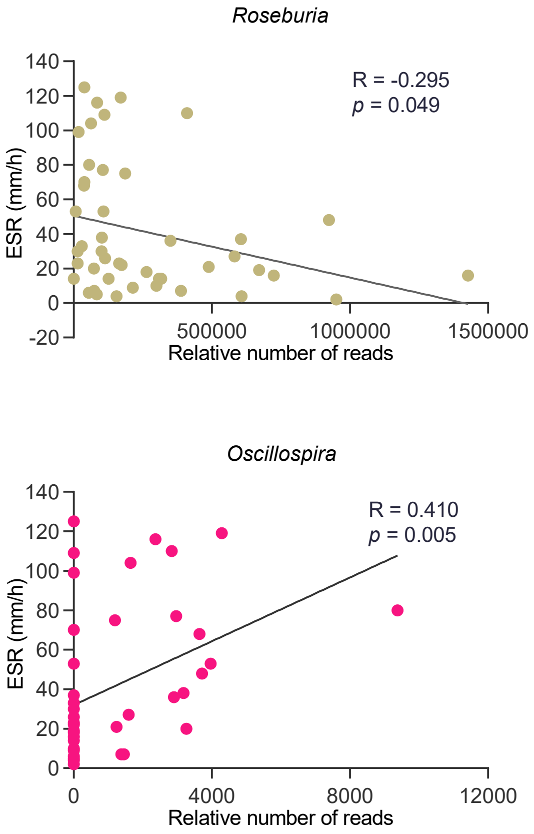
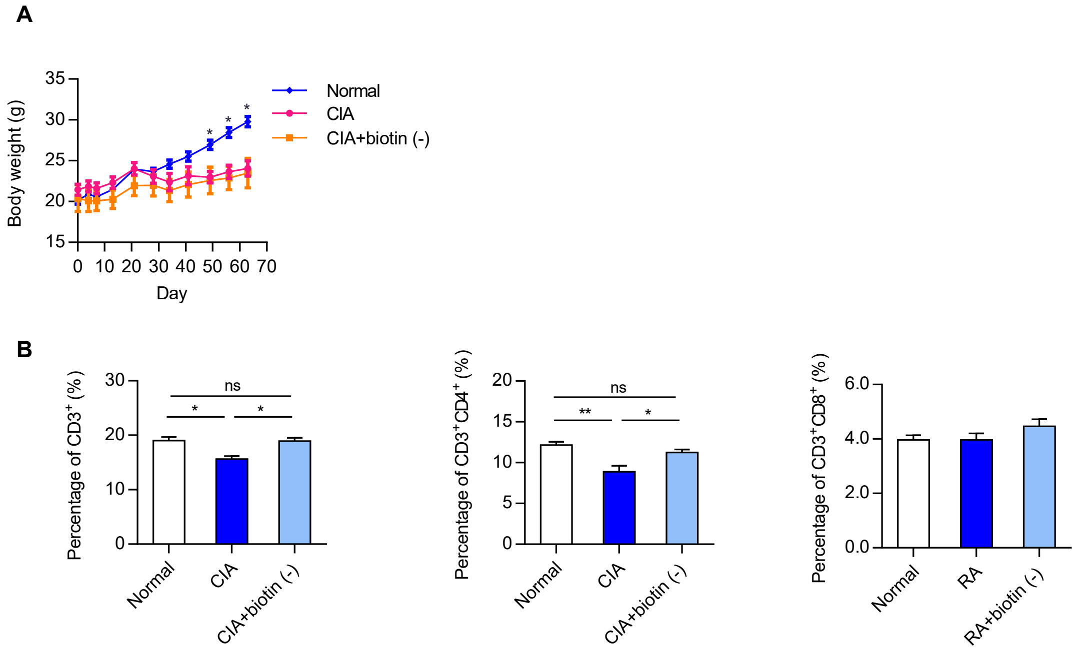
