

Supplementary table

Table S1. List of candidate gene SNPs successfully genotyped. The gene name, chromosomal location, coordinates according to Build 35

(<http://www.ncbi.nlm.nih.gov/mapview/stats/BuildStats.cgi?taxid=9606&build=35&ver=1>),

SNP name, nucleotide variation, and location of the variation are indicated.

Syn=synonymous. Nonsyn=nonsynonymous

Target Locus	Chr	Coordinates build 35	SNP Name	variation	variation type / Location other SNP name	
LEPR	1	65587872	rs3790436	C G	intron of DNAJC6	
LEPR	1	65597378	rs3806318	A G		
LEPR	1	65597590	rs1327118	C G	promoter	hCV3128062
LEPR	1	65598419	rs3790435	A G	5'UTR	exon1 noncoding +64 T>C
LEPR	1	65606363	rs3790433	A G	intron (UTR)	intron of OBRGRP
LEPR	1	65609972	rs7602	A G	UTR (intron1)	
LEPR	1	65618511	rs970468	A C		
LEPR	1	65647515	rs6588147	A G	intron	hCV29129972
LEPR	1	65661899	rs2025805	A G	UTR (intron)	
LEPR	1	65671418	rs1327120	A G	intron	
LEPR	1	65681083	rs2104563	A G	intron	hCV16095921
LEPR	1	65688072	rs1327116	A C		
LEPR	1	65699470	rs1171276	A G		
LEPR	1	65705369	rs1782754	A G		
LEPR	1	65747760	rs3790432	A T	intron	hCV518166
LEPR	1	65748462	rs1137100	A G	coding (nonsyn)	Lys109Arg
LEPR	1	65755040	rs3790426	A C	intron	
LEPR	1	65755133	rs3790425	A G	intron	
LEPR	1	65756034	rs3790424	A G	intron	
LEPR	1	65759288	rs1938487	A G	Intron	hCV12108671
LEPR	1		rs1137101	A G	coding (nonsyn)	Gln223Arg
LEPR	1	65774346	rs3828034	A G	intron	hCV25597196
LEPR	1	65777010	rs3790423	A G	intron	
LEPR	1	65778020	rs3790422	A G	intron	
						(=rs1805134) hCV11874781
LEPR	1	65779130	rs3790419	A G	coding (syn)	Ser343Ser
LEPR	1	65787973	rs8179183	C G	coding (nonsyn)	Lys656Asn
LEPR	1	65793303	rs1938484	A C	intron	
LEPR	1	65797454	rs3790437	A G	intron	hCV26465953
LEPR	1	65797595	rs3790439	A T	intron	A>T-36 intron16
LEPR	1	65814278	rs1805096	A G	coding (syn)	Pro1019Pro
LEPR	1	65960323	hCV1928197	A G	Intron	hCV1928197
LEPR	1	66033405	hCV1928241	A G	intron	hCV1928241
LEPR	1	66102255	hCV509173	A G	intron	hCV509173
LEPR	1	166152822	hCV429537	A G	intron	hCV429537
POMC	2	25232815	POMC236	C G	coding (cleavage site)	Arg236Gly
POMC	2	25232958	POMC188	A G	coding (syn)	Glu188Gly
POMC	2	25288980	rs2118404	A G	UTR of KIAA0953	6kb downstream
POMC	2	25292224	rs1866146	A G	3 flank	3kb downstream
POMC	2	25293121	rs4665285	C G	Intergenic	hCV11810742

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POMC	2	25296484	rs6713532	A	G	intron	
POMC	2	25301804	rs3769671	A	C	UTR	
POMC	2	25307663	rs6719226	C	G		n/a
POMC	2	25313931	rs874401	A	G		
GCG	2	162816754	rs2389681	A	C	Locus	
GCG	2	162823210	rs1990761	A	G	Locus	
GCG	2	162827605	rs5650	A	G	coding (nonsyn)	Val115Ala
GCG	2	162830665	rs5647	A	G	intron	
GCG	2	162831181	rs5645	A	G	coding (syn)	Tyr5Tyr
GCG	2	162836742	rs3761656	A	C	Locus	
BBS5	2	169784512	BBS5_SNP2	A	G		
BBS5	2	169797992	BBS5_A-Gsplice	A	G		A-G splice
BBS5	2	169798749	BBS5_N184S	A	G		N184S
BBS5	2	169802608	BBS5_R207H	A	G		R207H
BBS5	2	169809235	BBS5_SNP5	C	G		
BBS5	2	170164316	rs16823066	A	G		
GHRL	3	10303250	rs35683	A	C	intron	
GHRL	3	10303453	rs4684677	A	T	coding(nonsyn)	Gln90Leu
GHRL	3	10303782	rs35682	A	G	intron	
GHRL	3	10306457	rs696217	A	C	coding (nonsyn)	Leu72Met
GHRL	3	10307468	rs27647	A	G	promoter 5'UTR	
GHRL	3	10307858	rs26312	A	G	locus	
GHRL	3	10308364	rs3755777	C	G	locus	
GHRL	3	10311291	rs1629816	A	G	locus	
BBS3	3	98996956	rs10511163	A	G		
BBS3	3	98999808	rs4857294	C	G		
BBS3	3	99131522	BBS3_T31R	C	G		
BBS3	3	99132552	BBS3_SNP2	A	C		
BBS3	3	99144132	BBS3_SNP3	A	T		
BBS3	3	99148229	BBS3_SNP4	A	G		
BBS3	3	99155120	BBS3_G169A	C	G		G169A
GHSR	3	173636722	rs560994	A	T	n/a	
GHSR	3	173639812	rs558572	A	G	locus	
GHSR	3	173641099	rs1403637	A	G	intergenic	hCV2169202
GHSR	3	173641907	rs4144707	A	G	locus	
GHSR	3	173648429	rs572169	A	G	coding (syn)	Arg159Arg
GHSR	3	173648735	rs495225	A	G	coding (syn)	hCV1079488 Gly57Gly
GHSR	3	173649963	rs2922126	A	T	locus	
GHSR	3	173655071	rs11918879	A	G	n/a	
GHSR	3	173657776	rs863441	C	G	n/a	
APM1	3	188001838	rs1648703	A	C	Intron of RFC4	
APM1	3	188032397	rs10937273	A	G	Intron of LOC389184	
APM1	3	188038739	rs822387	A	G		
APM1	3	188042176	rs266729	C	G	promoter	-11377G/C
APM1	3	188043484	rs182052	A	G	intron1	
APM1	3	188049028	rs822393	A	G	intron1	
APM1	3	188049430	rs822394	A	C	intron1-4kbofATG	
APM1	3	188049509	rs822395	A	C	intron1-4kbofATG	-4041(-4034)A/C
APM1	3	188049579	rs822396	A	G	intron1-4kbofATG	-3971(-3964)A/G
							hCV26426077 +45T/G
APM1	3	188053594	rs2241766	A	C	coding(syn)	Gly15Gly
APM1	3	188053825	rs1501299	A	C	intron	+276G/TIVS2+62G/T
APM1	3	188053898	rs2241767	A	G	intron	+349A/G
APM1	3	188054261	rs3774261	A	G	intron	hCV27479710 +712G/A
APM1	3	188054516	rs3774262	A	G	intron	

