

# Supplementary materials

**Table S1.** Basic information of included children

Number	Diagnosis	Gender	Delivery	Age (month)	Number of erupted teeth
A1	RCCL, RCCP, RCCA	M	N	19	12
A2	BCCP	M	N	12	4
A3	BCCL after surgery, BCCP	M	C	12	3
A4	BCCL after surgery, BCLA, BCCP	F	C	15	7
A5	RCL after surgery, RCLA, BCCP	M	N	14	7
A6	BCCP	F	C	12	3
A7	BCCP	F	C	12	3
A8	BCL after surgery, LCCA, LCCP	M	N	12	4
A9	LCCA, LCL, LCCP	F	N	12	4
A10	RCCA, RCL after surgery, RCCP	M	N	12	3
B1	Control	M	C	12	4
B2	Control	F	N	12	4
B3	Control	M	N	12	5
B4	Control	F	C	12	3
B5	Control	M	N	12	5
B6	Control	M	N	12	4
B7	Control	F	C	15	8
B8	Control	M	C	12	8
B9	Control	M	N	12	2
B10	Control	F	N	12	2
P value		1.000 <sup>2</sup>	1.000 <sup>2</sup>	0.279 <sup>1</sup>	0.969 <sup>1</sup>

A1-A10: cleft palate children; B1-B10: healthy children

Diagnostic name notes: CCP, complete cleft palate; CCA, complete cleft alveolar; CCL, complete cleft lip; B, both sides; R, right side; L, left side.

Gender notes: M, male; F, female.

Delivery mode: N, natural labor; C, caesarean birth.

<sup>1</sup> Test by Mann-Whitney U; <sup>2</sup> Test by Fisher's exact

**Table S2.** Comparison of  $\alpha$ -diversity index in oral and nasal samples of two groups in children

Diversity index (M $\pm$ SD)	CP group		Healthy group	
	Saliva	Nasal	Saliva	Nasal
Ace	195.70 $\pm$ 42.88 <sup>b</sup>	155.6 $\pm$ 24.70 <sup>b</sup>	203.10 $\pm$ 39.00 <sup>c</sup>	129.90 $\pm$ 45.33 <sup>c</sup>
Chao1	196.80 $\pm$ 43.43 <sup>b</sup>	140.20 $\pm$ 17.42 <sup>ab</sup>	198.10 $\pm$ 30.49 <sup>c</sup>	114.60 $\pm$ 29.20 <sup>ac</sup>
Shannon	2.53 $\pm$ 0.49	2.68 $\pm$ 0.21 <sup>a</sup>	2.47 $\pm$ 0.46	2.18 $\pm$ 0.31 <sup>a</sup>

SD: Standard deviation, CP: Cleft palate

<sup>a</sup>There was significant difference in nasal microbiota between the two groups ( $p < 0.05$ )

<sup>b</sup>There was significant difference between salivary and nasal microbiota in CP group ( $p < 0.05$ )

<sup>c</sup>There was significant difference between salivary and nasal microbiota in healthy group ( $p < 0.05$ )

**Table S3.** Microbial biomarkers of oronasal bacteria of children

Microbial biomarkers of children	
Nasal	Saliva
Cleft palate > Healthy	Healthy > Cleft palate
<i>Granulicatella</i>	<i>Haemophilus</i>
<i>Actinomyces</i> <sup>*†</sup>	<i>Pseudomonas</i>
<i>Atopobium</i>	<i>Aggregatibacter</i>
<i>Gemella</i> <sup>*†</sup>	<i>Serratia</i>
<i>Veillonella</i> <sup>*†</sup>	<i>Achromobacter</i>
<i>Rothia</i> <sup>*†</sup>	
<i>Prevotella</i> <sup>*</sup>	
<i>Haemophilus</i>	
<i>Staphylococcus</i>	
<i>Streptococcus</i> <sup>*†</sup>	

