

Supplementary Information

Table S1. Baseline characteristics of the studies included in the meta-analysis.

Author (Year) [Ref.]	Country (Ethnicity)	Genotyping Method	Mean Age (Cases/Controls)	Source of Controls	Diagnose Criteria	BMI (Cases; Controls)	SNPs Studied
Thawnashom <i>et al.</i> (2005) [4]	Thailand (Asian)	PCR-RFLP	40/38	HB	BMI \geq 25	31.5 (25.1–56.2); 21.8 (18.52–24.97) *	<i>MTHFR</i> C677T
Terruzzi <i>et al.</i> (2007) [5]	Italy (Caucasian)	PCR-RFLP	43.3/35.2	HB	BMI \geq 30	34.1 \pm 7.1; 22.4 \pm 1.8 #	<i>MTHFR</i> C677T; <i>MTRR</i> A66G
Lewis <i>et al.</i> (2008) [6] ^a	English (Caucasian)	TaqMan	68.8 ^e	PB	BMI \geq 30	None	<i>MTHFR</i> C677T
Lewis <i>et al.</i> (2008) [6] ^b	English (Caucasian)	TaqMan	28.5 ^e (Young women)	PB	BMI \geq 30	None	<i>MTHFR</i> C677T
Lewis <i>et al.</i> (2008) [6] ^c	English (Caucasian)	TaqMan	9.9 ^e (Children)	PB	Females: BMI > 23.46 Males: BMI > 23.39	None	<i>MTHFR</i> C677T
Lewis <i>et al.</i> (2008) [6] ^d	Danish (Caucasian)	PCR-RFLP	57.6 ^e	PB	BMI \geq 30	None	<i>MTHFR</i> C677T
Settin <i>et al.</i> (2009) [7]	Saudi Arabia (Asian)	TaqMan	27/24	HB	BMI \geq 25	27 \pm 9.8; 24 \pm 8.8 #	<i>MTHFR</i> C677T
Bazzaz <i>et al.</i> (2010) [8]	Iran (Asian)	PCR-RFLP	44.8/41.6	HB	BMI \geq 30	33.8 \pm 3.4; 24.8 \pm 2.9 #	<i>MTHFR</i> C677T
Gara <i>et al.</i> (2011) [9]	Tunisia (African)	Pyrosequencing	4.6–14.3/NA	HB	BMI > 97% percentile	None	<i>MTHFR</i> C677T
Chauhan <i>et al.</i> (2012) [10]	India (Asian)	GoldenGate assay	44–64 ^e	PB	BMI \geq 23	None	<i>MTHFR</i> C677T
Yin <i>et al.</i> (2012) [11]	China (Asian)	PCR-RFLP	41.25/41.48	PB	BMI \geq 24	26.48 \pm 2.59; 21.23 \pm 1.68 #	<i>MTHFR</i> C677T
Tabassum <i>et al.</i> (2012) [12]	India (Asian)	GoldenGate assay	13.00/14.00	PB	BMI \geq 25	25.85 (23.97–28.97); 17.58 (15.86–19.44) *	<i>MTHFR</i> C677T, <i>MTRR</i> A66G

Abbreviation: *MTHFR*, methylenetetrahydrofolate reductase; *MTRR*, methionine synthase reductase; PCR-RFLP, polymerase chain reaction-restriction fragment length polymorphism; HB, hospital based; PB, population based; BMI, body mass index; NA, not available; ^a BWHHS cohort study; ^b ALSPAC women cohort study; ^c ALSPAC children cohort study; ^d CCHS cohort study; ^e The mean age of all subjects; * Data are presented as the median (25th–75th); # Data are presented as the mean \pm SD.

