

Supplementary Figure 1

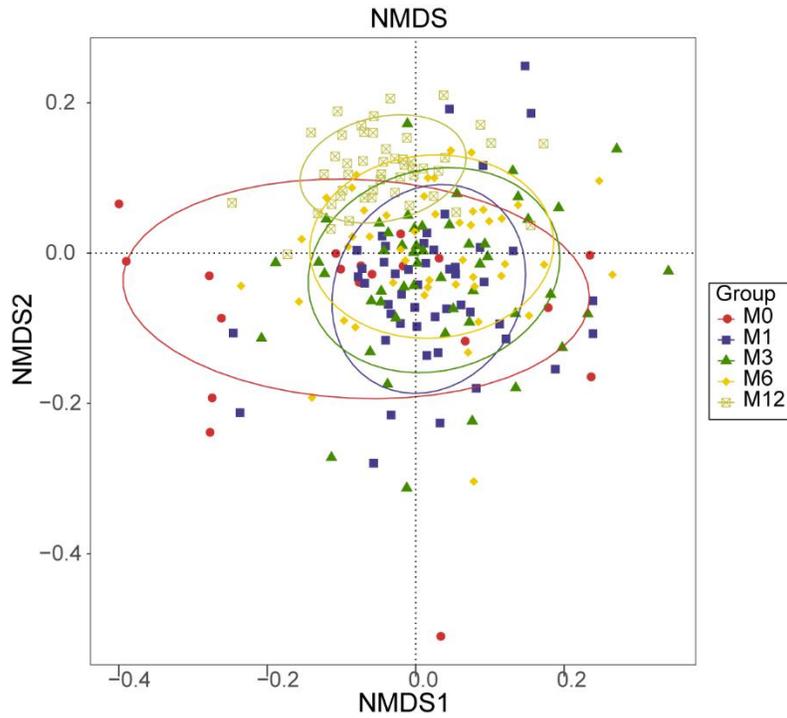


Figure S1: Overall diversity in bacterial composition was calculated using unweighted UniFrac distances by NMDS, and it indicated a notable separation of samples at 0, 1, 3, 6 and 12 months postpartum (Adonis $p < 0.005$, $R^2 = 0.08$). NMDS: non-metric multidimensional scaling; M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 2

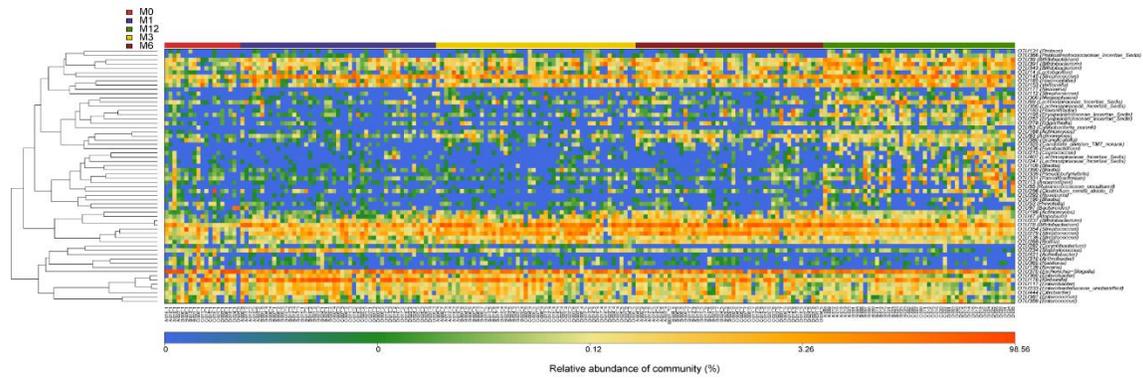


Figure S2: Heatmap showing the relative abundance of the discriminatory OTUs that drive the differences at 0, 1, 3, 6 and 12 months. Each vertical lane corresponds to one sample. Abundance values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units; M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 3

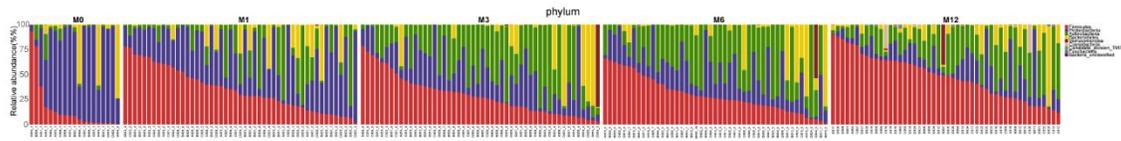


Figure S3: Composition of the fecal microbiota at the phylum level during the first year of life. M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 4

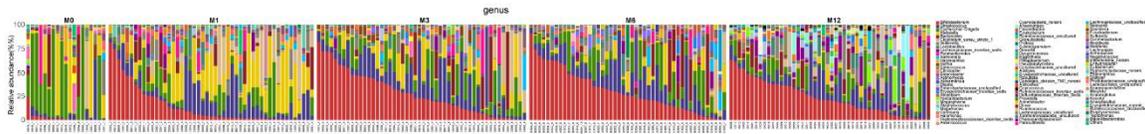


Figure S4: Composition of the fecal microbiota at the genus level during the first year of life. M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 5

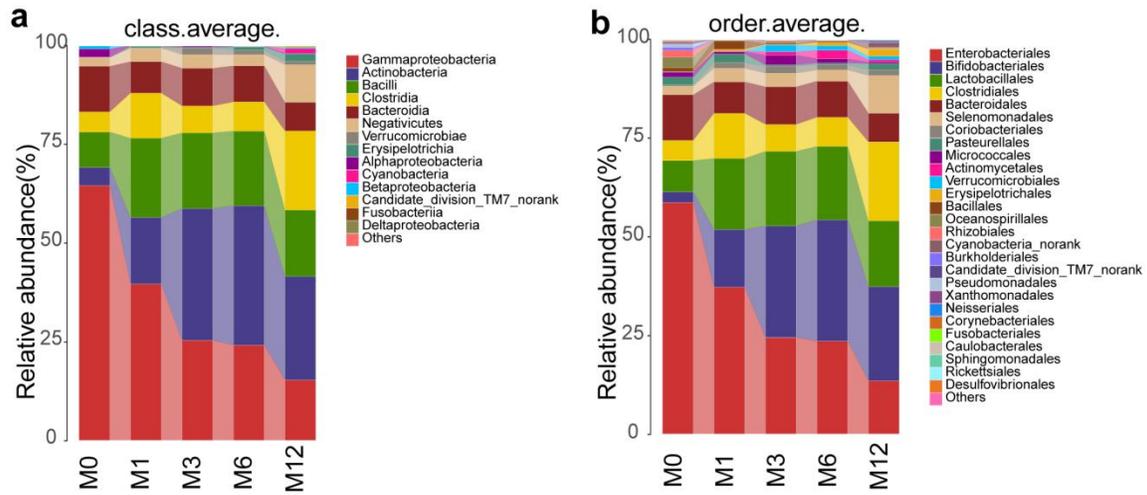


Figure S5: Gut microbiota community structure during the first year of life. Fecal microbiota composition at the class level **(a)** and order level **(b)** at 0, 1, 3, 6 and 12 months. M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 6

