SUPPORTING INFORMATION

Cyclic di-GMP contributes to adaption and virulence of *Bacillus thuringiensis* through a riboswitch-regulated collagen adhesion protein

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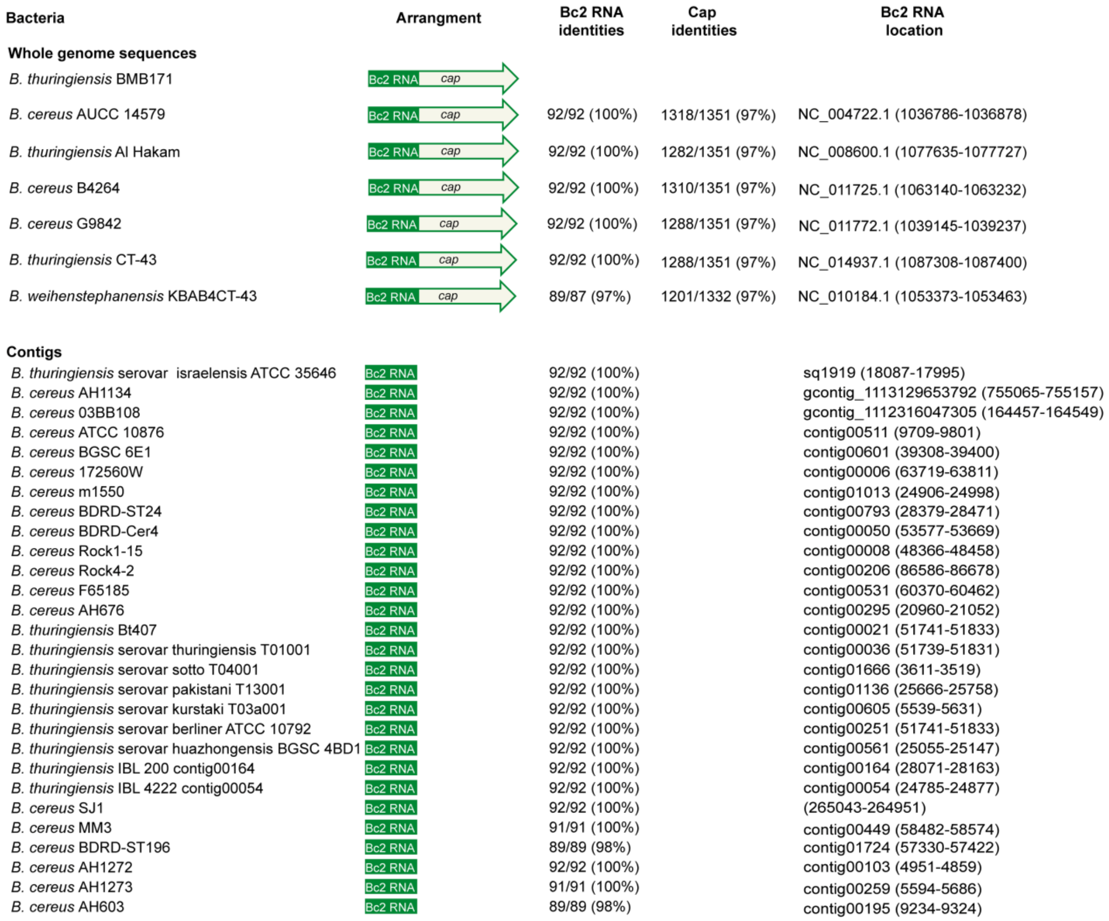
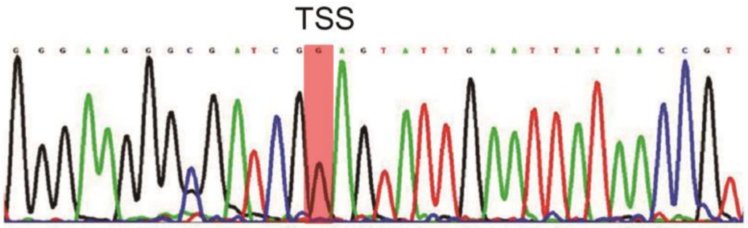
Supplementary Figures:



Bacteria	Arrangment	Bc2 RNA identities	Cap identities	Bc2 RNA location
Whole genome sequences				
B. thuringiensis BMB171	Bc2 RNA *cap*			
B. cereus AUCC 14579	Bc2 RNA *cap*	92/92 (100%)	1318/1351 (97%)	NC_004722.1 (1036786-1036878)
B. thuringiensis Al Hakam	Bc2 RNA *cap*	92/92 (100%)	1282/1351 (97%)	NC_008600.1 (1077635-1077727)
B. cereus B4264	Bc2 RNA *cap*	92/92 (100%)	1310/1351 (97%)	NC_011725.1 (1063140-1063232)
B. cereus G9842	Bc2 RNA *cap*	92/92 (100%)	1288/1351 (97%)	NC_011772.1 (1039145-1039237)
B. thuringiensis CT-43	Bc2 RNA *cap*	92/92 (100%)	1288/1351 (97%)	NC_014937.1 (1087308-1087400)
B. weihenstephanensis KBAB4CT-43	Bc2 RNA *cap*	89/87 (97%)	1201/1332 (97%)	NC_010184.1 (1053373-1053463)
Contigs				
B. thuringiensis serovar israelensis ATCC 35646	Bc2 RNA	92/92 (100%)		sq1919 (18087-17995)
B. cereus AH1134	Bc2 RNA	92/92 (100%)		gcontig_1113129653792 (755065-755157)
B. cereus 03BB108	Bc2 RNA	92/92 (100%)		gcontig_1112316047305 (164457-164549)
B. cereus ATCC 10876	Bc2 RNA	92/92 (100%)		contig00511 (9709-9801)
B. cereus BGSC 6E1	Bc2 RNA	92/92 (100%)		contig00601 (39308-39400)
B. cereus 172560W	Bc2 RNA	92/92 (100%)		contig00006 (63719-63811)
B. cereus m1550	Bc2 RNA	92/92 (100%)		contig01013 (24906-24998)
B. cereus BDRD-ST24	Bc2 RNA	92/92 (100%)		contig00793 (28379-28471)
B. cereus BDRD-Cer4	Bc2 RNA	92/92 (100%)		contig00050 (53577-53669)
B. cereus Rock1-15	Bc2 RNA	92/92 (100%)		contig00008 (48366-48458)
B. cereus Rock4-2	Bc2 RNA	92/92 (100%)		contig00206 (86586-86678)
B. cereus F65185	Bc2 RNA	92/92 (100%)		contig00531 (60370-60462)
B. cereus AH676	Bc2 RNA	92/92 (100%)		contig00295 (20960-21052)
B. thuringiensis Bt407	Bc2 RNA	92/92 (100%)		contig00021 (51741-51833)
B. thuringiensis serovar thuringiensis T01001	Bc2 RNA	92/92 (100%)		contig00036 (51739-51831)
B. thuringiensis serovar sotto T04001	Bc2 RNA	92/92 (100%)		contig01666 (3611-3519)
B. thuringiensis serovar pakistani T13001	Bc2 RNA	92/92 (100%)		contig01136 (25666-25758)
B. thuringiensis serovar kurstaki T03a001	Bc2 RNA	92/92 (100%)		contig00605 (5539-5631)
B. thuringiensis serovar berliner ATCC 10792	Bc2 RNA	92/92 (100%)		contig00251 (51741-51833)
B. thuringiensis serovar huazhongensis BGSC 4BD1	Bc2 RNA	92/92 (100%)		contig00561 (25055-25147)
B. thuringiensis IBL 200 contig00164	Bc2 RNA	92/92 (100%)		contig00164 (28071-28163)
B. thuringiensis IBL 4222 contig00054	Bc2 RNA	92/92 (100%)		contig00054 (24785-24877)
B. cereus SJ1	Bc2 RNA	92/92 (100%)		(265043-264951)
B. cereus MM3	Bc2 RNA	91/91 (100%)		contig00449 (58482-58574)
B. cereus BDRD-ST196	Bc2 RNA	89/89 (98%)		contig01724 (57330-57422)
B. cereus AH1272	Bc2 RNA	92/92 (100%)		contig00103 (4951-4859)
B. cereus AH1273	Bc2 RNA	91/91 (100%)		contig00259 (5594-5686)
B. cereus AH603	Bc2 RNA	89/89 (98%)		contig00195 (9234-9324)

Figure S1 Taxonomy of species containing Bc2 RNAs. The taxonomy of each organism containing a putative Bc2 RNA is listed. The identities of each Bc2 RNA and Cap with that in BMB171 are listed. Bc2 RNA-*cap* architecture in species whose genomes have been fully sequenced are demonstrated.



1 ACCATTGCTT CTTTAATGTA GTGGTGAATT GTTTTTTTTA TTAGAAAAAT AGAACAATTT

-35 -10

61 TATAGAGTAT TGAATTATAA CCGTCCAGAC GGTATAGTAA TATTTGGTTT AAGAGGAAAA

121 TGAAACAAAA AAAGAATAAA AGATATTTTT AGCACACTAT TCGAAAGGAT AGGCCGCAAA

181 GCTTAGAGTC TACGGTAATA CATATTGGTT ACTAAGATCG TCTGGTTGCA CATTTTTGAT

241 GCAACCGGAC GGTCTTTTTT TGTTATATAA ATATAAAAAA TAGGAGGGAA CT***ATGCAAAT***

301 ***GAAAAGTACT AAA***

Figure S2 Mapping the TSS of *cap*. The predicted -10 and -35 regions were underlined. The TSS of *cap* was highlight by a bent arrow. White letters shaded in black denotes the sequence of Bc2 RNA. Sequence in italic represents the coding sequence of *cap* gene.

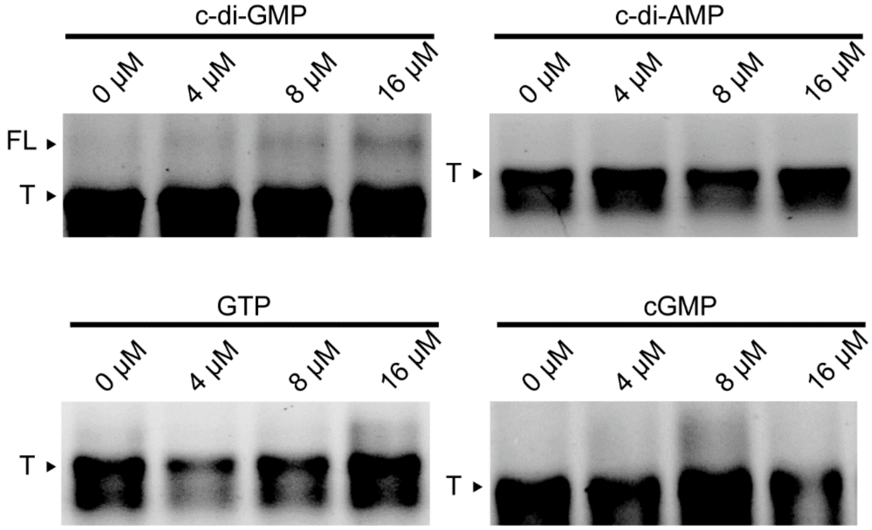


Figure S3 C-di-GMP specifically promotes Bc2 RNA transcription read-through. FL and T denote the full length transcripts and terminated transcripts of *in vitro* transcription termination assays, respectively. *In vitro* transcription was initiated by adding 0.25 U of *E. coli* RNA polymerase holoenzyme into transcription mixtures containing 0.1 pmol of DNA template, 5 mM ATP, CTP, GTP and UTP, 20 mM $MgCl_2$, 0.1 mM EDTA, 1 mM dithiothreitol and 10% glycerol. Reaction mixtures were also supplemented with c-di-GMP, c-di-AMP, GTP and cGMP at indicated concentrations. The reaction mixture was incubated at room temperature for 30 min and stopped by adding heparin at a final concentration of 0.5 mg/µl. The products were examined by 2% agarose gel and imaged by Molecular Imager (Bio-Rad, USA).

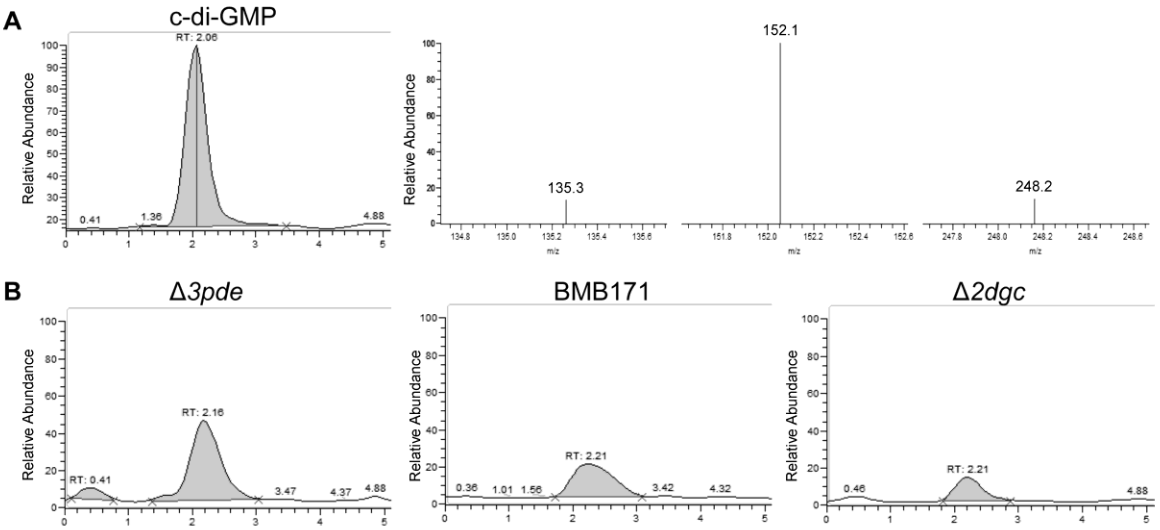


Figure S4 Quantification of intracellular c-di-GMP concentration by LC-MS/MS. (**a**) LC-MS/MS chromatogram of the c-di-GMP standard detected using the m/z fragments at 135.3, 152.25 and 248.2; (**b**) Determination of c-di-GMP extracted from Δ*3pde*, BMB171, and Δ*2dgc* culture.

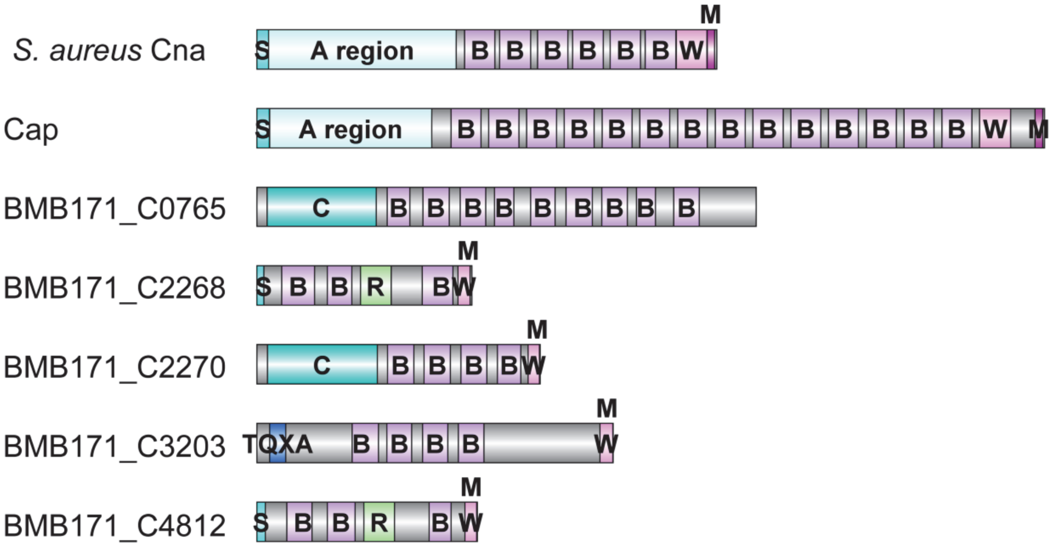


Figure S5 Domain organization of *S. aureus* Cna and collagen adhesion proteins in *B. thuringiensis* BMB171. The collagen binding A region is followed by B repeats. S, signal peptide; W, cell wall anchoring region containing the LPXTG motif; M, transmembrane segment; and C, choice-of-anchor A domain; TQXA, TQXA domain which occurs in surface-expressed proteins of Gram-positive bacteria; R, fimbrial isopeptide formation D2 domain. BMB171_C0765, BMB171_C2268, BMB171_C2270, BMB171_C3203, and BMB171_C4812 are encoded by *BMB171_C0765* (new tag *BMB171_RS04480*), *BMB171_C2268* (new tag *BMB171_RS12455*), *BMB171_C2270* (new tag *BMB171_RS12465*), *BMB171_C3203* (new tag *BMB171_RS17455*), and *BMB171_C4812* (new tag *BMB171_RS26025*), respectively. Prediction of transmembrane helices in proteins was performed by TMHMM Server v. 2.0. Signal peptide/non-signal peptide prediction was performed by SignalP 4.1 Server.

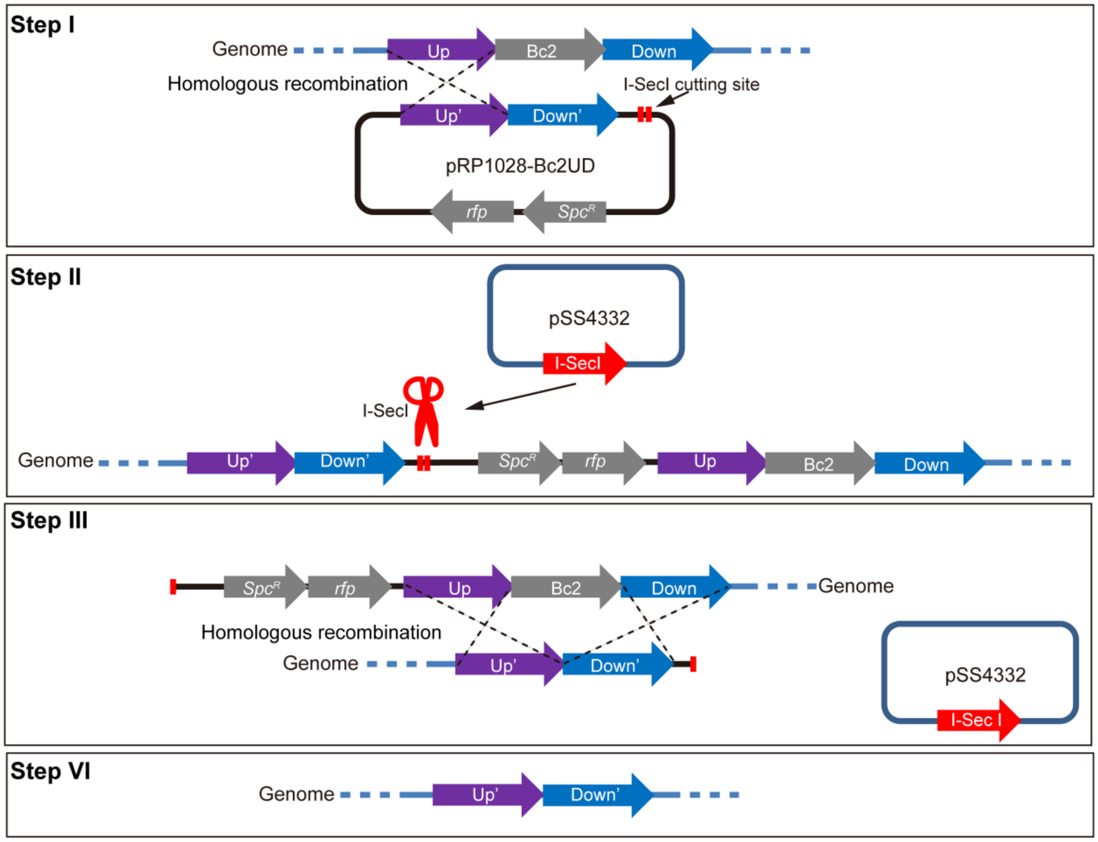


Figure S6 Scheme of the I-SceI mediated markless gene knockout procedure. Step I, the upstream and downstream of Bc2 RNA was fused together by overlap-PCR and cloned into pRP1028 to create recombinant plasmid pRP1028-Bc2UD. Then the recombinant plasmid was electroporated into BMB171 strain. Integration of plasmid pRP1028-Bc2UD into the chromosome through homologous recombination was induced by high temperature (37°C). Step II, plasmid pSS4332 was electroporated into the recombinant strain. I-SceI restriction enzyme synthesised by pSS4332 cleaved the recombination genome at I-SceI cutting site. Step III, homologous recombination was induced by the break DNA. Step VI, the redundant pSS4332 plasmid was removed using continuous passage at 28°C in LB broth, resulting in a markerless Bc2 RNA deletion strain.

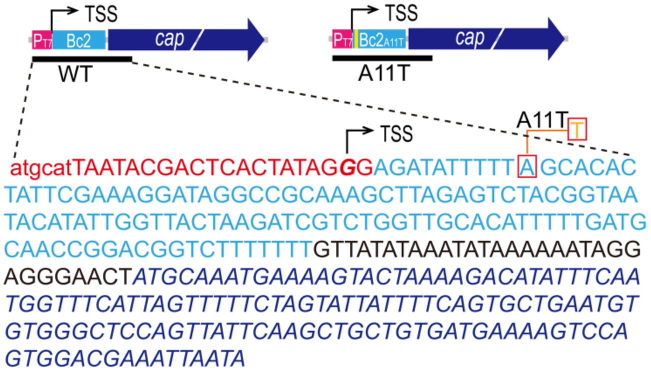


Figure S7 Schematic representation of the DNA templates used in *in vitro* transcription termination assays. Nucleotides in red denote T7 promoter, nucleotides in light blue denote Bc2 RNA sequence, and nucleotides in blue denote the coding region of *cap*. The TSS of *cap* was highlight by bent arrow.

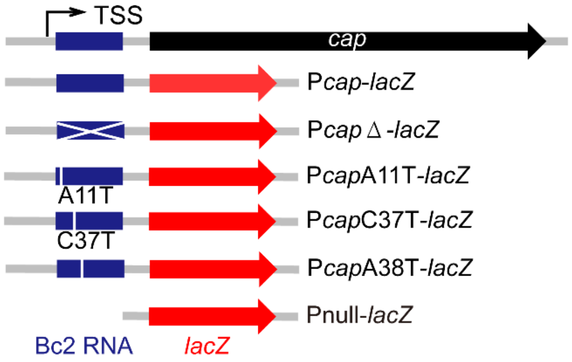


Figure S8 Schematic representation of the P*cap-lacZ*, P*cap*Δ*-lacZ* and Pnull-*lacZ* transcriptional reporter vectors. P*cap*-lacZ, pHT1K plasmid contains the 5´-UTR DNA region of *cap* gene encompassing Bc2 RNA sequence (-64—+249) which is fused with *lacZ*; P*cap*Δ-*lacZ*, pHT1K contains the 5´-UTR DNA region of *cap* gene lacking the Bc2 RNA sequence (-64—+76; +198—+249) which is fused with *lacZ*; P*cap*A11T-lacZ, P*cap*C37T-lacZ and P*cap*A38T-lacZ are pHT1Ks carrying 5´-UTR DNA region of *cap* with site mutants; Pnull-lacZ, pHT1K contains the promoterless *lacZ*.

Supplementary Tables :

Table S1 Primers used in this study

primers	Primer sequences (5´-3´)	Purposes	Origins
cap-U-F	ACATGGTACCTCAGAGAGGAAAGGGAGATGGGTT	*cap* gene knockout	This work
cap-U-R	ATTCGGATCCAGTTCCCTCCTATTTTTTATATT	*cap* gene knockout	This work
cap-D-F	ATACTCTAGATAAAGGTGAAAAGGTATCCTCAAAG	*cap* gene knockout	This work
cap-D-R	AGATAAGCTTAAACGATGATTCTCTTCCTCTTG	*cap* gene knockout	This work
cap-specific outer primer	GCATATCAATTGTGAATTGATCTCC	5´-RACE analysis	This work
cap-specific inner primer	GGCTTGATACGGTTCAGATGTCGTG	5´-RACE analysis	This work
5´-RACE Outer Primer	CATGGCTACATGCTGACAGCCTA	5´-RACE analysis	This work
5´-RACE Inner Primer	CGCGGATCC ACAGCCTACTGATGATCAGTCGATG	5´-RACE analysis	This work
P*cap*-F	CATGCCATGGACCATTGCTTCTTTAATGTAGTG	β-gal assays	This work
P*cap*-R	ACCGGATCCTTTAGTACTTTTCATTTGCATAGTTCCCTC	β-gal assays	This work
Bc2-Overlap-F	GAAACAAAAAAAGAATAAAGTTATATAAATATAAAAAATAGGAG	Overlap PCR	This work
Bc2-Overlap-R	TTTTATATTTATATAACTTTATTCTTTTTTTGTTTCATTTTCCTC	Overlap PCR	This work
RT*gap*-F	TTTTGCTAGCGCTTTCGCAG	qPCR assays	This work
RT*gap*-R	TAGCGCCTGTTGTGAAGGTG	qPCR assays	This work
RT*cap*-F	GACAGAGAGACCGAAGCCAC	qPCR assays	This work
RT*cap*-R	ACTCATGCCCAGGTCCTAATG	qPCR assays	This work
RTBc2-F	CGTCCAGACGGTATAGTAATATTTG	qPCR assays	This work
RTBc2-R	AGCTTTGCGGCCTATCCTTT	qPCR assays	This work
Bc2-U-F	CGACGCGTCTAAATTAACCTTAGAAGCAGTG	Bc2 knockout	This work
Bc2-D-R	CGGGATCCATTTACATATACAAGCCAATCAGC	Bc2 knockout	This work

A11T-b	CTTTCGAATAGTGTGCAAAAAAATATCT	Site mutation	This work
A11T-c	AGATATTTTTTTGCACACTATTCGAAAG	Site mutation	This work
C38T-b	CGAAAGGATAGGCCGTAAAGCTTAGAGTCTA	Site mutation	This work
C38T-c	TAGACTCTAAGCTTTACGGCCTATCCTTTCG	Site mutation	This work
A38T-b	CGTAGACTCTAAGCTTAGCGGCCTATC	Site mutation	This work
A38T-c	GTATGGCCGCTAAGCTTAGAGTCTACG	Site mutation	This work

Table S2 c-di-GMP-I riboswitch

Samples	Genome	Location	Sequence*
[Cellvibrio] gilvus ATCC 13127	CP002665.1	3443557-3443482	TCAGCGAAACGGCAAACCCTCCGCGAGGAGGGGACGCAAAGCCACGGGACCCACGACGGTCAGCCGGGCTACCGAA
[Cellvibrio] gilvus ATCC 13127	CP002665.1	1473921-1473997	CAGCGACAACGGCAAACCCTCCGCAAGGAGGGGACGCAAAGCCAACGGGACCCACGCAGGTCAGCCGAGCTACCGAA
Acaryochloris marina MBIC11017	CP000828.1	4797700-4797614	TCCTCGAAACGGCAACTTGTCTCGAAAGAGCAAGACGCAAATTAACGAGTCTAACCCTTTATAGGCATGATGGTCGTTAATACCGAA
Acaryochloris marina MBIC11017	CP000828.1	1721607-1721514	TCCCCGAAATGGCAACTTGCACCGAAAGGGTAAGGCGCAAATTAGCAGGCCTAAAATCCAAGCATTACGGGGTATGGATGCTGCTAGTGTCGAA
Acaryochloris sp. CCMEE 5410 contig00482	AFEJ01000324.1	22061-21975	TCCTCGAAACGGCAACTTGTCTCGAAAGAGCAAGACGCAAATTAACGAGTCTAACCCTTTATAGGCATGATGGTCGTTAATACCGAA
Acaryochloris sp. CCMEE 5410 contig00499	AFEJ01000341.1	4160-4067	TCCCCGAAATGGCAACTTGCACCGAAAGGGTAAGACGCAGATTAGCAGACCTAAAGTCCAAGCATTACGGGGTATGGATGCTGCTAGTGTCGAA
Acetivibrio cellulolyticus CD2 ctg00137	AEDB01000015.1	21591-21687	TATGAAACAGGGCAAAGTCGTTGAAAGACGGCGACGCAAAGCTGTGGGTCTAACGTTTGGGGAAGATGCCTTGAACTACGATTGCCAAGCTGCCATT
Acetivibrio cellulolyticus CD2 ctg00142	AEDB01000040.1	12119-12214	TATGAAACAGGGCAAAATCATTGAAAAATGATGACGCAAAGCTATGGGTCTAAGTTAAGGATTATATATCCTTGATATGATCGCCAAGTTGCCATT
Acetivibrio cellulolyticus CD2 ctg00148	AEDB01000011.1	99531-99625	TATGAAACAGGGCAAAGTTGTCGAAAGGCAATGACGCAAAGCCTTGGGTCTAAAGCTGAGACGAAAGTCAAAGCTAAGATAGCCGGGTTGCCATT
Acetivibrio cellulolyticus CD2 ctg00149	AEDB01000061.1	5161-5244	CATTTGAAATGGTAAACCTGGTGAAAACCAGTGACACAAAGCTACGGGTCTAAGGTCTTTGACTAAGACAGCCGAGTTGCCGAA

Acetivibrio cellulolyticus CD2 ctg00157	AEDB01000070.1	14624-14708	ATTTGTAAAAGGCAAATCTATCGAAAGATAGAGACGCAAAACTACGGGTCTACGGTCGCTTGACTACGACAGCCGGGTTGCCAAG
Acetivibrio cellulolyticus CD2 ctg00157	AEDB01000070.1	14797-14882	TTTCGAAAATGGCAAACTCAATGAAAATTGAGGACGCAAAACTACAGGTCTACGGGTTTCATTACTATGATGGCTGAGTTACCGAA
Acetohalobium arabaticum DSM 5501	CP002105.1	239557-239640	CCTCAAAAAAGGCACACTTGCTGAAAAGTAAGGTCGCAAAGTCTTGAGTCTAAAGCATAAAGCCATGACTGTCGGACTGCTGAA
Acetohalobium arabaticum DSM 5501	CP002105.1	1744836-1744745	AACTAGAAAGGGCACACTTATCGAAAGGTAAGGCCGCAAAGCTTCAAATCTACAGTGCAGTATAAAGGCACTATGATAGTTGGGCTACCACA
Acetonema longum DSM 6540 Contig00098	AFGF01000098.1	31377-31462	TAATAAACACGGCAAACTTATTGAAAAATAAGGACGCAAAGCTATGGGTCTACGTACTTTAAGTATATGGCTGCCAGGTTGCAAAA
Acholeplasma laidlawii PG-8A	CP000896.1	1183288-1183213	ATTAATATTTGGCAAACTATATGAAAATATAGGGCGCAAAACTATAGGGCCTTGAAAATGGTAGCCAGCTGCATAA
Acholeplasma laidlawii PG-8A	CP000896.1	1029409-1029330	AAGATTAAAAGGCAAACTTAAGGTAACTTAAGGACGCAAAACTAAAGGGTCTAATTAGTAATAGACAGCCAGTTGCATCG
Acholeplasma laidlawii PG-8A	CP000896.1	1036967-1036891	TAAAGTTTTTGGCAAAATTAGGGTAACCTAATGACGCAAAACTATAGGGCCTATATATTAGGCAGCCAGTTGCACTT
Acholeplasma laidlawii PG-8A	CP000896.1	1037127-1037052	TCATAAAAAAAGGCAAAATTAGGGTAACTTAATGACGCAAAACTACAGGGTCCAAATTAGGATAGCCAGTTGCTATA
Acidaminococcus fermentans DSM 20731	CP001859.1	1537998-1538074	AAAACCTTTTGGCAAACCTGGAGAAATCCAGCGACGCAAAGCTAACAGGGCCTGTAAAATGGCAGCCAGCTGCACAG
Activated sludge metagenome contig06636	AERA01006587.1	268-363	TTTCGAAAAAGGCAAACTGCGTGAAAGCGCAGGACGCAAAGCCACAAGCCTAAGGGCGCCGCTGAAATCGACGCCTATGGTGGTTGGGTTGCCGAT
Activated sludge metagenome contig19732	AERA01019441.1	138-228	AAGCGATAAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTTCGACCTAAGTGCTGAGAAATCAGCATACGGTGGCCGGGTTACCGAA

Activated sludge metagenome contig27665	AERA01026525.1	212-299	CACCGACAAGGGCAAACCATGCGAAAGCATGGGACGCAAAGCCAGCGGCCTAAGTCCCCCGCGGGGATAAGGCGGCAGGGTTGCCGAA
Aeromonas caviae Ae398	CACP01000024.1	108781-108867	TGTGCAAAAAGGCAAACCGGATGAAAGTCCGGGACGCAAAGCTTCCGGTCTAAGGGTCTGCGTACCTAGGATAGCGGGGCCACCACA
Aeromonas caviae Ae398	CACP01000017.1	7890-7805	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACAAGCTGTCCAGGATAGCGGGGTTGCAGCA
Aeromonas caviae Ae398	CACP01000095.1	68797-68714	CCAGGCAAAGGGCAAACCGGCAGTGATGCCGGGACGCAAAGCCTCCGATCTGTCCCATCCGGGCCAGACAGCGGGGTTACCCAG
Aeromonas hydrophila chiA gene for chitinase precursor	AB253741.1	579-665	TGTGCAAAAAGGCAAACCGGATGAAAGTCCGGGACGCAAAGCTTCCGGTCTAAGGGTCTGCGTACCTAGGATAGCGGGGCCACCACA
Aeromonas hydrophila chitinase 92 (chi92) gene	AF181852.1	295-381	TGTGCAAAAAGGCAAACCGGATGAAAGTCCGGGATGCAAAGCTTCCGGTCTAAGGGTCTGCGTACCTAGGATAGCGGGGCCACCACA
Aeromonas hydrophila chitinase gene	AF099928.1	353-438	GTGCAAAAAAGGCAAACGGATGAAAGTCCGGGACGCAAAGCCTCCGGTCTAAGGGTCAAAGCACCTAGGATAGCGGGGCCACCACA
Aeromonas hydrophila extracellular chitinase ChiA (chiA) gene	AF251793.1	101-188	GTGCAAAAAAGGCAAACCGGGATGAAAGTCCGGGACGCAAAGCCTCCGGTCTAAGGGTCAAAGCACCTAGGATAGCGGGGCCACCACA
Aeromonas hydrophila FliML (fliML)	DQ124694.1	7633-7720	GCATGATAAAGGCAAACTGAACTGAAAAGTCAGGACGCAAAGCCTCCGGTCTAATAGCTGCAATGCTAATGATAGCGGGGTTACCAAG
Aeromonas hydrophila subsp. hydrophila ATCC 7966	CP000462.1	551681-551596	TAGAGTAAAGGGCAAACCGGTCGAAAGGTCGGGACGCAAAGCCACCGGTCTAAGGGTTCATAACCTAAGACAGCGGAGCTGCCATC
Aeromonas hydrophila subsp. hydrophila ATCC 7966	CP000462.1	649413-649328	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Aeromonas hydrophila subsp. hydrophila ATCC	CP000462.1	1055622-1055709	TTGTGCAAAAGGCAAACCGGATGAAAGTCCGGGACGCAAAGCTTCCGGTCTAAGGGTCAGCAGTACCTAAGATAGCGGGGCCACCACA

7966			
Aeromonas hydrophila subsp. hydrophila ATCC 7966	CP000462.1	3873138-3873053	CCAGGTAAAGGGCAAACCGGTCGAGATGCCGGGACGCAATGCCTCCGGTCTTCAGATCGTGCGATCCAGATAGCGGGGCTTCCCAG
Aeromonas salmonicida subsp. salmonicida 01-B526 Contig016	AGVO01000016.1	110684-110771	TTGTGCAAAAGGCAAACCGGACGAAAGTCCGGGACGCAAAGCCTCCGGTCTAAGGGTCAGCAGTACCTAAGATAGCGGGGCCACCACA
Aeromonas salmonicida subsp. salmonicida 01-B526 Contig028	AGVO01000028.1	155902-155987	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Aeromonas salmonicida subsp. salmonicida 01-B526 Contig032	AGVO01000032.1	21104-21017	GCATGATAAAGGCAAACTGAACTGAAAAGTCAGGACGCAAAGCCTCCGGTCTAATAGCAGTAATGCTAATGATAGCGGGGTTACCAAG
Aeromonas salmonicida subsp. salmonicida 01-B526 Contig049	AGVO01000049.1	105007-105093	TAGAGTAAAGGGCAAACCGATCGAAAGGTCGGGACGCAAAGCCACCGGTCTAAGGGTGTAGATACCTAAGACAGCGGAGCTGCCAAC
Aeromonas salmonicida subsp. salmonicida 01-B526 Contig058	AGVO01000058.1	154133-154048	CCAGGTAAAGGGCAAACCGGTCGAAATGCCGGGACGCAATGCCTCCGGTCTCCAGATCAGTCGATCCAGATAGCGGGGCTTCCCAG
Aeromonas salmonicida subsp. salmonicida A449	CP000644.1	610702-610617	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Aeromonas salmonicida subsp. salmonicida A449	CP000644.1	365078-365165	GCATGATAAAGGCAAACTGAACTGAAAAGTCAGGACGCAAAGCCTCCGGTCTAATAGCAGTAATGCTAATGATAGCGGGGTTACCAAG
Aeromonas salmonicida subsp. salmonicida A449	CP000644.1	3594032-3593945	TTGTGCAAAAGGCAAACCGGACGAAAGTCCGGGACGCAAAGCCTCCGGTCTAAGGGTCAGCAGTACCTAAGATAGCGGGGCCACCACA

Aeromonas salmonicida subsp. salmonicida A449	CP000644.1	4016040-4015954	TAGAGTAAAGGGCAAACCGATCGAAAGGTCGGGACGCAAAGCCACCGGTCTAAGGGTGTAGATACCTAAGACAGCGGAGCTGCCAAC
Aeromonas salmonicida subsp. salmonicida A449	CP000644.1	899660-899745	CCAGGTAAAGGGCAAACCGGTCGAAATGCCGGGACGCAATGCCTCCGGTCTCCAGATCAGTCGATCCAGATAGCGGGGCTTCCCAG
Aeromonas veronii B565	CP002607.1	3993876-3993961	CTAGTCATTTGGCAAACTGACCGAAAGGTCGGGACGCAAAGCCTCCGGTCTACAGACGTTTTGTCCAGGATAGCGGGGTTGCCACA
Aeromonas veronii B565	CP002607.1	2331357-2331435	TATCCACCTCGCCACTCCCGATGTGAGTCGGGTTCGGAAAGCTACAGATCTCTACACCTGAGACGGCTGAGCTGCAGAT
Aeromonas veronii B565	CP002607.1	4488281-4488366	GGGTGAAAAAGGCAAAGTGACCCGAAAGGGCGCGACGCAAAGCCACCGGTCTAAGGGAAAACACCTATGACAGCGGGGCTGCCCCC
Aeromonas veronii B565	CP002607.1	933949-934036	TTGTGACAAGGGCAAACCGATTGAAAAGTCGGGACGCAAAGCTTCCGGTCTAAGGGTCAAGACGGCCTAGGATAGCGGGGCCACCACA
Aeromonas veronii B565	CP002607.1	945796-945878	CCAGGTAAAGGGCAAACCGGCAGTGATGTCGGGGCGCAATGCTTCCGGTCTCGATCGTGGATCCAGATAGCGGGGTTTCCCTG
Aeromonas veronii B565	CP002607.1	529899-529813	TAGAGTAAAGGGCAAACCGATCGAAAGGTCGGGACGCAAAGCCACCGGTCTAAGGGTTTTGATACCTAAGACAGCGGAGCTGCCATC
Aeromonas veronii B565	CP002607.1	929482-929569	GTAACCGAAGGGCAAACCGATCGCAAGATCGGGACGCAAAGCTTCCGGTCCAGGGATGAGCCGTACTTGAGATAGCGGGGCCACCACA
Alicyclobacillus acidocaldarius LAA1 ctg162	ACCS01000020.1	37515-37600	AGCGCATCAGGGCAAACCAACGGAAACGTTGGGACGCAAAGCTACGGGTCTACGGGGACTTGACCTAGGATCGCCGGGCTGCCGCT
Alicyclobacillus acidocaldarius LAA1 ctg162	ACCS01000020.1	42534-42619	TGTTGGCAAGGGCAAACCCGTCCGAAAGGCGGGGGCGCAAAGCCACGGGTCTACGGACGAAAGTCTATGGCAGCCGGGCTGCCGGA
Alicyclobacillus acidocaldarius LAA1 ctg48	ACCS01000010.1	51838-51922	GTCGGTCAAAGGCAAACTTCGCGAAAGCGGAGGACGCAAAGCTATAGGGACTCGACACGACGTGTCGTGCCAGCCAGCTGCCTGG
Alicyclobacillus acidocaldarius LAA1 ctg48	ACCS01000010.1	47507-47421	GGCGTTTCAGGGCAAACCAACGGAAACGTTGGGACGCAAAGCTACGGGTCTACGGGGACTTGGACCTAAGACCGCCGGGCTGCCGCT
Alicyclobacillus acidocaldarius LAA1 ctg6	ACCS01000033.1	24027-23944	GTCGGTCAAAGGCAAACTTCGCGCAAGCGGAGGACGCAAAGCTATAGGGGCTCGGCTATTATGCCGTGCCAGCCAGCTGCCTGA
Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446	CP001729.1	23541-23626	AGCGCATCAGGGCAAACCAACGGAAACGTTGGGACGCAAAGCTACGGGTCTACGGGGACTTGACCTAGGATCGCCGGGCTGCCGCT

plasmid pAACI02			
Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446 plasmid pAACI02	CP001729.1	28673-28758	TGTTGGCAAGGGCAAACCCGTCCGAAAGGCGGGGGCGCAAAGCCACGGGTCTACGGACGAAAGTCTATGGCAGCCGGGCTGCCGGA
Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1	CP002902.1	141355-141441	GGCGTTTCAGGGCAAACCAACGGAAACGTTGGGACGCAAAGCTACGGGTCTACGGGGACTTGGACCTAAGACCGCCGGGCTGCCGCT
Aliivibrio salmonicida LFI1238 chromosome 1 complete genome	FM178379.1	2124498-2124416	TCACGAACAGGGCAAACTGTGCGAAAGCTCAGGACGCAAAGCTTCCGGCCTACGTATTTATATAAGGTAGCAGGGTTGCCGAT
Alkaliphilus metalliredigens QYMF	CP000724.1	1508597-1508682	TAAATAAAAGGGCAAACTTATCGAAAGATAAGGGCGCAAAGCCAAGGGTCTTCATCAATTGATTGATATGACAGCCGGTTGCAGAG
Alkaliphilus metalliredigens QYMF	CP000724.1	2944881-2944796	AATAAGTAAAGGCAAAACCATCGAAAGATGGTGACGCAAAGCCACGAATCTAAGTCGTTTGACGATAGGATAGTCGGGTTGCCTAT
Alkaliphilus metalliredigens QYMF	CP000724.1	1528254-1528342	ACTTGATAAAGGCAAACTTATTGAAAAATAAGGACGCAAAGCTATGGATCTAAGGGGATCTTTATTCCTATGATTGCCAGGTTGCCAAA
Alkaliphilus metalliredigens QYMF	CP000724.1	608582-608671	CGTTGATAAGGGCAAACTTACTGAAAAGTAAGGACGCAAAGCCATGAGTCTAAGGGAAGTTTTTATTCCTATGATTGTCAGGTTGCAAAT
Alkaliphilus metalliredigens QYMF	CP000724.1	974342-974431	TGTTGGTAAGGGCAAACTTATTGAAAAATAAGGGCGCAAAGCTATGGATCTAAGGGAATATTATATTCCTATGATTGCCAGGTTGCCGAA
Alkaliphilus metalliredigens QYMF	CP000724.1	3297141-3297052	TATTGATAAGGGCAAACTTATTGAAAAATAAGGACGCAAAGCTATGGATATAAGGGAAAACATCATTCCTATGATTGCCAGGTTGCCGAA

Alkaliphilus metalliredigens QYMF	CP000724.1	3839765-3839670	AGAATGTAAAGGCAAACCATTGCAAACAATGGGACGCAAAGCCAGGAACCTAAAGTGTGTTATAAAAAAATATACCAAGATCGTCCGACTGCCATA
Alkaliphilus metalliredigens QYMF	CP000724.1	790814-790902	TGTTGATAAAGGCAAACTTATTGAAAAATAAGGACGCAAAGCTATGGATCTAAGGGAAGTTGTATTCCTATGATTGCCAGGTTGCCGAA
Alkaliphilus metalliredigens QYMF	CP000724.1	480071-480160	TGTTGATAAAAGCAAACTTATTGAAAAATAAGGGCGCAAAGCTATGGGTCTAAGGGAAGACACTATTCCTATGATTGCCAGGTTGCCGGA
Alkaliphilus metalliredigens QYMF	CP000724.1	1648997-1649082	GAATACAGAGGGCAAACTTATCGAAAGGTAAGGACGCAAAGCCATGGGCCTACATTCTAAACAGAAGATGGTAGCCGGTTGCAGAA
Alkaliphilus metalliredigens QYMF	CP000724.1	3306870-3306785	TATTAGTAAAGGCAAAACCATTGAAAGATGGTGACGCAAAGCCACGAGTCTAAGTCGTTATACGATATGATAGTCGGGTTGCCAAT
Alkaliphilus oremlandii OhILAs	CP000853.1	1736753-1736673	ACAATAAATGGGCAAACCTAGGGACGCAAAGCTTGAGTCTACGGTTATCTCAAAGATAATTACGATCGTTCAGCTGCATAG
Anaerofustis stercorihominis DSM 17244 A_stercorihominis-2.0.1_Cont214	ABIL02000006.1	978360-978435	ATTAAATATGGGCAAAACTGTGGAAACACAGTGACGCAAAACTATAGGGCCTGTAAAATGGCAGCCAGTTGCATTC
Anaeromyxobacter dehalogenans 2CP-1	CP001359.1	1969289-1969371	CACGCTTCAGGGCAATTCACCCGCACTTAGGGTGAAGCGCAAAGCCGCGGGTCCGGCGACGCCGGACGGCCGTGGCCGCCGTG
Anaeromyxobacter dehalogenans 2CP-C	CP000251.1	2466924-2466841	CACGCTTCAGGGCAATTCACCCGTACCCAGGGTGAAGCGCAAAGCCGCGGGTCCGGTGAACGCCGGACGGCCGTGGCCGCCGTG
Anaeromyxobacter sp. K	CP001131.1	1916166-1916248	CACGCTTCAGGGCAATTCACCCGCACGTAGGGTGAAGCGCAAAGCCGCGGGTCCGGCGACGCCGGACGGCCGTGGCCGCCGTG
Anaerostipes caccae DSM 14662	ABAX03000002.1	4791-4701	ATTATTCATCGGTAAAACTATTGAAAGATAGTGACACAAAGCCAAGGGTCTAAGGTCCTCCAAACGGGGATTATGACAGCCGGTTGCCACA

A_caccae-4.0.1_Cont13			
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont13	ABAX03000002.1	4503-4417	TTTAATATTTAGTAAAACTATCGAAAGGTAGTGACACAAAGCCAAGGGTCTAAGATCTCTAAGAGATTACGATAGCCGGTTGCCGCA
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont21	ABAX03000005.1	231872-231785	TTACATATTCAGTAAAACTGTCAAAAGGCAGTGGCACAAAGTCAAGGGTCTAAGATCTGATTACAGATTATGACAGCCGATTGCCGTA
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont21	ABAX03000005.1	232139-232052	AATTTTCATCGGTAAAGCTGCCGAAAGGCAGTGACACAAAGCCAAGGGTCTAAAGTCTTACATAAGACTATGACAGCCGGTTGCCACA
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont223	ABAX03000014.1	396556-396464	AAAATAAATAGGCAAAGCTGCCGAAAGGCAGTGACGCAAAGCTAAAGGGGCTATATCGTATAGGGAGTATGATCGTGCCAGCCAGCTGCCTCA
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont332	ABAX03000024.1	381353-381269	TTTATATTTTGGCAAAACCGGGGAAATCCGGTGACGCAAAGCCAAGGGCCTAAACCATTTACTGGTACGGCAGCCGGTTGCTCCA
Anaerostipes caccae DSM 14662 A_caccae-4.0.1_Cont7.1	ABAX03000037.1	71311-71226	TTACATATTGGGCAAAACAGGTGAAAGCCTGCGGCGCAAAGCTAAAGGGTCTAAGATTTTATTGATTATGACAGCCAGCTGCAGTT
Anaerostipes sp. 3_2_56FAA cont2.102	ACWB01000102.1	21326-21413	AATTTTCATCGGTAAAGCTGCCGAAAGGCAGTGACACAAAGCCAAGGGTCTAAAGTCTTACATAAGACTATGACAGCCGGTTGCCACA
Anaerostipes sp. 3_2_56FAA cont2.102	ACWB01000102.1	21593-21680	TTACATATTCAGTAAAACTGTCAAAAGGCAGTGGCACAAAGCCAAGGGTCTAAGATCTGATTACAGATTATGACAGCCGGTTGCCGTA
Anaerostipes sp. 3_2_56FAA cont2.103	ACWB01000103.1	8012-8104	AAAATAAATAGGCAAAGCTGCCGAAAGGCAGTGACGCAAAGCTAAAGGGGCTATATCGTATAGGGAGTATGATCGTGCCAGCCAGCTGCCTCA

Anaerostipes sp. 3_2_56FAA cont2.17	ACWB01000017.1	7965-7880	TTACATATTGGGCAAAACAGGTGAAAGCCTGCGGCGCAAAGCTAAAGGGTCTAAGATTTTATTGATTATGACAGCCAGCTGCAGTT
Anaerostipes sp. 3_2_56FAA cont2.30	ACWB01000030.1	779-865	TTTAATATTTAGTAAAACTATCGAAAGGTAGTGACACAAAGCCAAGGGTCTAAGATCTCTAAGAGATTACGATAGCCGGTTGCCGCA
Anaerostipes sp. 3_2_56FAA cont2.30	ACWB01000030.1	492-582	ATTATTCATCGGTAAAACTATTGAAAGATAGTGACACAAAGCCAAGGGTCTAAGGTCCTCAGAACGGGGATTATGACAGCCGGTTGCCACA
Anaerostipes sp. 3_2_56FAA cont2.65	ACWB01000065.1	60079-60163	TTTATATTTTGGCAAAACCGGGGAAATCCGGTGACGCAAAGCCAAGGGCCTAAACCATTTACTGGTACGGCAGCTGGTTGCTCCA
Anopheles gambiae str. PEST CRA_x9P1GAV4UD8 probable bacterial contamination	AAAB01002796.1	10989-10902	GCATGATAAAGGCAAACTGAACTGAAAAGTCAGGACGCAAAGCCTCCGGTCTAATAGCAGGAATGCTAATGATAGCGGGGTTACCAAG
Anopheles gambiae str. PEST whole genome shotgun sequencing project	AAAB01030370.1	270-355	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Anoxybacillus flavithermus WK1	CP000922.1	1599568-1599486	AAGAAGTAAAGGCACAGCTAAGGAAACTTAGCGTCGCAAAGCTATAGGGGCTAACGGGATACCTATGCCAGCCAGCTGCCATT
Anoxybacillus flavithermus WK1	CP000922.1	368638-368724	TTGAATAATCGGCAAACTACTCGAAAGGGTAGGGCGCAAAGCTATAGGGGCTACGTCTATTTGTAGATATGCCAGCCAGTTGCCCTT
Atta colombica fungus garden Bottom 2030640873	AGFT01130798.1	435-350	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGATGTCCAGGATAGCGGGGTTGCAACA
Atta colombica fungus	ADWX01004240.1	68-1	TCCCGATAATGGCAAACCTGGGGTGACCCAGGGGCGCAAAGCTACGGAACCGTTAACACGGTTGGCCG

garden FPBSU3X01A71RA			
Atta colombica fungus garden Top 2030348470	AGFS01046399.1	1-84	GACCAGGGCAAACCTGTGCGAAAGCCAGGGACGCAAAGCCACCGATCTACAGCCCGGAAGGGCCATGACCGCGGGGTTGCCAAG
Atta colombica fungus garden Top 2030376834	AGFS01071743.1	33-119	ATTGAATATGGGCAAATTTATCGAAAGATAAAGACGCAAAGCTATGGGTCTACGGACAATCTTGTCTAAGATCGCCAAGCTGCCAAC
Atta colombica fungus garden Top 2030402538	AGFS01094788.1	253-339	ATTGAATATGGGCAAATTTATCGAAAGATAAAGACGCAAAGCTATGGGTCTACGGACAATCTTGTCTAAGATCGCCAAGCTGCCAAC
Atta colombica fungus garden Top 2030455872	AGFS01142509.1	19-105	TGTGCAAAAAGGCAAACCGGATGAAAGTCCGGGACGCAAAGCCTCCGGTCTAAGGGTCAGAGTACCTAGGATAGCGGGGCCACCACA
Azoarcus aromaticum EbN1 complete genome	CR555306.1	718866-718950	CTCTGAAAAAGGCAAACCCGTCGAAAGGCGGGGACGCAAAATCACCGGTCTACAGGGGTCGCCCCATGACAGCGGGATTGCCAGG
Bacillus licheniformis lam and lchAA1 genes	X94148.1	1848-1934	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTACTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus licheniformis lchAA gene	Y10550.1	784-870	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTACTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus anthracis A2012 main chromosome	AAAC01000001.1	914180-914264	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0174 BAO.Contig121	ABLT01000026.1	56017-55933	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0193 BAQ.Contig113	ABKF01000028.1	10930-11014	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0248	CP001598.1	397192-397276	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0389 BAK.Contig141	ABLB01000011.1	135158-135074	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA

Bacillus anthracis str. A0442 BAH.Contig161	ABKG01000009.1	135148-135064	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0465 BAM.Contig83	ABLH01000025.1	55413-55329	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A0488 BAC.Contig147	ABJC01000008.1	11320-11404	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. A1055 cont245	AAEO01000030.1	151854-151938	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Ames	AE016879.1	397292-397376	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. 'Ames Ancestor'	AE017334.2	397292-397376	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Australia 94 cont54	AAES01000043.1	103414-103498	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. CDC 684	CP001215.1	397645-397729	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. CNEVA-9066 cont2232	AAEN01000023.1	138415-138499	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Kruger B cont1014	AAEQ01000043.1	90673-90589	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Sterne	AE017225.1	397305-397389	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Vollum cont55	AAEP01000046.1	103744-103828	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus anthracis str. Western North America USA6153 cont1978	AAER01000042.1	136402-136318	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA

Bacillus anthracis Tsiankovskii-I gcontig_1106600029418	ABDN02000009.1	88712-88628	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cellulosilyticus DSM 2522	CP002394.1	4574691-4574612	TTAATATTGGGGCAAACTGTGCGAAAGTGCAGGACGCAAAGCCACGGGTCTAAGCATAGTATGATAGCCGGGTTACCTAG
Bacillus cellulosilyticus DSM 2522	CP002394.1	2534514-2534426	TTTTGATAAAGGCAAACTATTTCGAAAGGATAGGACGCAAAGTCATGGGTCTAAAGCTAACGCATTGCAAAGACCGCCAGACTACCAAG
Bacillus cellulosilyticus DSM 2522	CP002394.1	2551967-2551883	ATTGTATAAAGGCAAACTTATTGAAAGATAAGGACGCAAAGCCAAGGGCCTAAATTATTTTATAATATGGCAGCCGGTTGCACAA
Bacillus cellulosilyticus DSM 2522	CP002394.1	2575578-2575493	AATACGAAACGGCAAAACCATCGAAAGTTGGTGACGCAAAGCTATAGGGGCTTCCTTCATCTAGAAGAAGCCAGCCAGTTACCGAA
Bacillus cellulosilyticus DSM 2522	CP002394.1	854055-854147	ACCAGATAAAGGCAAATCTATTGAAAAGTAGAGGCGCAAAACTACGGATCTAAGGGCTAAATGTTTAATGTCTATGATAGCCGGGTTACCTAG
Bacillus cellulosilyticus DSM 2522	CP002394.1	4239850-4239934	GTACGATAATAGCAAAGCTATCTGAAAAGTAGTGACGCAAAACTAAAGGGGCTAAAACGTTGAGTCATGCCAGCCAGTTGCCGAA
Bacillus cereus 03BB102	CP001407.1	416694-416778	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus 03BB108 gcontig_1112316047305	ABDM02000004.1	164457-164549	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus 03BB108 gcontig_1112316047309	ABDM02000008.1	106856-106940	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus 172560W contig00006	ACLV01000030.1	63719-63811	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus 172560W contig00919	ACLV01000013.1	36856-36940	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus 95/8201	ACMF01000010.1	108220-108304	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA

contig00017			
Bacillus cereus AH1134 gcontig_1113129653792	ABDA02000001.1	755065-755157	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus AH1134 gcontig_1113129653792	ABDA02000001.1	113216-113300	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus AH1271 contig00439	ACMR01000019.1	23756-23840	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus AH1272 contig00103	ACMS01000342.1	4951-4859	ACATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATATATATTGGTTACTAAGATCGTCTGGTTGCACTT
Bacillus cereus AH1272 contig00637	ACMS01000029.1	25218-25302	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGGGCTAAGGTCAAACGACTATGCTAGCCAGTTACCGGA
Bacillus cereus AH1273 contig00080	ACMT01000028.1	6612-6696	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGGGCTAAGGTCAAACGACTATGCTAGCCAGTTACCGGA
Bacillus cereus AH1273 contig00259	ACMT01000293.1	5594-5686	ACATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATATATATTGGTTACTAAGATCGTCTGGTTGCACTT
Bacillus cereus AH187	CP001177.1	464065-464149	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus AH603 contig00051	ACMP01000014.1	1595-1679	CAGCGAGAAAGGCAAACTTATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus AH603 contig00195	ACMP01000037.1	9234-9324	AAATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus AH621 contig00346	ACLX01000013.1	1595-1679	CAGCGAGAAAGGCAAACTTATGGAAACATGAGGACGCAAAACTACAGGGGCTAAGGTCGAAGGGCTAAGCTAGCCAGTTACCGGA
Bacillus cereus AH676 contig00042	ACMQ01000015.1	52028-52112	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus AH676	ACMQ01000033.1	20960-21052	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT

contig00295			
Bacillus cereus AH820	CP001283.1	413589-413673	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus ATCC 10876 contig00505	ACLT01000013.1	109234-109318	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus ATCC 10876 contig00511	ACLT01000029.1	9709-9801	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus ATCC 10987	AE017194.1	504284-504368	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus ATCC 14579	AE016877.1	408156-408240	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus ATCC 14579	AE016877.1	1036786-1036878	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus ATCC 4342 contig00056	ACLZ01000008.1	110907-110991	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAGAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus ATCC 4342 contig00081	ACLZ01000070.1	14309-14221	ACCTATATTTGGCACACTATTCGAAAGAATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus ATCC 4342 contig00081	ACLZ01000070.1	14149-14061	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus B4264	CP001176.1	1063140-1063232	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus B4264	CP001176.1	426372-426456	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus B4264	CP001176.1	4733162-4733074	ACCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus B4264	CP001176.1	4733001-4732913	AAAATAAATGGGCATACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus BDRD-Cer4 contig00006	ACME01000010.1	50668-50752	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus BDRD-Cer4 contig00050	ACME01000020.1	53577-53669	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus BDRD-ST196 contig00873	ACMD01000018.1	1598-1682	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTACAGGGGCTAAGGTCAAATGACTATGCTAGCCAGTTACCGGA

Bacillus cereus BDRD-ST196 contig01724	ACMD01000050.1	57330-57422	ACATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATATATATTGGTTACTAAGATCGTCTGGTTGCACTT
Bacillus cereus BDRD-ST24 contig00576	ACMB01000013.1	50679-50763	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus BDRD-ST24 contig00793	ACMB01000024.1	28379-28471	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus BDRD-ST26 contig00010	ACMC01000013.1	34673-34757	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus BGSC 6E1 contig00601	ACLU01000027.1	39308-39400	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus BGSC 6E1 contig00754	ACLU01000015.1	50013-50097	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus biovar anthracis str. CI	CP001746.1	393798-393882	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus E33L	CP000001.1	414665-414749	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus F65185 contig00099	ACMO01000012.1	50786-50870	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus F65185 contig00531	ACMO01000021.1	60370-60462	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus G9241 cont1845	AAEK01000003.1	195343-195254	AAATGTAATTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTTAAGAGTCTAAGGTAATACATATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus G9241 cont1845	AAEK01000003.1	195166-195078	GAAATAAATCGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATACATATTACTATGATAGTCTGGTTGCAATT
Bacillus cereus G9241 cont1847	AAEK01000015.1	90981-90897	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAGAGGCTACGCTAGCCAGTTACCGGA

Bacillus cereus G9842	CP001186.1	4695548-4695460	AAAATAAATGGGCACACTGTTCGAAAGAATAGGTCGCAAAGCTAAGAGTCTAAGGTAATAAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus G9842	CP001186.1	4695705-4695617	TCCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus G9842	CP001186.1	404495-404579	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus G9842	CP001186.1	4695392-4695304	AAAATAAATAGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus G9842	CP001186.1	1039145-1039237	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus H3081.97 gcontig2_1113133506686	ABDL02000002.1	149771-149855	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus m1293 contig01009	ACLS01000016.1	3286-3370	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus m1550 contig00016	ACMA01000078.1	13598-13510	AAAATGAATGGGCACACTATTTGAAAGAATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus m1550 contig00016	ACMA01000078.1	13758-13670	ACCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus cereus m1550 contig00043	ACMA01000009.1	110109-110193	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus m1550 contig01013	ACMA01000023.1	24906-24998	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus MM3 contig00449	ACLW01000034.1	58482-58574	AAATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus MM3 contig00530	ACLW01000014.1	4424-4508	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus NC7401 genomic DNA	AP007209.1	463937-464021	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus NVH0597-99	ABDK02000010.1	105183-105267	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA

gcontig2_1106432853405			
Bacillus cereus Q1	CP000227.1	463082-463166	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus R309803 contig01121	ACLY01000011.1	19476-19567	GGAATATCTTGGCACACTATTTGAAAGAATAGGTCGCAAAGCTTTGAGTCTAAGGTAATGAATCTTATTACTAGGATTGTCGAGTTGCAAAT
Bacillus cereus R309803 contig01156	ACLY01000012.1	2396-2480	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGGGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus Rock1-15 contig00008	ACMH01000027.1	48366-48458	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus Rock1-15 contig00038	ACMH01000013.1	50646-50730	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus Rock1-3 contig00001	ACMG01000012.1	114164-114248	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTATAGGGGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus Rock3-28 contig02794	ACMI01000055.1	114100-114184	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTATAGGGGCTAAGGTCGAGAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus Rock3-29 contig00189	ACMJ01000013.1	114104-114188	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTATAGGGGCTAAGGTCGAGAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus Rock3-42 contig00267	ACMK01000017.1	3213-3297	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus Rock4-18 contig00127	ACMN01000011.1	114220-114304	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTAAAGGGGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus cereus Rock4-2 contig00206	ACMM01000123.1	86586-86678	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus Rock4-2 contig00352	ACMM01000057.1	109136-109220	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus cereus SJ1	ADFM01000080.1	102098-102182	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA

Bacillus cereus SJ1	ADFM01000046.1	265043-264951	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus cereus subsp. cytotoxis NVH 391-98	CP000764.1	420958-421045	GGGCGAGAAAGGCAAACTCGTGGAAACATAAGGCTGCAAAACTGTAGGGCTTAAGGTCAAGAGAAGGCGAAGCTAGTCAGTTACCGAA
Bacillus cereus W gcontig_1112319163066	ABCZ02000007.1	116274-116358	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus coagulans 2-6	CP002472.1	265102-265187	ATATCAAAGGGGCAAATCCATTGAAAAATGGAGACGCAAAACTACAGGGGCTACCGGTTTTCCAATCATGCCAGCCAGTTGTTAAC
Bacillus coagulans 2-6	CP002472.1	2451009-2450925	AATTGAAAAAGGCAAATTCATCGAAAGGTGAAGACGCAAAGCTAAAGGGACTAAAGTCAGACGACCATGTCAGCCAGTTACCGAT
Bacillus coagulans 36D1	CP003056.1	2189771-2189855	AATTGAAAAAGGCAAATTCATCGAAAGGTGGAGACGCAAAGCTAAAGGGACTAAAGTCAGATGACCATGTCAGCCAGTTACCGAT
Bacillus coagulans 36D1	CP003056.1	1076897-1076812	ATATCAAAGGGGCAAATCCATTGAAAAATGGAGACGCAAAACTACAGGGGCTACCGGTTTTCTAACCATGCCAGCCAGTTGCTAAC
Bacillus coagulans XZL4 contig000210	AFWM01000210.1	19858-19770	ATATCAAAGGGGCAAATCCATTGAAAAATGGAGACGCAAAACTACAGGGGGCTTAAACAGTTTTTAATAACTTATAAAAAGTTATTAAA
Bacillus coahuilensis m4-4 1955101000018	ABFU01000018.1	9013-8932	AATATATAAGGGCAATCCAATTGATATATTGGTATGCAAAGCTATAGGGGCTTACTCATAGATCTGCCAGACAGCTGCAATT
Bacillus coahuilensis m4-4 1955101000045	ABFU01000045.1	13915-13831	TTTTATATTCGGCAAACTACTTGAAAGGGTAGGACGCAAAACTAAAGGGGCTAAATCATTCGTGACATGCCAGCCAGTTGCAGTC
Bacillus coahuilensis m4-4 1955101000063	ABFU01000063.1	11732-11649	TCACTATAAGGGCAAAATATTTGAAAAAATATGACGCAAAGCTACAGGGGCTTATGCTTACAGCAATGCTAGCCAGCTGCCGAA
Bacillus coahuilensis m4-4 1955101000064	ABFU01000064.1	66880-66963	AATTAGAAAGGGCAAACTCATTGAAAAATGAGGACGCAAAGTCACAGGTCTAAGGCATGTAGCTAGGATGGCTGGTCTGCCTCT
Bacillus halodurans C-125 DNA	BA000004.3	597582-597667	CCTTGAAAAAGGCGAGTGTTTGAAATGGAAAGACGCAAAGCTGCGAGTCTGAAATCCTTCTGAATAGGGATAGTCGAGTTGTCAAA
Bacillus licheniformis ATCC 14580	CP000002.3	378607-378693	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTGCTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus licheniformis BNP29 DNA for lichenysin	AJ005061.1	4393-4479	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTACTGACGGTGCTACGGTTGACAGGTTGCCGAA

A synthetase operon			
Bacillus licheniformis DSM 13	AE017333.1	378413-378499	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTGCTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus licheniformis lichenysin biosynthesis operon: lichenysin synthetase A (licA)	U95370.1	192-278	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTACTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus megaterium DSM319	CP001982.1	1084610-1084518	TTCAGAGAAAGGCAAAACTATTGAAAAGTAGTGACGCAAAGCCTCAGGTCTAAGGTTGTTTTCTCGATATACTATGACGGCTGGGCTCCCTGG
Bacillus megaterium QM B1551	CP001983.1	1077098-1077012	TCCAGATAAGGGCAAAACTATTGAAAAATAGTGACGCAAAGCTTCAGGTCTAAGGCCATTTTTGGCTACGACAGCTGGGTTCCCTGG
Bacillus megaterium WSH-002	CP003017.1	3889773-3889857	TACAGACAAGGGCAAACCAGTTGAAAGGCTGGGACGCAAAACCTCGGGTCTAAGGTCACAGGACTAGGACGGCCGGGTTTCCTGA
Bacillus megaterium WSH-002	CP003017.1	3878564-3878656	TTCAGATAAAGGCAAAGCTGCTGAAAAGCAGTGACGCAAAGCTTCAGGTCTAAGGTAATGTTTACAACATGCTAAGATGGCTGGGTTCCCTGA
Bacillus megaterium WSH-002	CP003017.1	3829336-3829420	TACAGAAAAAGGCAAACTAATTGAAAAGTTAGGACGCAAAACTACAGATCTACGGTTTTTACACTATGATGGCTGAGTTTCCTTT
Bacillus mycoides DSM 2048 contig00022	ACMU01000010.1	105768-105852	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGGCGCAAAACTACAGGGGCTAAGGTCAAATGACTATGCTAGCCAGTTACCGGA
Bacillus pumilus ATCC 7061 BAT.Contig112	ABRX01000003.1	451234-451142	AGAAGAAAAAGGCAAATCTATGGAAACGTAGAGACGCAAAGCCATGTCCTAAGGTAAATGTTGCTTTTTTACTAAGGTCGCCAGGTTACCGAA
Bacillus pumilus S-1 contig000007	AGBY01000007.1	15738-15830	AGAAGAAAAAGGCAAATCTATGGAAACATAGAGACGCAAAGCCATGTCCTAAGGTAAAAGTTGCTTTTTTACTATGGTCGGCAGGTTACCGAA
Bacillus pumilus SAFR-032	CP000813.1	318462-318554	AGAAGAAAAAGGCAAATCTATGGAAACGTAGAGACGCAAAGCCATGTCCTAAGGTAAATGTTGCTTTTTTACTATGGTCGCCAGGTTACCGAA
Bacillus selenitireducens	CP001791.1	807943-808025	TGGATAGATGGGCAAACCTGTTGAAAAGCAGGGACGCAAAGCCAAGGGTCTTCATCATGATGATATGACAGCCGGTTGCACCG