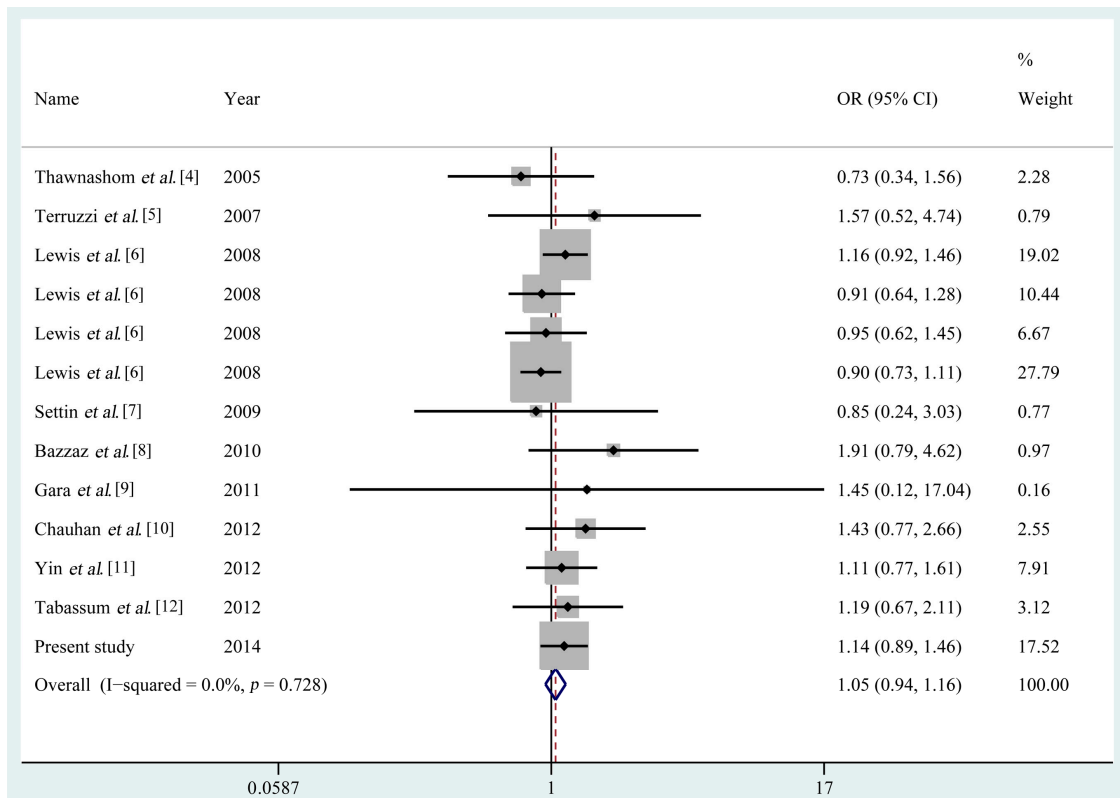


Figure S1. Forest plot of the association between the *MTHFR* C677T polymorphism and being overweight/obesity in the recessive model (TT vs. CT + CC).

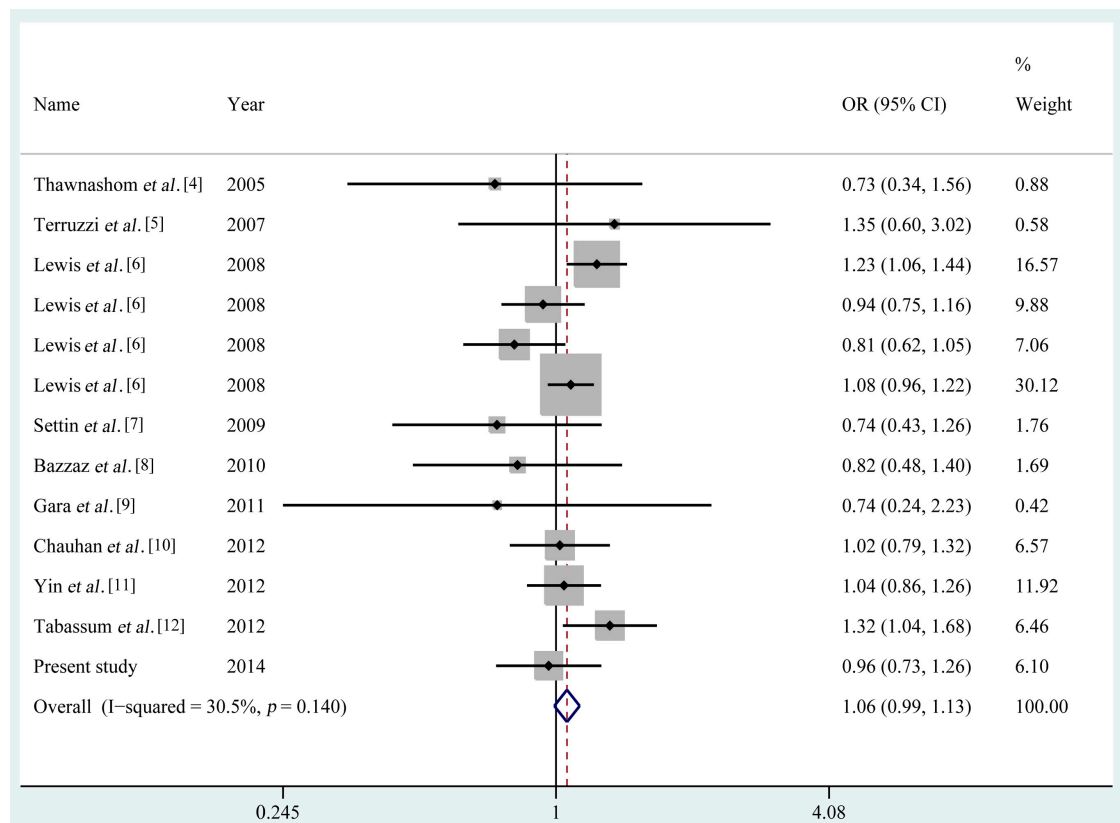


Figure S2. Forest plot of the association between the *MTHFR* C677T polymorphism and being overweight/obesity in the dominant model (TT + CT vs. CC).