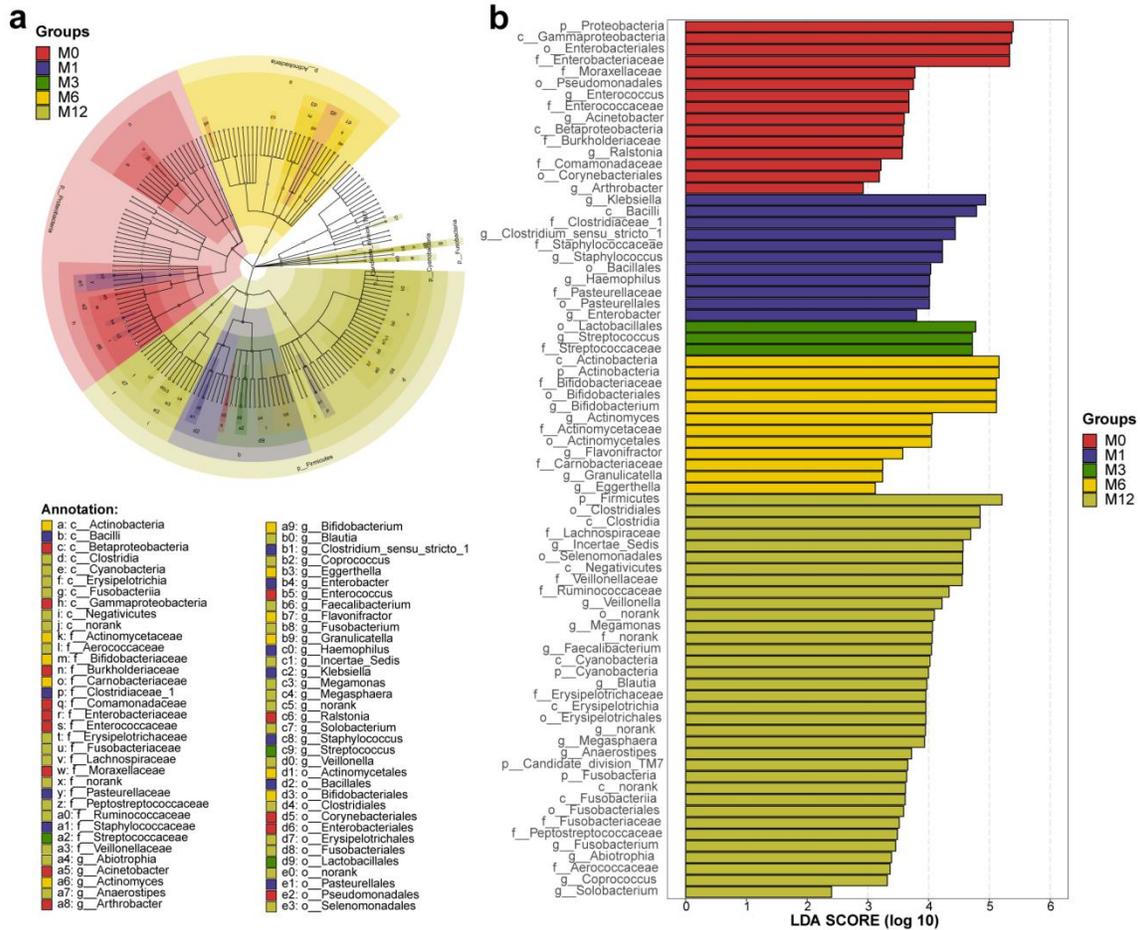


Figure S6: The gut microbiota differences during the first year of life were analyzed using the LefSe method. (a) The LefSe method identified the most differentially abundant taxa at 0, 1, 3, 6 and 12 months. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa at 0, 1, 3, 6 and 12 months are presented according to the LDA scores (log₁₀). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; M0: 0 months; M1: 1 month; M3: 3 months; M6: 6 months; M12: 12 months.

Supplementary Figure 8

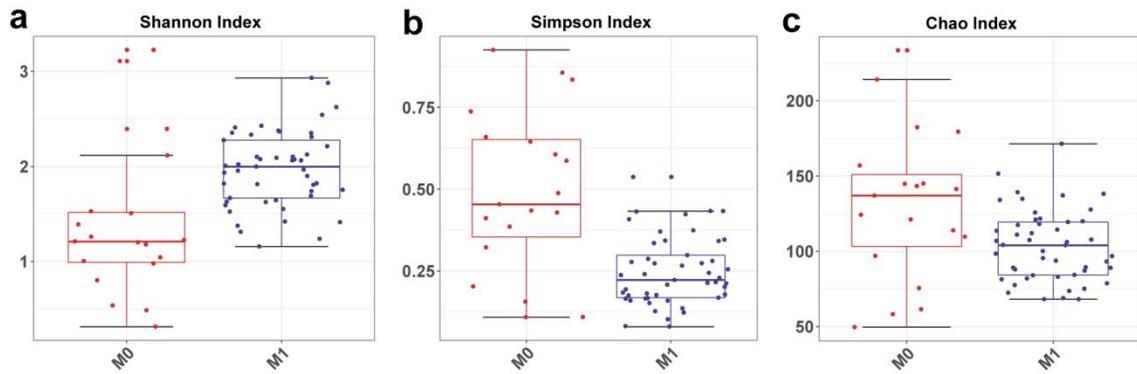


Figure S8: Infant gut microbial diversity between 0 months and 1 month. Gut microbial diversity, as estimated by the Shannon index **(a)**, Simpson index **(b)** and Chao1 index **(c)**, was significantly decreased at 0 months versus 1 month ($p < 0.001$, $p < 0.001$ and $p < 0.05$, respectively). M0: 0 months; M1: 1 month.

Supplementary Figure 9

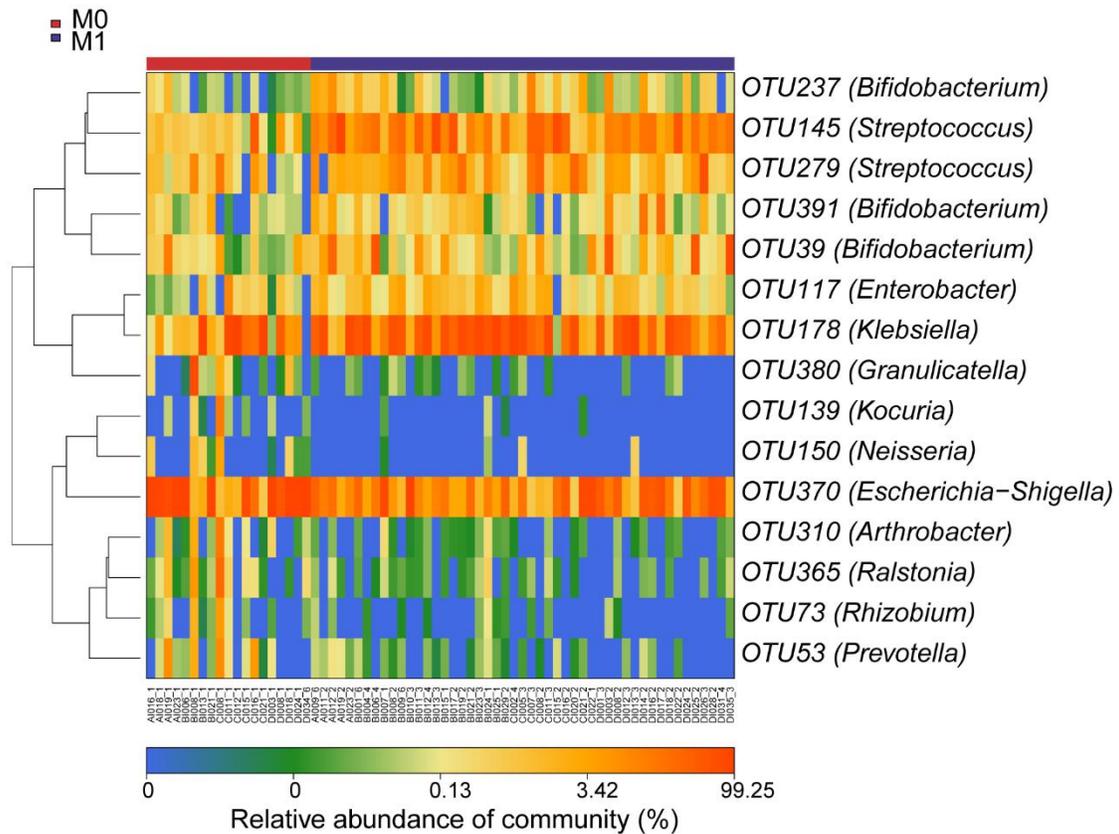


Figure S9: Heatmap showing the relative abundances of the discriminatory OTUs that drive the differences between 0 months and 1 month. Each vertical lane corresponds to one sample. Abundance values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units; M0: 0 months; M1: 1 month.

Supplementary Figure 10

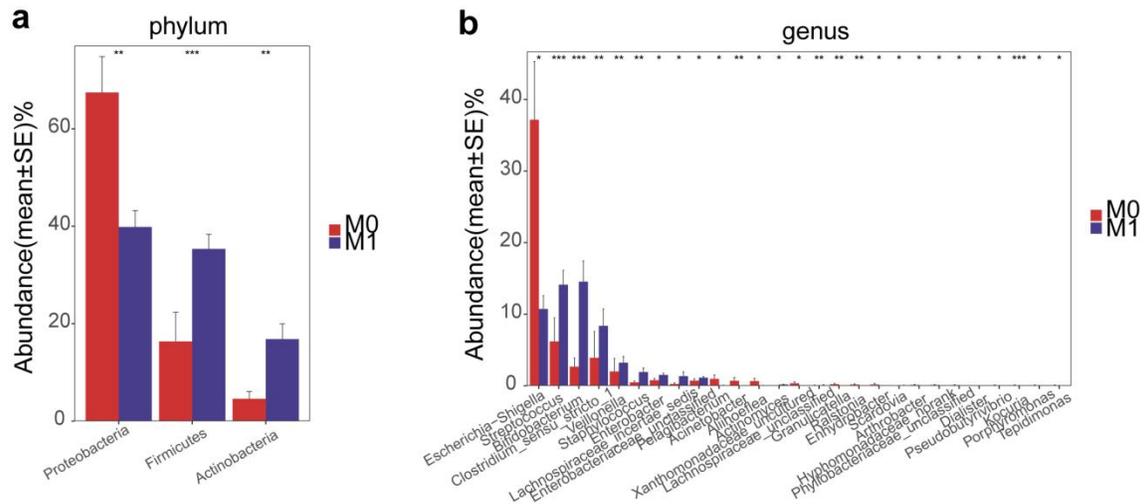


Figure S10: Gut microbial differences of infants between 0 months and 1 month. (a) One phylum was significantly increased, while 2 phyla were significantly decreased at 0 months compared with 1 month (all $p < 0.05$). **(b)** Fifteen genera were enriched, while 12 genera were decreased at 0 months versus 1 month (all $p < 0.05$). M0: 0 months; M1: 1 month.

