	Janez Prezelj	X		X	X
De novo	SLO-PREVAL	Janja Marc	X	X	X	X
De novo	SLO-PREVAL	Simona Mencej-Bedrac		X		X
De novo	UFO	Göran Hallmans			X	X
De novo	UFO	Olle Svensson			X	X
De novo	UFO	Ulrika Pettersson	X		X	X
De novo	deCODE	Gudmar Thorleifsson				X
De novo	deCODE	Gunnar Sigurdsson			X	
De novo	deCODE	Hrefna Johannsdottir		X		
De novo	deCODE	Kari Stefansson	X			
De novo	deCODE	Stefan Th. Palsson		X		
De novo	deCODE	Thorvaldur Ingvarsson			X	
De novo	deCODE	Unnur Styrkarsdottir	X	X	X	X
De novo	deCODE	Unnur Thorsteinsdottir	X			
EQTL	eQTL analytical center (deCODE)	Gudmar Thorleifsson				X
EQTL	eQTL analytical center (deCODE)	Unnur Styrkarsdottir	X	X	X	X
EQTL	eQTL analytical center (deCODE)	Unnur Thorsteinsdottir	X			
EQTL	eQTL analytical center (deCODE)	Kari Stefansson	X			
EQTL	eQTL analytical center (CA)	Dominique Verlaan		X	X	
EQTL	eQTL analytical center (CA)	Elin Grundberg		X	X	
EQTL	eQTL analytical center (CA)	Tomi Pastinen	X			
EQTL	eQTL analytical center (CA)	Tony Kwan		X		
EQTL	eQTL analytical center (NO)	Kaare M. Gautvik	X	X	X	
EQTL	eQTL analytical center (NO)	Sjur Reppe		X	X	X
GRAIL	Grail Analytical Support	Soumya Raychaudhuri				X

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