Table S1. Bacterial strains used for cell culture and genomic extraction.

Name	Genbank Accession	Ref
Escherichia coli BW25113	NZ_CP009273.1	Grenier et al. 2014
Vibrio coralliilyticus P1	NZ_AEQS00000000.1	Sussman et al. 2008; Santos et al. 2011
Vibrio sp. TOK8	MH807582.1	Miura et al. 2019
Vibrio sp. TOK14	MH807586.1	Miura et al. 2019
Vibrio sp. TOK79	MH807606.1	Miura et al. 2019
Vibrio sp. TOK88	MH807609.1	Miura et al. 2019
Ruegeria sp. TOK17	MH807589.1	Miura et al. 2019
Ruegeria sp. TOK19	MH807590.1	Miura et al. 2019
Ruegeria sp. TOK21	MH807591.1	Miura et al. 2019
Ruegeria sp. TOK22	MH807592.1	Miura et al. 2019
Ruegeria sp. TOK32	MH807597.1	Miura et al. 2019
Ruegeria sp. TOK38	MH807601.1	Miura et al. 2019
Ruegeria sp. TOK39	MH807602.1	Miura et al. 2019
Ruegeria sp. TOK44	MH807603.1	Miura et al. 2019
Ruegeria sp. TOK89	MH807610.1	Miura et al. 2019
Microbulbifer sp. TOK10	MH807584.1	Miura et al. 2019
Photobacterium sp. TOK16	MH807588.1	Miura et al. 2019
Tropicibacter sp. TOK31	MH807596.1	Miura et al. 2019
Pseudovibrio sp. TOK86	MH807607.1	Miura et al. 2019

Table S2. Bacterial genomic sequences downloaded from Genbank and used for primer design in this study. -: Unpublished.

Name	Genbank Accession No.	Ref.
Ruegeria sp. F75025	HQ908672.1	-
Bacterium 1H113	JF411452.1	Chiu et al. 2012
Ruegeria sp. TM1040	NC_008044.1	Moran et al. 2007
Ruegeria pomeroyi DSS-3	NC_003911.12	Moran et al. 2004
Vibrio coralliilyticus ATCC BAA-450	NR_117892.1	Hoffmann et al. 2012
Vibrio pelagius	LN832981.1	-
Vibrio breoganii FF50	NZ_CP016179.1	-
Vibrio anguillarum VIBI2	CP023310.1	-
Vibrio anguillarum MVAV6203	NZ_CP016095.1	-
Vibrio harveyi 345	CP025538.1	-
Vibrio natriegens CCUG16374	CP016351.1	-
Escherichia coli BW25113	NZ_CP009273.1	Grenier et al. 2014

Table S3. Previously Reported 16S Primers Used as References for Designing Universal Primers.

Primer name	Sequence (5'-3')	Target Group	Ref
8F	AGAGTTTGATCCTGGCTCAG	Universal	Turner et al. 1999
27F	AGAGTTTGATCMTGGCTCAG	Universal	Lane et al. 1991
CC[F]	CCAGACTCCTACGGGAGGCAGC	Universal	Rudi et al. 1997
357F	CTCCTACGGGAGGCAGCAG	Universal	Turner et al. 1999
515F	GTGCCAGCMGCCGCGGTAA	Universal	Turner et al. 1999
533F	GTGCCAGCAGCCGCGGTAA	Universal	Weisburg et al. 1991
895F	CRCCTGGGGAGTRCRG	Bacteria exc. plastids &	Hodkinson & Lutzoni 2009
16S. 1100. F16	CAACGAGCGCAACCCT	Universal	Turner et al. 1999
1237F	GGGCTACACACGYGCWAC	Universal	Turner et al. 1999
519R	GWATTACCGCGGCKGCTG	Universal	Turner et al. 1999
CD[R]	CTTGTGCGGGCCCCCGTCAATTC	Universal	Rudi et al. 1997
902R	GTCAATTCITTTGAGTTTYARYC	Bacteria exc. plastids &	Hodkinson & Lutzoni 2009
904R	CCCCGTCAATTCITTTGAGTTTYAR	Bacteria exc. plastids &	Hodkinson & Lutzoni 2009
907R	CCGTCAATTCMTTTRAGTTT	Universal	Lane et al. 1991
1100R	AGGGTTGCGCTCGTTG	Bacteria	Turner et al. 1999
1185mR	GAYTTGACGTCATCCM	Bacteria exc. plastids &	Hodkinson & Lutzoni 2009
1381R	CGGTGTGTACAAGRCCYGRGA	Bacteria exc. *Asterochloris* sp. plastids	Hodkinson & Lutzoni 2009
1381bR	GGGCGGTGTGTACAAGRCCYGRG	Bacteria exc. *Asterochloris* sp. plastids	Hodkinson & Lutzoni 2009
1391R	GACGGGCGGTGTGTRCA	Universal	Turner et al. 1999
1492R (i)	GGTTACCTTGTTACGACTT	Universal	Turner et al. 1999
1492 (s)	ACCTTGTTACGACTT	Universal	Lane et al. 1991

Primer sequences were downloaded from "LUTZONI LAB (http://lutzonilab.org/16s-ribosomal-dna/)".