Supplementary Figure 11

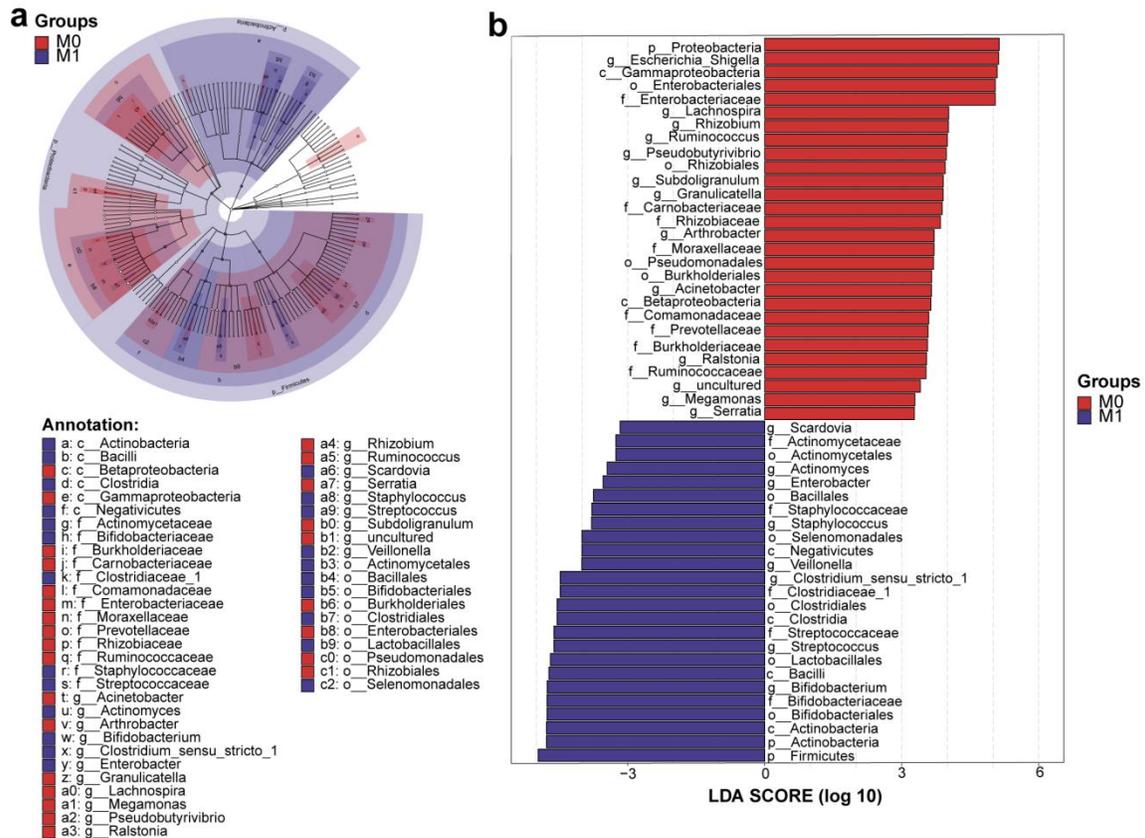


Figure S11: The gut microbiota differences between 0 months and 1 month were analyzed using the LEfSe method. (a) The LEfSe method identified the most differentially abundant taxa between 0 months and 1 month. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa between 0 months and 1 month are presented according to the LDA scores (log₁₀). LEfSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; M0: 0 months; M1: 1 month.

Supplementary Figure 12

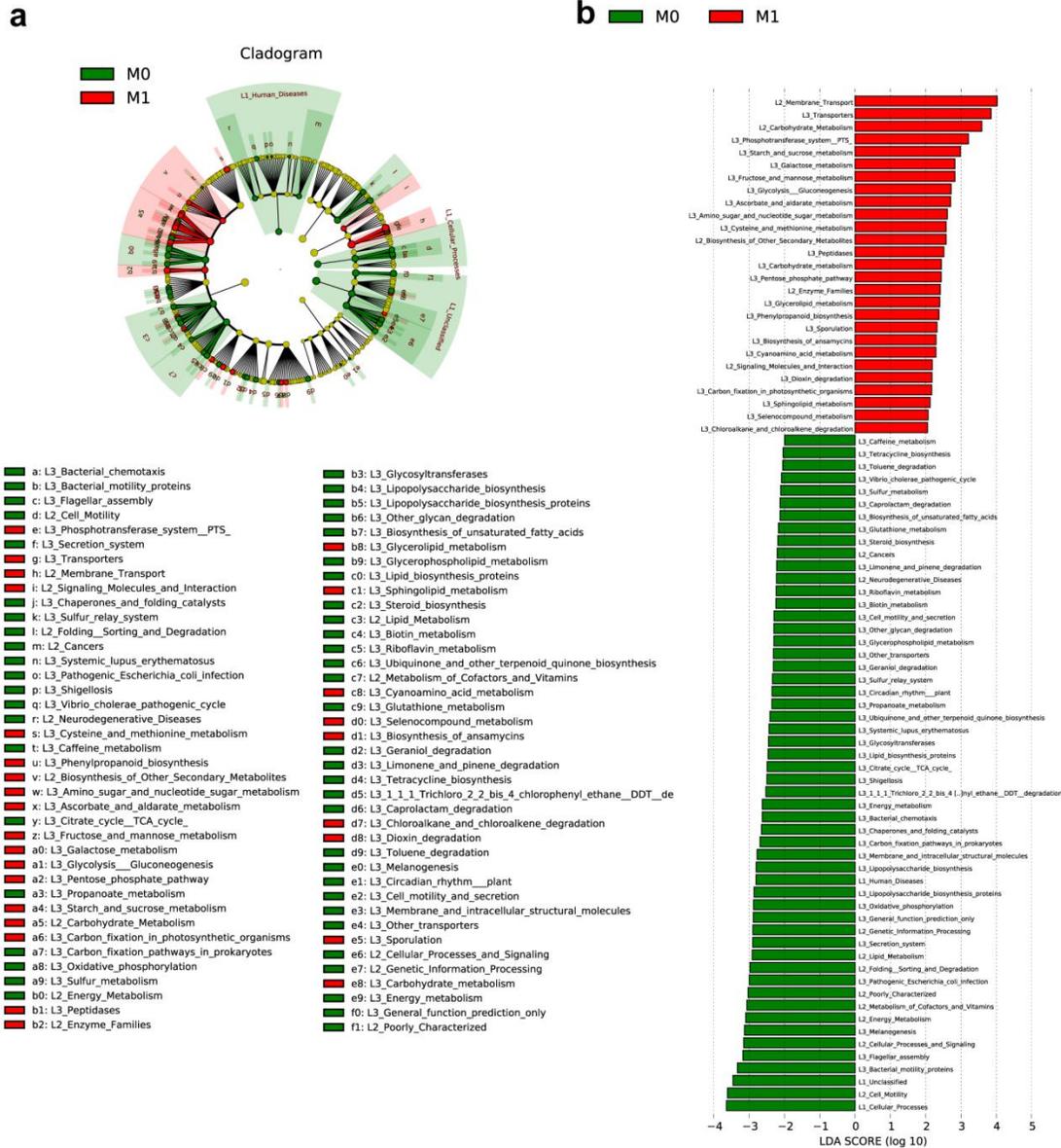


Figure S12: Functional prediction of microbial genes between 0 months and 1 month using PICRUSt. (a) A cladogram showing the gut microbial community function profiles between 0 months and 1 month and their predominant microbial functions. **(b)** Functional prediction of microbial genes showing significant differences between 0 months and 1 month according to the LDA scores (log₁₀). PICRUSt: phylogenetic investigation of communities by reconstruction of unobserved states; LDA: linear discriminant analysis; M0: 0 months; M1: 1 month.

Supplementary Figure 13

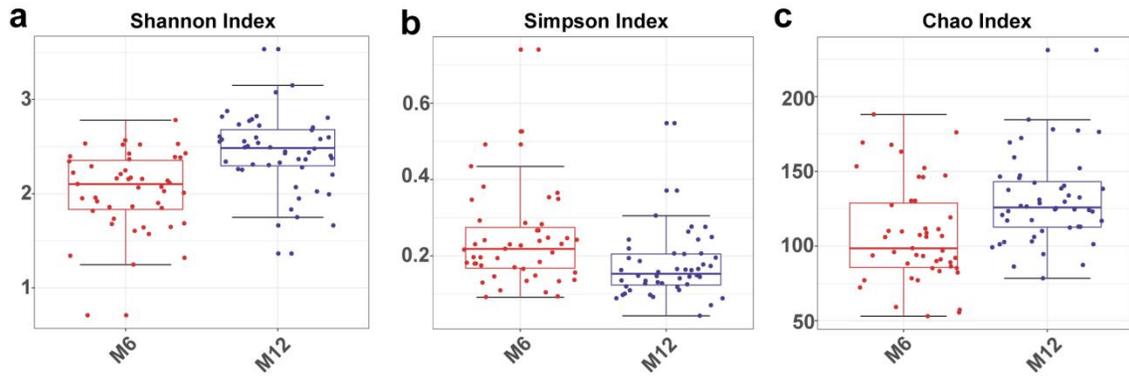


Figure S13: Infant gut microbial diversity between 6 months and 12 months. Gut microbial diversity, as estimated by the Shannon index **(a)**, Simpson index **(b)** and Chao1 index **(c)**, was significantly decreased at 6 months versus 12 months (all $p < 0.001$). M6: 6 months; M12: 12 months.

