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## Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding

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### AUTHOR CONTRIBUTIONS

M.G.D.B. designed the study.

M.G.D.B., S.J.S., J.W., P.R.H., C.D.H., N.H., E.A., D.N., C.G., V.M., W.S., M.J., J.C., H.S., M.C.C., I.G.M, F.G.R., J.I.R.V., M.C.R., J.F.R.C., R.K. collected and processed specimens.

M.G.D.B., R.K. sequenced and generated data.

M.G.D.B., S.J.S., J.W., C.M., L.J., W.K.T., L.S., D.McD., R.K. analyzed data including performing, and overseeing the bioinformatic and statistical analyses.

M.G.D.B. and R.K. have unrestricted access to all data.

M.G.D.B. S.J.S. and R.K. drafted the manuscript.

All authors reviewed, agreed to submit the final manuscript, read and approved the final draft and take full responsibility of its contents, including the accuracy of the data and the fidelity of the trial to the registered protocol and its statistical analyses.

### DECLARATION OF INTEREST

New York University has a U.S. patent (number 10357521) on behalf of M.G.D.B., related to methods for restoring the microbiota of newborns.

### INCLUSION AND DIVERSITY STATEMENT

We worked to ensure that the study questionnaires were prepared in an inclusive way. One or more of the authors of this paper self-identifies as an underrepresented ethnic minority in science. The author list of this paper includes contributors from the location where the research was conducted who participated in the data collection, design, analysis, and/or interpretation of the work.

### SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/xxx>

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## SUMMARY

**Background:** Early microbiota perturbations are associated with disorders that involve immunological underpinnings. Cesarean section (CS)-born babies show altered microbiota development in relation to babies born vaginally. Here we present the first statistically powered longitudinal study to determine the effect of restoring exposure to maternal vaginal fluids after CS birth.

**Methods:** Using *16S rRNA* gene sequencing, we followed the microbial trajectories of multiple body sites in 177 babies over the first year of life; 98 were born vaginally and 79 were born by CS, of which 30 were swabbed with a maternal vaginal gauze right after birth.

**Findings:** Compositional tensor factorization analysis confirmed that microbiota trajectories of exposed CS-born babies aligned closer to that of vaginally born babies. Interestingly, the majority of amplicon sequence variants from maternal vaginal microbiomes on the day of birth were shared with other maternal sites, in contrast to non-pregnant women from the HMP study.

**Conclusions:** The results of this observational study prompt the urgent need of randomized clinical trials to test whether microbial restoration reduces the increased disease risk associated with CS birth, and the underlying mechanisms. Also, it provides evidence for the pluripotential nature of maternal vaginal fluids to provide pioneer bacterial colonizers for the newborn body sites. This is the first study showing long term naturalization of the microbiota of CS-born infants by restoring microbial exposure at birth.

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### eTOC blurb

C-section alters the maturation of the infant microbiota. Song et al. show that restoring maternal microbes immediately after birth in Cesarean-born infants naturalizes their microbiota developmental trajectory. Perinatally, the maternal vaginal fluids appear pluripotential to provide pioneer bacterial colonizers for the newborn body sites.

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## INTRODUCTION

Over the past few decades, we have learned a great deal about the multitude of ways that microbiota affect the development of their hosts. Studies on model organisms show that fetal development can be modulated by microbial products from the pregnant mother's microbiota, and early colonization is critical for immune system development<sup>1,2</sup>.

Natural transmission and colonization of maternal microbes is impaired by delivery via Cesarean section (CS)<sup>3-7</sup>. Furthermore, CS birth is associated with reduced levels of various cytokines and their receptors<sup>8</sup>, increased risk of opportunistic neonatal infections<sup>6</sup>, immune diseases<sup>9,10</sup> and obesity<sup>11,12</sup>. These associations have been shown to be causal in mouse models for conditions such as obesity<sup>13,14</sup>, and immune disorders<sup>15,16</sup>. Neuroendocrine abnormalities including cognitive and behavioral disorders have also been associated with early microbiome perturbations<sup>17,18</sup>. Understanding the contribution of microbionts to healthy development remains a crucial challenge to address the current epidemic of immune and metabolic diseases in urban societies.

Although used without medical indication in many countries, CS delivery is often medically necessary and a life-saving procedure, and thus, restoration may be one solution to help reduce the risk of associated disorders related to the microbiome. Two proof of concept studies have demonstrated the principle of engraftment of maternal bacteria on CS born babies after deliberate microbial exposure: the first one by Dominguez-Bello et al. using maternal vaginal gauze as a source<sup>19</sup>, and the second recent pilot study by Korpela et al.

using maternal feces<sup>20</sup>. Here we present the first large observational study of the long-term effect of maternal vaginal seeding after CS delivery to restore microbial development during the first year of life.

## RESULTS

### Vaginal seeding of CS born infants

A total of 177 infants born to 174 mothers were studied (Figure S1a), of which 101 were born in USA, 50 in Chile, 6 in Bolivia, and 20 in Spain (Table 1). 98 infants were born vaginally and 79 were delivered by CS, of which 30, who complied with inclusion criteria (see Star Methods), were swabbed with a maternal vaginal gauze at birth (vaginal seeding<sup>19</sup>). The microbiota development was followed during the first year of life. A total of 8,104 samples from stool, mouth, and skin of infants and their mothers were obtained, with additional nasal and vaginal samples from mothers (Figure S1a–c). None of the seeded infants had any complications, and all children developed normally during the 12 months of the study.

### Vaginal seeding partly normalizes microbiome trajectories in C-section-delivered infants

Across the different body sites, the samples yielded good overall sequencing depth (mean depth of 63,035 paired-end reads per sample), with a low probability of sample contamination as indicated by a survey of negative controls (Figure S1d). Analysis of the vaginal gauzes stored in the vagina for an hour before the CS procedure with which the neonates were swabbed showed that ~76% of bacterial amplicon sequence variants (ASVs, see Star Methods) contained in maternal vaginal swabs were also present in the gauzes (Figure S2a).

Some studies have reported decreased alpha diversity in CS born versus vaginally-born infants<sup>21</sup><https://paperpile.com/c/vcRyUI/OTkm>. Yet, others have reported no differences by birth mode<sup>4,5</sup>. Using a linear mixed-effects model, we found inconsistent results depending on the body site and alpha-diversity metric (Supplementary Methods S1). One possibility for this inconsistency is that the dynamic nature of the developing microbiome can be highly non-linear, and often times, data collected longitudinally vary in frequency and timing across individuals. To account for these potential irregularities we applied a novel method called Bayesian Sparse Functional Principal Components Analysis (SFPCA; Jiang et al.<sup>22</sup> to estimate individual trajectories (see STAR Methods). Using SFPCA, we found that alpha diversity trajectories did not differ among birth modes when measured as Shannon diversity (Figure S3), or when accounting for phylogenetic relatedness (SFPCA on Faith's PD, data not shown).

However, significant birth group differences were found in beta diversity when using an unsupervised dimensionality reduction method called Compositional Tensor Factorization (CTF)<sup>23</sup>. CTF accounts for the repeated measurements allowing comparisons of beta-diversity over time ('trajectory') while accounting for the sparse, compositional nature of next-generation microbiome sequencing data<sup>24,25</sup>. The trajectory of gut microbiota development in CS born infants diverged from that of vaginally born infants through the

entire first year of life (Figure 1). These results are consistent with findings from previous studies that used more traditional analysis approaches<sup>4,5</sup>. CTF also detected measurable differences in the microbial development of the mouth (Figure 2) and skin (Figure 3), underscoring the importance of birth mode in affecting multiple microbial niches during human development.