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<i>APM1</i>	3	188203912	APM11426	A	G	promoter	-11426A/G
<i>APM1</i>	3	188216580	APM111	A	G	coding(nonsyn)	Tyr111His
<i>APM1</i>	3	188225331	hCV26426064	A	G	Intergenic	hCV26426064
<i>BBS7</i>	4	123006030	BBS7_SNP6	A	G		
<i>BBS7</i>	4	123032434	BBS7_T211I	A	G		T211I
<i>BBS7</i>	4	123039368	BBS7_SNP3	A	G		
<i>BBS7</i>	4	123048090	BBS7_SNP2	C	G		
<i>NPY5R</i>	4	164410779	Y5R1c52	A	G	UTR	
<i>NPY1R</i>	4	164599697	rs1574637	A	G	n/a	
<i>NPY1R</i>	4	164602658	rs4057797	A	T	locus (1R)	
<i>NPY1R</i>	4	164603010	rs9764	A	G	UTR	
<i>NPY1R</i>	4	164604094	rs5578	A	C	coding (nonsyn)	Thr374Lys
<i>NPY1R-5R</i>	4	164614340	rs6837793	A	G	n/a	
<i>NPY1R-5R</i>	4	164617881	rs4234955	A	G	n/a	
<i>NPY5R</i>	4	164629142	rs3967767	A	G	coding (nonsyn)	Asn38Asp
<i>NPY5R</i>	4	164630308	rs11946004	A	G	coding (syn)	Gly426Gly
<i>NPY5R</i>	4	164634502	rs6536721	A	G	n/a	
<i>NPY5R</i>	4	164637636	rs6826217	A	T	n/a	
<i>CPE</i>	4	166668633	rs1438109	A	T	intron	hCV7508762
<i>CPE</i>	4	166671752	rs1866217	A	G	intron	
<i>CPE</i>	4	166673330	rs6536912	A	G	intron	
<i>CPE</i>	4	166677307	rs1543915	A	G		
<i>CPE</i>	4	166682032	rs2164864	A	G	intron	hCV11243588
<i>CPE</i>	4	166689657	rs1866221	A	T	intron	hCV11243570
<i>CPE</i>	4	166698564	rs1946816	A	C	intron	
<i>CPE</i>	4	166710108	rs7699489	A	G	intron	
<i>CPE</i>	4	166716498	rs1370679	A	G	intron	hCV9460984
<i>CPE</i>	4	166717026	rs4481204	A	G	intron	
<i>CPE</i>	4	166720355	rs1898593	A	C	intron	
<i>CPE</i>	4	166727266	rs6841638	A	C	intron	
<i>CPE</i>	4	166733682	rs2118494	A	G	intron	hCV1582141
<i>CPE</i>	4	166739184	rs1001045	C	G	intron	
<i>CPE</i>	4	166744549	rs3775311	A	G	intron	
<i>CPE</i>	4	166747960	rs1370687	A	G	intron	
<i>CPE</i>	4	166753827	rs1583646	A	G	intron	
<i>CPE</i>	4	166761179	rs2289230	A	G	intron	hCV11252059
<i>CPE</i>	4	166763405	rs2304592	A	G	intron	
<i>CPE</i>	4	166766387	rs3822062	A	C	intron	hCV11252065
<i>CPE</i>	4	166774248	rs7692951	A	G	intron	
<i>CPE</i>	4	166777043	rs12200	A	G	UTR	
<i>CPE</i>	4	166785899	rs2280322	A	C	n/a	hCV11252077
<i>CARTPT</i>	5	71003920	CART3	A	G	UTR (+39bp STOP)	
<i>CARTPT</i>	5	71042167	rs2320165	A	G	n/a	
<i>CARTPT</i>	5	71049233	rs3763154	A	G	locus	hCV1561338
<i>CARTPT</i>	5	71049590	rs10515114	A	G	locus	
<i>CARTPT</i>	5	71049720	rs3857384	A	G	locus	
<i>CARTPT</i>	5	71059197	rs6874941	A	G	n/a	hCV1561333
<i>GLP1R</i>	6	39115518	rs7738586	A	C		
<i>GLP1R</i>	6	39118941	rs9380825	A	G	Locus	
<i>GLP1R</i>	6	39124335	rs880067	A	G	n/a	hCV8948755
<i>GLP1R</i>	6	39128520	rs2268657	A	G	intron	
<i>GLP1R</i>	6	39132734	rs2143734	A	G	intron	
<i>GLP1R</i>	6	39137812	rs742764	A	G	intron	hCV330391
<i>GLP1R</i>	6	39138379	rs2268650	A	G	intron	hCV2491167
<i>GLP1R</i>	6	39140393	rs910170	A	G	intron	hCV2491162