Supplementary Figure 14

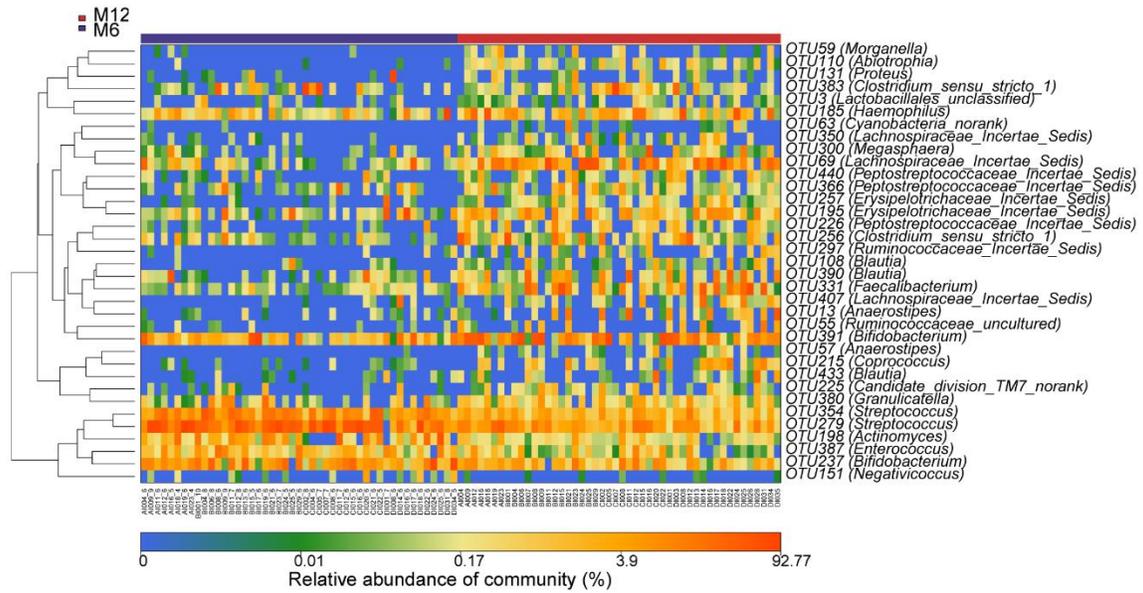


Figure S14: Heatmap showing the relative abundances of the discriminatory OTUs that drive the differences between 6 months and 12 months. Each vertical lane corresponds to one sample. Abundance values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units; M6: 6 months; M12: 12 months.

Supplementary Figure 16

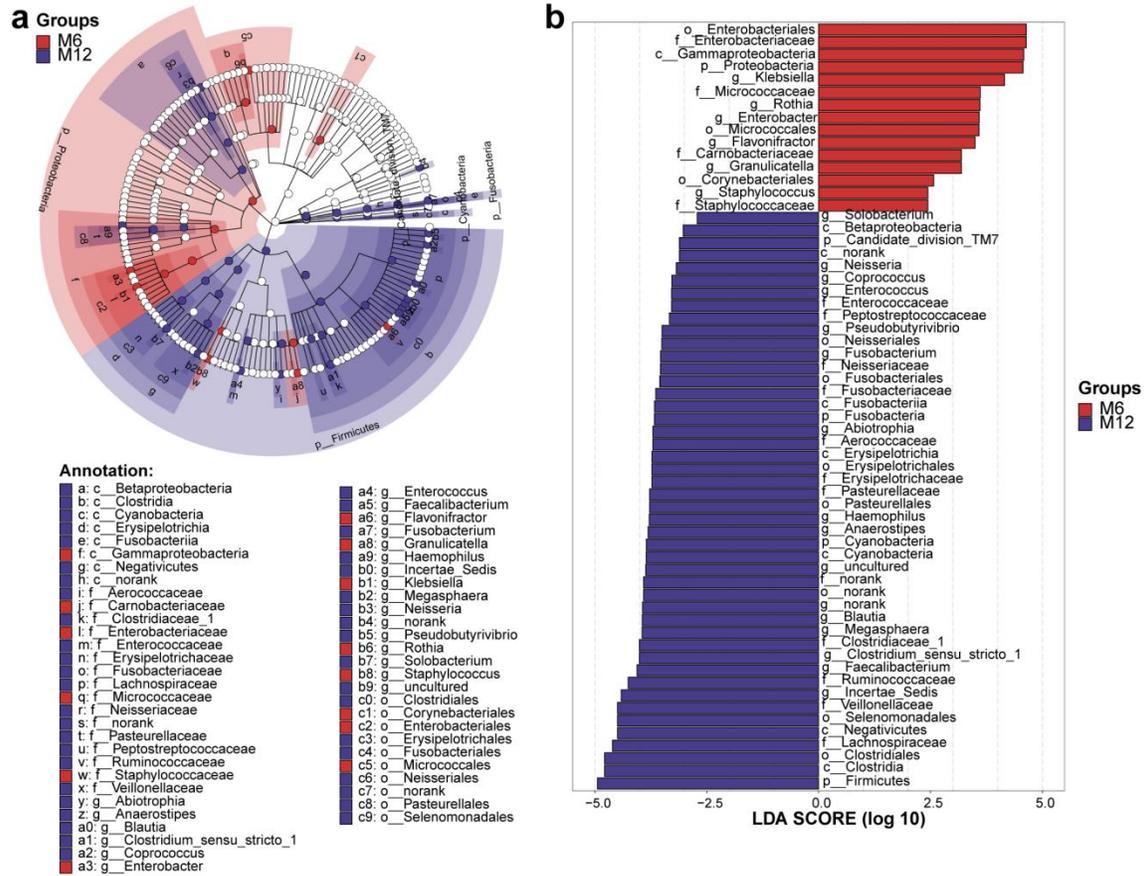
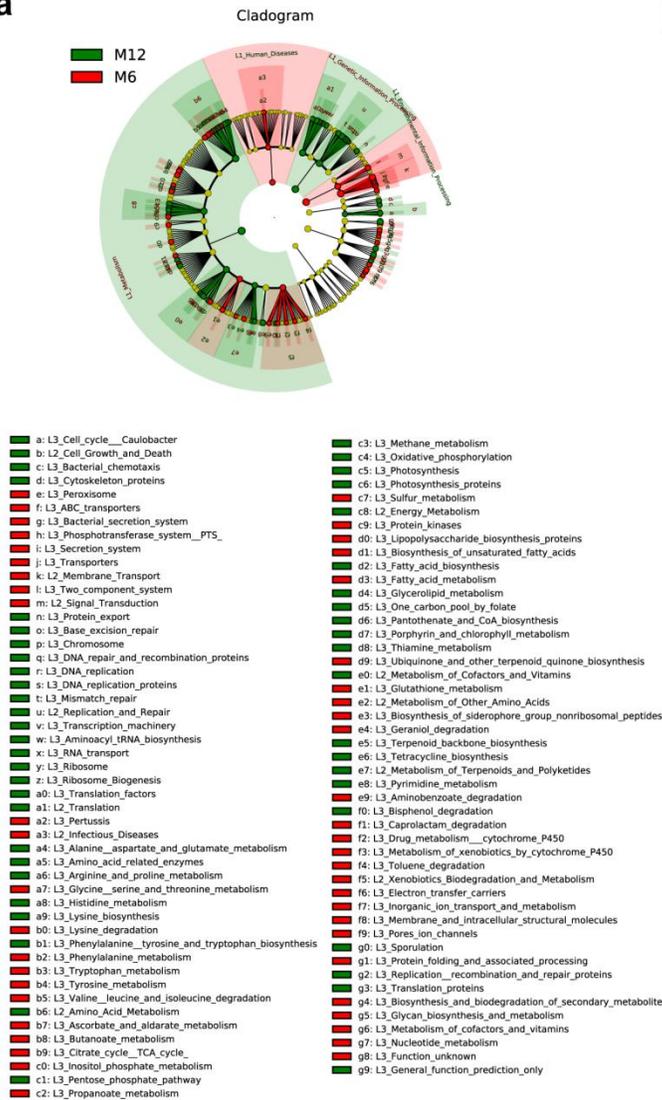


Figure S16: The gut microbiota differences between 6 months and 12 months were analyzed using the LEfSe method. (a) The LEfSe method identified the most differentially abundant taxa between 6 months and 12 months. The brightness of each dot is proportional to its effect size. (b) The greatest differences in taxa between 6 months and 12 months are presented according to the LDA scores (log₁₀). LEfSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; M6: 6 months; M12: 12 months.

Supplementary Figure 17

a



b

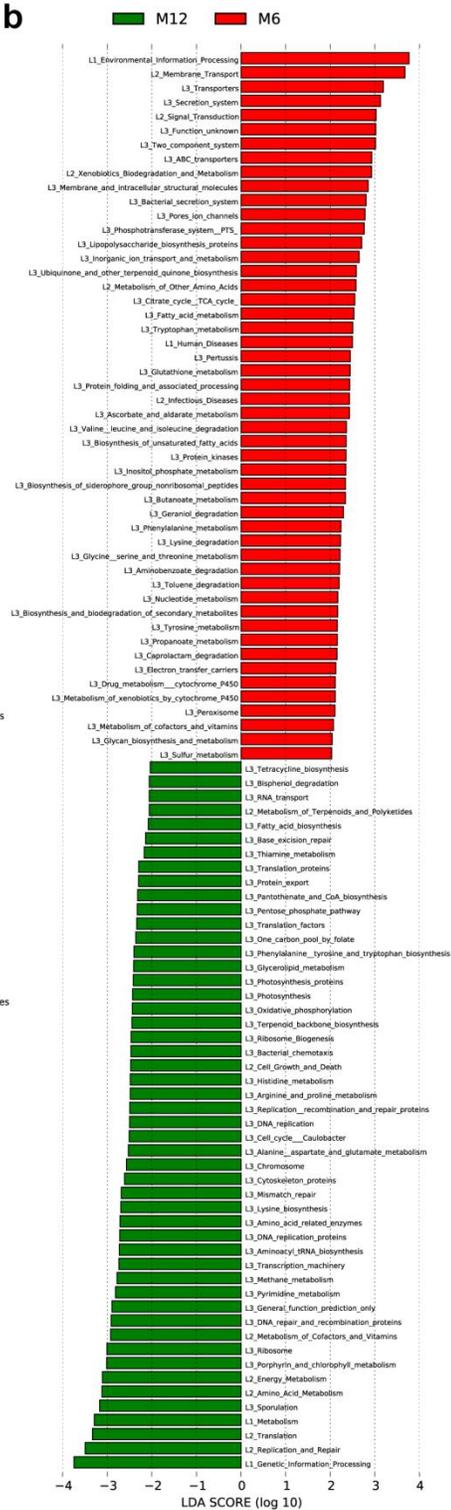


Figure S17: Functional prediction of microbial genes between 6 months and 12 months using PICRUSt. (a) A cladogram showing the gut microbial community function profiles between 6 months and 12 months and their predominant microbial functions. (b) Functional prediction of microbial genes showing significant differences between 6 months and 12 months according to the LDA scores (\log_{10}). PICRUSt: phylogenetic investigation of communities by reconstruction of unobserved states; LDA: linear discriminant analysis; M6: 6 months; M12: 12 months.