Seeding CS-born infants led to a developmental trajectory that more closely resembled that of vaginally-born infants most prominently in feces (Figure 1, S4a,b) and skin (Figure 3, S4a,b); this trend held when considering only the 101 babies born in the US (Figure S4c), while other countries lacked sufficient sample size for individual analysis. Furthermore, a stepwise redundancy analysis based on the first three principal components of CTF ordination<sup>26</sup> confirmed that birth mode significantly contributed to differences in microbial community structures in the gut and on skin, but not in the mouth, with effect sizes of 0.17 ( $R^2$ ) in fecal samples and 0.09 in skin samples (Supplementary Methods S2). Analyzing these data using more conventional tools for comparing beta diversity that do not account for interindividual variation in repeated measure studies (Supplementary Methods S3–S4), evaluated through PERMANOVA (on unweighted Unifrac distance) or RDA (on PCoA PCs), expectedly reveals individuals as the primary driver of variation (PERMANOVA F-statistic = 5.45, P-value  $\leq$  0.001; RDA adjusted  $R^2$  = 0.113, Supplementary Methods S5). High interindividual variation obscured the ability to detect differences due to more muted factors such as birth mode using these methods. Together, these findings reveal that birth mode affects the development of microbial communities, and that this effect may be undetected upon analyses with traditional bioinformatic tools.

Differences in microbial composition stability have been used to differentiate phenotypes in longitudinal studies<sup>27,28</sup>. Accordingly, we next compared variability across samples over time within a given individual. To leverage the dense sampling design, we calculated the volume of the shape determined by an individual's samples in the first 3 principal coordinates of unweighted UniFrac space using a convex hull analysis (see STAR Methods). As expected, the average variability of the microbiome over an infant's first year of life was much greater than the variability in the mother's microbiome (Figure 1b, 2b, 3b). CS born infants had significantly greater microbial variability than vaginally born infants, and the variability of seeded infants was intermediate (Figure 1b, 2b, 3b, Supplementary Methods S6). This finding held true for fecal, oral and skin samples, suggesting that vaginal seeding may also help stabilize microbiome development. This trend can also be observed using data within the first 6 months (Supplementary Methods S7). Possible confounders such as antibiotic consumption (which was similar between baby groups; Table 1) were discarded; in the CS born and restored babies, stepwise RDA did not recognize antibiotic consumption as a factor altering seeding efficiency. In summary, these results indicate that vaginal seeding resulted in partial recovery of the microbiome in CS-delivered infants.

### **Bacterial taxa associated with effective seeding**

To determine whether specific microbial taxonomies were being seeded well or the overall seeding across all microbes was partial, we first identified which taxa were most associated with a vaginal birth compared to a CS birth using Songbird<sup>25</sup>, and then calculated a seeding-

effectiveness score for those taxa (see STAR Methods; zero indicates poor seeding and one indicates effective seeding or effectively suppressed). Effectively seeded microbes are those shared by vaginal and CS-seeded infants. Effectively suppressed microbes are those highly associated only with unseeded CS infants, indicating that seeding excludes that microbe. Many taxa highly associated with CS-seeded infants had a seeding effectiveness score greater than 0.8, indicating that the vaginal seeding method was able to establish microbes missing in CS born babies (Figure 1, 2, 3, c–e). Notably, in the infant gut, ASVs from common gut-associated genera such as *Bacteroides*, *Streptococcus*, and *Clostridium* were identified to be enriched in CS-seeded infants and have high seeding effectiveness scores in early time points (Figure 1 c–e, Supplementary Methods S8–S9). Especially of note, *Bacteroides* was consistently identified as being associated with vaginal seeding (Supplementary Methods S10) using other algorithms such as ANCOM (Supplementary Methods S11), MaAsLin2 (Supplementary Methods S12) and LEfSe (Supplementary Methods S13). In the mouth, bacteria with high seeding effectiveness scores included ASVs from *Gemellaceae*, *Haemophilus*, and *Streptococcus* (Figure 2 c–e). In the skin, taxa included ASVs from *Streptococcus*, *Neisseria*, *Thermus*, and *Neisseriaceae* (Figure 3 c–e). However, across all three body sites, most of the taxa associated with CS had a moderate to low seeding effectiveness score, indicating that this method was not effective at attenuating the presence of microbes typically depleted in vaginally born babies.

### Maternal sites contribute to the infant microbiota

In order to determine which body sites from the mother were most likely to have the highest contributions towards shaping the infant microbiome, we also used the source-tracking tool FEAST<sup>29</sup>. The first 2 days of life showed a prominent maternal vaginal source in the oral and skin sites of infants exposed to vaginal fluids; however, within the first few days, a large proportion of the microbiota colonizing the infants' sites was shared with the corresponding maternal site, regardless of birth mode or seeding status (Figure 4). Selection by the specific body site was evidenced by the lack of overrepresentation of *Lactobacillus*, a dominant member of the mother's vagina, among infants born vaginally or exposed to the vaginal gauze when compared to CS-born babies. Unsurprisingly, we found that the infant oral microbiota most resembled that of the mother's mouth and areola (Figure 4 h, k), and that the infant skin microbiota resembled that of the mother's skin (Figure 4 o), consistent with exposure patterns and differential selection exerted by different body sites in the baby.

Interestingly, we observed a notable taxonomic overlap between the maternal vagina and other maternal body sites, especially feces, on the day of giving birth: nearly 30% of the bacterial ASVs in vaginal samples were shared with feces (5.5% with feces alone, and 24.5% with feces and some other body sites), and 22.3% with more distant body sites such as arm skin, mouth, and nose (Figure 5 a, Supplementary Methods S14). These trends showing the pluripotent nature of the perinatal vaginal microbiome held true when examining the mothers in different countries from this study, despite variations in specific proportions (Figure S2b,c, Supplementary Methods S15). In contrast, women who are not pregnant -from the HMP study- shared less than 20% of vaginal ASVs with other body sites, predominantly with skin, and none with fecal samples (Figure 5 b). Together, these

results point to the importance of maternal sources of microbes on the developing infant consortium.

## DISCUSSION

This intervention study expands the findings of previous smaller studies, further demonstrating that microbial differences associated with delivery mode can be reduced by exposure to a vaginal microbial source at birth. The study only included scheduled C-sections on healthy mothers (mostly due to multiple previous C-sections and to malposition presentations), since infants born by emergency C-section after rupture of the chorioamniotic membrane are likely exposed the maternal microbes, given enough time before the C-section procedure<sup>30</sup>.

Using advanced and longitudinally-aware methods, we found that birth mode significantly differentiated infant gut and skin microbiome development, and that seeding worked to adjust the trajectory of CS-delivered infants through partial restoration of microbiome features associated with a vaginal delivery. For example, differential abundance analyses confirmed previous findings that in the gut, *Bacteroides* and *Parabacteroides*-- both common gut-associated taxa--are highly associated with vaginally born infants. Our study further shows that seeding works to effectively restore these and other taxa associated with a vaginal birth. However, there are several other taxa that do not appear to establish well in the seeded infants (e.g. *Bilophila*). Also of interest, while we observed a significant association of *Enterococcus* with CS-born infants (which in previous studies has been noted as a potential opportunistic pathogen), we did not see a weakened association of this taxon, or most other CS-associated taxa, with seeded babies. Further research is needed to determine why certain gut taxa may show a higher effectiveness for seeding while other taxa may exhibit more resilience after a seeding procedure, and what roles these microbes may play in the developing infant microbiome.

