

Table S3: Prevalence and mean relative abundance of nasopharynx ASVs shared between OME patients and healthy controls. The healthy controls were considered cumulatively (HNPAI) and individually (HNPCI = Cochlear implant recipients, HNPDC = day-care children). To calculate the mean relative abundance, only samples in which the taxon was present was considered.

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Abiotrophia 1	defectiva	24%	25%	30%	24%	0,1%	0,1%	0,0%	0,1%	TACGTAGGTGGCGAGCGTTGTCCGATTATTGGGCGTAAAGGGAGTGTAGGCGGCTTTTAACTGATGTGAAAG CCCACGGCTCAACCTGGAGGGTTCATTGGAACTGGGAGACTTGTAGTGCAGAAGAGGAGAGCGGAATCCATGTGT AGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAAGTACGCTGAGGCT CGAAAGCGTGGGGAGCAACAGG
Acinetobacter 1	lwoffii/pseudolwoffii	3%	33%	20%	37%	0,3%	0,1%	0,1%	0,1%	TACAGAGGGTGCAAGCGTTAATCGAATTTACTGGGCGTAAAGCGCGCTAGGTGGCAATTAAGTCAAATGTGAAAT CCCCGAGCTTAACCTGGGAATTCGATTCGATACTGGTGGCTAGAGTATGGGAGAGGATGGTGAATCCAGGTGTA GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCTAATACTGACACTGAGGTG CGAAAGCATGGGGAGCAACAGG
Acinetobacter 3	johnsonii/oryzae	6%	12%	20%	10%	0,0%	0,1%	0,0%	0,1%	TACAGAGGGTGCGAGCGTTAATCGAATTTACTGGGCGTAAAGCGTGCCTAGGCGGCTTTTAACTCGGATGTGAAAT CCCTGAGCTTAACCTAGGAATTCGATTCGATACTGGGAAGCTAGAGTATGGGAGAGGATGGTGAATCCAGGTGTA GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCTAATACTGACGCTGAGGTA CGAAAGCATGGGGAGCAACAGG
Acinetobacter 4	baumannii	1%	10%	10%	10%	0,0%	0,1%	0,2%	0,1%	TACAGAGGGTGCGAGCGTTAATCGAATTTACTGGGCGTAAAGCGTGCCTAGGCGGCTTTAAGTTCGGATGTGAAAT CCCCGAGCTTAACCTGGGAATTCGATTCGATACTGGTGGCTAGAGTATGGGAGAGGATGGTGAATCCAGGTGTA GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCCATCTGGCTAATACTGACGCTGAGGTA CGAAAGCATGGGGAGCAACAGG
Actinobacillus 1 (Haemophilus or Conservatibacter)	H. parainfluenzae or C. flavescens	60%	57%	70%	54%	0,8%	0,7%	1,1%	0,5%	TACGGAGGGTGCGAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTGACTTAAGTGAAGTGTGAAA GCCCGGGCTTAACCTGGGAATTCGATTCGATACTGGTGGCTAGAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACGCTCATGTG CGAAAGCGTGGGGAGCAACAGG
Actinobacillus 2 (Haemophilus)	parahaemolyticus/paraphrohaemolyticus/sputorum	27%	10%	20%	7%	1,3%	0,3%	0,3%	0,2%	TACGGGGGGTGCGAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTGACTTAAGTGAAGTGTGAAA GCCCGGGCTTAACCTGGGAATTCGATTCGATACTGGTGGCTAGAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACGCTCATGTG CGAAAGCGTGGGGAGCAACAGG
Actinobacillus 3 (Haemophilus)	NA	34%	4%	10%	2%	0,9%	0,6%	0,9%	0,3%	TACGGGGGGTGCGAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTGACTTAAGTGAAGTGTGAAA GCCCGAGCTTAACCTGGGAATTCGATTCGATACTGGTGGCTAGAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACGCTCATGTG CGAAAGCGTGGGGAGCAACAGG
Actinomyces 1 (Schaalia)	odontolytica	25%	24%	30%	22%	0,1%	0,4%	0,2%	0,5%	TACGTAGGGGCGGAGCGTTGTCCGGAATTTATTGGGCGTAAAGGGCTTGTAGGCGGTTGGTCCGCTGTGCCGTGAAAT CCTCTGGCTTAACCTGGGGCGTGGTGGGTACGGGCTGACTTGTAGTGCAGTGGGGAGACTGGAATCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAAGAACCAGGCGGCGAAGGCGGCTCTGGGCGTACTGACGCTGAGGA GCGAAAGCGTGGGGAGCGAACAGG
Actinomyces 2	naeslundii/oris	21%	25%	10%	29%	0,2%	0,2%	0,1%	0,2%	TACGTAGGGGCGGAGCGTTGTCCGGAATTTATTGGGCGTAAAGGGCTTGTAGGCGGTTGTCCGCTGTGCCGTGAAAT CCTCTGGCTTAACCTGGGGCGTGGTGGGTACGGGCGGCTTGTAGTGCAGTGGGGAGACTGGAATCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAAGAACCAGGCGGCGAAGGCGGCTCTGGGCGTACTGACGCTGAGGA GCGAAAGCGTGGGGAGCGAACAGG
Actinomyces 5	NA	9%	4%	10%	2%	0,1%	0,1%	0,0%	0,2%	TACGTAGGGGCGGAGCGTTGTCCGGAATTTATTGGGCGTAAAGGGCTTGTAGGCGGTTGTCCGCTGTGCCGTGAAAT CCTCTGGCTTAACCTGGGGCGTGGTGGGTACGGGCGGCTTGTAGTGCAGTGGGGAGACTGGAATCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAAGAACCAGGCGGCGAAGGCGGCTCTGGGCGTACTGACGCTGAGGA GCGAAAGCGTGGGGAGCGAACAGG
Aggregatibacter 2	aphrophilus/kilianii	4%	4%	10%	2%	0,1%	0,4%	0,8%	0,0%	TACGGAGGGTGCGAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGACTTTAAGTGAAGTGTGAAA TCCCCGGGCTTAACCTGGGAATTCGATTCGATACTGGGCTAGAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACGCTCATGTG CGAAAGCGTGGGGAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Aggregatibacter 4	segnis	3%	4%	10%	2%	0,1%	0,1%	0,1%	0,2%	TACGGAGGGTGCAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGCGCGACTTTAAGTGAAGGTGTGAAA TCCC CGGGCTAACCTGGGAATTGCATTTCAGACTGGGAGTCTAGAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGCGAAGGCAGCCCTTGGGAATGACTGACGCTCATGTG CGAAGCGTGGGGAGCAACAGG
Alloiococcus 1	otitis	27%	14%	30%	10%	0,1%	0,0%	0,0%	0,0%	TACGTAGGTGACAAGCGTTGTCGGATTTATTGGGCGTAAAGCGAGCGCAGCGCGTCCGGTAAGTCTGATGTGAAAG CCCACGGCTCAACCGTGAACGGCATTGGAACTGGCGGACTTGAATGTAGCAGAGGAAAGTGAATCCATGTGTA GCGGTGGAATGCGTAGATATATGGAGGAACACCAGTGGCGAAAGCGACTTTCTGGGCTATGATTGACGCTGAGGCTC GAAAGCGTGGGGAGCAACAGG
Alloprevotella 1 (Ihuprevotella)	massiliensis	66%	57%	70%	54%	1,7%	0,5%	1,3%	0,3%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGATTATTAAGTCAGTGGTAAAAG ACGGTGGCTCAACCATCGTTAGCCATTGAACTGGTAGTCTTGAGTGCAGACAGGGATGCTGGAACCTGTTGGTGTAG CGGTGAAATGCTTAGATATCAGATGAAGTCCGATCGCGAAGGCAGGTGTCCGGGCTGCAACTGACGCTGAGGCTCG AAAGTGTGGGTATCAACAGG
Alloprevotella 10	rava	10%	4%	10%	2%	0,1%	0,1%	0,1%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGACGATTAAGTCAGTGTGAAAAG TTTGC GGCTCAACCGTAAAATTGCAGTTGAAACTGGTTGTCTTGAGTGCAGCAGGGATGTTGGAATTCATGGTGTAG CGGTGAAATGCTTAGATATCATGAAGAACTCCGATCGCGAAGGCATATGTCCGGAGTGAACACTGACGCTGAGGCTCG AAAGTGTGGGTATCAACAGG
Alloprevotella 2	NA	30%	8%	30%	2%	0,5%	0,4%	0,4%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGATTGTTAAGTCAGCGTTAAAAG GGTGTGGCTCAACCATGCATTGCCGTTGAACTGGCGATCTTGAGTGCAGACAGGGATGCCGGAATTCGTGGTGTAG CGGTGAAATGCTTAGATATCAGGAAGAACTCCGATCGCGAAGGCAGGTGTCCGGGCTGCAACTGACGCTGAGGCTCG AAAGTGTGGGTATCAACAGG
