

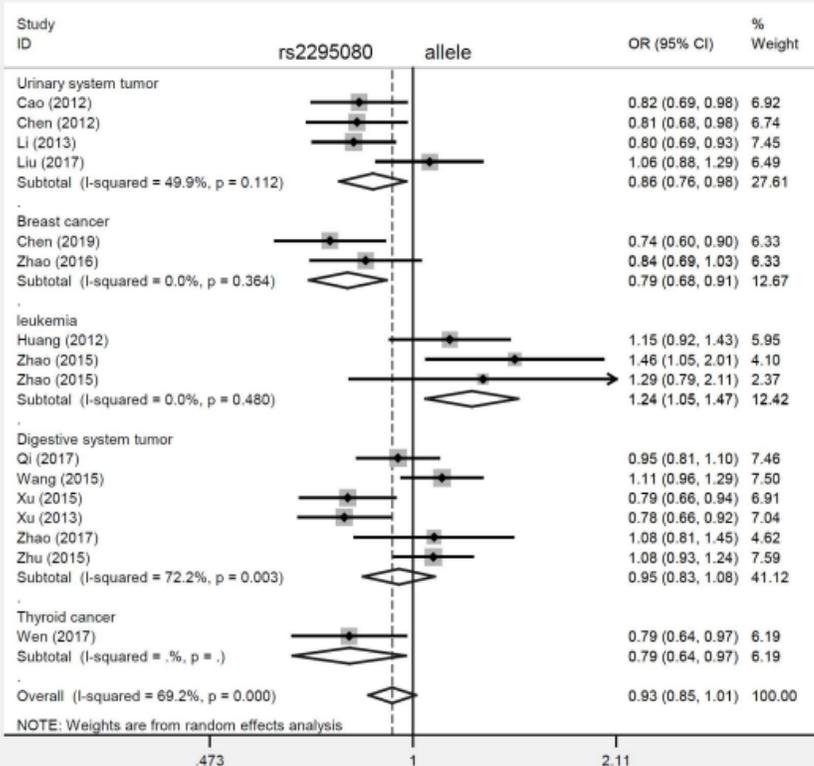
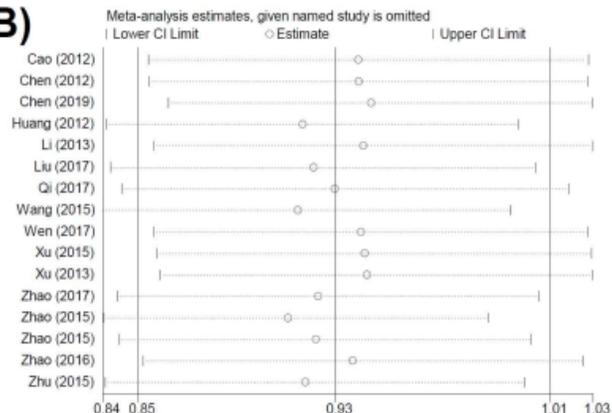
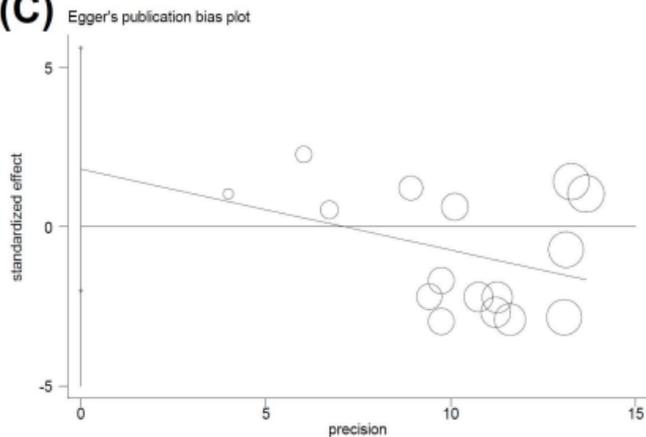
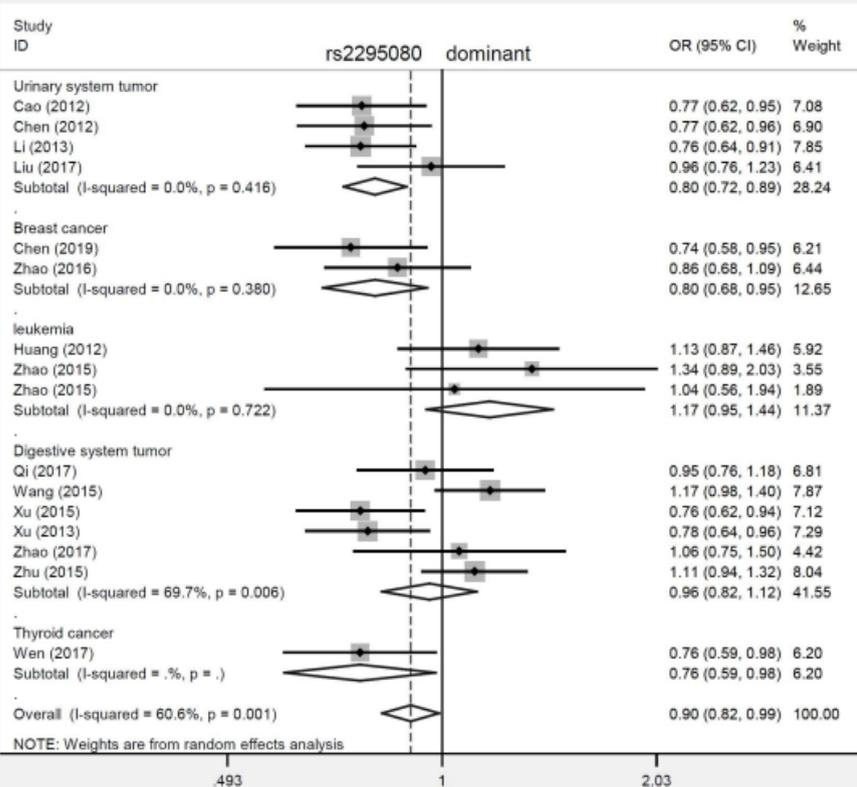
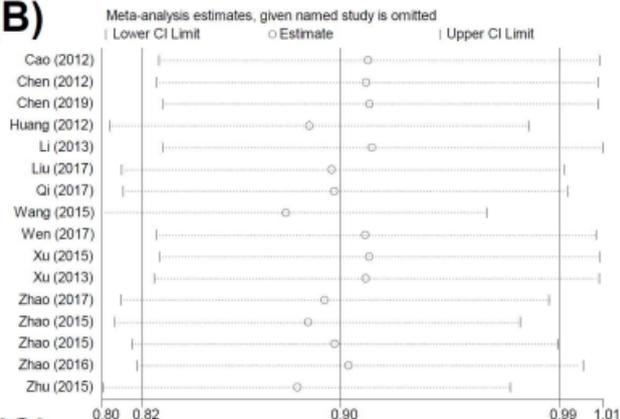
(A)**(B)****(C)****Figure S1**

Figure S1. Pooled analysis of *mTOR* rs2295080 via the allele comparison. (A) Forest plot of subgroup analyses by cancer type. (B) Begg's test. (C) Sensitivity analysis.

(A)**(B)****(C)**

Egger's publication bias plot

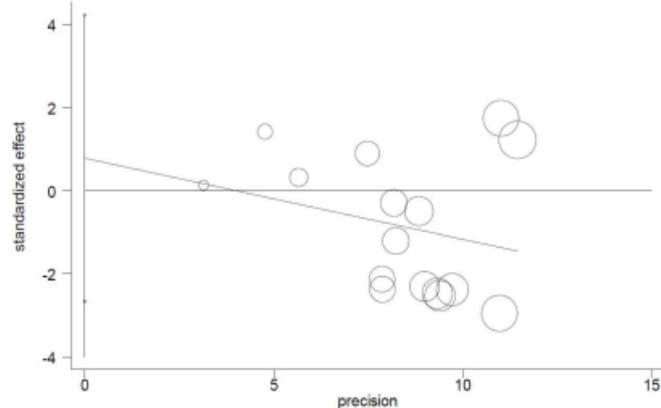
**Figure S2**

Figure S2. Pooled analysis of *mTOR* rs2295080 via the dominant comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.