An interesting facet of our study is the finding that vaginal seeding led to converging microbial compositions in the infant gut, despite the exposure coming from a vaginal source. The same pattern was observed in the skin environment. Our results clearly indicate that from very early timepoints, the microbiota of an infant largely resembles the same maternal site, supporting the idea of strong site selection occurring from very early ages (i.e. that different body sites will select for specific microbes out of a diverse population). This is further supported by the finding that *Lactobacillaceae*, the most dominant member of the mother's vagina, was not identified as one of the most differentially abundant taxa among infants at any of the three body sites observed. Site selection is also consistent with the recent evidence of successful engraftment after fecal microbiota transplant from the mother to CS neonates<sup>31</sup>, and with previous evidence of fecal bacteria in the infant gut<sup>32,33</sup>. Indeed, bacterial transfer from homologous sites from the mother and other family members surely occur after birth. However, this may only be a part of the story. Our results show that unlike in non-pregnant women, more ASVs from the vaginal microbiome from parturient women overlap with those in other body sites, mostly the proximal rectum (which in mammals is next to the reproductive canal), but also more distant sites. This strongly suggests a pluripotent capacity of vaginal fluids to seed different sites of the baby's body.

Transmission and colonization by these pioneer species may then modulate the succession that proceeds, influencing engraftment of later colonizers to each body site<sup>34</sup>. Major changes in the vaginal microbiota during pregnancy have been described<sup>35</sup>, although the changes in the last semester have not been deeply characterized. This begs the question of whether the vaginal microbiome becomes specifically primed during pregnancy to deliver key pioneer colonizers tailored towards multiple body sites of the infant. This hypothesis is supported by previous work demonstrating the by-phasic dynamics in gestational changes in which after decreasing diversity in the first two thirds of gestation, in the last gestational trimester diversity increases at the expense of *Lactobacillus* from week 24 of pregnancy until birth<sup>36</sup>; increase in vaginal diversity continues in the postpartum vaginal tract for up to 1 year following birth<sup>37</sup>.

This study provides solid evidence that deliberate, early microbial seeding can help naturalize the microbiome developmental trajectory of CS born infants. While overall trajectories do appear to head towards convergence over time, studies show that early perturbations during the crucial developmental window of very early life seem to have irreversible consequences<sup>38–41</sup>. Restoring natural exposures at birth may thus be one way to reduce the risk of CS-associated diseases such as obesity, asthma, allergies, and immune disfunctions. However, randomized clinical trials on large cohorts are needed to gain conclusive evidence for microbial restoration at birth improving health outcomes<sup>42</sup>. Moreover, in light of recent research showing that oral administration of maternal fecal microbes is also effective in restoring the microbiome in CS-delivered infants<sup>20</sup>, future research investigating the effects of exposure to both sources explicitly compared to either single source will help determine the best routes to restoring the neonate microbiome. In this study we exposed infants to freshly collected maternal vaginal/perineal microbes, but it is unknown how storage would alter the microbiota composition. More research is needed to determine whether it is optimum that they receive their own mother's microbiome or achieve defined universal cocktails that can be used to restore neonates.

### Limitations of study

This study is limited by the cohort size, particularly in countries outside of the United States, the follow up time of the first year of life, since any longer-term consequences of seeding were not assessed, and by the *16S rDNA* amplicon sequencing, which excludes functional characterizations as well as fungi and viruses. Future studies capturing longer timeframes, larger and broader cultural and geographic representations, and additional data types are needed to gain a more understanding of how seeding affects the microbiome and ultimately the health of CS-delivered infants.

## STAR \* METHODS

### RESOURCE AVAILABILITY

**Lead Contact**—Further information and requests for resources and reagents should be directed to and will be fulfilled by Dr. Maria Gloria Dominguez-Bello, mg.dominguez-bello@rutgers.edu



**Materials Availability**—DNA or samples that are available upon request, as collaboration, subject to availability.

**Data and Code Availability**—Sequence data have been deposited at European Bioinformatics Institute (EBI) under study accession number ERP120105, ERP016173 and ERP120109. Any Supplementary Information and Source Data files are available in the online version of the paper. Source codes, tests and notebooks to generate the figures are available at <https://github.com/knightlab-analyses/seeding-study>.

## EXPERIMENTAL MODEL AND SUBJECT DETAILS

**Human subjects**—The study recruitment was conducted in the period 2017 to 2019, at participating centers in the mainland US, Puerto Rico, Chile, Spain, and Bolivia. Physician-assessed healthy mothers who were set to deliver vaginally or by scheduled CS were offered to participate in this study during a physician's visit. Inclusion criteria included healthy, non-obese mothers with no pregnancy complications. Mothers delivering vaginally included GBS positive subjects who received antibiotics during labor. Mothers scheduled to have a CS were divided into two groups based on their willingness to have their newborns swabbed with the gauze: seeded CS (CS-seeded) and unseeded CS (CS). The mothers in the CS groups had intact amniotic membranes at the time of delivery. For the CS-seeded group, mothers had to have negative results for standard-of-care tests for Group B Streptococcus (GBS, standard test at 36 weeks by culturing) and STDs (including HIV and Chlamydia), no signs of vaginosis or viral infections as determined by their obstetrician, and a vaginal pH<4.5 at 1–2 h preceding the procedure. The infants from this group received swabbing of a gauze soaked with maternal vaginal fluids for microbial restoration at birth. No mock gauze was applied to the unseeded CS babies. All mothers received standard-of-care treatment, including preventive perinatal antibiotics (Beta lactams: mostly Cephalosporins or Penicillin) for mothers who underwent CS section or for vaginally delivering GBS positive mothers (Table 1). The study was approved by the Institutional Review Boards from New York University School of Medicine (S14–00377), University of Puerto Rico Rio Piedras (1011–107) campus, Pontificia Universidad Católica de Chile (180814027), and Hospital Universitario y Politécnico La Fe, Spain (2015/0024), Universidad Mayor, Real y Pontificia de San Francisco Xavier de Chuquisaca, Bolivia (02/2014). Written informed consent was obtained from all participants. This research did not require authorization from the FDA or an equivalent regulatory organization.

## METHOD DETAILS

**Microbial restoration procedure**—Restoration procedures were the same in all participating centers. Within the hour prior to the procedure, maternal vaginal pH was measured using a sterile swab and a paper pH strip (Fisher). Once the pH was confirmed to be <4.5, an 8×8 cm four-layered gauze (Fisherbrand Cat # 22028558) was folded like a fan, and then in half, inserted in a tampon applicator and wet with sterile saline solution using a sterile Pasteur pipette. The gauze was inserted in the maternal vagina for one hour. Immediately before the CS surgery started, the gauze was extracted and placed in a sterile collector and kept at room temperature. As soon as the baby was brought to the neonate lamp and within 1 minute after delivery, the infant was swabbed with the gauze, starting on

the lips, followed by the face, thorax, arms, legs, genitals and anal region, and finally the back. The swabbing took approximately 15 seconds. The neonatologist then proceeded to perform the standard detailed examination of the newborn.

