Supplemental Table 1: Results from prior association studies of obesity and BMI

SNP	*Gene*	*Risk allele*	*First author, reference number*	*Study*	*phenotype*	*Effect Size (95% CI)*	*Risk allele frequency*	*p-value*	*N*	*Effect Size used in power calculations*
rs2815752	NEGR1	T	Cotsapas, 7	case-control	obesity[a]	1.11 (0.98 - 1.25)[h]	0.65	0.035	775 cases, 3197 controls	0.10 (beta for BMI, Willer et al.)
			Renstrom, 16	case-control	obesity	1.10 (1.01 - 1.20)	0.58	0.028	353 cases, 1370 controls	
			Willer, 8	GWAS	BMI	0.10 (0.04 - 0.16)[c]	0.62	6.0E-08	83,499	
rs6548238	TMEM18	C	Cotsapas,7	case-control	obesity[a]	1.17 (1.01 - 1.37)[h]	0.82	0.016	775 cases, 3197 controls	0.26 (beta for BMI, Willer et al.)
			Renstrom, 16	case-control	obesity	1.10 (0.98 - 1.22)	0.82	0.095	353 cases, 1370 controls	
			Willer, 8	GWAS	BMI	0.26 (0.19 - 0.34)[c]	0.84	1.4E-18	84,823	
rs10938397	GNPDA2	G	Cotsapas,7	case-control	obesity[a]	1.18 (1.06 - 1.32)	0.43	1.7E-03	775 cases, 3197 controls	0.19 (beta for BMI, Willer et al.)
			Renstrom, 16	case-control	obesity	1.10 (1.00 - 1.20)	0.37	0.045	353 cases, 1370 controls	
			Willer, 8	GWAS	BMI	0.19 (0.13 - 0.25)[c]	0.45	3.4E-16	81,758	
rs10838738	MTCH2	G	Cotsapas,7	case-control	obesity[a]	1.09 (0.97 - 1.23)	0.35	0.063	775 cases, 3197 controls	0.07 (beta for BMI, Willer et al.)
			Willer, 8	GWAS	BMI	0.07 (0.01 - 0.13)[c]	0.34	4.6E-09	80,917	
rs7498665	SH2B1	G	Cotsapas,7	case-control	obesity[a]	1.12 (1.00 - 1.26)	0.37	0.022	775 cases, 3197 controls	0.15 (beta for BMI, Willer et al.)
			Thorleifsson, 12	GWAS	obesity	3.63 (2.49 - 4.77)	NR	3.0E-10	>68,000	
			Renstrom, 16	case-control	obesity	1.13 (1.04 - 1.24)	0.4	7.0E-03	353 cases, 1370 controls	
			Thorleifsson, 12	GWAS	BMI	3.63 (2.49 - 4.77)[g]	NR	1.0E-09	>68,000	
			Willer, 8	GWAS	BMI	0.15 (0.08 - 0.21)[c]	0.41	5.1E-11	86,677	
rs1121980	FTO	A	Hinney, 10	case-control	obesity[b]	1.66 (1.37 - 2.01)	.41 (controls)	1.0E-07	487 cases, 442 controls	0.59 (beta for BMI, Scuteri et al.)
			Renstrom, 16	case-control	obesity	1.15 (1.05 - 1.25)	0.42	2.0E-03	353 cases, 1370 controls	
			Scuteri, 11	GWAS	BMI	0.13 SD [f h]	0.45	1.4E-06	6,148; including 1407 imputed family members	
		NR	Loos , 6	GWAS	lnBMI	0.06 (0.04 - 0.08) [d]	NR	4.0E-08	77,228	
rs3751812	FTO	T	Thorleifsson, 12	GWAS	BMI	8.09 (6.99 - 9.19) [g]	NR	4.1E-47	>68,000	0.36 (beta for BMI, Thorleifsson et al.)
			Grant , 3	case-control	obesity[e]	1.27 (1.08 - 1.47)	.39 (controls)	2.2E-03	418 cases, 2270 controls	
rs8050136	FTO	A	Hinney, 10	case-control	obesity[b]	1.59 (1.31 - 1.92)	.39 (controls)	9.8E-06	487 cases, 442 controls	0.36 (beta for BMI, Thorleifsson et al.)
			Thorleifsson, 12	GWAS	obesity	1.27 (1.21 - 1.32)	NR	3.0E-26	>68,000	
			Bressler, 18[i]	case-control	obesity	1.21 (1.13 - 1.29)	.37 (controls)	<0.001	2470 cases, 4065 controls	
			Scuteri, 11	GWAS	BMI	0.13 SD [f h]	0.46	1.1E-06	6,148; including 1407 imputed family members	
			Thorleifsson, 12	GWAS	BMI	8.04 (6.96 - 9.12) [g]	NR	1.0E-47	>68,000	

Supplemental Table 1: (continued)

SNP	*Gene*	*Risk allele*	*Study*	*Study design*	*phenotype*	*Effect Size (95% CI)*	*Risk allele frequency*	*p-value*	*N*	*Effect Size used in power calculations*
rs9930506	FTO	G	Scuteri, 11	GWAS	BMI	0.13 SD [f h]	0.46	8.6E-07	6,148; including 1407 imputed family members	0.59 (beta for BMI, Scuteri et al.)
rs9939609	FTO	A	Cotsapas,7	case-control	obesity[a]	1.46 (1.31 - 1.64)	0.42	1.4E-11	775 cases, 3197 controls	0.33 (beta for BMI, Willer et al.)
			Hinney, 10	case-control	obesity[b]	1.57 (1.30 - 1.89)	.39 (controls)	1.9E-06	487 cases, 442 controls	
			Bressler, 18 [i]	case-control	obesity	1.22 (1.14 - 1.30)	.37 (controls)	<0.001	2470 cases, 4065 controls	
			Frayling, 17	meta-analysis	obesity	1.32 (1.26 - 1.39)	0.39	3.0E-26	38,759	
			Scuteri, 11	GWAS	BMI	0.13 SD [f h]	0.46	1.8E-06	6,148; including 1407 imputed family members	
			Willer, 8	GWAS	BMI	0.33 (0.27 - 0.39)[c]	0.41	4.3E-51	83,384	
rs12970134	MC4R	A	Thorleifsson, 12	GWAS	BMI	4.38 (3.16 - 5.60) [g]	NR	1.2E-12	>68,000	0.20 (beta for BMI, Thorleifsson et al.)
			Thorleifsson, 12	GWAS	obesity	1.12 (1.06 - 1.17)	NR	9.9E-06	>68,000	
rs17782313	MC4R	C	Cotsapas,7	case-control	obesity[a]	1.02 (0.90 - 1.17)	0.24	0.36	775 cases, 3197 controls	0.20 (beta for BMI, Willer et al.)
			Meyre, 13	case-control	obesity	1.22 (1.05 - 1.40)	NR	5.0E-15	1380 cases, 1416 controls	
			Renstrom, 16	case-control	obesity	1.11 (1.00 - 1.22)	0.26	0.042	353 cases, 1370 controls	
			Willer, 8	GWAS	BMI	0.20 (0.12 - 0.28)[c]	0.21	4.6E-18	80,747	
			Loos, 6	GWAS	BMI	0.05 (0.04 - 0.06) [d]	NR	3.0E-15	77,228	
rs11084753	KCTD15	G	Cotsapas,7	case-control	obesity[a]	1.15 (1.02 - 1.30) [h]	0.69	0.013	775 cases, 3197 controls	0.06 (beta for BMI, Willer et al.)
			Renstrom, 16	case-control	obesity	1.05 (0.96 - 1.14) [h]	0.63	0.330	353 cases, 1370 controls	
			Willer, 8	GWAS	BMI	0.06 (-0.01 - 0.13)[c]	0.67	2.3E-08	71,706	