Alloprevotella 3	NA	30%	27%	40%	24%	0,4%	0,5%	1,7%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGATTGTTAAGTCAGCGTTAAAAG GGTGTGGCTCAACCATACATTGCCGTTGAACTGGCGATCTTGAGTGCAGACAGGGATGCCGGAATTCGTGGTGTAG CGGTGAAATGCTTAGATATCAGGAAGAACTCCGATCGCGAAGGCAGGTGTCCGGGCTGCAACTGACGCTGAGGCTCG AAAGTGTGGGTATCAACAGG
Alloprevotella 4	NA	10%	12%	10%	12%	0,2%	2,8%	16,2%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGATTGTTAAGTCAGTGGTAAAAG ACGGTGGCTCAACCATCGTTAGCCATTGAACTGGTAGTCTTGAGTGCAGACAGGGATGCTGGAACCTGTTGGTGTAG CGGTGAAATGCTTAGATATCAGATGAAGTCCGATCGCGAAGGCAGGTGTCCGGGCTGTAAGTGCAGCTGAGGCTCG AAAGTGTGGGTATCAACAGG
Alloprevotella 7	NA	4%	4%	10%	2%	0,4%	0,1%	0,0%	0,2%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGATTGTTAAGTCAGCTGTTAAAT ATCAGGGCCCAACTCTGTATGCAGTTGAACTATATTTCTTGAGTACGCACAGGGATGGCGGAATTCAGGGTGTAGC GGTGAATGCTTAGATATCCTGAAGAACTCCGATCGCGAAGGCAGCCATCCGGAGCGTAACTGACGCTGAGGCTCGA AGGTGTGGGTATCAACAGG
AM420062_g	s	3%	6%	10%	5%	0,1%	0,0%	0,1%	0,0%	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAGGGAGCGCAGACGGCTTGGCAAGTCTGAAGTAAAA GCCCGGGGCTTAACCCCGGGACTGCTTTGAAACTGTGAAGCTAGAGTGTGCGGAGAGGTAAGTGAATTCACAGTGT AGCGGTGAAATGCGTAGATATTTGGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACGATAACTGACGTTGAGGC TCGAAGGCGTGGGGAGCAACAGG
Anaerococcus 1	murdochii/degeneri	3%	4%	10%	2%	0,1%	0,1%	0,2%	0,0%	TACGTAAGGTCCAGGCGTTGTCGGAAATCATTGGGCGTAAAGGGTACGTAGGCGGGTAAGCAAGTTAGAAGTGAAT CCTATAGCTCAACTATAGTAAGCTTTTAAACTGCTCATCTTGAGGTATGGAAGGGAAGTGAATTCCTAGTGTAGC GGTGAATGCGCAGATATTAGGAGGAATACCGGTGGCGAAGGCGACTTTCTGGCCATAACCTGACGCTGAGGTACG AAAGCGTGGGTAGCAACAGG
Atopobium 1	parvulum	16%	14%	30%	10%	0,1%	0,0%	0,1%	0,0%	TACGTAGGGGGCAAGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCGGCTGTTAAGTTCGGGAGTTAAAT CCGGGGCTCAACCCCGTTCGCTCCGATACCGGCAGACTTGTAGTTGGTAGGGGAAGTGAATTCCTAGTGTAG CGGTGAAATGCGCAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTCTGGCCATAACTGACGCTGAGGAGC GAAAGTGTGGGGAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Bergeyella 1	NA	36%	29%	10%	34%	0,3%	0,1%	0,2%	0,1%	TACGGAGGGTGCAAGCGTTATCCGGACTTATTGGGTTTAAAGGGTCCGTAGGCGGGTTATTAAGTCAGTGGTGAAT CTCATAGCTCAACTATGAACTGCCATTGATACTGATAGTCTTGAGTATATTTGAAGTAGCTGGAATAAGTAGTGTAGC GGTGAAATGCATAGATATTACTTAGAACACCAATTAGCGAAGGCAGGTTACTAAGATATTACTGACGCTGAGGGACGA GAGCGTAGGGAGCGAACAGG
Bergeyella 2	NA	12%	12%	20%	10%	0,1%	0,2%	0,5%	0,0%	TACGGAGGGTGCAAGCGTTATCCGGATTTATTGGGTTTAAAGGGTCCGTAGGTTGGGCTGATAAGTCAGCGGTGAAAT CCTGCAGCTTAAGTGTAGAAGTCCGCTTGATACTGTTAGTCTTGAGTGTATTTGAAGTGGCTGGAATAAGTAGTGTAGC GGTGAAATGCATAGATATTACTTAGAACACCAATTGCGAAGGCAGGTCACCTAAGATACAAGTACGCTGAGGGACGA AAGCGTGGGGAGCGAACAGG
Bergeyella 3	NA	16%	10%	20%	7%	0,1%	0,1%	0,1%	0,0%	TACGGAGGGTGCAAGCGTTATCCGGATTTATTGGGTTTAAAGGGTCCGTAGGTTGGTGTAGTAAAGTCAGTGGTGAATC CTGCAGCTTAAGTGTAGAATTGCCATTGATACTGCTAGTCTTGAGTGTATTTGAAGTAGCTGGAATAAGTAGTGTAGCG GTGAAATGCATAGATATTACTTAGAACACCAATTGCGAAGGCAGGTTACTAAGATACAAGTACGCTGATGGACGAA AGCGTGGGGAGCGAACAGG
Blautia 1	wexlerae	1%	4%	10%	2%	0,0%	0,0%	0,0%	0,0%	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAGGGGAGCGTAGACGGTGTGGCAAGTCTGATGTGAAAG GCATGGGCTCAACTCTGGACTGCATTGGAACTGTCACTTGAGTGCCGGAGGGGTAAGCGGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAGGAACACCAAGTGGCGAAGGCGGCTTACTGACGCTAAGTACGCTTGGAGGCT CGAAAGCGTGGGGAGCAACAGG
Bulleidia 1	NA	9%	14%	30%	10%	0,1%	0,0%	0,1%	0,0%	TACGTAGGTGGCAGCGTTATCCGGAAATTTGGGCGTAAAGGGTGCAGGCGGCTGTTAAGTAAAGTGGTTAAAT TGTTGGGCTCAACCAATCCAGCCACTTAACTGGCAGGCTAGAGTATTGGAGAGGCAAGTGAATTCATGTGTAG CGGTAAATGCGTAGATATATGAGGAAACACCAAGTGGCGAAGGCGGCTTACTAGCCAAAGACTGACGCTCATGCAC GAAAGCGTGGGGAGCAATAGG
Campylobacter 2	concisus	31%	22%	40%	17%	0,1%	0,1%	0,1%	0,0%	TACGGAGGGTGCAAGCGTTATCCGGAACTACTGGGCGTAAAGGACGCGTAGGCGGATTATCAAGTCTTTGAAAT CCTATGGCTTAACCATAGAACTGCTTGGGAACTGATAATCTAGAGTGAAGGAGAGGCAGATGGAATTTGGTGTGTA GGGGTAAATCCGTAGAGATACCAGGAATACCCATTGCGAAGGCGATCTGCTGGAATCAACTGACGCTAATGCGT GAAAGCGTGGGGAGCAACAGG
Capnocytophaga 1	leadbetteri	30%	14%	10%	15%	0,1%	0,2%	0,0%	0,2%	TACGGAGGATGCGAGCGTTATCCGGAACTATTGGGTTTAAAGGGTCCGTAGGCGGGCTAATAAGTCAGAGGTGAAAG CGCTCAGCTCAACTGAGCAACTGCCTTTGAACTGTCACTTGAATGTTGTAAGTGAAGTGAATGTTGAGTGTAG CGGTGAAATGCTTAGATATTACACAGAACACCGATAGCGAAGGCATATTACTAACAATTAATTGACGCTGATGGACGA AAGCGTGGGGAGCGAACAGG
Capnocytophaga 3	sputigena	24%	18%	20%	17%	0,1%	0,1%	0,1%	0,1%	TACGGAGGATGCGAGCGTTATCCGGAACTATTGGGTTTAAAGGGTCCGTAGGCGGGCTAATAAGTCAGAGGTGAAA GCGCTTAGCTCAACTAAGCAACTGCCTTTGAACTGTCACTTGAATGATTGTGAAGTGAAGTGAATGTTGAGTGTAG CGGTGAAATGCTTAGATATTACACAGAACACCGATAGCGAAGGCATATTACTAACAATTTATTGACGCTGATGGACGA AAGCGTGGGGAGCGAACAGG
Capnocytophaga 5	NA	12%	8%	20%	5%	0,1%	0,0%	0,1%	0,0%	TACGGAGGATGCGAGCGTTATCCGGAACTATTGGGTTTAAAGGGTCCGTAGGCGGGCTAATAAGTCAGGGGTGAAAG GTTTCAGCTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG GGTGAAATGCTTAGATATTACACAGAACACCGATTGCGAAGGCAGGGGACTAACAGACAATTGACGCTGAGAGACG AAAGCGTGGGGAGCGAACAGG
Conchiformibius 1 (Eikenella)	corrodens	4%	6%	20%	2%	0,2%	0,5%	0,7%	0,1%	TACGTAGGGTGCGAGCGTTAATCGGAATTAAGGGTCCGTAGGCGGCGAGCGGTTATTTAAGCAGGATGTGAAAT CCCCGGGCTTAAGTGGGAACTGCGTCTGAACTGGATAGCTAGAGTGTGTGAGAGGGGGGTAGAAATCCACGTGTA GCAGTGAATGCGTAGAGATGTGGAGGAATACCAGTGGCGAAGGCAGCCCCCTGGGATAACACTGACGTTTCATGCT CGAAAGCGTGGGTAGCAACAGG
