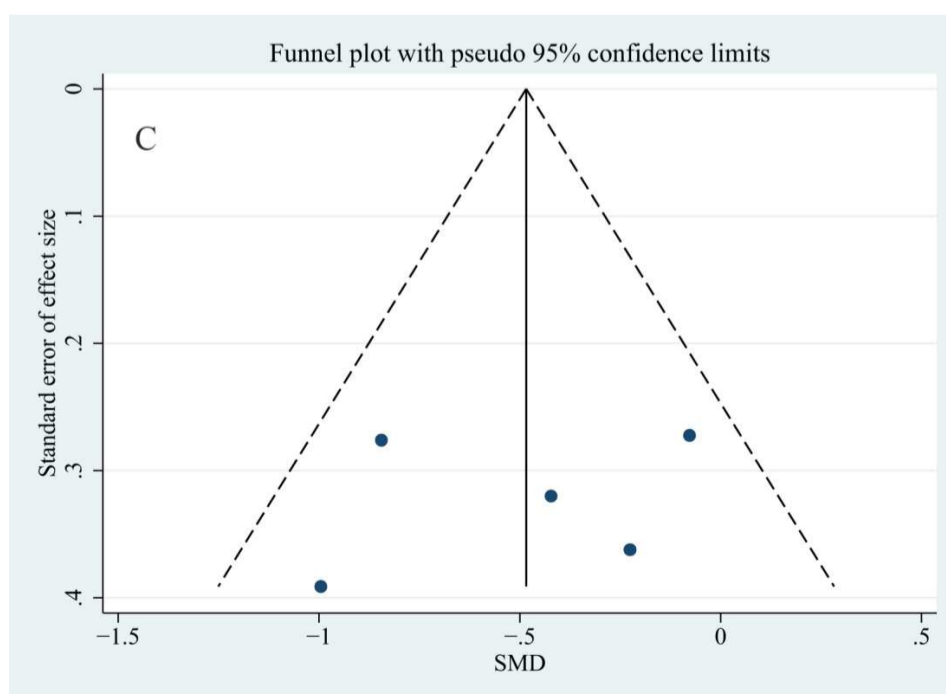
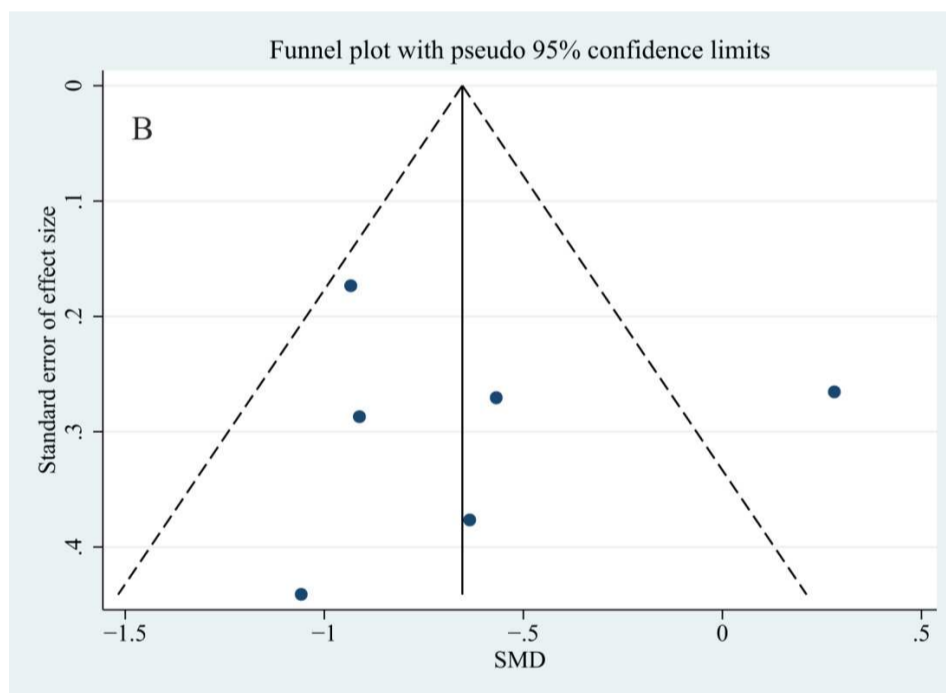
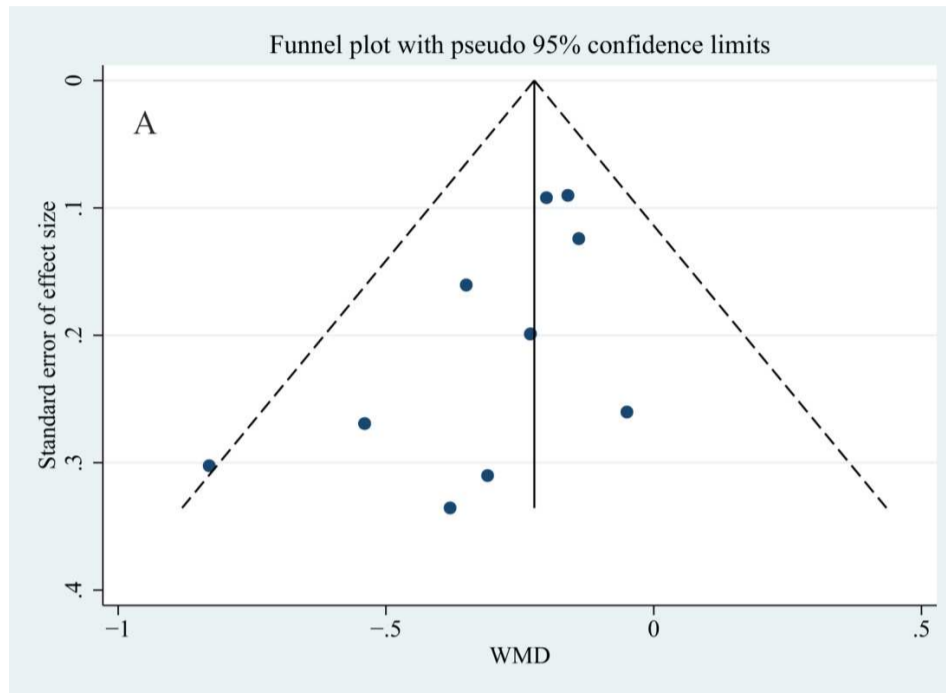
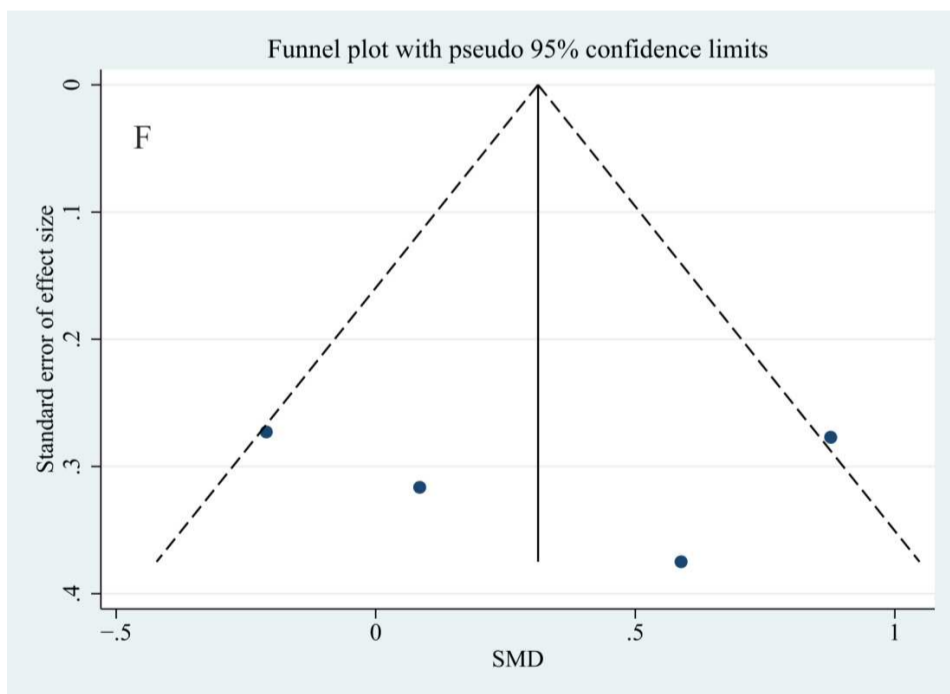
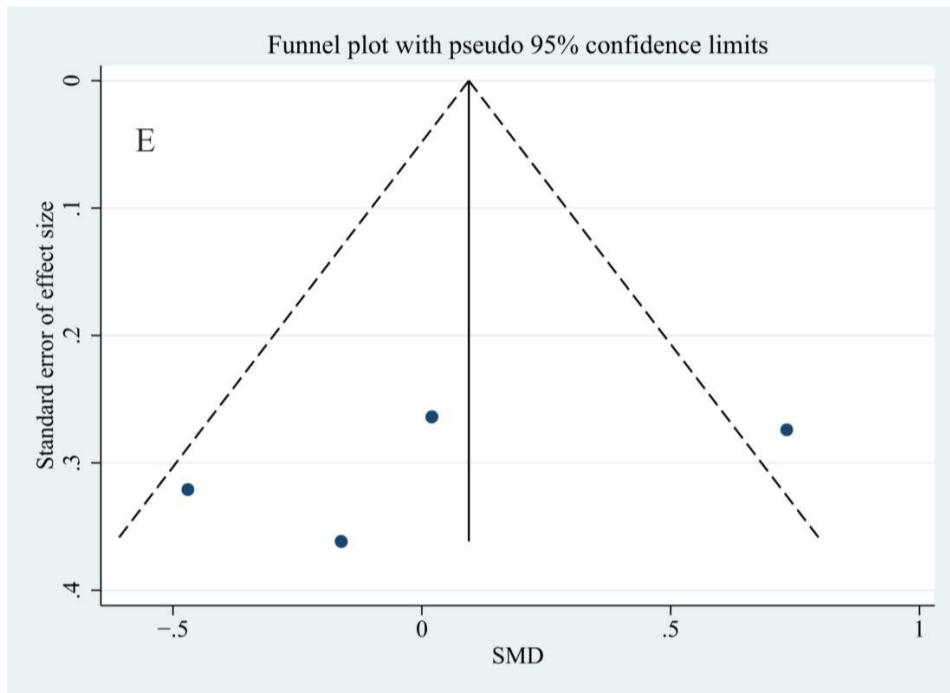
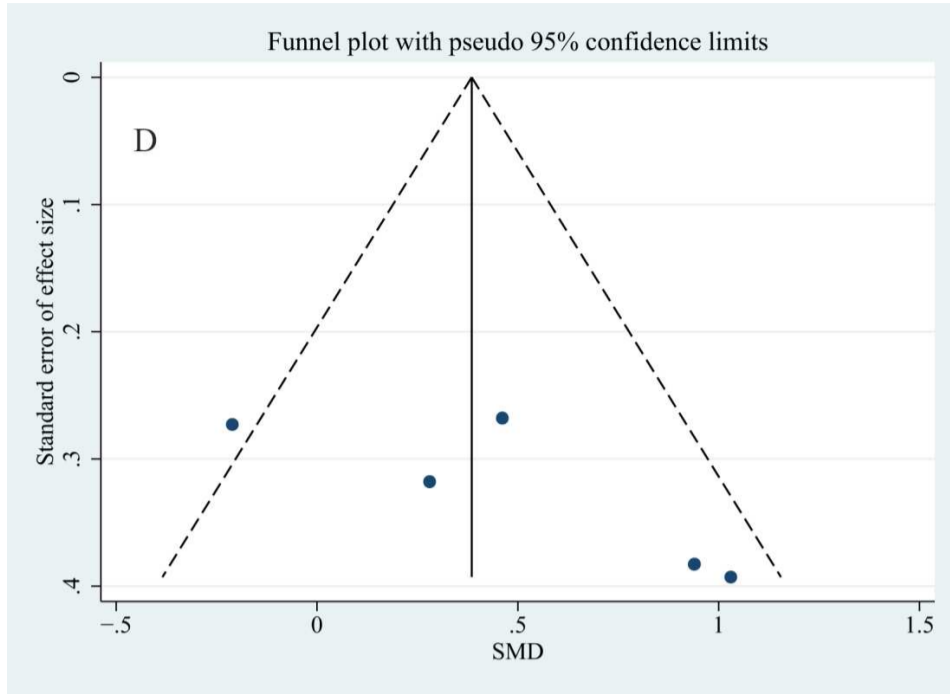
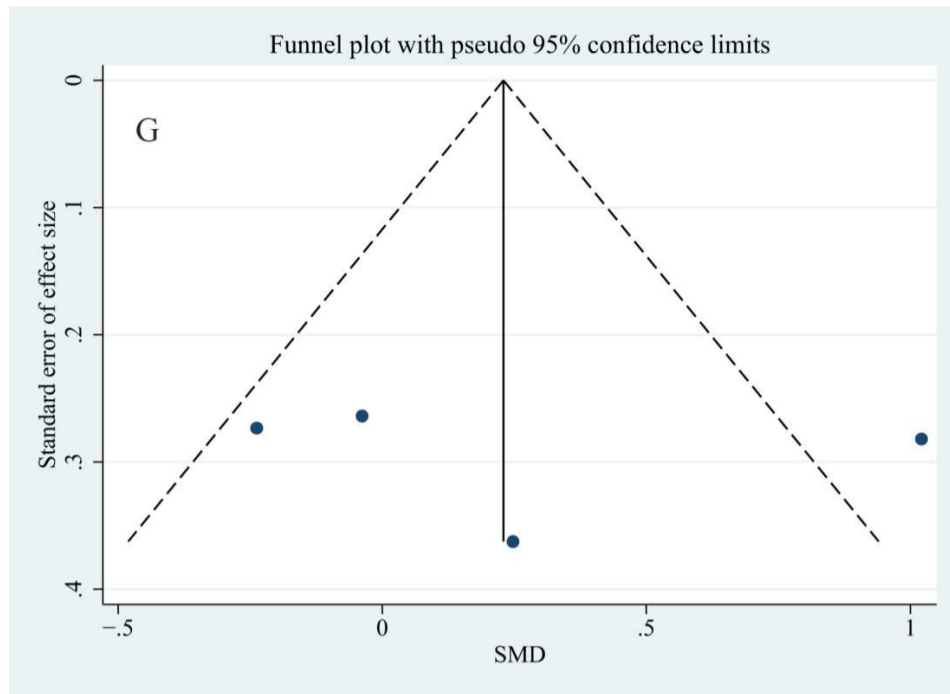


## Supplementary Information 2

**Figure S1. Funnel chart of the comparison of the