Table S4. Nucleotide area of Genbank no. HQ908672.1 sequence in reference with non-target strains.

Reference non-target strains (Genbank accession No.)	Selected nucleotide sequnence area of HQ908672.1 (start site–ending site)
Bacterium 1H113 (JF411452.1)	1251–1278
Vibrio coralliilyticus ATCC BAA-450 (NR_117892.1)	71–168, 482–513, 724–771, 903–944, 1014–1059, 1144–1178, 1214–1240
Vibrio pelagius (LN832981.1)	60–89, 118–143, 366–394, 482–505, 544–585, 717–772, 922–943, 1033–1053, 1219–1239, 1282–1310

ccode_53	date_mod	store	quantity	upc	geocode
2	05/08/2014	2708	192	245	33.5152,-79.0426,0.0,1.7,0.7,1.7,0.0,0.0,0.0

Table 56. Primers obtained after first selection

No	GC	Tm	Sequence
1	55.0	58.0	CCCGTGAGGATTACTCAGG
2	58.0	60.0	CCCGTGAGGATTACTCAGGC
3	58.0	60.0	CCGTGAGGATTACTCAGGCG
4	58.0	60.0	CCGTGAGGATTACTCAGGCG
5	58.0	60.0	CGTGAGGATTACTCAGGCGG
6	58.0	60.0	GTGAGGATTACTCAGGCGGG
7	57.0	55.0	GAGGATTACTCAGGCGGGTT
8	57.0	55.0	GAGGATTACTCAGGCGGGTT
9	57.0	55.0	AGGATTACTCAGGCGGGTTC
10	57.0	55.0	GGATTACTCAGGCGGGTTCT
11	55.0	60.0	GATTACTCAGGCGGGTTCTA
12	55.0	60.0	ATTACTCAGGCGGGTTCTAC
13	57.0	55.0	TTACTCAGGCGGGTTCTACC
14	58.0	55.0	TACTCAGGCGGGTTCTACGT
15	60.0	55.0	ACTCAGGCGGGTTCTACGTT
16	60.0	55.0	AATACGTTCCCGGGCCTTGT
17	59	60	GAATACGTTCCCGGGCCTTG
18	60.0	55.0	AATACGTTCCCGGGCCTTGT
19	58.0	55.0	ATACGTTCCCGGGCCTTGTA
20	60.0	60.0	ACGTTCCCGGGCCTTGTACA
21	62.0	60.0	ACGTTCCCGGGCCTTGTACA
22	61.0	60.0	GTTCCCGGGCCTTGTACACA
23	61.0	60.0	TTCCCGGGCCTTGTACACAT
24	64.0	60.0	TTGCGCTCGTTGCCGAACCT
25	57.0	55.0	CGAACTGCTGGCAACTAAGG
26	58.0	55.0	GAACTGCTGGCAACTAAGGA
27	58.0	60.0	ACTGCTGGCAACTAAGGATG
28	58.0	60.0	CTGCTGGCAACTAAGGATGT
29	58.0	60.0	TGCTGGCAACTAAGGATGTG
30	57.0	55.0	GCTGGCAACTAAGGATGTGG
31	61.0	59.0	GGAACGGGTCCAGAGATGGAACCT
32	61.0	59.0	GGAACGGGTCCAGAGATGGAACCT
33	61-62	57.0	GGACCGGTCCAGAGATGGAATCCT
34	61-62	54.0	GGACCGGTCCAGAGATGGAATCCTTT
35	57.0	58.0	GACCGGTCCAGAGATGGAT
36	58.0	57.0	GACCGGTCCAGAGATGGATC
37	58.0	57.0	GACCGGTCCAGAGATGGATCT
38	60.0	55.0	GACCGGTCCAGAGATGGATCTT
39	59-60	52.0	GACCGGTCCAGAGATGGATCTTTC
40	59-60	54.0	GACCGGTCCAGAGATGGATCTTTC
41	58.0	58.0	ACCGGTCCAGAGATGGATC
42	58-59	58.0	ACCGGTCCAGAGATGGATC
43	58.0	55.0	ACCGGTCCAGAGATGGATCT
44	58-59	55.0	ACCGGTCCAGAGATGGATCTT
45	60.0	55.0	ACCGGTCCAGAGATGGATCTTT
46	59-60	52.0	ACCGGTCCAGAGATGGATCTTTC
47	59-60	55.0	ACCGGTCCAGAGATGGATCTTTCA