NR: Not reported; OR: Odds Ratio; obesity defined as BMI≥ 30

[a] :"extreme obesity", defined as BMI > 40;

[b] :"early onset extreme obesity", defined as children and adolescents (mean age ~14) receiving inpatient hospital treatment for obesit

[c]: beta for per-allele change in BMI (kg/m2)

[d] : beta for per-allele change in lnBMI

[e]: "obese" defined as BMI ≥ 95th percentile

[f]: beta for change in standard deviations

[g]: beta for change in percentile of standard deviations

[h]: study used opposite risk allele as PAGE, therefore opposite effect size and CIs are presented in table

[i]: includes European American subjects from CALiCo also included in PAGE analyses

Supplementary Table 2: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group and adjusted for ancestry principal components

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	0.006 (0.001 - 0.01)	0.01	22774	0.62	0.0001 (-0.012 - 0.012)	0.98	2767	0.71	0.001 (-0.005 - 0.008)	0.67	7807	0.54
TMEM18	rs6548238	2p25.3	C	0.008 (0.003 - 0.014)	2.49E-03	22406	0.83	0.005 (-0.01 - 0.021)	0.50	2767	0.86	0.009 (-0.0001 - 0.018)	0.05	8541	0.88
GNPDA2	rs10938397	4p12	G	0.005 (0.001 - 0.009)	0.01	22753	0.43	0.009 (-0.003 - 0.020)	0.13	2744	0.39	0.013 (0.006 - 0.020)	4.88E-04	8479	0.25
MTCH2	rs10838738	11p11.2	G	0.005 (0.001 - 0.009)	0.02	22784	0.35	0.005 (-0.006 - 0.016)	0.37	2769	0.36	0.004 (-0.007 - 0.014)	0.51	8512	0.10
SH2B1	rs7498665	16p11.2	G	0.002 (-0.002 - 0.006)	0.37	22749	0.38	-0.011 (-0.022 - -0.0001)	0.05	2761	0.43	0.008 (0.001 - 0.014)	0.03	8518	0.27
FTO	rs1121980	16q12.12	A	0.015 (0.011 - 0.019)	1.05E-11	21426	0.43	0.008 (-0.045 - 0.061)	0.77	426	0.37	0.005 (-0.005 - 0.014)	0.32	3545	0.47
FTO	rs3751812	16q12.12	T	0.015 (0.011 - 0.020)	4.97E-12	21918	0.55	0.013 (-0.005 - 0.032)	0.17	1911	0.28	0.013 (-0.007 - 0.032)	0.20	3959	0.11
FTO	rs8050136	16q12.12	A	0.015 (0.011 - 0.019)	3.51E-12	22788	0.41	0.019 (0.007 - 0.030)	0.002	2874	0.29	0.005 (-0.001 - 0.012)	0.10	8028	0.43
FTO	rs9930506	16q12.12	G	0.014 (0.010 - 0.019)	4.71E-11	21783	0.44	0.017 (-0.002 - 0.035)	0.07	1912	0.32	0.005 (-0.005 - 0.014)	0.34	6610	0.21
FTO	rs9939609	16q12.12	A	0.015 (0.011 - 0.020)	4.92E-12	21769	0.41	-0.002 (-0.053 - 0.049)	0.93	449	0.33	0.003 (-0.006 - 0.012)	0.54	3588	0.47
MC4R	rs12970134	18q22	A	0.007 (0.002 - 0.012)	4.00E-03	21770	0.26	-0.027 (-0.077 - 0.022)	0.28	448	0.17	0.008 (-0.006 - 0.021)	0.25	3588	0.13
MC4R	rs17782313	18q22	C	0.006 (0.001 - 0.011)	0.02	22736	0.23	0.003 (-0.012 - 0.019)	0.69	2769	0.14	0.007 (0.0001 - 0.014)	0.05	7809	0.28
KCTD15	rs11084753	19q13.11	G	0.0004 (-0.004 - 0.005)	0.86	22748	0.67	0.007 (-0.004 - 0.018)	0.24	2767	0.66	0.002 (-0.005 - 0.008)	0.61	7806	0.64

Supplementary Table 2: Continued

				East Asians				Pacific Islanders			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	-0.004 (-0.022 - 0.014)	0.67	1902	0.93	-0.003 (-0.046 - 0.04)	0.89	321	0.84
TMEM18	rs6548238	2p25.3	C	0.001 (-0.014 - 0.017)	0.88	1902	0.90	0.002 (-0.057 - 0.06)	0.96	320	0.93
GNPDA2	rs10938397	4p12	G	-0.002 (-0.012 - 0.009)	0.77	1897	0.29	0.046 (0.013 - 0.079)	0.01	321	0.27
MTCH2	rs10838738	11p11.2	G	0.008 (-0.002 - 0.018)	0.10	1901	0.33	0.016 (-0.017 - 0.048)	0.34	321	0.31
SH2B1	rs7498665	16p11.2	G	0.020 (0.006 - 0.034)	0.01	1899	0.14	0.019 (-0.015 - 0.052)	0.28	320	0.29
FTO	rs1121980	16q12.12	A	0.005 (-0.022 - 0.033)	0.70	672	0.21				
FTO	rs3751812	16q12.12	T	0.012 (-0.017 - 0.041)	0.43	701	0.18				
FTO	rs8050136	16q12.12	A	0.018 (0.006 - 0.030)	2.31E-03	1930	0.20	0.017 (-0.017 - 0.051)	0.34	331	0.23
FTO	rs9930506	16q12.12	G	0.009 (-0.017 - 0.034)	0.51	699	0.22				
FTO	rs9939609	16q12.12	A	0.012 (-0.017 - 0.040)	0.42	696	0.18				
MC4R	rs12970134	18q22	A	0.025 (-0.007 - 0.056)	0.12	696	0.16				
MC4R	rs17782313	18q22	C	0.001 (-0.010 - 0.013)	0.82	1900	0.22	-0.027 (-0.071 - 0.018)	0.24	321	0.12
KCTD15	rs11084753	19q13.11	G	0.001 (-0.009 - 0.01)	0.91	1902	0.30	0.024 (-0.007 - 0.055)	0.13	319	0.45

CA: coded allele; AF: risk allele frequency; CI: confidence interva

Supplementary Table 3: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group and unadjusted for ancestry principal components