Supplementary Figure 18

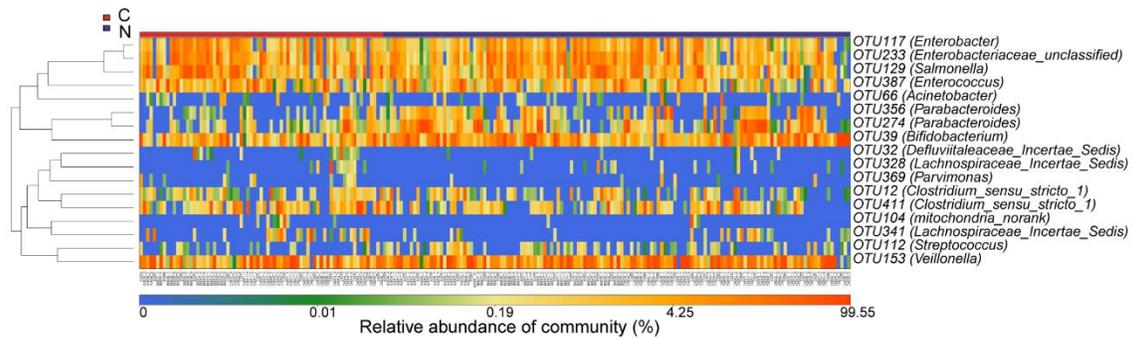


Figure S18: Heatmap showing the relative abundances of the discriminatory OTUs that drive the differences between vaginally delivered and cesarean sections. Each vertical lane corresponds to one sample. Abundances values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units; N: vaginally delivered; C: cesarean section.

Supplementary Figure 19

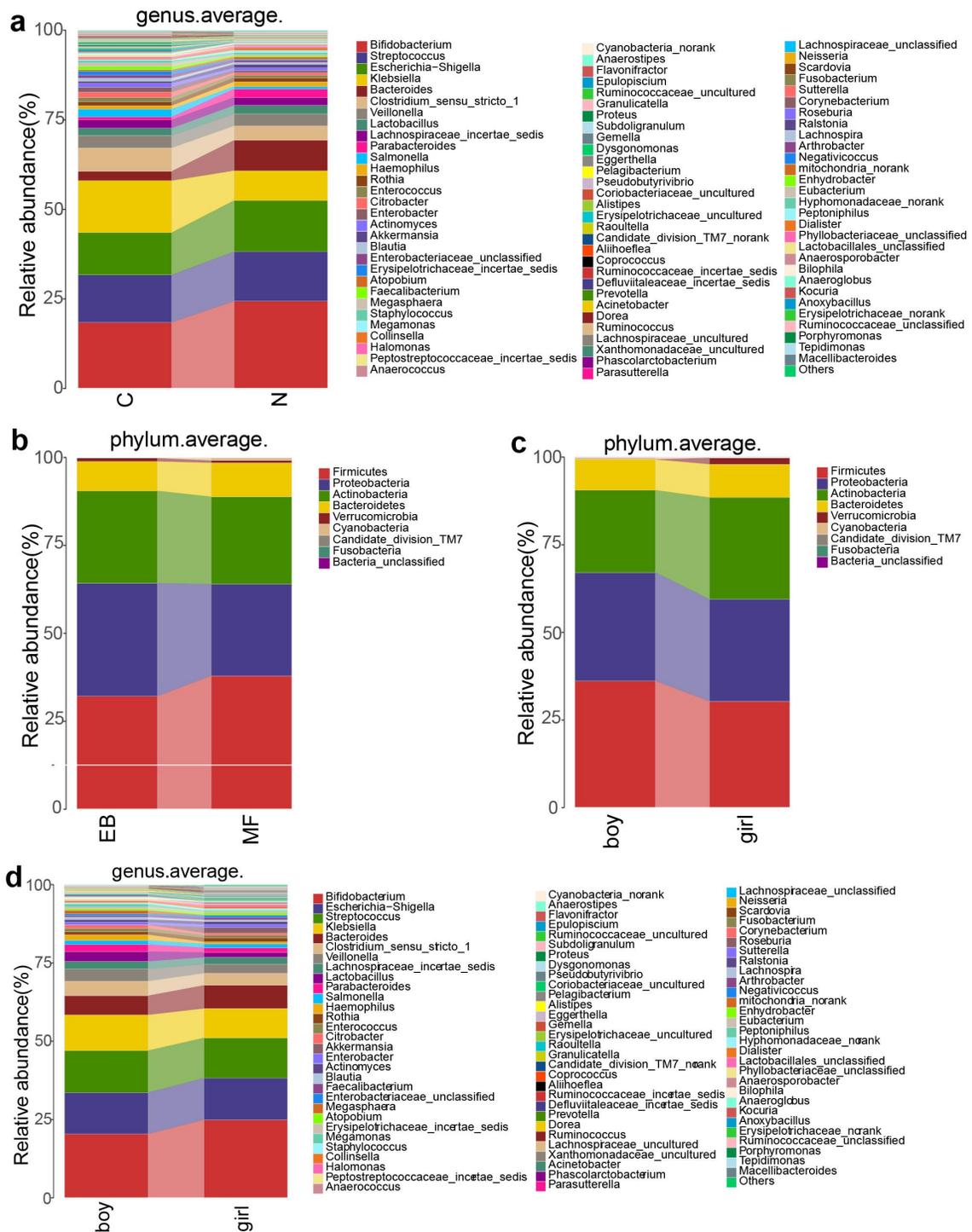


Figure S19: Differences in fecal microbial communities between groups. (a) Composition of the fecal microbiota at the genus level between vaginal delivery and

cesarean section. **(b)** Composition of the fecal microbiota at the phylum level between exclusive breastfeeding and combined feeding. **(c)** Composition of the fecal microbiota at the phylum level and **(d)** genus level between boys versus girls. N: vaginally delivered; C: cesarean section; EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 20

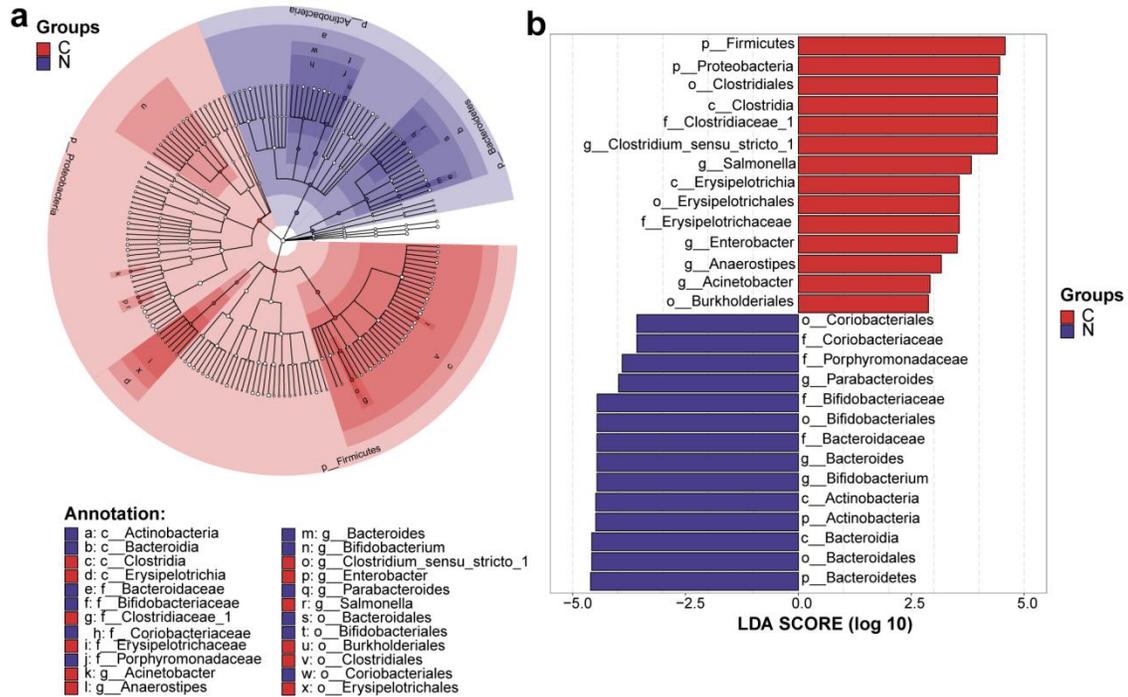


Figure S20: The gut microbiota differences between vaginal delivery and cesarean section were analyzed using the LefSe method. (a) The LefSe method identified the most differentially abundant taxa between vaginal delivery and cesarean section. The brightness of each dot is proportional to its effect size. (b) The greatest differences in taxa between vaginal delivery and cesarean section are presented according to the LDA scores (log10). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; N: vaginally delivered; C: cesarean section.