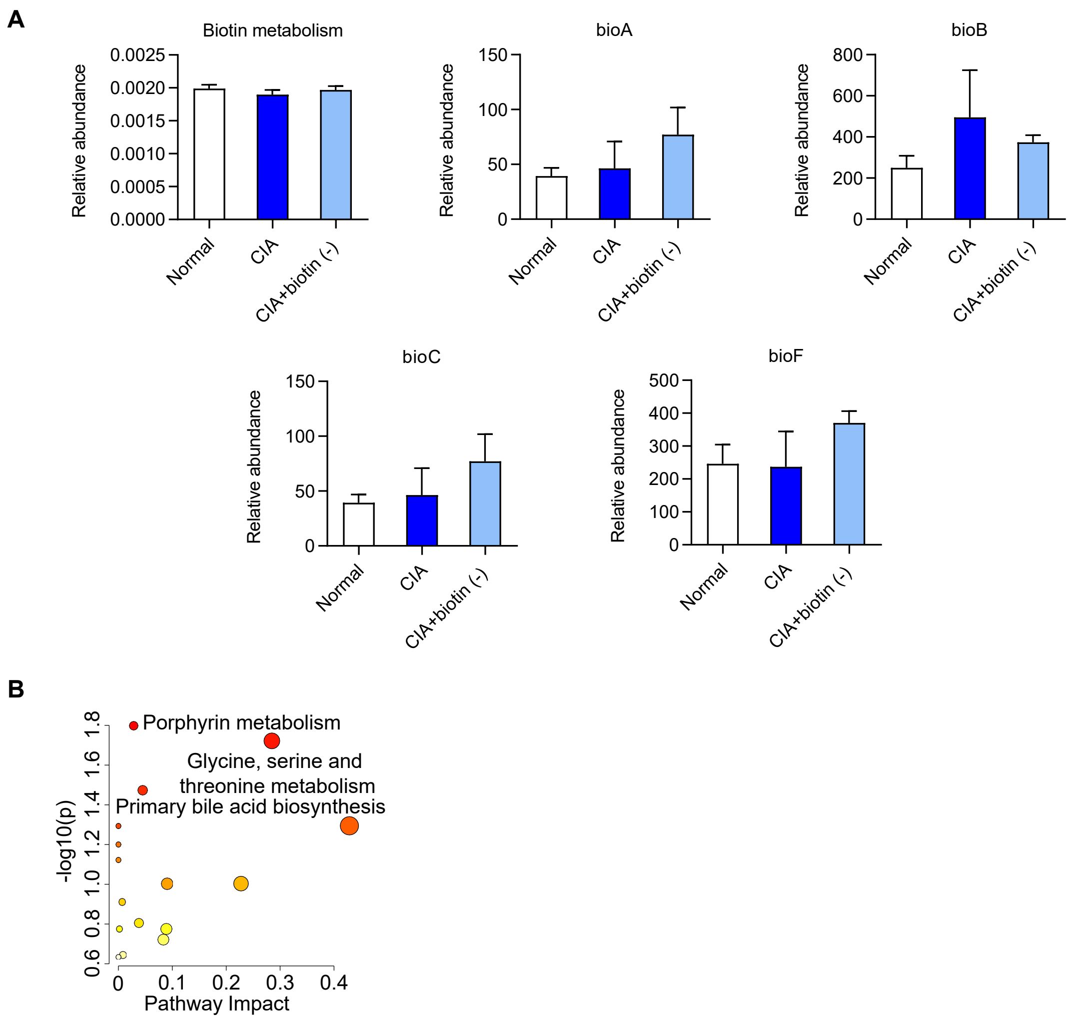


