

Appendix

Table A1: Genotype distribution and crude main effects of the different SNPs on the risk of obesity in the BVS II study.

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Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
IL-2 region 5'	rs4833248	0.30	GG	50.9	48.3	0.8876	1.00	0.6606
			AG	40.9	43.1		0.90 (0.58-1.39)	
			AA	8.2	8.6		0.91 (0.39-1.91)	
IL-2	rs2069779	0.07	CC	86.7	85.8	0.8649	1.00	0.7599
			CT	13.3	14.0		0.93 (0.49-1.65)	
			TT	0.0	0.2			
IL-2	rs2069778	0.16	CC	69.4	71.0	0.923	1.00	0.7846
			CT	28.8	27.0		1.09 (0.68-1.72)	
			TT	1.8	2.0		0.93 (0.14-3.69)	
IL-2	rs2069763	0.35	GG	38.9	43.2	0.0835	1.00	0.8331
			GT	54.0	43.9		1.37 (0.89-2.12)	
			TT	7.1	12.9		0.61 (0.25-1.31)	
IL-2	rs2069762	0.29	TT	51.8	49.6	0.9149	1.00	0.7005
			GT	40.2	42.0		0.91 (0.59-1.41)	
			GG	8.0	8.4		0.91 (0.40-1.92)	
IL-6 region 5'	rs1880241	0.50	AA	30.7	26.0	0.5736	1.00	0.3146
			AG	45.6	47.3		0.82 (0.50-1.33)	
			GG	23.7	26.7		0.75 (0.43-1.32)	
IL-6 region 5'	rs4719714	0.22	AA	59.8	61.6	0.0284	1.00	0.2056
			AT	30.4	34.6		0.90 (0.57-1.42)	
			TT	9.8	3.8		2.68 (1.17-5.94)	
IL-6 region 5'	rs12700386	0.19	CC	76.3	63.4	0.0327	1.00	0.0184
			CG	20.2	31.8		0.53 (0.31-0.86)	
			GG	3.5	4.9		0.60 (0.17-1.62)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
IL-6	rs1800797	0.42	GG	35.1	33.6	0.9132	1.00	0.6772
			AG	47.4	47.3		0.96 (0.61-1.52)	
			AA	17.5	19.1		0.88 (0.48-1.58)	
IL-6	rs1800795	0.43	GG	35.4	33.6	0.8814	1.00	0.6257
			CG	46.9	46.8		0.95 (0.60-1.52)	
			CC	17.7	19.6		0.86 (0.46-1.54)	
IL-6	rs2069840	0.35	CC	46.9	43.0	0.4942	1.00	0.8148
			CG	38.1	44.1		0.79 (0.50-1.24)	
			GG	15.0	12.9		1.07 (0.56-1.96)	
IL-6	rs2069861	0.10	CC	86.8	80.4	0.1825	1.00	0.2004
			CT	11.4	18.4		0.62 (0.33-1.10)	
			TT	1.8	1.1			
IL-6	rs2069833	0.43	TT	35.1	32.9	0.8205	1.00	0.5411
			CT	48.2	48.1		0.94 (0.60-1.49)	
			CC	16.7	19.0		0.82 (0.44-1.49)	
IL-6 region 3 ^c	rs10242595	0.30	AA	50.0	49.2	0.6341	1.00	0.7851
			AG	37.5	41.0		0.90 (0.57-1.40)	
			GG	12.5	9.8		1.26 (0.63-2.40)	
IL-10 region 5 ^c	rs17015767	0.19	GG	70.2	65.9	0.6464	1.00	0.5015
			CG	24.6	29.0		0.80 (0.49-1.27)	
			CC	5.3	5.1		0.97 (0.35-2.31)	
IL-10 region 5 ^c	rs3122605	0.16	AA	63.2	72.1	0.1351	1.00	0.0477
			AG	33.3	26.2		1.45 (0.92-2.26)	
			GG	3.5	1.8		2.26 (0.59-7.37)	
IL-10	rs3024498	0.22	AA	66.7	60.7	0.4964	1.00	0.306
			AG	28.1	33.6		0.76 (0.48-1.20)	
			GG	5.3	5.7		0.84 (0.30-1.98)	
IL-10	rs1554286	0.20	CC	59.6	63.7	0.5686	1.00	0.5872
			CT	37.7	32.7		1.23 (0.80-1.89)	