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	0.006 (0.002 - 0.01)	0.01	22774	0.62	0.001 (-0.011 - 0.013)	0.84	2767	0.71	0.0004 (-0.006 - 0.007)	0.91	7807	0.54
TMEM18	rs6548238	2p25.3	C	0.009 (0.003 - 0.014)	2.12E-03	22406	0.83	0.007 (-0.009 - 0.022)	0.41	2767	0.86	0.01 (-0.0005 - 0.019)	0.04	8541	0.88
GNPDA2	rs10938397	4p12	G	0.005 (0.001 - 0.009)	0.02	22753	0.43	0.007 (-0.004 - 0.019)	0.20	2744	0.39	0.011 (0.003 - 0.018)	3.90E-03	8479	0.25
MTCH2	rs10838738	11p11.2	G	0.005 (0.0004 - 0.009)	0.03	22784	0.35	0.006 (-0.005 - 0.018)	0.28	2769	0.36	-0.005 (-0.015 - 0.005)	0.33	8512	0.10
SH2B1	rs7498665	16p11.2	G	0.002 (-0.002 - 0.006)	0.42	22749	0.38	-0.009 (-0.020 - 0.002)	0.12	2761	0.43	0.005 (-0.002 - 0.012)	0.14	8518	0.27
FTO	rs1121980	16q12.12	A	0.015 (0.010 - 0.019)	1.84E-11	21426	0.43	-0.003 (-0.053 - 0.048)	0.91	426	0.37	0.005 (-0.004 - 0.014)	0.30	3545	0.47
FTO	rs3751812	16q12.12	T	0.015 (0.011 - 0.019)	6.91E-12	21918	0.55	0.006 (-0.012 - 0.023)	0.53	1911	0.28	0.001 (-0.017 - 0.020)	0.89	3959	0.11
FTO	rs8050136	16q12.12	A	0.015 (0.01 - 0.019)	4.80E-12	22788	0.41	0.014 (0.002 - 0.025)	0.02	2874	0.29	0.006 (-0.001 - 0.012)	0.08	8028	0.43
FTO	rs9930506	16q12.12	G	0.014 (0.01 - 0.019)	5.96E-11	21783	0.44	0.010 (-0.007 - 0.028)	0.24	1912	0.32	-0.0004 (-0.01 - 0.009)	0.92	6610	0.21
FTO	rs9939609	16q12.12	A	0.015 (0.011 - 0.019)	6.79E-12	21769	0.41	-0.013 (-0.060 - 0.034)	0.58	449	0.33	0.003 (-0.006 - 0.012)	0.48	3588	0.47
MC4R	rs12970134	18q22	A	0.007 (0.002 - 0.012)	3.49E-03	21770	0.26	-0.026 (-0.074 - 0.023)	0.30	448	0.17	0.005 (-0.009 - 0.018)	0.47	3588	0.13
MC4R	rs17782313	18q22	C	0.006 (0.001 - 0.011)	0.02	22736	0.23	0.001 (-0.014 - 0.016)	0.94	2769	0.14	0.008 (0.001 - 0.015)	0.04	7809	0.28
KCTD15	rs11084753	19q13.11	G	0.0003 (-0.004 - 0.005)	0.91	22748	0.67	0.007 (-0.005 - 0.018)	0.24	2767	0.66	0.001 (-0.005 - 0.008)	0.70	7806	0.64

Supplementary Table 3: Continued

				East Asians				Pacific Islanders			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	-0.005 (-0.023 - 0.014)	0.62	1902	0.93	0.002 (-0.039 - 0.042)	0.94	321	0.84
TMEM18	rs6548238	2p25.3	C	0.001 (-0.014 - 0.017)	0.86	1902	0.90	0.004 (-0.054 - 0.062)	0.89	320	0.93
GNPDA2	rs10938397	4p12	G	-0.002 (-0.011 - 0.008)	0.77	1897	0.29	0.042 (0.009 - 0.074)	0.01	321	0.27
MTCH2	rs10838738	11p11.2	G	0.009 (-0.001 - 0.018)	0.09	1901	0.33	0.015 (-0.017 - 0.047)	0.35	321	0.31
SH2B1	rs7498665	16p11.2	G	0.020 (0.006 - 0.033)	0.01	1899	0.14	0.025 (-0.009 - 0.058)	0.15	320	0.29
FTO	rs1121980	16q12.12	A	0.005 (-0.023 - 0.032)	0.73	672	0.21				
FTO	rs3751812	16q12.12	T	0.011 (-0.018 - 0.039)	0.46	701	0.18				
FTO	rs8050136	16q12.12	A	0.018 (0.007 - 0.030)	0.00	1930	0.20	0.014 (-0.019 - 0.048)	0.40	331	0.23
FTO	rs9930506	16q12.12	G	0.008 (-0.017 - 0.033)	0.53	699	0.22				
FTO	rs9939609	16q12.12	A	0.011 (-0.017 - 0.039)	0.45	696	0.18				
MC4R	rs12970134	18q22	A	0.025 (-0.006 - 0.056)	0.11	696	0.16				
MC4R	rs17782313	18q22	C	0.002 (-0.010 - 0.013)	0.80	1900	0.22	-0.035 (-0.079 - 0.009)	0.12	321	0.12
KCTD15	rs11084753	19q13.11	G	0.001 (-0.009 - 0.011)	0.89	1902	0.30	0.019 (-0.011 - 0.049)	0.21	319	0.45

CA: coded allele; AF: risk allele frequency; CI: confidence interva

Supplemental Table 4: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	0.005 (0.001 - 0.008)	9.16E-03	28261	0.63	-0.0001 (-0.011 - 0.011)	0.99	2891	0.71	0.001 (-0.004 - 0.006)	0.7	10576	0.54
TMEM18	rs6548238	2p25.3	C	0.01 (0.006 - 0.014)	8.59E-08	37061	0.83	0.002 (-0.008 - 0.012)	0.7	6398	0.87	0.013 (0.006 - 0.02)	2.41E-04	14492	0.88
GNPDA2	rs10938397	4p12	G	0.003 (0.0001 - 0.007)	0.04	31346	0.43	0.006 (-0.001 - 0.013)	0.11	6369	0.38	0.009 (0.003 - 0.014)	1.49E-03	14383	0.24
MTCH2	rs10838738	11p11.2	G	0.005 (0.002 - 0.008)	1.01E-03	34679	0.35	0.008 (0.001 - 0.014)	0.03	6406	0.37	-0.006 (-0.014 - 0.002)	0.15	13653	0.1
SH2B1	rs7498665	16p11.2	G	0.002 (-0.001 - 0.006)	0.22	31383	0.38	-0.0001 (-0.007 - 0.007) [a]	0.98	6391	0.45	0.005 (-0.001 - 0.01)	0.09	13642	0.27
FTO	rs1121980	16q12.12	A	0.015 (0.01 - 0.019)	7.60E-12	21645	0.43	-0.003 (-0.053 - 0.048)	0.91	426	0.37	0.004 (-0.005 - 0.012)	0.38	4005	0.47
FTO	rs3751812	16q12.12	T	0.014 (0.01 - 0.018)	4.21E-14	25776	0.52	0.006 (-0.012 - 0.023)	0.53	1911	0.275	0.004 (-0.011 - 0.02)	0.6	4549	0.118
FTO	rs8050136	16q12.12	A	0.014 (0.01 - 0.017)	2.78E-14	26544	0.41	0.013 (0.003 - 0.023)	9.91E-03	3674	0.29	0.006 (-0.0002 - 0.011)	0.06	9435	0.43
FTO	rs9930506	16q12.12	G	0.014 (0.01 - 0.019)	3.27E-11	21998	0.44	0.01 (-0.007 - 0.028)	0.24	1912	0.32	0.0001 (-0.009 - 0.009)	0.97	7065	0.21
FTO	rs9939609	16q12.12	A	0.013 (0.01 - 0.017)	4.61E-15	28286	0.4	-0.013 (-0.06 - 0.034)	0.58	449	0.33	0.001 (-0.005 - 0.008)	0.7	6492	0.47
MC4R	rs12970134	18q22	A	0.008 (0.003 - 0.012)	1.31E-03	21987	0.26	-0.026 (-0.074 - 0.023)	0.3	448	0.17	0.006 (-0.007 - 0.018)	0.38	4046	0.13
MC4R	rs17782313	18q22	C	0.002 (-0.0001 - 0.005)	0.08	35398	0.22	0.004 (-0.006 - 0.013)	0.41	6388	0.13	0.006 (0.0002 - 0.011)	0.04	13698	0.29
KCTD15	rs11084753	19q13.11	G	0.001 (-0.002 - 0.004)	0.61	29411	0.67	0.007 (-0.003 - 0.018)	0.18	2891	0.65	0.001 (-0.004 - 0.006)	0.72	10795	0.64

