## 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": $p > 0.05$, "*": $p <= 0.05$, "**": $p <= 0.01$, "***": $p <= 0.001$, "****": $p <= 0.0001$. 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": $p > 0.05$, "*": $p <= 0.05$, "**": $p <= 0.01$, "***": $p <= 0.001$, "****": $p <= 0.0001$. 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": $p > 0.05$, "*": $p <= 0.05$, "**": $p <= 0.01$, "***": $p <= 0.001$, "****": $p <= 0.0001$. Number in x-axis indicate the separate breastfeeding stages: 0-3 d, 13-15 d, 1 m, 2 m, 3 m, and 4 m.