MLS10			
Bacillus selenitireducens MLS10	CP001791.1	2058946-2059028	AATTAGAAAAGGCAAAATCTGTGAAATCAGATGACGCAAAGCCACGGACCTAACGGTTTTCCCACGGTCGCCGGGCTACCAAA
Bacillus sp. 2_A_57_CT2 cont1.20	ACWD01000020.1	177205-177119	TCTAATCCAGGGCAAATTTTACGAAAGTAAAAGACGCAAAGCTGCGGGCCTAAAGCAGGTTTCTGCCATGGCAGCCGGGCTGCACAG
Bacillus sp. 2_A_57_CT2 cont1.21	ACWD01000021.1	129677-129594	CTGGATAATCGGCAAACTTATTGAAAAGTAAGGACGCAAAGCCACGAGTCTAAGGTCATAGACTATGATAGTCGGGTTGCAGGT
Bacillus sp. 2_A_57_CT2 cont1.4	ACWD01000004.1	23734-23821	ATTTCCTCTGGGCAAATTTTACGAAAGTAAAAGACGCAAAGCCACGGGCCTAAAACAGCTTAATTGTCATGGCAGCCGGGTTGCACAA
Bacillus sp. 2_A_57_CT2 cont1.60	ACWD01000060.1	8590-8502	CGCAGAAAAAGGCAAACTCATTGAAAGATGAGGACGCAAAGTCACGGGTCTAAGGTATTGGATGATACTACGATGGCTGGGTTGCCTGG
Bacillus sp. 2_A_57_CT2 cont1.78	ACWD01000078.1	42006-41920	AAATTGAAAAGGCAAACTTATCGAAAGGTAAGGACGCAAAGCTACGAGTCTAAAATCCTCCAGGGTAATGACAGTCGGGTTGCCAAG
Bacillus sp. B14905 1101159007448	AAXV01000001.1	231054-230969	GGGAAAGATAGGCAAATTTACTAAAAAGTAAAGATGCAAAGCTACAGGTCTAAGGGAATAAGTACTTAGATGGCTAGGTTGCAAAA
Bacillus sp. BT1B_CT2 cont1.25	ACWC01000025.1	9229-9143	AGCAGATAAAGGCAAACCTGCGGAAACGCAGGGACGCAAAGCCATGGCCTAAGGTGCTGACGGTGCTACGGTTGACAGGTTGCCGAA
Bacillus sp. m3-13 Contig69	ACPC01000050.1	24677-24772	CATGGAAAAAGGCAAAACTAGTGAAAGCTAGTGACGCAAAACTAAAGGGACTTAAGTTTGCTTTCAATCGAGCAGACCAGTTAGCCAGTTACCCGC
Bacillus sp. m3-13 Contig74	ACPC01000020.1	181031-181143	AACAGTCAAAGGCAAACTTGCTGAAAGGCAAGGACGCAAAGTCAACAGATCTAAGATTATGTAAAAGAGATATAAAAAGTTCTTTTACCAATTAAGATGGCTGGGCTGCCTGA
Bacillus sp. NRRL B-14911 1099999053105	AAOX01000001.1	401431-401517	TTCTGTGAAACGCAAACTTATTGAAAGATAAGGGCGCAAAGCCTCAGGTCTAAGGCCATGTATGGTTAAGACGGCTGGGCTGCCGCA
Bacillus sp. NRRL B-14911 1099999053105	AAOX01000001.1	400824-400906	TATTGAAAAAGGCAAACTTATTGAAAAATAAGGACGCAAAGCCGCGAGTCTAAGGCGTAAGCTATGATAGTCGGGCTGCCAGG
Bacillus sp. NRRL B-14911	AAOX01000001.1	434573-434658	AAATACCAAAGGCAAAATCATTGAAAAATGATGACGCAAAGCTAAAGGGGCCTCTATTCAGTCGATAAGGCCAGCCAGCTGCCATC

1099999053105			
Bacillus sp. NRRL B-14911 1099999053105	AAOX01000001.1	422555-422642	GAATATCAAGGGCAAAATCACTGAAAAGTGATGACGCAAAGCTATAGGGGCTTATGTGGAAAAAAAACAATGCCAGCCAGCTGCCATC
Bacillus sp. NRRL B-14911 1099999053126	AAOX01000007.1	21294-21207	TCTTACTAAGGGCAAATTTTACGAAAGTAAAAGACGCAAAGCCACGGGCCTAAAACAAGTTATTTGTCATGGCAGCCGGGCCGCCAAG
Bacillus sp. NRRL B-14911 1099999053130	AAOX01000005.1	65987-65903	TAAATATACAGGCAAATTCATCGAAAGGTGAAGACGCAAAACTATAGGGGCTAAAGCCAAAAGGCTATGTCTGCCAGTTACCGAT
Bacillus sp. NRRL B-14911 1099999053130	AAOX01000005.1	210212-210294	CTATATAAGTGGCAAATTTTATGAAAGTAAAAGACGCAAAGCTGCGGGCCTAAGGCTTTTGCTATGGCAGCCGGGCTGCTTGC
Bacillus sp. NRRL B-14911 1099999053130	AAOX01000005.1	221613-221507	AGCAGAAAAAGGCAAACCTGTTGAAAGATAGGGACGCAAAGTCACAGGTCTACCGCGCCTATTGAGAGTAAAGTCGGATGAGGCGCCAGGACGGCTGGATTGCCTGG
Bacillus sp. NRRL B-14911 1099999053131	AAOX01000025.1	55956-55872	TACTGATAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTATGGGCCTTCCCGCATCAGCGGTTGGCTGCCAGGCTGCCGGG
Bacillus sp. SG-1 1101501000684	ABCF01000033.1	2268-2362	TGTTATAGAAGGCAAACTCATCTGAAAAGGGAGGACGCAAAGCCACGGGCCTACATGCAAAATATTATTTGTATATTGGCAGCCGGGTTACCTGT
Bacillus sp. SG-1 1101501000763	ABCF01000037.1	19041-19129	GCGACGAAAAGGTAAACTTATCGAAAGGTGAGGGCACAAAGCCGCGGGTCTAAGGTGACAGTAGTCACTATGACAGCCGGGTTGCCGAA
Bacillus sp. SG-1 1101501000765	ABCF01000117.1	1845-1935	GTCAGACAAAGGCAAACTCATTGAAAGATGGGGACGCAAAGTCACAGGTCTAAGGCAAGAGAAAACTTGTTAGGATGGCTGGGCTGCCTGA
Bacillus sp. SG-1 1101501000788	ABCF01000005.1	53556-53644	AGTAAATAAAGGCAACCTCTTCCGAAAGGAATTGGACGCAAAGCTAAAGGGGCTAACGTACATAAATACAATGCCAGCCAGTTGCAGAA
Bacillus sp. SG-1 1101501000788	ABCF01000005.1	23265-23355	TTAACGAAAAGGCAAACTTGCTGAAAGGCAAGGACGCAAAACCACAGATCTAAAGATTGCTAGAGCAATCCAAGATGGCTGGGTTACCGAA
Bacillus sp. SG-1 1101501000798	ABCF01000023.1	20598-20690	TATAAGAAAAGGCAAACTTGGCGAAAGCAAAGGACGCAAAGTCACAGACCTTCAATTTTTCATGTGAAAAATTATGGTGGCTGGATTACCGGA

Bacillus sp. SG-1 1101501000813	ABCF01000011.1	47422-47506	CGTACGAAAGGGCAAAATCATTGAAAAGTGACGACGCAAAACTATAGGGGCTAAAATCAACAGATGATGCCAGCCAGTTACCGAA
Bacillus sp. SG-1 1101501000813	ABCF01000011.1	46728-46643	ATTCGAGAAAGGCAAAGTCATTGAAAGATGGCGGCGCAAAACTATAGGGGCTACAGTCTGATCGACGATGCCAGCCAGTTGCCGAA
Bacillus sp. SG-1 1101501000813	ABCF01000011.1	25253-25167	TTTAAATATTGGCAAATCAGTCGAAAGGCTGGGACGCAAAACTACAGGGGCTACCATCCAATAAGGATATGCCAGCCAGTTGCACAC
Bacillus thuringiensis BMB171	CP001903.1	428508-428592	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis BMB171	CP001903.1	1051549-1051641	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis Bt407 contig00013	ACMZ01000107.1	13539-13451	AAAATAAATGGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis Bt407 contig00013	ACMZ01000107.1	13699-13611	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis Bt407 contig00013	ACMZ01000107.1	13859-13771	ACCTATTTTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis Bt407 contig00021	ACMZ01000030.1	51741-51833	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis Bt407 contig00126	ACMZ01000014.1	26338-26422	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis IBL 200 contig00157	ACNK01000011.1	128852-128936	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis IBL 200 contig00164	ACNK01000028.1	28071-28163	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis IBL	ACNK01000085.1	43451-43363	ACCTATTTTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT

200 contig00491			
Bacillus thuringiensis IBL 200 contig00491	ACNK01000085.1	43291-43203	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis IBL 200 contig00491	ACNK01000085.1	43135-43047	AAAATAAATGGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis IBL 4222 contig00054	ACNL01000037.1	24785-24877	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis IBL 4222 contig00080	ACNL01000013.1	45063-45147	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar andalousiensis BGSC 4AW1 contig00024	ACNG01000016.1	100871-100955	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGTCGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar berliner ATCC 10792 contig00063	ACNF01000103.1	13929-13841	ACCTATTTTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar berliner ATCC 10792 contig00063	ACNF01000103.1	13609-13521	AAAATAAATGGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar berliner ATCC 10792 contig00063	ACNF01000103.1	13769-13681	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar berliner ATCC 10792 contig00099	ACNF01000012.1	50751-50835	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis	ACNF01000032.1	51741-51833	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT

serovar berliner ATCC 10792 contig00251			
Bacillus thuringiensis serovar chinensis CT-43	CP001907.1	4753189-4753101	ACCTATTTTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar chinensis CT-43	CP001907.1	1087308-1087400	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar chinensis CT-43	CP001907.1	421335-421419	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar chinensis CT-43	CP001907.1	4753029-4752941	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar finitimus YBT-020	CP002508.1	508029-508113	CAGCGAGAAAGGCAAACTGGTGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar huazhongensis BGSC 4BD1 contig00178	ACNI01000012.1	108772-108856	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar huazhongensis BGSC 4BD1 contig00561	ACNI01000026.1	25055-25147	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar israelensis ATCC 35646 sq1869	AAJM01000107.1	5811-5723	AAAATAAATGGGCACACTGTTCGAAAGAATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCGGTT
Bacillus thuringiensis serovar israelensis ATCC 35646 sq1869	AAJM01000107.1	5655-5567	AAAATAAATAGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis	AAJM01000107.1	5968-5880	TCCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT

serovar israelensis ATCC 35646 sq1869			
Bacillus thuringiensis serovar israelensis ATCC 35646 sq1918	AAJM01000023.1	10970-11054	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar israelensis ATCC 35646 sq1919	AAJM01000012.1	18087-17995	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar konkukian str. 97-27	AE017355.1	421273-421357	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar kurstaki str. T03a001 contig00605	ACND01000297.1	5539-5631	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar kurstaki str. T03a001 contig01181	ACND01000016.1	13856-13940	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar monterrey BGSC 4AJ1 contig00061	ACNE01000010.1	108344-108428	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar pakistani str. T13001 contig00777	ACNC01000167.1	6779-6691	ACCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar pakistani str. T13001 contig00777	ACNC01000167.1	6460-6372	AAAATAAATGGGCACACTATTCGAAAGAATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAGTTACTATGATAGTCTGGTTGCAGTT

Bacillus thuringiensis serovar pakistani str. T13001 contig00777	ACNC01000167.1	6619-6531	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar pakistani str. T13001 contig01104	ACNC01000014.1	63876-63960	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar pakistani str. T13001 contig01136	ACNC01000043.1	25666-25758	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1 contig00141	ACNH01000011.1	108303-108387	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar pulsiensis BGSC 4CC1 contig00348	ACNJ01000012.1	117676-117760	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar sotto str. T04001 contig01666	ACNB01000274.1	3611-3519	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacillus thuringiensis serovar sotto str. T04001 contig01710	ACNB01000015.1	22111-22195	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar sotto str. T04001 contig01921	ACNB01000155.1	152-64	TCCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis	ACNA01000030.1	51739-51831	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT

serovar thuringiensis str. T01001 contig00036			
Bacillus thuringiensis serovar thuringiensis str. T01001 contig00037	ACNA01000101.1	13594-13506	AAAATAAATGGGCACACTGTTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar thuringiensis str. T01001 contig00037	ACNA01000101.1	13914-13826	ACCTATTTTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar thuringiensis str. T01001 contig00037	ACNA01000101.1	13754-13666	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar thuringiensis str. T01001 contig00064	ACNA01000012.1	26351-26435	CAGCGAGAAAGGCAAACTGATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar tochigiensis BGSC 4Y1 contig00501	ACMY01000012.1	29727-29811	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAGAGGCTACGCTAGCCAGTTACCGGA
Bacillus thuringiensis serovar tochigiensis BGSC 4Y1 contig00513	ACMY01000115.1	8768-8680	ACCTATATTTGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAAGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis serovar tochigiensis BGSC 4Y1 contig00513	ACMY01000115.1	8608-8520	AAAATAAATGGGCACACTATTCGAAAGGATAGGTCGCAAAGCTAAGAGTCTAAGGTAATGAAAATTACTATGATAGTCTGGTTGCAGTT
Bacillus thuringiensis str. Al Hakam	CP000485.1	1077635-1077727	AGATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATACATATTGGTTACTAAGATCGTCTGGTTGCACAT

Bacillus thuringiensis str. Al Hakam	CP000485.1	435376-435460	CAGCGAGAAAGGCAAACTGATGGAAACATTAGGACGCAAAACTACAGGAGCTAAGGCCGAAAGGCTATGCTAGCCAGTTACCGGA
Bacillus tusciae DSM 2912	CP002017.1	2855432-2855346	GTTGTATCAGGGCAAACTAGCGGAAACGCTAGGACGCAAAGCCACGGGTCTAAGGGCACATGTGCCTATGATCGCCGGGTTGCCACT
Bacillus weihenstephanensis KBAB4	CP000903.1	416914-416998	CAGCGAGAAAGGCAAACTTATGGAAACATGAGGACGCAAAACTACAGGAGCTAAGGTCGAAGGGCTAAGCTAGCCAGTTACCGGA
Bacillus weihenstephanensis KBAB4	CP000903.1	1053373-1053463	AAATATTTTTAGCACACTATTCGAAAGGATAGGCCGCAAAGCTTAGAGTCTACGGTAATATATTGGTTACTAAGATCGTCTGGTTGCACAT
Bacteroides capillosus ATCC 29799 B_capillosus-2.0.1_Cont29	AAXG02000004.1	120249-120340	GCGCGACAAAGGCAAACCGGCCGAAAGACCGGGACGCAAAGCCAGGAGGCTAAAGCGGACACAGTGTCCGCCATGCCGGTCCGGCCGCCGCA
Bacteroides capillosus ATCC 29799 B_capillosus-2.0.1_Cont30	AAXG02000005.1	128432-128342	ACCGACAAATGGCAAACCGGCTGAAAAACCGGGACGCAAAGCCAGGAGGCTAAAGCGGAGTCCGCTCCGCCACGCCCGTCCGGCCGCCGCA
Bacteroides capillosus ATCC 29799 B_capillosus-2.0.1_Cont30	AAXG02000005.1	131709-131618	GCGGGAAAAGGGCAAACCGGCTGAAAGGCCGGGACGCAAAGCCAGGAGGCTAAAGCGGAGGGAAACGCCGCCATGCCCGTCCGGTTGCCGCA
Bdellovibrio bacteriovorus complete genome	BX842649.1	31567-31484	TTTGCCTCAAGGCAAACCGTCGGAAACGGCGGGACGCAAAGCTAAAGGGGTGTCGGTGCAAAGCCACGCCAGCCAGCTGCCAAA
Bioreactor metagenome PBDCA2_contig03918	AGTN01366869.1	1264-1170	ACTTAATATTAGCACACTCGTTGAAAAGCGGGGTCGTTAAACTATCAGGGTCTATAGGGCGCAAAATTTGTAGCCTATGACTGCCAGTTGGTAAT
Bioreactor metagenome PBDCA2_contig06074	AGTN01645349.1	793-704	TCATCGAAAAGGCAAACCCGCCGAAAGGCGGGGACGCAAAGCCAACGATCTAAGGTGGCGTTGTTCCACTATGATGGCCGGGTTACCGAA

Bioreactor metagenome PBDCA2_contig11110	AGTN01458194.1	1542-1455	GTGTGTCAAGGGCAAACTTGCCGAAAGGCAAGGACGCAAAGCTACAGGGTCTAAGATGCGAGTGCATTATGACAGCCTGGCCGCTGTA
Bioreactor metagenome PBDCA2_contig11703	AGTN01155880.1	544-476	AATACTAAACCATTCGTGAGAATGGGACGGAAAGCCTATGGGTCTCACGGAGACAGCCGGGTCGCCGAA
Bioreactor metagenome PBDCA2_contig12947	AGTN01716158.1	156-64	AAGCGCTAAGGGTAAACCTGCCGAAAGGCAGGGACGCAAAGCCATAGGGTCTAAGGCGCCGTAAAGCGGCACTATGACAGCCTGGCTGCCGCG
Bioreactor metagenome PBDCA2_contig18731	AGTN01465683.1	2016-1907	CAGAGCAAACGGCAACCACGGCTGAAAAACGTGGGCGCAAAGCATGAAGTCTACGTCACGCACGATTCCGATCAGGATCGAATGTCTGATATGATGGTTCGGCTGCCTCC
Bioreactor metagenome PBDCA2_contig19259	AGTN01595931.1	1368-1281	GGCTGTGAAAGGCAAACCCGCGCGAAAGCCGGGGACGCAAAGCATGAAGTCTAAAGCGTATTAGCGCCATGACGGTTCGGCCGCCTCA
Bioreactor metagenome PBDCA2_contig19259	AGTN01595931.1	1544-1454	TTCAGTGAAAGGCAAACCCGCGCGAAAGCCGGGGACGCAAAACACGAAGTCTAAAGCGCGTTGTTTGCGCCATGATGGTTCGGTCGCCTCA
Bioreactor metagenome PBDCA2_contig24868	AGTN01172759.1	75-164	GTCATGATGGGGCAAACTTATCCGAAAGGTAAGGGCGCAAAGCTATGGGTCTAAAGGCGGGTTTTCGCCTACGATTGCCAGGTTGCGGCT
Bioreactor metagenome PBDCA2_contig30603	AGTN01163285.1	112-196	GGAGAACAAGGGCAAACCAGTTAAAAGACTGGGACGCAAAGTCAGGAATCTAAAGCGATGAGGCTATGATCGTCCGATCGCCGGA
Bioreactor metagenome PBDCA2_contig37261	AGTN01150342.1	175-87	CCGACGGGCAGGCAAACTCCGGGAAACCGGAGGACGCAAAGCTACGGGGCTAAAGACGGAGTACCGTCCATGCTCGCCGGGTTACCGAA
Bioreactor metagenome PBDCA2_contig44074	AGTN01004618.1	518-434	CAACTGACAAGGCAAACTTATCGAAAGGTAGGGACGCAAAGCCACGTATCTAAAGCGTGAAAGCCAGGATGGTCGGGCTGCCAAA
Bioreactor metagenome PBDCA2_FB2SNX102GIZS4	AGTN01439841.1	179-262	CGAGTAAAAGGGCAAACTCACCGAAAGGTGAGGACGCAAAGCGCGAAGTCTAAAGTTTTAAACTATGACCGTTCGGCTGCCTCT
Bioreactor metagenome PBDCA2_FB2SNX102H8I	AGTN01649706.1	188-81	TAGAATAAAGGGCAAACCCGGTAAAAGCCGGGGACGCAAAGCCGAGGATCTAAGGCCGTAGACGATTTATTATCTAATAATAGCTATCTGGTCGGACTGATTGACCCA

VK			
Bioreactor metagenome PBDCA2_FB2SNX102HH1FX	AGTN01535999.1	1-61	AAAATGATGACGCAAAGCTAAAGGGGCTACGGCGATAACGCTATGCCAGCCAGTTGCATCA
Bioreactor metagenome PBDCA2_FB2SNX102JH269	AGTN01266532.1	1-72	CTGTCGAAAAGCAGGGACGCAAAGCCAGGCGTCAAAGGTGCTTAACGACGCTATGACAACCCGGTTACCGCG
Bioreactor metagenome PBDCA2_FB2SNX102JP5D2	AGTN01203267.1	12-103	ACACGATAAGGGCAAAACTGTTAAAAGGCAGTGACGCAAAGCTATAGGGTCTAAAGTACTGCTCGAGGTACCATGACAGCCTGGTTACCGAA
Bioreactor metagenome PBDCA2_FBNLWBQ01B1WZJ	AGTN01513534.1	211-134	AAACCCATCAAAAGATGGGGACGCAAAGCCATAGGGTCTAAGGTGCTTTACTGCGCTATGATTAGCCTGGCTGCCAAA
Bioreactor metagenome PBDCA2_FBNLWBQ01B9FVX	AGTN01605802.1	262-173	ACACGCTCTTAGCAAACCGGTTGAAAAGCCGGGACGCAAAGCCATAGGGTCTACGTTAAGTTCTACTTAATACGACAGCCGGTTGCCGTG
Bioreactor metagenome PBDCA2_FBNLWBQ01BUFFA	AGTN01650811.1	204-130	GAATGACGTTGGCAAACGCGCTGAAAAGCGTGGACGCAAAGCTTTGGAACCTGAAATGGTAGTCCGGCTGCATTG
Bioreactor metagenome PBDCA2_FIDWTPW02P2XTH	AGTN01471828.1	237-154	AAGACGAAATGGCAAACCCGGTGAAAGCCGGTGACGCAAAGCTAAGAGGGGCTAAAACGAAAGTTATGCCAGCCAGCTGCCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02P7FK5	AGTN01509622.1	79-1	TTTTCGAAAAGGTAAATCCGGAAGAAATTCCGGAGGCACAAAGCTGACGGACCCGTTATGGAAATAACAGGTAGCCGGG

Bioreactor metagenome PBDCA2_FIDWTPW02PEZX4	AGTN01549269.1	123-34	TAAAATGTTTGGCAAAGCTTCCGAAAGGTAGTGACGCAAAGCTAGAGGGTCTAAGGGCGCTTAACCCGCCTATGACAGCCAGTTGCCCCG
Bioreactor metagenome PBDCA2_FIDWTPW02PTMIS	AGTN01077586.1	119-217	CTCCGATAATAGCAAACCCGGCGAAAGCCGGAGACGCAAAGCTGCGGGTCTAAAGCATACGCGTATCACGCGCTGTGCCACGACAGCCGGGCCGCCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02PUZ84	AGTN01298486.1	87-173	TTAAGCGTTAGGCAAACTTATCGAAAGATAGGGGCGCAAAGCTATGGGTCTAAGAGCGTAACTGTTTATGACCGCCAGGCTGCGAAT
Bioreactor metagenome PBDCA2_FIDWTPW02PW0H4	AGTN01380621.1	239-151	TTATAAAAGGGGCAAAACCGTCGAAAGACGGTGACGCAAAACTATAGGGGCTAAAGCCTGGCAACAGGTTATGCCTGCCAGTTGCGCTG
Bioreactor metagenome PBDCA2_FIDWTPW02Q0J4U	AGTN01152689.1	51-1	CAACCGAAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTACAGGACC
Bioreactor metagenome PBDCA2_FIDWTPW02Q1E79	AGTN01203929.1	411-336	TCCTCGAAACGGCAAAACCGCCGTGAGGCGGTGACGCAAAGTTCGGAGCCCCCTGTGGGCCGTCCGGGCTACCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02Q44V2	AGTN01337245.1	374-430	CGTGCGAAATGGCAAAGCTGGCGAAAGCCAGTGGCGCAAAGCTTCGAGACTACCACA
Bioreactor metagenome PBDCA2_FIDWTPW02Q5D4O	AGTN01305277.1	169-246	GTTTCGCAAAGGCAAACTACCATCGAAACGAGTAGGACGCAAAGCCATGGGTCTAAAGCGGTATTGTTCGGCTGCTAT
Bioreactor metagenome	AGTN01001772.1	4-93	AGCTGTGAAAGGCAAACCCGTGCGAAAGCCGGGGACGCAAAGCACGAAGTCTAAAGCGCACATCAGCGCCATGACGGTTCAGCCGCCTCA

PBDCA2_FIDWTPW02QK5PK			
Bioreactor metagenome PBDCA2_FIDWTPW02QKGSS	AGTN01723490.1	55-1	TAAAGCCAAGGGCAAACCCGGTGAAAACCGGCGGCGCAAAGCCACAGGGTCTACG
Bioreactor metagenome PBDCA2_FIDWTPW02QS1R9	AGTN01235706.1	282-196	AATTGATAAAGGCAAATCCATCAAAAGATGGAGACGCAAAGCCGCAAGTCTAAAGCAAGTAATTGCCATGACGGTTGGGTTGCCGGT
Bioreactor metagenome PBDCA2_FIDWTPW02R5FZX	AGTN01049784.1	95-180	CGTTGAAAAAGGCAAACCACCCGAAAGGGTGCGACGCAAAGCCACGGGCCTAAACAGCAAAGCTGTATGGCAGCCGGGCCGCCAAT
Bioreactor metagenome PBDCA2_FIDWTPW02RBM7S	AGTN01003536.1	379-461	CCGTTGCAAGGGCAAAGCGGCCGAAAGGCAGCGACGCAAAGCCACGGGCCTACAGCGGGCAACCGCCAGGGCAGCCGGGCCGC
Bioreactor metagenome PBDCA2_FIDWTPW02RBPNY	AGTN01667892.1	190-106	GATTGATAATAGCAAACTTACCGAAAGATAAGGACGCAAAGCCAAGGGTCTAAAGTCATTGTGACTATGACAGCCGGTTGCCAAA
Bioreactor metagenome PBDCA2_FIDWTPW02RDFOO	AGTN01149177.1	333-256	AAATTGGCAAACCTGTCGAAAGACGGCGGTGACAAACCTGCGGGTCTAAGGCTTATGCTATGACAGCCAGTTGCAAAA
Bioreactor metagenome PBDCA2_FIDWTPW02RHMLH	AGTN01354186.1	102-194	TCGCGCCAAGGGCACACCGCGGAAAGCCGGGGGCCGCAAAGCCATGGGTCTACACGGGCCTGAGAGGGCCCGTACGACTGCCAGGTTGCCGTC
Bioreactor metagenome PBDCA2_FIDWTPW02RL	AGTN01527726.1	243-362	CAGAGAAACTGGCTACCATCGCCGAAAGGCAATGGGCGCAAAGCATGAAGTCTAAAGCTTGATATGCGTCTCAAAATGGCATTTTGGGACAGTAACGGCTATGACGGTTCGGCTGCCTCA

FUX			
Bioreactor metagenome PBDCA2_FIDWTPW02RQ1CC	AGTN01268828.1	48-132	AAACGACAATAGTAAACCTGCCGAAAGGCAGCGACACAAAGCTACAGGGCCTACAGGCGAAAGCCCATGGCAGCCAGTTGCCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02RUIZD	AGTN01616185.1	50-135	CAGTGATAAAGGCAAACCCCGCGAAAGCGGGCGACGCAAAGCTACAGGGCCTAAAGGGATATACCCGATGGCAGCCAGTTACCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02RYB7J	AGTN01556829.1	74-159	CCACGTTAATGGCTAAACCTGTGAAAACAGGCGGCGCAAAGCTAAAAGGGCCTAAAGGCGGAAGCCTATGGTAGCCAGCTGTCGGT
Bioreactor metagenome PBDCA2_FIDWTPW02RZYK8	AGTN01386429.1	375-480	TTAGGGTTTTGGCAAAACTTTTTGTAAAGAAAAGGACGCAAAGTGTGGAATCTAAAGTAATATAATTAGTAAAAGATTAGCTTACTATGATTGTCCTACTGCATTA
Bioreactor metagenome PBDCA2_FIDWTPW02S1HW1	AGTN01322048.1	380-296	TAATAACTGGGGCAAACTTATCGAAAGGTAAGGACGCAAAGCTATGGGTCTACGGACAGCCGTCCATGATTGCCAGGCCGCCGAC
Bioreactor metagenome PBDCA2_FIDWTPW02SCX3J	AGTN01015665.1	80-163	TTGAAGAAAAGGCAAACTTACCGAAAGGTAAGGACGCAAAGCCACGGATCTGATACACTCTCCAAAGATAGCCGGGTTGCCACG
Bioreactor metagenome PBDCA2_FIDWTPW02SGGE5	AGTN01686469.1	273-171	AAAGCAAGAGGGCAAACCCGCCGAAAGGCGGGGACGCAAAGCTCAGGAGCCTGACATTGAAAGCGAGTGACACCGTCTTCAATATGGCAGTCCGGCCGCATTA
Bioreactor metagenome PBDCA2_FIDWTPW02SKMDE	AGTN01074107.1	340-257	ATATTGTAAAGGCAAACTTATTGAAAAGTAAGGGCGCAAAGCTATAGGGCCTTGTAGGAAACTATGTGGTAGCCAGTTGCCATT

Bioreactor metagenome PBDCA2_FIDWTPW02SMLNC	AGTN01313719.1	78-181	AAGTGATAAAGGCAAATTTACTGAAAAGTAAAGACGCAAAGCCAAGGGTCTAAGGTCCCGGCTCCGAATGGGGCGGAACGGGGCTATGACAGCCGGTTACCAAA
Bioreactor metagenome PBDCA2_FIDWTPW02SUQS2	AGTN01050262.1	241-327	TCACGATAAAGGCAAACTTGATGAAAATCAAGGACGCAAAGCCATGGGTCTAAGGCAAGAGATTGCTATGATTGCCAAGCCGCCGAA
Bioreactor metagenome PBDCA2_FIDWTPW02T4385	AGTN01254918.1	53-1	CTTTTGCAAGGGCATACCTGTCCGAAAGGCAGGGACGCAAAGCCTCCGGTCTA
Bioreactor metagenome PBDCA2_FIDWTPW02TI4FN	AGTN01072540.1	70-1	TAAAGCCAAGGGCAAACCTGCCAAAAGGCAGGGACGCAAAGCCGTAGGGTCTAAGGCGCATTAAGCGCTA
Bioreactor metagenome PBDCA2_FISUTAU01A3WRC	AGTN01735905.1	207-120	CAATAATTTTGGCAAACACGTTTAAAAACGTGGGCGCAAAGCTTTGGAGCCTAATCTGAGTTTTCGGAATGGCAGTCCGGCCGCATTG
Bioreactor metagenome PBDCA2_FISUTAU01A76SY	AGTN01522678.1	196-282	AAGAGTTATGGGCAGATCAGTCGAAAGGCTGAGGCGCAAAGTATGGAGCCTAAGGCACGTTTGTGCTATGGCAGTCCGGCTGCAATT
Bioreactor metagenome PBDCA2_FISUTAU01AIZSH	AGTN01572059.1	414-330	AAAACGAACTGGCAAATCTGCTGAAAGGCAGAGACGCAAAACCACGGGTCTAAAGTCTTTCGACCATGACCGCCGGGTTGCCGAA
Bioreactor metagenome PBDCA2_FISUTAU01AMUT4	AGTN01234163.1	72-1	TAATATTACTGGCAAACCCGTTAAAAGACGGGGACGCAAAGCCACGGGTCTAAGGTGAAAGCTATGACAGCC
Bioreactor metagenome	AGTN01410772.1	216-132	AAACGATAATAGCAAACCTGCCGAAAGACAGGGACGCAAAGCCACGGGTCTAAAGTCCTTCGACCATGACAGCCGGGTTGCCGAA

PBDCA2_FISUTAU01APBP9			
Bioreactor metagenome PBDCA2_FISUTAU01AY37T	AGTN01471933.1	218-303	CAACGATAAAGGCAAACCCGATGAAAGTCGGGGACGCAAAGCCGTGAGTCTAAAGCTGAAACAGCTATGATAGTCAGGTTGCCGTA
Bioreactor metagenome PBDCA2_FISUTAU01AYUZH	AGTN01513783.1	196-270	GGCCGAAAAGGGCAAACCACCGGAGACGGTGGGACGCAAAGCCTCCGGTCCCAGAAGGATAGCGGGGTTGCCGAA
Bioreactor metagenome PBDCA2_FISUTAU01AZMRJ	AGTN01441826.1	192-274	AAAAGATACTAGCAAATCCAGCGAAAGTTGGAGACGCAAAGCTATGGGTCTAAAGCGCAAGCCACGATTGCCAGGTTGCCTAA
Bioreactor metagenome PBDCA2_FISUTAU01B1AN5	AGTN01431825.1	259-343	TAATGAAAAGAGCAAAGTTGCCGAAAGGTAACGACGCAAAGCTAAAGGGCCTTATTGAATACCAATATGGCAGCCAGTTGCCATT
Bioreactor metagenome PBDCA2_FISUTAU01B3ZLG	AGTN01720335.1	303-390	ATATTCCAAGGGCAAACTTGCCGAAAAGCAAGGACGCAAAGCCATAGGGTCTAAGATGCGAATGCATGATGACAGCCTGCCCGCCGCA
Bioreactor metagenome PBDCA2_FISUTAU01BG2ZQ	AGTN01336270.1	184-270	GGAGGTCATGGGCAAATCAGCCGAAAGTCTGAGACGCAAAGTAAGGAGCCTAAAGCGCGCTTGTGTTATGGCAGTCCGGCTGCAAAT
Bioreactor metagenome PBDCA2_FISUTAU01BG4G6	AGTN01524214.1	410-523	ATCTGCCAATAGCAAATCCGATTAAAGTCGGAGACGCAAAGCCATGGGTCTAAAGCAAATAGGTACGTATAACCAAAATGCCTATTAATTTGCCATGATTGCCAGGTTGCCAAG
Bioreactor metagenome PBDCA2_FISUTAU01BHF	AGTN01286121.1	151-67	AGTTGTGAAATGCAAAATAGACGAAAGTCTGTGACGCAAAACTACAGGGCCTAATTCCGTATGGAAATGGCAGCCAGTTGCCGCT

MZ			
Bioreactor metagenome PBDCA2_FISUTAU01BO2GY	AGTN01296642.1	473-528	GATCTGAAATAGCAAACCTGGTGAAAACTAGGGACGCAAAGCTATTGGGTCTAAGG
Bioreactor metagenome PBDCA2_FISUTAU01BSCR6	AGTN01347944.1	413-317	AATCGATAATAGCAAACCTGCCGAAAGACAGGGACGCAAAGCTCAGGGCCTAAGACAAGCGTTTGACAGCGCTATGTTATGGCAGCCAGTTGCCGAA
Bioreactor metagenome PBDCA2_FISUTAU01BTM4W	AGTN01299684.1	305-399	GCACGATCAGGGCTAAACAGGCGAAAGCCTGTGGCGCAAAGCTATAGGGTCTAAGTCCATTTGTCATGGTATGGATATGACAGCCGGTTGCCACT
Bioreactor metagenome PBDCA2_FISUTAU01C0WPN	AGTN01205960.1	307-382	AACTGAAAAAGGCAAAGCCGACTGAAAAGCGGCGACGCAAAGCCACGGGCCTAAACCATCGCATGGTATGGCAGCC
Bioreactor metagenome PBDCA2_FISUTAU01C2P2K	AGTN01466698.1	241-147	TTTCGCAAAAGGCAAACTACCATCGAAAGAGTAGGACGCAAAGCCATGGGTCTAAAGCGGTATTGTTCGGCTGCTATGATTGCCAGGTTGCGGTA
Bioreactor metagenome PBDCA2_FISUTAU01C4LQ8	AGTN01411135.1	20-110	TAAAGCCAAGGGCAAACCCATCAAAAGATGGGGACGGCAAAGCCATAGGGTCTAAGGTGCTTTACTGCGCTATGATAGCCTGGCTGCCAAA
Bioreactor metagenome PBDCA2_FISUTAU01CLE6U	AGTN01473584.1	39-123	TTCCTGTAAAGGCAAACCGCTTGAAAAATCGGGACGCAAAGTCAGGAATCTAAAGCTTATCAGCAATGATCGTCCGGCTGCCATA
Bioreactor metagenome PBDCA2_FISUTAU01CUIR3	AGTN01212763.1	249-161	TAAAGCAGAGGGCCACCCCGTTGAAAAACGGGGGTACAAAGCCATAGGGCCTAAGGCGTTTTAAACGCTATGATAGATTGGCTGTCAAG

Bioreactor metagenome PBDCA2_FISUTAU01D02UM	AGTN01695387.1	105-19	AACTGAAAAGAGCAAACCTGTCGAAAGGCGGGGACGCAAAGCCGCAAGTCTAAGGCATGTGGGTGCTATGACCGTTGGGTTGCCAGG
Bioreactor metagenome PBDCA2_FISUTAU01D2YJ2	AGTN01306259.1	34-123	TAGAGAAAAGGGCAAACTTGCCGAAAGGTAAGGACGCAAAGCCAAAGGGTCTAAAATGGCAAAAGCCATTACGATAGCCTGGTTGCCAAA
Bioreactor metagenome PBDCA2_FISUTAU01DLUA2	AGTN01190950.1	355-271	GTACGATAAAGGCAAAGCTGCCGAAAGGCTGCGACGCAAAACTAGAGGGTCTAAGGGTGTCCGCCTATGACAGCCAGTTGCTCCG
Bioreactor metagenome PBDCA2_FISUTAU01DSI3S	AGTN01139688.1	81-1	AACCGATAATCGCAAACCCAATGAAAGTTGGGGACGCAAAGCCACGGATCTAAAGCGAAACGCCATGATCGCCGGGTTGCC
Bioreactor metagenome PBDCA2_FISUTAU01DTCF3	AGTN01745846.1	434-518	TGACGAAAAGGGCAAACCCGGTGAAAGCCGGGGATGCAAAGCCATAGCCTGACCTGTGCAAATATAATCATGCAGGATTGCAGTA
Bioreactor metagenome PBDCA2_FISUTAU01EDBV7	AGTN01545926.1	106-30	ATGCGATACTACTAAACCATCCGCGAGGGTGGGGCGGAAAGCCCATCGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Bioreactor metagenome PBDCA2_FISUTAU01EGW1X	AGTN01453008.1	177-263	AACTGAAAAGAGCAAACCTGTCGAAAGGCGGGGACGCAAAGCCGCAAGTCTAAGGCATGTGGGTGCTATGACCGTTGGGTTGCCAGG
Bioreactor metagenome PBDCA2_FISUTAU01EYXSC	AGTN01552693.1	1-79	TAATAGCAAACCTGCCGAAAGACAGGGGCGCAAAGCCACGGGTCTAAAGTCCTTCGACCATGACAGCCGGGTTGCCGAA
Bioreactor metagenome	AGTN01557057.1	304-212	CGTTGAAAAAGGCAAGGTTGCGCCGAAAGGCCTTCCACGCAAAGCCACGGGCCTAATCTGCAATCCATGCAGCATGGCAGCCGGGCCACCAAT

PBDCA2_FUFP16434_b2			
Bioreactor metagenome PBDCA2_FUFP23154_g1	AGTN01211212.1	98-191	CTGTGACAAGGGCAAACCCGTCGCAAGACGGGGGCGCAAAACCAGGGGTCCAACCGCGGCAAATAGCTGGGGCTTGGATGGCCCGGCTCCCGAA
Bioreactor metagenome PBDCA2_FUFP24611_g1	AGTN01688783.1	715-637	AGCCGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCTCGTTCAGACAGCCGGGTTGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401A0OBL_right	AGTN01095788.1	193-98	TAAATATAATAGCAAAACGGGTGAAAGCCCGCGACGCAAAGCTATAGGGTCTTAATTATTCATAATATTTGAATAATATGATAGCCAGTTACCGTA
Bioreactor metagenome PBDCA2_GBB5CE401A0ZK3	AGTN01611988.1	218-276	GAACGACAATAGTAAACCTGCCGAAAGGCAGCGACACAAAGCTACAGGGCCTACAGGCG
Bioreactor metagenome PBDCA2_GBB5CE401A6EZV	AGTN01425959.1	331-247	TTTATAAAAAGGCAAAACTTTCGAAAGGAAGTGACGCAAAGCTACGAGTCTAAAGCAGTAATGCGATGACAGTCGGGTTGCATGA
Bioreactor metagenome PBDCA2_GBB5CE401A9FZ8_left	AGTN01748236.1	201-103	AGCAATATTTGGCAAAACCGGGGAAACCCGGCGACGCAAAGCTAAAGGGTCTAAAGCCTGAAGCCTTGAGGGCTAAGGTTATGACAGCCGGTTGCGCGA
Bioreactor metagenome PBDCA2_GBB5CE401AKRYJ_left	AGTN01582068.1	157-61	AAGCGACAATGGCAAACCCTGGCGAAAGCCAGGGGACGCAAAGCCACGGGGCTTAAGGCCGGATGTATCGAACGGACCAGCCAGCCGGGTTGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401B32AJ_left	AGTN01312481.1	218-124	TCCTCGAACCGGCAAACCCGTCGTAAGGCGGGGACGCAAAGCTATGGGTCCGTTCCAAAGTGCGTAGCCGAACAACGGATCGCCAGGCTACCAAA
Bioreactor metagenome PBDCA2_GBB5CE401B5	AGTN01040078.1	57-146	GGACGAAAAGGACAAACCCAGCGAAAGCCGGAGACGCAAAGCTACAGGGCCTAAAATGCAGACAAGCATGATGACAGCCTGGCTGCCGTA

WYJ_left			
Bioreactor metagenome PBDCA2_GBB5CE401BBMMA_right	AGTN01709558.1	143-23	AAATGTGAAAAGCAAAGCTGGCGAAAGCCAGCGACGCAAAGCCAAGGGTCTAAACCTCTTTAATTTTTAGTGCTTTTAGGTGAAAAGCTCCGTAAAAGAGATACGACAGCCGGTTGCCGCT
Bioreactor metagenome PBDCA2_GBB5CE401BEHNU	AGTN01502987.1	157-60	AAGCGATAATAGCAAACTTGCTGAAAAGCAAGGACGCAAAGCCAAGGGTCTAAGGTCTTGAGAGACGGCTCAAAAGACGATGACAGCCGGTTGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401BNZ0A_right	AGTN01727425.1	139-224	CGTTGAAAAAGGCAAAGCCGCCGAAAGGCGGCGACGCAAAGCCACGGGCCTAAAGCGTGAAACGCAACGGCGGCCGGGCCGCCAAT
Bioreactor metagenome PBDCA2_GBB5CE401BPA20_right	AGTN01607320.1	263-172	ACTCCGAAACGGCAAACCTGTCGAAAGACTGGGACGCAAAGCTAAGGGTCTAAGTCCCATCCGCAGTGGGATATGATCGCCTGGCTGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401BSA0K_left	AGTN01189980.1	21-107	AAGCGTTAATAGCAAACTTGTTGAAAGGCAAGGACGCAAAGCCGTTGGGTCTAAGGTGCTTAGCACTATGACAGCCTGGTTGCCGTA
Bioreactor metagenome PBDCA2_GBB5CE401BTMHU_left	AGTN01299357.1	67-1	AATCGATAATAGCAAAACCGGCGAAAGCCGGCGACGCAAAGCTAAGGGTCTAAGGCCTGTGAAAATG
Bioreactor metagenome PBDCA2_GBB5CE401BWY5C	AGTN01411218.1	91-165	CCTCGATAAGGGCAAACCATCCGCGAGGGTGGGACGCAAAGCCATGGGTCCCTCTGGGATCGCCAGGTTGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401BXBYB_right	AGTN01686969.1	79-259	ACCCGATAATAGCAAATCCTGCGAAAGCTTGAGACGCAAAGCCACGGATCTAACGCTAAGGTTAGCTAAATGATTATTTACACTTTTTCTGAAATGCACATGGACTAATGTGTGTTTCAGAAAAATATTAGTGGAAGTTATCATTTAGCAAATCCTAACTGCCATGATCGCCGGGCTACCG

Bioreactor metagenome PBDCA2_GBB5CE401C563G_left	AGTN01179694.1	209-123	TATTGGCAAACTTATCCGAAAGGTAAGGACGCAAAGCCATGGGTCTAACGGCCCTGACGCCGGGCTTATGACTGCCAGGTTGCGGAC
Bioreactor metagenome PBDCA2_GBB5CE401CK44J_left	AGTN01244058.1	145-61	CCCACGTTGTGGCAAAGCCCGCGAAAACGGGTGACGCAAAGCTAAAGGGCCTAAGGGCGCAAGCCTATGGCAGCCAGTTGCCGGG
Bioreactor metagenome PBDCA2_GBB5CE401CKUO6_right	AGTN01446196.1	198-86	TCACGATAATGGCAAACCTATGGGAAACCATGGGGACGCAAAGCACAGGGGCCTAAACATCCGACCAATGCGTACAAATATGCGATCGGATGCACGGCAGCCCGGCCGCCGAA
Bioreactor metagenome PBDCA2_GBB5CE401CYRX7_left	AGTN01303612.1	188-272	TCGAATAATGGGCAAACTCATCGAAAGGTGAGGGCGCAAAGCTAAAGGGGCTACGGTGCTCGAAGAGACACTAAGCATTTCAGTC
Bioreactor metagenome PBDCA2_GBB5CE401D1QSL	AGTN01519402.1	238-177	GGCAGCGACGCAAAGCTAAAGGGCCTGAAGGGCGTTTTCGTCTATGGCAGCCAGTTGCCGCA
Bioreactor metagenome PBDCA2_GBB5CE401D4U4E_right	AGTN01166220.1	137-43	CGTTGAAAAAGGCAAAGCCGCCGAAAGGCGGCGACGCAAAGCCACGGGCCTAAATCGCTCCCAATTGAAAGCGATATGGCAGCCGGGTCGCCAGC
Bioreactor metagenome PBDCA2_GBB5CE401DKLJ3_right	AGTN01197001.1	281-367	TATTTCATTAGGCAAACCCCGTCGAAAGAGAGGGACGCAAAAGCCATGGGTCTTCAAACATTTGTTTATGACTGCCAGGTTGCATGT
Bioreactor metagenome PBDCA2_GBB5CE401E4FM3	AGTN01177985.1	7-83	TCACGATAATACTAAACCATTCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTTACTGAGACAGCCGGGTTGCCGAA
Bioreactor metagenome	AGTN01221495.1	19-103	AATATCGTTTAGTAAACCCGTCGAAAGGCGGGGACACAAAGCTACGGGTCTAAAGCATTTTTGCTATGACAGCCGAGTTGCAAGA

PBDCA2_GBB5CE401E5ZYF_left			
Bioreactor metagenome PBDCA2_GBB5CE401EI4ZX_left	AGTN01237493.1	104-1	AACGACAAACGGCAAACCTGGCGAAAGTCAGGGGCGCAAAGCTAAAGGGCCTGAAAACGTTATTCCGCGAGGACACAAGGAAACGTATAATGGCAGCCAGTTAC
Bioreactor metagenome PBDCA2_GBB5CE401ERGHN	AGTN01570293.1	75-1	TAGAGAAAAGGGCAAACCAACTGAAAAGTTGGGACGCAAAGCCAAGGGTCTACTGTGGCGAAAGCCACTATGATA
Blastopirellula marina DSM 3645 1099463000698	AANZ01000050.1	14174-14099	CCTCGAAAAAGGCAAACCGATCGTGAGGTCGGGACGCAAAGCCAAGGGCCACGTAAGTGGACGCCAGGCTGCCGAA
blood disease bacterium R229	FR854083.1	151902-151982	CTGTTGCATTTGCAAAGCTGGAGTGACCCGGCGACGCAAAGCCAGGGGGACTTCCGTATCGGAAGTCAGCCAGTTGTCCGC
Brevibacillus brevis NBRC 100599 DNA	AP008955.1	1128088-1128005	AAATGCAAAAGGCAAAGTCATCGAAAGGTGGCGACGCAAAACCACGGGTCTACAGTCTTTGACCATGATAGCCGGGTTGCCATC
Brevibacillus brevis NBRC 100599 DNA	AP008955.1	5867835-5867923	ATATCGAAACGGCATACCCGGGGAAATCCGGCGACGCAAAGCTACAGGGGCTACCTCCGCAACAGCGGACACGCTTGCCAGCTACCGAA
Brevibacillus brevis NBRC 100599 DNA	AP008955.1	5961464-5961364	GAATGACAAAGGCAAACTTGCTGAAAGGCAGGGACGCAAAGCCACGGGTCTAAGGACGAAGGTCAAATGACTTTCGCAGCTAGGACAGCCGGGTTGCCATA
Brevibacillus brevis NBRC 100599 DNA	AP008955.1	4601883-4601798	GCTATGAATGGGCAAACCCATTGAAAAGTGGGGACGCAAAGCCACGGGCCTAATGTACACGTTACGATGGCAGCCGGGTTGCCAAC
Burkholderia phytofirmans PsJN chromosome 1	CP001052.1	1667937-1667858	GCGCAGTTTGGGCAAACCCGGAGCGATCCGGCGACGCAAAGCTACAGGGACTCCCTTGCGGGAGTTTGCCAGTTGCCCGC

Burkholderia sp. Ch1-1 ctg00164	ADNR01000015.1	78057-77978	GCGCAGTTTGGGCAAACCCGGAGCGATCCGGCGACGCAAAACTATAGGGACTCCCTTGCGGGAGTTTGCCAGTTGCCCGC
Butyrivibrio crossotus DSM 2876 B_crossotus-1.0_Cont20.1	ABWN01000030.1	140002-139920	TTGAACAATGGGCAAACCAATCGAAAGATTGGGACGCAAAGCCAAGGACCTTTCCCTTAACAGGATGGTAGCCGGTTGCACGG
Butyrivibrio crossotus DSM 2876 B_crossotus-1.0_Cont20.1	ABWN01000030.1	140139-140057	TTGAATATTAGGCAAACCAATCGAAAGGTTGGGACGCAAAGCCAAGGGCCTTTCCCTTAACAGGGTGGCAGCCGGTTGCATAT
Butyrivibrio crossotus DSM 2876 B_crossotus-1.0_Cont22.1	ABWN01000043.1	4363-4275	ATTATGAATGGGCATACCCGCAGAAATGTGGGGTCGCAAAGCTAGGGGTCTAAGGGGATTTATATTTCTATGATAGCTCGGCTGCAACA
Butyrivibrio proteoclasticus B316 chromosome 1	CP001810.1	2398853-2398928	TTTGATATCGGGCAAAGCAAGCGAAAGCTTGTGGCGCAAAGCTATAGGGACTTTAACATGTCAGCCAGTTGCATCT
Butyrivibrio proteoclasticus B316 chromosome 1	CP001810.1	1091136-1091221	ATCAAATAAAGGCAAAGCCATTGGAAAATGGTGACGCAAAGCTATAGGGTCTCAATCGCATATGCGACAGACAGCCAGTTGCTGGC
Caldalkalibacillus thermarum TA2.A1 ctg178	AFCE01000088.1	17-103	AACCGATAAAGGCAAAACTGTGGAAACGCAGTGACGCAAAGCTACAGGGGCTAAGGTCCGCCAGGGCTATGCCAGCCAGCTACCGGT
Caldalkalibacillus thermarum TA2.A1 ctg242	AFCE01000160.1	14647-14734	CGTTTGAAAGGGCAAAGCTACGGAAACGTAGTGACGCAAAGCTACAGGGGCTAAGGTTGTTCAACAACTATGCCAGCCAGCTGCCGTT
Caldicellulosiruptor bescii DSM 6725	CP001393.1	1980616-1980527	ATATCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGTAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor bescii	CP001393.1	1919845-1919748	TGTCGATAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGTCTGTCGGAAAAGGGTTTTTACCTTTTCCTATGATTGCCAGGCTGCCGAA

DSM 6725			
Caldicellulosiruptor bescii DSM 6725	CP001393.1	1974651-1974562	TAGTCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor hydrothermalis 108	CP002219.1	943671-943760	TGTCGACAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGTACAGCTTCCTATGGTCGCCAGGCTGCCGAA
Caldicellulosiruptor hydrothermalis 108	CP002219.1	2712272-2712180	TCCTGAAAAGGGCAAACACAGGGAAACCTGGGGCGCAAAGCCATGGGCCTATCGTGGGAAGTTTACCTCCCCTATGGTCGCCAGGCTGCCTGC
Caldicellulosiruptor kristjanssonii 177R1B	CP002326.1	897466-897555	TGTCGACAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAGCCTTCCTATGGTCGCCAGGCTGCCGAA
Caldicellulosiruptor kronotskyensis 2002	CP002330.1	989712-989801	ATATCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAATCTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor kronotskyensis 2002	CP002330.1	996348-996437	TAGTCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor kronotskyensis 2002	CP002330.1	1045800-1045897	TGTCGATAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGTCTGTCGGAAAAGGGTTTTTACCTTTTCCTATGATTGCCAGGCTGCCGAA
Caldicellulosiruptor lactoaceticus 6A	CP003001.1	1572387-1572298	TGTCGACAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAGCCTTCCTATGGTCGCCAGGCTGCCGAA
Caldicellulosiruptor obsidiansis OB47	CP002164.1	2488995-2488906	TCCTGAAAAAGGCAAACACAGGGAAACCTGTGGGCGCAAAGCCATGGGCCTGTCGGGGGAAAAACCCCCTATGGTTGCCAGGCTGCCAGG
Caldicellulosiruptor obsidiansis OB47	CP002164.1	1810549-1810460	ATATCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCTTGTCGGAAGTAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor obsidiansis OB47	CP002164.1	1806882-1806793	TGGTCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor obsidiansis OB47	CP002164.1	1764638-1764548	TGTCGACAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAGAAAACTTCCTATGGTTGCCAGGCTGCCGAA

Caldicellulosiruptor owensensis OL	CP002216.1	1656306-1656217	TGTCGAGAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGAAAATCTTCCTATGGTCGCCAGGCTGCCGAA
Caldicellulosiruptor owensensis OL	CP002216.1	2385548-2385460	TCCTGAAAAAGGCAAACACAGGGAAACCTGTGGGCGCAAAGCCATGGGCCTGTCGGGGAAAAGTCCCCTATGGTCGCCAGGCTGCCAGG
Caldicellulosiruptor saccharolyticus DSM 8903	CP000679.1	1205666-1205755	TGGTCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGGAGTAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor saccharolyticus DSM 8903	CP000679.1	912898-912799	TGTCGACAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGTCTGTCGGAAAAGGTATAGAGGACCTTTTCCTATGATCGCCAGGCTGCCGAA
Caldicellulosiruptor saccharolyticus DSM 8903	CP000679.1	1202000-1202089	ATATCGAAAGGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTGTCGGAAGTAAAACTTCCTATGGTTGCCAGGCTGCCGAA
Caldicellulosiruptor saccharolyticus DSM 8903	CP000679.1	2504398-2504301	TGTCGATAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGTCTGTCGGAAAAGGGTTTTTACCTTTTCCTATGATCGCCAGGCTGCCGAA
Campylobacterales bacterium GD 1 ctg_1106149034614	ABXD01000002.1	14206-14295	ATTGTATTTAGCCAAACTTATTGCGAAATAAGGACGGAAAGCTGTGAGTCTTAAATTTTGTGTAAAATTGAAGATTGTCTAGTTGCACTT
Candidatus Accumulibacter phosphatis clade IIA str. UW-1	CP001715.1	1004038-1004135	CTGATTTAAAGGCAAACGGAGGGAAACCTCCGGACGCAAAGCCGCGGACCCTACCCTGAGTTGTCAGATGAGCTCAGAAGGGTGGCCGGGTTGCCCGA
Candidatus Desulforudis audaxviator MP104C	CP000860.1	1941831-1941917	TCTGATTCAGGGCAAAGTCGCCGAAAGGTGACGGCGCAAAACTAGAGGGGCTACAGCGATAATACGCCAAGCCAGCCAGTTGCCGGA
Candidatus Desulforudis audaxviator MP104C	CP000860.1	470626-470536	TCCTAGAAAGGGCAAACCTGGCGAAAGCCAGGGACGCAAAGCTACGGGTCTAAAGCTTTCAGGCGAAAGCCAGGACCGCCGGGCCGCCACT
Candidatus Desulforudis	CP000860.1	1860186-1860097	ACCCCGAAAGGGCAAACCGGTACGAAAGTCCGGGACGCAAAGCTACGGGTCCTTAAGTTCCATGGGGAATAGGACGGCTGAGCCGCTGGG

audaxviator MP104C			
Candidatus Methylomirabilis oxyfera complete genome.	FP565575.1	196276-196197	TTCCGATAAAGGCAAACCAGTCGCGAGGCTGGGACGCAAAGCCACCGGTCAGCAAACGGGCTGACAGCGGGGTTACCGAA
Carboxydibrachium pacificum DSM 12653 ctg_1106511212248	ABXP01000171.1	25651-25564	CTTCGATAAGGGCAAACCCGTCGAAAGGCGGGGGCGCAAAGCCACGGGCCTAAATCCCTGATTGGGACATGGTAGCCGGGCTGCCGAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	900392-900476	AAACGTTAAGGGCAAACCCGGCGAAAGCCGGCGACGCAAAGCTACAGGGGCTAAAGCCGTAAGGCTATGCCAGCCAGCTGCCAAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	851296-851384	TTCCGAAAAAGGCAAACCCGGCGAAAGCCGGGGACGCAAAGCTACAGGGGCTAAAGCAGGTTGTCCTGCTATGCCAGCCAGCTGCCGAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	777679-777763	TACCGATAAAGGCAAACCCGGCGAAAGCCGGCGACGCAAAGCTACAGGGGCTAAGGCCGTAAGGCTATGCCAGCCAGCTGCCGAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	90445-90359	TGTCGATAAAGGCAAAACCGGCGAAAGCCGGTGACGCAAAGCTACAGGGGCTAAAGCGAATTTTCGCCATGCCAGCCAGCTGCCGAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	906921-907004	CTTTGTCAAAGGCAAACCCGGTGAAAGCCGGGGGCGCAAAGCTACAGGGGCTAAAGCTTAAAGCTAAGCCAGCCAGCTGCCAAA
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	875560-875646	CGAAAAGTTTGGCAAAACCGGCGAAAGCCGGCGACGCAAAGCTAAAGGGGCTAAGGCGGGTAACCGCTATGCCAGCCAGCTGCCGGG
Carboxydothermus hydrogenoformans Z-2901	CP000141.1	785822-785906	CTTTGTCAATAGCAAACCCGGCGAAAGCCGGCGACGCAAAGCTACAGGGGCTAAAGCCGTAAGGCTATGCCAGCCAGCTGCCGAA
Cellulomonas fimi ATCC 484	CP002666.1	2316135-2316209	GTCAGACAAGGGCACACCCGTCGCGAGGCGGGGCCGCAAAGCCACGGGACCCACGCGGTCAGCCGGGCTGCCGAC

Cellulomonas fimi ATCC 484	CP002666.1	243861-243935	TCAGCGAAACGGCAAACCCTCCGCAAGGGGGGGACGCAAAGCCACGGGACCCACGAGGTCAGCCGGGCTACCGAA
Cellulomonas fimi ATCC 484	CP002666.1	2514437-2514363	CAGCGACAACGGCAAACCCGCCGCAAGGTGGGGACGCAAAGCCACGGGACCCACGAGGTCAGCCGAGCTACCGAA
Cellulomonas flavigena DSM 20109	CP001964.1	3848833-3848759	TCAGCGAAACGGCAAACCCTCCGCAAGGAGGGGACGCAAAGCCACGGGACCCACGCGGTCAGCCGGGCTACCGAA
Cellulomonas flavigena DSM 20109	CP001964.1	2407306-2407232	AGCGACAAACGGCAAACCCGCCGCAAGGTGGGGACGCAAAGCCACGGGGCCCACGAGGTCAGCCGAGCTACCGAA
Clostridiales bacterium 1_7_47_FAA cont2.6	ABQR01000006.1	160585-160491	TTGAAGACCGGGCATAGCTGTCGAAAGGCAGTGTCGCAAAGCTATAGGGGTTTCGCCTTTCCGCAGTGCGGAAGGAAAGCCAGCCAGTTGTATAT
Clostridiales sp. SSC/2 draft genome.	FP929061.1	2108567-2108642	AAAGATTCTAGGCAAAACAGACGAAAGTCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGCAGAA
Clostridiales sp. SSC/2 draft genome.	FP929061.1	1293086-1293176	TTATTTTAAAGGCAAACCTGTTGAAAAGCAGGGGCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGCTTGACCATGTCAGCCGGTTGCCACT
Clostridiales sp. SSC/2 draft genome.	FP929061.1	1054036-1054123	TTATTCATAGGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAGAAGGGTCTAAGGTCTTATTGGACTATGACAGCCGGTTGCCACA
Clostridium asparagiforme DSM 15981 C_asparagiforme-1.0_Cont5.9	ACCJ01000143.1	25178-25272	GTGAATAACGGGCACAACTGTCGAAAGGCAGTGTCGCAAAGCTATAGGGGCTTCTCCTTCCGGCCGTGACCAGGGAAAGCCAGCCAGTTGTCTGA
Clostridium asparagiforme DSM 15981 C_asparagiforme-1.0_Cont6.295	ACCJ01000366.1	4015-3933	TGAAAGATTGGGCAAACCCGTCGAAAGGCGGCGACGCAAAGCTACAGGGGCTTCACCGGATGGTAAGCCAGCCAGCTGCTCTC

Clostridium asparagiforme DSM 15981 C_asparagiforme-1.0_Cont6.295	ACCJ01000366.1	3755-3673	AGACTATAAAGGCAAACCCGTCGAAAGGCGGCGGCGCAAAGCTACAGGGGCTAAACCGAACGGTATGCCAGCCAGTTGCAGGA
Clostridium asparagiforme DSM 15981 C_asparagiforme-1.0_Cont6.357	ACCJ01000435.1	32235-32148	CTACATACTTGGCAAAACTGATGAAAGTCAGCGACGCAAAGCTAAAGGGTCTAAATCATAGTATATGATATGACAGCCAGTTGCCCCT
Clostridium beijerinckii NCIMB 8052	CP000721.1	1066054-1066144	AATATCAATAGGCACACTTATTGAAAAATAGGGTCGCAAAGCTATGAGTCTAAGGAAAAATTTAATTTTCTATGATTGTCAGGTTGCCAAA
Clostridium beijerinckii NCIMB 8052	CP000721.1	4931184-4931096	AAATGTTACTAGCACACTTATTGAAAGATAAGGCCGCAAAGCCATGAGTCTAAGGGAATTTACATTTCTATGATTGTCAGGTTGCCAAA
Clostridium beijerinckii NCIMB 8052	CP000721.1	646595-646680	ATATTGAATTGGCAAAGCAGTTGAAAAACTGTGACGCAAAGCTAGAGGGCCTTTTCCTTTTGAAAGGATGGCAGCCAGTTGCAAGT
Clostridium beijerinckii NCIMB 8052	CP000721.1	4634346-4634259	TATTGATAATAGCACACTTGCCGAAAGGTAGGGCCGCAAAGCTATGGGTCTAAAGAAATTCATTTTCAATGATTGCCAGGTTGCCAAA
Clostridium bolteae ATCC BAA-613 C_bolteae-3.0.1_Cont118	ABCC02000009.1	273209-273134	TAAATATTGGGGCAAAGCACGTGAAAACGTGTGACGCAAAACTAGAGGGCCTGTAAGATGGCAGCCAGTTGCATTT
Clostridium bolteae ATCC BAA-613 C_bolteae-3.0.1_Cont22	ABCC02000002.1	64098-64013	AAAAATAATTAGCAAAACTGGTGAAAGCTAGTGACGCAAAGCTACAGGGATTTCTCTCTAAAAAGAGGTGTCAGCCAGCTGCATGA
Clostridium bolteae ATCC BAA-613 C_bolteae-3.0.1_Cont270	ABCC02000037.1	177159-177084	ATATTCAGGTAGCAAAGTAGTTGAAAGTCTATGACGCAAAGCTAAAAGGCCTGTGAAATGGTAGCCAGTTGCACGT

Clostridium botulinum B str. Eklund 17B	CP001056.1	2563878-2563794	AAATTTAATAGGCATAGCTAGGGAAATCTAGTGACGCAAAGCTAAAGGGGCTAAAGAAGAAATTCCATGCCAGCCAGTTGCCGAT
Clostridium botulinum B str. Eklund 17B	CP001056.1	3268396-3268305	ATATGATAATAGCACACTTGTTGAAAAATAAGGTCGCAAAGCTTATGAGTCTAAGGGAAAGAATTATTTTCTATGATCGTCAGGTTACCAAA
Clostridium botulinum B str. Eklund 17B	CP001056.1	856609-856691	TAACTGAATAGGCAAAACTAATTAAAGTTAGTGACGCAAAGCTATAGGGGCTAAGGAATAATCTATGTCAGCCAGTTGCCGAA
Clostridium botulinum E1 str. 'BoNT E Beluga' CLO.Contig141	ACSC01000002.1	444804-444895	ATATGATAATAGCACACTTGTTGAAAAATAAGGTCGCAAAGCTTATGAGTCTAAGGGAAAGAATTATTTTCTATGATCGTCAGGTTACCAAA
Clostridium botulinum E1 str. 'BoNT E Beluga' CLO.Contig141	ACSC01000002.1	3011343-3011261	CAATTGAATAGGCAAAATTAACGAAAGTTAGTGACGCAAAGCTATAGGGGCTAAAGAGGAATCTATGCCAGCCAGTTGCCGAA
Clostridium botulinum E3 str. Alaska E43	CP001078.1	834905-834987	CAATTGAATAGGCAAAATTAACGAAAGTTAGTGACGCAAAGCTATAGGGGCTAAAGAGGAATCTATGCCAGCCAGTTGCCGAA
Clostridium botulinum E3 str. Alaska E43	CP001078.1	3080253-3080162	ATATGACAATAGCACACTTGTTGAAAAATAAGGTCGCAAAGCTTATGAGTCTAAGGGAAAAAATTATTTTCTATGATCGTCAGGTTGCCAAA
Clostridium butyricum 5521 gcontig_1106103650290	ABDT01000010.2	7909-7989	TTTCATATTGGGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAGAGGGCCTTTCTTATAGAATGGCAGCCAGTTGCATAA
Clostridium butyricum 5521 gcontig_1106103650320	ABDT01000066.2	102117-102027	TAATTGAATACGCAAAGTTAATGAAAGTTAATGACGCAAAGCTATAGGGACTAAGAATTTTATTAAGAATTTATGTCAGCCAGTTGCCGGG
Clostridium butyricum 5521 gcontig_1106103650426	ABDT01000056.2	21523-21607	AAGTATTAATGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGAGCTAAAGTTAAAAAACTATGCTAGCCAGTTGCTAAC
Clostridium butyricum E4 str. BoNT E BL5262 CLP.Contig62	ACOM01000004.1	102356-102266	TAATTGAATACGCAAAGTTAATGAAAGTTAATGACGCAAAGCTATAGGGACTAAGAATTTTATTAAGAATTTATGTCAGCCAGTTGCCGGG

Clostridium butyricum E4 str. BoNT E BL5262 CLP.Contig65	ACOM01000005.1	1063771-1063856	AGTATGTTTTAGCAAAGCTAGAGAAATCTAGCGACGCAAAGCTATAGGGACTAAGGTTGTGAAAACTATGTCAGCCAGTTGCCGAA
Clostridium butyricum E4 str. BoNT E BL5262 CLP.Contig65	ACOM01000005.1	1474542-1474462	TTTCATATTGGGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAGAGGGCCTTTCTTATAGAATGGCAGCCAGTTGCATAA
Clostridium butyricum E4 str. BoNT E BL5262 CLP.Contig69	ACOM01000007.1	60367-60451	AAGTATTAATGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGAGCTAAAGTTAAAAAACTATGCTAGCCAGTTGCTAAC
Clostridium carboxidivorans P7 CLCAR0098	ADEK01000045.1	183990-183902	AATTGAAAAAGGCAAACCCATTGAAAAGTGGGGACGCAAAGCCATGAGTCTAAAGCAATTTTAACTGCTATGACAGTCAGGTTGCCAAT
Clostridium carboxidivorans P7 ctg00030	ACVI01000170.1	5733-5645	AATTGAAAAAGGCAAACCCATTGAAAAGTGGGGACGCAAAGCCATGAGTCTAAAGCAATTTTAACTGCTATGACAGTCAGGTTGCCAAT
Clostridium cellulovorans 743B	CP002160.1	1445176-1445086	AAGTGAAAAAGGCAAATCATGGGAAATCATGAGACGCAAAGCCATGGGCCTGTACCACACATTATATGTTGGATGGCAGCCGGTTACCACG
Clostridium cellulovorans 743B	CP002160.1	296693-296772	ATAAATTAAAGGCAAACTATGCGGGAGCATAGGACGCAAAGCCACGGGTCTGAACATTAAAAGATAGCCGGGTTGCATGT
Clostridium cellulovorans 743B DNA	BABR01000261.1	16724-16645	ATAAATTAAAGGCAAACTATGCGGGAGCATAGGACGCAAAGCCACGGGTCTGAACATTAAAAGATAGCCGGGTTGCATGT
Clostridium cellulovorans 743B DNA	BABR01000333.1	1081-1171	AAGTGAAAAAGGCAAATCATGGGAAATCATGAGACGCAAAGCCATGGGCCTGTACCACACATTATATGTTGGATGGCAGCCGGTTACCACG
Clostridium citroniae WAL-17108 cont1.4	ADLJ01000004.1	176443-176357	ATGATCGATCAGCAAAACTAGCGAAAGCTAGTGACGCAAAGCTACAGGGATTTCCCCTTTTAACAGGGATGTCAGCCAGCTGCAGGA
Clostridium difficile 002-P50-2011	AGAA01000002.1	63452-63362	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACATGAACTATGTCAGCCAGTTGCCAAA