			TT	2.6	3.5		0.79 (0.18-2.47)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
IL-10	rs3021094	0.10	AA	84.2	79.9	0.3698	1.00	0.2204
			AC	15.8	19.0		0.74 (0.42-1.27)	
			CC	0.0	1.1			
IL-10	rs1800896	0.44	AA	25.4	31.3	0.3532	1.00	0.5466
			AG	57.9	50.6		1.41 (0.87-2.31)	
			GG	16.7	18.2		1.13 (0.59-2.12)	
IL-10 region 3'	rs3024505	0.16	CC	63.2	70.4	0.1416	1.00	0.0783
			CT	33.3	28.3		1.31 (0.84-2.03)	
			TT	3.5	1.3		2.94 (0.74-10.57)	
IL-18	rs3882891	0.42	AA	32.5	35.0	0.7613	1.00	0.8617
			AC	50.9	47.0		1.17 (0.74-1.86)	
			CC	16.7	18.0		1.00 (0.53-1.83)	
IL-18	rs5744280	0.33	CC	45.1	43.8	0.9581	1.00	0.8547
			CT	45.1	46.7		0.94 (0.61-1.45)	
			TT	9.7	9.6		0.98 (0.45-1.98)	
IL-18	rs549908	0.30	TT	44.2	49.1	0.6455	1.00	0.367
			GT	46.0	42.4		1.20 (0.78-1.86)	
			GG	9.7	8.5		1.27 (0.59-2.59)	
IL-18	rs5744256	0.26	TT	54.0	54.7	0.9818	1.00	0.9464
			CT	39.8	38.9		1.04 (0.67-1.59)	
			CC	6.2	6.4		0.97 (0.38-2.21)	
IL-18	rs360722	0.11	CC	82.5	77.5	0.5139	1.00	0.2638
			CT	16.7	21.4		0.73 (0.42-1.22)	
			TT	0.9	1.1			
IL-18	rs795467	0.27	GG	51.8	53.1	0.9414	1.00	0.7426
			AG	40.4	39.8		1.04 (0.67-1.60)	
			AA	7.9	7.1		1.14 (0.49-2.44)	
IL-18	rs1946519	0.39	CC	38.1	36.7	0.7115	1.00	0.5333
			AC	48.7	46.9		1.00 (0.64-1.57)	
			AA	13.3	16.4		0.78 (0.40-1.46)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
TNF- α	rs3093662	0.07	AA	87.6	85.9	0.8051	1.00	0.5965
			AG	12.4	13.9		0.86 (0.45-1.55)	
			GG	0.0	0.2			
TNF- α	rs3093668	0.05	GG	92.9	90.0	0.5996	1.00	0.329
			CG	7.1	9.7		0.69 (0.29-1.43)	
			CC	0.0	0.2			
TNFRSF1A	rs4149579	0.06	GG	90.4	88.3	0.6836	1.00	0.4742
			AG	9.6	11.3		0.81 (0.39-1.54)	
			AA	0.0	0.4			
TNFRSF1A	rs4149577	0.48	TT	28.1	24.3	0.4424	1.00	0.216
			CT	55.3	54.1		0.88 (0.55-1.44)	
			CC	16.7	21.6		0.67 (0.35-1.24)	
TNFRSF1A	rs4149576	0.45	GG	24.6	31.2	0.354	1.00	0.3468
			AG	55.3	48.9		1.44 (0.88-2.38)	
			AA	20.2	19.9		1.29 (0.69-2.37)	
TNFRSF1A	rs4149570	0.39	GG	43.4	34.4	0.2057	1.00	0.1269
			GT	44.2	51.4		0.68 (0.44-1.06)	
			TT	12.4	14.2		0.69 (0.35-1.31)	
TNFRSF1B	rs652625	0.05	AA	88.6	91.2	0.3895	1.00	0.5686
			AT	11.4	8.2		1.33 (0.66-2.51)	
			TT	0.0	0.7			
TNFRSF1B	rs496888	0.32	AA	49.1	46.7	0.7928	1.00	0.5235
			AG	41.2	41.6		0.94 (0.61-1.45)	
			GG	9.6	11.7		0.78 (0.37-1.55)	
TNFRSF1B	rs3766730	0.16	CC	69.9	71.0	0.1012	1.00	0.4355
			CT	25.7	27.7		0.94 (0.58-1.49)	
			TT	4.4	1.3		3.38 (0.95-11.48)	
TNFRSF1B	rs1061622	0.21	TT	61.1	62.9	0.1445	1.00	0.3269
			GT	31.9	34.0		0.97 (0.61-1.50)	
			GG	7.1	3.1		2.36 (0.91-5.74)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