STable 4: Continued

				East Asians				Pacific Islanders				American Indians			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
NEGR1	rs2815752	1p31.1	T	-0.007 (-0.023 - 0.01)	0.43	2041	0.91	-0.004 (-0.038 - 0.031)	0.84	392	0.81	-0.004 (-0.013 - 0.005)	0.39	6153	0.76
TMEM18	rs6548238	2p25.3	C	-0.001 (-0.015 - 0.014)	0.94	2041	0.9	0.014 (-0.035 - 0.064)	0.57	392	0.92	0.002 (-0.007 - 0.011)	0.61	6186	0.78
GNPDA2	rs10938397	4p12	G	-0.001 (-0.01 - 0.009)	0.92	2037	0.28	0.02 (-0.008 - 0.047)	0.16	392	0.27	0.01 (0.001 - 0.018)	0.03	6125	0.24
MTCH2	rs10838738	11p11.2	G	0.007 (-0.003 - 0.016) [b]	0.16	2041	0.34	0.024 (-0.005 - 0.053)	0.11	392	0.34	-0.004 (-0.011 - 0.003)	0.25	6147	0.46
SH2B1	rs7498665	16p11.2	G	0.019 (0.005 - 0.032)	5.77E-03	2038	0.13	0.028 (-0.001 - 0.056)	0.06	392	0.25	0.012 (0.004 - 0.02)	2.00E-03	6149	0.59
FTO	rs1121980	16q12.12	A	0.005 (-0.023 - 0.032)	0.73	672	0.21								
FTO	rs3751812	16q12.12	T	0.011 (-0.018 - 0.039)	0.46	701	0.18								
FTO	rs8050136	16q12.12	A	0.016 (0.005 - 0.026)	3.14E-03	2325	0.19	0.017 (-0.008 - 0.042)	0.18	574	0.24	0.01 (-0.0004 - 0.021)	0.06	6193	0.13
FTO	rs9930506	16q12.12	G	0.008 (-0.017 - 0.033)	0.53	699	0.22								
FTO	rs9939609	16q12.12	A	0.011 (-0.017 - 0.039)	0.45	696	0.18					0.011 (0.00002 - 0.022)	0.05	6168	0.14
MC4R	rs12970134	18q22	A	0.025 (-0.006 - 0.056)	0.11	696	0.16								
MC4R	rs17782313	18q22	C	0.004 (-0.007 - 0.015)	0.46	2040	0.22	-0.024 (-0.065 - 0.016)	0.24	392	0.14	0.01 (-0.006 - 0.027)	0.21	6163	0.07
KCTD15	rs11084753	19q13.11	G	0.008 (-0.002 - 0.018)	0.1	2041	0.62	-0.001 (-0.03 - 0.027)	0.93	392	0.52	0.001 (-0.007 - 0.008)	0.89	6163	0.69

CA: coded allele; AF: risk allele frequency; CI: confidence interval; [a] = heterogeneity I^2 = 72.5, p-value = 0.03; [b] = heterogeneity I^2 = 87.2, p-value = 0.005

Supplementary Table 5: Meta-analysis results for 7 SNPs not reaching genome-wide significance in prior GWAS of BMI and obesity

Supplementary Table 5a: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	0.0003 (-0.004 - 0.004)	0.9	27929	0.67	0.008 (-0.001 - 0.017)	0.07	3950	0.72	0.001 (-0.007 - 0.008)	0.83	6935	0.75
none identified	rs748192	chr3	A	0 (-0.006 - 0.006)	0.99	21775	0.17	0.028 (-0.031 - 0.086)	0.35	435	0.21	-0.013 (-0.028 - 0.002)	0.09	4030	0.09
none identified	rs10498767	chr6	C	0.001 (-0.003 - 0.005)	0.62	21998	0.48	0.011 (-0.031 - 0.054)	0.6	449	0.55	-0.005 (-0.014 - 0.004)	0.31	4049	0.61
none identified	rs1106683	7q32.3	A	0.0002 (-0.006 - 0.006)	0.96	22124	0.14	-0.014 (-0.045 - 0.017)	0.38	1913	0.09	-0.005 (-0.015 - 0.005)	0.31	7096	0.16
PFKP	rs6602024	10p15.2	A	0.003 (-0.003 - 0.01)	0.35	21727	0.11	0.027 (-0.028 - 0.082)	0.34	449	0.12	0.001 (-0.008 - 0.01)	0.83	3961	0.28
none identified	rs1333026	13q21.32	A	0.006 (-0.002 - 0.014)	0.15	16148	0.14	0.003 (-0.023 - 0.029)	0.82	1912	0.11	-0.005 (-0.017 - 0.006)	0.36	4550	0.25
CTNNBL1	rs6013029	20q11.23	T	0.007 (-0.003 - 0.016)	0.15	22124	0.06	0.007 (-0.026 - 0.041)	0.66	1913	0.07	0.008 (0.0001 - 0.016)	0.05	7079	0.27

				East Asians			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	-0.002 (-0.024 - 0.02)	0.88	695	0.65
none identified	rs748192	chr3	A	-0.006 (-0.033 - 0.021)	0.69	674	0.14
none identified	rs10498767	chr6	C	0.001 (-0.02 - 0.021)	0.94	696	0.61
none identified	rs1106683	7q32.3	A	0.03 (-0.006 - 0.066)	0.1	702	0.09
PFKP	rs6602024	10p15.2	A	0.046 (-0.033 - 0.125)	0.26	696	0.01
none identified	rs1333026	13q21.32	A	-0.034 (-0.066 - -0.002)	0.04	700	0.08
CTNNBL1	rs6013029	20q11.23	T	0.051 (-0.059 - 0.16)	0.36	702	0.01

Supplementary Table 5b: Meta-analysis of logistic regression of putative obesity-related SNPs and obesity, stratified by racial/ethnic group

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	1.004 (0.957 - 1.055)	0.85	27929	0.67	1.007 (0.902 - 1.125)	0.90	3950	0.72	1.035 (0.952 - 1.125)	0.41	6935	0.75
none identified	rs748192	chr3	A	0.998 (0.926 - 1.075)	0.95	21775	0.16	1.322 (0.818 - 2.136)	0.25	435	0.21	0.840 (0.709 - 0.996)	0.05	4030	0.09
none identified	rs10498767	chr6	C	1.031 (0.976 - 1.089)	0.27	21998	0.50	1.213 (0.848 - 1.735)	0.29	449	0.55	0.958 (0.868 - 1.057)	0.39	4049	0.61
none identified	rs1106683	7q32.3	A	0.961 (0.889 - 1.039)	0.32	22124	0.14	0.916 (0.692 - 1.213)	0.54	1913	0.09	0.937 (0.845 - 1.040)	0.22	7096	0.16
PFKP	rs6602024	10p15.2	A	1.030 (0.944 - 1.125)	0.50	21727	0.11	1.265 (0.755 - 2.119)	0.37	449	0.12	0.999 (0.898 - 1.111)	0.98	3961	0.28
none identified	rs1333026	13q21.32	A	1.022 (0.923 - 1.131)	0.68	16148	0.14	1.115 (0.862 - 1.441)	0.41	1912	0.11	0.895 (0.793 - 1.010)	0.07	4550	0.25
CTNNBL1	rs6013029	20q11.23	T	1.022 (0.908 - 1.151)	0.72	22124	0.05	1.029 (0.742 - 1.427)	0.86	1913	0.07	1.045 (0.958 - 1.140)	0.32	7079	0.27