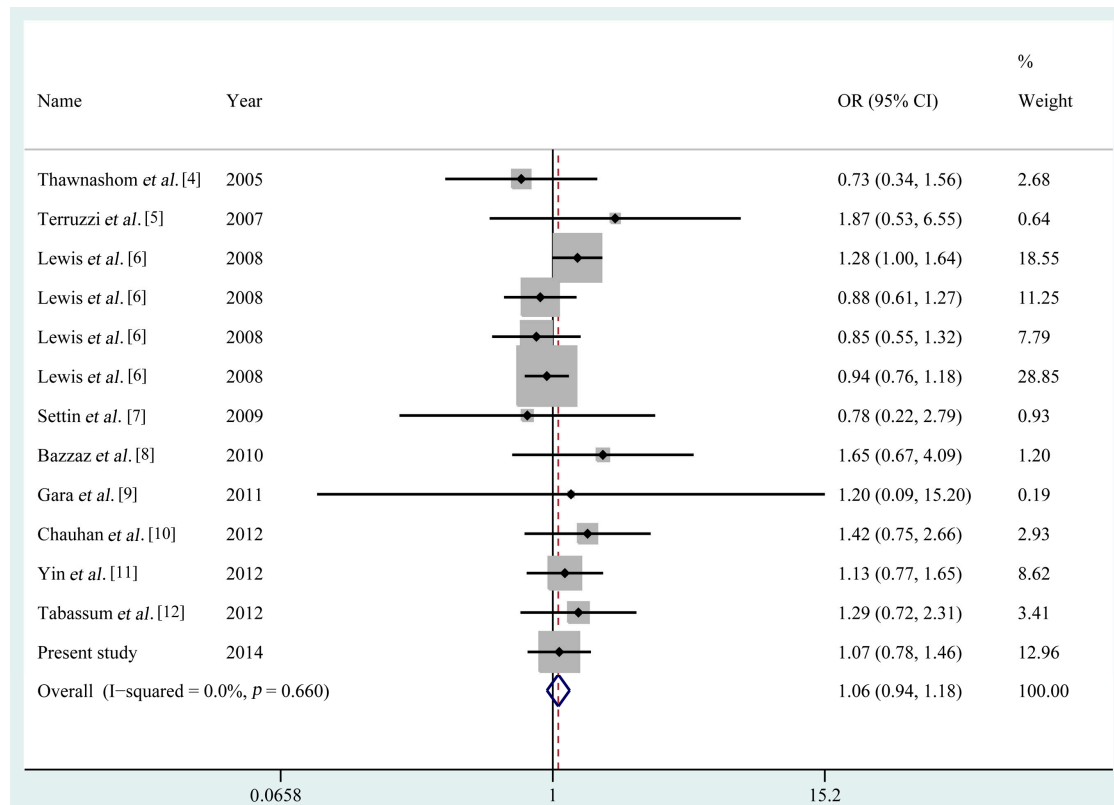


Figure S3. Forest plot of the association between the *MTHFR* C677T polymorphism and being overweight/obesity in the homozygous codominant model (TT vs. CC).