TNFRSF1B	rs2275416	0.18	GG	62.8	67.9	0.2342	1.00	0.1668
			AG	31.9	29.7		1.16 (0.73-1.81)	
			AA	5.3	2.5		2.34 (0.78-6.36)	
TNFRSF1B	rs235219	0.10	GG	82.1	81.4	0.9817	1.00	0.8626
			AG	17.0	17.7		0.95 (0.54-1.60)	
			AA	0.9	0.9			
TNFRSF1B	rs1061624	0.41	GG	42.9	38.2	0.6605	1.00	0.4479
			AG	37.5	40.8		0.82 (0.51-1.30)	
			AA	19.6	21.0		0.83 (0.47-1.45)	
TNFRSF1B	rs1061628	0.40	CC	32.1	36.4	0.0219	1.00	0.5483
			CT	58.9	46.1		1.45 (0.92-2.29)	
			TT	8.9	17.5		0.58 (0.26-1.18)	
TNFRSF21	rs9473029	0.05	GG	92.0	90.1	0.6198	1.00	0.4332
			CG	8.0	9.3		0.78 (0.35-1.59)	
			CC	0.0	0.7			
TNFRSF21	rs2236039	0.28	AA	49.1	53.3	0.6287	1.00	0.6086
			AG	43.0	38.1		1.23 (0.80-1.89)	
			GG	7.9	8.6		0.99 (0.43-2.09)	
TNFRSF21	rs2295266	0.19	CC	61.9	66.4	0.6331	1.00	0.4735
			CG	34.5	29.9		1.24 (0.79-1.92)	
			GG	3.5	3.8		1.01 (0.28-2.83)	
TNFRSF21	rs714373	0.36	AA	44.7	40.3	0.649	1.00	0.5459
			AG	41.2	45.8		0.81 (0.52-1.26)	
			GG	14.0	13.9		0.91 (0.47-1.67)	
TNFRSF21	rs9473045	0.34	GG	45.1	43.0	0.7653	1.00	0.9333
			AG	41.6	45.2		0.88 (0.56-1.36)	
			AA	13.3	11.8		1.08 (0.55-2.03)	
TNFRSF21	rs16875844	0.08	GG	81.6	86.3	0.3809	1.00	0.274
			AG	17.5	12.6		1.42 (0.81-2.42)	
			AA	0.9	1.1			

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
TNFRSF21	rs2017424	0.48	CC	29.8	27.6	0.5536	1.00	0.8808
			CG	43.9	49.4		0.82 (0.51-1.34)	
			GG	26.3	23.0		1.06 (0.61-1.85)	
TNFRSF21	rs6458555	0.34	GG	44.2	46.8	0.8817	1.00	0.6226
			AG	41.6	40.1		1.10 (0.70-1.71)	
			AA	14.2	13.1		1.14 (0.59-2.12)	
TNFRSF21 region 3'	rs9381530	0.43	TT	35.1	30.7	0.6516	1.00	0.3818
			GT	49.1	51.7		0.83 (0.53-1.32)	
			GG	15.8	17.7		0.78 (0.41-1.44)	
NPY region 5'	rs16480	0.32	TT	56.3	52.9	0.3693	1.00	0.2632
			CT	30.4	28.0		1.02 (0.63-1.62)	
			CC	13.4	19.1		0.66 (0.35-1.19)	
NPY	rs16148	0.34	TT	43.4	43.5	0.3535	1.00	0.5282
			CT	48.7	43.9		1.11 (0.72-1.72)	
			CC	8.0	12.6		0.64 (0.28-1.32)	
NPY	rs16141	0.49	AA	25.0	23.6	0.6322	1.00	0.78
			AC	50.0	54.8		0.86 (0.52-1.45)	
			CC	25.0	21.6		1.09 (0.60-1.98)	
NPY	rs9785023	0.50	AA	23.7	23.2	0.7098	1.00	0.6878
			AG	50.9	54.6		0.91 (0.55-1.54)	
			GG	25.4	22.1		1.13 (0.62-2.04)	
NPY	rs16138	0.26	GG	56.1	53.0	0.4733	1.00	0.3394
			CG	40.4	40.6		0.94 (0.61-1.43)	
			CC	3.5	6.4		0.52 (0.15-1.37)	
NPY	rs16135	0.07	CC	90.4	84.7	0.2342	1.00	0.099
			CT	9.6	14.4		0.59 (0.29-1.11)	
			TT	0.0	0.9			
NPY	rs16131	0.15	AA	68.4	73.7	0.4935	1.00	0.2354
			AG	28.1	23.8		1.27 (0.79-2.01)	
			GG	3.5	2.4		1.56 (0.42-4.69)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
