

Supplementary Materials

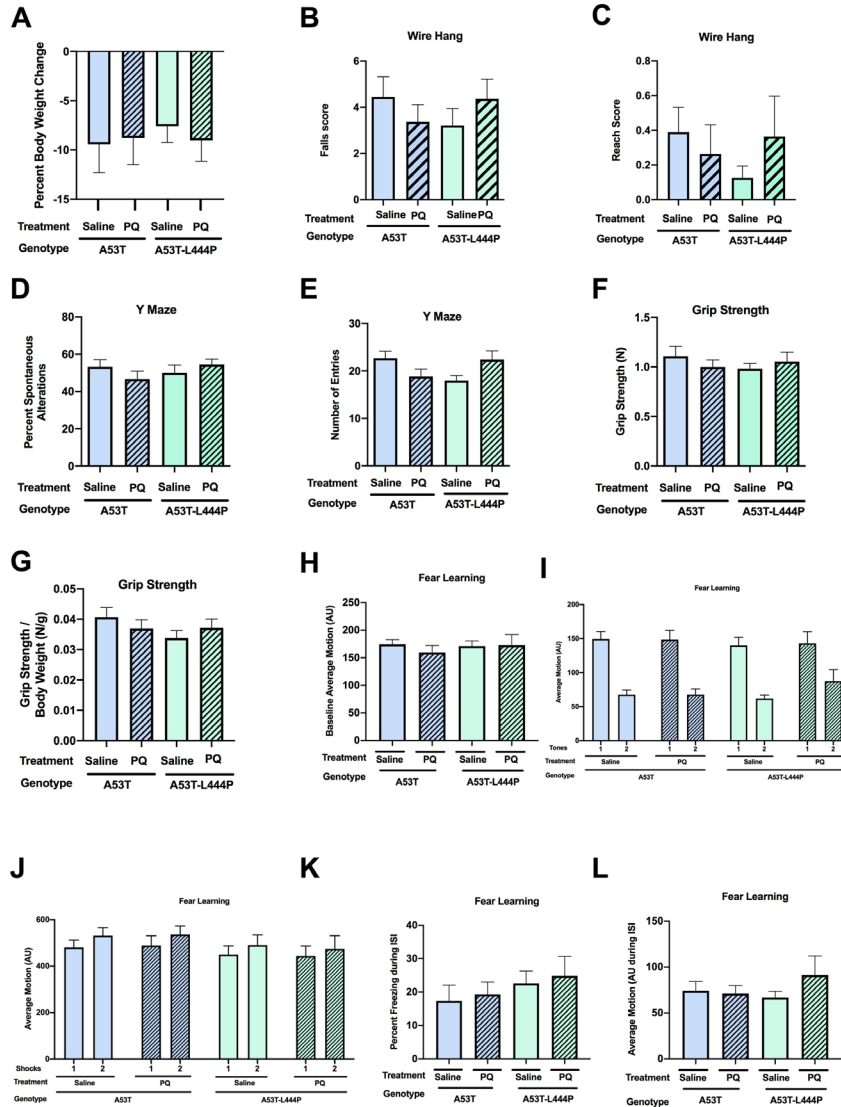


Figure S1. A. There was no effect of genotype or treatment on the percent body weight change. **B.** There was no effect of genotype or treatment on fall scores in the wire hang test. **C.** There was no effect of genotype or treatment on reach scores in the wire hang test. **D.** In the grip strength test, there was no effect of genotype or treatment. **E.** When grip strength per body weight was analyzed, there was no effect of genotype or treatment.

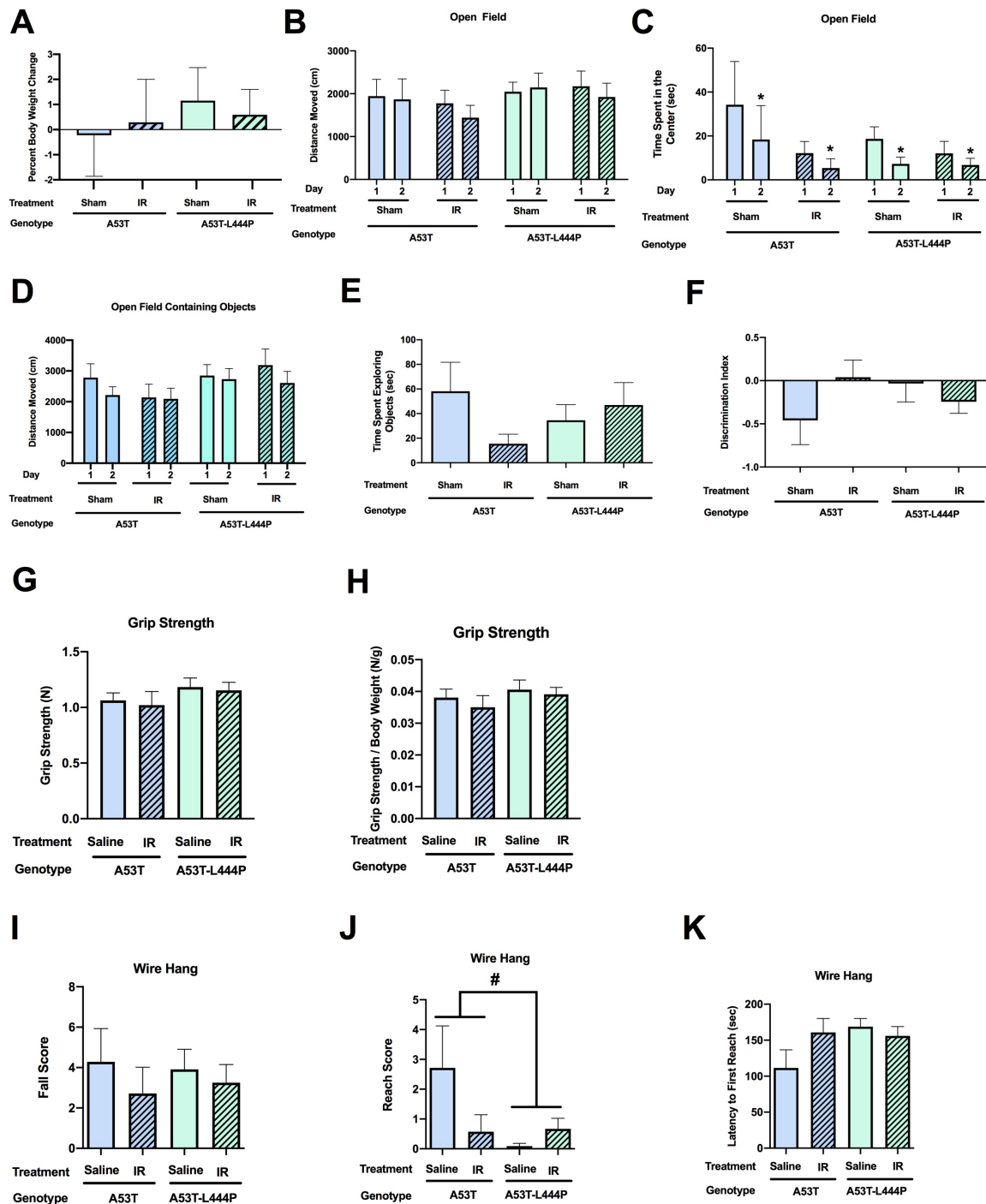


Figure S2. A. There was no effect of genotype or treatment on the percent body weight change. **B.** There was no effect of genotype or treatment on activity levels during open field testing. **C.** When time spent in the center of the open field was analyzed, there was an effect of day ($F(1,29) = 6.309$, $*p = 0.018$). **D.** There was no effect of genotype or treatment on

activity levels in the open field containing objects. **E.** There was no effect of genotype or treatment on time spent exploring the objects in the object recognition test. **F.** There was no effect of genotype or treatment on the discrimination index in the object recognition test. **G.** There was no effect of genotype or treatment on grip strength. **H.** There was no effect of genotype or treatment on grip strength per body weight. **I.** There was no effect of genotype or treatment on fall scores in the wire hang test. **J.** There was a trend towards an effect of genotype for reach scores ($F(1,29) = 3.271$, $^{\#}p = 0.081$), with a trend towards higher reach scores in A53T than A53T-L444P mice. **K.** There was a no effect of genotype or treatment on latency to first reach in the wire hang test.

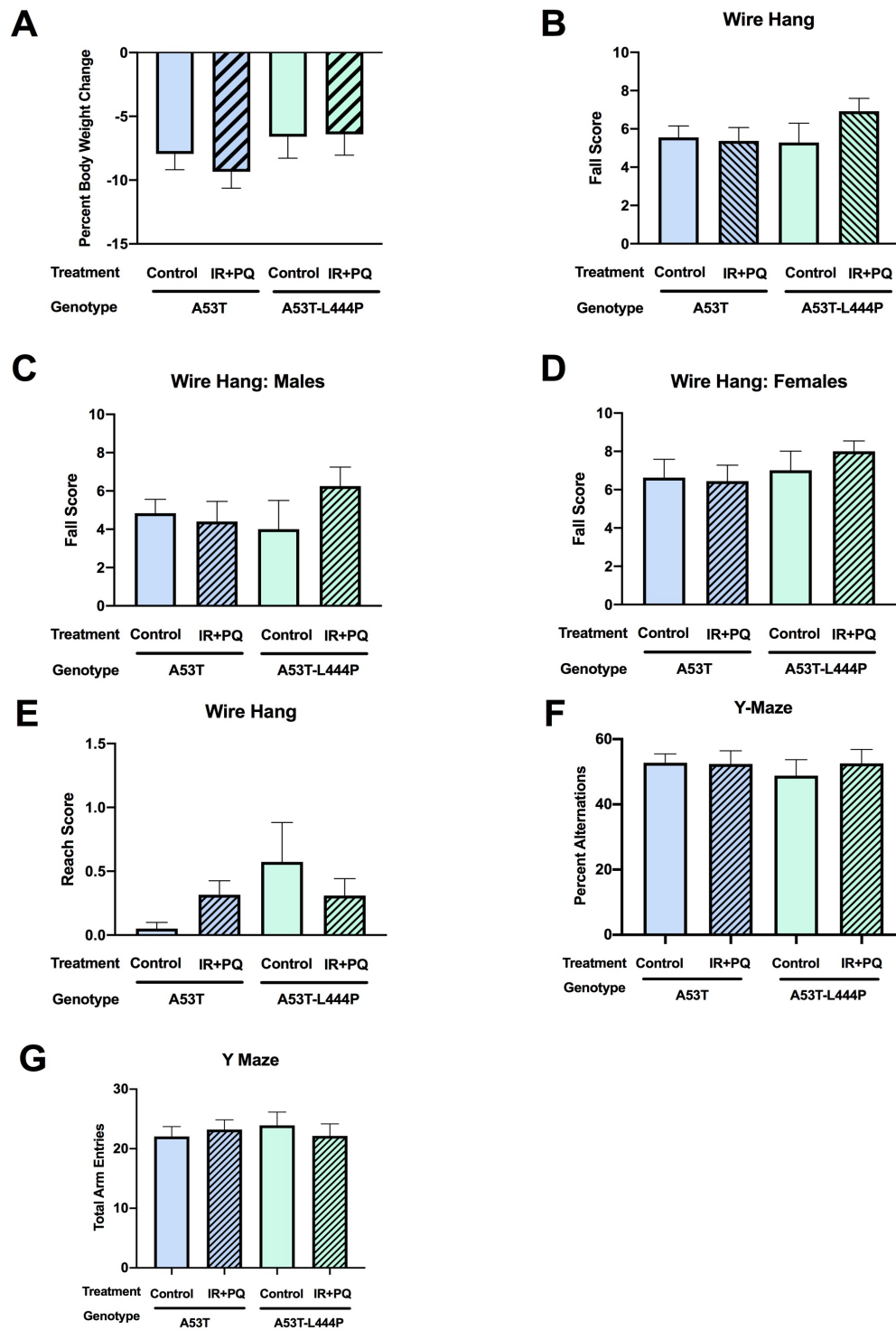


Figure S3.A. There was no effect of genotype or treatment on the percent body weight change. **B.** There was an effect of sex for fall scores in the wire hang test ($F(1,58) = 8.345$, $p = 0.005$). **C.** Fall scores in males. **D.** Fall score in females were higher than those in males (C).

E. For reach scores, there was a trend towards a treatment x sex x genotype interaction

($F(1,58) = 3.248$, $p = 0.077$). F. There was no effect of genotype or treatment on spontaneous alternation in the Y maze. There was no effect of genotype or treatment for the number of entries in the Y maze ($F(1,58) = 3.949$, $p = 0.052$).

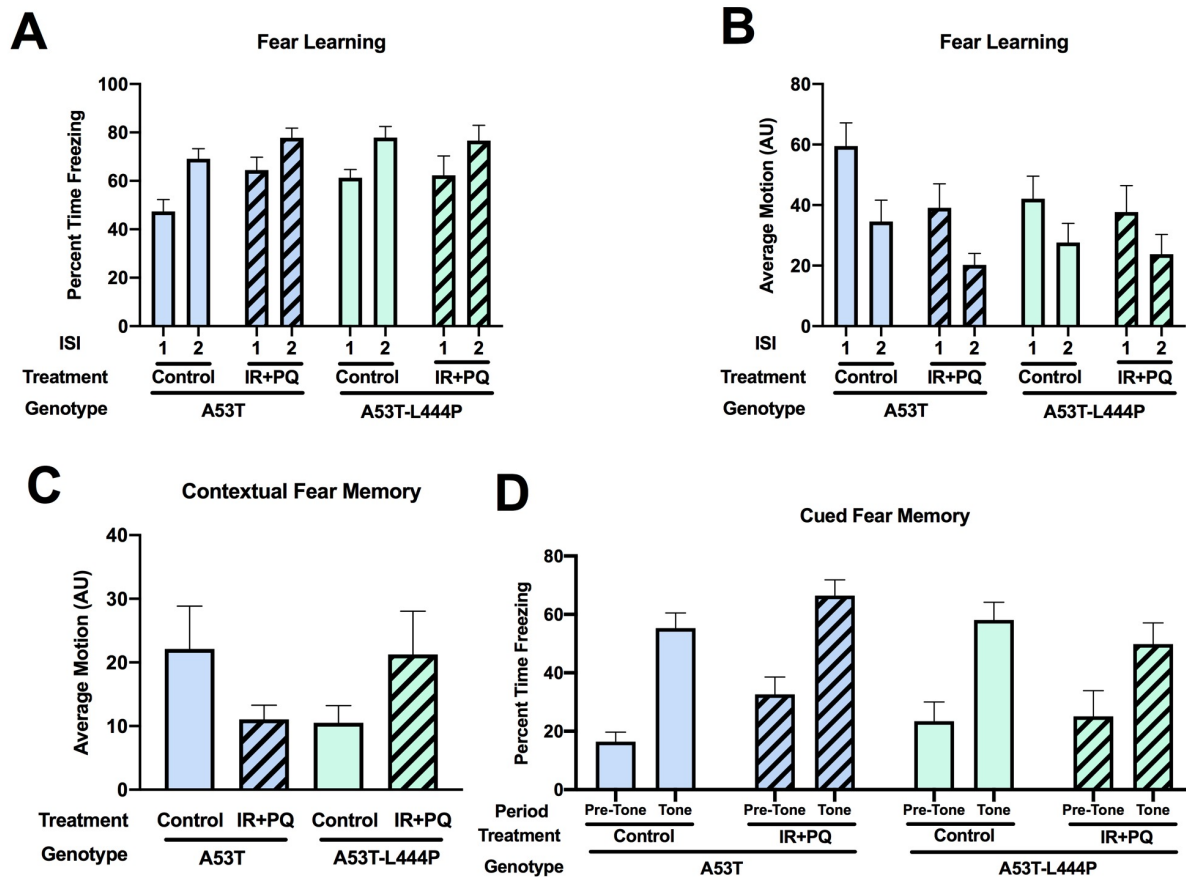


Figure S4. A. There was no effect of genotype or treatment on freezing levels during the ISIs. B. There was no effect of genotype or treatment on activity levels during the ISIs. C. There was no effect of genotype or treatment on activity levels during the contextual fear memory test. D. There was no effect of genotype or treatment on freezing levels during the cued fear memory test.

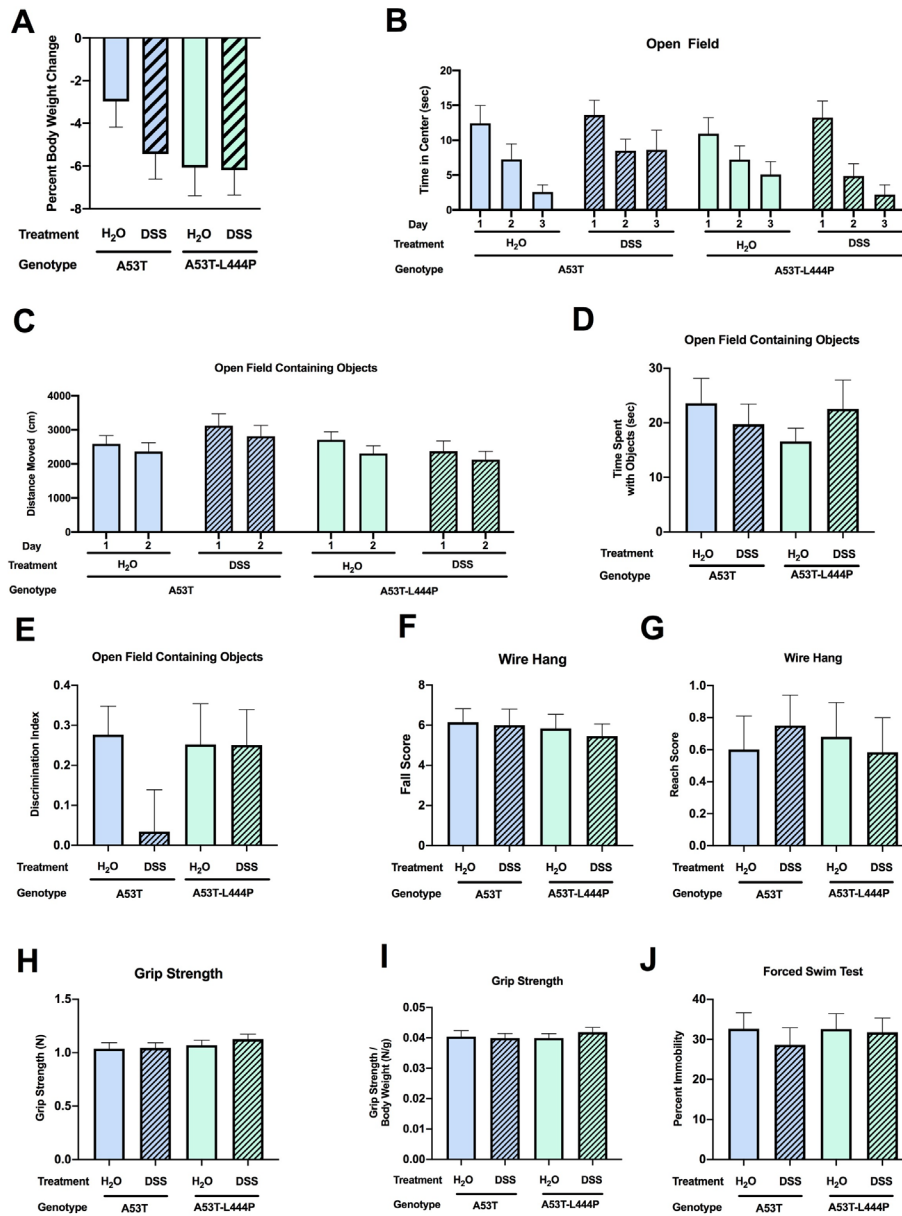


Figure S5. A. There was no effect of genotype or treatment on the percent body weight change. **B.** There was no effect of genotype or treatment on anxiety levels in the open field. **C.** There was no effect of genotype or treatment on activity levels in the open field containing objects. **D.** There was no effect of genotype or treatment on time spent exploring the objects in the object recognition test. **E.** There was no effect of genotype or treatment on the discrimination index. **F.** There was no effect of genotype or treatment on fall scores in

the wire hang test. **G.** There was no effect of genotype or treatment on reach scores in the wire hang test. **H.** There were no effects of genotype or treatment on performance in grip strength test. **I.** There was no effect of genotype, treatment on grip strength per body weight. **J.** There were no effects of genotype or treatment on depressive-like behavior in the forced swim test.

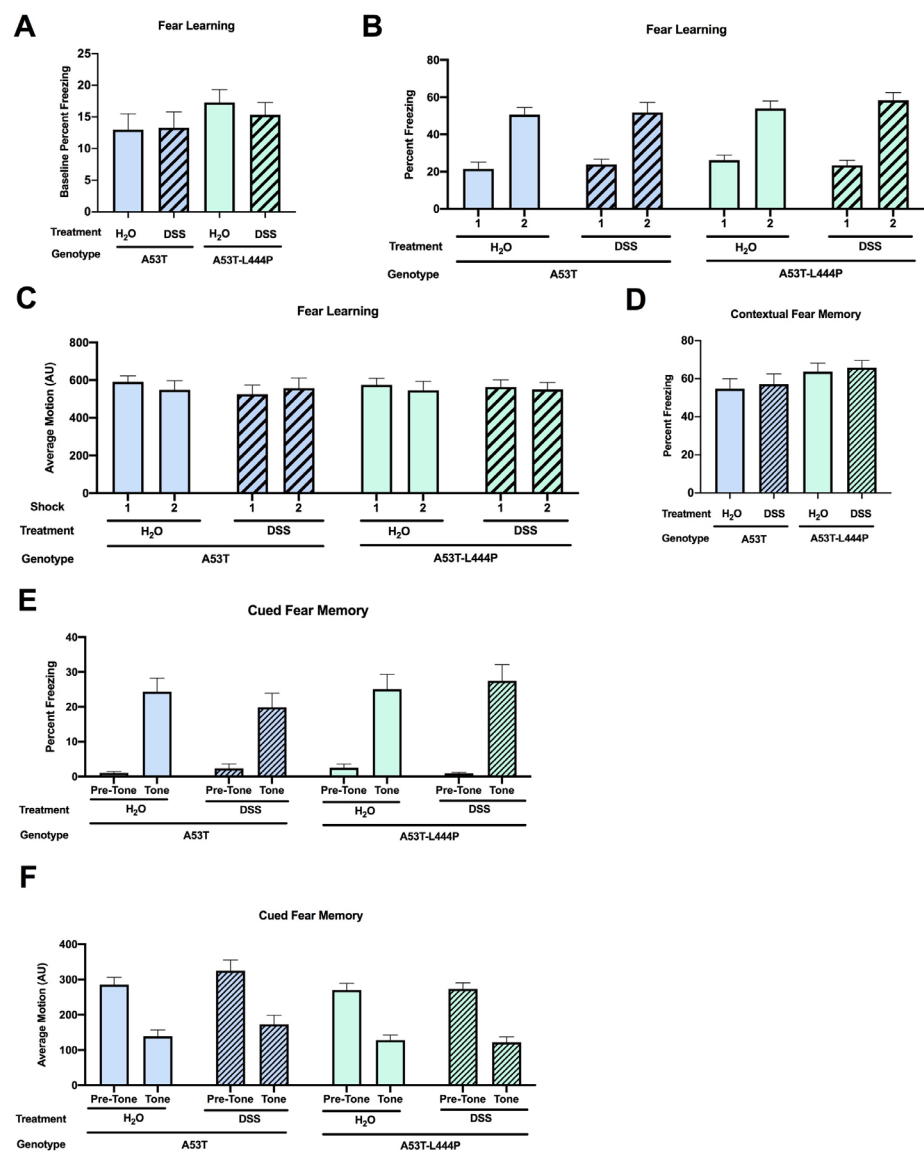


Figure S6. A. There were no effects of genotype or treatment on percent freezing during the baseline period in the fear conditioning test. **B.** There was no effect of genotype or treatment

on freezing during the tones. **C.** There was no effect of genotype or treatment on response to the shocks. **D.** There was no effect of genotype or treatment on freezing levels during the contextual fear memory test. **E.** There was no effect of genotype or treatment on freezing levels during the cued fear memory test. **F.** There was no effect of genotype or treatment on activity levels during the cued fear memory test.

Table S1. PQ_sample_data.

	Ki ng do m	Phyl um	Class	Order	Family	Genus	Taxon
ASV015A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGGGCAAGTCTGATG TGAAAGTCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGTCCGGCTAGAGTGCAGGAGAGGTAAGTGGA ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV360A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTATGGTAAGTCAGATGT GAAAGCCCCGGGGCTTAACCCCGGAACTGCATTGAAACTATCAAAGTGTAGAGTGTCCGAGAGGTAAGTGGA TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGAT AACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV098A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTATGGTGCAAGCGTTATCCGGAATGACTGGGTGTAAAGGGAGCGTAGACGGTTGTACAAGTCTGATGT GAAAGCCCACGGCTCAACTGTGGGAGTGCATTGGAAACTGTAGAAGTGTAGAGTATCGGAGAGGCAAGTGGA TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGTCTGGACGAA AACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV286A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	XBB1006	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCAGGATGAGTCTGATG TGAAAACCCGCGGCTCAACCACGGGATTGCATTGGAAACTGTCCAGCTAGAGTGTCCGAGAGGTAAGCGGA ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA TGACTGACGCTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV571A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAGAGGGAGCGCAGGCGGCAGGATGAGTCTGATG TGAAAACCCGCGGCTCAACCACGGGATTGCATTGGAAACTGTAGAAGTGTAGAGTATCGGAGAGGCAAGTGGA ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGTCTGGACGA AAACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV069A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGTCTGATGT GAAAACCCGGGGCTCAACCCCGGGACTGCATTGAAACTGTGCGGCTGGAGTGTCCGAGAGGCAAGTGGA TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGTCTGGACGAC GACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG
ASV069A	Bacteri	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-006	TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT GAAAGGCCGGGGCCCAACCCCGGGAGTGTCTTGGAAACTGTGCGGCTAGAGTGTCCGAGAGGCAAGTGGA ATTCCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCGTCTTGTCTGGACGA TGACTGACGTTGAGGCTCGAAAGCGTGCGGAGCAAAACAGG

18							
8							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGGAGT
V	ct	Firm					GAAAGGCATGGGGCTCAACCTGTGGACTGCTTTGGAAACTGTGCGGCTTGAGTGTGCGAGAGGGCAAGTGGAA
11	eri	icute	Clostr	Lachnos	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGAT
4	a	s	idia	pirales	raceae	Dorea	GACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGTGCAAGTCTGAAG
V	ct	Firm				Lachnospira	TGAAAGGCAAGGGCTCAACCCCTGGACTGCTTTGGAAACTGTGCTGCTGGAGTGTGCGAGAGGGCAAGTGGAA
21	eri	icute	Clostr	Lachnos	Lachnospi	ceae_UCG-	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGA
5	a	s	idia	pirales	raceae	006	TGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
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V	ct	Firm					GAAAGCCCGGGGCTCAACCTCGGGACTGCATTTGGAAGTGTATGGCTGGAGTGTGCGAGAGGGCAGGCGGAA
37	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGAT
9	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
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V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCATTTGGAAGTGTATGGCTGGAGTGTGCGAGAGGGCAGGCGGA
24	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGA
5	a	s	idia	pirales	raceae	idium	TGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGGTGCAAGCCAGATG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCATTTGGAAGTGTATAGCTAGAGTGTGCGAGAGGGCAGGCGGA
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V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCATTTGGAAGTGTATGGCTGGAGTGTGCGAGAGGGCAGGCGGA
35	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGA
4	a	s	idia	pirales	raceae	idium	TGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG

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	V	ct	Firm					GAAAGCCCCGGGGCTCAACCCCGGGACTGCATTTGGAAGTGTGTGGCTAGAGTGTGCGAGAGGCAGGCGGAA
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2	a	s	idia	pirales	raceae	ceae_Genus		GACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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	V	ct	Firm					TGAAAGCCCCGGGGCTCAACCCCGGGACTGCATTTGGAAGTGTGTGGCTGGAGTGTGCGAGAGGCAGGCGGA
18	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGA
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	S	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	GAAAAACCCGGGGCTCAACCCCGGGACTGCATTGGAAGTGTGAGGCTAGAGTGTGCGAGAGGCAAGTGGA
V	a	s	idia	pirales	raceae	ceae_Genus		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGTGGACGA
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28							
1							
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S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTATGGCAAGTCTGATGT
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6	a	s	idia	pirales	raceae	Roseburia	TGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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V	ct	Firm					GAAAATCCGGGGCCCAACCCCGGAACTGCATTGGAAACTGTATTTCTAGAGTGTCTGGAGAGGCAAGTGGAA
09	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi	TTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGAT
7	a	s	idia	pirales	raceae	006	GACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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1	a	s	idia	pirales	raceae	006	TGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGACTTGCAAGTCTGATGT
V	ct	Firm					GAAAATCCGGGGCCCAACCCCGGAACTGCATTGGAAACTGTATATCTAGAGTGTCTGGAGAGGCAAGTGGAA
14	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi	TTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGAT
2	a	s	idia	pirales	raceae	006	GACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGAGGAGCAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGCGGCTCAACTGCGGGACTGCTTTGGAAACTGTTTCATCTAGAGTGTCTGGAGAGGTAAGTGGAA
25	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGAT
8	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGCGGTAAGTCTGATG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGTCTGTCTGGAGTGTCTGGAGGGGCAAGTGGAA
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9	a	s	idia	pirales	raceae	Roseburia	CAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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04	eri	icute	Clostr	Lachnos	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
5	a	s	idia	pirales	raceae	Roseburia	TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTCACTGGGCGTAAAGGGAGCGCAGGCGGGCGGGCAAGTCTGATG
	V	ct	Firm					TGAAAGCTCGGGGCTCAACCCCGGGTCTGCATTGAAAAGTGTGAGCTAGAGTGTGCGAGGGGTAAGCGGA
30	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
9	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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02	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
4	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGCGTAAAGGGAGCGCAGGCGGGCACGGCAAGTCCGGTG
	V	ct	Firm					TGAAAGCCCGGGGCCAACCCCGGGACTGCACTGAAAAGTGTGCGGGCTGGAGTGTGCGAGGGGCAGGCGG
02	eri	icute	Clostr	Lachnos	Lachnospi			AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGACG
7	a	s	idia	pirales	raceae	Roseburia		ACGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
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07	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGA
3	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTCTGGCAAGTCTGATGT
	V	ct	Firm					GAAAGGCCGGGGCTCAACTCCGGGACTGCATTGAAAAGTGTGAGACTGGAGTGTGCGAGAGGTAAGCGGAA
12	eri	icute	Clostr	Lachnos	Lachnospi			TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGAT
8	a	s	idia	pirales	raceae	Roseburia		GACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTCTGGCAAGTCTGATGT
	V	ct	Firm					GAAAGGCCGGGGCTCAACCCCGGGACTGCATTGAAAAGTGTGAGACTGGAGTGTGCGAGAGGTAAGCGGA
16	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
4	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTCTGGCAAGTCTGGTGT
	V	ct	Firm					GAAAGGCCGGGGCTCAACCCCGGGACTGCATTGAAAAGTGTGAGACTGGAGTGTGCGAGAGGCAAGCGGA
02	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
8	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTAAGGCAAGTCTGATGT
	V	ct	Firm					GAAAGGCCAGGGCTCAACCCCTGGGACTGCATTGAAAAGTGTGAGACTGGAGTGTGCGAGAGGCAAGTGAA
09	eri	icute	Clostr	Lachnos	Lachnospi			TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGAT
	a	s	idia	pirales	raceae	Roseburia		GACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	Ba							TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCTTGGCAAGTCTGATGT
	ct	Firm						GAAAGGCTGGGGCTCAACCCAGGACTGCATTGAAAAGTGTGAGGCTGGAGTGTGCGAGAGGTAAGCGGAA
S	eri	icute	Clostr	Lachnos	Lachnospi			TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGAC
V	a	s	idia	pirales	raceae	Roseburia		AAGTGTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

19								
7								
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGCAGGCGGGCGGCCAAGTCTGATGT
V	ct	Firm						GAAACCCCGGGGCTCAACCCCGGGCATGCATTGAAACTGGCGGGCTGGAGTGCCGGAGAGGTAAGCGGA
09	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTACTGGACGG
1	a	s	idia	pirales	raceae	Roseburia		CAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGGCGGCTTAAGTCTGATGT
V	ct	Firm						GAAAACCCCGGGGCTCAACTGCGGGACTGCATTGAAACTGGCGGGCTTGAGTGCCGGAGAGGCAAGCGGA
25	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTGCTGGACGG
2	a	s	idia	pirales	raceae	Roseburia		TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGGCGGCTTAAGTCTGATGT
V	ct	Firm						GAAAACCCCGGGGCTCAACTGCGGGACTGCATTGAAACTGGCGGGCTTGAGTGCCGGAGAGGCAAGCGGA
39	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGGCGGGCAAGTCAGATGT
V	ct	Firm						GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGAAACTGCCGGGCTAGAGTATCGGAGAGGCAAGTGGAA
10	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTGCTGGACGAT
4	a	s	idia	pirales	raceae	ceae_Genus		CACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGGCGGGCAAGTCAGATGT
V	ct	Firm						GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGAAACTGCCGGGCTAGAGTATCGGAGAGGCAAGGCGGA
56	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTGCTGGACAG
6	a	s	idia	pirales	raceae	ceae_Genus		CAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTTCTGCAAGTCTGATGT
V	ct	Firm						GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGAAACTGCCGGGACTGGAGTGTCCGAGGGGTAAGCGGA
18	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGCGCAAGGCGGCTTACTGGACGA
6	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTGCGGCAAGTCTGATGT
V	ct	Firm						GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGAAACTACCGAAGTGTGCGAGAGGTAAGTGGGA
36	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTACTGGACGA
2	a	s	idia	pirales	raceae	Roseburia		TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTACGGCAAGTCCGATGT
V	ct	Firm						GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGAAACTGCCGCACTAGAGTGCCGGAGAGGTAAGTGGGA
28	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGCAAGGCGGCTTACTGGACGG
8	a	s	idia	pirales	raceae	001		TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

ASV347	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTACGGCAAGTCCGATGTGAAAACCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGCCGCTAGAGTGCCGGAGAGGTAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV057	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Roseburia	TACGTATGGTGC AAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTGCGGCAAGTCTGATGTGAAAGCCCGGGGCCAACCCCGGTACTGCATTGGAAACTGCCGTACTTGAGTGTCCGAGGGGTAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGACAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV348	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Agathobacter	TACGTATGGTGC AAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTGCGGCAAGTCTGATGTGAAAGCCCGGGGCTCAACCCCGGTACTGCATTGGAAACTGTCTGCTACTAGAGTGTCCGAGGGGTAAGCGGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGATAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV125	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTATGGCAAGTCAGATGTGAAAACCCAGGGCTCAACCCCTGGGACTGCATTGAAACTGCCATACTGGAGTGCCGGAGAGGTAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV173	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTATGGCAAGTCAGATGTGAAAACCCAGGGCCCCAACCCCTGGGACTGCATTGAAACTGCCATACTGGAGTGCCGGAGAGGTAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV308	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGTGCGCAAGTCAGATGTGAAAACCCGGGGGCCAACCCCGGGACTGCATTGAAACTGCCATGCTGGAGTGCCGGAGAGGCAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGGAGGCGGCTTGCTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV036	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGTGCGCAAGTCAGATGTGAAAACCCGGGGGCCAACCCCGGGAGTGCATTGAAACTGCCATGCTGGAGTGCCGGAGAGGTAAGCGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGGAGGCGGCTTACTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV327	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-001	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGTGCGCAAGTCAGATGTGAAAACCCGGGGGCCAACCCCGGGAGTGCATTGAAACTGCCATGCTGGAGTGCCGGAGAGGTAAGTGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGGAGGCGGCTTACTGGACGGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
ASV	Bacterial Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_Genus	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGAGCGCAAGTCTGATGTGAAAGCCCGGGGCCAACCCCGGGACTGCATTGAAACTGCGCAGCTGGAGTGCCGGAGGGGTAAGCGGAATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGCAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

35							
5							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGATGGACAAGTCTGATG
V	ct	Firm					TGAAAGGCTGGGGCTCAACCCCGGGACTGCATTGGAAACTGCCCGTCTTGAGTGCCGGAGAGGTAAGCGGA
35	eri	icute	Clostr	Lachnos	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG
7	a	s	idia	pirales	raceae	Blautia	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGATGTGCAAGTCTGATGT
V	ct	Firm					GAAAGGCGGGGCTCAACCCCTGGACTGCATTGGAAACTGTAAATCTTGAGTGCCGGAGAGGTAAGCGGAA
05	eri	icute	Clostr	Lachnos	Lachnospi	Marvinbrya	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT
3	a	s	idia	pirales	raceae	ntia	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGATCTGCAAGTCTGATGT
V	ct	Firm					GAAAGGCGGGGCTCAACTCCTGGACTGCATTGGAAACTGTAGATCTTGAGTGCCGGAGAGGTAAGCGGAA
13	eri	icute	Clostr	Lachnos	Lachnospi	Marvinbrya	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT
7	a	s	idia	pirales	raceae	ntia	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGTGCCAAGTCTGATGT
V	ct	Firm					GAAAGGCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGGCATGCTGGAGTGCCGGAGGGGCAAGCGGA
03	eri	icute	Clostr	Lachnos	Lachnospi	Marvinbrya	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGG
1	a	s	idia	pirales	raceae	ntia	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGGCAAGTCTGATGT
V	ct	Firm					GAAAGGCATGGGCTCAACCTGTGGACTGCATTGGAAACTGTCATACTTGAGTGCCGGAGGGGTAAGCGGAA
29	eri	icute	Clostr	Lachnos	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT
0	a	s	idia	pirales	raceae	Blautia	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGCAGCAAGTCTGATG
V	ct	Firm					TGAAAGGCAGGGGCTTAACCCCTGGACTGCATTGGAAACTGCTGTGCTTGAGTGCCGGAGGGGTAAGCGGA
37	eri	icute	Clostr	Lachnos	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG
4	a	s	idia	pirales	raceae	Blautia	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATTGCAAGTCTGATGT
V	ct	Firm				Lachnospira	GAAAGATTGGGGCTCAACCCAGGCCTGCATTGGAAACTGTAAAGCTGGAGTACAGGAGAGGTAAGCGGA
03	eri	icute	Clostr	Lachnos	Lachnospi	ceae_NK4A1	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
9	a	s	idia	pirales	raceae	36_group	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATAGCAAGTCTGATGT
V	ct	Firm					GAAAGATCGGGGCTCAACCCCGGGCTGCATTGGAAACTGTAAAGCTGGAGTACAGGAGAGGTAAGCGGAA
04	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
8	a	s	idia	pirales	raceae	ceae_Genus	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATGGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACCGCGGGACTGCTTTGGAACTGTAAAGCTGGAGTGCAGGAGAGGTAAGTGGAA
40	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
1	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGTAGGCGGCAAAAATAAGTCTGAAG
	V	ct	Firm		Erysipel			TAAAAGGCGTTGGCTCAACCAACGTAAGCTTTGGAACTGTAAAGCTAGCGTGCAGGAGAGGTTAGTGGAA
26	eri	icute		otrichal	Erysipelot			TTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTAACTGGCCTGT
4	a	s	Bacilli	es	richaceae	Breznakia		AACGGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCGAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGCGCATTAAGTTTGAAGT
	V	ct	Firm		Erysipel			AAAAGGTAGCGGCTCAACCGCTGCAAGCTTCGAAAACCTGGTGTGCTGGAGTGCAGGAGAGGGCAGTGGAA
23	eri	icute		otrichal	Erysipelot	Erysipelotric		TCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGCCTGTA
3	a	s	Bacilli	es	richaceae	us		ACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCGAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGTAGGTGGCAGAACAAAGTCTGGAG
	V	ct	Firm		Erysipel			TAAAAGGTATGGGCTCAACCCGTAAGCTTTGGAACTGTTCAGCTAGAGAACAGAAGAGGACGGCGGAA
47	eri	icute		otrichal	Erysipelot	Holdemanel		CTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGCCGTCTGGTCTGTT
2	a	s	Bacilli	es	richaceae	la		GCTGACACTGAAGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCGAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGTCTGCAAGTCTGGAGT
	V	ct	Firm		Erysipel			GAAACGCATGAGCTCAACTCATGCATGGCTTTGGAACTGGAGGACTGGAGAGCAGGAGAGGGCGGTGGA
38	eri	icute		otrichal	Erysipelot	Faecalibacul		ACTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGCCCTGGCCTG
0	a	s	Bacilli	es	richaceae	um		TTGCTGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGATGTATAAGTCTGAAG
	V	ct	Firm		Erysipel			TAAAAGCCATCGGCTCAACCGATGTAAGCTTTGGAACTGTAGATCTAGAGTGCAGGAGAGGACAGTGGAA
30	eri	icute		otrichal	Erysipelot	Erysipelotric		TTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTGTCTGGCCTGTA
5	a	s	Bacilli	es	richaceae	us		ACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGAACCATAAGTCTGAAG
	V	ct	Firm		Erysipel			TAAAAGCCATCGGCTCAACCGATGTAAGCTTTGGAACTGTGGATCTAGAGTGCAGGAGAGGACAGTGGAA
16	eri	icute		otrichal	Erysipelot	Erysipelotric		TTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTGTCTGGCCTGTA
3	a	s	Bacilli	es	richaceae	us		ACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATGATTGGGCGTAAAGGGTGCGCAGGCGGAACCATAAGTCTGAAG
	V	ct	Firm		Erysipel			TAAAAGCCATCGGCTCAACCGATGTAAGCTTTGGAACTGTGGATCTGGAGTGCAGGAGAGGACAGTGGAA
24	eri	icute		otrichal	Erysipelot	Erysipelotric		TTCCATGTGTAGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTGTCTGGCCTGTA
4	a	s	Bacilli	es	richaceae	us		ACTGACGCTGAGGCACGAAAGCGTGGGGAGCAAATAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGAGTAGGTGGCAGAGCAAGTCCGAAG
	V	ct	Firm		Erysipelot	Erysipelotoc		TGAAAACCCAAAGCTCAACTATGGGAATGCTTTAGAACTGCTCAGCTAGAGTGCAGTAGAGGATCGTGGAA
AS	eri	icute		otrichal	oclostridia	lostridiaceae		ATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGACGATCTGGGCTG
V	a	s	Bacilli	es	ceae	_Genus		CAACTGACGCTCAGTCCCGAAAGCGTGGGGAGCAAACAGG

52							
2							
A							
S	Ba	Firm er a	Bacilli	Erysipel otrichal es	Erysipelat oclostridia ceae	Erysipelatoc lostridiaceae _Genus	TACGTAGGTGGCGAGCGTTATCCGGAATTATTGGGCGTAAAGAGGGAGCAGGCGGCAGCTAAGGTCTGCGG
V	ct						TGAAAGCCCCGAAGCTAAACTTCGGTAAGCCGTGGAAACCGGAGCAGCTAGAGTGCAGTAGAGGATCGTGGA
13	eri						ATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGACGATCTGGGCTG
6	a	s					CAACTGACGCTCAGTCCCGAAAGCGTGGGGAGCAAATAGG
A							
S	Ba	Firm er a	Bacilli	Erysipel otrichal es	Erysipelat oclostridia ceae	Erysipelatoc lostridium	TACGTAGGTGGCGAGCGTTATCCGGAATCATTGGGCGTAAAGAGGGAGCAGGCGGCCTGGAGGGTCTATTG
V	ct						TTAAAAGGCAGTGGCTTAACCATTGCAAGGCGAAGAAACCGGAGGCTAGAGTTCTAAAGAGGATCGTGGA
33	eri						ATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGACGATCTGGGAAG
7	a	s					AAACAGACGCTGAGTCCCGAAAGCGTGGGGAGCAAATAGG
A							
S	Ba	Firm er a	Bacilli	Erysipel otrichal es	Erysipelat oclostridia ceae	Erysipelatoc lostridium	TACGTAGGTGGCGAGCGTTATCCGGAATCATTGGGCGTAAAGAGGGAGCAGGCGGCCTGGAGGGTCTATTG
V	ct						TTAAAAGGCATGGCTTAACCATTGTAAGGCGAAGAAACCGGAGGCTAGAGTTCTAAAGAGGATCGTGGA
35	eri						ATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGACGATCTGGGAAG
6	a	s					AAACAGACGCTGAGTCCCGAAAGCGTGGGGAGCAAATAGG
A							
S	Ba	Firm er a	Bacilli	Lactoba cillales	Leuconost ocaceae	Weissella	TACGTATGTTCCAAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGACGGTTATTTAAGTCTGAAGTG
V	ct						AAAGCCCTCAGCTCAACTGAGGAATTGCTTTGGAAACTGGATGACTTGAGTGCAGTAGAGGAAAGTGGAAAC
37	eri						TCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTAA
0	a	s					CTGACGTTGAGGCTCGAAAGTGTGGGTAGCAAACAGG
A							
S	Ba	Firm er a	Bacilli	Lactoba cillales	Streptococ caceae	Streptococcu s	TACGTAGGTCCCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTGGATAAGTCTGAAGT
V	ct						TAAAGGCTGTGGCTCAACCATAGTATGCTTTGGAAACTGTTCAACTTGAGTGCAGAAGGGGAGAGTGGAATT
24	eri						CCATGTGTAGCGGTGGAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAAC
9	a	s					TGACGCTGAGGCTCGAAAGCGTGGGTAGCGAACAGG
A							
S	Ba	Firm er a	Bacilli	Lactoba cillales	Streptococ caceae	Streptococcu s	TACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGT
V	ct						TAAAGGCTGTGGCTCAACCATAGTTCGCTTTGGAAACTGTCAAACCTTGAGTGCAGAAGGGGAGAGTGGAATT
37	eri						CCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTGTAAC
6	a	s					TGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A							
S	Ba	Firm er a	Bacilli	Lactoba cillales	Lactobacill aceae	Lactobacillu s	TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGTGCAGGCGGTTCAATAAGTCTGATGT
V	ct						GAAAGCCTTCGGCTCAACCGGAGAATTGCATCAGAAACTGTTGAACCTTGAGTGCAGAAGAGGAGAGTGGA
00	eri						CTCCATGTGTAGCGGTGGAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGCA
1	a	s					ACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG
A							
S	Ba	Firm er a	Bacilli	Lactoba cillales	Enterococ caceae	Enterococcu s	TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGT
V	ct						GAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGA
04	eri						ATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGT
7	a	s					AACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGATTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTTAAGTCTGATGT
V	51	ct	Firm			Carnobacteri		GAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGGGGAGAGTGGAA
	2	eri	icute	Lactoba	Carnobact	aceae_Genu		ATTCCATGTGTAGCGGTAGAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGACTTGCTGGGCCA
A		a	s	Bacilli	eriales	s		TCACTGACGGTCAGGGACGAAAGCGTGGGGAGCGAATAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTAATTAAGTCTGATGT
	44	ct	Firm		Bacilli_Or	Bacilli_Orde		GAAAGCCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGTGGAAGTGGAGTGTGGAGAGGCAAGCGGA
A	5	eri	icute	Bacilli	der_Famil	r_Family_Ge		ATTCCATGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGCGCAAGGCGGCTTGCTGGACTA
		a	s		Order	nus		AAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTAATTAAGTCTGATGT
	22	ct	Firm	Erysipel				GAAAGCCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAAGTGGAA
A	6	eri	icute	otrichal	Erysipelot			TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGTA
		a	s	Bacilli	richaceae	Turicibacter		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTGATTAAGTCTGATGT
	08	ct	Firm	Erysipel				GAAAGCCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAAGTGGAA
A	4	eri	icute	otrichal	Erysipelot			TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGCA
		a	s	Bacilli	richaceae	Turicibacter		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTAATTAAGTCTGATGT
	00	ct	Firm	Erysipel				GAAAGCCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAAGTGGAA
A	3	eri	icute	otrichal	Erysipelot			TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGCA
		a	s	Bacilli	richaceae	Turicibacter		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	V	Ba						TACGTAGGTGGTAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCGCGCAGGTGGTTAATTAAGTCTGATGT
	07	ct	Firm	Erysipel				GAAAGCCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAAGTGGAA
A	7	eri	icute	otrichal	Erysipelot			TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGCA
		a	s	Bacilli	richaceae	Turicibacter		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTCTTAAGTCTGATGT
	17	ct	Firm	Staphyl				GAAAGCCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAACTTGAGTGCAGAAGAGGAAAGTGGAA
A	6	eri	icute	ococcale	Staphyloc	Staphylococ		ATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTCTCTGGTCTGT
		a	s	Bacilli	occaceae	cus		AACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGG
S	V	Ba						TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTCTTAAGTCTGATGT
	30	ct	Firm	Staphyl				GAAAGCCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGGAACTTGAGTGCAGAAGAGGAGAGTGGAA
A	1	eri	icute	ococcale	Staphyloc	Staphylococ		ATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGT
		a	s	Bacilli	occaceae	cus		AACTGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGG
S	V	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGTGCGCCAAGTCTGGAG
	3	ct	Firm					TGAAATGCCGCAGCTTAACTGCGGAACTGCTTTGGAAACTGGCGAACTAGAGTGCAGAAGAGGAGAGTGGAA
A	1	eri	icute	Clostr	Lachnos	Lachnospira		ACTCCATGTGTAGCGGTGAAATGCGTAGATATATGAAAGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGC
V	1	a	s	idia	pirales	ceae_Genus		AACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG

46							
6							
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGACGGTGCGCCAAGTCTGGAGT
V	ct	Firm					GAAATGCCGCAGCTTAACTGCGGAACTGCTTTGGAACTGGCGAACTAGAGTGCGGGAGGGGTAAGCGGAA
49	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGACTTTCTGGACAGTA
8	a	s	idia	pirales	raceae	ceae_Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGCGCCAAGTCTGGAG
V	ct	Firm					TGAAATGCCGCAGCTTAACTGCGGAACTGCTTTGGAACTGGCGAACTAGAGTGCGGGAGGGGTAAGCGGA
01	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACCG
2	a	s	idia	pirales	raceae	36_group	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCGTAGGCGGCTTTGCAAGTCAGAAAGT
V	ct	Firm					GAAATCCATGGGCTTAACCCATGAAGTCTTTGAACTGCAGAGCTTGAGTGGAGTAGAGGTAGGCGGAAT
09	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc	TCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGCGGAAGGCGGCCTGCTGGGCTCTA
3	a	s	idia	pirales	ccaceae	s	ACTGACGCTGAGGCACGAAAGCGTGGGTAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCGTAGGCGGCTTTGCAAGTCAGAAAGT
V	ct	Firm					GAAATCTATGGGCTTAACCCATAAACTGCTTTGAACTGCAGGGCTTGAGTGAAGTAGAGGTAGGCGGAAT
06	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc	TCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGCGGAAGGCGGCCTACTGGGCTTTA
4	a	s	idia	pirales	ccaceae	s	ACTGACGCTGAGGCACGAAAGCGTGGGTAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCGTAGGCGGCTTTGCAAGTCAGATGT
V	ct	Firm					GAAATCTATGGGCTCAACCCATAAACTGCATTTGAACTGTAGAGCTTGAGTGAAGTAGAGGCAGGCGGAA
30	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc	TTCCCGGTGTAGCGGTGAAATGCGTAGAGATGGGGAGGAACACCAGTGCGGAAGGCGGCCTGCTGGGCTTT
2	a	s	idia	pirales	ccaceae	us	AACTGACGCTGAGGCACGAAAGCGTGGGTAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCGAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCGTAGGCGGCCGAGCAAGTCAGTTGT
V	ct	Firm					GAAAACCTATGGGCTTAACCCATAACGTGCAATTGAACTGTCCGGCTTGAGTGAAGTAGAGGTAGGCGGAA
49	eri	icute	Clostr	Oscillos	Ruminoco	CAG-352	TTCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGCGGAAGGCGGCCTACTGGGCTTT
9	a	s	idia	pirales	ccaceae		AACTGACGCTGAGGCACGAAAGCATGGGTAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGTGCGTAGGCGGCCTTGCAAGTCAGGCGT
V	ct	Firm					GAAAACCATGGGCTCAACCCGTGGACTGCGTTTGAAGTGTGAGGCTTGAGTGAAGTAGAGGTAGGCGGAA
16	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc	TTCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGCGGAAGGCGGCCTACTGGGCTTT
0	a	s	idia	pirales	ccaceae	s	AACTGACGCTGAGGCACGAAAGCATGGGTAGCAAACAGG
A							
S	Ba						TACGTAGGGGAGCGAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCGCAGGCGGCTCTGCAAGTCAGGCGT
V	ct	Firm					GAAAGCTAGGGGCTCAACCCCTAACTGCGCTTGAAGTGTGGAGCTTGAGTGAAGTAGAGGCAGGCGGAA
31	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc	TTCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGCGGAAGGCGGCCTGCTGGGCTTT
5	a	s	idia	pirales	ccaceae	s	AACTGACGCTCAGGCACGAAAGCATGGGTAGCAAACAGG

A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGTGCGCAGGCGGCTCTGCAAGTCAGGCGT
	V	ct	Firm			Ruminococ		GAAAGCTAGGGGCTCAACCCCTAAATTGCGCTTGAAACTGTGGAGCTTGAGTGAAGTAGAGGCAGGCGGAA
35	eri	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TTCCCGGTGTAGCGGTGAAATGCGTAGAGATCGGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTT
1	a	s	idia	pirales	ccaceae	s		AACTGACGCTCAGGCACGAAAGCATGGGTAGCAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGGATAAGTTGAATG
	V	ct	Firm		Oscillospir	Oscillospir		TGAAATCTATGGGCTCAACCCATAGCTGCGTTCAAACTGTTCTTCTTGAGTGCAGAAGAGGGAAGCGGAAT
48	eri	icute	Clostr	Oscillos	ales_Famil	es_Family_G		TCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCCTTCTGGTCTGCA
7	a	s	idia	pirales	y	enus		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGGATAAGTTGAATG
	V	ct	Firm			Ruminococ		TGAAATCTATGGGCTCAACCCATAGCTGCGTTCAAACTGTTCTTCTTGAGTGAAGTAGAGGCAGGCGGAAT
07	eri	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
8	a	s	idia	pirales	ccaceae	s		CTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAAAAGCAAGTTGAATG
	V	ct	Firm			Ruminococ		TTTAAGGTACGGGCTCAACCTGTACAAGCGTTCAAACTGTTTTCTTGAGTGGAGTAGAGGTAAGCGGAAT
23	eri	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TCCTAGTGTAGCGGTGAAATGCGTAAATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTTACTGGGCTTTAA
6	a	s	idia	pirales	ccaceae	s		CTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGGATAAGTTGGACG
	V	ct	Firm			Ruminococ		TATAAACTATCGGCTCAACCGGTAGAGGCGTTCAAACTGTCCTTCTTGAGTGAAGTAGAGGTAAGCGGAAT
35	eri	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TCCTAGTGTAGCGGTGAAATGCGTAAATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTTACTGGGCTTTAA
3	a	s	idia	pirales	ccaceae	s		CTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGCGAGAAAAGTTGAATG
	V	ct	Firm					TTAAATCTACCGGCTTAACTGGTAGCTGCGTTCAAACTTCTTGCTTGAGTGAAGTAGAGGCAGGCGGAATT
12	eri	icute	Clostr	Oscillos	Ruminoco	Anaerotrunc		CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTAA
3	a	s	idia	pirales	ccaceae	us		CTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGCTTGTAAGTTGAATGT
	V	ct	Firm			Anaerotrunc		CTAATCCACCGGCTCAACCGGTGATCGCGTTCAAACTGCAGGTCTTGAGTGAAGTAGAGGCAGGCGGAATT
19	eri	icute	Clostr	Oscillos	Ruminoco	us		CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTAA
0	a	s	idia	pirales	ccaceae			CTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGCTTGTAAGTTGAATGT
	V	ct	Firm			Anaerotrunc		CTAATCCACCGGCTCAACCGGTGATCGCGTTCAAACTGCAGGTCTTGAGTGAAGTAGAGGCAGGCGGAATT
47	eri	icute	Clostr	Oscillos	Ruminoco	us		CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGGAGGCGGCCTTACTGGACGGTAA
4	a	s	idia	pirales	ccaceae			CTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
	Ba							TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGACTGCAAGTTGGGTG
A	ct	Firm				Ruminococ		TCAAATCTACCGGCTCAACCGGTAGCCGCACTCAAACTGCAGTTCTTGAGTGAAGTAGAGGCAGGCGGAA
	S	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTT
V	a	s	idia	pirales	ccaceae	s		ACTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAACAGG

26								
9								
A								
S	Ba	Firm				Ruminococ		TACGTAGGGAGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGGATGCAAGTTGGGTG
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TCAAAACTACCGGCTCAACCGATAGTCGCACTCAAAACTGCAGCTCTTGAGTGAAGTAGAGGCAGGCGGAA
20	eri	s	idia	pirales	ccaceae	s		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTT
0	a							ACTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAACAGG
A								
S	Ba	Firm				Ruminococ		TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGGATGCAAGTTGGGTG
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TTAAATCTACCGGCTCAACTGGTAGTCGCACTCAAAACTGCAGCTCTTGAGTGAAGTAGAGGCAGGCGGAAT
13	eri	s	idia	pirales	ccaceae	s		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
2	a							CTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAACAGG
A								
S	Ba	Firm				Ruminococ		TACGTAGGGAGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGATGGCAAGTTGGGTG
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TTAAATCTACCGGCTCAACTGGTAGTCGCACTCAAAACTGCTATTCTTGAGTGAAGTAGAGGCAGGCGGAAT
38	eri	s	idia	pirales	ccaceae	s		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
1	a							CTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAACAGG
A								
S	Ba	Firm						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGGATGCAAGTTGGATG
V	ct	icute	Clostr	Oscillos	Ruminoco	Anaerotrunc		TTTAAACTATCGGCTCAACCGGTAATTGCAACCAAACTGCAACTCTTGAGTGAAGTAGAGGCAGGCGGAAT
24	eri	s	idia	pirales	ccaceae	us		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
7	a							ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba	Firm				Ruminococ		TACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGATATTAAGTTGAATGT
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		ATAAACTACCGGCTTAACCGATAGAAGCGTTCAAAACTGATATTCTTGAGTGAAGTAGAGGCAGGCGGAAT
32	eri	s	idia	pirales	ccaceae	s		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
2	a							ACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A								
S	Ba	Firm				Ruminococ		TACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGTGCAAGTTGAATG
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TATAAACTATCGGCTCAACTGATAGAAGCGTTCAAAACTGCACCTCTTGAGTGAAGTAGAGGCAGGCGGAAT
32	eri	s	idia	pirales	ccaceae	s		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
1	a							ACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A								
S	Ba	Firm						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAATGCAAGTTGAATG
V	ct	icute	Clostr	Oscillos	Ruminoco	Negativibaci		TTTAAACTATGGGCTCAACCCATAGTCGCTTCAAAACTGCATTTCTTGAGTGGAGTAGAGGCAGGCGGAAT
33	eri	s	idia	pirales	ccaceae	llus		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTCTA
4	a							ACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG
A								
S	Ba	Firm				Ruminococ		TACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGAGCAAGTCGACTG
V	ct	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TGAAATCTATGGGCTTAACCCATAGCTGCGATCGAAACTGTTTCATCTTGAGTGAAGTAGAGGCAGGCGGAAT
23	eri	s	idia	pirales	ccaceae	s		TCCTAGTGTAGCGGTGAAATGCGTAAATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTA
0	a							ACTGACGCTGAGGCTCGAAAGCGTGGGTAGCAAACAGG

A	S	Ba						AACGTAGGTCACAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGAAGACAAGTTGGAAG
	V	ct	Firm					TGAAATCTATGGGCTCAACCCATAAACTGCTTTCAAAACTGTTTTCTTGAGTAGTGCAGAGGTAGGCGGAAT
36	eri	icute	Clostr	Oscillos	Ruminoco	Faecalibacte		TCCCGGTGTAGCGGTGGAATGCGTAGATATCGGGAGGAACACCAGTGGCGAAGGCGGCCTACTGGGCACCA
6	a	s	idia	pirales	ccaceae	rium		ACTGACGCTGAGGCTCGAAAGTGTGGGTAGCAAACAGG
A	S	Ba						AACGTAGGTCACAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGAAGACAAGTTGGAAG
	V	ct	Firm					TGAAATCCATGGGCTCAACCCATGAACCTGCTTTCAAAACTGTTTTCTTGAGTAGTGCAGAGGTAGGCGGAAT
37	eri	icute	Clostr	Oscillos	Ruminoco	Faecalibacte		TCCCGGTGTAGCGGTGGAATGCGTAGATATCGGGAGGAACACCAGTGGCGAAGGCGGCCTACTGGGCACCA
3	a	s	idia	pirales	ccaceae	rium		ACTGACGCTGAGGCTCGAAAGTGTGGGTAGCAAACAGG
A	S	Ba						AACGTAGGGTGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGAAGACAAGTTGGAAG
	V	ct	Firm					GTGAAAACCATGGGCTCAACCCATGAATTGCTTTCAAAACTGTTTTCTTGAGTAGTGCAGAGGTAGATGGA
47	eri	icute	Clostr	Oscillos	Ruminoco	Subdoligran		ATTCCCGGTGTAGCGGTGGAATGCGTAGATATCGGGAGGAACACCAGTGGCGAAGGCGGTCTACTGGGCAC
3	a	s	idia	pirales	ccaceae	ulum		CAACTGACGCTGAGGCTCGAAAGCATGGGTAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCCGGGATGTCAAGTCAGAAG
	V	ct	Firm					TGAAAATTATGGGCTCAACTCATAACCTGCTTTTGAAGTATTTCTTGAGTGAAGTAGAGGCAAGCGGAA
07	eri	icute	Clostr	Oscillos	Ruminoco	Ruminococc		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGTCTGGGCTTTT
4	a	s	idia	pirales	ccaceae	s		ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGTCCGTTAAGTCAGCGGT
	V	ct	Firm					AAAATTGCGGGGCTCAACCCCGGGACTGCATTGGAAGTGGCATGCTGGAGTGCCGGAGGGGCAAGCGGAA
42	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACCGT
7	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGTCCGTTAAGTCAGCGGT
	V	ct	Firm					AAAATTGCGGGGCTCAACCCCGGGGCTGCATTGGGAAGTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
50	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGACTG
9	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGGGAGCCAAGTCAGCGGT
	V	ct	Firm					AAAATCGTGGGGCTCAACCCCATCCCGCCGTTGAAACTGTATTTCTTGAGTGCTGGAGAGGCAATCGGAATT
47	eri	icute	Clostr	Oscillos	Oscillospir	Pseudoflavo		CCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTAA
6	a	s	idia	pirales	aceae	nifactor		CTGACGCTGAGGCACGAAAGCGTGGGTAGCAAATAGG
A	S	Ba	Bact	Bacter	Bacteria_P	Bacteria_Ph		TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGGCTTTTAAAGTCAGCGGT
	V	ct	eria_Ph	ia_Ph	hylum_Cl	ylum_Class_		AAAAATCCGGGGCCCAACCCCGGAAGTGCATTGGAAGTGTATTTCTAGAGTGTCCGAGAGGCAGACGGAA
57	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		TTCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGC
7	a	um	Class	_Order	_Family	y_Genus		AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCGAACAGG
	Ba	Bact	Bacter	Bacteria	Bacteria_P	Bacteria_Ph		TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGGGAGCCAAGTCAGCGGT
A	ct	eria_Ph	ia_Ph	_Phylu	hylum_Cl	ylum_Class_		AAAATTGAGAGGCTCAACCTCTTCGAGCCGTTGAAACTGGTTGACTTGAGTGCAGAAGAGGGAAGTGAAT
S	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		TCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAAGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGCA
V	a	um	Class	_Order	_Family	y_Genus		ACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG

56							
9							
A							
S	Ba	Firm		Oscillospir	Oscillospir		TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGAGGTGCAAGTCAGCGGT
V	ct	icute	Clostr	ales_Famil	es_Family_G		CAAAATTGCGGGGCTCAACCTCGTACTGCCGTTGAAACTGCAGAGCTTGAGTGGAGTAGAGGTAGGCGGAATT
58	eri	s	idia	pirales	y		CCCGGTGTAGCGGTGAAATGCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTCTAA
8	a						CTGACGCTGAGGCACGAAAGCGTGGGTAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGGCTTTTAAGTCAGCGGT
V	ct	Bact			Bacteroidale		AAAAATTGCGGGGCTCAACCCCGTCCGGCCGTTGAAACTGGGGGCTTGAGTGAAGTGGAGGTTGGCGGAAT
44	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	TCCGAGTGTAGCGGTGAAATGCGTAGATATTCGGAGGAACACCAGTGGCGAAGGCGGCCAACTGGGCTTTA
2	a	ota	oidia	dales	les_Family	nus	ACTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGATTTTAAAGTCAGCGGT
V	ct	Bact					AAAATGTCCGGGCTCAACCCGGGCCGCGTTGAAACTGGGGATCTTGAGTGGGCGAGAAGTATGCGGAAT
45	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGTGGTGTAGCGGTGAAATGCGTAGATATTAGGGGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGCA
0	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGTTGAGGCTCGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGGGCAGGCGGCGAGTTAAGTCAGCGGT
V	ct	Bact				Bacteroidale	AAAATTTGCGGGGCTCAACCCCGACAAGCCGTTGAAACTGGCTTGCTAGAGTGGGCGAGAAGTATGCGGAAT
41	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	GCGTGGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTACTGGACGATG
1	a	ota	oidia	dales	les_Family	nus	ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTAGGTTTAAAGGGTGCGCAGGCGGCGAGTTAAGTCAGCGGT
V	ct	Bact				Bacteroidale	AAAATTTGCGGGGCTCAACCCCGACAAGCCGTTGAAACTGGCTTGCTAGAGTGGGCGAGAAGTATGCGGAAT
43	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	GCGTGGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGCA
3	a	ota	oidia	dales	les_Family	nus	ACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGCGAGTTAAGTCAGCGGT
V	ct	Firm					AAAATTTGCGGGGCTCAACCCCGACAAGCCATTGAAACTGGCTTGCTAGAGTGGGCGAGAAGTATGCGGAAT
47	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGCA
1	a	s	idia	pirales	raceae	ceae_Genus	ACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGAGGTGCAAGTCAGCGGT
V	ct	Bact				Bacteroidale	CAAAATTGCGGGGCTCAACCCCGTACTGCCGTTGAAACTGCATCCCTTGAGTGC GCGAGAAGTATGCGGAATG
42	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	CGTG GTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGCAA
5	a	ota	oidia	dales	les_Family	nus	CTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGACGGAGCGTTAAGTCAGTGGT
V	ct	Bact				Bacteroidale	CAAAATTGAGGGGCTCAACCCCTTCCCGCCATTGAAACTGGCGCTCTTGAGTGGAAGAGAAGTATGCGGAATG
38	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	CGTG GTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGTGA
3	a	ota	oidia	dales	les_Family	nus	CTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGGCTTTAAGTCAGCGGT
V	ct	Bact						AAAAATTCGGGGCTCAACCCCGTCCGGCCGTTGAAACTGGGGGCCTTGAGTGGGCGAGAAGAAGGCGGAAT
41	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculu		GCGTGGTGTAGCGGTGAAATGCATAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGACTGAA
0	a	ota	oidia	dales	aceae	m		ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGGCTTTAAGTCAGCGGT
V	ct	Bact						AAAAATTCGGGGCTCAACCCCGTCCGGCCGTTGAAACTGGGGGCCTTGAGTGGGCGGGAAGAAGGCGGAAT
56	eri	eroid	Bacter	Bacteroi	Bacteroida	Bacteroidale		GCGTGGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTGCTGGACAGTA
3	a	ota	oidia	dales	les_Family	s_Family_Ge	nus	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGAGTAGGCGGGCTGGCAAGTTGGGAG
V	ct	Firm						TGAAATCCCGGGCTTAACCCCGGAACTGCTTTCAAACACTGCTGGTCTTGAGTGATGGAGAGGCAGGCGGAA
35	eri	icute	Clostr	Oscillos	Butyricico	Butyricicocc		TTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGACATT
9	a	s	idia	pirales	ccaceae	us		AACTGACGCTGAGGAGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGCTGCAAGTCAGAAG
V	ct	Firm						TGAAATCTGGGGCTTAACCCCAAACACTGCTTTTGAAACTGTGGGTCTTGAGTGATGGAGAGGCAGGCGGAA
06	eri	icute	Clostr	Oscillos	Butyricico	Butyricicocc		TTCCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGACATT
6	a	s	idia	pirales	ccaceae	us		AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGCTGCAAGTCAGAAG
V	ct	Firm						TGAAATCTGGGGCTTAACCCCAAACACTGCTTTTGAAACTGTGGATCTTGAGTGATGGAGAGGCAGGCGGAA
23	eri	icute	Clostr	Oscillos	Butyricico	Butyricicocc		TTCCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGACATT
9	a	s	idia	pirales	ccaceae	us		AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGCGAGTAGGCGGACTGACAAGTCAGAAG
V	ct	Firm						TGAAATCTAGGGGCTCAACCCCTAAACACTGCTTTTGAAACTGTCCGCCTTGAGTGCCGGAGAGGAAAGCGGA
50	eri	icute	Clostr	Monogl	Monoglob	Monoglobus		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACGGT
5	a	s	idia	obales	aceae			AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGATTTACTGGGTGTAAAGGGCGTGTAGGCGGAGCTGCAAGTCAGAAG
V	ct	Firm						TGAAATCTCCGGGCTCAACCCGGAACACTGCTTTTGAAACTGTAGCCCTTGAGTATCGGAGAGGCAGGCGGAA
32	eri	icute	Clostr	Oscillos	Oscillospir			TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTGCTGGACGAC
5	a	s	idia	pirales	aceae	UCG-005		AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGATTTACTGGGTGTAAAGGGCGTGTAGGCGGAGCTGCAAGTCAGAAG
V	ct	Firm						TGTAATCTCCGGGCTCAACCCGGAACACTGCTTTTGAAACTGTAGCCCTTGAGTATCGGAGAGGCAGGCGGAA
51	eri	icute	Clostr	Oscillos	Oscillospir			TTCTAGTGTAGCGGTGAAATGCGCAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAGT
3	a	s	idia	pirales	aceae	UCG-005		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGTGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGGAAGCAAGTCAGATG
S	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac		TGAAAACACGGGCTCAACCTGTGCCTGCATTTGAAACTGTTTTCTTGAGTGCTGGAGAGGCAATCGGAA
V	a	s	idia	pirales	aceae	eae_Genus		TTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGT
								AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

11							
5							
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGGAGGCAAGTCAGATGT
V	ct	Firm					GAAAACCACGGGCTCAACCTGTGGCCTGCATTTGAAACTGTTTTCTTGAGTGCTGGAGAGGCAATCGGAAT
32	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
3	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGCGTGTAGGCGGGAAAGCAAGTCAGATGT
V	ct	Firm					GAAAACCTCAGGGCTCAACCTGAGCCTGCATTTGAAACTGTTTTCTTGAGTGCTGGAGAGGCAATCGGAAT
41	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGCAA
2	a	s	idia	pirales	aceae	eae_Genus	CTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGCGTGTAGGCGGGAAAGCAAGTCAGATGT
V	ct	Firm					GAAAACCTCAGGGCTCAACCTGAGCCTGCATTTGAAACTGTTTTCTTGAGTGCTGGAGAGGCAATCGGAAT
15	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
1	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGCGTGTAGGCGGGAGCGCAAGTCAGATGT
V	ct	Firm					GAAAACCTCAGGGCTCAACCTGAGCCTGCATTTGAAACTGTGTTTCTTGAGTGCTGGAGAGGCAATCGGAAT
14	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
4	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGCGTGTAGGCGGGAAATGCAAGTCAGATGT
V	ct	Firm					GAAAACCTCAGGGCTCAACCTGAGCCTGCATTTGAAACTGTATTTCTTGAGTGCTGGAGAGGCAATCGGAAT
05	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
5	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGCGTGTAGGCGGGAAATGCAAGTCAGATGT
V	ct	Firm					GAAAACCTATGGGCTCAACCCATAGCCTGCATTTGAAACTGTATTTCTTGAGTGCTGGAGAGGCAATCGGAAT
13	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
3	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGATTGCAAGTCAGATGT
V	ct	Firm					GAAAACCTATGGGCTCAACCCATAGCCTGCATTTGAAACTGTAGTTCTTGAGTGCTGGAGAGGCAATCGGAAT
27	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
9	a	s	idia	pirales	aceae	eae_Genus	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAGTGCAAGTCAGATGT
V	ct	Firm					GAAAACCTATGGGCTCAACCCATAGCCTGCATTTGAAACTGTACTTCTTGAGTGCTGGAGAGGCAATCGGAAT
18	eri	icute	Clostr	Oscillos	Oscillospir	Intestinimon	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA
2	a	s	idia	pirales	aceae	as	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAGAGCAAGTCAGACG
V	11	ct	Firm					TGAAATTCAGGGCTCAACCCTGGAAGTGC GTTTGAAACTGTTCTTCTTGAGTGATGGAGAGGCAGGCGGAA
	9	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATT
A		a	s	idia	pirales	aceae	cter	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	19	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
V	1	ct	Firm					GAAATTCAGGGCTCAACCCTGGAAGTGCATTTGAAACTGTAGTTCTTGAGTGATGGAGAGGCAGGCGGAAT
	1	eri	icute	Clostr	Oscillos	Oscillospir	Intestinimon	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATTA
A		a	s	idia	pirales	aceae	as	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	22	Ba						TACGTAGGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGCGTAGGCGGGATGGCAAGTCAGATG
V	7	ct	Firm					TGAAATCCAGGGGCTCAACCCCTGAACTGCATTTGAAACTGTCGTTCTTGAGTACTGGAGAGGTTGACGGAA
	7	eri	icute	Clostr	Oscillos	Oscillospir	NK4A214_g	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCAACTGGACAGC
A		a	s	idia	pirales	aceae	roup	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	15	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGAGTGCAAGTCAGATGT
V	2	ct	Firm					GAAATCCC GCGGCTCAACCGCGGAAGTGCATTTGAAACTGTGCTTCTTGAGTGCTGGAGAGGCAGACGGAAT
	2	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGTA
A		a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	09	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGTTGACAAGTCAGATGT
V	9	ct	Firm					GAAATCCTGCGGCTTAACCGCAGAACTGCATTTGAAACTGTTGATCTTGAGTACTGGAGAGGCAGACGGAAT
	9	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
A		a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	17	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGTTTATAAGTCAGATGT
V	4	ct	Firm					GAAATCCC GCGGCTCAACCGCGGAAGTGCATTTGAAACTGTAGATCTTGAGTACTGGAGAGGCAGGCGGAA
	4	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACAGC
A		a	s	idia	pirales	aceae	eae_Genus	AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S	44	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGTTTATAAGTCAGATGT
V	6	ct	Firm					GAAATCCC GCGGCTCAACCGCGGAAGTGCATTTGAAACTGTAGATCTTGAGTACTGGAGAGGCAGGCGGAA
	6	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGC
A		a	s	idia	pirales	aceae	eae_Genus	AACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
S	20	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGAAGGCAAGTCAGATGT
V	4	ct	Firm					GAAATCCGGAGGCTCAACCTCCGAATTGCATTTGAAACTGTTTTTCTTGAGTACTGGAGAGGCAGACGGAAT
	4	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTTGTTAGCGGTGAAATGCGTAGATATAAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
A		a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
S		Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGCTGACAAGTCAGATGT
V		ct	Firm					GAAATCCC GCGGCTCAACCGCGGAAGTGCATTTGAAACTGTGCGTCTTGAGTATCGGAGAGGCAGGCGGAA
		eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGAC
A		a	s	idia	pirales	aceae	eae_Genus	AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

27							
3							
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGCTGACAAGTCAGATGT
V	ct	Firm					GAAATCCCGTGGCTCAACCACGGAAGTGCATTTGAAACTGTCTGGTCTTGAGTATCGGAGAGGCAGGCGGAA
42	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGT
1	a	s	idia	pirales	aceae	eae_Genus	GACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGCTGACAAGTCAGATGT
V	ct	Firm					GAAATCCGGGGGCTCAACCCCGAACTGCATTTGAAACTGTTGGTCTTGAGTATCGGAGAGGCAGGCGGAAT
11	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGACA
0	a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGCTGACAAGTCAGATGT
V	ct	Firm					GAAATCCGGGGGCTCAACCCCGACCTGCATTTGAAACTGTTGGTCTTGAGTATCGGAGAGGCAGGCGGAAT
16	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGACA
8	a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGCCGGGCGCGCAAGTCAGATGT
V	ct	Firm					GAAATCCCAAGGCTCAACCTTGGAAGTGCATTTGAAACTGTTGGTCTTGAGTATCGGAGAGGCAGGCGGAAT
27	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGACA
1	a	s	idia	pirales	aceae	eae_Genus	ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGAAGACAAGTCAGATG
V	ct	Firm					TGAAATCCCGCGGCTCAACCGCGGAAGTGCATTTGAAACTGTTTTTCTTGAGTACCGGAGAGGTCATCGGAA
05	eri	icute	Clostr	Oscillos	Oscillospir		TTCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAGTGGCGAAGGCGGATGACTGGACGGC
9	a	s	idia	pirales	aceae	Oscillibacter	AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGCTGACAAGTCAGATGT
V	ct	Firm					GAAATCCCGCGGCTCAACCGCGGAAGTGCATTTGAAACTGTTAGTCTTGAGTACCGGAGAGGTCATCGGAAT
14	eri	icute	Clostr	Oscillos	Oscillospir	Oscillibacter	TCCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAGTGGCGAAGGCGGATGACTGGACGGCA
3	a	s	idia	pirales	aceae		ACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGAAGACAAGTCAGATG
V	ct	Firm					TGAAATCCCGCGGCTCAACCGCGGAAGTGCATTTGAAACTGTTTTTCTTGAGTATCGGAGAGGTAACCGGAA
22	eri	icute	Clostr	Oscillos	Oscillospir		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGTTACTGGACGAC
9	a	s	idia	pirales	aceae	Oscillibacter	AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGAAGACAAGTCAGATG
V	ct	Firm					TGAAATCCCGCGGCTCAACCGCGGAAGTGCATTTGAAACTGTTTTTCTTGAGTATCGGAGAGGTAATCGGAA
28	eri	icute	Clostr	Oscillos	Oscillospir		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGATTACTGGACGAC
7	a	s	idia	pirales	aceae	Oscillibacter	AACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

ASV293	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	UCG-003	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGAGAGGCAAGTCAGATGTGAAATCCGCGGGCTCAACCCGCGAACTGCATTTGAAACTGCTTCCCTTGAGTATCGGAGAGGTAATCGGAAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGATTACTGGACGACAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV205	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGACTGCAAGTCAGATGTGAAATCCGCGGGCTTAACCCGCGAACTGCATTTGAAACTGCGGATCTTGAGTACCGGAGAGGTTATCGGAATTCCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAGTGGCGAAGGCGGATAACTGGACGGCAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV248	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGCCGACAAGTCAGATGTGAAATCCGCGGGCTTAACCCGCGAACTGCATTTGAAACTATTGGTCTTGAGTACCGGAGAGGTCATCGGAATTCCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAGTGGCGAAGGCGGATGACTGGACGGCAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV278	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGAGAGACAAGTCAGATGTGAAATCCGCAGGCTCAACCTGCGAACTGCATTTGAAACTGTTTCCCTTGAGTATCGGAGAGGTCATCGGAAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGATGACTGGACGACAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV231	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGAGAGACAAGTCAGATGTGAAATCCGCGGGCTCAACCCGCGAACTGCATTTGAAACTGTTTCCCTTGAGTATCGGAGAGGTCATCGGAAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGATGACTGGACGACAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV058	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGAGAGACAAGTCAGATGTGAAATCCACGGGCTCAACCCGTGAACCTGCATTTGAAACTGTTTCCCTTGAGTGTCCGAGAGGTAATCGGAAATTCCTTGTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAGTGGCGAAGGCGGATTACTGGACGATAACTGACGGTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV275	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Colidextribacter	TACGTAGGTGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAGAGCAAGTCAGATGTGAAAACCTACAGGCTTAACCTGTAGCCTGCATTTGAAAACCTGTTCTTCTTGAGTGATGGAGAGGCAGGCCGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATTAACTGACGCTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV405	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Colidextribacter	TACGTAGGTGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAGAGCAAGTCAGATGTGAAAACCTACAGGCTTAACCTGTAGCCTGCATTTGAAAACCTGTTTTCTTGAGTGATGGAGAGGCAGGCCGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATTAACTGACGCTGAGGCGCGAAAAGCGTGGGGAGCAAACAGG
ASV	Bacterial Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillospiraceae Genus	TACGTAGGTGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGATTGCAAGTCAGATGTGAAAACCTATGGGCTCAACCCATAGCCTGCATTTGAAAACCTGTAGTTCTTGAGTGCTGGAGAGGCAATCGGAATTCCTGTGTAGCGGTGAAATGCTTAGATATCAAGAAGAACCTCCGATTGCGAAGGCAGCCTGCTGGACTGTAACTGACGCTGATGCTCGAAAGTGTGGGTATCAAACAGG

44							
9							
A							
S	Ba						TACGTAGGGAGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGATGGCAAGTCAGGCG
V	ct	Firm					TGAAAACCTATGGGCTCAACCCATAGCCTGCGTTTAAAAGTGTCTTCTGAGTGATGGAGAGGCAAGCGGAA
36	eri	icute	Clostr	Oscillos	Oscillospir	Oscillospirac	TTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACATT
8	a	s	idia	pirales	aceae	eae_Genus	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
V	ct	Firm					GAAAACCATGGGCTCAACCCATGGCCTGCATTTGAAAGTGTAGTTCTTGAGTGATGGAGAGGCAGGCGGAAT
14	eri	icute	Clostr	Oscillos	Oscillospir	Intestinimon	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATTA
7	a	s	idia	pirales	aceae	as	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGAGTAGGCGGGATTGCAAGTCAGATGT
V	ct	Firm					GAAAACCTATGGGCTCAACCGATAGAGTGCATTTGAAAGTGCAGTTCTTGAGTGATGGAGAGGCAGGCGGAA
12	eri	icute	Clostr	Oscillos	Butyricico		TTCCCGTGTAGCGGTGGAATGCGTAGATATCGGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACATT
6	a	s	idia	pirales	ccaceae	UCG-009	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAAGTGTAGTTCTTGAGTACTGGAGAGGCAGACGGAAT
10	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
9	a	s	idia	pirales	aceae	cter	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAGTGCAAGTCAGATGT
V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAAGTGTACTTCTTGAGTACTGGAGAGGCAGACGGAAT
33	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
1	a	s	idia	pirales	aceae	cter	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGGACGCAAGTCAGATGT
V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAAGTGTGTTTTCTTGAGTACTGGAGAGGCAGACGGAAT
24	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
3	a	s	idia	pirales	aceae	cter	ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAAAGCAAGTCAGATG
V	ct	Firm					TGAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAAGTGTGTTTTCTTGAGTACTGGAGAGGCAGACGGAA
08	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGC
1	a	s	idia	pirales	aceae	cter	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAAAGCAAGTCAGATG
V	ct	Firm					TGAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAAGTGTGTTTTCTTGAGTACTGGAGAGGCAGACGGAA
37	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba	TTCCCTGTGTAGCGGTGAAATGCGTAGATATGAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGC
2	a	s	idia	pirales	aceae	cter	AACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
	V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAACTGTAGTTCTTGAGTACTGGAGAGGCAGACGGAAT
19	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
2	a	s	idia	pirales	aceae	cter		ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
	V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAACTGTAGTTCTTGAGTACTGGAGAGGCAGACGGAAT
36	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGCCTGCTGGACGGTG
9	a	s	idia	pirales	aceae	cter		ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGACTGCAAGTCAGATGT
	V	ct	Firm					GAAAACCATGGGCTCAACCTGTGGCCTGCATTTGAAACTGTAGTTCTTGAGTACTGGAGAGGCAGACGGAAT
33	eri	icute	Clostr	Oscillos	Oscillospir	Colidextriba		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACAGCA
0	a	s	idia	pirales	aceae	cter		ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGCCTGCCAAGTCTGATGT
	V	ct	Firm					GAAATACCGGGGCTCAACCCAGGCCTGCATTGGAAACTGTAAAGCTGGAGTACAGGAGAGGTAAGCGGA
53	eri	icute	Clostr	Lachnos	Lachnospira	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCAGCGTACCGGCGCC
4	a	s	idia	pirales	raceae	ceae_Genus		AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGCAGGCGGCGGCCAAGTCTGATGT
	V	ct	Bact					GAAACCCCGGGGCTCAACCCCGGGCATGCATTGGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGAA
56	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac		TGCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCATAACTCCGATTGCGAAGGCAGCATGCCGGCTCCAC
2	a	ota	oidia	dales	aceae	eae_Genus		ACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGTGCCAAGTCTGATGT
	V	ct	Bact					GAAAGGCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGAA
44	eri	eroid	Bacter	Bacteroi	Muribacul			TGCGCGGTATAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCACCA
0	a	ota	oidia	dales	aceae	CAG-873		GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGCGTTAAGCCTGGTGT
	V	ct	Bact					GAAAGCCCGCGGCCCAACCGCGGGACTGCATTGGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGA
55	eri	eroid	Bacter	Bacteroi	Muribacul			ATGCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCT
4	a	ota	oidia	dales	aceae	CAG-873		AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGTGGTGATTTAAGTCAGCGGT
	V	ct	Bact					GAAAGTTTGTGGCTCAACCATAAAATTGCCGTTGAAACTGGGTTACTTGAGTGTGTTTGAAGTAGGCGGAAT
58	eri	eroid	Bacter	Bacteroi	Tannerella	Parabacteroi		GCGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCTTACTAAACCATA
9	a	ota	oidia	dales	ceae	des		ACTGACACTGAAGCACGAAAGCGTGGGGATCAAACAGG
A	ct	Bact						TACGGAGGATCCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGATGGATGTTTAAAGTCAGTTGTG
	S	eri	Bact					AAAAGTTTGGCGCTCAACCGTAAAAATTGCAGTTGATACTGGATATCTTGAGTGCAGTTGAGGCAGGCGGAATT
	V	a	eroid	Bacteroi	Bacteroida			CGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAACTCCGATTGCGAAGGCAGCCTGCTAAGCTGCAA
		ota	oidia	dales	ceae	Bacteroides		CTGACATTGAGGCTCGAAAGTGTGGGTATCAAACAGG