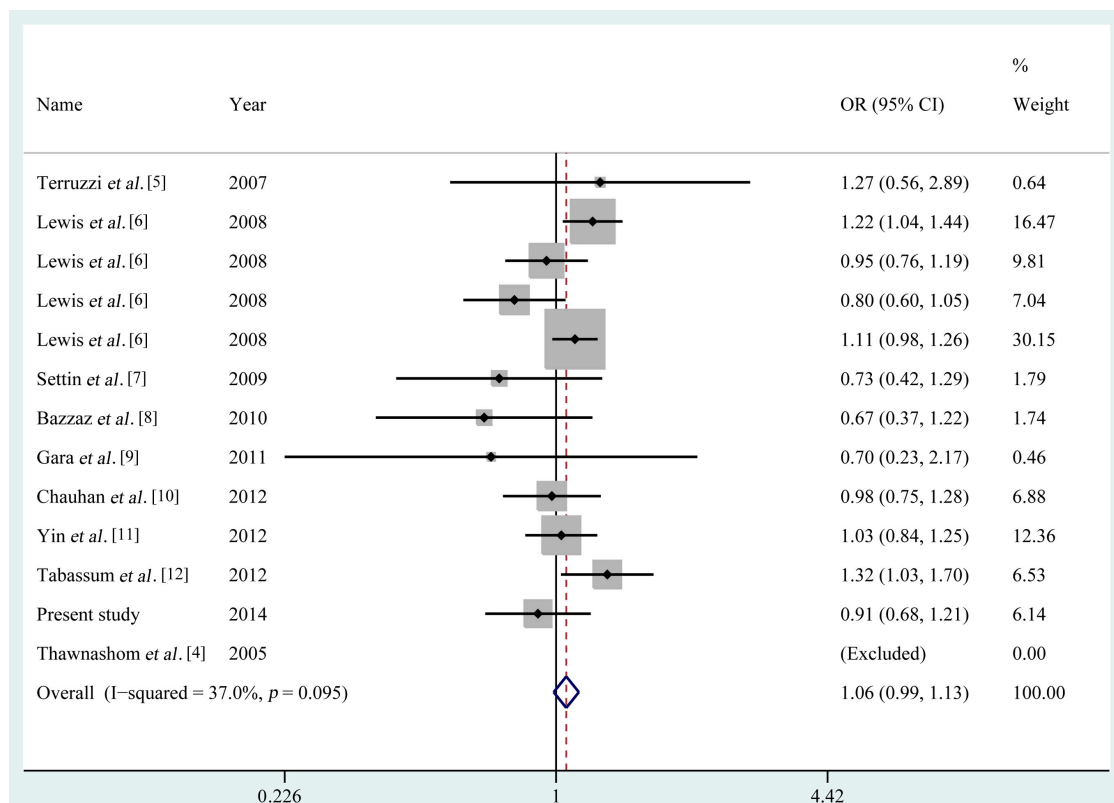


Figure S4. Forest plot of the association between the *MTHFR* C677T polymorphism and being overweight/obesity in the heterozygous codominant model (CT vs. CC).

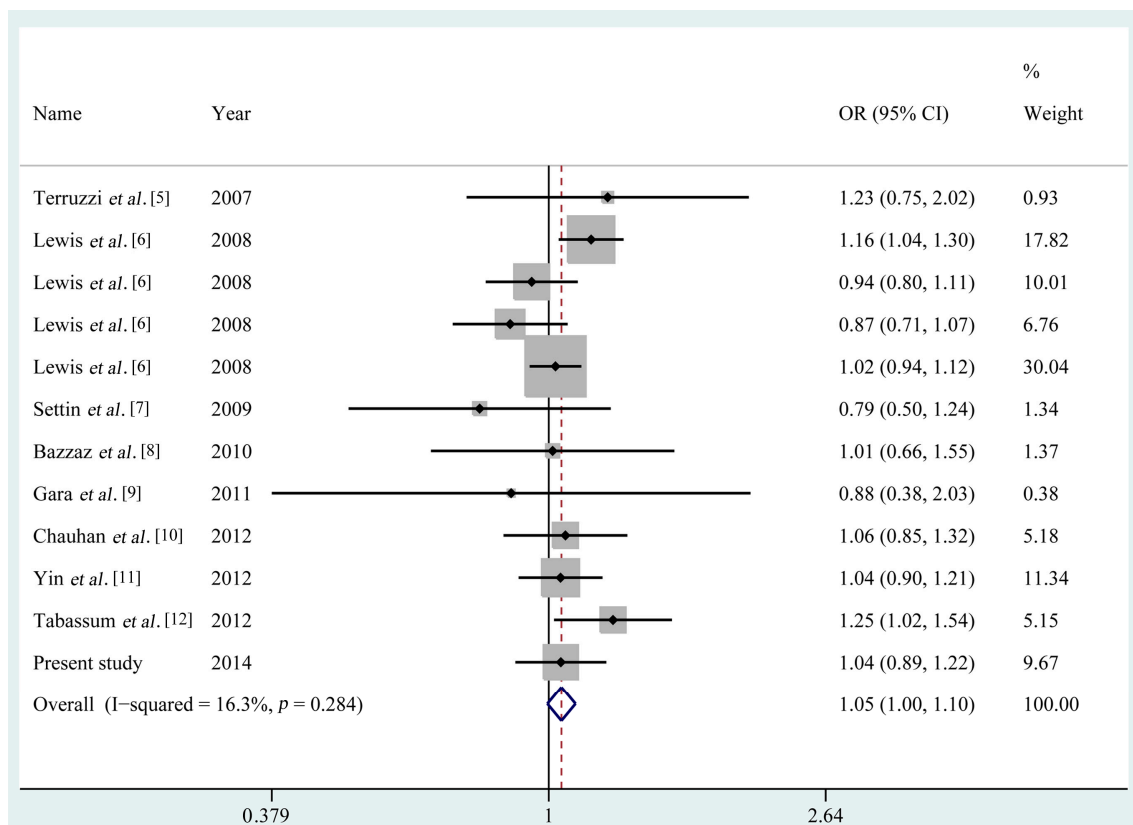


Figure S5. Forest plot of the association between the *MTHFR* C677T polymorphism and being overweight/obesity in the allelic model (T vs. C).