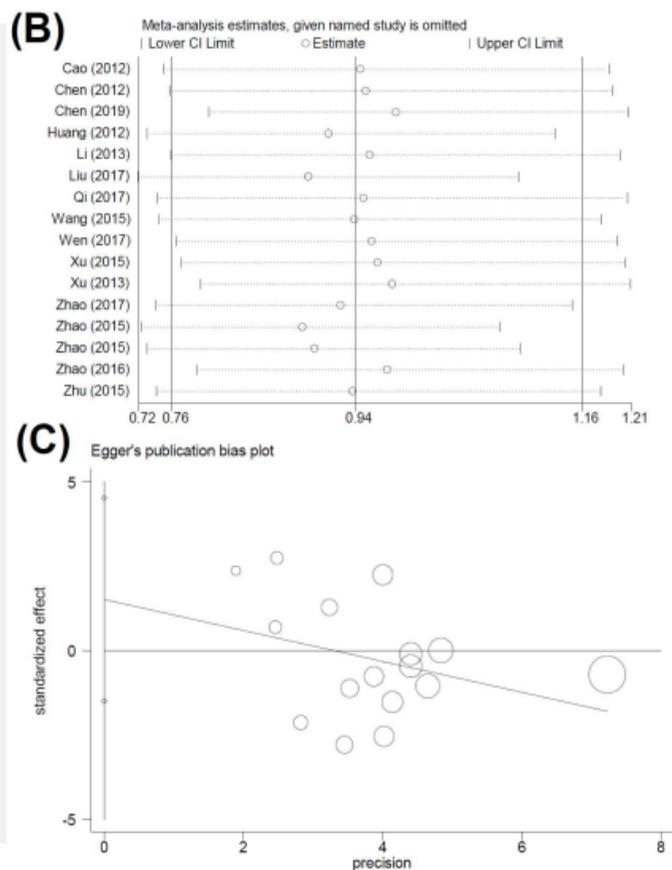
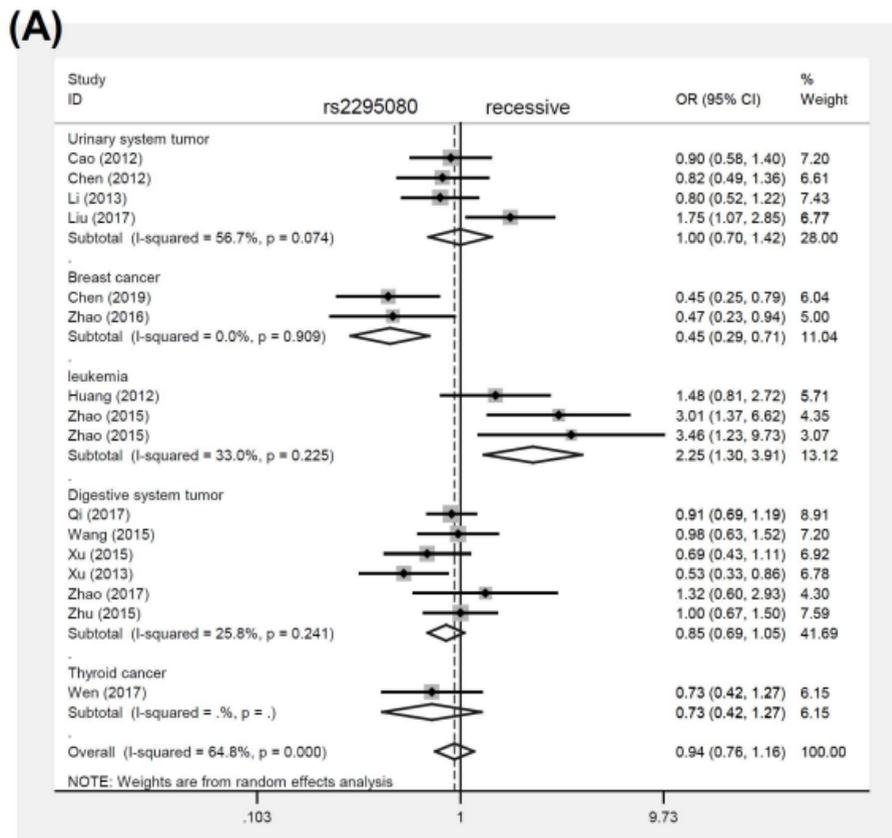


Figure S3

Figure S3. Pooled analysis of *mTOR* rs2295080 via the recessive comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.

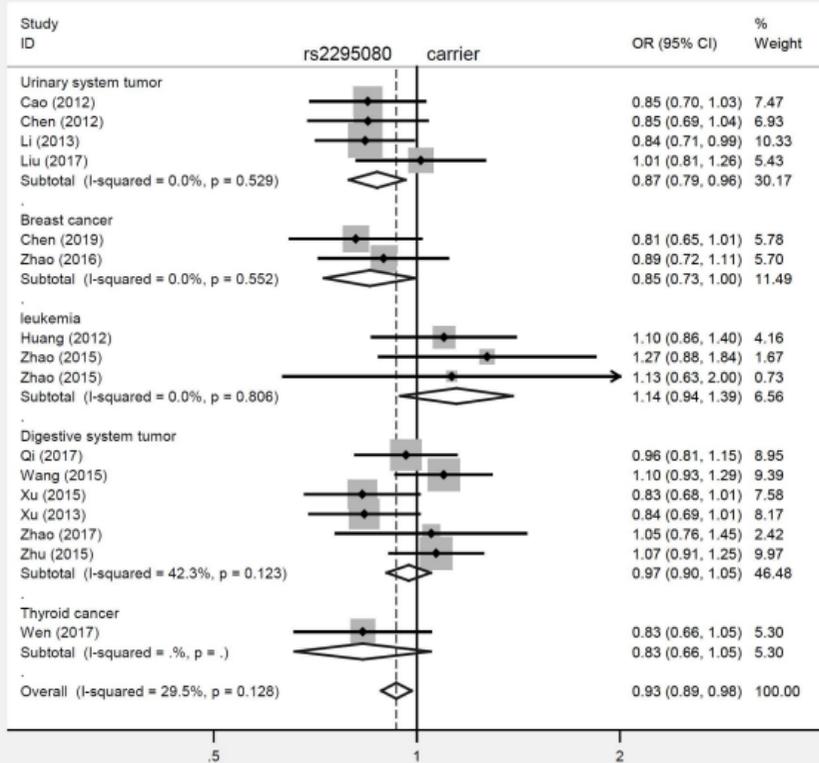
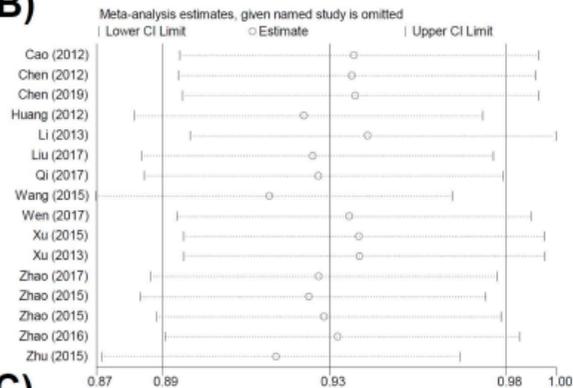
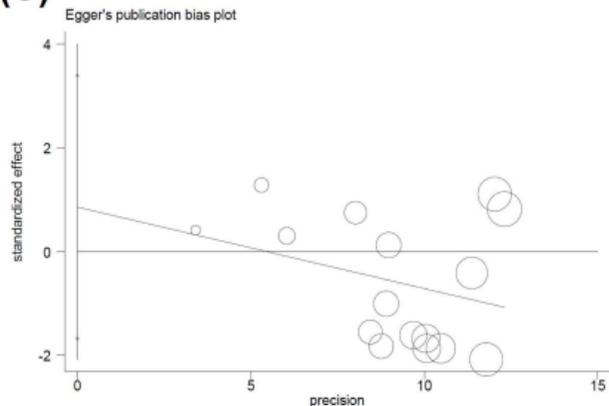
(A)**(B)****(C)****Figure S4**

Figure S4. Pooled analysis of *mTOR* rs2295080 via the carrier comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.