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<i>GLP1R</i>	6	39141109	rs910167	A	G	intron	
<i>GLP1R</i>	6	39142050	rs6923761	A	G	coding (nonsyn)	Ser168Gly
<i>GLP1R</i>	6	39148632	rs2235868	A	C	coding (syn)	Arg176Arg
							hCV2491143
<i>GLP1R</i>	6	39149480	rs1042044	A	C	coding (nonsyn)	Phe260Leu
<i>GLP1R</i>	6	39150312	rs932443	A	G	intron	hCV2491141
<i>GLP1R</i>	6	39151156	rs2268647	A	G	intron	hCV2491138
<i>GLP1R</i>	6	39151970	rs2268645	A	G	intron	
<i>GLP1R</i>	6	39156469	rs8192681	A	C	coding (syn)	Ile400Ile
<i>GLP1R</i>	6	39158244	rs2268641	A	G	intron	hCV2491125
<i>GLP1R</i>	6	39158362	rs2268640	A	G	intron	hCV2491124
<i>GLP1R</i>	6	39159672	rs2268635	A	G	intron	
<i>GLP1R</i>	6	39161166	rs2235866	A	G	intron	hCV15953203
<i>GLP1R</i>	6	39163463	rs4714210	A	G	UTR	
<i>GLP1R</i>	6	39169474	rs2143733	A	C	UTR	
<i>CNR1</i>	6	88902668	rs806365	A	G	n/a	hCV1652594
<i>CNR1</i>	6	88904154	rs7766029	A	G	n/a	
<i>CNR1</i>	6	88904308	rs806366	A	G	n/a	
<i>CNR1</i>	6	88906819	rs806368	A	G	UTR	
							hCV1652590
<i>CNR1</i>	6	88910354	rs1049353	A	G	coding (syn)	Thr392(453)Thr
<i>CNR1</i>	6	88913082	rs806371	A	C	locus	
<i>CNR1</i>	6	88915442	rs806377	A	G	intron ?	hCV1652585
<i>CNR1</i>	6	88916270	rs806378	A	G	n/a	
<i>CNR1</i>	6	88921372	rs806380	A	G	intron	hCV1652583
<i>CNR1</i>	6	88929649	rs6454674	A	C	n/a	hCV11418433
<i>LEP</i>	7	127460064	rs791601	A	C	intergenic	H1328090-15.3kb
<i>LEP</i>	7	127466943	rs791608	A	G		
<i>LEP</i>	7	127472049	rs12535708	A	C	5'flank/TFBS	H1328082-3.3kb
<i>LEP</i>	7	127472218	rs11770725	A	G	5'flank/TFBS	H1328081-3.1kb
							hCV15966471 exon1 +19G>A A19G
<i>LEP</i>	7	127475300	rs2167270	A	G		
<i>LEP</i>	7	127475802	rs2278815	A	G	UTR	
<i>LEP</i>	7	127481090	rs12706832	A	G	intron1	H1432615
<i>LEP</i>	7	127482640	rs10244329	A	T	intron1	H1328076
<i>LEP</i>	7	127484013	rs11763517	A	G	intron1	H3001671
<i>LEP</i>	7	127485391	rs10954173	A	G	intron1	C1328073
<i>LEP</i>	7	127486166	rs1800583	A	G	coding(Syn)	hCV11609920 Thr48Thr
<i>LEP</i>	7	127486931	rs2071045	A	G	intronIVS2	
<i>LEP</i>	7	127488256	rs3828942	A	G	intronIVS2-152	
<i>LEP</i>	7	127493080	rs2060715	A	G	3flank	hCV3001667 +4.2kb
<i>LEP</i>	7	127511684	H1328083	A	G	5'flank/TFBS	H1328083-3.6kb
<i>LEP</i>	7	127512207	hCV1328081	A	G	Intergenic	hCV1328081 -3.1kb
<i>LEP</i>	7	127514638	LEP633	A	G	UTR	C-633T-0.7kb
<i>LEP</i>	7	127522868	hCV1328075	A	G	intron	hCV1328075
<i>LEP</i>	7	127528791	LEPUTR	A	G	3'UTR	33bp after TGA C>T
<i>LEP</i>	7	127531017	hCV1328071	A	C	UTR3	hCV1328071+2.2kb
<i>LEP</i>	7	127533304	hCV3001666	A	G	Intergenic	hCV3001666 +4.5kb
<i>JAK2</i>	9	4969730	rs1887427	A	G	n/a	
<i>JAK2</i>	9	4973311	rs3808850	A	T	n/a	
<i>JAK2</i>	9	4975542	rs2274472	A	G	UTR	
<i>JAK2</i>	9	4975879	rs2274471	A	G	UTR	
<i>JAK2</i>	9	4983082	rs1327493	C	G	UTR	
<i>JAK2</i>	9	5039065	rs1328917	A	C	intron	
<i>JAK2</i>	9	5040706	rs2230722	A	G	coding (syn)	His163His

