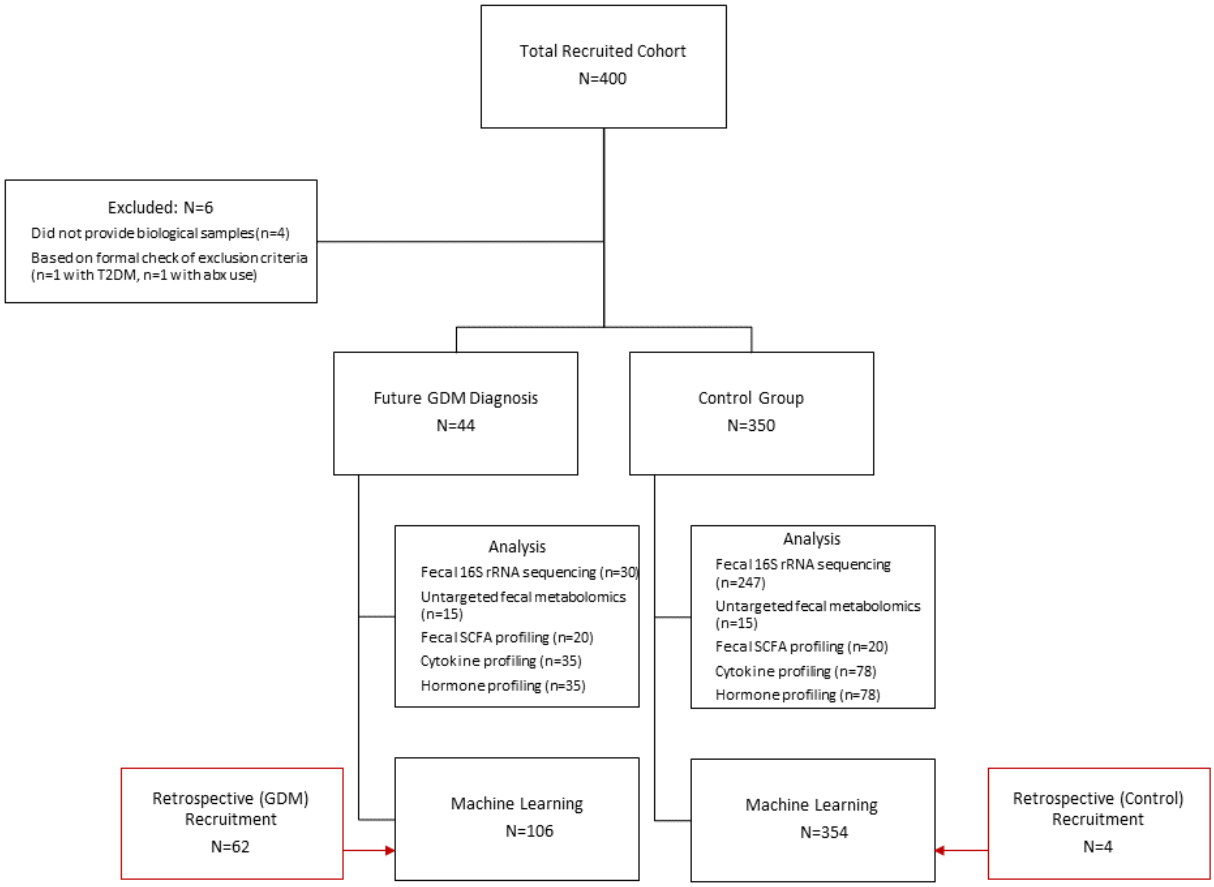
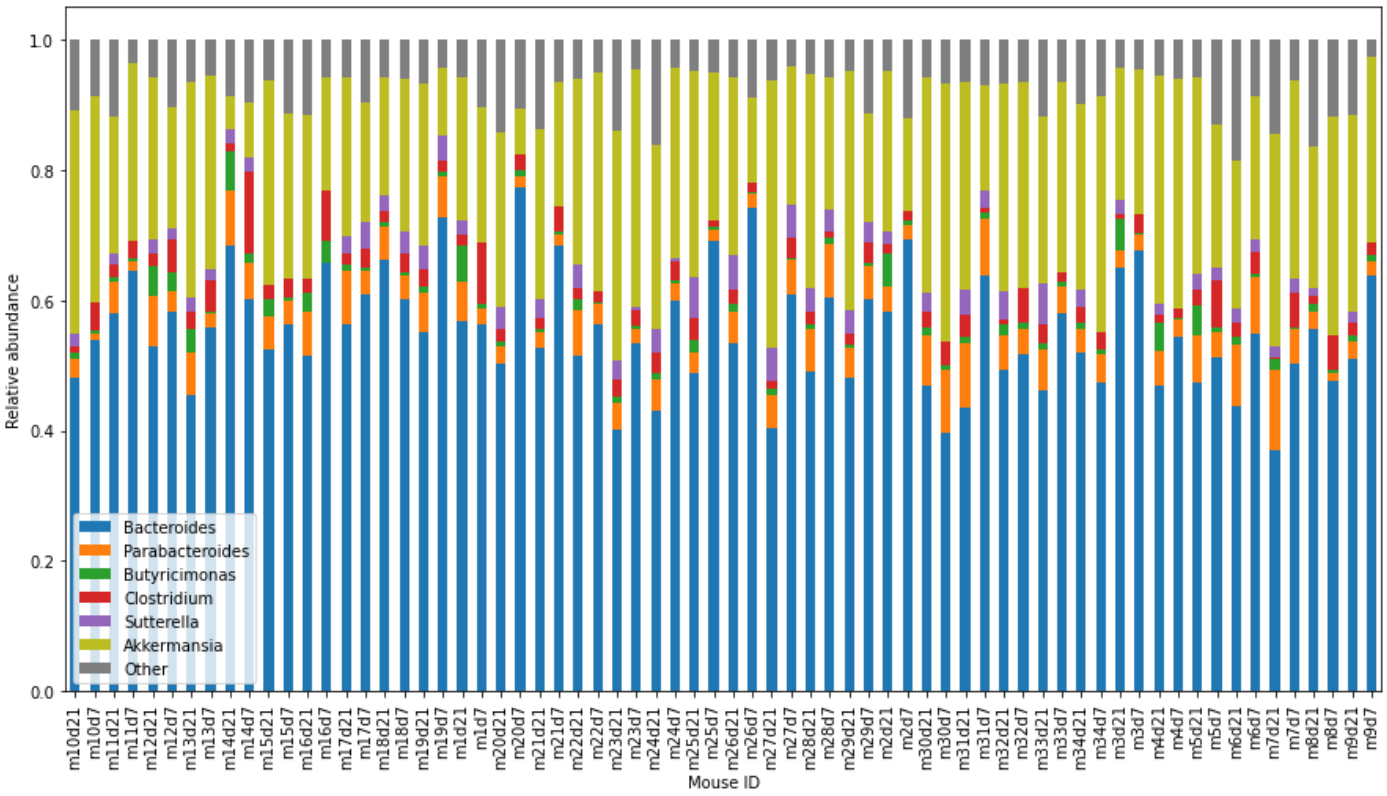
Supplementary Figures for