NPY	rs16475	0.11	TT	86.7	86.5	0.498	1.00	0.7838
			CT	2.7	4.9		0.54 (0.13-1.61)	
			CC	10.6	8.6		1.22 (0.59-2.36)	
NPY region 3′	rs2023890	0.22	TT	57.7	61.7	0.3871	1.00	0.2594
			CT	35.1	34.1		1.10 (0.70-1.71)	
			CC	7.2	4.2		1.82 (0.72-4.22)	
NPY region 3′	rs16472	0.08	CC	84.7	83.3	0.7242	1.00	0.724
			CT	15.3	16.7		0.90 (0.49-1.57)	
NPY region 3′	rs17374047	0.15	AA	73.2	70.8	0.6333	1.00	0.4807
			AG	25.9	27.0		0.93 (0.57-1.47)	
			GG	0.9	2.2		0.39 (0.02-2.08)	
NPY region 3′	rs16468	0.40	CC	33.0	33.9	0.8188	1.00	0.8685
			AC	54.5	51.7		1.08 (0.69-1.72)	
			AA	12.5	14.5		0.88 (0.44-1.72)	
NPY region 3′	rs16110	0.50	GG	26.5	23.7	0.8191	1.00	0.6479
			CG	50.4	52.8		0.85 (0.52-1.42)	
			CC	23.0	23.5		0.87 (0.48-1.58)	
NPY1R region 5′	rs4234955	0.23	AA	59.3	60.1	0.1041	1.00	0.3521
			AG	31.0	35.2		0.89 (0.56-1.40)	
			GG	9.7	4.7		2.11 (0.94-4.51)	
NPY1R region 5′	rs4691076	0.23	CC	58.4	59.0	0.2458	1.00	0.4733
			CT	32.7	36.1		0.91 (0.58-1.42)	
			TT	8.8	4.9		1.83 (0.80-3.96)	
NPY1R	rs9764	0.27	TT	53.6	50.6	0.8303	1.00	0.6456
			TC	42.0	45.2		0.88 (0.57-1.34)	
			CC	4.5	4.3		0.99 (0.32-2.57)	
NPY1R	rs4691075	0.11	TT	78.6	80.1	0.3085	1.00	0.4762
			CT	18.8	19.0		1.10 (0.65-1.80)	
			CC	2.7	0.9			

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
NPY1R	rs7687423	0.35	GG	40.4	41.3	0.9668	1.00	0.9305
			AG	48.2	46.9		1.05 (0.68-1.64)	
			AA	11.4	11.8		0.99 (0.48-1.93)	
NPY1R	rs12507653	0.30	AA	53.1	47.9	0.6132	1.00	0.3763
			AT	38.1	42.4		0.81 (0.52-1.25)	
			TT	8.8	9.8		0.82 (0.37-1.66)	
NPY5R	rs4632602	0.10	TT	74.6	82.1	0.1896	1.00	0.0779
			CT	24.6	17.2		1.57 (0.95-2.52)	
			CC	0.9	0.7			
NPY5R	rs7678265	0.08	CC	85.0	85.2	0.969	1.00	0.9122
			CT	14.2	14.2		1.02 (0.56-1.78)	
			TT	0.9	0.7			
NPY5R	rs11100494	0.08	CC	89.4	82.9	0.169	1.00	0.0692
			AC	10.6	15.7		0.58 (0.29-1.06)	
			AA	0.0	1.3			
NPY5R region 3′	rs6536721	0.34	GG	47.8	43.5	0.2032	1.00	0.9922
			AG	36.3	44.8		0.74 (0.47-1.15)	
			AA	15.9	11.7		1.24 (0.66-2.26)	
POMC region 5′	rs874401	0.18	CC	73.7	65.6	0.1012	1.00	0.2296
			CT	22.8	32.5		0.63 (0.38-1.00)	
			TT	3.5	2.0		1.57 (0.42-4.96)	
POMC	rs6713532	0.21	TT	69.9	60.0	0.1127	1.00	0.1282
			CT	24.8	35.1		0.61 (0.37-0.96)	
			CC	5.3	4.9		0.94 (0.34-2.26)	
POMC	rs934778	0.30	TT	50.4	46.8	0.6555	1.00	0.699
			CT	40.7	45.5		0.83 (0.54-1.28)	
			CC	8.8	7.8		1.06 (0.47-2.19)	
MC4R region 5′	rs8097783	0.06	GG	89.5	87.6	0.7778	1.00	0.5455
			AG	10.5	12.2		0.83 (0.41-1.56)	
			AA	0.0	0.2			

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