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JAK2	9	5045434	rs1536800	A	G	intron	
JAK2	9	5055003	rs2230723	C	G	coding (nonsyn)	Leu Val
JAK2	9	5058520	rs3780365	A	G	intron	
JAK2	9	5071780	rs2230724	A	G	coding (syn)	rs7048717 Leu830Leu
JAK2	9	5073173	rs1410779	A	G	intron	
JAK2	9	5081675	rs3824432	A	G	intron	
JAK2	9	5087544	rs3780372	A	G	intron	
JAK2	9	5099531	rs10491652	A	G	intron	
JAK2	9	5102519	rs3780379	A	G	intron	
JAK2	9	5111070	rs966871	A	T	intron	
TUB	11	8009735	rs4758272	A	G	n/a	
TUB	11	8013375	rs2178152	A	G		
TUB	11	8018502	rs1406094	A	C	intron	
TUB	11	8024027	rs2141322	A	G	intron	
TUB	11	8029812	rs7949880	A	G	intron	
TUB	11	8035280	rs11041723	A	C	intron	
TUB	11	8039305	rs2280726	A	G	intron	
TUB	11	8046522	rs7114018	A	G	intron	
TUB	11	8048000	rs1881240	C	G	intron	
TUB	11	8051258	rs1406095	A	G	intron	
TUB	11	8054010	rs3794018	A	G	intron	
TUB	11	8057749	rs4758040	A	G	intron	
TUB	11	8072275	rs4758289	A	G	coding (syn)	Gly120(175)Gly
TUB	11	8074679	rs2242501	A	G	intron	
TUB	11	8075048	rs2242503	A	G	intron	
TUB	11	8082818	rs3750955	A	G	UTR	
TUB	11	8084071	rs1055233	A	G	UTR	
TUB	11	8089461	rs1569128	A	T	intron of RIC3	
BBS1	11	66014368	BBS1_SNP1	A	G		
BBS1	11	66016028	BBS1_SNP2	A	G		
BBS1	11	66026525	BBS1_SNP5	C	G		
BBS1	11	66031444	BBS1_M390R	A	C		
BBS1	11	66038671	rs2298806	A	G		
BBS1	11	66039833	rs2276406	A	G		
BBS1	11	66050355	rs3819247	A	G		
BBS1	11	66053939	rs3816492	A	G		
BBS1	11	66056924	rs3741360	A	G		
HTR2A	13	46307035	rs6314	A	G	coding (nonsyn)	Tyr452His
HTR2A	13	46307127	rs1058576	A	G	coding (nonsyn)	Phe421Ser
HTR2A	13	46309662	rs1923882	A	G	intron	hCV11696918
HTR2A	13	46313002	rs977003	A	C	intron	
HTR2A	13	46317578	rs3742278	A	G	intron	
HTR2A	13	46319837	rs1923884	A	G	intron	hCV11696916
HTR2A	13	46321087	rs1923885	A	G	Intron	hCV1619744
HTR2A	13	46322813	rs1745837	A	G	intron	
HTR2A	13	46324723	rs9316232	A	G	intron	
HTR2A	13	46326472	rs2296972	A	C	intron	
HTR2A	13	46326612	rs643627	A	G	intron	hCV2711061
HTR2A	13	46328480	rs2246127	A	G	intron	
HTR2A	13	46335217	rs1928042	A	C	intron	
HTR2A	13	46338561	rs2770296	A	G	intron	
HTR2A	13	46343704	rs9316235	A	G	intron	
HTR2A	13	46343878	rs582854	A	C	intron	
HTR2A	13	46343995	rs582385	A	G	intron	
HTR2A	13	46345237	rs1928040	A	G	intron	