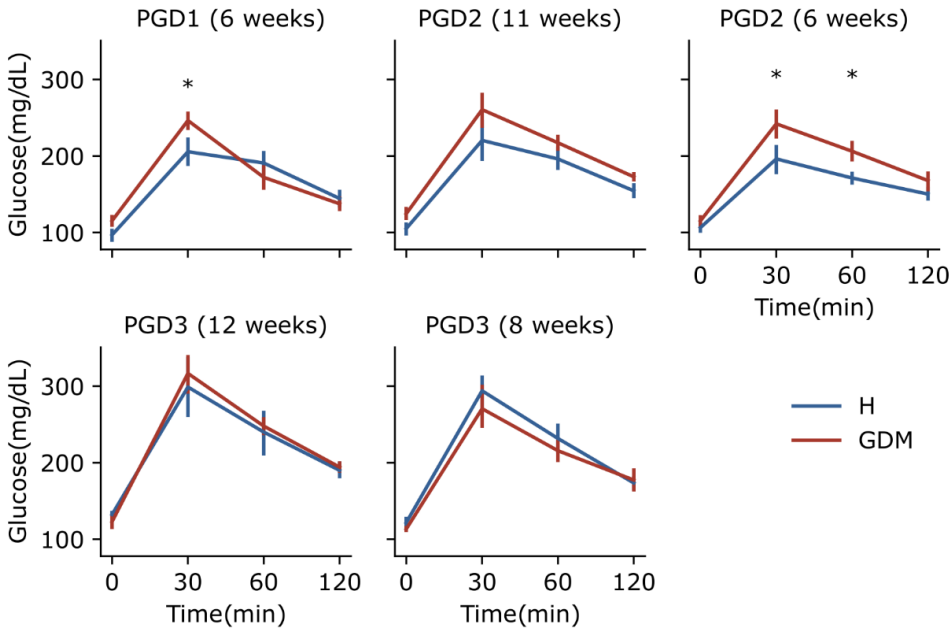
Gestational diabetes is driven by microbiota-induced inflammation months before diagnosis



