

Supplementary Figure legends

Fig.S1 Scatter plots for the causal association between 18 bacterial traits and GC.

(A) GCST90027571, “PWY.6147:6-hydroxymethyl dihydropterin diphosphate biosynthesis I”; (B) GCST90027510, “POLYAMSYN.PWY:superpathway of polyamine biosynthesis I”; (C) GCST90027629, “PWY_ARG.POLYAMINE.SYN:superpathway of arginine and polyamine biosynthesis”; (D) GCST90027552, “PWY.5659: GDP mannose biosynthesis”; (E) GCST90027726, “g_Oxalobacter”; (F) GCST90027602, “PWY.6897: thiamin salvage II”; (G) GCST90027781, “s_Alistipes_sp_AP11”; (H) GCST90027681, “f_Oxalobacteraceae”; (I) GCST90027810, “s_Oxalobacter_formigenes”; (J) GCST90027733, “g_Haemophilus”; (K) GCST90027576, “PWY.6284:superpathway of unsaturated fatty acids biosynthesis(E.coli)”; (L) GCST90027450, “ARO.PWY:chorismate biosynthesis I”; (M) GCST90027618, “PWY.724:superpathway of L lysine, L threonine and L methionine biosynthesis II”; (N) GCST90027646, “TRNA.CHARGING.PWY:tRNA.charging”; (O) GCST90027743, “o_Burkholderiales”; (P) GCST90027664, “f_Bacteroidaceae”; (Q) GCST90027843, “s_Coproccoccus_catus”; (R) GCST90027816, “s_Escherichia_coli”.

Fig.S2 Forest plot of the causal effect of 18 bacterial traits on GC.

(A) GCST90027571, “PWY.6147:6-hydroxymethyl dihydropterin diphosphate biosynthesis I”; (B) GCST90027510, “POLYAMSYN.PWY:superpathway of polyamine biosynthesis I”; (C) GCST90027629, “PWY_ARG.POLYAMINE.SYN:superpathway of arginine and polyamine biosynthesis”; (D) GCST90027552, “PWY.5659: GDP mannose biosynthesis”; (E) GCST90027726, “g_Oxalobacter”; (F) GCST90027602, “PWY.6897: thiamin salvage II”; (G) GCST90027781, “s_Alistipes_sp_AP11”; (H) GCST90027681, “f_Oxalobacteraceae”; (I) GCST90027810,

“s_Oxalobacter_formigenes”; (J) GCST90027733, “g_Haemophilus”; (K) GCST90027576,
 “PWY.6284:superpathway of unsaturated fatty acids biosynthesis(E.coli)”; (L) GCST90027450,
 “ARO.PWY:chorismate biosynthesis I”; (M) GCST90027618, “PWY.724:superpathway of L lysine, L
 threonine and L methionine biosynthesis II”; (N) GCST90027646,
 “TRNA.CHARGING.PWY:tRNA.charging”; (O) GCST90027743, “o_Burkholderiales”; (P)
 GCST90027664, “f_Bacteroidaceae”; (Q) GCST90027843, “s_Coproccoccus_catus”; (R)
 GCST90027816, “s_Escherichia_coli”.

Fig.S3 Funnel plot of the causal effect of 18 bacterial traits on GC.

(A) GCST90027571, “PWY.6147:6-hydroxymethyl dihydropterin diphosphate biosynthesis I”; (B)
 GCST90027510, “POLYAMSYN.PWY:superpathway of polyamine biosynthesis I”; (C)
 GCST90027629, “PWY_ARG.POLYAMINE.SYN:superpathway of arginine and polyamine
 biosynthesis”; (D) GCST90027552, “PWY.5659: GDP mannose biosynthesis”; (E) GCST90027726,
 “g_Oxalobacter”; (F) GCST90027602, “PWY.6897: thiamin salvage II”; (G) GCST90027781,
 “s_Alistipes_sp_AP11”; (H) GCST90027681, “f_Oxalobacteraceae”; (I) GCST90027810,
 “s_Oxalobacter_formigenes”; (J) GCST90027733, “g_Haemophilus”; (K) GCST90027576,
 “PWY.6284:superpathway of unsaturated fatty acids biosynthesis(E.coli)”; (L) GCST90027450,
 “ARO.PWY:chorismate biosynthesis I”; (M) GCST90027618, “PWY.724:superpathway of L lysine, L
 threonine and L methionine biosynthesis II”; (N) GCST90027646,
 “TRNA.CHARGING.PWY:tRNA.charging”; (O) GCST90027743, “o_Burkholderiales”; (P)
 GCST90027664, “f_Bacteroidaceae”; (Q) GCST90027843, “s_Coproccoccus_catus”; (R)
 GCST90027816, “s_Escherichia_coli”.

Fig.S4 Leave-one-out plots for the causal association between 18 bacterial traits and GC.

(A) GCST90027571, “PWY.6147:6-hydroxymethyl dihydropterin diphosphate biosynthesis I”; (B) GCST90027510, “POLYAMSYN.PWY:superpathway of polyamine biosynthesis I”; (C) GCST90027629, “PWY_ARG.POLYAMINE.SYN:superpathway of arginine and polyamine biosynthesis”; (D) GCST90027552, “PWY.5659: GDP mannose biosynthesis”; (E) GCST90027726, “g_Oxalobacter”; (F) GCST90027602, “PWY.6897: thiamin salvage II”; (G) GCST90027781, “s_Alistipes_sp_AP11”; (H) GCST90027681, “f_Oxalobacteraceae”; (I) GCST90027810, “s_Oxalobacter_formigenes”; (J) GCST90027733, “g_Haemophilus”; (K) GCST90027576, “PWY.6284:superpathway of unsaturated fatty acids biosynthesis(E.coli)”; (L) GCST90027450, “ARO.PWY:chorismate biosynthesis I”; (M) GCST90027618, “PWY.724:superpathway of L lysine, L threonine and L methionine biosynthesis II”; (N) GCST90027646, “TRNA.CHARGING.PWY:tRNA.charging”; (O) GCST90027743, “o_Burkholderiales”; (P) GCST90027664, “f_Bacteroidaceae”; (Q) GCST90027843, “s_Coproccoccus_catus”; (R) GCST90027816, “s_Escherichia_coli”.

Fig.S5 MR analyses show causal effects between 16 immune cell traits and GC.

(A) Forest plot for the causal effect of 16 immune cell traits on GC via IVW method,
 (B) The name of the immune cell associated with the risk of GC, and the name of the gut microbiota that regulates that immune cell.

Fig.S6 Forest plots showed the causal associations between 12 bacterial traits and 16 immune cell traits by using different methods.

The names of immune cells associated with the risk of GC, as well as the names of the gut microbiota that regulate this immune cell, were shown in Figure 5.

Fig.S7 Scatter plots for the causal association between 12 bacterial traits and 16 immune cell

traits.

Fig.S8 Forest plot of the causal effect of 12 bacterial traits on 16 immune cell traits.

Fig.S9 Funnel plot of the causal effect of 12 bacterial traits on 16 immune cell traits.

Fig.S10 Leave-one-out plots for the causal association between 12 bacterial traits and 16 immune cell traits.

Fig.S11 Forest plots showed the causal associations between 16 immune cell traits and GC by using different methods.

Fig.S12 Scatter plots for the causal association between 16 immune cell traits and GC.

Fig.S13 Forest plot of the causal effect of 16 immune cell traits on GC.

Fig.S14 Funnel plot of the causal effect of 16 immune cell traits on GC.

Fig.S15 Leave-one-out plots for the causal association between 16 immune cell traits and GC.