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<i>HTR2A</i>	13	46349287	rs912127	A	G	intron	
<i>HTR2A</i>	13	46353864	rs985933	A	G	intron	
<i>HTR2A</i>	13	46354052	rs927544	A	G	intron	
<i>HTR2A</i>	13	46362858	rs4941573	A	G	intron	
<i>HTR2A</i>	13	46364450	rs2070035	A	C	intron	
<i>HTR2A</i>	13	46365627	rs2070040	A	G	intron	
<i>HTR2A</i>	13	46367941	rs6313	A	G	coding (syn)	hCV3042197 102T/C Ser34Ser
<i>HTR2A</i>	13	46369479	rs6311	A	G	UTR	hCV8695278 -1438G/A
<i>HTR2A</i>	13	46371551	rs4142900	A	C	UTR	
<i>HTR2A</i>	13	46371922	rs9534512	A	C	UTR	hCV3042190
<i>HTR2A</i>	13	46376345	rs2149434	A	C	UTR	
<i>HTR2A</i>	13	46381178	rs2026690	A	C	UTR	
<i>HTR2A</i>	13	46387077	rs1410659	A	G	UTR	
<i>BBS8</i>	14	88377073	rs17700296	A	G		
<i>BBS8</i>	14	88388987	rs2273657	A	G		
<i>BBS8</i>	14	88402295	rs17124926	A	G		
<i>BBS8</i>	14	89494213	BBS8_SNP5	A	G		
<i>BBS4</i>	15	70816321	rs2277596	A	G		Met472Val
<i>BBS4</i>	15	70834939	BBS4_SNP1	A	G		
<i>BBS4</i>	15	70836841	BBS4_SNP3	A	G		
<i>BBS4</i>	15	70863028	BBS4_SNP4	A	G		
<i>BBS4</i>	15	70867497	BBS4_SNP5	A	G		
<i>BBS4</i>	15	70885766	BBS4_SNP6	A	G		
<i>BBS4</i>	15	70888063	BBS4_SNP7	A	G		
<i>PLIN</i>	15	87999043	rs11637802	A	G	n/a	
<i>PLIN</i>	15	88009314	rs1052700	A	T	UTR	
<i>PLIN</i>	15	88012827	rs894160	A	G	intron	
<i>PLIN</i>	15	88014138	rs2304794	A	T	intron	
<i>PLIN</i>	15	88014233	rs6496589	C	G	coding (nonsyn)	Pro194Ala
<i>PLIN</i>	15	88018100	rs2289487	A	G	intron	
<i>PLIN</i>	15	88088686	Plin82	A	G	coding (nonsyn)	Thr82Ile
<i>PLIN</i>	15	88088812	Plin40	C	G	coding (nonsyn)	Thr40Ser
<i>BBS2</i>	16	53854869	BBS2_SNP7	A	G		
<i>BBS2</i>	16	53868279	BBS2_T560I	A	G		
<i>BBS2</i>	16	53870304	BBS2_SNP5	A	C		
<i>BBS2</i>	16	53876482	BBS2_SNP4	A	G		
<i>BBS2</i>	16	53876690	BBS2_SNP3	C	G		
<i>BBS2</i>	16	53881675	BBS2_SNP2	A	G		
<i>BBS2</i>	16	53884899	BBS2_D104A	A	C		
<i>BBS2</i>	16	53890618	BBS2_SNP1	A	G		
<i>AGRP</i>	16	66074446	rs5030980	A	G	coding (nonsyn)	760G/A Thr67Ala
<i>AGRP</i>	16	66074556	rs11575892	A	G	intron	650 C/T
<i>STAT3</i>	17	37713088	rs2272087	A	G	intron	
<i>STAT3</i>	17	37713263	rs16967659	A	G	coding (syn)	Asp634Asp
<i>STAT3</i>	17	37719142	rs1053023	A	G	n/a	
<i>STAT3</i>	17	37719436	rs1053005	A	G	n/a	
<i>STAT3</i>	17	37719618	rs1053004	A	G	n/a	
<i>STAT3</i>	17	37735055	rs2293152	C	G	intron	
<i>STAT3</i>	17	37743267	rs12721576	C	G	intron	
<i>STAT3</i>	17	37745206	rs2306580	C	G	intron	
<i>STAT3</i>	17	37746413	rs3869550	A	G	intron	
<i>STAT3</i>	17	37748428	rs8069645	A	G	intron	
<i>STAT3</i>	17	37751799	rs3816769	A	G	intron	
<i>STAT3</i>	17	37753791	rs2306581	A	C	intron	

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STAT3	17	37755105	rs6503697	A	T	UTR	
STAT3	17	37767727	rs744166	A	G	UTR	
STAT3	17	37773451	rs957971	C	G	UTR	
STAT3	17	37783361	rs1026916	A	G	UTR	
STAT3	17	37794757	rs12721585	A	C	locus	
STAT3	17	37795736	rs4796793	C	G	locus	
SOCS3	17	73855196	rs11077357	C	G	n/a	
SOCS3	17	73861445	rs8069976	A	C	n/a	
SOCS3	17	73865388	rs4969168	A	G	locus	
SOCS3	17	73866399	rs1061489	A	G	coding (nonsyn)	Tyr125His
SOCS3	17	73872133	rs4969170	A	G	UTR of LOC388421	
SOCS3	17	73876088	rs8074003	A	G		
MC4R	18	56074460	rs1379444	A	C	Intergenic	hCV26141745
MC4R	18	56076486	rs8085887	A	C	Intergenic	hCV1659552
MC4R	18	56160406	rs1943214	A	G		
MC4R	18	56170414	hCV2747897	A	G	Intergenic	hCV2747897
MC4R	18	56191823	hCV27864867	A	C	coding (nonsyn)	L251I Leu251Ile
MC4R	18	56192751	MC4R178	A	C	promoter	-178A/C
MC4R	18	56195804	rs1943220	A	G		
MC4R	18	56202634	rs1943223	A	G	Intergenic	hCV11962324 +12.1kb
MC4R	18	56245389	rs1943232	A	G		
MC4R	18	56251779	rs1539984	A	G		
BBS6	20	10286678	BBS6_SNP5	A	G		
BBS6	20	10287159	BBS6_SNP4	A	G		
BBS6	20	10294262	BBS6_SNP2	A	C		
BBS6	20	10294539	BBS6_A242S	A	C		
BBS6	20	10297201	BBS6_SNP1	A	G		
HTR2C	X	113641096	rs498207	A	G	locus	
HTR2C	X	113641562	rs518147	C	G	UTR	
HTR2C	X	113643340	rs569959	A	G	UTR	
HTR2C	X	113644329	rs539748	A	G	UTR	
HTR2C	X	113647670	rs498177	A	G	UTR	
HTR2C	X	113668627	rs12558586	A	T	Intron, UTR	hCV339374
HTR2C	X	113699082	rs7055144	A	G	UTR	
HTR2C	X	113714753	rs2192372	A	G	UTR	
HTR2C	X	113719806	rs11798698	A	C	UTR	
HTR2C	X	113723589	rs12844109	A	G	Intron, UTR	hCV2672776
HTR2C	X	113742127	rs2069237	A	G	UTR	hCV15858653
HTR2C	X	113787202	rs2497543	A	G	intron	hCV346619
HTR2C	X	113788715	rs6318	C	G	coding (nonsyn)	Ser23Cys
HTR2C	X	113820006	rs2497523	A	G	intron	hCV15890899
HTR2C	X	113820120	rs4911871	A	G	intron	
HTR2C	X	113821110	rs2497522	A	G	intron	
HTR2C	X	113829656	rs2497514	A	G	intron	hCV15890836
HTR2C	X	113961124	rs1414334	C	G	intron	
HTR2C	X	113963553	rs1360852	A	G	intron	