<sup>\*</sup>O-N bacs in the nasal microbial biomarkers of CP children

<sup>†</sup>TS O-N bacs in the nasal microbial biomarkers of CP children

**Table S4.** Basic information of included adolescents

Number	Diagnosis	Palatoplasty (yes/no)	Gender	Age (year)	DMFT
C1	BCCP	no	M	15	0
C2	LCCL after surgery, LCCA, LCCP	no	M	18	0
C3	LCCL after surgery, LCCA, LCCP	no	M	18	1
C4	LCCP	no	M	18	0
C5	RCCL after surgery, RCCA, RCCP	no	F	13	0
D1	BCCL after surgery, BCCP after surgery, BCCA	yes	M	13	3
D2	LCCL after surgery, LCCP after surgery, LCCA	yes	F	18	0
D3	LCCL after surgery, LCCP after surgery, LCCA	yes	M	18	0
D4	LCCP after surgery, LCCA	yes	M	15	0
D5	BCCL after surgery, BCCP after surgery BCCA	yes	M	16	2
D6	BCCL after surgery, BCCP after surgery BCCA	yes	M	18	0
D7	BCCP after surgery	yes	M	16	0
D8	LCCL after surgery, LCCP after surgery LCCA	yes	F	15	0
D9	LCCL after surgery, LCCP after surgery LCCA	yes	M	15	0
D10	RCCP after surgery, RCCA	yes	M	18	2
E1	Control	-	M	16	0
E2	Control	-	F	18	0
E3	Control	-	F	17	0
E4	Control	-	F	18	0
E5	Control	-	M	14	2
E6	Control	-	M	14	0
E7	Control	-	M	14	1
E8	Control	-	M	18	0
E9	Control	-	M	18	0
E10	Control	-	M	18	0
P			1.000 <sup>2</sup>	0.873 <sup>1</sup>	0.618 <sup>1</sup>

C1-C5: cleft palate adolescents; D1-D10: postoperative adolescents; E1-E10: healthy adolescents

Diagnostic name notes: CCP, complete cleft palate; CCA, complete cleft alveolar; CCL, complete cleft lip; B, both sides; R, right side; L, left side.

Gender notes: M, male; F, female.

<sup>1</sup> Test by independent-sample Kruskal-Wallis test;

<sup>2</sup> Test by Fisher's exact

**Table S5.** Comparison of  $\alpha$ -diversity index in oral and nasal samples of three adolescence groups

		Nasal		Saliva	
		M	SD	M	SD
<b>Ace</b>	CP group	219.4 <sup>a</sup>	83.54	346.8	46.27
	Postoperative group	180.6 <sup>a</sup>	78.61	332	44.81
	Healthy group	113.6	49.16	337	96.01
<b>Chao1</b>	CP group	182.2 <sup>a</sup>	72.95	342	37.98
	Postoperative group	161.9 <sup>a</sup>	67.52	307.7	50.15
	Healthy group	106.2	33.83	331.5	91.32
<b>Shannon</b>	CP group	2.82 <sup>a</sup>	0.58	3.29	0.85
	Postoperative group	2.66	0.42	3.02 <sup>b</sup>	0.67
	Healthy group	2.33	0.24	3.71	0.56

<sup>a</sup>There was significant difference in nasal microbiota between the tag and healthy group

( $p < 0.05$ )

<sup>b</sup>There was significant difference in salivary microbiota between the tag and healthy group

( $p < 0.05$ )

**Table S6.** Microbial biomarkers in the nasal cavity of adolescents

Microbial biomarkers in the nasal cavity of adolescents				
Cleft palate-Healthy		Postoperative-Healthy		Cleft palate- Postoperative
Cleft palate > Healthy	Healthy > Cleft palate	Postoperative > Healthy	Healthy > Postoperative	Cleft palate > Postoperative
<i>Atopobium</i> <sup>*</sup>	<i>Serratia</i>	<i>Streptococcus</i> <sup>#†</sup>	<i>Escherichia_Shigella</i>	<i>Dolosigranulum</i>
<i>Oribacterium</i> <sup>*</sup>	<i>Escherichia_Shigella</i>	<i>Haemophilus</i> <sup>#</sup>	<i>Serratia</i>	<i>Achromobacter</i>
<i>Mycoplasma</i> <sup>*</sup>	<i>Rhodococcus</i>	<i>Parvimonas</i> <sup>#</sup>		<i>Lautropia</i>
<i>Catonella</i> <sup>*</sup>		<i>Gemella</i> <sup>#†</sup>		<i>Sphingomonas</i>
<i>Campylobacter</i> <sup>*</sup>		<i>Peptostreptococcus</i> <sup>#</sup>		
<i>Klebsiella</i>		<i>Rothia</i> <sup>*†</sup>		
<i>Rothia</i> <sup>*†</sup>		<i>Dialister</i> <sup>#</sup>		
<i>Dialister</i> <sup>*</sup>		<i>Porphyromonas</i>		
<i>Alloprevotella</i> <sup>*†</sup>		<i>Catonella</i> <sup>#</sup>		
<i>Veillonella</i> <sup>*†</sup>		<i>Fusobacterium</i>		
<i>Sphingomonas</i>		<i>Campylobacter</i> <sup>#</sup>		
<i>Solobacterium</i>		<i>Actinobacillus</i> <sup>#</sup>		
<i>Selenomonas</i> <sup>*</sup>		<i>Oribacterium</i> <sup>#</sup>		
<i>Slackia</i>		<i>Alloprevotella</i> <sup>#†</sup>		
<i>Gemella</i> <sup>*†</sup>				
<i>Parvimonas</i> <sup>*</sup>				
<i>Peptostreptococcus</i> <sup>*</sup>				
<i>Filifactor</i> <sup>*</sup>				
<i>Prevotella</i> <sup>*</sup>				
<i>Porphyromonas</i> <sup>*</sup>				
<i>Streptococcus</i> <sup>*†</sup>				