C_difficile002-P50-2011-1.0 _Cont1.1			
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0 _Cont10.1	AGAA01000010.1	145624-145539	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0 _Cont10.1	AGAA01000010.1	108336-108251	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0 _Cont54.1	AGAA01000037.1	145393-145482	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0 _Cont54.1	AGAA01000037.1	156002-155909	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0 _Cont673.1	AGAA01000091.1	2504-2593	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0	AGAA01000092.1	239408-239505	AGACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA

_Cont673.2			
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont81.1	AGAA01000044.1	38449-38353	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont87.1	AGAA01000047.1	36787-36691	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont101.1	AGAB01000041.1	38449-38353	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont30.2	AGAB01000015.1	2816-2901	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont30.2	AGAB01000015.1	39977-40062	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont347.1	AGAB01000067.1	141-44	AGACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA

Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_ Cont347.2	AGAB01000068.1	534-445	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_ Cont396.2	AGAB01000070.1	212-305	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_ Cont396.2	AGAB01000070.1	10821-10732	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_ Cont43.1	AGAB01000022.1	36787-36691	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_ Cont81.1	AGAB01000036.1	143786-143876	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACATGAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	3936239-3936335	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	1142665-1142570	AAACTAAATCGGCAAAACTAGAGAAAATTAGTGACGCAAAGCTATAGGGACTAAGATTTATAAAATTCTTATAAATTATGCCAGCCAGTTGCCAAA
Clostridium difficile 630	AM180355.1	3303460-3303375	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA

complete genome			
Clostridium difficile 630 complete genome	AM180355.1	2285922-2286011	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	308777-308867	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTATATACATAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	2671808-2671897	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	2297491-2297588	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	3379980-3380075	AAACTAAATCGGCAAAACTAGAGAAAATTAGTGACGCAAAGCTATAGGGACTAAGATTTATAAAATTCTTATAAATTATGCCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	2296528-2296435	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	1653917-1653821	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	2907225-2907322	AAACTAAATCGGCAAAACTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 630 complete genome	AM180355.1	3266964-3266879	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 6407 contig_1379	ADEH01001379.1	80-1	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTC
Clostridium difficile 6407 contig_1494	ADEH01001494.1	16-106	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACACAAGCTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6407 contig_1836	ADEH01001836.1	435-350	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA

Clostridium difficile 6407 contig_3336	ADEH01003336.1	1335-1424	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6466 contig_117	ADDE01000117.1	10523-10610	AAACTTAATAGGCAAACCTAGAGAAATCTAGGGACGCAAAGCTATAGGGGTTAAGGTCTTAAAAAGATTATGCCTGCCAGTTACTAAA
Clostridium difficile 6466 contig_222	ADDE01000222.1	24-113	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6466 contig_319	ADDE01000318.1	32015-32100	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 6466 contig_321	ADDE01000320.1	2506-2599	TTCATATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATATAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile 6466 contig_356	ADDE01000355.1	2030-2119	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6466 contig_89	ADDE01000089.1	21755-21851	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAAATATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_1	ADEI01000001.1	38408-38312	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_15	ADEI01000015.1	65161-65064	AGACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_18	ADEI01000018.1	420-513	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_30	ADEI01000030.1	31786-31876	AAACTAAATAGGCAAAACTAGAGAAATCTAGCGACGCAAAGCTATAGGAGCTAAGGTTTGTATATACGAACTATGCTAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_43	ADEI01000043.1	91888-91799	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503	ADEI01000047.1	77878-77781	AAACTAAATCGGCAAAACTAGAGAAATCTAGCGACGCAAAGCTATAGGGACTAAGACTTATATAAATATATTATGAGTTATGTCAGCCAGTTGCCAAA

contig_47			
Clostridium difficile 6503 contig_66	ADEI01000066.1	6535-6438	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_69	ADEI01000069.1	37387-37472	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 6503 contig_69	ADEI01000069.1	89-174	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 6503 contig_89	ADEI01000089.1	54279-54183	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6503 contig_99	ADEI01000099.1	174961-175050	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6534 contig_1131	ADEJ01001131.1	177-81	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6534 contig_1175	ADEJ01001175.1	145-56	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6534 contig_235	ADEJ01000235.1	251-340	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 6534 contig_281	ADEJ01000281.1	143-47	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGACCAA
Clostridium difficile 6534 contig_458	ADEJ01000458.1	9065-8980	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 6534 contig_487	ADEJ01000487.1	23911-24008	AAACTAAAACGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTTAGCCAGTTGCCAAA
Clostridium difficile 6534 contig_679	ADEJ01000679.1	216-309	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA

Clostridium difficile 6534 contig_907	ADEJ01000907.1	7812-7738	GCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 6534 contig_922	ADEJ01000922.1	4100-4190	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTATATACATAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont1012.4	AGAC01000130.1	4271-4360	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont1012.5	AGAC01000131.1	234656-234753	AAACTAAATCGGCAAAACTAGAGAAATCTAGTGACGCAAAGCTATAGAGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont191.2	AGAC01000081.1	8105-8009	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont25.3	AGAC01000021.1	504-407	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont25.3	AGAC01000021.1	1484-1577	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile	AGAC01000021.1	12121-12032	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA

70-100-2010 C_difficile70-100-2010-1.0_ Cont25.3			
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont35.1	AGAC01000033.1	64556-64466	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTATATACATAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont38.1	AGAC01000036.1	16390-16475	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont38.1	AGAC01000036.1	52929-53014	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_ Cont44.1	AGAC01000040.1	22320-22416	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00008_2	ABKJ02000008.1	57627-57717	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACACAAGCTATGTAAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00008_2	ABKJ02000008.1	241-144	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTTAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00016_2	ABKJ02000016.1	132491-132395	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA

Clostridium difficile ATCC 43255 contig00018_2	ABKJ02000018.1	443359-443266	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00018_2	ABKJ02000018.1	812858-812947	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00018_2	ABKJ02000018.1	444323-444420	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00018_2	ABKJ02000018.1	1047597-1047694	AAACTAAATCGGCAAAACTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTTAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00018_2	ABKJ02000018.1	432755-432844	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00019_2	ABKJ02000019.1	654797-654894	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile ATCC 43255 contig00019_2	ABKJ02000019.1	145198-145113	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile ATCC 43255 contig00019_2	ABKJ02000019.1	108651-108566	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile ATCC 43255 contig00020_2	ABKJ02000020.1	105117-105213	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile bacteriophage phi CD119	AY855346.1	29246-29151	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGATTTATAAAATTCTTATAAATTATGCCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	1522481-1522385	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	2151966-2152055	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1	FN668941.1	2165422-2165519	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA

chromosome			
Clostridium difficile BI1 chromosome	FN668941.1	3758256-3758352	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	3144610-3144525	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile BI1 chromosome	FN668941.1	2164456-2164363	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	2510128-2510217	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	320244-320334	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI1 chromosome	FN668941.1	3104136-3104051	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile BI9 chromosome	FN668944.1	2629381-2629478	AAACTAAATCGGCAAAACTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTTAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	3019045-3018960	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile BI9 chromosome	FN668944.1	3608604-3608700	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	2044462-2044369	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	2982499-2982414	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile BI9 chromosome	FN668944.1	2045442-2045539	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA

Clostridium difficile BI9 chromosome	FN668944.1	1429802-1429706	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	2033855-2033944	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	270216-270306	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTATATACATGAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile BI9 chromosome	FN668944.1	2390875-2390964	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	3750238-3750334	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	310584-310674	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	2143958-2144047	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	2157412-2157509	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	2156446-2156353	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	1512707-1512611	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	2502116-2502205	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CD196 complete genome	FN538970.1	3136658-3136573	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile CD196	FN538970.1	3096184-3096099	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA

complete genome			
Clostridium difficile CIP 107932 contig00005_2	ABKK02000005.1	159700-159790	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00021_2	ABKK02000021.1	218694-218598	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00025_2	ABKK02000025.1	226346-226435	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00026_2	ABKK02000026.1	10476-10383	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00026_2	ABKK02000026.1	11442-11539	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00027_2	ABKK02000027.1	118-207	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile CIP 107932 contig00030_2	ABKK02000030.1	108717-108632	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile CIP 107932 contig00032_2	ABKK02000032.1	5335-5250	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile CIP 107932 contig00036_2	ABKK02000036.1	22585-22681	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665653.1	3160669-3160584	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile complete genome	FN665653.1	2145097-2145004	TTCATATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATATAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665653.1	2134493-2134582	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA

Clostridium difficile complete genome	FN665653.1	3343645-3343732	AAACTTAATAGGCAAACCTAGAGAAATCTAGGGACGCAAAGCTATAGGGGTTAAGGTCTTAAAAAGATTATGCCTGCCAGTTACTAAA
Clostridium difficile complete genome	FN665653.1	2533656-2533745	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665653.1	3731801-3731897	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAAATATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	1548193-1548097	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	2198836-2198925	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	3198352-3198267	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile complete genome	FN665652.1	2209445-2209352	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	284001-284091	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACATGAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	2560642-2560731	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	2800330-2800427	AGACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665652.1	3161064-3160979	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile complete genome	FN665652.1	3833856-3833952	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile	FN665654.1	3087657-3087572	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA

complete genome			
Clostridium difficile complete genome	FN665654.1	1506125-1506029	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	2148097-2148004	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	2149063-2149160	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	303777-303867	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	3128131-3128046	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile complete genome	FN665654.1	2493763-2493852	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	2135608-2135697	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile complete genome	FN665654.1	3769710-3769806	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	3838915-3839011	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	2777561-2777658	AGACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	2537871-2537960	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	2186681-2186588	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	1527335-1527239	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	2176075-2176164	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	242414-242504	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTGTATACATGAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile M68	FN668375.1	3138201-3138116	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA

Clostridium difficile M68	FN668375.1	3175448-3175363	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile NAP07 contig00006	ADVM01000002.1	7478-7391	AAACTTAATAGGCAAACCTAGAGAAATCTAGGGACGCAAAGCTATAGGGGTTAAGGTCTTAAAAAGATTATGCCTGCCAGTTACTAAA
Clostridium difficile NAP07 contig00010	ADVM01000006.1	65172-65257	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile NAP07 contig00034	ADVM01000029.1	193174-193085	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP07 contig00044	ADVM01000039.1	154161-154250	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP07 contig00044	ADVM01000039.1	164766-164673	TTCATATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATATAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP07 contig00216	ADVM01000060.1	25133-25229	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAAATATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP08 contig00033	ADNX01000031.1	165170-165081	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP08 contig00041	ADNX01000039.1	53861-53954	TTCATATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATATAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP08 contig00041	ADNX01000039.1	64466-64377	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP08 contig00099	ADNX01000073.1	38633-38537	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAAATATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile NAP08 contig00110	ADNX01000084.1	7475-7388	AAACTTAATAGGCAAACCTAGAGAAATCTAGGGACGCAAAGCTATAGGGGTTAAGGTCTTAAAAAGATTATGCCTGCCAGTTACTAAA
Clostridium difficile NAP08 contig00115	ADNX01000089.1	65151-65236	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA

Clostridium difficile QCD-23m63 contig00024_2	ABKL02000024.1	185065-185154	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-23m63 contig00024_2	ABKL02000024.1	195670-195577	TTCATATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATATAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-23m63 contig00025_2	ABKL02000025.1	123335-123424	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-23m63 contig00031_2	ABKL02000031.1	19674-19589	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-23m63 contig00032_2	ABKL02000032.1	53675-53762	AAACTTAATAGGCAAACCTAGAGAAATCTAGGGACGCAAAGCTATAGGGGTTAAGGTCTTAAAAAGATTATGCCTGCCAGTTACTAAA
Clostridium difficile QCD-23m63 contig00039_2	ABKL02000039.1	21221-21317	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAAATATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00003	AAML04000003.1	159704-159794	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00010	AAML04000010.1	412864-412768	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00013	AAML04000013.1	108853-108760	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00013	AAML04000013.1	109821-109918	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile	AAML04000013.1	96368-96457	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA

QCD-32g58 C_difficile_bld4_cont00013			
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	1065-1154	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	635378-635293	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	594909-594824	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	1246925-1247021	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-37x79 contig00003_2	ABHG02000003.1	159789-159879	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-37x79 contig00015_2	ABHG02000015.1	218853-218757	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-37x79 contig00017_2	ABHG02000017.1	557084-557173	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-37x79 contig00018_2	ABHG02000018.1	10504-10411	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-37x79 contig00018_2	ABHG02000018.1	11470-11567	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile	ABHG02000019.1	692-781	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA

QCD-37x79 contig00019_2			
Clostridium difficile QCD-37x79 contig00023_2	ABHG02000023.1	108586-108501	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile QCD-37x79 contig00023_2	ABHG02000023.1	149059-148974	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-37x79 contig00025_2	ABHG02000025.1	140267-140363	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00006_2	ABHD02000006.1	63126-63216	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGGTTTATATACATGAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00014_2	ABHD02000014.1	122952-122856	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00025_2	ABHD02000025.1	543312-543401	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00025_2	ABHD02000025.1	178678-178775	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00025_2	ABHD02000025.1	167089-167178	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00025_2	ABHD02000025.1	177698-177605	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00025_2	ABHD02000025.1	781818-781915	AAACTAAATCGGCAAAACTAGAGAAATCTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTTAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00026_2	ABHD02000026.1	145149-145064	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-63q42 contig00026_2	ABHD02000026.1	108601-108516	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA

Clostridium difficile QCD-63q42 contig00027_2	ABHD02000027.1	217626-217723	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-63q42 contig00029_2	ABHD02000029.1	23174-23270	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00003_2	ABFD02000003.1	159708-159798	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00008_2	ABFD02000008.1	415686-415590	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00010_2	ABFD02000010.1	454536-454625	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00010_2	ABFD02000010.1	109828-109925	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00010_2	ABFD02000010.1	108862-108769	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00010_2	ABFD02000010.1	96374-96463	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-66c26 contig00011_2	ABFD02000011.1	110690-110605	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile QCD-66c26 contig00011_2	ABFD02000011.1	151162-151077	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-66c26 contig00012_2	ABFD02000012.1	238844-238940	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-76w55 contig00004_2	ABHE02000004.1	159958-160048	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile	ABHE02000023.1	219622-219526	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA

QCD-76w55 contig00023_2			
Clostridium difficile QCD-76w55 contig00026_2	ABHE02000026.1	354921-355010	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-76w55 contig00027_2	ABHE02000027.1	10811-10718	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-76w55 contig00027_2	ABHE02000027.1	11777-11874	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-76w55 contig00028_2	ABHE02000028.1	1261-1350	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-76w55 contig00032_2	ABHE02000032.1	27252-27167	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile QCD-76w55 contig00034_2	ABHE02000034.1	6392-6307	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-76w55 contig00037_2	ABHE02000037.1	202629-202725	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00006_2	ABHF02000006.1	63218-63308	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00026_2	ABHF02000026.1	218696-218600	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00030_2	ABHF02000030.1	96509-96598	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00031_2	ABHF02000031.1	9736-9643	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00031_2	ABHF02000031.1	10702-10799	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA

Clostridium difficile QCD-97b34 contig00032_2	ABHF02000032.1	118-207	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile QCD-97b34 contig00035_2	ABHF02000035.1	108615-108530	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile QCD-97b34 contig00037_2	ABHF02000037.1	5331-5246	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile QCD-97b34 contig00040_2	ABHF02000040.1	327991-328087	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	2237000-2236907	TTCAGATATAGGCAATATTAGATAAATCTAATGACGCAAAACTATAGGGACTAAAATCTTTATGTAATAAAGGTCATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	1510328-1510232	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	3217186-3217101	AATTAAATGAGGCAAAACTAGGGAAACCTAGTCACGCAAAGCTATAGGGGCTAAAGTTTAGTAAACCATGCCAGCCAGTTGCCGAA
Clostridium difficile R20291 complete genome	FN545816.1	2224510-2224599	AAACTAAATAGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATGAAATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	2237966-2238063	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAAGACTTATATAAATATCTTATGAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	308010-308100	AAACTAAATAGGCAAATCTAGAGAAATCTAGTGACGCAAAGCTATAGGGGCTAAGGTTTGTATACACAAACTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	2582672-2582761	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAGTTATGTCAGCCAGTTGCCAAA
Clostridium difficile R20291 complete genome	FN545816.1	3176712-3176627	AAAATTAAATGGCAAAATTAGGGAAATCTAATGACGCAAAACTATAGGGATTAAAGCTTTTAAAGCCATATCAGCCAGTTGCTAAA
Clostridium difficile R20291	FN545816.1	3831022-3831118	AAACTAAATCGGCAAAACTAGAGAAATTTAGTGACGCAAAGCTATAGGGACTAACGCTTATAAAATAAACTATGAGTTATGTCAGCCAGTTGCCAAA

complete genome			
Clostridium hathewayi DSM 13479 C_hathewayi-2.0_Cont164.3	ACIO01000620.1	655-727	ATATAGTAATGGCAAAACTGTCGAAAGGCAGTGACGCAAAGCTAAAGGGCCGTATGGGCAGCCAGCTGCTAAA
Clostridium hathewayi WAL-18680 cont1.75	ADLN01000075.1	7720-7628	TTACATATTCGGCACATCTGTTGAAAAGCAGAGTCGCAAAACTTTAGGGGCTAACCCATTTGGAAACGAATGGTATGCCAGCCAGTTGCACAT
Clostridium hylemonae DSM 15053 C_hylemonae-2.0.1_Cont0.16	ABYI02000008.1	20274-20192	TGAACAGATGGAAATATATAGAAATATTTGACAAAGCCAGAGGGCCTAAGCAGAAATGACATGTATGGCAGCCGGCTGCACTC
Clostridium kluyveri DSM 555	CP000673.1	2377705-2377793	TATTGATAATAGCACACTTATCGAAAGGTAGGGTCGCAAAGCTATGGGTCTTAAGAAAATTATTTTTCTATGATTGCCAGGTTGCCAAA
Clostridium kluyveri DSM 555	CP000673.1	3562398-3562309	TATTGATAATAGCACACTTATTGAAAAATAAGGTCGCAAAGCTATGGGTCTAAAGAAAAGTTATTTTTCTATGATTGCCAGGTTGCCAAA
Clostridium kluyveri DSM 555	CP000673.1	3897171-3897085	TCCGACAAAGGGCAAACTTGCCGAAAGGTAAGGACGCAAAGCCGAGGGTCTAAAGTGCGAGAGCATTATGACAGTCTGGCTGCCGTA
Clostridium kluyveri NBRC 12016 DNA	AP009049.1	3828674-3828588	TCCGACAAAGGGCAAACTTGCCGAAAGGTAAGGACGCAAAGCCGAGGGTCTAAAGTGCGAGAGCATTATGACAGTCTGGCTGCCGTA
Clostridium kluyveri NBRC 12016 DNA	AP009049.1	2309208-2309296	TATTGATAATAGCACACTTATCGAAAGGTAGGGTCGCAAAGCTATGGGTCTTAAGAAAATTATTTTTCTATGATTGCCAGGTTGCCAAA
Clostridium kluyveri NBRC 12016 DNA	AP009049.1	3493900-3493811	TATTGATAATAGCACACTTATTGAAAAATAAGGTCGCAAAGCTATGGGTCTAAAGAAAAGTTATTTTTCTATGATTGCCAGGTTGCCAAA
Clostridium ljungdahlii DSM 13528	CP001666.1	2698829-2698742	CATTGATAATAGCACATTTATCGAAAGGTAAAGTCGCAAAGCTATGGGTCTAAAGAAAATTATTTTCTATGATTGCCAGGTTACCAAA
Clostridium novyi NT	CP000382.1	1871611-1871526	CAACGATAAAGGCAAATTTAGTGAAAACTAGAGACGCAAAGCTAAAGGGCCTTCCTTAGTTATTAAGATGGCAGCCAGTTACCGAA

Clostridium papyrosolvens DSM 2782 ctg49	ACXX02000016.1	57333-57416	TAATGTTAAGGGCAAACTTGCTGAAAAGCAAGGACGCAAAGCTACGAGTCTAAAGCGTAATGCCAGGATGGTCGGGTTGCCAAA
Clostridium papyrosolvens DSM 2782 ctg65	ACXX02000001.1	388494-388577	ATGGATTTTTAGTAAATCTGTCGAAAGGCAGAGACACAAAGCTACGAGTCTAAAGCATGATGCTATGACAGTCGGGTTGCAGAT
Clostridium papyrosolvens DSM 2782 ctg65	ACXX02000001.1	460758-460840	CACCGACAAAGGCAAACTAATCGAAAGATTAGGACGCAAAACTATAGGGTCTTACTCATTTGAGTTGATAGCCAGTTACCGAA
Clostridium perfringens ATCC 13124	CP000246.1	1218268-1218355	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGCCAGTTGCCGAA
Clostridium perfringens ATCC 13124	CP000246.1	1695696-1695613	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens B str. ATCC 3626 gcontig_1106202601658	ABDV01000039.1	10616-10703	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGCCAGTTGCTGAA
Clostridium perfringens B str. ATCC 3626 gcontig_1106202601684	ABDV01000006.1	21251-21334	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens C str. JGS1495 gcontig_1106166513243	ABDU01000076.2	6941-6854	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGTCAGTTGCTGAA
Clostridium perfringens C str. JGS1495 gcontig_1106166513253	ABDU01000065.2	900-817	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens CPE str. F4969 gcontig_1106202596926	ABDX01000004.1	24814-24897	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA

Clostridium perfringens CPE str. F4969 gcontig_1106202599046	ABDX01000001.1	131078-130991	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGCCAGTTGCTGAA
Clostridium perfringens D str. JGS1721 gcontig_1108490430993	ABOO01000003.1	113271-113188	AAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens D str. JGS1721 gcontig_1108490431123	ABOO01000024.1	23728-23815	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGCCAGTTGCCGAA
Clostridium perfringens E str. JGS1987 gcontig_1106202897252	ABDW01000004.1	131179-131263	ATAATATATTGGCAAATCTAGAGAAATTTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATAACTATGCTAGCCAGTTGCCAAA
Clostridium perfringens E str. JGS1987 gcontig_1106202899234	ABDW01000037.1	13611-13528	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens NCTC 8239 gcontig_1106202603774	ABDY01000002.1	211393-211306	ATAATATATTGGCAAACCTAGGGAAATCTAGAGACGCAAAGCTAAAGGGGCTAAGGTTATATGATAACTATGCTAGCCAGTTGCCGAA
Clostridium perfringens NCTC 8239 gcontig_1106202603786	ABDY01000007.1	25749-25832	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens SM101	CP000312.1	1445209-1445126	TTTAAAATTCGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA
Clostridium perfringens str. 13 DNA	BA000016.3	1510292-1510209	TAAAAAAATGGGCAAAATTAGAGAAATCTAATGACGCAAAGCTATAGGGACTAAGGTTTATAACTATGTCAGCCAGTTGCCAAA

Clostridium phage phiCD27	EU719189.1	33053-32958	AAACTAAATCGGCAAAACTAGAGAAAATTAGTGACGCAAAGCTATAGGGACTAAGATTTATAAAATTCTTATAAATTATGCCAGCCAGTTGCCAAA
Clostridium phytofermentans ISDg	CP000885.1	1913586-1913673	CAACGATAATAGCAAACCTAGTGAAAACTAGCGACGCAAAACTATAGGGTCTTCCTTAGATATTCTAAGATGATAGCCAGTTACCGAA
Clostridium phytofermentans ISDg	CP000885.1	1430070-1430158	TTATAAATTTAGCAAACTAATTGAAAGATTAGGACGCAAAGCTATGGGTCTAAGGATATCATAATATCAACGATTGCCAGGTTACAGAA
Clostridium ramosum DSM 1402 C_ramosum-2.0.1_Cont104	ABFX02000002.1	244990-244905	TCATAAATATGGCAAACTCTTTGAAAAAAGAAGTACGCAAAGCTATAGGGCCTTCATCAATTATGATATGGCAGCCAGTTGCATTC
Clostridium saccharolyticum WM1	CP002109.1	3771078-3770990	ATAAGCCAAGGGCAAACCCGGCAAAAGCCGGGGACGCAAAGCCGAGGGTCTAAGGTGTCTTAGGACGCTATGATAGTCTGGCTGCTGAC
Clostridium saccharolyticum WM1	CP002109.1	1527906-1527991	ATAAGTCAAAGGAAAACCTGTTAAAAAAGGGACGCAAAGCCGAAGGTCTAAGGCGTTTCTTGTACTATGTTTGCCCAGTTGTCAGA
Clostridium saccharolyticum WM1	CP002109.1	1872800-1872887	TTGAATTAAGGGCAAACCCATCTAAAGATGGGGACGCAAAGCCGAGGGTCTAAGGCGCACATTGTGCTATGATAGTCTGGCTGCAAAA
Clostridium saccharolyticum WM1	CP002109.1	2969431-2969517	TAATTTTAAGGGCAAACTTGCCGAAAGACAAGGACGTAAAGCCAAGGGTCTAAGATGTGAATGCATTATGATAGCCTGGCTGCCGTT
Clostridium saccharolyticum WM1	CP002109.1	3799466-3799379	TTGAATTAAGGGCAAACCCATCAAAAGATGGGGACGCAAAGCCGAGGGTCTAAGGCGCACATTGTGCTATGATAGTCTGGCTGCAAAA
Clostridium saccharolyticum WM1	CP002109.1	3784391-3784303	ATAAGCTATGGGCAAACCCGGCAAAAGCCGGGGACGCAAAGCCGAGGGTCTAAGGTGTCTTAGGACGCTATGATAGTCTGGCTGCTGAC
Clostridium saccharolyticum WM1	CP002109.1	3402847-3402933	TCCGACAAAGGGCAAACTTGCCGAAAGGTAAGGACGCAAAGCCGAGGGTCTAAAGTGCGAGAGCATTATGACAGTCTGGCTGCCGTA
Clostridium sp. 7_2_43FAA cont1.6	ACDK01000006.1	9767-9850	AAATTAAATAGGCAAACTTAGAGAAATTTAAGGACGCAAAGCTATAGGGACTAAGGTGTATAACTATGTCAGCCAGTTGCCAAA
Clostridium sp. 7_3_54FAA	ACWK01000098.1	37547-37629	TATTATATTTGGCAAACCCGTCGAAAGGCGGTGGCGCAAAGCTAAAGGGTCTAAGTAGAAGTATATGACAGCCAGTTGCAATC

cont1.98			
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont1	AFWX01000001.1	1668071-1668159	TGATGTTAATAGCATACTTATCGAAAGGTAAGGACGCAAAGCTTTGAGTCTAAGGGAAAGTTTTTTTCTATGATCGTCAGGTTGCCAAA
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	1635028-1634940	AAATGTAAATAGCAAATTCATTGAAAGGTGAAGACGCAAAGCCATGAGTCTAAAGTAATTTCGATTGCCATGATAGTCAGGTTGCCAAA
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	2302511-2302425	TATTGATAATAGTACACTTATTGAAAGGTAAGGTCACAAAGCCATGGGTCTAAGGAATGTTATGTCTATGATTGCCAGGCTACTAAG
Clostridium sp. SS2/1 Clostridium_sp_SS21-1.0.1_Cont764	ABGC03000028.1	1552-1465	TTATTCATAGGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAGAAGGGTCTAAGGTCTTATTGGACTATGACAGCCGGTTGCCACA
Clostridium sp. SS2/1 Clostridium_sp_SS21-1.0.1_Cont879	ABGC03000034.1	274477-274387	TTATTTTAAAGGCAAACCTGTTGAAAAGCAGGGGCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGCTTGACCATGTCAGCCGGTTGCCACT
Clostridium sp. SS2/1 Clostridium_sp_SS21-1.0.1_Cont916	ABGC03000042.1	79558-79633	AAAGATTCTAGGCAAAACAGACGAAAGTCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGCAGAA
Clostridium sp. SY8519 DNA	AP012212.1	1618715-1618640	TGCTGATCATGGCAAAACAGATGAAAATCTGTGACGCAAAGCTGCAGGGTCTTTGTCATGGCAGCCAGTTGCGCTT
Clostridium sticklandii str. DSM 519 chromosome	FP565809.1	1005537-1005454	TCACGACAATGGCAAAGTAGTAGAAATGCTATGACGCAAAGCTATAGGGCCTTACCGTAACTGGTTGGCAGCCTAGCTACCGAA
Clostridium sticklandii str. DSM 519 chromosome	FP565809.1	513404-513496	GTATGAAAAAGGCAAACTACAGGAAACTGTAGGACGCAAAGCGAGGAGTCTAAGACTGAATACTAACTCAGTTATGATAGTCCAGCCGCCATA
Clostridium sticklandii str. DSM 519 chromosome	FP565809.1	515076-515164	TAATGAAAAAGGCAAACTATGGGAAACTGTAGGACGCAAAGCAAGGAGTCTAAAGCTTAGTTTTAAGCAATGATAGTCCAGCCGCCATA
Clostridium symbiosum	ADLQ01000045.1	19424-19506	TATTATATTTGGCAAACCCGTCGAAAGGCGGTGGCGCAAAGCTAAAGGGTCTAAGTAGAAGTATATGACAGCCAGTTGCAATC

WAL-14163 cont1.45			
Clostridium symbiosum WAL-14673 cont1.40	ADLR01000040.1	5906-5988	TATTATATTTGGCAAACCCGTCGAAAGGCGGTGGCGCAAAGCTAAAGGGTCTAAGTAGAAGTATATGACAGCCAGTTGCAATC
Clostridium tetani E88	AE015927.1	477013-477088	CCACGATAAAGGCAAAACTATTGAAAGATAGTGACGCAAAGCTATAGGGTCTGTAAAATGACAGCCAGTTATCGAA
Clostridium thermocellum ATCC 27405	CP000568.1	1772116-1772199	ACATTACAAAGGCAAACCCATCAAAAGATGGCGACGCAAAGCTAAAGGGGCTAAAGCATTATGCCATGCCAGCCAGTTGCAATG
Clostridium thermocellum ATCC 27405	CP000568.1	3637613-3637528	TTTTGAAAAGGGCAAATCTATCGAAAGATAGAGACGCAAAGCCAACGAGTCTAAGGTGGAAACACTATGACGGTCGGGTTGCCAAA
Clostridium thermocellum ATCC 27405	CP000568.1	1273271-1273368	TATGAAACAGGGCAAAATCATCGAAAGGTGATGACGCAAAGCCATGGGTCTACTGTTTTAAAACAATGTTTTAAAGCTATGATCGCCAGGCTGCCATT
Clostridium thermocellum ATCC 27405	CP000568.1	3637352-3637262	TTTCGACAAAGGCAAACTCAATGAAAATTGAGGACGCAAAGCTCCAGGTCTTCGGTTTGGTATTCCAAACCATGACGGCTGAGTTACCGAA
Clostridium thermocellum DSM 1313	CP002416.1	719109-719024	TTTTGAAAAGGGCAAATCTATCGAAAGATAGAGACGCAAAGCCAACGAGTCTAAGGTGGAAACACTATGACGGTCGGGTTGCCAAA
Clostridium thermocellum DSM 1313	CP002416.1	1366547-1366450	TATGAAACAGGGCAAAATCACCGAAAGGTGATGACGCAAAGCCATGGGTCTACTGTTTTAAAACAATGTTTTAAAGCTATGATCGCCAGGCTGCCATT
Clostridium thermocellum DSM 1313	CP002416.1	718848-718758	TTTCGACAAAGGCAAACTCAATGAAAATTGAGGACGCAAAGCTCCAGGTCTTCGGTTTGGTATTCCAAACCATGACGGCTGAGTTACCGAA
Clostridium thermocellum DSM 1313	CP002416.1	923160-923077	ACATTACAAAGGCAAACCCATCAAAAGATGGCGACGCAAAGCTAAAGGGGCTAAAGCATTATGCCATGCCAGCCAGTTGCAATG
Clostridium thermocellum DSM 2360 ctg00038	ACVX01000002.1	111354-111451	TATGAAACAGGGCAAAATCACCGAAAGGTGATGACGCAAAGCCATGGGTCTACTGTTTTAAAACAATGTTTTAAAGCTATGATCGCCAGGCTGCCATT
Clostridium thermocellum DSM 2360 ctg00048	ACVX01000041.1	17586-17669	ACATTACAAAGGCAAACCCATCAAAAGATGGCGACGCAAAGCTAAAGGGGCTAAAGCATTATGCCATGCCAGCCAGTTGCAATG
Clostridium thermocellum	ACVX01000049.1	8906-8996	TTTCGACAAAGGCAAACTCAATGAAAATTGAGGACGCAAAGCTCCAGGTCTTCGGTTTGGTATTCCAAACCATGACGGCTGAGTTACCGAA

DSM 2360 ctg00052			
Clostridium thermocellum DSM 2360 ctg00052	ACVX01000049.1	8645-8730	TTTTGAAAAGGGCAAATCTATCGAAAGATAGAGACGCAAAGCCAACGAGTCTAAGGTGGAAACACTATGACGGTCGGGTTGCCAAA
Clostridium thermocellum JW20 ctg299	ABVG02000001.1	31537-31447	TTTCGACAAAGGCAAACTCAATGAAAATTGAGGACGCAAAGCTCCAGGTCTTCGGTTTGGTATTCCAAACCATGACGGCTGAGTTACCGAA
Clostridium thermocellum JW20 ctg299	ABVG02000001.1	31798-31713	TTTTGAAAAGGGCAAATCTATCGAAAGATAGAGACGCAAAGCCAACGAGTCTAAGGTGGAAACACTATGACGGTCGGGTTGCCAAA
Clostridium thermocellum JW20 ctg299	ABVG02000001.1	1525336-1525433	TATGAAACAGGGCAAAATCATCGAAAGGTGATGACGCAAAGCCATGGGTCTACTGTTTTAAAACAATGTTTTAAAGCTATGATCGCCAGGCTGCCATT
Clostridium thermocellum JW20 ctg299	ABVG02000001.1	1978266-1978349	ACATTACAAAGGCAAACCCATCAAAAGATGGCGACGCAAAGCTAAAGGGGCTAAAGCATTATGCCATGCCAGCCAGTTGCAATG
Colwellia psychrerythraea 34H	CP000083.1	807375-807459	AATTGAAAAGAGCAAAACTTTCGAAAGAAAGTGGCGCAAAGTCACCGGTCTACGGGAATAATTCTACGACAGCGGAACTGCCAAC
Colwellia psychrerythraea 34H	CP000083.1	4612611-4612693	GCTTGATAAGGGCAAATCTAATGAAAGTTAGAGACGCAAAGTTACCGGTCTAATGGGAAACCTATGATAGCGGGACTGCAAAT
Colwellia psychrerythraea 34H	CP000083.1	1642525-1642430	ACAAAGAAAAGGCAAAGCACGCGAAAACGTGTTACGCAAAACCACCGGTCTAAGGGTAAAGTTTAATTATTTATCTATGACAGCGGAGTCACCTCG
Compost metagenome contig09248	ADGO01009203.1	510-424	AATTGTCAAGGGCAAACCCGTCGAAAGACGGGGACGCAAAGCCTCCGATCTTCCGGGTACACACCCAAAGACAGCGGGGCTGCCAAA
Compost metagenome contig09410	ADGO01009365.1	22-111	CACTGCTCAGGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCTTCCGGTCTAAGGGTCGCTCCGGCGACCACGATAGCGGGGCTGCCAGG
Compost metagenome contig09783	ADGO01009737.1	332-253	CGGTGCCAAAGGCAAACCCACCGCGAGGTGGTGACGCAAAGCCACGGGTCTTCCCGACGGAAGACAGCCGGGCTGCCACC

Compost metagenome contig10756	ADGO01010708.1	491-407	CGCGTCGAAGGGCAAACCTGCCGCAAGGCGGGACGCAAAGCCTCCGGTCCCGGGTGGTCGCTTCCGGGATAGCGGGGTTGCCGGG
Compost metagenome contig15785	ADGO01015725.1	238-333	AACTGCTAAAGGCAAACCCGTCGAAAGGCGGGACGCAAAGCCACCGGTCTAAGGGGAGCTCGGATACCGAGCTGCCACGATAGCGGGGTTGCCAGG
Compost metagenome contig18000	ADGO01017929.1	447-364	CGCTGACAAGGGCACACCTTTCGAAAGAAAGGGCCGCAAAGCCACCGGTCTAAGGGGATTTCCTATGACAGCGGGGTTACCAGC
Compost metagenome contig21071	ADGO01020994.1	1911-1830	TTTTGCTAAGGGCAAACCCATCGACAGGTGGGGACGCAAAGCCATCGGTCCTTCTTTCGAGAAGGAAAGCGAGGCTGCCGAA
Compost metagenome contig23786	ADGO01023703.1	1993-1907	AATTGTCAAGGGCAAACCCGTCGAAAGACGGGGACGCAAAGCCTCCGATCTTCCGGGTGAATACCCAAAGACAGCGGGGCTGCCAAG
Compost metagenome contig30245	ADGO01030145.1	398-312	CGAGCTCAAGGGCAAACTCGTCGAAAGGCGAGGACGCAAAGCTTCCGGTCTAACGGAGATTTCTCCCAAGACAGCGGGGTTGCCTCA
Compost metagenome contig32980	ADGO01032870.1	448-362	GCGAGCTCAGGGCAAACTCGCCGAAAGGCGGGGACGCAAAGCTTCCGGTCTAACGGAGATCTCTCCTAAGACAGCGGGGTTGCCACA
Compost metagenome contig34365	ADGO01034251.1	177-273	CGTCGACAAGGGCAAAGCCGTCGTAAGGCGGTGACGCAAAGCCTCCGGTCCTCTTTACGCCGCTCGCGGTTGAAAAGGGGATAGCGGGGTTCCCGCT
Compost metagenome contig38268	ADGO01038152.1	352-267	GCGTGAAAAGGGCAAACCCGTCGAAAGACGGGGACGCAAAGCCACCGGTCTAACGGACGAGGTCCTATGACGGCGGGGCTGCCACG
Compost metagenome contig39546	ADGO01039427.1	398-301	CACTGCTAAAGGCAAACCCGTCGAAAGCGGGACGCAAAGCCACCGGTCTAAGGTCGCTCTCGGGGTACTGAGGCGATCACGATAGCGGGGTTGCCAGG
Compost metagenome contig42419	ADGO01042296.1	256-173	ACGTGAAAAGGGCAAACCCGCCGAAAGGCGGGGACGCAAAGCCACCGGTCTACGGCGAGGAGCTATGACAGCGGGGTTGCCACG
Compost metagenome contig44784	ADGO01044656.1	301-390	CATCGAGATCGGCAAACCCGTCGCAAGTCGGGGACGCAAAGCCTCCGGTCCGAGAGCAGAGTCGGCTCTCGTGATAGCGGGGCTGCCAGC
Compost metagenome	ADGO01047296.1	215-289	GCTCGTGAAAGGCAAACTCGTCGCAAGGCGAGGACGCAAAACCTCCGGTCTTTCAGAGATAGCGGGGTTGCCGCC

contig47429			
Compost metagenome contig48987	ADGO01048849.1	1114-1215	GTCGAACAAGGGCAAAACCACCGCAAGGTGGTGACGCAAAGCCTCCGGTCCGTTCCGTAGATGTGCACTCGTGAAGCACACACGGATAGCGGGGTTGCCGCG
Compost metagenome contig53246	ADGO01053096.1	238-332	GTCGAACAAGGGCAAAGCCGTCGAAAGGCGGCGACGCAAAGCTTCCGGTCCTCGGCCGACTCGCAACAGTCGGCACGGATAGCGGGGTTGCCGCG
Compost metagenome contig57478	ADGO01057323.1	186-272	AATTGAACAGGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCCACCGGTCTACGAGACGAATGTCTTACGACAGCGGGGTTGCCAAT
Compost metagenome contig60023	ADGO01059865.1	46-128	GCTAAGCAAAGGCAAACTCACTGAAAAGTGGGGACGCAAAGCCACCGGTCTAAAGGGCTTCCTAAGACAGCGGGGTTGCCAAG
Compost metagenome contig60269	ADGO01060111.1	255-161	CGAACGCGAGGGCAAACCCGTCGCGAGGCGGGGACGCAAAACTTCCGGTCTCGGCATGTTCTGTCGCTTGATGCCGAGATAGCGGGGTCGCCGCC
Compost metagenome contig61860	ADGO01061699.1	82-168	CGGACGCAAAGGCAAACCCACCGAAAGGTGGGGGCGCAAAACTTCCGGTCTAACGGCTGAAAGGCCCAGGACAGCGGGGTTGCCGGG
Compost metagenome FHNL2OP03Q1TLP	ADGO01094978.1	72-1	CGACACGAAGGGCAAACCCGCCGTGAGGCGGGGACGCAAAGCCTCCGGTCTTCGTGCCGAAGATAGCGGGGT
Compost metagenome FHNL2OP03Q42V9	ADGO01114571.1	201-118	AACTGATCAAGGCACACTCTTCGAAAGAAGGGGCCGCAAAGCCACCGGTCTAAGGGGATCTCCTATGACAGCGGGGTTGCCAGC
Compost metagenome FHNL2OP03Q4P0S	ADGO01080467.1	313-228	ATTGAAAACGGGCAAACCCGTCGAAAGGCGGGACGCAAAGCCTCCGGTCTACGGGATCCACATCCTATGACAGCGGGGTTGCCACA
Compost metagenome FHNL2OP03Q8CX0	ADGO01109231.1	385-473	CGTCTGCAGGGGCAAATTCGTCGAAAGGCGAAGACGCAAAGCCGCGGGCCTGAAGCTCGATCGAGAGCGATGGCAGCCGGGCCGCCAGA
Compost metagenome FHNL2OP03QJ2T7	ADGO01117420.1	298-211	AACAGATAAAGGCAAACCTATTGAAAAATTGGGACGCAAAGTCACAGGTCTAATGTATCGTACATACTATGACGGCTGGACTGCCTGG
Compost metagenome FHNL2OP03QK2Q1	ADGO01108465.1	424-499	GCAATCCGAGGGCAAACCCACCAAAAGGTGGGGCGCAAAGCTTCCGGTCTAAAGGAGAGATCCCATGACAGCGGGG

Compost metagenome FHNL2OP03R4P5H	ADGO01101996.1	100-182	CAATTGAAAGGGCAAACTTGCCGAAAGGCAAGGGCGCAAAGCCACAGGCCTAAGGGATTACCTATGGCAGCTGGGTTGCCGAA
Compost metagenome FHNL2OP03RFVLV	ADGO01131224.1	198-114	GGCACCGAAGGGCAAACCCGCCGTGAGGTGGGGACGCAAAGCCTCCGGTCTTCAGCCTATCTCTGAAGATAGCGGGGTTGCCGAA
Compost metagenome FHNL2OP03RRNLR	ADGO01084780.1	372-276	GCGGCCAGTGGGCAAACCCATCGAAAGGTGGGACGCAAAGCCACCGGTCTAAGGGCGGGAATCTGAGTGCAAAGCCTAGGATAGCGGGGCTGCCGAA
Compost metagenome FHNL2OP03RSZI1	ADGO01080028.1	491-440	GACGCAAAGCCACCGGTCTAACGGAGCTTCCTAAGACAGCGGGGTTGCCAGC
Compost metagenome FHNL2OP03RT805	ADGO01092221.1	481-395	GAGCTGACAAGGCAAAGCCGCCGAAAGGCGGCGACGCAAAACCACCGGGTCTACGGGGAGTCGCCCTACGATAGCGGGGTTGCCAGC
Compost metagenome FHNL2OP04X0ZJR	ADGO01176494.1	302-390	CTACGTCAAGGGCAAACCCGTCGAAAGTCGGGGACGCAAAGCCACCGGTCTAAAAAGGGCGCAAGCCTTCAGACAGCGGGGCTGCCAAA
Compost metagenome FHNL2OP04XU6ZK	ADGO01203309.1	19-105	AATTTGAAAAGGCAAACTCATTGAAAAATGGGGACGCAAAGCCACGGGTCTAAGGTTTGAAAAAACTATGATAGCCGGGTTGCCGAA
Compost metagenome FHNL2OP04Y53EU	ADGO01167617.1	243-151	CGCTGCTCAGAGCAAACCTCGCGAAAGCGGGGGGCGCAGAGCTTCGGGGCTACAGCCGGCGCAAGCCGATGCCACGCCAGCCGGGCCGCCAGC
Compost metagenome FHNL2OP04Y5FV7	ADGO01170350.1	2-79	AAGGGCAAACTCGTCGAGAGGCGAGGACGCAAAGCTTCCGGTCCGGACGTTGCGGTCCGAGATAGCGGGGTTGCCGGT
Compost metagenome FHNL2OP04Y5JTI	ADGO01180502.1	408-316	ATTGAATAAAGGCAAACTCATCGAAAGGTGAGGACGCAAAGCCACAGGTCTAAAGTAATTCTTCGGAATTACTATGACGGCTGGGTTGCTGAG
Compost metagenome FHNL2OP04YIMPF	ADGO01167563.1	227-316	TGCTGCCAAGAGCAAAGCCGCTGAAAGGCGGTGGCGCAGAGCTAAGGGGCTACCGCGGCTGAATGCCGCCATGCTCGCCTGGCCGCCAGC
Compost metagenome FHNL2OP04YRLMG	ADGO01171289.1	106-20	AACTGAAAAAGGCAAACTTATCGAAAGGTAGGGACGCAAAGCTACGAGTCTAAAATCCTATTGGGTAAAGATAGTCGGGTTGCCAAT
Compost metagenome	ADGO01162073.1	9-95	GGCTGCTAAGGGTAAACCTGGCGAAAGCCAGCGACACAAAACTTCCGGTCTAAGGGACTTCCGTCCTACGATAGCGGGGTTGCAGGC

FHNL2OP04YSHV2			
Compost metagenome FHNL2OP04ZDDFH	ADGO01182347.1	453-503	TCCGAACAAAGGCAAACCCACCGAAAGGTGGGACGCAAAGCCACCGGTCTA
Coprobacillus sp. 29_1 cont1.33	ADKX01000033.1	77622-77699	TATAAAAATAGGCAAAACTATTGAAAGATAGTGACGCAAAGCTATAGGGCCTCTTTAACGTGGCAGCCAGTTGCACAA
Coprobacillus sp. 29_1 cont1.39	ADKX01000039.1	155454-155538	ATATGTAAATAGCAAAACTATTGAAAAATAGTGACGCAAAGCTATAGGGTCTAATCTCATATGAGAATGACAGCCAGTTGCCAAT
Coprobacillus sp. 29_1 cont1.41	ADKX01000041.1	89095-89010	ATATGTAAATAGCAAGCCCATTGAAAAATGGAGTACGCAAAACTATAGGGTCTAAGCTTGTTGAAGTAGGATAGCCAGTTGCCAAT
Coprobacillus sp. D7 cont1.177	ACDT01000177.1	506-591	TCATAAATATGGCAAACTCTTTGAAAAAAGAAGTACGCAAAGCTATAGGGCCTTCATCAATTATGATATGGCAGCCAGTTGCATTC
Coprococcus catus GD/7 draft genome.	FP929038.1	3189627-3189717	TAAGGAAAACGGCAAACCAGATGAAAGTCTGGGACGCAAAGCCAGAAGAGGCTAAAGTCAGAAAGTTTGACCAGGTCAGCCGGTTGCAACT
Coprococcus catus GD/7 draft genome.	FP929038.1	3107441-3107515	AAGATTCGTCGGCAAATCAGTCGAAAGGCTGAGACGCAAAGCTATAGGGTCTGTAAAATGACAGCAAATGCATTT
Coprococcus catus GD/7 draft genome.	FP929038.1	1519054-1519139	TATTTATAGGGGCAGAGCTGTCGAAAGGCAGTGACGCAAAGCCAAAGGGACTAAGGTGTTAGAAACTATGTCAGCCGGTTGCGATA
Coprococcus catus GD/7 draft genome.	FP929038.1	3205275-3205350	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATAA
Coprococcus comes ATCC 27758 C_comes-1.0.1_Cont2257	ABVR01000028.1	31655-31572	TGTTTATAGGGGCAAAGCTGTTGAAAAACTGTGACGCAAAGCCAAAGGGACTAAGGCAGTACGCTATGTCAGCCGGTTGCAATA
Coprococcus comes ATCC	ABVR01000042.1	89198-89123	TAAGGAAAACGGCAAAACAGATCAAAGTCTGCGACGCAAAGCTATAGTGCCTGTAAAATGGTAGCCAGTTGCCACG

27758 C_comes-1.0.1_Cont2289			
Coprococcus comes ATCC 27758 C_comes-1.0.1_Cont2289	ABVR01000042.1	56233-56143	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGAGCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGCTTGACCATGTCAGCCGGTTGCCACT
Coprococcus sp. ART55/1 draft genome.	FP929039.1	120750-120648	ATAAATATTTAGTAAACCCGTTGAAAAGCGGTGACACAAAGCCATATGGGTCTAAGGTCTGAAAACAGAGAACTGTTTCGGACTATGACAGCCGGTTGCAGTA
Coriobacteriaceae bacterium JC110	CAEM01000034.1	24791-24864	TTTTCGAATCGGCAAAATCATCGAAAGGTGATGACGCAAAGCTATAGGGCCTGAAATGGCAGCCAGTTGCACAG
Culex pipiens quinquefasciatus	AC167560.3	117624-117709	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Culex pipiens quinquefasciatus	AC167664.4	1129-1044	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Culex pipiens quinquefasciatus	AC167663.3	117631-117716	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Curvibacter putative symbiont of Hydra magnipapillata genomic scaffold HmaUn_WGA69518_1	FN543104.1	1410700-1410616	AGTGCTTATGGGTAAACCCGTTGAAAGACGGGGACACAAAGCCACCGACCTACAGCATCAATGCCATGGTAGCGGGGCCGCCAAT
Cyanothece sp. PCC 7425	CP001344.1	107070-106982	GTCCCGAAAAGGCAACTTGCTCCGAAAGGGTAAGACGCAAATTGGTAATCCTGTAGCCAGGGTGTCGGTATGGATGTGTCAATGCCGAA

Cyanothece sp. PCC 7425	CP001344.1	3682885-3682978	CCCCGAAAATGGCAAGTTATTCCGAAAGGGTAATACGCAAATCCGAGATCCTGAAGCCACTCTTTCCAGGGGTATGGACGTCTCTGATGCCGAA
Cyanothece sp. PCC 7425	CP001344.1	5088371-5088464	GTCCCGAAAAGGCAACTTGCTCCGAAAGGGTAAGGCGCAAATTAGTGGTCCTGTAGCCAGAGTTAGGTGTCGGTATGGATGTGCTAATGCCGAA
Cyanothece sp. PCC 7425	CP001344.1	2022506-2022600	GTCCCGAAAAGGCAACTTGTTCCGAAAGGACAAGACGCAAATTAGGAGTCCTGTAGCCAACCTTTGATTGCGGTATGGACAGCACTAATGCCGAA
Cyanothece sp. PCC 7425 plasmid pP742501	CP001345.1	191915-191827	GTCCCGAAAAGGCAACTTACTCCGAAAGGGTAAGGCGCAAATTGGTAATCCTGTAGCCAAGGTGCCGGTATGGATGTGCCAATGCCGAA
Cyanothece sp. PCC 7425 plasmid pP742501	CP001345.1	189896-189808	GTCCCGAAAAGGCAACTTACTCCGAAAGGGTAAGGCGCAAATTGGTAATCCTGTAGCCAAGGTGCCGGTATGGATGTGCCAATGCCGAA
Cyanothece sp. PCC 7425 plasmid pP742501	CP001345.1	193383-193295	GTCCCGAAAAAGCAACTTACTCCGAAAGGGTAGGGCGCAAATTGGTAAGCCTGCAGCCAGGGTATCGGTATGGCTGTGCCAATGCCGAA
Cyanothece sp. PCC 7425 plasmid pP742502	CP001346.1	134259-134171	GTCCCCAAAAGGCAACTTGCTCCGAAAGGGTAAGACGCAAATTGGTAATCCTGTAGCCAAAGTGTCGGTATGGATGTGCCAATGCCGAA
Cyanothece sp. PCC 7425 plasmid pP742502	CP001346.1	31148-31236	GTCCCGAAAAGGCAACTTGCTCCGAAAGGGTAAGACGCAAATTGGTAATCCTGCAGCCAGGGTGTCGGTATGGATGTGTCAATGCCGAA
Daphnia pulex DAPPUscaffold_11575_Cont18181	ACJG01018181.1	934-1025	ATGTGACAAAGGCAAACCACTCGAGAGGGTGGGACGCAAAGCCAAGGGACCTAACGAGGGACACATGTTCCAGGGTCAGCCTAGCCGCCACA
Dechlorosoma suillum PS ctg77	ADDK02000002.1	364061-364156	CATTGATAAAGGCAAACCCGTACGAAAGGCGGGGGCGCAAAGTCACCGGTCTACCGGGCGTCGGCAAGGGCGCTCCATGACGGCGGGACTGCCATA
Deinococcus deserti VCD115 plasmid 1	CP001115.1	26820-26745	AACCGAAAAAGGCAAATCCGCCGCGAGACGGAGACGCAAAGCTACCGGGACCCACGAGGTCGGCCGAGTTACCGAA
Deinococcus deserti VCD115 plasmid 1	CP001115.1	240205-240130	CACCGAAAAAGGCAAACCCGTCGCGAGGCGGGGACGCAAAGCTCCCGGGACCCCTGAGGTCGGCCGAGCTACCGAA

Deinococcus deserti VCD115 plasmid 1	CP001115.1	217020-216945	AACCGAAAAAGGCAAATCCGCCGCGAGACGGAGACGCAAAGCTACCGGGACCCACGAGGTCGGCCGAGTTACCGAA
Deinococcus maricopensis DSM 21211	CP002454.1	420719-420644	CACACGAACAGGCAACCCCGTCGCAAGGCGGTGACGCAAAGCCAACGGGACCCACGCGGTCGGCCGGGCTACCGAA
Deinococcus proteolyticus MRP plasmid pDEIPR03	CP002539.1	70077-69973	TCTCGACAAAGGCAAACCCTCCGCGAGGGGGGGACGCAAAGCCCACGGAACTCCGCTGCTCCGCTCTTCTCTCAGGGCAGCACGGAAGTTGGCCGGGCCACCGAA
Delftia acidovorans SPH-1	CP000884.1	4023666-4023571	TTTGCGCACCAGCACACCCGTACGAAAGGCGGGGTCGCAAAGCCTCCGGTCTACCCCCGCCCTTTGACGGGCGGGCATGACAGCGGGGTTGCCAGG
Delta proteobacterium NaphS2 ctg_1101087565953	ADZZ01000720.1	9715-9635	ATCTGAAAAAGCCAAACCTCAAGTAATTGAGGGACGGAAAGCCGCGGATCCTTACAACGCAAGGACAGCCGGGTTGCCTGG
Delta proteobacterium NaphS2 ctg_1101087565953	ADZZ01000720.1	12250-12158	GTTCGAAAAAGGCAAACCACTCGAAAGGGTGGGACGCAAAGCCAGCGGCCTACGTCCTCAAATACCAAAGGATAAGGCGGCAGGGTTGCCGGG
Delta proteobacterium NaphS2 ctg_1101087565953	ADZZ01000720.1	9107-9027	ATCAGCAAAGGCCAAACCCCAAGCAATTGGGGGACGGAAAGCCACGGATCCTCAAAAAGCAAGGACAGCCGGGTTGCCTGG
Delta proteobacterium NaphS2 ctg_1101087565963	ADZZ01000513.1	780-856	CAGAGATAAAGCTAAACCCGTCGTGAGGCGGGGACAGAAAGTTTCGGGTCTCAAAGGAAGGCGGCCGGGCTGCCTTA
Delta proteobacterium NaphS2 ctg_1101087568010	ADZZ01000749.1	84356-84436	ACAGAAAAATGCCAAGCCCATCGTGAAGTGGGTACGGAAAGCCGCGAGCCCCTTTTTTCAAGGGATAGTCGGGTTGCCTGT
Desulfarculus baarsii DSM	CP002085.1	3203430-3203341	GGTGTGAAAGGGCAAACCCGCGCGAAAGCCGGGGGCGCAAAGTCACCGGCCTACAGCCGCCCGGGCGGCCACGGCGGCGGGACTGCCAAC

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Desulfatibacillum alkenivorans AK-01	CP001322.1	5865666-5865587	AATTAGTTTTGCCAAACCGGTCGCGAGGCCGGGACGGAAAGCCACGGGTCTTGATCATAAAAGACAGCCGGGTTGCGCAT
Desulfatibacillum alkenivorans AK-01	CP001322.1	3523916-3523993	TTTGTTCTCAGCCAAACCTGTTGCAAAGCGGGGACGGAAAGCCACGGGTCCGCGTCCGCGGACAGCCGGGTTGCCTGC
Desulfatibacillum alkenivorans AK-01	CP001322.1	4141190-4141274	GAAAGACAAAGCCAAACCTGCTGCGAGGCAGGGACGGAAAGCCACGGGTCCCATAAACAGACATGCGGATAGCCGGGTTACCATT
Desulfatibacillum alkenivorans AK-01	CP001322.1	4141109-4141188	GTCTCTTTTTGCCAAACCTGCCGCAAGGCAGGGACGGAAAGCTCCGGGTCCCCCATGAGGGGGACGGCCGAGCCGCCGGC
Desulfitobacterium hafniense DCB-2	CP001336.1	3634475-3634381	TGATGGTTGGAGCAAACTTTGTGAAAGCAAAGGACGCTAAAGCTATGGGTCTAAGGCCGTCGCGCAAGACCGGCTAGGATCGCCAGGCTACAAGT
Desulfitobacterium hafniense DCB-2	CP001336.1	4958095-4958179	TTGCGACAAAGGCAAACTTAGTGAAAGCTAAGGACGCAAAGCTATGGGCCTTCCTGATCAAGCTGATGGCCGCCAAGCTACCGAA
Desulfitobacterium hafniense DCB-2	CP001336.1	2632813-2632901	TATAGCTATGGGCAAACCCGGTTAAAGCCGGGGACGCAAAGCCGAGGGTCTAAGGTGTCTTAGGACGCTATGATAGTCTGGCTGCTGAC
Desulfitobacterium hafniense DCB-2	CP001336.1	2615723-2615811	TAAAGCTATGGGCAAACCCGGCTAAAGCCGGGGACGCAAAGCCGAGGGTCTAAGGTGTCTTAGGACGCTATGATAGTCTGGCTGCTGAC
Desulfitobacterium hafniense DCB-2	CP001336.1	1127881-1127794	ATTCGACAATAGCAAACCTGGCGAAAGCCAGGGACGCAAAGCTATGGGTCTTCCTGGATACACTCCTGATGATCGCCAAGCTACCGAA
Desulfitobacterium hafniense Y51 DNA	AP008230.1	2621237-2621143	TGATGGTTGGAGCAAACTTTGTGAAAGCAAAGGACGCTAAAGCTATGGGTCTAAGGCCGTCGCGCAAGACCGGCTAGGATCGCCAGGCTACAAGT
Desulfitobacterium hafniense Y51 DNA	AP008230.1	15633-15544	TAGAGCCAAGGGCAAACCCGGTGAAAGCCGGGGGCGCAAAGCTACAGGGTCTACGGCATTTTCGGATGCTATGATAGCCTGGCTGCCAAA
Desulfitobacterium hafniense Y51 DNA	AP008230.1	4879337-4879424	ATTCGACAATAGCAAACCTAGCGAAAGCCAGGGACGCAAAGCTATGGGTCTTCCTGGATACACTCCTGATGATCGCCAAGCTACCGAA

Desulfitobacterium hafniense Y51 DNA	AP008230.1	5437254-5437338	TTGCGACAAAGGCAAACTTAGTGAAAGCTAAGGACGCAAAGCTATGGGCCTTCCTGATCAAGCTGATGGCCGCCAAGCTACCGAA
Desulfitobacterium hafniense Y51 DNA	AP008230.1	3900342-3900252	TAAAATCAAGGGCAAACCGGCCTAAAGGTAGGGACGCAAAGCCGTAGGATTTAAGGTGCTCAAAAAGTGCTATGATAGCCTGGTTGCCAAA
Desulfitobacterium hafniense Y51 DNA	AP008230.1	5220217-5220127	TAAAGTCAAGGGCAAACCTGCCTAAAGGCAGGGACGCAAAACCGTAGGATCTAAGGTGCTTAAAAGGTGCTATGATAGCCTGGTTGCCAAT
Desulfitobacterium metallireducens DSM 15288 ctg103	AGJB01000012.1	86191-86109	CAAAGAAAAAGGCAAACCCGTTGAAAAGCGGGGACGCAAAGCGATGGGTCTAAGGCTTTTGCTAAGACTGCCAAGCTGCCATA
Desulfitobacterium metallireducens DSM 15288 ctg104	AGJB01000010.1	48317-48229	CATTTGTAAAGGCAAACTCAGTGAAAGCCGAGGACGCAAAGCTACGAGTCTAAAGCCTCGGCAGAGGTAAAGATAGTCGGGTTGCCATG
Desulfitobacterium metallireducens DSM 15288 ctg107	AGJB01000007.1	134456-134546	TTCTGATAAAGGCAAAACATCTGAAAAGGTGTGACGCAAAGCCATGGGTCTACAGCAGGAAAGACACTGCCATGATCGCCAGGTTGCCGGA
Desulfitobacterium metallireducens DSM 15288 ctg111	AGJB01000003.1	15355-15440	CATCGACAAGAGCAAACTTGGCGAAAGCCAAGGACGCAAAGCTATGGGTCTTCCAGAGTTCTTCTGATGACTGCCAAGCCACCGAA
Desulfitobacterium metallireducens DSM 15288 ctg111	AGJB01000003.1	90831-90914	CAATGACAAAGGCAAACCTGGCGAAAGTCAGGGACGCAAAGCTATGGGTCGTCCAGTGTGGCTGACGATTGCCAGGTCGCTAAT
Desulfitobacterium metallireducens DSM 15288 ctg111	AGJB01000003.1	240759-240842	CAATGACAAGAGCAAACCTGGCGAAAGTCAGGGACGCAAAGCTATGGGTCGTCCAGTTTGGCTGACGATTGCCAGGTTACCAAA
Desulfitobacterium	AGJB01000001.1	246363-246463	ATTGTGTTGGGGTAAACTTCGTGAAAGCGAAGGACGCTAAAGCTATGGGTCTACGGTTGATTACATGAGCAAACATCAGCTAAGATCGCCAAGCTACAA

metallireducens DSM 15288 ctg113			GT
Desulfobacca acetoxidans DSM 11109	CP002629.1	903566-903641	TCGTGAAGAAGCCACACCCCGGGCGACCGGGGGCCGGAAAGCCGCGGGTCTCAGCAGAGACGGCCGGGTTGCCACC
Desulfobacca acetoxidans DSM 11109	CP002629.1	900580-900658	CCCTGATAAAGCCACACACCGGGCGACCGGGGGCCGGAAAGCTACGGGTCTCACCAGAGACAGCCTTGTAGCTGCCAGG
Desulfobacca acetoxidans DSM 11109	CP002629.1	901334-901409	TCGTGAACAAGCCACACCCCGGGCGACCGGGGGCCGGAAAGCCGCGGGTCTCAGCAGAGACGGCCGGGTTGCCACC
Desulfobacca acetoxidans DSM 11109	CP002629.1	907011-907086	CCGTGAAAAAACCACACCTCGGGCGACCGGGGGCCGGAAAGCCGCGGGTCTCAAAGGAGATGGCCGGGTTGCCAGA
Desulfobacter postgatei 2ac9 ctg440	AGJR01000015.1	18301-18375	AGACGACAAAGCCAAACCTGCCGAAAGACAGGCACGGAAAGGCGCGGTTCCATTGATTATAACTGGGTTGCCATT
Desulfobacter postgatei 2ac9 ctg445	AGJR01000009.1	114910-114826	AATAGAAAATACCAAACCTGTTGTGAAGCAGGGACGGAAAGCCACGGGTCTTAAAGTTGCATCAATAGAAAGCCGGGTTGCCTTT
Desulfobacter postgatei 2ac9 ctg446	AGJR01000008.1	43629-43708	AACAGTCAAAGCCAAACCTGACGAAAGTCAGGGACGGAAAGACACGGATTCTAATTAAAGGGGACAGCCGGGTTGCCTGA
Desulfobacter postgatei 2ac9 ctg450	AGJR01000004.1	208953-208876	AAATAGAAAAGCCAATTCTGCACAGATGCAGAAACGGAAAGCCATAGGGTCTATGATTTAGATAGCCGGGTTGCCTCG
Desulfobacterium autotrophicum HRM2	CP001087.1	3010098-3010019	TTCCGACAAAGGTAACCCGTGGGTAACCACGGTTCACAAAGCTTATGGGTCCGTCATTGGCGGATAGCCGAGTTGCCGAA
Desulfobulbus propionicus	CP002364.1	1829443-1829363	TTGATAACTGGGCAAACATACCGAAAGGTATGGGCGCAAAGTCTCCGGCCTACGGGAAACTATGGTAGCGGGACTGCGGCA

DSM 2032			
Desulfococcus oleovorans Hxd3	CP000859.1	2080979-2081056	TCATGCTAAAGCCAAACTCCGGGCGACCGGAGGACGGAAAGCAACGGGTCTTAATATAAAGACAGCCGGGCTGCCATG
Desulfohalobium retbaense DSM 5692	CP001734.1	427624-427550	GACTGACAAAGCCAAACCCGTCGTGAGGCGAGGACGGAAAGCCACGGGTCTCAATGAGACAGCCGGGTTGCCGGA
Desulfohalobium retbaense DSM 5692	CP001734.1	1118070-1118144	GACTGACAAAGCCAAACCCGTCGTGAGGCGGGGACGGAAAGCCACGGGTCTCAATGAGACAGCCGGGTTGCCGGA
Desulfonatronospira thiodismutans ASO3-1 ctg19	ACJN02000003.1	250966-251062	TACATATCCAGCCAAACCCGCCGCAAGGCGGGGACGGAAAGCCACGGGCCCCCGGGATTTAAAAGTCATAGCATACGCGGGCAGCCGGGTTGCCGGA
Desulfonatronospira thiodismutans ASO3-1 ctg21	ACJN02000001.1	84539-84450	GTCTGACAAAGGCAACACAGCCTGAAAAGGTGTGACGCAAAGCCACCGGCCTGGATTTTTTTTTGGGAGTATGGCAGCGGGGTTTCCGGA
Desulfosporosinus meridiei DSM 13257 ctg108	AGJA01000012.1	5783-5697	TTATTGACAAGGCAAACTGAGCGAAAGCTCAGGACGCAAAGCTACGGATCTTCCACTCTTAGGGGTAAAGATGGCCGAGTTACCAAT
Desulfosporosinus meridiei DSM 13257 ctg109	AGJA01000009.1	122495-122577	CTGCGATAAAGGCAAACTCAGTGAGAACTGAGGACGCAAAGCCACGGGTCTTACACATGTGTGAAGACAGCCGGGTTATCGAA
Desulfosporosinus meridiei DSM 13257 ctg117	AGJA01000003.1	459792-459896	AAACGGTTGGGGTAAACTTCGCGAAAGCGAAGGACGCTAAAATCATGGGTCTAAGGCTGCTAATTTCACACATGGAAATTAGGCTAGGATCGCCAGATTACAAGC
Desulfosporosinus meridiei DSM 13257 ctg117	AGJA01000003.1	75111-75197	TAATGAGAAAAGTAAACTTACTGAAAGGTAAGGACACAAAGCCATGAGTCTAAGGTATGAAGATACTATGATTGTCAGGTTGCCAAA
Desulfosporosinus meridiei DSM 13257 ctg117	AGJA01000003.1	457715-457825	GTTCGGTTGGGGTAAACTTCGCGAAAGCGAAGGACGCTAAAGTCATGGGTCTAAGGCTAAATTCAAAGGGCTGCTAATACCTTTGAGGGCTATGATCGCCAGACTACAAGC