Table S2. SNPs associated with adiposity in the Yup'ik participants. The p-values without testing for multiple correction are listed. If not indicated, p-values were not statistically significant at level of 0.05. **None of the p-values translated to FDR values below 0.05.**

<i>Gene</i>	<i>SNP Name</i>	<i>Chromosome</i>	<i>Map</i>	<i>percent body fat</i>	<i>triceps skinfold</i>	<i>abdominal skinfold</i>	<i>BMI</i>	<i>Sub-scapular -skinfold</i>	<i>thigh skinfold</i>	<i>waist circum</i>	<i>Composite Score</i>
<i>ADIPOQ</i>	rs1648703	3	188001838	0.008	0.080	0.066	0.256	0.047	0.036	0.023	0.033
<i>ADIPOQ</i>	rs10937273	3	188032397	0.031	0.060	0.302	0.482	0.048	0.430	0.019	0.180
<i>ADIPOQ</i>	rs182052	3	188043484	0.088	0.044	0.101	0.029	0.136	0.105	0.181	0.038
<i>ADIPOQ</i>	rs3774261	3	188054261	0.003	0.007	0.006	0.044	0.003	0.006	0.002	0.019
<i>ARL6</i>	rs4857294	3	98999808	0.014	0.068	0.002	0.012	0.275	0.674	0.200	0.053
<i>BBS4</i>	BBS4_SNP4	15	70863028	0.062	0.316	0.710	0.453	0.324	0.049	0.463	0.114
<i>BBS5</i>	BBS5_SNP5	2	169809235	0.204	0.101	0.174	0.018	0.047	0.201	0.023	0.061
<i>CNR1</i>	rs806365	6	88902668	0.726	0.376	0.045	0.235	0.667	0.484	0.098	0.301
<i>CNR1</i>	rs806378	6	88916270	0.941	0.590	0.903	0.869	0.769	0.626	0.012	0.868
<i>CNR1</i>	rs806380	6	88921372	0.804	0.753	0.952	0.478	0.793	0.664	0.004	0.603
<i>CPE</i>	rs2164864	4	166682032	0.173	0.624	0.356	0.236	0.079	0.037	0.228	0.171
<i>CPE</i>	rs1898593	4	166720355	0.030	0.133	0.014	0.019	0.011	0.037	0.013	0.022
<i>CPE</i>	rs6841638	4	166727266	0.122	0.117	0.015	0.039	0.101	0.389	0.045	0.039
<i>CPE</i>	rs2118494	4	166733682	0.026	0.090	0.012	0.019	0.008	0.023	0.008	0.010
<i>CPE</i>	rs3775311	4	166744549	0.485	0.110	0.042	0.072	0.476	0.140	0.313	0.164
<i>CPE</i>	rs1370687	4	166747960	0.125	0.097	0.037	0.050	0.055	0.064	0.104	0.033
<i>CPE</i>	rs2304592	4	166763405	0.105	0.067	0.256	0.453	0.025	0.014	0.418	0.160
<i>CPE</i>	rs7692951	4	166774248	0.037	0.029	0.046	0.293	0.024	0.004	0.161	0.032
<i>CPE</i>	rs2280322	4	166785899	0.031	0.027	0.044	0.308	0.017	0.003	0.130	0.030
<i>GHRL</i>	rs3755777	3	10308364	0.190	0.563	0.089	0.046	0.139	0.352	0.135	0.149
<i>GHSR</i>	rs560994	3	173636722	0.681	0.615	0.489	0.548	0.686	0.004	0.981	0.558
<i>GHSR</i>	rs558572	3	173639812	0.253	0.037	0.052	0.045	0.191	0.035	0.300	0.077
<i>GHSR</i>	rs4144707	3	173641907	0.726	0.644	0.436	0.612	0.769	0.004	0.962	0.599
<i>GHSR</i>	rs572169	3	173648429	0.411	0.770	0.101	0.488	0.631	0.026	0.771	0.254
<i>GHSR</i>	rs495225	3	173648735	0.726	0.644	0.436	0.612	0.769	0.004	0.962	0.599
<i>GHSR</i>	rs2922126	3	173649963	0.283	0.184	0.036	0.069	0.255	0.0002	0.525	0.064
<i>GHSR</i>	rs11918879	3	173655071	0.600	0.381	0.206	0.335	0.493	0.001	0.928	0.310
<i>GHSR</i>	rs863441	3	173657776	0.485	0.824	0.095	0.590	0.691	0.030	0.785	0.288