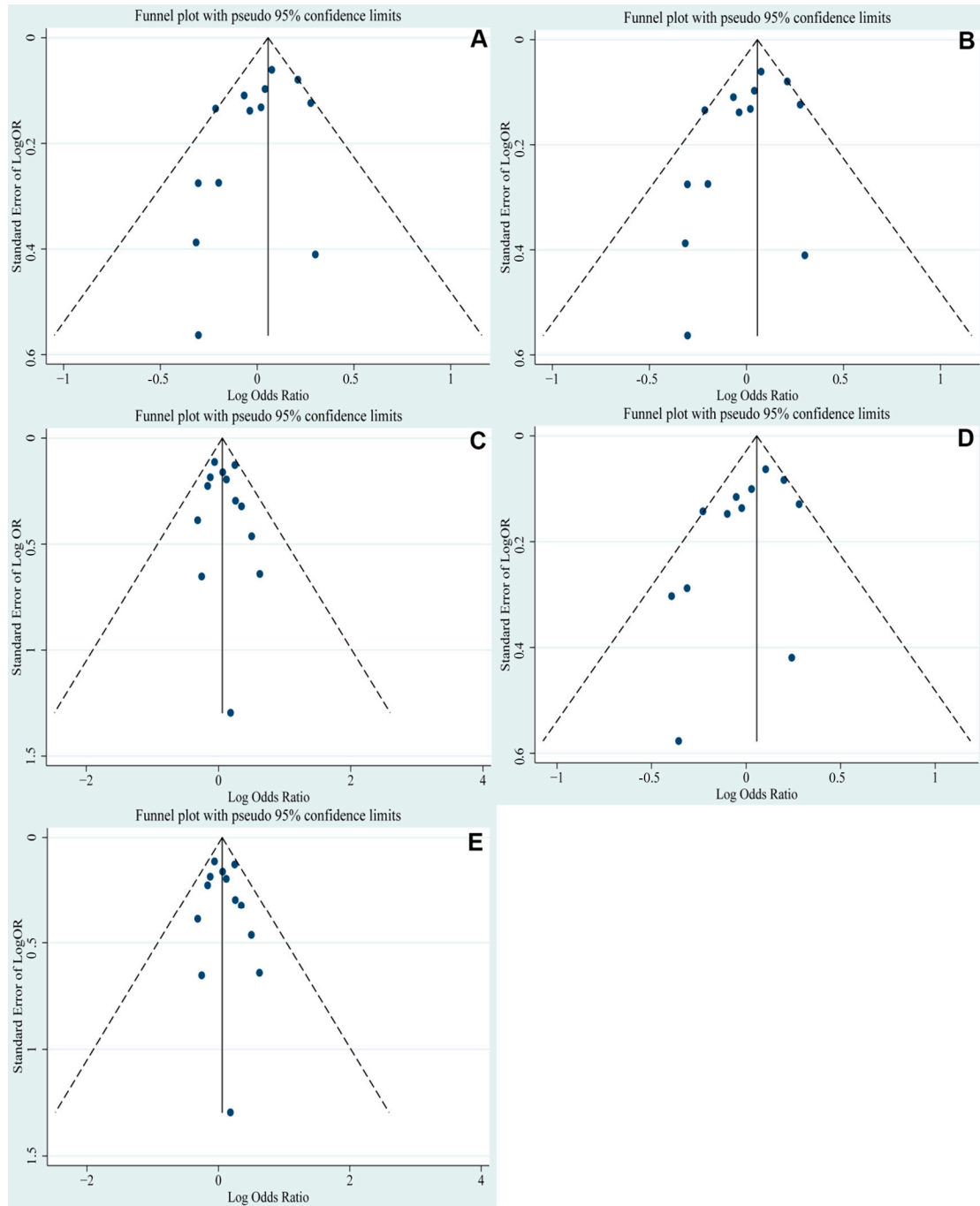


Figure S6. Funnel plot analysis on the detection of publication bias in the meta-analysis of the associations between MTHFR polymorphisms and being overweight/obesity: (A) recessive model; (B) dominant model; (C) homozygous codominant model; (D) heterozygous codominant model; (E) allelic model.

