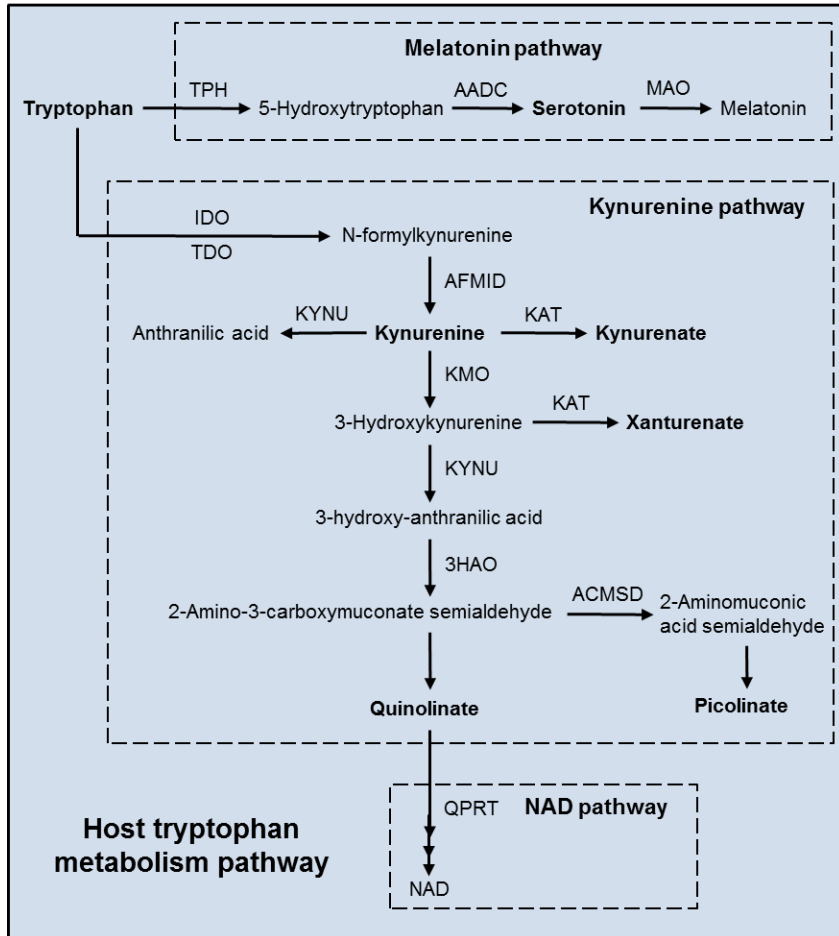


Supplemental Figures

Figure S1 Host and microbial tryptophan metabolism pathways

A total of 11 tryptophan metabolites (in **Bold**) were measured in this study. This figure was adapted from Polyzos et al.¹, Badawy et al.², and Roager et al.³.



Host enzymes

AADC, Aromatic amino acid decarboxylase
 ACMSD, 2-amino-3-carboxymuconate semialdehyde decarboxylase
 AFMID, Kynurenine formamidase
 CYP2E1, Cytochrome P450 2E1
 3HAO, 3-hydroxyanthranilic acid oxygenase
 IDO, Indoleamine-2,3-dioxygenase
 KAT, Kynurenine aminotransferase
 KMO, Kynurenine 3-hydroxylase
 KYNU, Kynureninase
 MAO, Monoamine oxidase
 QPRT, Quinolinic acid phosphoribosyl transferase
 SULT, Sulfotransferase
 TDO, Tryptophan-2,3-dioxygenase
 TPH, Tryptophan hydroxylase

Microbial enzymes

AAT, Aromatic amino acid aminotransferase
 ACD, Acyl-CoA dehydrogenase
 IAD, Indoleacetate decarboxylase
 IADH, Indoleacetaldehyde dehydrogenase
 IAH, Indoleacetamide hydrolase
 IAR, Indoleacetaldehyde reductase
 ID, Indolepyruvate decarboxylase
 ILD, Indolelactate dehydratase
 ILDH, Indolelactate dehydrogenase
 TMO, Tryptophan monooxygenase
 TNA, Tryptophanase
 TRPD, Tryptophan decarboxylase