Supplementary Figure 1 Correlation analysis of the relative abundance of the genera and the blood levels of the clinical indices of disease activity, erythrocyte sedimentation rate (ESR), in RA patients. Spearman rank correlation test was performed to determine correlations between the variables.



Supplementary Figure 2 Effects of biotin on CIA mice. (A) Changes of body weight. (B) Percentages of $CD3^+CD4^+$ T cell, $CD3^+$ and $CD8^+$ T cell in spleen. One-way ANOVA was performed to assess the significance of differential abundance ($*p < 0.05$, $** p < 0.01$, $^{ns} p > 0.05$).



Supplementary Figure 3 Effects of biotin on CIA mice. (A) Relative abundance of microbial genes related to biotin metabolism and biotin biosynthesis (bioA, bioB, bioC, bioF). Data is expressed as mean ± SEM. One-way ANOVA was performed to assess the significance of differential abundance. (B) Altered pathway annotated by serum metabolites.

Supplementary Table 1 Altered genera in RA patients compared to control subjects .

Genus	Fold change (RA/control)	*p* value
Bacteroides	1.70	0.001
Faecalibacterium	0.58	0.013
Prevotella	2.15	0.010
Roseburia	0.56	0.006
Blautia	0.79	0.018
Escherichia-Shigella	0.35	<0.001
Parabacteroides	2.65	<0.001
Pseudobutyrivibrio	0.24	<0.001
Subdoligranulum	0.58	0.006
Coprococcus	0.65	0.027
Phascolarctobacterium	3.17	0.002
Anaerostipes	0.18	<0.001
Megamonas	2.24	0.028
Enterobacter	0.34	0.001
Dorea	0.35	<0.001
Bacillus	0.25	<0.001
Klebsiella	0.60	<0.001
Lactobacillus	4.62	0.002
Bifidobacterium	0.27	<0.001
Sutterella	1.38	0.016
Paraprevotella	3.32	0.016
Carnobacterium	14.52	<0.001
Candidatus_Nitrososphaera	2.22	0.010
Anaerotruncus	2.28	0.023
Butyricimonas	2.04	0.033
Bilophila	1.23	0.040
Desulfovibrio	2.29	0.016
Odoribacter	2.08	0.039
Acinetobacter	2.71	<0.001
Anderseniella	2.22	0.007
Serratia	0.69	0.033
Collinsella	0.53	0.032
Pseudomonas	1.88	0.007
Lactococcus	1.88	0.010
Weissella	4.99	0.002
Psychrobacter	10.21	<0.001
Burkholderia	0.62	0.043
Acidaminococcus	32.89	0.006
Massilia	0.30	0.012
Paenibacillus	0.21	<0.001
Vagococcus	8.07	<0.001
Macrococcus	8.04	0.004

Genus	Fold change (RA/control)	*p* value
Brochothrix	5.87	0.001
Raoultella	1.14	<0.001
Aeromonas	1.29	<0.001
Vibrio	0.43	0.012
Kluyvera	0.31	0.013
Cetobacterium	8.13	<0.001
Candidatus_Saccharimonas	0.25	<0.001
Staphylococcus	2.98	0.006
Caulobacter	13.07	<0.001
Clostridium_sensu_stricto_11	0.08	0.027
Myroides	9.11	<0.001
Chryseobacterium	2.75	<0.001
Paludibacter	5.60	0.041
Acidovorax	1.08	0.030
Shewanella	3.63	0.048
Ralstonia	0.19	<0.001
Stenotrophomonas	11.50	<0.001
Bosea	9.07	0.001
Gemella	0.72	0.015
Ochrobactrum	12.00	0.002
Sediminibacterium	0.10	<0.001
Alkaliphilus	0.32	0.009
Zoogloea	7.58	<0.001
RC9_gut_group	0.23	0.021
Cedecea	8.22	<0.001
Oscillospira	3.39	0.024
Longilinea	1.14	0.044
Aerococcus	6.33	0.001
Cronobacter	0.07	<0.001
Methylocaldum	12.75	0.003
Victivallis	2.60	0.002
Opitutus	0.11	0.026
Rahnella	13.00	0.003
Caldithrix	4.43	0.008
Lysinibacillus	0.44	0.025
Albidiferax	15.00	0.001
Microbacterium	6.25	0.002
Luteimonas	8.00	0.024
Pleomorphomonas	0.86	0.039
Buttiauxella	0.36	0.041
Solibacillus	0.07	0.002
Brevibacillus	0.09	0.002