				East Asians			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	0.795 (0.496 - 1.276)	0.34	695	0.65
none identified	rs748192	chr3	A	1.044 (0.579 - 1.883)	0.89	674	0.14
none identified	rs10498767	chr6	C	0.935 (0.593 - 1.474)	0.77	696	0.61
none identified	rs1106683	7q32.3	A	1.400 (0.720 - 2.722)	0.32	702	0.09
PFKP	rs6602024	10p15.2	A	0.373 (0.092 - 1.509)	0.17	696	0.01
none identified	rs1333026	13q21.32	A	0.664 (0.256 - 1.722)	0.40	700	0.08
CTNNBL1	rs6013029	20q11.23	T	1.270 (0.162 - 9.938)	0.82	702	0.01

CA: coded allele; AF: risk allele frequency; CI: confidence interva

Supplementary Table 6a: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group and adjusted for ancestry principal components

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	-0.0002 (-0.005 - 0.004)	0.94	21659	0.67	-0.01 (-0.057 - 0.037)	0.67	449	0.72	0.002 (-0.008 - 0.012)	0.68	3556	0.75
none identified	rs748192	chr3	A	-0.001 (-0.006 - 0.005)	0.84	21558	0.17	0.031 (-0.024 - 0.085)	0.27	435	0.21	-0.012 (-0.028 - 0.005)	0.17	3570	0.09
none identified	rs10498767	chr6	C	0.001 (-0.003 - 0.005)	0.70	21779	0.48	0.008 (-0.035 - 0.051)	0.72	449	0.55	-0.004 (-0.014 - 0.005)	0.39	3590	0.61
none identified	rs1106683	7q32.3	A	0.001 (-0.005 - 0.007)	0.80	21906	0.14	-0.011 (-0.041 - 0.020)	0.48	1913	0.09	-0.006 (-0.017 - 0.004)	0.23	6636	0.16
PFKP	rs6602024	10p15.2	A	0.001 (-0.005 - 0.008)	0.71	21518	0.11	0.024 (-0.026 - 0.074)	0.35	449	0.12	-0.002 (-0.012 - 0.008)	0.71	3523	0.28
none identified	rs1333026	13q21.32	A	0.004 (-0.009 - 0.017)	0.53	12857	0.15	0.005 (-0.021 - 0.031)	0.68	1912	0.11	-0.007 (-0.021 - 0.006)	0.29	3959	0.25
CTNNBL1	rs6013029	20q11.23	T	0.007 (-0.002 - 0.016)	0.15	21905	0.06	0.009 (-0.024 - 0.043)	0.59	1913	0.07	0.006 (-0.002 - 0.015)	0.15	6620	0.27

				East Asians			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	-0.002 (-0.024 - 0.021)	0.88	695	0.65
none identified	rs748192	chr3	A	-0.006 (-0.033 - 0.021)	0.67	674	0.14
none identified	rs10498767	chr6	C	0.001 (-0.019 - 0.021)	0.92	696	0.61
none identified	rs1106683	7q32.3	A	0.031 (-0.005 - 0.067)	0.09	702	0.09
PFKP	rs6602024	10p15.2	A	0.046 (-0.035 - 0.127)	0.26	696	0.01
none identified	rs1333026	13q21.32	A	-0.033 (-0.066 - -0.0005)	0.05	700	0.08
CTNNBL1	rs6013029	20q11.23	T	0.049 (-0.062 - 0.161)	0.39	702	0.01

Supplementary Table 6b: Meta-analysis of linear regression of putative obesity-related SNPs and natural log BMI, stratified by racial/ethnic group and unadjusted for ancestry principal components

				European Americans				Hispanics				African Americans			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	-0.0003 (-0.005 - 0.004)	0.91	21659	0.67	-0.009 (-0.057 - 0.039)	0.72	449	0.72	0.003 (-0.007 - 0.013)	0.57	3556	0.75
none identified	rs748192	chr3	A	-0.001 (-0.006 - 0.005)	0.88	21558	0.17	0.028 (-0.031 - 0.086)	0.35	435	0.21	-0.013 (-0.029 - 0.004)	0.13	3570	0.09
none identified	rs10498767	chr6	C	0.001 (-0.003 - 0.005)	0.67	21779	0.48	0.011 (-0.031 - 0.054)	0.60	449	0.55	-0.004 (-0.013 - 0.006)	0.46	3590	0.61
none identified	rs1106683	7q32.3	A	0.001 (-0.005 - 0.006)	0.87	21906	0.14	-0.014 (-0.045 - 0.017)	0.38	1913	0.09	-0.006 (-0.016 - 0.004)	0.26	6636	0.16
PFKP	rs6602024	10p15.2	A	0.002 (-0.005 - 0.008)	0.65	21518	0.11	0.027 (-0.028 - 0.082)	0.34	449	0.12	0.0003 (-0.010 - 0.010)	0.96	3523	0.28
none identified	rs1333026	13q21.32	A	0.005 (-0.009 - 0.018)	0.50	12857	0.15	0.003 (-0.023 - 0.029)	0.82	1912	0.11	-0.006 (-0.020 - 0.008)	0.39	3959	0.25
CTNNBL1	rs6013029	20q11.23	T	0.007 (-0.002 - 0.016)	0.14	21905	0.06	0.007 (-0.026 - 0.041)	0.66	1913	0.07	0.010 (0.001 - 0.018)	0.03	6620	0.27

				East Asians			
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**AF**
INSIG2	rs7566605	2q14.2	G	-0.002 (-0.024 - 0.02)	0.88	695	0.65
none identified	rs748192	chr3	A	-0.006 (-0.033 - 0.021)	0.69	674	0.14
none identified	rs10498767	chr6	C	0.001 (-0.020 - 0.021)	0.94	696	0.61
none identified	rs1106683	7q32.3	A	0.030 (-0.006 - 0.066)	0.10	702	0.09
PFKP	rs6602024	10p15.2	A	0.046 (-0.033 - 0.125)	0.26	696	0.01
none identified	rs1333026	13q21.32	A	-0.034 (-0.066 - -0.002)	0.04	700	0.08
CTNNBL1	rs6013029	20q11.23	T	0.051 (-0.059 - 0.160)	0.36	702	0.01

CA: coded allele; AF: risk allele frequency; CI: confidence interva

Supplementary Table 7: Ranges of pairwise correlation (r2) for putative obesity-related SNPs in FTO and MC4R, stratified by racial/ethnic group. Based on WHI, EAGLE, ARIC, MEC, and CHS data

European Americans

Gene	SNP	rs1121980	rs3751812	rs8050136	rs9930506	rs9939609	rs17782313
FTO	rs1121980	1	0.85 - 0.87	0.86 - 0.89	0.83 - 0.86	0.86 - 0.88	na
	rs3751812		1	0.94 - 0.99	0.86	0.96 - 0.99	na
	rs8050136			1	0.82 - 0.85	0.97 - 0.99	na
	rs9930506				1	0.83 - 0.85	na
	rs9939609					1	na
MC4R	rs12970134	na	na	na	na	na	0.76

Hispanics

Gene	SNP	rs1121980	rs3751812	rs8050136	rs9930506	rs9939609	rs17782313
FTO	rs1121980	1	0.63	0.75	0.7	0.77	na
	rs3751812		1	0.84	0.78	0.76	na
	rs8050136			1	0.66	0.91	na
	rs9930506				1	0.66	na
	rs9939609					1	na
MC4R	rs12970134	na	na	na	na	na	0.57

African Americans

Gene	SNP	rs1121980	rs3751812	rs8050136	rs9930506	rs9939609	rs17782313
FTO	rs1121980	1	0.15	0.73 - 0.76	0.18 - 0.20	0.59 - 0.62	na
	rs3751812		1	0.12 - 0.40	0.46	0.14 - 0.36	na
	rs8050136			1	0.09 - 0.12	0.84 - 0.92	na
	rs9930506				1	0.07 - 0.09	na
	rs9939609					1	na
MC4R	rs12970134	na	na	na	na	na	0.11 - 0.13