<sup>\*</sup>O-N bacs in the nasal microbial biomarkers of CP adolescents

<sup>#</sup>O-N bacs in the nasal microbial biomarkers of postoperative adolescents

<sup>†</sup>TS O-N bacs in the nasal microbial biomarkers of CP adolescents and postoperative adolescents

**Table S7.** Microbial biomarkers in the saliva of adolescents

Microbial biomarkers in the saliva of adolescents			
Cleft palate-Healthy	Postoperative - Healthy		Cleft palate- Postoperative
Healthy > Cleft palate	Postoperative > Healthy	Healthy > Postoperative	Cleft palate > Postoperative
<i>Pseudomonas</i>	<i>Streptococcus</i>	<i>Achromobacter</i>	<i>Campylobacter</i>
<i>Serratia</i>	<i>Granulicatella</i>	<i>Stenotrophomonas</i>	<i>Leptotrichia</i>
<i>Stenotrophomonas</i>		<i>Veillonella</i>	
<i>Achromobacter</i>		<i>Solobacterium</i>	
<i>Kingella</i>		<i>Serratia</i>	
<i>Rhodococcus</i>		<i>Burkholderia</i>	
		<i>Pseudomonas</i>	

**Table S8.** Translocation bacteria between oral and nasal cavity CP children

Direction	Genera	Proportion (%)			
		CP-nasal	H-nasal	CP-saliva	H-saliva
Nasal— Oral	<i>Cyanobacteria_norank</i>	0.023%	0.003%	0.012%	0.002%
	<i>Dolosigranulum</i>	8.865%	15.488%	0.015%	0.000%
	<i>Staphylococcus</i>	4.132%	0.048%	0.012%	0.002%
	<i>Acinetobacter</i>	0.017%	0.037%	0.008%	0.000%
Oral— Nasal	<i>Actinomyces</i>	0.340%	0.005%	1.347%	0.503%
	<i>Prevotella</i>	0.987%	0.008%	2.993%	1.238%
	<i>Rothia</i>	1.018%	0.013%	1.262%	0.983%
	<i>Streptococcus</i>	11.300%	0.502%	57.372%	54.840%
	<i>Neisseria</i>	0.147%	0.058%	9.580%	7.768%
	<i>Veillonella</i>	0.833%	0.027%	3.675%	3.943%
	<i>Gemella</i>	0.432%	0.017%	3.883%	2.332%
	<i>Alloprevotella</i>	0.293%	0.015%	2.962%	4.272%
	<i>Lautropia</i>	0.005%	0.000%	0.338%	0.098%

