**A graph showing different types of diabetes

AI-generated content may be incorrect.Figure 1. Two-sample forward MR results on Hughes et al. microbial traits and T2DM related outcomes.**

**Figure 1.** Abbreviations: AB = abundance; P/A = presence versus absence; HbA1c = Glycated Haemoglobin; MR = Mendelian randomization; T2DM = Type two diabetes Mellitus. Bracketed letters in the microbial trait name represent the taxon classification level from which that microbial trait was observed, with “C”, “F”, “G”, “O” and “P” representing “class”, “family”, “genus”, “order” and “phylum”, respectively. Some microbial traits are organised into ‘unclassified groups’ within higher classification levels. X-axis represents the effect estimates (Beta values – calculated using Wald ratio) and y-axis represents the strength of the association for microbial traits on T2DM (purple), fasting insulin (orange), glucose (pink), and HbA1c (green). Each point represents a microbial taxon tested (labelled with taxon name). The vertical dashed line represents the null (no effect).MR effect estimates for T2DM represent the log odds ratio for T2DM risk per SD higher relative abundance (for continuous microbial traits (labelled as “AB” in brackets)) or approximate doubling of the genetic liability to presence (versus absence) of each binary microbial trait (labelled as “P/A” in brackets). MR effect estimates for insulin, glucose and HbA1c represent the pmol/l(insulin), mmol/m(HbA1c), mmol/l (glucose) change in insulin/HbA1c/glucose respectively, per SD higher relative abundance (for continuous microbial traits (labelled as “AB” in brackets)) or approximate doubling of the genetic liability to presence vs. absence of binary microbial traits (labelled as “P/A” in brackets).

**Figure 2.** **Two-sample forward MR results on Kurilshikov et al. microbial traits and T2DM related outcomes.**

A diagram of a type of diabetes

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**Figure 2.** Abbreviations: AB = abundance; HbA1c = Glycated Haemoglobin; MR = Mendelian randomization; T2DM = Type two diabetes Mellitus; Inverse variance weighted =IVW. “class”, “family”, “genus”, “order” and “phylum”, in the microbial trait name represent the taxon classification level from which that microbial trait was observed respectively. All traits are measured as AB of microbe in the gut microbiome. X-axis represents the effect estimates (Beta values – calculated using Wald ratio and IVW) and y-Axis represents the strength of the association for microbial traits on T2DM (purple), fasting insulin (orange), glucose (pink), and HbA1c (green). Each point represents a microbial taxon tested (labelled with taxon name). The vertical dashed line represents the null (no effect). MR effect estimates for T2DM represent the log odds ratio for T2DM risk per SD higher relative abundance (for continuous microbial traits (“AB”)). MR effect estimates for insulin, glucose and HbA1c represent the pmol/l(insulin), mmol/m(HbA1c), mmol/l(glucose) change in insulin/HbA1c/glucose respectively, per SD higher relative abundance (for continuous microbial traits ( “AB” traits)).