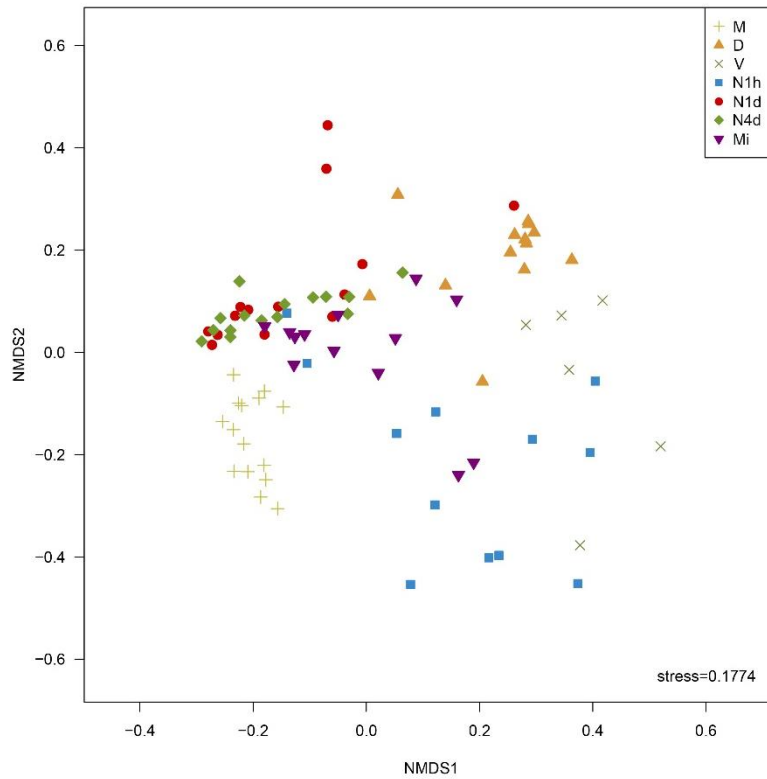


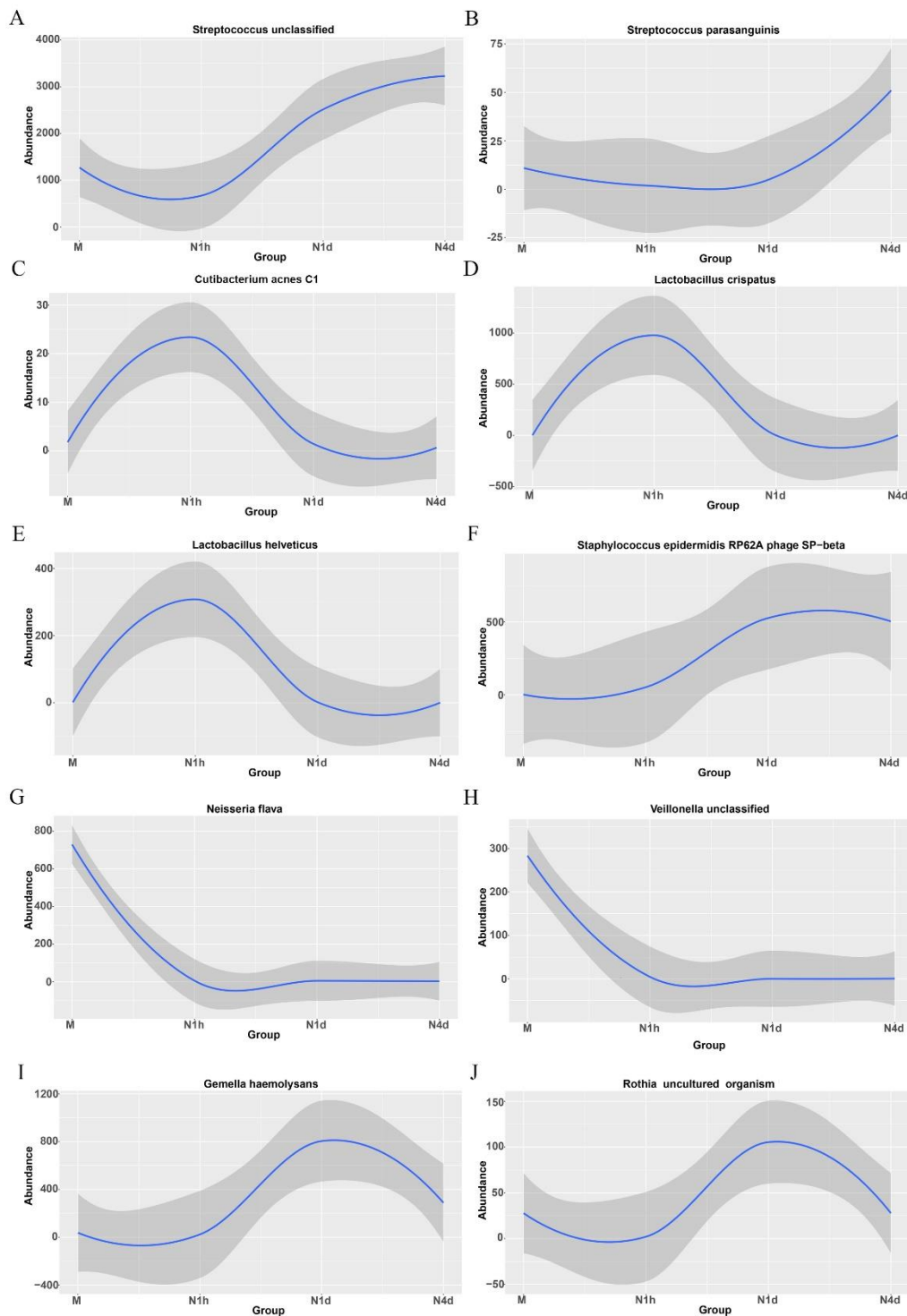
## Supplementary Material

Supplementary Figure 1



**NMDS analysis of microbiomes in the neonates and their mothers.** NMDS based on the Bray–Curtis distances illustrating the beta diversity of the microbiomes of all the groups. Each point represented a single sample.

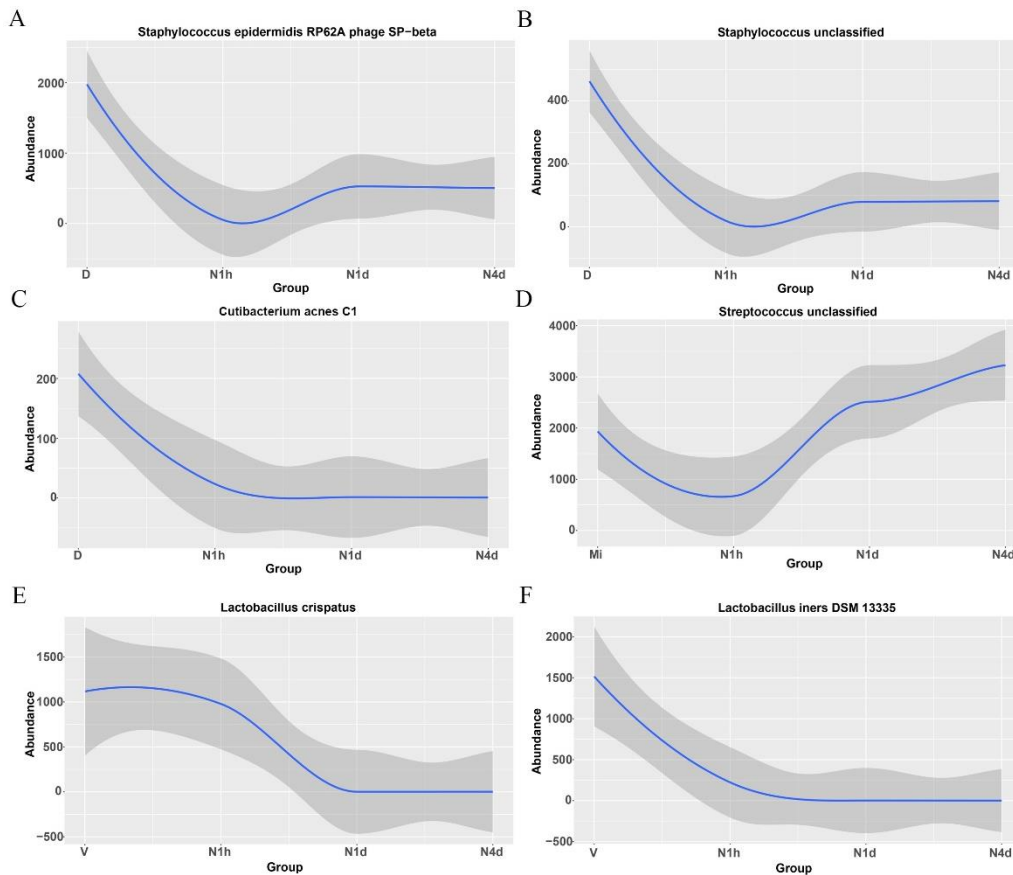
## Supplementary Figure 2



**STAMP analysis of microbiomes to investigate different bacteria among maternal oral microbiome and neonatal oral microbiomes.** STAMP analysis of neonatal groups in comparison with the M group, and then all the significant bacteria in each comparison were fit linearly. The y-coordinate represented the relative abundance of the species, and the x-coordinate represented the

name of sample groups. The relative abundances of the top 20 taxa at the species level of each group were shown.