Corynebacterium 1	propinquum/pseudodiphtheriticum	60%	63%	50%	66%	2,3%	2,5%	6,3%	1,8%	TACGTAGGGTGCAAGCGTTGTCGGAAATTAAGGGTCCGTAGGCGGCTGATAGTGGTGTGTCACGTCGCTGTGAAAT CCACAGCTTAAGTGTGGGCTGCAGGCGATACGGGCTGACTTGAAGTGTAGTGGGTAAGTGAATTCCTGGTGTAG CGGTGAAATGCGAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTTACTGGGCAGTACTGACGCTGAGGAGC GAAAGCATGGGTAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Corynebacterium 10	matruchotii	12%	14%	10%	15%	0,2%	0,2%	0,2%	0,2%	TACGTAGGGTGCAGCGTTGTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGTGGTTTGTTCGCTCGTCTGTGAAATT CCGGGGCTTAACTTCGGGGTGGCAGGCGATACGGGCATAACTAGAGTGTGTAGGGGAGACTGGAATTCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTCTCTGGGCAGTAACTGACGCTGAGGA GCGAAAGCATGGGGAGCGAACAGG
Corynebacterium 3	tuberculostearicum	4%	18%	10%	20%	0,5%	2,0%	0,3%	2,3%	TACGTAGGGTGCAGCGTTGTCCGGAATTACTGGGCGTAAAGGGCTCGTAGGTGGTTTGTTCGCTCGTCTGTGAAATT CCGGGGCTTAACTTCGGGGTGCAGGCGATACGGGCATAACTGAGTACTGTAGGGGTAAGTGAATTCCTGGTGT GCGGTGAAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTACTGGGCAGTAACTGACGCTGAGGAG CGAAAGCATGGGTAGCGAACAGG
Corynebacterium 9	durum	10%	14%	10%	15%	0,2%	0,2%	0,0%	0,2%	TACGTAGGGTGCAGCGTTGTCCGGAATTTACTGGGCGTAAAGAGCTCGTAGGTGGTGTTCGCTCGTCTGTGAAATT CCGGGGCTTAACTTCGGGGTGCAGGCGATACGGGCACGACTAGAGTGTGTAGGGGTAAGTGAATTCCTGGTGT AGCGGTGAAATGCGCAGATATCAGGAGGAACACCGATGGCGAAGGCAGGTACTGGGCAGTAACTGACGCTGAGGA GCGAAAGCATGGGGAGCGAACAGG
CP009312_g (Lawsonella)	clevelandensis	3%	6%	20%	2%	0,2%	0,0%	0,0%	0,0%	TACGTAGGGTGCAGCGTTGTCCGGAATTACTGGGCGTAAAGAGCTCGTAGGCGGTTTGTACGCTCGTCTGTGAAAT CCTAGGGCTTAACTTCGGGGTGCAGGCGATACGGGCCTGACTTGTAGTACTACAGGGGAGACTGGAATTCCTGGTGT GCGGTGGAATGCACAGATATCAGGAAGAACACCGATGGCGAAGGCAGGTCTCTGGGTAGTAACTGACGCTGAGGAG CGAAAGCATGGGTAGCGAACAGG
Dolosigranulum 1	pigrum	70%	71%	60%	73%	3,8%	5,5%	11,9%	4,2%	TACGTAGGGTGCAGCGTTGTCCGGAATTTACTGGGCGTAAAGAGCTCGTAGGTGGCACCCTTAAAGCGCAGGGTTAAG CCCACGGCTTAACTTCGGGGTGCAGGCGATACGGGCACGACTAGAGTGTGTAGAGAGGAAAAAGTGAATTCCTGGTGT GCGGTGGAATGCGTAGATATTTGGAGGAACACCGATGGCGAAGGCAGTTTCTGGTCTAACATTGACGCTGAGGCTC GAAAGCGTGGGGAGCGAACAGG
Eubacterium_g10 1	sulci	6%	4%	10%	2%	0,0%	0,0%	0,0%	0,0%	TACGTAGGGGCGAGCGTTATCCGGAATTTACTGGGCGTAAAGAGCTCGTAGGTGGCACCCTTAAAGCGCAGGGTTAAG GCAATGGCTCAACCATTGTTGCGCTTGCGAAGTGGGGTCTTGTAGTGCAGGAGGGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAGGAACACCGATGGCGAAGGCAGCTTCTGGACTGTTACTGACACTGAGGCACG AAAGCGTGGGGAGCAAACAGG
Eubacterium_g11	brachy	6%	8%	30%	2%	0,0%	0,1%	0,2%	0,1%	TACGGAGGGGCAAGCGTTATCCGGAATTTACTGGGCGTAAAGGGTACGTCAGGCGGTTTAAAGTGAATGTTAAAG GCAATGGCTCAACCATTGTTGCGCTATGAAGTGAAGGCTTGTAGTGCAGGAGAGGAAAGCGGAATTCCTAGTGTAG CGGTGAAATGCATAGATATTAGGAGGAACATCAGCGGCGAAGGCAGCTTCTGGACTGCAACTGACACTGAGGTAC GAAAGCGTGGGGAGCAAACAGG
Finegoldia	magna	4%	8%	10%	7%	0,1%	0,1%	0,1%	0,0%	TACGTATGGAGCGAGCGTTGTCCGGAATTTACTGGGCGTAAAGGGTACGTCAGGCGGTTTAAAGTGAATGTTAAAG ATCGGGGCTCAACCCCGGAAGTGTGAAACTGATAACTTGTAGTGTGAGGAGGAAAGTGAATTCCTAGTGTAG TGGTGAATACGTAGATATTAGGAGGAATACCAGTAGCGAAGGCAGCTTCTGGACACAACTGACGCTGAGGTACG AAAGCGTGGGGAGCAAACAGG
FJ705147_g 1	NA	37%	18%	40%	12%	0,3%	1,4%	2,9%	0,1%	TACGTAGGGGCAAGCGTTATCCGGAATTTACTGGGCGTAAAGGGGAGCGTAGACGGCATAGCAAGTCTGAAGTGAAG GCCCGGGGCTCAACCCCGGAAGTGTGAAACTGTTAAGCTAGAGTGTGCGGAGAGGTAAGTGAATTCCTAGTGTAG AGCGGTGAAATGCGTAGATATTGGGAGGAACACCGTGGCGAAGGCAGGCTTACTGGACGATAACTGACGTTGAGGC TCGAAGGCGTGGGGAGCAAACAGG
FM873692_g 1	s	18%	35%	40%	34%	0,9%	0,3%	0,5%	0,2%	TACGTAGGGTGCAGCGTTAATCCGGAATTTACTGGGCGTAAAGCGAGTGCAGACGGTACTTAAAGCCAGATGTGAAAT CCCCAAGCTTAACTTCGGGACGTGCATTTGGAAGTGGGTGACTAGAGTGTGCAGAGGGAGGTAGAATTCACATGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCAGTGGCGAAGGCAGCCTCTGGGATAACTGACGTTGAGGCT CGAAAGCGTGGGGAGCAAACAGG
FM873692_g 2	NA	1%	12%	20%	10%	0,1%	0,3%	0,8%	0,0%	TACGTAGGGTGCAGCGTTAATCCGGAATTTACTGGGCGTAAAGCGAGTGTAGACGGTAAAGCCAGATGTGAAAT ACCCGAGCCTAAGTGGGAGGTGCATATGGAAGTGGGTAGCTAGAGTGTGCAGAGGGAGGTAGAATTCACGCTGTA GCAGTGAATGCGTAGAGATGTGGAAGAATACCAGTGGCGAAGGCAGCCTCTGGGATAACTGACGTTGAGGCT CGAAAGCGTGGGGAGCAAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
FM873692_g 3	NA	1%	6%	10%	5%	0,1%	0,0%	0,0%	0,0%	TACGTAGGGTGCAAGCGTTAATCGGAATATTGGGCGTAAAGCGAGTGCAGACGGTTACTTAAGCCAGATGTGAAAT CCCCAAGCTTAACCTGGGACGTGCATTTGGAAGTGGGTAAGTGCAGAGTGTGCAGAGGGAGGTAGAATCCACATGTA GCGGTGGAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCTCTGGGATAACACTGACGTTGAGGCT CGAAGCGTGGGGAGCAACAGG
Fusobacterium 1	necrophorum subsp. necrophorum/funduliforme	21%	20%	40%	15%	13,5%	2,6%	4,7%	1,2%	TACGTATGTCGAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGCGGGCAAGGAAAGTCTGATGTGAAAA TGCGGAGCTCAACTCCGTATGGCGTTGGAAGTGCCTACTAGAGTACTGGAGAGGTAGGCGGAAGTACAAGTGTAG AGGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGGGAAGCCAGCCTACTGGACAGATACTGACGCTAAAGCGCG AAAGCGTGGGTAGCAACAGG
Fusobacterium 3	periodonticum	37%	29%	40%	27%	0,7%	0,3%	0,6%	0,2%	TACGTATGTCACAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGGTGGTTATGTAAGTCTGATGTGAAAA GCAGGGCTCAACTCTGATTGCGTTGGAAGTGCATGACTAGAGTACTGGAGAGGTAAAGCGGAAGTACAAGTGTAGA GGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGGGAAGCCAGCCTACTGGACAGATACTGACGCTAAAGCGCGA AAGCGTGGGTAGCAACAGG
Fusobacterium 5	massiliense	46%	14%	30%	10%	0,3%	0,3%	0,6%	0,1%	TACGTATGTCACAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGCGGGCTATGTAAGTCTGATGTGAAAA GCGGGCTCAACTCCGTATTGCGTTGGAAGTGTGTAGCTAGAGTATCGGAGAGGTAAGCGGAAGTACAAGTGTAGA GGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGGGAAGCCAGCCTACTGGACGAATACTGACGCTAAAGCGCGA AAGCGTGGGTAGCAACAGG
Fusobacterium 6	NA	33%	20%	20%	20%	0,2%	0,3%	1,2%	0,1%	TACGTATGTCACAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGGTGGTTATGTAAGTCTGATGTGAAAA GCGGAGCTCAACTCCGTATTGCGTTGGAAGTGGTAACTAGAGTACTGGAGAGGTAAAGCGGAAGTACAAGTGTAGA GGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGGGAAGCCAGCCTACTGGACAGATACTGACGCTAAAGCGCGA AAGCGTGGGTAGCAACAGG