Desulfosporosinus meridiei DSM 13257 ctg118	AGJA01000001.1	182645-182558	TGACGACATTAGCAAACTTGAGCGAAAGCCAAGGACGCAAAGCCATGGGTCTTCCAGTTGTATAACTGATGATTGCCAGGTTACCGAA
Desulfosporosinus meridiei DSM 13257 ctg118	AGJA01000001.1	435027-435109	CTGCGATAAGAGCAAACCCAGTGAGAACTGGGGACGCAAAGCCACGGGTCTTCATTTATTTATAAGATAGCCGGGTTACCGAA
Desulfosporosinus orientis DSM 765	CP003108.1	4122117-4122032	ATGCGATAAAGGCAAACTCCGCGAAAGCTGGGGACGCAAAGCCACGGGTCTTAGCATGATTGGGTGAAGACAGCCGGGTTACCGAA
Desulfosporosinus orientis DSM 765	CP003108.1	5825576-5825492	TAAAGACAAAGGCAAACCCAGCTAAAGCTGGGGACGCAAAGCCACGGATCTTACACGTAAGGGTGATGATGGCCGGGCTGCCTAC
Desulfosporosinus orientis DSM 765	CP003108.1	644558-644650	TCAAATAGTAGGCAAATCTATTGAAAAATAGAGACGCAAAGCCACGGGTCTAAAGCAGGCCTTTCTGCCTGTCATGACGGCCGGGTTGCAGAA
Desulfosporosinus orientis DSM 765	CP003108.1	4078740-4078656	CTGCGATAATGGCAAACCCAGTGAGAGTTGGGGACGCAAAGCCACGGGTCTGACCACAGAATGTGAAGATAGCCGGGTTATCGAA
Desulfosporosinus orientis DSM 765	CP003108.1	466066-465952	GTTCGGTTGGAGCAAACTTCGCGAAAGCGTAGGACGCTAAAGTCATGGGTCTAAGGCCCGCCTGAGAGAATATTACTATACTCTTCAGACAGGTTATGATCGCCAGACTACAAGC
Desulfosporosinus orientis DSM 765	CP003108.1	1268377-1268463	GACGATAAATAGCAAACTTGAGTGAAAGCCAAGGCGCAAAGCCTTGGGTCTTCCAGTTGTCTAACTGATGATTGCCAGGTTACCGAT
Desulfosporosinus orientis DSM 765	CP003108.1	5373108-5373024	TTGCGATAAAGGCAAACTTAGTGAAAACTAAGGACGCAAAGCTATGGGTCTTCCGGGTAAAGCTGATGACTGCCAAGCCACCGAA
Desulfosporosinus sp. OT TOU.assembly.114	AGAF01000016.1	5315-5399	GGTTGATAAAGGCAAACTTAGCGAAAGTTAAGGACGCAAAGCCACGGGTCTTCTGCTTACAAGTAATGATCGCCGGGCTACCGAG
Desulfosporosinus sp. OT TOU.assembly.146	AGAF01000050.1	9055-8966	TAGCGCTAAGGGCAAACCTGTCAAAAGATAGGGACGCAAAGCCATAGGGTCTAAGGTGCTTACCAGCACTATGATAGCCTGGCTACCGCA
Desulfosporosinus sp. OT TOU.assembly.149	AGAF01000053.1	65276-65397	GTTCGGTTGGGGTAAACTTTGCGAAAGCGAAGGACGCTAAAGTCATGGGTCTAAGGCTTAAGAAAACCAAAGTACTTTTTCAAGTAACTTGGAACTTAAGCTAAGATCGCCAGATTACAAGA
Desulfosporosinus sp. OT	AGAF01000059.1	30745-30836	TATTATTAAGGGCAAACCTGTCTAAAGACAAGGGACGCAAAGCCATAGGGTCTAAAGTGCTATAGCGGTACTATGATAGCCTGGTTGCATAG

TOU.assembly.155			
Desulfosporosinus sp. OT TOU.assembly.203	AGAF01000111.1	50366-50277	TCAGCCTAAGGGCAAACTTGTTAAAAGGCAGGGACGCAAAGCCATCGGATCTAAAGCGCTTATGAGTACTATGACAGCCTGGCTGCCGCA
Desulfosporosinus sp. OT TOU.assembly.203	AGAF01000111.1	28402-28318	AAACGATAAAGGCAAACTTGGTGAAAGCCAAGGACGCAAAGCCATGGGTCTTCCATGTTAAGGTGAAGATAGCCGGGTTACCATA
Desulfosporosinus sp. OT TOU.assembly.252	AGAF01000165.1	46546-46463	AGATGAAAAAGGTAAACCCGTTGAAAGACGGGGACACAAAGCTATGGGTCTAAGGCTATACGCTATGACTGCCAGGTTGCCACT
Desulfosporosinus sp. OT TOU.assembly.27	AGAF01000192.1	19086-19005	TAACGATAAAGGCAAACTTGGTGAGAGCCAAGGACGCAAAGCCACGGGTCTTCATTAAGCTGAAGATAGCCGGGTTACCACA
Desulfosporosinus sp. OT TOU.assembly.275	AGAF01000187.1	39470-39383	TTCTTTTAAGGGCAAACTTACTTAAAGGTGAGGACGCAAAATCACAGGTCTAAGGTTCCTTCAGAACTATGACGGCTGGATTGAACAA
Desulfosporosinus sp. OT TOU.assembly.4	AGAF01000229.1	60313-60227	CAGCGATAAAGGCAAACTCAGTGAGAACTGAGGACGCAAAGCCACGGGTCTCCTATTTGCTTTACGGAAGATAGCCGGGTTACCGAA
Desulfosporosinus sp. OT TOU.assembly.47	AGAF01000226.1	5987-6068	TAACGACAAAGGCAAACTTGGTGTAAACCAAGGACGCAAAGCCACGGGTCTTCCTTAAGCTGAAGATAGCCGGGTTACCGTA
Desulfosporosinus sp. OT TOU.assembly.61	AGAF01000242.1	59563-59476	CTGCGATAAAGGCAAACTCAGTGAGAGCTGAGGACGCAAAGCCACGGGTCTCCCACACCTTAGAGTGGAAGATAGCCGGGTTACCGAA
Desulfosporosinus sp. OT TOU.assembly.62	AGAF01000243.1	2481-2397	TTCTGAAAATGGCAAACTTAGCGAAAGCTAAGGACGCAAAGCCATAGATCGTACAGGGAAGGCTGACGACAGCTAGGCTACCAAA
Desulfotomaculum acetoxidans DSM 771	CP001720.1	4469519-4469430	AAACAGGAAGAGCAAACCTGGCGAAAGTCGGAGACACAAAGCTACATGGTCTAAAATGCAGACAAGTATTACGACAGCCTGGCCGCCGTA
Desulfotomaculum acetoxidans DSM 771	CP001720.1	1572818-1572907	TATTAGTAAGGGCAAACCTATTTAAAAATAGGGACGCAAAGCCTAGGGTCTAAGGTGCTGAATAAGCGCTATGATAGCCTGGTTGCCGCA
Desulfotomaculum	CP001720.1	3575661-3575571	ATAACTAATGGGCAAAACCATACGAAAGATGGTGACGCAAAACCTTGGATCTAAGGTCATAAAATATGGCTATGATTGCCAGGCTGCAAAT

acetoxidans DSM 771			
Desulfotomaculum acetoxidans DSM 771	CP001720.1	4175329-4175242	AGCCTTAGAGGGCAAATCTGGCGAAAGCCAGAGACGCAAAGCCAAGGGTCTAAGTTGCATTAAGCGATAAGATAGCCTGGTTGCAAAA
Desulfotomaculum carboxydivorans CO-1-SRB	CP002736.1	682909-682822	GGTTGAAAAAGGCAAACCTATCCGAAAGGTAGGGGCGCAAAACCATGGGTCTAAATCGTTTCTGCGATATGATCGCCAGGTTGCCAAC
Desulfotomaculum carboxydivorans CO-1-SRB	CP002736.1	2301344-2301268	ATACGATAAGGGCAAACCTATTGAAAGATAGGGACGCAAAGCCACGGGCCTAAAACGATGGCAGCCGGGTTACCGAA
Desulfotomaculum carboxydivorans CO-1-SRB	CP002736.1	2837937-2837853	AGTTAAAAAGGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCCGGGGTCTAAAGTTTAAATAAACCATGACAGCCGGTTGCTGAT
Desulfotomaculum gibsoniae DSM 7213 ctg381	AGJQ01000021.1	60589-60677	CCACGGGTTAGGCAAACCTGGTGAAAGCCAGGGACGCTAAAGCTATGGGTCTAATGGTTTGAAAAACCTATGATTGCCAGGCTATAACG
Desulfotomaculum gibsoniae DSM 7213 ctg384	AGJQ01000019.1	72207-72109	GTTTCACAAAGGCAAACTACATCGAAAGATTAGGGCGCAAAGCCATGGGTCTAAAGCGCTTGAGCTTATTAATAGTGCAATGATTGCCAGGTTGCGGGA
Desulfotomaculum gibsoniae DSM 7213 ctg385	AGJQ01000018.1	12827-12915	TTTCTGAAAAGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCATGAGTCTAAGGTTTTTGAAAGGGCTATGACAGTCAGGCTGCCGGA
Desulfotomaculum gibsoniae DSM 7213 ctg402	AGJQ01000001.1	21022-20935	TAAAGTTAAGGGCAAACCTGTCTAAAGGCAGGGACGCAAAGCCGAGGGTCTAAAGCGTTTGCCGCGCTATGACAGCCTGGCTGCCGAT
Desulfotomaculum gibsoniae DSM 7213 ctg402	AGJQ01000001.1	33891-33805	AATTGATAAAGGCAAATCCGTCGAAAGGCGGAGACGCAAAGCCGCAAGTCTAAAGCAAGAGATTGCTATGATAGTTGGGCTGCCAAT
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	1790648-1790561	ATTGTCCAGGGGCAAACTTCACCGAAAGGGAGGGGCGCAAAGCCACGGGCCTAAAGCGGACTCCCGCTAAGGCAGCCGGGTTGCGACA
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	569329-569414	TTGTGTTAAAGGCAAACCACTCGAAAGGGTGGGGCGCAAAGCCATGGGTCTGCAGCCCTAAAGGGTATGACTGCCAGGCTGCCGCG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	3293408-3293316	AATCCCGGTGGGCAAACCCGGCAAAAGCCGGGGACGCAAAGCCACAGGTCTAAAGTTACCCATTGAGGTAACCATGACGGCTGGGTTGCAAGG

Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	2737106-2737195	TTACGGGTTGGGCAAACCGGGCGAAAGCCCGGGACGCTAAAGCCATGGGTCTAAGGTCCTTTTCAGGACTATGATCGCCAGGCTGCAACG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	668125-668210	CCCGATTAAAGGCAAAGCCATTGAAAAATGGCGGCGCAAAGCTATAGGGGCTAAGGCGAACAACGCTATGCCAGCCAGCTGCCGGG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	771180-771270	CTTTCCGGAGGGCAAACCCGGCGAAAGCCGGGGACGCAAAGCCACAGGTCTAAAGTTCCCCGCGGGGAACCATGACGGCTGGGTTGCAAGG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	1050220-1050361	AATCCTGGAGGGCAAACTCGGCGAAAGCCGGGGGCGCAAAGCCACAGGTCTAAGGTTCCCCAAAAGCGCTCGAAGGCAAAGCCACAGGTCTAAGGTTCCCCAAAAGGTTGCCACGGGGAACTATGACGGCTAGGTTGCAAGG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	239178-239089	GGGCGTCAAGGGCAAACCCATTGGTGGGGACGCAAAGCTACAGGGTCTAAGGTGCTTATGCGATGGCACTACGACAGCCTGGCCGCCGCG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	885656-885746	GCCCGAAAATAGCAAACCCGTGCGAAAGCCGGGGACGCAAAGCCATGGGCCTACAGCGGTGTTGTGCCGCTACGGTTGCCAGGTTGCCGAA
Desulfotomaculum nigrificans DSM 574 ctg00018	AEVP01000018.1	9627-9714	ATGTATATTGGGCAAACCCGTCGAAAGGCGGTGGCGCAAAGCCAAGGGCCTAAGGAGTAAAGAAATTCTATGGCAGCCGGTTGCAGCA
Desulfotomaculum nigrificans DSM 574 ctg00084	AEVP01000043.1	15009-15096	GGTTGAAAAAGGCAAACCTATCCGAAAGGTAGGGGCGCAAAACCATGGGTCTAAATCGTTTCTGCGATATGATCGCCAGGTTGCCAAC
Desulfotomaculum nigrificans DSM 574 ctg00101	AEVP01000014.1	784-868	AGTTAAAAAGGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCCGGGGTCTAAAGTTTAAATAAACCATGACAGCCGGTTGCTGAT
Desulfotomaculum reducens MI-1	CP000612.1	2518598-2518516	AATAAAGAAAGGCAAACCTACTGAAAGGTAGGGGCGCAAAGCTAGAGGGTCTAAGGGGGAACCTATGACAGCCAGTTGCTCCG
Desulfotomaculum reducens MI-1	CP000612.1	1256280-1256362	TAACAAACAGGGCAAACCTGGTGAAAGTCAGGGACGCAAAGCCATGGGTCTAAAGCGAATGCCAGGACGGCTAGGCTACTAAA

Desulfotomaculum reducens MI-1	CP000612.1	3257014-3256933	TTCCGACAAAGGCAAACCCTCCGAAAGGGTGGGGCGCAAAACCACGGGCCTAAGGTGTAGCTAGGGTAGCCGGGTTGCCGAG
Desulfotomaculum reducens MI-1	CP000612.1	2231434-2231354	TTCAAAAATGGGTAAATCTTGAAAGGTAGGGACGCAAAGCCATGGGTCTAATGCATTTGCAATGATAGCCAGGCAGCATAA
Desulfotomaculum reducens MI-1	CP000612.1	1107064-1107147	AAAATTAAAAGGCAAACTTTCCGAAAGGAAAGGACGCAAAGCCACGGGCCTAAGGACATTGTCTATGGTAGCCGGGCCGCCTTA
Desulfotomaculum reducens MI-1	CP000612.1	416215-416306	GAAACTGAAGGGCAAACCCGAACGAAAGACGGGGACGCAAAACCTTGGGTCTAAGGTTCTAGGAATGAACTATTGATTGCCAGGCTGCAAAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	3531132-3531049	AGACGATAAAGGCAAACTTATCGAAAGGTAAGGACGCAAAGCCATGGGCCTAATCCCGAAGGGAACGGTTGCCAGGCTGCCAAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	3171783-3171704	AATACGAAAAGGCAAACCTAGCGAAAGTTAGGGACGCAAAGCCACGGGCCTCATTTTCATGTGGCGGCCGGGCTGCCGAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	1842846-1842762	TTAAATATCGGGCAAATCTGTCGAAAGGCAGAGACGCAAAGCTATGGGCCTAAGGCAGAAATGCTATGGTTGCCAGGTTGCTTAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	1614085-1613996	GTCAGATACTGGCAAACTGGTGGAAACACCGGGACGCAAAGCAATAGGGCCTAATCCTCCGGCAGGAGGGACGGCAGCCTGGCCGCCGAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	668160-668076	AGTATGAAAAGGCAAATCCATTGAAAAATGGGGGCGCAAAGCCATGGGTCTAAGCCAAGTTCGGTATGATTGCCAGGCTGCCAAA
Desulfotomaculum ruminis DSM 2154	CP002780.1	3181084-3181173	TAATCCAAAAGGCAAACCATCCGAAAGGTTGGGACGCAAAGCCATGGATCTAAGGCAGGTTTTATATGCTAAGATTGCCAGGTTGCGGAG
Desulfovibrio aespoeensis Aspo-2	CP002431.1	3315258-3315128	GGTAAGACAAGCCAAACCCGTCGCGAGACGGGGACGGAAAGCCACGGGTCTTTGCCCGCTTCGGTCTCTGTCCGGCATCGGTGCCGGGACATGGGAGCGAAGGGGTACGCAAAGACAGCCGGGTTGCCAGA
Desulfovibrio aespoeensis Aspo-2	CP002431.1	2774858-2774783	TGTTATTAAAGCCAAATTCGTCGTGAGGCGGAGACGGAAAACCACGGATCTCAGAAGAGATAGCCGGGTTACCGAT

Desulfovibrio africanus str. Walvis Bay ctg406_Cont2	AFHE01000002.1	381807-381895	ACTCGCTAAAGGCAAACCACTTTAAAGAGTGGGACGCAAAGTCTTCTGCCTACGTTCCCTTCGGGGAATATGGTCGTGAGGCTGCCGAG
Desulfovibrio alaskensis G20	CP000112.1	841128-841197	CGAGAATCAAGCCAACCCGCCTCAGGCGGGACGGAAAGCCACGGGTCTTTCAGACAGCCGGGTTGCCTCG
Desulfovibrio desulfuricans ND132 ctg54_1_Cont4	AEUJ01000004.1	187919-187845	TAGAGAAACTGCCAAACCCGCCGCGAGGCGGGGACGGAAAGCCACGGGCCTCACGCAGGCAGCCGGGTTGCCTAC
Desulfovibrio fructosovorans JJ ctg00015	AECZ01000036.1	40498-40584	CACTGAAAAAGGCAAACCCTTCGAAAGAAGGGGACGCAAAGCCACGGGCCTACGTCCCGCAAGGGATACGGTAGCCGGGCCGCCAAT
Desulfovibrio magneticus RS-1 DNA	AP010904.1	3289058-3288977	AGTCTGTAAAGCCAACCCCGTCGTGAGGCGGGTGCGTACGGAAAGCCACGGGCCTCACGGTTGAGGCAGCCGAGCCGCCATG
Desulfovibrio magneticus RS-1 DNA	AP010904.1	4339624-4339540	GCCCAATAACGCCACCCCTGCCGCGAGGCAGGTCCGGAAAGCCGCGGGTCTCGACGGCCGTCGTCGAGACAGCCGGGCCGCTGGG
Desulfovibrio sp. A2 tab.contig.37	AGFG01000038.1	17557-17631	CGAGACAAATGCCAAACCTGCCGTGAGGTAGGGACGGAAAGCCACGGGTCTCTCGAAGACAGCCGGGCCGCCTTG
Desulfovibrio sp. A2 tab.contig.41	AGFG01000042.1	88257-88181	TCAAGAGAAAGCCAAACCCGCCGCGAGGCGGGGACGGAAAGCCACGGATCTCGCGCAGAGACAGCCGGGTTGCCTGC
Desulfovibrio vulgaris str. 'Miyazaki F'	CP001197.1	2307925-2307849	ACAAGCGAAAGCCAAACCCGCTGCGAGGCGGGGACGGAAAGCCACGGATCTCGCGTAGAGACAGCCGGGTTGCCTGC
Desulfurivibrio alkaliphilus AHT2	CP001940.1	469814-469735	CTCTGATAAGGGTAAACCCATCGTAAGGTGGGGACACAAAGCCAACGGGTCCTGGAGCACAGGACGGCCGGGTTGCCGGA
Desulfurivibrio alkaliphilus AHT2	CP001940.1	2075224-2075133	CCACGAAAAAGGCAAACCATCGCGAAAGCATGGGACGCAAAGCCACCGGCCTTCTTCCTGTTAAGACAGGAAATGGCAGCGGGGTTGCCGAA
Desulfuromonas acetoxidans	AAEW02000011.1	10503-10578	GCAAGATAAAGGCAAAACCGAAGTAATTCGGTGACGCAAAGCCACGGGTCCATAACTGGATCGCCGGGTTGCTCAA

DSM 684 ctg54			
Desulfuromonas acetoxidans DSM 684 ctg66	AAEW02000001.1	146764-146686	CTCCGATAAAGGCAAAACCGGAGTAATCCGGTGACGCAAAGCCACGGGTCCTGTTTGACAGGATCGCCGGGTTCCCGAA
Dethiobacter alkaliphilus AHT 1 ctg11	ACJM01000001.1	102217-102302	CAGTATAAAAGGCAAATCCGTTGAAAAGCGGGGACGCAAAGCTATGGGTCTAAGGCGGAATGCCGCTATGACAGCCGGTTGCCAAA
Dethiobacter alkaliphilus AHT 1 ctg13	ACJM01000030.1	1847-1764	CCTTGATAAGGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTACAGGTCTAAAGCATTTTGCTAAGACAGCTGGGTTGCCGGG
Dethiobacter alkaliphilus AHT 1 ctg16	ACJM01000018.1	13988-14074	AGGTGAAAAAGGCAAACGTTCTGAAAGGAACGGGCGCAAAGCCACGGGTCTAAAGCCTTAAAAGGCCATGATAGCCGGGTTGCCCCA
Dethiobacter alkaliphilus AHT 1 ctg21	ACJM01000017.1	32821-32734	GCTTGAAAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCAAGGGTCTAATGCTGTTTTTACAGCGATGACAGCCGGTTGCCGGG
Dethiobacter alkaliphilus AHT 1 ctg27	ACJM01000016.1	42135-42050	GTCGAATAAAGGCAAACTCGCCGAAAGGCGGGGACGCAAAGCCACAGGCCTACGGTTGTAATGACTATGGCGGCTGGGTTGCCGGC
Dethiobacter alkaliphilus AHT 1 ctg28	ACJM01000007.1	61666-61582	AACTGTTAAAGGCAAGCTCGTCGAAAGGCGGGTACGCAAAGCCATGGGTCTAATGCTATTGTAGCGATGACAGCCGGTTGCCAGG
Dethiobacter alkaliphilus AHT 1 ctg28	ACJM01000007.1	39998-40079	CCTTGATAAAGGCAAACCCGTCGAAAGACGGGGACGCAAAGCCACGGGCCTAAAGCATTGCTATGGCAGCCGGGTCGCCGGG
Dethiobacter alkaliphilus AHT 1 ctg36	ACJM01000005.1	37784-37870	ATTCGCTCAGGGCAAACCTGTTGAAAGGCAGGGACGCAAAGCCAAGGGTCTAACACTGCAAAGCAGTCATGACAGCCGGTTGCCGAA
Dethiobacter alkaliphilus AHT 1 ctg4	ACJM01000010.1	93366-93279	ACTGGATAATGGCAAACCTGTTGAAAAGCAGGGACGCAAAGCTAAGGGTCTACGGCACATTTTGTGTCATGACAGCCTGGTTATCGAA
Dethiobacter alkaliphilus AHT 1 ctg9	ACJM01000004.1	66132-66048	ATCCGACAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGCCATGGGTCTAAGGGCACACGCCTACGATCGCCAGGTTGCCGAA

Dorea formicigenerans 4_6_53AFAA cont1.37	ADLU01000037.1	19561-19636	TAATATTTTGGGCAAAACAGACGAAAGTCTGCGACGCAAAGCTATAGGACCTGTAAAATGGTAGCCAGTTGTAAAA
Dorea formicigenerans 4_6_53AFAA cont1.66	ADLU01000066.1	25331-25406	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATAA
Dorea formicigenerans ATCC 27755 D_formicigenerans-3.0.1_Cont150	AAXA02000010.1	13807-13732	TAATATTTTGGGCAAAACAGACGAAAGTCTGCGACGCAAAGCTATAGGACCTGTAAAATGGTAGCCAGTTGTAAAA
Dorea formicigenerans ATCC 27755 D_formicigenerans-3.0.1_Cont399	AAXA02000015.1	880668-880758	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGGCGCAAAGCCAGAAGGGACTAAAGTCAGAAAACTTGACCATGTCAGCCGGTTGCCACT
Eggerthella sp. YY7918 DNA	AP012211.1	612893-612976	TATTTTCACGAGCAAACCTGCCGGAAAGCAGGGACGCAAAGCTATAGGGGCCGAACCCCTTGGGGCGGCTAGCCAGTTGCGATC
Eggerthella sp. YY7918 DNA	AP012211.1	493503-493586	ATATTCTCAAGGCAAACCCGCCGTAAGGCGGCGACGCAAAGCTACAGGGGCCATATCGGTTCGATGGGTCAGCCAGCTGCGGTC
Eggerthella sp. YY7918 DNA	AP012211.1	141116-141199	ATGTCTTCAAGGCAAACCTGCCGGAAGGCAGCGGCGCAAAGCTAAAGGGGCCCATTCTAAGAAGAAGGCCAGCCAGTTGCACGT
Eggerthella sp. YY7918 DNA	AP012211.1	882367-882451	ATCGGCTACGGGCAAACCCGTCGAAAGACGGTGACGCAAAGCTAAAGGGCCTTCGCCGCGTGCGGCATGGCAGCCAGTTGCAAAG
Environmental sequence 2662324_fasta.screen.Contig11497	AAFX01114411.1	145-238	CCATCGAACGGGCAAACCCACTGAGAGGTGGGGACGCAAAGCCTCCGGTCCCGAGAGTCTAGTAAGACATTCTTCGGATAGCGGGGTTGCCAGG

Environmental sequence 2662324_fasta.screen.Contig20358	AAFX01070808.1	1034-948	TCTGAAACAGGGCAAACCCGCCGAGAGACGGGGACGCAAAGCCAAGGATCTTCGCGACGAGAGTCGGCAAGACCGCCCGGTACCAGG
Environmental sequence 2662324_fasta.screen.Contig24218	AAFX01084845.1	258-332	AAAGGAAAAAGGCAAACTTACCGTGAGGTAAGGACGCAAAGCCACGGGACTCGAGGAGTCAGCCGGGTTACCCAT
Environmental sequence 2662324_fasta.screen.Contig32687	AAFX01108761.1	554-467	TTCCGCAAAGGGCAAACCGCGCGAAAGCGCGGGACGCAAAGCCGCTGGCCTAAGTCTCTCAGCGAGATACGGCAGCAGGGTTGCCGGA
Environmental sequence 2662324_fasta.screen.Contig34285	AAFX01084815.1	828-726	GCGCGACAAGGGCAAACCGGGCGAAAGCTTGGGACGCAAAGCCACGAGGCTAAAGCAGGACTGTCCGAAGACGGCGGTCGGCCAAGCCAGTCGGGTCGCCGAG
Environmental sequence 2662324_fasta.screen.Contig3511	AAFX01100921.1	226-134	CGACGACAAAGGCAACCCCTTCGGAAACGAGGGTGGGCGCAAAGCAAACGGGGCTAACGCACGCACGCGTGCTATGCCGGCTGAGCCGCCAAA
Environmental sequence 2662324_fasta.screen.Contig42409	AAFX01003619.1	286-206	TAACCGAAAAGGCAACCGCCGCAGCAAAAAGCGGTGGGCGCAAAGCCAGGAGTTCCGTTAAAGAACCGTCCGGCCGCCGAA
Environmental sequence ctg11473	AATN01000135.1	4211-4308	CTGATTTAAAGGCAAACGGAGGGAAACCTCCGGACGCAAAGCCGCGGACCCTACCCTGAGTTGTCAGATAAGCTCAGAAGGGTGGCCGGGTTGCCCGA
Environmental sequence ctg1449	AATO01014039.1	335-238	CTGATTTAAAGGCAAACGGAGGGAAACCTCCGGACGCAAAGCCGCGGACCCTACCCTGAGTTGTCAGATAAGCTCAGAAGGGTGGCCGGGTTGCCCGA
Environmental sequence ctg16200	AATO01000161.1	2779-2876	CTGATTTAAAGGCAAACGGAGGGAAACCTCCGGACGCAAAGCCGCGGACCCTACCCTGAGTTGTCAGATGAGCTCAGAAGGGTGGCCGGGTTGCCCGA
Environmental sequence	AATO01013153.1	264-167	CTGATTTAAAGGCAAACGGAGGGAAACCTCCGGACGCAAAGCCGCGGACCCTACCCTGAGTTGTCAGATGAGCTCAGAAGGGTGGCCGGGTTGCCCG

ctg6129			A
Environmental sequence GutlessWorm_Cont1000	AASZ01001000.1	4254-4168	ATAGCGAAAGGGCAAAGTCACCGAAAGATGGCGACGCAAAACCGTGGATCTAAAGCCATTTATGGCCAAGATAGCCAGGTTACCGAA
Environmental sequence GutlessWorm_Cont1127	AASZ01001127.1	10703-10603	GCTCGATAAAGGCAAACCACTCGAAAGGGTGGGACGCAAAGCCACTAATCCACCCTTGTTCCGTTGACATCGGAAGAATGGCGGACAGCAGGGCTGCCGGG
Environmental sequence GutlessWorm_Cont1200	AASZ01001200.1	1265-1043	TTAAGCAAAGGCCAACTCTCGGGGGATCGGGGGGCGGAAAGCCACGGGTCTTAAGTTAGTTGAATGGTTTATCGGTTGATTTCGGTGAAATTCGCTGCGCTGTCATATACCTGAACTTCACTGGATAAATTAGTTGACTGGTAAGGACGGGTAAATACCCCTCAACTAATTTAGCGTTTTACAAATCAACTATTCAACGAAAAAAGATAGCCGGGTTACCTTA
Environmental sequence GutlessWorm_Cont1208	AASZ01001208.1	1150-1033	TGCCATAAAAGCCACACCCATCGTGAGATGGGGTCGGAAAGCAACGGGTCTTGAAATATTCAAATTGACTATCAGCTAAATATTCTCCACGTGTGGATAAGACAGCCGGGCTGCCGAG
Environmental sequence GutlessWorm_Cont1260	AASZ01001260.1	516-606	GCTTGATAATAGCAAACCACTTGAAAGGGTGGGACGCAAAGCCACTGGCCTAAATCTCGATTCGGCGGGATATGGCAGCAGGGTTGCCGGG
Environmental sequence GutlessWorm_Cont1693	AASZ01001693.1	1787-1864	AACAGAAAAAGCCAAACCCCGAGAGATCGGGAGACGGAAAGCCACGGGTCTGAACTTAAAGATAGCCGGGCTGCCTTA
Environmental sequence GutlessWorm_Cont2655	AASZ01002655.1	5432-5343	TTTACTGAAGGGCAAACCTTCCGAAAGGAGGGGGCGCAAAGCTTCCGGTCTAAGTTCGTATCAGACGAATAAGATAGCGGGGTTGCTAGG
Environmental sequence GutlessWorm_Cont2817	AASZ01002817.1	8015-7939	TATTGATAAAGCCAAACCCACCGGGAGGTGGGGGCGGAAAGCCACGGGTCTTGAACAGAGACAGCCGGGTTGCCAGG
Environmental sequence GutlessWorm_Cont2941	AASZ01002941.1	1174-1264	GCTTGATAATAGCAAACCACTTGAAAGGGTGGGACGCAAAGCCACTGGCCTAAATCTCGATTCGGCGGGATATGGCAGCAGGGTTGCCGGG
Environmental sequence GutlessWorm_Cont3026	AASZ01003026.1	2488-2400	CTAGCCGCAGGGCAAAACTTCCGAAAGGAAGCGGCGCAAAGCTTCCGGCCTAAATCCTTAAACCGGGACACGGCAGCGGGGCTGCATGG
Environmental sequence GutlessWorm_Cont316	AASZ01000316.1	1765-1675	GCTTGAAAAGGGCAAACCGCTCGAAAGAGCGGGACGCAAAGCCACTGGCCTAAGTTCTGATATCGCGGAATACGGCAGCAGGGCTGCCGGG
Environmental sequence	AASZ01000761.1	11028-10947	TAAACGAAAAGGCAAAGCTGCCGAGCAGTCACGCAAAGCCACGGGTTTCTATATTTGAGTTTGTGATAGCCGGGCTGCCGAA

GutlessWorm_Cont761			
Environmental sequence s8_160359	AAQL01001872.1	853-778	TAGGATAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGTCTTTAAAATGGCAGCCAGCTGCATGA
Environmental sequence s8_163345	AAQL01003639.1	4195-4101	TTTATATTTGGGTAAAACTGTCGAAAGGCAGCGACACAAAGCCAAATGGGTCTAAGGTTCATTTTTTAAGAGAATTATGACAGCCGGTTGCATCA
Environmental sequence s8_175521	AAQL01009711.1	838-751	TTATTCATAGGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAGAAGGGTCTAAGGTCTTATTGGACTATGACAGTCGGTTGCCACA
Environmental sequence s8_176510	AAQL01009925.1	3116-3200	GAAGGATAATAGCAAAATTAGTGAAAGCTAATGACGCAAAGCTACGGGTCTAAGTACAAAAGTATATGATTGCCGGGCCGCCCAA
Environmental sequence s8_177602	AAQL01010251.1	934-853	ATATTTTAAAGGCAAAACTRTTGAAAAATAGTGACGCAAAGCTACAGAACTGAACCGTAAGGAAGTTGGCTGAGTTGCAGAT
Environmental sequence s8_179529.1	AAQL01011659.1	1058-1133	TATGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Environmental sequence XZS102136.b1	AAFX01019087.1	306-393	TTTTGACAAGGGCAAAGCCATCGAAAGGTGGCGACGCAAAGTCACCGGCCTAACGGGCGCAGCGCCCCACGGCAGCGGGACCGCCGGA
Environmental sequence XZS115708.b1	AAFX01022269.1	808-886	TTTCGACAAAGGCACCCCGGTCGTGAGGCCGGTCCGCAAAGCAAGGGATCTCCGAGGTGGAGACAGCCCTGCCGCCGAA
Environmental sequence XZS24728.x1	AAFX01065385.1	658-754	AGCGACAAAAGGCAAACCCGCCTAAAGGCGGGGACGCAAAGCTCCGAAGCTAAAGCTGTGTACTCCGGAAAGCAGCCAGGCTGGTCGAGCTACCGAA
Environmental sequence XZS29341.x1	AAFX01072742.1	371-297	CTTCCGAAACGGCAAACCGGTCGCGAGGCCGGGACGCAAAGCAACGGATCTCCTCGAGATAGCCGTGCTACCGAA
Environmental sequence XZS29341.x1	AAFX01072742.1	782-707	CTTCCGAAAGGGCCAACCAGTCGCGAGGCTGGTGCGCAAAGTCAGACTTCTCACGCAGAAGTGGCTGACTGCCGAA
Environmental sequence XZS29341.y1	AAFX01051910.1	90-183	TCGCGATAAGGGCAAACCCGCTGAAAGGCGGGGACGCAAAGCTCCGAGGCTAAAGCGGTGGAAAGTCCATCGCCATGCCGGTCGAGTTACCGAA

Environmental sequence XZS29962.y1	AAFX01119316.1	250-171	TTTCGACGAGGGCACCCCGGCCGCGAGGCCGGTCCGCAAAGCCACGGGTCTCCTGACCGGGAGATGGCCGGGTTGTCGAA
Environmental sequence XZS33963.y1	AAFX01103928.1	230-153	CCCCGACAAGAGCAAACCCACGGTGACGTGGGGACGCAAAGTCACGGGCCAGCGAAAGCTGATAGCCGGACTGCCGAA
Environmental sequence XZS34958.b1	AAFX01035207.1	214-290	CTTCCGAAAAGGCAATCCGGCTGCGAGGCTGGTGCGCAAAGCTGATTTCTCACGCAGAGAAACGTCCAGCTGCCGAA
Environmental sequence XZS34958.b1	AAFX01035207.1	567-643	CTTCCGAAAAGGCACCCCGGCTGTGAAGCCGGTCCGCAAAGCCCAGGATCTCAATCCGAGACAGCCGGGTTTCCGAA
Environmental sequence XZS39783.b1	AAFX01042002.1	359-448	TCCGATAAAAAGCAAACCTGAGGAAACTCAGCGACGCAAAGTCATGGGTCTACGTCTCGTTCTACGGGATATGATCGCCAGACTACCGAT
Environmental sequence XZS39783.b1	AAFX01042002.1	540-624	CTAACCGAAAGGCAAACACAGGGAAACCTGTGGGCGCAAAGTTATGGGTCTAAAGTCGGATGACCAGGACTGCCAGACTGCCGAA
Environmental sequence XZS43929.x1	AAFX01029204.1	425-527	TTTTGATAAGGGCAAACTGAACCGAAAGGTTCTGCGCGCAAAGTTACCGGTCTAACGATCGAGCGTCTGCAAGATGCCGATCCATGATTGCGGGGCTGCCGAA
Environmental sequence XZS45527.y1	AAFX01035547.1	121-212	TCGCGACAAAGGCAAAGTCGCTGAAAGGCGGTGACGCAAAGCCTCGGGGCTACAGCGTGCGCAGGGCACGCCATGCCAGCCGGGCCGCCGAC
Environmental sequence XZS47381.b1	AAFX01060826.1	640-727	CGCTGCCCAGAGCAAACCGGTTGGAAACACCGGGACGCAGAGCCACGGAGCTTCGGCGCACACGCGCCATGCCAGCCGGGCCGCCAGC
Environmental sequence XZS52754.b1	AAFX01027005.1	533-615	CGACGACAAAGGCAAACCCATCGCGAGGTGGGGACGCAAAGCTTCCGGTCTTGCGCAGAGCGTAAGACAGCGGAGTTACCGAA
Environmental sequence XZS56734.b1	AAFX01068332.1	106-22	AAACGACAAGGGCACACCTCGTGTGAACGAGGCTCGCAAAGCCGACAGAGGTCATGGACCGTTATTGACCTGGCTGGGTACCGAA
Environmental sequence XZS57554.b1	AAFX01029657.1	103-193	GTTCGATAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCATGGGTCTACCGTCACACGTTTGTGACTACGATAGCCAGGTTGCCGAA
Environmental sequence	AAFX01027420.1	114-37	ACACGACAAAGGCAAACCCTCGGTGACGGGGGGGCGCAAAGCCCACGGGTCTGCACGTCAGACGGCCGGGCTGCCGAA

XZS72112.b1			
Environmental sequence XZS89381.y1	AAFX01098341.1	792-705	ATCGGATGAAGCCAAAACCGGTGAAAGCCGGCGACGCAAAACCATGGTCTAACCGTCACAAAGTGACTATGACCCCAAGGCCGCCGAA
Environmental sequence XZS92507.b1	AAFX01019119.1	769-857	GCGCCTCAAGGGCAAACCCATCGAAAGGTGGGGACGCAAAGCCTCCGGGCTAATGGTTCGCGAGAACCAATGCTAGCGGGGCCGCCGGC
Epibiont metagenome Alv_AA_004_C11.y01	AAUQ01088527.1	217-136	GAGCTACAAGGCCAAACCCGTCGTGAGACGGGGACGGAAAACCATGGGTCTCCAGCTTGCTGGAGATCGCCAGGTTGCCGGT
Epibiont metagenome Alv_AB013_F01.y01	AAUQ01123481.1	377-303	TTTTGTTAAAGCCAAACCTGCCGTGAGGTAGGGACGGAAAGTCACAGGTCTTACCAAGACAGCTGGACTGCCTTC
Epibiont metagenome Alv_LSA_034_B05.x01	AAUQ01060006.1	83-158	TTTTGTTAAAGCCAAACCGTGCTGTGAGGTAGGGACGGAAAGTCACAGGTCTTACCAAGATAGCTGGACTGCCTTT
Epibiont metagenome Alv_LSA_098_F08.y01	AAUQ01032159.1	251-325	CTATGTCAAAGCCAAACTCGTTGCGAAACGGGGACGGAAAGCTACGGGTCTCTAGCAGATAGCCGGGTTACCATG
Epibiont metagenome ALV_LSA_109_E13.X01	AAUQ01123772.1	205-122	AACTGTTAAAGCTAAACCTATTGTGAAATAGGGACAGAAAGTCACAGGTCTTTTTAACTTATACTAAGACGGCTGGCTGCCCTT
Epibiont metagenome Alv_LSA_178_B02_D03.y01	AAUQ01126501.1	26-100	TAAGATAGTCGCCAAACTGGTCGAGAGGTCAGGACGGAAAGCCACGGGTCTTGTAGAGATAGCCGGGTTGCAACA
Epibiont metagenome Alv_LSA_182_N11.x01	AAUQ01051993.1	754-636	AAGGTTAGTCCCCAAATCTGTTGTGAAGCAGGGACGGAAAGCTATGGGTCTTATCCTCAAATAACAATAATATCCAAATCTAGATTGGTCGAAGTGGATAAGATTGCCAGGTTGCCATC
Epibiont metagenome Alv_LSA_184_J16.x01	AAUQ01020220.1	33-117	GGTAAGTGTGGCCAACCTATCGCAAGGTAGGGACGGAAAGCCACGGGACTCTGCAAATTTTAAAAGAGTTAGCCGGGTTGCCTCT
Epibiont metagenome Alv_LSA_247_G12.y01	AAUQ01039183.1	600-681	GTAGTAAATAGCCAAACCAATCGCGAGGTTGGGACGGAAAGCCTTGGGTCTTAATTAAATAGAAGATTGCCAGGTTGCCACT

Epibiont metagenome ALV_LSA_347_I06.y01	AAUQ01059428.1	79-2	GTGTTTATTTGCCAAACCTATCGCGAGGTAGGGACGGAAAGGCCATGTAAAGCTCAAGGAGATCGACAGGTTGCTAAA
Epibiont metagenome ALV_LSA_396_J12.x01	AAUQ01061271.1	74-1	TAATGAAAAGGCCAAACCTGTTGCAAAATAGGGACGGAAAGCCACGGAGGTCTTGTAGATAGCCGGGTTGACCA
Epibiont metagenome ALV_LSB_173_A09.x01	AAUQ01090257.1	93-175	GAGCTACAAGGCCAAACCCGTCGTGAGAGCGGGGACGGAAAACCATGGGTCTCCAGCTTGCCTGGAATCGCCAGGTTGCCGGT
Epibiont metagenome Ctg1022.2	AAUQ01001550.1	1553-1638	GTAAAGTGTGGCCAAACCTATCGCAAGGTAGGGACGGAAAGCCACGGGACTCTGCAAATTTTAAAAGAGTTAGCCGGGTTGCCTCT
Epibiont metagenome Ctg1316.1	AAUQ01021274.1	921-1002	GTAGTAAATAGCCAAACCAATCGCGAGGTTGGGACGGAAAGCCTTGGGTCTTAATTAAATAGAAGATTGCCAGGTTGCCACT
Epibiont metagenome Ctg19241.1	AAUQ01076621.1	419-497	ATTTGAAAAGGCCAAACCATCCGTGAGGGTGGGACGGAAAGCCACGGATCTTAATTAATAAGACAGCCGGGTTGCCAAA
Epibiont metagenome Ctg2012.2	AAUQ01016272.1	1214-1140	CTGTGTTAAAGCCAAATTCGTCGCGAGGCGGGGACGGAAAGCCACGGGTCTCTCTGAGATAGCCGGGTTGCCATA
Epibiont metagenome Ctg2036.2	AAUQ01029484.1	925-999	CTATGTTGTGGCCAAATTCGTCGCGAGGCGGGGACGGAAAGCCACGGGTCTCTCTGAGATAGCCGGGTTGCCATA
Epibiont metagenome Ctg2354.2	AAUQ01092265.1	84-10	CTATGTTAAAGCCAAATTCGTCGCGAGGCGGGGACGGAAAGCCACGGGTCTCTCTGAGATAGCCGGGTTGTCATA
Epibiont metagenome Ctg3910.1	AAUQ01009368.1	695-621	CTACGTTAAGGCCAAATTCGTCGTGAGGTGGGGACGGGAAGCCACGGGTTTCTCTGAGATAGCCGGGTTATCATA
Epibiont metagenome Ctg4370.1	AAUQ01032061.1	278-359	GAGCTACAAGGCCAAACCCGTCGTGAGACGGGGACGGAAAACCATGGGTCTCCAGCTTGCTGGAGATCGCCAGGTTGCCGGT
Epibiont metagenome Ctg647.2	AAUQ01000252.1	5041-4952	AACTGTTAAAGCTAAACCTATTGTGAAATAGGGACAGAAAGTCACAGGTCTTTTTAACTTAAATGTAACTAAGACGGCTGGACTGCCCTT
Epibiont metagenome	AAUQ01011702.1	1423-1349	TAATGAAAAGGCCAAACCTGTTGCAAAATAGGGACGGAAAGCCACGGATCTCTTGTAGATAGCCGGGTTGCCATA

Ctg866.3			
Epibiont metagenome Ctg908.1	AAUQ01000609.1	4009-3927	AAATGTAGTTGCCAAACCTACTGTGAAGTGGGGACGGAAAGCCAATGAGTCTTGATTAAGTACAAGATAGTCAGGTTGCCACT
Epibiont metagenome Ctg9365.1	AAUQ01069258.1	333-249	AGGCATTAAAGCCAAACCATTCGTGAGAATGGGACGGAAAGCTACGGGTCTCTCGATGTTTTGAAGAGATAGCCGGGTTGCCATA
Ethanoligenens harbinense YUAN-3	CP002400.1	58174-58090	AAAATGTATCGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAATGTTTCATCACGATGATAGCCGGGTTGCCTTT
Ethanoligenens harbinense YUAN-3	CP002400.1	2083110-2083198	TATCAGAAAAGGCAAACTGACCGAAAGGCAGGGGCATAAAGCCAAGAGTCTAAGGTAAATAAACGTACTATGATAGTCTGGTTGCAAAA
Ethanoligenens harbinense YUAN-3	CP002400.1	44570-44660	TATTGTAAATAGCAAACTTGTCGAAAGGCAGGGGCGCAAAGCTACGGGTCTAATGCTTCCGTTCGGAAGCGATGATCGCCGGGTTGCCATT
Eubacterium cellulosolvens 6 ctg00005	AEOA01000041.1	2611-2529	TTAATTGCATAGCAAACCTGTAGTGATGCAGGGACGCAAAACCGTGAGTCACGAGGTTGTTTCGTGATTGTCTGGCTGCATTC
Eubacterium cellulosolvens 6 ctg00006	AEOA01000049.1	5379-5297	TTAATTACATAGCAAACCTGTAGTGATGCAGGGACGCAAAACCGTGAGTCACGCGTTCGGTGCGTGATTGTCTGGCTGCATTC
Eubacterium cellulosolvens 6 ctg00012	AEOA01000061.1	3000-3082	TTAATTGCATAGCAAACCTGTAGTGATGCAGGGACGCAAAACCGTGAGTCACGAGGCAGTTTCGTGATTGTCTGGCTGCAATC
Eubacterium cellulosolvens 6 ctg00051	AEOA01000012.1	47756-47830	TCAAATCAAAGGCAAAACAGACGAAAGTCTGTGACGCAAAACTATAGGGGCCGAAATAGCCAGCCAGTTGCATTC
Eubacterium cellulosolvens 6 ctg00060	AEOA01000026.1	43622-43547	AATAGTGTATGGCAAAACAGACGAAAGTCTGCGACGCAAAGCTAAAGGGACTGTAAAATGTCAGCCAGCTGCAATA
Eubacterium eligens ATCC 27750	CP001104.1	398951-399037	TTAATATGTTGGCAAAGTAGTCGAAAGGCTATGACGCAAAGCCAAGGGTCTTAACTGATTTTATCAGAATGACAGCCGGTTGCATTA

Eubacterium eligens ATCC 27750	CP001104.1	1345607-1345470	AAGTAAATATGGCAAACTTATAGAAATATAAGGACGCAAAACTAGAAGTCTAGAGGTATAAAGCTGAAAAACACTATTTTCAGTTGAGAGATTCACATAAGCATAAGTCTCTAATACTATGATAGTTCGGTTGCATTA
Eubacterium eligens ATCC 27750	CP001104.1	545635-545750	ACAAAAGAGGGGTAAACCTGCAGAAATGCAGGGACACAAAGCTACAAGTCTAAGTTGATTCAGTAGTCTGGGGAGTATTGGATATATTGAAGATATAAGATGGTTGAGTTGCAGAT
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont31.1	ACEP01000029.1	46847-46922	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGATGCATAA
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont365.1	ACEP01000106.1	6720-6802	TGTTCTAGTGGGCAAACCTTGTGAAAGCAGGGGACGCAAAGCCAAGGGTCTAAGGGCATAGCCTATGACAGCCGGTTGCCGCG
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont53.1	ACEP01000048.1	3328-3234	TTTATATTTGGGTAAAACTGTCGAAAGGCAGCGACACAAAGCCAAATGGGTCTAAGGTTCATTTTTTAAGAGAATTATGACAGCCGGTTGCATCA
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont54.1	ACEP01000049.1	11891-11966	TAGGATAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGTCTTTAAAATGGCAGCCAGCTGCATGA
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont78.1	ACEP01000072.1	439-349	ATTATTTAAAGGCAAATCTGCTGAAAGGCAGGGACGCAAAGTTAGAAGGGGCTAAAGTCAGAAAGATTGACCAGGTCAGCCAGTTGCCACT
Eubacterium hallii DSM 3353 E_hallii-1.0_Cont78.1	ACEP01000072.1	10388-10313	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTACATGA
Eubacterium limosum KIST612	CP002273.1	3827128-3827035	TTGTTCAAAAGGCAAAGCGGTGCGAAAGCCCGTGGCGCAAAACTACAGGGTCTACGTCGGAAGCTCCAGGCCGATATGACAGCCAGATGCCACA
Eubacterium limosum KIST612	CP002273.1	2529297-2529210	ACGTAAAAAGGGCAAATCTGTTGAAAGGCAGAGACGCAAAACTAAAGGGCCTAAAACCGGTAACCGGTAATGGCAGCCAGCTGCTACG
Eubacterium limosum KIST612	CP002273.1	1003350-1003430	TTAATATCAGGGCAAATCTGTTGAAAGACAGAGACGCAAAGCTAAAGGGCCTAAACAACCACTATCAACTGGGCTGCAGTT
Eubacterium limosum KIST612	CP002273.1	4247327-4247414	TTTGAAATAGGGCAAAACTACTGAAAGGTAGTGACGCAAAGCCAAGGGTCTAATTCATCTCAAGATGAAACGACAGCCGGTTGCTCGG

Eubacterium rectale ATCC 33656	CP001107.1	255854-255958	ATCAAATTAGGGCAAACTTATGGAAACGTAAGGACGCAAAACATGAAGTCTAAGTAATAAAATAAAATACACGTATTTTATTATATTGACGGTTCGGTTGCAATG
Eubacterium rectale ATCC 33656	CP001107.1	551418-551509	TGTATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACGGAGTAACATTTATGTAATGACAGATCGGCTGCAACA
Eubacterium rectale ATCC 33656	CP001107.1	553720-553811	CGTATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACGGAGTAACATTTATGTAATGACAGATCGGCTGCAACA
Eubacterium rectale ATCC 33656	CP001107.1	549360-549451	CATATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACGGAGTAACATTTATGTAATGACAGATCGGCTGCAACA
Eubacterium rectale ATCC 33656	CP001107.1	3157371-3157283	TAACCATAAAGGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Eubacterium rectale ATCC 33656	CP001107.1	3151655-3151567	TAACCATAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Eubacterium rectale ATCC 33656	CP001107.1	769967-770055	TAACCATAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Eubacterium rectale DSM 17629 draft genome.	FP929042.1	237482-237573	CGTATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACGGAGTAACATTTATGTAATGACAGATCGGCTGCAACA
Eubacterium rectale DSM 17629 draft genome.	FP929042.1	505578-505666	TAACCATAAAGGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Eubacterium rectale DSM 17629 draft genome.	FP929042.1	169765-169853	TAACCATAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Eubacterium rectale DSM 17629 draft genome.	FP929042.1	235157-235248	CGTATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACAGAGTAATATTTATGTAATGACAGATCGGCTGCAACA
Eubacterium rectale M104/1 draft genome.	FP929043.1	1314013-1313914	ATGAAATATGGGCAAACTTATGGAAACATAAGGACGCAAAGCATGAAGTCTAAGTAATAAAATGTGCACATTTTATTATATTGATGGTTCGGTTGCAATG
Eubacterium rectale M104/1	FP929043.1	2434515-2434427	CACCTATCAAGGCACACTTATGGAAACATAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACACGATGTAATGACAGATCGGCTGCATCA

draft genome.			
Exiguobacterium sp. AT1b	CP001615.1	1052296-1052220	CACTGATAATGGCAAAACTACGCGAAAGCTAGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTTCCAAA
Exiguobacterium sp. AT1b	CP001615.1	1190640-1190725	TATCGAGACGGGCAAACTTACTGAAAAGTAAGGGCGCAAAGACATGGGTCGTCGATCTTTTAGATACCGATCGCCAGTCTGCAATA
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont1.5	ACOP02000031.1	16629-16554	GAATATCCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont1.5	ACOP02000031.1	16830-16755	GAATATTCTCGGCAAAACAGTCGAAAGGCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGCTGCTTCT
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont2.7	ACOP02000047.1	24777-24703	CAGAAGAATCGGCAAACCAGCTGGAAGGCTGCGACGCAAAGCTAAAGGGCCCAGACCGGGCAGCCAGCTGCACTT
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont3.16	ACOP02000057.1	13486-13411	TTGAAGAACCGGCAAACCAGCCGAAAGGCTGCGACGCGAAGCTATAGGGCCTGTAAGATGGCAGCCAGTTGTATTT
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont4.4	ACOP02000073.1	63838-63914	CTGAAGAATCGGCAAGCCAGTCGAAAGGCTGCGACGCAAAGCTACAAGGGCCTGTAATATGGCAGCCAGCCGCACGT
Faecalibacterium prausnitzii A2-165 F_prausnitzii-1.0.1_Cont6.6	ACOP02000082.1	2089-2164	AGAAAAAAACGGCAAACCAGTCGAAAGGCTGCGACGCAAAGCTACAGGGCCTGTAATATGGCAGCCAGCCGCACTT
Faecalibacterium prausnitzii	FP929045.1	3143612-3143705	AATCGTTGTTGGCAAACCTGATGTGAGTCAGGGACGCAAAGCCAGGAGCTTTCTGCTTTATTTCCTGCAAGCAGAAGGTAGTTCGGCTGCAATA

L2/6 draft genome.			
Faecalibacterium prausnitzii L2/6 draft genome.	FP929045.1	2779134-2779225	CTTAATACTTGGTAAACCTACCGAAAGATAGGGCAACAAAGCCAAATGAGTCTAAAATCTCATATACGAGGTCATGGCAGCTGGTTGCTTTT
Faecalibacterium prausnitzii L2/6 draft genome.	FP929045.1	2072446-2072371	TAGAATATTTAGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGTAGCCAGTTGCATTT
Faecalibacterium prausnitzii M21/2 F_prausnitzii_M212-2.0.1_ Cont30.1	ABED02000012.1	2557-2651	GCAATTTTTTGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCCATAGGGGCTAAGGTTCGGGGCATTTCCCGGATGATGCCAGCCGGTTGCTTCC
Faecalibacterium prausnitzii SL3/3 draft genome.	FP929046.1	1805030-1805124	GCAATTTTTTGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCCATAGGGGCTAAGGTTCGGGGCATTTCCCGGATGATGCCAGCCGGTTGCTTCC
Ferrimonas balearica DSM 9799	CP002209.1	739797-739890	ACGTGATAAAGGCAAACCCGGCGAAAGCCGGTGACGCAAAGCCACCGGCCTAAGGTGCCCCTGTAGGGGGTGCGATGGCAGCGGGGCTACCGCA
Ferrimonas balearica DSM 9799	CP002209.1	2762199-2762116	CGACGAAAAAGGCAAACCAGGTGAAAGCCTGGGACGCAAAGCCTCCGGTCTAAGGTGAACGCTATCGATAGCGGGGCTGCCGAG
Ferrimonas balearica DSM 9799	CP002209.1	2783819-2783902	CTGTGATAAAGGCAAACCGGTCGAAAGGCCGGGACGCAAAGCCTCCGGTCTAAGGGCATCGCCTAAGATAGCGGGGATACCATA
Filifactor alocis ATCC 35896	CP002390.1	860021-859940	TAATTTTTCCGTCAAAGCATTTGAAAGAATGTGACGCAAAGCTAAAGTGCTTAAGTTAATTATATGGTTGCCAGTTGCACGT
Fish metagenome 9220464	ABMZ01023210.1	1-92	CGACAAAGGCAAAGCTGGCGAAAGCCAGTGACGCAAAGCTAAAGGGGCTTCCTTGTCCTGCAAATCGGACTCGCAGCCAGCCAGCCGCCGAA
Fish metagenome 9485294	ABMZ01002837.1	12-92	CCACGATAATGGCAAAACCGTTTAAAGGCGGTGACGCAAAGCTAGAGGGGCTAAGGGAAACTATGCCAGCCAGCTATTAAA
Fish metagenome 9503073	ABNA01040436.1	45-101	AATGAACAAAGGCAAATCCATCGAAAGGTGGAGACGCAAAGCCACGGGTCTAAGCCA

Fish metagenome 9509352	ABNA01033708.1	1-82	AAGCTGGCGAAAGCCAGTGACGCAAAGCTAAAGGGGTCTTCCTTGTCCTGCAAATCGGACTCGCAGCCAGCCAGCCGCCGAA
Fossil metagenome sequence DNPX6MG02DRVOW	CAAM02049685.1	66-1	CACTGAAAATGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCAACGGGCCTACGGGCCGGCACTGA
Freshwater metagenome 43458779	ABMW01042130.1	42-1	TGATGAAAATGGCAAACTACGTGAAAGCGTAGGACGCAAAAC
Freshwater metagenome 43885243	ABMW01041290.1	3-76	GGCAAACTTGTCGAAAGACAAGGACGCAAAGCTTCCGGCCTAAGGTCTTCGATCATGGTAGCGGGGTTTCCAAG
Freshwater metagenome 43888827	ABMW01158621.1	80-1	TATTTTAAAAGGCAAACTGTATGAAAATGCAGGGCGCAAAGCCACATATCTGACGGTACAAGTTACACAAGAACGATGAG
Freshwater metagenome June_2007_contig01412	ADVU01001405.1	171-231	TACTGACAAAGGCAAACCCGCCGAAAGGCGGCGGCGCAAAGCTACAGGGCCTACCGGCGCG
Freshwater sediment metagenome lwFormaldehyde_BCIB16902_y1	ABSN01036975.1	361-279	TTTGACTAAGACCAAACCTGCCGTAAGGCAGAGACGGAATGTTACGGGTCTTGGCCTAATTCCAAGATAGCCGGACTGCCGAG
Freshwater sediment metagenome lwFormaldehyde_BCIB27858_b1	ABSN01046431.1	108-182	GTTATGGAAGGCCAAACCTATCGCAAGGTAGGGGCAGAAAGTCGCGGATCCCATGCGGAAAGCCGGACTGCCGAA
Freshwater sediment metagenome	ABSN01015815.1	21186	CACCGATAAAGGCAAACCCTGAGTGATCGGGGGGCGCAAAGTAAAGGGTCTTAAACTT

lwFormaldehyde_BCIB2841_b1			
Freshwater sediment metagenome lwFormaldehyde_BCIB29667_b1	ABSN01049753.1	226-311	CCTCGATAAGGGCAAACCGACAGCAATGTCGGGGCGCAAAGCCAAGGGCCGACGTTCTTCGGAGCGGCGGCAGCCTGGTTGCCGAA
Freshwater sediment metagenome lwFormaldehyde_BCIB32539_b1	ABSN01055035.1	510-595	AGTAAAAAAGGGTAAACCCGACTGAAAAGCGGGGACGCAAAGCTACCGGTCTAAAGGAGAAATTCCATGACAGCGGGGTCACCGAA
Freshwater sediment metagenome lwFormaldehyde_BCIB34510_b1	ABSN01058586.1	679-604	GACACGAAAAGGCACACCCGTCGCGAGACGGGGCCGCAAAGCTACGGGCCTGGAAACAGGCGGCCGAGCTGCCGAT
Freshwater sediment metagenome lwFormaldehyde_BCIB42387_b1	ABSN01070577.1	628-706	AATATTTAAAGCCAAACCTAACGTAAGTTAGGGACGGAATGTTACGAATCCAAACGGTTTGGAAAGTCGGACTGCCGAG
Freshwater sediment metagenome lwFormaldehyde_BCIB7115_y1	ABSN01023000.1	411-491	TAAATTAAATGCCAAACCTATTGTAAAGTAGGGACGGAAAGCCACGGGTCCTAAGATGTTCAGGATGGCCGGGTTACGATT
Freshwater sediment metagenome lwFormaldehyde_BHFI7763	ABSN01004832.1	594-507	GTCTGAAAAGGGCAAACCCGCCGCAAGGCGGGGACGCAAAGCCTCCGGTCCGGGCCGCAAGTGAGCGACGGATAGCGGGGTTGCCAGC

_g1			
Freshwater sediment metagenome lwFormaldehyde_BHFI8094_b1	ABSN01005451.1	71-1	CTGGCGAAATGGCACACCCGCTGCGAGGCGGGGTCGCAAAGCCACGGGTCTCCTGCTCCAGGACGACCGCC
Freshwater sediment metagenome lwFormaldehyde_BHFI8094_b1	ABSN01005451.1	214-302	TTCGTACAAGGGCAAACCCATCGAAAGGTGGGGACGCAAAGCTTCCGGGCTACCGACTGAAATCAGTCCATGCCAGCGGGGTTGCCGGC
Freshwater sediment metagenome lwFormaldehyde_BHFI8452_b1	ABSN01006073.1	811-732	ATAACGCCAACCACGCCGAAAGGCGTGCACGAAAAGCCGCGGATCTCCCAGAACTGATCTGAGACAGCCGGGCTGCCGAA
Freshwater sediment metagenome lwFormaldehyde_BHFI9017_g1	ABSN01007106.1	521-597	TTTTTTTAAGGCCAAACCTATTGTAAGGTAGGGGCAGAAAGTCGCGGGTCCTATCAACGGAAAGCCGGACTACCGAA
Freshwater sediment metagenome lwFormaldehyde_C1055	ABSN01001055.1	373-288	ATATTTAAAGGGCAAACTCGACTGAAAAGCGAGGACGCAAAGCCTCCGGTCTAAAGGAGAAATCCTATGACAGCGGGGCCACCGTA
Freshwater sediment metagenome lwFormate_BCIX894_g1	ABSO01011129.1	274-348	AGGCGTAAAGGGCAAACCACTTGCGAAGGTGGGGCGCAAAGCTACAGGGCTCTCAGAGCCGGCTGGGCTGCCGCC
Freshwater sediment metagenome	ABSO01011567.1	290-395	AACAAGAAAAGGCACACCCGTTGAAAGGCGGGGCCGCAAAGCCACGGAGCCTCATCGCATCCGCCACAACGACGTGGCGGCCGCGACGGCGAGCCGAGCTGCCGAG

lwFormate_BCIX9362_b1			
Freshwater sediment metagenome lwMethane_BCGO10124_x1	ABSP01016915.1	460-546	TCCTGCACAGAGCAAACCCGGGGCGACCCGGGGACGCAGAGCCACGGGGCCCCCGCGAAGAGGGCGGGGGTCAGCCGAGCCGCCGGG
Freshwater sediment metagenome lwMethane_BCGO11720_x1	ABSP01019593.1	117-24	CTGAAAACAGGGCAAACCCGCCGAAAGGCAGGGGCGCAAAGTCACCCGCCTAAAGGACGCAGCAAGCGCGTCACATGGCAGCGGAACCACCAGG
Freshwater sediment metagenome lwMethane_BCGO15226_y1	ABSP01025478.1	869-792	TTTTACTAAAGCCAAACCTATTGTAAGTTAGGGGCAGAAAGTCGCGGATCCAGAATAACGGAAAGCCGGACTGCCGAA
Freshwater sediment metagenome lwMethane_BCGO20968_y1	ABSP01035114.1	135-57	AAAAATTAAAGCTAAACCCACCGTGAGTTGGGGGCAGAAAGTTGCGAATCCAGAATGTTTGGAAAGTCGGACTGCCGAG
Freshwater sediment metagenome lwMethane_BCGO23047_x1	ABSP01038606.1	131-221	CCTCGATAACGGCACGACGATCGAAAGGTCGCTCACGCAAAGCTTTGGAGCCTCGCGGCGCTCGCGCGCCTACGGCAGTCCGGCCGCCGAA
Freshwater sediment metagenome lwMethane_BCGO25644_y1	ABSP01042952.1	785-700	TCTTGATCGCGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCTCCGGTCCGAGGGACGGATGTCCTGGATAGCGGGGTTGCCCAG

Freshwater sediment metagenome lwMethane_BCGO26278_y1	ABSP01044018.1	238-321	TGATAGCAACGCCAAACCTATCGTAAATTAGGGACGGAAAGTCGCGTATCCAGACTAAGAATAATGGAAAGCCGGACTGCCGAA
Freshwater sediment metagenome lwMethane_BCGO26841_y1	ABSP01044985.1	654-567	ACTGATCAAGGGCAAACCCGCCGGAAGGCGGGGACGCAAAGCCTCCGGTCCTCGGGCGTGACGCGCCACGGATAGCGGGGTTGCCAGT
Freshwater sediment metagenome lwMethane_BCGO27296_x1	ABSP01045765.1	124-41	TGCATTTAAGGTCAAACCTGTTGAAAAACAGGGGCGCAAAGTTACCAGTCTAAGGGTTTATACCTAAGACAGTGGGGTGCCGTT
Freshwater sediment metagenome lwMethane_BCGO27771_x1	ABSP01046580.1	581-504	GATAATCAATACTATACCTATGGTAACGTAGGGACAGAAAGTCACGGGTCCTAAATTTAGGAAAGCCGAACTGCCGAG
Freshwater sediment metagenome lwMethane_BCGO27843_y1	ABSP01046708.1	295-373	AAATAATAACGCCAAACCTATCGTAAGGTAGGGACAGAAAGTTGCGGATCCTCTGATTCAGGAAAGCCGGACTGCCGAA
Freshwater sediment metagenome lwMethane_BCGO28164_x1	ABSP01047252.1	410-495	TCTGATAAAGGGCAAACCCGATCGAAAGGCGGGCTCGCAATGTCACCGGTCTAAAGGCGAAAGCCAATGACGGCGGGACTGCCAGA
Freshwater sediment	ABSP01051733.1	671-745	ATCAGAAAACGCCAAACCTGTCGCGAGGCAGGGACGGAAAGCCACGGATCTCTCGAAGACCGCCGGGTTGCCTGA

metagenome lwMethane_BCGO31799_y1			
Freshwater sediment metagenome lwMethane_BCGO31910_x1	ABSP01051928.1	584-507	AAATAATAAAGCTAAACCTATCGGAAGGTAGGGACAGAAAGTCGCGGATCCCGAATCACGGAAAGCCGGACTACCGAG
Freshwater sediment metagenome lwMethane_BCGO9377_y1	ABSP01016195.1	210-130	TTCCCGAAAAGCCAACCGCGCCGTGAGACGCGTGCGGAAAGCCACGGATCCCGCGAGACGCGGGACAGCCGGGTTGCCGAA
Freshwater sediment metagenome lwMethane_C384	ABSP01000384.1	580-658	ATTTATTAAAGCCAAACTTATTGTAAGGTAGGGGCAGAAAGTTACGGATTCCATACAAACGGAAAGCCGAACTGACGAA
Freshwater sediment metagenome lwMethenol_BCHA11409_y1	ABSQ01018261.1	232-145	GTCTTGCGGGGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCCAGCGGGCCTTCGGTCCTCAGGGATCAAGGTGGCCGGGCTGCCAGG
Freshwater sediment metagenome lwMethenol_BCHA13039_y1	ABSQ01020420.1	401-315	TGTTTCAATGGGCAAAACCATCGAGAGATGGTGACGCAAAGCCTCCGGCCCACACGCTCGCACGCGATGGGTAGCGGGGTTGCCAGT
Freshwater sediment metagenome lwMethenol_BCHA14489_y1	ABSQ01022178.1	248-172	TAAAAATCATACTAAACCTATGGTAACGTAGGGACAGAAAGTTATGGATCCTGATTCAGGAAAGCCGAACTGCCGAG

Freshwater sediment metagenome lwMethenol_BCHA14514_x1	ABSQ01022225.1	607-519	CCGGTCGAAGGGCACACCCGCCGCGAGNCGGGGCCGCAAAGCCACAGCTCTTGATCGTCAATTGAGAACAAGAGGGCTGGGCTGCCGCC
Freshwater sediment metagenome lwMethenol_BCHA20496_y1	ABSQ01031933.1	655-731	ATAAAAAAAAGCCAAACCTATTGTAAGGTGGGGGCAGAAAGTCGCGAGTCCTATCAGCGGAAAGCCGGACTGCCGAG
Freshwater sediment metagenome lwMethenol_BCHA22305_x1	ABSQ01033693.1	429-503	TGCCGATCAAGCCAAACCCGTCGTGAGACGGGGACGGAAAGCCACGGGTCCACCGGGGATAACCGGGTTGCCGAA
Freshwater sediment metagenome lwMethenol_BCHA23196_y1	ABSQ01035196.1	249-340	GCACGAAAAAGGCAAACCATCCGAAAGGGTGGGACGCAAAACTACGAGGGCCTTCGTCGCTCGAGAGAGCGAAAAGGCAGCCAGTTGCCGAA
Freshwater sediment metagenome lwMethenol_BCHA23557_x1	ABSQ01035821.1	535-449	GTCTGTAAAGGGCAAACCCAGCGAAAGCTGGGGACGCAAAGTCACCGGTCTAAGGGGCGCAGGCCCTACGATAGCGGGATTGCCGGA
Freshwater sediment metagenome lwMethenol_BCHA31557_x1	ABSQ01047381.1	903-787	AAGGGCATACCCGCCGAAAGNCGGGGACGCAAAGCCACCGGTCTAACGACGGTGCGCGCTGGCGCGGCGAGGGATCGCTGCGGCATCGACACCGTCCACGACAGCGGGGCTGCCGAG
Freshwater sediment	ABSR01014820.1	687-770	AGTTGTTAAAAGCAAACTTATCGAAAGGTAAGCACGCAAAATTACCGGTCTACAGGCTTATGCCATGACAGCGGGATTGCCGGC

metagenome lwMethylamine_BCHP12100_g1			
Freshwater sediment metagenome lwMethylamine_BCHP30330_g1	ABSR01027696.1	351-425	TCACCGAACAGGCACACCCGGAGCGATCCGGGGTCGCAAAGCCGAGGGTCTCTCAGAGACAGCCTGGCTATCGAA
Freshwater sediment metagenome lwMethylamine_BCHP41198_g1	ABSR01034994.1	779-862	AGTTGTTAAAAGCAAACTTATCGAAAGGTAAGCACGCAAAATTACCGGTCTACAGGCTTACGCCATGACAGCGGGATTGCCGGC
Freshwater sediment metagenome lwMethylamine_C1984	ABSR01001984.1	4860-4773	ATTTGAAAAAGGCAAACTCTGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTCAGTTCTAAGATAGCGGGAGTACCAGA
Freshwater sediment metagenome lwMethylamine_C340	ABSR01000340.1	798-885	ATTTGAAAAAGGCAAACTCTGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTAAGTTCTAAGATAGCGGGAGTACCAGA
Freshwater sediment metagenome lwMethylamine_C3444	ABSR01003444.1	717-630	ATTTGAAAAAGGCAAACTCAGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTAAGTTCTAAGATAGCGGGAGTACCAGA
Freshwater sediment metagenome lwMethylamine_C4760	ABSR01004760.1	1664-1751	ATTTGAAAAAGGCAAACTCTGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGCAAGTTCTAAGATAGCGGGAGTACCAGA
Freshwater sediment metagenome	ABSR01000491.1	1307-1220	ATTTGAAAAAGGCAAACTCTGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTAAGTTCTAAGATAGCGGGAGTACCAGA

lwMethylamine_C491			
Freshwater sediment metagenome lwMethylamine_C5141	ABSR01005141.1	613-700	ATTTGAAAAAGGCAAACTCAGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTAAGTTCTAAGATAGCGGGAGTACCAGA
Freshwater sediment metagenome lwMethylamine_C5455	ABSR01005455.1	1071-1154	AGTTGTTAAAAGCAAACTTATCGAAAGGTAAGCACGCAAAATTACCGGTCTACAGGCTTATGCCATGACAGCGGGATTGCCGGC
Fusobacterium ulcerans ATCC 49185 cont1.5	ACDH01000005.1	9304-9229	ATTATAATTTAGCAAAATAACAGAAATGCTATGACGCAAAGCTATAGGGCCTGTAAGATGGCAGCCAGTTGCAATT
Fusobacterium ulcerans ATCC 49185 cont1.5	ACDH01000005.1	11055-10980	TTATATCCTTGGCAAAATAACAGAAATGTTATGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCAATT
Fusobacterium ulcerans ATCC 49185 cont1.5	ACDH01000005.1	20810-20735	CATTTTTTATGGCAAAGTAATGGAAACATTACGACGCAAAGCTATAGGGCCTGTAAAGTGGCAGCCAGTTGCAATT
Fusobacterium varium ATCC 27725 cont2.1	ACIE02000001.1	78742-78667	GTTAAAATTCGGCAAAGTAATGGAAACATTATGACGCAAAGCTATAGGGCCTGTAAAATGGTAGCCAGTTGCAATT
Fusobacterium varium ATCC 27725 cont2.1	ACIE02000001.1	80448-80373	TTAATTTCTTGGCAAAGTAATGGAAACATTATGACGCAAAGCTATAGGGCCTTTTAAATGGCAGCCAGTTGCAATT
Fusobacterium varium ATCC 27725 cont2.1	ACIE02000001.1	90203-90128	GATATTTTACGGCAAAGTAATGGAAACATTATGACGCAAAGCTATAGGGCCTGTTAAATGGTAGCCAGTTGCAATT
Gamma proteobacterium NOR51-B ctg_1109846220915	ACCY01000019.1	226517-226430	GCTGCTTAAAGGCAACCCCGCTGAAAGGCGGGCAACGCAAAGTCACGGGTCTAACGGGCGCATGCCCTATGACAGCCGGACTGCCGAT
Gamma proteobacterium	ACCY01000023.1	22592-22505	GCTGCTTAAAGGCAACCCCGCTGAAAGGCGGGCAACGCAAAGTCACGGGTCTAACGGGCGCATGCCCTATGACAGCCGGACTGCCGAT