34							
3							
A							
S	Ba						TACGGAGGATCCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGATGGATGTTTAAGTCAGTTGTG
V	ct	Bact					AAAGTTTGCGGCTCAACCGTAAAATTGCAGTTGATACTGGATGTCTTGAGTGCAGTTGAGGCAGGCGGAATT
36	eri	eroid	Bacter	Bacteroi	Bacteroida		CGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAAGCTCCGATTGCGAAGGCAGCCTGCTAAGCTGCAA
5	a	ota	oidia	dales	ceae	Bacteroides	CTGACATTGAGGCTCGAAAAGTGTGGGTATCAAACAGG
A							
S	Ba						TACGGAGGATCCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCGGACGCTTAAGTCAGTTGT
V	ct	Bact					GAAAGTTTGCGGCTCAACCGTAAAATTGCAGTTGATACTGGGTGTCTTGAGTACAGTAGAGGCAGGCGGAAT
44	eri	eroid	Bacter	Bacteroi	Bacteroida		TCGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAAGCTCCGATTGCGAAGGCAGCCTGCTGGACTGTAA
1	a	ota	oidia	dales	ceae	Bacteroides	CTGACGCTGATGCTCGAAAAGTGTGGGTATCAAACAGG
A							
S	Ba						TACGGAGGATCCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCGGGTGTTAAGTCAGTTGT
V	ct	Bact					GAAAGTTTGCGGCTCAACCGTAAAATTGCAGTTGATACTGGCATCCTTGAGTACAGTAGAGGTAGGCGGAAT
01	eri	eroid	Bacter	Bacteroi	Bacteroida		TCGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAAGCTCCGATTGCGAAGGCAGCCTGCTGGACTGTAA
1	a	ota	oidia	dales	ceae	Bacteroides	CTGACGCTGATGCTCGAAAAGTGTGGGTATCAAACAGG
A							
S	Ba						TACGGAAGGTCCGGGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCCGGAGATTAAGCGTGTGT
V	ct	Bact					GAAATGTAGACGCTCAACGTCTGCAGTCAGCGGAAGTGGTTTCCTTGAGTACGCACAAAGTGGGCGGAAT
43	eri	eroid	Bacter	Bacteroi	Prevotella		TCGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAAGCTCCGATTGCGAAGGCAGCTACTGGAGCGCA
0	a	ota	oidia	dales	ceae	Prevotella	ACTGACGCTGAAGCTCGAAAGTGCGGGTATCGAACAGG
A							
S	Ba						TACGGAAGGTCCGGGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCCGGAGATTAAGCGTGTGT
V	ct	Bact					GAAATGTAGATGCTCAACATCTGAAGTGCAGCGGAAGTGGTTTCCTTGAGTACGCACAAAGTGGGCGGAAT
44	eri	eroid	Bacter	Bacteroi	Prevotella		TCGTGGTGTAGCGGTGAAATGCTTAGATATCACGAAGAAGCTCCGATTGCGAAGGCAGCTACTGGAGCGCA
7	a	ota	oidia	dales	ceae	Prevotella	ACTGACGCTGAAGCTCGAAAGTGCGGGTATCGAACAGG
A							
S	Ba						TACGGAGGATTCAAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCCGTTTGATAAGTTAGAGGT
V	ct	Bact					GAAATCCCGGGGCTTAACTCCGGAAGTGCCTCTAATACTGTTAGACTAGAGAGTAGTTGCGGTAGGCGGAAT
49	eri	eroid	Bacter	Bacteroi	Rikenellac		GTATGGTGTAGCGGTGAAATGCTTAGAGATCATACAGAACACCGATTGCGAAGGCAGCTTACCAAATATAT
4	a	ota	oidia	dales	eae	Alistipes	CTGACGTTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATTCAAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCCGTTTGATAAGTTAGAGGT
V	ct	Bact					GAAATTTCCGGGCTCAACCTGAACGTGCCTCTAATACTGTTAGCTAGAGAGTAGTTGCGGTAGGCGGAAT
45	eri	eroid	Bacter	Bacteroi	Rikenellac		GTATGGTGTAGCGGTGAAATGCTTAGAGATCATACAGAACACCGATTGCGAAGGCAGCTTACCAAATATAT
9	a	ota	oidia	dales	eae	Alistipes	CTGACGTTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATCCAAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCCGTTTGATAAGTTAGAGGT
V	ct	Bact					GAAAGCTCGGGGCTTAACTCCGAGACTGCCTCTAATACTGTTAGCTAGAGAGTAGTTGCGGTAGGCGGAAT
47	eri	eroid	Bacter	Bacteroi	Rikenellac		GTATGGTGTAGCGGTGAAATGCTTAGAGATCATACAGAACACCGATTGCGAAGGCAGCTTACCAAATATA
8	a	ota	oidia	dales	eae	Alistipes	TCTGACGTTGAGGCACGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGTCTGTAAAGTCAGCGGT
	V	ct	Bact					CAAAGCCCCGGGGCTCAACCCCGGCCCGCCGTTGAAACTGGCAGTCTCGAGTTGGAGAGAAAGTATGCGGAAT
25	0	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGCGGTGTAGCGGTGAAATGCATAGATATCTCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCAC
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGTCTGTAAAGTCAGCGGT
	V	ct	Bact					CAAAGCCCCGGGGCTCAACCCCGGCCCGCCGTTGAAACTGGCAGTCTCGAGTTGGAGAGAAAGTATGCGGAAT
00	8	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCAC
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGTCCGTAAAGTCAGCGGT
	00	ct	Bact					AAAATTGCGGGGCTCAACCCCGTCGAGCCGTTGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGAAT
2	2	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCAG
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGTCCGTAAAGTCAGCGGT
	17	ct	Bact					AAAATTGCGGGGCTCAACCCCGTCGAGCCGTTGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGAAT
9	9	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCAC
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGTCCGTAAAGTCAGCGGT
	02	ct	Bact					AAAATTGCGGGGCTCAACCCCGTCGAGCCGTTGAAACTGGCAGACTTGAGTTGGCGAGAAGTACGCGGAAT
2	2	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGTGCCAC
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGCGAGTTAAGTCAGCGGT
	01	ct	Bact					AAAATTTGCGGGGCTCAACCCCGACAAGCCGTTGAAACTGGCTTGCTAGAGTGGGCGAGAAGTATGCGGAAT
4	4	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	GCGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCCCA
	A	a	ota	oidia	dales	aceae	eae_Genus	ACTGACGCTCAGGCACGAAAGCGTGGGTATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGAAGATCAAGTCAGCGGT
	00	ct	Bact					AAAATTGAGAGGCTCAACCTCTTCGAGCCGTTGAAACTGGTTTTCTTGAGTGAGCGAGAAGTATGCGGAATG
4	4	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	CGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTCAA
	A	a	ota	oidia	dales	aceae	eae_Genus	CTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGCAGGCGGAGGTGCAAGTCAGCGGT
	00	ct	Bact					CAAATTGCGGGGCTCAACCCCGTACTGCCGTTGAAACTGCATCCCTTGAGTGCGCGAGAAGTATGCGGAATG
5	5	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	CGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCGCAA
	A	a	ota	oidia	dales	aceae	eae_Genus	CTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
S	V	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGGAGCCAAGTCAGCGGT
	00	ct	Bact					AAAATCGTGGGGCTCAACCCCATCCCGCCGTTGAAACTGGTTTTCTTGAGTGAGTGGATGAGAAGTATGCGGAATG
5	5	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac	CGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCATCCAA
	A	a	ota	oidia	dales	aceae	eae_Genus	CTGACGCTGAAGCACGAAGGCGTGGGTATCAAACAGG

00								
6								
A								
S	Ba							TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGAGCGTTAAGTCAGTGGT
V	ct	Bact						CAAATTGAGGGGCTCAACCCCTTCCCGCCATTGAAACTGGCGCTCTTGAGTGGAAGAGAAGTATGCGGAAT
04	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac		CGTGTTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCATGCCGGCTTCCTAC
6	a	ota	oidia	dales	aceae	eae_Genus		TGACGCTGAAGCACGAAAGCGTGGGGATCGAACAGG
A								
S	Ba							TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGATCGTTAAGTCAGTGGT
V	ct	Bact						CAAATTGAGGGGCTCAACCCCTTCCCGCCATTGAAACTGGCGATCTTGAGTGGAAGAGAAGTATGCGGAAT
01	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac		GCGTGTTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCATGCCGGCTTCCT
8	a	ota	oidia	dales	aceae	eae_Genus		ACTGACGCTGAAGCACGAAAGCGTGGGGATCGAACAGG
A								
S	Ba							TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGATTTTTAAGTCAGCGGT
V	ct	Bact						AAAATGTCCGGGCTCAACCCGGGCCGCGTTGAAACTGGGGATCTTGAGTGGGCGAGAAGTATGCGGAAT
03	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac		GCGTGTTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCCCC
8	a	ota	oidia	dales	aceae	eae_Genus		ACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A								
S	Ba							TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCGTAGGCGGGCTTTTAAGTCAGCGGT
V	ct	Bact						AAAAATTCGGGGCTCAACCCCGTCCGGCCGTTGAAACTGGGGCCTTGAGTGGGCGAGAAGAAGGCGGAAT
00	eri	eroid	Bacter	Bacteroi	Muribacul	Muribaculac		GCGTGTTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCCTTCCGGCGCCCT
7	a	ota	oidia	dales	aceae	eae_Genus		ACTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG
A								
S	Ba							TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGTGAGCGCAGGCGGTTTCTTAAGTCTGATGTG
V	ct	Bact				Bacteroidale		AAAGCCCCCGGCTCAACCGGGGAGGGTCATTGAAACTGGTTTTCTTGAGTGGATGAGAAGTATGCGGAAT
50	eri	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge		GCGTGTTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCATCCA
2	a	ota	oidia	dales	les_Family	nus		ACTGACGCTGAAGCACGAAGGCGTGGGTATCAAACAGG
A								
S	Ba							TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGGCAAGTTAGTTGT
V	ct	Firm						GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAACTATCTTTCTTGAGTGCTGGAGAGGAAAGTGAAT
39	eri	icute						TCCTAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTCA
9	a	s	Clostr	Clostrid	Clostridia	Clostridia_O		ATTGACGCTCATGCACGAAAGTGTGGGTATCAAACAGG
A			idia	ia_Orde	_Order_Fa	rd_Family		
S	Ba							TACGTAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAGCAAGTTAGTTGT
V	ct	Firm						GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAACTACTTTTCTTGAGTGCAGGAGAGGTAAGTGAAT
49	eri	icute						TCCTAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTCA
0	a	s	Clostr	ia_UCG	014_Famil	014_Family_		ACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A			idia	-014	y	Genus		
S	Ba	Bact	Bacter	Bacteria	Bacteria_P	Bacteria_Ph		TACGTAGGGAGCAAGCGTTGTTCGGAATGACTGGGCGTAAAGGGTGCGTAGGCGGTTGTACAAGTTAGAAG
V	ct	eria_	ia_Ph	_Phylu	hylum_Cl	ylum_Class		TGAAATACCCAGGGCTTAAGTGGGTGCTGCTTCTAAACTGTATGACTTGAGTGCAGAAGAGGGAAGTGAAG
60	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		ATTCCATGTGTAGCGGTGAAATGCGTAGATATCGGCAGAACTCCGATTGCGAAGGCAGCGTACCGGTGCCA
5	a	um	Class	_Order	_Family	y_Genus		CACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG

A	S	Ba						TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCCTAGGTGGTTTGACAAGTTAGTAG
	V	ct	Bact		Porphyro	Porphyromo		CGCAACTCCGGAGCTTAACCTTCGGAAGCTACTACTAAAAGCTGTTGGAGCTTGAAGTGCAGGAGGGGCAATCGGA
55	eri	eroid	Bacter	Bacteroi	monadace	nadaceae_G		ATTCCATGTGTAGCGGTGGAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCG
0	a	ota	oidia	dales	ae	enus		CAACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGTGGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGAGAGCAAGTCGACTG
	V	ct	Firm			Ruminococc		TGAAATCTATGGGCTTAACCCATAGCTGCGATCGAAACTGTTTCATCTTGAGTGAAGTAGAGGCAGGCGGAAT
55	eri	icute	Clostr	Oscillos	Ruminoco	aceae_Genu		TCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCACA
7	a	s	idia	pirales	ccaceae	s		CTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGCGAGAAAGTTGAATG
	V	ct	Firm			Anaerotrunc		TTAAATCTACCGGCTTAACCTGGTAGCAGCGTTCAAACTTCTTGTCTTGAGTGAAGTAGAGGCAGGCGGAAT
55	eri	icute	Clostr	Oscillos	Ruminoco	us		TCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCAG
9	a	s	idia	pirales	ccaceae			ACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGGAAGCCAAGTCAGCTG
	V	ct	Bact		Bacteroidale	Bacteroidale		TGAAAAGCTACGGGCTTAACCTGTAGACTGCAGTTGAAAGCTGGTTTTCTTGAGTGAAGTGGAGGTTGGCGGAA
50	eri	eroid	Bacter	Bacteroi	les_Family	s_Family_Ge		TTCCGAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCGC
4	a	ota	oidia	dales		enus		AACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGGAAGCCAAGTCAGCTG
	V	ct	Bact		Bacteroidale	Bacteroidale		TGAAAAGCTACGGGCTTAACCTGTAGACTGCAGTTGAAAGCTGGTTTTCTTGAGTGAAGTAGAGGTTGGCGGAA
51	eri	eroid	Bacter	Bacteroi	les_Family	s_Family_Ge		TTCTGTGTAGCGGTGAAATGCTTAGATATCAGGAAGAACTCCGATTGCGAAGGCAGCCTGCTGGACTGTA
6	a	ota	oidia	dales		enus		ACTGACGCTGATGCTCGAAAGTGTGGGTATCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGCAGGCGGGGAAGCCAAGTCAGCTG
	V	ct	Firm		Oscillospir	Oscillospir		TGAAAAGCTACGGGCTTAACCTGTAGACTGCAGTTGAAAGCTGGTTTTCTTGAGTGAAGTAGAGGTTGGCGGAA
03	eri	icute	Clostr	Oscillos	ales_Famil	es_Family_G		TTCCGAGTGTAGCGGTGAAATGCGTAGATATTCGGAGGAACACCGGTGGCGAAGGCGGCCAACTGGGCTTT
5	a	s	idia	pirales	y	enus		AACTGACGCTGAGGCTCGAAAGTGTGGGGAGCAAAACAGG
A	S	Ba						TACGTAGGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGCTGCAAGTCAGAAG
	V	ct	Firm		Butyricico	Butyricicocc		TGAAATCTGGGGGCTTAACCCCCAAAGCTGCTTTTGAAAGTGTGGGTCTTGAGTGTAGGAGAGGCAGGCGGAA
50	eri	icute	Clostr	Oscillos	ccaceae	aceae_Genu		TTCCAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCA
7	a	s	idia	pirales		s		GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGTGCCTAGGCGGCTTTGCAAGTCAGAAGT
	V	ct	Firm		Ruminococc	Ruminococc		GAAATCCATGGGCTTAACCCATGAAGTGTCTTTTGAAAGTGCAGAGCTTGAGTGGAGTAGAGGTAGGCGGAAT
45	eri	icute	Clostr	Oscillos	ccaceae	aceae_Genu		TCCCGGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACCCCGATTGCGAAGGCAGCCTTCCGGCGCCCTA
4	a	s	idia	pirales		s		CTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG
A	Ba	Bact	Bacter	Bacteria	Bacteria_Ph	Bacteria_Ph		TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGTGCCTAGGCGGCTTTGCAAGTCAGAAGT
	ct	eria_P	ia_Ph	_Phylu	ylum_Cl	ylum_Class_		GAAATCTATGGGCTTAACCCATAAAAGTGTCTTTTGAAAGTGCAGGGCTTGAGTGAAGTAGAGGTAGGCGGAAT
S	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		TCCCGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCCTTCCGGCGCCCTA
V	a	um	Class	_Order	_Family	y_Genus		CTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG

49							
3							
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGCCGGGTTTATAAGTCAGATGT
V	ct	Firm		Clostrid	Clostridia	Clostridia_O	GAAATCCCGCGGGCTCAACCGCGGAACTGCATTTGAAACTGTAGATCTTGAGTACTGGAGAGGCAGGCGGAA
48	eri	icute	Clostr	ia_Orde	_Order_Fa	Order_Family	TTCCTAGTGTAGCGGTGAAATGCGTAGATATCGCGCAGGACTCCGATTGCGAAGGCAGCATGCCGGCTCCAC
1	a	s	idia	r	mily	_Genus	ACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGCAGTCGGGAAGACAAGTCAGATGT
V	ct	Firm					GAAATCCCGCGGGCTCAACCGCGGAACTGCATTTGAAACTGTTTTCTTGAGTACCGGAGAGGTCATCGGAAT
49	eri	icute	Clostr	Oscillos	Oscillospir		TCCTTGTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCACA
5	a	s	idia	pirales	aceae	Oscillibacter	CTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGGAATGCAAGTCAGATGT
V	ct	Firm					GAAACTCAGGGCTCAACCCCTGAGCCTGCATTTGAAACTGTATTTCTTGAGTGCTGGAGAGGCAATCGGAAT
43	eri	icute	Clostr	Oscillos	Oscillospir	Pseudoflavo	TCCGTGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTCA
7	a	s	idia	pirales	aceae	nifactor	ACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGCAGGCGGCACGGCAAGTCTGGTG
V	ct	Firm					TGAAAACCCGGGGCTCAACCCCGGACTGCATTGGAAACTGCCGGGCTGGAGTGTCGGAGGGGTAAGCGGA
42	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCATGCCGGCTCC
2	a	s	idia	pirales	raceae	ceae_Genus	TACTGACGCTGAAGCACGAAGGCGTGGGGATCGAACAGG
A							
S	Ba	Bact	Bacter	Bacteria	Bacteria_P	Bacteria_Ph	TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGCAGGCGGCACGGCAAGTCCGGTG
V	ct	eria_	ia_Ph	_Phylu	hylum_Cl	ylum_Class_	TGAAAGCCCGGGGCCCAACCCCGGGACTGCACTGGAAACTGCCGGGCTGGAGTGTCGGAGGGGTAAGCGG
45	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil	AATTCCTGTTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGC
8	a	um	Class	_Order	_Family	y_Genus	CAGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTCTGGCAAGTCTGGTG
V	ct	Firm					GAAAGCCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGCCGGGCTGGAGTGCCGGAGAGGTAAGCGGA
42	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
4	a	s	idia	pirales	raceae	ceae_Genus	AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGGGCAAGTCTGATG
V	ct	Firm					TGAAATACCGGGGCCCAACCCCGGGGCTGCATTGGGAAGTGCAGGCTGGAGTGCCGGAGAGGCAGGCGG
46	eri	icute	Clostr	Lachnos	Lachnospi		AATTCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACCCCGATTGCGAAGGCAGCCTTCCGGCGCC
3	a	s	idia	pirales	raceae	A2	CTACTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG
A							
S	Ba						TACGTATAGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCATGGCAAGTCAGATG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCATTTGAAACTGTCAGGCTGGAGTGCCAGGAGAGGCAGGCGGA
51	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACCCCGATTGCGAAGGCAGCCTTCCGGCGCC
9	a	s	idia	pirales	raceae	ceae_Genus	TACTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG

A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
V	ct	Firm						GAAATACCGGGGGCCCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
43	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
6	a	s	idia	pirales	raceae	A2		AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
V	ct	Firm						GAAATACCGGGGGCCCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
45	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATAACCGGCGCTC
1	a	s	idia	pirales	raceae	A2		AACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A	S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCACGGCAAGCCTGATG
V	ct	Bact			Porphyro	Porphyromo		TGAAAGCCCGCGGCCCAACCGCGGGACTGCATTGGGAACTACCGGGCTGGAGTGCCGGAGAGGTAGGCGG
40	eri	eroid	Bacter	Bacteroi	monadace			AATTCCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATAACCGGCGC
8	a	ota	oidia	dales	ae	enus		GCAACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCCATGGCAAGCCCGGT
V	ct	Firm		Clostrid	Clostridia	Clostridia_O		GTGAAAGGCAGGGGCATAACCCCTGGACTGCACTGGGAACTGTCAGGCTGGAGTGCCGGAGGGGTAAAGCG
46	eri	icute	Clostr	ia_Orde	_Order_Fa	Order_Family		GAATTCCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAAACCCCGATTGCGAAGGCAGCCTTCCGGCGC
8	a	s	idia	r	mily	_Genus		CCTACTGACGCTGAGGCACGAAAGTGCGGGGATCGAACAGG
A	S	Ba	Bact	Bacteria	Bacteria_P	Bacteria_Ph		TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCCATGGCAAGCCCGGT
V	ct	eria_Ph	ia_Ph	_Phylu	ylum_Cl	ylum_Class_		GTGAAAGGCAGGGGCATAACCCCTGGACTGCACTGGGAACTGTCAGACTGGAGTGTCCGGAGAGGCAAGCG
51	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		GAATTCCTAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTC
0	a	um	Class	_Order	_Family	y_Genus		CACACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGGGCAAGTCTGATG
V	ct	Firm						TGAAAGTCCGGGGCTCAACCCCGGGACTGCATTGGAAGTGTCCGGCTAGAGTGAGGAGAGGTAAGTGGA
40	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
3	a	s	idia	pirales	raceae	ceae_Genus		AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGGGCAAGTCTGATG
V	ct	Firm						TGAAAGTCCGGGGCTCAACCCCGGGACTGCATTGGAAGTGTCCGGCTAGAGTGAGGAGAGGTAAGTGGA
50	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTACGCAGAACTCCGATTGCGAAGGCAGCATAACCGGCGCTC
1	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGGGCAAGCCAGAAAG
V	ct	Firm						TGAAACGCAGAGCTTAACCTTTGCGACTGCTTTTGGAACTGCCAGCTAGAGTACAGGAGAGGTAAGTGGA
46	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGTGCCA
7	a	s	idia	pirales	raceae	28-4		CACCTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	Ba							TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGAGTAGGCGGCAAGGTAAGCGATATG
V	ct	Firm						TGAAAGCCTTAAGCTTAACCTTAAGGATGGCATAACGAACTATCTAGCTAGAGTACAGGAGAGGAAAGCGGA
46	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
7	a	s	idia	pirales	raceae	ASF356		AGACTGACGCTGAGGCACAAAAGCGTGGGGATCGAACAGG

54							
0							
A							
S	Ba	Bact			Bacteroidale		TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGACGGCGATGCAAGTCTGAAGT
V	ct	eroid	Bacter	Bacteroi	Bacteroida	s_Family_Ge	GAAAGGCGGGGGCCCAACCCCGGACTGCTTTGAAACTGTATGGCTGGAGTGCAGGAGAGGTAAGTGAA
53	eri	ota	oidia	dales	les_Family	nus	TGCGTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCA
9	a						CACTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTAAGTGGAGTGCAGGAGAGGTAAGCGGA
40	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTTCC
4	a	s	idia	pirales	raceae	ceae_Genus	TACTGACGCTGAAGCACGAAAGCGTGGGGATCGAACAGA
A							
S	Ba						TACGTAGGGGGCAAGCGTTTCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGCAAGTCAGAAGT
V	ct	Firm					GAAAGCCCGGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTGACTGGAGTGCAGGAGAGGTAAGCGGAA
45	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TGCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCA
5	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTGACTGGAGTGCAGGAGAGGTAAGCGGA
49	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCATGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCTA
6	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACGGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCGATGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTGACTGGAGTGCAGGAGAGGTAAGCGGA
39	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTGGTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
6	a	s	idia	pirales	raceae	ceae_Genus	AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGATGTGCAAGTCTGATGT
V	ct	Firm					GAAAGGCGGGGGCTCAACCCCTGGACTGCATTGAAACTGTAAATCTTGAGTGCCCGAGAGGTAAGCGGAA
41	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCA
6	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCTGTGCAAGTCTGGAG
V	ct	Firm					TGAAAGGCGGGGGCCCAACCCCGGACTGCTCTGAAACTGTATGGCTGGAGTGCAGGAGAGGTAAGCGGA
38	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCC
7	a	s	idia	pirales	raceae	ceae_Genus	AGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A							
S	Ba						TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCTGTGCAAGTCTGGAGT
V	ct	Firm					GAAAGCCCGGGGCTCAACCCCGGACTGCTTTGAAACTGTAGGGCTGGAGTGCAGGAGGGGTAAGCGGA
52	eri	icute	Clostr	Lachnos	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCGTACCGGTGCCA
8	a	s	idia	pirales	raceae	UC5-1-2E3	CACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG

A	S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT
	V	ct	Firm					GAAATGCCGGGGCTCAACCCCGGAAGTCTTTGGAACTGTACAGCTGGAGTGCAGGAGGGGTGAGCGGAA
39	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCATAGATATCAGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCA
3	a	s	idia	pirales	raceae	ceae_Genus		GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGAGGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGGGCTTAACCGCGGACTGCTTTGGAACTGTCTGACTGGAGTGTGGAGAGGTAAGTGGAA
45	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCCAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCC
7	a	s	idia	pirales	raceae	ceae_Genus		CAACTGACGCTCAGGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATTGCAAGTCTGAAGT
	V	ct	Firm					GAAAGCCCGTGGCTTAACCGCGGAACGGCTTTGGAACTGTGGAAGTGGAGTGTGGAGAGGCAAGCGGAA
48	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCGTACCGGCGCCA
4	a	s	idia	pirales	raceae	ceae_Genus		GACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGAATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCCGAAG
	V	ct	Firm					TGAAAGCCCGGGGCCAACCCCGGACTGCTTTGGAACTGTGAAGCTGGAGTGCAGGAGGGGCAGGCGG
54	eri	icute	Clostr	Lachnos	Lachnospi	Acetatifactor		AATTCCTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGC
7	a	s	idia	pirales	raceae			CCGACTGACGCTGAGGCACGAAAGCGTGGGGATCGAACAGG
A	S	Ba	Bact	Bacter	Bacteria	Bacteria_Ph		TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTAAGGCAAGTCTGATG
	V	ct	eria_Ph	ia_Ph	_Phylu	ylum_Cl		TGAAAGGCCAGGGCTCAACCCTGGGACTGCATTGGAACTGTGTTAACTGGAGTGTGCGAGAGGCAAGTGGAA
59	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		ATTCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCG
6	a	um	Class	_Order	_Family	y_Genus		CAACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba	Bact	Bacteroi	Bacteroidi	Bacteroidia_		TACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGCGCAAGTCTGGAGT
	V	ct	eroid	dia_Ord	a_Order_F	Order_Famil		GAAATGCCGCAGCTTAAGTGTGCGGAACTGCTTTGGAACTGGCGAACTAGAGTGTGCGGAGGGGTAAAGCGGAA
41	eri	ota	oidia	er	amily	y_Genus		TTCCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTCA
7	a							ACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGTGTAAGTCTGGAGT
	V	ct	Firm					GAAAGCCCGGGGCCAACCCCGGACTGCTTTGGAACTGTGTAAGTGGAGTACAGGAGGGGCAGGCGGA
38	eri	icute	Clostr	Lachnos	Lachnospi	Acetatifactor		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCG
2	a	s	idia	pirales	raceae			CAACTGACGCTCATGCACGAAAGCGTGGGTATCGAACAGG
A	S	Ba	Bact	Bacter	Bacteria	Bacteria_Ph		TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTATGTAAGTCTGGAGT
	V	ct	eria_Ph	ia_Ph	_Phylu	ylum_Cl		GAAAGCCCGGGGCCAACCCCGGACTGCTTTGGAACTGTGTAAGTGGAGTACAGGAGGGGCAGGCGGA
43	eri	Phyl	ylum_	m_Class	ass_Order	Order_Famil		ATTCTGGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCATCC
9	a	um	Class	_Order	_Family	y_Genus		AACTGACGCTGAAGCACGAAGCGTGGGTATCAAACAGG
	Ba			Bacteroi	Bacteroido	Bacteroidota		TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCACGCAAGTCAGAAG
A	ct	Bact	Bacter	dota_Cl	ta_Class_	_Class_Orde		TGAAAACCCGGGGCTCAACCCTGGGAGTGTCTTTGAACTGTGCGGCTAGAGTGTGCGAGGGGTAAGTGGAA
	S	eroid	oidota	ass_Ord	Order_Fa	r_Family_Ge		ATTCTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTC
V	a	ota	_Class	er	mily	nus		AACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG

45							
6							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTCACTGGGCGTAAAGGGAGAGTAGGTGGCAGAGCAAGTCCGAAG
V	ct	Bact			Porphyro	Porphyromo	TGAAAACCCAAAGCTCAACTATGGGAATGCTTTAGAAACTGCTCAGCTAGAGTGCAGGAGAGGCAAGTGGA
46	eri	eroid	Bacter	Bacteroi	monadace	nadaceae_G	ATTCTTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTC
0	a	ota	oidia	dales	ae	enus	AACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGACTTACTGGGTGTAAAGGGAGAGTAGGTGGCAGAGCAAGTCCGAAG
V	ct	Bact			Porphyro	Porphyromo	TGAAAACCCAAAGCTCAACTATGGGAATGCTTTAGAAACTGCTCAGCTAGAGTGCAGGAGAGGCAAGTGGA
52	eri	eroid	Bacter	Bacteroi	monadace	nadaceae_G	ATTCTTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCGCTC
5	a	ota	oidia	dales	ae	enus	AACTGACGCTCATGCACGAAAGTGTGGGTATCGAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCAGGGCAAGTCAGATG
V	ct	Firm					TGAAAACCCGGGGCTCAACTCCGGGAGTGCATTTGAAACTGTCCAGCTAGAGTGCAGGAGAGGTAAGCGGA
41	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTTAGTGTAGCGGTGAAATGCATAGATATCACGCAGAACTCCGATTGCGAAGGCAGCATACCGGCATCC
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGCTGAAGCACGGAGGCGTGGGTATCAAAACAGG
A							
S	Ba						TACGCATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTGCGGCAAGTCTGATGT
V	ct	Firm					GAAAGCCCCGGGGCCCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
53	eri	icute	Clostr	Lachnos	Lachnospi	A2	ATTCTTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCAGCATACCGGCGCC
8	a	s	idia	pirales	raceae		CAACTGACGCTCAGGCACGAAAGCGTGGGTATCGAACAGG
A							
S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCGGGCAAGTCAGATGT
V	ct	Firm					GAAAGCCCCGGGGCTCAACCCCGGGACTGCATTTGAAACTGTATTCTTGAGTGCTGGAGAGGCAATCGGAAT
58	eri	icute	Clostr	Oscillos	Oscillospir	Pseudoflavo	TCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCAGCATACCGGCATCCA
6	a	s	idia	pirales	aceae	nifactor	ACTGACGCTGAAGCACGAAGGCGTGGGTACCAAACAGG
A							
S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGTGCGTAGGTGGCAAGGCAAGTCTGAAGT
V	ct	Firm					GAAAATCCGGGGCTCAACCCCGGAACTGCTTTGGAAACTGTTTAGCTGGAGTACAGGAGAGGTAAGTGGA
29	eri	icute	Clostr	Lachnos	Lachnospi	Coprococcus	TTCTTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTACTGGACTGCT
8	a	s	idia	pirales	raceae		ACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCATGGCAAGTCAGATG
V	ct	Firm				Lachnospira	TGAAAGCCCCGGGGCTCAACCCCGGGACTGCATTTGAAACTGTCAGGCTGGAGTGCAGGAGAGGCAGGCGGA
04	eri	icute	Clostr	Lachnos	Lachnospi	ceae_NK4B4	ATTCTTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTG
1	a	s	idia	pirales	raceae	_group	TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
V	ct	Firm					GAAATACCGGGGCTCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
07	eri	icute	Clostr	Lachnos	Lachnospi	A2	ATTCTTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
0	a	s	idia	pirales	raceae		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
	V	ct	Firm					GAAATACCGGGGCCCCAACCCCGGACTGCTCTGAAACTGTATGGCTGGAGTGCAGGAGAGGTAAGCGGAA
53	eri	icute	Clostr	Lachnos	Lachnospi			TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGT
0	a	s	idia	pirales	raceae	A2		GACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG
A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
	V	ct	Firm					GAAATACCGGGGCCCCAACCCCGTCTCGTTCTATAAACTGATAGACTAGAGTGTGGTAGAGGCAAGTGAATT
57	eri	icute	Clostr	Lachnos	Lachnospi			TCTAGTGTAGCGGTAGAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGTGA
4	a	s	idia	pirales	raceae	A2		CTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCCTGGCAAGCCTGATGT
	V	ct	Firm					GAAATACCGGGGCCCCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
21	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
6	a	s	idia	pirales	raceae	A2		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCTGGCAAGCCTGATGT
	V	ct	Firm					GAAATACCGGGGCCCCAACCCCGGGGCTGCATTGGGAACTGCCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
00	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
9	a	s	idia	pirales	raceae	A2		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCAGGGCAAGCCTGATG
	V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGGACTGCATTGGGAACTGCCCGCTCGAGTGCCGGAGGGGCAGGCGGA
08	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
2	a	s	idia	pirales	raceae	A2		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCACGGCAAGCCTGATGT
	V	ct	Firm					GAAAGCCCCGCGGCCCAACCGCGGACTGCATTGGGAACTACCGGGCTGGAGTGCCGGAGAGGTAGGCGGA
03	eri	icute	Clostr	Lachnos	Lachnospi			ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTACTGGACGG
3	a	s	idia	pirales	raceae	Roseburia		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCAGGCTTAAGCCTGGTGT
	V	ct	Firm					GAAAGCCCCGCGGCCCAACCGCGGACTGCATTGGGAACTGGCGGCTGGAGTGCCGGAGGGGTAGGCGGA
06	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTACTGGACGG
0	a	s	idia	pirales	raceae	ceae_Genus		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGCACGCTAAGCCTGATGT
	V	ct	Firm					GAAAACCCGCGGCCCAACCGCGGAGTGCATTGGGAACTGGCGGGCTGGAGTACCGGAGGGGCAGGCGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
7	a	s	idia	pirales	raceae	ceae_Genus		AGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCTCTGTAAGTCTGATGT
	S	eri	icute	Clostr	Lachnos	Lachnospi		GAAAATTTGGGGCTCAACCCCAAACGTGCATTGGAACTGCAGGGCTTGAGTGCCGGAGAGGCAGGCGGAA
V	a	s	idia	pirales	raceae	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGT
						ceae_Genus		AAGTACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

22							
5							
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCTCTGTAAGTCTGATGT
V	ct	Firm					GAAAATTTGGGGCTCAACTCCAAACGTGCATTGGAAACTGCAGGGCTTAGAGTGTCCGAGAGGCAGGCGGAA
41	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGGT
9	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGCCTGCCAAGTCTGATGT
V	ct	Firm					GAAAGTCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGTCCGGCTAGAGTGCAGGAGGGGCAGGCGGA
54	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
4	a	s	idia	pirales	raceae	ceae_Genus	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGCCTGCCAAGTCTGATGT
V	ct	Firm					GAAATACCGGGGGCTCAACCCCGGGGCTGCATTGGAAACTGGCAGGCTGGAGTGCCGGAGAGGCAGGCGGA
03	eri	icute	Clostr	Lachnos	Lachnospi	A2	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
4	a	s	idia	pirales	raceae		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGTGTAGGTGGCATCACAAGTCAGAAGT
V	ct	Firm					GAAAGCCCCGGGGCTCAACCCCGGGACTGCTTTTGAAGTGTGGAGCTGGAGTGCAGGAGAGGCAAGTGGAA
47	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGTA
5	a	s	idia	pirales	raceae		ACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGAGTAGGTGGCAGAGCAAGTCCGAAG
V	ct	Firm					TGAAAACCCAAAGCTCAACTATGGGAATGCTTTAGAAACTGCTCAGCTAGAGTGCAGGAGAGGCAAGTGGAA
01	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGT
0	a	s	idia	pirales	raceae	ceae_Genus	AACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTATGGAGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGTGTAGGTGGCCAGGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCCGGGGCTCAACCCCGGGACTGCTTTTGAAGTGCAGGGCTAGAGTGCAGGAGGGGCAAGTGGAA
46	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTGT
1	a	s	idia	pirales	raceae		AACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCGAGCGTTATCCGGAATTACTGGGTGTAAAGGGTGAGTAGGCGGCTGTGCAAGTCATATGT
V	ct	Firm					GAAATACAGGGGGCTTAACCCCTGTGCCGATAAGAAACTGTACAGCTTAGAGTGCAGGAGAGGCAAGCGGA
19	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAAGAACACCGGTGGCGAAGGCGGCCTGCTGGACTGT
6	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGCTGAGTCACGAAAGCGTGGGGAGCGAACAGG
A				Peptostr			
S	Ba			eptococ			TACGTAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTCTTAAGTCAGAGGT
V	ct	Firm		cales-	Peptostrep		GAAAGGCTACGGCTCAACCGTAGTAAGCCTTTGAAACTGGGAAACTTGAGTGCAGGAGAGGAGAGTGGAAT
20	eri	icute	Clostr	Tissierel	tococcacea		TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTTGCGAAGGCGGCCTCTCTGGACTGTAA
7	a	s	idia	lales	e	Romboutsia	CTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG

A					Peptostr				
S	Ba				eptococ				
V	ct	Firm			cales-	Peptostrep			
20	eri	icute	Clostr		Tissierel	tococcacea			
9	a	s	idia		lales	e	Romboutsia		TACGTAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTCTTAAGTCAGAGGT GAAAGGCTACGGCTCAACCGTAGTAAGCCTTTGAAACTGGGGAACCTTGAGTGCAGGAGAGGAGAGTGGAAT TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTTGCGAAGGCGGCTCTCTGGACTGTAA CTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ				
V	ct	Firm			cales-	Peptostrep			
44	eri	icute	Clostr		Tissierel	tococcacea			
3	a	s	idia		lales	e	Romboutsia		TACGCAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTCTTAAGTCAGAGGT GAAAGGCTACGGCTCAACCGTAGTAAGCCTTTGAAACTGGGGAACCTTGAGTGCAGGAGAGGAGAGTGGAAT TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTTGCGAAGGCGGCTCTCTGGACTGTAA CTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ				
V	ct	Firm			cales-		Anaerovorac		
24	eri	icute	Clostr		Tissierel	Anaerovor	aceae_Genu		
0	a	s	idia		lales	acaceae	s		TACGTAGGGGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTACGTAGGCGGTTCTTTAAGCGCAGGGT TTAAGGCGATAGCTTAACCTATCGTTCGCCCTGTGAACTGGGGGACTTGAGTATCGGAGAGGAAAGCGGAATT CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACGAAAA CTGACGCTGAGGTACGAAAGCGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ		Anaerovorac		
V	ct	Firm			cales-		aceae_Genu		
33	eri	icute	Clostr		Tissierel	Anaerovor	s		CACGTAGGGGGCGAGCGTTATCCGGAATCATTGGGCGTAAAGGGTGCGTAGGCGGCCCTTTAAGCGCGGGG TCTAAGGCGGTGGCCCAACCACCGTTTCGCCCCGCGAAGTGGAGGGCTAGAGTGTGCGGAGAGGGAAAGCGGAA TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGACGAA GACTGACGCTGAGGCACGAAAGCGTGGGGAGCGAACAGG
A					Peptostr				
S	Ba				eptococ		Anaerovorac		
V	ct	Firm			cales-		aceae_Genu		
15	eri	icute	Clostr		Tissierel	Anaerovor	s		TACGTAGGGGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTACGTAGGTGGCAACCTAAGCGCAGGG TTTAAGGCAATGGCTCAACCATTGTTCCGCCCTGCGAAGTGGGATGCTTGAGTGCAGGAGAGGAAAGCGGAAT TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTAA CTGACACTGAGGTACGAAAGCGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ		Family_XIII		
V	ct	Firm			cales-		_AD3011_gr		
23	eri	icute	Clostr		Tissierel	Anaerovor	oup		TACGTAGGGGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGCCTAGGTGGTTACCTAAGCAGGGGG TGAAAGGCAATGGCTCAACCATTGTTAGCCCTCTGAACTGGGTTACTTGAGTGCAGGAGAGGAAAGCGGAA TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGAA ACTGACACTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ		Family_XIII		
V	ct	Firm			cales-		_AD3011_gr		
29	eri	icute	Clostr		Tissierel	Anaerovor	oup		TACGTAGGGGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGCCTAGGTGGTTACTTAAGCGCGGGGT TTAAGGCAATGGCTCAACCATTGTTCCGCCCTGCGAAGTGGGTTACTTGAGTGCAGGAGAGGAAAGCGGAATT CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTAC TGACACTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A					Peptostr				
S	Ba				eptococ				
V	ct	Firm			cales-				
30	eri	icute	Clostr		Peptoco	Peptococc	Peptococcac		
7	a	s	idia		ccales	aceae	eae_Genus		TACGTAGGGGAGCGAGCGTTGTCCGGAATTACTGGGCGTAAAGGGCGCGTAGGCGGGAACTTAAGTTAGATG TGAAAACTCCGGGCTTAACCTGGAGACTGCATTTAAACTGGGTTTCTTGAGGGCAGGAGAGGAAAGTGGA ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGACTTTCTGGACTGT ACCTGACGCTGAGGCGCGAAAGCATTGGGGAGCGAACAGG
A	Ba								
ct	Firm								
S	eri	icute	Clostr		Peptoco	Peptococc	Peptococcac		
V	a	s	idia		ccales	aceae	eae_Genus		TACGTAGGGAGCAAGCGTTGTCCGGAATTACTGGGCGTAAAGGGCGCGTAGGTGGGCGCTTAAGTCAGGTG TGAAAACTCCGGGCTCAACCTGGAGACTGCACCTGAAACTGGGTGTCTTGAGGGCAGGAGAGGAAAGTGGA ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGACTTTCTGGACTGT ACCTGACGCTGAGGCGCGAAAGCGTGGGTAGCGAACGGG

22							
1							
A							
S	Ba	Firm icute	Clostr idia	Peptoco ccales	Peptococc aceae	Peptococcac eae_Genus	TACGGAGGATGCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGCGCGTAGGTGGGCGCTTAAGTCAGGTGT
V	ct						GAAACTCCGGGCTCAACCTGGAGACTGCACTTGAAACTGGGTGTCTTGAGGGCAGGAGAGGAAAGTGGAA
51	eri						TTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACTGTA
7	a	s					CCTGACGCTGAGGCGCGAAAGCGTGGGTAGCGAACGGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridiace ae_Genus	TACGTAGGGGGCAAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGATTTTTAAGTGGGATGT
V	ct						GAAATACCCGGGCTCAACTTGGGTGCTGCATTCCAAACTGGAAGTCTAGAGTGCAGGAGAGGAAAGTGGAA
46	eri						TTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTA
4	a	s					ACTGACACTGAGGTACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridium _sensu_strict o_1	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGATTTTTAAGTGGGATGT
V	ct						GAAATACCCGGGCTCAACTTGGGTGCTGCATTCCAAACTGGAAGTCTAGAGTGCAGGAGAGGAAAGTGGAA
52	eri						TTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGACTTTCTGGACTGTA
7	a	s					ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridium _sensu_strict o_1	TACGTAGGTGGCGAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGACTTTTTAAGTGAGATGT
V	ct						GAAATACTCGGGCTCAACTTGAGTGCTGCATTCCAAACTGGAAGTCTAGAGTGCAGGAGAGGAGAATGGAA
08	eri						TTCTTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGATTCTCTGGACTGTA
0	a	s					ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridium _sensu_strict o_1	TACGTAGGTGGCGAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGACTTTTTAAGTGAGATGT
V	ct						GAAATACTCGGGCTCAACTTGAGTGCTGCATTCCAAACTGTAAGTCTAGAGTGCAGGAGAGGAGAATGGAA
15	eri						TTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGATTCTCTGGACTGTA
5	a	s					ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridium _sensu_strict o_1	TACGTAGGTGGCGAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGACTTTTTAAGTGAGATGT
V	ct						GAAATACTCGGGCTCAACTTGAGTGCTGCATTCCAAACTGGAAGTCTAGAGTGCAGGAGAGGAGAATGGAA
02	eri						TTCTTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGATTCTCTGGACTGTA
5	a	s					ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Clostr idia	Clostrid iales	Clostridia ceae	Clostridium _sensu_strict o_6	TACGTAGGTGGCAAGCGTTGTCCGGATTTACTGGGCGTAAAGGGAGCGTAGGCGGACCTTTAAGTGAGATGT
V	ct						GAAATACCCGAGCTCAACTTGGGTGCTGCATTCCAAACTGGAGGTCTAGAGTGTGCGAGAGGTAAGTGGAA
60	eri						TCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACCCCGGTGGCGAAGGCGACTTACTGGACGATA
7	a	s					ACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm icute	Firmic utes_ Class	Firmicut es_ _Order	Firmicutes _Class_ _Order	Firmicutes_ _Class_ _Order _Family_ _Genus	TACGTAGGGGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCCTAGGTGGTTTGGCAAGTTAGTAGC
V	ct						GTAACCTCCGGGGCTCAACTCCGGAATACTACTAAAACTGTCGGACTTGAGTGCAGAAGAGGGAAGTGGAA
43	eri						TTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGCA
4	a	s					ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG

A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTAGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGCAACTCCGGAGCTTAACCTTCGGAATACTACTAAAACTGTTGGACTTGAGTGCAGGAGGGGCAATCGGA
06	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGATTGCTAGACTGT
1	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGATAAGTTAGTAGC
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	GCAACTCCGGAGCTTAACCTTCGGAATACTACTAAAACTGTCGGACTTGAGTGCAGAAGGGGCAACCGGAA
35	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGGTTGCTAGGCTGTA
0	a	s	idia	group	amily	_Genus	ACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTGGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAACTCCGGGGCTCAACCTCGGCACTACTACCAAACTGTTGGACTTGAGTGCAGGAGGGGCAAATGGA
13	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGATTGCTGGACTGT
8	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTGGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAACTCCGAGGCTTAACCTCGGCACTACTACCAAACTGTTGGACTCGAGTGCAGGAGGGGCAAATGGA
12	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGATTGCTGGACTGT
7	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTGGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAAATCCGAGGCTCAACCTCGGCACTACTACCAAACTGTTGGACTTGAGTGCAGGAGGGGCAACTGGA
21	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGAGTTGCTGGACTGT
0	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGGAAGTTAGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAACTCCGGGGCTCAACTCCGGAATACTACTAAAACTGTCGGACTTGAGTGCAGGAGGGGCAATTGGA
06	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGAATTGCTGGACTGT
5	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTAGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAAATCCGGGGCTCAACTTCGGAATACTACTAAAACTGTTGGGCTTGAGTGCAGGAGAGGTGAATGGAA
26	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGCGGCGAAAGCGATTCACTGGACTGT
3	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGACAAGTTGGTAG
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	CGTAACTCCGGGGCTCAACCTCGGATCTACTACCAAACTGTTGGGCTTGAGTGCAGGAGGGGTGAATGGAA
22	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGCGGCGAAGGCGATTCACTGGACTGT
2	a	s	idia	group	amily	_Genus	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGGAAGTTGGTAGC
	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	GTAATCCCGGGGGCTCAACCTCGGTGCTACTACCAAACTGTTGAACTTGAGTGCAGGAGGGGTGAATGGAA
S	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TCCCAGTGTAGCGGTGGAATGCGTAGATATTGGGAAGAACACCAGCGGCGAAGGCGATTCACTGGACTGT
V	a	s	idia	group	amily	_Genus	ACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG

25							
5							
A							
S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGAGGCAAGCGTTATCCGGAATGACTGGGCGTAAAGGGTGCGTAGGTGGTTTGGCAAGTTGGTAGC
V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	GTAATTCGGGGGCTCAACCTCGGCGCTACTACCAAACTGCTGGACTTGAGTGCAGGAGGGGTGAATGGAAT
32	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAAGAACACCAGTCGGCGAAGGCGATTCACTGGACTGTA
9	a	s	idia	group	amily	_Genus	ACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACGTAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAGCAAGTTAGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAATCCCTCGGCTTAACCTGAGGAACTGCAACTAAAACACTATTTTCTTGAGTGCAGGAGAGGTAAGTGGAAAT
14	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTACTGGACTGTA
6	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACGTAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAACAAGTTAGTTG
V	ct	Firm		Clostrid	_UCG-	CG-	TGAAATCCCTCGGCTTAACCTGAGGAACTGCAACTAAAACACTATTTTCTTGAGTGCAGGAGAGGTAAGTGGAA
20	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTACTGGACTGTA
1	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACGTAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAACAAGTTAGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAATCCCTCGGCTTAACCTGAGGAACTGCAACTAAAACACTATTTTCTTGAGTGCAGGAGAGGTAAGTGGAAAT
28	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTACTGGACTGTA
3	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGCTAACAAGTTAGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAATCCCTCGGCTTAACCTGAGGAACTGCAACTAAAACACTATTAGTCTCTGAGTGCGGGAGAGGAAAGTGGAA
16	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACCGT
2	a	s	idia	-014	y	Genus	AACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAACAAGTTAGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAATCCCTCAGCTTAACCTGAGGAACTGCAACTAAAACACTATTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
24	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
1	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACATAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAATACAAGTTGGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAATCCCTCGGCTCAACCGAGGAACTGCAACCAAACTATATTTCTTGAGTACTGGAGAGGAAAGTGGAA
21	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGA
7	a	s	idia	-014	y	Genus	AACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A							
S	Ba				Clostridia	Clostridia_U	TACATAGGGAGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAATACAAGTTGGTTGT
V	ct	Firm		Clostrid	_UCG-	CG-	GAAAGCCCTCGGCTTAACCGAGGAACTGCAACCGAACTATATTTCTTGAGTATCGGAGAGGAAAGTGGAA
36	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACGAA
4	a	s	idia	-014	y	Genus	AACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG

A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCGAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGTATACAAGTTGGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTGTATATCTTGAGTACAGGAGAGGTAAGTGGAA
34	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTACTGGACTGA
0	a	s	idia	-014	y	Genus	AACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGATGGATAAACAAGTTGTTTGT
	V	ct	Firm		_UCG-	CG-	GAAATACCTCGGCTCAACTGAGGAACTGCAAGCAAAACTGTATATCTTGAGTACTGGAGGGGAAAGCGGAA
18	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCGGTGGCGAAGGCGGCTTTCTGGACAGA
4	a	s	idia	-014	y	Genus	AACTGACATTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGGCAAGTTGGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTATCTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
13	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
9	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGGCAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAACATCTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
12	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
1	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGTCAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAACATCTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
31	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
6	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGGCAAGTTGGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTATCTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
33	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
9	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGGCAAGTTGGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTACATTTCTTGAGTGCTGGAGAGGAAAGTGGAA
13	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
4	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATGCAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAACATCTTTCTTGAGTGCTGGAGAGGAAAGTGGAAAT
20	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
6	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATGCAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTACATTTCTTGAGTGCTGGAGAGGAAAGTGGAA
13	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
4	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG

34							
6							
A							
S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAGACAAGTTGGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTATCTTCTTGAGTGCTGGAGAGGAAAAGTGGAAAT	
39	eri	icute	Clostridia	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA	
0	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAAACAAGTTGGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACCAAACTATTTTCTTGAGTGCTGGAGAGGAAAAGTGGAAAT	
30	eri	icute	Clostridia	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA	
0	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACATAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAAATTAAGTTAGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAAGTATTTTCTTGAGTACTGGAGAGGAAAAGTGGAAAT	
18	eri	icute	Clostridia	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA	
5	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACATAGGGGGCGAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAATTAAGTTAGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTTGGCTTAAGTGAAGAACTGCAACTAAAAGTATTTTCTTGAGTATTGGAGAGGAAAAGTGGAAAT	
20	eri	icute	Clostridia	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAAAA	
3	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACATAGGGGGCAAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAATTAAGTTAGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATACCTTGGCTCAACTAAGGAAGTCAACTAAAAGTGGTTTCTTGAGTACTGGAGAGGAAAAGTGGAAAT	
32	eri	icute	Clostridia	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGAA	
4	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATTTAAGTTAGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAAGTCAACTAAAAGTGGATTCTTGAGTGCTGGAGAGGAAAAGCGGAA	
36	eri	icute	Clostridia	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACAGTA	
7	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACATAGGGAGCGAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATTTAAGTTGGTTGT	
V	ct	Firm		_UCG-	CG-	GAAATCCCTCAGCTCAACTGAGGAAGTCAACCAAAAGTGGATTCTTGAGTGCTGGAGAGGAAAAGTGGAA	
15	eri	icute	Clostridia	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA	
7	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba			Clostridia	Clostridia_U	TACATAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATTTAAGTTGGTTGT	
V	ct	Firm		_UCG-	CG-	GAAAGCCCTCGGCTCAACTGAGGAAGTCAACCAAAAGTGGATTCTTGAGTATTGGAGAGGAAAAGTGGAA	
31	eri	icute	Clostridia	014_Famil	014_Family_	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACAATA	
3	a	s	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	

A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAATTTAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAGTGAATTTCTTGAGTGCGGGAGAGGAAAGTGGAA
17	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACCGTA
2	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAAATTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAATAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAACTGCAACTAAAGTGAATTTCTTGAGTGACAGGAGAGGAAAGTGGAA
36	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACTGTA
1	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAAATTATTGGGTGTAAAGGGTGCGTAGACGGGAGTCTAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAACTGCAACTAAAGTGGGCATCTTGAGTGACAGGAGAGGAAAGTGGAA
29	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACTGTA
1	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCGAGCGTTATCCGGAAATTATTGGGTGTAAAGGGTGCGTAGACGGGTAAATAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAACTGCAACTAAAGTGTATATCTTGAGTGCGGGAGAGGAAAGTGGAA
38	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACCGTA
6	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGTATATAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAACTGCAACTAAAGTGTAAATCTTGAGTGCGGGAGAGGAAAGTGGAA
27	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACCGTA
4	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGGAAAAACAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAGTATTTTTCTTGAGTGCTGGAGAGGAAAGTGGAA
19	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAGTA
8	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACATAGGGGGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGAGAAAAACAAGTTGGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTCAACTGAGGAACTGCAACCAAAACTATTTCCCTTGAGTGTCGGAGAGGAAAGTGGAA
26	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGACTTTCTGGACGATA
0	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGATTTATTGGGTGTAAAGGGTGCGTAGACGGAGAAAGCAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAATCCCTCGGCTTAAGTGAAGAACTGCAACTAAAGTACTTCCCTTGAGTGTTGGAGAGGAAAGTGGAA
39	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGACAATA
2	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG
A	S	Ba			Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAAATTATTGGGTGTAAAGGGTGCGTAGACGGGAATACAAGTTAGTTGT
	V	ct	Firm		_UCG-	CG-	GAAAGCCCTCGGCTTAAGTGAAGAACTGCAACTAAAGTATATTTCTTGAGTGACAGGAGAGGAAAGCGGAA
3	eri	icute	Clostr	ia_UCG	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGTA
S	a	s	idia	-014	y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG

26							
8							
A							
S	Ba	Firm		Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGACAGCAAGTTAGTTGT	
V	ct	icute		_UCG-	CG-	GAAAGCCCTCGGCTTAAGTGAAGAACTGCAACTAAAACTATTGTTCTTGAGTGCAGGAGAGGAAAGCGGAA	
37	eri	s	Clostridia	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTTCTGGACTGTA	
7	a			y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTATTGGGTGTAAAGGGTGCGTAGACGGGATAACAAGTTGGTTGT	
V	ct	icute		_UCG-	CG-	GAAACCCCTCGGCTCAACTGAGGAACTGCAACCAAACTATTATTCTTGAGTGCAGGAGAGGAAAGTGGAA	
21	eri	s	Clostridia	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCGGTGGCGAAGGCGACTTTCTGGACTGTA	
2	a			y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTTATTGGGTGTAAAGGGTGCGTAGACGGGATTACAAGTTGGTTGT	
V	ct	icute		_UCG-	CG-	GAAACCCCTCAGCTCAACTGAGGAACTGCAACCAAACTATAATTCTTGAGTGCAGGAGAGGAAAGTGGAA	
41	eri	s	Clostridia	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTGCTGGACGGT	
4	a			y	Genus	GACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTTATTGGGTGTAAAGGGTGCGTAGACGGGATTACAAGTTGGTTGT	
V	ct	icute		_UCG-	CG-	GAAACCCCTCAGCTCAACTGAGGAACTGCAACCAAACTATAATTCTTGAGTGCAGGAGAGGAAAGTGGAA	
32	eri	s	Clostridia	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCGGTGGCGAAGGCGACTTTCTGGACTGTA	
8	a			y	Genus	ACTGACGTTGAGGCACGAAAGTGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_U	TACGTAGGGAGCAAGCGTTATCCGGAATTTATTGGGTGTAAAGGGTGCGTAGACGGGATAACAAGTTGGTTGT	
V	ct	icute		_UCG-	CG-	GAAACCCCTCGGCTCAACTGAGGAACTGCAACCAAACTATTATTCTTGAGTGCAGGAGAGGAAAGTGGAA	
42	eri	s	Clostridia	014_Famil	014_Family_	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACTGTA	
3	a			y	Genus	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_v	TACGTAGGGGGCGAGCGTTGTCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTGTGCAAGTTAGATG	
V	ct	icute		_vadinBB6	adinBB60_gr	TGAAATCCCATGGCTTAACCATGGAAGTGCATCTAAAAGTGCATAGCTGGAGTGCAGGAGAGGTGAGTGGAA	
31	eri	s	Clostridia	nBB60_	oup_Family_	ATTCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGAGGCGAAGGCGACTCACTGGACTG	
2	a		group	family	_Genus	TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_v	TACGTAGGGGGCAAGCGTTGTCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTTATCAAGTTAGATG	
V	ct	icute		_vadinBB6	adinBB60_gr	TGAAATCCCGCGGCTTAACCGCGGAAGTGCATCTAAAAGTGGTGGAGTGCAGGAGAGGTGAGTGGAA	
21	eri	s	Clostridia	nBB60_	oup_Family_	ATTCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGAGGCGAAGGCGACTCACTGGACTG	
1	a		group	family	_Genus	TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG	
A							
S	Ba	Firm		Clostridia	Clostridia_v	TACGTAGGGGGCAAGCGTTGTCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTTGTAAAGTTAGATGT	
V	ct	icute		_vadinBB6	adinBB60_gr	GAAATCCTACGGCTTAACCGTAGAAGTGCATCTAAAAGTGTGAGGCTGGAGTGCAGGAGAGGTGAGTGGAA	
27	eri	s	Clostridia	nBB60_	oup_Family_	TTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGAGGCGAAGGCGACTCACTGGACTGT	
0	a		group	family	_Genus	AACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG	

A	S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGGGGCGAGCGTTGTCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTCTTTAAGTTATATGT
	V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	GAAATCCCGCGGCTTAACCGTGGAAGTGCATATAAACTGGGAGCTGGAGTGCAGGAGAGGTGAGTGGAA
25	1	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	TTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAAGAACACCGGTGGCGAAGGCGGCTCACTGGACTGT
A		a	s	idia	group	amily	_Genus	AACTGACGCTGAGGCTCGAAAGCGTGGGAGCAAACAGG
A	S	Ba			Clostrid	Clostridia	Clostridia_O	TACGTAGGGGGCGAGCGTTGTCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTCTTTAAGTTATGTGT
	V	ct	Firm		ia_Orde	_Order_Fa	order_Family	GAAAGCCCACGGCTCAACTGTGGAATTGCACATAAACTGGGAGGCTGGAGTGCAGGAGAGGTAAGCGGA
30	6	eri	icute	Clostr	ia_Orde	_Order_Fa	_Genus	ATTTCCAGTGTAGCGGTGGAATGCGTAGATATTGGGAAGAACACCGGAGGCGAAGGCGGCTTACTGGACTG
A		a	s	idia	r	mily		TAACTGACGCTGAGGCTCGAAAGCGTGGGAGCAAACAGG
A	S	Ba			Clostrid	Clostridia	Clostridia_O	TACGTAGGGGGCGAGCGTTATCCGGAATGACTGGGCGTAAAGGGAGTGTAGGCGGCTCTTTAAGTTATGTGT
	V	ct	Firm		ia_Orde	_Order_Fa	order_Family	GAAAGCCCACGGCTCAACTGTGGAATTGCACATAAACTGGGAGGCTGGAGTGCAGGAGAGGTAAGCGGA
53	1	eri	icute	Clostr	ia_Orde	_Order_Fa	_Genus	ATTTCCAGTGTAGCGGTGGAATGCGTAGATATTGGGAAGAACACCGGAGGCGAAGGCGGCTTACTGGACTG
A		a	s	idia	r	mily		TAACTGACGCTGAGGCTCGAAAGCGTGGGAGCAAACAGG
A	S	Ba						TACGTAGGTGGCAAGCGTTGTTCGGAATAACTGGGCGTAAAGGATGCGTAGGCGGTTAAACAAGTTATATGT
	V	ct	Firm					TAAATATATAGGCTTAACCTGTAGAAAGCATATAAACTGTTTAACTAGAGTGCAGGAGAGGTAAGTGGAA
17	5	eri	icute	Clostr	Clostrid	Clostridia	Candidatus_	TTCCTAGTGTAGCGGTGAAATGCGTAGAGATTAGGAAGAACACCAGTGGCGAAGGCGACTTACTGGACTGT
A		a	s	idia	iales	ceae	Arthromitus	AACTGACGCTGAGGCATGAGAGCATGGGAGCAAACAGG
A	S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGGAGCAAGCGTTGTTCGGAATGACTGGGCGTAAAGGGTGCCTAGGCGGTTGTACAAGTTAGAAG
	V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	TGAAATACCCAGGGCTTAACCTCGGGTGCTGCTTCTAAAACTGTATGACTTGAGTGCAGTAGAGGTTAGTGA
16	7	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGAGGCGAAGGCGGCTAACTGGACTG
A		a	s	idia	group	amily	_Genus	CAACTGACGCTGAGGCACGAAAGTGTGGGAGCAAACAGG
A	S	Ba			Clostrid	Clostridia	Clostridia_v	TACGTAGGGAGCAAGCGTTGTTCGGAATGACTGGGCGTAAAGGGTGCCTAGGCGGTTATACAAGTTAGAAG
	V	ct	Firm		ia_vadi	_vadinBB6	adinBB60_gr	TGAAATACCCAGGGCTTAACCTCGGGTGCTGCTTCTAAAACTGTAAGACTTGAGTACAGTAGAGGTTAGTGA
25	9	eri	icute	Clostr	nBB60_	0_group_F	oup_Family	ATTCCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGAGGCGAAGGCGGCTAACTGGACTG
A		a	s	idia	group	amily	_Genus	AAACTGACGCTGAGGCACGAAAGTGTGGGAGCAAACAGG
A	S	Ba	Acti					TACGTAGGGTGCAAGCGTTATCCGGAATTATTGGGCGTAAAGGGCTCGTAGGCGGTTTCGTCGCGTCCGGTGT
	V	ct	noba	Actin				GAAAGTCCATCGCTTAACGGTGATCCGCGCCGGGTACGGGCGGGCTTGAGTGCGGTAGGGGAGACTGGAA
45	2	eri	acteri	obacte	Bifidoba	Bifidobact	Bifidobacteri	TTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGCAGGTCTCTGGGCCGT
A		a	ota	ria	cteriales	eriaceae	um	CACTGACGCTGAGGAGCGAAAGCGTGGGAGCGAACAGG
A	S	Ba	Acti					TACGTAGGGTGCAAGCGTTATCCGGAATTTATTGGGCGTAAAGGGCTCGTAGGCGGTTTCGTCGCGTCCGGTGT
	V	ct	noba	Actin				GAAAGTCCATCGCTTAACGGTGATCCGCGCCGGGTACGGGCGGGCTTGAGTGCGGTAGGGGAGACTGGAA
11	6	eri	acteri	obacte	Bifidoba	Bifidobact	Bifidobacteri	TTCCCGGTGTAACGGTGGAATGTGTAGATATCGGGAAGAACACCAATGGCGAAGGCAGGTCTCTGGGCCGT
		a	ota	ria	cteriales	eriaceae	um	ACTGACGCTGAGGAGCGAAAGCGTGGGAGCGAACAGG
A		Ba						TACGTAGGTGGCGAGCGTTATCCGGAATTTATTGGGCGTAAAGCGTGCGCAGGCGGCTTATTAAGTCTAAGAT
		ct	Firm					TAAAGCCCGGAGCTTAACCTCCGGTTCGTCTTAGAAACTGGTAGGCTTGAGTATGGTAGAGGCAAACGGAATT
S		eri	icute			RF39_Fam	RF39_Famil	CCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTTTGCTGGGCCATTAC
V		a	s	Bacilli	RF39	ily	y_Genus	TGACGCTCATGCACGAAAGCGTGGGAGCAAATAGG

23									
7									
A									
S	Ba								TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGCGCAGGCGGTTTGTTAAGTCTAAAATT
V	ct	Firm							AAAGTCCGAAGCTTAACTTCGGTTCGTTTTAGAACTGGCAGGCTTGAGTATGGTAGAGGCAAACGGAATTT
34	eri	icute			RF39_Fam	RF39_Famil			CTAGTGTAGCGGTAAAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGTTTGCTGGGCCATTACT
1	a	s	Bacilli	RF39	ily	y_Genus			GACGCTCATGCACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGCGCAGGCGGTTTGTTAGGTCTAAAATT
V	ct	Firm							AAAGCCCGAAGCTTAACTTCGGTTCGTTTTAGAAACCGGCAGGCTTGAGTATGGTAGAGGCAAACGGAATTT
48	eri	icute			RF39_Fam	RF39_Famil			CTAGTGTAGCGGTAAAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGTTTGCTGGGCCATTACT
9	a	s	Bacilli	RF39	ily	y_Genus			GACGCTCATGCACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGCGCAGGCGGTTTGTTAGGTCTAAAATT
V	ct	Firm							AAAGTCCGAAGCTTAACTTCGGTTCGTTTTAGAAACCGGCAGGCTTGAGTATGGTAGAGGCAAACGGAATTT
21	eri	icute			RF39_Fam	RF39_Famil			CTAGTGTAGCGGTAAAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGTTTGCTGGGCCATTACT
4	a	s	Bacilli	RF39	ily	y_Genus			GACGCTCATGCACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGGGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGGGTGTGTAGGCGGTTTGTTAAGTCTAAAAT
V	ct	Firm							CAAAGCCCGAGGCTTAACTTCGGTTCGTTTTAGAACTGGCAAACCTAGAGTACAGTAGAGGCAAAGTGAAT
39	eri	icute			RF39_Fam	RF39_Famil			TTCTAGTGTAGCGGTTAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGCTTGCTGGGCTGTTA
7	a	s	Bacilli	RF39	ily	y_Genus			CTGACGCTGAGACACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGGGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGTGTAGGCGGTTTATTAAGTCTAAGATT
V	ct	Firm							AAAGCCTGGAGCTTAACTTCAGTTCGTCTTAGAACTGGTAGACTTGAGTGTGGTAGAGGCAAAGTGAATTT
26	eri	icute			RF39_Fam	RF39_Famil			CTAGTGTAGCGGTAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGACTTGCTGGGCCATTACT
6	a	s	Bacilli	RF39	ily	y_Genus			GACGCTGAGACACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGGGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGTGTAGGCGGTTTATTAAGTATAAGATT
V	ct	Firm							AAAGCCCGAGGCTTAACTTCGGTTCGTCTTATAAACTGGTAGACTTGAGTGTGGTAGAGGCAAAGTGAATTT
37	eri	icute			RF39_Fam	RF39_Famil			CTAGTGTAGCGGTTAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGCTTGCTGGGCCATTACT
1	a	s	Bacilli	RF39	ily	y_Genus			GACGCTGAGACACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGGAGGGGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGTGTAGGCGGTTTATTAAGTATAAGAT
V	ct	Firm							TAAAGCCCGAGGCTTAACTTCGGTTCGTCTTATAAACTGGTAGACTTGAGTGTGGTAGAGGCAAAGTGAATTT
50	eri	icute			RF39_Fam	RF39_Famil			TCTAGTGTAGCGGTTAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCGGCTTGCTGGGCCATTAC
8	a	s	Bacilli	RF39	ily	y_Genus			TGACGCTGAGACACGAAAGCGTGGGGAGCAAATAGG
A									
S	Ba								TACGTAGGTGGCGAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGCGCAGGCGGTTTGATAAGTCTAAAAT
V	ct	Firm			Bacilli_Or	Bacilli_Orde			AAAAGCCCGAAGCTTAACTTCGGTTCGTTTTAGAACTGTCAGACTAGAGTGTGGTAGAGGCAAATGGAATTT
60	eri	icute			der_Famil	r_Family_Ge			TCTAGTGCAGCGTAAAAATGCGTAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCACA
4	a	s	Bacilli	Order	y	nus			CTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
A	Ba	Bact	Bacter	Bacteria	Bacteria_P	Bacteria_Ph			TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGCGCAGGCGGCTTATTAAGTCTAAGAT
S	ct	eria_	ia_Ph	_Phylu	hylum_Cl	ylum_Class_			TAAAGCCCGAGCTTAACTCCGGTTCGTCTTAGAACTGGTAGGCTTGAGTATGGTAGAGGCAAACGGAATT

V583A	eri a	Phylum	ylum_Class	m_Class_Order	ass_Order_Family	Order_Family_Genus	CCTAGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACTCCGATTGCGAAGGCAGCATGCCGGCTCCACA CTGACGCTGAGGCACGAAAGCGTGGGTATCGAACAGG
V037A	Bacteria	Firmicutes	Bacilli	RF39	RF39_Family	RF39_Family_Genus	TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTCCGCAGCCGGTTTATTAAGTATAGAAT AAAACCTTCGGGGCTCAACCCGCTCTCGTTCTATAAACTGATAGACTAGAGTGTGGTAGAGGCAAATGGAATT TCTAGTGTAGCGGTAGAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCCGACTTGCTGGGCCATCA CTGACGGTCAGGGACGAAAGCGTGGGGAGCGAATAGG
V599A	Bacteria	Firmicutes	Bacilli	Bacilli_Order	Bacilli_Order_Family	Bacilli_Order_Family_Genus	TACGTAGGTGGCGAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGCGCAGGCGGTTTGATAAGTCTAAAAAT AAAAGCCCGAAGCTTAACCTTCGGTTCGTTTTAGAACTGTCAGACTAGAGTGTGGTAGAGGCAAATGGAATT TCTAGTGTAGCGGTAAAAATGCGTAGATATTAGGAGGAACACCAGATTGCGAAGGCAGCCTGCTGGACTGTAA CTGACGCTGATGCTCGAAAAGTGTGGGTATCAAACAGG
V262A	Bacteria	Firmicutes	Bacilli	RF39	RF39_Family	RF39_Family_Genus	TACGTAGGTGGCGAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGCGCAGGCGGTTTGATAAGTCTAAAAAT AAAAGCCCGAAGCTTAACCTTCGGTTCGTTTTAGAACTGTCAGACTAGAGTGTGGTAGAGGCAAATGGAATT TCTAGTGTAGCGGTAAAAATGCGTAGATATTAGAAGGAACACCAGTGGCGAAGGCCGATTTGCTGGGCCACAA CTGACGCTCATGCACGAAAGCGTGGGGAGCAAATAGG
V553A	Bacteria	Firmicutes	Bacilli	RF39	RF39_Family	RF39_Family_Genus	TACGTAGGTGGCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTGCGCAGGCGGCTTATTAAGTCTAAGAT TAAAGCCCGGAGCTTAACCTCCGGTTCGTCTTAGAACTGGTAGGCTTGAGTATGGTAGAGGCAAACGGAATT CCTAGTGTAGCGGTGGAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCCGGCTTACTGGACCGTAA CTGACGTTGAGGCTCGAAAAGCGTGGGGAGCAAACAGG
V238A	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Eggerthellaceae	Enterorhabdus	TACGTAGGGGGCGAGCGTTATCCGGATTCATTGGGCGTAAAGCGCGCGTAGGCGGCCGCTAAGCGGAACC TCTAACCCCGGGGCTCAACCTCGGGCCGGGTTCCGGACTGGGCGGCTCGAGTGCGGTAGAGGAGAGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTCTCTGGGCCGT CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
V336A	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Eggerthellaceae	Enterorhabdus	TACGTAGGGAGCGAGCGTTATCCGGATTCATTGGGCGTAAAGCGCGCGTAGGCGGCTGCCTAAGCGGAACC TCTAACCCCGGGGCTCAACCTCGGGCCGGGTTCCGAACTGGGCGGCTCGAGTGCGGTAGAGGAGAGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTCTCTGGGCCGG CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
V253A	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Eggerthellaceae	Parvibacter	TACGTAGGGAGCGAGCGTTATCCGGATTCATTGGGCGTAAAGCGCGCGTAGGCGGCTGCCTAAGCGGAACC TCTAATCCCGGGGCTCAACCTCGGGCCGGGTTCCGAACTGGGCGGCTCGAGTGCGGTAGAGGCAGGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCCTGCTGGGCCGT CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
V193A	Bacteria	Actinobacteria	Coriobacteriia	Coriobacteriales	Eggerthellaceae	Adlercreutzia	TACGTAGGGGGCGAGCGTTATCCGGATTCATTGGGCGTAAAGCGCGCGTAGGCGGCCGCTAAGCGGAACC TCTAATCCCGGGGCTCAACCTCGGGCCGGGTTCCGAACTGGGCGGCTCGAGTGCGGTAGAGGCAGGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCCTGCTGGGCCGG CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG

ASV187A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	DNF00809	TACGTAGGGGGCAAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGCAGGCGGGCCGCTAAGCGGGACC TCTAATCTTGGGGCTCAACCTCAAGCCGGGTCCCGAAGTGGCAGCCTCGAGTGCGGTAGGGGTAAAGCGGAAT TCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTTACTGGGCCGAC ACTGACGCTGAGGCGCGAAAGCTAGGGGAGCGAACAGG
ASV332A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	DNF00809	TACGTAGGGGGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGCAGGCGGACCGTTAAGCGGGACC TCTAATCTTGGGGCTCAACCTCAGGCCGGGTCCCGAAGTGGCGGTCTCGAGTGCGGTAGGGGAGGTCGGAAT TCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGACCTCTGGGCCGAC ACTGACGCTGAGGCGCGAAAGCTAGGGGAGCGAACAGG
ASV292A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	Enterorhabdus	TACGTAGGGGGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGCAGGCGGGCTTGAAGCGGGGCC TTAATCTTGGGGCTTAACCTCAAGTCGGGTTCGGAAGTCAAGCCTCGAGTGTGGTAGGGGAAGGCGGAAT TCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCCTTCTGGGCCACT ACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
ASV153A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	Eggerthellaceae_Genus	TACGTATGGGGCAAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGCAGGCGGGCGCCTAAGCGGGACC TCTAATCTCGGGGCTCAACCCCGAGCCGGGTTCGGAAGTGGGCACCTCGGGTTCGGTAGGGGTAGACGGAAT TCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGTCTACTGGGCCGCA ACCGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
ASV223A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	DNF00809	TACGTAGGGGAGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGTAGGCGGGCATCTAAGCGGGACC TCTAATCTCGGGGCTCAACCTCGAGCCGGGTTCGGAAGTGGATGCCTCGAGTCCGGTAGGGGCAAGTGAAT TCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTTGCTGGGCCGCG ACTGACGCTGAGGCGCGAAAGCTAGGGGAGCGAACAGG
ASV564A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	Eggerthellaceae_Genus	TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGCGCGTAGGCGGCGCGTCAAGCGGGACCT CTAACCCCGGGGCTCAACCCCGGGCCGGGTCCCGGACTGGCGCGCTCGAGTGCGGTAGAGGCGAGTGAAT TCCCGGTGTAGCGGTGGAATGCGTAGATATATGGAAGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGCA ACTGACGCTGAGGCTCGAAAGCATGGGTAGCGAACAGG
ASV400A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	DNF00809	TACGTAGGGGGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGTAGGCGGCGCGTCAAGCGGGACC TCTAACCCCGGGGCTCAACCCCGGGCCGGGTCCCGGACTGGCGCGCTCGAGTGCGGTAGAGGCGAGTGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTCGCTGGGCCGA CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
ASV113A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	Enterorhabdus	TACGTAGGGGGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGTAGGCGGCGCGTCAAGCGGGACC TCTAACCCCGGGGCTCAACCCCGGGCCGGGTCCCGGACTGGCGCGCTCGAGTGCGGTAGAGGAGAGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATCGGGAAGAACACCGATGGCGAAGGCAGCTCTCTGGGCCGT CACTGACGCTGAGGCGCGAAAGCTGGGGGAGCGAACAGG
ASV113A	Bacteria	Actinobacteria	Coriobacteriales	Coriobacteriales	Eggerthellaceae	Enterorhabdus	TACGTAGGGGGCGAGCGTTATCCGGATTCAATTGGGCGTAAAGCGCGCGTAGGCGGCGCGTCAAGCGGGACC TCTAACCCCGGGGCTCAACCCCGGGCCGGGTCCCGGACTGGCGCGCTCGAGTGCGGTTAGAGGAGAGCGGAA TTCCCGGTGTAGCGGTGGAATGCGCAGATATGGAAGTACCAACAGTGGCGAAGGCAGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

48								
0								
A			Gam					
S	Ba	Prot	mapr			Comamona		TACGTAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGTGCGCAGGCGGTTATGTAAGACAGAGG
V	ct	eoba	oteob			daceae_Gen		TGAAATCCCCGGGCTCAACCTGGGAAGTGCCTTTGTGACTGCATGACTAGAGTACGGTAGAGGGGGATGGA
60	eri	cteri	acteri	Burkhol	Comamon			ATTCCACGTGTAGCAGTGAAATGCGTAGATATGTGGAGGAACACCGATGGCGAAGGCAATCCCCTGGACCT
3	a	a	a	deriales	adaceae	us		GTACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTAGGATCCGAGCATTATCCGGAGTGACTGGGTGTAAAGAGTTGCGTAGGTGGCATAATAAGTAGCTAG
V	ct	Pates	Sacch	Sacchari		Candidatus_		TGAAATCTGGTGGCTCAACCTCAGACTATTAGCTAAACTGTAAAGCTCGAGACCGTTAGGGGTAAGTGA
42	eri	cibac	arimo	monada	Saccharim	Saccharimon		ATTTCTAGTGTAGGAGTGAAATCCGTAGATATTAGAAAGAACACCAATAGCGTAGGCAGGTTACTGGGACG
8	a	teria	nadia	les	onadaceae	as		GTTCTGACACTAAGGCACGAAAGCGTAGGGAGCAAACGGG
A								
S	Ba							TACGTAGGACCCGAGCATTATCCGGAGTGACTGGGTGTAAAGAGTTGCGTAGGTGGCATAATAAGTAGCTAG
V	ct	Pates	Sacch	Sacchari		Candidatus_		TGAAATCTGGTGGCTCAACTATTCAGACTATTAGCTAAACTGTAAAGCTCGAGACCGTTAGGGGTAAGTGA
48	eri	cibac	arimo	monada	Saccharim	Saccharimon		ATTTCTAGTGTAGGAGTGAAATCCGTAGATATTAGAAAGAACACCAATAGCGTAGGCAGGTTACTGGGACG
6	a	teria	nadia	les	onadaceae	as		GTTCTGACACTAAGGCACGAAAGCGTAGGGAGCAAACGGG
A		Verr						
S	Ba	uco						TACGGAGGGTGCTAGCGTTAATCCGATTTATTGGGCGTAAAGGGCGTGAGGCGGAAAGGTAAGTTAGTTGT
V	ct	micr	Chla					CAAATCTCGGGGCTCAACCCGAATCGGCATCTAAACTATTTTCTAGAGGGTAGATGGAGAAAAGGGAA
21	eri	obiot	mydia	Chlamy	Chlamydi			TTTCACGTGTAGCGGTGAAATGCGTAGATATGTGGAAGAACACCAAGTGGCGAAGGCGCTTTTCTAATTTATA
3	a	a	e	diales	aceae	Chlamydia		CCTGACGCTAAGGCGCGAAAGCAAGGGGAGCAAACAGG
A		Verr						
S	Ba	uco						TACAGAGGTCTCAAGCGTTGTTCCGAATCACTGGGCGTAAAGCGTGCGTAGGCTGTTTCGTAAGTCGTGTGTG
V	ct	micr	Verru	Verruco				AAAGGCGCGGGCTCAACCCGCGGACGGCACATGATACTGCGAGACTAGAGTAATGGAGGGGGAAACCGGAA
56	eri	obiot	comic	microbi	Akkerman	Akkermansi		TTCTCGGTGTAGCAGTGAAATGCGTAGATATCGAGAGGAACACTCGTGCGAAGGCGGGTTCTTGACATTA
7	a	a	robiae	ales	siaceae	a		ACTGACGCTGAGGCACGAAGGCCAGGGGAGCGAAAGGG
A								
S	Ba							TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTTGGAAGCCAGATG
V	ct	Firm						TGAAAGGCTGGGGCTCAACCCAGGACTGCATTTGAAACTGTTTTCTTGAGTACCGGAGAGGTCATCGGAA
54	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCTTGTTGTAGCGGTGAAATGCGTAGATATAAGGAAGAACACCAAGTGGCGAAGGCGGCTTCTGGTCTGCA
2	a	s	idia	pirales	raceae	ceae_Genus		ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTATGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCATGCAAGTCAGAAG
V	ct	Firm						TGAAAACCCGGGGCTCAACCTGGGAGTGCTTTTGAAACTGTGCGGCTAGAGTGTGCGAGGGGTAAGTGA
42	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAAGTGGCGAAGGCGGCTTCTGGTCTGC
9	a	s	idia	pirales	raceae	ceae_Genus		AACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A								
S	Ba							TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCCATGCAAGTCAGAAG
V	ct	Firm						TGAAAACCCGGGGCTCAACCTGGGAGTGCTTTTGAAACTGTGCGGCTAGAGTGTGCGAGGGGTAAGTGA
05	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAAGTGGCGAAGGCGGCTTACTGGACGA
2	a	s	idia	pirales	raceae	ceae_Genus		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCCGCCACGCAAGTCAGAAG
	V	ct	Firm					TGAAAACCCGGGGCTCAACCCTGGGAGTGCTTTTGAAACTGTGCGGCTAGAGTGTCCGAGGGGTAAGTGGA
06	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGA
8	a	s	idia	pirales	raceae	ceae_Genus		TGACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCCGCCAGTGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCAAGGCTCAACCATGGGACTGCTTTTGAAACTGTACAGCTAGATTGCAGGAGAGGTAAGTGGA
11	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
7	a	s	idia	pirales	raceae	900066575		AAATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCCGCCAAGGTAAGCCAGAAG
	V	ct	Firm					TGAAAGCCCGCGGCTCAACTGCGGGACTGCTTTTGAAACTATCTAGCTAGATTGCAGGAGAGGTAAGTGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGA
4	a	s	idia	pirales	raceae	ceae_Genus		AATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCCGCCATGGTAAGCCAGATG
	V	ct	Firm					TGAAAGCCCGCGGCTTAACCGCGCGGATTGCATTTGGAACATCAAGCTAGAGTACAGGAGAGGAAAGCGG
41	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTG
5	a	s	idia	pirales	raceae	ceae_UCG-		AAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCCGCCATGGTAAGCCAGATG
	V	ct	Firm					TGAAAGCCCGCGGCTTAACCGCGCGGATTGCATTTGGAACATCAAGCTAGAGTACAGGAGAGGAAAGCGG
27	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTG
7	a	s	idia	pirales	raceae	ceae_UCG-		AAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCCGCCATGGTAAGCCAGATG
	V	ct	Firm					TGAAAGCCCGCGGCTTAACCGCGCGGATTGCATTTGGAACATCAAGCTAGAGTACAGGAGAGGAAAGCGG
51	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		AATTCCTAGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGCGGCGAAGGCGGCCTGCTGGACT
1	a	s	idia	pirales	raceae	ceae_UCG-		GAAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGTGAGTAGGCCGCCATGGTAAGCCAGATG
	V	ct	Firm					TGAAAGCCTTGGGCTTAACCCGAGGATTGCATTTGGAACATCAAGCTAGAGTACAGGAGAGGAAAGCGGA
27	eri	icute	Clostr	Lachnos	Lachnospi	Tuzzerella		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGA
2	a	s	idia	pirales	raceae			AACTGACGCTGAGGCACGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGAGTAGGCCGCCAAGGTAAGCGATATG
	V	ct	Firm					TGAAAGCCTTAGGCTTAACCAAAGGATTGCATAACGAACATCTAGCTAGAGTACAGGAGAGGAAAGCGGA
08	eri	icute	Clostr	Lachnos	Lachnospi	ASF356		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGA
7	a	s	idia	pirales	raceae			AACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	Ba							TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGAGTAGGCCGCCAAGGTAAGCGATATG
	ct	Firm						TGAAAGCCTTAAGCTTAACCTAAGGATGGCATAACGAACATCTAGCTAGAGTACAGGAGAGGAAAGCGGA
S	eri	icute	Clostr	Lachnos	Lachnospi	ASF356		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTTCTGGACTGA
V	a	s	idia	pirales	raceae			AACTGACGCTGAGGCTCGAAAGCGTGGGGAGCGAACAGG