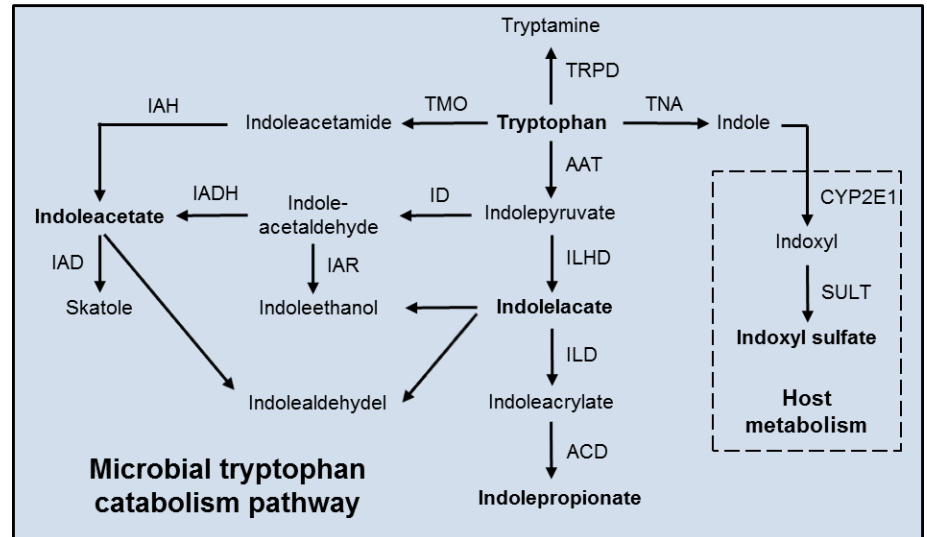


Figure S2 Correlation Heatmap among tryptophan metabolites

Data are partial Spearman correlation coefficients (r) among tryptophan metabolites in 2821 SOL participants free of diabetes at baseline, adjusted for age, sex and field center. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