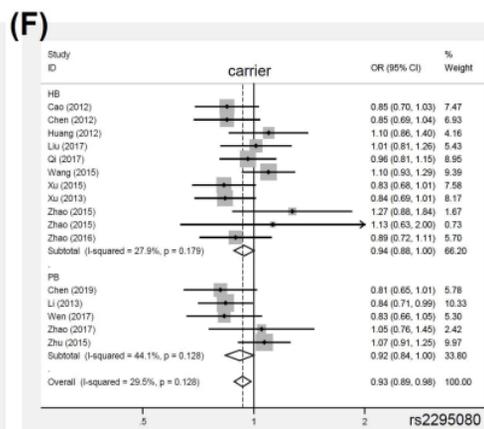
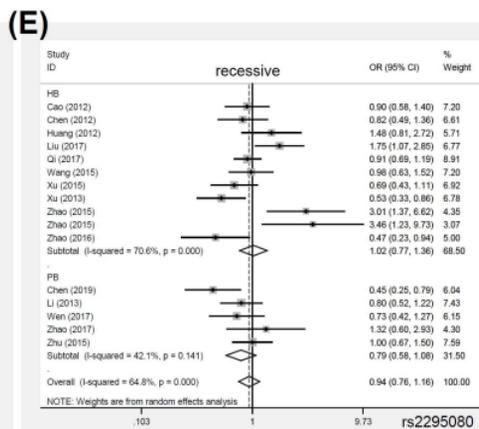
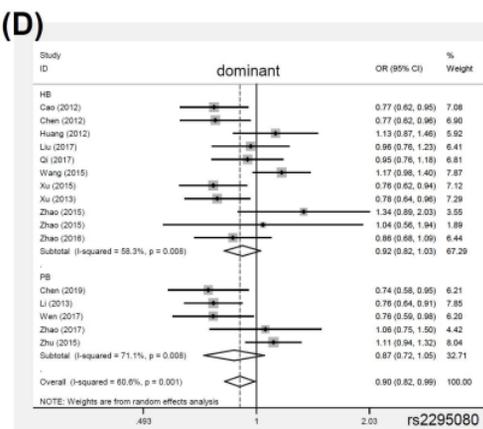
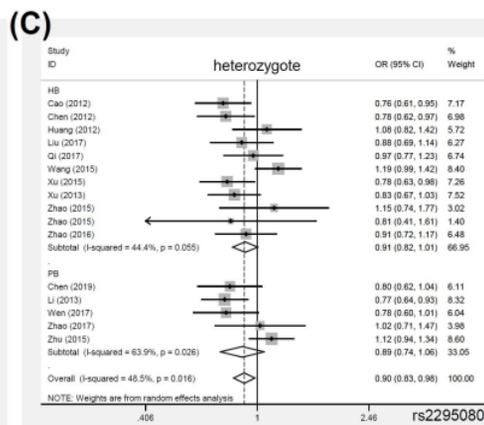
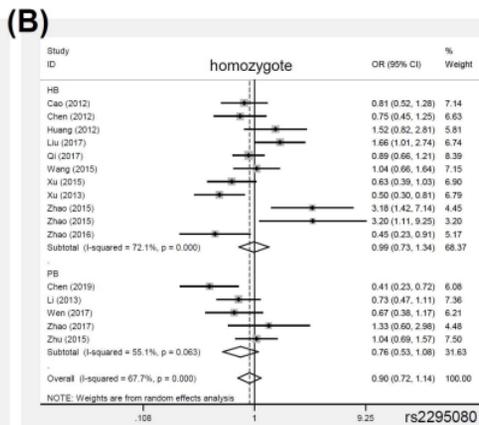
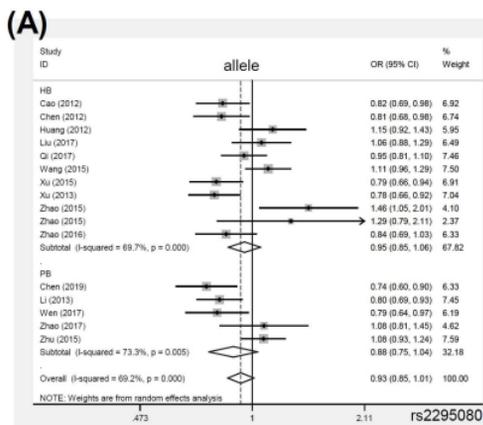


Figure S5

Figure S5. Forest plot of subgroup analyses of *mTOR* rs2295080 by control source. (A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.

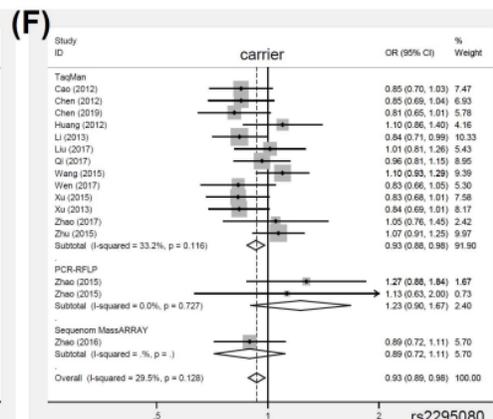
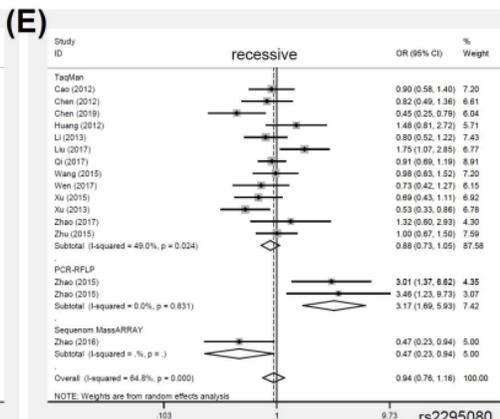
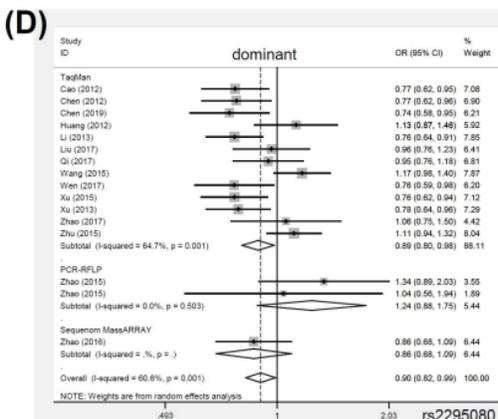
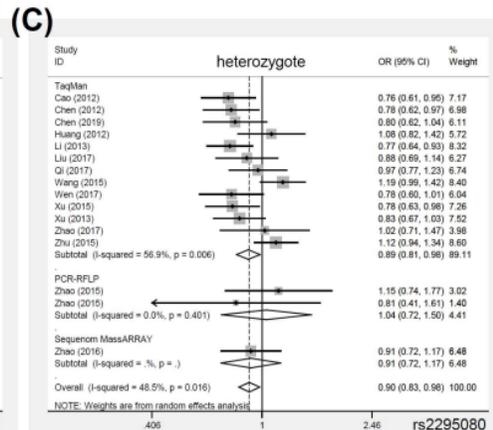
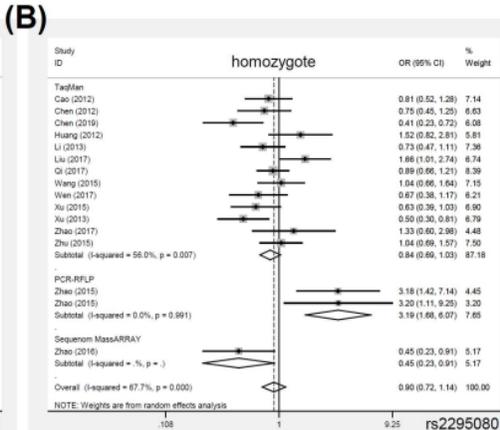
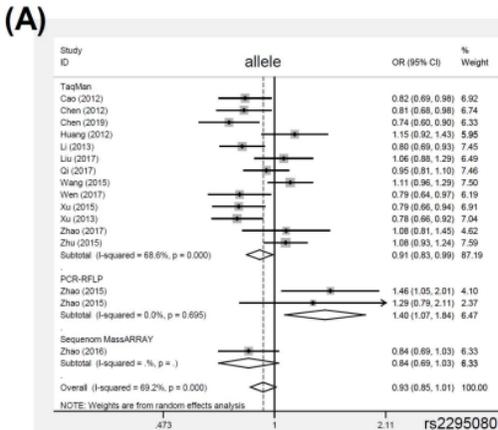


Figure S6

Figure S6. **Forest plot of subgroup analyses of *mTOR* rs2295080 by genotyping method. (A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.**