**Sample collection and processing**—Sampling with sterile swabs in different body sites took place within the first hours after birth in all babies (including the vaginal gauze exposed CS group, who were sampled after the gauze swabbing procedure), then at day 1–3, weekly for the first month and monthly up to the first year. Sampled body sites included oral mucosa, right arm region and feces of the baby, and the same sites of the mother plus nasal, right areola, vaginal swabs. All samples were transported to the laboratory with ice packs within two hours of collection and stored at  $-80^{\circ}\text{C}$  until further processing. Gauze samples for microbiota determination were obtained from one  $\text{cm}^2$  from the center of the gauze. Together with swabs and gauzes, 399 control blanks and 249 reagent blanks were included and processed.

**Sequencing and data processing**—DNA extraction, amplicon generation, and sequencing were performed as described in the protocols for the Earth Microbiome Project<sup>43,44</sup>. Briefly, DNA was from samples using the DNeasy PowerSoil HTP 96 Kit (<http://www.earthmicrobiome.org/emp-standard-protocols/dna-extraction-protocol/>), and the V4 region of the 16S rRNA gene was amplified using the 515f/806r primers and prepared for sequencing (<http://press.igsb.anl.gov/earthmicrobiome/protocols-and-standards/16s/>). Sequencing was performed at the University of Colorado Biofrontiers Sequencing Facility, New York University Genome Technology Center, or UC San Diego Institute for Genomic Medicine Genomics Facility using the Illumina MiSeq or HiSeq sequencing instrument. Raw reads were de-multiplexed and quality filtered using QIIME2 v2019.10 with default parameters<sup>45</sup>. Quality-filtered reads were clustered into amplicon sequence variants (ASVs) using deblur v1.1.0<sup>46</sup>. A phylogenetic tree was constructed through insertion<sup>47</sup> with the Greengenes v13\_8 as a reference backbone<sup>48</sup>.

Data used from the human microbiome project (HMP) included 16S rRNA gene sequence data from 105 women (Supplementary Methods S14) identified based on metadata provided in the HMP16SData R package<sup>49</sup>. Sequences, which spanned the of V3-V5 region of 16S rRNA gene, were downloaded, trimmed to the corresponding 100nt of the V4 region generated in the current study, and processed as described above.

**Bacterial source tracking**—To estimate the sources of the microbial communities observed in each of the three infant groups at different body sites and time points, we used FEAST<sup>29</sup>, based on expectation-maximization (EM) estimation, for bacterial source tracking. Samples from each body site in the infants were designated as sinks, and samples collected within the first month after birth from the vagina, stool, skin, mouth and nose of the corresponding mother were tagged as sources. The analysis was performed on rarified count tables with 5000 reads per sample with 1000 EM iterations.

**Alpha Diversity**—Shannon Diversity was calculated on rarified count tables with 5000 reads/sample using QIIME2 v2019.10<sup>45</sup>. The birth mode effect over time in Shannon diversity was analyzed initially using a linear mixed-effect model and then using a

novel longitudinal method, Bayesian Sparse Functional Principal Components Analysis (SFPCA)<sup>22</sup>. Generally, a functional principal components analysis is used to investigate longitudinal data with highly non-linear temporal trends<sup>50</sup>, and Bayesian SFPCA performs dimensionality reduction on longitudinal alpha diversity measurements to reveal changes in microbial diversity over time, estimating both mean trajectories, as well as subject-level variation around this mean. Bayesian SFPCA expresses repeated measurements from each baby in the form of a smooth function that represents the entire time course as a single observation, and then uses a reduced rank mixed-effects framework to handle scenarios where datapoints are collected at irregular and sparse time points. The final inference on birth mode effect is done based on the estimated weights that each baby receives on the first principal component function, which captures the different growth rates in alpha diversity among babies with different birth modes.

**Beta Diversity and Convex Hull**—The infant microbiome variability over time of infants for each birth mode were compared to the mothers through a calculation of the per subject convex hull volume from Principal Coordinates derived from unweighted UniFrac distances<sup>51</sup>. The convex hull is the volume produced by considering a set of points to define the outer surface of a shape (like stretching wrapping paper around those points), so a larger convex hull volume indicates greater variability across the set of samples around which the convex hull is built. The unweighted UniFrac distance was calculated on rarefied tables with 1000 reads/sample and dimensionality reduction on the distances was performed through Principal Coordinates Analysis (PCoA) for each body site. Per subject convex hull volume from the individuals' data points in each ordination using `scipy v1.3.1`<sup>52</sup>. The resulting volumes were assessed by body-site pairwise for statistical significance between mothers and infants of different birth modes with a Bonferroni corrected Mann-Whitney rank test using `scipy v1.3.1`<sup>52</sup>.

**Dimensionality reduction**—We used compositional tensor factorization (CTF) to produce a dimensionality reduction aware of the repeated measure structure of the longitudinal experimental design and the compositional nature of microbiome data<sup>23</sup>. To reduce sparsity data was split into two time periods being days 0–2 and 7–360 of life and subjects with more than two missing timepoints were removed. CTF was run on the filtered data through `gemelli v0.0.6` (<https://github.com/biocore/gemelli>) on default parameters. The resulting ordinations first principal component (i.e. Axis 1) was plotted for each sample type across time. To evaluate the statistical significance, a permutational multivariate analysis of variance (PERMANOVA)<sup>53</sup> was performed on the CTF based Aitchison distances<sup>54</sup> separately for each time point and sample type using `scikit-bio v0.5.5`. Bonferroni p-value correction was applied to each comparison with PERMANOVA to correct for multiple comparisons.

**Effect Size Analysis**—In order to calculate the relative effect size of all recorded metadata within the CTF ordinations, a stepwise redundancy analysis was performed (stepwise RDA). The stepwise analysis was performed on the first three principal components of the CTF sample ordination through the `ordistep` function in `vegan v2.4–2`<sup>55</sup>.

The ordiR2step function was run with 5000 permutation steps, with a permutation  $p$ -values limit of 0.1 and otherwise following the procedure of Falony et al.<sup>26</sup>.

**Differential Abundance and Effectiveness Score**—Differential abundance analysis was performed through Songbird at days 2, 30, and 180 on each infant body site (i.e. feces, mouth, and skin)<sup>25</sup>. Optimized model parameters were determined for each model with respect to the main factor of birth mode and the covariate of country by the cross-validation (CV) minimization. The models were then compared by a  $Q^2$ -value defined as  $1 - \text{model CV} / \text{baseline CV}$ . A positive  $Q^2$ -value was observed for all models indicating good predictive accuracy (Supplementary Methods S16). Differentials were obtained with the reference class as vaginal and contrast variables as CS and CS-seeded, producing the columns  $\log(\text{CS}/\text{Vaginal})$  and  $\log(\text{CS-seeded}/\text{Vaginal})$ . The differentials from Songbird in this contrast setup can give a rank of how much each ASV is associated with a contrast variable relative to the reference variable. For example, for  $\log(\text{CS}/\text{Vaginal})$ , positive valued ASVs are more associated with a CS birth and negative values with vaginal birth. However, in order to describe the probability of association of a given ASV relative to all three groups (vaginal, CS, CS-seeded), the inverse additive log-ratio (alr) transformation<sup>56</sup> was applied to the songbird differentials. We then defined a score for each microbe's "seeding effectiveness" as a measure of efficacy of seeding. We defined the score as

$$\text{seeding effectiveness} = \beta_{\text{vaginal}}^* - \beta_{\text{CS-seeded}}^* + \frac{\beta_{\text{CS}}^*}{1 + N_{\text{classes}}}$$

where the score can range from zero to one, with zero indicating the least effective seeding and one indicating the most effective seeding. Effectively seeded microbes would be those shared by vaginal and CS-seeded infants. Effectively seeded microbes can also be associated with only Caesarean infants, indicating that seeded infants no longer contained that microbe after seeding. Poorly seeded microbes would be those shared between CS and CS-seeded infants. Poorly seeded microbes can also be associated only with Vaginal birth indicating that seeding did not graft that microbe effectively.