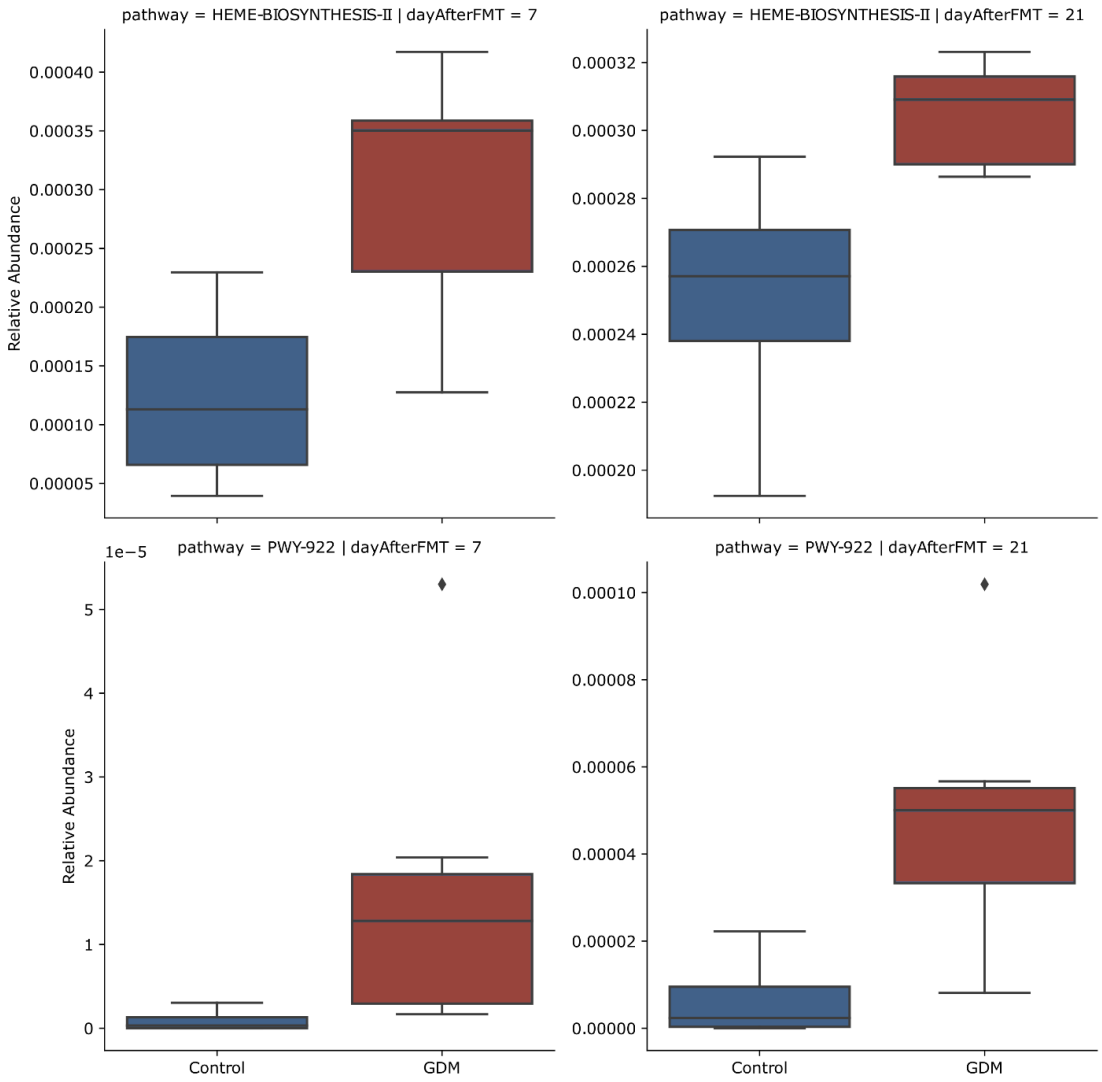
Supplementary Figure S1. The study design for the multi-omics and prediction modeling arms of this research. Initially, a Primary Cohort of 400 women was recruited prospectively and 394 were included in the study - 44 who would go on to develop GDM and 350 who would not (the "healthy control group"). To increase power in our predictive models, we recruited a Secondary Cohort retrospectively which included 62 women with GDM and 4 without. Clinical data from their first trimester of pregnancy was retroactively extracted from the medical records following their recruitment in their second trimester of pregnancy (after GDM status was already known).



Supplementary Figure S2. Relative abundances of transplanted mice at the genus level. Columns are labeled by the mouse number and day after transplantation (e.g. m1d7 is mouse number 1, 7 days post transplantation).



Supplementary Figure S3. intraperitoneal glucose tolerance test (ipGTT) exhibit impaired glucose sensitivity in mice transplanted with feces from GDM women in the Finnish cohort (upper row) and in the American STORK cohort (lower row). *p<0.05 Mann Whitney U test. Combined p=0.15, 0.022, 0.10, 0.24 for timepoints 0,30,60,120 minutes respectively, Fisher's method.



Supplementary Figure S4. Relative abundances of the MetaCyc heme pathway (up) and mevalonate pathway (down) as predicted by PICTUSt2 for the transplanted mice, 7 days post transplantation (left) or 21 days post transplantation (right). FDR corrected $p<0.05$, linear mixed model (see methods).