Figure S1. Association of microRNA-126 expression with type 2 diabetes mellitus risk in 7 epidemiological studies (5 analytical and 2 cross-sectional studies). The pooled estimates were obtained using a random-effects model, and the dotted lines represent the corresponding pooled results. RR, relative ratio.

Study	RR (95% CI)	Weight %
Al-Kafaji, et al, 2017	0.69 (0.55, 0.76)	14.62
Al-Kafaji, et al, 2016	0.80 (0.61, 0.96)	13.81
Liu, et al, 2014	0.63 (0.62, 0.64)	15.72
Zampetaki, et al, 2010	0.57 (0.37, 0.86)	10.55
Zhang, et al, 2015	0.97 (0.94, 0.99)	15.70
Weale, et al, 2021	1.43 (1.21, 1.69)	14.60
Wang, et al, 2014	1.08 (0.95, 1.23)	15.01
Overall (I-squared = 99.3%, P < 0.001)	0.85 (0.67, 1.08)	100.00

NOTE: Weights are from random effects analysis
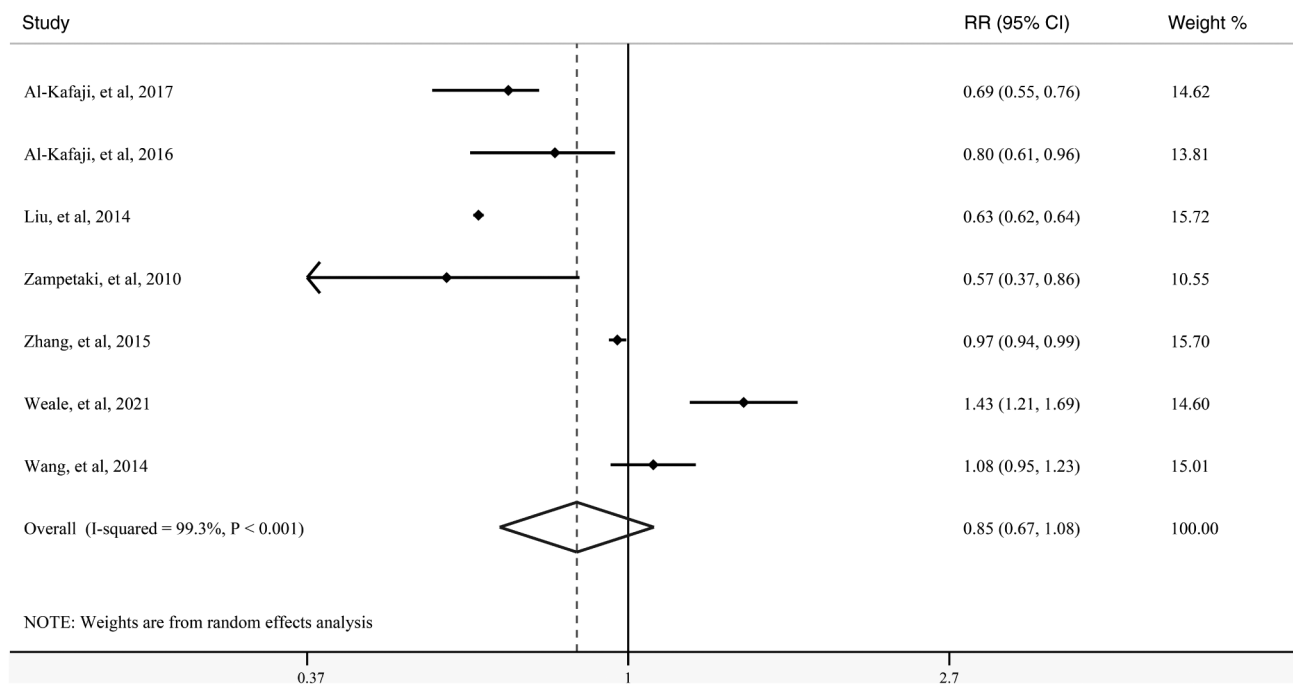
0.37   1   2.7