gut microbiota diversity and the relative abundance of some flora between patients with SLE and HCs. (A) Shannon-wiener diversity index, (B) Chao1 richness estimator, (C) *Ruminococcaceae*, (D) *Enterobacteriaceae*, (E) *Lachnospiraceae*, (F) *Enterococcaceae*, (G) *Bacteroides*.**







**Table S1. Egger test and Begg test identifying the publication bias for the association between the gut microbiota and SLE**

	P >   t   (bias)	
	Egger's test	Begg's test
<b>Alpha diversity</b>		
Shannon-wiener diversity	0.057	0.057
Chao1 richness estimator	0.775	0.775
<b>Gut microbiota</b>		
<i>Ruminococcaceae</i>	0.653	0.653
<i>Enterobacteriaceae</i>	0.116	0.116
<i>Lachnospiraceae</i>	0.434	0.434
<i>Enterococcaceae</i>	0.819	0.819
<i>Bacteroides</i>	0.833	0.833

**Figure S2. One-study-removed analysis on the association of the gut microbiota diversity and the relative abundance of some flora between patients with SLE and HCs. (A) Shannon-wiener diversity index, (B) Chao1 richness estimator, (C) *Ruminococcaceae*, (D) *Enterobacteriaceae*, (E) *Lachnospiraceae*, (F) *Enterococcaceae*, (G) *Bacteroides*.**