East Asians

Gene	SNP	rs1121980	rs3751812	rs8050136	rs9930506	rs9939609	rs17782313
FTO	rs1121980	1	0.81	0.81	0.9	0.81	na
	rs3751812		1	0.99	0.77	0.99	na
	rs8050136			1	0.77	0.98	na
	rs9930506				1	0.75	na
	rs9939609					1	na
MC4R	rs12970134	na	na	na	na	na	0.64

American Indians

Gene	SNP	rs9939609
FTO	rs8050136	0.98

Supplemental Table 8: PAGE site-specific linear regression of putative obesity-related SNPs and natural log BMI, using a range of BMI exclusion criteria

European Americans, ARIC

				BMI 18.5 - 40 only			BMI 18.5 - 50 only			BMI 18.5 - 70 only		
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**Effect Size (95% CI)**	**p-value**	**N**	**Effect Size (95% CI)**	**p-value**	**N**
NEGR1	rs2815752	1p31.1	T	0.005 (0.001 - 0.01)	0.02	9092	0.007 (0.002 - 0.012)	0.01	9243	0.007 (0.002 - 0.012)	0.004	9256
TMEM18	rs6548238	2p25.3	C	0.006 (0.0002 - 0.011)	0.04	10617	0.007 (0.001 - 0.013)	0.02	10795	0.008 (0.002 - 0.014)	0.01	10810
GNPDA2	rs10938397	4p12	G	0.01 (0.001 - 0.019)	0.02	2126	0.01 (0.0004 - 0.019)	0.04	2166	0.009 (-0.0002 - 0.019)	0.05	2168
MTCH2	rs10838738	11p11.2	G	-0.003 (-0.013 - 0.006)	0.46	2128	-0.002 (-0.012 - 0.008)	0.66	2168	-0.001 (-0.011 - 0.009)	0.81	2170
SH2B1	rs7498665	16p11.2	G	0.002 (-0.007 - 0.012)	0.61	2122	0.004 (-0.006 - 0.014)	0.47	2161	0.004 (-0.006 - 0.014)	0.44	2163
FTO	rs1121980	16q12.12	A									
FTO	rs3751812	16q12.12	T									
FTO	rs8050136	16q12.12	A	0.016 (0.011 - 0.02)	5.6E-12	9092	0.017 (0.012 - 0.022)	5.9192E-12	9243	0.017 (0.013 - 0.022)	2.4095E-12	9256
FTO	rs9930506	16q12.12	G									
FTO	rs9939609	16q12.12	A	0.016 (0.012 - 0.021)	3.9489E-12	9082	0.017 (0.012 - 0.022)	4.9931E-12	9233	0.017 (0.013 - 0.022)	2.0512E-12	9246
MC4R	rs12970134	18q22	A									
MC4R	rs17782313	18q22	C	0.005 (-0.0001 - 0.011)	0.05	9088	0.007 (0.002 - 0.013)	0.01	9239	0.007 (0.001 - 0.013)	0.02	9252
KCTD15	rs11084753	19q13.11	G	0.002 (-0.002 - 0.007)	0.34	9070	0.002 (-0.003 - 0.007)	0.49	9221	0.001 (-0.004 - 0.007)	0.60	9234

African Americans, ARIC

				BMI 18.5 - 40 only			BMI 18.5 - 50 only			BMI 18.5 - 70 only		
Gene	**SNP**	**Location**	**CA**	**Effect Size (95% CI)**	**p-value**	**N**	**Effect Size (95% CI)**	**p-value**	**N**	**Effect Size (95% CI)**	**p-value**	**N**
NEGR1	rs2815752	1p31.1	T	-0.004 (-0.012 - 0.004)	0.28	2949	-0.003 (-0.011 - 0.006)	0.56	3105	-0.003 (-0.012 - 0.006)	0.52	3134
TMEM18	rs6548238	2p25.3	C	0.003 (-0.008 - 0.015)	0.54	3664	0.003 (-0.01 - 0.015)	0.65	3869	0.006 (-0.007 - 0.018)	0.40	3897
GNPDA2	rs10938397	4p12	G	0.002 (-0.006 - 0.011)	0.58	3626	0.004 (-0.006 - 0.013)	0.44	3827	0.003 (-0.006 - 0.013)	0.50	3855
MTCH2	rs10838738	11p11.2	G	-0.002 (-0.014 - 0.011)	0.77	3626	-0.005 (-0.018 - 0.009)	0.49	3830	-0.0004 (-0.014 - 0.014)	0.96	3858
SH2B1	rs7498665	16p11.2	G	0.003 (-0.005 - 0.011)	0.41	3639	0.005 (-0.004 - 0.014)	0.25	3840	0.006 (-0.003 - 0.015)	0.20	3868
FTO	rs1121980	16q12.12	A									
FTO	rs3751812	16q12.12	T									
FTO	rs8050136	16q12.12	A	0.008 (0.0001 - 0.016)	0.05	2949	0.008 (-0.0003 - 0.017)	0.06	3105	0.006 (-0.003 - 0.015)	0.22	3134
FTO	rs9930506	16q12.12	G									
FTO	rs9939609	16q12.12	A	0.008 (0.001 - 0.016)	0.04	2949	0.01 (0.001 - 0.019)	0.03	3105	0.007 (-0.002 - 0.016)	0.13	3134
MC4R	rs12970134	18q22	A									
MC4R	rs17782313	18q22	C	0.002 (-0.007 - 0.011)	0.66	2946	0.004 (-0.006 - 0.014)	0.40	3102	0.004 (-0.006 - 0.014)	0.43	3131
KCTD15	rs11084753	19q13.11	G	0.0002 (-0.008 - 0.009)	0.96	2944	-0.0003 (-0.009 - 0.009)	0.94	3100	-0.003 (-0.013 - 0.006)	0.52	3129

Supplemental Table 8: Continued

European Americans, WHI

Gene	SNP	Location	CA	BMI 18.5 - 40 only			BMI 18.5 - 50 only			BMI 18.5 - 70 only		
				Effect Size (95% CI)	p-value	N	Effect Size (95% CI)	p-value	N	Effect Size (95% CI)	p-value	N
NEGR1	rs2815752	1p31.1	T	0.002 (-0.006 - 0.01)	0.64	11894	0.001 (-0.008 - 0.01)	0.82	12752	0.002 (-0.007 - 0.011)	0.71	12871
TMEM18	rs6548238	2p25.3	C	0.005 (-0.005 - 0.015)	0.32	11896	0.007 (-0.005 - 0.018)	0.26	12754	0.005 (-0.007 - 0.017)	0.41	12873
GNPDA2	rs10938397	4p12	G	0.002 (-0.006 - 0.009)	0.69	11875	0.007 (-0.002 - 0.015)	0.12	12727	0.005 (-0.004 - 0.014)	0.24	12846
MTCH2	rs10838738	11p11.2	G	0.003 (-0.005 - 0.011)	0.50	11896	0.0003 (-0.009 - 0.01)	0.94	12754	-0.001 (-0.011 - 0.008)	0.81	12873
SH2B1	rs7498665	16p11.2	G	0.009 (0.001 - 0.016)	0.03	11863	0.009 (-0.0002 - 0.017)	0.06	12719	0.009 (-0.001 - 0.018)	0.07	12838
FTO	rs1121980	16q12.12	A	0.007 (-0.001 - 0.015)	0.08	11450	0.01 (0.001 - 0.02)	0.03	12273	0.009 (-0.0004 - 0.018)	0.06	12388
FTO	rs3751812	16q12.12	T	0.006 (-0.002 - 0.014)	0.13	11896	0.01 (0.001 - 0.019)	0.03	12752	0.008 (-0.001 - 0.018)	0.07	12871
FTO	rs8050136	16q12.12	A	0.006 (-0.002 - 0.014)	0.14	11896	0.009 (0.0003 - 0.018)	0.04	12754	0.008 (-0.001 - 0.017)	0.09	12873
FTO	rs9930506	16q12.12	G	0.007 (-0.001 - 0.015)	0.08	11842	0.01 (0.001 - 0.019)	0.03	12699	0.009 (-0.001 - 0.018)	0.07	12817
FTO	rs9939609	16q12.12	A	0.006 (-0.002 - 0.014)	0.15	11774	0.009 (0.0003 - 0.019)	0.04	12622	0.008 (-0.001 - 0.017)	0.09	12741
MC4R	rs12970134	18q22	A	0.007 (-0.002 - 0.015)	0.13	11773	0.006 (-0.003 - 0.016)	0.18	12621	0.003 (-0.006 - 0.013)	0.50	12740
MC4R	rs17782313	18q22	C	0.01 (0.001 - 0.019)	0.03	11865	0.01 (-0.00003 - 0.02)	0.05	12720	0.007 (-0.003 - 0.017)	0.18	12839
KCTD15	rs11084753	19q13.11	G	0.005 (-0.003 - 0.013)	0.21	11893	0.006 (-0.003 - 0.015)	0.19	12751	0.007 (-0.002 - 0.017)	0.13	12870