Figure S21: Functional prediction of microbial genes between vaginal delivery and cesarean section using PICRUSt. (a) A cladogram showing the gut microbial community function profiles between vaginal delivery and cesarean section and their predominant microbial functions. (b) Functional prediction of microbial genes showing significant differences between vaginal delivery and cesarean section according to the LDA scores (log10). PICRUSt: phylogenetic investigation of communities by reconstruction of unobserved states; LDA: linear discriminant analysis; N: vaginally delivered; C: cesarean section.

Supplementary Figure 22

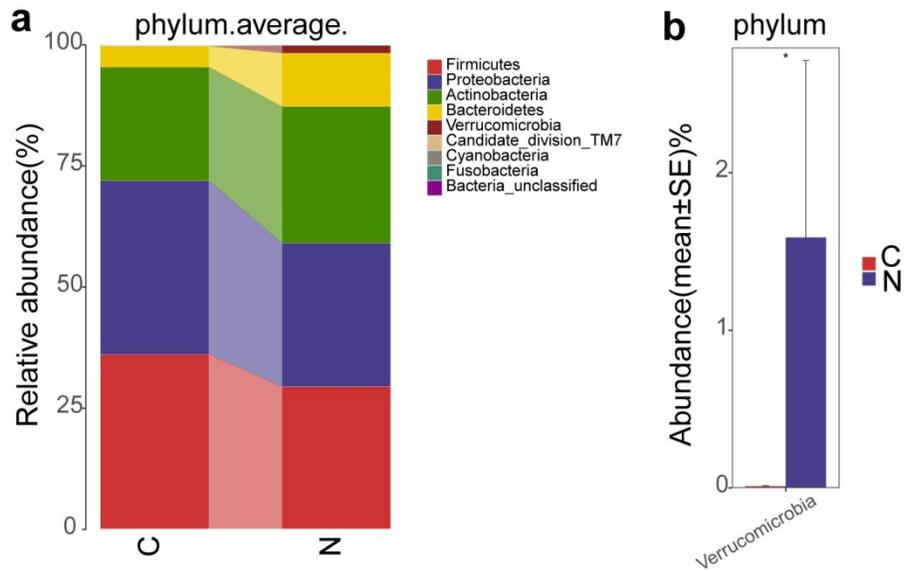


Figure S22: Differences in fecal microbial communities between vaginally delivered and cesarean sections under fixed exclusive breastfeeding conditions. (A) Composition of the fecal microbiota at the phylum level between vaginal delivery and cesarean section under fixed exclusive breastfeeding conditions. **(B)** Under fixed exclusive breastfeeding conditions, 1 phylum was significantly increased in vaginal delivery versus cesarean section ($p < 0.05$). N: vaginally delivered; C: cesarean section.

Supplementary Figure 23

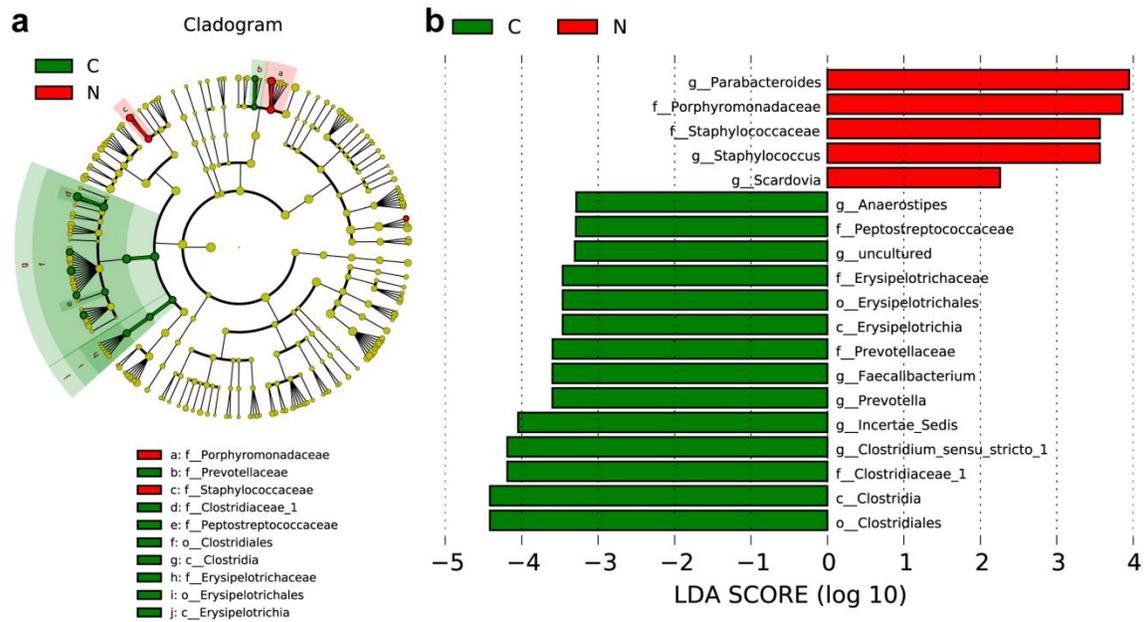


Figure S23: The gut microbiota differences between vaginal delivery and cesarean section under fixed exclusive breastfeeding conditions were analyzed using the LefSe method. (a) The LefSe method identified the most differentially abundant taxa between vaginal delivery and cesarean section under fixed exclusive breastfeeding conditions. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa between vaginal delivery and cesarean section under fixed exclusive breastfeeding conditions are presented according to the LDA scores (log₁₀). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; N: vaginally delivered; C: cesarean section.

Supplementary Figure 24

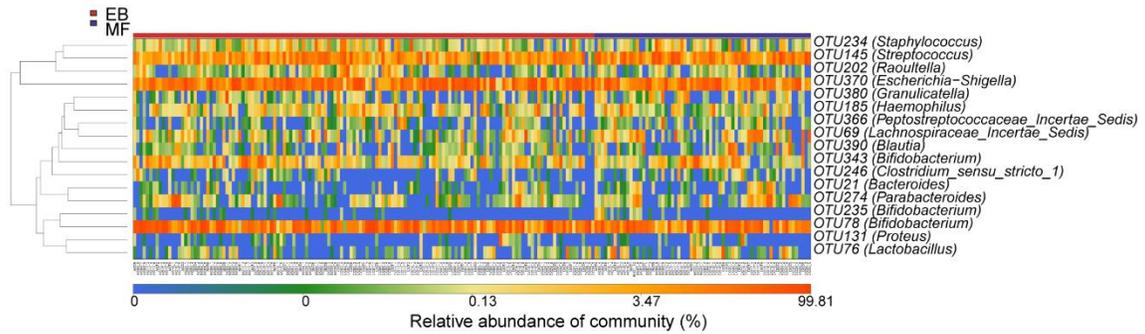


Figure S24: Heatmap showing the relative abundances of the discriminatory OTUs that drive the differences between exclusive breastfeeding and combined feeding. Each vertical lane corresponds to one sample. Abundances values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units; EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 25

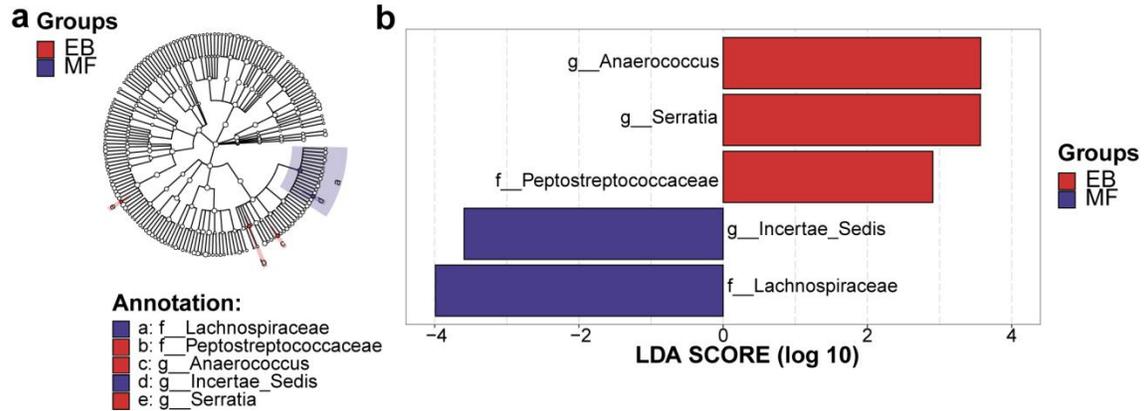
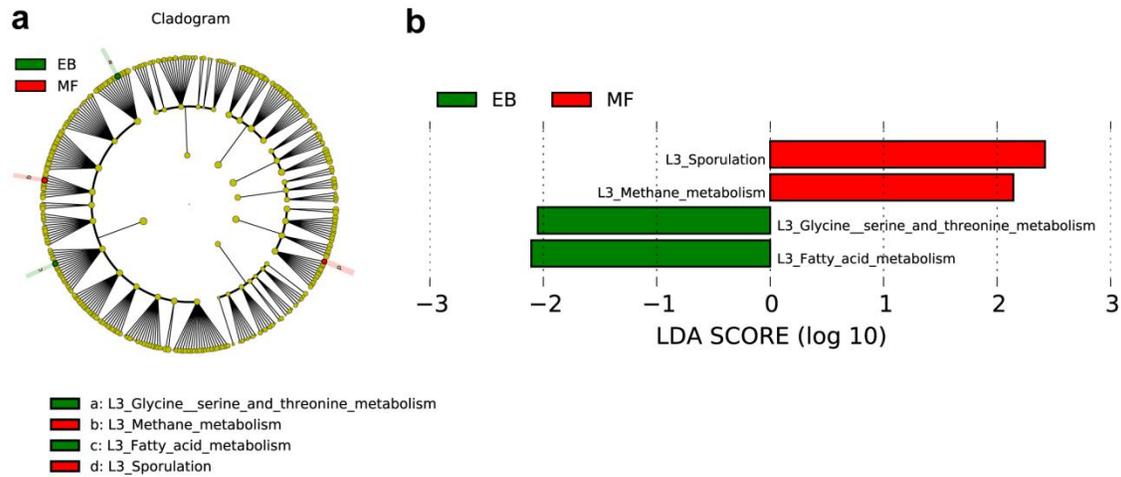