### Supplementary Figure 3



**STAMP analysis of microbiomes to investigate different bacteria among maternal microbiomes and neonatal oral microbiomes.** STAMP analysis of neonatal groups in comparison with D group (A, B and C), Mi group (D) and V group (E and F), and then all the significant bacteria in each comparison were fit linearly. The y-coordinate represented the relative abundance of the species, and the x-coordinate represented the name of sample groups. The relative abundances of the top 20 taxa at the species level of each group were shown.

### Supplementary Table 1 The shared OTUs among the maternal samples

OTU ID	Taxonomy
OTU11	<i>s_Staphylococcus epidermidis RP62A phage SP_beta</i>
OTU13	<i>g_Cutibacterium</i>
OTU19	<i>g_Haemophilus</i>
OTU25	<i>s_Lactobacillus helveticus</i>
OTU26	<i>s_Aeromonas hydrophila YL17</i>
OTU41	<i>s_Lactobacillus iners DSM 13335</i>
OTU56	<i>s_Prevotella bivia</i>
OTU82	<i>s_Lonsdalea quercina subsp. populi</i>
OTU84	<i>g_Curvibacter; s_unidentified</i>

OTU85	<i>g_Gardnerella; s_uncultured bacterium</i>
OTU87	<i>g_Staphylococcus</i>
OTU96	<i>s_Capnocytophaga gingivalis</i>
OTU98	<i>s_Bifidobacterium breve</i>
OTU100	<i>g_Gemella</i>
OTU113	<i>g_Granulicatella</i>
OTU128	<i>s&gt;Weissella hellenica</i>
OTU130	<i>s_Streptococcus salivarius subsp. salivarius</i>
OTU136	<i>s_Streptococcus parasanguinis</i>
OTU146	<i>s_Lactobacillus crispatus</i>
OTU147	<i>s_Bradyrhizobium denitrificans</i>
OTU148	<i>s_Kocuria marina</i>
OTU168	<i>s_Cutibacterium avidum 44067</i>
OTU182	<i>s_Neisseria oralis</i>
OTU187	<i>g_Vibrio</i>
OTU193	<i>s_Prevotella jejuni</i>
OTU207	<i>g_Escherichia_Shigella</i>
OTU209	<i>s_Porphyrromonas gingivalis</i>
OTU210	<i>g_Rothia; s_uncultured organism</i>
OTU223	<i>g_Lactobacillus</i>
OTU229	<i>s_Pseudomonas aeruginosa VRFPA04</i>
OTU232	<i>s_Lactobacillus delbrueckii subsp. bulgaricus ND02</i>
OTU252	<i>g_Veillonella</i>
OTU255	<i>s_Cutibacterium acnes C1</i>
OTU262	<i>s_Atopobium vaginae DSM 15829</i>
OTU264	<i>g_Streptococcus</i>
OTU266	<i>g_Vibrio</i>
OTU275	<i>s_Brevundimonas vesicularis</i>
OTU277	<i>s_Bacteroides fragilis</i>
OTU290	<i>s_Gemella haemolysans</i>
OTU291	<i>s_Sphingomonas panni</i>
OTU292	<i>g_Prevotella 9</i>
OTU295	<i>s_Neisseria elongata subsp. glycolytica ATCC 29315</i>
OTU310	<i>g_norank</i>
OTU330	<i>g_Erwinia</i>
OTU343	<i>s_Micrococcus luteus</i>
OTU349	<i>s_Enterococcus mundtii ATCC 882</i>
OTU364	<i>g_Streptococcus</i>
OTU368	<i>s_Aerococcus christensenii</i>
OTU370	<i>f_Neisseriaceae; g_uncultured; s_uncultured organism</i>
OTU380	<i>s_Neisseria flava</i>
OTU385	<i>s_Staphylococcus epidermidis RP62A phage SP_beta</i>
OTU416	<i>s_Colocasia esculenta taro</i>

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**Supplementary Table 2 The shared OTUs among the neonate oral groups**