The class probabilities were plotted as a ternary plot and colored by their 'seeding effectiveness' score (Figure 1, 2, 3 c–e). The differentials for Vaginal vs. Caesarean born infants were plotted at the genus taxonomic level for the top and bottom 20% of ASVs based on the centered songbird differentials and colored by the mean 'seeding effectiveness' score (Figure 1, 2, 3 c–e).

## QUANTIFICATION AND STATISTICAL ANALYSIS

Details on statistical tests,  $n$  numbers can be found in the figure legends and further details can be found in the method details for specific measurement.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

## ACKNOWLEDGMENTS

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## DATA AVAILABILITY

**Accession codes.** European Bioinformatics Institute (EBI): sequence data have been deposited under study accession number ERP120105, ERP016173 and ERP120109.

Note: Any Supplementary Information and Source Data files are available in the online version of the paper. Source codes, tests and notebooks to generate the figures are available at <https://github.com/knightlab-analyses/seeding-study>

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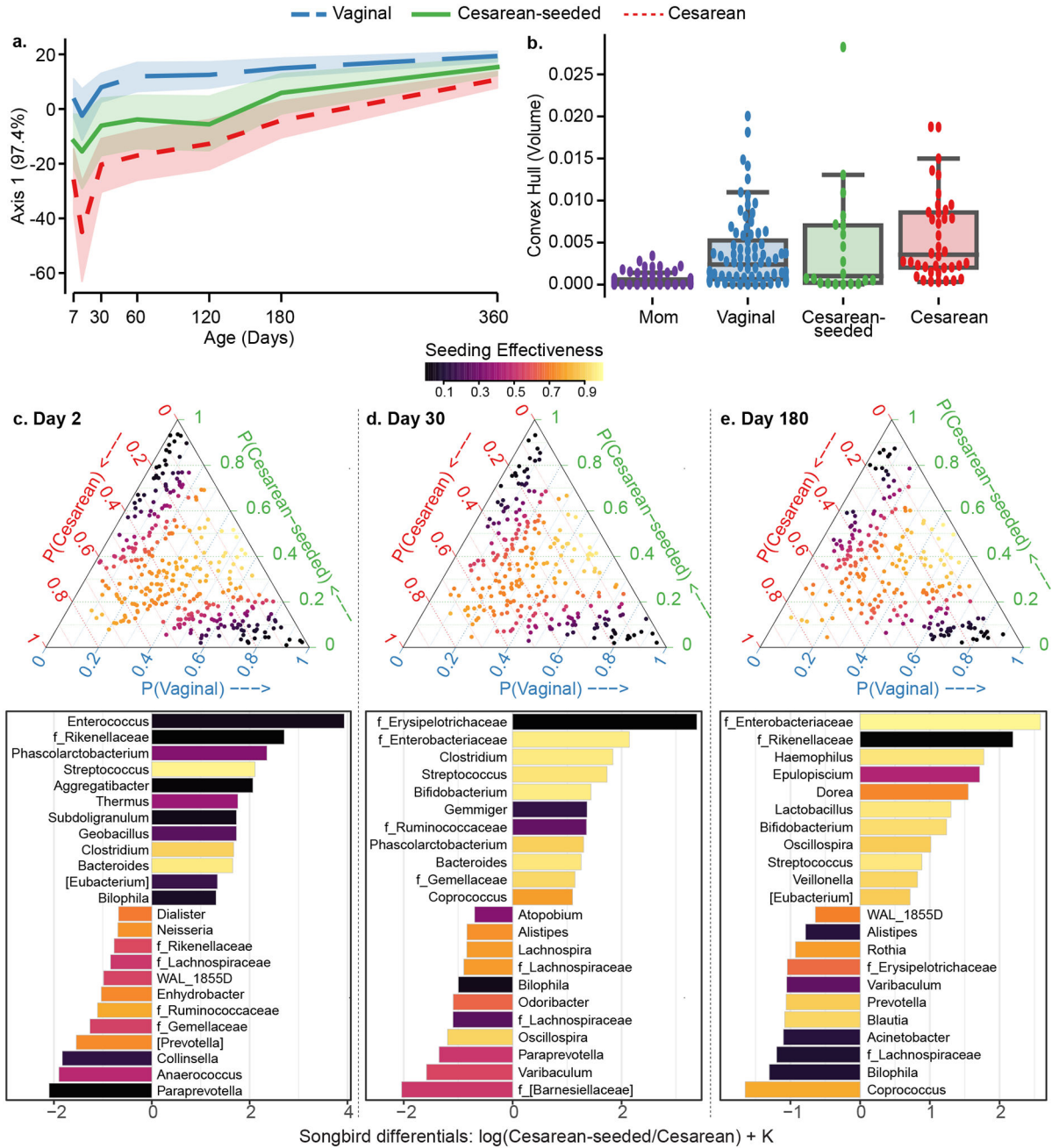


### Highlights

- Vaginal seeding of Cesarean born babies naturalizes their microbiota
- Bacteria from multiple body sites compose the perinatal maternal vaginal microbiome
- Bacteria typical in vaginal birth engraft different sites of Cesarean born babies