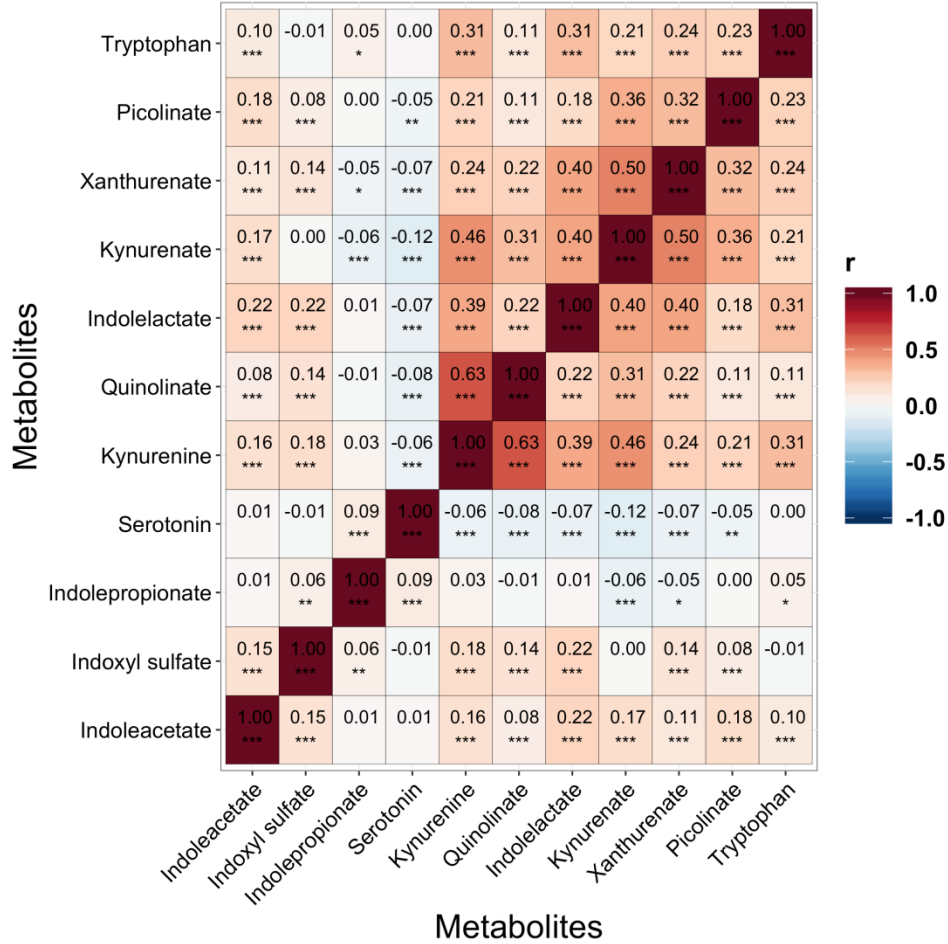


Figure S3 Correlation Heatmap between tryptophan metabolites and cardiometabolic traits
 Data are partial Spearman correlation coefficients (r) between tryptophan metabolites and cardiometabolic traits in 2821 SOL participants free of diabetes at baseline, adjusted for age, sex, field center, lipid-lowering medication use and anti-hypertensive medication use. Results were similar after excluding participants with lipid-lowering medication use or anti-hypertensive medication use (data not shown). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