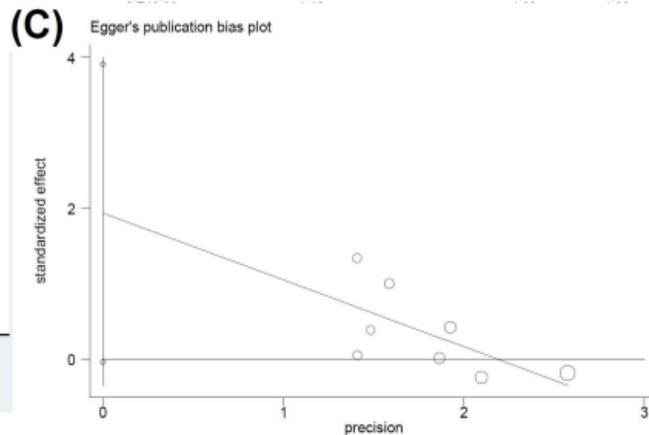
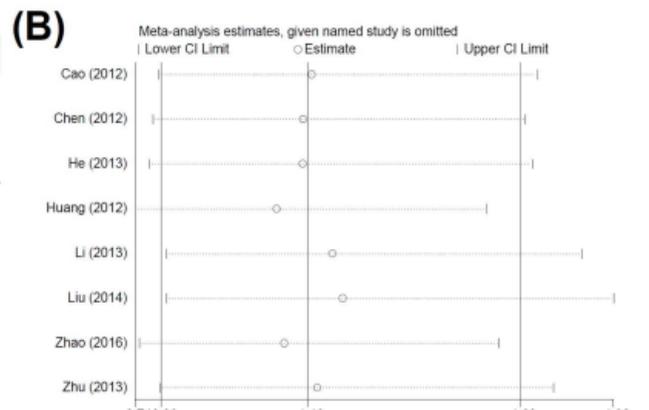
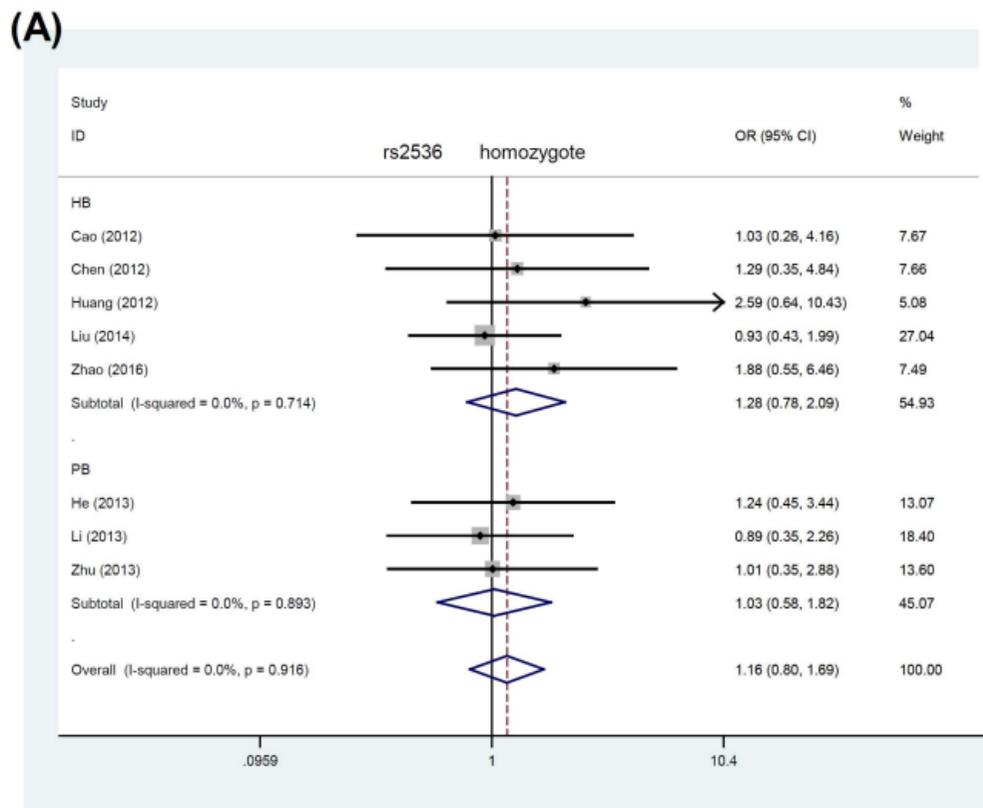


Figure S7

Figure S7. Pooled analysis of *mTOR* rs2536 via the homozygote comparison. (A) Forest plot of subgroup analyses by control source. (B) Begg's test. (C) Sensitivity analysis.

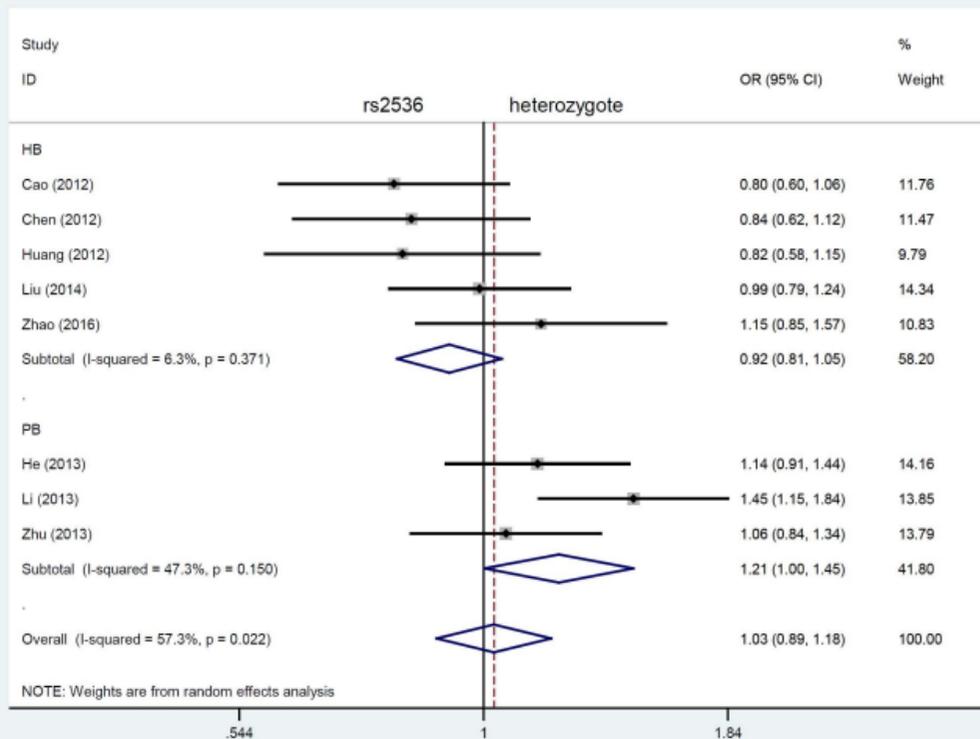
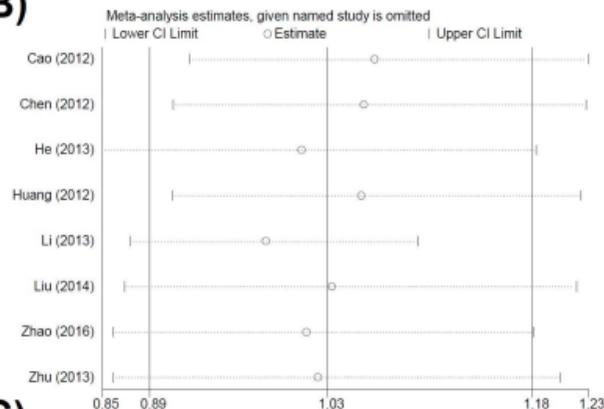
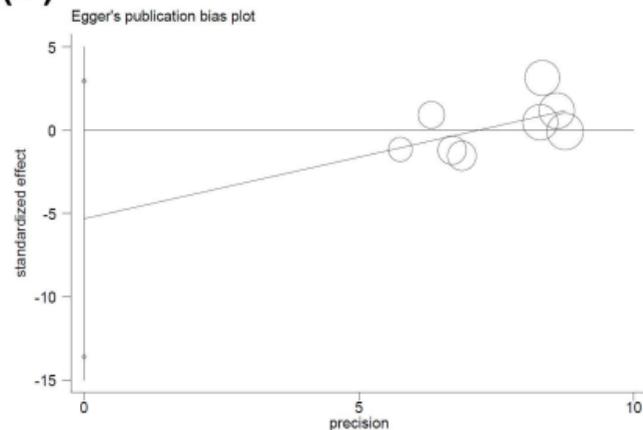
(A)**(B)****(C)****Figure S8**

Figure S8. Pooled analysis of *mTOR* rs2536 via the heterozygote comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

