Supplementary Table 1. Information of peroxisome proliferator activated receptor-γ (PPAR-γ) single nucleotide polymorphisms (SNPs) used in this study. Valid SNPs used in statistical analysis are marked with #

SNP	rs number	Position on chr3	Intervening seq. & exon	Nucleotide change	Minor allele	MAF	Amino acid change
1#	rs6785890	12335816	5’UTR	A/C	C	0.475	-
2#	rs12631819	12342861	5’UTR	G/T	T	0.321	-
3	rs7620165	12344441	5’UTR	A/G	G	0.025	-
4#	rs10510410	12346738	5’UTR	A/C	C	0.320	-
5#	rs13061415	12349924	5’UTR	C/T	C	0.383	-
6#	rs12485478	12351223	5’UTR	A/G	G	0.269	-
7	rs9310401	12352468	5’UTR	C/T	T	0.415	-
8	rs17793951	12370737	5’UTR	A/G	G	0.015	-
9#	rs12496005	12371082	5’UTR	C/G	C	0.383	-
10#	rs12490265	12384542	5’UTR	A/G	A	0.170	-
11#	rs1801282	12393125	Exon B	C/G	G	0.047	Pro12Ala
12#	rs17817276	12397392	Intron B	A/G	G	0.111	-
13	rs2938397	12408278	Intron B	A/G	G	0.293	-
14#	rs13306745	12421056	Intron B	G/T	T	0.079	-
15	rs1805192	12421238	Exon 1	C/G	G	0	Pro12Ala
16	rs1800571	12422848	Exon 2	A/C	A	0	Gln85Pro
17#	rs4135268	12437237	Intron 3	C/G	G	0.044	-
18#	rs2959272	12442833	Intron 3	T/G	T	0.373	-
19#	rs1875796	12443657	Intron 3	C/T	C	0.441	-
20#	rs4135275	12443844	Intron 3	A/G	G	0.469	-
21#	rs12489347	12443877	Intron 3	C/G	C	0.383	-
22	rs4135352	12458208	Exon 5	C/T	T	0	Phe247Phe
23#	rs13306747	12458274	Exon 5	C/G	G	0.057	Pro269Pro
24	rs28936407	12458330	Exon 5	A/G	A	0	His288Arg
25	rs13306746	12458334	Exon 5	A/G	T	0	Ser289Ser
26#	rs1175544	12467044	Intron 5	C/T	T	0.362	
27	rs28763894	12475440	Exon 6	A/G	G	0	Gln410Gln
28	rs41516544	12475497	Exon 6	A/G	G	0	Ser429Ser
29#	rs3856806	12475557	Exon 6	C/T	T	0.212	His449His

Genotype distributions of SNP-7 and -13 deviated from the Hardy-Weinberg Equilibrium. SNP-3 and -8 had MAFs of 0.025 and 0.015, while SNP-15, -16, -22, -24, -25, -27 and -28 were monomorphic. Chr.: chromosome, seq.: sequence, MAF: minor allele frequency, 5’UTR: 5’un-translated region