48	57.0	58.0	CCGGTCCAGAGATGGATCT
49	58-59	55.0	CCGGTCCAGAGATGGATCTT
50	58.0	52.0	CCGGTCCAGAGATGGATCTTT
51	58-59	55.0	CCGGTCCAGAGATGGATCTTTC
52	60.0	55.0	CCGGTCCAGAGATGGATCTTTCA
53	60-61	54.0	CCGGTCCAGAGATGGATCTTTCAC
54	55.0	56.0	CGGTCCAGAGATGGATCT
55	55.0	53.0	CGGTCCAGAGATGGATCTT
56	56.0	50.0	CGGTCCAGAGATGGATCTTT
57	56-57	52.0	CGGTCCAGAGATGGATCTTTC
58	56-57	52.0	CGGTCCAGAGATGGATCTTTCA
59	56-58	52.0	CGGTCCAGAGATGGATCTTTCAC
60	58.0	50.0	GGTCCAGAGATGGATCTTTCA
61	58.0	50.0	GGTCCAGAGATGGATCTTTCAC
62	57-58	48.0	GGTCCAGAGATGGATCTTTCACT
63	58.0	46.0	GGTCCAGAGATGGATCTTTCACTT
64	56-57	46.0	TCCAGAGATGGATCTTTCACTTCG
65	57.0	48.0	CCAGAGATGGATCTTTCACTTCG
66	57-58	48.0	CCAGAGATGGATCTTTCACTTCG
67	56-60	50.0	CCAGAGATGGATCTTTCACTTC
68	57.0	48.0	CAGAGATGGATCTTTCACTTCG
69	57.0	48.0	CAGAGATGGATCTTTCACTTCGG
70	58-59	48.0	CAGAGATGGATCTTTCACTTCGGT
71	56-57	45.0	AGAGATGGATCTTTCACTTCGG
72	58.0	43.0	AGAGATGGATCTTTCACTTCGGT
73	58.0	45.0	AGAGATGGATCTTTCACTTCGGT
74	55-56	48.0	GAGATGGATCTTTCACTTCGG
75	58.0	45.0	GAGATGGATCTTTCACTTCGGT
76	56-57	46.0	GAGATGGATCTTTCACTTCGGTG
77	56-57	46.0	GAGATGGATCTTTCACTTCGGTGA
78	58.0	43.0	AGATGGATCTTTCACTTCGGT
79	57.0	45.0	AGATGGATCTTTCACTTCGGTG
80	56-57	43.0	AGATGGATCTTTCACTTCGGTGA
81	56-57	46.0	AGATGGATCTTTCACTTCGGTGAC
82	55-56	48.0	GATGGATCTTTCACTTCGGT
83	57-58	48.0	GATGGATCTTTCACTTCGGTG
84	56-57	45.0	ATGGATCTTTCACTTCGGTGA
85	56-57	45.0	ATGGATCTTTCACTTCGGTGAC
86	56-58	43.0	ATGGATCTTTCACTTCGGTGACT
87	58.0	46.0	ATGGATCTTTCACTTCGGTGACTC
88	55-56	48.0	TGGATCTTTCACTTCGGTGAC
89	58.0	46.0	TGGATCTTTCACTTCGGTGACT
90	56-57	48.0	TGGATCTTTCACTTCGGTGACTC
91	58.0	50.0	TGGATCTTTCACTTCGGTGACTCG
92	56-57	48.0	GGATCTTTCACTTCGGTGACT
93	57.0	50.0	GGATCTTTCACTTCGGTGACTC
94	58.0	50.0	GGATCTTTCACTTCGGTGACTCG
95	60-61	54.0	GGATCTTTCACTTCGGTGACTCGG
96	57.0	50.0	GATCTTTCACTTCGGTGACTCG
97	58.0	50.0	ATCTTTCACTTCGGTGACTCG
98	60.0	50.0	GATCTTTCACTTCGGTGACTCGGT
99	57.0	48.0	ATCTTTCACTTCGGTGACTCG
100	58-59	50.0	ATCTTTCACTTCGGTGACTCGG
101	60-61	48.0	ATCTTTCACTTCGGTGACTCGGT
102	59-60	50.0	ATCTTTCACTTCGGTGACTCGGTG
103	59-61	52.0	TCTTTCACTTCGGTGACTCGGTG
104	59-60	50.0	CTTTCACTTCGGTGACTCGGTG
105	58.0	50.0	TTCACTTCGGTGACTCGGTG
106	58.0	50.0	TTGACTTCGGTGACTCGGTG
107	57.0	58.0	TCACTTCGGTGACTCGGTG
108	56-58	61.0	CACTTCGGTGACTCGGTG
109	62.0	60.0	AGCGTCGTCGGGTGAACCCA
