Additional Materials

Additional Table 1. a, Correlation of human breast milk sn-2 fatty acids with infant’s gut microbiome by Spearman correlation; b, Partial correlation of human breast milk sn-2 fatty acids with infant’s gut microbiome at 13-15 d; c, Partial correlation of human breast milk sn-2 fatty acids with infant’s gut microbiome at 1 m; d, Partial correlation of human breast milk sn-2 fatty acids with infant’s gut microbiome at 2 m.

Additional Figure 1. Rarefaction curves of 16S rRNA gut microbiome samples.

Additional Figure 2. Differences of gut microbiome taxa at phylum level by phases using Kruskal-Wallis test with posthoc analysis. The star symbol indicates a significant difference ($P < 0.05$). “ns”: $p > 0.05$, “*”: $p \leq 0.05$, “**”: $p \leq 0.01$, “***”: $p \leq 0.001$, “****”: $p \leq 0.0001$. Number in x-axis indicate the separate breastfeeding stages: 0-3 d, 13-15 d, 1 m, 2 m, 3 m, and 4 m.

Additional Figure 3. Differences of gut microbiome taxa at family level by phases using Kruskal-Wallis test with posthoc analysis. The star symbol indicates a significant difference ($P < 0.05$). “ns”: $p > 0.05$, “*”: $p \leq 0.05$, “**”: $p \leq 0.01$, “***”: $p \leq 0.001$, “****”: $p \leq 0.0001$. Number in x-axis indicate the separate breastfeeding stages: 0-3 d, 13-15 d, 1 m, 2 m, 3 m, and 4 m.

Additional Figure 4. Differences of gut microbiome taxa at genus level by phases using Kruskal-Wallis test with posthoc analysis. The star symbol indicates a significant difference ($P < 0.05$). “ns”: $p > 0.05$, “*”: $p \leq 0.05$, “**”: $p \leq 0.01$, “***”: $p \leq 0.001$, “****”: $p \leq 0.0001$. Number in x-axis indicate the separate breastfeeding stages: 0-3 d, 13-15 d, 1 m, 2 m, 3 m, and 4 m.