Correction: Genetic Polymorphisms and Weight Loss in Obesity: A Randomised Trial of Hypo-Energetic High- versus Low-Fat Diets

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The numbering of the reference citations in Table 2 is incorrect. The correct numbering is shown in the table below.

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Presumed Function of Genes	Normal Name	Gene Name	Locus ID	Location	Rs	SNP	Genotype			Hardy-Weinberg Equilibrium ^b	
							Non-carrier	Hetero-zygote	Homo-zygote	Allele Frequency	p-Value
Hypothalamic regulation of appetite	Solute carrier family 6 member 14 [15] Women ^a	SLC6A14	11254	Xq23	2011162	+22510 C>G	79	219	153	0.58	0.70
	Solute carrier family 6 member 14 [15] Men ^a	SLC6A14	11254	Xq23	2011162	+22510 C>G	66	—	80	0.55	—
	Cocaine- and amphetamine-regulated transcript [16]	CART	9607	5q13.2	7379701	−3608 T>C ²	150	305	170	0.52	0.58
					6453132	−1702 C>T ²	221	292	122	0.42	0.19
					—	−175 A>G ²	155	303	163	0.51	1.00
					5868607	−1336delA	512	105	6	0.094	0.53
	Growth hormone secretagogue receptor [17,18]	GHSR	2693	3q26.3	2232169	Leu149Leu	599	25	0	0.022	1.00
	Glutamate decarboxylase 2 [19]	GAD2	2572	10p11.23	928197	+83897 T>A	426	169	31	0.18	0.0065
					992990	+61450 C>A	318	257	57	0.29	0.12
					2236418	−243 A>G	416	173	30	0.19	0.30
	Ghrelin [20,21]	GHLR	51738	3p25.3	696217	Leu72Met	552	69	4	0.062	0.56
8195					20p12	1547	Arg517Cys	505	120	1	0.097
McKusick-Kaufman syndrome [22]	MKKS	8195	20p12								
Leptin receptor overlapping transcript-like 1 [23]	LEPROTL1	23484	8p21.2–1			−2625 C>T	551	54	1	0.046	0.48
Proprotein convertase subtilisin/kexin type 1 [24]	PCSK1	5122	5q15	6235	T690S C>G	360	215	47	0.25	0.074	
Efficiency of energy expenditure	Uncoupling protein 2 [25]	UCP2	7351	11q13	6593669	−866 G>A	250	307	81	0.37	0.50
	Uncoupling protein 3 [26]	UCP3	7352	11q13	1900849	−55 C>T	351	239	46	0.26	0.94
Regulation of adipocyte differentiation and function	Forkhead box C2 [27,28]	FOXC2	2303	16q22–24	—	−512 C>T	86	288	227	0.62	0.31
	Peroxisome proliferative activated receptor. Gamma coactivator 1. alpha [29–31]	PPARGC1A	10891	4p15.1	8192678	Gly482Ser	74	276	276	0.66	0.83
					2932963	+2962 A>G	178	298	151	0.48	0.73
	Peroxisome proliferative activated receptor. Gamma isoform 2 [31–35]	PPARG2	5468	3p25	1801282	Pro12Ala	475	151	12	0.14	0.30
					3856806	1431 C>T	474	144	11	0.13	0.66
					7649970	−820 C>T	465	147	13	0.14	0.64
	Peroxisome proliferative activated receptor. Gamma isoform 3 [36]	PPARG3	5468	3p25	10865710	−681C>G	346	258	37	0.26	0.57
	Sterol regulatory element binding transcription factor 1 [37]	SREBF1	6720	17p11.2	—	17 C>G	248	304	83	0.37	0.59
	WW domain containing adaptor with coiled-coil [38]	WAC	51322	10p12.1	2807761	−829 A>G	142	274	157	0.51	0.16

Table 2. Continued

Presumed Function of Genes	Normal Name	Gene Name	Locus ID	Location	Rs	SNP	Genotype			Hardy-Weinberg Equilibrium ^b		
							Non-carrier	Hetero-zygote	Homo-zygote	Allele Frequency	p-Value	
Regulation of lipid and glucose metabolism	Hydroxysteroid (11-beta) Dehydrogenase 1 [39–40]	HSD11B1	3290	1q32.2	846919	–2940 G>A	525	70	1	0.060	0.97	
	Hepatic lipase C [41]	LIPC	3990	15q21–23	6082	Asn215Ser	280	282	71	0.33	0.91	
					1800588	–514 C>T	369	225	21	0.22	0.51	
					3168310	1926 C>G	308	256	59	0.30	0.88	
	Insulin-like growth factor 2 [42,43]	IGF2	3481	11p15.5	680	Apal A>G	320	257	55	0.29	0.99	
					3842759	–6815 A>T	325	251	55	0.29	0.78	
					5219	Glu23Lys	241	300	73	0.36	0.26	
	Potassium inwardly rectifying channel J11 (KIR6.2) [44,45]	KCNJ11	3767	11p15.1	5219	Glu23Lys	241	300	73	0.36	0.26	
	Ectonucleotide pyrophosphatase/ phosphodiesterase 1 [46]	ENPP1	5167	6q23.2	—	IVS20delT-11	374	232	27	0.23	0.30	
					1044498	Lys121Gln	433	171	12	0.16	0.84	
					7754561	1044 A>G	318	244	40	0.27	0.34	
	Production of adipocytokines	Adiponectin [47,48]	ADIPOQ	9370	3q27.3	266729	–11377 C>G	356	236	38	0.25	0.32
						2241766	+45 T>G	477	130	21	0.14	0.052
1501299						+276 T>G	76	233	323	0.70	0.021	
17300539						–11391 G>A	525	101	3	0.085	0.78	
CD36 antigen [49]		CD36	948	7q11.2	2232169	–178 A>C	110	294	189	0.57	0.68	
					1800795	–174 G>C	184	326	116	0.45	0.62	
					1800629	–308 G>A	459	159	14	0.15	0.011	
					1799889	–675insG	157	259	140	0.49	0.099	

The table is based on those obese individuals among the 771 enrolled in the NUGENOB study who completed the dietary intervention ($n = 648$), who have been genotyped ($n = 643$) and who had a body mass index <60 ($n = 642$).

The genes are grouped according to their known or presumed function leading to the association with the obesity-related phenotypes.

^aFor SLC6A14, results are presented separately for women and men since the SNP is located on chromosome X. One male individual was identified as heterozygote on SLC6A14, and was excluded.

^bAll tests for Hardy-Weinberg equilibrium are based on the sum of the Pearson test statistics for each centre. The p -value is calculated from a χ^2 distribution with 8 degrees of freedom.

SNP, single nucleotide polymorphism; Rs, Reference SNP accession ID.

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