110	60.0	60.0	CGTCGTCGGGTGAACCAC
111	58.0	60.0	CGTCGTCGGGTGAACCAAC
112	57.0	55.0	GTCGTCGGGTGAACCAACT
113	58.0	60.0	CGTCGTCGGGTGAACCAACT
114	58.0	60.0	CGTCGGGTAGAACCAACTCC
115	58.0	60.0	GTCGGGTAGAACCAACTCCC
116	58.0	55.0	TCGGGTAGAACCAACTCCCA
117	58.0	55.0	CGGGTAGAACCAACTCCCAT
118	58.0	55.0	GGGTAGAACCAACTCCCATG
119	58.0	55.0	GGTAGAACCAACTCCCATGG
120	58.0	42.0	GGGTTAATCCCAAAAACTGTCTC
121	58.0	45.0	ATGCCCAAAGGTACGGAATT
122	55-57	41.0	ATGCCCAAAGGTACGGAATT
123	55.0	45.0	ATGCCCAAAGGTACGGAATA
124	58.0	45.0	AACGCGGGCTAATCCAAAGG
125	62.0	60.0	ACGCGGGCTAATCCAAAGGC
126	57.0	52.0	TATCGCCTTTGGATTAGCCCG
127	57-58	52.0	TATCGCCTTTGGATTAGCCCG
128	57.0	53.0	ATCGCCTTTGGATTAGCCC
129	58.0	53.0	ATCGCCTTTGGATTAGCCCG
130	62.0	57.0	ATCGCCTTTGGATTAGCCCGC
131	58-59	58.0	TCGCCTTTGGATTAGCCCG
132	60.0	60.0	TCGCCTTTGGATTAGCCCGC
133	62-63	60.0	GCCTTTGGATTAGCCCGCGT
134	60.0	58.0	CCTTTGGATTAGCCCGCGT
135	60.0	58.0	CCTTTGGATTAGCCCGCGT
136	60-61	55.0	CCTTTGGATTAGCCCGCGTT
137	60.0	55.0	CCTTTGGATTAGCCCGCGTT
138	62.0	60.0	AGRCTGGAGCGGTGTCTCAGT
139	58.0	55.0	CGTGTCTCAGTCCCAGTGTT
140	58.0	55.0	GTGTCTCAGTCCCAGTGTT
141	58-59	58.0	CGTAGCCGGATCCGGAAAGT
142	58.0	57.0	GTAGCCGGATCCGGAAAGT
143	59-60	57.0	CGTAGCCGGATCCGGAAAGTTG
144	56-57	55.0	GTAGCCGGATCCGGAAAGTTG
145	61.0	60.0	CGGATCCGGAAAGTTGGGGGT
146	58-59	58.0	GGATCCGGAAAGTTGGGGGT
147	57-58	55.0	GATCCGGAAAGTTGGGGGTGA
148	57-58	55.0	GATCCGGAAAGTTGGGGGTGAA
149	57-58	60.0	ATCGGAAAGTTGGGGGTGAA
150	58.0	55.0	AGAGTTCGAAGAAGGTGAAGT
151	55.0	55.0	AGAGTTCGAAGAAGGTGAAGT
152	55.0	55.0	GAGTTCGAAGAAGGTGAAGTG
153	57.0	55.0	AGTTCGAAGAAGGTGAAGTGG
154	57.0	55.0	GTTCGAAGAAGGTGAAGTGGA
155	58.0	55.0	TCGAAGAAGGTGAAGTGGAAT
156	58.0	55.0	TCGAAGAAGGTGAAGTGGAAT
157	55.0	55.0	CGAGAAGAGGTGAGTGGAATT
158	58.0	55.0	CGAGAAGAGGTGAGTGGAATT
159	61-62	60.0	AATGCACGTCCTCGGGTAGC
160	62.0	57.0	AATGCCAGTCCTCGGGTAGCA
161	62-63	60.0	ATTGCCAGTCCTCGGGTAGCA
162	63.0	57.0	ATGCCAGTCCTCGGGTAGCAT
163	61-62	60.0	ATGCCAGTCCTCGGGTAGCAT
164	61-62	60.0	CAGTCCTCGGGTAGCATGCT
165	60.0	57.0	CAGTCCTCGGGTAGCATGCTA
166	60-61	57.0	CAGTCCTCGGGTAGCATGCTAT
167	58.0	55.0	GTCCTCGGGTAGCATGCTAT
168	57-58	50.0	TCGTCGGGTAGCATGCTATT
169	57-58	55.0	CGTCGGGTAGCATGCTATTC
170	56-57	55.0	GTCGGGTAGCATGCTATTCG
171	57.0	55.0	TCGGGTAGCATGCTATTCGC
172	57.0	60.0	AGCATGCTATTCGGTGACAC
173	57.0	60.0	AGCATGCTATTCGGTGACACA
174	58.0	55.0	GCATGCTATTCGGTGACACA