**Context and Significance paragraph**

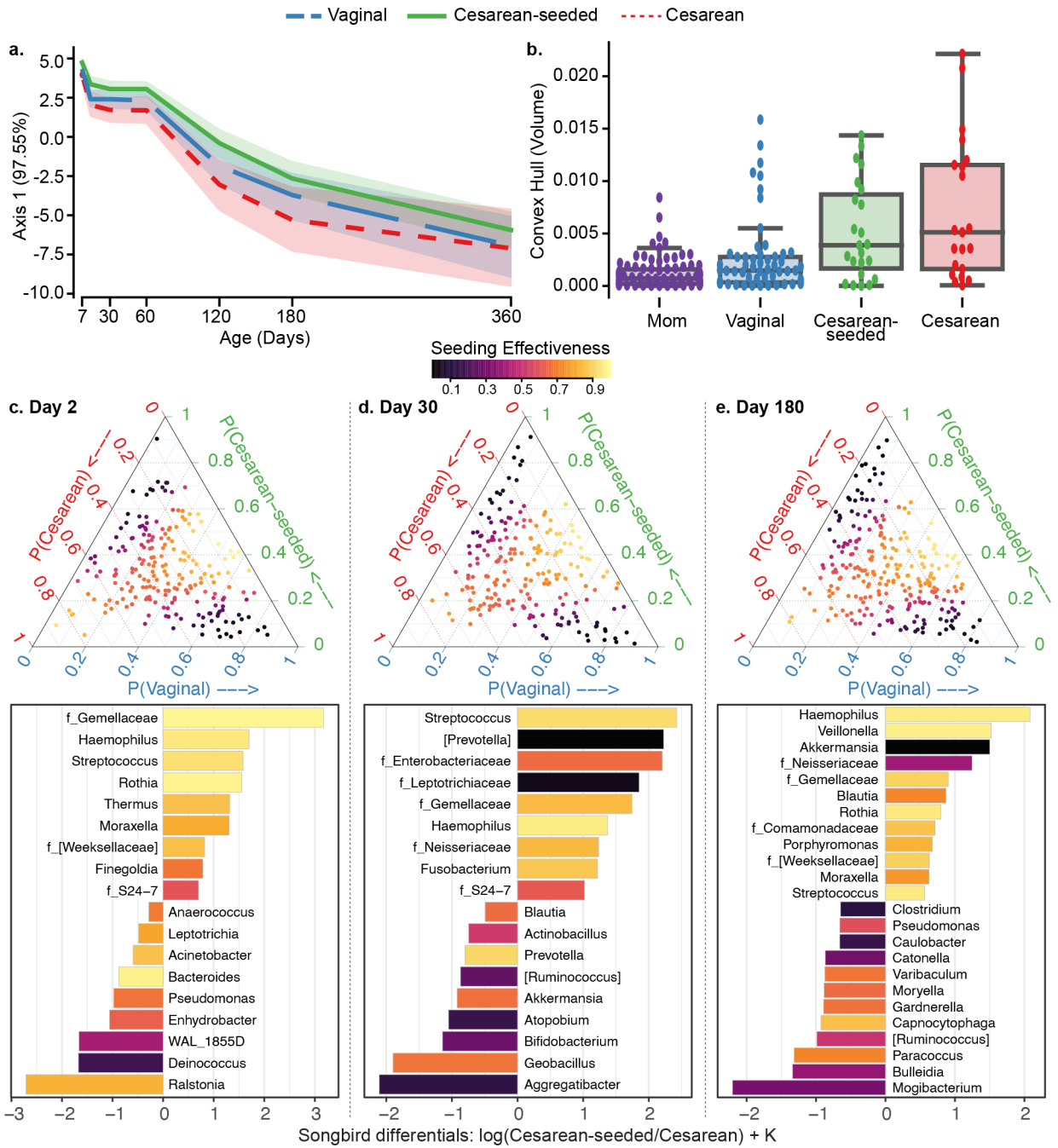
Cesarean birth alters the infant microbiota and is associated with increased risk of immune and metabolic disorders. We restored the natural microbial exposure of babies to their mothers' birth canal fluids right after Cesarean birth, and found that perinatally, the maternal birth canal contains very high proportions of bacteria typical of other body sites, and engraftment of these maternal bacteria normalizes microbiota development in different infant sites. In the context of risks and benefits of Cesarean procedures, normalizing the infant microbiota from birth might mitigate the collateral effects of missing colonization by important early bacteria, and reduce the increased risk to immune and metabolic diseases associated with Cesarean birth.



**Figure 1. Fecal microbiota development during the first year of life in babies discordant to birth mode/exposure.**

(a) Compositional Tensor Factorization (CTF) first principal component (Y-axis) of infant samples over age in days (X-axis). (b) Convex hull volume (Y-axis) on the first three Principal Coordinates (unweighted UniFrac distances) in mothers (purple) and infants by birth mode or exposure (X-axis). Infants show highest volumes in Cesarean born and lowest in Vaginally born, with Cesarean-seeded babies showing intermediate volumes; all pairwise comparisons are significant using Mann-Whitney test with Bonferroni corrections at 0.05 level (Table S3). (c-e) Songbird differentials shown for day 2, 30, and 180 after birth; ternary plots of the inverse additive log-ratio transform (inverse-ALR) of Songbird

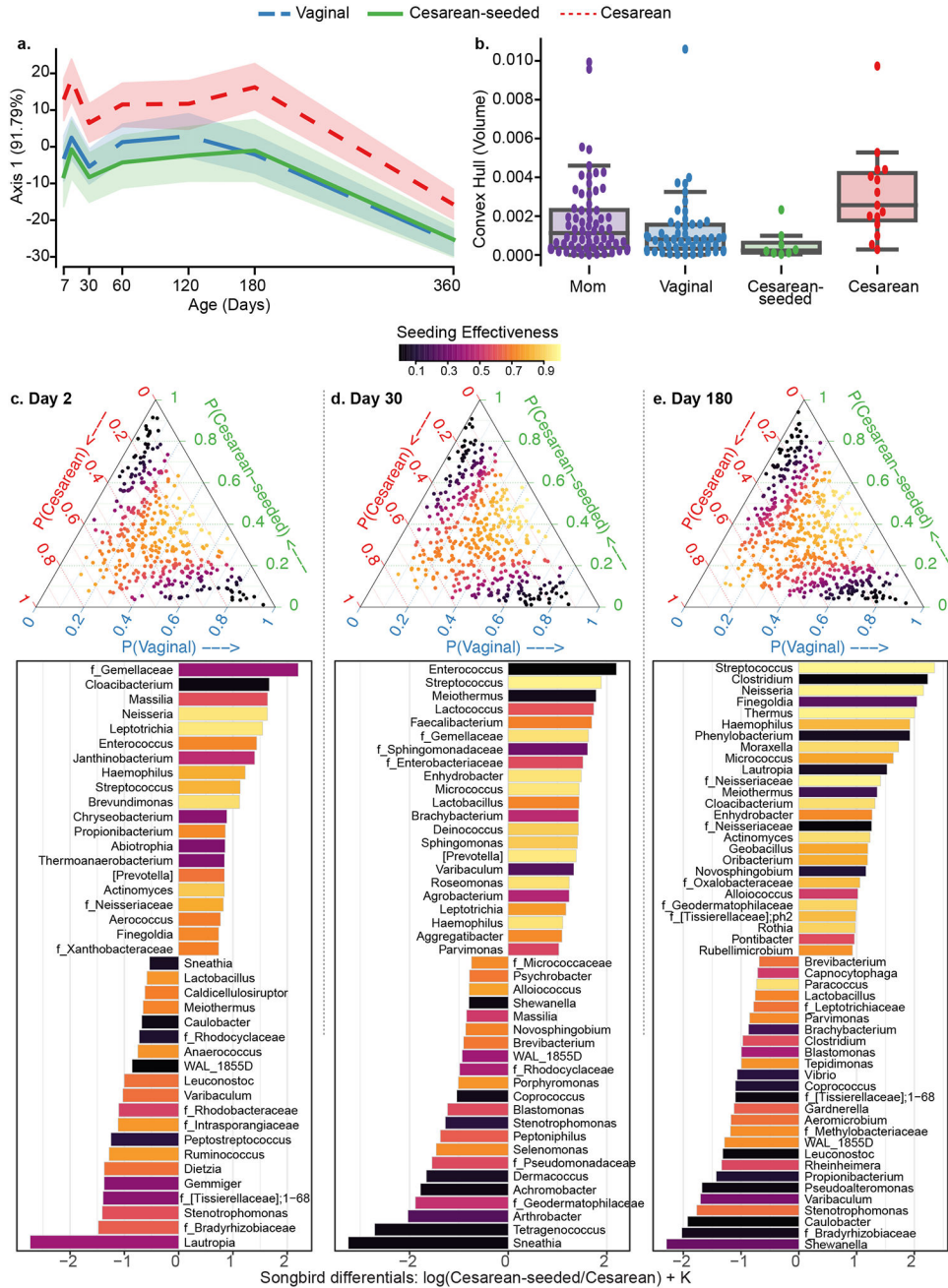
differentials give the estimated probability of a microbe being observed in Cesarean (left-axes; red), Vaginal (bottom-axes; blue), or Cesarean-seeded (right-axes; green). The color of the dots depicts the seeding effectiveness, with yellow color indicating effectively seeded/suppressed and black indicating not effectively seeded. Below each triangle, bar plots of top and bottom 20% Songbird differentials summarized at genus-level taxa between Cesarean-seeded and Cesarean born babies; a positive value indicates higher association with the Cesarean-seeded group, a negative value indicates higher with Cesarean. Bars are colored by the ASVs' seeding effectiveness. The majority of taxa discordant overrepresented in the Cesarean-seeded group over the Cesarean group are yellow-orange, indicating ASVs effectively seeded in the Cesarean seeded group, and these are observed at all ages. *See also* Figure S4, Supplementary Methods S2–S7.



