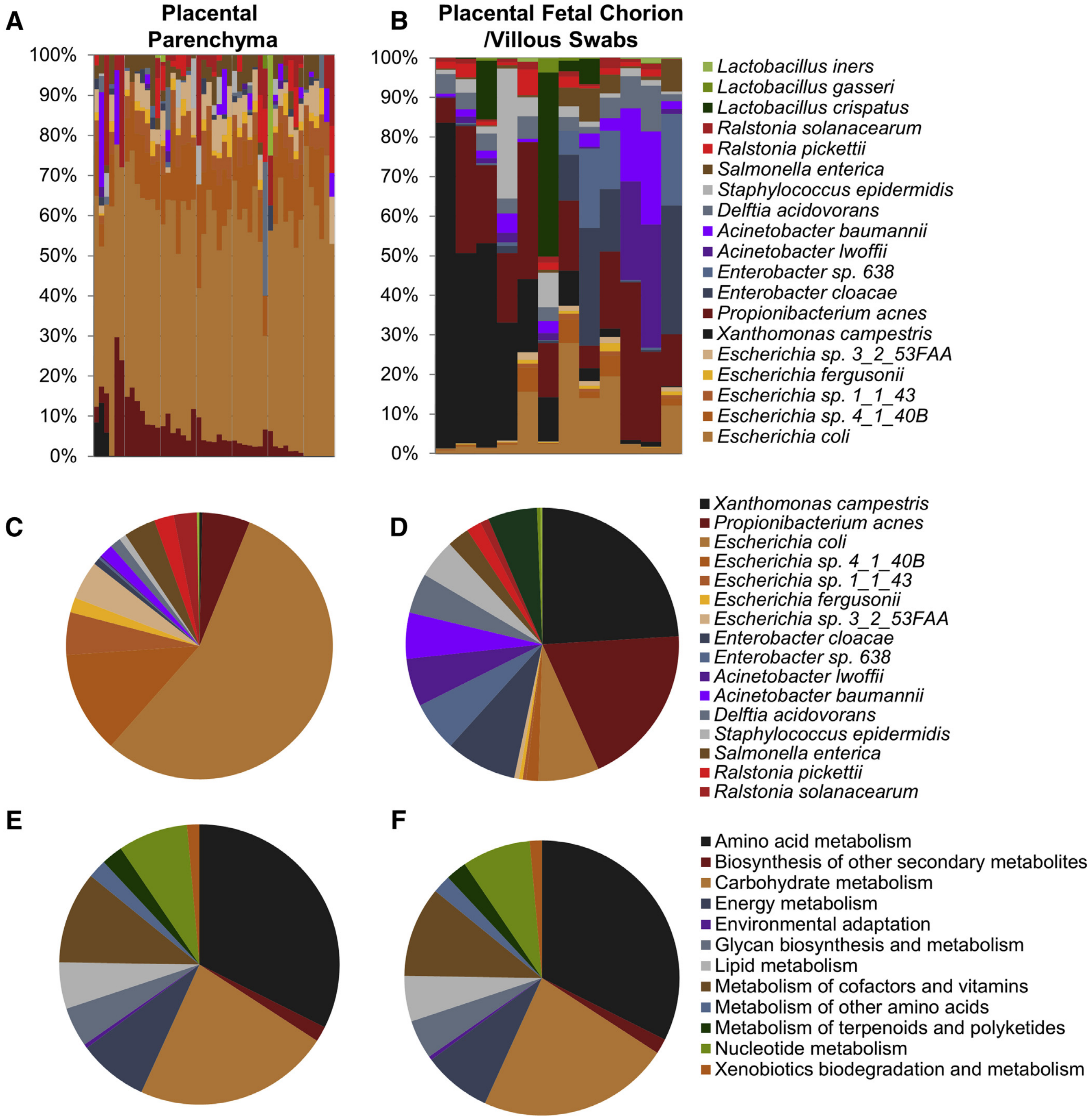
SUPPLEMENTAL FIGURE 1

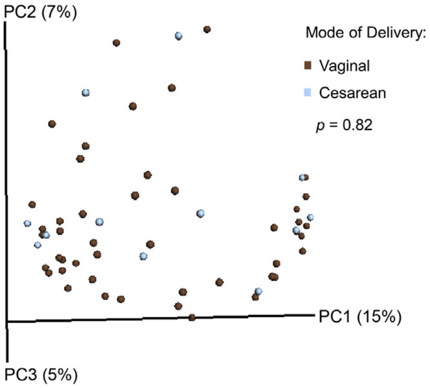
Niche specificity of the placental microbiome



A—D, Bacterial taxa and **E—F,** metabolic pathways were compared between our previous cohort examining the placental parenchyma microbiome and our current study examining the placental membrane microbiome. **A,** When examining individual subjects, we find that the placental parenchyma microbiome has a high abundance of *Escherichia coli*. **B,** Although the placental membrane microbiome also had a high abundance of *E. coli*, *Xanthamonas campestris, Propionibacterium acnes*, and *Lactobacillus* species also were highly prevalent in the placental membrane microbiome. **C—D,** Overall abundance comparison of pie charts reflects similar results to individual bar plots in **A—B**. **E—F,** Despite some differences in overall bacterial taxa, inferred metabolic pathways are remarkably similar between the 2 placental sites.

Prince et al. Placental microbiota and their metabolic pathways in PTB and chorioamnionitis. Am J Obstet Gynecol 2016.

SUPPLEMENTAL FIGURE 2
Beta diversity of subjects cluster independent from mode of delivery



PCoA plot of all subjects (both term and preterm) demonstrate that clustering of beta diversity is independent of mode of delivery ($P = .82$ by PERMANOVA, *brown*: vaginal delivery, *blue*: cesarean delivery).

PCoA, principal coordinates analysis; *PERMANOVA*, permutational multivariate analysis of variance.

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