MC4R region 5'	rs8091237	0.23	CC	54.9	59.7	0.5989	1.00	0.4611
			CG	39.8	34.7		1.25 (0.81-1.92)	
			GG	5.3	5.5		1.05 (0.38-2.50)	
MC4R region 5'	rs1943225	0.26	TT	53.1	58.3	0.3252	1.00	0.6525
			GT	39.8	32.6		1.34 (0.86-2.07)	
			GG	7.1	9.2		0.85 (0.35-1.82)	
MC4R region 5'	rs7228573	0.31	CC	45.9	47.5	0.503	1.00	0.825
			CT	47.7	43.2		1.14 (0.74-1.76)	
			TT	6.3	9.3		0.70 (0.27-1.56)	
MC4R region 5'	rs1943228	0.22	AA	56.9	61.4	0.4261	1.00	0.6171
			AG	40.4	34.3		1.27 (0.82-1.96)	
			GG	2.8	4.3		0.70 (0.16-2.13)	
MC4R	rs8087522	0.32	GG	42.5	45.2	0.5264	1.00	0.9645
			AG	50.4	45.2		1.19 (0.77-1.83)	
			AA	7.1	9.5		0.79 (0.33-1.71)	
MC4R region 3'	rs17066829	0.35	TT	41.6	42.9	0.7242	1.00	0.9011
			AT	47.8	44.2		1.11 (0.72-1.73)	
			AA	10.6	12.8		0.85 (0.41-1.67)	
MC4R region 3'	rs1943226	0.10	TT	85.0	80.5	0.3931	1.00	0.2191
			GT	15.0	18.6		0.73 (0.40-1.26)	
			GG	0.0	0.9			
PPY	rs231471	0.44	AA	39.5	29.9	0.0621	1.00	0.3392
			AG	38.6	50.6		0.58 (0.36-0.92)	
			GG	21.9	19.5		0.85 (0.48-1.48)	
PPY	rs1642603	0.34	CC	46.0	43.4	0.7247	1.00	0.4614
			CT	43.4	43.4		0.94 (0.61-1.46)	
			TT	10.6	13.3		0.75 (0.36-1.46)	
PYY region 5'	rs17611995	0.18	CC	66.7	68.1	0.8208	1.00	0.9245
			AC	29.8	27.4		1.11 (0.70-1.74)	
			AA	3.5	4.4		0.81 (0.23-2.22)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
PYY region 5′	rs497847	0.07	AA	87.6	86.7	0.5218	1.00	0.9523
			AG	11.5	13.1		0.92 (0.48-1.68)	
			GG	0.9	0.2			
PYY	rs9907468	0.10	CC	81.4	80.1	0.5998	1.00	0.6236
			CT	18.6	19.0		0.92 (0.53-1.54)	
			TT	0.0	0.9			
PYY	rs918242	0.34	TT	43.8	43.0	0.8146	1.00	0.6827
			CT	46.4	45.0		1.01 (0.65-1.57)	
			CC	9.8	12.0		0.81 (0.38-1.61)	
PYY	rs1684668	0.24	CC	58.4	57.4	0.9807	1.00	0.8464
			CT	36.3	37.1		0.96 (0.62-1.48)	
			TT	5.3	5.5		0.95 (0.34-2.26)	
PYY	rs1859223	0.15	CC	71.1	71.7	0.7638	1.00	0.9592
			CG	28.1	26.5		1.03 (0.65-1.61)	
			GG	0.9	1.8			
PYY region 3′	rs1662754	0.47	AA	23.9	28.4	0.2685	1.00	0.95
			AT	58.4	49.9		1.39 (0.85-2.32)	
			TT	17.7	21.7		0.97 (0.51-1.82)	
PYY region 3′	rs8079623	0.13	CC	74.6	76.1	0.9068	1.00	0.6876
			CG	23.7	22.6		1.09 (0.67-1.73)	
			GG	1.8	1.3			
LEP	rs2167270	0.40	GG	36.0	36.2	0.8447	1.00	0.738
			AG	45.6	47.6		0.97 (0.61-1.53)	
			AA	18.4	16.2		1.14 (0.62-2.05)	
LEP	rs2278815	0.46	AA	27.2	32.2	0.5427	1.00	0.2784
			AG	47.4	45.6		1.23 (0.76-2.03)	
			GG	25.4	22.1		1.36 (0.77-2.40)	
LEP	rs11763517	0.47	CC	29.8	28.2	0.7577	1.00	0.945
			CT	46.5	50.3		0.87 (0.54-1.42)	
			TT	23.7	21.5		1.04 (0.58-1.84)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