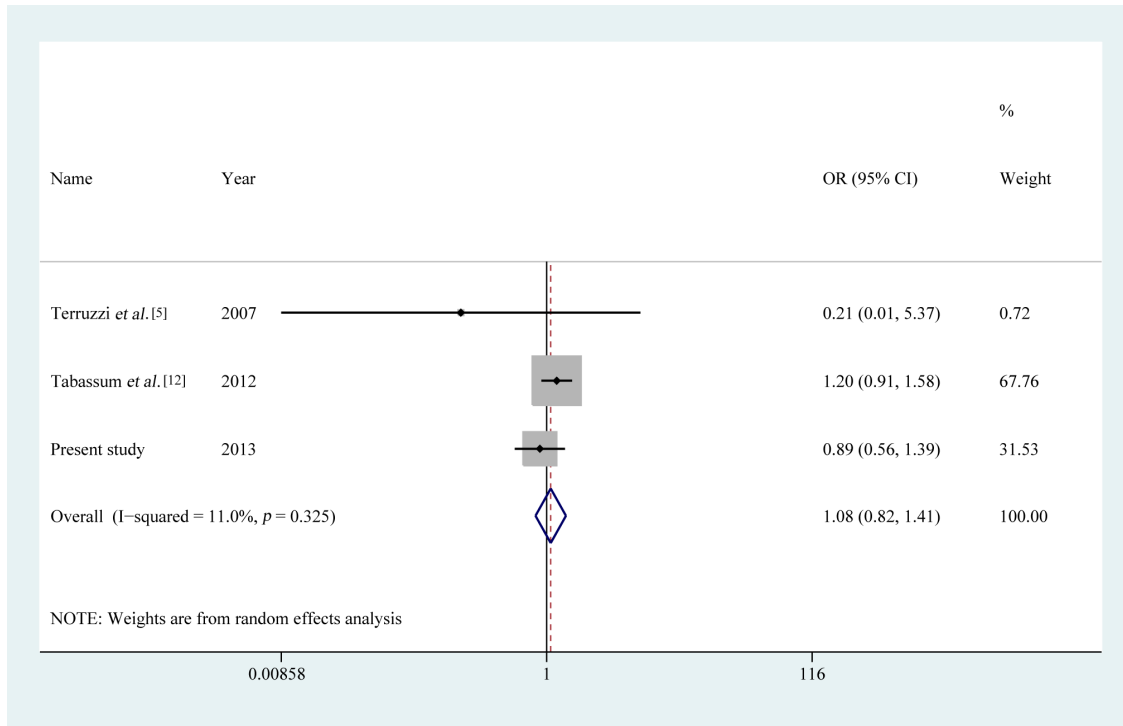


Figure S7. Forest plot of the association between the *MTRR* A66G polymorphism and being overweight/obesity in the recessive model (TT vs. CT + CC).