**Figure 2. Oral microbiota development during the first year of life in babies discordant to birth mode/exposure.**

(a) Compositional Tensor Factorization (CTF) first principal component (Y-axis) of infant samples over age in days (X-axis). (b) Convex hull volume (Y-axis) on the first three Principal Coordinates (unweighted UniFrac distances) in mothers (purple) and infants by birth mode or exposure (X-axis). Infants show highest volumes in Cesarean born and lowest in Vaginally born, with Cesarean-seeded babies showing intermediate volumes; all pairwise comparisons are significant using Mann-Whitney test with Bonferroni corrections at 0.05 level (Table S3). (c-e) Songbird differentials shown for day 2, 30, and 180 after

birth; ternary plots of the inverse additive log-ratio transform (inverse-ALR) of Songbird differentials give the estimated probability of a microbe being observed in Cesarean (left-axes; red), Vaginal (bottom-axes; blue), or Cesarean-seeded (right-axes; green). The color of the dots depicts the seeding effectiveness, with yellow color indicating effectively seeded/suppressed and black indicating not effectively seeded. Below each triangle, bar plots of top and bottom 20% Songbird differentials summarized at genus-level taxa between Cesarean-seeded and Cesarean born babies; a positive value indicates higher association with the Cesarean-seeded group, a negative value indicates higher with Cesarean. Bars are colored by the ASVs' seeding effectiveness. The majority of taxa discordant overrepresented in the Cesarean-seeded group over the Cesarean group are yellow–orange, indicating ASVs effectively seeded in the Cesarean seeded group, and these are observed at all ages. *See also* Figure S4, Supplementary Methods S2–S7.

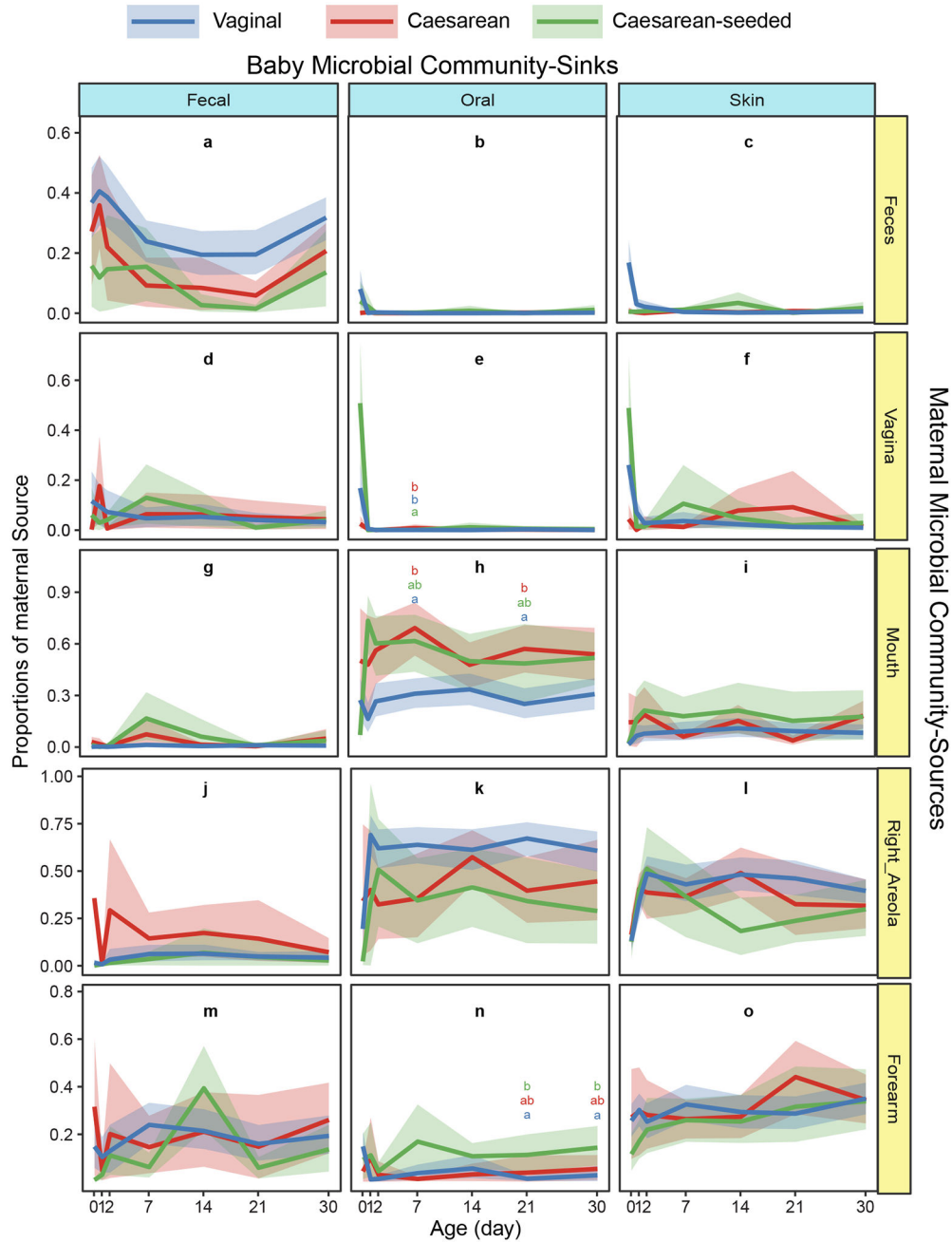


**Figure 3. Skin microbiota development during the first year of life in babies discordant to birth mode/exposure.**

(a) Compositional Tensor Factorization (CTF) first principal component (Y-axis) of infant samples over age in days (X-axis). (b) Convex hull volume (Y-axis) on the first three Principal Coordinates (unweighted UniFrac distances) in mothers (purple) and infants by birth mode or exposure (X-axis). Infants show highest volumes in Cesarean born and lowest in Vaginally born, with Cesarean-seeded babies showing intermediate volumes; all but one pairwise comparison are significant using Mann-Whitney test with Bonferroni corrections at 0.05 level (Table S3). (c-e) Songbird differentials shown for day 2, 30, and 180 after birth; ternary plots of the inverse additive log-ratio transform (inverse-ALR) of Songbird

differentials give the estimated probability of a microbe being observed in Cesarean (left-axes; red), Vaginal (bottom-axes; blue), or Cesarean-seeded (right-axes; green). The color of the dots depicts the seeding effectiveness, with yellow color indicating effectively seeded/suppressed and black indicating not effectively seeded. Below each triangle, bar plots of top and bottom 20% Songbird differentials summarized at genus-level taxa between Cesarean-seeded and Cesarean born babies; a positive value indicates higher association with the Cesarean-seeded group, a negative value indicates higher with Cesarean. Bars are colored by the ASVs' seeding effectiveness. The majority of taxa discordant overrepresented in the Cesarean-seeded group over the Cesarean group are yellow–orange, indicating ASVs effectively seeded in the Cesarean seeded group, and these are observed at all ages. *See also* Figure S4, Supplementary Methods S2–S7.