LEP	rs7795794	0.05	GG	89.5	91.4	0.1278	1.00	0.3672
			AG	9.6	8.6		1.25 (0.61-2.40)	
			AA	0.9	0.0			
LEP	rs10954173	0.40	GG	36.0	36.1	0.6991	1.00	0.6587
			AG	44.7	47.8		0.94 (0.59-1.49)	
			AA	19.3	16.2		1.20 (0.66-2.14)	
LEP region 3'	rs10954176	0.47	TT	24.6	30.6	0.1173	1.00	0.8758
			CT	55.3	44.4		1.55 (0.95-2.57)	
			CC	20.2	25.0		1.00 (0.54-1.84)	
LEP region 3'	rs1116656	0.46	GG	27.2	30.8	0.0144	1.00	0.3721
			AG	59.6	45.8		1.48 (0.92-2.40)	
			AA	13.2	23.4		0.64 (0.32-1.22)	
LEPR	rs3790433	0.25	GG	50.9	58.1	0.3229	1.00	0.1334
			AG	40.4	35.8		1.29 (0.83-1.98)	
			AA	8.8	6.2		1.62 (0.71-3.42)	
LEPR	rs4655811	0.34	GG	44.6	42.3	0.8564	1.00	0.5812
			CG	45.5	46.5		0.93 (0.60-1.44)	
			CC	9.8	11.3		0.82 (0.38-1.65)	
LEPR	rs1327120	0.41	GG	32.5	32.7	0.5787	1.00	0.6174
			AG	55.3	51.3		1.08 (0.69-1.72)	
			AA	12.3	16.0		0.77 (0.38-1.49)	
LEPR	rs1327116	0.27	CC	50.4	52.1	0.7634	1.00	0.5888
			AC	42.5	42.6		1.03 (0.67-1.58)	
			AA	7.1	5.3		1.37 (0.55-3.10)	
LEPR	rs1782763	0.05	TT	89.3	91.3	0.5182	1.00	0.5185
			CT	10.7	8.7		1.25 (0.61-2.41)	
LEPR	rs6673324	0.48	AA	21.1	26.0	0.542	1.00	0.4375
			AG	57.0	52.7		1.34 (0.81-2.28)	
			GG	21.9	21.3		1.27 (0.68-2.37)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
LEPR	rs3790428	0.28	CC	50.9	49.0	0.6817	1.00	0.9737
			AC	42.1	45.7		0.89 (0.58-1.36)	
			AA	7.0	5.3		1.26 (0.51-2.85)	
LEPR	rs1137101	0.46	AA	29.8	26.4	0.367	1.00	0.1988
			AG	55.3	53.0		0.92 (0.58-1.49)	
			GG	14.9	20.6		0.64 (0.33-1.20)	
LEPR	rs4655537	0.33	GG	41.2	43.7	0.8253	1.00	0.5467
			AG	48.2	47.3		1.08 (0.70-1.68)	
			AA	10.5	9.0		1.24 (0.59-2.50)	
LEPR	rs3790419	0.22	AA	65.8	60.0	0.5004	1.00	0.3475
			AG	28.9	34.7		0.76 (0.48-1.19)	
			GG	5.3	5.3		0.90 (0.32-2.15)	
LEPR	rs8179183	0.20	GG	62.7	65.4	0.6831	1.00	0.8065
			CG	33.6	29.8		1.17 (0.74-1.83)	
			CC	3.6	4.8		0.79 (0.23-2.16)	
LEPR	rs1938484	0.19	CC	69.3	64.7	0.5503	1.00	0.2901
			AC	28.9	32.2		0.84 (0.53-1.31)	
			AA	1.8	3.1		0.53 (0.08-1.94)	
LEPR	rs1805096	0.39	CC	36.8	37.5	0.9541	1.00	0.9855
			CT	48.2	46.7		1.05 (0.67-1.66)	
			TT	14.9	15.7		0.97 (0.50-1.79)	
ADIPOQ region 5'	rs1648707	0.34	AA	45.9	43.1	0.7352	1.00	0.818
			AC	41.4	45.5		0.85 (0.55-1.33)	
			CC	12.6	11.4		1.04 (0.52-1.98)	
ADIPOQ region 5'	rs10937273	0.44	GG	30.1	31.6	0.9484	1.00	0.7506
			AG	50.4	49.8		1.06 (0.66-1.72)	
			AA	19.5	18.6		1.10 (0.59-1.99)	
ADIPOQ	rs16861194	0.07	AA	89.5	86.7	0.5573	1.00	0.3562
			AG	10.5	12.6		0.77 (0.38-1.43)	
			GG	0.0	0.7			

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