175	55-58	55.0	GCATGCTATTCGGTGACACA
176	58.0	52.0	GCATGCTATTCGGTGACACAC
177	55.0	50.0	CATGCTATTCGGTGACACAC
178	56-57	50.0	ATGCTATTCGGTGACACACC
179	58.0	50.0	TGCTATTCGGTGACACACC
180	58.0	55.0	CCCCCCGTCAATTCCTTTGG
181	57.0	55.0	CCCCCCGTCAATTCCTTTGAG
182	58.0	55.0	CCCCCCGTCAATTCCTTTGAGC
183	60-61	58.0	ACGCGTGGGAATATGCCCA
184	61-62	55.0	ACGCGTGGGAATATGCCCAA
185	60-62	52.0	ACGCGTGGGAATATGCCCAAA
186	59-60	58.0	CGCGTGGGAATATGCCCAA
187	60-61	55.0	CGCGTGGGAATATGCCCAAA
188	60-62	57.0	CGCGTGGGAATATGCCCAAAG
189	57-58	55.0	GCGTGGGAATATGCCCAAAG
190	58.0	55.0	GCGTGGGAATATGCCCAAAGT
191	56-57	50.0	GTGGGAATATGCCCAAAGT
192	55.0	50.0	GGGAATATGCCCAAAGGTAC
193	57-58	52.0	GGGAATATGCCCAAAGGTACG
194	55.0	50.0	GGAATATGCCCAAAGGTACG
195	55.0	50.0	GAATATGCCCAAAGGTACGG
196	55.0	50.0	GAATATGCCCAAAGGTACGG
197	55-58	48.0	GAATATGCCCAAAGGTACGGA
198	58.0	50.0	GGGCTAATCCAAAGGGATA
199	58.0	50.0	AGGCGATAAACTTTCCCCC
200	58.0	50.0	GCGATAAACTTTCCCCCG
201	58.0	50.0	GCGATAAACTTTCCCCCGA
202	55.0	50.0	TAAACTTTCCCCCGAAGGG
203	55.0	50.0	TAAACTTTCCCCCGAAGGGC
204	60.0	55.0	AATCCTTTCCCCGAAGGGCA
205	61.0	60.0	ATCCTTTCCCCGAAGGGCAC
206	62.0	60.0	TCTTTCCCCGAAGGGCACA
207	61.0	60.0	CTTTCCCCGAAGGGCACAT
208	61.0	60.0	TTTCCCCGAAGGGCACATT
209	57-58	55.0	TATGTCCCCTTCGGGGGAAA
210	60.0	58.0	ATGTGCCCTTCGGGGGAAA
211	61-62	57.0	ATGTGCCCTTCGGGGGAAAG
212	61-62	57.0	ATGTGCCCTTCGGGGGAAAGA
213	61.0	60.0	TGTGCCCTTCGGGGGAAAGA
214	61-62	57.0	TGTGCCCTTCGGGGGAAAGAT
215	61-62	60.0	GTGCCCTTCGGGGGAAAGAT
216	60.0	55.0	TGCCCTTCGGGGGAAAGATT
217	60.0	55.0	TGCCCTTCGGGGGAAAGATT
218	55.0	50.0	GCCTGTGAAGATATGACGG
219	55.0	50.0	GCCTGTGAAGATATGACGGC
220	55.0	45.0	AATTCCGAACAAGCCTAACC
221	57.0	50.0	ATTCCGAACAAGCCTAACCC
222	58.0	55.0	TTCCGAACAAGCCTAACCCC
223	61.0	60.0	TCCGAACAAGCCTAACCCCC
224	58.0	60.0	CCGAACAAGCCTAACCCCTC
225	58.0	60.0	CGAACAAGCCTAACCCCTCC
226	58.0	60.0	GAACAAGCCTAACCCCTCCC
227	58.0	60.0	AACAAGCCTAACCCCTCCCT
228	62.0	60.0	ACAACGCTAACCCCTCCCGT
229	60.0	60.0	CAACGCTAACCCCTCCCGTA
230	58-59	58.0	CGTAGCCGGATCCGGAAAGT
231	58.0	55.0	CGTAGCCGGATCCGGAAAGTT
232	56-57	55.0	GTAGCCGGATCCGGAAAGTTG
233	61.0	60.0	CTAGCTGCGCTTTACGCCCA
234	61.0	60.0	CTAGCTGCGCTTTACGCCCAA
235	58.0	60.0	ACGTTGCGCTTTACGCCCAGT
236	58.0	60.0	ACGTTGCGCTTTACGCCCAGTA
237	61.0	60.0	CGTGCGCTTTACGCCCAGTA
238	58.0	55.0	GTGCGCTTTACGCCCAGTAA
239	58.0	60.0	TGCGCTTTACGCCCAGTAAT