**Figure 4. Microbial source tracking of the neonate microbiome (first month) through fast expectation-maximization microbial source tracking (FEAST).** Contributions (y-axes) of various maternal sources (rows) to the infant microbial community (columns) are estimated across age in days (x-axes) for the first month of life, in 15 mother-baby pairs. Error bars show 95% confidence interval of the mean calculated by bootstrapping; Dunn test based on Kruskal-Wallis were performed on each time points by each maternal source for each baby sink, significant differences are marked by different letters in each panel. The vaginal source -prominent in day “0” for oral and skin in babies exposed to vaginal fluids (vaginal and CS-seeded; panel e, f)- as not prominent later in any baby site. Baby site specific communities resemble the corresponding maternal site (panels

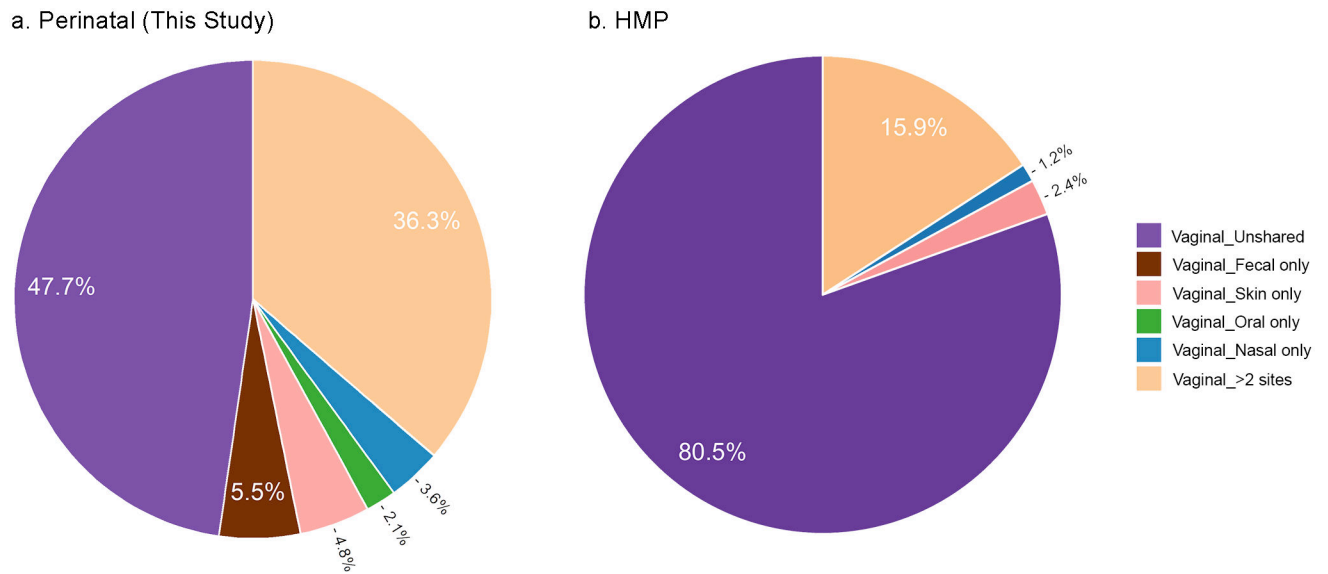
a, h, o), consistent with specific site selection of bacteria. The maternal right areola appears as a source for baby oral bacteria (panel k), which likely means that baby oral bacteria is transmitted to the mother's areola during lactation.

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**Figure 5. Proportions of bacterial vaginal ASVs shared with other body sites in the mothers of the current study, at the day of delivery (a) and in non-pregnant women (b).**

(a) V4 sequences from vaginal swabs and gauzes obtained from 97 parturient mothers from this study at the day of birth. Current study data were sequenced by Illumina HiSeq and processed by QIIME2 using the same pipeline as for the HMP data. (b) HMP V4 data from vaginal swabs obtained from 105 non-pregnant women; ASVs included in the analyses were present in at least 10% of the samples in the respective body site. Roche 454 V3V5 sequences were trimmed to obtain the V4 region. *See also* Figure S2 b–c, Supplementary Methods S13–S14.

**Table 1.**

Key characteristics of families included in this study for analysis.

		Vaginal	Cesarean	Cesarean-Seeded
Number of Families		97	49	28
Number of Babies	Total	98	49	30
	USA	62	23	16
	Spain	7	5	8
	Chile	26	18	6
	Bolivia	3	3	0
Baby female sex (%)		52.0	38.8	46.7
Mean baby follow-up, months (standard deviation)		6.2 (5.1)	8.8 (4.7)	7.1(5.2)
Baby antibiotics use within the Study Period (after week 1)				
Any (%)		18.4	20.4	16.7
1 dose (%)		7.1	14.3	3.3
>1 doses (%)		11.3	6.1	13.4
Breast Feeding Dominant within first 4 month <sup>1</sup> (%)		75.5	69.4	53.3
Mother tested positive to Group B Streptococcus (%)		8.9	11.1	0
Use of Perinatal Antibiotics in Mother <sup>2</sup> (%)		13.3	95.6	95.8
Any Use of Antibiotics during Pregnancy (%)		20	26.7	16.7

<sup>1</sup>Breast feeding dominant is defined as the mothers who reported breastfeeding exclusively or >50% of breastfeeding in at least 60% of follow-up visits.

<sup>2</sup>Use of perinatal antibiotics is part of the standard-of-care for women underwent Cesarean birth.

## KEY RESOURCE TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Biological Samples		
Stool, mouth, and skin specimen from infants	This Study	
Stool, mouth, skin, vagina, nasal specimen from mothers	This Study	
Critical Commercial Assays		
DNeasy PowerSoil HTP 96 Kit	Qiagen	12955-4
illumine MiSeq/HiSeq sequencing PE150	New York University Genome Technology Center, or UC San Diego Institute for Genomic Medicine Genomics Facility	-
Deposited Data		
Raw sequencing data	European Bioinformatics Institute	ERP120105, ERP016173 and ERP120109
Raw sequencing data and processed data	Qiita	Study 10894, 10249, and 1718
Source codes, tests and notebooks to generate the figures	This study	<a href="https://github.com/knightlab-analyses/seedling-study">https://github.com/knightlab-analyses/seedling-study</a>
Oligonucleotides		
515f forward primer: GTGYCAGCMGCCGCGTAA	EMP protocol	
806r reverse primer: GGACTACNVGGGTWTCTAAT	EMP protocol	
Software and Algorithms		
Qiime2-2019.8	Bolyen et al. (2019)	
FEAST	Shenhav et al. (2019)	<a href="https://github.com/ETaSky/FEAST.gitbranch:removewritingfiles">https://github.com/ETaSky/FEAST.gitbranch:removewritingfiles</a>
BayestTime	Jiang et al. (2020)	<a href="https://github.com/biocore/bayestime">https://github.com/biocore/bayestime</a>
Gemelli	Martino et al. (2020)	<a href="https://github.com/biocore/gemelli">https://github.com/biocore/gemelli</a>
stepwise-rda.R	This study	<a href="https://github.com/knightlab-analyses/seedling-study">https://github.com/knightlab-analyses/seedling-study</a>
Songbird	Morton et al. (2019)	<a href="https://github.com/biocore/songbird">https://github.com/biocore/songbird</a>