11							
1							
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCATGGTAAGCCAGAAG
V	ct						TGAAAACCCAGGGCTCAACTCTGTGGATTGCTTTTGAACTATCAAGCTAGAGTGCTGGAGGGGTAAGCGGA
12	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACAG
9	a	s	idia	pirales	raceae	ceae_Genus	AAACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCATGGTAAGCCAGAAG
V	ct						TGAAAACCCAGGGCTCAACTCTGTGGATTGCTTTTGAACTATCAAGCTAGAGTGCCGGAGGGGCAAGCGG
53	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGTCTGCTGGACA
2	a	s	idia	pirales	raceae	ceae_Genus	GCAACTGACGGTGAGGCGCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm				Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCATGGCAAGCCAGAAG
V	ct					ceae_FCS020	TGAAAACCCGGGGCTTAACCCCGCGGATTGCTTTTGAACTGTCAGGCTGGAGTGCAGGAGGGGCAGGCGG
14	eri	icute	Clostr	Lachnos	Lachnospi	_group	AATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGCCTGCTGGACT
9	a	s	idia	pirales	raceae		GTAAGTACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm				Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCAAGGCAAGCCAGAAG
V	ct					ceae_FCS020	TGAAACCCCGGGGCTTAACCCCGCGGATTGCTTTTGAACTGTCTGGCTGGAGTGCAGGAGGGGCAGGCGG
29	eri	icute	Clostr	Lachnos	Lachnospi	_group	AATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACT
9	a	s	idia	pirales	raceae		GTAAGTACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGTGCGTAGGTGGTATGGCAAGTCAGAAG
V	ct						TGAAAACCCAGGGCTTAACCTCTGGGACTGCTTTTGAACTGTCAGACTGGAGTGCAGGAGAGGTAAGCGGA
38	eri	icute	Clostr	Lachnos	Lachnospi	Anaerostipe	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACATCAGTGGCGAAGGCGGCTTACTGGACTGA
8	a	s	idia	pirales	raceae	s	AACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCAGGGCAAGTCAGATG
V	ct						TGAAAACCCGGGGCTCAACTCCGGGAGTGCAATTTGAACTGTCCAGCTAGAGTGCAGGAGAGGTAAGCGGA
04	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCATAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
3	a	s	idia	pirales	raceae	ceae_Genus	AACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGTGCGTAGGTGGCAGGGCAAGTCAGATGT
V	ct						GAAAGCCCCGGGGCTCAACCCCGGTACTGCATTTGAACTGTCCAGCTGGAGTGCAGGAGAGGTAAGCGGAA
06	eri	icute	Clostr	Lachnos	Lachnospi	Anaerostipe	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
7	a	s	idia	pirales	raceae	s	ACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGG
A							
S	Ba	Firm					TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCGTGCCAAGTCAGGAG
V	ct						TGAAAACCCAGGGCCCAACCCTGGGACTGCTCTTGAACTGGCAGGCTTGAGTGTCTGGAGAGGTAAGCGGA
16	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
5	a	s	idia	pirales	raceae	ceae_Genus	TGACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGTGGCAAGGCAAGTCAGAAG
	V	ct	Firm					TGAAACCCTCGGGCTCAACCTGAGGCATGCTTTTGAAACTGTCAAGCTGGAGTGCTGGAGAGGTAAGCGGA
28	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACAG
4	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACACTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGGGCAAGCCAGAAG
	V	ct	Firm					TGAAAACGCAGAGCTTAACTTTGCGACTGCTTTTGAAACTGCCCAGCTAGAGTACAGGAGAGGTAAGTGGA
01	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTG
9	a	s	idia	pirales	raceae	ceae_Genus		AGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTAATGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTTGCTAGATTGCAGGAGAGGTAAGTGGA
24	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
6	a	s	idia	pirales	raceae	900066575		AATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTGATGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGCAGCTCAACTGCGGGACTGCTTTTGAAACTGTATGACTAGATTGCAGGAGAGGTAAGTGGA
20	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	900066575		AAATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTTTACGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGAACTAGATTGCAGGAGAGGTAAGTGGA
10	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	900066575		AAATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGTGCAGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGAACTAGATTGCAGGAGAGGTAAGTGGA
20	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
2	a	s	idia	pirales	raceae	900066575		AAATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGGCGGCGATGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTATGGCTAGATTGCAGGAGAGGCAAGTGGA
10	eri	icute	Clostr	Lachnos	Lachnospi	GCA-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACTGT
7	a	s	idia	pirales	raceae	900066575		AAATGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGATGCAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTAAGTGGAGTGACAGGAGAGGTAAGCGGA
18	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTG
9	a	s	idia	pirales	raceae	_group		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGATGCAAGTCAGAAG
	S	eri	icute	Lachnos	Lachnospi	Lachnospira		TGAAAGCCCGGGCTCAACTCCGGGACTGCTTTTGAAACTGTGTGACTGGAGTGACAGGAGAGGTAAGCGGA
V	a	s	idia	pirales	raceae	_group		ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTG
								TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

02							
1							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCGCGGGACTGCTTTTGAAACTGTGTAGCTGGAGTGCAGGAGAGGTAAGTGG
14	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGCGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCGCGGGACTGCTTTTGAAACTGTGTAGCTAGAGTGCAGGAGAGGTAAGTGG
19	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT
9	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCGCGGGACTGCTTTTGAAACTGTGTAGCTAGAGTGCAGGAGAGGTAAGTGG
34	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT
5	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGACAAGTCAGAAG
V	ct	Firm					TGAAAACCCGCGGCTCAACTGCGGGAGTGCTTTTGAAACTGTGTGGCTGGAGTGCAGGAGAGGTAAGTGG
37	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAATGCAAGCCAGATG
V	ct	Firm					TGAAAACCCGCGAGCTCAACTGGGGGAGTGCAATTTGAAACTGTGTAGCTGGAGTGCAGGAGAGGTAAGCGGA
05	eri	icute	Clostr	Lachnos	Lachnospi	Eisenbergiell	ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTG
4	a	s	idia	pirales	raceae	a	TAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGATGCAAGCCAGATG
V	ct	Firm					TGAAAGCCCGCGGCTCAACTGCGGTAGTGCAATTTGAAACTGTATGGCTGGAGTGCAGGAGAGGCAGGCGGA
07	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACTG
5	a	s	idia	pirales	raceae	ceae_Genus	TAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGGTCAAGTCTGAAGT
V	ct	Firm					GAAAGCCCGGGGCTTAACCCCGGAACGGCTTTGAAACTGAGCAGCTAGAGTGTGAGAGGTAAGCGGA
21	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
9	a	s	idia	pirales	raceae	ceae_Genus	TAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGGTCAAGTCTGAAGT
V	ct	Firm					GAAAGCCCGGGGCTTAACCCCGGAACGGTTTTGAAACTGAGCAGCTAGAGTGTGAGAGGTAAGCGGAA
43	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGGAGGCGGCTTACTGGACAGT
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTCTGCAAGTCTGAAAGT
	V	ct	Firm					GAAAGCCCGTGGCTTAACCGCGGAACGGCTTTGGAAACTGTGGAAGTGGAGTGTCTGGAGAGGCAAGCGGAA
09	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACAGT
2	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGTGCAAGTCTGAAAGT
	V	ct	Firm					GAAAGCCCGCGGCTCAACTGCGGAACGGCTTTGGAAACTGTGTAAGTGGAGTGTCTGGAGAGGTAAGCGGAA
07	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		TTCCTGGTGTAGCGGTGAAATGCGTAGAGATCAGGAGGAACACCGGCGGCGAAGGCGGCTTACTGGACAGT
9	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGTCGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGTGGCTCAACCGCGGAACCGCTTTGGAAACTGCGAGGCTGGAGTGTCTGGAGAGGTAAGCGGA
12	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACAG
0	a	s	idia	pirales	raceae	ceae_Genus		TGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGTCGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGTGGCTCAACTGCGGAACCGCTTTGGAAACTGCGAGGCTGGAGTGTCTGGAGAGGTAAGCGGA
34	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACAG
2	a	s	idia	pirales	raceae	ceae_Genus		TGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAAGT
	V	ct	Firm					GAAAGCCCGTGGCTCAACCGCGGAAGTGTCTTTGGAAACTGTATAGCTTGAGTACTGGAGAGGCAGGCGGAA
10	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACAGA
8	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTACAAGTCTGAAAGT
	V	ct	Firm					GAAAGCCCGTGGCTCAACCGCGGAAGTGTCTTTGGAAACTGTAAAGCTGGAGTACTGGAGAGGCAGGCGGAA
11	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACAGA
8	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGTGCAAGTCTGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCCAACCCCGGAAGTGTCTGGAAGTGTGCGGCTAGAGTACTGGAGGGGCAGGCGGA
10	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACAG
5	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCAGCGCAAGTCTGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCCAACCCCGGAAGTGTCTGGAAGTGTGCGGCTAGAGTACTGGAGGGGCAGGCGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACAG
9	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGCTGCAAGTCCGGAG
	S	eri	icute	Clostr	Lachnos	Lachnospi		TGAAAGCCCATGGCTTAACCATGGTACTGCTCTGGAAGTGTGAGCTTGAGTGCAGGAGGGGCAGGCGGA
V	a	s	idia	pirales	raceae	Acetatifactor		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGGCGGCGAAGGCGGCTTGCTGGACCG
								TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

06							
2							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCCGAAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTTTGGAAACTGTGAAGCTGGAGTGCGGGAGGGGCAGGCGG
07	eri	icute	Clostr	Lachnos	Lachnospi		AATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACC
6	a	s	idia	pirales	raceae	Acetatifactor	GTAAGTACGTTGAGGCTCGAAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCCGAAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTTTGGAAACTGTGTAAGTGGAGTACAGGAGGGGCAGGCGGA
36	eri	icute	Clostr	Lachnos	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACTG
3	a	s	idia	pirales	raceae	Acetatifactor	AAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTATGTAAGTCTGGAGT
V	ct	Firm					GAAAGCCCGGGGCCCAACCCCGGGACTGCTTTGGAAACTGTGTAAGTGGAGTACAGGAGGGGCAGGCGGA
02	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACTG
6	a	s	idia	pirales	raceae	ceae_Genus	AAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTATAAGTCTGGAGT
V	ct	Firm					GAAAGCCCGGGGCCCAACCCCGGGACTGCTTTGGAAACTGTGTAAGTGGAGTACAGGAGGGGCAGGCGGA
38	eri	icute	Clostr	Lachnos	Lachnospi		TTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACTGA
4	a	s	idia	pirales	raceae	Acetatifactor	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGAGCAAGTCCGGAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTGGAAACTGTGTAAGCTGGAGTGCGGGAGGGGCAGGCGGA
09	eri	icute	Clostr	Lachnos	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
6	a	s	idia	pirales	raceae	Acetatifactor	TGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGAGCAAGTCCGGAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTGGAAACTGTGTAAGCTGGAGTACGGGAGGGGCAGGCGGA
24	eri	icute	Clostr	Lachnos	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
2	a	s	idia	pirales	raceae	Acetatifactor	TGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGCCTGGAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTGGAAACTGTGAAGCTGGAGTGCGGGAGGGGCAGGCGG
40	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	AATTCCTGGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACT
9	a	s	idia	pirales	raceae	ceae_Genus	GTAAGTACGTTGAGGCTCGAAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGCCTGGAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTGGAAACTGTGCGGCTGGAGTGCGGGAGGGGCAGGCGG
05	eri	icute	Clostr	Lachnos	Lachnospi		AATTCCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACC
6	a	s	idia	pirales	raceae	Acetatifactor	GCGACTGACGTTGAGGCTCGAAAAGCGTGCGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCGTGCAAGCCAGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTTGAACTGTGCGGCTGGAGTGCGGGAGGGGCAGGCCGA
25	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
7	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCGTGCAAGCCAGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTTGAACTGTGCGACTGGAGTGCGGGAGGGGCAGGCCGA
33	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
5	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGCCAGGGG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCCCTTGAACTGTGCGGCTAGAGTGCGGGAGGGGCAGGCCGA
23	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
5	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGCCAGGGG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCCCTTGAACTGCATGGCTGGAGTGCGGGAGGGGCAGGCCGA
10	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
2	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCAAGCAAGCCAGGGG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCCCTTGAACTGCATGGCTGGAGTGCGGGAGGGGCAGGCCGA
23	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
2	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTCACTGGGTGTAAAGGGAGCGTAGACGGCCAGGCAAGCCTGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTGGGAACTGTCCGGCTGGAGTGCGGGAGGGGCAGGCCGA
30	eri	icute	Clostr	Lachnos	Lachnospi			ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCCTGCTGGACCG
4	a	s	idia	pirales	raceae	Acetatifactor		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCGATGCAAGCCAGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTTGAACTGCGCGGCTGGAGTGCAAGAGGGGCAGGCCGA
37	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGCCTGCTGGACTG
5	a	s	idia	pirales	raceae	ceae_Genus		CGACTGACGTTGAGGCCCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCGATGCAAGCCAGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTTGAACTGCGTGGCTGGAGTGCAAGAGGGGCAGGCCGA
07	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGTGGCGAAGGCGGCCTGCTGGACTG
2	a	s	idia	pirales	raceae	ceae_Genus		CAACTGACGTTGAGGCCCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCAATGCAAGCCAGGAG
	S	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TGAAAGCCCGGGGCCCAACCCCGGGACTGCTCTTGAACTGCATGGCTGGAGTACAGGAGGGGCAGGCCGA
	V	a	s	idia	pirales	raceae	ceae_Genus	ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCCTGCTGGACTGT
								GACTGACGTTGAGGCCCGAAGGCGTGGGGAGCAAACAGG

11							
2							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTATAAAGGGGGCGCAGACGGCAATGCAAGCCAGGAG
V	ct	Firm					TGAAAGCCCGGGGCCCAACCCCGGGACTGCTTTGGAACTGCATGGCTGGAGTACAGGAGGGGCAGGCGGA
29	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTCTGGACTGT
6	a	s	idia	pirales	raceae	ceae_Genus	GACTGACGTTGAGGCCCGAAGGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGCGCAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCTTTGGAACTGTGTAGCTAGAGTGTCTGGAGAGGCAAGCGGA
17	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTGTCTGGACAG
8	a	s	idia	pirales	raceae	idium	TAACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGAGACAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCTTTGGAACTGCCTGACTGGAGTGTCTGGAGAGGCAAGCGGA
08	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTGTCTGGACAG
6	a	s	idia	pirales	raceae	ceae_Genus	TAACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGATGCAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGGGGCTCAACCCCGGGACTGCTTTGGAACTGTATGGCTGGAGTGTCTGGAGAGGCAAGCGGA
14	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTGTCTGGACAG
0	a	s	idia	pirales	raceae	idium	TAACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGAGAAAAGTCTGAAG
V	ct	Firm				Lachnospira	TGAAAGCCCGCGGCTCAACCGCGGAAGTCTTTGGAACTTTTCGGCTAGAGTACCGGAGAGGTAAGCGGA
35	eri	icute	Clostr	Lachnos	Lachnospi	ceae_UCG-	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG
8	a	s	idia	pirales	raceae	002	TAACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGAAGAAAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGCGGCTCAACCGCGGAAGTCTTTGGAACTTTTGTCTGGAGTACCGGAGAGGTAAGCGGAA
13	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT
0	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGAAGAAAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGCGGCTTAACCGCGGAAGTCTTTGGAACTTTTGTCTGGAGTACCGGAGAGGTAAGCGGAA
30	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT
3	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGAGCAAGTCTGAAG
V	ct	Firm					TGAAAGCCCGCGGCCCAACTCGGGACTGCTTTGGAACTGCCCGGCTAGAGTGTCTGGAGAGGTAAGCGGA
07	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
1	a	s	idia	pirales	raceae	ceae_Genus	TAACTGACGTTGAGGCTCGAAAAGCGTGCGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTAGAGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGGGCTCAACTGCGGGACTGCTTTGGAACTGTTCAACTGGAGTGCTGGAGAGGTAAGCGGA
22	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAG
4	a	s	idia	pirales	raceae	idium		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGGGCAAGTCTGGAG
	V	ct	Firm					TGAAAGCCCGGGGCCAACCCCGGGACTGCTTTGGAACTGCCATGCTGGAGTGCTGGAGAGGTAAGCGGA
21	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAG
8	a	s	idia	pirales	raceae	idium		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGCGGCAAGTCTGAAG
	V	ct	Firm					TGAAAGGCAGGGGCTTAACCCCTGAACTGCTTTGGAACTGCCATGCTAGAGTGCTGGAGAGGTAAGTGGGA
04	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAG
2	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGAGGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGGGGCTTAACCCCGGGACTGCTTTGGAACTGTCTGACTGGAGTGCTGGAGAGGTAAGTGGGA
16	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAG
1	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGAGGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCGGGGCTTAACCCCGGGACTGCTTTGGAACTGTCTGACTGGAGTGCTGGAGAGGTAAGTGGGA
19	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAG
4	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGCGTCAAGTCTGAAGT
	V	ct	Firm					GAAAGCCCGGGGCTTAACCCCGGGACTGCTTTGGAACTGGCGCGCTAGAGTGCTGGAGAGGTAAGTGGAA
14	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCTTACTGGACAGT
5	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAAGGCAAGTCTGATG
	V	ct	Firm					TGAAAACCCAGGGCTTAACCCCTGGGACTGCATTGGAACTGTCTGGCTCGAGTGCCGGAGAGGTAAGCGGA
39	eri	icute	Clostr	Lachnos	Lachnospi	Fusicateniba		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGCGGAAGGCGGCTTACTGGACGG
1	a	s	idia	pirales	raceae	cter		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGACAAGTCTGAAG
	V	ct	Firm					TGAAAATCCAGCGCTTAACGTTGGAAGTGCTTTGGAACTGCCGGGCTAGAGTGCCAGAGGGGCAGGCGGA
04	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGGGGAACACCAGTGCGGAAGGCGGCCTGCTGGACTG
4	a	s	idia	pirales	raceae	36_group		CAACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGACAAGTCTGAAG
	S	eri	icute	Clostr	Lachnos	Lachnospi		TGAAAATCCAGCGCTTAACGTTGGAAGTGCTTTGGAACTGCCGGGCTAGAGTGCCAGAGGGGCAGGCGGA
V	a	s	idia	pirales	raceae	36_group		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGCGGAAGGCGGCCTGCTGGACTG
								CAACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG

01							
3							
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTAGTCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCAGGGCTCAACCTTGGGACTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTAATCAAGTCAGAAG
V	ct	Firm					TGAAAACCCAGGGCTCAACCTTGGGACTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
22	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTAATCAAGTCAGAAG
V	ct	Firm					TGAAAACCCAGGGCTCAACCTTGGGACTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
15	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGGAGGATGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTAATCAAGTCAGAAG
V	ct	Firm					TGAAAACCCAGGGCTCAACCTTGGGAGTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
48	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTCTGGTCTGC
8	a	s	idia	pirales	raceae	ceae_Genus	AACTGACACTGAGGCGCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTAATCAAGTCAGAAG
V	ct	Firm					TGAAAACCCAGGGCTCAACCTTGGGAGTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
1	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTAATCAAGTCAGAAG
V	ct	Firm					TGAAAACCCAGGGCTCAACCTTGGGAGTGCTTTTGAAACTGAGTAGCTAGAGTGCAGGAGAGGTAAGCGGA
25	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
6	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGGCAAGTCAGAAG
V	ct	Firm					TGAAAGCCCAGGGCTCAACCTTGGGACTGCTTTTGAAACTGCCGGGCTGGAGTGCAGGAGAGGTAAGCGGA
27	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
6	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A							
S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCTGACAAGTCAGAAG
V	ct	Firm					TGAAAGCCCAGGGCTCAACCTTGGGACTGCTTTTGAAACTGCCGGGCTGGAGTGCAGGAGAGGTAAGCGGA
28	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	ceae_Genus	AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGACAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCAGGGCTCAACCCTGGGACTGCTTTTGAAACTGCCGGGCTGGAGTGCAGGAGAGGTAAGCGGA
06	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
3	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGACAAGTCAGAAG
	V	ct	Firm					TGAAAGCCCAGGGCTCAACTCTGGGACTGCTTTTGAAACTGCCGGGCTGGAGTGCAGGAGAGGTAAGCGGA
33	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
3	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAATACAAGTCGGAAG
	V	ct	Firm			Lachnospira		TGAAATACCCGGGCTCAACCTGGGAACTGCTTTGGAAACTGTATGGCTGGAGTGTCTGGAGAGGTAAGCGGA
09	eri	icute	Clostr	Lachnos	Lachnospi	ceae_UCG-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
5	a	s	idia	pirales	raceae	004		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAATACAAGTCGGAAG
	V	ct	Firm			Lachnospira		TGAAATACCCGGGCTTAACCTGGGAACTGCTTTGGAAACTGTATGGCTGGAGTGTCTGGAGAGGTAAGCGGA
29	eri	icute	Clostr	Lachnos	Lachnospi	ceae_UCG-		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
4	a	s	idia	pirales	raceae	004		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATAGCAAGTCTGAAG
	V	ct	Firm					TGAAAGCCCAAGGCTCAACCATGGGACTGCTTTGGAAACTGTAAAGCTAGAGTGTCTGGAGAGGTAAGCGGA
08	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGGCGGCTTACTGGACAG
5	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTATGCAAGTCTGAAGT
	V	ct	Firm			Lachnospira		GAAAGCCCCAAGGCTCAACCATGGGACTGCTTTGGAAACTGTAAAAGTGGAGTGCAGGAGAGGTAAGCGGA
31	eri	icute	Clostr	Lachnos	Lachnospi	ceae_NK4A1		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	36_group		AACTGACGTTGAGGCTCGAAGGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT
	V	ct	Firm					GAAAGCCCAGGGCTCAACCCTGGGACTGCTTTGGAAACTGTGGAGCTAGAGTGTCTGGAGAGGTAAGTGGA
34	eri	icute	Clostr	Lachnos	Lachnospi	Lachnoclostr		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACAGT
4	a	s	idia	pirales	raceae	idium		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT
	V	ct	Firm			Lachnospira		GAAATGCCGGGGCTCAACCCCGGAAGTCTTTGGAAACTGTACAGCTAGAGTGCAGGAGGGGTGAGCGGAA
05	eri	icute	Clostr	Lachnos	Lachnospi	ceae_NK4A1		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGACTGT
1	a	s	idia	pirales	raceae	36_group		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Firm						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT
	S	eri	icute	Clostr	Lachnos	Lachnospi		GAAATGCCGGGGCTCAACCCCGGAAGTCTTTGGAAACTGTACAGCTAGAGTGCAGGAGGGGTGAGCGGAA
V	a	s	idia	pirales	raceae	ceae_NK4A1		TTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGTGGCGAAGGCGGCTCACTGGACTGT
						36_group		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

04								
9								
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
02	eri	a	idia	pirales	raceae	ceae_NK4A1		
3	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGT GAAATGCCGGGGCCCAACCCCGGAAGTCTTTGGAAACTGTACAGCTAGAGTGCAGGAGGGGTGAGCGGAA TTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTCACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
02	eri	a	idia	pirales	raceae	ceae_NK4A1		
0	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATCCCATGGCTTAACCATGGAAGTCTTTGGAAACTGTGCAGCTAGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
01	eri	a	idia	pirales	raceae	ceae_NK4A1		
6	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATCCCATGGCTTAACCATGGAAGTCTTTGGAAACTGTGCAGCTGGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
12	eri	a	idia	pirales	raceae	ceae_NK4A1		
2	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATGCCGGGGCCCAACCCCGGAAGTCTTTGGAAACTGTGCAGCTCGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
34	eri	a	idia	pirales	raceae	ceae_NK4A1		
9	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATGCCGGGGCCCAACCCCGGAAGTCTTTGGAAACTGTGCAGCTCGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
28	eri	a	idia	pirales	raceae	ceae_NK4A1		
5	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATGCCGGGGCCCAACCCCGGAAGTCTTTGGAAACTGTGCGGCTCGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACCG TAACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
26	eri	a	idia	pirales	raceae	ceae_NK4A1		
5	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGTCTGGAG TGAAATGCCGGGGCTCAACCCCGGAAGTCTTTGGAAACTGTGCAGCTCGAGTGCAGGAGAGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTGT AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
A								
S	Ba	Firm						
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospi		
03	eri	a	idia	pirales	raceae	ceae_NK4A1		
2	a	s				36_group		TACGTAGGGGGCAAGCGTTATCCGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCAGGCAAGTCTGGAG TGAAAGCCCGGGGCTCAACCCCGGGAAGTCTTTGGAAACTGTAGGGCTGGAGTGCAGGAGGGGTAAGCGGA ATTCCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTTACTGGACTG CAACTGACGTTGAGGCTCGAAGGCGTGCGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGCAGACGGCTGTGCAAGTCTGGAG
	V	ct	Firm					TGAAAGGCGGGGGCCCAACCCCGGACTGCTCTGGAAGTGTAAAGCTGGAGTGCAGGAGAGGTAAAGCGG
04	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACT
0	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	GCAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGTGATGTAAGTCTGGAG
	V	ct	Firm					TGAAAGGCGGGGGCCCAACCCCGGACTGCTCTGGAAGTATGTGACTGGAGTGCAGGAGAGGTGAGCGGA
42	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTCACTGGACTG
6	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGCGCAAGTCTGGAGT
	V	ct	Firm					GAAAGGCGGGGGCCCAACCCCGGACTGCTCTGGAAGTGTGTAAGTGGAGTGCAGGAGAGGTAAGTGGAA
16	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
6	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	AAGTACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGCGCAAGTCTGGAGT
	V	ct	Firm					GAAAGGCGGGGGCTCAACCCCGGACTGCTCTGGAAGTGTGTAAGTGGAGTGCAGGAGAGGTAAGTGGAA
17	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
1	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGCGCAAGTCTGGAGT
	V	ct	Firm					GAAAGGCGGGGGCTCACCCCGGACTGCTCTGGAAGTGTGTAAGTGGAGTGCAGGAGAGGTAAGTGGAA
38	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
9	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTGTGCAAGTCTGGAGT
	V	ct	Firm					GAAAGGCGGGGGCCCAACCCCGGACTGCTTTGGAAGTGTATAACTGGAGTGCAGGAGAGGTAAGTGGAA
10	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
3	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTACGCAAGTCTGAAGT
	V	ct	Firm					GAAAGGCGGGGGCCCAACCCCGGACTGCTTTGGAAGTGTGAAAGTGGAGTGCAGGAGAGGTAAGTGGAA
18	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	AAGTACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTACGCAAGTCTGGAGT
	V	ct	Firm					GAAAGGCGGGGGCCCAACCCCGGACTGCTTTGGAAGTGTGAAAGTGGAGTGCAGGAGAGGTAAGTGGAA
22	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospira		ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
8	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	AAGTACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	ct	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTACGCAAGTCTGGAGT
	S	eri	Firm					GAAAGGCGGGGGCCCAACCCCGGACTGCTTTGGAAGTGTATAACTGGAGTGCAGGAGAGGTAAGTGGAA
V	a	s	Clostr	Lachnos	Lachnospi	Lachnospira		TTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGTA
			idia	pirales	raceae	ceae_NK4A1	36_group	ACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