ADIPOQ	rs822391	0.21	TT	63.2	61.9	0.7309	1.00	0.6241
			CT	33.3	32.7		1.00 (0.64-1.54)	
			CC	3.5	5.3		0.65 (0.19-1.74)	
ADIPOQ	rs16861210	0.09	GG	83.3	83.4	0.9751	1.00	0.9711
			AG	15.8	15.5		1.01 (0.57-1.71)	
			AA	0.9	1.1			
ADIPOQ	rs822395	0.35	AA	47.4	41.4	0.3662	1.00	0.1607
			AC	43.0	44.9		0.84 (0.54-1.29)	
			CC	9.6	13.7		0.61 (0.29-1.21)	
ADIPOQ	rs822396	0.19	AA	68.5	65.2	0.7134	1.00	0.4385
			AG	28.8	30.7		0.89 (0.56-1.41)	
			GG	2.7	4.1		0.63 (0.15-1.93)	
ADIPOQ	rs12495941	0.35	GG	41.2	43.2	0.8475	1.00	0.5893
			GT	44.7	44.6		1.05 (0.68-1.64)	
			TT	14.0	12.2		1.21 (0.62-2.26)	
ADIPOQ	rs17366568	0.12	GG	78.9	77.0	0.9051	1.00	0.6962
			AG	19.3	21.2		0.89 (0.52-1.47)	
			AA	1.8	1.8		0.97 (0.14-3.95)	
ADIPOQ	rs2241766	0.11	TT	85.1	77.8	0.2306	1.00	0.1049
			GT	14.0	21.1		0.62 (0.34-1.05)	
			GG	0.9	1.1			
ADIPOQ	rs1501299	0.28	CC	51.8	51.7	0.9954	1.00	0.9557
			AC	40.4	40.2		1.00 (0.65-1.54)	
			AA	7.9	8.2		0.96 (0.42-2.03)	
ADIPOQ	rs3821799	0.45	CC	37.7	28.5	0.1589	1.00	0.1004
			CT	43.9	50.1		0.66 (0.42-1.05)	
			TT	18.4	21.4		0.65 (0.36-1.15)	
ADIPOQ	rs17366743	0.11	TT	84.1	81.7	0.8112	1.00	0.6611
			CT	11.5	13.8		0.81 (0.41-1.49)	
			CC	4.4	4.5		0.97 (0.31-2.46)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
ADIPOQ	rs6773957	0.39	GG	42.1	36.8	0.5817	1.00	0.3651
			AG	43.9	47.9		0.80 (0.51-1.25)	
			AA	14.0	15.3		0.80 (0.42-1.48)	
ADIPOQ	rs1063539	0.13	GG	80.5	72.7	0.1881	1.00	0.0755
			CG	19.5	26.6		0.64 (0.38-1.06)	
			CC	0.0	0.7			
RETN region 5'	rs2081075	0.27	GG	59.3	54.4	0.5533	1.00	0.5421
			AG	31.0	36.4		0.78 (0.49-1.22)	
			AA	9.7	9.1		0.98 (0.46-1.95)	
RETN	rs1862513	0.28	GG	54.9	50.3	0.6693	1.00	0.3745
			CG	38.9	42.2		0.85 (0.55-1.30)	
			CC	6.2	7.5		0.76 (0.30-1.70)	
RETN	rs3745367	0.23	GG	64.9	56.4	0.2546	1.00	0.1083
			AG	31.6	38.7		0.71 (0.45-1.10)	
			AA	3.5	4.9		0.63 (0.18-1.70)	
RETN	rs3745369	0.50	GG	25.4	26.3	0.86	1.00	0.8851
			CG	50.9	48.1		1.09 (0.67-1.82)	
			CC	23.7	25.6		0.96 (0.53-1.71)	
PPAR γ	rs2972164	0.47	CC	24.1	28.1	0.5491	1.00	0.2757
			CT	51.8	51.8		1.17 (0.71-1.95)	
			TT	24.1	20.1		1.40 (0.77-2.54)	
PPAR γ	rs6809631	0.29	AA	53.5	50.0	0.5309	1.00	0.3255
			AT	40.4	40.7		0.93 (0.60-1.42)	
			TT	6.1	9.3		0.62 (0.24-1.36)	
PPAR γ	rs17793951	0.31	AA	44.1	47.8	0.3464	1.00	0.2421
			AG	42.3	43.3		1.06 (0.68-1.65)	
			GG	13.5	9.0		1.63 (0.82-3.14)	
PPAR γ	rs12497191	0.14	AA	78.1	73.2	0.5658	1.00	0.2914
			AG	20.2	24.3		0.78 (0.46-1.27)	
			GG	1.8	2.4		0.68 (0.10-2.58)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
