


Figure S1

Figure S1. Pooled analysis of $\boldsymbol{m T O R}$ rs2295080 via the allele comparison. (A) Forest plot of subgroup analyses by cancer type. (B) Begg's test. (C) Sensitivity analysis.

## (A)



OR (95\% CI)
$0.77(0.62,0.95) \quad 7.08$ $0.77(0.62,0.96) \quad 6.90$ $0.76(0.64,0.91) 7.85$ $0.96(0.76,1.23) 6.41$ $0.80(0.72,0.89) \quad 28.24$
$0.74(0.58,0.95) 6.21$ $0.86(0.68,1.09) 6.44$ $0.80(0.68,0.95) \quad 12.65$
$1.13(0.87,1.46) 5.92$ $1.34(0.89,2.03) 3.55$ $1.04(0.56,1.94) \quad 1.89$ $1.17(0.95,1.44) \quad 11.37$
$0.95(0.76,1.18) 6.81$ $1.17(0.98,1.40) 7.87$ $0.76(0.62,0.94) 7.12$ 0.78 (0.64, 0.96) 7.29 $1.06(0.75,1.50) 4.42$ $1.11(0.94,1.32) 8.04$ $0.96(0.82,1.12) 41.55$
$0.76(0.59,0.98) 6.20$ $0.76(0.59,0.98) \quad 6.20$
$0.90(0.82,0.99) \quad 100.00$ 2.03
(B)

Meta-analysis estimates, given named study is omitted | Lower Cl Limit Lower Cl Limit Estimate

Upper CI Limit
Cao (2012) Chen (2012) Chen (2019) Huang (2012) Li (2013) Liu (2017) Qi (2017) Wang (2015) Wen (2017) Xu (2015) Xu(2013) Zhao (2017) Zhao (2015) Zhao (2015) Zhao (2016) Zhu (2015)

## (C)




Figure S2

Figure S2. Pooled analysis of $\boldsymbol{m} T O R$ rs2295080 via the dominant comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.

## (A)


(B)

Meta-analysis estimates, given named study is omitted | Lower Cl Limit Estimate
| Upper CI Limit
(C)


Egger's publication bias plot


Figure S3

Figure S3. Pooled analysis of $\boldsymbol{m T O R}$ rs2295080 via the recessive comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.

## (A)




## Figure S4

Figure S4. Pooled analysis of $\boldsymbol{m}$ TOR rs2295080 via the carrier comparison. (A) Forest plot of subgroup analysis by cancer type. (B) Begg's test. (C) Sensitivity analysis.
(A)

| ${ }_{10}^{\text {ssudy }} \quad$ allele | OR (95\% Cl) | $\%$ |
| :---: | :---: | :---: |
| HB |  |  |
| Cao (2012) $\longrightarrow$ | 0.82 (0.69, 0.98) | 6.92 |
| Chen (2012) | 0.81 (0.68, 0.98) | 674 |
| Huang (2012) | 1.15 (0.92, 1.43) | 5.95 |
| Lu (2017) | 1.06 (0.88, 129) | 6.49 |
| ai (2017) | 0.95 (0.81, 1.10) | 7.46 |
| Wang (2015) | 1.11 (0.96, 129) | 7.50 |
| Xu (2015) | $0.79(0.66 .0 .94)$ | 6.91 |
| Xu (2013) | 0.78 (0.66, 0.92) | 7.04 |
| Zhao (2015) | 1.46 (1.05, 2.01) | 4.10 |
| Zhao (2015) | $1.29(0.79 .211)$ | 237 |
| Zhao (2016) | 0.84 (0.69, 1.03) | 6.33 |
| Sutiotal (1-squared $=69.7 \%, \mathrm{p}=0.000$ ) | 0.95 (0.85, 1.06) | 67.82 |
| P8 |  |  |
| Chen (2019) | $0.74(0.60 .0 .90)$ | 6.33 |
| Li (2013) | $0.80(0.69 .0 .93)$ | 7.45 |
| Wen (2017) | $0.79(0.64,0.97)$ | 6.19 |
| Zhao (2017) | 1.08 (0.81, 1.45) | 4.62 |
| Zhu (2015) | $1.08(0.93,124)$ | 7.59 |
| Subtotal (1-squared $=73.3 \%, \mathrm{p}=0.005$ ) | 0.88 (0.75, 1.04) | 32.18 |
| Overall ( 1 -squared $=69.2 \%, \mathrm{p}=0.000$ ) | 0.93 (0.85, 1.01) | 100.00 |
| NOTE: Weights are from random effects analysis |  |  |
| . 473 | 11 rs22 | 95080 |

## (D)


(B)

(C)
(F)


| Study <br> ID |  | OR (95\% CII) |
| :--- | :--- | :--- | :--- | :--- |

Figure S5

Figure S5. Forest plot of subgroup analyses of $\boldsymbol{m T O R}$ rs2295080 by control source. (A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.


