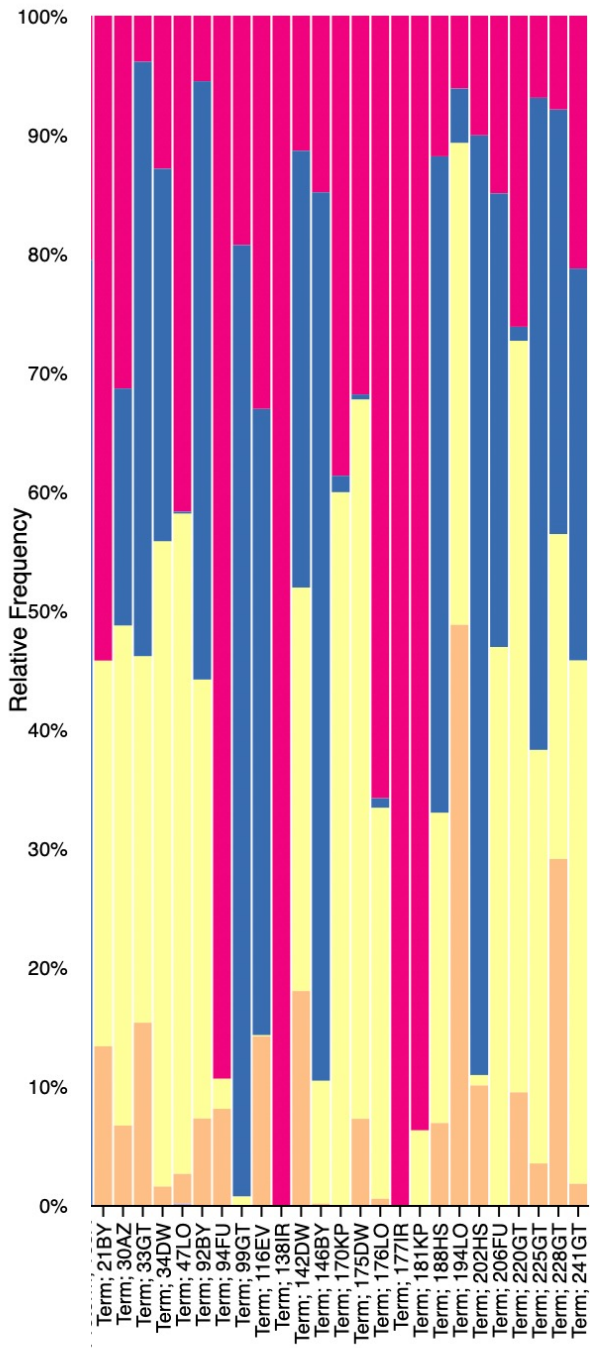


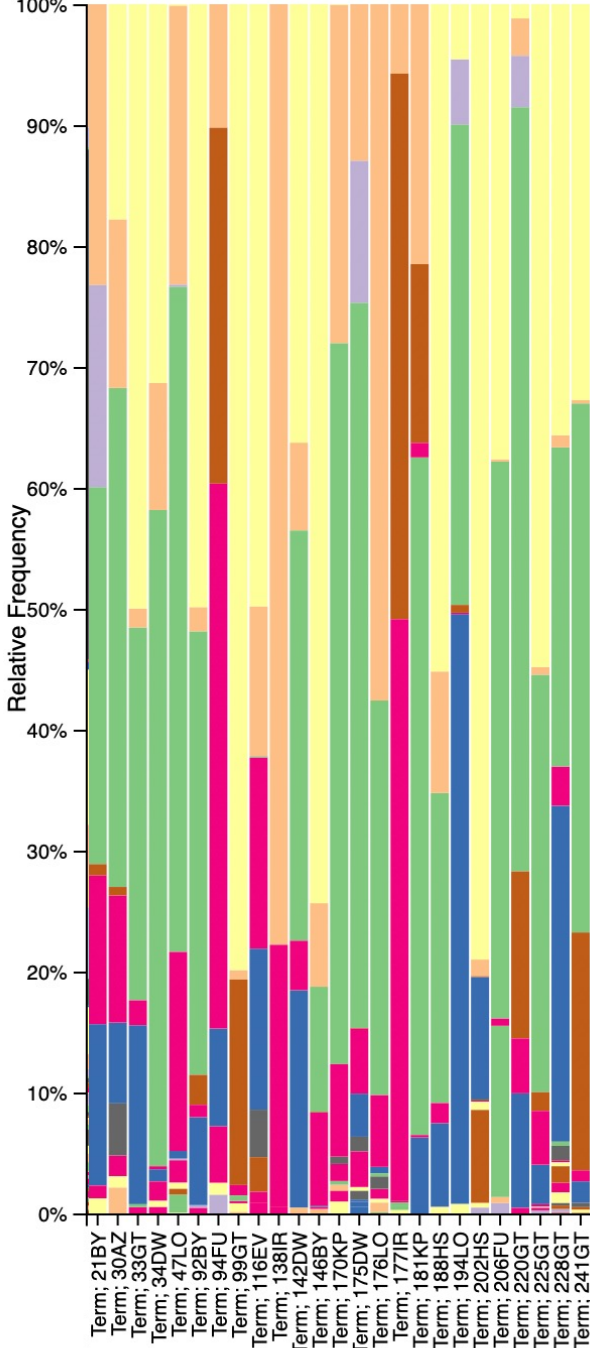
Supplementary Figure 1

A



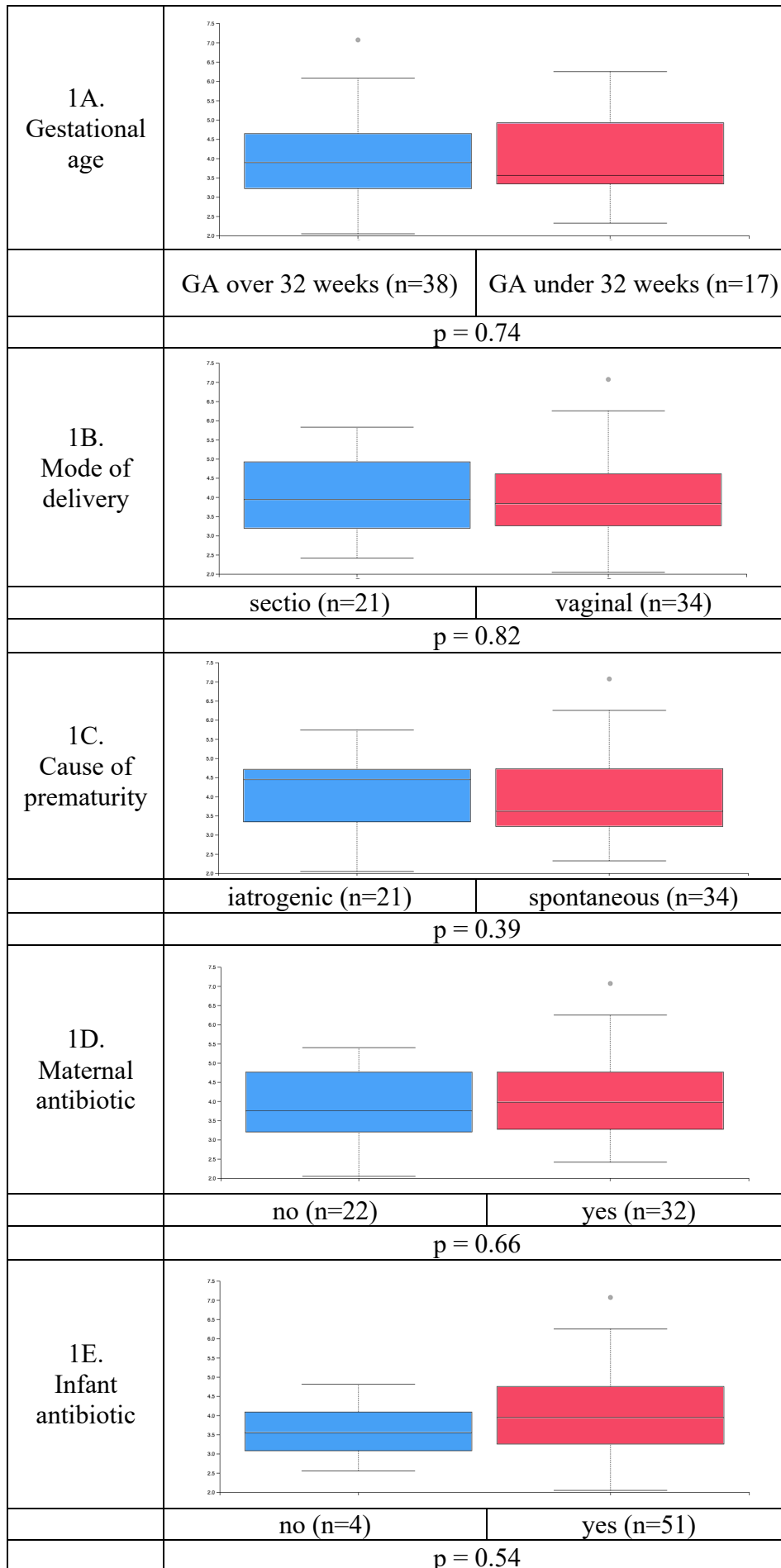
- k__Bacteria;p__Firmicutes
- k__Bacteria;p__Proteobacteria
- k__Bacteria;p__Actinobacteria
- k__Bacteria;p__Bacteroidetes
- k__Bacteria;__
- k__Bacteria;p__Tenericutes
- k__Bacteria;p__Verrucomicrobia
- Unassigned;__
- k__Bacteria;p__Cyanobacteria
- k__Bacteria;p__TM7
- k__Bacteria;p__Fusobacteria
- k__Bacteria;p__Chloroflexi
- k__Bacteria;p__
- k__Bacteria;p__GN02