NOR51-B ctg_1109846220919			
Gamma proteobacterium NOR51-B ctg_1109846220919	ACCY01000023.1	38522-38439	TAGCAAAAAGGGCATGACCATCGAAAGGTGGTGGCGCAAAGTTACCGGCCTAAGGGCAAAACCTACGGCAGCGGGATTACCGGA
Gamma proteobacterium NOR51-B ctg_1109846220919	ACCY01000023.1	33529-33444	CATGCACAAGGGCAAACCCATCGAAAGGTGGGGACGCAAAGTTTCCGGCCTACCGAGCAAGCCTCCAAGGTCGCGGGATTGCAACG
Gemmata obscuriglobus UQM 2246 gcontig_1106221708081	ABGO01000202.1	369-275	TCCTCGAAAGGGCTAACCCGCTGCGAAGCGGGGGCGCAAAGCCACGGGCCTGCGGTCTCCCCACCACACCGACCGCAGGTCGCCTGGTTGCCGAA
Geobacillus sp. C56-T3	CP002050.1	3363364-3363282	TCATGATAAAGGTACAGCTAAGGAAACTTAGCGTCACAAAGCTACAGGGGCTAAGGGGAAACCTATGCCAGCCAGCTGCCATT
Geobacillus sp. C56-T3	CP002050.1	3278494-3278579	ACGGCGAAAAGGCAAAGCGCTGGAAACAGCGTGGCGCAAAGCTAAAGGGGCTACGGCGAAAGACGCTATGCCAGCCAGCTGCCGAA
Geobacillus sp. Y412MC52	CP002442.1	3342925-3342843	CATGATGAAAGGTACAGCTAAGGAAACTTAGCGTCACAAAGCTACAGGGGCTAAGGGGAAACCTATGCCAGCCAGCTGCCATT
Geobacillus sp. Y412MC52	CP002442.1	3240798-3240883	ACGGCGAAAAGGCAAAGCGCTGGAAACAGCGTGGCGCAAAGCTAAAGGGGCTACGGCGAAAGACGCTATGCCAGCCAGCTGCCGAA
Geobacillus sp. Y412MC61	CP001794.1	3336956-3336874	CATGATGAAAGGTACAGCTAAGGAAACTTAGCGTCACAAAGCTACAGGGGCTAAGGGGAAACCTATGCCAGCCAGCTGCCATT
Geobacillus sp. Y412MC61	CP001794.1	3234829-3234914	ACGGCGAAAAGGCAAAGCGCTGGAAACAGCGTGGCGCAAAGCTAAAGGGGCTACGGCGAAAGACGCTATGCCAGCCAGCTGCCGAA
Geobacillus thermoglucosidasius C56-YS93	CP002835.1	3310199-3310288	AATATAAATCAGCAAACTACTCGAAAGGGTAGGACGCAAAACTAAAGGGGCTAAATCTATTCTCAATAGACATGCCAGCCAGTTGCCCTT
Geobacter bemidjiensis Bem	CP001124.1	2736237-2736160	CACACGAAAAGGCAAACCCAGGGTAACCTGGGGACGCAAAGCCACCTGTCCAGCATTCTGGAAAGAGGGGTTGTCGAA
Geobacter bemidjiensis Bem	CP001124.1	3197829-3197905	AGACGACAATACTAAACCATCCGCGAGGATGGGACGGAAAGCCTACAGGGTCTCCAAGAGACAGCCGGGTCGCCGAA

Geobacter bemidjiensis Bem	CP001124.1	649730-649654	ACACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTATAGGGTCTCCCTGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	2079950-2080025	CAACGACAATACTAAACCATCCGTGAGGATGGGACGGAAAGCCCACGGGTCTCCCTGAGACAGCCGGGTCGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	2499141-2499065	ACACGATAATACTCAACCACTCGCGAGGGTGGGGCGGAAAGCCTACAGGGTCTCCTTGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	382539-382615	ATACGACAATACTAAACCTTCCGCGAGGATGGGACGGAAAGCCTATAGGGTCTCACTGAGACAGCCGGGTCGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	1256047-1255971	ACACGACAATACTAAAACTTTCGCGAGAAAGTGACGGAAAGCCTATTGGGTCTCACGAAGACAGCCGGGTCGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	4525108-4525184	AGACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTATAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	2076757-2076832	CAACGACAATACTAAACCACCTGCGAAGGTGGGACGGAAAGCCCACGGGTCTCCCTGAGACAGCCGGGTCGCCGAT
Geobacter bemidjiensis Bem	CP001124.1	1375451-1375527	AAACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACAGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	2179000-2178925	GACGACAAATGCTAAACCATCCGCGAGGATGGGGCGGAAAGCCCAAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	2179188-2179112	AGACGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCCACGAGACAGCCGGGTCGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	4525294-4525370	ACACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTATTGGGTCTCTCTGAGACAGCCGGGTTGCCGAA
Geobacter bemidjiensis Bem	CP001124.1	3434379-3434303	TAACGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACTGGGTCTCATAGAGACAGCCGGGTCGCCGAA
Geobacter lovleyi SZ	CP001089.1	2534834-2534760	TCACCGAAAAGGCAAAATCCAGGGGACTGGATGACGCAAAGCCACCTACCCGGACCGGGAAGAGGGGTTACCGAA
Geobacter lovleyi SZ	CP001089.1	2146051-2145975	ACACGATAATACTAAACCATTCGCGAGGATGGGACGGAAAGCCTACAGGATCTCTCTGAGACAGCCGGGTCGCCGAA
Geobacter lovleyi SZ	CP001089.1	1534181-1534105	TATCGATACTACTAAACTATCCGTGAGGATAGGACGGAAAGCCTACAGGGTCTCACCGAGACAGCCAGGTCGCCGAA
Geobacter lovleyi SZ	CP001089.1	645064-645139	ATACGAAAATACTCAACTACCCGCGAGGGTAGGGCGGAAAACCCACGGGTCTCTCTGAGACAGCCGGGCTACCGAA
Geobacter lovleyi SZ	CP001089.1	213210-213134	CCCTTTAAAGAGCAAAATCAGGGTGACCTGATGGCGCAAAATCACGGGTCCCATGAAAGGATAGCCGGATTACTGAT
Geobacter metallireducens GS-15	CP000148.1	2280692-2280768	AGACGACAATACTCAACCATCCGTGAGGATGGGGCGGAAAGCCTATTGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	2447619-2447695	ACACGACAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCCAGCAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	265065-264989	AGACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCATAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	158170-158246	AGACGATAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCCCCGAGACAGCCGGGTCGCCAAA

Geobacter metallireducens GS-15	CP000148.1	1324478-1324402	AGTCGATAATACTAAACCATTCGTGAGAATGGGGCGGAAAGCCTACAGGGTCTTACTGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	325755-325831	AGACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCTTCGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	3913272-3913348	AGACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCCCTGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	3913064-3913140	AGACGACAATACTTAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCATGGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1911272-1911348	AGACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAACCCACAGGGTCTCCCTGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1212049-1211973	TAGCGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCATCGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	827292-827209	TTTCCGAGAGGGCAAACTTCGGGTAACCGGAGGACGCAAAGCCACGGGTCCTGACTCCATGGTCAGGATAGCCGGGTTGTCGAA
Geobacter metallireducens GS-15	CP000148.1	1079465-1079541	TATCGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCTCTGAGACAGCCGGGATGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1977793-1977869	AGACGATAATACTCAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCATGCAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1623888-1623688	ACCAGTAAAGGCCAAAACACGGGTAACCGTGTGACGGAAAGCCTACGGGTCCACGAGACGGATTCGATTTTTGACGGAGACCAAGGCGGCGAGGAGGAGGCGACGGAGGCGTACCTGAAGGTACGTTGAGGAGCCCCGCACGAGCCAACGCCGGTATACGTCAGAAGGCGAATCCGGCCGATGGATGGCCGGGTTGCCTGG
Geobacter metallireducens GS-15	CP000148.1	824437-824354	TTTCCGAAAGGGCAAACTTCGGGTAACCGGGGGACGCAAAGCCACGGGTCCTGACTCCATGGTCAGGATAGCCGGGTTGTCGAA
Geobacter metallireducens GS-15	CP000148.1	271494-271418	ACACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA

Geobacter metallireducens GS-15	CP000148.1	1334239-1334315	AGACGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCCCCGAGACAGCCGGGTCGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1212229-1212153	TAGCGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCATCGAGACAGCCGGGTTGCCGAA
Geobacter metallireducens GS-15	CP000148.1	1324617-1324541	AGACGACAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTACAGGGTCTTATTGAGACAGCCGGGTTGCCGAA
Geobacter sp. FRC-32	CP001390.1	1962097-1962021	AGACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTAAAGGGTCTCTCTGAGACAGCCGGGTTGCCGAA
Geobacter sp. FRC-32	CP001390.1	1198050-1198127	TTGACGAAAAGGCAAAGCACGGGTAATCGTGTGACGCAAAGCTACCTGTCCAGAAGCCTGGAAAGAGGGGCCGCCGAA
Geobacter sp. FRC-32	CP001390.1	3538288-3538364	AGACGACAATACTAAACCATTCGCAAGGGTGGGACGGAAAGCCTACAGGGTCTTACTGAGACAGCCGGGACGCCGAA
Geobacter sp. FRC-32	CP001390.1	3356677-3356601	TAACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCAAGCAGACAGCCGGGTTGCCGAA
Geobacter sp. FRC-32	CP001390.1	158336-158260	AGACGATAATACTCAACCATTTGCAAGAATGGGGCGGAAAGCCTATAGGGTCTTACTGAGACAGCCGGGTTGCCGAA
Geobacter sp. FRC-32	CP001390.1	2319947-2320023	AGACGATAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCCATTGGGTCTCATCGAGATAGCCGGGTCGCCGAA
Geobacter sp. FRC-32	CP001390.1	1868595-1868511	TTTCCGAAAGGGTAATCTGGAAGAAATTCCAGTGACACAAAGCATACGGATCTGTTATTAACTAACAGATAGCCGGGCTGCCGAA
Geobacter sp. FRC-32	CP001390.1	3607979-3607903	AGACGATAATACTAAACCACCTGCGAAGGTGGGGCGGAAAGCCTAATGGGTCTCAAGGAGACAGCCGGGTTGCCGAA
Geobacter sp. FRC-32	CP001390.1	3014666-3014591	AGACGACAATACTAAACCATTCGCGAGAATGGGGCGGAAAACCCATGGGTCTCCTGTAGACAGCCGGGCTGCCGAA
Geobacter sp. M18	CP002479.1	4751536-4751459	TCTCCGAACGGGCAAAGCCAGAGTGATCTGGTGACGCAAAGCCACGGGTCCTGACACAAGGATAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	2018597-2018673	ACACGACAATACTAAACCATTCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCTCTGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	4032452-4032528	ACACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCATTGGGTCTCAAGGAGACAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	5044342-5044266	TAACGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCATCGGGTCTCACGCAGACAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	1280784-1280873	TTTCCGAAACGGTAAACTTGGAAGAAATTCCAAGGGCACAAAGCTGACGGACCCGTTACCTAAAAAATAACAGGTAGCCGAGCTACCGAA
Geobacter sp. M18	CP002479.1	1214376-1214301	AAACGATAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTAAGGGTCTCAACGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	315514-315436	GTGAGATAAGGGCAAACCGGAGCAATCCGGCGACTCAAAGCCACGGGTCCCCTGCAGCGGGGACAGCCGGGTTACCGAA
Geobacter sp. M18	CP002479.1	3835282-3835206	AAACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTATTGGGTCTCCCTGAGACAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	1214179-1214103	ACACGATAATACTAAACCACTCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCAACGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	5044142-5044066	AGACGATAATACTAAACCGCCCGCGAGGGTGGGGCGGAAAGCCCATAGGGTCTCACTGAGACAGCCGGGTTGCCGAA

Geobacter sp. M18	CP002479.1	1337425-1337504	ACACCGAAAAGGCAAACCTGGGGTGACCCGGGGACGCAAAGCCACCTATCCAGGAAAGCCTGGAAAGAGGGGCTATCGAA
Geobacter sp. M18	CP002479.1	4751318-4751240	TCTCCGAACGGGCAAAGCCAGAGTAATCTGGTGACGCAAAGCCACGGGTCCTGACACAAGGGACAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	3146404-3146480	AGACGATAATACTAAACCATCCGCGAGGATGGGACGGAAAGCCTACAGGGTCTCAACGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	1576719-1576643	AAACGACAATACTAAACCATCCGCGAGGATGGGACGGAAAACCTACAGGGTCTCACAGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	4751085-4751008	TCTCCGAACGGGCAAAGCCAGAGTAATCTGGTGACGCAAAGCCACGGGTCCTGAGACAAGGATAGCCGGGTTGCCGAA
Geobacter sp. M18	CP002479.1	2017161-2017237	AGACGATAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACAGGGTCTCACTGAGACAGCCGGGTCGCCGAA
Geobacter sp. M18	CP002479.1	4501775-4501699	TAACGATAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTACTGGGTCTCATAGAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	1725760-1725684	AGACGACAATACTAAACCATCCGCGAGGATGGGACGGAAAGCCTACAGGGTCTCCAAGAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	675289-675213	AGACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTATAGGGTCTCCCTGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	3585644-3585568	AGACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCCCAGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	513439-513518	TCTCCGAACTGGCAAACCCAGAGTAATCTGGTGACGCAAAGCCACGGGTCCTGAACTTACAGGATAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	2163539-2163616	CACACGAAAAGGCAAACCCAGGGTAACCTGGGGACGCAAAGCCACCTGTCCAGCATTCTGGAAAGAGGGGTTGTCGAA
Geobacter sp. M21	CP001661.1	2404320-2404396	ACACGATAATACTCAACCACTCGCGAGGGTGGGGCGGAAAGCCTACAGGGTCTCCTTGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	3691135-3691211	TAACGACAATACTAAAACTTTCGCGAGGAAGTGACGGAAAGCCTATTGGGTCTCACGCAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	1448421-1448497	ACACGACAATACTAAACCACTCCGCAAGGGTGGGACGGAAAGCCTAAGGGTCTCACCGAGACAGTCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	359887-359963	ATACGACAATACTAAACCTTCCGCGAGGATGGGACGGAAAGCCTATAGGGTCTCACTGAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	2863132-2863057	CCGCGACAATACTAAACCATCTGCGAAGATGGGACGGAAAGCCCAAGGGTCTCTCTGAGACAGCCGGGTCGCCGAT
Geobacter sp. M21	CP001661.1	2709731-2709807	AGACGAAAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCTAAAGGGTCTCCACGAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	2709923-2709998	GACGACAAATGCTAAACCATCCGCGAGGATGGGGCGGAAAGCCCAAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	512997-513076	TCTCCGAACGGGCAAAACCAGAGTAATCTGGTGACGCAAAGCCACGGGTCCTGATGTTACAGGATAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	513975-514054	TCTCCGAACGGGCAAAGCCAGAGTGATCTGGTGACGCAAAGCCACGGGTCCTGGACTGACAGGATAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	4660637-4660713	AGACGATAATACTCAACCATCCGCGAGGGTGGGGCGGAAAGCCTATAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	4660821-4660897	AGACGATAATACTCAACCATTCGCGAGGATGGGGCGGAAAGCCTATTGGGTCTCTCTGAGATAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	378592-378668	ACACGACAATACTAAACCATCCGTGAGGGTGGGACGGAAAGCCTATTGGGTCTCACCGAGACAGCCGGGTCGCCGAA
Geobacter sp. M21	CP001661.1	1448204-1448280	ACACGACAATACTAAACCATCCGTGAGGGTGGGACGGAAAGCCCATAGGGTCTCAACGAGACAGCCGGGTCGCCGAA

Geobacter sp. M21	CP001661.1	2863574-2863498	AGACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCAACGAGACAGCCGGGTTGCCGAA
Geobacter sp. M21	CP001661.1	513222-513301	TCTCCGAACAGGCAAAGCCAGAGTGATCTGGTGACGCAAAGCCACGGGTCCTGCACTTACAGGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	166135-166059	AAACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	1681079-1681003	ACACGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCACCGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	1889823-1889898	ACACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTAAGGGTCTCCCTGAGACAGCCGGGTCGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	1117928-1117852	ACACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCACCGAGACAGCCGGGTCGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	2104756-2104666	TTTCCGAAGGGGTAAACCCAGGGTAACCTGGGGACACAAAGCTACGGGTCCTGAAATGTCCTAGGGTTTTCAGGATAGCCGGGTTGGCGAG
Geobacter sulfurreducens KN400	CP002031.1	1070932-1070849	TTTTCGAAGAGGTAAACCCCGGGCAACCGGGGGGCACAAAGCTGCGGGTCCCGCCAGAAACAGCGGGACAGCCGGGTTGGCGAA
Geobacter sulfurreducens KN400	CP002031.1	2195974-2195898	TATCGATAATACTAAACCATCCGTGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	1319879-1319954	AGACGATAAGACTAAACCACCCGCGAGGGTGGGGCGGAAAGCCCACGGGTCTCTCTGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	2107501-2107410	TTTCCGAAGAGGTAAAACCAGGGTAACCTGGTGACACAAAGCCACGGGTCCTGAAATCGTCCTAGGTATTTCAGGATGGCCGGGTTGGCGAA
Geobacter sulfurreducens KN400	CP002031.1	2105023-2104947	ACACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	1052331-1052407	ACACGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCCACAGGGTCTCTCTGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens	CP002031.1	166334-166258	AGACGACAATACTCAACCATTCGCGAGAATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA

KN400			
Geobacter sulfurreducens KN400	CP002031.1	3063293-3063219	ACACGATAAGACTAAACCGTCCGCGAGGGCGGGGCGGAAAGCCTAGGGTCTCCTAGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	2107711-2107635	AGACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCCACGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	3063478-3063404	AGCCGATAAGACTAAACCATCCGCGAGGGTGGGGCGGAAAGCCCAGGGTCTCAAGGAGATGGCCGGGATGCCGAA
Geobacter sulfurreducens KN400	CP002031.1	2659769-2659689	CTCCGAAAAGAGTAAACCCATCGCAAGGTGGGGACACAAAGCCGACGGGTGCCGCTGGAGCGGGACGGCCGGGTTGCCGGA
Geobacter sulfurreducens PCA	AE017180.1	1348999-1349074	AGACGATAAGACTAAACCACCCGCGAGGGTGGGGCGGAAAGCCCACGGGTCTCTCTGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	2133695-2133619	ACACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACAGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	1922655-1922730	ACACGACAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTAAGGGTCTCCCTGAGACAGCCGGGTCGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	2760060-2759980	CTCCGAAAAGAGTAAACCCATCGCAAGGTGGGGACACAAAGCCGACGGGTGCCGCTGGAGCGGGACGGCCGGGTTGCCGGA
Geobacter sulfurreducens PCA	AE017180.1	3169147-3169073	AGCCGATAAGACTAAACCATCCGCGAGGGTGGGGCGGAAAGCCCAGGGTCTCAAGGAGATGGCCGGGATGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	2133429-2133339	TTTCCGAAGGGGTAAACCCAGGGTAACCTGGGGACACAAAGCTACGGGTCCTGAAATGTCCTAGGGTTTTCAGGATAGCCGGGTTGGCGAG
Geobacter sulfurreducens PCA	AE017180.1	2773389-2773465	TAGCGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCACGAAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	2225994-2225918	TATCGATAATACTAAACCATCCGTGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA

Geobacter sulfurreducens PCA	AE017180.1	2136377-2136301	AGACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTATAGGGTCTCCACGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	1081543-1081619	ACACGACAATACTAAACCATCCGCGAGGGTGGGACGGAAAGCCCACAGGGTCTCTCTGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	198072-197996	AGACGACAATACTCAACCATTCGCGAGAATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	3168962-3168888	ACACGATAAGACTAAACCGTCCGCGAGGGCGGGGCGGAAAGCCTAGGGTCTCCTAGAGACAGCCGGGATGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	1147037-1146961	ACACGACAATACTAAACCATCCGCGAGGATGGGACGGAAAGCCCACAGGGTCTCACCGAGACAGCCGGGTCGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	1100143-1100060	TTTTCGAAGAGGTAAACCCCGGGTAACCGGGGGGCACAAAGCTGCGGGTCCCGCCTGAAACAGCGGGACAGCCGGGTTGGCGAA
Geobacter sulfurreducens PCA	AE017180.1	197873-197797	AAACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter sulfurreducens PCA	AE017180.1	2136167-2136076	TTTCCGAAGAGGTAAAACCAGGGTAACCTGGTGACACAAAGCCACGGGTCCTGAAATCGTCCTAGGTATTTCAGGATGGCCGGGTTGGCGAA
Geobacter sulfurreducens PCA	AE017180.1	1711433-1711357	ACACGATACTACTAAACCATCCGCGAGGATGGGGCGGAAAGCCCACAGGGTCTCACCGAGACAGCCGGGATGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2694571-2694495	AGACGATAATACTAAACCATTCGCGAGAATGGGACGGAAAGCCTAAAGGGTCTCACCGAGACAGCCAGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	247508-247587	CCGACGAAAAGGCAAAGCACGGGCAACCGTGTGACGCAAAGCTACCTGTCCAGTTGCAACTGGATAGAGGGGCTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	458192-458116	ACGCGATACTACTAAACCACCCGCGAGGGTGGGGCGGAAAGCCCACAGGGTCTTTAAAAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens	CP000698.1	2980387-2980463	TCTAGATAAAGCCAAAACCCGGGTAACCGGGTGACGGAAAGCCACGGGCCCTGCGAATGGGCAGCCGGGTTGCCTGG

Rf4			
Geobacter uraniireducens Rf4	CP000698.1	3544154-3544233	TCCCGACAAAGCCAACCCCTTCGTGAGGGGGGGAACGGAAAGCCACGGGCCTCCGGAATGGAGACAGCCGAGCCGCCAAA
Geobacter uraniireducens Rf4	CP000698.1	2785587-2785665	TTCCGACAAAGCCAAACCCTTCGCGAGGAGGGGGCGGAAAGCGGCGGGTCTTCGCGACGAAGATGGCCGAGCTGCCGAG
Geobacter uraniireducens Rf4	CP000698.1	2843136-2843059	TACCGAAAAAGCCAAACCTTTCGTGAGAGGGGGGCGGAAAGCAACGGGTCTTCAGATGAAGATGGCCGGGCTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	838672-838748	AGACGATAATACTAAACCATTCGTGAGAATGGGGCGGAAAGCCTATAGGGTCTCGAAGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	838444-838520	AGACGATAATACTAAACCATTCGCGAGAATGGGGCGGAAAGCCTAATGGGTCTCGAAGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2005281-2005205	AAACGATAATACCAAACCATCCGCGAGGATGGGACGGAAAGCCTACAGGGTCTCAAGAAGACAGCCGGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2097368-2097444	TAACGATAATACTAAACCATCCGCGAGGATGGGGCGGAAAGCCTATAGGGTCTCACGCAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	3601373-3601294	TCTCCGAACGGGCAAAACCAGAGTAATCTGGTGACGCAAAGCTACGGGTCCTGACCTAAAAGGATAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	323123-323198	AGACGATACTACTAAACCATCCGCGAGGATGGGACGGAAAGCCACAGGATCTCCAGAAGACAGCCGGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2356611-2356687	AGACGATAATACTTAACCATCCGCGAGGGTGGGGCGGAAAGCCTAAAGGGTCTCCATGAGATAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	626595-626519	AGACGATAATACTAAACCATCCGCGAGGATGGGACGGAAAGCCTACAGGGTCTCATGAAGACAGCCGGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2790589-2790512	AGACGATAATACTAAACCATCCGTGAGGATGGGGCGGAAAGCCTAAAGGGTCTCAAGCCAGACAGCCGGGTTGCCGAA

Geobacter uraniireducens Rf4	CP000698.1	626391-626315	AAACGATAATACTAAACCATCCGTGAGGATGGGACGGAAAGCCTATAGGGTCTCATGAAGACAGCCGGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2518900-2518824	AAACGATAATACTCAACCATCCGCGAGGGTGGGGCGGAAAGCCTACAGGGTCTCACTGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2885785-2885709	AGACGATAATACTAAACCACCTGTGAAGGTGGGGCGGAAAGCCTATTGGGTCTCCAGGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2697411-2697487	AGACGATAATACTAAACCATCCGCAAGGATGGGGCGGAAAGCCTAAAGGGTCTCACTGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2035506-2035430	AGCCGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACTGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2356837-2356914	ACACGATAATACTAAACCATCCGTGAGGGTGGGGCGGAAAGCCTATAGGGTCTCAAGTCAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	3600589-3600510	TCTCCGAACGGGCAAAACCAGAGCAATCTGGTGACGCAAAGCCACGGGTCCTGACCTAAAAGGATAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2692038-2691962	AGACGAAAATACTAAACCATTCGCGAGAATGGGACGGAAAGCCTAAAGGGTCTCACCGAGACAGCCGGGTCGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	463577-463498	TCACGATAAAGCCGAACCCTCCGCAAGAAGGGGGCGGAAAGTCGCGGGTCTTCGCAGTGGAAGACGGCCGGACTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	3898438-3898514	AGACGACAAGGCTCAACCATTCGTGAGAATGGGGCGGAAAGCCCATCGGGTCTCCACGAGACAGCCGGGTTACCGAA
Geobacter uraniireducens Rf4	CP000698.1	2519084-2519009	AGACGATAATACTTAACCATTCGCAAGAATGGGGCGGAAAGCCTACGGGTCTTACTGAGACAGCCGGGTTGCCGAA
Geobacter uraniireducens Rf4	CP000698.1	2025185-2025022	GACTTGAAATGCCAAACCTTGAGCAATCAGGGGACGGAAAGCCAACGGGACTTGGGTTCCAATGAATTCCAATGAATTGACTCCGTCTGTCATTGAATCTGCTTTCCCTTGTTAATATAGTTTCTCCACAAGATGTTATTCTCCAAGTTGGCCGGGTTGCCGTT
Geobacter uraniireducens	CP000698.1	3601129-3601051	TCTCCGAACGGGCAAAACCAGAGTAATCTGGTGACGCAAAGCCACGGGTCCTGACCTAAAGGATAGCCGGGTTGCCGAA

Rf4			
Grimontia hollisae CIP 101886 VHA.Contig67	ADAQ01000013.1	435861-435954	TCAAGAAAAAGGCAAACCATGGCGAAAGCCTGGGACGCAAAGCTTCCGGCCTCACACGGTATATATTTTACGTGTTGGTAGCGGAGTTACCGAA
Grosmannia clavigera kw1407 contig_10856.0	ACYC01000191.1	501-591	ATTATTCATCGGTAAAACTATTGAAGATAGTGACACAAAGCCAAGGGTCTAAGGTCCTTCCAAACGGGATTATGACAGTCCGGTTGCCACA
Halanaerobium hydrogeniformans	CP002304.1	314539-314628	TAAATATAAAAGCAAAATAGTTGAAAGACTATCACGCAAAAGCTTGAGTCTAAAGGGTTTTAATATTCTATGATCGTCAAGCCTGCCTCG
Halanaerobium hydrogeniformans	CP002304.1	299132-299215	AAAAATAAAAGGCAATTCAATCGAAAGGTTGTTACGCAAAAGTCTGAATCTACGGGGGTACCCTATGATTGTCAGCTTGCCTCA
Halanaerobium hydrogeniformans	CP002304.1	2552413-2552502	TAATATTAATAGCAAAATATTCGAAAGATTATTACGCAAAAGCTTGAATCTAAGGAGTTTTAATATTCTATGATTGTCAAGCCTGCCTCA
Halanaerobium praevalens DSM 2228	CP002175.1	611770-611857	AATAAATATTAGCAAAATTAGCGAAAGTTGATGACGCAAAGTTATGGGTCTAAGATATTTAATATATTATGATTGCCAAACTGCACAG
Halanaerobium praevalens DSM 2228	CP002175.1	187732-187818	TTTTAATAAAAGCAAAACAATTGAAAAATTGTGACGCAAAGATCTGAATCTAAAGCTAAATTAGCAATGATTGTCAGATTCACCTCA
Halanaerobium praevalens DSM 2228	CP002175.1	937363-937448	TAAAATAAAAAGCAAAACAACCTAAAGGTTGTTACGCAAAAACATAGGTCTAAAGCTTTTAAGCCATGACTGTTATGTCTGCCTCA
Haloplasma contractile SSD-17B Contig22	AFNU01000022.1	54226-54303	TAATGTAAAAGGCAGCGTTAGAGAAATCTAAGCGTACGCAAAGCTATAGGGCCTGTAAAATGGTAGCCAGTTGTCATT
Haloplasma contractile SSD-17B Contig22	AFNU01000022.1	53497-53571	GTATGACAAAGCTAAACCCGGAGCGATCCGGCGGCAGAAAACTATAGGGTCTCACGTAGATAGCCAGTTACCTTA

Halothermothrix orenii H 168	CP001098.1	769989-769887	GACCGATAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAACCACGGGCCTGTAGCCTTATATAAAAAAAACTTATATAAGGTATGGCAGCCGGGTTACCGAA
Halothermothrix orenii H 168	CP001098.1	769828-769735	CTCCGGAAATGGTAAACCCATCGAAAGGTGGGGACACAAAGTCACGGGCCTGTAGCCGGTTATTTTTAACCGGTATGGCAGCCGGACTGCCGAA
Heliobacterium modesticaldum Ice1	CP000930.2	120402-120314	CCGTGACAAGGGCAAACCTGCCTAAAGGCCGGGACGCAAAGCCATAGGGTCTAAGGTGCTTAAAGCGCTATGACAGCCTGGTTGCCGCA
Hot springs metagenome ctg6135	AFSR01006659.1	13392-13476	AGCAGAAAAGGGCAAACCTGTAGCGATGCAGGGGCGCAAAGCCTACGGGTCTGTCGTACTCGCGGCAGATGGCTGGGTTGCCTGC
Human gut metagenome DNA	BAAU01014367.1	523-611	TACCCATAAGAGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAGAACAGTTACATGTAGTCCTGACCGTTCGGCTGCAACA
Human gut metagenome DNA	BAAV01015941.1	250-162	TAACCATAAGGGCACACTTATGGAAACGTAAGGCCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Human gut metagenome DNA	BAAV01003376.1	1495-1610	ACAAAAGAGGGGTAAACCTGCAGAAATGCAGGGACACAAAGCTACAAGTCTAAGTTGATTCAGTGGTCTGGGGAGTATTGGATATATTGAAGATATAAGATGGTTGAGTTGCAGAT
Human gut metagenome DNA	BAAV01001975.1	1028-1116	TAACCATAAGGGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Human gut metagenome DNA	BAAW01004042.1	393-479	AAATTTAATAGGCAAACTTAGGGAAATCTAAGGGCGCAAAGCTATAGGGACTAATGTTTTAATAAACTATGTCAGCCAGTTGCCAAA
Human gut metagenome DNA	BAAZ01012664.1	144-218	CAAGTCCACAGGCAAACCCGGTGCAAACCGGCGACGCAAAGCTATAGGGGCCCATCGGGTCAGCCAGTTGCCAAC
Human gut metagenome	BABG01012220.1	305-215	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGTCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGCTTGACCATGTCAGCCGGTTGCCACT

DNA			
Human gut metagenome DNA	BAAY01018648.1	293-368	TAGAATATTTAGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGTAGCCAGTTGCATTT
Human gut metagenome DNA	BAAY01003288.1	2-77	GAATATCCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Human gut metagenome DNA	BAAU01021153.1	820-737	TGTTAAAAGGGGCAAAGCTGTTGAAAAACTGTGACGCAAAGCCAAAGGGACTAAGGCAGTACGCTATGTCAGCCGGTTGCAATA
Human gut metagenome DNA	BAAX01009490.1	528-603	TGAAAACGATGGCAAAGCAGGCGAAAGCCTGTGACGCAAAGCTATAGGGCCTTTCAAATGGCAGCCAGCTGCAACC
Human gut metagenome DNA	BAAW01006249.1	293-212	AATTTAATAGGGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAAAGGGCCTTTTCCTAATGGATGGCAGCCAGTTGCATTT
Human gut metagenome DNA	BAAY01009326.1	687-613	AAATGCTATCGGCAAACCCGGCGCAAGCCGGCGGCGCAAAGCTACAGGGACCCATTGGGTCAGCCAGCTGCAATC
Human gut metagenome DNA	BAAY01001440.1	1679-1604	GAATATCCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Human gut metagenome DNA	BABG01032311.1	322-234	TAACCATAAGGGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAAAGCAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Human gut metagenome DNA	BABE01017342.1	975-887	ATTAGGAAAAGGCAACCGGTGAAAGACAGGGACGCAAAGCCAGAAGGGACTAAAGTCAGAAAGTTGGACCAGGTCAGCCGGTTGCCACG
Human gut metagenome DNA	BABD01024787.1	545-457	CACCTATCAAGGCACACTTATGGAAACATAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACACGATGTAATGACAGATCGGCTGCATCA
Human gut metagenome DNA	BAAY01001646.1	1865-1939	CAGAAGAATCGGCAAACCAGCTGGAAGGCTGCGACGCAGAGCTAAAGGGCCCAGACCGGGCAGCCAGCTGTACTT
Human gut metagenome DNA	BABE01019247.1	234-157	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGTCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGTTTGACCGACGTA

Human gut metagenome DNA	BAAY01001122.1	2291-2382	CTTAATACTTGGTAAACCTACCGAAAGATAGGGCAACAAAGCTAAATGAGTCTAAAATCTCATATACGAGGTCATGGCAGCTGGTTGCTTTT
Human gut metagenome DNA	BABB01000152.1	8484-8568	TTAGCATGATAGCAAACTTATAGAAATATAAGGACGCAAAGTTAGAAATCTAAGGCATATAAGCATAGATAGTTCGGTTGCAATG
Human gut metagenome DNA	BABB01000610.1	5225-5313	TAACCATAAAGGCACACTTATGGAAACATAGGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Human gut metagenome DNA	BAAY01002056.1	2733-2635	CTCATATTTTGGCAAAACCGCCGAAAGGCGGCGACGCAAAGCCAGATGGGTCTAACGCCTCTCCGAATGGAGAATACGCTATGACAGCCGGTTGCACCC
Human gut metagenome DNA	BAAU01015418.1	148-74	CAAGTCCACAGGCAAACCCGGTGCAAACCGGCGACGCAAAGCTATAGGGGCCCATCGGGTCAGCCAGTTGCCAAC
Human gut metagenome DNA	BAAU01005913.1	1649-1574	GAACATTCTTGGCAAAACAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Human gut metagenome DNA	BABG01006932.1	741-829	TAACCATAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACATGTAGTAATGACAGTTCGGCTGCAACA
Human gut metagenome DNA	BAAY01027138.1	877-802	TCAAAGAATCGGCCAACCAGTCGAAAGGCTGCGACGCAAAGCTAAAGGGCCTGTAATATGGCANCCAGCTGCACTT
Human gut metagenome DNA	BABG01009184.1	345-270	TTTATAAATGGGCAAAGCAGTCGAAAGGCTGTGACGCAAAACTATAGGGCCTGTAAAATGGCAGCCAGCTGCAGAA
Human gut metagenome DNA	BABB01000032.1	11550-11638	CACCTATCAAGGCACACTTATGGAAACATAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACACGATGTAACGACAGATCGGCTGCATCA
Human gut metagenome DNA	BAAU01012059.1	639-714	TTGAAGAATCGGCAAACCAGTCGAAAGGCTGCGACGCAAAGCTACAGGGCCTGTAATATGGCAGCTAGCTGCCCTT
Human gut metagenome DNA	BAAV01025425.1	340-265	AAATATATTTAGCAAAGCAGGTGAAAACCTGTGACGCAAAGCTATAGGGCCTTTAAAATGGCAGCCAGTTGCACTT
Human gut metagenome	BABG01008815.1	532-444	AAACGATAATAGCAAACCCACCGAAAGGTGGCGACGCAAAGCTATAGGGCCTTACCCCTCATCGAGAGGGCTGGCAGCCAGTTACCGAA

DNA			
Human gut metagenome DNA	BAAV01008805.1	235-321	TTAATATATTGGCAAAGTAGTCGAAAGGCTATGACGCAAAGCCAAGGGTCTTAACTGATTTTATCAGAATGACAGCCGGTTGCATTA
Human gut metagenome DNA	BAAV01000762.1	3032-3107	TTAAAAATACAGCAGAGCAGCAAAAATCTTGTGACACAAAGCTATAGGGCCTGATATATGGCAGCCAGTTGCAACA
Human gut metagenome DNA	BAAX01001792.1	39-114	TAGAAAGATCAGCAAGCCAGTCGAAAGGCTGCGACGCAAAGCGAAAGGGCCTGTAATATGGCAGCCAGCCGCACGT
Human gut metagenome DNA	BAAV01002604.1	131-55	CTGAAGAATCGGCAAACCAGTCGAAAGGCTGCGACGCAAAGCTACAAGGGCCTGTAATATGGCAGCCAGCCGCACGT
Human gut metagenome DNA	BAAV01005638.1	523-614	TGTATAAAAGGGCACACTTATGGAAACGTAAGGTCGCAAAGCTAGAGTCTAACACGGAGTAACATTTATGTAATGACAGATCGGCTGCAACA
Human gut metagenome DNA	BABB01013864.1	347-435	CACCTATCTTGGCACACTTATGGAAACTTAAGGTCGCAAAGCCTGAGTCTAAAACAGTTACACGATGTAATGACAGATCGGCTGCGTCA
Human gut metagenome DNA	BAAV01015471.1	827-740	AAACGATAATAGCAAACCCGGTGAAAACCGGCGACGCAAAGCTATAGGGCCTTACCCCTGGGAACAGGGCTGGCAGCCAGTTACCGAA
Human gut metagenome DNA	BABA01033305.1	96-171	TAGAATATATAGCAAAGCAGTTGAAAAGCTGTGACGCAGAGCTAAAGGGCCTGTAAAATGGTAGCCAGTTGCATAT
Human gut metagenome DNA	BABD01001177.1	2901-2825	CTGAAGAATCGGCAAGCCAGTCGAAAGGCTGCGACGCAAAGCTACAAGGGCCTGTAATATGGCAGCCAGCCGCACGT
Human gut metagenome DNA	BAAV01014501.1	515-652	AAGTAAATATAGCAAACTTATAGAAATATAAGGACGCAAAACTAGAAGTCTAGAGGTATAAAGCTGAAAAACACTATTTTCAGTTGAGAGATTCACATAAGCATAAGTCTCTAATACTATGATAGTTCGGTTGCATTA
Human gut metagenome DNA	BAAZ01002932.1	945-1031	TTAATATATTGGCAAAGTAGTCGAAAGGCTATGACGCAAAGCCAAGGGTCTTAACTGATTTTATCAGAATGACAGCCGGTTGCATTA
Human gut metagenome DNA	BABA01009840.1	878-803	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA

Human gut metagenome DNA	BABA01028447.1	760-850	CTGAGAGATAGGCAAACCCATCGAAAGATGGGGGACGCAAAGCCGGAAGGGTCTAAGGCGGCGAACGCCGCAATGACAGCCGGTTGTAAGC
Human gut metagenome DNA	BAAY01014683.1	171-95	CTGAAGAATCGGCAAGCCAGTCGAAAGGCTGCGACGCAAAGCTACAAGGGCCTGTAATATGGCAGCCAGCCGCACGT
Human gut metagenome DNA	BABF01002553.1	73-1	TATTAGTAATGGCAAAACTGTCGAAAGGCAGCGACGCAAAGCTAAAGGACGAATTCACCCGGGAAGTCTGCTA
Human gut metagenome DNA	BABB01000741.1	1023-935	CACCTATCAAGGCACACTTATGGAAACATAAGGTCGCAAAGCCAGAGTCTAAAACAGTTACACGATGTAATGACAGATCGGCTGCATCA
Human gut metagenome DNA	BAAU01027867.1	102-27	CTGAAGAATCGGCAAACCAGTCGAAAGGCTGCGACGCAAAGCTACAGGGCCTGTAACATGGCAGCCAGCTGCACGG
Human gut metagenome DNA	BAAX01030081.1	526-451	GAATATTCTCGGCAAAACAGTCGAAAGGCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGCTGCTTCT
Human gut metagenome DNA	BAAX01030081.1	325-250	GAATATCCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Human gut metagenome DNA	BAAU01000896.1	3213-3288	TAGAATATTTAGCAAAGCAGTTGAAAAGCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGTAGCCAGTTGCATTT
Human gut metagenome DNA	BABD01006876.1	1215-1140	AGATATATTCAGCAAAGTAATCGAAAGGTTATGACGCAAAGCTAAAGGGGCTTTAAAATGCTAGCCAGTTGCAATA
Hydra magnipapillata strain 105 ctg1101284715335	ABRM01031829.1	2234-2318	AGTGCTTATGGGTAAACCCGTTGAAAGACGGGGACACAAAGCCACCGACCTACAGCATCAATGCCATGGTAGCGGGGCCGCCAAT
Hydrothermal vent metagenome FOSS10795.x2	ACQI01022275.1	167-70	ATACGATAAAGGCAAACTTGCTGAAAAACAGGGGCGCAAAGTTTCGGGCCTAATGCATTAGTGCTTTAGCTCAATGTAAGGGCGGCCGGACTGCCGAA
Hydrothermal vent	ACQI01023578.1	1-62	GATAAGGGCGCAAGCTATAGGGGCTAAGGCAGTTTTTTCTGCTATGCCAGCCAGCTGCCGGT

metagenome FOSS12552.x2			
Hydrothermal vent metagenome FOSS14305.y2	ACQI01024947.1	716-625	TCCCGATAATGGCAAACCGCCTGAAAAGGCGGGACGCAAAGCTACCGGCCTAAATACCTGATCATCCGGTGTATGGCAGCGGGGCTATCGAA
Hydrothermal vent metagenome LCHCB.C2194	ACQI01002194.1	2641-2719	ATTTAACATGGGCAAACCGGTCGAAAGGCTGGGGCGCAAAGCTATGGGCCTAAATCTTTTTTGATATGGTTGCCAGGTT
Hydrothermal vent metagenome LCHCB.C235	ACQI01000235.1	99-19	CAACATTGAAGCCAAACTTATTGTGAGATAAGGACGGAAAGCCGTGGATCTTGTAGTCAACAAGACTGCCTGGTTACTCAA
Hydrothermal vent metagenome LCHCB.C3667	ACQI01003667.1	1152-1233	AACTTGATGTGCCAAACTTGTTGTGAAGCAGGGACGGAAAGCCATGGGTCTCGGTCTGAATCGAGATCGCCAGGTTGCAAAA
Hydrothermal vent metagenome LCHCB.C4499	ACQI01004499.1	1203-1294	ACAATCTATTGCCAAACTTCGTGTGAACGTAGGACGGAAAGTTACAGGTCTTAATTGCTTTAAAAACAATTCAAGATGGCTGAACTGCATTT
Hydrothermal vent metagenome LCHCB.C762	ACQI01000762.1	1971-1897	ATAATGCTGTGCCAAACTTGCTGTGAAGCAGGGACGGAAAGCCATGGGTCTCCTCGAGATCGCCAGGTTGCCATA
Hylemonella gracilis ATCC 19624 Contig33	AEGR01000054.1	7557-7473	CATGAGGCAAGGCACACCTGCGCGAAAGCCAGGGTCGCAAAGCTACCGGTCTACGTCCAGACGACACGACAGCGGGGTTGCCAGA
Hylemonella gracilis ATCC 19624 Contig42	AEGR01000064.1	1711-1614	TTCTTCCCAAGGCACACCTGTCCGAAAGGCGGGGTCGCAAAGCCACCGGTCTAACGCAGCGGCGCGAAGCGCACTGACACGATAGCGGGGCTGCCAGG
Hylemonella gracilis ATCC 19624 Contig8	AEGR01000102.1	86229-86131	ATCACACAAAGGCACACCCGAGCGAAAGCCGGGGTCGCAAAGCTTCCAGTCTAAAGTAGCTCGCGGACCGCGAGCCGCCAAGATCGTGGGGCCGCTGTC
Hypersaline lake metagenome contig00001	AGBJ01000001.1	35352-35278	TATTGAAAAAGCCAAGTTCATCGCGAGGTGGGTACGGAAAGTCATGGGTCTCACGTAGATCGCCAGACTACCAAT
Hypersaline lake metagenome contig00051	AGBJ01000051.1	14847-14773	TTTTGAAAAAGCCAAACTTATCGTGAGGTAAGGACGGAAAGCCACGGATCTCAAGAAGATAGCCGGGTCACCAAA

Hypersaline lake metagenome contig00129	AGBJ01000129.1	6923-6849	TAGTTTAACAGCTAAACGCATTGTGAAGTGGGGGCAGAAAACCATAGGTCTTTTCACGATTGCTGGGTTCCAGAC
Hypersaline lake metagenome contig00741	AGBK01000741.1	410-336	GGCCGACAAAGGCAAACTCGGGGTAACCCGAGGGCGCAAAACCACGGGTCCTTACAGGACAGCCGAGTTACCGTA
Hypersaline lake metagenome contig00741	AGBK01000741.1	1237-1159	ACCTGAAAAGGGCAAAACTGCGGCAACGCAGTGACGCAAAGCTCAGGATCCTTACAAAAAGGACGGCCGGGCTGCCAAG
Hypersaline lake metagenome contig01078	AGBJ01001078.1	1926-2004	ATTTTGTTGTGCCAAACTTGTTGTGAAGCAAGGACGGAAAGCTATGGGTCTTAAACATGAAGATCGCCAGGCTGCCAAA
Hypersaline lake metagenome contig01078	AGBJ01001078.1	1771-1848	TATTTGTTGTGCCAAACTTGTTGTGAAGCAAGGACGGAAAGCCATGGGTCTTAACTGCAAGATCGCCAGGTTGCCAAA
Hypersaline lake metagenome contig01178	AGBK01001178.1	944-1031	TCCCGAGAAGGGTAACCCCGCCGGAAGGTGGGCGCACAAAGTCAACGGGCCCCAACCTCGTATAGAGGCGGGCGGCCAGGCTGCCGAA
Hypersaline lake metagenome contig03642	AGBK01003642.1	572-493	TCCCGAGAAGGGTAACCCCGCCGAAAGGTGGGCGCACAAAGTCAACGGGCCCCAACCTCGTATAGAGGCGGGCTGCCGAA
Hypersaline lake metagenome contig05180	AGBK01005180.1	593-506	TGCCGAGAAGGGTAACCCCACTGAAAGGTGGGCGCACAAAGTCAACGGGCCCCAACTTCGTATAGAGGCGGGCGGCCGGGCTGCCGAA
Hypersaline lake metagenome contig05904	AGBK01005904.1	90-3	TCCCGAGAAGGGTAACCTCGCCGGAAGGCGGGCGCACAAAGTCGACGGGCCCCAACCTCGTATAGAGGCGGGCGGCCGGGCTGCCGAA
Hypersaline lake metagenome contig05954	AGBK01005954.1	266-188	TTCACGAAAAGGCAAACTCGGGGTAACCTGAGGACGCAAAACCACGGGTCCTCTCAAAGAGGATAGCCGGGCTGCCGTG
Hypersaline lake metagenome contig05954	AGBK01005954.1	326-272	ATCTATAAATGGCAAACCGGGGGCAACCCCGGGGCGCAAAGCTACGGCCTCTAAG
Hypersaline lake metagenome contig07839	AGBK01007839.1	435-339	CCTTGAAAAAGGCTAAGTTATCGTGAGATAACCTCGCAAAGCCACGGGTCAGTTCATGAGGTGAAGTTTTACAGGAACTGATAGCCGGGTTGCCAGG
Hypersaline lake	AGBK01007888.1	346-438	TCCCGAGAAGGGTAACCCCGCCGGAAGGCGGGCGCACAAAGTCACGGGCCCTACCCTCTAGAAGGAAAAGAGGCGGGCAGCCGGGCTGCCGAA

metagenome contig07888			
Hypersaline lake metagenome contig08518	AGBK01008518.1	398-311	TCCCGAGAAGGGTAACCCCACCGAAAGGTGGGCGCACAAAGTCACGAGCCCTACTCCTTTTAATAGGAAGGGCAGCCGGGCTGCCGAA
Hypersaline lake metagenome contig09049	AGBK01009049.1	120-196	TTCACGAAAAGGCAAACTCCGGGCAACCTGGGGGCGCAAAACCACGGGTCCTCGTAGAGGATAGCCGGGCTGCCGTG
Hypersaline lake metagenome contig09750	AGBK01009750.1	240-153	TCCCGAGAAGGGTAACCCCGCCGGAAGGTGGGCGCACAAAGTCAACGGGCCCCAACCTCGTATAGAGGCGGGCGGCCGGACTGCCGAA
Hypersaline lake metagenome contig11975	AGBK01011975.1	21-102	TGGTCGAAAAGGTAAACCGGACGAACTCCGGGGCACAAAGCTTCCGGGTCCGACAACGATTACGGGCCGCGGAGCTGCCGAA
Idiomarina baltica OS145 1099451322285	AAMX01000014.1	21204-21112	TTGTTTAACTGCCAAACTCATCGCGAGATGAGGACGGAAAGCCACGGGTCTCAGAGTGTGTTGAGATGTATCTCAGATAGCCGGGTTGCGGAA
Idiomarina baltica OS145 1099451322285	AAMX01000014.1	21303-21217	ACTTGAGTCGGCCAAACCCTCCGTGAGGCGGGGACGGAAAGCTTCGGGTCTTCTAAAAATAAAAACGAAGATAGCCGGGTTGCAGCT
Ilyobacter polytropus DSM 2926 plasmid pILYOP01	CP002282.1	410241-410316	TATAGAAAAAAGCAAACCTTTGGAAACAAAGGGACGCAAAGCTATAGGGCCTGTAAGATGGTAGCCAGTTGCCGAA
Ilyobacter polytropus DSM 2926 plasmid pILYOP01	CP002282.1	419280-419205	AAAAAATATCGGCAAACCATTGGAAACAATGGGACGCAAAACTATAGGGCCTTTAAAATGGCAGCCAGTTCCCGAG
Ilyobacter polytropus DSM 2926 plasmid pILYOP02	CP002283.1	7971-8046	CTATATTAATAGCAAACCATTGGAAACGATGGGACGCAAAGCTATAGGGCCTTTAATGTGGCAGCCAGTTACCAAA
Ilyobacter polytropus DSM 2926 plasmid pILYOP02	CP002283.1	47080-47005	AAAAATATTCGGCAAACTAATGGAAATGTTAGGACGCAAAACTATAGGGCCTTTAAAATGGCAGCCAGTTGCAAAA
Ilyobacter polytropus DSM 2926 plasmid pILYOP02	CP002283.1	122888-122974	CTCCGAAAAAGGTAAAACAGGAGAAATCCTGTGACACAAAACTATAGGGTCTAATTCTTTCTTAAGATATGACAGCCAGTTGTCGAG

Ilyobacter polytropus DSM 2926 plasmid pILYOP02	CP002283.1	7218-7143	TGAATTATTTGGCAAACTAATGGAAACGTTAGGACGCAAAGCTATAGGGCCTTTAAAATGGTAGCCAGTTGCAGAA
Kuenenia stuttgartiensis genome fragment KUST_C (3 of 5).	CT573073.1	544510-544431	TTTGAAAAAAGGCAAACCAATTGTGAGGCTGGGACGCAAAGCCATGGGTCTTCAGGAAAGAAGAATGCCAGGTCGCCAAA
Kuenenia stuttgartiensis genome fragment KUST_C (3 of 5).	CT573073.1	545352-545273	TTTGAAAAAAGGTAAACCAATCGTGAGGTTGGGACACAAAGCCATGGGTCTTTCTTAAAGAAGAATGCCAGGTTGCCAGA
Kuenenia stuttgartiensis genome fragment KUST_D (4 of 5).	CT573072.1	134369-134453	TATCGATAAAGGCAAACCCTGAGCAATCAGGGGACGCAAAGTAAAAGGTCTTTACTTACAGTACAAAGATAGCCTTACTACCGAT
Kuenenia stuttgartiensis genome fragment KUST_D (4 of 5).	CT573072.1	491002-491095	GATTGAAAAAGGCAAACCAACCGCAAGTTTGGGACGCAAAGCCATGGGTCTTAAGCGTGAGTTCTTTATACGTAAAGATTGCCAGGTTGCCGAA
Kuenenia stuttgartiensis genome fragment KUST_E (5 of 5).	CT573071.1	309575-309657	ATGTGAAAAAGGCAAACCAATCGTGAGGTTGGGGCGCAAAGCCATGGGGCTTCGGAAATACCGAAGCTCGCCAGGTCGCCATG
Kuenenia stuttgartiensis genome fragment KUST_E (5 of 5).	CT573071.1	153651-153732	TGCATACAAAGGCAAACCAATCGTGAGGTTGGGACGCAAAGCCATGGGTCTTATTTTTTGGAAAGAATGCCAGGTTGCCACC
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.109	ACTP01000109.1	333-248	AACTACATTCGGCAAACTTATTGAAAAGTAAGGACGCAAAAGCTACAGGGCCTTCCCCTTAAAAAGGATGGCAGCCAGCTGCCGGT
Lachnospiraceae bacterium	ACTP01000109.1	519-436	TTTAATACTTGGCAAACTTGCTGAAAAGCAAGGACGCAAAGCTACAGGGCCTTCCCTCAAAGAGGATGGCAGCCAGTTGCCTGA

3_1_57FAA_CT1 cont1.109			
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.141	ACTP01000141.1	673-600	GGCAAACTTGCTGAAAAGCAAGGACGCAAAGCTACAGGGCCTTCCCTCAAAGAGGATGGCAGCCAGTTGCCTGA
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.141	ACTP01000141.1	497-413	AACTACATTCGGCAAACTTATTGAAAAGTAAGGACGCAAAGCTACAGGGCCTTCCCCTTAAAAAGGATGGCAGCCAGCTGCCGGT
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.36	ACTP01000036.1	150469-150544	TATAAATTTTAGCAAAACAGTCGAAAGATTGTGACGCAAAGCTATAGGGCCTGTAATATGGTAGCCAGTTGCAAAT
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.92	ACTP01000092.1	157520-157431	GATTTCATTTGGCAAAGCCGGCGAAAGCCGGTGACGCAAAGCTAGAGGGCCTTGTATCCGTTATTCGGTATGTGGCAGCCAGTTGCAAAA
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.93	ACTP01000093.1	127-42	AACTACATTCGGCAAACTTATTGAAAAGTAAGGACGCAAAGCTACAGGGCCTTCCCCTTAAAAAGGAATGGCAGCCAGCTGCCGGT
Lachnospiraceae bacterium 3_1_57FAA_CT1 cont1.93	ACTP01000093.1	313-230	TTTAACACTTGGCAAACTTGCTGAAAAGCAAGGACGCAAAGCTACAGGGCCTTCCCTCAAAGAGGATGGCAGCCAGTTGCCTGA
Lachnospiraceae bacterium 5_1_63FAA cont1.34	ACTS01000034.1	700-610	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGGCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGATTGACCATGTCAGCCGGTTGCCACT
Lachnospiraceae bacterium 5_1_63FAA cont1.4	ACTS01000004.1	225017-224942	TAAGGAAATTGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Lachnospiraceae bacterium 5_1_63FAA cont1.4	ACTS01000004.1	53398-53311	TTATTCATAGGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAGAAGGGTCTAAGGTCTTATTGGACTATGACAGCCGGTTGCCACA
Lachnospiraceae bacterium 5_1_63FAA cont1.55	ACTS01000055.1	28133-28058	AAAGATTCTAGGCAAAACAGACGAAAGTCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGCAGAA
Leptothrix cholodnii SP-6	CP001013.1	4180402-4180494	TCAATCACAAGGCAAACGGCGTGAAAGCGCCGGACGCAAAGCCACGGGCCCTCAGGCGATTCATCCGATCGCACGGGCAGCCGGGTTGCTTGC
Listeria monocytogenes	CP001602.1	1849552-1849466	TTGTGTTAAGGGTAAACTTGCCGAAAGGCAAGGACGCAAAGCCGAGGGTCTAAGATGCAAACGCATTATGACAGCCTAGCTGCCGTG

08-5578			
Listeria monocytogenes 08-5923	CP001604.1	1816283-1816197	TTGTGTTAAGGGTAAACTTGCCGAAAGGCAAGGACGCAAAGCCGAGGGTCTAAGATGCAAACGCATTATGACAGCCTAGCTGCCGTG
Lysinibacillus fusiformis ZC1 contig00014	ADJR01000014.1	47207-47122	GGGAAATATAGGCAAATTTACTGAAAAGTAAAGACGCAAAGCTACAGGTCTAAGGCAATAAATGCTATGGCGGCTGGGTTGCAAAA
Lysinibacillus fusiformis ZC1 contig00051	ADJR01000049.1	117800-117891	AACTGAAAAAGGCAAACTTCACCGAAAGGGAGGGACGCAAAGCCATGAGTCTAAACACTATAATTTCAGTGCAAGATTGTCAGGTTGCCAGG
Lysinibacillus sphaericus C3-41	CP000817.1	272148-272233	GGAAAATATAGGCAAATTTACTAAAAAGTAAAGATGCAAAGCTACAGGTCTAAGGGAATATTTACTTAGATAGCTAGGTTGCAAAA
Marine metagenome 1091141731174	AACY021822495.1	361-273	GCAGCGAAACGGCACCCTTGAGGGAAACCCAAGCTCGCAAAGTTACTGACCTAAACGCCTGACGGCGCACGGTTTGAAGAACCACCGAA
Marine metagenome 1092963530478	AACY020820783.1	446-363	GCGCTCGAAAGGCAAGTCTCCCGAAAGGGAGTACACGCAAAGCTTCAGATCTAAGGGGAAACCTATGATGGCTGGGCTGCCGTA
Marine metagenome 1096626182008	AACY020159240.1	754-829	CATCCGAAAAGGCAAACCAGCCGCGAGGCTGGGACGCAAAGCCAGGGGTCTCGTCAGAGACAGCCCCGCTACCGAA
Marine metagenome 1096626364222	AACY024044040.1	795-878	TATGTAACAAGGCACACCAGGAGTAATCCTGGGCCGCAAAGTCATGGGCCCGGCCGAGCGTTGCAAAGCAGGGTTGCCAGACCG
Marine metagenome 1096626423965	AACY020343240.1	4-92	TTGTGCAAAAGGCAAACCCGGATGAAAGTCCGGGACGCATAGCTTCCGGTCTAAGGGTCAGCAGTACCTAAGATAGCGGGGCCACCACA
Marine metagenome 1096626431952	AACY020350093.1	241-329	GAAATTAAAAGGCAAACTGGCCTAAAGGTCAGGACGCAAAGCCTCCGGTCTAAGGATCCAAAAGGATCTACGATAGCGGGGTTGCATTA
Marine metagenome 1096626457847	AACY020364809.1	409-494	CCAGGTAAAGGGCAAACCGGTCGAGATGCCGGGACGCAATGCCTCCGGTCTTCAGATCGTGCGATCCAGATAGCGGGGCTTCCCAG

Marine metagenome 1096626458271	AACY020366890.1	1618-1705	TTGTGCAAAAGGCAAACCGGATGAAAGTCCGGGACGCAAAGCTTCCGGTCTAAGGGTCAGCAGTACCTAAGATAGCGGGGCCACCACA
Marine metagenome 1096626470692	AACY020374334.1	900-983	GCGCTCGAAAGGCAAGTCTCCCGAAAGGGAGTACACGCAAAGCTGCAGATCTAAGGGGAAACCTATGATGGCTGGGCTGCCGTA
Marine metagenome 1096626541226	AACY020420574.1	1022-938	ACACCATGAAATCAAACTTCTTGAAAAAGAAGGTCGTAAAACTATTATCATTGGGGATCATGGTCATGATGAGGTAGTTGCAATA
Marine metagenome 1096626782921	AACY020349431.1	1659-1744	GTAGTCATTTGGCAAACTGGTTGAAAGGCCAGGACGCAAAGCCTCCGGTCTAAAGACATGTCGTCCAGGATAGCGGGGTTGCCACA
Marine metagenome 1096626783697	AACY020365487.1	1679-1764	TAGAGTAAAGGGCAAACCGGTCGAAAGGTCGGGACGCAAAGCCACCGGTCTAAGGGTTCATAACCTAAGACAGCGGAGCTGCCATC
Marine metagenome 1096626842707	AACY020557263.1	8816-8723	CACCGTATTGGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAAGGATGTTAACTAAGATAGCGGGGTTGCTGTA
Marine metagenome 1096626842779	AACY020557419.1	5169-5082	TTGTGTGAAAGGCAAACCAATCGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGTTGTTAGTACCTATGATAGCGGGGATACCGCA
Marine metagenome 1096626843902	AACY020562586.1	34421-34509	TAGTGTAAAAGGCAAACCAATCGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTTTGTACCTATGATAGCGGGGATACCACA
Marine metagenome 1096626844163	AACY020563665.1	59398-59303	CACCGTATTTGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTGAAACTAAGATAGCGGGGTTGCCTAA
Marine metagenome 3599078	ABMK01018861.1	71-131	AATCGATAAAGGTAAACCTAAGGCAACTTAGGGGCACAAAGCAATGGATCCTTGTTTAGGG
Marine metagenome 4197540	ABMC01102009.1	14-90	CGTCGATAATGGCAAACCGGCCGTGAGGTCGGGACGCAAAGCCATGGGTCTGGATCTCAGATCGCCAGGCTACCGAA
Marine metagenome 4211022	ABMC01017149.1	47-131	CCCAGACAAAGGCAAACCGAACCGAAAGGTCGGGGCGCAAAGCCGCGGGTCCGTGGGTAGCGCGAAGGTGTTACTCGAAGGATAG
Marine metagenome 625093	AACY021348332.1	498-403	CACCGTATTTGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTGTAACTAAGATAGCGGGGTTGCCTCT

Marine metagenome ctg_1101667168567	AACY022761216.1	356-262	CTTTGAAAAAGGCAACCCGGCCGAAAGGCCGGTTACGCAAAGCTACGGAGCTAAGGACTGCAACCCCGACAGTCTACGCTAGCCGAGCTGCCAAA
Marine metagenome ctg_1101667302988	AACY022895637.1	446-373	CTGGCGAACGGGCAAACCTCGAGTGATCGGGGGACGCAAAGCTTCGGGTCTCACTAGACTGCCGAGCTGCCGAC
Marine metagenome ctg_1101667373295	AACY022965944.1	914-962	TAGAGTAAAGGGCAAACCGGTCGAAAGGTCGGGACGCAAAGCCACCGGT
Marine metagenome ctg_1101668159085	AACY023351734.1	1378-1304	TACTGAGAACGCCACACCCCGCGTGAGCGGGGGTCGGAAAGCCACGGGCCCCGAGAGGGTAGCCGGGTTGCCAAA
Marine metagenome ctg_1101668551357	AACY023744006.1	1400-1547	CTTTGAAAAAGGCAAACCAAAGGAAACTTTGGGACGCAAAACCACCGGTCCTAGCAAAATCGCCCTATCGCATCTAGGTATTTTCTTTCGATTTTGCGTACTCCGTCAGCGGAGCTGACGGAGCCTAACGGATAGCGGGGTTGCCAGG
Marine metagenome ctg_1101668555221	AACY023747870.1	1258-1117	TCCCGAGAAAGGCAAACTTCCGCCAGCACGAACGGCGGACCCGTCATAAGAGCGCGAAGGTCGCGGGGACGGTAACGTCAGGGCGCAAAGCCACGGGCTTTAAGAAAGCAATGGGATTTCTTAAGGTAGCCGGGTTGCCGAA
Marine metagenome ctg_1101668556430	AACY023749079.1	142-247	GTATCAGGGTGGCGTGCACGGTAACGTGGGGGCGCAAAGCCACGGGTCCTAGCTTCGAGGATCGCCGGGTTGCCGAGCGGTCAAGAAGGATAGCCGGGTTGCCAAG
Marine metagenome ctg_1101668562533	AACY023755182.1	872-707	AGCCGATAAAGGTAAACTCGGAGAAATCCGAGGACACAAAATCACAGGCCTACGTTGTCCGAAGACCGGGAAGGCCCGTTCAGCCGGCCAGGCGCCCCCAAGCCGGCGGGGCAAGATCAGATGAGTTTCGGGGTTTGTAGGATGATATGGCGGCTGGGTTGCCGAA
Marine metagenome ctg_1101668564545	AACY023757194.1	143-55	AGTTGTAAAGGGTAAACCATTCGAAAGAATGGGGCACAAAGCTTTAGAGCCTAACGGTCCGGACGGACTTACGGCTGTCAGCTGCCAAA
Marine metagenome ctg_1101668569597	AACY023762246.1	300-201	TGCGCGACTTGGCAAACCCATTGAAAAATGGGGACGCAAAGCCACCGGTCTAAGGGTCCCGCGGCCAGCGTTGCGGACCTAGGATAGCGGGGCTGCCCGA
Marine metagenome ctg_1101668573352	AACY023766001.1	1556-1454	CTCCGATAATAGCAAACCATGAGTAATCATGGGGCGCAAAACATCGGGTCCCCAATTACTTTTGATAATGCCAAAAGTAGTTGGGGATAGCCGAGTTGCCGAA
Marine metagenome ctg_1101668584191	AACY023776840.1	1049-1131	TCGCGAGAAGGGCACACCTACCGCAAGGTAGGGTCGCAAAGCCGCGGATCCGATTCCCGATACCGGACAGCCGGGCTGCCGAA
Marine metagenome	AACY023777537.1	1038-1155	CCCCGATAAGGGCAACTTCCGGCGCAAGCCGGAAGACGCAAAGCCATGAGTCCCGGTTTTGGGACGCCGCCGTACGGACGTGGGCGCTCGAAAAAGC

ctg_1101668584888			CGGGATCGTCAGGTCGCCGAG
Marine metagenome ctg_1101668586529	AACY023779178.1	631-716	AATTGATGAGGGCAAACTTAGAGTAATCTAGGGACGCAAAGACACAGTCCCGTACCTACCTCGGTACGGGGGGCTGGTCCGCCGAC
Marine metagenome ctg_1101668586988	AACY023779637.1	657-582	AAGTGATAAAGGCACACCCGAAGCAATTCGGGGTCGCAAAGTCATGGGTCCTTAGGAGGATCGCCAGACCGCCACT
Marine metagenome ctg_1101668587231	AACY023779880.1	137-220	TGACGATAAAGGCAGATTACGCGAAAGCGTAGCGCGCAAAACTCAAGAGCCTAAAGCTTAAAGCTATGGCAGTCAGTTACCGAA
Marine metagenome ctg_1101668588666	AACY023781315.1	624-704	ACTCGAAAAAGGCAATCCTTGGCATCAAGGGATGCCAAGGAGCGCAAAGCCACGGGCCAGAAAGGCAGCCGGGTTACCGAG
Marine metagenome ctg_1101668588758	AACY023781407.1	697-610	AGTCGAAAATGGCAAAACCGGGAAAACCCGGCGGCGCAAAGCTACAGAACCTAAGGTCTCAAGAGGACTATGGTAGTCAGTTACCGAA
Marine metagenome ctg_1101668614096	AACY023806745.1	1046-903	GCCTGAAAAGGGCAAACCTGTTGAAAAACAGGGGCGCAAAGCTACAGACCAGTTAGTTGCTAGATAATAGCTATTGGCTTCTAGTCGTAGATTACTAACCAAGAGCTGACTGCTAACAACCAAAATGGTAGCTGGGTTGCCAGG
Marine metagenome HOTS_Contig12129	ABEF01012129.1	805-713	TTCCGAAAAAGGCAAACCGTCGGTAACGGCGGGACGCAAAGTTACCGGTCCCAAAGCGATTTTAGACACCTTTGGGACAGCGGGACCGCCGGG
Marinobacter adhaerens HP15	CP001978.1	2000844-2000918	TTTCCCCGCCGCCAAACCTCTCGCGAGAGGGGGACGGAAAGCCACGGATCTCTCTGAGATAGCCGGGTTGCACGG
Marinobacter sp. ELB17 1101232001221	AAXY01000014.1	263-343	CTAACCAGCAGCCAAACCATTTGTGAGGATGGGACGGAAAGCCAAGGATCTCTGGGGAAAAGAGACAGCCTGGTTGCCTAG
Marinobacter sp. MnI7-9 contig00025	AGTR01000027.1	928-1010	CCGTTCGGGAGCCAAACCATTCGCGAGGATGGGACGGAAAGCCAAGGATCTCTAGAAGAATAAGAGACAGCCTGGTTGCAAAG
Marinobacterium stanieri S30 contig00063	AFPL01000054.1	32927-32851	CTCCCGAAAAGGCAACTGCCCCAAGAGCGGCAGACGCAAAGCCAAGGGCCAATTGGATTGGCTGCCTGGCTACCGAA

