

Table S1. Detailed information of sequencing data

Raw Data(Gb)			Clean Data(Gb)		
Mean	Min	Max	Mean	Min	Max
14.00	10.77	22.20	7.01	0.92	13.76

Table S2. The genomic information and G4 analysis results of five enriched oral bacteria genera

	numbers of species	Median (Gb)	GC %	PQS	Mean f
Actinomyces	8	2.88	68.75	5144	1.75
Neisseria	3	2.25	51.86	1139	0.51
Prevotella	6	3.14	44.51	623	0.20
Streptococcus	15	2.13	39.33	156	0.07
Veillonella	1	2.13	38.63	130	0.06

Table S4. G4 analysis of *Acinetobacter baumannii* and *Actinomyces odontolyticus*

	complete Sequences	Median (b)	mean GC %	mean PQS	Mean f
<i>Acinetobacter baumannii</i>	244	4039492	39	282	0.070
<i>Actinomyces odontolyticus</i>	2	2393960	65	2543	1.063

Table S5. G4 sequence information related to MFS gene of *A. odontolyticus*

G4ID	sequence	cGcC	G4H	G4NN
AO-1	AAACGAGGGGCGGTGGCGCGGGGATGCAAC	8.50	1.20	0.91
AO-2	ATGAGGAAGAAGAGGGTGTGCGGGGCTTCG	13.33	1.07	0.56
AO-3	GTGTGCGGGGCTTCGCGCTTGAGGGTTCGC	5.29	0.90	0.68
AO-4	ACCTTCTTGGGCAGCGGGGGGTTTCACGATG	7.67	0.90	0.79
AO-5	GGGGGGTTCACGATGACGGGGATCGCGAAG	16.20	1.33	0.96
AO-6	AGGACGGAGGCGGGGTGCACGAAGTACATG	7.20	0.93	0.86
AO-7	GTGATGACCGATGCGGGGTGGCGGGAGTA	10.25	1.07	0.83
AO-8	GGGGTGGCGGGAGTAGCGCTCATGGGATCG	9.60	1.30	0.91
AO-9	GGAGGATCGTGCGCAGACGGGGAGCGCGGC	5.43	0.90	0.70
AO-10	AGAGGATGATGGGGAGGAACTGCAGTGCGG	12.33	1.00	0.76
AO-11	TGGGGAAAGGGGCGCGCGGGGTCTACGC	9.14	1.50	0.96
AO-12	AAGAGCGGCGGGCACGGGGGTGTCGAGGTC	9.50	1.17	0.78
AO-13	GGGGGTGTCGAGGTCGCGGATGCGGGGGAT	20.50	1.60	0.98
AO-14	GCGGATGCGGGGGATGGCATACATAGCGGC	8.33	0.97	0.94
AO-15	GATGAGGGTCATCAGGGGGGCGTGGAACCA	10.43	1.13	0.95
AO-16	GATGGCGGGGGAACCGATGTTGGCGATGGA	8.50	1.00	0.89
AO-17	TCGAGGGGCAGTTCGGGCGCGGGCGCGGCG	6.13	1.17	0.78
AO-18	GTCATCGTGGGGGCGCAGGTCAGGCCGGTG	5.67	0.90	0.79
AO-19	ACGGA CT CGC GAGGAACATCGGGGTCTGTGG	5.00	0.93	0.78
AO-20	ACATCGGGGTCTGTGGGGAACGATCGCGGGC	7.57	1.23	0.97
AO-21	TCGGAGGAGCGACGCGACAGGAAGAGGGGG	10.40	1.07	0.66
AO-22	AGCATGAGGGCGGTGACGGAAACGGCGGGC	5.83	0.90	0.77
AO-23	AGTGCAACGAGGACGAAGACGGGGGTGGCG	9.80	0.97	0.77
AO-24	AAGACGGGGGTGGCGTGCACGGGGCCATAA	7.75	1.17	0.95
AO-25	AGCGTCTGGTGTGGGTGGGGCGAGGCTCGGG	10.40	1.37	0.87
AO-26	GGCGGTGAGCAGATACGCCAGGGGAGGGGC	6.50	1.20	0.84