Fusobacterium 8	canifelinum	16%	10%	20%	7%	0,4%	0,1%	0,2%	0,1%	TACGTATGTCACAAGCGTTATCCGGATTATTGGGCGTAAAGCGCGTCTAGGTGGTTATGTAAGTCTGATGTGAAAA GCAGGGCTCAACTCTGATTGCGTTGGAAGTGTGTAAGTACTAGAGTACTGGAGAGGTAAAGCGGAAGTACAAGTGTAGA GGTGAAATTCGTAGATATTTGTAGGAATGCCGATGGGGAAGCCAGCCTACTGGACAGATACTGACGCTGAAGCGCGA AAGCGTGGGTAGCAACAGG
Gemella 1	haemolysans/morbillorum/sanguinis/t aiwanensis/parahaemolysans	84%	69%	70%	68%	0,7%	1,1%	3,2%	0,5%	TACGTAGGTGGCAAGCGTTGTCCGGAATATTGGGCGTAAAGCGCGCAGGCGGTTTAAAGTCTGATGTGAAAG CCCACGGCTCAACCGTGGAGGGTCAATGGAACTGTTAACTGAGTGCAGGAGAGAAAAGTGAATTCCTAGTGTGA GCGGTGAAATGCGTAGAGATATTAGGAGGAACACCAGTGGCGAAGGCGCTTTTGGCTGTAAGTACTGACTGAGGCG CGAAGCGTGGGGAGCAACAGG
GQ422727_g 1	s	15%	10%	30%	5%	0,2%	0,9%	1,5%	0,0%	AACATAGGGGGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGGCGCGCAGGCGGTAATTAAGTCAAGTGTGAAA GTTCCGGGGCTCAACCCCGTATTGCACCTGATACTGATAAAGTACTAGAGTGTGGAGAGGTAAAGTGAATTCCTAGTGTGA GCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAAGTACTGACGCTGAGGCTC CGAAGCGTGGGGAGCAACAGG
Granulicatella 1	elegans	70%	53%	60%	51%	0,5%	0,6%	0,9%	0,5%	TACGTAGGTGGCAAGCGTTGTCCGGAATATTGGGCGTAAAGCGAGCGCAGGCGGTTCAATTAAGTCTGATGTGAAAG CCCCGGCTCAACCGGGGAGGGTCAATGGAACTGGTTGACTTGTAGTGCAGAAGAGGAGAGTGAATTCATGTGTA GCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAAGTACTGACGCTGAGGCTC GAAAGCGTGGGTAGCAACAGG
Granulicatella 2	adiacens	39%	43%	50%	41%	0,2%	0,4%	0,2%	0,5%	TACGTAGGTGGCAAGCGTTGTCCGGAATATTGGGCGTAAAGCGAGCGCAGGCGGTTCTTAAGTCTGATGTGAAAG CCCCGGCTCAACCGGGGAGGGTCAATGGAACTGGGGAAGTGTAGTGCAGAAGAGGAGAGTGAATTCATGTGT AGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAAGTACTGACGCTGAGGCT CGAAGCGTGGGTAGCAACAGG
GU410548_g 1	NA	4%	6%	10%	5%	0,1%	0,1%	0,1%	0,0%	TACGTAGGTTCGAAGCGTTATCCGGATTACTGGGCGTAAAGTGTCCGTAAGTCTGATGTGAAATTC TACGACTCAATCGTAGAAAGGAATGGACTGCAGATCTAGAAGTACTAGGGGTTAGTGAATTTCCGGTGGAGC GGTGAAATGCGTTGATATCGGAAGGAACCGGAAAGCGAAGCAGTAACTATAGAACTGACGATGAGGGACG ACAGTTTGGGGAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
GU410548_g 2	NA	21%	6%	10%	5%	0,1%	0,0%	0,1%	0,0%	TACGTAGGTTCTCAAGCGTTATCCGGATTACTGGGCGTAAAGTGTCCGTAGTCTGAATTGTAAGTCTGTTTCAAATCC TACGACTCAATCGTAGAAAGGGAGTGGACTGCAATTCTAGAATATCTAGGGGTAGTGGAAATTCGGGTGGAGC GGTGAAATGCGTTGATATCGGAAGGAACGCCGAAAGCGAAAGCAGTAACATAGAATACTTGACGATGAGGGACG ACAGTTTGGGGAGCAAACAGG
Haemophilus 1	influenzae/seminalis	90%	82%	70%	85%	17,2%	14,2%	6,2%	15,8%	TACGGAGGGTGCAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTTATTTAAGTGAGGTGTGAAA GCCCGGGCTTAACCTGGGAATTCATTTAGACTGGGTAAGTACTAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACTGACGCTCATGTG CGAAAGCGTGGGGAGCAAACAGG
Haemophilus 2	aegyptius	67%	71%	70%	71%	27,8%	16,2%	18,3%	15,7%	TACGGAGGGTGCAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTTATTTAAGTGAGGTGTGAAA GCCCTGGGCTTAACCTAGGAATTCATTTAGACTGGGTAAGTACTAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACTGACGCTCATGTG CGAAAGCGTGGGGAGCAAACAGG
Haemophilus 3	quentini/influenzae	34%	14%	10%	15%	6,6%	12,0%	2,7%	13,6%	TACGGAGGGTGCAGCGTTAATCGGAATAACTGGGCGTAAAGGGCACGCAGGCGGTTATTTAAGTGAGGTGTGAAA GCCCTGGGCTTAACCTGGGAATTCATTTAGACTGGGTAAGTACTAGTACTTTAGGGAGGGGTAGAATCCACGTGTA GCGGTGAAATGCGTAGAGATGTGGAGGAATACCGAAGGCGAAGGCAGCCCTTGGGAATGTAAGTACTGACGCTCATGTG CGAAAGCGTGGGGAGCAAACAGG
JN713389_g 1	NA	16%	6%	10%	5%	0,1%	0,1%	0,0%	0,1%	TACATATGGGGCGAGCGTTATCCGGAAATTTGGGTGTAAAGGGTGCAGTGGCGGAATAGCAAGTCAAGTGTGAAA TCTCTCGGCTCAACCGAGAACTGCGACTGAACTACTATTCTTGTAGTGTGGAGGGGAAAGTGAATTCCTAGTGTGTA GCGGTGAAATGCGTAGATATTAGGAGGAACACCGAGTGGCGAAGGCGACTTTCTGGACAACAAGTACTGACGCTGAGGCA CGAAAGCGTGGGTAGCAAACAGG
Lachnoanaerobaculum 1	gingivalis	34%	16%	20%	15%	0,1%	0,1%	0,1%	0,1%	TACGTAGGGGCAAGCGTTATCCGGATTACTGGGTGTAAAGGGAGCGCAGACGGCAATGCAAGTCTGAAGTGAAA GGCGTGGGCTCAACCCATGAAGTCTTTGGAACTGTATAGCTTGTAGTGTGCGAGGGGTAAAGCGGAATTCCTAGTGT AGCGGTGAAATGCGTAGATATTAGGAGGAACACCGAGGCGAAGGCGGCTTACTGGACGACAAGTACTGACGTTGAGGC TCGAAGGCGTGGGGAGCAAACAGG
Lachnoanaerobaculum 2	orale	13%	8%	20%	5%	0,1%	0,0%	0,1%	0,0%	TACGTAGGGGCAAGCGTTATCCGGATTACTGGGTGTAAAGGGAGCGCAGACGGCAAGTCTGAAGTGAAA TGCAATGGGCTCAACCCATGAATTCATTTGGAACTGTTGGCTTGTAGTGTGCGAGGGGTAAAGCGGAATTCCTAGTGTGTA GCGGTGAAATGCGTAGATATTAGGAGGAACACCGAGGCGAAGGCGGCTTACTGGACGACAAGTACTGACGTTGAGGCT CGAAGGCGTGGGGAGCAAACAGG
Lactobacillus 3	iners	1%	4%	10%	2%	0,0%	0,0%	0,0%	0,0%	TACGTAGGGTGCAGCGTTATCCGGATTACTGGGCGTAAAGGGAGTGCAGGCGGCTCGATAAGTCTGATGTGAAAG CCTTCGGCTCAACCGGAGAATGCATCAGAACTGTCGAGCTTGTAGTACAGAAGAGGAGAGTGGAACTCCATGTGTA GCGGTGAAATGCGTAGATATTAGGAGGAACACCGGAGGCGAAGGCGGCTCTGTGCTTACTGACGCTGAGGCTC GAAAGCATGGGTAGCAAACAGG
Lautropia 1	mirabilis	21%	27%	40%	24%	0,1%	0,1%	0,1%	0,1%	TACGTAGGGTGCAGCGTTAATCGGAATAACTGGGCGTAAAGAGTGCAGGCGGTTTTCGAAGACCGATGTGAAAT CCCCGGGCTTAACCTGGGAAGTGCATTGGTACTGCAAGGCTAGAGTGTGTCAGAGGGAGGTGGAATTCGCGATGTA GCAGTGAATGCGTAGATATCGGGAGGAACACCGATGGCGAAGGCAGCCCTTGGGATAACTGACGCTCATGCA CGAAAGCGTGGGGAGCAAACAGG
Leptotrichia 1	NA	22%	10%	20%	7%	0,8%	0,0%	0,0%	0,0%	TACGTATGTCGCGAGCGTTATCCGGAAATTTGGGCATAAAGGGCATCTAGGCGGTTATGCAAGTCAAGGGGTGAAAA CTTACGGCTCAACCGTGAAGTTCGCTTTGAAACTGTGTACTAGAGTACTGGAGAGGTGGGCGGAACTACACGAGTA GAGGTGAAATTCGATAGATATGTGAGGAATGCCGATGATGAAGTAGTCTACTGGACGAAAGTACTGACGCTGAAGTGC GAAAGCTAGGGGAGCGAACAGG