Nasal-Oral: Common nasal bacteria translocated to oral microbiota

Oral-Nasal: Common oral bacteria translocated to nasal microbiota

CP: Cleft palate group

H: Health group

**Table S9.** Translocation bacteria between oral and nasal cavity in CP adolescents

Directi on	Genera	Proportion (%)					
		CP-nasal	Post- nasal	H-nasal	CP- saliva	Post- saliva	H-saliva
Nasal	<i>Staphylococcus</i>	3.420%	7.573%	3.868%	0.040%	0.022%	0.002%
—Oral	<i>Corynebacterium</i>	3.397%	2.792%	3.868%	1.147%	0.560%	0.913%
Oral— Nasal	<i>Actinobacillus</i>	0.037%	0.095%	0.003%	1.410%	0.470%	0.352%
	<i>Actinomyces</i>	0.103%	0.113%	0.008%	1.230%	2.103%	2.637%
	<i>Alloprevotella</i>	0.177%	0.118%	0.002%	0.407%	0.548%	0.340%
	<i>Atopobium</i>	0.027%	0.020%	0.000%	0.033%	0.067%	0.060%
	<i>Campylobacter</i>	0.097%	0.032%	0.000%	0.183%	0.130%	0.157%
	<i>Catonella</i>	0.083%	0.050%	0.002%	0.177%	0.298%	0.233%
	<i>Dialister</i>	0.017%	0.017%	0.000%	0.060%	0.045%	0.038%
	<i>Family_XIII_incertae_sedis</i>	0.430%	0.028%	0.000%	0.143%	0.128%	0.222%
	<i>Filifactor</i>	1.347%	0.040%	0.000%	0.173%	0.102%	0.202%
	<i>Lachnoanaerobaculum</i>	0.030%	0.035%	0.003%	0.927%	0.327%	0.502%
	<i>Leptotrichia</i>	0.040%	0.067%	0.003%	3.433%	0.743%	1.430%
	<i>Mogibacterium</i>	0.013%	0.012%	0.000%	0.017%	0.010%	0.025%
	<i>Mycoplasma</i>	0.013%	0.020%	0.000%	0.017%	0.003%	0.012%
	<i>Oribacterium</i>	0.063%	0.027%	0.000%	0.277%	0.487%	0.470%
	<i>Parvimonas</i>	0.677%	1.662%	0.002%	0.067%	0.070%	0.088%
	<i>Peptostreptococcaceae_incer tae_sedis</i>	0.110%	0.025%	0.003%	0.130%	0.055%	0.228%
	<i>Peptostreptococcus</i>	0.953%	0.800%	0.000%	0.167%	0.210%	0.512%
	<i>Rothia</i>	0.137%	0.510%	0.000%	2.093%	2.245%	4.073%
	<i>Tannerella</i>	0.140%	0.017%	0.002%	0.793%	0.140%	0.183%
	<i>Treponema</i>	0.133%	0.023%	0.002%	0.287%	0.137%	0.353%
	<i>Streptococcus</i>	2.850%	4.412%	0.100%	45.413%	56.365%	29.637%
	<i>Gemella</i>	0.627%	1.207%	0.012%	4.663%	3.263%	2.208%
	<i>Neisseria</i>	0.187%	0.238%	0.045%	6.343%	5.913%	6.130%
	<i>Veillonella</i>	0.070%	0.025%	0.020%	1.740%	1.095%	2.803%
	<i>Bergeyella</i>	0.020%	0.008%	0.002%	0.750%	1.475%	1.028%
	<i>Candidate_division_TM7_no rank</i>	0.027%	0.007%	0.000%	0.767%	0.133%	0.632%
	<i>Eikenella</i>	0.023%	0.008%	0.008%	0.233%	0.108%	0.120%
	<i>Family_XIII_uncultured</i>	0.073%	0.005%	0.000%	0.017%	0.023%	0.163%
	<i>Johnsonella</i>	0.123%	0.010%	0.002%	0.557%	0.105%	0.160%
	<i>Peptococcus</i>	0.247%	0.003%	0.000%	0.050%	0.017%	0.045%
	<i>Pseudoramibacter</i>	0.033%	0.000%	0.000%	0.007%	0.005%	0.008%
	<i>Selenomonas</i>	0.020%	0.005%	0.002%	0.763%	0.212%	0.670%
	<i>Synergistaceae_uncultured</i>	0.023%	0.003%	0.000%	0.030%	0.025%	0.018%
	<i>Fusobacterium</i>	1.503%	0.400%	0.017%	2.687%	1.698%	2.800%
	<i>Porphyromonas</i>	1.380%	0.405%	0.013%	2.500%	2.233%	2.577%
	<i>Prevotella</i>	1.320%	0.747%	0.052%	2.757%	3.382%	3.637%
	<i>Abiotrophia</i>	0.003%	0.017%	0.002%	0.720%	0.355%	0.347%

<i>Actinobaculum</i>	0.003%	0.012%	0.000%	0.063%	0.143%	0.027%
<i>Aggregatibacter</i>	0.003%	0.043%	0.007%	0.600%	0.398%	0.552%
<i>Neisseriaceae_norank</i>	0.000%	0.023%	0.003%	0.020%	0.205%	0.385%
<i>Haemophilus</i>	0.657%	4.183%	0.072%	2.077%	2.960%	4.417%

Nasal-Oral: Common nasal bacteria translocated to oral microbiota

Oral-Nasal: Common oral bacteria translocated to nasal microbiota

CP: Cleft palate group

H: Health group

Post: Postoperative group

In the oral-nasal part, black font: Exchange genera of CP and postoperative adolescents