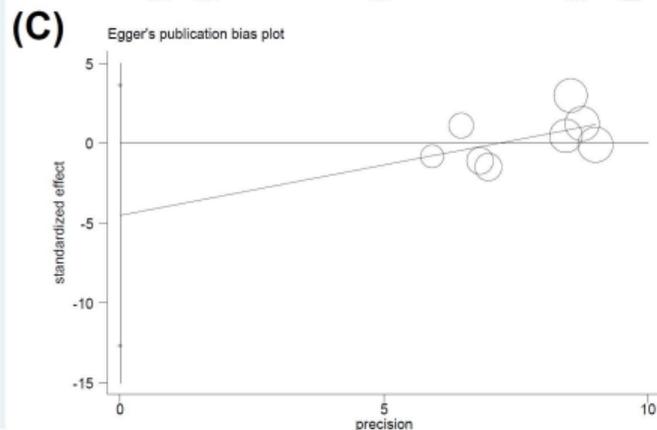
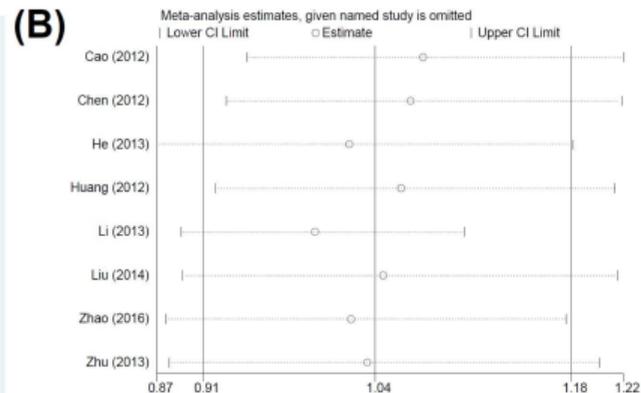
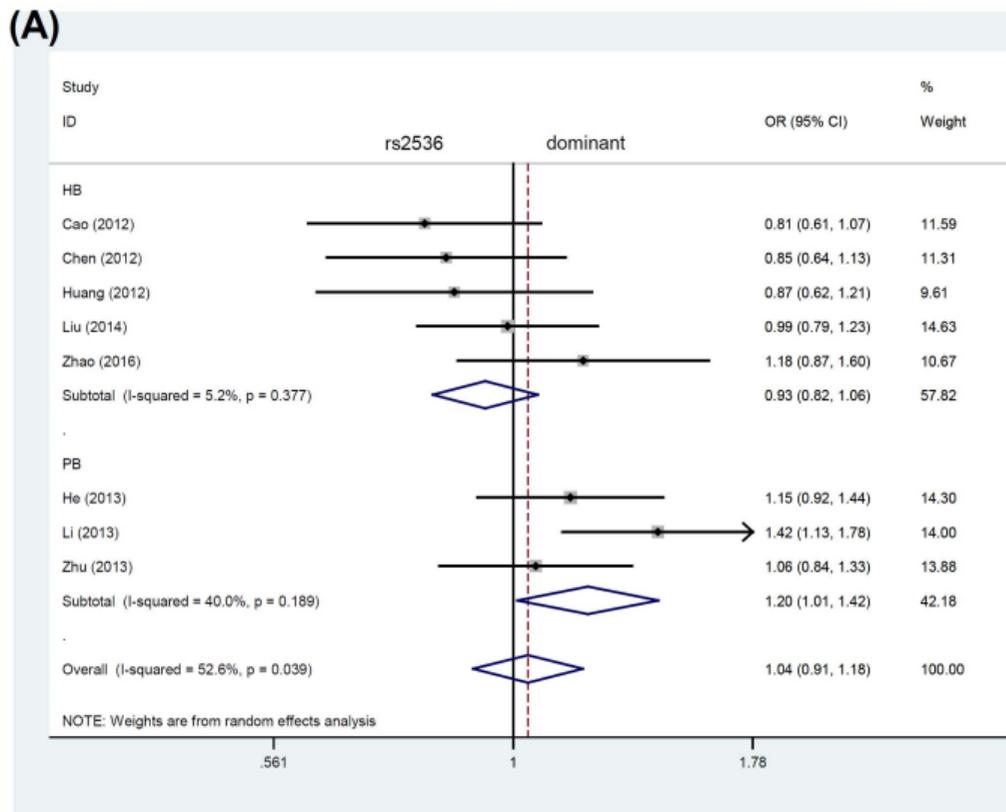


Figure S9

Figure S9. Pooled analysis of *mTOR* rs2536 via the dominant comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

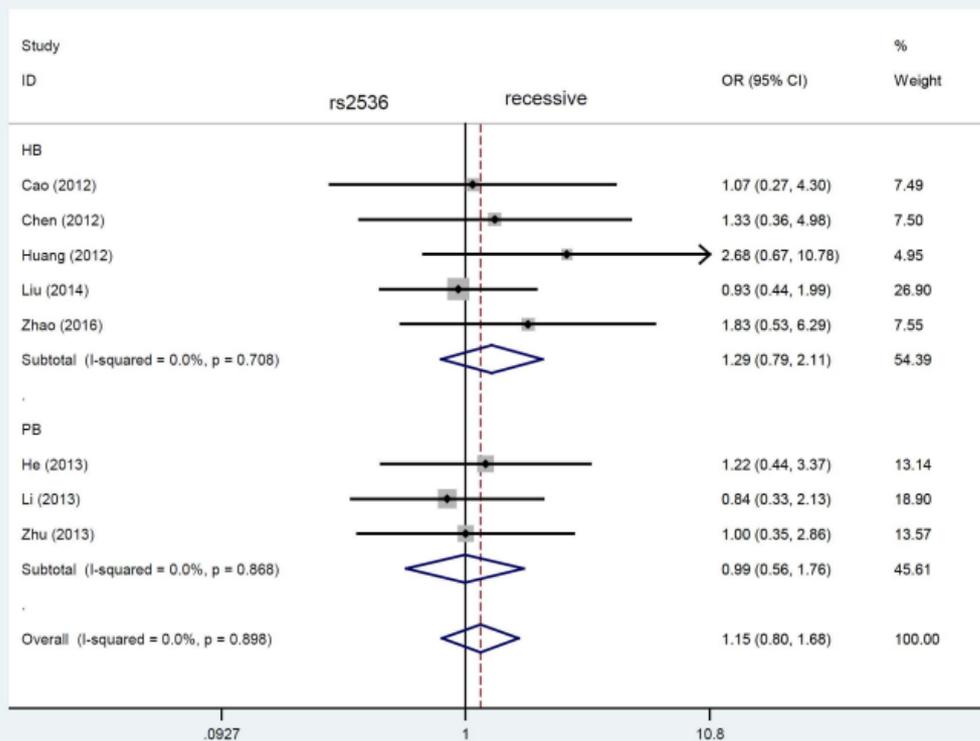
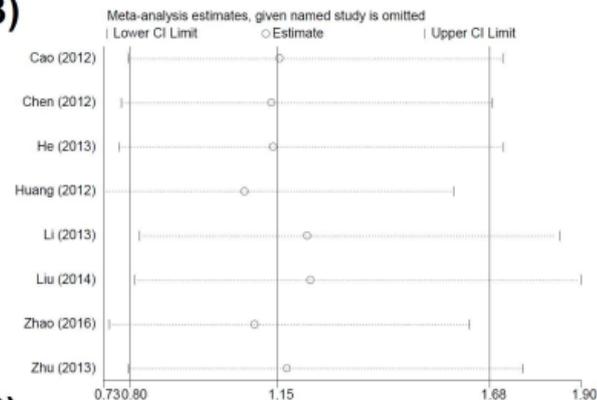
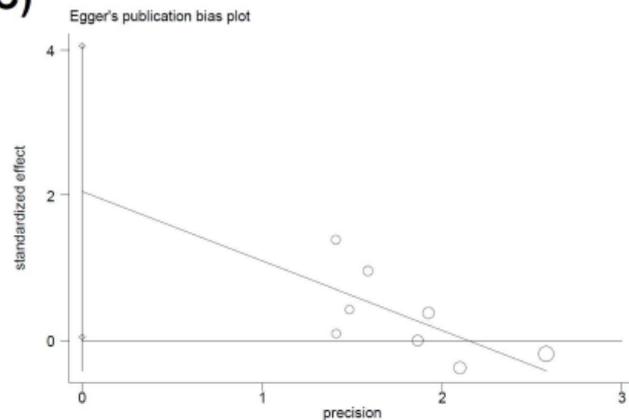
(A)**(B)****(C)****Figure S10**

Figure S10. Pooled analysis of *mTOR* rs2536 via the recessive comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