240	58.0	60.0	GCGCTTTACGCCCAGTAATC
241	55.0	60.0	CGCTTTACGCCCAGTAATCC
242	55.0	50.0	GCTTTACGCCCAGTAATCCC
243	55.0	50.0	CGCTTTACGCCCAGTAATCCC
244	55.0	45.0	TTACGCCCAGTAATCCCGAA
245	56.0	50.0	TACGCCCAGTAATCCCGAAC
246	58.0	50.0	ACGCCCAGTAATCCCGAACA
247	57.0	50.0	CGCCCAGTAATTCCCGAACAA
248	58.0	50.0	GCGCCCAGTAATTCCCGAACA
249	55-58	48.0	ACTATCGGCTTAAGATTCGAAG
250	55.0	48.0	ATCGGCTTCGAGATTCGAAGA
251	55.0	50.0	TCGGCTTCGAGATTCGAAGAG
252	55-56	50.0	CGGCTTCGAGATTCGAAGAG
253	57-58	57.0	CGGCTCTAGATTCCGAGAGAG
254	55-58	52.0	GGTCTGAAGTTCGAGAGAGGT
255	55.0	52.0	GTCTGAAGTTCGAGAGAGGTG
256	57.0	52.0	GAGTTCGAGAGAGGTGAAGT
257	57.0	52.0	AGAGTTCGAGAGAGGTGAAGTG
258	55.0	53.0	GAGTTCGAGAGAGGTGAAGT
259	56-57	55.0	GAGTTCGAGAGAGGTGAAGTG
260	58-59	57.0	GAGTTCGAGAGAGGTGAAGTGG
261	57.0	55.0	AGTTCGAGAGAGGTGAAGTGG
262	57.0	55.0	AGTTCGAGAGAGGTGAAGTGG
263	58.0	52.0	AGTTCGAGAGAGGTGAAGTGGA
264	58.0	55.0	GTTCGAGAGAGGTGAAGTGGA
265	56-57	55.0	GTTCGAGAGAGGTGAAGTGGA
266	57.0	52.0	GTTCGAGAGAGGTGAAGTGGAA
267	55-58	55.0	TTCGAGAGAGGTGAAGTGGAA
268	58.0	60.0	TTCGAGAGAGGTGAAGTGGAAT
269	58.0	60.0	TCGAGAGAGGTGAAGTGGAATT
270	56-57	60.0	TCGAGAGAGGTGAAGTGGAATT
271	55-58	53.0	CGAGAGAGGTGAAGTGGAAT
272	56-57	52.0	CGAGAGAGGTGAAGTGGAATT
273	56-57	52.0	CGAGAGAGGTGAAGTGGAATTC
274	58.0	52.0	AGAGAGGTGAATGGAATTCCG
275	56-58	55.0	GAGAGGTGAATGGAATTCCG
276	57-58	55.0	AAGAATGAATGCCAATCGCC
277	58-59	55.0	AAGAATGAATGCCAATCGCC
278	60-61	60.0	CGATGAATGCCAATCGTCCGG
279	57-58	58.0	GATGAATGCCAATCGTCCGG
280	58-59	60.0	GATGAATGCCAATCGTCCGGT
281	60-62	57.0	GATGAATGCCAATCGTCCGGGT
282	59-60	58.0	ATGAATGCCAATCGTCCGGG
283	57.0	55.0	ATGAATGCCAATCGTCCGGGTA
284	58.0	52.0	ATGAATGCCAATCGTCCGGGTAA
285	57.0	52.0	TGAATGCCAATCGTCCGGGTA
286	57.0	52.0	TGAATGCCAATCGTCCGGGTAA
287	59-60	57.0	TGAATGCCAATCGTCCGGGTAG
288	58.0	60.0	GAATGCCAATCGTCCGGGTAG
289	58-60	60.0	GAATGCCAATCGTCCGGGTAG
290	58.0	58.0	AATGCCAATCGTCCGGGTAG
291	61-62	60.0	AATGCCAATCGTCCGGGTAGC
292	61-63	57.0	AATGCCAATCGTCCGGGTAGCA
293	60.0	55.0	ATGCCAATCGTCCGGGTAGCA
294	60-61	60.0	TGCCAATCGTCCGGGTAGCA
295	61-62	60.0	CAATCGTCCGGGTAGCATGCT
296	60.0	55.0	CAATCGTCCGGGTAGCATGCT
297	58.0	55.0	CAATCGTCCGGGTAGCATGCTA
298	58-60	55.0	GTCCGGGTAGCATGCTATTC
299	58-60	55.0	GTCCGGGTAGCATGCTATTCG
300	57-58	55.0	GTCGGGTAGCATGCTATTCGC
301	58.0	55.0	TCGGGTAGCATGCTATTCGCC
302	58.0	52.0	TCGGGTAGCATGCTATTCGCCT