Leptotrichia 12	NA	7%	6%	20%	2%	0,1%	0,1%	0,1%	0,1%	TACGTATGTCGCGAGCGTTATCCGGAAATTTGGGCATAAAGGGCATCTAGGCGGATATACAAGTCAAGGGGTGAAAA CTTAGGGCTCAACTCAAAGTTCGCTTTGAAACTGTATCTAGAGTGTGAGAGGTGGACGGAAGTACTACACGAGTAG AGGTGAAATTCGATAGATATGTGAGGAATGCCGATGATGAAGTAGTCCACTGGACGACAAGTACTGACGCTGAAGTGC AAAGCTAGGGGAGCAAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Leptotrichia 2	wadei	10%	10%	10%	10%	0,2%	0,2%	0,6%	0,1%	TACGTATGTCGCAAGCGTTATCCGGAATTATTGGGCATAAAGGGCATCTAGGCGGCCAGATAAGCTGGGGTGAAAA CTTGGCGCTCAACCGCAAGCCTGCGCTGAAACTATGTGGCTAGAGTACTGGAGAGGTGGACGGAACTGCACGAGTA GAGGTGAAATTCGTAGATATGTGCAGGAATGCCGATGATGAAGATAGTTCACTGGACGGTAACTGACGCTGAAGTGC GAAAGCTAGGGGAGCAACAGG
Leptotrichia 3	NA	19%	8%	20%	5%	0,3%	0,3%	0,4%	0,3%	TACGTATGTCGCGAGCGTTATCCGGAATTATTGGGCATAAAGGGCATCTAGGCGGCCCTTCAAGTCAGGGGTGAAAA CCTGCGGCTCAACCGCAGGCTGCCTTTGAAACTGATAGGCTGGAGTACCGGAGAGGTGGACGGAACTGCACGAGT AGAGGTGAAATTCGTAGATATGTGCAGGAATGCCGATGATGAAGATAGTTCACTGGACGGTAACTGACGCTGAAGTG CGAAAGCCGGGGAGCGAACAGG
Leptotrichia 4	NA	9%	6%	10%	5%	0,1%	0,1%	0,1%	0,1%	TACGTATGTCGCGAGCGTTATCCGGAATTATTGGGCATAAAGGGCATCTAGGCGGCCGTACAAGTCAGGGGTGAAAA CCTGCGGCTCAACCGCAGGCTGCCTTTGAAACTGTGAGGCTGGAGTACCGGAGAGGTGGACGGAACTGCACGAGT AGAGGTGAAATTCGTAGATATGTGCAGGAATGCCGATGATGAAGATAGTTCACTGGACGGTAACTGACGCTGAAGTG CGAAAGCCGGGGAGCGAACAGG
Megasphaera 1	micronuciformis	24%	10%	20%	7%	0,1%	0,1%	0,2%	0,1%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCGCGCAGGCGGCTTCTAAGTCTGTCTTAAAG TGCGGGGCTTAACCCGCTGATGGGATGGAAGCTGGAAGCTCAGAGTATCGGAGAGGAAAGCGGAATTCCTAGTGT AGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAAGCGGCTTCTGGACGAAACTGACGCTGAGGC GCGAAAGCCAGGGGAGCGAACGGG
Moraxella 1	catarrhalis/nonliquefaciens	84%	92%	80%	95%	25,1%	29,1%	18,7%	31,3%	TACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCTAGGTGTTATTTAAGTCAGATGTGAAAG CCCCGGGCTTAACCTGGAACTGCATCTGATACTGGATAACTAGAGTAGGTGAGAGGGGAGTAGAATCCAGGTGTA GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCTCCCTGGCATCACTGACACTGAGGTG CGAAAGCGTGGGTAGCAACAGG
Moraxella 2	lincolnii	22%	41%	10%	49%	2,9%	16,7%	7,0%	17,2%	TACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGTAGGTGTTTATTAAGTCAGATGTGAAAT CCCTGGGCTTAACCTAGGAACTGCATCTGATACTGATAACTAGAGTAGGTGAGAGGAAAGTAGAATCCAGGTGTA GCGGTGAAATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCTTCTGGCATCACTGACACTGAGGTTG GAAAGCGTGGGTAGCAACAGG
Moryella 1	NA	13%	8%	20%	5%	0,1%	0,1%	0,0%	0,1%	TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGCAGACGGTTCGCAAGTCTGAAGTGAAT CCCGAGGCTTAACCCAGGACTGCTTTGAAACTGTGCGACTTGAGTATCGGAGGGGAGCGGAAATTCCTAGTGTA GCGGTGAAATGCGTAGATATTAGGAAGAACCAGGTTGGCGAAGGCGGCTCTGGACGAAACTGACGTTGAGGCT CGAAGCGTGGGGAGCAACAGG
Neisseria 1	cinerea/perflava/subflava	61%	59%	60%	59%	3,7%	1,6%	4,1%	0,9%	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGCAGACGGTACTTAAGCAGGATGTGAAAT CCCCGGGCTCAACCTGGAACTGCGTTCTGAACTGGGTGACTAGAGTGTGTCAGAGGGAGGTAGAATCCACGTGTA GCAGTGAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCTCCTGGGATAAAGTACGCTTATGCTC GAAAGCGTGGGTAGCAACAGG
Neisseria 11	polysaccharea	3%	4%	10%	2%	1,2%	0,6%	0,3%	1,0%	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGGGCGCAGACGGTACTTAAGCAGGATGTGAAAT CCCCGGGCTCAACCCGGAACTGCGTTCTGAACTGGGTGACTCAGTGTGTCAGAGGGAGGTAGAATCCACGTGTA GCAGTGAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCTCCTGGGATAAAGTACGCTTATGCTC CGAAAGCGTGGGTAGCAACAGG
Neisseria 3 (Neisseria or Morococcus)	N. mucosa/macacae/flava or M. cerebrosus	39%	31%	60%	24%	1,9%	0,7%	0,7%	0,8%	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGGGCGCAGACGGTACTTAAGCAGGATGTGAAAT CCCCGGGCTCAACCTGGAACTGCGTTCTGAACTGGGTGACTAGAGTGTGTCAGAGGGAGGTAGAATCCACGTGTA GCAGTGAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCTCCTGGGATAAAGTACGCTTATGCTC CGAAAGCGTGGGTAGCAACAGG
Neisseria 4	lactamica	24%	6%	10%	5%	2,2%	0,5%	1,1%	0,1%	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGGGCGCAGACGGTACTTAAGCAGGATGTGAAAT CCCCGGGCTCAACCCGGAACTGCGTTCTGAACTGGGTGGCTAGAGTGTGTCAGAGGGAGGTAGAATCCACGTGTA GCAGTGAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCTCCTGGGATAAAGTACGCTTATGCTC CGAAAGCGTGGGTAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Neisseria 8 (Neisseria or Kingella)	N. elongata subsp. elongata/glycolytica/nitroreducens or K. denitrificans	10%	12%	10%	12%	0,4%	0,1%	0,1%	0,1%	TACGTAGGGTGCAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGCAGACGGTTACTTAAGCAGGATGTGAAAT CCCCGGCTCAACCTGGGAACCTCGTCTGAACCTGGGTAGCTAGAGTATGTCAGAGGGGGGTAGAATCCACGTGTA GCAGTAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGCCCCCTGGGATAATACTGACGTTTCATGCTC GAAAGCGTGGGTAGCAAACAGG
Oribacterium 1	sinus	22%	20%	30%	17%	0,1%	0,1%	0,1%	0,1%	TACGTAGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAGGGGAGCGTAGACGGAATGGCAAGTCTGAAGTGAAAT ACCCGGCTCAACCTGGGAACCTGCTTGGAACTGTTGTTCTAGAGTGTGGAGAGGTAAGTGAATTCCTGGTGTAG CGGTGAAATGCGTAGATATCAGGAAGAACCACCGAGGCGAAGGCGGCTTACTGGACAATAACTGACGTTGAGGCTC GAAAGCGTGGGATCAAACAGG
Oribacterium 2	parvum	4%	4%	10%	2%	0,1%	0,0%	0,0%	0,0%	TACGTAGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAGGGGAGCGTAGACGGAATGGCAAGTCTGAAGTGAAA ACCCGGCTCAACCTGGGACTGCTTGGAACTGTTGTTCTAGAGTGTGGAGAGGTAAGTGAATTCCTGGTGTGTA GCGGTGAAATGCGTAGATATCAGGAAGAACCACCGAGGCGAAGGCGGCTTACTGGACAATAACTGACGTTGAGGCT CGAAGCGTGGGATCAAACAGG
Parvimonas 2	micra	7%	4%	10%	2%	0,1%	0,7%	1,4%	0,0%	TACGTATGGGCGAGCGTTGTCGGGAATTATTGGGCGTAAAGGGTACGTAGGCGGTTTTTAAAGTCAAGTGTGAAAG CGTGAGGCTCAACCTCATTAAAGCACTTGAACCTGGAAGACTTGAGTGAAGGAGAGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAGGAATACCGGTGGCGAAGGCGACTTTCTGGACTTTTACTGACGCTCAGGTACG AAAGCGTGGGAGCAAACAGG
Parvimonas 3	NA	3%	8%	10%	7%	0,0%	0,0%	0,0%	0,0%	TACGTATGGGCGAGCGTTGTCGGGAATTATTGGGCGTAAAGGGTACGTAGGCGGCTTTTAAAGTCAAGTGTGAAAG CGTGAGGCTCAACCTCATTAAAGCACTTGAACCTGGAAGGCTTGAAGTGAAGGAGAGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAGGAATACCGGTGGCGAAGGCGACTTTCTGGACTTTTACTGACGCTCAGGTACG AAAGCGTGGGAGCAAACAGG