<i>Gene</i>	<i>SNP Name</i>	<i>Chromosome</i>	<i>Map</i>	<i>percent body fat</i>	<i>triceps skinfold</i>	<i>abdominal skinfold</i>	<i>BMI</i>	<i>Sub-scapular-skinfold</i>	<i>thigh skinfold</i>	<i>waist circum</i>	<i>Composite Score</i>
<i>GCG</i>	rs1990761	2	162823210	0.042	0.058	0.096	0.041	0.018	0.045	0.032	0.034
<i>GLP1R</i>	rs7738586	6	39115518	0.025	0.030	0.022	0.012	0.026	0.008	0.039	0.004
<i>GLP1R</i>	rs9380825	6	39118941	0.217	0.170	0.224	0.088	0.257	0.756	0.191	0.155
<i>GLP1R</i>	rs2268657	6	39128520	0.036	0.023	0.067	0.062	0.048	0.228	0.058	0.011
<i>GLP1R</i>	rs6923761	6	39142050	0.044	0.379	0.320	0.880	0.304	0.584	0.372	0.376
<i>GLP1R</i>	rs2143733	6	39169474	0.079	0.085	0.074	0.122	0.112	0.259	0.177	0.032
<i>HTR2A</i>	rs1923885	13	46321087	0.123	0.165	0.042	0.295	0.317	0.083	0.331	0.084
<i>HTR2C</i>	rs7055144	13	113699082	0.517	0.795	0.649	0.515	0.322	0.050	0.293	0.495
<i>JAK2</i>	rs3808850	9	4973311	0.411	0.196	0.669	0.268	0.199	0.560	0.357	0.248
<i>JAK2</i>	rs1327493	9	4983082	0.446	0.610	0.012	0.289	0.546	0.476	0.432	0.331
<i>JAK2</i>	rs2230722	9	5040706	0.291	0.260	0.118	0.650	0.460	0.198	0.579	0.227
<i>JAK2</i>	rs1536800	9	5045434	0.085	0.036	0.046	0.078	0.210	0.044	0.211	0.052
<i>LEPR</i>	hCV1928197	1	65960323	0.283	0.016	0.270	0.095	0.163	0.046	0.466	0.119
<i>LEPR</i>	hCV1928241	1	66033405	0.315	0.028	0.410	0.094	0.246	0.194	0.401	0.177
<i>MC4R</i>	MC4R178	18	56192751	0.146	0.236	0.169	0.017	0.392	0.047	0.269	0.043
<i>MC4R</i>	rs1943232	18	56245389	0.253	0.020	0.469	0.358	0.110	0.070	0.342	0.179
<i>NPY1R</i>	rs1574637	4	164599697	0.340	0.082	0.294	0.120	0.323	0.048	0.388	0.116
<i>NPY5R</i>	rs6837793	4	164614340	0.339	0.082	0.283	0.117	0.322	0.048	0.384	0.114
<i>NPY5R</i>	rs4234955	4	164617881	0.165	0.022	0.298	0.168	0.075	0.160	0.124	0.077
<i>PLIN</i>	rs2304794	15	88014138	0.415	0.031	0.029	0.121	0.187	0.078	0.379	0.178
<i>PLIN</i>	rs6496589	15	88014233	0.415	0.031	0.029	0.121	0.187	0.078	0.379	0.178
<i>PLIN</i>	rs2289487	15	88018100	0.283	0.182	0.674	0.487	0.033	0.268	0.150	0.292
<i>SOCS3</i>	rs8074003	17	73876088	0.239	0.328	0.170	0.573	0.051	0.130	0.017	0.200
<i>STAT3</i>	rs2272087	17	37713088	0.907	0.791	0.955	0.846	0.861	0.019	0.868	0.801
<i>STAT3</i>	rs16967659	17	37713263	0.906	0.783	0.958	0.822	0.860	0.019	0.854	0.781
<i>STAT3</i>	rs1053023	17	37719142	0.906	0.783	0.958	0.822	0.860	0.019	0.854	0.781
<i>STAT3</i>	rs1053005	17	37719436	0.961	0.838	0.936	0.704	0.937	0.014	0.918	0.840
<i>STAT3</i>	rs2306580	17	37745206	0.699	0.723	0.844	0.951	0.449	0.013	0.629	0.730
<i>TUB</i>	rs4758272	11	8009735	0.081	0.059	0.133	0.376	0.019	0.515	0.218	0.080
<i>TUB</i>	rs1406094	11	8018502	0.015	0.223	0.237	0.082	0.002	0.932	0.009	0.052
<i>TUB</i>	rs7949880	11	8029812	0.023	0.031	0.085	0.362	0.005	0.350	0.094	0.048