303	57.0	53.0	TCGTCGGGTAGCATGCTAT
304	58.0	55.0	TCGTCGGGTAGCATGCTATT
305	58.0	58.0	TCGTCGGGTAGCATGCTATTC
306	57-58	53.0	CGTCGGGTAGCATGCTATT
307	57-58	55.0	CGTCGGGTAGCATGCTATTC
308	59-61	57.0	CGTCGGGTAGCATGCTATTCG
309	58.0	55.0	GTCGGGTAGCATGCTATTCG
310	58.0	57.0	GTCGGGTAGCATGCTATTCGG
311	58.0	55.0	TCGGGTAGCATGCTATTCGG
312	59-60	52.0	TCGGGTAGCATGCTATTCGGT
313	57-58	58.0	CGGGTAGCATGCTATTCGG
314	58-59	58.0	CGGGTAGCATGCTATTCGGT
315	60-61	57.0	CGGGTAGCATGCTATTCGGTG
316	55-58	53.0	CGGGTAGCATGCTATTCGGT
317	58.0	55.0	GGGTAGCATGCTATTCGGTG
318	56-57	52.0	GGGTAGCATGCTATTCGGTGA
319	56-57	52.0	GGTAGCATGCTATTCGGTGAC
320	58.0	48.0	TAGCATGCTATTCGGTGACAC
321	57.0	50.0	AGCATGCTATTCGGTGACAC
322	58.0	50.0	GCATGCTATTCGGTGACAC
323	58.0	53.0	GCATGCTATTCGGTGACAC
324	55-58	50.0	GCATGCTATTCGGTGACACA
325	55.0	50.0	CATGCTATTCGGTGACACA
326	55.0	50.0	CATGCTATTCGGTGACACAC
327	57-58	52.0	CATGCTATTCGGTGACACACC
328	56-57	50.0	ATGCTATTCGGTGACACACC
329	58-59	48.0	ATGCTATTCGGTGACACACCT
330	58.0	50.0	TGCTATTCGGTGACACACC
331	58.0	50.0	AATCTTCGCAACCGATACTCCC
332	55.0	53.0	CTTTCAACTTCGGTGACTCG
333	55.0	50.0	CTTTCAACTTCGGTGACTCGG
334	58.0	53.0	CTTTCAACTTCGGTGACTCGGT
335	58.0	53.0	TTTCACTTCGGTGACTCGG
336	56-58	55.0	TTTCACTTCGGTGACTCGGT
337	58.0	55.0	ACTAAGGATGTGGGTTGCGCC
338	58.0	55.0	CTCGTCCGTTGCCGGACCTTA
339	58.0	55.0	CCCGTCCAGCATCGGGAGTT
340	62.0	60.0	AAGGATGTGGGTTGCGCTCG
341	58.0	60.0	CTGGCTCGTTGCCGGACCTT
342	64.0	60.0	TTGGCTCGTTGCCGGACCTT
343	63.0	60.0	TGCGCTCGTTGCCGGACCTTA
344	58.0	60.0	GTGTAGCCCAACCATGGAAGTT
345	60.0	60.0	TGTAGCCCAACCCGTAAGGG
346	58.0	60.0	CCCGTAAGGGCCATGTCCAG
347	58.0	60.0	CAACCCGTAAGGGCCATGAG
348	58.0	60.0	CCGTGAGGATTACTCAGGCG
349	58.0	60.0	CGTGAGGATTACTCAGGCGG
350	58.0	60.0	GTGAGGATTACTCAGGCGGG
351	58.0	55.0	TGAGGATTACTCAGGCGGGT
352	57.0	55.0	GAGGATTACTCAGGCGGGTT
353	57.0	55.0	AGGATTACTCAGGCGGGTTC
354	58.0	55.0	GGATTACTCAGGCGGGTTC
355	55.0	50.0	GATTACTCAGGCGGGTTCTA
356	55.0	50.0	ATTACTCAGGCGGGTTCTAC
357	58.0	55.0	TTACTCAGGCGGGTTCTACG
358	58.0	55.0	TACTCAGGCGGGTTCTACGT
359	60.0	60.0	ACTCAGGCGGGTTCTACGTG
360	61.0	60.0	CCCGTCACACATCGGGAGTT
361	58.0	60.0	CCGTCACACATCGGGAGTTG
362	58.0	60.0	CGTCACACATCGGGAGTTGT
363	58.0	60.0	GTCACACATCGGGAGTTGTT
364	58.0	50.0	TCACACATCGGGAGTTGTTC
365	55.0	60.0	ACACCATGGGAGTTGTTCTA
366	58.0	60.0	CACCATGGGAGTTGTTCTAC
367	58.0	60.0	CCATGGGAGTTGTTCTACC