4
(D)

(B)
(A)

## (A)

$\square$

Figure S6

(C)

(F)


$0.76(0.61,0.95) 7.17$

$0.78(0.62,0.97) 6.98$ $0.80(0.62,1.04) 6.11$ $0.77(0.64,0.93) 8.3$ $0.88(0.69,1.14) 6.27$ | $0.97(0.77,1.123) 6.74$ |
| :--- |
| $119(0.99 .142)$ |
| 8.40 |
| $0.78(0)$ | $0.78(0.60,1.01) 6.04$

$0.78(0.63,0.98) 7.26$ $0.83(0.67,1.03) 7.52$ $1.12(0.94,1.34) 8.60$

$1.15(0.74,1.77) 3.02$ | $0.81(0.41,1.6)$ |
| :--- |
| 1.04 |

$0.91(0.72,1.17) 6.48$
$0.91(0.72,1.17) 6.48$ 46 rs229508

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\begin{aligned}
& \text { Study } \\
& 10
\end{aligned}
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r rs2295080


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Figure S6. Forest plot of subgroup analyses of $\boldsymbol{m T O R}$ rs2295080 by genotyping method. (A) Allele; (B) homozygote; (C) heterozygote; (D) dominant; (E) recessive; (F) carrier.

## (A)

| Study |  |  |  | \% |
| :---: | :---: | :---: | :---: | :---: |
| ID | rs2536 | homozygote | OR (95\% Cl) | Weight |
| HB |  | ! |  |  |
| Cao (2012) |  | , | 1.03 (0.26, 4.16) | 7.67 |
| Chen (2012) |  |  | 1.29 (0.35, 4.84) | 7.66 |
| Huang (2012) |  | ! | 2.59 (0.64, 10.43) | 5.08 |
| Liu (2014) |  | ! | 0.93 (0.43, 1.99) | 27.04 |
| Zhao (2016) |  |  | 1.88 (0.55, 6.46) | 7.49 |
| Subtotal ( 1 -squared $=0.0 \%, \mathrm{p}=0.714$ ) |  |  | 1.28 (0.78, 2.09) | 54.93 |
| . |  | I |  |  |
| PB |  | $1$ |  |  |
| He (2013) |  |  | 1.24 (0.45, 3.44) | 13.07 |
| Li (2013) |  | I | 0.89 (0.35, 2.26) | 18.40 |
| Zhu (2013) |  |  | 1.01 (0.35, 2.88) | 13.60 |
| Subtotal ( 1 -squared $=0.0 \%, \mathrm{p}=0.893$ ) |  |  | 1.03 (0.58, 1.82) | 45.07 |
| . |  |  |  |  |
| Overall (l-squared $=0.0 \%, \mathrm{p}=0.916$ ) |  |  | 1.16 (0.80, 1.69) | 100.00 |
| 1 |  |  |  |  |
| . 0959 |  | 1 |  |  |

(B)

Meta-analysis estimates, given named study is omitted I Lower CI Limit - Estimate | Upper CI Limit
(C) Egger's publication bias plot


Figure S7

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

## (A)





Figure S8

Figure S8. Pooled analysis of $m T O R$ rs2536 via the heterozygote comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

## (A)




Figure S9

Figure S9. Pooled analysis of $m T O R$ rs2536 via the dominant comparison. (A) Forest plot of subgroup analysis by control source. (B) Begg's test. (C) Sensitivity analysis.

## (A)

Study
ID
HB
Cao (2012)
Chen (2012)
Huang (2012)
Liu (2014)
Zhao (2016)
Subtotal (l-squared $=0.0 \%, \mathrm{p}=0.708$ )
PB
He (2013)
Li (2013)
Zhu (2013)
Subtotal (l-squared $=0.0 \%, \mathrm{p}=0.868)$
(B) Meta-analysis es
Lower CI Limit
Cao (2012)
C)


## Figure S10

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

(B)
Meta-analysis estimates, given named study is omitted | Lower CI Limit
Upper CI Limit

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

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Figure S13
(B)

(D)

(A)


(A)




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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 $\boldsymbol{m T O R}$ 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; (F) 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 <br> FKBP12-rapamycin complex-associated protein | $((()(((($ Polymorphism) OR  <br> Polymorphism, Genetic $)$ OR <br> Polymorphisms, Genetic) OR <br> Genetic   <br> Polymorphisms) OR Genetic <br> Polymorphism) OR Polymorphism  <br> (Genetics)) OR Polymorphisms <br> (Genetics)) OR Polymorphisms) OR <br> 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' |  | '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 <br> Polymorphism') OR ('rs2536') <br> OR ('rs2295080') (Word <br> variations have been <br> 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 |


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