This study utilized the metabolite database from a highly comprehensive metabolite study for exposure assessment. A systematic two-sample MR analysis was employed, using the GECCO, CORECT, CCFR, and other European Cohorts' Genome-Wide Association Studies (GWAS) data as the phenotypic data for colorectal cancer\cite{1}. Ethical approval was obtained from the FinnGen steering committee for all selected genome-wide association studies GWASs in the FinnGen Consortium, and individuals provided written informed consent.