Peptoniphilus 1	grossensis/vaginalis/harei	1%	8%	30%	2%	0,3%	0,3%	0,4%	0,0%	TACGTAGGGGCTAGCGTTGTCGGGAATCACTGGGCGTAAAGGGTTCGAGGCGGAAATGCAAGTCAAGTGTGAAAA GGCAGTAGCTTAACCTACTGTAAGCATTGAAACTGCATATCTTGAGAAGAGTAGAGGTAAGTGAATTTTTAGTGTAG CGGTGAAATGCGTAGATATTAAGAAGAAATACCGGTGGCGAAGGCGACTTACTGGCTCATTCTGACGCTGAGGAACG AAAGCGTGGGTAGCAAACAGG
Peptostreptococcus 1	stomatis	18%	12%	20%	10%	0,1%	0,0%	0,1%	0,0%	TACGTAGGGGCTAGCGTTATCCGGATTTACTGGGCGTAAAGGGTGCAGTGGTCTTCAAGTCAAGTGGTGTAAAG GCTACGGCTCAACCTAGTAAGCCGCGAAACTGGAGGACTTGAGTGCAGGAGAGGAAAGTGAATTCACAGTGTGTA GCGGTGAAATGCGTAGATATTGGGAGGAACACAGTAGCGAAGGCGGCTTTCTGGACTGCAACTGACACTGAGGCA CGAAGCGTGGGTAGCAAACAGG
Porphyromonas 1	NA	60%	33%	60%	27%	1,7%	0,6%	1,4%	0,1%	TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCAGTGGCGGCTGTTAAGTCAAGCGGTGAAAT CTAGGAGCTCAACTCCTAAATGGCATTGAAACTGGCGGGCTTGAAGTGTAGATGAGGTAGGCGGAATGCGTGGTGTGTA GCGGTGAAATGCATAGATATCACGAGAACTCCAATTGCGAAGGCGACTTACTAAGGTACAACCTGACGCTGAAGCAC GAAAGCGTGGGTATCAAACAGG
Porphyromonas 2	NA	49%	20%	30%	17%	0,5%	0,3%	0,9%	0,1%	TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCAGTGGCGGTTGTTAAGTCAAGCGGTGAAATC TAGAGGCTCAACCTCGAACTGCGGTTGAAACTGGCGAAGTGAAGTGTAGATGAGGTAGGCGGAATTCGTTGGTGTAG CGGTGAAATGCATAGATATCACGAGGAACTCCGATTGCGAAGGCGACTTACTAAGGTACAACCTGACGCTGAAGCACG AAAGCGTGGGTATCAAACAGG
Porphyromonas 3	NA	27%	14%	40%	7%	0,3%	0,6%	0,4%	0,9%	TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCAGTGGCGGTTGTTAAGTCAAGCGGTGAAATC TAGAGGCTCAACCTCGAACTGCGGTTGAAACTGGCGAAGTGAAGTGTAGATGAGGTAGGCGGAATTCGTTGGTGTAG CGGTGAAATGCATAGATATCACGAGGAACTCCAATTGCGAAGGCGACTTACTAAGGTACAACCTGACGCTGAAGCACG AAAGCGTGGGTATCAAACAGG
Porphyromonas 4	pasteri	6%	4%	10%	2%	0,4%	0,2%	0,4%	0,0%	TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCAGTGGCGGCTGTTAAGTCAAGCGGTGAAAT CTAGGAGCTCAACTCCTAAATGGCATTGATACTGGCGGGCTTGAAGTGTAGATGAGGTAGGCGGAATGCGTGGTGTGTA GCGGTGAAATGCATAGATATCACGAGAACTCCGATTGCGAAGGCGACTTACTAAGGTACAACCTGACGCTGAAGCAC GAAAGCGTGGGTATCAAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Prevotella 1	melaninogenica	54%	41%	70%	34%	1,2%	0,8%	1,9%	0,2%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCTGGAGATTAAGTGTGTTGTGAAAT GTAGACGCTCAACGTCTGAATTGCAGCGCATACTGGTTTCCTTGAGTACGCACAACGTTGGCGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCAACTGACGCTTAAGCTCG AAGGTGCGGGTATCGAACAGG
Prevotella 10	salivae	25%	12%	30%	7%	0,2%	0,2%	0,3%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTGGATTAAGCGTGTGTTGTGAAAT GTAGACGCTCAACGTCTGAATTGCAGCGCAACTGGTTCACCTGAGTACGACAACGTAGGCGGAATTCGTCGTGTAG GCGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTTACGGGAGCACAACCTGACGCTGAAGCTC GAAGGTGCGGGTATCGAACAGG
Prevotella 11	NA	18%	20%	10%	22%	0,4%	0,3%	0,2%	0,4%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGGAGATTAAGTGTGTTGTGAAAT GTAGACGCTCAACGTCTGACTTGCAGCGCATACTGGTTTCCTTGAGTACGCACAACGTTGGCGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCAACTGACGCTTAAGCTCG AAGGTGCGGGTATCGAACAGG
Prevotella 12	NA	10%	4%	10%	2%	0,3%	0,1%	0,1%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGGTGAGGCCGTTGTTAAGCGTGTGTTGTGAAAT TAGATGCTCAACATTAACCTGCAGCGCAACTGCAGACTTGAGTACACGCAACGATGCGGAATTCATGGTGTAGC GGTGAAATGCTTAGATATCATGAAGAAGCTCCGATTGCGAAGGCAGCATACGGGAGTGAAGTACGCTTAAGCTCGA AGGTGCGGGTATCGAACAGG
Prevotella 13	melaninogenica	13%	16%	10%	17%	0,4%	0,4%	0,6%	0,3%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGCCCTTAAGCGTGTGTTGTGAAAT GTAGACGCTCAACGTCTGAATTGCAGCGCATACTGGTTTCCTTGAGTACGCACAACGTTGGCGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCAACTGACGCTTAAGCTCG AAGGTGCGGGTATCGAACAGG
Prevotella 15	NA	13%	4%	10%	2%	1,0%	4,7%	9,2%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTTGATAAGCGTGTGTTGTGAAAT GCGGGTGCTCAACATCCGACTTGCAGCGCAACTGGGGGCTTGAGTGCGCCGAAAGTAGGCGGAATTCGTCGTGTAG AGCGGTGAAATGCTTAGATATCAGGAAGAAGCTCCGATTGCGAAGGCAGCTTACTGTAGCGCAACTGACGCTGATGCT CGAAAGCGGGTATCGAACAGG
Prevotella 19	NA	21%	12%	10%	12%	0,2%	0,2%	0,5%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTTGATAAGCGTGTGTTGTGAAAT TAGAGGCTCAACCTTACCCTGCAGCGCAACTGCAGACTTGAGTGCCTAGTAGGAGGCGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATCAGGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGTATCGCAACTGACGCTGATGCTCG AAGGTGCGGGTATCGAACAGG
Prevotella 2	histicola	25%	8%	20%	5%	0,7%	0,4%	0,5%	0,2%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCTGGAGATTAAGTGTGTTGTGAAAT GTAGACGCTCAACGTCTGACTTGCAGCGCATACTGGTTTCCTTGAGTACGCACAACGTTGGCGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCAACTGACGCTGAAGCTC GAAGGTGCGGGTATCGAACAGG
Prevotella 21	NA	19%	10%	20%	7%	0,1%	0,0%	0,1%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTTGATAAGCGTGTGTTGTGAAAT TAGGCGCCCAACGTCTGCCTTGCAGCGCAAACTGGTTACTTGAGTACGCACAACGAGCGGGAATTCGTCGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCATTGCGAAGGCAGCTTACGGGAGCGTTACTGACGCTGAAGCTCG AAAGTGCGGTATCGAACAGG
Prevotella 27	shahii	15%	6%	20%	2%	0,1%	0,0%	0,1%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGCTTAAAGCGTGTGTTGTGAAAT CGGTGCTCAACATCCGACTTGCAGCGCAACTGGGGGCTTGAGTGCGCCGAAAGTAGGCGGAATTCGTCGTGTAG GCGGTGAAATGCTTAGATATCAGGAAGAAGCTCCGATTGCGAAGGCAGCTTACTGTAGCGCAACTGACGCTGATGCTC GAAAGCGTGGTATCGAACAGG