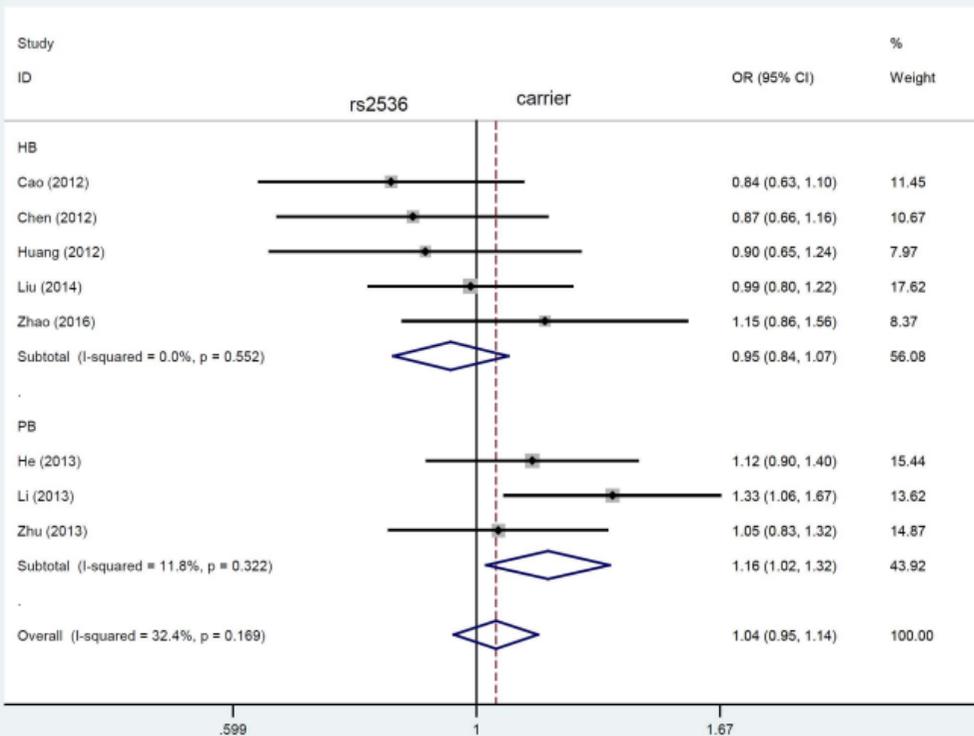
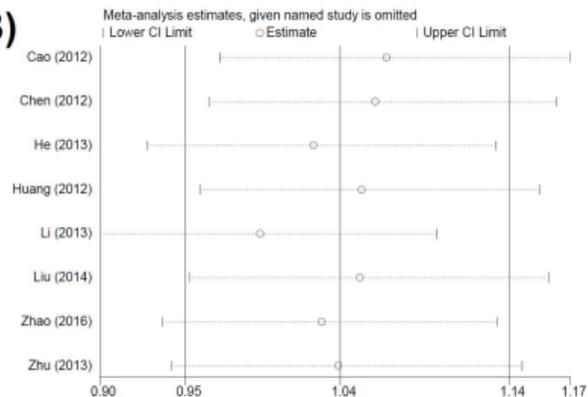
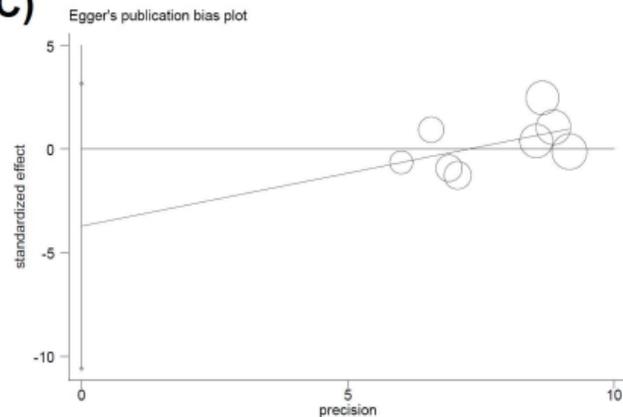
(A)**(B)****(C)****Figure S11**

Figure S11. Pooled analysis of *mTOR* rs2536 via the carrier comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

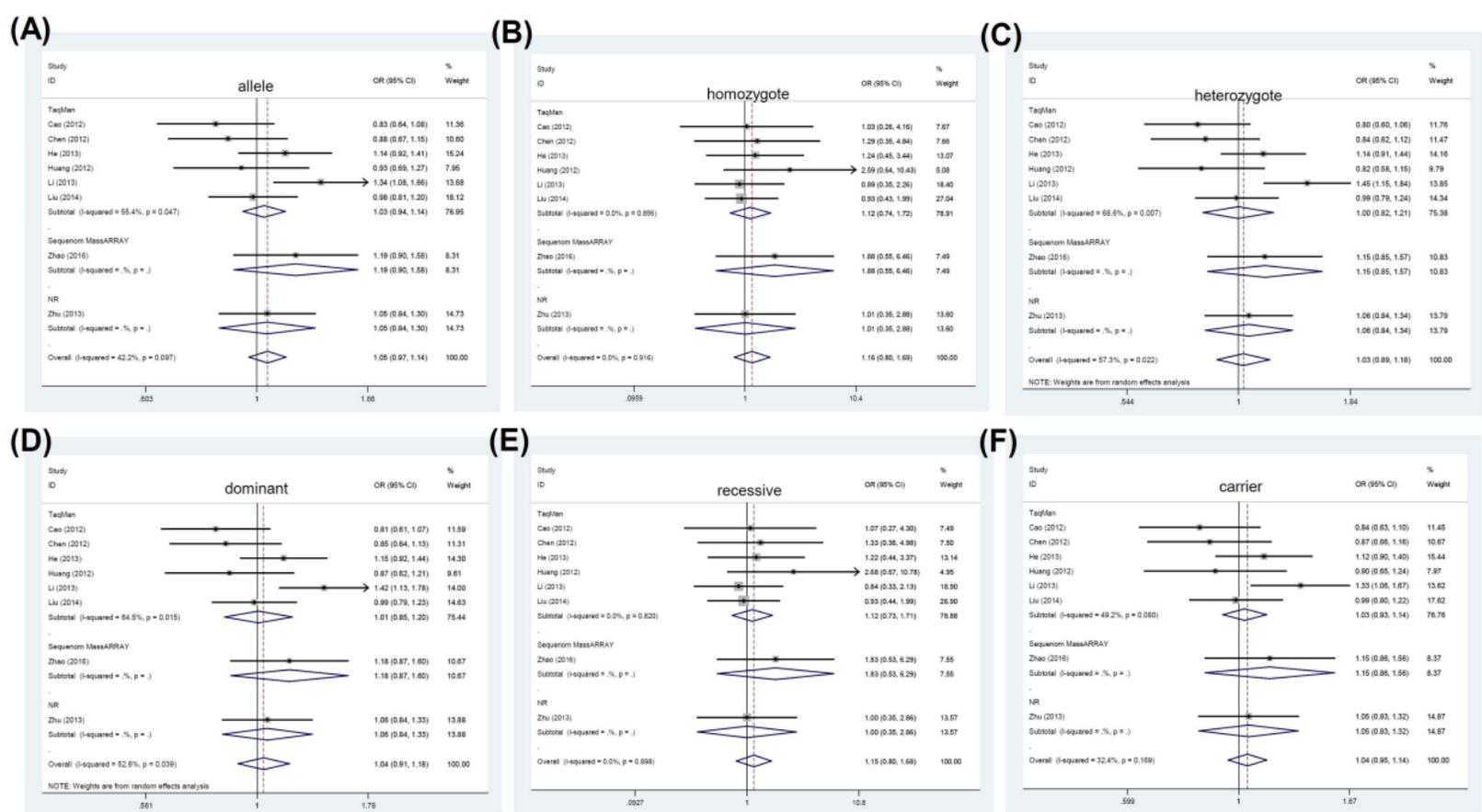


Figure S12

Figure S12. **Forest plot of subgroup analyses of *mTOR* rs2536 by genotyping method.**
(A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.