PPAR γ	rs1801282	0.15	CC	72.8	72.6	0.9028	1.00	0.9392
			CG	24.6	25.4		0.96 (0.59-1.54)	
			GG	2.6	2.0		1.32 (0.29-4.53)	
PPAR γ	rs12629751	0.09	CC	83.9	82.8	0.9115	1.00	0.7262
			CT	15.2	15.8		0.92 (0.51-1.59)	
			TT	0.9	1.4			
PPAR γ	rs2028759	0.48	AA	29.5	26.4	0.6772	1.00	0.8333
			AG	45.5	50.1		0.81 (0.50-1.34)	
			GG	25.0	23.5		0.95 (0.54-1.68)	
PPAR γ	rs1151996	0.36	TT	38.6	41.7	0.8223	1.00	0.6575
			GT	48.2	45.2		1.15 (0.74-1.80)	
			GG	13.2	13.1		1.09 (0.55-2.06)	
PPAR γ	rs7645903	0.18	AA	67.9	66.5	0.7513	1.00	0.6389
			AT	30.4	30.4		0.98 (0.62-1.53)	
			TT	1.8	3.1		0.56 (0.09-2.08)	
PPAR γ	rs1175540	0.34	CC	39.8	44.4	0.3925	1.00	0.7579
			CA	51.3	44.4		1.29 (0.84-2.00)	
			AA	8.8	11.3		0.88 (0.39-1.79)	
PPAR γ	rs6782475	0.17	TT	69.0	68.1	0.6231	1.00	0.6289
			GT	29.2	28.3		1.02 (0.64-1.59)	
			GG	1.8	3.6		0.49 (0.08-1.77)	
PPAR γ	rs3856806	0.14	CC	72.6	73.8	0.4017	1.00	0.5333
			CT	23.9	24.6		0.99 (0.60-1.59)	
			CC	3.5	1.6		2.30 (0.59-7.80)	
PPAR γ C1	rs6821591	0.48	CC	21.9	25.8	0.6696	1.00	0.5795
			CT	56.1	52.3		1.26 (0.76-2.14)	
			TT	21.9	21.9		1.18 (0.64-2.19)	

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
PPAR γ C1	rs3736265	0.05	GG	89.5	90.2	0.8394	1.00	0.8647
			AG	10.5	9.5		1.09 (0.53-2.07)	
			AA	0.0	0.2			
PPAR γ C1	rs3755863	0.40	GG	35.1	34.7	0.8476	1.00	0.7283
			AG	51.8	50.0		1.02 (0.66-1.62)	
			AA	13.2	15.3		0.85 (0.43-1.62)	
PPAR γ C1	rs8192678	0.35	GG	39.8	43.6	0.7172	1.00	0.6385
			AG	48.7	44.5		1.20 (0.77-1.87)	
			AA	11.5	11.9		1.05 (0.51-2.05)	
PPAR γ C1	rs2970849	0.33	TT	48.2	42.5	0.4445	1.00	0.2045
			CT	43.9	46.5		0.83 (0.54-1.28)	
			CC	7.9	10.9		0.64 (0.28-1.32)	
PPAR γ C1	rs2932976	0.27	GG	59.6	51.8	0.2763	1.00	0.1101
			AG	35.1	40.3		0.76 (0.49-1.16)	
			AA	5.3	8.0		0.57 (0.21-1.33)	
PPAR γ C1	rs4697046	0.33	TT	39.5	45.6	0.3565	1.00	0.1567
			CT	46.5	44.2		1.21 (0.78-1.89)	
			CC	14.0	10.2		1.58 (0.81-3.01)	
PPAR γ C1	rs4235308	0.41	TT	30.1	34.8	0.3145	1.00	0.1555
			CT	49.6	50.3		1.14 (0.71-1.84)	
			CC	20.4	14.9		1.59 (0.86-2.88)	
PPAR γ C1	rs7677000	0.16	CC	71.9	69.9	0.9124	1.00	0.6985
			CT	26.3	28.3		0.90 (0.56-1.43)	
			TT	1.8	1.8		0.96 (0.14-3.93)	
PPAR γ C1	rs4469064	0.08	AA	81.6	84.1	0.7239	1.00	0.4678
			AG	17.5	15.5		1.19 (0.69-2.01)	
			GG	0.9	0.4			
PPAR γ C1	rs3774902	0.05	CC	91.2	89.6	0.7184	1.00	0.5342

Gene	SNP	MAF	Allele	obese	non-obese	p-value*	OR (95% CI)	p-trend†
			CT	8·8	10·0		0·83 (0·38-1·63)	
			TT	0·0	0·4			

* p-value of the Kruskal-Wallis Test.

† p-value derived from the continuous model .