Figure S25: The gut microbiota differences between exclusive breastfeeding and combined feeding were analyzed using the LefSe method. (a) The LefSe method identified the most differentially abundant taxa between exclusive breastfeeding and combined feeding. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa between exclusive breastfeeding and combined feeding are presented according to the LDA scores (log₁₀). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 26



Supplementary figure 26: Functional prediction of microbial genes between exclusive breastfeeding and combined feeding using PICRUST. (A) A cladogram shows the gut microbial community function profiles between exclusive breastfeeding and combined feeding and their predominant microbial functions. **(B)** Functional prediction of microbial genes showing significant differences between exclusive breastfeeding and combined feeding according to the LDA scores (log₁₀). PICRUST: phylogenetic investigation of communities by reconstruction of unobserved states; LDA: linear discriminant analysis; EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 27

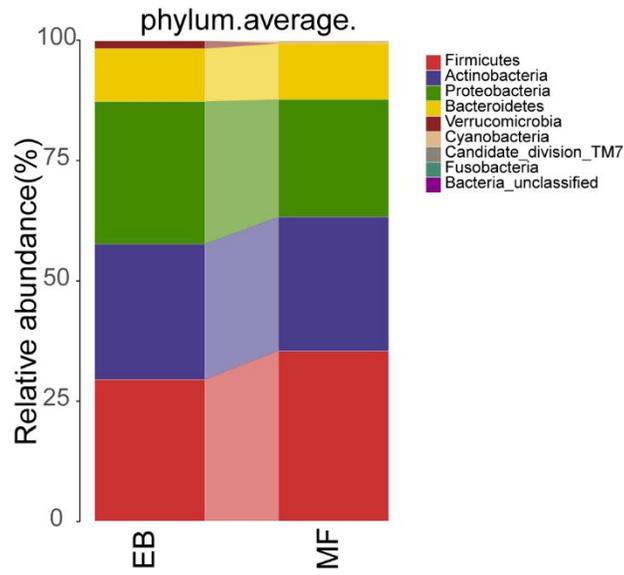


Figure S27: Composition of the fecal microbiota at the phylum level between exclusive breastfeeding and combined feeding under fixed vaginal delivery conditions. EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 28

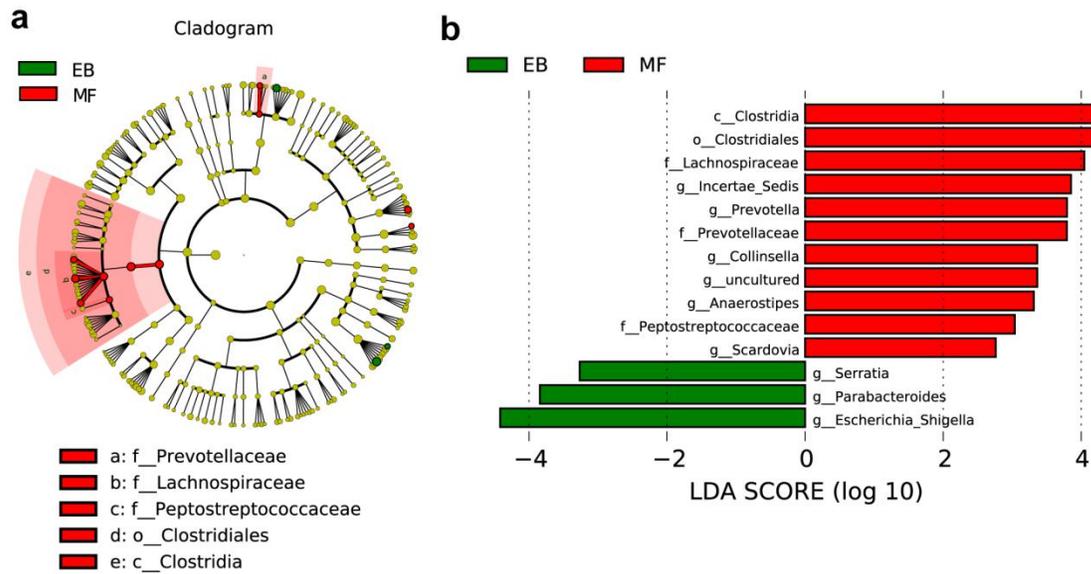


Figure S28: The gut microbiota differences between exclusive breastfeeding and combined feeding under fixed vaginal delivery conditions were analyzed using the LefSe method. (A) The LefSe method identified the most differentially abundant taxa between exclusive breastfeeding and combined feeding under fixed vaginal delivery conditions. The brightness of each dot is proportional to its effect size. **(D)** The greatest differences in taxa between exclusive breastfeeding and combined feeding under fixed vaginal delivery conditions are presented according to the LDA scores (log10). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis; EB: exclusive breastfeeding; MF: combined feeding.

Supplementary Figure 29

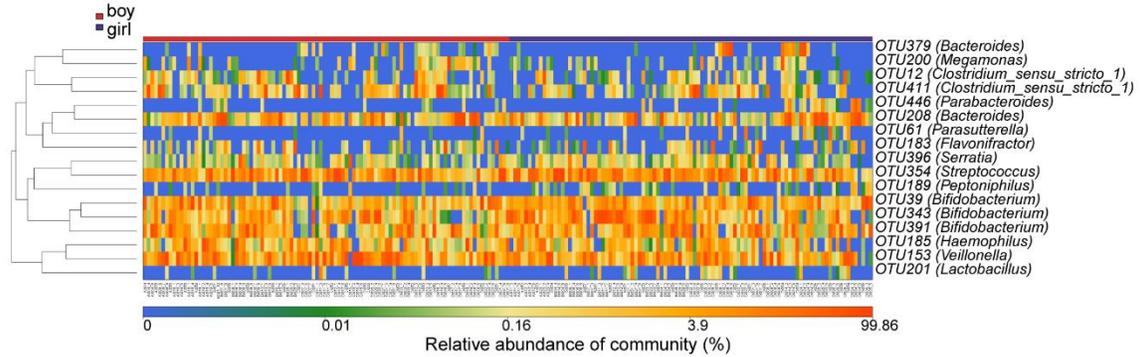


Figure S29: Heatmap showing the relative abundances of the discriminatory OTUs that drive the differences between boys and girls. Each vertical lane corresponds to one sample. Abundances values increase from blue (low abundance) to red (high abundance). OTUs: operational taxonomic units.

Supplementary Figure 30

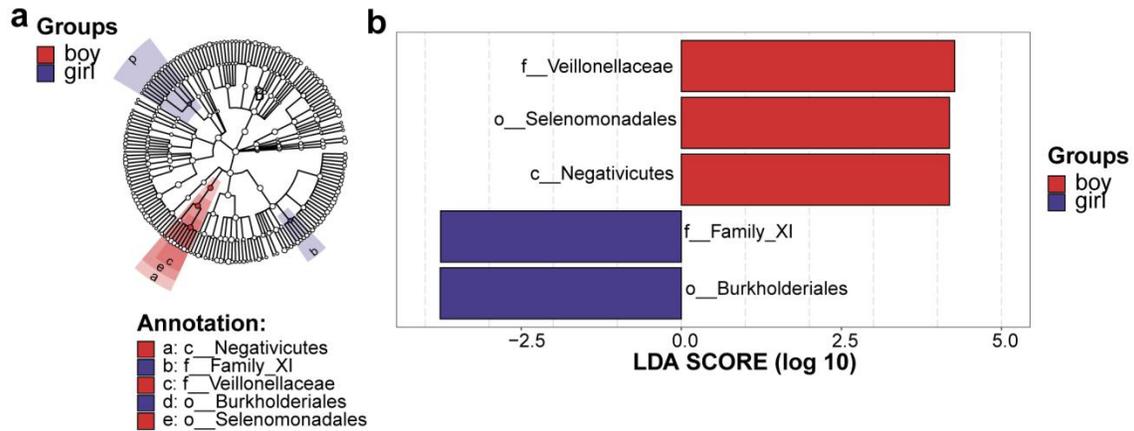


Figure S30: The gut microbiota differences between boys and girls were analyzed using the LefSe method. (a) The LefSe method identified the most differentially abundant taxa between boys and girls. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa between boys and girls are presented according to the LDA scores (log₁₀). LefSe: linear discriminant analysis effect size; LDA: linear discriminant analysis.