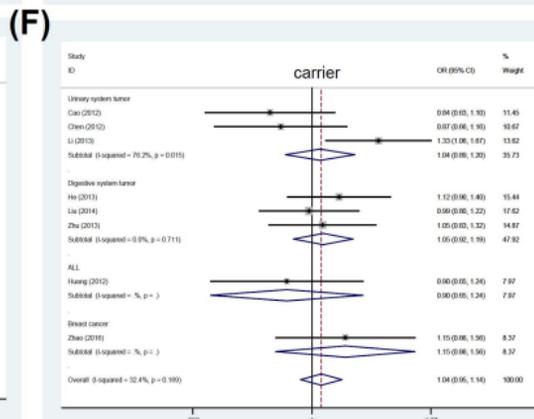
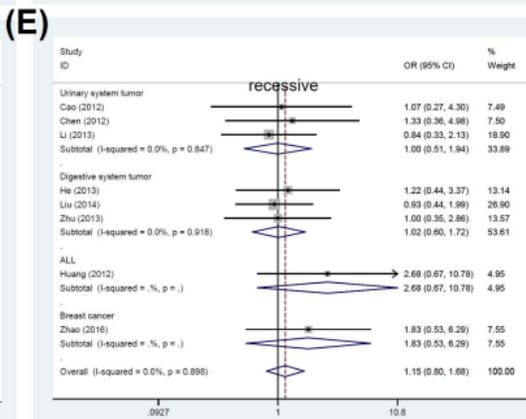
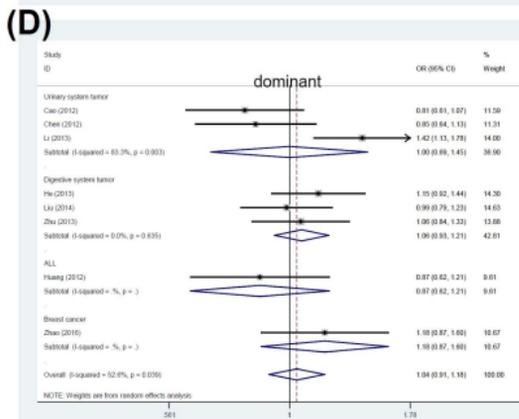
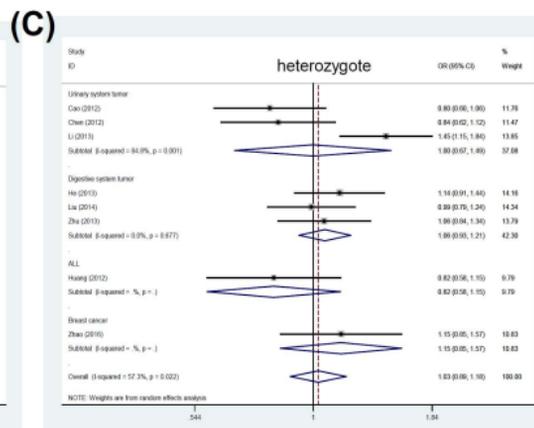
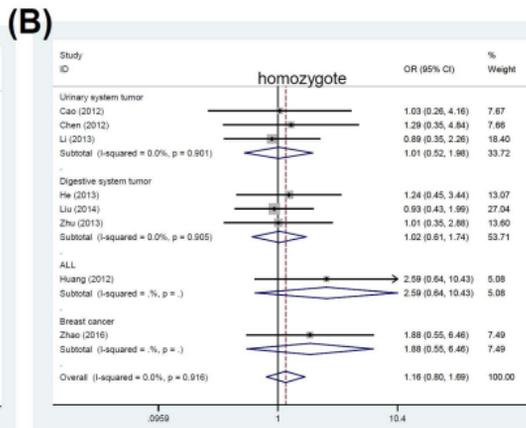
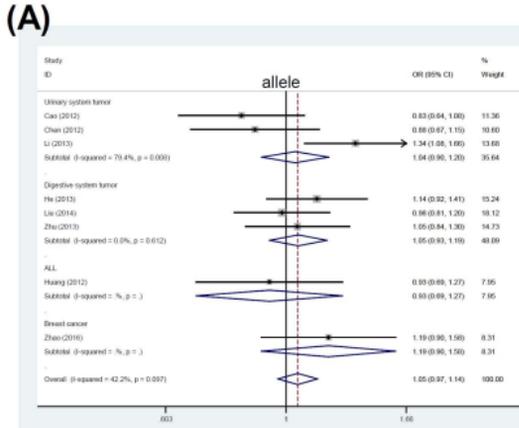


Figure S13

Figure S13. Forest plot of subgroup analyses of *mTOR* rs2536 by cancer type. (A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.

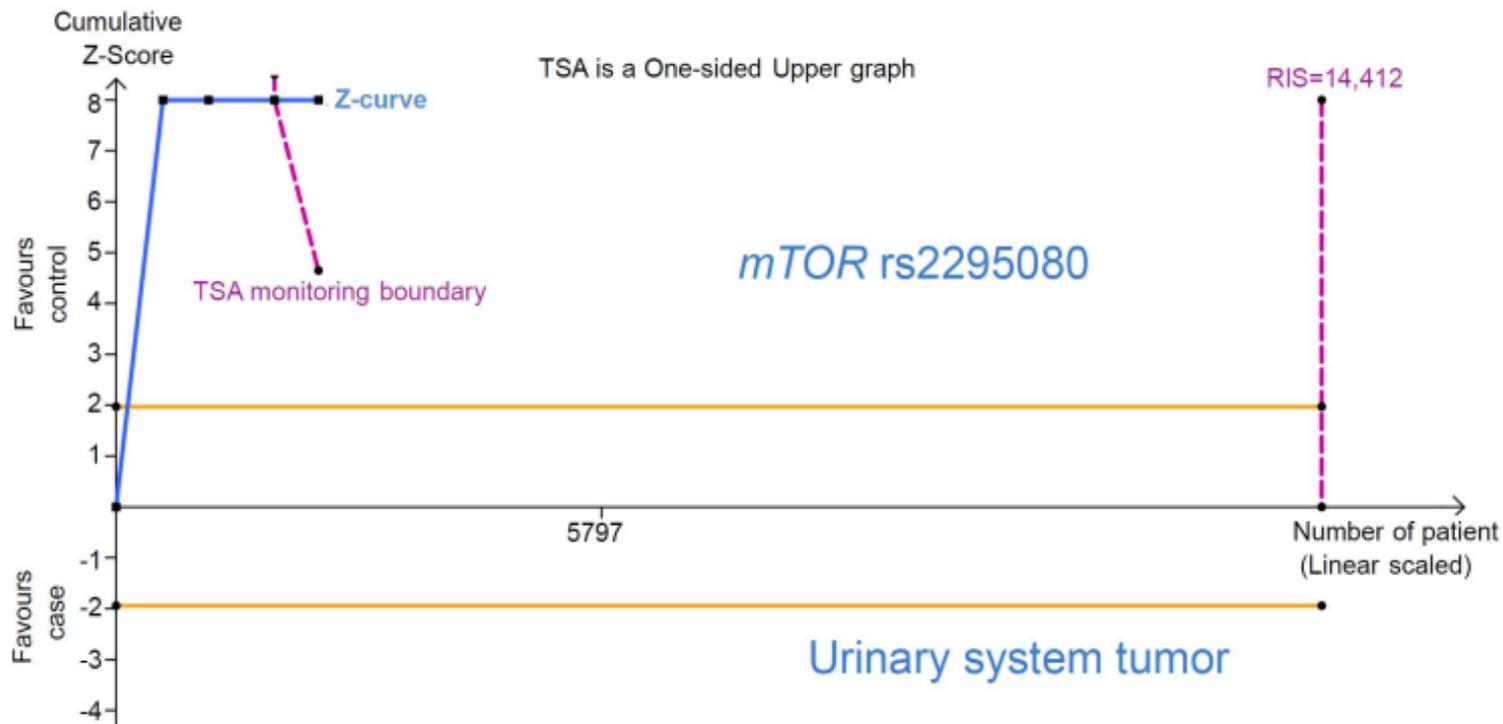


Figure S14

Figure S14. Trial sequential analysis of the association between *mTOR* rs2295080 and urinary system tumor risk via the dominant comparison.