African Americans, WHI

Gene	SNP	Location	CA	BMI 18.5 - 40 only			BMI 18.5 - 50 only			BMI 18.5 - 70 only		
				Effect Size (95% CI)	p-value	N	Effect Size (95% CI)	p-value	N	Effect Size (95% CI)	p-value	N
NEGR1	rs2815752	1p31.1	T	-0.001 (-0.011 - 0.009)	0.84	3143	-0.0004 (-0.012 - 0.011)	0.94	3847	0.002 (-0.009 - 0.014)	0.67	3956
TMEM18	rs6548238	2p25.3	C	0.015 (0.001 - 0.03)	0.04	3146	0.023 (0.007 - 0.039)	0.005	3851	0.021 (0.004 - 0.038)	0.02	3960
GNPDA2	rs10938397	4p12	G	0.012 (0.001 - 0.024)	0.03	3124	0.017 (0.005 - 0.03)	0.01	3825	0.02 (0.006 - 0.033)	0.004	3934
MTCH2	rs10838738	11p11.2	G	0.001 (-0.015 - 0.016)	0.94	3147	-0.001 (-0.018 - 0.016)	0.90	3852	0.004 (-0.015 - 0.022)	0.71	3961
SH2B1	rs7498665	16p11.2	G	0.002 (-0.009 - 0.014)	0.69	3141	0.005 (-0.007 - 0.018)	0.41	3845	0.007 (-0.006 - 0.02)	0.28	3954
FTO	rs1121980	16q12.12	A	-0.022 (-0.044 - 0.001)	0.06	687	-0.015 (-0.039 - 0.009)	0.22	848	-0.017 (-0.042 - 0.007)	0.17	870
FTO	rs3751812	16q12.12	T	0.004 (-0.013 - 0.02)	0.67	3145	0.012 (-0.006 - 0.031)	0.19	3850	0.013 (-0.007 - 0.032)	0.20	3959
FTO	rs8050136	16q12.12	A	0.0001 (-0.01 - 0.011)	0.98	3146	0.002 (-0.009 - 0.014)	0.69	3851	0.002 (-0.01 - 0.014)	0.72	3960
FTO	rs9930506	16q12.12	G	0.002 (-0.011 - 0.014)	0.79	3144	0.008 (-0.006 - 0.021)	0.27	3847	0.009 (-0.005 - 0.023)	0.21	3956
FTO	rs9939609	16q12.12	A	-0.013 (-0.035 - 0.009)	0.24	724	-0.015 (-0.038 - 0.009)	0.22	888	-0.015 (-0.039 - 0.009)	0.21	914
MC4R	rs12970134	18q22	A	-0.001 (-0.032 - 0.029)	0.94	724	0.016 (-0.018 - 0.05)	0.36	889	0.012 (-0.023 - 0.047)	0.49	915
MC4R	rs17782313	18q22	C	0.004 (-0.007 - 0.015)	0.50	3144	0.006 (-0.006 - 0.019)	0.30	3849	0.009 (-0.004 - 0.022)	0.17	3957
KCTD15	rs11084753	19q13.11	G	-0.002 (-0.012 - 0.009)	0.75	3146	-0.007 (-0.019 - 0.004)	0.21	3851	-0.008 (-0.02 - 0.004)	0.18	3959

CA: coded allele; AF: risk allele frequency; CI: confidence interval

Title: Influence of population diversity on replication of obesity-related GWAS findings: The PAGE Consortium.

Supplementary Methods

PAGE Cohort Descriptions

Causal Variants Across the Life Course (CALiCo): CALiCo is a consortium of well characterized population based studies and a central genotyping and resequencing core laboratory. This collaborative network includes six of the most informative and demographically diverse population-based studies extant, contributing approximately 58,000 men and women from the main ethnic and racial groups in the U.S., ranging in age from childhood to old adulthood. Four CALiCo studies are involved in this analysis: Atherosclerosis Risk in Communities Study (ARIC), Coronary Artery Risk in Young Adults (CARDIA), Cardiovascular Health Study (CHS), and Strong Heart Family Study (SHFS) and Strong Heart Cohort Study (SHCS).

ARIC is a multi-center prospective investigation of atherosclerotic disease in a predominantly bi-racial population conducted in four U.S. communities, involving both cohort and community surveillance components[1]. European American and African American men and women aged 45-64 years at baseline were recruited from 4 communities: Forsyth County, North Carolina; Jackson, Mississippi; suburban areas of Minneapolis, Minnesota; and Washington County, Maryland. A total of 15,792 individuals participated in the baseline examination in 1987-1989, with follow-up examinations in approximate 3-year intervals, during 1990-1992, 1993-1995, and 1996-1998. Weight and height were measured. Current smoking was dichotomized as yes/no according to the question “Do you now smoke cigarettes?”

CARDIA multicenter longitudinal study of the development and determinants of cardiovascular disease over time in 5115 young adults initially aged 18 to 30 years from 1985 to 1986 [2]. African American and European American adults were recruited from four US cities (Birmingham, Ala; Chicago, Ill; Minneapolis, Minn; and Oakland, Calif) with population-based samples approximately balanced within center by sex, age (18 to 24 or 25 to 30 years), Racial/ethnic group (European American or African American), and education (high school graduate or less or greater than high school graduate). Participants have been reexamined 2, 5, 7, 10, 15, and 20 years after baseline; and retention rates across examinations were 91%, 86%, 81%, 79%, 74%, and 72%, respectively.

The CHS is a prospective, population-based cohort study of cardiovascular disease in older adults[3]. In 1989/1990, a group of 5201 men and women 65 years of age and older was recruited from a random sample of Medicare-eligible residents in 4 US communities: Forsyth County, NC; Sacramento County, CA; Washington County, MD; and Allegheny County, PA. To be considered eligible, persons had to meet the following criteria: 1) age at least 65 years; 2) not institutionalized; 3) expected to remain in the current community for 3 years or longer; 4) not under active treatment for cancer; and 5) provided informed consent without requiring a proxy respondent. To increase the number of African American participants, a supplemental cohort of 687 predominantly African American men and women was recruited in 1992/1993 from three of the same communities (excepting Washington County) using the same sampling and recruitment methods. CHS participants completed standardized clinical examinations and questionnaires at study baselines and at up to 9 annual follow-up visits.