Figure S2. Begg's funnel plot for the association of microRNA-126 with type 2 diabetes mellitus risk. Asymmetry suggested the presence of a potential publication bias.
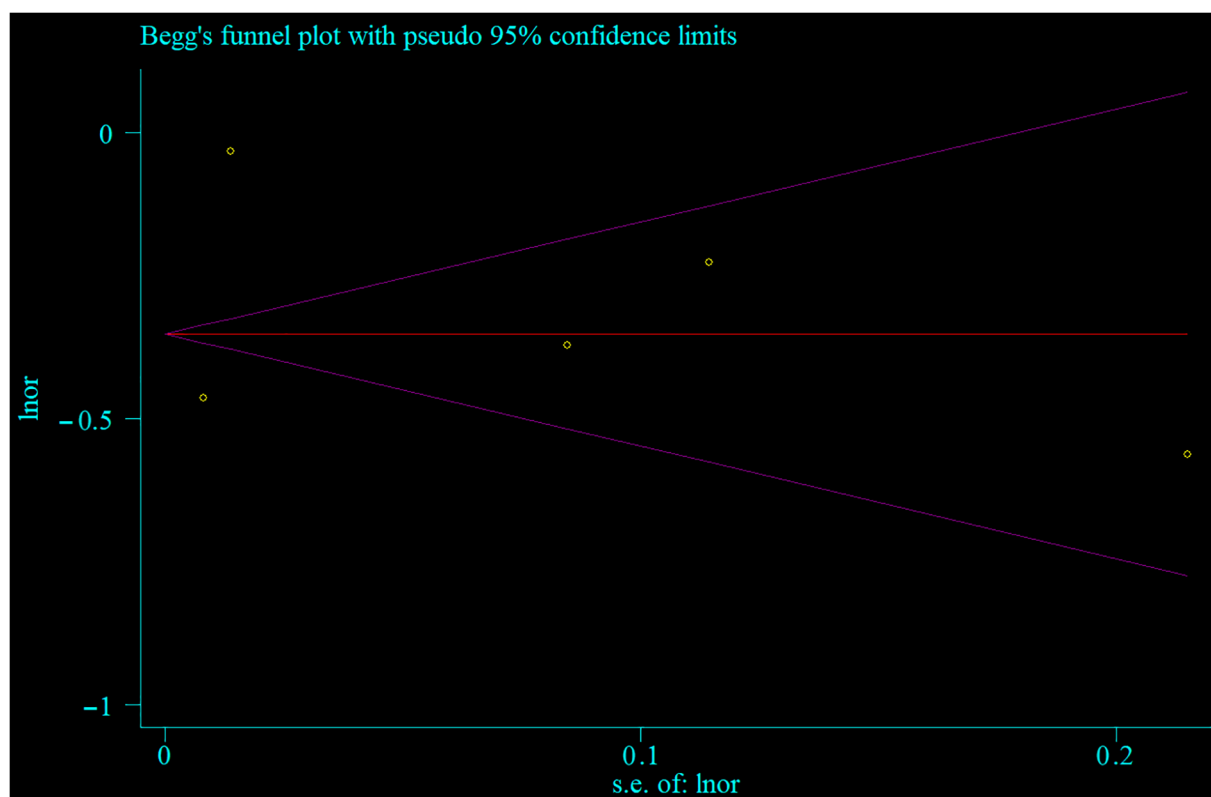
Figure S3. Begg's funnel plot for the association of miR-126 and miR-122 with FBG level and HOMA-IR index. (A) A total of 22 studies for the association of miR-126 with FBG level. (B) A total of 10 studies for the association of miR-122 with FBG level. (C) A total of 9 studies for the association of miR-126 with HOMA-IR index. (D) A total of 9 studies for the association of miR-122 with HOMA-IR index. Asymmetry suggested the presence of a potential publication bias. miR, microRNA; FBG, fasting blood glucose; HOMA-IR, homeostasis model assessment of insulin resistance.