Table S7. Primers obtained after seond selection

No.	Tm	GC%	length	Sequence (5'-3')
1	57	55	20	GGATTACTCAGGCGGGTTCT
2	55	50	20	GATTACTCAGGCGGGTTCTA
3	55	50	20	ATTACTCAGGCGGGTTCTAC
4	57	55	20	TTACTCAGGCGGGTTCTACG
5	59	55	20	TACTCAGGCGGGTTCTACGT
6	60	60	20	ACTCAGGCGGGTTCTACGTG
7	60	55	20	AATACGTTCCCGGGCCTTGT
8	59	60	20	GAATACGTTCCCGGGCCTTG
9	60	55	20	AATACGTTCCCGGGCCTTGT
10	59	55	20	ATACGTTCCCGGGCCTTGTA
11	57	55	20	GCTGGCAACTAAGGATGTGG
12	63-64	58	24	GGGACCGGTCCAGAGATGGATCTT
13	61	59	22	GGACCGGTCCAGAGATGGATCT
14	61-62	57	23	GGACCGGTCCAGAGATGGATCTT
15	61-62	54	24	GGACCGGTCCAGAGATGGATCTTT
16	57	58	19	GACCGGTCCAGAGATGGAT
17	57-58	60	20	GACCGGTCCAGAGATGGATC
18	59	57	21	GACCGGTCCAGAGATGGATCT
19	60	55	22	GACCGGTCCAGAGATGGATCTT
20	59-60	52	23	GACCGGTCCAGAGATGGATCTTT
21	58-59	50	22	ATCTTTCACTTCGGTGACTCGG
22	60-61	48	23	ATCTTTCACTTCGGTGACTCGGT
23	60-61	50	24	ATCTTTCACTTCGGTGACTCGGTG
24	59-61	52	23	TCTTTCACTTCGGTGACTCGGTG
25	59-60	55	22	CTTTCACTTCGGTGACTCGGTG
26	57-58	52	21	TTTCACTTCGGTGACTCGGTG
27	58	55	20	TTCACTTCGGTGACTCGGTG
28	57	58	19	TCACTTCGGTGACTCGGTG
29	56-58	61	18	CACTTCGGTGACTCGGTG
30	62	60	20	AGCGTCGTCGGGTAGAACCA
31	55	45	20	TATGCCCAAAGGTACGGAAT
32	56-57	47	19	ATGCCCAAAGGTACGGAAT
33	55	45	20	ATGCCCAAAGGTACGGAATA
34	59	55	20	AACGCGGGCTAATCCAAAGG
35	62	60	20	ACGCGGGCTAATCCAAAGGC
36	61	60	20	GCGGGCTAATCCAAAGGCGA
37	55	53	19	CTTTCACTTCGGTGACTCG
38	57	55	20	CTTTCACTTCGGTGACTCGG
39	58	52	21	CTTTCACTTCGGTGACTCGGT
40	56	53	19	TTTCACTTCGGTGACTCGG
41	56-58	50	20	TTTCACTTCGGTGACTCGGT
42	59	55	20	ACTAAGGATGTGGGTTGCGC
43	59	55	20	CTAAGGATGTGGGTTGCGCT
44	59	55	20	TAAGGATGTGGGTTGCGCTC
45	62	60	20	AAGGATGTGGGTTGCGCTCG
46	57	55	20	GAGGATTACTCAGGCGGGTT
47	57	55	20	AGGATTACTCAGGCGGGTTC
48	57	55	20	GGATTACTCAGGCGGGTTCT
49	55	50	20	GATTACTCAGGCGGGTTCTA
50	55	50	20	ATTACTCAGGCGGGTTCTAC
51	57	55	20	TTACTCAGGCGGGTTCTACG
52	59	55	20	TACTCAGGCGGGTTCTACGT
53	60	60	20	ACTCAGGCGGGTTCTACGTG
54	61	60	20	CCCGTCACACCATGGGAGTT
55	59	60	20	CCGTCACACCATGGGAGTTG

Table S8. Feature table of the NGS reads after denoise using DADA2 on QIIME2 platform. See also supplemental FASTA file for nucleotide sequences.

Sequence Count	Min Length	Max Length	Mean Lengtr	Range	Standard Deviation
514	389	436	420.54	47	9.87

Table S9. Results of *in silico* PCR of the NGS reads

Primer set	Total number of sequences tested	Number of amplified sequences	Percentage amplified
U357'F- U515'R		429	83
r445F-r446R	514	26	5.1
r38F-r30R		0	0