<b>OTU ID</b>	<b>Taxonomy</b>
OTU1	<i>f_Caulobacteraceae; g_uncultured</i>
OTU11	<i>s_Staphylococcus epidermidis RP62A phage SP_beta</i>
OTU13	<i>g_Cutibacterium</i>
OTU19	<i>g_Haemophilus</i>
OTU25	<i>s_Lactobacillus helveticus</i>
OTU34	<i>f_Planococcaceae</i>
OTU41	<i>s_Lactobacillus iners DSM 13335</i>
OTU84	<i>g_Curvibacter; s_unidentified</i>
OTU85	<i>g_Gardnerella; s_uncultured bacterium</i>
OTU87	<i>g_Staphylococcus</i>
OTU98	<i>s_Bifidobacterium breve</i>
OTU100	<i>g_Gemella</i>
OTU107	<i>g_Pelomonas; s_uncultured bacterium</i>
OTU113	<i>g_Granulicatella</i>
OTU118	<i>g_Faecalibacterium</i>
OTU123	<i>g_Streptococcus</i>
OTU130	<i>s_Streptococcus salivarius subsp. salivarius</i>
OTU136	<i>s_Streptococcus parasanguinis</i>
OTU138	<i>g_Curvibacter; s_unidentified</i>
OTU141	<i>g_Parasutterella; s_uncultured organism</i>
OTU146	<i>s_Lactobacillus crispatus</i>
OTU149	<i>g_Streptococcus</i>
OTU178	<i>g_Mesorhizobium</i>
OTU179	<i>g_Bacteroides</i>
OTU198	<i>g_Stenotrophomonas</i>
OTU209	<i>s_Porphyrmonas gingivalis</i>
OTU210	<i>g_Rothia; s_uncultured organism</i>
OTU219	<i>g_Streptococcus</i>
OTU226	<i>g_Bradyrhizobium</i>
OTU227	<i>g_Streptococcus</i>
OTU231	<i>s_Ralstonia insidiosa</i>
OTU232	<i>s_Lactobacillus delbrueckii subsp. bulgaricus ND02</i>
OTU240	<i>g_Undibacterium; s_uncultured bacterium</i>
OTU247	<i>s_uncultured Bosea sp.</i>
OTU252	<i>g_Veillonella</i>
OTU255	<i>s_Cutibacterium acnes C1</i>
OTU262	<i>s_Atopobium vaginae DSM 15829</i>
OTU264	<i>g_Streptococcus</i>
OTU277	<i>s_Bacteroides fragilis</i>
OTU287	<i>g_Bacillus</i>
OTU290	<i>s_Gemella haemolysans</i>
OTU292	<i>g_revotella 9</i>
OTU300	<i>s_Clostridium butyricum</i>
OTU304	<i>g_Bacteroides</i>

OTU310	<i>g_norank</i>
OTU327	<i>s_Bacillus] thermocloacae</i>
OTU330	<i>g_Erwinia</i>
OTU349	<i>s_Enterococcus mundtii ATCC 882</i>
OTU352	<i>g_Actinobacillus</i>
OTU360	<i>s_Corynebacterium suicordis</i>
OTU364	<i>g_Streptococcus</i>
OTU373	<i>s_Bacteroides dorei</i>
OTU380	<i>s_Neisseria flava</i>
OTU385	<i>s_Staphylococcus epidermidis RP62A phage SP_beta</i>
OTU387	<i>s_Algoriphagus sp. JJ018</i>
OTU395	<i>s_human gut metagenome</i>
OTU411	<i>g_Acinetobacter</i>
OTU414	<i>g_Lawsonella; s_uncultured organism</i>
OTU416	<i>s_Colocasia esculenta taro</i>

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Supplementary Table 3 The shared OTUs among all groups

OUT ID	Taxonomy
OTU11	<i>s_Staphylococcus epidermidis RP62A phage SP_beta</i>
OTU13	<i>g_Cutibacterium</i>
OTU19	<i>g_Haemophilus</i>
OTU25	<i>s_Lactobacillus helveticus</i>
OTU41	<i>s_Lactobacillus iners DSM 13335</i>
OTU84	<i>g_Curvibacter; s_unidentified</i>
OTU85	<i>g_Gardnerella; s_uncultured bacterium</i>
OTU87	<i>g_Staphylococcus</i>
OTU98	<i>s_Bifidobacterium breve</i>
OTU100	<i>g_Gemella</i>
OTU113	<i>g_Granulicatella</i>
OTU130	<i>s_Streptococcus salivarius subsp. salivarius</i>
OTU136	<i>s_Streptococcus parasanguinis</i>
OTU146	<i>s_Lactobacillus crispatus</i>
OTU209	<i>s_Porphyrmonas gingivalis</i>
OTU210	<i>g_Rothia; s_uncultured organism</i>
OTU232	<i>s_Lactobacillus delbrueckii subsp. bulgaricus ND02</i>
OTU252	<i>g_Veillonella</i>
OTU255	<i>s_Cutibacterium acnes C1</i>
OTU262	<i>s_Atopobium vaginae DSM 15829</i>
OTU264	<i>g_Streptococcus</i>
OTU277	<i>s_Bacteroides fragilis</i>
OTU290	<i>s_Gemella haemolysans</i>
OTU292	<i>g_Prevotella 9</i>
OTU310	<i>g_norank</i>
OTU330	<i>g_Erwinia</i>

OTU349 s\_*Enterococcus mundtii* ATCC 882  
OTU364 g\_*Streptococcus*  
OTU380 s\_*Neisseria flava*  
OTU385 s\_*Staphylococcus epidermidis* RP62A phage SP\_beta  
OTU416 s\_*Colocasia esculenta taro*

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