Red font: Exchange genera of CP adolescents only

Green font: Exchange genera of postoperative adolescents only

**Table S10.** Dominant oral bacteria ( > 1%) in each group

Children			Adolescents	
CP-saliva	H-saliva	Post-saliva	CP-saliva	H-saliva
<i>Streptococcus</i> (57.37%)* <sup>†</sup>	<i>Streptococcus</i> (54.84%)	<i>Streptococcus</i> (56.37%)* <sup>†</sup>	<i>Streptococcus</i> (45.41%)* <sup>†</sup>	<i>Streptococcus</i> (29.6%)
<i>Neisseria</i> (9.58%)* <sup>†</sup>	<i>Neisseria</i> (7.77%)	<i>Neisseria</i> (5.91%)* <sup>†</sup>	<i>Neisseria</i> (6.34%)* <sup>†</sup>	<i>Pseudomonas</i> (10.00%)
<i>Granulicatella</i> (4.12%)	<i>Granulicatella</i> (5.57%)	<i>Prevotella</i> (3.38%)	<i>Gemella</i> (4.66%)* <sup>†</sup>	<i>Serratia</i> (6.64%)
<i>Gemella</i> (3.88%)* <sup>†</sup>	<i>Bergeyella</i> (4.66%)	<i>Gemella</i> (3.26%)* <sup>†</sup>	<i>Leptotrichia</i> (3.43%)* <sup>†</sup>	<i>Neisseria</i> (6.13%)
<i>Veillonella</i> (3.68%)* <sup>†</sup>	<i>Alloprevotella</i> (4.27%)	<i>Haemophilus</i> (2.96%)* <sup>†</sup>	<i>Granulicatella</i> (3%)	<i>Haemophilus</i> (4.42%)
<i>Prevotella</i> (2.99%)*	<i>Veillonella</i> (3.94%)	<i>Granulicatella</i> (2.58%)	<i>Prevotella</i> (2.76%)* <sup>†</sup>	<i>Rothia</i> (4.07%)
<i>Alloprevotella</i> (2.96%)* <sup>†</sup>	<i>Haemophilus</i> (3.17%)	<i>Pseudomonas</i> (2.37%)	<i>Fusobacterium</i> (2.69%)* <sup>†</sup>	<i>Prevotella</i> (3.64%)
<i>Bergeyella</i> (2.57%)	<i>Porphyromonas</i> (2.34%)	<i>Rothia</i> (2.25%)* <sup>†</sup>	<i>Capnocytophaga</i> (2.63%)	<i>Veillonella</i> (2.80%)
<i>Porphyromonas</i> (1.75%)	<i>Gemella</i> (2.33%)	<i>Porphyromonas</i> (2.23%)	<i>Porphyromonas</i> (2.5%)* <sup>†</sup>	<i>Fusobacterium</i> (2.80%)
<i>Actinomyces</i> (1.35%)* <sup>†</sup>	<i>Pseudomonas</i> (1.95%)	<i>Actinomyces</i> (2.10%)* <sup>†</sup>	<i>Rothia</i> (2.09%)* <sup>†</sup>	<i>Actinomyces</i> (2.64%)
<i>Rothia</i> (1.26%)* <sup>†</sup>	<i>Prevotella</i> (1.24%)	<i>Fusobacterium</i> (1.70%)	<i>Haemophilus</i> (2.08%)	<i>Porphyromonas</i> (2.58%)
<i>Haemophilus</i> (1.01%)		<i>Bergeyella</i> (1.48%)	<i>Veillonella</i> (1.74%)* <sup>†</sup>	<i>Stenotrophomonas</i> (2.40%)
		<i>Serratia</i> (1.38%)	<i>Pseudomonas</i> (1.66%)	<i>Gemella</i> (2.21%)
		<i>Veillonella</i> (1.10%)* <sup>†</sup>	<i>Actinobacillus</i> (1.41%)* <sup>†</sup>	<i>Achromobacter</i> (1.82%)
			<i>Actinomyces</i> (1.23%)* <sup>†</sup>	<i>Lautropia</i> (1.59%)
			<i>Corynebacterium</i> (1.15%)	<i>Leptotrichia</i> (1.43%)
				<i>Capnocytophaga</i> (1.41%)
				<i>Granulicatella</i> (1.25%)
				<i>Bergeyella</i> (1.03%)

\*O-N bacs in the oral dominant bacteria of CP children

\*O-N bacs in the oral dominant bacteria of postoperative adolescents

#O-N bacs in the oral dominant bacteria of CP adolescents

<sup>†</sup>TS O-N bacs in the oral dominant bacteria

CP: Cleft palate group

H: Health group

Post: Postoperative group