The SHCS is a community-based study of CVD and its risk factors among American Indians, supported by the National Heart, Lung, and Blood Institute (NHLBI) [4, 5]. The family component of the study (SHFS) began in 1998 (phase III) with a pilot study that recruited and examined at least 300 members of 9-2 extended families in each of the three centers (Arizona, South Dakota, Oklahoma). In phase IV of the

SHFS, an additional ~900 family members were recruited from each center yielding sample sizes of more than 1,200 participants at each site. In all centers, some individuals are descended from more than one tribe and/or from non-Indian ancestors.

The Women's Health Initiative (WHI) is a prospective cohort study investigating post-menopausal women's health in the U.S [6]. WHI was funded by the National Institutes of Health and the National Heart, Lung, and Blood Institute to study strategies to prevent heart disease, breast cancer, colon cancer, and osteoporotic fractures in women aged 50-79. WHI consists of two parts: randomized clinical trials of hormone therapy, dietary modification, and calcium/Vitamin D supplementation, and an observational cohort study. Subjects for this analysis are 21,000 women drawn from the pool of over 161,000 women involved in either the clinical trial or observational study components of WHI. The 21,000 women were chosen using several selection criteria, which resulted in oversampling women with a BMI > 40, and women belonging to non-white ancestry groups. All selected women were required to have DNA available for analysis.

The Multiethnic Cohort (MEC) is a population-based prospective cohort study of over 215,000 men and women in Hawaii and California aged 45-75 at baseline (1993-1996) and primarily of five ancestries[7]. The MEC was funded by the National Cancer Institute in 1993 to examine lifestyle risk factors and genetic susceptibility to cancer. Cohort members who develop cancer are identified via the California and Hawaii state cancer registries, and all eligible cohort members completed baseline and follow-up questionnaires. Participants eligible for the current analysis were controls in nested case-control studies of breast, colorectal, or prostate cancer or for biomarker studies (N=7,216).

Epidemiologic Architecture for Genes Linked to Environment (EAGLE) accesses the genetic component of three National Health and Nutrition Examination Surveys (NHANES; n~15,000): NHANES III (phase 2 collected between 1991 and 1994), NHANES 1999-2000, and NHANES 2001-2002[8-10]. NHANES is a

U.S. population-based, cross-sectional survey of Americans ranging in age from infants to the elderly ascertained regardless of health status, conducted by the National Center for Health Statistics at the Centers for Disease Control and Prevention. In general, DNA samples collected for NHANES on participants 12 years of age or older are linked to survey responses related to demographic, health, and lifestyle as well as data from a physical examination and >100 laboratory measures.

Data collection

BMI: In EAGLE, all CALiCo studies, and WHI, BMI was calculated from height and weight measured at time of study enrollment in a clinic setting. In WHI only, measurements collected 1 or 3 years after enrollment were substituted for 140 participants missing enrollment height and/or weight. In the MEC, self-reported height and weight were used to calculate baseline BMI.

Smoking status: Current smokers were identified in the MEC, WHI, and ARIC by asking subjects whether they were current smokers and in CHS by asking subjects whether they had smoked in the past 30 days. In EAGLE, current smoking for NHANES participants was defined by the answer "yes" to the question "do you smoke cigarettes now?" or if cotinine levels were >15ng/ml. In SHS and SHFS, Tobacco exposure was quantified using standardized questionnaires.

Racial/ethnic group: In all studies, self-reported Racial/ethnic group was collected via questionnaire at baseline.

DNA extraction

In the MEC and WHI, DNA was purified from buffy coat samples. A subset of MEC DNA samples were whole-genome amplified by Molecular Staging Inc. following their standard protocol [11]. For CALiCo, DNA was extracted from blood samples drawn at baseline. For EAGLE, NHANES III DNA samples are

crude cell lysates obtained from Epstein-Barr Virus transformed lymphocyte cell lines [12]. DNA samples from NHANES 1999-2000 and 2001-2002 were purified from blood using standard methods.

Genotyping

MEC: Genotyping was conducted at the Cancer Research Center of Hawaii (CRCH) and at the University of Southern California (USC). Genotyping at CRCH was performed using the AB OpenArray genotyping while genotyping at USC was performed using the TaqMan platform. To assess inter-study (within PAGE) and inter-lab (within the MEC) concordance, all SNPs were typed on 375 HapMap samples. The concordance between the CRCH and USC labs was 99.9% for the 8 BMI SNPs genotyped in MEC. In addition, 8.8% blinded duplicate samples were included: resulting in >99.3% concordance.

WHI: Genotyping was performed at the Translational Genomics Research Institute (Phoenix, AZ) on Illumina's BeadXpress Reader using Illumina's Veracode GoldenGate genotyping assay, following the manufacturer's recommended protocol (Reference: www.illumina.com). Image data were imported into Illumina's GenomeStudio software. Genotype calls were made using a GenCall cutoff of 0.25. Each batch of ~500 samples included 12 pairs of blind duplicate controls for quality control, with a total of 376 pairs. Overall concordance between pairs was 96.3%.

CALiCo: The majority of genotyping for all sites was performed at the CALiCo central laboratory in Houston, TX using the TaqMan platform using appropriate duplicates and controls. Genotypes were called using the Applied Biosystem Autocaller 3.1 software, subject to manual review. A subset of CHS and ARIC genotypes (rs10838738, rs1333026, rs2815752, rs3751812, and rs8050136) was obtained from previous GWAS studies[13] using either the Illumina 370CNV BeadChip system (CHS) or the Affymetrix Genome-Wide Human SNP Array 6.0 (Santa Clara, CA) (ARIC). For all genotyping platforms, SNPs were excluded if the minor allele frequency was less than 1%, or if they deviated from Hardy-Weinberg expectations ($p < 5x10^{-5}$). Participants were excluded if their genotypes exhibited discordance with prior

genotyping, or call rate < 95%. Imputation for four SNPs (rs10838738, rs10938397, rs7498665, and rs3751812) in European American ARIC subjects only was performed using BIMBAM v0.99 with reference to HapMap CEU using release 22, build 36 using one round of imputations and the default expectation-maximization warm-ups and runs. Allele frequencies for imputed SNPs were estimated using the averaged frequencies reported by the other PAGE sites.

EAGLE: For NHANES participants, genotyping was performed by the Vanderbilt DNA Resources Core and the laboratory of Dr. Jonathan Haines, both in Nashville, Tennessee. Genotyping was performed using Sequenom's iPLEX® Gold coupled with MassARRAY MALDI-TOF MS detection (San Diego, CA) and Illumina's BeadXpress with a custom GoldenGate assay (San Diego, CA). All NHANES experimental DNA samples and blinded duplicates supplied by CDC were genotyped, and SNPs reported here passed CDC quality control measures and are available for secondary analyses through the National Center for Health Statistics (NCHS) CDC.

Statistical Analysis

For EAGLE, all statistical analyses for NHANES data (i.e., genetic data linked to NHANES data) were conducted remotely with SAS software v9.2 [14](SAS Institute, Cary, NC) using the Analytic Data Research by Email (ANDRE) portal of the CDC Research Data Center (RDC) in Hyattsville, Maryland. Data from CHS was analyzed using R[15] (R Foundation for Statistical Computing, Vienna, Austria), data from SHFC was analyzed using SOLAR [16](San Antonio, TX), data from WHI was analyzed using Stata 10 [17] (StataCorp, College Station, TX), and data from all other sites was analyzed using SAS software v9.2. LD plots and blocks were constructed in HaploView 4.2 (Broad Institute, Cambridge, MA) [18] using data from the International HapMap Project (Version 3, Release R2)[19] and the confidence intervals method for blocks described in Gabriel et al.[20].

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