B

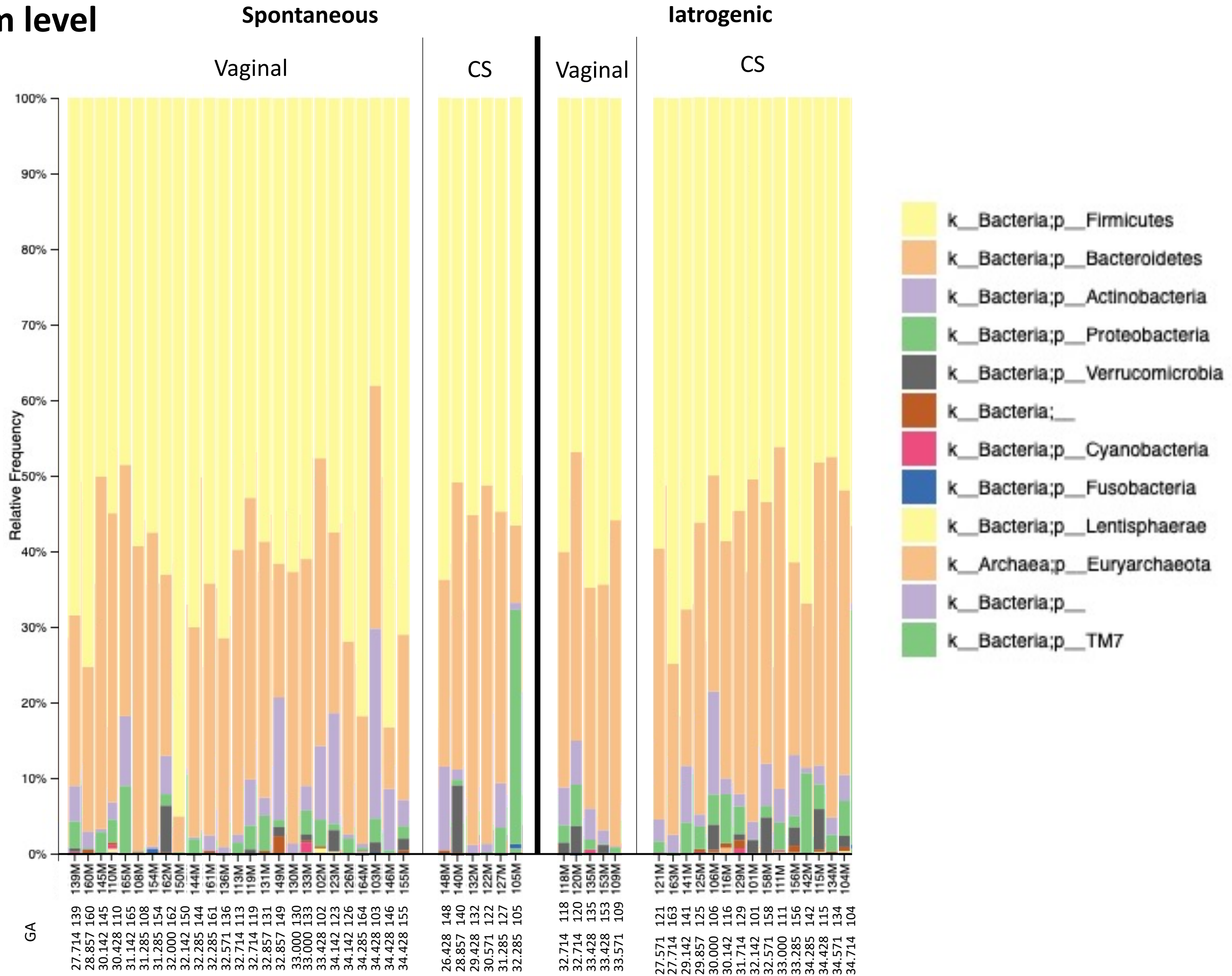


- k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae
- k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae
- k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae
- k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae
- k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;__
- k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae
- k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae
- k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae
- k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cytophagaceae
- k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;__
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae
- k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae
- k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Propionibacteriaceae
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae
- k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae
- k__Bacteria;__;__;__
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Corynebacteriaceae
- k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Alcaligenaceae
- k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae
- k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;__
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;__
- k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae
- k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;__
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Microbacteriaceae
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae]
- k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae
- k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae
- k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae
- k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__
- k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Gordoniaceae

Supplementary Figure 2.



A Phylum level



Supplementary Figure 1. Term microbiota taxa plots at (A) phylum and (B) family levels.

At the phylum level, the most abundant were Proteobacteria, Firmicutes and Actinobacteria.

The three most abundant bacterial families were Bifidobacteriaceae, Enterobacteriaceae and

Planococcaceae. The 35 most abundant families are included.

Supplementary Figure 2. Preterm neonate gut microbiota alpha diversity (Shannon). P-

values are presented below each figure and calculated with Kruskal-Wallis test. None of the

results were statistically significant.

Supplementary Figure 3. Maternal gut microbiota taxa plots in (A) phylum and (B) family

levels grouped by gestational age (GA), cause of prematurity and mode of delivery.

Firmicutes, Bacteroidetes and Actinobacteria were the most abundant phyla and

Bacteroidaceae, Lachnospiraceae and Ruminococcaceae the most abundant bacterial families.

The 24 most abundant families are included.