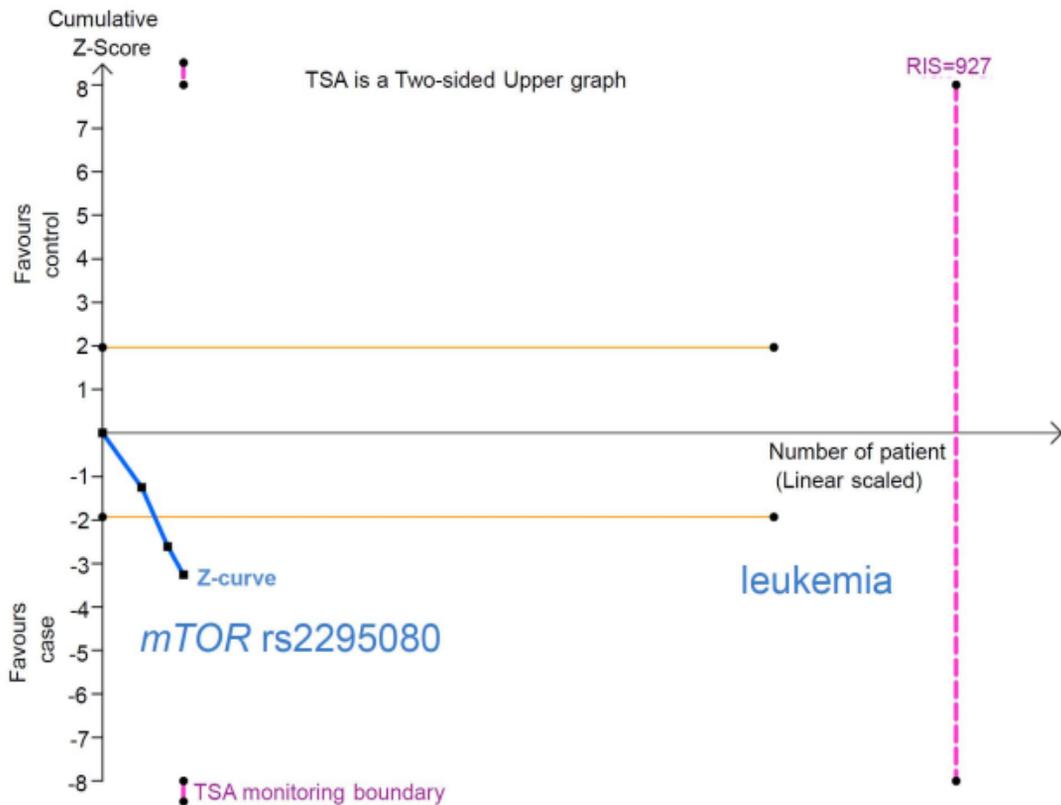


Figure S15

Figure S15. Trial sequential analysis of the association between *mTOR* rs2295080 and leukemia risk via the recessive comparison.

mTOR (ENSG00000198793.12) and rs2536 (chr1_11106656_T_C_b38)

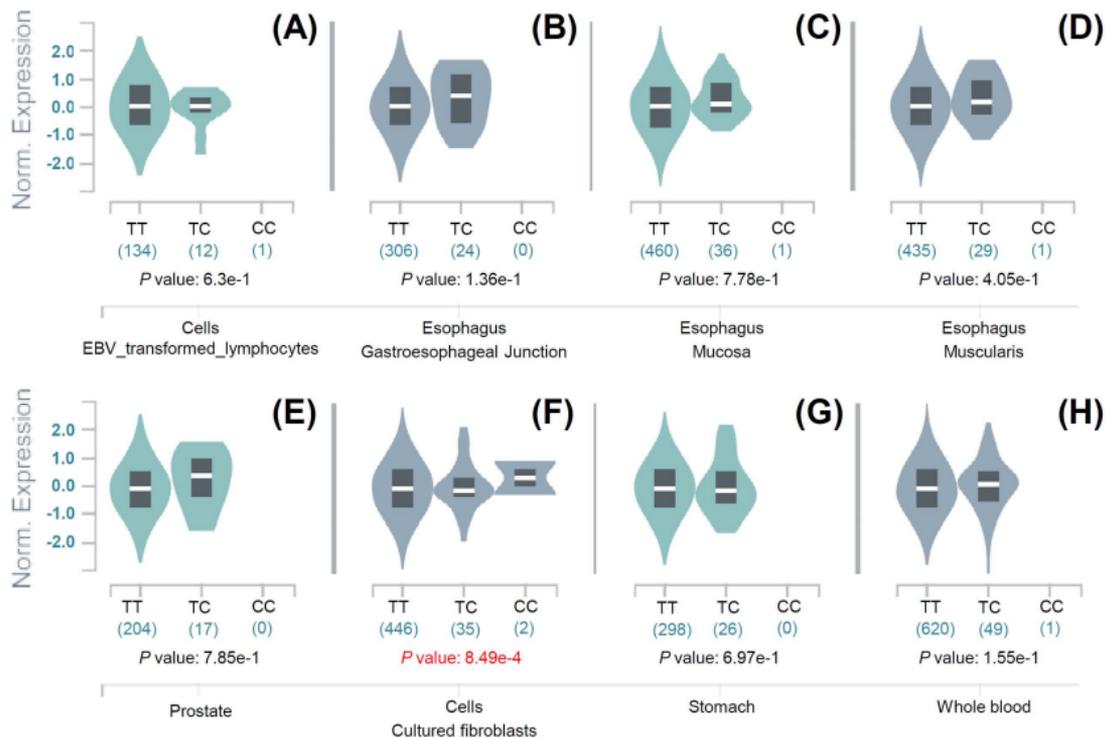


Figure S16

Figure S16. eQTL analysis of *mTOR* rs2536 in selected cells or tissues within the GTEx database. (A) EBV_transformed_lymphocytes; (B) Esophagus_Gastroesophageal_Junction; (C) Esophagus_Mucosa; (D) Esophagus_Muscularis; (E) Prostate; (F) cultured_fibroblasts; (G) Stomach; (H) whole blood.

Table S1. Database search terms.

(1) PubMed database			
#1	#2	#3	#4
(((((((Neoplasms) OR Neoplasia) OR Neoplasias) OR Neoplasm) OR Tumors) OR Tumor) OR Cancer) OR Cancers	((mTOR) OR Mammalian target of rapamycin) OR FRAP) OR FKBP12-rapamycin complex-associated protein	(((((((Polymorphism) OR Polymorphism, Genetic) OR Polymorphisms, Genetic) OR Genetic Polymorphisms) OR Genetic Polymorphism) OR Polymorphism (Genetics)) OR Polymorphisms (Genetics)) OR Polymorphisms) OR rs2536) OR rs2295080	((((mTOR) OR Mammalian target of rapamycin) OR FRAP) OR FKBP12-rapamycin complex-associated protein)) AND (((((((Neoplasms) OR Neoplasia) OR Neoplasias) OR Neoplasm) OR Tumors) OR Tumor) OR Cancer) OR Cancers)) AND (((((((Polymorphism) OR Polymorphism, Genetic) OR Polymorphisms, Genetic) OR Genetic Polymorphisms) OR Genetic Polymorphism) OR Polymorphism (Genetics)) OR Polymorphisms (Genetics)) OR Polymorphisms) OR rs2536) OR rs2295080)
4,553,668	45,424	341,334	233
(2) Embase database			
#1	#2	#3	#4
'neoplasms'/exp OR 'neoplasms' OR 'neoplasia'/exp OR 'neoplasia' OR 'neoplasias' OR 'neoplasm'/exp OR 'neoplasm' OR 'tumors'/exp OR 'tumors' OR 'tumor'/exp OR 'tumor' OR 'cancer'/exp OR 'cancer' OR 'cancers'/exp OR 'cancers'	'mtor'/exp OR 'mtor' OR 'mammalian target of rapamycin'/exp OR 'mammalian target of rapamycin' OR 'frap' OR 'fkbp12-rapamycin complex-associated protein'	'polymorphism'/exp OR 'polymorphism' OR 'polymorphisms' OR 'genetic polymorphisms' OR 'genetic polymorphism'/exp OR 'genetic polymorphism' OR 'rs2536' OR 'rs2295080'	#1 AND #2 AND #3

6,343,682	78,916	521,258	848
(3) Cochrane			
#1	#2	#3	#4
('mTOR') OR ('Mammalian target of rapamycin') OR ('FRAP') (Word variations have been searched)	('Polymorphism') OR ('Genetic Polymorphism') OR ('rs2536') OR ('rs2295080') (Word variations have been searched)	('Neoplasia') OR ('Neoplasm") OR ('Tumor') OR ('Cancer') (Word variations have been searched)	#1 and #2 and #3
1,436	8,689	196,203	8
(4) WANFANG			
mTOR and Polymorphism and cancer			
25			

Table S2. Quality assessment score.

Study	Representativeness of case	Representativeness of control	Ascertainment of case	Control selection	Genotyping examination	HWE	Total sample size	Score
Cao, 2012	1	1	2	2	1	1	3	11
Chen, 2012	1	1	2	1	2	1	3	11
Chen, 2019	1	3	2	0	1	1	2	10
He, 2013	1	3	1	2	1	1	3	12
Huang, 2012	1	1	2	2	1	1	2	10
Li, 2013	1	3	2	1	1	1	3	12
Liu, 2017	1	1	2	1	1	1	3	10
Liu, 2014	1	1	0	2	2	1	3	10
Qi, 2017	1	1	2	2	0	1	3	10
Wang, 2015	1	1	2	2	1	1	3	11
Wen, 2017	1	3	2	2	2	1	3	14
Xu, 2015	1	1	2	2	1	1	3	11
Xu, 2013	1	1	2	2	2	1	3	12
Zhao, 2017	1	3	2	2	1	1	2	12
Zhao, 2015	1	1	2	2	1	1	2	10
Zhao, 2016	1	1	2	2	0	1	3	10
Zhu, 2015	1	3	2	2	1	1	3	13
Zhu, 2013	1	3	2	2	1	1	3	13