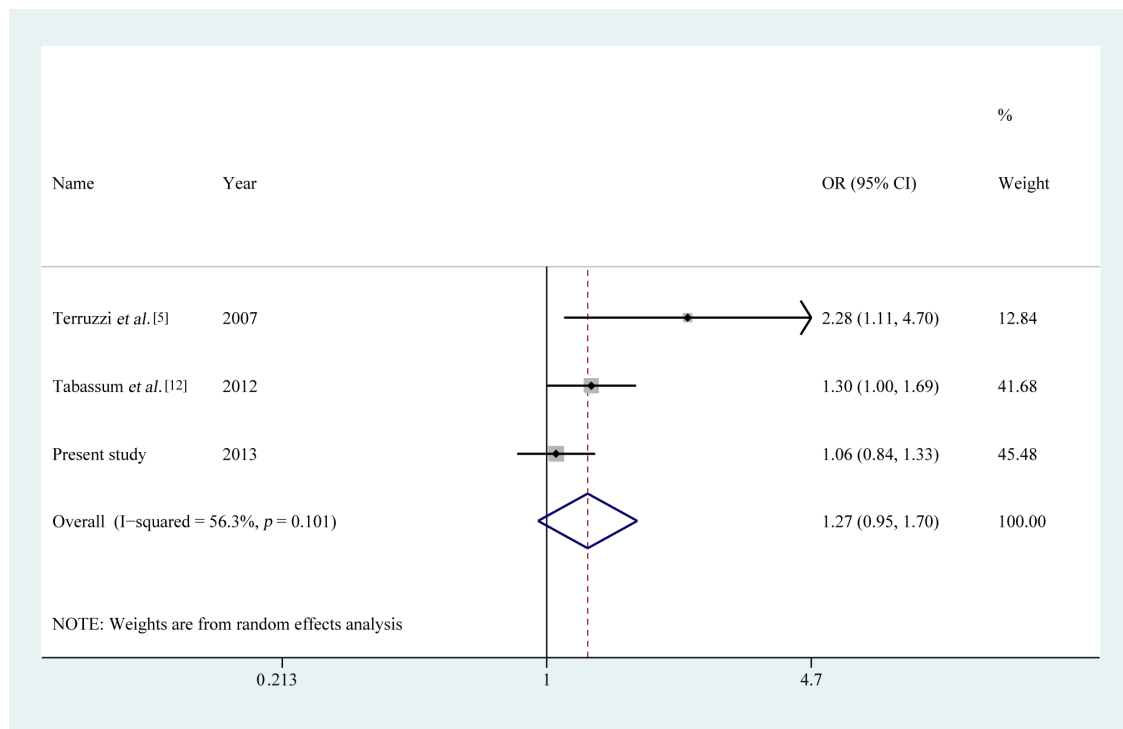


Figure S8. Forest plot of the association between the *MTRR* A66G polymorphism and being overweight/obesity in the dominant model (TT + CT vs. CC).

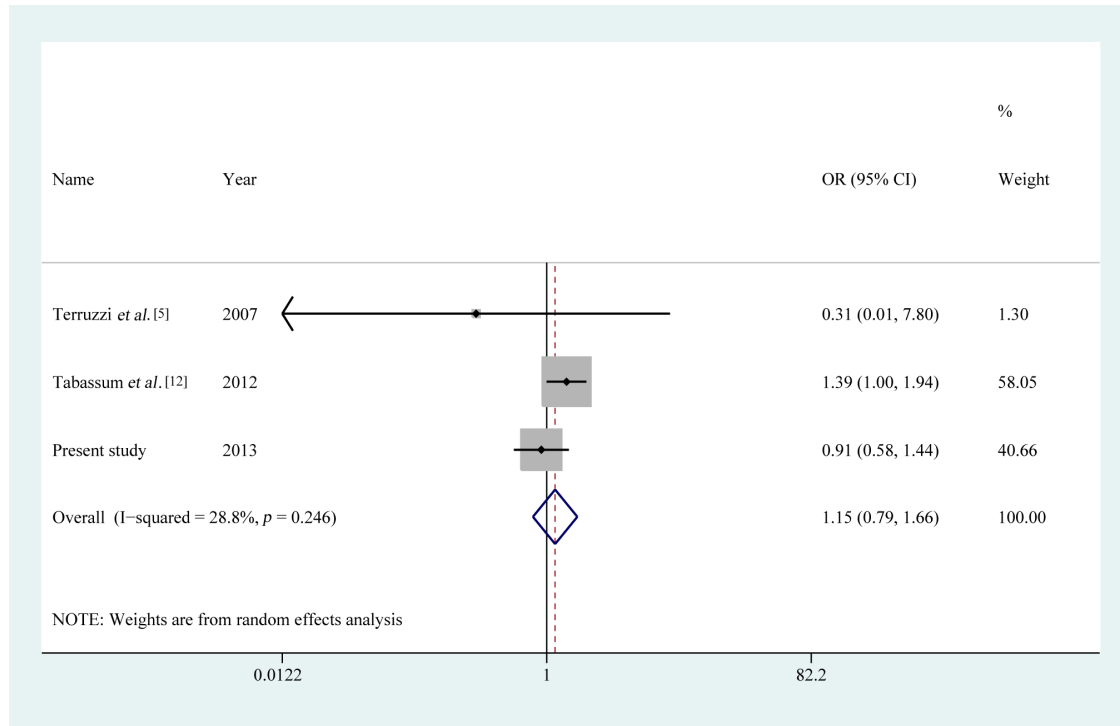


Figure S9. Forest plot of the association between the *MTRR* A66G polymorphism and being overweight/obesity in the homozygous codominant model (TT vs. CC).