Megasphaera elsdenii strain DSM 20460 draft genome	HE576794.1	199821-199748	CATTAAATTCGGCAAACCCGGGGAAACCCGGCGACGCAAAGCTATAGGGCCTCTGCTGGCAGCCAGTTGCAATC
Metagenome sequence 3634298_fasta.screen.Contig6294	AAFY01000350.1	1255-1332	GATACAAATAGCCAAACTTACTGTGAAGTAAGGACGGAAAGCTACGGATCTTGATTTAAAGATGGCCGAGTTGCAACT
Metagenome sequence AGZO12498.g2	AAFY01007332.1	747-673	ATCCGACAATAGCAAACCCGGAGTAATCCGGGGACGCAAAACCACGGGTCCTATTTGGATAGCCGGGTTACCGAA
Metagenome sequence AGZO9529.g2	AAFY01019596.1	653-567	CCACGAAAAAGCCAAACCTGTTTAAACGCAGGGACGGAAAGCCACGGGTCTTTTCTACGATACGACCAAGACAGCCGAGCTGCCGAA
Metagenome sequence AGZO9766.g2	AAFY01014293.1	531-604	TTTATTTAAAGCCAAACCTGTTGTAAGGCAGGGACGGAAAACTACGGGTCTATCAAGATAGCCGAGTTGCCAGA
Methylobacillus flagellatus KT	CP000284.1	503076-502984	AAATGTTAAGGGCAACCTTGGTTGAAAAACCAAGGACGCAAAGTCACCGGTCTAAGGTAAGCAGCTTGCTACTATGACAGCGGAACCGCCATA
Methylobacter tundripaludum SV96 Mettuscaffold_1_Cont6	AEGW02000006.1	60848-60922	AATAAATAAAGCTAAACCTATTGAAAGGTAGGGACAGAAAGTTACGGTTCCAAAACGGAAAGCCGGACTGCCGAA
Methylobacter tundripaludum SV96 Mettuscaffold_2_Cont9	AEGW02000009.1	242664-242740	ACACGATAAAGCCAATCCTGCCGAAAGACAGGAGCAGAAAGTCGCGGATCCTATTAACGGAAAGCCGGACTGCCGAA
Methylomicrobium	FO082060.1	3219719-3219804	ATCATAAAAGGGCAAAACCACCGAAAGGTGGTGACGCAAAGTTTCCAGTCTAACGGAGTTATTCCTATGACAGTGGGATTGCTAAA

alcaliphilum str. 20Z chromosome			
Methylomonas methanica MC09	CP002738.1	3052770-3052683	TTTAACGTTTGCCACTCCCGTTGCGAGGCGGGGCCGGAAAGCCACGGTTCTTGAGAAACAACAAAAACAAGAAGGCCGGGCTGCCTCC
Methylomonas methanica MC09	CP002738.1	477526-477609	GACATCTATCGCCAAACCCGCTGCGAAGTGGGGGCGGAAAGTCTCGGGTCTTGAGATTCGTTACAAGACGGCTGGATTGCTCCC
Methylomonas methanica MC09	CP002738.1	3378100-3378022	TTGCAACCCCGCCACATCCGCCGCGAGACGGAGCCGGAAAGCCACGGGTCTTGGGAAGTAAGACAGCCGGGTTACCTTC
Methylomonas methanica MC09	CP002738.1	990642-990719	AATAACCATGGCCAAACTCGTCGCGAGGCGGGGGCGGAAAGCTGCGGGTCTTGTTTGCAAGACGGCCGGGTTGCCAAC
Methylomonas methanica MC09	CP002738.1	986079-986231	GCGTGTAAAAGCCAAACCCGTCGCGAGGCGGGGACGGAAAGTCACGGGTCTTGAATGGTTAGTCATGCTCGCTTGCGAGTAGCCTGAAATGGGGCTTGCCGCCTACGGGCGGCAATGACAGGGACCGCTGTAAAAGACGGCCGGATCGTCACC
Methylomonas methanica MC09	CP002738.1	4651110-4651029	TACCCAATTTGCCACAGCCGTCGTGAGGCGGCGTCGGAAAGCCTAGGGTCTGGTTAGGATGCCAGATAGCCGGGCCGCCTCC
Methylomonas methanica MC09	CP002738.1	4842565-4842484	GCATAAATTCGCCATCCCCGTCGCAAGGCGGGTTCGGAAAGCCGCGGGTCTTGCCGCTCAGCGAGATAGCCGGGCTGCTTTC
Methylophaga aminisulfidivorans MP 54_1	AFIG01000001.1	1881455-1881378	GAACAGTTAAGCCAACCTTGGTGTGAGCCATGTGACGGAAAGCCACGGATCTTTTTTAAAGATGGCCGGGTTGCATAG
Methylophaga aminisulfidivorans MP 54_1	AFIG01000001.1	1615961-1616039	TTTAATCGAAGCCAAACTCGTCGTGAGGCGGGGTCGGAAAGCTACAGGTCTTCCAAGTGAAGATGGCTGGGTTGCATTG
Methylophaga aminisulfidivorans MP 54_1	AFIG01000001.1	1236852-1236771	TATTTAATCGGCCAAACTTGGTGTGAATCAGGGACGGAAAGCCACAGGCCTTGTTGTTTAACAAGGTGGCTGGGTTGCACAA
Methylophaga	AFIG01000003.1	355044-354968	TTTAACAAAAGCCAAACTCGTCGTGAGGCGGGGTCGGAAAGCCACAGATCTTTTTTAAAGATGGCTGGGTTGCATTG

aminisulfidivorans MP 54_3			
Methylophaga aminisulfidivorans MP 54_3	AFIG01000003.1	123988-124076	AATTATCGGAGCCAACCTTGGTGCGAGCCAAGTACGGAAAGCTACAGATCTCGGCTGATGTACTTAGTTGAGATGGCTGAGTTGCATTT
Methylophaga aminisulfidivorans MP 54_3	AFIG01000003.1	123622-123540	TTTTTTTAAAGCCAAACTCGTCGTGAGGCGGGGTCGGAAAGCCACGGGTCTCTGGTTTGATTAGAGATGGCTGGGTTGCATTG
Methylophaga aminisulfidivorans MP 54_3	AFIG01000003.1	631345-631263	ACATATTATCGCCAAACCTGATGTGAGTCAGGGACGGAAAACCTACAGCTGTGCATTAGTGGCATCAGGGCTGGGCTGCATGA
Methylophaga aminisulfidivorans MP 54_3	AFIG01000003.1	355846-355761	TGTAATTAAAGCCAAACTCGCTGTGAGGCGGGGTCGGAAAGCCACAGATCTTTAAATCTACATTTAAAGATGGCTGGGTTGCATTG
Methylophaga aminisulfidivorans MP 54_3	AFIG01000003.1	233715-233636	TATCATTATTGCCAAACTCAGCGTGAGCTGAGGACGGAAAGCTACAGACCTTAAGCTCTTAAGGTGGCTGAGTTACATAG
Methylotenera mobilis JLW8	CP001672.1	134556-134643	ATTTGAAAAAGGCAAACTCAGCTGAAAAGCGAGGGCGCAAAATCACCGGTCTAAGGGGCGTAAGTTCTAAGATAGCGGGAGTACCAGA
Methylotenera versatilis 301	CP002056.1	2547134-2547237	ATTAAATAAAGGCAAATCCAAATGAAAATTGGAGACGCAAAGTTACCGGTCTAAAGAAAGCATATTCAATATGAAATGCTATCAATGGCAGCGGGGCCGCAAAT
Methyloversatilis universalis FAM5 contig00047	AFHG01000030.1	202545-202633	GCTGAACCAGGGCAAACCCGTCGAAAGGCGGCGACGCAAAGTTTCCGGTCTAACGGGTGACAACACCCCATGACAGCGGGGCCGCCGCT
Methyloversatilis universalis FAM5 contig00071	AFHG01000053.1	92847-92759	AGCTGAAAAAGGCAAACCCGTCGAAAGGCGGGGACGCAAAGTCACCGGTCTAATCCGCGCGTGCGCGGGATGACGGCGGGACCGCCACT
Methylovorus glucosetrophus SIP3-4	CP001674.1	417524-417440	GTTATTGAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGTTTCCGACCTAAGGGCGCATGCCTAAGGTAGCGGGACTGCCGTT
Methylovorus	CP001674.1	111009-111093	TGCATGAAAAGGCAAACCCGTTTGAAAGAACGGAGACGCAAAGCTACCGGTCTAAGGAGCAATCTATGACAGCGGGGCCGCCAAT

glucosetrophus SIP3-4			
Methylovorus sp. MP688	CP002252.1	110948-111032	TGCATGAAAAGGCAAACCCGTTTGAAAGAACGGAGACGCAAAGCTACCGGTCTAAGGAGCAATCTATGACAGCGGGGCCGCCAAT
Methylovorus sp. MP688	CP002252.1	419887-419803	GTTATTGAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGTTTCCGACCTAAGGGCATATGCCTACGGTAGCGGGACTGCCGTT
Microbial mat metagenome hsmat03_BHWI2563_y1	ABPR01002897.1	790-715	TTCCGACAAGGGCAAACCCAGGGTGACTTGGGGACGCAAAGCCACGGGCCAAAAATTTGGCGGCCGGGTTGCCGAG
Microbial mat metagenome hsmat03_BHWI3290_y1	ABPR01004227.1	569-481	GGTGTAGAAGGGCAAAGCTGCCGAAAGGCTGTGACGCAAAGCCACGGGTCTACCGCTCAACCACGAGCAATGATCGCCGGGCTGCCGAA
Microbial mat metagenome hsmat03_BHWI6167_y1	ABPR01008458.1	695-769	CAATGTAAAAGCCAAACCTGTCGCGAGGCAGAGACGGAAAGCCACGGGTCTTTCAGAGACAGCCGGGTTGCCATT
Microbial mat metagenome hsmat04_BHWN6261_x1	ABPS01008260.1	844-784	CCTATTGTGAAGTAGGGACGGAAAGCCACGGGTCTCACGGTGAGACCGCCGGGTTGCCTTC
Microbial mat metagenome hsmat05_BHWO2906_x1	ABPT01003066.1	331-415	CTATGACAAGGCCGAACCATTCGCAAGTTTGGGGCGGAAAGCTGCGGGTCTTGATGATTTCCGAAAAGACAGCCGGGCCGCCATA
Microbial mat metagenome hsmat05_BHWO3072_x1	ABPT01003325.1	49-123	CAATGTAAAAGCCAAACCTGTCGCGAGGCAGAGACGGAAAGCCACGGGTCTTTCAGAGACAGCCGGGTTGCCATT
Microbial mat metagenome hsmat05_BHWO4321_y1	ABPT01005252.1	327-402	TTCCGACAAGGGCAAACCCAGGGTGACTTGGGGACGCAAAGCCACGGGCCAAAAATTTGGCGGCCGGGTTGCCGAG
Microbial mat metagenome hsmat06_BHWP4406_y1	ABPU01005130.1	28-109	ATCAGCCAACGCCAAACCCGCCGCGAGGCGGGGACGGAAAGCCACGGGTCCGCAAAAAGGGGCGGGGAGCCGGGTTGCCTGA
Microbial mat metagenome hsmat06_BHWP8728_y1	ABPU01012127.1	338-263	TTCAGCAAAAGCCAAACCTACTGTGAAGTGGGGACGGAAAGCTACGGGTCTTAAGTAAGATAGCCGGGTTACCTCA
Microbial mat metagenome hsmat08_BHWT2991_x1	ABPW01003212.1	199-273	TCAAGACAAAGCTAAACTTGTCGCGAGGCAAGGGCAGAAAGCCACGGGTCTCACTGAGACAGCCGGGCTACCAGG
Microbial mat metagenome	ABPW01003599.1	136-60	GAACAACAAGGCCAAACCTGCTGCAAGGCAGGGACGGAAAGCCGCGGGCCCCTGACTCACTTTTCAGCGCTGCCGCC

hsmat08_BHWT3971_b1			
Microbial mat metagenome hsmat10_BHWZ1487_x1	ABPY01000821.1	130-210	CCATGCAAATGGCAAACCGGCCGTAAGGCCGGGACGCAAATCCACGGGTTCGCCTCAGAGGTGGACAGCCGGGCTGCCTTG
Mine drainage metagenome 27894568	ABLU01025776.1	127-41	GCAAACCTCACCGAAAGGAAGGGACGCAAAGCCACTGGCCTAAATCACAGTGTAAAAAGTTGTGATTATGGTAGCAGGGTTGCCTCT
Mine drainage metagenome 27898624	ABLU01110618.1	90-16	AGAAGAAAAAGCCAAACCTGCTGAGAAGCACGGGCGGAAAGTCACGGGTCTTCCAAAGATAGCCGAGCTGCCTTT
Mine drainage metagenome 27902334	ABLU01098556.1	31-104	TTGAGATAAAGCCAACCCTGTTGCAAAGCGGGGACGGAAAGCCACGGGTCTGAATTGATAGCCGGGTTGCCTTG
Mine drainage metagenome 27951665	ABLU01050434.1	61-1	TTGAGATAAAGCCAACCCTGTTGCAAAGCGGGGACGGAAAGCCACGGGTCTGAATTGATAG
Mine drainage metagenome 28065084	ABLU01137524.1	84-1	ATCAGAGAAAAGCAAACCTCACCGAAAGGAAGGGACGCAAAGCCACTGGCCTAAATCACAGTGTAAAAGTTGTGATATGGTAGC
Mine drainage metagenome 28071833	ABLU01037732.1	113-40	TGCAGGTAAAGCCAAACCCTTCGCGAGGAGGGGACGGAAAACTACGGATCTCTCGAGACAGCCGGGTAACCTTG
Mitsuaria sp. H24L5A	CAFG01000465.1	3433-3332	GGCTGACCAGGGCAAAACCGGCGCGAGCCGGCGACGCAAAGCCTCCGGTCTCGGCGCCGACATCCCAAAGATGTCACGACTCGAGATAGCGGGGTTGCCGTA
Moorella thermoacetica ATCC 39073	CP000232.1	774359-774445	TCCCCGAAAGGGCAAACCTGCTGAAAGGCAGGGGCGCAAAACTAGAGGGTCTACAGCCTTCACGGGCCATGACAGCCAGTTACCACG
Moorella thermoacetica ATCC 39073	CP000232.1	1536251-1536164	ATCAACAAAGGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCATGGGCCTAAAGCCCGACAAGGGCTATGGTTGCCAGGTTGCCGGT
Moorella thermoacetica	CP000232.1	1595675-1595592	CCTTGTTAAGGGCAAACCTGGTGAAAGCCAGGGGCGCAAAGCCACGGGCCTGCAGACGCAAGTCATGGCCGCCGGGCTGCCGGG

ATCC 39073			
Moorella thermoacetica ATCC 39073	CP000232.1	394734-394819	TAGTGTAAAAGGCAAACCACCTGAAAGGGTGGGACGCAAAGCCATGGGTCTACAGCCGTTACCGGTATGACTGCCAGGCTGCCGCT
Moorella thermoacetica ATCC 39073	CP000232.1	543022-543109	AACCGCTAAAGGCGAACCTGACCGAAAGGCGGGGGCGCAAAGCCACGGGCCTAAAGCCTCAACAGGCCATGGCAGCCGGGTTGCCGGA
Moorella thermoacetica ATCC 39073	CP000232.1	805514-805611	GGGCGTCAAAGGCAAGCTCTCCGAAAGGGGATGCGCGCAAAGCCATGGGTCTAAGGCCTGGTAGATACAGACCGGGCTATGGCTGCCAGGCTACCGTA
Moorella thermoacetica ATCC 39073	CP000232.1	2598937-2598849	TGCTCAAAAGGGTAAACCCATCGAAAGGTGGGGACACAAAGCCATGGGTCTAAGGTCCTTAAAAGGGCTATGATCGCCAGGCTGCCGGC
Moritella sp. PE36 1099400000563	ABCQ01000007.1	1346-1265	GTTGTAAAAAGGCAAACAAATCGTGAGGTTTGGACGCAAAGTTACCAGTCTGTATTTTATTACAGATAGTGGAACCGCCAAA
Mosquito metagenome 6386792	ABNJ01050198.1	115-47	GTTGAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATTCCACA
Mosquito metagenome 6397033	ABNJ01021441.1	41-121	GTGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGG
Mouse gut metagenome LEAN2_U_FF-aaa66d09.b1	AATB01007711.1	352-262	GGAAACTTTTGGCAATTCATTCGAAAGAATGGCCGCGCAAAGTCAGGAGGCTAAAACGCCGTCACGGCGTCATGCTCGTCCGGCTGCCGGA
Mouse gut metagenome LEAN3_U_BK-aaa60d10.b1	AATC01005788.1	229-145	TTTTGTAAAAGGCAAAATAAATGAAAATTTATGACGCAAAGCCAAGGTCTAAGAGCTATATGCTTATGATAGCTAGGTTGCACAA
Myxococcus fulvus HW-1	CP002830.1	7444138-7444058	CCTGTTCAAGGGCAATCCCGGGCGAAAGCCCGGGTGCGCAAAGCCGCGGGGCCTGAAGTCCGGCCGGCCGTGACCGCCGTG

Natranaerobius thermophilus JW/NM-WN-LF	CP001034.1	2311743-2311659	TCTTGATAAAGGCAAACCTATCGCGAGGTGGGGGCGCAAAGCCACGAGTCTTTACGATTATTATAAAGACAGTCGGGCTGCCAAG
Natranaerobius thermophilus JW/NM-WN-LF	CP001034.1	2319081-2318999	CCTTGACAAGGGCAAACCTATCGTGAGGTAGGGGCGCAAAGCTACGAGTCTTTACAGTTTGTAAAGACAGTCGGGCCGCCAAG
Natranaerobius thermophilus JW/NM-WN-LF	CP001034.1	2633390-2633298	TCTTGAAAATGGCAAACCTGCCGTGAGGTGGGGGCGCAAAGCCACGAGTCTTTTGTTGACAAAACGTCAATAAAAGACAGTCGGGTTGCCAAG
Natranaerobius thermophilus JW/NM-WN-LF	CP001034.1	2260763-2260660	TTGTTATCGGGGCAAACCTAATGAAAGTTAGGGACGCAAAGCCATGGGTCTAAGGCACTTTATTGTATATATAATTAAATTGCTAGGACTGCCAGGCTGCCGCA
Nitratifractor salsuginis DSM 16511	CP002452.1	740503-740601	ACTAGAAAATGCCACCCCTGTTGCGAGGCAGGTTCGGAAAGCCATGGGTCTTTGATACTGTCACTTGGCAGTAAATGAGAAGATCGCCAGGTTGCCTAA
Nitratifractor salsuginis DSM 16511	CP002452.1	1496875-1496792	CGATGTTAAGGCCAAACCCGCCGTGAGACGGGGACGGAAAGCCATGGGTCTAAGGAGAGTGTCTTAGATCGCCAGGTTGCCAGA
Nitrosococcus halophilus Nc4	CP001798.1	3391739-3391824	AACCGAAAAAGGCAAACTATCCGAAAGGATGGGACGCAAAGCCTCTGGCCTAAGTCCTTTAAGGATAAGGTAGCAAGGCTACCGTA
Nitrosococcus watsoni C-113	CP002086.1	3042769-3042683	TTATTTAAAAGCTAAACCGACCGCAAGGTTGGGGCAGAAAGTCACGGGTCCTTATTTCCATGAGAAGCGGATAGCCGGACTGTCGGA
Nitrosococcus watsoni C-113	CP002086.1	3036682-3036607	TATTCATAAAGCTAAACCAGCTGAGAGGCTGGGGCGGAAAGTTACGGGTCCGTTAACGGAGAGCCGAGCTACCGAG

Nitrosomonas europaea ATCC 19718	AL954747.1	1707540-1707622	AACCGACAAAGGCTAATCTGTCGTAAGGCAGGGGCGCAAAGTTTCCGGTCCTGATCCATGATCAGGAAAGCGGGACTGCCGAA
Nitrosomonas eutropha C91	CP000450.1	861386-861306	AACCGACAAAGGCCAACCTGTCGTGAGGCAGGGGCGCAAAGTTTCCGATCCTGATTGCATCAGGAAAGCGGGACTGCCGAA
Nitrosomonas sp. AL212	CP002552.1	1184435-1184356	ATTTGATATTGCCACTCTTGTCGCGAGGCAAGTTCGGAAAGCCTACGGATCTCCGCAAACGAGACGGCTGGGTTGCCTCT
Nitrosomonas sp. AL212	CP002552.1	2586175-2586089	CTATGAAAAAGGCAAACTCTGCGAAAGCGGGGGACGCAAAGTCACTGATCTAAAGGGCAAATGCCCCAGGATGGCAGGACTGCCAGG
Nitrosomonas sp. AL212	CP002552.1	2586415-2586329	AGATGAAAAAGGCAAACCCTGCGAAAGCAGGGGACGCAAAGTCACTGATCTAAAGGGTAAATACCCCAGGATGGCAGGGCCGCCAGA
Nitrosomonas sp. AL212	CP002552.1	2587963-2587877	AACTTGAAAAGGCAAACTTTGCGAAAGCAGAGGGCGCAAAGTCACTGATCTAAAGGGAAAGCTCCCAATGATAGCAGGACTGCCAGG
Nitrosomonas sp. Is79A3	CP002876.1	1763093-1763171	CAAAGTTAATGCCACCCTTACTGCAAAGTAAGTCCGGAAAGCCAACGGATCTCTTCATTGAGATGGCCGGGTTGCCTCT
Nitrosomonas sp. Is79A3	CP002876.1	1942496-1942582	ATTTGAAAAAGGCAAACTCTGCGAAAGCAGGGGACGCAAAGTCACTGATCTAAAGGGCAAATACCCCACGATGGCAGGACTGCCATG
Nitrosospira multiformis ATCC 25196	CP000103.1	3131016-3131108	TACCGTAAAAGCCACACCCGTCGCGAGGCGGGGCCGGAAAGTCCCGGATTTGCGCAATTGAAGGGAACTCGCGCAGGTAGCCGGACTGCCAGT
Nitrosospira multiformis ATCC 25196	CP000103.1	2175552-2175465	ATCTGTAAAAGGCAAATCTCGCGAAAGCGGGGGACGCAAAGTCATCGGTCTACCGGGCTCAAGGCCCCAGGACGGCAGGACTGCCAGA
Nitrosospira multiformis ATCC 25196	CP000103.1	2965168-2965087	CAGGAACAAAGCCAAACCCGTTGCGAAGCGGGGACGGAAAGCTGCGGGTCTCCAAGCAAGCGGAGGTAGCCGGGTTGCTCCA
Oceanobacillus iheyensis HTE831 DNA	BA000028.3	2580327-2580243	CTCAGAAAAAGGCAAACCTATTGAAAGATGGGGACGCAAAGTCACAGATCTAAGGTATTTTTACTAAGATGGCTGGACTATCTGG
Oceanospirillum sp. MED92 1099521380308	AAOW01000025.1	38985-39059	TCTCGATAATGGCAAACCAGAAGCGATTCTGGGGCGCAAAGTCACAGGTCCCTTGTGGATGGCTGGGCTACCGAA
Oceanospirillum sp. MED92 1099521380376	AAOW01000010.1	54987-54913	CTCTCGAAAAGGCAAAACCCGAGTAATCGGGTGACGCAAAGTCACGGGTCCCAATGGGACAGCCGGACCGCCACA

Oceanospirillum sp. MED92 1099521380380	AAOW01000017.1	31244-31159	AACCCTAATGGCCAAACCTGCCGTGAGACAGGGACGGAAAGCTACAGGTCTATGTTTTGATGTCATTAGATGGCTGAGCTGCGCAG
Olsenella sp. oral taxon 809 str. F0356 cont1.8	ACVE01000008.1	68265-68366	AATTAAACTTGGCAAACCTGCCGAAAGGCAGCGACGCAAAGCTATAGGGCCTTAACTGGTAACCAGCTGCATTCTCCGCAAGGGGGGCAGCCGGCTGTTTTT
Olsenella uli DSM 7084	CP002106.1	604544-604621	AATATGTCCTGGCAAACCCATCGAAAGGTGGGGACGCAAAGCTATAGGGCCTTGTGCGCATGGCAGCCAGCTGCGGTT
Olsenella uli DSM 7084	CP002106.1	789919-789992	ATTTCAGCTAAGTAAAACTGTCGAAAGGCAGTGACGTAAAGCTATAGGGCCTGGAATGGCAGCCAGCTGCAATT
Oribacterium sinus F0268 contig00315	ACKX01000177.1	5327-5252	GTAGGACATCGGCAAACCCGGGGAAATCCGGCGACGCAAAGCTATAGGGACTGTAAAATGTCAGCCAGCTGCAATC
Oribacterium sinus F0268 contig00316	ACKX01000178.1	159-84	GATCTGTTTGAGCAAAATCGGGGAAACCCGGTGACGCAAAGCTATAGGGCCTGTAATATGGCAGCCAGTTGCGATC
Oribacterium sp. oral taxon 108 str. F0425 noncontiguous_finished_chromosome	AFIH01000001.1	637037-637112	GATCTGTTTGAGCAAAATCGGGGAAACCCGATGACGCAAAGCTATAGGGCCTGTAACATGGCAGCCAGTTGCGATC
Oribacterium sp. oral taxon 108 str. F0425 noncontiguous_finished_chromosome	AFIH01000001.1	637271-637346	GTTGGACATCGGCAAACCCGGGGAAATCCGGCGACGCAAAGCTATAGGGACTGTAAAATGTCAGCCAGCTGCAATC
Ornithinibacillus sp. TW25 contig00027	AEWH01000012.1	10584-10499	TTACGAAAAAGGCAAACTTATCGAAAGGTAAGGACGCAAAGCCAAAGGGCCTAATACATCACTGTAATGGCAGCCTAGCTACCGAA
Ornithinibacillus sp. TW25 contig00072	AEWH01000024.1	131228-131315	TAATGAAAAAGGCAAACTATTCGAAAGGGTAGGACGCAAAGCTTAGGGTCTAATGGCACACAAAGCCAACGATCGCCTGGCTACCAAA

Ornithinibacillus sp. TW25 contig00116	AEWH01000060.1	92407-92325	TCTATTAAAAGGCAAACCCATTGTGAAGTGGGGACGCAAAGTCACAGATCCAAGCTTTTGGCTAGGATGGCTGGATTACATAG
Ornithinibacillus sp. TW25 contig00190	AEWH01000074.1	6929-6845	TTTGTATAAAGGCAAACTATCTGAAAGGGTAGGACGCAAAGCTAAGGGTCTAAGGTTGAAAAACTATGATCGCCTGGTTGCCAAG
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	2922659-2922578	TAAAATCATTGGCAAAACCGTCGAAAGACGGCGTCGCAATGTTAAAGGGCCTGTACCGTTTGGATGGCAGCCAGTTGCGGAA
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	780090-780177	TAAAAAAATGGGCGAACTTACTGAAAGATAAGGGCGCAAAGCTAAAGGGCCTAAAGTGCAAGCGCATGACGCCATATAGGATTGCGTA
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	81299-81385	CTCCGATACGAGCAAACTTGGCGAAAGTCCAGGACGCAAAGCCACGGGTCTAAGGCATTGTTATGCTATGACAGCCGGGCTGCCGAA
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	1215747-1215829	ATCTTGAAGGGGCAAACCGCCTGAAAAGACGGGACGCAAAGCCAGGGGGCTAAGGCGAAAGCTATGCCAGCCCGGCTGCCACG
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	4000699-4000608	AAATGTTAAGAGCAAACCTGCCCAAAGGCAGGGACGCAAAGCCATAGGATCTAAGGTGCTGATGTAAGCGCTACGACAGCCTGGCTGCCAAT
Oscillibacter valericigenes Sjm18-20 DNA	AP012044.1	3430294-3430206	TAAAGCCAAGGGCAAACCCGGTGAAAACCGGGGCCGCAAAGCCGCAGGGTCTAAGGTGCTGAATGCGCTATGATAGTCTGGCTGCAAAA
Oxalobacteraceae bacterium IMCC9480 ctg_1037	AEPR01000467.1	1255-1332	CAGTTACCCCCGCAAACCTGGAGCGATCCAGCGACGCAAAGCTACAGGGACTTCCCCCGAAGTCAGCCAGCTACCTGA
Oxalobacteraceae bacterium IMCC9480 ctg_4647	AEPR01000974.1	220-306	ATTGCGGCTGGGCAAACTTACTGAAAAGTAAGGACGCAAAGCCTCCGGCCTACGGTCTTCACGGATCACGGTAGCGGGGTTGCCAGC
Paenibacillus curdlanolyticus YK9 ctg105	AEDD01000006.1	3984-3890	GAACGATAATGGCAAACTTGCTGAAAAGCAAGGACGCAAAGCCATAGGGCCTAATCGCCGCCGTAGACGGGGCATTTGGCAGCCTGGTTACCGAA

Paenibacillus curdlanolyticus YK9 ctg106	AEDD01000012.1	51621-51535	TTAAATACTTGGCAAAGCTATAGAAATATAGTGACGCAAAGCTATGGGTCTTCGCACATTTTAGTGAAAGATCGCCAGGTTGCCCAT
Paenibacillus curdlanolyticus YK9 ctg106	AEDD01000012.1	237420-237345	GACCGATAATGGCAAACTCGTCGCGAGGCGAGGACGCAAAGTCATGGGTCCCTAGATGGATCGCCAGACTGCCGAA
Paenibacillus elgii B69 Contig1	AFHW01000001.1	90436-90349	CACTGATAAAGGCAAACCTGTTGAAAAGCGGGGACGCAAAGCTCCGGGTCTAAGGCATAAGTTATGCGATGACGGCCGAGCCGCCAAA
Paenibacillus elgii B69 Contig138	AFHW01000138.1	4918-4830	ATTCGTTCATGGCAAACCTGCCGAAAGGCAGCGACGCAAAGCTTAGGGTCTAAGGTCCGCAAACGGACTACGACAGCCTGGCCGCCGAA
Paenibacillus elgii B69 Contig28	AFHW01000028.1	124886-124969	TCACAGACATGGCAAACTTGGCGAAAGTCAAGGACGCAAAGCTATAGGGACTAAGGTGTATCACGATGTCAGCCAGCTGCCGAA
Paenibacillus elgii B69 Contig3	AFHW01000003.1	20681-20591	GCTCGATAAAGGCAAACCGGGCGAAAGCTCGCAGGCGCAAAGCGATAGGGATAATGCGCCGAGGTTGCGTGATGCCAGCCAGTTTACCGAA
Paenibacillus elgii B69 Contig31	AFHW01000031.1	107104-107011	ACATGAAAAAGGCAAACTATTTGAAAGAATAGGACGCAAAACTAGAGGGGCTAAGGCTGCTATCCTATAGCGGCTATGCCAGCCAGCTACCTGT
Paenibacillus elgii B69 Contig8	AFHW01000008.1	14783-14692	TGAGTAAAAAGGCACACCTGTCTGAAAAGCGGGGACGCAAAGCCATGGGTCTGCCCTTCCCGAACGGGAAGAACGATCGCCAGGTTGCCACT
Paenibacillus elgii B69 Contig94	AFHW01000094.1	37876-37966	AACCGATAAAGGCAAACCTAACGAAAGTTGGGGACGCAAAGCTACAGGGCCTTCCTTAGTTTAGTAACTAAGATGGCAGCCAGTTACCGAA
Paenibacillus lactis 154 ctg186	AGIP01000013.1	159170-159257	CTACGATAACGGCAAACTTGTCGAAAGATAAGGACGCAAAGCCACAGGGCCTTCTTGATGAACCGTCAATGGCAGCCTGGCTACCGAA
Paenibacillus lactis 154 ctg186	AGIP01000013.1	123475-123569	GTACGACAATAGCAAACCCACCGAAAGGTGGCGACGCAAAGCTATAGGGGCTAATGCGGGACCTACTGCAACCGCAATGCCAGCCAGTTGCCGAA
Paenibacillus lactis 154 ctg186	AGIP01000013.1	159021-159107	CACGATAAATGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCTATAGGGCCTTCTTGATGAACCATCAATGGCAGCCAGCTACCGAA
Paenibacillus lactis 154	AGIP01000003.1	298175-298081	GTACGATAATCGCAAACCCACTGAAAAGTGGCGACGCAAAGCTATAGGGGCTAATGGGGTTCTGCATAGAACCGCGATGCCAGCCAGTTGCCGAA

ctg196			
Paenibacillus lactis 154 ctg196	AGIP01000003.1	297812-297718	GTACGATAATAGCAAACCCACTGAAAAGTGGCGACGCAAAGCTATAGGGGCTAATGCGAATCTGCTAAGATACGTGATGCCAGCCAGTTGCCGAA
Paenibacillus mucilaginosus KNP414	CP002869.1	8527198-8527102	TAGTGAAAAGGGCAAAACGCAGGAAACTGCGTGACGCAAAGCCACAGGGCCTGAACCCTCAAGAGATTCTCTTGATGGAAGGCAGCCGGTTGCCACA
Paenibacillus mucilaginosus KNP414	CP002869.1	2325919-2325827	CTTGTTCAATAGCAAACTTATTGAAAAATAAGGACGCAAAGCCTCGGGCCTAAGGAATGAACCTTCTCATTCTATGGCAGCCGGGCTGCCTTA
Paenibacillus mucilaginosus KNP414	CP002869.1	3205243-3205331	TCTCGATAAAGGCAAACCTGGTGAAAACCAGCGACGCAAAGCTACAGGGGCTACAGCGACAAGGTGCGCTATGCCAGCCAGCTACCGAA
Paenibacillus mucilaginosus KNP414	CP002869.1	8482134-8482045	CACACGTCAGGGCTAACTTGATGAAAGTCAGGGGCGCAAAGTCACGGGCCTGTAATCCGTTCCGCGGATTATGGCAGCCGGGCTGCATTC
Paenibacillus mucilaginosus KNP414	CP002869.1	980457-980542	ATCCGACAAAGGCAAAACTGGTGAAAGCCAGTGACGCAAAGCTACAGGGGCTACAGTCTTTAGGACCATGCCAGCCAGTTGCCGGT
Paenibacillus mucilaginosus KNP414	CP002869.1	30540-30627	TTCGTTTCATGGCAAACCTGCCGAAAGGCAGGGACGCAAAGCTTAGGGTCTACGGTCCTGCAGGGACTATGACAGCCTGGCCGCCGAA
Paenibacillus mucilaginosus KNP414	CP002869.1	2865292-2865388	TTACGATAAAGGCAAACTCATCGAAAGGTGGGGACGCAAAGCCACAGATCTAAAGCCTTCAGTCCCGCTGACAGGCAATGACCGCTGGGTTACCGAA
Paenibacillus mucilaginosus KNP414	CP002869.1	6097648-6097735	TTCCGACAAAGGCAAACTCCTCTAAAGGGGAGGACGCAAAGCCACGGGCCTACCGAACATCCTGTTCCACGGCTGCCGGGCTGCCGTT
Paenibacillus mucilaginosus KNP414	CP002869.1	8482460-8482363	ACGCGAGATTGGCAAACTTAAATGAAAATCAAGGGCGAAAAGTCATGGTCCTAAAGTCTTAACCACTTACATAAGATCATGGCAGCCGGGCTGCATTC
Paenibacillus mucilaginosus KNP414	CP002869.1	7702453-7702369	GATCGAAAAAGGCAAACCATGCGAAAGCATGGGACGCAAAGCCACGGGTCTACAGCGTTATGCGCATGACAGCCGGGCTGCTGCA
Paenibacillus polymyxa ATCC 842 contig16	AFOX01000016.1	286231-286312	CAACGATAAACGCAGCCCTGTCGAAAGGCAGGTACGCAAAGCTAAAGGGCCTTCCCGTAAGGATGGCAGCCTGGCTACCGAA

Paenibacillus polymyxa ATCC 842 contig7	AFOX01000007.1	174-94	TCAAGCTAATGGCAAAGCTGTCGAAAGACAGTGACGCAAAACTATAGGGCCTTCCTACTCGGATGGCAGCCAGTTACCAAG
Paenibacillus polymyxa E681	CP000154.1	1235056-1235136	CAACGATAAACGCAGCCCTGTCGAAAGGCAGGTACGCAAAGCTAAAGGGCCTTCCACAAGGATGGCAGCCTGGCTACCGAA
Paenibacillus polymyxa E681	CP000154.1	444495-444415	TCAAGTTAATGGCAAAACTGTCGAAAGGCAGTGACGCAAAACTATAGGGCCTTCCTATCCGGATGGCAGCCAGCTACCAGA
Paenibacillus polymyxa M1 main chromosome	HE577054.1	506219-506141	CAGGATAAATGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCTACAGGGCCTTCTGTATGATGGCAGCCAGCTACCGGT
Paenibacillus polymyxa M1 main chromosome	HE577054.1	506100-506019	TATACGAAATGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTATAGGGCCTTCTATTGATGATGGCAGCCTGGCCACCGAA
Paenibacillus polymyxa M1 main chromosome	HE577054.1	1357088-1357169	CAACGATAAACGCAGCCCTGTCGAAAGACTGGTACGCAAAGCTAAAGGGCCTTCCCGTAAGGATGGCAGCCTGGCTACCGAA
Paenibacillus polymyxa SC2	CP002213.1	1358460-1358541	CAACGATAAACGCAGCCCTGTCGAAAGACTGGTACGCAAAGCTAAAGGGCCTTCCCGTAAGGATGGCAGCCTGGCTACCGAA
Paenibacillus polymyxa SC2	CP002213.1	507707-507626	TATACGAAATGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTATAGGGCCTTCTATTGATGATGGCAGCCTGGCCACCGAA
Paenibacillus polymyxa SC2	CP002213.1	507826-507748	CAGGATAAATGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCTACAGGGCCTTCTGTATGATGGCAGCCAGCTACCGGT
Paenibacillus riograndensis SBR5 Contig153g	AGBD01000202.1	1315-1235	CTACGACAAAGGCAAACCTAATCGAAAGATAGGGACGCAAAGCTATAGGGCCTCCGAAAGAGTGGCAGCCTGGCTACCGAA
Paenibacillus riograndensis SBR5 Contig207a	AGBD01000315.1	3941-3848	TCCAGTAAAGGGTAAACCTGCCGAAAGGCAGGGACACAAAGTCTCGGGTCTACTGTAGAGATGCTGGAGCTACTACGACGGCCGGACTGCCTGG
Paenibacillus riograndensis SBR5 Contig341c	AGBD01000709.1	7511-7420	ATTTCATAACGGCAAACTATCTGAAAGGATAGGACGCAAAGCAATGGGCCTAAAGATGCAAACATCGCATCCATGGCTGCCAGGCTGCCAAG
Paenibacillus riograndensis SBR5 Contig407a	AGBD01000972.1	9517-9608	TATTCCTAAAGGCAAACTGTCCGAAAGGGCAGGACGCAAAGCCATGGGCCTAAGAGCGCAATTGCTGCATTTATGGCCGCCAGGCTGCCAAT
Paenibacillus riograndensis SBR5 Contig430c	AGBD01001042.1	575-667	TTGGAACAAGGGCAAATCCGTACGAAAGTCGGAGACGCAAAGCCACGGGCCTACTTCATCCGGGAGGGATGTCAGGGCAGCCGGGCCGCTCAA

Paenibacillus riograndensis SBR5 Contig498	AGBD01001299.1	1042-955	CATGTATAAACGCAAACCGTCTGAAAGGACGGGACGCAAAGTCAGGAATCTAATGCCCGACCAGGGCTATGATCGTCCGGCCGCCGTG
Paenibacillus riograndensis SBR5 Contig510e	AGBD01001363.1	10160-10241	ATACGATAACGGCAAACCTATCGAAAGGTAGGGACGCAAAGCTAAAGGGCCTTCCCAATACGAATGGCAGCCAGCTACCGAA
Paenibacillus riograndensis SBR5 Contig510e	AGBD01001363.1	10004-10085	GCACGACAACGGCAAACCTATCGAAAGGTAGGGACGCAAAGCTAAAGGGCCTTCCCGCTATGGATGGCAGCCAGCTACCGAA
Paenibacillus sp. HGF7 contig00172	AFDH01000004.1	14990-15071	ACTCGATAAAGGCAAACTATCGCGAAAGCATAGGACGCAAAGCCACGGGTCTAAAGCGCAGCTAGACAGCCGGGTTACCGAA
Paenibacillus sp. JDR-2	CP001656.1	4481333-4481246	AACTGAAAAAGGCAAACTTGCCGAAAGGCAAGGACGCAAAGTTATGGGCCTAATGCTGCATAGAAGCGATGGCTGCCAGACCGCCGGA
Paenibacillus sp. oral taxon 786 str. D14 cont1.121	ACIH01000121.1	24181-24265	ACCAGATAAGGGTAAACCTGTTGAAAAGCAGGGGCACAAAGTCTCAGATCTAAGGTAGGAATACTAAGATGGCTGGACTGCCTGG
Paenibacillus sp. oral taxon 786 str. D14 cont1.121	ACIH01000121.1	49416-49501	AAGGAAAAATGGCAAACCCGCTCGAAAGACGGGGACGCAAAGCCACGGGTCTGCGGCCGTAAGGCTATGATCGCCGGGTTACCCTA
Paenibacillus terrae HPL-003	CP003107.1	3006386-3006466	CCACGATAAACGCAGCCCTGTTGAAAGGCAGGTACGCAAAGCTAAAGGGCCTTCCGTGAGGATGGCAGCCTGGCTACCGAA
Paenibacillus terrae HPL-003	CP003107.1	2098534-2098453	ATACGATAATAGCAAACCTGTCGAAAGGCAGGGACGCAAAGCTATAGGGCCTTCTTTTTAAGATGGCAGCCTGGCCGCCGAA
Paenibacillus terrae HPL-003	CP003107.1	2098656-2098576	CAGGATAAATGGCAAACCTGTCGAAAGGCGGGGACGCAAAGCTACAGGGCCTTCTTTTTAAGATGGCAGCCAGCTACCGGT
Paenibacillus terrae HPL-003	CP003107.1	4653410-4653325	ACCAGTAAAGGGTAAACCTGCCCGAAAAGCAGGGGCACAAAGTCCCAGATCTAAGGTAGAGATACTAGGATGGCTGGTCTGCCCGG
Paenibacillus terrae HPL-003	CP003107.1	4365885-4365974	TCCCGTTAATCGTAAACACCTCGAAAGTGGTGGACACAAAGCCATGGGTCTAAAGCTGGATTAAACAGCCATGATTGCCAGGTTGCCGAA
Pelobacter carbinolicus	CP000142.2	2400104-2400022	CTCCGATAAGAGCACAGCCAGATTCTTCTGGTGTCGCAAAGTCACGGGTTCGCTTTTAAAGAGCGGATGGCCGGTCTGCCGAA

DSM 2380			
Pelobacter carbinolicus DSM 2380	CP000142.2	2380546-2380623	TTCCGACAATGGCAAAATCGGGGTGACCCGATGACGCAAAGCCACGGGTCCCATTGCAAGGACAGCCGGGTTATCGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	1141626-1141702	TTTAACATAGGGCAAAACTGGAGTAATCCAGTGACGCAAAGCCACGGGTCCTTGCCGAGGATAGCCGGGTTGCTGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	1141853-1141929	AGGATATATCGGCAAAGCCGGAGTAATCCGGTGACGCAAAGCCACGGGTCCTCATTGAGGATAGCCGGGTTGCTGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	1987037-1987116	TCCCGATAAAACCAAACCTGTCGCAAGACAGGGACGGAAAGCAACGGATCTTCGAACCAGAAGATGGCCGAGCTGCCGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	1774619-1774697	TTTCGTTCAAGGCAAAGTCAGAGTAATCTGGCCACGCAAAACCACGGGTCCATGGTTCATGGATAGCCGGGTTGCCGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	2399816-2399735	TTCCGATAAGGGCAAAACTGGAGTAATCCAGTGACGCAAAGCTGCGGGTGCGTGGGAAACCACGGATAGCCGGGCTACCGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	668521-668443	TTCCGAAAATAGCAAACTCGGGGTAACTCGGGGACGCAAAGCCATGGACCCGTTGCAGGCGGGCCGCCAGGCTACCGAA
Pelobacter carbinolicus DSM 2380	CP000142.2	2648195-2648117	CCGACGAAAAGGTAAACCCCGGGCAACCGGGGGGCGCAAAGCCGCTCATCCGGATCTTCCGGAAAGGAGGGCTGTCGAA
Pelobacter propionicus DSM 2379	CP000482.1	3117927-3118003	AGACGACAATACTAAACCATTCGCGAGAATGGGACGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTCGCCGAA
Pelobacter propionicus DSM 2379	CP000482.1	3118185-3118275	GCCTGAAAAAGGCAAACCATTCGAAAGGATGGGGCGCAAAACCACTGGTCTAAATCCCGGAAATTCGGGACATGACAGCAGGGCTGCCGGG
Pelobacter propionicus DSM 2379	CP000482.1	1047089-1047165	TCACCGATAGGGCACAGCAGGGGCAACCCTGTGTCGCAAAGCTACCATCCTCGGGAGGGGATAGAGGGGTTGTCGAA
Pelobacter propionicus DSM 2379	CP000482.1	2712839-2712914	ACACGACACTACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTCAGGATCTCCAGAAGACAGCCGGGTTGCCGAA

Pelobacter propionicus DSM 2379	CP000482.1	315395-315321	TCACCGAAAAGGCAAAATCCGGGGGACCGGATGACGCAAAGCCACCTACCCAGAACGGGAAGAGGGGTTGTCGAA
Pelobacter propionicus DSM 2379	CP000482.1	3445254-3445331	TCTATGAAAAGGCAAACTCAGGGCAACCTGGGGACGCAAAGCCACGGGTCCGCAGCAGCGGACAGCCGGGACATCAAG
Pelobacter propionicus DSM 2379	CP000482.1	609688-609613	AGACGATACTACTTAACCATTCGCAAGAATGGGGCGGAAAGCCTAAGGGTCTTACTGAGACAGCCGGGTTGCCGAA
Pelobacter propionicus DSM 2379	CP000482.1	609469-609393	ACACGATAATACTCAACCATCCGCGAGGATGGGGCGGAAAGCCTACAGGGTCTCACCGAGACAGCCGGGTTGCCGAA
Pelobacter propionicus DSM 2379	CP000482.1	306485-306561	TCACCGAAAGGGCACAGCAGGGGCAACCCTGTGTCGCAAAGCTACCATCCCTGAGCGGGGATAGAGGGGTTATCGAA
Pelobacter propionicus DSM 2379	CP000482.1	3251882-3251809	AAACCGAAAAGGCAAAATCCGGGGAACCGGATGACGCAAAGCCACCTCCCAGGCCGGGCAGAGGGGCCGCCGAA
Pelobacter propionicus DSM 2379	CP000482.1	2368974-2369055	TTTTGAAAAGGCCAAACCCTTCGCGAGGAGGGGGCGGAAAGCGAGGGATCTTCCCTGAAGAGAAGATGGCCGAGCTGCCAAA
Pelobacter propionicus DSM 2379	CP000482.1	2576366-2576288	TCGCCGAAAGGGTAAAGCACGGGTAACCGTGTGGCACAAAGCCACCATCCAGAATGGTCTGGATAGCGGGGCTGTCGAA
Pelobacter propionicus DSM 2379	CP000482.1	2787031-2787107	AATCGATACTACTAAACCATCCGCGAGGATGGGACGGAAAGCCCACAGGGTCTCCAGAAGACAGCCGGGTCGCCGAA
Pelobacter propionicus DSM 2379	CP000482.1	2645554-2645467	TTTCCGAAGGGGTAAACCCAGGGTAACCTGGGGACACAAAGCCGCGGGTCCTGATTGGTGGATCGGTCAGGATAGACGGGTTGGCGAG
Pelobacter propionicus DSM 2379	CP000482.1	2448471-2448396	CCACCGACGGTGCACAGCACGGGTAACCGTGTGTCGCAAAACTACCATCCCGAAGAGGGATAGAGGGGTTGTCGAA
Pelobacter propionicus DSM 2379	CP000482.1	2353262-2353340	TCGCCGAAAGGGTAAAGCACGGGTAACCGTGTGGCACAAAGCCACCACCCAGCACAAGCTGGGCAGAGGAGCTGCCGAA

Pelotomaculum thermopropionicum SI DNA	AP009389.1	1635122-1635210	AACAAGAAAAGGCAAACCCGGGCGAAAGCCGGGGGCGCAAAGCCATGTGTCCAAAGCCGCGGGGAGGCTACTATCGCCAGGCTGCCGCA
Pelotomaculum thermopropionicum SI DNA	AP009389.1	1981930-1982019	CTACGTTAAGGGCAAACCCATTGAAAGGTGGGGACGCAAAGCTATAGGGTCTAAGGTACTTCCCGGCACTATGATAGCCTGGCTGTCGCT
Pelotomaculum thermopropionicum SI DNA	AP009389.1	201391-201476	CAATGATAATGGCAAATCCACTCGAAAGATGGAGACGCAAAGCCGCGGGTCTAAAGCAATTACGCCATGACAGCCGGGCTGCCGTG
Pelotomaculum thermopropionicum SI DNA	AP009389.1	357790-357871	TTCCGACAAAGGTAAACCCGGCGAAAGCCGGGGGCACAAAGCCAGGGGCCTAAAGCGAAAGCCAGGGCAGCCGGCTGCCGGA
Pelotomaculum thermopropionicum SI DNA	AP009389.1	2800899-2800816	GCAAGATAAAGGCAAACCCAGTCGAAAGATGGGGACGCAAAGCCACGGGTCTAAAGCACATGCTATGACAGCCGGGTTGCCGTG
Pelotomaculum thermopropionicum SI DNA	AP009389.1	804550-804637	TTCCTAAAAGGGCAAACCATTCGAAAGAATGGGACGCAAAACCTTGGGTCTAAGGCAGCAAAGCTGCTATGATTGCCAGGTTGCAGGA
Pelotomaculum thermopropionicum SI DNA	AP009389.1	1181119-1181203	AACTGTAAAAGGCAAACAGTCCGAAAGGGCTGGGCGCAAAACCACGGGCCTAAGGCATTGCTGCTATGGTCGCCTGGTTGCCAGT
Pelotomaculum thermopropionicum SI DNA	AP009389.1	2201437-2201300	TCCACGGAAGGGCAAACCTCCCGAAAGGGTGGGACGCAAAGCTATCGGGCCTAAAGCCGGGTATTGGCGCAAGGACAGCTGCCTTAAAAAGGTGCGGCCTTGGCGCCTGTATTTGGCCAGGGCGGCCGGGTTGCCAAG
Photobacterium damselae subsp. damselae CIP 102761 Contig58	ADBS01000001.1	1452434-1452528	TTACGAACAGGGCAAACTATCTTGAAAGAGATGGGACGCAAAGCTTCCGGCCTAAAAGTTTATTTACATAAGCTCATGGTAGCGGGGTTGCCGAT
Photobacterium leiognathi subsp. mandapamensis svers.1.1. DNA	BACE01000011.1	604993-605083	GTCACGAACAGGCAAATTAATTGAAAGATTAAGACGCAAAACTTCCGGCCTAAAAATTAATTTTTTAATTCATGGTAGCGGAGTTACCGAA
Photobacterium profundum 3TCK 1099451005265	AAPH01000029.1	24025-23938	GTATGTAAAGGGCAAACTAGTCGAAAGGCTAGGACGCAAAGCTACCGGTTTAAGGGTTACACAGACCTATGACAGCGGAGCCGCCATA
Photobacterium profundum	AAPH01000007.1	119243-119159	CCACATTATTGGCAAACTATCCTAAAGGGTAGGACGCAAAGCTTCCGGTCTGTCGACGCCAGTCTATGATAGCGGGGTTACCGTC

3TCK 1099451005275			
Photobacterium profundum 3TCK 1099451005285	AAPH01000002.1	334491-334597	CACGAAACAAGGCAAACTATTCGAAAGAATAGGACGCAAAGCTTCCGGCCTAAAAAGGTATTATTTGTATCTTAAATAATAACCCTCATGGTAGCGGGGTTGCCGAT
Photobacterium profundum SS9 chromosome 2; segment 2/7	CR378676.1	6047-6131	CCACATTGTTGGCAAACTATCCTAAAGGGTAGGACGCAAAGCTTCCGGTCTGTCGACGTCAGTCTATGATAGCGGGGTTACCGTC
Photobacterium profundum SS9; segment 7/12	CR378669.1	339100-339205	CACGAAACAAGGCAAACTATTCGAAAGAATAGGACGCAAAGCTTCCGACCTAAAAGGTATTATTTGTGTCTTAAATAATAAACCTCATGGTAGCGGGGTTGCCGAT
Photobacterium profundum SS9; segment 8/12	CR378670.1	196774-196861	GTATGTAAAGGGCAAACTAGTCGAAAGGCTAGGACGCAAAGCTACCGGTTTAAGGGTTATTAAGACCTATGACAGCGGAGCCGCCATA
Photobacterium sp. SKA34 1099521381155	AAOU01000011.1	39728-39638	GTCACGAACTGGCAAATTAATTGAAAGATTAAGACGCAAAACCACCGGCCTAAAAATTATGTTAATAATTCAAGGTAGCGGGGTTACCGAA
Phytophthora infestans T30-4 cont1.15137	AATU01015137.1	982-1065	AAATGACAAAGGCAAAACCATCGAAAGATGGTGACGCAAAACTATAGGGGCTAAAGCGATTCGCTAAGCCAGCCAGTTACCCGA
Phytophthora infestans T30-4 cont1.15137	AATU01015137.1	1224-1311	TATTGAAAAAGGCAAACTCATCGAAAGGTGAGGGCGCAAAGCTACAGGAGCTAAAGCGATTCAATCGCCATGCTAGCCAGCTACCAGT
Pirellula staleyi DSM 6068	CP001848.1	2667852-2667960	CCTCGATAAGGGCAAACCGGTAGAGATGCCGGGGCGCAAAGCAAAGGGCCTTTGGCCCGCTGGGATCACGCAAGTGAACTGGTGGGCCGATGGTAGCCTGGCTGCCGAA
Planococcus donghaensis MPA1U2 contig00001	AEPB01000001.1	112419-112506	ATCTGAAAAAGGCAAACTCCATCGAAAGAGGAGGACGCAAAGCCATGAGCCTAACCGTTGAAAAACGCAAGGTCGTCAGGTTGCCAGG
Planococcus donghaensis MPA1U2 contig00061	AEPB01000057.1	65090-65179	AAAACGAAAAGGCAAATTTGTCGAAAGACAAAGACGCAAAACCACAGATCTACGGATTGGTAAACAATCTACGATGGCTGGGTTACCGAA

Pseudoalteromonas haloplanktis ANT/505 PH505aq	ADOP01000017.1	55100-55013	CCGCATTGCTGGCAAACTAGCCGAAAGGTTAGGACGCAAAGTTTCCGGTCTAAGGCTTTTTAAAAGCTATGGTAGCGGGACTACTGCA
Pseudoalteromonas sp. BSi20429 DNA	BADV01000004.1	32064-32152	CCGCATTGCTGGCAAACTAATCGAAAGATTAGGGCGCAAAGTTTCCGGTCTAAGGCTTTTTATAAAGCTATGGTAGCGGGACTACTGCA
Pseudoalteromonas sp. BSi20652 DNA	BADT01000169.1	30238-30326	CTGCATTGCAAGCAAACTAATCGAAAGATTAGGGCGCAAAGTTCCCGGTCTAATACTTTTTATAAAGCGATTTTAGCGGGACTACTGAA
Pseudoalteromonas sp. SM9913 chromosome I	CP001796.1	971601-971683	TAAATTAAATGGCAAACTATGCGAAAGCATAGGACGCAAAGCTTCCAGTCTAAGGCAATCGCTACGATCGTGGGGTTACATTA
Pseudoalteromonas tunicata D2 1099591001413	AAOH01000011.1	15155-15071	GTTCGTAAAGGGCAAACTTAGTGAAAATTAAGGACGCAAAGCTATTGGTCTAAGGGTATTTACCTATGATTGCAAAGCTGCCAAC
Pseudoalteromonas tunicata D2 1099591001414	AAOH01000001.1	581796-581713	GCAAGTCAAAGGCAAGCCACTTGAAAAAGTAGTCACGCAAAGTTACAGATCTAAGGGGAAACCTATGATGGCTGAACTACCAAA
Pseudoalteromonas tunicata D2 1099591001417	AAOH01000007.1	198689-198776	GCACCTATTTGGCAAACTAACCGAAAGGTTAGGACGCAAAGCTTCCGGTCTACCATCATTTTATGATCATGATAGCGGGGTTGCCGCA
Pseudomonas fluorescens HK44 Contig7	AFOY01000007.1	5453-5369	ATACGATAATGGCAAACCCGTCGAAAGGCGGGGACGCAAAACTTCCGGTCTAAAGGCTTCGGCCTATGACAGCGGGGTTACCGAA
Psychromonas ingrahamii 37	CP000510.1	3759112-3759037	GAAGTTGATTCGCAAACCTGGGGAAACCTTGGGGCGCAAAGCTATAGGGCCTGTAAAATGGTAGCCAGTTGCCGAA
Psychromonas ingrahamii 37	CP000510.1	3752582-3752507	GAAAGTCATTCGCAAACTTGGGGAAATTCAAGGACGCAAAACTATAGGGCCTGTAAAATGGCAGCCAGTTGCCAAA
Psychromonas ingrahamii	CP000510.1	1867279-1867369	GCTGGAAAAAAGCAAATTAAGGGAAACCTTAATACGCAAAACCACCGGCCTGTTGATTGACTATTTAGTCTATGGCAGCGGAGTTACCAAG

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Psychromonas ingrahamii 37	CP000510.1	3759584-3759509	ATAACTAATTCGCAAACCTGGGGAAACCCTGGGGCGCAAAGCTATAGGGCCTGTAAAATGGTAGCCAGTTGCCAAG
Ralstonia pickettii 12D chromosome 2	CP001645.1	592517-592437	CAGAGGTCTGGGCAAAACCGGAGTGATCCGGCGACGCAAAGCTACAGGGACTTCTCCAGAAGAAGTCAGCCAGTTGCCCGC
Ralstonia pickettii 12J chromosome 2	CP001069.1	148723-148643	CAGAGGTCTGGGCAAAACCGGAGTGATCCGGCGACGCAAAGCTACAGGGACTTCTCCAGAAGAAGTCAGCCAGTTGCCCGC
Ralstonia solanacearum PSI07 megaplasmid mpPSI07	FP885891.2	25748-25828	CTGTTGCATTTGCAAAGCTGGAGTGATCCGGCGACGCAAAGCCAGGGGGACTTCCGTATCGGAAGTCAGCCAGTTGTCCGC
Ralstonia sp. 5_2_56FAA cont1.4	ACTT01000004.1	7007-6927	CAGAGGTCTGGGCAAAACCGGAGTGATCCGGCGACGCAAAGCTATAGGGACTTCGCTGGACGAAGTCAGCCAGTTGCCCGC
Ralstonia sp. 5_7_47FAA cont1.11	ACUF01000011.1	80800-80880	CAGAGGTCTGGGCAAAACCGGAGTGATCCGGCGACGCAAAGCTATAGGGACTTCGCTGGACGAAGTCAGCCAGTTGCCCGC
Ralstonia syzygii R24	FR854092.1	652037-652117	CTGTTGCATTCGCAAAGCTGGAGTGATCCGGCGACGCAAAGCCAGGGGGACTTCCGTATCGGAAGTCAGCCAGTTGTCCGC
Rheinheimera sp. A13L DRAFT__contig00003	AFHI01000023.1	163830-163744	ACTCAGCAGTGGCACGTCAGCTGAAAAGCTGCACACGCAAAACTATGGGCCTAAGGTTGGATCAACTAAGGTTGCCAGGTTGCAGCA
Rheinheimera sp. A13L DRAFT__contig00004	AFHI01000034.1	24932-24849	GCGCTCGAAAGGCAAGTCTCCCGAAAGGGAGTACACGCAAAGCTGCAGATCTAAGGGGAAACCTATGATGGCTGGGCTGCCGTA
Rhodoferax ferrireducens T118	CP000267.1	4400341-4400428	CAAGTTCAAAAGCACACCCGATCGAAAGACGGGGTCGCAAAGCTTCCGGCCTGACGCATTCGTGCGAAGTGGTAGCGGGGTTGCCCAA

Rhodopirellula baltica SH 1 complete genome; segment 9/24	BX294141.1	222899-223010	CCCTGACAAAGGCAAACCGTTCGAGAGGACGGCACGCAAAACCACGGGTCCGTGAGTCGGTCGATCGCATTGTTTGCGTTCGGCTTGGCTTCAGGAAAGCCGAGTTGCCGTG
Rhodopirellula baltica WH47 cWH470135	AFAR01000123.1	12527-12610	TCAAGAAAACGGCAAACCACGTGTAAACGTGGGACGCAAAGTCATGGATCCATGTTGAAAAACATAGACTGCCAGACCGCCCTG
Rhodopirellula baltica WH47 cWH470162	AFAR01000149.1	3066-2955	CCCTGACAAAGGCAAACCGTTCGAGAGGACGGCACGCAAAACCACGGGTCCGTGAGTCGGTCGATCGCATTGTTTGCGTTCGGCTTGGCTTCAGGAAAGCCGAGTTGCCGTG
Ricinus communis ctg_1100012291151	AASG02030143.1	332-249	TAGTAACAAGGGCAAATCCATCGAAAGATGGAGACGCAAAATCACCGGTCTACGGGCTTATGCCACGACAGCGGGATTGCCGGC
Rubrivivax benzoatilyticus JA2 contig_67	AEWG01000067.1	15417-15331	GCGGCCGATGGGCAAACCCGGCGAAAGCCGGGGACGCAAAGCTTCCGGGCTACGGGCGGCAACGCCTACGCCAGCGGGGTTGCCGTC
Ruminococcus albus 7	CP002403.1	1557401-1557482	ATAGTAAAAAAGCAAAACTACTGAAAAGCAGTGACGCAAAGCCAAGGGTCTAAGCCGAAAGGTATGACAGCCGGTTGCCATG
Ruminococcus albus 7 plasmid pRUMAL01	CP002404.1	212912-212830	ATATCACAAAGGCAAAATTGCTGAAAGGCAGTGACGCAAAGCTAAGGGTCTAAGCTCGAAGAGTATGACAGCCGGTTGCATAG
Ruminococcus albus 7 plasmid pRUMAL01	CP002404.1	269767-269848	AAAATATAAAAGCAAAATTGCTGAAAAGCAGTGACGCAAAGCCAAGGGTCTAAACCGTATGGTATGACAGCCGGTTGCTATA
Ruminococcus lactaris ATCC 29176 R_lactaris-2.0.1_Cont512	ABOU02000033.1	53420-53326	AAGTTATACGGGCAAACTTGACGAAAGTCAGGGACGCAAAGCCAGATGGGGCTAAAATCCAGAGAGATTTTGGATAATGCCAGCCGGTTACAAGA
Ruminococcus obeum A2-162 draft genome.	FP929054.1	771178-771253	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTTTAAAATGGCAGCCAGTTGCATGA
Ruminococcus obeum	FP929054.1	909571-909654	TAAATTCAAAGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCATGGGTCTAAGGTCGTGAGATTATGACAGCCGGTTGCCGCA

A2-162 draft genome.			
Ruminococcus obeum A2-162 draft genome.	FP929054.1	341399-341474	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATAA
Ruminococcus obeum A2-162 draft genome.	FP929054.1	2343838-2343928	TTATTTTAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGCCAGAAGGGGCTAAAGTCAGAAAGTTTGACCAGGTCAGCCGGTTGCCACT
Ruminococcus obeum A2-162 draft genome.	FP929054.1	2384071-2384151	TTAATAAAAAGGCATAGCCGGGGAAATCTGGTGACGCAAAACTATAGGGTCTAAGCAAATGTATGACAGCCAGTTGCAGGA
Ruminococcus obeum ATCC 29174 R_obeum-MSIQ_Cont105	AAVO02000002.1	48259-48176	ATAGCATAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGCCACGGGTCTAAGGTCGTGAGACTAAGGCAGCCGGTTGCCGCA
Ruminococcus obeum ATCC 29174 R_obeum-MSIQ_Cont209	AAVO02000011.1	91921-91996	TAAGGAAATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Ruminococcus obeum ATCC 29174 R_obeum-MSIQ_Cont29.1	AAVO02000031.1	25601-25676	GAAAATAATTGGCAAAGCAGACGAAAGTCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATAA
Ruminococcus obeum ATCC 29174 R_obeum-MSIQ_Cont64.1	AAVO02000044.1	1325-1245	TTTAAAAAAAGGCATAGCCGGGGAAATCCGGTGGCGCAAAACTATAGGGTCTAAGCAAATGTATGACAGCCAGTTGCAGGA
Ruminococcus sp. 5_1_39B_FAA cont1.118	ACII01000118.1	6788-6713	ATACAGTATCAGCAAAACAGTCGAAAGGCTGCGGCGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGCATTT
Ruminococcus sp. 5_1_39B_FAA cont1.121	ACII01000121.1	26274-26181	GGCATTTATTGGCAAACCGGTTGAAAAGCCGGGGCGCAAAGCCAGAAGGAGCTAAAGTCAGATTGAAATCTGGCCATGCCAGCCGGTTGCATCA
Ruminococcus sp. 5_1_39B_FAA cont1.45	ACII01000045.1	245-155	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGACGCAAAGCCAGAAGGGACTAAAGTCAGAAAGTTTGACCATGTCAGCCGGTTGCCACT

Ruminococcus sp. 5_1_39B_FAA cont1.47	ACII01000047.1	8271-8196	TATGGAAATTGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Ruminococcus sp. SR1/5 draft genome.	FP929053.1	1999710-1999623	TATATATAAAGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCATGGGTCTAAGGTCCGAAGGATGACTATGACAGCCGGTTGCCGCA
Ruminococcus sp. SR1/5 draft genome.	FP929053.1	1653120-1653195	AAGGATGATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Ruminococcus sp. SR1/5 draft genome.	FP929053.1	79312-79402	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGTCGCAAAGCCAGAAGGGACTAAAGTCAGAAAGTTTGACCATGTCAGCCGGTTGCCACT
Saccharophagus degradans 2-40	CP000282.1	787494-787401	CACTCTAAATGGCTAACCGTCGCGAAAGCGCGGCCACGCAAAGCTTCCGGTCTAAGGGTATGTAAACCATATCTACGATAGCGGGGTTGCTGGA
Saccharophagus degradans 2-40	CP000282.1	989437-989348	CAACGATAAAGGCAAACCCGCGGTAACGTGGGGACGCAAAGCCAGTGCCCAACTACTTGTAATTTAAGATTGGGTCGAACGGTTACCGAA
Sediment metagenome	ADZX01000355.1	56-1	AACCCGAAAAGGCAAATCCGCCGCGAGACGGAGGCGCAAAACTACGGGCCGCCAAT
Sediment metagenome	ADZX01000355.1	222-140	TACCCGAAAAGGCAAACCCGCCGTGAGGCGGGGGCGCAAAACTGCGGGTCCCGAAAAGGATTTGGGAAAGCCGAGTTGCCGAA
Shewanella baltica BA175	CP002767.1	3998688-3998589	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica BA175	CP002767.1	1523461-1523549	GCATGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS117	CP002811.1	3702523-3702435	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS117	CP002811.1	1124968-1125067	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS155	CP000563.1	3606440-3606352	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS155	CP000563.1	1022723-1022822	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS183 ctg588	AECY01000004.1	145226-145127	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA

Shewanella baltica OS183 ctg589	AECY01000003.1	303129-303041	GCATGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS185	CP000753.1	4117744-4117645	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS185	CP000753.1	3685694-3685606	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS195	CP000891.1	4224626-4224527	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS195	CP000891.1	3806662-3806574	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS223	CP001252.1	4025248-4025149	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS223	CP001252.1	1519289-1519377	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS625 ctg153	AGEX01000004.1	490432-490344	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS625 ctg156	AGEX01000001.1	127426-127327	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella baltica OS678	CP002383.1	3754926-3754838	GCGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTCTGTACCTATGATAGCGGGGATACCACA
Shewanella baltica OS678	CP002383.1	4172590-4172491	TACCGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAATGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella denitrificans OS217	CP000302.1	2534228-2534317	TGCTGTGGAAGGCAAACCAGTTTTAAAGACTGGGACGCAAAGCCTCCGATCTAAAGGTTTGCTTGTACCTATGATAGCGGGGATCCCACA
Shewanella halifaxensis HAW-EB4	CP000931.1	4237453-4237540	ACAGCGAAAAGGCAAACCAGTTGAAAGACTGGGACGCAAAACCACCGGTCTAAGGGTCAATTGTACCTATGATAGCGGGGATGCCATT
Shewanella halifaxensis HAW-EB4	CP000931.1	4546741-4546656	TGATGAAAAAGGCAAAACCTGTGAAAGCGGGTGACGCAAAGCATCCAGCCTAACGGAGCAACTCCTACGGCAGTGGCGCTACCGCA
Shewanella loihica PV-4	CP000606.1	1879203-1879288	CTCTCGAAACGGCAAGCATTAAGTAATTAATGTACGCAAAGCCACAGGCCCTAATTGCATAGCAAAAGGGTGGCTGGGTTACCGAA
Shewanella oneidensis MR-1	AE014299.1	1112481-1112574	CACCGTATTGGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTAACTAAGATAGCGGGGTTGCTTAA
Shewanella pealeana ATCC 700345	CP000851.1	4449140-4449058	TGATGAAAAAGGCAAAACCTGTGAAAGCAGGTGACGCAAAGCATCCAGCCTAAGGGGACACCTATGGCAGTGGCGCTACCGCA

Shewanella putrefaciens 200	CP002457.1	712651-712733	CTGACGAACAGGTACACCCGTTGTGAGACGGGGTCGCAAAGCTTCGGGTCTTGATTTTTTATTAAGATAGCCGGGTTGCCGAA
Shewanella sediminis HAW-EB3	CP000821.1	3858383-3858465	CTACGATAAAGGCAAAACCGGGGTAACCCGGCGACGCAAAACCAGTGCCCAGGCAGAGATGCGGGGGTCGAACGGTTACCGAA
Shewanella sp. ANA-3 chromosome 1	CP000469.1	3587317-3587229	TAGTGTAAAAGGCAAACCAATCGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGTTCGTTTGTACCTATGATAGCGGGGATACCACA
Shewanella sp. ANA-3 chromosome 1	CP000469.1	1061668-1061763	CACCGTATTTGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTGTAACTAAGATAGCGGGGTTGCCTCT
Shewanella sp. HN-41 44_14	AFOZ01000014.1	232524-232623	TACTGTATTTGGCAAACTAATTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTTGTAAAGGGATTTTTTAGTGAACTAAGATAGCGGAGTTGCCGCA
Shewanella sp. HN-41 44_15	AFOZ01000015.1	27168-27256	ATGTGTAAAAGGCAAACCAGTTGAAAAACTGGGACGCAAAGCCTCCGGTCTAAGGGCTCGTCCGTACCTATGATAGCGGGGATACCACA
Shewanella sp. MR-4	CP000446.1	3621627-3621532	CACCGTATTTGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTGAAACTAAGATAGCGGGGTTGCCTCA
Shewanella sp. MR-4	CP000446.1	3357377-3357290	TATTGTGAAAGGCAAACCAATTGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGTCGTTTGTACCTATGATAGCGGGGATACCGCA
Shewanella sp. MR-4	CP000446.1	4029417-4029328	CTGACGAACAGGCACACCCGTTGTGAAACGGGGTCGCAAAGCTTCGGATCTTATTGTACAGGCTGTTATTAAGATGGCTGAGTTGCCGAA
Shewanella sp. MR-7	CP000444.1	675036-675125	CTGACGAACAGGCACACCCGTTGTGAAACGGGGTCGCAAAGCTTCGGATCTTATTGTACAGGCTGTTATTAAGATGGCTGAGTTGCCGAA
Shewanella sp. MR-7	CP000444.1	3427742-3427655	TATTGTGAAAGGCAAACCAATTGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGTCGTTTGTACCTATGATAGCGGGGATACCGCA
Shewanella sp. MR-7	CP000444.1	1084468-1084563	CACCGTATTTGGCAAACTAATTGAAAAATTAGGACGCAAAGCCTCCGGTCTAAGGTTGTAAAGGGATGTTGAAACTAAGATAGCGGGGTTGCCTGA
Shewanella sp. W3-18-1	CP000503.1	3966333-3966251	CTGACGAACAGGTACACCCGTTGTGAGACGGGGTCGCAAAGCTTCGGGTCTTGATTTTTTATTAAGATAGCCGGGTTGCCGAA
Shewanella violacea DSS12 DNA	AP011177.1	990519-990638	TTGAATAAAAGGCAAACCAATCGAAAGATTGGGACGCAAAGCCTCCGGTCTAAGGGGATAGTGTTGAGGCGGTCGTTGTCTCAGTATTATCGCAGTACCTAAGATAGCGGGGATACTTCA
Shewanella woodyi ATCC 51908	CP000961.1	1418939-1419059	AATGTACAAAGGCAAACCAATCGAAAGGTTGGGACGCAAAGCTTCCGGTCTAAGGGGATAGTGTTTGAGAGGGTCGCACTCTTAACGTTATTTTGGTACCTATGATAGCGGGGATGTTACA
Shewanella woodyi ATCC 51908	CP000961.1	4728867-4728769	CCATGTATTTGGCAAACTAGCTGAAAAGTTAGGACGCAAAGCTTCCGGTCTAAGGTGCAGGACTCACTGAGTGCTCATTAAGATAGCGGGGTTGCCACG

Sideroxydans lithotrophicus ES-1	CP001965.1	1136910-1137012	CGCCTGCAAGGGCAAACCCGTCGAAAGGCGGGGACGCAAAGTTTCCGGGCTAAAGGACATGTTCCTATTCGACATCAGGTCGAGTGCCAGCGGGGCTGCCAGG
Sideroxydans lithotrophicus ES-1	CP001965.1	2226794-2226883	GTAAACTAATAGCAAACCTATTGAAAGGTAGGGACGCAAAGTTTCCGGTCTAAGGGGTCTGCAAAGCCCTATGACAGCGGGATTGCCGGT
Sideroxydans lithotrophicus ES-1	CP001965.1	1143960-1144044	TATTGATAAAGGCAAACCTGTTGAAAAGCAGCGACGCAAAGTTTCCGGTCTAAGGCAAAAAACCTTTGATAGCGGGGCCGCCAAA
Sideroxydans lithotrophicus ES-1	CP001965.1	1575864-1575784	TCTTCAACTTGGCAAACATGCTGAAAAGTATGGACGCAAAGTCTCCGGCCTAAGGGAAGCTATGGCAGCGGGACTGCGATA
Slackia exigua ATCC 700122 S_exigua-2.0.1_Cont0.5	ACUX02000006.1	76573-76498	GCAATTACTCGGCAAACCCGTCGAAAGGCGGCGACGCAAAGCTACAGGGCCTTTCATATGGCAGCCAGCTGCAACT
Slackia exigua ATCC 700122 S_exigua-2.0.1_Cont1.6	ACUX02000016.1	4891-4816	CAAATATAATGGCAAACCCGTCGAAAGACGGCGACGCAAAGCTATAGGGCCTTTCGCATGGCAGCCAGCTGCGATT
Sphaerobacter thermophilus DSM 20745 chromosome 2	CP001824.1	1166952-1166875	AGCTGAAAAGGGCAAACCCGTCGCGAGGCGGGGGCGCAAAGCCATGGACCTCCACCCGGAGGCCGCCAGGCTGCCAGC
Sphingobium chlorophenolicum L-1 chromosome 2	CP002799.1	74281-74206	TCCCGACAGGGGCAAACTGCCGGTGACGGCAGGACGCAAAGCTTCCGGGCTGTCAACAGCTAGCGGGGTTGCGAAG
Sphingobium sp. SYK-6 DNA	AP012222.1	431488-431561	CTTCGCCAAGGGCAAACCGTCGGTAACGGCGGGACGCAAAGCCTCCGGCCCCATGGGGTAGCGGGGTTGCCGGA

Sphingomonas sp. KC8 contig05	AFMP01000005.1	19735-19660	TTCGTTGAAGGGCAAACTGTCGGCGACGGCAGGGCGCAAAGCCTCCGGGCTCCAAGGAGCTAGCGGGGCCGCCAGC
Sporolactobacillus inulinus CASD contig000045	AFVQ01000045.1	158-241	TAATCGAAATGGCACACTTATTGAAAGATAAGGTCGCAAAGCCACGGGCCTAAGGCAATGAGCTAGGGTAGCCGGGCTGCCGAA
Sporosarcina newyorkensis 2681 contig00077	AFPZ01000077.1	28087-27977	AGAAGTTAAAGGCAAACTGATCTGAAAGGGCAGGACGCAAAGCTTAGGGTCTAAAGTTTAGGGATTATTTAAAAGTCCTGCAATCTAAACAATGATCGCCTGGTTACCAAG
Streptococcus sobrinus TCI-157 contig00006	AGHO01000006.1	8967-8882	CTTCGAAAATAGCAAACTCATTGAAAAATGAGGACGCAAAGCTGCGGGCCTAAAGAAGTATTTCCATGGTAGCCAGGGTTGCCAAA
Streptococcus sobrinus TCI-157 contig00006	AGHO01000006.1	11648-11562	AATTGAAAAAGGCAAACTTATCGAAAGGTAAGGACGCAAAGCTACGAGTCTAAAATCCTTCTGGATAATGATAGTCGGGTTGCCAGG
Streptococcus sobrinus TCI-157 contig00162	AGHO01000162.1	658-743	AAATGTAAAAGGCAAACCAATACGAAAGTTTGGGACGCAAAGTCACGGATCTAATGTCTTAAAACAATGATGGCCGGACTGCCAAA
Streptococcus sobrinus TCI-157 contig00508	AGHO01000508.1	2825-2913	AACAGATAAAGGCAAACCATCTGAAAGGGTGGGACGCAAAGCTTCGGGTCTAAGGTAGATTTTTTTACTATGATGGCTGGGCCACCTTA
Streptococcus sobrinus TCI-157 contig00601	AGHO01000601.1	995-910	AAATGATAAAGGCAAATTCATCGAAAGGTGAAGACGCAAAGCTATAGGGACTAAGATCGTGGAGATTAAGTCAGCCAGTTACCGAT
Streptococcus sobrinus TCI-157 contig00961	AGHO01000961.1	927-797	TCGACGAAAGGGCAAAATCATTGAAAAGTGATGACGCAAAGCTATAGGGGCTTAGGGGTAACGAAGATCGATTTTTTCTACATGATAGCAAAAGTTATGACATTCATTACGCTTGCCAGCCAGTTACCGAA
Streptococcus sobrinus TCI-157 contig02613	AGHO01002613.1	128-211	ATTAAGTTTGGGCAAATTTTACGAAAGTAAAAGACGCAAAGCCACGGGCCTAAAGCGAAATGCTATGGCAGCCGGGTTGCCAAG
Stromatolite metagenome	ABMV01167972.1	1-100	AAAGCAAACTGCTCGAAAGCGCAGGACGCAGAGCCACGGAGCTAACGACCGAAAGCGGACGTTTCCGTCCGCTCAGGTACATGCCCGCCGGGCCGCC

10218074			ATG
Sulfobacillus acidophilus TPY	CP002901.1	2801999-2801912	TGTCGTTCAAGGCACAACATCCGAAAGGGTGTGTCGCAAAGCCAGAGGGTCTAAGCCCTGAAGGGGGTATGACAGCCGTGCTGCCGAC
Sulfobacillus acidophilus TPY	CP002901.1	1797527-1797611	GAACGATAAAGGCAAACCATGCGAAAGCATGGGACGCAAAGCTAGAGGGGCTTATCGCATCCGCGATTGCCAGCCAGCTGCCGAA
Sulfuricurvum kujiense DSM 16994	CP002355.1	1608921-1608845	AAAATTCAAAGCCAAACCTGCTGTGAAGCAGGGACGGAAAGCCGCGGGTCTCAAAGCGAGATAGCCGGGTTGTCATT
Sulfurimonas autotrophica DSM 16294	CP002205.1	2068864-2068781	ACTATAATTTGCCAAACTTATTGTGAAATAAGGACGGAAAGCTTTGAGTCTTAATTAGTAAATTAAGATTGTCGGGTTGCGATT
Sulfurovum sp. NBC37-1 genomic DNA	AP009179.1	2164685-2164587	GAAAGAAAACGCCACCCCTGTTGCGAAGCAGGTTCGGAAAGCTATGGGTCTTTGATGCTGTCGCCTGGCAGCAGACGAGAAGATCGCCAGGTTGCCTAA
Sulfurovum sp. NBC37-1 genomic DNA	AP009179.1	1220413-1220339	TCTAATATATGCCAAACCTGTTGCGAAACAGGGACGGAAAGCCACGGGTCTCATGAAGATAGCCGGGTTGCCAGA
Sulfurovum sp. NBC37-1 genomic DNA	AP009179.1	1968269-1968348	ACGATGAAAAGCCAAACCTGCTGTGAAAGCAGGAGCGGAAAGTTGTGGGTCTTCATTTTGAAGACAGCCAGACTGCCAAG
Sulfurovum sp. NBC37-1 genomic DNA	AP009179.1	1900452-1900372	AAATGAAAAAGCCAAACTTGTTGTGAGACAGGGACGGAAAGTTATGGGACTTTAGAATATCAAGTTTACCAGACTGCCATA
Symbiobacterium thermophilum IAM 14863 DNA	AP006840.1	3227495-3227385	CAGCGATAAAGGCACACCCGCCGAAAGACGGGGCCGCAAAGCCACGGGGCTACAGGAAGCGGGCGCCGCCCTGCCGGGTCTCCCGCCTCCCATGCTAGCCGGGCTGCCGCT

Syntrophobacter fumaroxidans MPOB	CP000478.1	611274-611193	GTTAGAAAAAGCCAAATCCATCGCAAGGTGGAGACGGAAAGCCGCGGGTCTCCTTCCCATTCGAGACGGCCGGGTTGCCTGA
Syntrophobacter fumaroxidans MPOB	CP000478.1	4137263-4137350	GTTCGATAATGGCAAACTGGTCGAAAGACCGGGACGCAAAGCCACTGGCCTAAGTCCCCTCTGAGGATACGGTAGCAGGGTCGCCGGG
Syntrophobacter fumaroxidans MPOB	CP000478.1	4310866-4310955	ACCCGAAAAAGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCACTGGCCTACGTCTTCCGAGGGAGGATAGGGCGGCAGGGTTGCCGGA
Syntrophobacter fumaroxidans MPOB	CP000478.1	4434364-4434438	GTCAGAAAACGCCAACCCTGTTGCGAGACGGGGACGGAAAGCCGCGGGTCTCATGGAGATGGCCGGGTTGCCTGA
Syntrophobacter fumaroxidans MPOB	CP000478.1	4546395-4546307	ACCTGTAAAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCGCTGGCCTAAGTCCCCCGCGTGGGATATGGCAGCAGGGTTGCCAGG
Syntrophobacter fumaroxidans MPOB	CP000478.1	4864953-4864879	TTGTGAAAAAGCCAAACCTCCCGCGAGGGGGGGACGGAAAACCGCGGGTCTCACGTAGACGGCCGGGTTGCCTGA
Syntrophobacter fumaroxidans MPOB	CP000478.1	3150567-3150651	GTTTGGAAAAGGCAAACTATTCGAAAGACTGGGACGCAAAGCTTCTGGCCTAAGTCCAAAAGGATATGGCAGCAGAGCCGCCGAG
Syntrophobotulus glycolicus DSM 8271	CP002547.1	1225438-1225527	TATCGCTAAGGGCAAACCCGCTGAAAAACGGGGATGCCAAAGCTATAGGGTCTAAGGCGCATCTAACGCTATGATAGCTTGGCTGCCAAA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	1642369-1642294	TACTGACAATGGCAAACCTGCTGAAAAGCAGCGACGCAAAGCTAAAGGGCCTGTAACATGGCAGCCAGCTACCAAA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	1070289-1070372	GAGCGATAAGAGTAAACCTGTCCAAAGACAGGGACGCAAAGCTATAGGGTCTAGGTGCTTACAGTTCAAAAGTCAGTTATTAAC
Syntrophobotulus glycolicus DSM 8271	CP002547.1	1516492-1516575	TGACGATAAGAGCACACCTTCCGAAAGGATGGGCCGCAAAGTCACGGGTCTAAAGCGATTTGCCAGGATTGCCGGACTGCCGAA
Syntrophobotulus glycolicus	CP002547.1	829966-830072	GAACTGAAAAGGCAAACTTGCCGAAAGGCAAGGACGCAAAGCTACGGGTCTAAAGCCCGGCATTTTCTTGAGAAAAAATGCCGGGCCAGGACCGCCG

DSM 8271			GGCCGCCGAA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	20507-20418	TAAAGCCAAGGGCAAACCCATCAAAAGATGGGGACGCAAAGCCATAGGGTCTAAGGTGCTTTACTGCGCTATGATAGCCTGGCTGCCAAA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	3225788-3225704	ATATGATAAGAGTAAACCTGTCGAAAGACAGGGACACAAAGCCACGGGTCTAAAGTAATCTAACCATGATAGCCGGGTTGCCATA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	3349441-3349353	GAATATTAAGGGCAAACCTGTGGAAATGCAGGGACGCAAAGCTATGGGTCTAAAGATATGAGAGTATCAATGACTGCCAGGCCGCTATT
Syntrophobotulus glycolicus DSM 8271	CP002547.1	1642478-1642403	TATTGACAATGGCAAACCTGCTGAAAAGCAGCGACGCAAAGCTAAAGGGCCTGTAACATGGCAGCCAGCTACCAAA
Syntrophobotulus glycolicus DSM 8271	CP002547.1	3108266-3108357	TATTGCCAAGGGCAAACCCGGTGAAAGCCGGGGGCGCAAAGCTACAGGGTCTAAGGCGTTTGATAAAACGCTACGATAGCCTGGCTGCCAAA
Syntrophothermus lipocalidus DSM 12680	CP002048.1	1229385-1229300	AACAACTAAGGGCAAACTCACCGAAAGGTGAGGGCGCAAAGCCTCGGGCCTAAGGGCGAGGAGTCTATGGCGGCCGGGTTGCCTTA
Syntrophothermus lipocalidus DSM 12680	CP002048.1	1301529-1301443	TCCTGATAAAGGCAAAACCATCCAAAGATGGTGACGCAAAGCTATAGGGGCTAAAGCGAACATTCGCTATGCCAGCCAGCTGCCGGG
Tepidanaerobacter sp. Re1	CP002728.1	939896-939796	GATATAATTTGGCAAACTCCTCCAAAGAGGTGGGCGCAAAGCCATGGGCCTAAAGTTTTTCTGGCTTTTTCGCGAAAAACTATGGCAGCCAGGCTGCTGGT
Teredinibacter turnerae T7901	CP001614.2	634901-634815	CTGATAAAAAGGCACGCTGACGCGAAAGCCCAGCACGCAAAATTACCGGTCTAAGGACTCAAGGTCTACGACAGCGGGATCGCCAGA
Thauera selenatis AX	CACR01002012.1	2225-2139	CGAGTACAAAGGCAAACGGGGTGGAAGCCCCGGACGCAAAGCCACGGACCCAAAGCTGGTTTCCAGACGGGTGGCCGGGTTCCCTCG
Thauera selenatis AX	CACR01001638.1	11522-11608	CGAGTCCAAAGGCAAACGGGGCGGAAGCCCCGGACGCAAAGCTACAGGCCCGATCCTGGATGTCAGGGGGGCGGCTGGGTTTCCTCG

Thermaerobacter marianensis DSM 12885	CP002344.1	198923-199054	GCCGCGAACGGGCAAACCCGCCGAAAGGCGGGGGCGCAAAGCCACGGGTCTACCGCGCGGCGGGAGCGGAAGGCGGCGACGGGCAGCCGCCGCGCCTCCGGCCCCGCCGGCTACGACGGCCGGGCTGCCGAA
Thermaerobacter marianensis DSM 12885	CP002344.1	1187425-1187517	CAGCGACAAAGGCACCCCTGCCGAAAGGCAGGCTCGCAAAGTCACGGGTCTACGGTCCCGCTCCGGCGGGACTATGACGGCCGGACTGCCGAA
Thermaerobacter subterraneus DSM 13965 Tsubt_Contig168	AENY01000069.1	35051-35143	CAGCGACAAAGGCACCCCTGTCGAAAGGCAGGTTCGCAAAGTCACGGGTCTAAGGTCCCGCCAGCACGGGACTATGACGGCCGGACTGCCGAA
Thermaerobacter subterraneus DSM 13965 Tsubt_Contig194	AENY01000095.1	131782-131726	CCGCGATAAAGGCAAACCCGCCGAAAGGCGGGGGCGCAAAGCCACGGGTCTACCGCA
Thermincola sp. JR	CP002028.1	2870835-2870749	TATAAAAGTTGGCAAACTTCGCGAAAGTGAAGGACGCAAAGCTATGGGTCTACGGCCAGGGGAGGTTATGATTGCCAGGTTGCGGTT
Thermincola sp. JR	CP002028.1	434673-434757	TATATCGTTTGGCAAACCATGCGAAAGCATGGGGCGCAAAGCCATGGGTCTACGGCCGAAGGGCCAGGATTGCCAGGTTGCAGTA
Thermincola sp. JR	CP002028.1	2921021-2920938	CCACGATAAAGGCTAAGCCGTCGAAAGACGGTGGCGCAAAGCCATGGGTCTAAAGCTTATTGCTATGATCGCCAGGCTGCCGAA
Thermincola sp. JR	CP002028.1	891749-891848	TGGTGAAAAGGGTAAACTTATCGAAAGATAAGGACACAAAGCCATGGGTCTACGGAATGGTGTCCAGTGGTCATTATTCTATGATTGCCAGGCTGCCGAA
Thermincola sp. JR	CP002028.1	1107721-1107812	AAGTCATTTTGGCAAACTCCGCGAAAGTGGGGGACGCAAAGCATGGGTCCTGGATACGCCGCGGGAAAGGCAGGGATCGCCAGGTTGCAGCA
Thermincola sp. JR	CP002028.1	728265-728363	TTTCGAAAAAGGCAAACCTGTCGAAAGGCGGGGACGCAAAGCTGCGGGTCTAAGGAATTAGTGGCCGGTCCACTACTCTATGACAGTCGGGCTGCCGAA
Thermincola sp. JR	CP002028.1	1610190-1610104	CTTTGATAAAGGCAACTTTATCGAAAGATAAAGGCGCAAAACTACGGGCCTAAAGCGACATAACGCAATGGTTGCCGGGTTGCCGAA
Thermincola sp. JR	CP002028.1	2160379-2160275	TCAGTGTTGGTGTAAACCCAGTGAAAGCTGGGGGCGCTAAAGCCCAAGGGCCTAAGGATACAGTGGGGCCAATGACCGCTGATCTACGGCAGCCGGGATGCAAGG
Thermincola sp. JR	CP002028.1	2411555-2411433	GATAATATTGGGCAAACCCGTACGAAAGACGGGGGCGCAAAGCCGTGGGTCTACGAATTAGTGACCAGTGGCCGGTGACTATGTGGCTACTGACCACTGATTTATGACAGCCTGGTTGCCGCA

Thermincola sp. JR	CP002028.1	1656944-1657065	GACTGACAAAGGCAAACTTGTCGAAAGACAGTGACGCAAAGCTATTGATCTAAGGCACAGCAGCAGTTGGCAACCATATGATTTTCCAACTGCCCGGTTGCTATGACCGCAGGGCTGCCAAC
Thermincola sp. JR	CP002028.1	1894931-1894781	GTCCCGAAACGGCAAACCAGGTGAAAATCTGGGACGCAAAGCCACGGGTCTACGAATTGGTGACTAGTGACCAGTGACCGGTAAATAAAAAATAGACCGGTTACTGGCTGTGGACCACTGGTCGCTGATTTACGACAGCCGGGTTACCGAA
Thermoanaerobacter brockii subsp. finnii Ako-1	CP002466.1	1533383-1533296	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter ethanolicus CCSD1 ctg00037	ACXY01000004.1	66574-66487	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter ethanolicus JW 200 ctg1011	AEYS01000015.1	35189-35102	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCTACGGGTCTAATGCAACAGTTTTGCTATGATAGCCGGGCTACCAAC
Thermoanaerobacter ethanolicus JW 200 ctg1018	AEYS01000011.1	74563-74493	TATTGAAAAAGGCAAGGGCGCAAAGCCACAGGTCTACAGTATGCAAATACTATGACGGCTGGGTTGCCAAT
Thermoanaerobacter italicus Ab9	CP001936.1	837524-837611	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCAATAATCTTGCTATGACAGCCGGGCTGCCAAC
Thermoanaerobacter italicus Ab9	CP001936.1	1888656-1888744	TGTCGATAAGGGCACACTTATCGAAAGGTAAGGTCGCAAAGCCATGGGTCTAAGGGAATGAATATTCCTATGATCGCCAGGCTGCCGAA
Thermoanaerobacter italicus Ab9	CP001936.1	2124854-2124940	TTATGAGAAAGGCAAACCTACCGAAAGGTAAGGACGCAAAGCCACAGGTCTAAGGCATGCAGATGCTATGACGGCTGGGTTGCCAAT
Thermoanaerobacter mathranii subsp. mathranii str. A3	CP002032.1	1839377-1839465	TGTCGATAAGGGCACACTTATCGAAAGGTAAGGTCGCAAAGCCATGGGTCTAAGGGAATGAATATTCCTATGATCGCCAGGCTGCCGAA
Thermoanaerobacter mathranii subsp. mathranii	CP002032.1	851894-851981	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCAATAATCTTGCTATGACAGCCGGGTTGCCAAC

str. A3			
Thermoanaerobacter mathranii subsp. mathranii str. A3	CP002032.1	2041185-2041271	TTATGAGAGAGGCAAACCTACCGAAAGGTAAGGGCGCAAAGCTACAGGTCTGAGTCATGCAGATGCTATGACGGCTGGGTTGCCAAT
Thermoanaerobacter mathranii subsp. mathranii str. A3	CP002032.1	2214234-2214145	TGGCGTTAAAGGCAAACCCATTGAAAAATGGGGACGTAAAGCTACAGGGTCTAAGGTGCCCACAGGCACTATGACAGCCTGGCTGCCGCT
Thermoanaerobacter pseudethanolicus ATCC 33223	CP000924.1	1541170-1541083	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter sp. X513	CP002210.1	763697-763784	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter sp. X514	CP000923.1	2190645-2190558	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter sp. X561 ctg62	ACXP02000002.1	787740-787653	TGTTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCCACGGGTCTAAAGCGATAGTTTTGCTATGATAGCCGGGCTGCCAAC
Thermoanaerobacter tengcongensis MB4	AE008691.1	706140-706227	CTTCGATAAGGGCAAACCCGTCGAAAGGCGGGGGCGCAAAGCCACGGGCCTAAATCCCTGATTGGGACATGGTAGCCGGGCTGCCGAA
Thermoanaerobacter wiegelii Rt8.B1	CP002991.1	948288-948375	TGCTGAAAAAGGCAAACTCGTCGAAAGGCGGGGACGCAAAGCTACGGGTCTAATGCAACAGTTTTGCTATGATAGCCGGGTTACCAAC
Thermoanaerobacterium xylanolyticum LX-11	CP002739.1	2097303-2097218	ACTTGAAAAGAGCAAACTTATCGAAAGATAAGGACGCAAAGCCACGGGTCTAAAGCAGATTCTGCTAAGATGGCCGGGTTGCCAGC
Thermobacillus composti KWC4 ctg146	AGFE01000025.1	68011-68098	ATCAGCAAAGGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCTAAGGGTCTACGGCTCCGCACGAGCTATGATCGCCTGGTTACCGGG

Thermobacillus composti KWC4 ctg154	AGFE01000013.1	14027-14110	AGCTGATAAAGGCAAACCATATGAAAATATGGGACGCAAAGCTACGGGTCTAAGGCGGAATGCTATGACAGCCGGGCTGCCGGA
Thermobacillus composti KWC4 ctg157	AGFE01000012.1	86144-86271	TTGGGATCAAGGCAACCTGCGCGAAAGCGCAAGGGCGCAAAGCTACAGGGGCTAATCGGCGGGATGGACCGGACCTCCGCAATTCGGGCGGACGGGCGGTTCGCGCCGGATGCCAGCCAGCTGCCGAA
Thermobacillus composti KWC4 ctg160	AGFE01000005.1	138345-138242	AAAGAAAAGAGGTAAACCCGTACGAAAGTCGGGGACGCAAAGCCACGGGTCTAAAGCGTGGGACTATGACGTCCGGATCACGCCATGACAGCCGGGCTGCTCTA
Thermobaculum terrenum ATCC BAA-798 chromosome 1	CP001825.1	394631-394557	CCCAGAAAAGGGCAAACCCGTCGTGAGATGGGGACGCAAAGCCACGGGACTCTAAGAGTCAGCCGGGCTGCCTGG
Thermobaculum terrenum ATCC BAA-798 chromosome 2	CP001826.1	961185-961111	CCCAGAAAAAGGCAAACCTGTCGCGAGGCAGGGGCGCAAAGCCACGGAGCTCTCGAAGCTAGCCGGGCTGCCTGG
Thermosediminibacter oceani DSM 16646	CP002131.1	1935923-1935836	CCCTGTAAAGGGCAAACCCGGTGAAAGCCGGGGGCGCAAAGCTACGGGCCTAAGGGTAATAAAGCCTATCGGCCGCCGGGCTGCCGGG
Thermosediminibacter oceani DSM 16646	CP002131.1	1748978-1748891	CAGCGAAAAGGGCAAACTCACCGAAAGGTGGGGGCGCAAAGCCATAGGGTCTAAGGTGCTTTTGCACTATGACAGCCTGGTTGCCGCT
Thermosediminibacter oceani DSM 16646	CP002131.1	1606753-1606665	CAGAGAAAAGGGTAAACTCAATGAAAGGTAGGGGTGCAAAAGCCATAGGGTCTAAGGTGCATTTACATTATAACAGCATGGCTGCCGCT
Thermosediminibacter oceani DSM 16646	CP002131.1	472224-472131	GCCGATAAAAGGCAAACCTGTCGAAAGGCAGGGGCGCAAAGCCATGGGCCTACGGCTCCATTGATGATGGAGCTACGGCTGCCAGGTTGCCGGC
Thermosediminibacter oceani DSM 16646	CP002131.1	2216288-2216203	TATACCAAAGTGCAAACCAGCCGAAAAGCTGGAGTGCCAAGCTGCGGATATAAAGCTTTTAATGCTATGGTAGCCGGGCTGCCGAT
Thermosediminibacter	CP002131.1	1785307-1785219	TTCCGTCAAGGGCAAACCGTCGAAAGGTAGGGACGCAAAGCCACGGGCCTACGAAGAGACAAGCTCTTCATAGCAGCCGGGCTGCCGGG

oceani DSM 16646			
Thermosinus carboxydivorans Nor1 ctg43	AAWL01000017.1	11338-11251	ACATAAGTTGGGCAAACCCGGCGAAAGCCGGGGACGCAAAGCCATGGGTCTAAGGACATTGGGTGTCTATGATCGCCAGGTTGCCAAT
Thermosinus carboxydivorans Nor1 ctg45	AAWL01000008.1	69995-70080	CTGAATATTGGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCTAAAGGGTCTAAGGACTTCGTGTCTATGATTGCCAGCTGCCGGT
Thermosinus carboxydivorans Nor1 ctg53	AAWL01000002.1	59937-60025	ATTATCCAAGGGCAAACCTGTCGAAAGGCAGGGACGCAAAGCCAAGGGCCTAAGGAATAGAAATTATTCTATGGCAGCCGGTTGCATGA
Thermovirga lienii DSM 17291	CP003096.1	134111-134022	AGCTGACAAGGGCAAAGCAGGCGAAAGCCTGCGGCGCAAAGCCCAGGGTCTAAGGCGCACATTTCGCGCTATGACAGCCTGGCTGCCGGC
Thermovirga lienii DSM 17291	CP003096.1	1717110-1717196	AACCCGAAAGGGCAAAACCGTCGAAAGGCGGCGACGCAAAGCCGAGGGTCTAAAGCCTTTAAAGGCCATGACAGCCAGGCTGCCGAA
Thermovirga lienii DSM 17291	CP003096.1	1716907-1716993	AATCCGAAAGGGCAAAACCGCCGAAAGGCGGTGGCGCAAAGCCAAGGGTCTAAAGCCTTTAAAGGCCATGACAGCCAGGCTGCCGAA
Thioalkalivibrio sulfidophilus HL-EbGr7	CP001339.1	2479059-2479143	TCTCGACAAAGGCATACCCAGCCGAAAGGCGGGGACGCAAAGCTACCGGTCTACGGGACTTTCCCACGACAGCGGGGTTACCGAA
Thioalkalivibrio sulfidophilus HL-EbGr7	CP001339.1	1221167-1221084	AAACGACAAGGGCATACCCGACCGAAAGGCGGGGACGCAAAACCACCGGTCTACGGCAAACGCCACGACAGCGGAGTTACCGAA
Thioalkalivibrio sulfidophilus HL-EbGr7	CP001339.1	3208761-3208679	ACAGGACAAAGGCAAACCCGTCGAAAGGCGGGGACGCAAAGCCACCGGTCTCACGGAACATCCAAGACAGCGGGGTTGCCCAC
Thioalkalivibrio sulfidophilus HL-EbGr7	CP001339.1	1219780-1219697	TCATCGAAAGGGCATACCCGACCGAAAGGCGGGGACGCAAAACCACCGGTCTACGGCTTCGGCCATGACAGCGGAGTTACCGAA
Thioalkalivibrio	AGFB01000006.1	139895-139987	TCGAGACAAAGGTAAACCCGTCGCAAGGCGGGGACACAAAGCCGCCGGTCCCCGGATTCAAGAACGACAATGGGGGACAGCGGGGCTGCCGCT

thiocyanoxidans ARh 4 ctg49			
Thiobacillus denitrificans ATCC 25259	CP000116.1	532900-532975	ATCCCGAAAGGGCAAACCCGCCGCGAGGCGGGGGCGCAAAGCGACCGGTCTCGAAAGAGATAGCGGCGCTGCCGTG
Thiocapsa marina 5811 ctg455	AFWV01000020.1	58886-58979	TAAGCGAAAGGCCAAACCTACCGAGAGGTAGGGGCGGAAAGTCGCGGATCCTAAGATCCCGGATTCTGGGATCAAGGACAGCCGGACTGCCGAG
Thiomicrospira crunogena XCL-2	CP000109.2	1051066-1051149	ATGTAGATTTGCCAAACTTACTGTGAAGTAAGGACGGAAAGCCACGGGTCTTTGTCATCAAATAAAGATAGCCGGGTTGCGTAG
Thiomicrospira crunogena XCL-2	CP000109.2	325943-326021	AGAAAATTTTGCCAAACTTGTTGTGAAGCAAGGACGGAAAGCCATGGGTCTCAATGGTTGAGATCGCCAGGTTGCCAAA
Thiomicrospira crunogena XCL-2	CP000109.2	1048651-1048725	ATTTGATAAAGCTAAATTCGTCGCGAGGCGAAGACAGAAAGCCACGGATCTCCCTGAGATGGCCGGGTTACCTTT
Thiomicrospira crunogena XCL-2	CP000109.2	326120-326199	GTTTTTAATTGCCAAACTTGTTGTGAAGCAGGGACGGAAAGCCATGGGTCTCAATGTTTTGAGATCGCCAGGTTGCATAC
Tolumonas auensis DSM 9187	CP001616.1	1034201-1034287	CTCCCGAAACGGCAAACTCCGGGTAACCGGATGTACGCAAAGCCACAGGTCCTTTTGAGTCATCATCAGGACAGCTGAGCTACCGAA
Turicibacter sanguinis PC909 contig00032	ADMN01000047.1	7214-7128	AAATTTTATAGGCAAATTTGGAGAAATCCAAAGACGCAAAGCTAAAGGGGCTAAGGTCAATCGAGACTATGCTAGCCAGTTGCCGAA
Turicibacter sanguinis PC909 contig00107	ADMN01000030.1	91543-91459	CAATCAAATAGACAAACTTAAGGAAATTTAAGGACGCCAAGCTACAGGGCTTAACTCAAGATGATGATGCTAGCTAGTTGCCATA

Turicibacter sp. HGF1 contig00066	AEXQ01000078.1	7191-7105	AAATTTTATAGGCAAATTTGGAGAAATCCAAAGACGCAAAGCTAAAGGGGCTAAGGTCAATTGAGACTATGCTAGCCAGTTGCCGAA
Turicibacter sp. HGF1 contig00089	AEXQ01000012.1	51729-51645	CAATCAAATAGACAAACTTAAGGAAATTTAAGGACGCCAAGCTACAGGGCTTAACTCAAGATGATGATGCTAGCTAGTTGCCATA
Uncultured bacterium 9F08 genomic fragment.	GU177851.1	4045-3951	ATTCCCACTTGGTAAACCTGCACGAAAGTCGGGGACACAAAGTTACCGGTCTAAGGGGCATATATACTATGCCCTATGACAGCGGGATTGCCGGA
Uncultured bacterium clone pSM9 penicillin-binding protein gene	DQ898548.1	1361-1448	CCCGTTTCAGGGCAAACTCACCGAAAGGTGGGGACGCAAAGCCTCCGGTCTACGGGACGCATGTGCCTATGACAGCGGGGTTGCCGGT
Uncultured Clostridium sp. TS28_contig59277	ADJS01005390.1	1670-1580	GGGAATATTGGGCAAACCCAGTGAAAGCTGGTGACGCAAAGCTATAGGGTCTACGTTTCTCCGCACGGAAGCATGACAGCCAGTTGCAGCA
Uncultured Clostridium sp. TS29_contig117344	ADJT01003581.1	2726-2613	ATTAAATATTGGCAAACTATTTGAAAAAATAGGTCGCAAAGCTTTAGAGACTAAGTTGACCATTATAAGCAATATGCTTTTATGGAAGTTTCAATATGTCAGTCAGCTGCCTCC
Uncultured Clostridium sp. TS29_contig16032	ADJT01002700.1	296-211	AAGTTTAAAAGGCAAACCTGCCGAAAGACAGGGACGCAAAGCCAAGGGTCTAAGGTCCGTATGGACTATGACAGCCGGTTGCCGCA
Uncultured Desulfobacterium sp. genomic DNA	FR695874.1	304930-305040	TTCTGATAAAGCCAAACTGCCTGTGATCTTAAAACTAAATTGATCTTTTATAGAAAAAAGGCAGAACGGGAAGCCACGGGTTCTCAAAGAAAGAATAGCCGGGTTGCCAGA
Uncultured Dorea sp. TS28_contig06379	ADJS01006855.1	390-303	TTATTCATAGGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAGAAGGGTCTAAGGTCTTATTGGACTATGACAGCCGGTTGCCACA

Uncultured Eubacterium sp. TS28_contig06066	ADJS01007775.1	25128-25046	TGTTCTAGTGGGCAAACCTTGTGAAAGCAGGGGACGCAAAGCCAAGGGTCTAAGGGCATAGCCTATGACAGCCGGTTGCCGCG
Uncultured Eubacterium sp. TS28_contig185480	ADJS01009048.1	1948-2023	GAAAATAATTGGCAAAGCAGACGAAAGTCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATAA
Uncultured Eubacterium sp. TS28_contig197515	ADJS01009351.1	4318-4412	TTTATATTTGGGTAAAACTGTCGAAAGGCAGCGACACAAAGCCAAATGGGTCTAAGGTTCATTTTTTAAGAGAATTATGACAGCCGGTTGCATCA
Uncultured Eubacterium sp. TS28_contig44402	ADJS01008438.1	4304-4393	CTGAGAAATAGGCAAACCCGTCGAAAGACGGGGACGCAAAGCCAGAAGGGTCTAAAGCGGCGAAAGCTGCAATGACAGCCGGTTGCAAGC
Uncultured Faecalibacterium sp. TS28_contig08302	ADJS01010440.1	217-143	AAATGCTATCGGCAAACCCGGCGCAAGCCGGCGGCGCAAAGCTACAGGGACCCATTGGGTCAGCCAGCTGCAATC
Uncultured Faecalibacterium sp. TS28_contig178696	ADJS01012342.1	19372-19278	GCAATTTTTTGGCAAACTTGTCGAAAGGCAAGGACGCAAAGCCATAGGGGCTAAGGTTCGGGGCATTTCCCGGATGATGCCAGCCGGTTGCTTCC
Uncultured Faecalibacterium sp. TS28_contig181382	ADJS01012479.1	956-1044	TGCAGACAAGGGCACGATCGGTGAAAGCCGGTTTCGCAAAGCCAGGGGCCTAAACGGAAGACTTTTCCGCATGGCAGCCGGTTTCCTGA
Uncultured Faecalibacterium sp. TS28_contig181382	ADJS01012479.1	726-817	TACAGATAAAGGCACAGCCGGTGAAAGCCGGTGCCGCAAAGCCAGATGGGCCTAAACGGAGCTTGTCCTCCGCATGGCAGCCGGCTGCCAAC
Uncultured Faecalibacterium sp. TS28_contig186573	ADJS01012807.1	3734-3659	GAATATCCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT

Uncultured Faecalibacterium sp. TS28_contig186573	ADJS01012807.1	3935-3860	GAATATTCTCGGCAAAACAGTCGAAAGGCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGCTGCTTCT
Uncultured Faecalibacterium sp. TS29_contig132743	ADJT01006955.1	9-74	GGCAAGACAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCTTCT
Uncultured Faecalibacterium sp. TS29_contig142890	ADJT01007769.1	7522-7613	CTTAATACTTGGTAAACCTACCGAAAGATAGGGCAACAAAGCTAAATGAGTCTAAAATCTCATATACGAGGTCATGGCAGCTGGTTGCTTTT
Uncultured Ruminococcaceae bacterium TS28_contig09421	ADJS01015797.1	2218-2143	TTCATAAACCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTATAGGGCCTGTAAAATGGCAGCCAGTTGCACCT
Uncultured Ruminococcus sp. TS28_contig09634	ADJS01017175.1	1544-1624	TTTAAAAAAAGGCATAGCCGGGGAAATCCGGTGGCGCAAAACTATAGGGTCTAAGCAAATGTATGACAGCCAGTTGCAGGA
Uncultured Ruminococcus sp. TS28_contig163554	ADJS01019394.1	465-540	ATACAGTATCGGCAAAACAGTCGAAAGGCTGCGGCGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGCATTT
Uncultured Ruminococcus sp. TS28_contig164519	ADJS01019441.1	69-1	ACAGCATAAAGGCAAACCTGCTGAAAGGCAGGGACGCAAAGCCACGGGTCTAAGGTCGTGAGACTAAGG
Uncultured Ruminococcus sp. TS28_contig173278	ADJS01019690.1	4275-4182	GGCATTTATTGGCAAACCGGTTGAAAAGCCGGGGCGCAAAGCCAGAAGGAGCTAAAGTCAGATTGAAATCTGGCCATGCCAGCCGGTTGCATCA
Uncultured Ruminococcus sp. TS28_contig177606	ADJS01019823.1	2162-2237	AAAGATTCTAGGCAAAACAGACGAAAGTCTGTGACGCAAAGCTAAAGGGCCTGTAAAATGGCAGCCAGTTGTAGAA
Uncultured Ruminococcus sp. TS28_contig186038	ADJS01020268.1	394-469	AAAGAATCTCGGCAAAGCAGTCGAAAGGCTGTGACGCAAAGCTACAAGGCCTGTAAAATGGCAGCCAGTTGCGTAA

Uncultured Ruminococcus sp. TS29_contig00514	ADJT01008988.1	413-338	AAGGATGATCGGCAAACCAGATGAAAGTCTGGGACGCAAAGCTATAGGGCCTGTAAAATGGTAGCCAGTTGCATGA
Uncultured Ruminococcus sp. TS29_contig118902	ADJT01011779.1	2006-1913	GGCATTTATTGGCAAACCGGTTGAAAAGCCGGGGCGCAAAGCCAGAAGGAGCTAAAGTCAGATTGAAATCTGGCCATGCCAGCCGGTTGCATCA
Uncultured Ruminococcus sp. TS29_contig126743	ADJT01012312.1	17871-17961	TTATTTTAAAGGCAAACCTGTTGAAAGGCAGGGACGCAAAGCCAGAAGGGACTAAAGTCAGAAAGCTTGACCATGTCAGCCGGTTGCCACT
Uncultured Ruminococcus sp. TS29_contig136355	ADJT01012865.1	2681-2756	TAAGAAAATCGGCAAAACAGACGAAAGTCTGTGACGCAAAGCTACAGGGCCTGTAAAATGGCAGCCAGTTGCATGA
Uncultured Ruminococcus sp. TS29_contig139182	ADJT01013011.1	11568-11655	TATATATAAAGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCATGGGTCTAAGGTCCGAAGGATGACTATGACAGCCGGTTGCCGCA
Uncultured Ruminococcus sp. TS29_contig18840	ADJT01010127.1	1258-1341	GTGAATAAAAGGCAAACCTGTTGAAAGACAGGGACGCAAAGCCAAGGGTCTAAGGTCTCAGGACTATGACAGCCGGTTGCCGCA
Vibrio alginolyticus 12G01 1100007009578	AAPS01000039.1	21459-21548	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTGAACCATATTACGATATGGAAGGTAGCGGGGTTACCGAT
Vibrio alginolyticus 12G01 1100007009659	AAPS01000001.1	220352-220252	ATCACATTTCGGCAAACCATTCGAAAGGGTGGGACGCAAAGCTTCCGGTCTGTCAGCATTTAAAAATCTAAAAGAATGCTCATGATAGCGGGGTTACCATG
Vibrio alginolyticus 40B Cont24	ACZB01000024.1	14116-14216	ATCACATTTCGGCAAACCATTCGAAAGGGTGGGACGCAAAGCTTCCGGTCTGTCAGCATTTAAAAATCTAAAAGAATGCTCATGATAGCGGGGTTACCATG
Vibrio alginolyticus 40B Cont70	ACZB01000069.1	74260-74171	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTGAACCATATTACGATATGGAAGGTAGCGGGGTTACCGAT
Vibrio anguillarum 775 chromosome I	CP002284.1	1996187-1996272	TCACGCACAGGGCAAACCATTTGAAAAGATGGGACGCAAAGCCTCCGGCCTAAACCGACTATTCGGTAGGTAGCGGGGTTGCCGAT
Vibrio anguillarum 96F contig00011	AEZA01000009.1	247884-247799	TCACGCACAGGGCAAACCATTTGAAAAGATGGGACGCAAAGCCTCCGGCCTAAACCGACTATTCGGTAGGTAGCGGGGTTGCCGAT

Vibrio anguillarum RV22 contig00057	AEZB01000056.1	34556-34641	TCACGCACAGGGCAAACCATTTGAAAAGATGGGACGCAAAGCCTCCGGCCTAAACCGACTATTCGGTAGGTAGCGGGGTTGCCGAT
Vibrio angustum S14 1099604003192	AAOJ01000002.1	319461-319551	GTCACGAACTGGCAAATTAATTGAAAGATTAAGACGCAAAACCACCGGCCTAAAAATTATGTTAATAATTCAAGGTAGCGGGGTTACCGAA
Vibrio brasiliensis LMG 20546 VIBR0546_32	AEVS01000059.1	18437-18350	CTGCACTTCAGGCAAACTATCCGAAAGGTTAGGACGCAAAGCCACCGGTCTGTCGACACTCGATGTCTATGATAGCGGGGCCGCCGCT
Vibrio brasiliensis LMG 20546 VIBR0546_61	AEVS01000091.1	2986-3071	CCACGAACAGGGCAAACCACTCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTTCAACATTTTATGTCAGGTAGCGGGGTTGCCGAT
Vibrio campbellii DS40M4 contig00041	AGIE01000036.1	12296-12385	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCGTCGAATTAGATGGAAGGTAGCGGGGTTACCGAT
Vibrio caribbenthicus ATCC BAA-2122 VIBC2010_95	AEIU01000122.1	2635-2721	CCACGAACAGGGCAAACCATTTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTTAAACATGATAATGTCTGGTAGCGGGGTTGCCGAT
Vibrio cholerae 12129(1) VCG.Contig178	ACFQ01000009.1	839950-839844	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGTCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae 12129(1) VCG.Contig179	ACFQ01000010.1	734747-734661	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae 1587 gcontig_1103206002954	AAUR01000056.1	3604-3710	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae 1587 gcontig_1103206003212	AAUR01000002.1	72158-72244	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae 2740-80 gcontig_1103206066802	AAUT01000003.1	5810-5896	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae 2740-80 gcontig_1103206067204	AAUT01000081.1	11064-10958	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae 623-39	AAWG01000002.1	25205-25291	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT

gcontig_1104444419539			
Vibrio cholerae 623-39 gcontig_1104444419597	AAWG01000058.1	6725-6831	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae AM-19226 gcontig_1101953438548	AATY01000002.1	114977-114891	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae AM-19226 gcontig_1101953438552	AATY01000001.1	2527-2633	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCACTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae B33 gcontig_1104196056141	AAWE01000144.1	2848-2742	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae B33 gcontig_1104196062761	AAWE01000118.1	3454-3368	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae B33 VCE.Contig124	ACHZ01000016.1	248017-248123	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae B33 VCE.Contig125	ACHZ01000017.1	1070903-1070989	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae BJG-01 vcoBJG01.contig.155_1	AFOU01000213.1	41348-41434	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae BJG-01 vcoBJG01.contig.64_2	AFOU01000085.1	43059-43165	GTCACACTTTGGCAAACCCTTTGGAAAAATGGACGCAAAGCCTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGTCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae bv. albensis VL426 Contig238	ACHV01000002.1	827242-827136	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae bv. albensis VL426 Contig239	ACHV01000001.1	439542-439628	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae BX 330286 VCF.Contig78	ACIA01000003.1	289201-289095	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT

Vibrio cholerae BX 330286 VCF.Contig96	ACIA01000006.1	1070688-1070602	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae CIRS101 strain CIRS 101 VCH.Contig85	ACVW01000011.1	76131-76045	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae CIRS101 strain CIRS 101 VCH.Contig89	ACVW01000014.1	686172-686066	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae CT 5369-93 VIH.Contig345	ADAL01000127.1	2628-2714	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-02A1 vcoHO2A1.contig.116_3	AFOT01000135.1	49923-50009	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-02A1 vcoHO2A1.contig.163_2	AFOT01000201.1	47235-47341	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACATCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-06A1 vcoHC06A1.contig.109_2	AGUI01000118.1	49808-49894	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-06A1 vcoHC06A1.contig.53_1	AGUI01000054.1	18311-18417	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-19A1 vcoHC19A1.contig.102_1	AGUJ01000122.1	18315-18421	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-19A1 vcoHC19A1.contig.48_2	AGUJ01000062.1	49879-49965	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-21A1 vcoHC21A1.contig.108_1	AGUK01000119.1	121693-121779	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-21A1	AGUK01000064.1	18309-18415	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGG

vcoHC21A1.contig.60_1			GTTACCAAT
Vibrio cholerae HC-22A1 vcoHC22A1.contig.47_1	AGUL01000063.1	18307-18413	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-22A1 vcoHC22A1.contig.79_1	AGUL01000104.1	121691-121777	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-23A1 vcoHC23A1.contig.10	AGUM01000011.1	276151-276237	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-23A1 vcoHC23A1.contig.9	AGUM01000010.1	653247-653141	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-28A1 vcoHC28A1.contig.101_1	AGUN01000124.1	121695-121781	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-28A1 vcoHC28A1.contig.56_1	AGUN01000058.1	18311-18417	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-32A1 vcoHC32A1.contig.37_2	AGUO01000048.1	49859-49945	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-32A1 vcoHC32A1.contig.92_1	AGUO01000111.1	18311-18417	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-33A2 vcoHC33A2.contig.40_2	AGUP01000049.1	49847-49933	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-33A2 vcoHC33A2.contig.75_1	AGUP01000102.1	18307-18413	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-38A1 vcoHC30A1.contig.134_1	AFOV01000164.1	18301-18407	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-38A1 vcoHC30A1.contig.63_2	AFOV01000072.1	49847-49933	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT

Vibrio cholerae HC-40A1 vcoHC40A1.contig.167_1	AFOK01000206.1	122404-122490	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-40A1 vcoHC40A1.contig.61_1	AFOK01000081.1	12000-12106	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-43A1 vcoHC43A1.contig.16	AGUQ01000017.1	653087-652981	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-43A1 vcoHC43A1.contig.17	AGUQ01000018.1	278535-278621	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-48A1 vcoHC48A1.contig.181_1	AFOL01000209.1	121685-121771	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-48A1 vcoHC48A1.contig.64_1	AFOL01000083.1	12007-12113	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-48B2 vcoHC48B2.contig.144_1	AGUR01000163.1	31932-32018	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-48B2 vcoHC48B2.contig.49_1	AGUR01000066.1	12004-12110	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-49A2 vcoHC49A2.contig.17	AFOM01000018.1	278193-278279	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-49A2 vcoHC49A2.contig.9	AFOM01000010.1	319891-319997	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-61A1 vcoHC61A1.contig.3	AGUS01000004.1	320785-320891	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HC-61A1 vcoHC61A1.contig.9	AGUS01000010.1	281448-281534	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HC-70A1	AFON01000157.1	121689-121775	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT

vcoHC70A1.contig.139_1			
Vibrio cholerae HC-70A1 vcoHC70A1.contig.60_1	AFON01000071.1	18305-18411	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HCUF01 vcoHCUF01.contig.18	AFOO01000017.1	641313-641207	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HCUF01 vcoHCUF01.contig.19	AFOO01000018.1	278540-278626	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HE-09 vcoHE09.contig.143_1	AFOP01000172.1	79925-80011	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HE39 vcoHE39.contig.8	AFOQ01000008.1	321581-321475	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACATCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae HE39 vcoHE39.contig.9	AFOQ01000009.1	1091825-1091911	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTCACCGAT
Vibrio cholerae HE48 vcoHE48.contig.14	AFOR01000015.1	268838-268924	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HE48 vcoHE48.contig.4	AFOR01000005.1	828904-828798	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTGCCAAT
Vibrio cholerae HFU-02 vcoHFU02.contig.40_2	AFOS01000056.1	49781-49867	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae HFU-02 vcoHFU02.contig.99_1	AFOS01000130.1	18305-18411	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae INDRE 91/1 VIG.Contig303	ADAK01000048.1	2725-2831	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae INDRE 91/1 VIG.Contig313	ADAK01000056.1	255725-255811	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT

Vibrio cholerae LMA3894-4 chromosome I	CP002555.1	1730416-1730502	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae LMA3894-4 chromosome II	CP002556.1	639801-639907	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGTCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae M66-2 chromosome I	CP001233.1	1807824-1807910	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae M66-2 chromosome II	CP001234.1	729240-729346	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae MAK 757 cont1.11	AAUS02000011.1	440458-440564	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae MAK 757 cont1.5	AAUS02000005.1	126675-126589	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae MJ-1236 chromosome 1	CP001485.1	1806545-1806459	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae MJ-1236 chromosome 2	CP001486.1	590578-590472	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae MO10 cont1.29	AAKF03000029.1	18237-18343	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae MO10 cont1.4	AAKF03000011.1	97017-97103	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae MZO-2 gcontig_1104435214482	AAWF01000029.1	2517-2603	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae MZO-2 gcontig_1104435214484	AAWF01000100.1	2245-2139	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTATGATAGCGGGGTTACCAAT
Vibrio cholerae MZO-3	AAUU01000047.1	27433-27347	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT

gcontig_1103200937837			
Vibrio cholerae MZO-3 gcontig_1103200937997	AAUU01000070.1	19554-19448	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae NCTC 8457 gcontig_1104196174555	AAWD01000198.1	2303-2217	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae NCTC 8457 gcontig_1104196176147	AAWD01000128.1	3808-3702	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O1 biovar El Tor str. N16961 clone Vc_npcR_4589 non-coding RNA	HQ442188.1	8-94	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O1 biovar eltor str. N16961 chromosome I	AE003852.1	1860690-1860776	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O1 biovar eltor str. N16961 chromosome II	AE003853.1	755256-755362	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O1 str. 2010EL-1786 chromosome 1	CP003069.1	1332090-1332176	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O1 str. 2010EL-1786 chromosome 2	CP003070.1	455786-455892	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O1 str. 2010EL-1792 contig00014	AELJ01000010.1	121619-121705	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT

Vibrio cholerae O1 str. 2010EL-1792 contig00094	AELJ01000077.1	218015-217909	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O1 str. 2010EL-1798 contig00015	AELI01000014.1	121619-121705	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O1 str. 2010EL-1798 contig00100	AELI01000084.1	18238-18344	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O1 str. Amazonia Contig19	AFSV01000007.1	32864-32778	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O1 str. Amazonia Contig2	AFSV01000029.1	311-417	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACATCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O395 chromosome 1	CP000626.1	469864-469758	GTCACACTTTGGCAAACCCTTTGGAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCACTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae O395 chromosome 2	CP000627.1	1413802-1413888	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O395 chromosome I	CP001235.1	1945221-1945307	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae O395 chromosome II	CP001236.1	794078-794184	GTCACACTTTGGCAAACCCTTTGGAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCACTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae RC27 VIJ.Contig960	ADAI01000039.1	58394-58500	GTCACACTTTGGCAAACCCTTTGGAAAAATGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCACTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae RC27 VIJ.Contig963	ADAI01000041.1	281046-281132	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae RC385 cont1.18	AAKH03000018.1	618060-617954	GTCACACTTTGGCAAACCCTTTGAAAAAATGGACGCAAAGCCTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae RC385	AAKH03000009.1	28640-28726	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT

cont1.9			
Vibrio cholerae RC9 VCC.Contig60	ACHX01000009.1	660097-659991	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTATTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae RC9 VCC.Contig62	ACHX01000011.1	282853-282939	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae TM 11079-80 VIF.Contig82	ACHW01000019.1	33510-33424	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae TM 11079-80 VIF.Contig91	ACHW01000026.1	153407-153513	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACATCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae TMA 21 VCB.Contig128	ACHY01000016.1	146188-146294	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio cholerae TMA 21 VCB.Contig158	ACHY01000017.1	281216-281302	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACATGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae V51 gcontig_1101953397202	AAKI02000145.1	2735-2841	GTCACACTTTGGCAAACCCTTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTACACTTAGGATAGCGGGGTTACCAAT
Vibrio cholerae V51 gcontig_1101953399652	AAKI02000072.1	12068-12154	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae V52 gcontig_1103206895372	AAKJ02000030.1	26337-26423	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAAGACGTGGTAGGTAGCGGGGTTACCGAT
Vibrio cholerae V52 gcontig_1103206896866	AAKJ02000083.1	10246-10140	GTCACACTTTGGCAAACCCTTTGGAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCACTCTTACACCTAGGATAGCGGGGTTACCAAT
Vibrio coralliilyticus ATCC BAA-450 VIC.Contig71	ACZN01000018.1	915382-915468	CCACGAACAGGGCAAACCACTTCGAAAGAGTGGGACGCAAAGCTTCCGGCCTGACTCAGGAGACTGAAAGGTAGCGGGGTTGCCGAT
Vibrio coralliilyticus P1 contig00235	AEQS01000211.1	9090-9176	CCACGAACAGGGCAAACCACTTCGAAAGAGTGGGACGCAAAGCTTCCGGCCTGACTCAGGAGACTGAAAGGTAGCGGGGTTGCCGAT

Vibrio fischeri ES114 chromosome I	CP000020.2	1762259-1762341	TCACGAACATGGCAAACTACATGAAAATGTAGGACGCAAAGCTTCCGGCCTAAGTATTTATATAAGGTAGCGGGGTTGCCGAC
Vibrio fischeri MJ11 chromosome I	CP001139.1	1780753-1780835	TCACGAACATGGCAAACTACATGAAAATGTAGGACGCAAAGCTTCCGGCCTAAGTATTTATATAAGGTAGCGGGGTTGCCGAC
Vibrio furnissii CIP 102972 VFA.Contig90	ACZP01000013.1	323533-323448	TCACGCACAGGGCAAACCATCTGAAAAGGTGGGACGCAAAGCCTCCGGCCTAAACCCAATTTCGGGTAGGTAGCGGGGTTACCGAT
Vibrio furnissii NCTC 11218 chromosome 1	CP002377.1	1685128-1685043	TCACGCACAGGGCAAACCATCTGAAAAGGTGGGACGCAAAGCCTCCGGCCTAAACCCAATTTTGGGTAGGTAGCGGGGTTACCGAT
Vibrio harveyi 1DA3 Cont13	ACZC01000013.1	188423-188499	ACTCATTAAGGGCAAACCAATCGTGAGGTTGGGACGCAAAGTGACAGCACAGGGATACTGTGGGCTGCATTGCTGAG
Vibrio harveyi 1DA3 Cont50	ACZC01000050.1	13231-13142	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACTATCTTATTAGATGGAAGGTAGCGGGGTTACCGAT
Vibrio harveyi ATCC BAA-1116 chromosome I	CP000789.1	1588082-1587993	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATCGAATTAGATGGAAGGTAGCGGGGTTACCGAT
Vibrio harveyi HY01 gcontig_1104549820419	AAWP01000006.1	124156-124245	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATCGAATTAGATGGAAGGTAGCGGGGTTACCGAT
Vibrio ichthyoenteri ATCC 700023 VII00023_104	AFWF01000007.1	54192-54105	ACACACTGTCGGCAAACCATTTGAAAAAATGGGACGCAAAGCTTCCGGTCTAACGATAATTCTTATCTACGATAGCGGAGCCGCCACT
Vibrio ichthyoenteri ATCC 700023 VII00023_281	AFWF01000175.1	38395-38307	TCACGCACAGGGCAAACCATTCTGAAAAGATGGGACGCAAAGCCACCGACCTACACATTGAATAAATGCACGGCAGCGGGGTTACCGAT
Vibrio metschnikovii CIP 69.14 VIB.Contig146	ACZO01000006.1	562466-562384	TCACGCACAGGGCAAACCATTTGAAAAGATGGGACGCAAAGCCTCCGGCCTAAACCATAGTGGTAGGTAGCGGGGTTGCCGAT
Vibrio mimicus MB-451 Contig42	ADAF01000002.1	1275675-1275785	ATCACATTTCGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGTCTGTGGGTTAAAGAGGTTCCCGACGAACACGACTTCAAACCTATGATAGCGGGGTTGCCATA
Vibrio mimicus MB-451	ADAF01000001.1	1074675-1074589	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAGTTCATGGTAGGTAGCGGGGTTACCGAT

Contig43			
Vibrio mimicus SX-4 Contig1	ADOO01000001.1	11561-11647	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAGTTCATGGTAGGTAGCGGGGTTACCGAT
Vibrio mimicus SX-4 Contig8	ADOO01000008.1	207644-207754	ATCACATTTCGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGTCTGTGGGTTAAAGAGGTTCCCGACGAACACGACTTCAAACCTATGATAGCGGGGTTGCCATA
Vibrio mimicus VM223 VMA.Contig52	ADAJ01000007.1	980657-980547	ATCACATTTCGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGTCTGTGGGTTAAAGAGGTTCCCGACGAACACGACTTCAAACCTATGATAGCGGGGTTGCCATA
Vibrio mimicus VM223 VMA.Contig53	ADAJ01000008.1	1115356-1115442	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAGTTCATGGTAGGTAGCGGGGTTACCGAT
Vibrio mimicus VM573 Cont32	ACYV01000032.1	4409-4299	ATCACATTTCGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGTCTGTGGGTTAAAGAGGTTCCCGACGAACACGACTTCAAACCTATGATAGCGGGGTTGCCATA
Vibrio mimicus VM573 Cont8	ACYV01000008.1	760138-760052	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAGTTCATGGTAGGTAGCGGGGTTACCGAT
Vibrio mimicus VM603 Cont30	ACYU01000014.1	139538-139648	ATCACATTTCGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGTCTGTGGGTTAAAGAGGTTCCCGACGAACACGACTTCAAACCTATGATAGCGGGGTTGCCATA
Vibrio mimicus VM603 Cont474	ACYU01000186.1	66718-66804	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAGTTCATGGTAGGTAGCGGGGTTACCGAT
Vibrio nigripulchritudo ATCC 27043 VINI7043_164	AFWJ01000073.1	9690-9783	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCTTCCGGCCTAAATGGATGTATAAAAAATCCAAATGGTAGCGGGGTTGCCGAT
Vibrio nigripulchritudo ATCC 27043 VINI7043_6	AFWJ01000289.1	14509-14601	ACGCTCAAAAGGCAAACTTGCTTAAAAGCAGGGACGCAAAATGACAGTGCCACTGATTTTTGGAGAGGATTATTGGCAGGCTGCATTACAAGA
Vibrio nigripulchritudo ATCC 27043 VINI7043_6	AFWJ01000289.1	16356-16452	CGACTCTTAGGGCAAACCCATTGAGAAGTGGGGGCGCAAAATGACAGTACCTAGTTTAACTTTAGGACGTTCAATTTAGGTAGGCTGCATTGCTGAG
Vibrio nigripulchritudo	AFWJ01000289.1	18174-18339	TCGCTCTAAGGGCAAACTGGCTGTAAAGTCAGGGCGCAAAATGACAGTGCCTGATGGCAGTGGTCGCTGAGTTTAAGTCATTCAGCTGTGTTGATTTTT

ATCC 27043 VINI7043_6			CACAATAAGTCGCGTTAACGCTCAATGGAAACATCAACAGTCCAATCAGGCAGGCTGCATTGCTGAG
Vibrio ordalii ATCC 33509 contig00150	AEZC01000128.1	5972-5887	TCACGCACAGGGCAAACCATTTGAAAGGATGGGACGCAAAGCCTCCGGCCTAAACTGAATATTCAATAGGTAGCGGGGTTGCCGAT
Vibrio orientalis CIP 102891 = ATCC 33934 strain CIP 102891 VIA.Contig79	ACZV01000004.1	867727-867816	CGGCACTTTTGGCAAACTATTCGAAAGGATAAGACGCAAAGCTTCCGGTCTGTCGGTACATATCGTACCTATGATAGCGGGGTTGCCACT
Vibrio orientalis CIP 102891 = ATCC 33934 strain CIP 102891 VIA.Contig80	ACZV01000005.1	451367-451280	CCACGAACAGGGCAAACCATTTCGAAAGGATGGGACGCAAAGCCTCCGGCCTTCAACAAGTTAATTGTTTGGTAGCGGGGTTGCCGAT
Vibrio orientalis CIP 102891 = ATCC 33934 strain CIP 102891 VIOR3934_1	AFWH01000001.1	264756-264667	CGGCACTTTTGGCAAACTATTCGAAAGGATAAGACGCAAAGCTTCCGGTCTGTCGGTACATATCGTACCTATGATAGCGGGGTTGCCACT
Vibrio orientalis CIP 102891 = ATCC 33934 strain CIP 102891 VIOR3934_40	AFWH01000041.1	15003-14916	CCACGAACAGGGCAAACCATTTCGAAAGGATGGGACGCAAAGCCTCCGGCCTTCAACAAGTTAATTGTTTGGTAGCGGGGTTGCCGAT
Vibrio parahaemolyticus 10329 VP10329_21	AFBW01000012.1	426847-426936	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus 10329 VP10329_38	AFBW01000028.1	268312-268416	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTGCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus 16 ctg_1108854221719	ACCV01000017.1	11091-11005	CCACGAACAGGGCAAACCATTTCGAAAGGATGGGACGCAAAGCCTCCGGCCTTAAGTATACTTATACAAGGTAGCGGGGTTGCCGAT
Vibrio parahaemolyticus 16 ctg_1108854221733	ACCV01000124.1	3623-3535	CTGCACTTCTGGCAAACTATCTGAAAAGTTAGGACGCAAAGTCTCCGGTCTGTCGACTCACTCAAGTCTATGATAGCGGGACCGCCACC
Vibrio parahaemolyticus AN-5034	ACFO01000050.1	596713-596817	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCAGTCTGCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAACGGGGTTGCCACT

gcontig_1113976711500			
Vibrio parahaemolyticus AN-5034 gcontig_1113976711502	ACFO01000009.1	100724-100635	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus AQ3810 gcontig_1104296539730	AAWQ01000012.1	171-275	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTTCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus AQ3810 gcontig_1104296540634	AAWQ01000045.1	17416-17505	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus AQ3810 gcontig_1104296542148	AAWQ01000571.1	193-89	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTTCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus AQ3810 gcontig_1104296547160	AAWQ01000114.1	171-275	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTTCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus AQ3810 gcontig_1104296555802	AAWQ01000087.1	9659-9555	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTTCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus AQ4037 gcontig_1113976701954	ACFN01000028.1	32858-32962	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCGGTCTTCCAGCACTGCTTAACTAGTCAACATTAGTGCTTAAGATAGCGGGGTTGCCACT
Vibrio parahaemolyticus AQ4037 gcontig_1113976703408	ACFN01000044.1	10796-10707	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT

Vibrio parahaemolyticus K5030 gcontig_1118352721751	ACKB01000125.1	18296-18385	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus K5030 gcontig_1118352721827	ACKB01000054.1	343148-343252	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCAGTCTGCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAACGGGGTTGCCACT
Vibrio parahaemolyticus Peru-466 gcontig_1113329539760	ACFM01000057.1	29049-29153	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCAGTCTGCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAACGGGGTTGCCACT
Vibrio parahaemolyticus Peru-466 gcontig_1113348543590	ACFM01000141.1	9244-9155	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus RIMD 2210633 DNA	BA000031.2	1078742-1078653	TCACGCACAGGGCAAACCATCCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAGTAGTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio parahaemolyticus RIMD 2210633 DNA	BA000032.2	1695926-1696030	ATCACATTTCGGCAAACCATTCGAAAGGATGGGACGCAAAGCTTCCAGTCTGCCAGCACTGCTTAACTAGTCAACACTAGTGCTTAAGATAACGGGGTTGCCACT
Vibrio rotiferianus DAT722 contig00056	AFAJ01000025.1	99303-99213	TCACGCACAGGGCAAACCACTCTAAAGGGTGGGACGCAAAGCTTCCGGCCTAAACTATCGCATGAGATAGCATGGTAGCGGGGTTACCGAT
Vibrio scophthalmi LMG 19158 VIS19158_176	AFWE01000073.1	62760-62673	ACACACTGTCGGCAAACCATTTGAAAAAATGGGACGCAAAGCTTCCGGTCTAACGATAAAATTTATCCACGATAGCGGAGCCGCCACT
Vibrio scophthalmi LMG 19158 VIS19158_9	AFWE01000220.1	3180-3101	AACGAGAAAAGCCAAACCTATCGCGAGGTAGGGACGGAAAGCTGCAGGTCTCATTCCATTGAGATGGCTGAGCCGCCTCA
Vibrio scophthalmi LMG 19158 VIS19158_95	AFWE01000226.1	43115-43203	TCACGCACAGGGCAAACCAAACTGAAAAGTTGGGACGCAAAGCCACCGACCTAAACATTGTAATGATGTACGGCAGCGGGGTTACCGAT
Vibrio shilonii AK1	ABCH01000059.1	9246-9159	TCACGCACAGGGCAAACCACTTGAAAGGGTGGGACGCAAAGCCACCGGCCTAAACCAAATTTATTTGATAGGTAGCGGGGTTACCGAT

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Vibrio sinaloensis DSM 21326 VISI1226_47	AEVT01000083.1	27776-27690	ATGCACTTCTGGCAAACTATCTGAAAAGATAGGACGCAAAGCCACCGGTCTGTCGACAATTTTGTCTATGATAGCGGGGCCGCCGCT
Vibrio sinaloensis DSM 21326 VISI1226_68	AEVT01000105.1	24695-24782	CCACGAACAGGGCAAACCACTCCGAAAGGATGGGACGCAAAGCCACCGGCCTTAAGTAATGTGTTTACAAGGTAGCGGGGTTGCCGAT
Vibrio sp. AND4 1103602000573	ABGR01000006.1	118490-118579	TCACGCACAGGGCAAACCTCTCGAAAGGGGGGGACGCAAAGCCTCCGGCCTGAACCATCGAATTAGATGGAAGGTAGCGGGGTTACCGAT
Vibrio sp. Ex25 chromosome 1	CP001805.1	2580794-2580883	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAATACTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio sp. Ex25 chromosome 2	CP001806.1	1291324-1291224	ATCACATTTCGGCAAACCATTCGAAAGGGTGGGACGCAAAGCTTCCGGTCTGTCAGCATTCCATCATCAAAAGTAATGCTCATGATAGCGGGGTTGCCATG
Vibrio sp. Ex25 gcontig_1102407882090	AAKK02000061.1	16343-16432	TCACGCACAGGGCAAACCATTCGAAAGGGTGGGACGCAAAGCCTCCGGCCTGAACCATAATACTATATGGAAGGTAGCGGGGTTACCGAT
Vibrio sp. MED222 1099517005443	AAND01000010.1	47376-47291	TCACGCACAGGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGCCTAAACCACTCGTTGGTATGGTAGCGGGGTTACCGAT
Vibrio sp. N418 VIBRN418_13	AFWD01000016.1	79627-79548	AACGAGAAAAGCCAAACCTATCGCGAGGTAGGGACGGAAAGCTGCAGGTCTCATTCCATTGAGATGGCTGAGCCGCCTCA
Vibrio sp. N418 VIBRN418_140	AFWD01000022.1	16289-16377	TCACGCACAGGGCAAACCAAACTGAAAAGTTGGGACGCAAAGCCACCGGCCTAAACATTGTAATGATGTACGGCAGCGGGGTTACCGAT
Vibrio sp. N418 VIBRN418_89	AFWD01000095.1	82012-82099	ACACACTGTCGGCAAACCATTTGAAAAAATGGGACGCAAAGCTTCCGGTCTAACGATAATATTTATCCACGATAGCGGAGCCGCCACT
Vibrio sp. RC341 VCJ.Contig153	ACZT01000023.1	296971-297056	TCACGCACAGGGCAAACCATTCGAAAGAGTGGGACGCAAAGCCTCCGGCCTAAACCAGAACATAGGTAGGTAGCGGGGTTACCGAT
Vibrio sp. RC341 VCJ.Contig161	ACZT01000025.1	262127-262237	ATCACATTTCGGCAAACCATTTGAAAAAATGGGACGCAAAGCCTCCGGTCTGTCGGTTCGAGAAAAGCTCAACAAACGGTTTTCTCAATCTATGATAGCGGGGCCGCCATA

Vibrio sp. RC586 VOA.Contig110	ADBD01000010.1	477413-477519	GTCACACTTCGGCAAACCATTTGAAAAAATGGGACGCAAAGCTTCCGGTCTGTCGGTCAAGAAAGCTCATAAAGCCCTCTTAAACCTATGATAGCGGGGTTGCCAAT
Vibrio sp. RC586 VOA.Contig114	ADBD01000013.1	222759-222846	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAAAAGTTTATGGTAGGTAGCGGGGTTACCGAT
Vibrio splendidus 12B01 1099451319034	AAMR01000021.1	11847-11762	TCACGCACAGGGCAAATCACTTGAAAGAGTGAGACGCAAAGCTTCCGGCCTAAACCACTCGTTGGTATGGTAGCGGGGTTACCGAT
Vibrio splendidus 12B01 1099451319042	AAMR01000015.1	100102-100013	ACGCACTTCTGGCAAACTATTTGAAAGAATAGGACGCAAAGCCACCGGTCTGTCGACAATTATTCTGTCTATGATAGCGGGGCCGCCACT
Vibrio splendidus ATCC 33789 VISP3789_12	AFWG01000004.1	132090-132005	TCACGCACAGGGCAAATCACTTGAAAAGGTGAGACGCAAAGCTTCCGGCCTAAACCACTCGTTGGTATGGTAGCGGGGTTACCGAT
Vibrio splendidus ATCC 33789 VISP3789_9	AFWG01000089.1	45553-45464	ACGCACTTCTGGCAAACTATTTGAAAGAATAGGACGCAAAGCCACCGGTCTGTCGACAATTATTCTGTCTATGATAGCGGAGCTGCCACT
Vibrio splendidus LGP32 chromosome 1	FM954972.2	1146263-1146178	TCACGCACAGGGCAAACCACTTGAAAAAGTGGGACGCAAAGCTTCCGGCCTAAACCACTCGTTGGTATGGTAGCGGGGTTACCGAT
Vibrio tubiashii ATCC 19109 VITU9109_20	AFWI01000113.1	53825-53911	CCACGAACAGGGCAAACCATTCCGAAAGGATGGGACGCAAAGCCTCCGGCCTTAAACAATTTATTGTCTGGTAGCGGGGTTGCCGAT
Vibrio tubiashii ATCC 19109 VITU9109_88	AFWI01000214.1	14803-14890	CTGCACTTCAGGCAAACTATCCGAAAGGTTAGGACGCAAAGCCACCGGTCTGTCGACATCTTATGTCTATGATAGCGGGGTTGCCATT
Vibrio vulnificus CMCP6 chromosome I	AE016795.3	2138086-2137998	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGACGTTTTTTGGTAGGTAGCGGGGTTACCGAT
Vibrio vulnificus CMCP6 chromosome II	AE016796.2	45972-45881	ATCACACATAGGCAAACCTTCTGAAAAGATGGGACGCAAAGCTTCCGGTCTGTCGGTATTTTTATCATACCCAAGATAGCGGGGCCGCCGCT
Vibrio vulnificus MO6-24/O chromosome I	CP002469.1	1123237-1123149	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGACGTTTTTTGGTAGGTAGCGGGGTTACCGAT
Vibrio vulnificus MO6-24/O	CP002470.1	602641-602550	ATCACACATAGGCAAACCTTCTGAAAAGATGGGACGCAAAGCTTCCGGTCTGTCGGTATTTTTACCATACCCAAGATAGCGGGGCCGCCGCT

chromosome II			
Vibrio vulnificus YJ016 DNA	BA000037.2	2327906-2327994	TCACGCACAGGGCAAACCATTTGAAAAAGTGGGACGCAAAGCCTCCGGCCTAAACCAGACGTTTTTTGGTAGGTAGCGGGGTTACCGAT
Vibrio vulnificus YJ016 DNA	BA000038.2	624584-624493	ATCACACATAGGCAAACCTTCTGAAAAGATGGGACGCAAAGCTTCCGGTCTGTCGGTATTTTTATCATACCCAAGATAGCGGGGCCGCCGCT
Vibrionales bacterium SWAT-3 1101732140710	AAZW01000020.1	21384-21469	TCACGCACAGGGCAAATCACTTGAAAAGGTGAGACGCAAAGCTTCCGGCCTAAACCACTCGTTGGTATGGTAGCGGGGTTACCGAT
Vibrionales bacterium SWAT-3 1101732140720	AAZW01000005.1	50241-50330	ACGCACTTCTGGCAAACTATTTGAAAGAATAGGACGCAAAGCCACCGGTCTGTCGACAAATGTTCTGTCTATGATAGCGGAGCTGCCACT
Wallaby gut metagenome FWYF9480.b1	ADGC01050767.1	157-231	TCAAGAATAGGGCAAAGCATCTGAAAAGATGTGACGCAAGCTAAAGGGCCTGTAAAATGGCAGCCAGCTGCACCA
Wallaby gut metagenome MeugComb_C12011	ADGC01012011.1	2308-2383	TGAATAAAATCGCACACTTGGAGAAATCCAGGGTCGCAAAGCTATAGGACCTTTCACATGGTAGCCAGTTGCAATG

*The original RNA qequences were downloaded from Rfam FTP site

Table S3 c-di-GMP-II riboswitch

Samples		Location	Sequence*
Acetohalobium arabaticum DSM 5501	CP002105.1	21848-21766	TTAATAATGAGAACGTTGAAGTATAACTTGTATTTGGTCACCTAAGTTATATGGAGTTAGTGGTGAAACCTCCTCATATTTAT
Actinosynnema mirum DSM 43827	CP001630.1	6488894-6488813	GGCCGAAGGCGAAGCGATGAACCACCGGGCGTGTCTGGTCGCCGGTCCGATGGGGAGCTAGCGGCGAACCCACCGCCTGGGC
Alicyclobacillus acidocaldarius LAA1 ctg1	ACCS01000001.1	83237-83153	ACGTCTGGTGGACGCGAAGATCTCAGGTCGTCACGTGGGCACATAAGGCCTGAGGGAGCGAGTTGTGCAACCGGCCACCCGCGCA
Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446	CP001727.1	379758-379674	CACGACGGTGGACGCGAAGATCTCAGGTCGTCATCTGGGCACATAAGGCCTGAGGGAGCGAGTTGTGCAACCGGCCACCCGCGTA
Alicyclobacillus acidocaldarius subsp. acidocaldarius Tc-4-1	CP002902.1	450249-450167	CATGACGGTGGACGCGAAGATCTCAGGTCGTCATCTGGGCACATAAGGCCTGAGGGAGCGAGTTGTGCAACCGGCCACCCGCG
Alkaliphilus metalliredigens QYMF	CP000724.1	3560727-3560645	AAAAATGTAGAGCAAATGAACTGCAGGTATACATGGACGCCTTAAACTGCAGGGATGTAGTGGCGTAACCGACTAACAATATT
Anaerobaculum hydrogeniformans ATCC BAA-1850 A_SpOS1-1.0.1_Cont1.5	ACJX02000017.1	195834-195922	GGTTTAGGGGAAACGATGATCCCTTTGCATCTCTGATGACGGGCGCAAGAGCGAAGGGGGAGTGAGTAGCGCGACCGGCCCCGTAGAGC
Anaerolinea thermophila UNI-1 DNA	AP012029.1	2238146-2238247	TGAAAAAGTGGAGGCGATGACTCGAGGTCTGTAAACTGGTCGCTTGCTCGAAATTCTGGGCAAAGACCTCGACGAGCCAATGGCGAAACCGTCCACTTGACA
Anaerolinea thermophila UNI-1 DNA	AP012029.1	1764854-1764753	TTATTTTGTGGAGGCGTTGACTCAGAACGGGATAGTTGGTCGCTTTCCCAAGAATTTGGGAAGTGTTCTGATGAGCCAGTAGCGAAACCGACCACAAAAAGG
Anaerolinea thermophila UNI-1 DNA	AP012029.1	1525234-1525130	CATTTTTGTGGAGGCGTTAATCCACAGGATGAGTTTGGTCGCTCATCTGTCAAACGGGCAGAGAAATTCTGTGGGGAGTCAATAGCGAA

			ACCGGTCCTGAGGATG
Bacillus cellulosilyticus DSM 2522	CP002394.1	3293603-3293521	TTATATTAAGGAGCGATGAAAAATGATCTACATGTGGGCACTTGGATCATTAGGAGCGAGTAGTGCAACCGGACTTTATATAT
Bacillus cellulosilyticus DSM 2522	CP002394.1	3192859-3192776	AATTTAAAAGGTAGCGAAGAATATATGTCTTGATTTGGGCACTTGGACATACAGGAGCTAGTAGTGCAACCGACCTTGTTATTT
Bacillus coahuilensis m4-4 1955101000007	ABFU01000007.1	19777-19861	ACAAATTGTGGAAGCGATGAGGGATTTGACGGCAACTGGGCACTTAGTCAAACCTTAGCTTATAGTGCAACCGGCCACATCCTAT
Bacillus coahuilensis m4-4 1955101000013	ABFU01000013.1	89831-89915	TTGCAATGAGGAATGCTACGACCCTAAATTAGTACTTGGGCGCTTTGATTTAGGATAGCTAATAGCGCAACCGGCCACATTGAGA
Bacillus halodurans C-125 DNA	BA000004.3	387918-387999	AATCAATAGGGAAGCAACGAAGCATAGCCTTTATATGGACACTTGGGTTATGTGGAGCTACTAGTGTAACCGGCCCTCCTTT
Bacillus pseudofirmus OF4	CP001878.2	854191-854275	TAAATTGACGGATACGTTGAAAACTTCTCTGTAAATTGGGCGCTTTGAGAAGTTGGAGTAAGTAGCGCAACCGGCCGATAAAGGG
Bacillus pseudofirmus OF4	CP001878.2	2833763-2833680	TTTCATATGGAACGTGATGAAAAGCTATCTGTACATGGGCACTTGGGTAGTTTGGAGCAGCTAGTGCAACCGGCCAATTTTGTC
Bacillus selenitireducens MLS10	CP001791.1	1643284-1643367	ACGACAATTGGATGCTGAGAAGAAATGGGTACTATCTGGGCACTTAACCATTTTGGAGCTGCTAGTGCAACCGGCCGGAGACAT
Bacillus selenitireducens MLS10	CP001791.1	652937-653016	TGCCCGAATGGAAACGTTGATGAGATGACTGTATGTGGGCACTTGGTCATTTCGGAGTGAGTAGTGCAACCGGCCGAGCA
Bacillus sp. 2_A_57_CT2 cont1.22	ACWD01000022.1	14544-14461	GGACAAGTTGGAAGCAATGAGAATTCAAGGAAAAATGGGCGCTTTAATGAATTCGAGCTAGTAGCGCAACCGGCCAGCACTTAC
Bacillus sp. NRRL B-14911 1099999053126	AAOX01000007.1	31274-31356	AAGAATATAGAACACTGTGATGAGCGGTTTTTATTTGCACTTTAAACCGCTTGGAGTGACTAGTGCAGCCGGCCAATGATCTA
Bacillus tusciae DSM 2912	CP002017.1	2052455-2052535	GTCTGGTTTGGAGGCAATGAAAAACTGTCTGGAATTGGGCGCTTGGACAGTTGGGAGCCAGTAGCGCAACCGGCCAATGTC
Bioreactor metagenome PBDCA2_FIDWTPW02QBO29	AGTN01455485.1	501-449	ACCTGGGCACTTTGGGCTATATGGAGCAAGTGGTGCAACCGGCAATCTTTTTT
Bioreactor metagenome PBDCA2_FIDWTPW02RWU4G	AGTN01346032.1	500-419	TAAATATAGGGATACCTTGATGGAAATTGTGTATATGGGCACTTTCAATTTCCGGAGTATATAGTGCAACCGACCCTGCTTA
Bioreactor metagenome PBDCA2_FIDWTPW02RY3K3	AGTN01199440.1	195-276	CAGTAATGTGGAAGCTATGAAGCATGACCTGTATCTGGTTGCCTGGGTCATGATGAGCTAATGGCAAACCCACCCACTTTGG
Bioreactor metagenome	AGTN01413439.1	514-432	AGACAGTGGGATGCAATGACGTGTAAAAACACTATGTGGTCACTATTTACACCGAGCTAATAGTGAACCCCTCCGGACTGTAA

PBDCA2_FIDWTPW02RYRLV			
Bioreactor metagenome PBDCA2_FIDWTPW02TG8FK	AGTN01151901.1	40-123	ATTTAATAATGAAACAATGAAGTCGGGTTTGTATGTGGTCACTTAAACCTGATGGAGTTAGTAGTGAAACCGGCGATGTTAAAT
Bioreactor metagenome PBDCA2_FISUTAU01CWAZC	AGTN01652160.1	197-114	AAAAAAAGTGGAAACTATGAAAAATTCTCTTTATTTGGGCACTTGGAGAATTTAGAGTTAGTAGTGCAACCGACCAATAGATAG
Bioreactor metagenome PBDCA2_GBB5CE401AO6U7	AGTN01001494.1	194-110	AAACGAGATTGATGCGAAGACATATAGCTTGTATTTGGGCACTTTGGGCTGTATTGAGCGAGTGGTGCAACCGGCATTTTTTTA
Bioreactor metagenome PBDCA2_GBB5CE401EDRAX_right	AGTN01137125.1	306-155	AAACTAAGCGGATGCGATAATATACAGCTTTTATTGGTCACTTAGAGTGATAGGAGATGCTCAGTTCAGAGGGATCTCTCAAGCACTCCTGGGGGAGAAAGTTGACTTCCAGAGAGCTGTATGGAGCAAGAGTGAAACCGACCGTGCTGATA
Brevibacillus brevis NBRC 100599 DNA	AP008955.1	5612470-5612389	AGGTAGGAAAGAAGCGAAGAAGTACGGACTGTATCTGGTCGCTTGGTCCGTATGGAGCCAGTAGCGAATCCAGCCTTTTCCG
Caldalkalibacillus thermarum TA2.A1 ctg246	AFCE01000164.1	32300-32383	TAGTGCAAAGGATGTGATGAAGTGCAACTCTTAGTTGGGCGCCTGAGTTGCATGGAGCGAGTGGCGCAACCGGCCTTTACTTTT
Clostridium acetobutylicum ATCC 824	AE001437.1	3752962-3752879	TTAAGCGTTGGAGACTGTGAAGAATTTCTTGTATTTGGGCACCTTAGAAATTTGGAGTTAGTGGTGCAACCTGCCAACAATAAT
Clostridium acetobutylicum ATCC 824	AE001437.1	648479-648561	TATTTGTTTGGAAACAATGATGAATTTCTTTAAATTGGGCACTTGAGAAATTTTGAGTTAGTAGTGCAACCGACCAACGATTA
Clostridium acetobutylicum DSM 1731	CP002660.1	3754545-3754462	TTAAGCGTTGGAGACTGTGAAGAATTTCTTGTATTTGGGCACCTTAGAAATTTGGAGTTAGTGGTGCAACCTGCCAACAATAAT
Clostridium acetobutylicum DSM 1731	CP002660.1	648465-648547	TATTTGTTTGGAAACAATGATGAATTTCTTTAAATTGGGCACTTGAGAAATTTTGAGTTAGTAGTGCAACCGACCAACGATTA
Clostridium acetobutylicum EA 2018	CP002118.1	3752314-3752231	TTAAGCGTTGGAGACTGTGAAGAATTTCTTGTATTTGGGCACCTTAGAAATTTGGAGTTAGTGGTGCAACCTGCCAACAATAAT

Clostridium acetobutylicum EA 2018	CP002118.1	648092-648174	TATTTGTTTGGAAACAATGATGAATTTCTTTAAATTGGGCACTTGAGAAATTTTGAGTTAGTAGTGCAACCGACCAACGATTA
Clostridium beijerinckii NCIMB 8052	CP000721.1	1272636-1272718	TGTATATAAGGAAACTGTGATTCGAATATTTACTTGGGCACTTTATATTCGATGAGTTAATAGTGCAACCGACCTTTTTATTA
Clostridium beijerinckii NCIMB 8052	CP000721.1	2207052-2207135	ACAAAGATTGGGAACTATGAAGAATTCTCTGTATTTGGGCATCTTGAGAATTTAGAGTTAATGATGCAACCCACCAATCAAAAC
Clostridium beijerinckii NCIMB 8052	CP000721.1	3552610-3552527	AGAACAATTGGAAGCGATGAAAAATTCTCTATATCTGGGCACTTTGAGAATTTGGAGCTAGTTGTGCAACCGACCAATTAAAAC
Clostridium beijerinckii NCIMB 8052	CP000721.1	4369760-4369677	ATAGTAATTGAGAGCTATGAAGAATTCTTTTTATGTGGATATTTTAAGAATTTCGAGCTATCTGTGCAGTCGACCAATTTAAAC
Clostridium beijerinckii NCIMB 8052	CP000721.1	4868651-4868568	TTGTCATAAGGAAACTTTGATCCATATATTTTAATTGGGCACTTTATATATGGTGAGTTAGTAGTGCAACCGACCTTTATATTT
Clostridium beijerinckii NCIMB 8052	CP000721.1	2550212-2550295	ATTACAATTGGAAGCTATGAAGAATTCTTTCTAAGTGGGCACTTTAAGAGTTTGGAGCTAGTTGTGCAACCGACCAATTAAGAT
Clostridium botulinum B str. Eklund 17B	CP001056.1	3474048-3473965	TATAAAGTTGGAGATTGTGAATAGTTCTCTTTATTTGGGCACCTTGAGAACTAGGAGTCAGTGGTGCACCCGGCCAACAAATTA
Clostridium botulinum E1 str. 'BoNT E Beluga' CLO.Contig141	ACSC01000002.1	226862-226945	TATAAAGTTGGAGATTATGAATAGTTCTCTTTATTTGGGCACCTTGAGAACTAGGAATCAGTGGTGCACCCGGCCAACAAATTA
Clostridium botulinum E3 str. Alaska E43	CP001078.1	3290558-3290475	TATAAAGTTGGAGATTATGAATAGTTCTCTTTATTTGGGCACCTTGAGAACTAGGAATCAGTGGTGCACCCGGCCAACAAATTA
Clostridium butyricum 5521 gcontig_1106103650464	ABDT01000076.2	17918-17835	CATGTAGTTGGAAACGAAGAATAGTTCTCTCAATCTGGGCACCTTGGGAACTAGGAGTTAGTGGTGCAACCCGCCAGCAAATTA
Clostridium butyricum E4 str. BoNT E BL5262 CLP.Contig65	ACOM01000005.1	2090470-2090387	CATGTAGTTGGAAACGAAGAATAGTTCTCTCAATCTGGGCACCTTGGGAACTAGGAGTTAGTGGTGCAACCCGCCAGCAAATTA
Clostridium carboxidivorans P7 CLCAR0068	ADEK01000030.1	38999-39081	ATTAAAAAGGAGACAAAGAAGTATACTTATATTTGGGCACCTTAAAGTATACAGAGTCAATGGTGCAACCGACCTGATTTTAC
Clostridium carboxidivorans P7 CLCAR0092	ADEK01000042.1	6399-6480	TATTATATTGGAAGCGTTGAACTACATACTTAATTGGGCACTTTGTATGTAGGAAGCAGCTAGTGCAACCGGCCAAATATTG
Clostridium carboxidivorans P7 CLCAR0098	ADEK01000045.1	227536-227619	AAAAAAAGTGCAAACTGTGAAAAATTATCTTTATTTGGGCACTTGGAGAATTTAGAGTTAGTAGTGCAGCCGGCCAATAATTAG
Clostridium carboxidivorans P7 CLCAR0098	ADEK01000045.1	229397-229480	TTAAAAAAATGGAAACTGTGAAAAATTCTCTTTACTTGGGCACTTGGAGAATTTAGAGTTAGTAGTGCAACCGGCCAATAATTAG

Clostridium carboxidivorans P7 ctg00111	ACVI01000071.1	13890-13972	ATTAAAAAGGAGACAAAGAAGTATACTTATATTTGGGCACCTTAAAGTATACAGAGTCAATGGTGCAACCGACCTGATTTTAC
Clostridium carboxidivorans P7 ctg00119	ACVI01000016.1	6410-6491	TATTATATTGGAAGCGTTGAACTACATACTTAATTGGGCACTTTGTATGTAGGAAGCAGCTAGTGCAACCGGCCAAATATTG
Clostridium carboxidivorans P7 ctg00129	ACVI01000032.1	43884-43967	TTAAAAAATGGAAACTGTGAAAAATTCTCTTTACTTGGGCACTTGGAGAATTTAGAGTTAGTAGTGCAACCGGCCAATAATTAG
Clostridium carboxidivorans P7 ctg00129	ACVI01000032.1	42023-42106	AAAAAAAGTGCAAACTGTGAAAAATTATCTTTATTTGGGCACTTGGAGAATTTAGAGTTAGTAGTGCAGCCGGCCAATAATTAG
Clostridium carboxidivorans P7 ctg00174	ACVI01000001.1	117963-117880	TATGTCTTGGGAAATTATGAGCTATATACTTAATTTGGGCACTTTGTATATAGGGAGTTATTAGTGCAACCGGCCGAATATTTA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont10.1	AGAA01000010.1	148931-148846	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont29.1	AGAA01000024.1	52133-52216	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont29.1	AGAA01000024.1	81221-81306	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 002-P50-2011 C_difficile002-P50-2011-1.0_Cont4.1	AGAA01000005.1	96603-96518	TAATAAAATAGAAACGTTGATTTATGTTCTGCAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont30.1	AGAB01000014.1	95548-95633	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont38.1	AGAB01000020.1	885-800	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA

Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont402.1	AGAB01000071.1	96600-96515	TAATAAAATAGAAACGTTGATTTATGTTCTGCAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 050-P50-2011 C_difficile050-P50-201-1.0_Cont73.1	AGAB01000034.1	29728-29645	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 630 complete genome	AM180355.1	3801149-3801064	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 630 complete genome	AM180355.1	4105882-4105797	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 630 complete genome	AM180355.1	3306767-3306682	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 630 complete genome	AM180355.1	3826693-3826610	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6407 contig_1271	ADEH01001271.1	574-491	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6407 contig_2804	ADEH01002804.1	453-368	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6407 contig_3694	ADEH01003694.1	909-824	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 6407 contig_511	ADEH01000511.1	3693-3778	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 6466 contig_124	ADDE01000124.1	18557-18640	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6466 contig_241	ADDE01000240.1	16776-16861	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 6466 contig_27	ADDE01000027.1	30384-30469	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 6466 contig_319	ADDE01000318.1	28737-28822	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6503 contig_1	ADEI01000001.1	126371-126454	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA

Clostridium difficile 6503 contig_48	ADEI01000048.1	13134-13219	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6503 contig_7	ADEI01000007.1	41296-41381	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 6503 contig_82	ADEI01000082.1	16823-16908	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 6534 contig_293	ADEJ01000293.1	9201-9284	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 6534 contig_84	ADEJ01000084.1	1487-1572	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 6534 contig_880	ADEJ01000880.1	9852-9937	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 6534 contig_962	ADEJ01000962.1	5974-6059	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_Cont169.1	AGAC01000077.1	95005-94920	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_Cont28.1	AGAC01000024.1	77687-77772	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_Cont28.1	AGAC01000024.1	52149-52232	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile 70-100-2010 C_difficile70-100-2010-1.0_Cont38.1	AGAC01000036.1	13084-13169	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile ATCC 43255 contig00019_2	ABKJ02000019.1	632185-632100	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile ATCC 43255 contig00019_2	ABKJ02000019.1	148505-148420	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile ATCC 43255 contig00020_2	ABKJ02000020.1	17357-17274	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile ATCC 43255 contig00021_2	ABKJ02000021.1	96423-96338	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile BI1 chromosome	FN668941.1	3663876-3663793	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA

Clostridium difficile BI1 chromosome	FN668941.1	3147948-3147863	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile BI1 chromosome	FN668941.1	3913917-3913832	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile BI9 chromosome	FN668944.1	3814731-3814646	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile BI9 chromosome	FN668944.1	3022353-3022268	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile BI9 chromosome	FN668944.1	3514141-3514058	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile BI9 chromosome	FN668944.1	3488594-3488509	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile CD196 complete genome	FN538970.1	3905897-3905812	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile CD196 complete genome	FN538970.1	3139996-3139911	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile CD196 complete genome	FN538970.1	3655856-3655773	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile CIP 107932 contig00032_2	ABKK02000032.1	8674-8589	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile CIP 107932 contig00035_2	ABKK02000035.1	46456-46373	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile CIP 107932 contig00038_2	ABKK02000038.1	57364-57279	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile complete genome	FN665653.1	3637731-3637648	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile complete genome	FN665653.1	3163955-3163870	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile complete genome	FN665653.1	3612592-3612507	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile complete genome	FN665653.1	3870483-3870398	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile complete genome	FN665652.1	3717144-3717059	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile complete genome	FN665652.1	3973905-3973820	TAATAAAATAGAAACGTTGATTTATGTTCTGCAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile complete genome	FN665652.1	3201659-3201574	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA

Clostridium difficile complete genome	FN665652.1	3746232-3746149	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile complete genome	FN665654.1	3675328-3675245	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile complete genome	FN665654.1	3975213-3975128	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile complete genome	FN665654.1	3159482-3159397	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile M68	FN668375.1	3178755-3178670	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile M68	FN668375.1	3694212-3694127	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile M68	FN668375.1	3978970-3978885	TAATAAAATAGAAACGTTGATTTATGTTCTGCAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile M68	FN668375.1	3723299-3723216	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile NAP07 contig00010	ADVM01000006.1	61886-61971	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile NAP07 contig00213	ADVM01000057.1	19350-19265	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile NAP07 contig00215	ADVM01000059.1	209-126	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile NAP07 contig00217	ADVM01000061.1	94959-94874	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile NAP08 contig00002	ADNX01000002.1	90348-90263	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile NAP08 contig00102	ADNX01000076.1	39666-39749	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile NAP08 contig00103	ADNX01000077.1	14622-14707	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile NAP08 contig00115	ADNX01000089.1	61865-61950	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-23m63	ABKL02000031.1	22961-22876	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA

contig00031_2			
Clostridium difficile QCD-23m63 contig00036_2	ABKL02000036.1	888-803	CCTATTTATAGAAACTGTGAAGTATATCTTAAACTTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile QCD-23m63 contig00037_2	ABKL02000037.1	208-125	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-23m63 contig00040_2	ABKL02000040.1	94961-94876	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	1152543-1152460	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00014	AAML04000014.1	638715-638630	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-32g58 C_difficile_bld4_cont00015	AAML04000015.1	157646-157561	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-37x79 contig00023_2	ABHG02000023.1	152397-152312	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-37x79 contig00025_2	ABHG02000025.1	45887-45804	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-37x79 contig00027_2	ABHG02000027.1	57971-57886	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-63q42 contig00026_2	ABHD02000026.1	148456-148371	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-63q42 contig00027_2	ABHD02000027.1	195004-194919	CCTATTTATAGAAACTGTGAAGTATATCTTAAACCTGGGCACTTAAAAGATATATGGAGTTAGTAGTGCAACCTGCTATAAATATA
Clostridium difficile QCD-63q42 contig00028_2	ABHD02000028.1	4862-4779	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTAGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA

Clostridium difficile QCD-63q42 contig00030_2	ABHD02000030.1	99563-99478	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTGGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-66c26 contig00011_2	ABFD02000011.1	154500-154415	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-66c26 contig00012_2	ABFD02000012.1	144463-144380	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-66c26 contig00014_2	ABFD02000014.1	57540-57455	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-76w55 contig00034_2	ABHE02000034.1	9730-9645	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-76w55 contig00037_2	ABHE02000037.1	108247-108164	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-76w55 contig00039_2	ABHE02000039.1	57574-57489	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile QCD-97b34 contig00037_2	ABHF02000037.1	8669-8584	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-97b34 contig00040_2	ABHF02000040.1	233611-233528	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile QCD-97b34 contig00042_2	ABHF02000042.1	57542-57457	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile R20291 complete genome	FN545816.1	3986683-3986598	TAATAAAATAGAAACGTTGATTTATGTTCTGTAATGTGGGCACCTTAGAGCATATTGAGTTAGTGGTGCAACCGGCTATGAAATTG
Clostridium difficile R20291 complete genome	FN545816.1	3220524-3220439	AAATATTATAGAGATGTTGAAGTATATTCTATTATTGGGCACCTTATGGATATACTGAGTCAGTGGTGCAACCGGCTATGAATATA
Clostridium difficile R20291 complete	FN545816.1	3736631-3736548	AATATTTTAGAAACTGAGAAGTATATCTTATTATTGGGCATCTGGAGATATATGGAGTTAGTGGTGCAACCGGCTATGAATATA

genome			
Clostridium kluyveri DSM 555	CP000673.1	1160200-1160286	CAAATTGAGGGGAACGATGAGGTACACACTTTAATTTGGGCATCCTTGTGTGTATTGGAGTTAGTGATGCAACCGACCCTGTATTCA
Clostridium kluyveri NBRC 12016 DNA	AP009049.1	1160074-1160160	CAAATTGAGGGGAACGATGAGGTACACACTTTAATTTGGGCATCCTTGTGTGTATTGGAGTTAGTGATGCAACCGACCCTGTATTCA
Clostridium ljungdahlii DSM 13528	CP001666.1	409921-410004	TAATGTAAAGGAAACTATGATATATATGCCGTAATTTGGGTATCAGACATATACGGAGTTAATGATACAACCGACCTTACATCT
Clostridium ljungdahlii DSM 13528	CP001666.1	1584482-1584399	GAAAATATGGGAAACTATGAAAAATTTCTTCTAATTGGGCACTTTGGAAATTTGGAGTTAATAGTGCAACCGGCCAGCTATATA
Clostridium ljungdahlii DSM 13528	CP001666.1	990420-990503	TTAAAAGTTGAAAACAATGAAAAATTCTCTATAATTGGGCACCTGGAGGATTTGGAGTTAGTGGTGCAACCTGCCAATAGTCGA
Clostridium novyi NT	CP000382.1	1875256-1875172	TTTTTAAAAGGAGACATTTGAACTATATACTTTATTTGGGCACTTTGTATATAGGGAGTCATTAGTGCAACCGACCTTATTTTAT
Clostridium perfringens ATCC 13124	CP000246.1	171340-171423	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens B str. ATCC 3626 gcontig_1106202603824	ABDV01000011.1	27277-27360	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens C str. JGS1495 gcontig_1106166512733	ABDU01000054.2	14999-15082	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens CPE str. F4969 gcontig_1106202596980	ABDX01000006.1	72290-72207	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens D str. JGS1721 gcontig_1108490431717	ABOO01000009.1	68696-68613	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens E str. JGS1987 gcontig_1106202897272	ABDW01000009.1	70792-70709	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens NCTC 8239 gcontig_1106202603744	ABDY01000009.1	15518-15601	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium perfringens SM101	CP000312.1	175590-175672	ATATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTAT
Clostridium perfringens str. 13 DNA	BA000016.3	197260-197343	AAATGTTATAGAAACGTTGATGTATATTCTGTATTTGGGCATCTGGAATATGCTGAGTTAGTGATGCAACCGACTATATTTATA
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont1	AFWX01000001.1	1837525-1837609	TTTTATTAAGGAAACTATGATCCATATATTTTATTTTGGGCACTTTATATATGGTGAGTTAGCAGTGCAACCGACCTTTATGATT

Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	2459932-2459851	AATCAATATGGAAACAATGATTCATATATTTATTTTGGGCACTTTATATATGAGGAGTTAGTAGTGCAACCGGCCTTTGTTT
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	560316-560399	ATATAAATTGGACACTATGATAAGTTTTCTGTATTTGGGTACCTGGATAACTTTGAGTGATTGGTACAACCGACCAGCATAAAA
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	2392283-2392202	AATTAAGTTGGAAATGTTGAAGGATCTCCTTATTTTGGGCACCTTGGGGATTTGGAGTTAATGGTGCAACCGGCCAATGATT
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	2464246-2464163	ACACGGATTGGGAACTGTGAGGGATTCTCTCTATTTGGGCATCTGGAGGATTCTTAGTTAATGATGCAACCCGCCAATCAAAAC
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	1791131-1791049	ATAAAACTTGGAAGCTGTGAAGAATTCTTTTATGTGGGCACTTTAGGAATTTGGAGCTAGTTGTGCAACCGGCCAATTTAAAC
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	1580959-1580876	AAAAAATGTGGAAACGGTGAAAAATTCTCTCTATATGGGCACTTTGAGAATTTGGAGTTAATAGTGCAACCGACCAATTTAAGC
Clostridium sp. DL-VIII CDLVIIIscaffold_1_Cont2	AFWX01000002.1	1699465-1699382	ATGTAAATTGGAAGCTGTGAAAAACTTTCTTATTTTGGGCACATTGAGAGTTTAGAGCTAGTTGTGCAACCGACCAATTAAATT
Clostridium sticklandii str. DSM 519 chromosome	FP565809.1	218088-218170	ACATAATAAGAGCAGATGAACTATAGCTAGATATGGACGCCTTACGCTATAGGGATGCAGTGGCGTAACCGGCTGAATTATAA
Clostridium tetani E88	AE015927.1	474745-474827	ATTTTAAGAGGAAATTTTGAACTATATACTTATTTGGGCACTTTGTATATAGGGAGTTAGTAGTGCAACCGACCTTGATTAAT
Compost metagenome contig19871	ADGO01019795.1	335-417	ACCGACCCGGCGGCAATGACACACGGTCCGTATCTGGGCACCTGGGCCGTGTCGAGCTAGTGGTGCAACCGGCCGACATCCGT
Dehalococcoides sp. CBDB1 complete genome	AJ965256.1	1260708-1260792	AAATTAAGGGGAAGCGTTGAGCCGCTACCCATATGTGGTTCACTCGGATAGCGGGGAGCTAATAGTGAAACCGGCCCTTTAGGGG
Dehalococcoides sp. GT	CP001924.1	1225340-1225424	AAATTAAGGGGAAGCGTTGAGCCGCTACCCATATGTGGTTCACTCGGATAGCGGGGAGCTAATAGTGAAACCGGCCCTTTAGGGG
Dehalococcoides sp. VS	CP001827.1	205125-205209	AAAATTAAGGGAAGCGTTGAGCCGCTACCCATATTTGGTTCACTCGGATAGCGGGGAGCTAATAGTGAAACCGGCCCTTTAGGGG

Dehalogenimonas lykanthroporepellens BL-DC-9	CP002084.1	961690-961774	ATAACAACAGGAAGCGTTGAACCGTCACCTGTAATGTGGTCACTTGGGTGACGGGGAGCCCCTAGTGAAACCGGCCTGATATTTT
Deinococcus deserti VCD115	CP001114.1	488794-488900	AAGCACTCGGGACGCGATGACCCCCACCCCTCTCCGGCGCCTGTCATTCGGGTGCACGCGGTCACCTCAGGTGGGGCGAGCCAGTGGTGAGACCGACCCGTGTGGGG
Deinococcus deserti VCD115	CP001114.1	1034721-1034638	ACTGTACTGAGATGCATCGACGCTTGCCCTGTATACGGTCACCTGGGTCAAGCCGAGCGAATGGTGAGCCCGACTCAATGGAGA
Deinococcus deserti VCD115	CP001114.1	1166571-1166489	AACTAAAGGGGAGCTATGAACGCCGTCTTTTAACCCGGTCACCTGGGACGGCTGGAGCAGTGGTGAGACCGACCCCAGGAGGC
Deinococcus deserti VCD115	CP001114.1	617472-617555	CACAACTTGGTAGGCTAAGAAACTCGTCCTGTAACAGGTCACCTGGGGCGAGTAGAGCTAGTGGTGATTCTACCCCAGGTTAAG
Deinococcus deserti VCD115 plasmid 2	CP001116.1	102374-102291	ATAACGGCACGAAGCAATGAAATGTTCGATGTAACCGGGCACCTATCGAACATGGAGCTAGTGGTGCGACCGACGTTTCATACG
Deinococcus deserti VCD115 plasmid 2	CP001116.1	87607-87689	CTGATGGGGAGCGCGAAGAGCCCTGTTCTGTATTCGGGCACCTGGGACAGGGGGAGCTAGTGGTGCGACCGGCTTTTCGTCTG
Deinococcus geothermalis DSM 11300	CP000359.1	298588-298671	TTCTTGTTCCGGGGCGAAGAGGCGTGTGGTGTATCCGGGCACCTGCCACACGCGGAGCCAGTGGTGCGACCGACGAACCGTGAA
Deinococcus maricopensis DSM 21211	CP002454.1	2352368-2352449	CTTCACAGACGAGGCAAGGAAACGCGCAGTGCATCCGGGCACCTGCTGCGCGTCGAGCCAGTGGTGCGACCGACGTCCCCCG
Deinococcus maricopensis DSM 21211	CP002454.1	2009832-2009748	CTGACTGGTAGAGGCTGCGACGCGCGCTCCCGTACTCGGGCACCTGGGACGCGCAGAGCCAGTGGTGCGACCGACTATTGGTTCC
Deinococcus maricopensis DSM 21211	CP002454.1	388333-388413	CTGAACCAGCGACGCGACGACTCCCGTTCTCCATCCGGGCACCTGGAACGGGCCGAGCCAGTGGTGCGCCCACCGCTTCGC
Deinococcus maricopensis DSM 21211	CP002454.1	1046404-1046488	AACTAGTTCAGGAGCAATGAAACATCTGGCGTTACACGGGCGCCTGCCAGATGCGGAGCGAGTGGCGCGACCGACAGAACCGAGG
Deinococcus maricopensis DSM 21211	CP002454.1	314698-314782	CTGGCGAACAGATGCAAAGATCCTCGTCCCGTAATTCGGGCACCTCAGGCGAGGGGAGCAAGTGGTGCGACCGGCTCTTCGTTTC
Deinococcus maricopensis DSM	CP002454.1	445427-445510	TTCAACCTGCGACGCAACGACGTCTGTTCAGTATCCGGGCACCTTGAACGGACCGAGCCAGTGGTGCGCCCACCGCGGTCATCA

21211			
Deinococcus proteolyticus MRP	CP002536.1	513083-513167	TCTGTGGAGGGAGGTGATGATTCCCGTCCTGTAATCCGGGCACCTCGGACGGGAGGAGCCAGTGGTGCGACCGACTTTTCGTTGC
Deinococcus radiodurans R1 chromosome 1	AE000513.1	1919839-1919755	CTGTCGAAGAGACGCGATGAATCCCGCCCTGTAATTCGGGCACCTCGGACGGGAGGAGCAAGTGGTGCGACCGGCTTTTCGTTGG
Deinococcus radiodurans R1 chromosome 1	AE000513.1	692045-692129	AAGTGGTTTTGAAGCAGGGAAGCATCTGACGCATTCGGGCGCCTTGTCAGATGTGGAGCGAGTGGCGCGACCGGCAAAGCTGTGG
Desulfosporosinus sp. OT TOU.assembly.134	AGAF01000038.1	1437-1354	AAGCATGTGTGAGACAATGATTTGCAGTTAGAATTGGTCACGTTAAATTGCAAGGAGTCAAACGTGAACCCGGCACACTCATAT
Desulfosporosinus sp. OT TOU.assembly.26	AGAF01000182.1	569-487	TGTAAAGAGGAAATTTTGAAGCATGTATCTTATTTGGGCGCTTGATACATGTGGAGTAAGTAGCGCAACCGGCCTGGTTTATA
Desulfotomaculum acetoxidans DSM 771	CP001720.1	3609158-3609242	ATTTATACGGGATACTATGAAGTGAACTCTATAATTTGGGCATCTGGGGTTTACTGAGTAAGTGATGCAACCGGCCACTATTTTA
Desulfotomaculum acetoxidans DSM 771	CP001720.1	3973350-3973434	GAGTTTCTTGGGAACTATGACATCAACTCTTTATCTGGGCATCTTAGAGTTGATTGAGTTAGTGATGCAACCGACCTTGAAGAAA
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	2086514-2086431	TATAAGAGCGGAGGCCGTGAACCGCTGCCTGTAACTGGGCGCCTGGGCAGCGGGGAGCCGCTGGCGCACCCGGCCGCTTACCAG
Desulfotomaculum kuznetsovii DSM 6115	CP002770.1	2268897-2268980	GTAAAAAGGTGAGCGATGAACTGCGGTCTGTAACGTGGGCGCTTGGACCGGAGTGAGCCAGTAGCGCAACCGCCGCCTGCCAGT
Dethiobacter alkaliphilus AHT 1 ctg22	ACJM01000003.1	182391-182476	ATCAACCATAGAAGCAATGACCAACCTCTTACAAATCGGGCGCCTTGAGAGGTTGAGAGCTGGCGGCGCAACCGGCTATGGCAGGC
Dethiobacter alkaliphilus AHT 1 ctg28	ACJM01000007.1	48473-48391	AATTTTTGTGGGGGCAATGATTTTTGGGCTGATTTGGACGCTTTGCCTGGAATGAGCCGGTAGCGTAACCGACCACTTGTGGT
Dethiobacter alkaliphilus AHT 1 ctg36	ACJM01000005.1	89134-89216	CCCGTTTATGGGGGCTGTGATTTCAGGGCTTATATGGACGCTTTGCCCGGGAGGAGCCAGTAGCGTAACCGACCATATATTAA
Dethiobacter alkaliphilus AHT 1 ctg36	ACJM01000005.1	88429-88511	TTAGTTCTTGGGGGCTGTGATTTCAGGGCTTATATGGACGCTTTGCCCTGGGGGAGCCAGTAGCGTAACCGACCACTTATGGT

Dethiobacter alkaliphilus AHT 1 ctg9	ACJM01000004.1	62456-62538	CAAGTGTGCGGAATCAATGACCGCGACTCTCATTTGGTCACTTTAGGGTCGCGCGAGATAGAGTGAAACCGGCTGCACACGGG
Environmental sequence 2662324_fasta.screen.Contig17117	AAFX01105197.1	106-204	GTTAGTTCGGGCGGCGAAGATCCGGTGACTGGCATGGTCGCTCCATCCTTTCGGGATACGGTCACTGAGGAGCCAGTAGCGAAACCGGCCCTATGGGTC
Environmental sequence 2662324_fasta.screen.Contig5218	AAFX01131626.1	2-107	TATTGTTTGGGATGCGTAGACCCCGAGACGAAATCTGGTCGCAAAACCCTCCATGATAGGTGGGTGTAGTCTCTGGTGAGCAATAGCGAAACCGACCCTGCCCGGG
Environmental sequence XZS39253.g1	AAFX01078109.1	475-391	TCACCCTTCAGAGGCTTAGATGCCTACCCCGCAACTTGGGCGCTTGGGGTACGCGGAGCCAGTAGCGCAACCGGCCGAGGGCTTC
Environmental sequence XZS76186.x1	AAFX01082705.1	413-331	ATCGATTTCGGATGCCTTGATCCGACCGCTGAATGTGGGCACTTAGGCGGCCGGGGAGCAGGTAGTGCAACCGACCGTTCCGC
Environmental sequence XZS84852.b1	AAFX01050824.1	22-122	CGATTCTGTGGAGGCCTGATCCATAGCGGTACTGGTCGCAGCTCTTTCTGGATAGAAAGAACGCTATTGGGGAGCCAGTTGCGAAACCGGCCACGTAGCCG
Environmental sequence XZS94218.g1	AAFX01024083.1	557-455	CACCACTGTGGACGCTTTGATCCGGTGTCTTGATTTGGTCGCTTAACGTCTGGAACTTTTGACGAGGGCGCCGGGGAGCGAGTAGCGAAACCGGCCACTGGTA
Epibiont metagenome Alv_LSA_172_B08.y01	AAUQ01013182.1	230-147	ACAAACTTGGGATGCGTCGAAGTCCAGTTAAATTTGGTTGCCATAGACTGGATGGAGCAAATGGCAAAACCGGCCCAAGTGATT
Freshwater sediment metagenome lwFormaldehyde_BCIB32736_g1	ABSN01055388.1	86-2	GTACGCGTGGGAGGCTCTGACACGCGGTCCAAACCCCGGCCGCCGGGACCGCGCTGAGCCACTGGCGAGACCGACCCGCGCATGC
Freshwater sediment metagenome lwFormate_BCIX11931_g1	ABSO01013207.1	629-713	ACGGGTGCGGGAGGCGATGACACGCGGCTCGCATGACGGCCGCCTGAGCCGCGCCGAGCCACTGGCGAGACCGAGCCGCTCTGAT
Freshwater sediment metagenome lwFormate_BCIX16035_g1	ABSO01016797.1	548-464	CCGCGTGCGGGAGGTTGAGACGCGCGGTCCACACCCCGGCCGCCGGGACCGCGCCGAGCCACTGGCGAGACCGACCCGCGCGTGC
Freshwater sediment metagenome	ABSO01017373.1	256-341	ACGCACACGGGAGGCGATGACGTCGCGGCTTGCACCCTGGTCGCCTGAGCCGCGCCGAGCCACTGGCGAGACCGACCCGCTTGTTG

lwFormate_BCIX16653_b1			
Freshwater sediment metagenome lwFormate_BCIX3308_g1	ABSO01005747.1	296-213	GTCAATATCGGACGCGCGGATGCCTCGCCTGAAATGGGCACTTAGGGTGAGGCGGAGCGAGTAGTGCAACCGACCGACCCCAGT
Freshwater sediment metagenome lwFormate_BCIX8145_b1	ABSO01010315.1	425-508	AAGACGCTCGGACGCGCAGATGCCTCTCCTGAAATGGGCACTTAGGGAGAAGCGGAGCGAGTAGTGCAACCGACCGACCTAATC
Freshwater sediment metagenome lwFormate_BCIX9830_g1	ABSO01020038.1	334-252	TCGTACGTGGGAGGCTGTGACGCGCGGCCCATGCAATGGGCGCCCGGACCGCGCCGAGCCACTGGCGAGACCGGCCTGCGCGA
Freshwater sediment metagenome lwMethane_BCGO16849_y1	ABSP01028201.1	593-677	TCGTACGCGGGAGGCTGAGACACGCGGTCCGAATTCGTGCCGCCGGGACCGCGCCGAGCCACTGGCGAGACCGACCCACGCTGGC
Freshwater sediment metagenome lwMethenol_BCHA14774_x1	ABSQ01022675.1	554-638	GGGCGAGCGGGAGGCTCTGACGTGCGGNCCACACCCTGGCCGCCGGGACTGCGTCGAGCCACTGGCGGACCCGACCCGCGCATCA
Freshwater sediment metagenome lwMethenol_BCHA21047_x1	ABSQ01032870.1	364-280	GTCGTCGCGGGAGGCCATGACACGCGGCCCGAACCCCGGCCGCCGGGACCGCGCCGAGCCACTGGCGAGACCGACCCGCGAATGC
Freshwater sediment metagenome lwMethenol_BCHA27458_x1	ABSQ01040898.1	118-201	TCCGCAGCGGGAAGCTCTGACGCGCGGCCCATCTACGGCCGCCGGGACCGCGCCGAGCCACTGGCGAGACCGACCCGCGAGTCA
Freshwater sediment metagenome lwMethenol_C1513	ABSQ01001513.1	702-619	CGGTCTGCGGGAGGCGATGACGCGCGGGCCAATGCCGGCCGCCGGGACCGCGCGGAGCCACTGGCGAGACCGACCCGCGGGTGC
Freshwater sediment metagenome lwMethenol_C2548	ABSQ01002548.1	1348-1264	CCGAAAGCGGGAGGCTACGACGCACGGTCCACACTCCGGCCGCCGGGACCGCGCCGAGCCACTGGCGAGACCGACCCGCGTACGT
Freshwater sediment metagenome lwMethenol_C2845	ABSQ01002845.1	828-909	CGGTTGGCGGGAGGCTCTGACACGCGGTCCATACCCGGCCGCCGGGACCGCGCCGAGCTACTGGCGAGACCGACCCGCGCCG
Freshwater sediment metagenome lwMethenol_C298	ABSQ01000298.1	1345-1256	CCACAAACGGGAGGCCGTGATCCGCCGGACGTACCACTTCGGCCACCGCGGTCCGGCGGGGAGCCACTGGTGAGACCGGCCCGCGGGCCG
Freshwater sediment metagenome lwMethylamine_C5836	ABSR01005836.1	444-360	CGGTTGGCGGGAGGCTATGACACGCGGCCCATACTCTGGCCGCCCGGACCGCGCCGAGCCACTGGCGAGACCGACCCGTTGGATC

Geodermatophilus obscurus DSM 43160	CP001867.1	492880-492797	CACGAACGGGTAGTGATGATCCGCCGGGCGCACCTGGTCGCCATAGCCCGGCGGGGAGCAGAGGCGAAACCGGGCCCGTCCTAG
Halanaerobium hydrogeniformans	CP002304.1	1331049-1331135	AAACTTATTGGATGCTGAGATCTGCCAGGATAAAATGGTCACCAGATTAATTGGCAGTGAGCTAAATGGTGAAACCGGCCAAAATTG
Halothermothrix orenii H 168	CP001098.1	2206138-2206055	TATTGAATGGGAAGCTATGAACTCTTCTTTGTACGTGGTCACTTGAAGGAGAGGGAGCTAGTAGTGAAACCGCCCCGACCGGGG
Hot springs metagenome ctg_1106445192553	ADKJ01000386.1	1697-1612	CCTCTGAGGGGAGGCGATGAACCCTCGAGCCCAAGATGGGCGCCATGGGACGAGGGGGAGCCAGTGGCGCAACCGGCCCCTAAAGC
Human gut metagenome DNA	BAAW01001404.1	566-484	ATAAATCTGGAAGTAATGATAAATTCTCTTTATTTGGGCACTTTGAGGATTTTGAACTAGTAGTGCAACCCGCCAACAATTAA
Marine metagenome 1096626368917	AACY020292692.1	343-428	GAGGCGTCCGGAGGCGATGACCCGCTGATCCCCATTTGGGCATCAAGGGACGCGGCGAGCCAGTGATGCAACCGGCCGGACGGCTA
Marine metagenome 1096626368917	AACY020292692.1	175-258	TCGCGATTCGAGGGCGATGACGCTCGTTCTGCAACATGGGCGCTTGGAACGAGCCGAGCCAGTAGCGCAACCGATCGGTCGACG
Marine metagenome ctg_1101668569280	AACY023761929.1	1009-1091	ATAATTTGGTGGGCGTTGATGTGCCCTTTGTATCTGGTCGCTTGAGGGGTACGGAGCCAATAGCGAAACCGCCGCCGTCATAG
Marinithermus hydrothermalis DSM 14884	CP002630.1	142650-142566	GGAGCGTTCGGAGGCGATGAACCGTACTCCCAACCTGGGCACCAAGGGATACGGGGAGCCAGTGGTGCAACCGGCCGAACGCCGT
Marinithermus hydrothermalis DSM 14884	CP002630.1	1070287-1070204	GCTTCCCCTAGCGGCGAGGAAGCCTGTCCTGTACGTGGGCGCCTGGGGCAGGTGGAGCCAGTGGCGCAACCGGCTAGGGGATCT
Marinithermus hydrothermalis DSM 14884	CP002630.1	142912-142999	GGAGCCGTAAGCGGCGATGACCCGCCCATTCCCAACTCGGGCGCCAAGGGAGGGCGGCGAGCCAGTGGCGCGACCGGCTTGCGGCCTC
Marinithermus hydrothermalis DSM	CP002630.1	142803-142719	CGTCCCCTCGGAAGCGATGAAGCCTGTCCTGCACGTTGGGCGCCTGGGGCAGGTGGAGCGGGTGGCGCAACCGGCCGAGGGCGTA

14884			
Marinithermus hydrothermalis DSM 14884	CP002630.1	2135386-2135469	CGGGCCCTTGGAGGCGATGAACCCTGCCCGTGAACTGGGCGCCTGGGGCGGGGGAGCCAGTGGCGCAACCGGCCAAGGGAGGG
Meiothermus ruber DSM 1279	CP001743.1	2770688-2770773	ACCAAGTTCGGAGGTGATGATCCGTGATTCCCAATCTGGGCACCAAGGGAAACGGGGAGCCAGTGGTGCAACCGGCCGAACCCAAA
Meiothermus silvanus DSM 9946	CP002042.1	3024809-3024724	GGGGGGTTCGGAGGCGACGAACTGTGTCACCCAATATGGGCACCAAGGGGCACAGGGAGCTAGTGGTGCAACCGGCCGAACACCGC
Mine drainage metagenome Contig10238	ACXJ01008876.1	95-14	ATCCGTTAGTGAAGCGTTGAATCGTTCGGTTGCATGGTCGCCTTACCGAGCGGTGAGCTAATGGCGAAACCGGCACTTTGTT
Mine drainage metagenome Contig6680	ACXJ01005483.1	595-679	ATAGATGGGTAATGCAATGATCCCTGGGTGCGCAATGGTCGCTTTAGCCCAGGGGGAGTAAGTAGCGAAACCGGTACCCATAAAA
Oceanithermus profundus DSM 14977	CP002361.1	164383-164467	TGAAGAGCAGGAGGCAGTGAACCGTCTTCCGCAACGCGGGCGCCTGGAAGACGGGGAGCCAGTGGCGCGACCGGCCTCGTCCGCG
Oceanithermus profundus DSM 14977	CP002361.1	232155-232069	TCAAATCTTGGAGGCGATGAACCGTGTGTCCCCAATCTGGGCACCAAGGGGCACGGGGAGCCAGTGGTGCAACCGGCCAAGAAGATG
Oceanithermus profundus DSM 14977	CP002361.1	232367-232455	TGTGTAGTTGGAGGCGATGACCCGCCAGGTCCCTATACGGGCGCCAAGGGACGAGCGGCGAGCCAGTGGCGCGACCGACCAAACCCCTA
Ornithinibacillus sp. TW25 contig00142	AEWH01000068.1	172333-172251	ACTTATGTAGGAGGCTAGGAATAATTACCTGTATTTGGGCACTTGGGTAGTTAGGAGCCAGTAGTGCAACCGACCAACTATGT
Paenibacillus elgii B69 Contig4	AFHW01000004.1	83677-83757	GAGAACTAGGTAGGCAATGAGTTCGAATCTGTATATGGGCACTTGGATTCGAAGGAGCTAGTAGTGCAACCGGACCATCTT
Paenibacillus elgii B69 Contig94	AFHW01000094.1	32614-32695	AAACACATGGTAAGCGATGATTTCGAATCTGTATCTGGGCACTTGGATTCGACGGAGCTAGTAGTGCAACCGGACCACCTTT
Paenibacillus mucilaginosus KNP414	CP002869.1	472797-472880	ATACGACATGGGAGCTATGACTTTGAATCCGTATCTGGGCACTTGGATTCAAACGAGCCAGTAGTGCAACCGACCATCTTCCTT
Paenibacillus mucilaginosus KNP414	CP002869.1	6120416-6120499	AAAAGTTTTGGGAGCTATGACTTCGACATCCGCAACGTGGGCACTTGGATGCGAACGAGCTGGTAGTGCAACCGACCATCTTCT
Pelotomaculum thermopropionicum SI	AP009389.1	2908378-2908465	GAGATAGTGTGAAGCAGTGATCTTGCAGCTAATATGGTCACTTTTTACGGCTGCAAGTGAGCTAATAGTGAAACCGGCACACTGATGC

DNA			
Solibacillus silvestris StLB046 DNA	AP012157.1	868334-868251	TTTACAATGGGAGACTATGAAGTACATCCTTTAATTGGGCACCTTGGATGTATGGAGTCAGTGGTGCAACCGGCCTCACAACAT
Sphaerobacter thermophilus DSM 20745 chromosome 1	CP001823.1	2685771-2685688	CTGACCTGCGGACGTGATGACCCCTGTGGTGAGCATGGACGCCGTGCCACCGGGCGAGCGAGTGGCGTACCCGGCCTCGGTCAG
Sphaerobacter thermophilus DSM 20745 chromosome 2	CP001824.1	1154934-1155017	CGTGAGCGCGGAGGCGATGACGCGCGGGCTGTAATTTGGGCACCTCGCCCGCGCCGAGCCTGGGGTGCAACCGGCCGGCTAAGA
Sphaerobacter thermophilus DSM 20745 chromosome 2	CP001824.1	1154769-1154853	CGAAACGTCGGAGACGTTGAGGCGCAGGCTGTAATCTGGGCACCTCGCCTGCGCCGAGTCTGAGGTGCAACCGGCCGACCCTTTG
Streptococcus sobrinus TCI-157 contig00390	AGHO01000390.1	4173-4091	TGAAAGGTAGAAAGCTATGATTAATCAACTTATTTGGGCGCTTTGTTGATTATGAGCTACTAGCGCAACCGGCTAACCAAACT
Thermoanaerobacter brockii subsp. finnii Ako-1	CP002466.1	1121256-1121339	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter ethanolicus CCSD1 ctg00026	ACXY01000031.1	16323-16240	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter ethanolicus JW 200 ctg1020	AEYS01000008.1	66877-66959	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTAGTGCAACCGGCTTATGTCGG
Thermoanaerobacter italicus Ab9	CP001936.1	1106970-1107052	ATTTTATAAAGAGAGATGAAGTGAGGCTATAGGGGGGCACTTTACGCCTCATGGATTGAATGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter mathranii subsp. mathranii str. A3	CP002032.1	1134808-1134888	ATTTTATAGAGAGATGAAGTGAGGCTATAGGGGGGCACTTTACGCCTCATGGATTGAATGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter pseudethanolicus ATCC 33223	CP000924.1	1129065-1129148	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG

Thermoanaerobacter sp. X513	CP002210.1	1378865-1378782	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter sp. X514	CP000923.1	1535517-1535600	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter sp. X561 ctg62	ACXP02000002.1	172572-172655	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGTGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTTATGTCGG
Thermoanaerobacter wiegelii Rt8.B1	CP002991.1	1237154-1237236	ATTTTATAAAGAGTAGATGAAGTGAGGCTATATGCGGGCACTTTATGCCTCACGGATACAGTGGTGCAACCGGCTTATGTCGG
Thermoanaerobacterium saccharolyticum strain JW/SL-YS485 PilB (pilB)	GU479453.1	3423-3505	GATTTGATTGAGATAGATGATGTGAGTCTATATTTGGGCGCTTTATGACTCATTGATATAGTGGCGCAACCGGCATCATTGTC
Thermoanaerobacterium thermosaccharolyticum DSM 571	CP002171.1	2615418-2615336	GATAAAATAGGATTCTATGAAGTATAACCTGTATTTGGGCACCTGGGTTATGCGGAGATAGTGGTGCAACCGGCCGTAGTATC
Thermoanaerobacterium thermosaccharolyticum DSM 571	CP002171.1	1298918-1298999	GAATTGATAGACGTAGATGATGTGAGTCTATATTTGGGCGCTTTACGACTCATTGATATAGTGGCGCAACCGGCATCATTGT
Thermoanaerobacterium xylanolyticum LX-11	CP002739.1	2362968-2362885	AAATATATAGGATTCTGTGAAGCATAACCTGTATTTGGGCACCTGGGTTATGCGGAGATAGTGGTGCAACCGGCCGTAGTTTTT
Thermoanaerobacterium xylanolyticum LX-11	CP002739.1	1231285-1231367	GATTTGATTGAGATAGATGATGTGAGTCTATATTTGGGCGCTTTATGACTCATTGATATAGTGGCGCAACCGGCATCATTGTC
Thermobaculum terrenum ATCC BAA-798 chromosome 1	CP001825.1	388010-388096	AATTAGCGTAGAGGCGACGAAGTCCGCTTACCTATATGGGCACCATGGGAGCGGATGGAGCCACTGGTGCAACCGGCTACTGAGAAG
Thermomicrobium roseum DSM 5159 plasmid	CP001276.1	419946-420032	CGACACCCCGGAGGCGAAGAAGCGCTGCCTGAGCGTTGGGCGCCAGTGGGCAGCGTGGAGCCAGTGGCGCACCCGGCCGGGATATCC
Thermosinus carboxydivorans Nor1 ctg50	AAWL01000006.1	67971-67888	ACTGCAATGGGTGTGATGAAGTCCGGACAGTAATGTGGGCACTTAGTCCGGACCGAGCAAGTAGTGCAACCGACCAGATGCAAA
Thermus aquaticus Y51MC23 ctg62	ABVK02000002.1	96520-96603	AGGCACCTCGGAGGCGACGAAGCCTGTCCTGCAATCTGGGCGCCTGGGACAGGTGGAGCCAGTGGCGCAACCGGCCGAGGGCGG

Thermus aquaticus Y51MC23 ctg62	ABVK02000002.1	96672-96757	AGGGCGTTCGGAGGCGAGGAACCGTGATACCCAAGATGGGCGCCAAGGACACGGGGAGCCAGTGGCGCAACCGGCCGGACGCTAT
Thermus aquaticus Y51MC23 ctg74	ABVK02000011.1	69647-69731	CCTCTGAGGGGAGGCGATGAACCCTCGAGCCCAAGATGGGCGCCATGGGCCGAGGGGACCCAGTGGCGCAACCGGCCCCTAAAGC
Thermus scotoductus SA-01	CP001962.1	1792927-1792844	AGGTACCTCGGAGGCGAAGAAGCCTGCCCTGTAGTTGGGCGCCTGGGGCAGGTGGAGCCAGTGGCGCAACCGGCTGAGGGTTAG
Thermus scotoductus SA-01	CP001962.1	1638632-1638717	AGGGCGTTCGGAGGCGAGGAACCGTGAGTCCCAAGATGGGCGCCAAGGACACGGGGAGCCAGTGGCGCAACCGGCCGGACGCATG
Thermus scotoductus SA-01	CP001962.1	1792779-1792694	AGGGCGTTCGGAGGCGATGAACCGTGGAACCCAAGATGGGCGCCAAGGACACGGGGAGCCAGTGGCGCAACCGGCCGAACGTCGA
Thermus scotoductus SA-01	CP001962.1	1638487-1638571	AGGCACCTCGGAGGCGAGGAAGCCTGCCCTGCAATCTGGGCGCCTGGGGCAGGTGGAGCCAGTGGCGCAACCGGCCGAGGGCGGT
Thermus scotoductus SA-01	CP001962.1	1792216-1792129	GCCTTGAGGGGAGGCGAGGAACCCCCGATCTCCCAGATGGGCGCCAAGGAGCGGGGGGGAGCCAGTGGCGCAACCGGCCCCTAATCCT
Truepera radiovictrix DSM 17093	CP002049.1	2322363-2322277	CCGCCCCTCGGAGGCTTTGACACCCGTTTCCTGTATATGGGCGCTTGGGAGCGGGTCGAGCCAGTAGCGCAACCGGCCGAGGGGAGC
Turicibacter sanguinis PC909 contig00019	ADMN01000014.1	3259-3334	ATTTTAGTTGGAAATGTTGAAATATGTCCTGTATTTGGGTACCTGGGACATATGGAGTTATTGGTACAACTGTAGT
Turicibacter sanguinis PC909 contig00029	ADMN01000011.1	58945-58863	GAATTAAAAGAAACGATGAAGTATATTCTGTATTTGGGCACCTGGAATATATGGAGTTAGTGGTGCAACCGGCTTTATAAATT
Turicibacter sanguinis PC909 contig00047	ADMN01000018.1	10516-10597	TTCTGCCTAAGAATCGATGAAATATATTCTGTATATGGGTACCTGGAATATATCGAGATATTGGTACAACCGGCTTTTTAAA
Turicibacter sp. HGF1 contig00008	AEXQ01000067.1	3225-3308	ATTTTAGTTAGAAATGTTGAAATATGTCCTGTATTTGGGTACCTGGGGCATATGGAGTTATTGGTACAACCGGCTGCCTTTTTT
Turicibacter sp. HGF1 contig00092	AEXQ01000089.1	3700-3619	TTCTGCCTAAGAATCGATGAAATATATTCTGTATATGGGTACCTGGAATATATCGAGATATTGGTACAACCGGCTTTTTAAA

*The original RNA qequences were downloaded from Rfam FTP site