

Supplementary information

The vaginal microbiome of pregnant women is less rich and diverse, with lower prevalence of Mollicutes, compared to non-pregnant women

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Supplementary Methods

Comparison between microbiological and demographic characteristics of the pregnant cohort.

Microbiological and demographic characteristics were compared to CST (I, II, III, IVC, IVD, V), presence of Mollicutes (yes/no) and *Ureaplasma* (yes/no), microbiome richness (continuous variable) and diversity (continuous variable). Each of these five observations were compared to the following metadata: Nugent score category (BV-, intermediate BV, BV+), 16S RNA gene copy number ($<10^4$, 10^5 - 10^6 , 10^7 - 10^8 , $>10^9$), maternal age (18-25, 26-35, 36-45), maternal age (18-35, 35-45), BMI category (underweight, normal, overweight, obese), BMI (<25 , ≥ 25), ethnicity (White, East Asian, South Asian, Black, Hispanic, Other), ethnicity (White, East Asian, South Asian, Other), ethnicity (White, Asian, Other), natural conception (yes/no), folic acid intake before conception (yes/no), folic acid intake during pregnancy (yes/no), vitamins before

conception (yes/no), vitamins during pregnancy (yes/no), unprotected sex in the past 4 days (yes/no), parity (0-6), parity (0, >1), pre-existing conditions (yes/no), surgeries in the past 10 years (yes/no), smoking (yes/no), drinking alcohol (yes/no), antibiotics at enrolment (yes/no), gestational age at delivery (<37, ≥37), mode of delivery (vaginal, C-section), mode of delivery (vaginal, C-section, C-section-elective), fetal sex (male, female), neonate in level 2 care nursery (yes/no), birth weight (continuous variable) and Apgar score at 5 minutes (0-9).

Supplementary Table S1 (.xls)

Summary of OTU analyzed in this study. Best database match, percentage of identity, cpnDB name, taxonomic lineage and abundance in each library are shown.