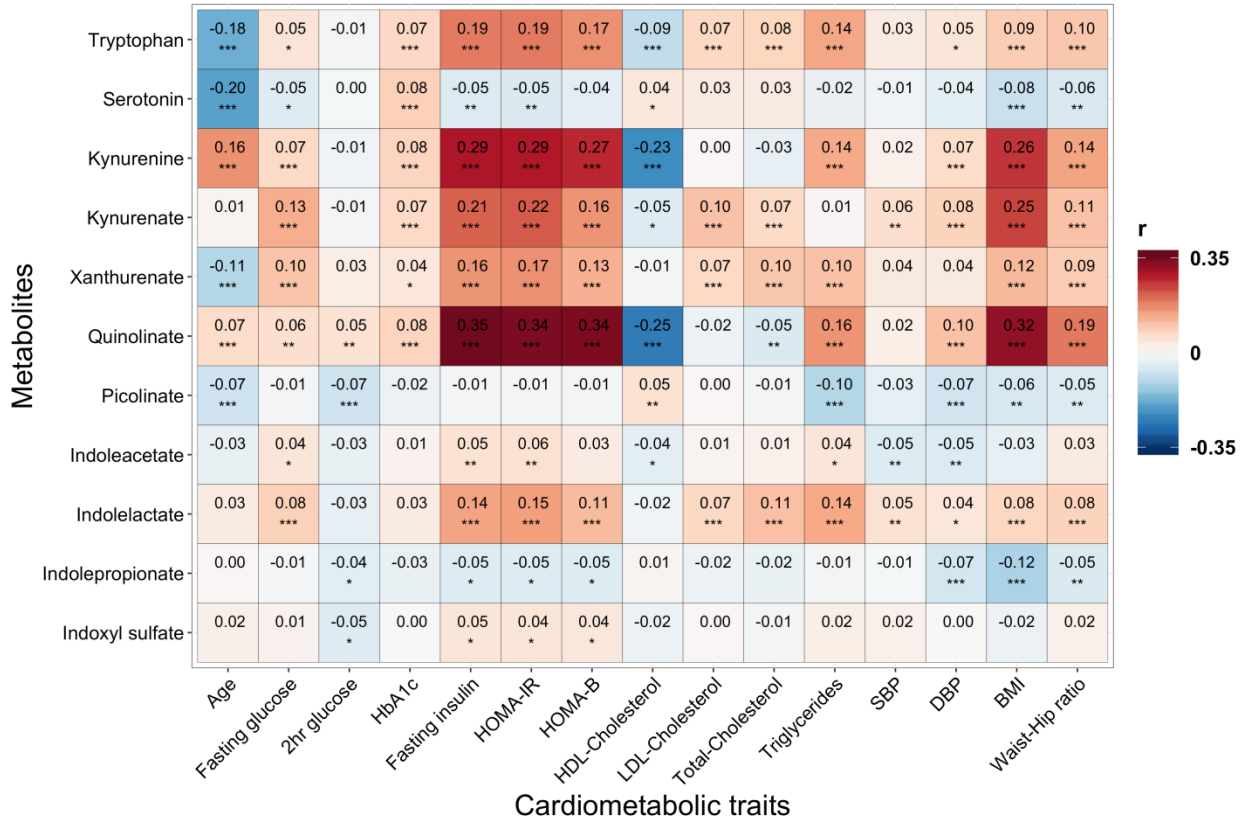
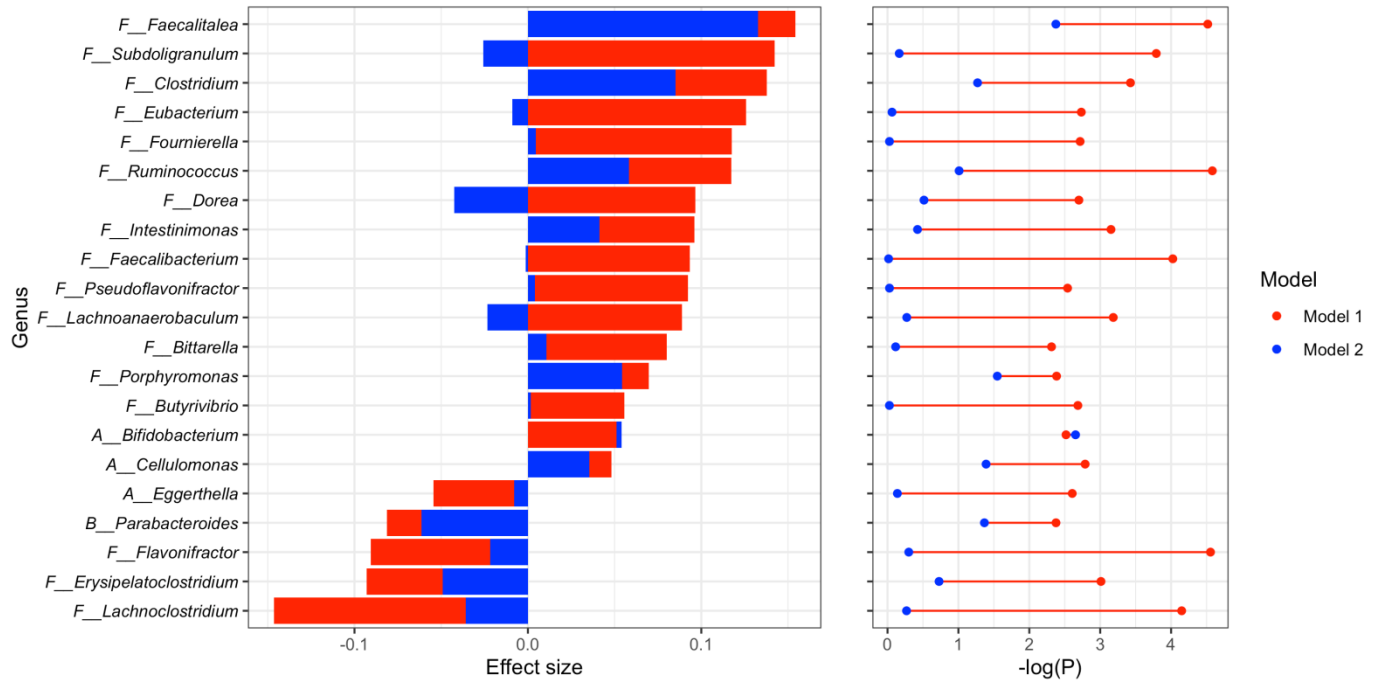


Figure S4 Associations of 22 gut bacterial genera and serum indolepropionate before and after mutual adjustment.

Model 1: adjusting for age, sex, study center, smoking, education, family income, physical activity, AHEI-2010, use of antibiotics, and use of probiotics;

Model 2 (mutual adjustment): further adjusting for other 21 bacterial genera based on Model 1 (all 22 bacterial genera were included in the model simultaneously).



References

1. Polyzos KA, Ketelhuth DF. The role of the kynurenine pathway of tryptophan metabolism in cardiovascular disease. An emerging field. *Hamostaseologie* 2015;35:128-36.
2. Badawy AA. Kynurenine Pathway of Tryptophan Metabolism: Regulatory and Functional Aspects. *Int J Tryptophan Res* 2017;10:1178646917691938.
3. Roager HM, Licht TR. Microbial tryptophan catabolites in health and disease. *Nat Commun* 2018;9:3294.