



**Figure S1.** Schematic representation of 2SMR analysis using Bonder microbiome and Trynka CeD GWASs as exposure and outcome datasets, respectively. **(a)** Flowchart of step-by-step analysis: after preparing exposure data (Step 1), outcome data is extracted (Step 2), both datasets are harmonized (Step 3), and 2SMR analysis is performed (Step 4). **(b)** Diagram, representing the number of SNPs selected in each category (taxa, pathway, GO) after performing each step of the analysis. **(c)** Venn-diagrams, illustrating the number of SNPs in harmonized datasets derived from Bonder vs. Dubois (orange) or Bonder vs. Trynka (purple) analyses.