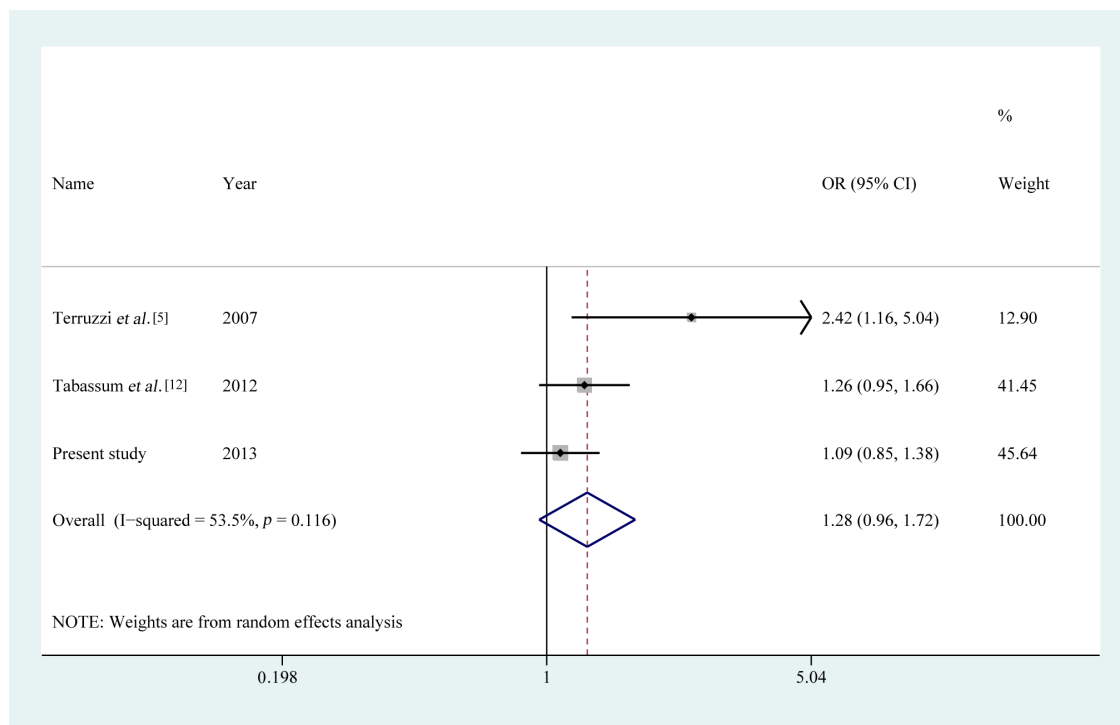


Figure S10. Forest plot of the association between the *MTRR* A66G polymorphism and being overweight/obesity in the heterozygous codominant model (CT vs. CC).

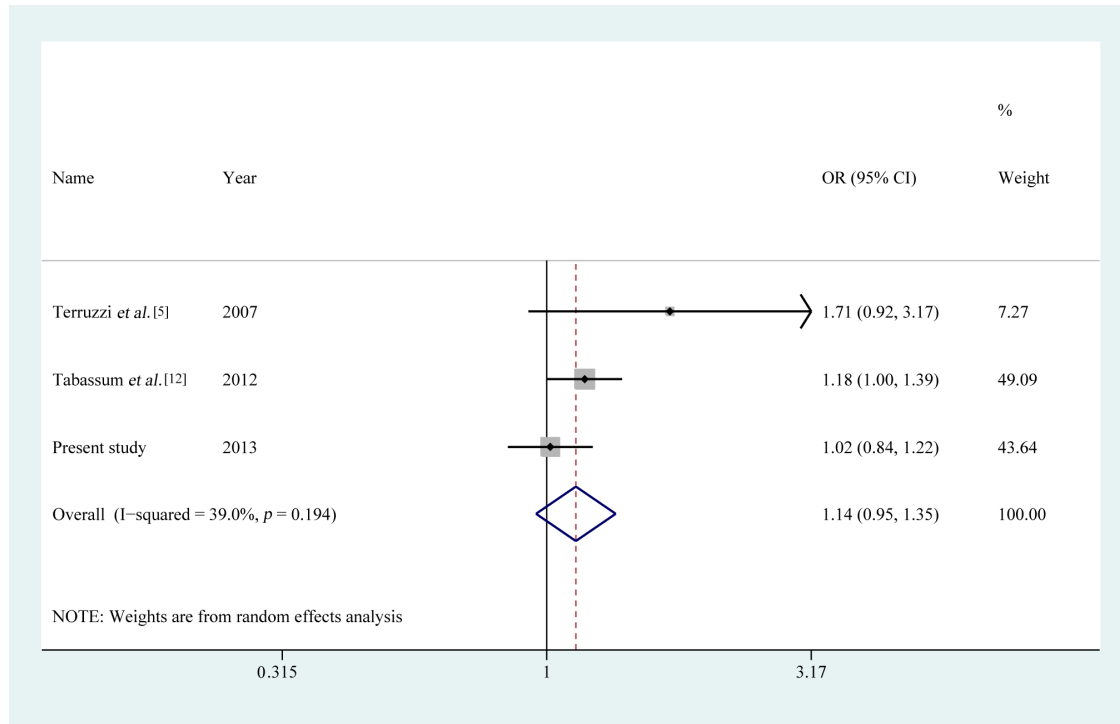


Figure S11. Forest plot of the association between the *MTRR* A66G polymorphism and being overweight/obesity in the allelic model (T vs. C).