Prevotella 3	nigrescens	24%	4%	10%	2%	1,9%	4,6%	8,9%	0,3%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGGTGAGGCCGTGTTAAGCGTGTGTTGTGAAAT TAGGTGCTCAACATTAACCTGCAGCGCAACTGCAGACTTGAGTACACGCAGCGAGCGGGAATTCATGGTGTAG CGGTGAAATGCTTAGATATCATGAGGAAGCTCCGATTGCGAAGGCAGCTGCGGGAGTGTACTGACGCTTAAGCTCG AAGGTGCGGGTATCGAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Prevotella 4	nanceiensis	36%	25%	30%	24%	0,5%	0,4%	1,3%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGTGCCTAGGCCGTTTGATAAGCGTGTGTGAAATA TAGTGGCTCAACCTCTATCGTGCAGCGCAACTGTTGAACCTGAGTGCCTAGTAGTAGGCCGGAATTCGTGGTGTAGC GGTGAAATGCTTAGATATACGGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGTAACGTTACTGACGCTTAAGCACGA AGGTGCGGGTATCGAACAGG
Prevotella 42	veroralis	4%	4%	10%	2%	0,2%	0,9%	1,8%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGAGATTAAGTGTGTTGTGAAAT GTAGACGCTCAACGCTGACTTGCAGCGCATACTGGTTTCTTGTAGTACGCACAACGTTGGCGGAATTCGTGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCCACTGACGCTTAAGCTCG AAGGTGCGGGTATCGAACAGG
Prevotella 45	NA	3%	8%	20%	5%	0,1%	0,2%	0,2%	0,2%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGTGCCTAGGCCGTTTGATAAGCGTGTGTGAAATA TAGTGGCTCAACCTCTATCGTGCAGCGCAACTGTGCAACTTGTAGTGCCTAGTAGTAGGCCGGAATTCGTGGTGTAG CGGTGAAATGCTTAGATATCAGGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGTAACGTTACTGACGCTTAAGCACGA AGGTGCGGGTATCGAACAGG
Prevotella 49	NA	1%	4%	10%	2%	0,0%	0,1%	0,0%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTAGATTAAGCGTGTGTGAAATG TAGATGCTCAACATCTGACTTGCAGCGCAACTGGTTTACTTGTAGTGTGCGCAACGTAGGCCGGAATTCGTGTGTAGC GGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGGAGCACAACTGACGCTGAAGCTCGA AGGTGCGGGTATCGAACAGG
Prevotella 5	NA	40%	18%	20%	17%	0,5%	0,1%	0,1%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGTGCCTAGGCCGTTTGATAAGCGTGTGTGAAATA TAGTGGCTCAACCTCTATCGTGCAGCGCAACTGTGCAACTTGTAGTGCCTAGTAGTAGGCCGGAATTCGTGGTGTAG CGGTGAAATGCTTAGATATCAGGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGTAACGTTACTGACGCTTAAGCACGA AGGTGCGGGTATCGAACAGG
Prevotella 54	NA	3%	4%	10%	2%	0,1%	0,1%	0,1%	0,2%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGTGATTAAGCGTGTGTGAAAT GCAGGTCTCAACGCTGCACTGCAGCGCAACTGGTTCACTTGTAGTGTGCGCAACGCAAGCGGAATTCGTGTGTAG GCGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTTACCGGAGCACAACTGACGCTGAAGCTC GAAAGTGCGGTATCGAACAGG
Prevotella 74	NA	1%	4%	10%	2%	0,0%	0,0%	0,1%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGTGTAGGCCGTTTGTAAAGCGTGTGTGAAAT TAGTGGCTCAACATTTAAGTGCAGCGCAACTGGCGAAGCTTGTAGTGCACACAACGTATGCGGAATTCATGGTGTAGC GGTGAAATGCTTAGATATCATGAAGAAGCTCCGATTGCGAAGGCAGCATACGGGAGTGTAACTGACGCTTAAGCTCGA AGGTGCGGGTATCGAACAGG
Prevotella 8	pallens	28%	12%	30%	7%	0,3%	0,2%	0,4%	0,0%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGTGTAGGCCGTTTGTAAAGCGTGTGTGAAAT TAGGTGCTCAACATTTAAGTGCAGCGCAACTGTCAGACTTGTAGTACACGCAACGTATGCGGAATTCATGGTGTAGC GGTGAAATGCTTAGATATCATGAAGAAGCTCCGATTGCGAAGGCAGCATACGGGAGTGTAACTGACGCTTAAGCTCGA AGGTGCGGGTATCGAACAGG
Prevotella 9	NA	16%	12%	30%	7%	0,4%	0,2%	0,3%	0,1%	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTAAAGGGAGCGTAGGCCGAGATTAAGTGTGTTGTGAAAT GTAGACGCTCAACGCTGACTTGCAGCGCATACTGGTTTCTTGTAGTACGCACAACGTTGGCGGAATTCGTGTGTAG CGGTGAAATGCTTAGATATGACGAAGAAGCTCCGATTGCGAAGGCAGCTGACGGGAGCGCAACTGACGCTGAAGCTC GAAGGTGCGGGTATCGAACAGG
Pseudoxanthomonas 4	kaohsiungensis/koreensis	1%	4%	10%	2%	0,0%	0,0%	0,0%	0,0%	TACGAAGGGTCAAGCGTTACTCGGAATTAAGGCGTAAAGCGTGCCTAGGTGGTTGTTAAGTGTGCTGTGAAAG CCCTGGGCTCAACCTGGGAATTCGATGATACTGGGCAACTAGAGTGTGGTAGAGGGTGGCGGAATTCGGGTGTA GCAGTGAATGCGTAGAGATCGGGAGGAACATCCGTTGCGAAGGCAGCTGACGGGAGCGCAACTGACACTGAGGC ACGAAAGCGTGGGGAGCAACAGG
Romboutsia 1	timonensis	1%	14%	10%	15%	0,0%	0,1%	0,0%	0,1%	TACGTAGGGGGCTAGCGTTATCCGGAAATTAAGTGGGCTAAAGGGTGCCTAGGTGGTTTCTTAAGTGTGAGGTGAAAG GCTACGGCTCAACCGTAGTAAGCCTTTGAAACTGGGAACTTGTAGTGCAGGAGAGGAGTGTGAAATTCATGTGTAG CGGTGAAATGCTTAGATATGAGGAGAACACAGTTGCGAAGGCAGCTTCTGGACTGTAAGTGTGAGGAGGAGGAGG AAAGCGTGGGGAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Rothia 1	mucilaginoso	16%	16%	30%	12%	0,1%	0,4%	0,4%	0,4%	TACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTTGTAGGCGGTTTGTCCGCTCTGCTGTGAAAAG GCCGGGGCTTAACCCCGTATTGTCAGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTG TAGCGGTGGAATGCGCAGATATCAGGAGGAACCCGATGGCGAAGGCAGGTCTCTGGGCTGTAACCTGACGCTGAGAA AGCGAAAGCATGGGGAGCGAACAGG
Rothia 2	NA	31%	14%	30%	10%	0,3%	0,3%	0,5%	0,1%	TACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTTGTAGGCGGTTTGTCCGCTCTGCTGTGAAAAG GCCGGAGCTTAACCTCGTATTGTCAGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAGGAACACCCGATGGCGAAGGCAGGTCTCTGGGCTGTAACCTGACGCTGAGAA GCGAAAGCATGGGGAGCGAACAGG
Rothia 4	mucilaginoso	10%	16%	10%	17%	0,1%	0,3%	0,1%	0,3%	TACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTTGTAGGCGGTTTGTCCGCTCTGCTGTGAAAAG GCCGGGGCTTAACCTCGTATTGTCAGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTGT AGCGGTGGAATGCGCAGATATCAGGAGGAACACCCGATGGCGAAGGCAGGTCTCTGGGCTGTAACCTGACGCTGAGAA GCGAAAGCATGGGGAGCGAACAGG
Rothia 7	mucilaginoso	1%	6%	20%	2%	0,2%	0,3%	0,3%	0,4%	TACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTTGTAGGCGGTTTGTCCGCTCTGCTGTGAAAAG GCCGGGGCTTAACCCCGTATTGTCAGTGGGTACGGGCAGACTAGAGTGCAGTAGGGGAGACTGGAATTCCTGGTGT TAGCGGTGGAATGCGCAGATATCAGGAAAGAACCCGATGGCGAAGGCAGGTCTCTGGGCTGTAACCTGACGCTGAGAA AGCGAAAGCATGGGGAGCGAACAGG
Selenomonas 1	NA	21%	14%	40%	7%	0,1%	0,0%	0,1%	0,0%	TACGTAGGTGGCGAGCGTTGTCCGGAATCATTGGGCGTAAAGGAGCGCAGGCGGGCGGTAAGTCTTACTTAAAA GTGCGGGGCTCAACCCCGTATGGGAGAGAACTATCGGTCTTGTAGTACAGGAGAGGAAAGCGGAATTCCTAGTGT AGCGGTGAAATGCGTAGATATTGGGAAGAACCAGTGGCGAAGGCAGGCTTCTGGACTGCAACTGACGCTGAGGC TCGAAAGCCAGGGGAGCGAACGGG
Selenomonas 2	sputigena	15%	8%	20%	5%	0,1%	0,0%	0,0%	0,0%	TACGTAGGTGGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGGAGCGCAGGCGGACATATAAGTCCATCTTAAAAAG TGCGGGGCTCAACCCCGTATGGGGATGGAACCTGTATGCCTTGTAGTGCAGGAGAGGAAAGCGGAATTCCTAGTGT GCGGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCAGGCTTCTGGACTGTAACCTGACGCTGAGGCT CGAAAGCCAGGGGAGCGAACGGG