Supplementary Figure 31

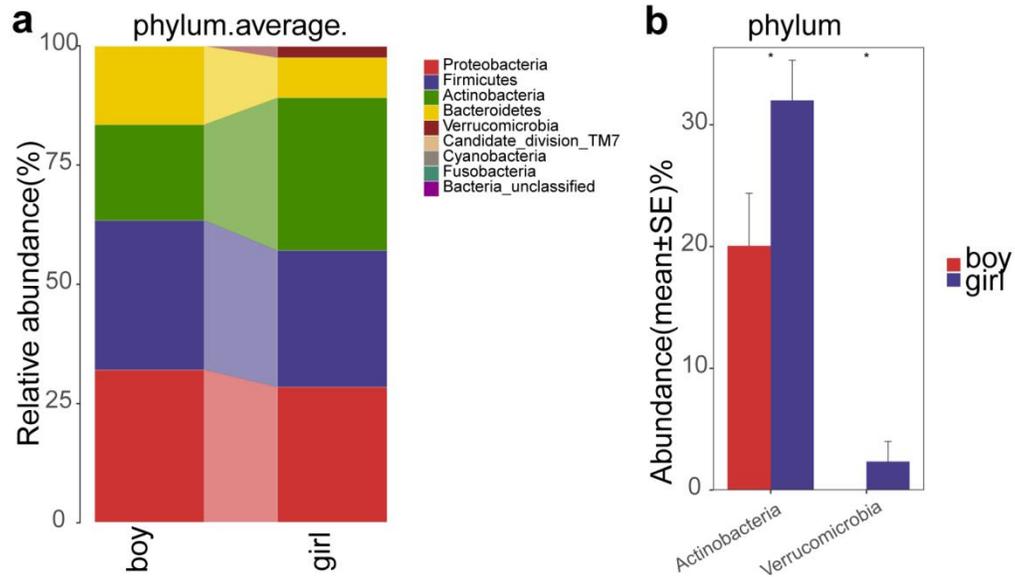


Figure S31: Differences in fecal microbial communities between boys and girls in vaginally delivered infants who were fed exclusively milk. (A) Composition of the fecal microbiota at the phylum level between boys and girls in vaginally delivered infants who were fed exclusively milk. **(B)** Two phyla were significantly increased in girls versus boys in vaginally delivered infants who were fed exclusively milk (all $p < 0.05$).

Supplementary Figure 32

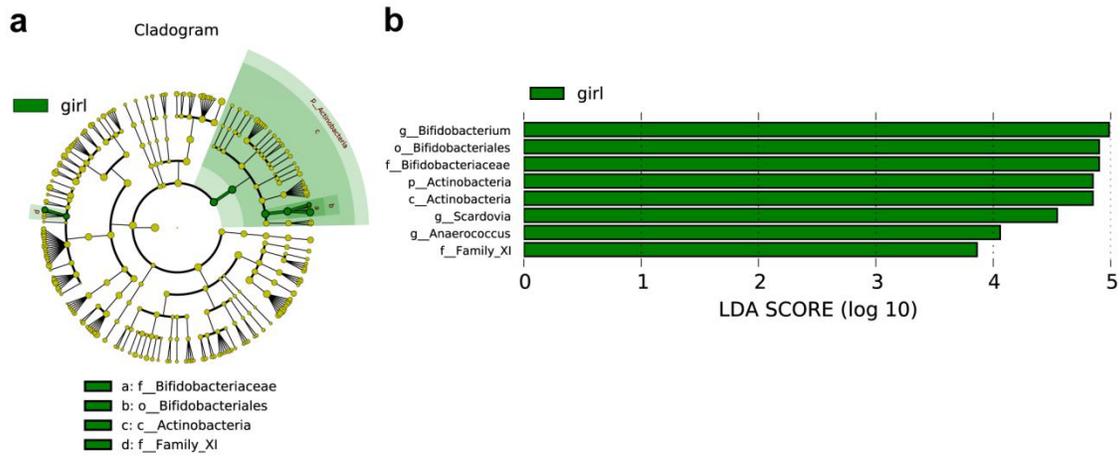


Figure S32: The gut microbiota differences between boys and girls in vaginally delivered infants who were fed exclusively milk were analyzed using the LEfSe method. (a) The LEfSe method identified the most differentially abundant taxa between boys and girls in vaginally delivered infants who were fed exclusively milk. The brightness of each dot is proportional to its effect size. **(b)** The greatest differences in taxa between boys and girls in vaginally delivered infants who were fed exclusively milk are presented according to the LDA scores (log10). LEfSe: linear discriminant analysis effect size; LDA: linear discriminant analysis.

Supplementary Figure 33

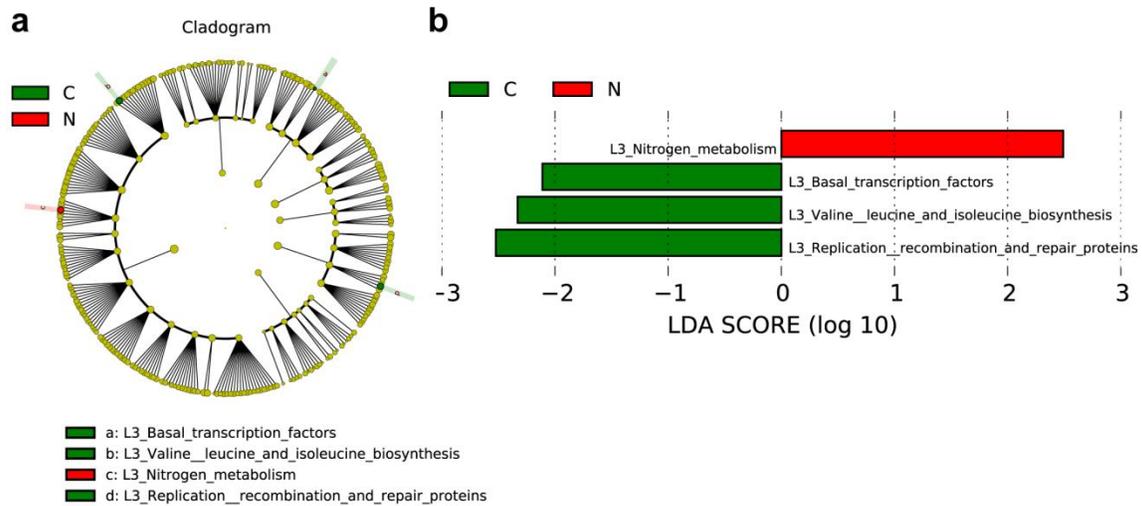


Figure S33: Functional prediction of microbial genes associated with delivery mode at 12 months. (a) A cladogram showing the gut microbial community function profiles of vaginal delivery and cesarean section at 12 months and their predominant microbial functions. **(b)** Functional prediction of microbial genes showing significant differences between vaginal delivery and cesarean section at 12 months. N: vaginally delivered; C: cesarean section.

Supplementary Figure 34

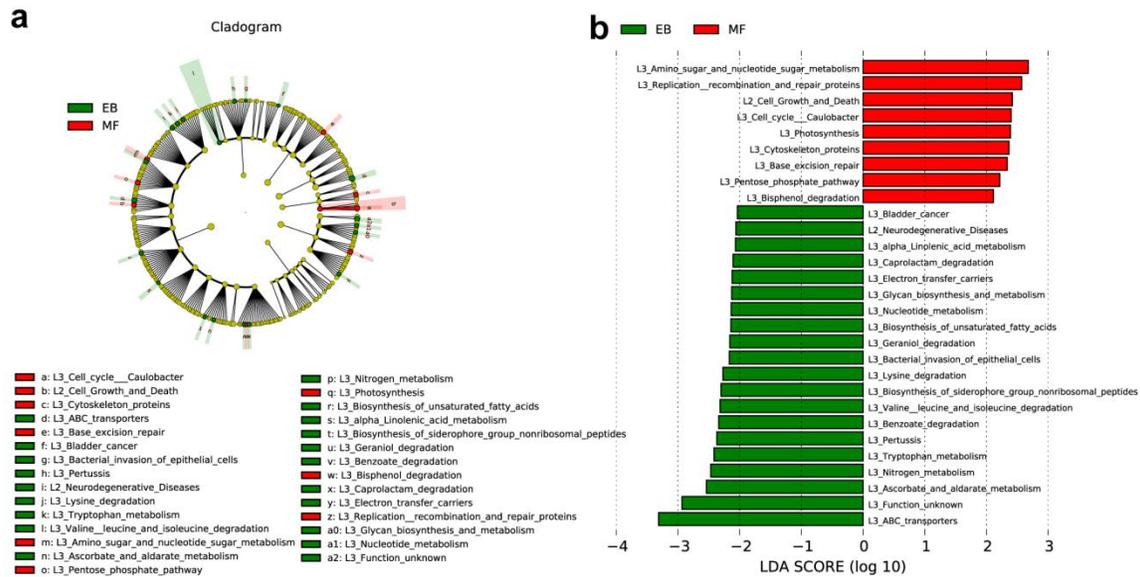


Figure S34: Functional prediction of microbial genes associated with feeding mode at 12 months. (a) A cladogram showing the gut microbial community function profiles of exclusive breastfeeding and combined feeding at 12 months and their predominant microbial functions. **(b)** Functional prediction of microbial genes showing significant differences between exclusive breastfeeding and combined feeding at 12 months. EB: exclusive breastfeeding; MF: combined feeding.