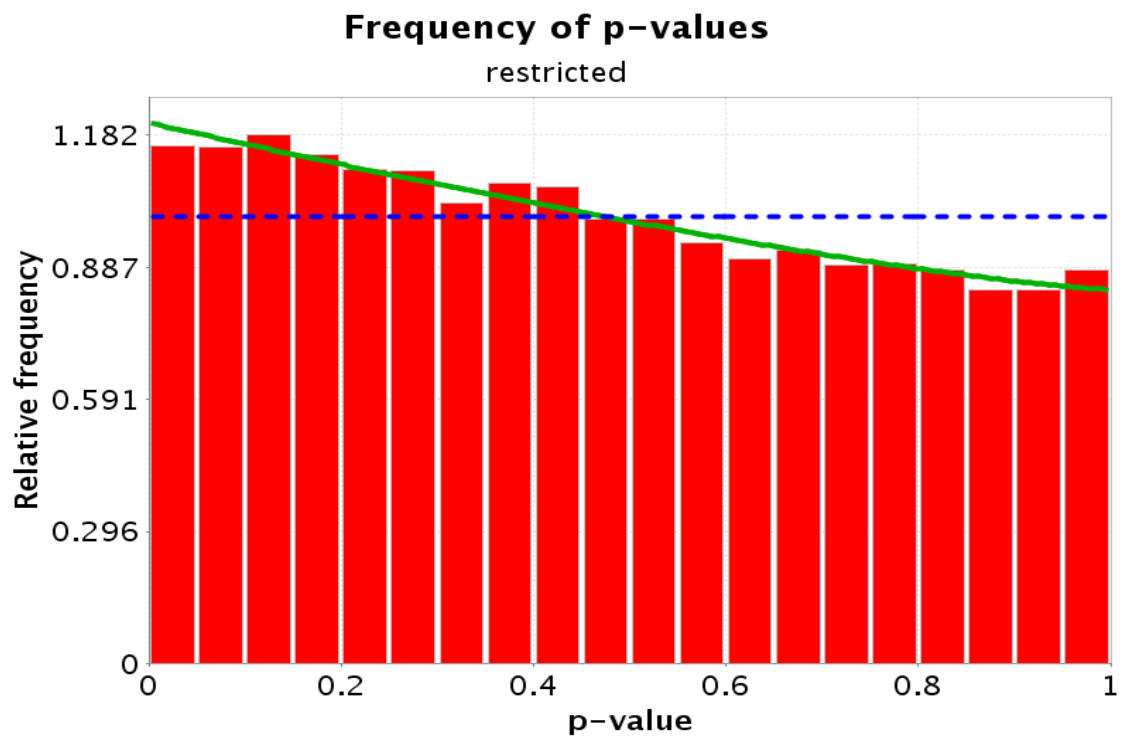
<i>Gene</i>	SNP Name	Chromosome	Map	percent body fat	triceps skinfold	abdominal skinfold	BMI	Sub-scapular-skinfold	thigh skinfold	waist circum	Composite Score
<i>TUB</i>	rs11041723	11	8035280	0.063	0.107	0.122	0.574	0.012	0.572	0.190	0.112
<i>TUB</i>	rs2280726	11	8039305	0.023	0.031	0.085	0.362	0.005	0.350	0.094	0.048
<i>TUB</i>	rs2242503	11	8075048	0.145	0.264	0.047	0.316	0.288	0.033	0.422	0.175
<i>TUB</i>	rs1055233	11	8084071	0.304	0.041	0.175	0.134	0.278	0.262	0.413	0.107
<i>TUB</i>	rs1569128	11	8089461	0.369	0.046	0.214	0.140	0.319	0.300	0.452	0.125

Table S3. Genes associated with obesity in Yup'ik participants using all SNPs genotyped within the gene. **For none of the genes were the FDR values less than 0.05.** There was no significant p-value corresponding to the phenotype subscapular-skinfold.

Phenotype	ADIPOQ			MC4R			NPY5R			TUB		
	Raw p-value	R ²	Adjusted R ²	Raw p-value	R ²	Raw p-value	R ²	Adjusted R ²	Raw p-value	Raw p-value	R ²	
Percent bodyfat	0.04	0.071	0.026	0.14	Percent bodyfat	0.04	0.071	0.026	0.14	Percent bodyfat	0.04	0.071
Triceps skinfold	0.21	0.055	0.010	0.04	Triceps skinfold	0.21	0.055	0.010	0.04	Triceps skinfold	0.21	0.055
Abdominal skinfold	0.51	0.044	-0.002	0.54	Abdominal skinfold	0.51	0.044	-0.002	0.54	Abdominal skinfold	0.51	0.044
BMI	0.11	0.061	0.017	0.08	BMI	0.11	0.061	0.017	0.08	BMI	0.11	0.061
Thigh skinfold	0.63	0.041	-0.005	0.14	Thigh skinfold	0.63	0.041	-0.005	0.14	Thigh skinfold	0.63	0.041
Waist circumference	0.02	0.074	0.031	0.12	Waist circumference	0.02	0.074	0.031	0.12	Waist circumference	0.02	0.074
Composite Score	0.10	0.061	0.018	0.07	Composite Score	0.10	0.061	0.018	0.07	Composite Score	0.10	0.061

Table S4. Summary of the ten pairwise interactions with the highest posterior probability of true positive interaction association.

<i>Gene × gene</i>	<i>SNP × SNP</i>	<i>Observed p-value</i>	<i>Posterior probability of true positive</i>
<i>TUB × JAK2</i>	rs11041723 x rs2274471	6.1×10^{-05}	0.31
<i>BBS8 × GLPIR</i>	rs17700296 x rs2268641	7.0×10^{-05}	0.31
<i>CPE × APM1</i>	rs1866217 x rs3774261	1.0×10^{-04}	0.31
<i>LEPR × LEPR</i>	rs3790423 x rs3790439	1.2×10^{-04}	0.31
<i>MC4R × APM1</i>	rs1543915 x rs3774261	1.2×10^{-04}	0.31
<i>LEPR × LEPR</i>	rs3790422 x rs3790439	1.3×10^{-04}	0.31
<i>NPY5R × GLP1R</i>	Y5R1c52 x rs9380825	1.3×10^{-04}	0.31
<i>TUB × SOCS3</i>	rs4758289 x rs4969168	2.3×10^{-04}	0.31
<i>JAK2 × JAK2</i>	rs10491652 x rs1410779	2.6×10^{-04}	0.31
<i>GHRL × CPE</i>	rs3755777 x rs6536912	2.6×10^{-04}	0.31



Supplemental Figure 1. The proportion of pairwise interaction tests. The proportion of truly null hypotheses is represented by the area under the green solid line and the blue broken horizontal line. This area is approximately 16 % of the total area.