Selenomonas 3	NA	7%	4%	10%	2%	0,1%	0,0%	0,0%	0,0%	TACGTAGGTGGCGAGCGTTGTCCGGAATCATTGGGCGTAAAGGAGCGCAGGCGGGCATGTAAGTCTTCTTAAAAAG TTCGGGGCTCAACCCCGTATGGGAAAGAACTACATGTCTTGTAGTACAGGAGAGGAAAGCGGAATTCCTAGTGT CGGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCAGGCTTCTGGACTGCAACTGACGCTGAGGCTC GAAAGCCAGGGGAGCGAACGGG
Staphylococcus 1	aureus subsp. aureus/anaerobius argenteus/caprae/epidermidis/haemol yticus/lugdunensis/pasteuri/saccharol yticus/schweitzeri/simiae/warneri petrasii subsp. croceilyticus/petrasii/pragensis/jettens is capitis subsp. capitis hominis subsp. novobiosentis	42%	61%	50%	63%	2,7%	0,8%	0,4%	0,9%	TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCTAGGCGGTTTTTAAAGTCTGATGTGAAAGC CCACGGCTCAACCGTGGAGGGTATTGGAACCTGGAACCTTGTAGTGCAGAAGGAAAGTGGAAATTCATGTGTAG CGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCAGCTTCTGGTCTGTAACCTGACGCTGATGTGCG AAAGCGTGGGGATCAACACAGG
Streptobacillus 1 (Pseudostreptobacillus)	hongkongensis	36%	12%	30%	7%	0,4%	0,1%	0,1%	0,0%	TACGTATGTCGCAAGCGTTATCCGGAATTATTGGGCTTAAAGGGCATCTAGGCGGTTAAACAAGTACAGGGGTGAAAA CTTGACGCTCAACTGCAAGCTTGCCTTTGAAACTGATTAAGTACTGAGTACTGAAAGGTTGGGTGGAACCTACACGAGTAG AGGTGAAATTCGTAGATATGTGTAGGAATGCCGATGATGAAGATAAAGTACTGACAGAAACTGACGCTGAAGTGCG AAAGCTAGGGGAGCAACAGG
Streptobacillus 2	NA	25%	8%	20%	5%	0,3%	1,0%	2,0%	0,1%	TACGTATGTCGCAAGCGTTATCCGGAATTATTGGGCTTAAAGGGCATCTAGGCGGTTTCAAGTACAGGGGTGAAAA TTATGGCTCAACATAAGCTTGCCTTTGAAACTGAAAGACTAGAGTACTGAAAGGTTGGGTGGAACCTACACGAGTAG AGGTGAAATTCGTAGATATGTGTAGGAATGCCGATGATGAAGATAAAGTACTGACAGAAACTGACGCTGAAGTGCG AAAGCTAGGGGAGCAACAGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Streptobacillus 3	NA	30%	16%	30%	12%	0,2%	0,2%	0,3%	0,1%	TACGTATGTCGCAAGCGTTATCCGGAATTATTGGGCTTAAAGGGCATCTAGGCGGTTTTCAAGTCAGGGGTGAAAAC TTATGGCTCAACTATAAGCTTGCCTTTGAAACTGAAAGACTAGAGTACTGGAAGGTGGGTGGAACACACAGTAGA GGTGAAATCGCTAGATATGTAGGAATGCCGATGATGAAGATAACTCACTGGACAGAAAAGTACGCTGAAGTGCGA AAGCTAGGGGAGCAACAGG
Streptococcus 1	pneumoniae/pseudopneumoniae	66%	55%	60%	54%	8,0%	9,5%	6,7%	10,3%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCAACAGG
Streptococcus 11	intermedius	9%	6%	10%	5%	0,2%	0,9%	2,7%	0,0%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCAGTGGCTCAACCATTGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCGAACAGG
Streptococcus 19	anginosus subsp. anginosus/whileyi	1%	4%	10%	2%	0,1%	0,3%	0,2%	0,4%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGAAAAGTCTGAAGTAAAG GCAGTGGCTCAACCATTGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCGAACAGG
Streptococcus 2	mitis/infantis oralis subsp. oralis/tigurinus/dentisani	70%	69%	80%	66%	1,9%	2,9%	2,7%	2,9%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCAACAGG
Streptococcus 4	NA	4%	16%	20%	15%	12,9%	8,9%	4,0%	10,6%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCAACAGG
Streptococcus 5	salivarius/thermophilus/vestibularis	45%	73%	60%	76%	0,2%	0,4%	0,2%	0,4%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAG CGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCG AAGCTGGGGAGCGAACAGG
Streptococcus 7	parasanguinis/australis/rubneri	24%	24%	30%	22%	0,2%	0,5%	0,3%	0,5%	TACGTAGGTCCTCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCAACAGG
Streptococcus 8	sanguinis	9%	16%	20%	15%	0,2%	0,1%	0,3%	0,1%	TACGTAGGTCCTCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTAGATAAGTCTGAAGTTAAAG GCTGTGGCTTAACCATAGTAGGCTTTGAAACTGTTAACTTGAGTGCAGAGGGGAGAGTGGAAATCCATGTGTAGC GGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGCTGTAAGTACGCTGAGGCTCGA AAGCTGGGGAGCAACAGG
Veillonella 1	dispar/infantium	60%	37%	60%	32%	1,0%	0,6%	1,3%	0,3%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCAGGCGGATTGGTCAGTCTGTCTTAAAAG TTCGGGCTTAACCCCGTATGGGATGGAACACTGCAACTTAGAGTATCGGAGAGGAAAGTGGAAATCCTAGTGTAG CGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGACGAAAAGTACGCTGAGGCGC GAAAGCCAGGGGAGCGAACGGG
Veillonella 2	NA	72%	55%	60%	54%	0,9%	0,7%	1,1%	0,6%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCAGGCGGCTATCCAAGTCTGTCTTAAAAG TTCGGGCTCAACCCCGTATGGGATGGAACACTAGTAGGCTAGAGTATCGGAGAGGAAAGCGGAATCCTAGTGTAG CGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGACGAAAAGTACGCTGAGGCGC GAAAGCCAGGGGAGCGAACGGG

Taxon Name	Species	Prevalence				Mean Relative Abundance				Sequence
		DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} n=10	HNP _{DC} (n=41)	DNP (n=67)	HNP _{All} (n=51)	HNP _{CI} (n=10)	HNP _{DC} (n=41)	
Veillonella 3	parvula/tobetsuensis	42%	43%	40%	44%	0,8%	0,7%	0,6%	0,7%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGATCAGTCAGTCTGTCTTAAAAG TTCGGGGCTTAACCCCGTATGGGATGGAACTGCTGATCTAGAGTATCGGAGAGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAAGAACCACAGTGGCGAAGGCGACTTCTGGACGAAAACTGACGCTGAGGCGC GAAAGCCAGGGGAGCGAACGGG
Veillonella 4	NA	10%	14%	10%	15%	0,6%	0,7%	0,1%	0,8%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGATAGTTCAGTCTGTCTTAAAAG TTCGGGGCTTAACCCCGTATGGGATGGAACTGCCAATCTAGAGTATCGGAGAGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAAGAACCACAGTGGCGAAGGCGACTTCTGGACGAAAACTGACGCTGAGGCGC GAAAGCCAGGGGAGCGAACGGG
Veillonella 5	atypica/rogosae	12%	12%	20%	10%	0,5%	0,5%	0,6%	0,5%	TACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGCGCGCGCAGGCGGATCAGTTAGTCTGTCTTAAAAG TTCGGGGCTTAACCCCGTATGGGATGGAACTGCTGATCTAGAGTATCGGAGAGGAAAGTGAATTCCTAGTGTAG CGGTGAAATGCGTAGATATTAGGAAGAACCACAGTGGCGAAGGCGACTTCTGGACGAAAACTGACGCTGAGGCGC GAAAGCCAGGGGAGCGAACGGG