PICRUST analysis demonstrating differential abundance of bacterial genes in week 1 compared to later weeks in the NICU.

SUPPLEMENTAL DIGITAL CONTENT

Figure S1

Longitudinal analyses of rectal swab samples at the OTU level. Richness (a) and diversity (b,c,d) were similar over time at the OTU level.

Figure S2

Jackknifed estimates of the principal coordinates analysis with an unweighted Unifrac metric. Week 1 samples are shown in red, Week 2 samples are shown in blue, and Week 3-5 samples are shown in yellow. The jackknifed estimates are represented by the confidence ellipsoids around each sample point, representing the degree of variation from one replicate to the next.

Figure S3

Weekly core microbiome. Number of OTUs present in at least 50% of samples for each time period.

Figure S4

Principal coordinates analysis of antibiotics and microbiota. (a) samples collected off antibiotics during week 1 (red), week 2 (blue) and weeks 3-5 (orange); (b) samples collected on antibiotics during week 1 (green), week 2 (purple) and weeks 3-5 (yellow).

Figure S5

Network analysis of samples obtained over time in the NICU. OTUs are represented by small white dots. Large dots represent patient sample nodes obtained on antibiotics in red, and sample nodes obtained off antibiotics in blue. Sample nodes are connected to the OTU nodes in which their sequences are found via lines.

Figure S6

PICRUST analysis controlling for antibiotic treatment. Enhancement of multiple predicted pathways in week 1 on antibiotics (shown in green) versus those obtained in week 3 off antibiotics (shown in red).