13							
5							
A							
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGATGCAAGTCTGAAG
02	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTTTGGGAACTGTATGGCTGGAGTGCAGGAGAGGTAAGTGG
9	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGAATCACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGCCTGAAG
16	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTTTGGGAACTGTACGGCTGGAGTGCAGGAGAGGTAAGTGG
9	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGAATCACTGGGTGTAAAGGGAGCGTAGACGGCTGAGCAAGCCTGAAG
15	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTTTGGGAACTGTACGGCTGGAGTGCAGGAGAGGTAAGTGG
4	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGAATCACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGCCTGAAG
19	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTTTGGGAACTGTACGGCTGGAGTGCAGGAGAGGTAAGTGG
5	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGAATCACTGGGTGTAAAGGGAGCGTAGACGGCTGAGCAAGCCTGAAG
09	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTTTGGGAACTGTACGGCTGGAGTGCAGGAGAGGTAAGTGG
4	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGGAG
01	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCGGGGGCCCCAACCCCGGACTGCTCTGGGAACTGTATGGCTGGAGTGCAGGAGAGGTAAGCGGA
7	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
A							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGGGGCAAGTCTGGAG
13	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCCGGGGCCCCAACCCCGGGACCGCTCTGGGAACTGCCCGGCTGGAGTGCGGGAGAGGTAAGCGG
1	a					36_group	AATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGCGGCGAAGGCGGCTTACTGGACC
A							GTGACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG
S	Ba	Firm					
V	ct	icute	Clostr	Lachnos	Lachnospi	Lachnospira	TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGAGACAAGTCTGGAG
26	eri	s	idia	pirales	raceae	ceae_NK4A1	TGAAAGGCCGGGGCCCCAACCCCGGGACTGCTCTGGGAACTGCCTGGCTGGAGTACAGGAGAGGTAAGTGG
1	a					36_group	ATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
							AACTGACGTTGAGGCTCGAAAGCGTGCGGGAGCAAACAGG

A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGGGCAAGTCTGGAG
	V	ct	Firm					TGAAAGGCGGGGCTCAACCCCGGACTGCTCTGGAACTGCCAGGCTGGAGTGCAGGAGAGGTAAGTGGA
14	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
1	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGGGCAAGTCTGGAG
	V	ct	Firm					TGAAAGGCGGGGCCCCAACCCCTGGACTGCTCTGGAACTGTCCGGCTGGAGTGCAGGAGAGGTAAGTGGA
03	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
0	a	s	idia	pirales	raceae	ceae_NK4A1	36_group	AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGCGAGGTAAGCCTGAAG
	V	ct	Firm					TGGAAGCCCGCGGCCAACCGCGGAAGTCTTTGGGAACTGTTTGTCTGGAGTATGGGAGGGGTAAGCGGA
18	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACCA
3	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGCGTAGACGGCAATGCAAGTCCGGAG
	V	ct	Firm					TGGAATGCGGCAGCTCAACTGCCGAAGTCTCTGGAACTGTATGGCTTGAGTGCAGGAGGGGTAAGCGGA
26	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACTGT
7	a	s	idia	pirales	raceae	ceae_Genus		AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCAGCGCAAGCCTGGAG
	V	ct	Firm					TGAAAGGATGGGGCCCCAACCCCATGACTGCTCTGGGAACTGTGCGGCTAGAGTGCCGGAGGGGTAAGCGGA
17	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG
0	a	s	idia	pirales	raceae	ceae_Genus		TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCCATGCAAGCTCGGTGT
	V	ct	Firm					GAAAGGTGCGGGCACAACCCGCAGACTGCACTGAGAACTGTATGGCTGGAGTGCCGGAGGGGCAGGCGGA
08	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		ATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGACGG
9	a	s	idia	pirales	raceae	ceae_Genus		CGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCCATGGCAAGCCCGGT
	V	ct	Firm					GTGAAAGGCAGGGGCATAACCCCTGGACTGCACTGGGAACTGTCAGGCTGGAGTGCCGGAGGGGTAAGCG
05	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		GAATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCGGCGGCGAAGGCGGCTTACTGGAC
0	a	s	idia	pirales	raceae	ceae_Genus		GGCAACTGACGTTGAGGCCCGAAAGCGTGGGGAGCGAACAGG
A	S	Ba						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCCATGGCAAGCCCGGT
	V	ct	Firm					GTGAAAGGTGCGGGCACAACCCGCAGACTGCACTGGTAAGTGCCTGGCTGGAGTGCCGGAGGGGTAAGCGG
17	eri	icute	Clostr	Lachnos	Lachnospi	Lachnospi		AATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACG
7	a	s	idia	pirales	raceae	ceae_Genus		GCAACTGACGTTGAGGCCCGAAAGCGTGGGGAGCGAACAGG
A	ct	Firm						TACGTAGGGGGCGAGCGTTATCCGGATTTACTGGGTGTAAAGGGGGCGCAGACGGCCATGGCAAGCCCGGT
	S	eri	icute	Clostr	Lachnos	Lachnospi		GTGAAAGGTGCGGGCACAACCCGCAGACTGCACTGGTAAGTGTCTGGCTGGAGTGCCGGAGGGGTAAGCGG
V	a	s	idia	pirales	raceae	ceae_Genus		AATTCTGGTGTAGCGGTGAAATGCGTAGATATCAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACG
								GCAACTGACGTTGAGGCCCGAAAGCGTGGGGAGCGAACAGG

Table S2. PQ metadata.

Mous eID	Sex	Genot ype	Treat ment	SeqI D	Barcode	Time point	FC.train_basel ine_motion	FC.train_fr z_tone1	FC.train_fr z_tone2	FC.context_t otalfrzing	GS.S core	OF1.T otDist	OF2.T otDist	OF3.T otDist	YM.Pct.S pon.Alt
m01	m01	M	A53T- L444P	P	T3-1	CTATATTA TCCG	t3	121.75	26.78	75.22	93.36	2.1	-	1117.93532.314	57.1429
m02	m02	M	A53T	S	T3-2	CAAACGTG CGTTG	t3	139.75	13.78	64.56	73.98	1.7	-	202.998215.412	80
m03	m03	M	A53T- L444P	S	T3-3	CTGACAC GAAT A	t3	140.5	10.67	46	82.44	1.3	-	349.655 399.71	50
m04	m04	M	A53T- L444P	P	T3-4	AGCAGTG CGGTG	t3	180.47	0	33.67	66.13	1	-	1108.7 933.338	55
m05	m05	M	A53T	P	T3-5	GTTGGAC GAAGG	t3	67.28	38.44	44.33	80.41	1	852.929960.736563.017		50
m06	m06	M	A53T	S	T3-6	CAGGAAC CAGGA	t3	163.99	0	43.67	88.58	1.7	1504.351109.91739.297	61.5385	
m07	m07	M	A53T	P	T3-7	CAAAGGA GCCCCG	t3	199.31	0	10.78	65.59	0.6	1156.42 980.74 812.412	56.5217	
m08	m08	M	A53T- L444P	S	T3-8	GAATCTG ACAAC	t3	240.31	0	43.44	65.28	1	1602.871089.14782.335	47.8261	
m09	m09	M	A53T- L444P	P	T3-9	CTCATCA TGTTT	t3	69.92	40.22	92.22	91.2	0.9	1241.981151.33789.642	50	
m10	m10	M	A53T	S	T3-10	TTATCCA GTCCT	t3	189.71	0	45.78	86.8	1	1733.361351.121489.86	65	
m11	m11	M	A53T- L444P	S	T3-11	GAGTCTT GGTAA	t3	189.62	0	64.11	62.99	1	1067.79 677.85 941.056	54.5455	
m12	m12	M	A53T- L444P	P	T3-12	CATTTAC ATCAC	t3	155.47	32.33	49.67	96.07	1.1	1013.65813.405608.691	72.2222	
m13	m13	M	A53T	S	T3-13	TTCTTAAC GCCT	t3	114.08	18.22	89.67	57.1	0.9	2270.812133.111034.78	46.6667	
m14	m14	M	A53T	P	T3-14	AGTAGTT TCCTT	t3	185.89	3.67	42	60.77	1.2	905.01 630.722589.561	35.7143	
m15	m15	M	A53T- L444P	S	T3-15	GACCCGT TTCGC	t3	174.97	23.56	33.44	79.31	1	938.8441542.261238.26	75	
m16	m16	M	A53T- L444P	P	T3-16	ATTGCCTT GATT	t3	43.08	41.33	59.89	85.52	1.1	331.979284.807285.339	50	
m17	m17	M	A53T- L444P	S	T3-17	TTAGGAT TCTAT	t3	183.22	4.78	27.56	69.74	1	2838.361959.58 1482.3	50	
m18	m18	M	A53T	P	T3-18	GTTTATCT TAAG	t3	105.87	0	0	12.82	1	1844.261626.561302.19	41.6667	

m19	m19	M	A53T	P	T3-19	CAGTCTA GTACG	t3	87.16	70.11	93.56	67.43	0.8	1443.081039.73763.291	36.3636
m20	m20	M	A53T- L444P	P	T3-20	GTGGGAC TGCGC	t3	174.71	0	11	71.89	0.9	1806.961674.511503.08	58.8235
m21	m21	M	A53T- L444P	S	T3-21	CTCCCGA GCTCC	t3	101.12	41.89	33.78	92.38	0.8	1789.061732.73902.119	59.0909
m22	m22	F	A53T- L444P	P	T3-22	CAGATCC CAACC	t3	79.44	85.67	67.33	-	0.9	1039.29608.882340.988	69.2308
m23	m23	F	A53T	P	T3-23	TGACTGC GTTAG	t3	148.06	13.89	65.11	-	0.9	955.228899.387232.513	50
m24	m24	F	A53T	S	T3-24	GAGCCCA AAGAG	t3	137.45	0	36.22	-	1	1540.7 996.2561133.99	64.5161
m25	m25	F	A53T- L444P	S	T3-25	CAACGAA CCATC	t3	131.04	31.33	42.78	-	0.9	1002.37842.106722.568	56.25
m26	m26	F	A53T- L444P	P	T3-26	GTTCGCC GCATC	t3	NA	NA	NA		NA	NA NA NA	NA
m27	m27	F	A53T	P	T3-27	GTTCGAG TGAAT	t3	244.95	0	6.67	43.81	0.7	2647.242022.931655.36	51.7241
m28	m28	F	A53T	S	T3-28	CGGCCTA AGTTC	t3	163.57	0	19.44	25.3	0.9	1442.621094.92424.456	58.8235
m29	m29	F	A53T- L444P	S	T3-29	TAGACTT CAGAG	t3	270.83	0	63.44	70.76	0.8	1676.791012.16 878.96	39.1304
m30	m30	F	A53T- L444P	S	T3-30	GATAGCA CTCGT	t3	76.57	12.89	93.44	98.66	0.7	711.639454.562272.101	14.2857
m31	m31	F	A53T	P	T3-31	ACGTTAA TATTC	t3	186.25	0	21.33	79.8	1.1	815.788579.348377.979	66.6667
m32	m32	F	A53T	S	T3-32	CCATGTG GCTCC	t3	178.32	0	54.78	48.44	0.7	1883.721835.541900.51	75
m33	m33	F	A53T- L444P	P	T3-33	ACACGTT TGGGT	t3	224.41	0	9.44	64.79	0.7	2064.45 1927 1213.36	66.6667
m34	m34	F	A53T	P	T3-34	AGACTAT TTCAT	t3	112.39	13.11	57.56	78.23	1	1027.68643.202630.387	52.381
m35	m35	F	A53T	S	T3-35	AGTCCGA GTTGT	t3	194.07	0	52.22	59.49	0.9	1490.911165.871066.95	58.8235
m36	m36	F	A53T	P	T3-36	GCTGAGC CTTIG	t3	251.28	0	55.78	64.69	1.2	1071.27 958.29 914.974	52.1739

Table S3. DSS taxon.

	Kin gdo m	Phylum	Class	Order	Family	Genus
raber- 2020- dss_ ASV0 01	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 02	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 03	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Turicibacter
raber- 2020- dss_ ASV0 04	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV0 05	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV0 06	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 07	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p

raber- 2020- dss_ ASV0 08	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	A2
raber- 2020- dss_ ASV0 09	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 10	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 11	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 12	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV0 13	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _FCS020_group
raber- 2020- dss_ ASV0 14	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 15	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p

raber- 2020- dss_ ASV0 16	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 17	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV0 18	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 19	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 20	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 21	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV0 22	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 23	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia

raber- 2020- dss_	ASV0 24	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raber- 2020- dss_	ASV0 25	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_	ASV0 26	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_	ASV0 27	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_	ASV0 28	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raber- 2020- dss_	ASV0 29	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_	ASV0 30	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_	ASV0 31	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia

raher- 2020- dss_ ASV0 32	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV0 33	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV0 34	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV0 35	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 36	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Faecalibaculum
raher- 2020- dss_ ASV0 37	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV0 38	Bact eria	Firmicu tes	Bacilli	Staphylococca les	Staphylococcac eae	Staphylococcus
raher- 2020- dss_ ASV0 39	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia

raber- 2020- dss_ ASV0 40	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 41	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 42	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Marinifilaceae	Odoribacter
raber- 2020- dss_ ASV0 43	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes
raber- 2020- dss_ ASV0 44	Bact eria	Firmicu tes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sen su_stricto_1
raber- 2020- dss_ ASV0 45	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes
raber- 2020- dss_ ASV0 46	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	A2
raber- 2020- dss_ ASV0 47	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes

raber- 2020- dss_ ASV0 48	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Marvinbryantia
raber- 2020- dss_ ASV0 49	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV0 50	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4B4_group
raber- 2020- dss_ ASV0 51	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Butyricicoccace ae	Butyricicoccus
raber- 2020- dss_ ASV0 52	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV0 53	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV0 54	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001
raber- 2020- dss_ ASV0 55	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raher- 2020- dss_ ASV0 56	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raher- 2020- dss_ ASV0 57	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raher- 2020- dss_ ASV0 58	Bact eria	Firmicu tes	Clostridia	Clostridia_vad inBB60_grou p	NA	NA
raher- 2020- dss_ ASV0 59	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Bacteroidaceae	Bacteroides
raher- 2020- dss_ ASV0 60	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiraceae	Oscillibacter
raher- 2020- dss_ ASV0 61	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Dubosiella
raher- 2020- dss_ ASV0 62	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV0 63	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculaceae	NA

raher- 2020- dss_ ASV0 65	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raher- 2020- dss_ ASV0 66	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	NA	NA
raher- 2020- dss_ ASV0 67	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV0 68	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiraceae	NA
raher- 2020- dss_ ASV0 69	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raher- 2020- dss_ ASV0 70	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Roseburia
raher- 2020- dss_ ASV0 71	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raher- 2020- dss_ ASV0 72	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes

raher- 2020- dss_ ASV0 73	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV0 74	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raher- 2020- dss_ ASV0 75	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 76	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raher- 2020- dss_ ASV0 77	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raher- 2020- dss_ ASV0 78	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 79	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raher- 2020- dss_ ASV0 80	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raher- 2020- dss_ ASV0 81	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV0 82	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 83	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV0 84	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 85	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 86	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV0 87	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV0 88	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter

raher- 2020- dss_ ASV0 89	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV0 90	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Prevotellaceae	Prevotellaceae_ UCG-001
raher- 2020- dss_ ASV0 91	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raher- 2020- dss_ ASV0 92	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV0 93	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	GCA-900066575
raher- 2020- dss_ ASV0 94	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raher- 2020- dss_ ASV0 95	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	ASF356
raher- 2020- dss_ ASV0 96	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV0 97	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV0 98	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	Muribaculum
raber- 2020- dss_ ASV0 99	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV1 00	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV1 01	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 02	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raber- 2020- dss_ ASV1 03	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 04	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor

raber- 2020- dss_ ASV1 05	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 06	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raber- 2020- dss_ ASV1 07	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 08	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 09	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Butyricicoccace ae	Butyricicoccus
raber- 2020- dss_ ASV1 10	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV1 11	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raber- 2020- dss_ ASV1 12	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raher- 2020- dss_ ASV1 13	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV1 14	Bact eria	Firmicu tes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sen su_stricto_1
raher- 2020- dss_ ASV1 15	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV1 16	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raher- 2020- dss_ ASV1 17	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raher- 2020- dss_ ASV1 18	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV1 19	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV1 20	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	ASF356

raber- 2020- dss_ ASV1 21	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Marvinbryantia
raber- 2020- dss_ ASV1 22	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 23	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 24	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 25	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Butyricicoccace ae	UCG-009
raber- 2020- dss_ ASV1 26	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raber- 2020- dss_ ASV1 27	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 28	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV1 29	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Turicibacter
raber- 2020- dss_ ASV1 30	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV1 31	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raber- 2020- dss_ ASV1 32	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Anaerotruncus
raber- 2020- dss_ ASV1 33	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 34	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 35	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 36	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA

raber- 2020- dss_ ASV1 37	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _FCS020_group
raber- 2020- dss_ ASV1 38	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV1 39	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 40	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 41	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 42	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 43	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV1 44	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Prevotellaceae	Alloprevotella

raber- 2020- dss_ ASV1 45	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001
raber- 2020- dss_ ASV1 46	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001
raber- 2020- dss_ ASV1 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	GCA-900066575
raber- 2020- dss_ ASV1 48	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Intestinimonas
raber- 2020- dss_ ASV1 49	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raber- 2020- dss_ ASV1 50	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 51	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Bacteroidaceae	Bacteroides
raber- 2020- dss_ ASV1 52	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Eisenbergiella

raher- 2020- dss_ ASV1 53	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV1 54	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-006
raher- 2020- dss_ ASV1 55	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raher- 2020- dss_ ASV1 56	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV1 57	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV1 58	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV1 59	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV1 60	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Butyricicoccace ae	Butyricicoccus

raher- 2020- dss_	ASV1 61	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_	ASV1 62	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raher- 2020- dss_	ASV1 63	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_	ASV1 64	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-004
raher- 2020- dss_	ASV1 65	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Bacteroidaceae	Bacteroides
raher- 2020- dss_	ASV1 66	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_	ASV1 67	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Anaerotruncus
raher- 2020- dss_	ASV1 68	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia

raber-2020-dss_	ASV1	Bacteria	Firmicutes	Bacilli	RF39	NA	NA
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillibacter
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-006
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	NA
raber-2020-dss_	ASV1	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	NA

raher- 2020- dss_ ASV1 77	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV1 78	Bact eria	Firmicu tes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sen su_stricto_1
raher- 2020- dss_ ASV1 79	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV1 80	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV1 81	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV1 82	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV1 83	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV1 84	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m

raber- 2020- dss_ ASV1 85	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV1 86	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	GCA-900066575
raber- 2020- dss_ ASV1 87	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV1 88	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelatoclos tridiaceae	NA
raber- 2020- dss_ ASV1 89	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Anaerostipes
raber- 2020- dss_ ASV1 90	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV1 91	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV1 92	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV1 93	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Dorea
raber- 2020- dss_ ASV1 94	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raber- 2020- dss_ ASV1 95	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV1 96	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	NA
raber- 2020- dss_ ASV1 97	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Marvinbryantia
raber- 2020- dss_ ASV1 98	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	A2
raber- 2020- dss_ ASV1 99	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV2 00	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-006

raber- 2020- dss_ ASV2 01	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raber- 2020- dss_ ASV2 02	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Rikenella
raber- 2020- dss_ ASV2 03	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 04	Bact eria	Proteob acteria	Gammapr oteobacteri a	Burkholderial es	Sutterellaceae	Parasutterella
raber- 2020- dss_ ASV2 05	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 06	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 07	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 08	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter

raber- 2020- dss_ ASV2 09	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 10	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV2 11	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Butyricicoccace ae	Butyricicoccus
raber- 2020- dss_ ASV2 13	Bact eria	Desulfo bacterot a	Desulfovib rionia	Desulfovibrio nales	Desulfovibrion aceae	Bilophila
raber- 2020- dss_ ASV2 14	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 15	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV2 16	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV2 17	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA

raber-2020-dss_ASV2_18	Bacteria	Firmicutes	Bacilli	Staphylococcales	Staphylococcaceae	Staphylococcus
raber-2020-dss_ASV2_19	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_ASV2_20	Bacteria	Firmicutes	Bacilli	Acholeplasmatales	Acholeplasmataceae	Anaeroplasma
raber-2020-dss_ASV2_21	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Roseburia
raber-2020-dss_ASV2_22	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium_sensu_stricto_1
raber-2020-dss_ASV2_23	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	GCA-900066575
raber-2020-dss_ASV2_24	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_ASV2_25	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Acetatifactor

raher- 2020- dss_ ASV2 26	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raher- 2020- dss_ ASV2 27	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV2 28	Bact eria	Firmicu tes	Clostridia	Peptostreptoc occales- Tissierellales	Anaerovoracac eae	NA
raher- 2020- dss_ ASV2 29	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raher- 2020- dss_ ASV2 30	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	UCG-003
raher- 2020- dss_ ASV2 31	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV2 32	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV2 33	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001

raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_NK4A136_group
raber-2020-dss_	ASV2	Bacteria	Cyanobacteria	Vampirivibrionia	Gastranaerophilales	NA	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_NK4A136_group
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Clostridia_UCG-014	NA	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_	ASV2	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Muribaculaceae	NA
raber-2020-dss_	ASV2	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Muribaculaceae	NA

raher- 2020- dss_ ASV2 42	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	Adlercreutzia
raher- 2020- dss_ ASV2 43	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV2 44	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV2 45	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Faecalibaculum
raher- 2020- dss_ ASV2 46	Bact eria	Cyanob acteria	Vampirivi brionia	Gastranaerop hilales	NA	NA
raher- 2020- dss_ ASV2 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raher- 2020- dss_ ASV2 48	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Rikenella
raher- 2020- dss_ ASV2 49	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter

raber- 2020- dss_ ASV2 50	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV2 51	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raber- 2020- dss_ ASV2 52	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	Enterorhabdus
raber- 2020- dss_ ASV2 53	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV2 54	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV2 55	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV2 56	Bact eria	Firmicu tes	Clostridia	Peptostreptoc occales- Tissierellales	Anaerovoracac eae	NA
raber- 2020- dss_ ASV2 57	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p

raber- 2020- dss_ ASV2 58	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV2 59	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV2 60	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV2 61	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Paludicola
raber- 2020- dss_ ASV2 63	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Intestinimonas
raber- 2020- dss_ ASV2 64	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV2 65	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV2 66	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raher- 2020- dss_ ASV2 67	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV2 68	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	UC5-1-2E3
raher- 2020- dss_ ASV2 69	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV2 70	Bact eria	Proteob acteria	Gammapr oteobacteri a	Burkholderial es	Sutterellaceae	Parasutterella
raher- 2020- dss_ ASV2 71	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV2 72	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-010
raher- 2020- dss_ ASV2 73	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raher- 2020- dss_ ASV2 74	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber- 2020- dss_ ASV2 75	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV2 76	Bact eria	Firmicu tes	Bacilli	Staphylococca les	Staphylococcac eae	Jeotgalicoccus
raber- 2020- dss_ ASV2 77	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Dubosiella
raber- 2020- dss_ ASV2 78	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV2 80	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV2 81	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809
raber- 2020- dss_ ASV2 82	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV2 83	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p

raher- 2020- dss_ ASV2 84	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Anaerotruncus
raher- 2020- dss_ ASV2 85	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Marvinbryantia
raher- 2020- dss_ ASV2 86	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NK4A214_group
raher- 2020- dss_ ASV2 87	Bact eria	Firmicu tes	Clostridia	Peptococcales	Peptococcaceae	NA
raher- 2020- dss_ ASV2 89	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV2 90	Bact eria	Firmicu tes	Clostridia	Peptostreptococcales- Tissierellales	Anaerovoracaceae	Family_XIII_AD 3011_group
raher- 2020- dss_ ASV2 91	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raher- 2020- dss_ ASV2 92	Bact eria	Firmicu tes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus

raber-2020-dss_	ASV2	Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnoclostridium
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Colidextribacter
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Bacilli	RF39	NA	NA
raber-2020-dss_	ASV2	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	GCA-900066575
raber-2020-dss_	ASV3	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnoclostridium
raber-2020-dss_	ASV3	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Marvinbryantia

raber- 2020- dss_ ASV3 02	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	NA
raber- 2020- dss_ ASV3 03	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV3 04	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raber- 2020- dss_ ASV3 05	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV3 06	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes
raber- 2020- dss_ ASV3 07	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Marinifilaceae	Odoribacter
raber- 2020- dss_ ASV3 08	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV3 09	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber-2020-dss_ASV3 10	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Marinifilaceae	Odoribacter
raber-2020-dss_ASV3 11	Bacteria	Firmicutes	Clostridia	Oscillospirales	Ruminococcaceae	Incertae_Sedis
raber-2020-dss_ASV3 12	Bacteria	Firmicutes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raber-2020-dss_ASV3 13	Bacteria	Firmicutes	Clostridia	NA	NA	NA
raber-2020-dss_ASV3 15	Bacteria	Bacteroidota	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides
raber-2020-dss_ASV3 16	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_ASV3 17	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_NK4A136_group
raber-2020-dss_ASV3 18	Bacteria	Firmicutes	Clostridia	Clostridia_UCG-014	NA	NA

raber- 2020- dss_ ASV3 19	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV3 20	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV3 21	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV3 22	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV3 23	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV3 24	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-006
raber- 2020- dss_ ASV3 25	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV3 26	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Enterococcacea e	Enterococcus

raher- 2020- dss_ ASV3 27	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	GCA-900066575
raher- 2020- dss_ ASV3 28	Bact eria	Firmicu tes	Clostridia	Clostridia_v adinBB60_grou p	NA	NA
raher- 2020- dss_ ASV3 29	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV3 30	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV3 31	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-004
raher- 2020- dss_ ASV3 32	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raher- 2020- dss_ ASV3 33	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV3 34	Bact eria	Firmicu tes	Clostridia	Clostridia_v adinBB60_grou p	NA	NA

raher- 2020- dss_ ASV3 35	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV3 36	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV3 37	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV3 38	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV3 39	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-006
raher- 2020- dss_ ASV3 40	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raher- 2020- dss_ ASV3 41	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV3 42	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raiber- 2020- dss_ ASV3 43	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raiber- 2020- dss_ ASV3 44	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raiber- 2020- dss_ ASV3 45	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raiber- 2020- dss_ ASV3 46	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Rikenella
raiber- 2020- dss_ ASV3 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raiber- 2020- dss_ ASV3 48	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raiber- 2020- dss_ ASV3 49	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raiber- 2020- dss_ ASV3 50	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA

raber- 2020- dss_ ASV3 51	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV3 52	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	A2
raber- 2020- dss_ ASV3 53	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Breznakia
raber- 2020- dss_ ASV3 54	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV3 55	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	NA
raber- 2020- dss_ ASV3 56	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes
raber- 2020- dss_ ASV3 57	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	NA
raber- 2020- dss_ ASV3 58	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raher- 2020- dss_ ASV3 59	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV3 60	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raher- 2020- dss_ ASV3 61	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raher- 2020- dss_ ASV3 62	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV3 63	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV3 64	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raher- 2020- dss_ ASV3 65	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raher- 2020- dss_ ASV3 66	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA

raber- 2020- dss_ ASV3 67	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV3 68	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raber- 2020- dss_ ASV3 69	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV3 70	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raber- 2020- dss_ ASV3 71	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV3 72	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raber- 2020- dss_ ASV3 73	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raber- 2020- dss_ ASV3 74	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV3 75	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raber- 2020- dss_ ASV3 76	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV3 77	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV3 78	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV3 79	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raber- 2020- dss_ ASV3 80	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV3 81	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV3 82	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p

raher- 2020- dss_ ASV3 83	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raher- 2020- dss_ ASV3 84	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	NA
raher- 2020- dss_ ASV3 85	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV3 86	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raher- 2020- dss_ ASV3 87	Bact eria	Firmicu tes	Clostridia	Peptostreptoc occales- Tissierellales	Anaerovoracac eae	Family_XIII_UC G-001
raher- 2020- dss_ ASV3 88	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV3 89	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NK4A214_group
raher- 2020- dss_ ASV3 90	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA

raher- 2020- dss_ ASV3 91	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV3 93	Bact eria	Firmicu tes	Clostridia	Peptococcales	Peptococcaceae	NA
raher- 2020- dss_ ASV3 94	Bact eria	Actinob acteriot a	Actinobact eria	Bifidobacteria les	Bifidobacteriac eae	Bifidobacterium
raher- 2020- dss_ ASV3 95	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV3 96	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV3 97	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Tuzzerella
raher- 2020- dss_ ASV3 98	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV3 99	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA

raber- 2020- dss_ ASV4 00	Bact eria	Firmicu tes	Clostridia	Clostridia_vad inBB60_grou p	NA	NA
raber- 2020- dss_ ASV4 01	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001
raber- 2020- dss_ ASV4 02	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV4 03	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV4 04	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	GCA-900066575
raber- 2020- dss_ ASV4 05	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	UCG-005
raber- 2020- dss_ ASV4 06	Bact eria	Cyanob acteria	Vampirivi brionia	Gastranaerop hilales	NA	NA
raber- 2020- dss_ ASV4 07	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor

raber- 2020- dss_ ASV4 08	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV4 09	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnospiraceae _NK4A136_group
raber- 2020- dss_ ASV4 10	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV4 11	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnoclostridium
raber- 2020- dss_ ASV4 12	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculaceae	NA
raber- 2020- dss_ ASV4 13	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Negativibacillus
raber- 2020- dss_ ASV4 14	Bact eria	Proteob acteria	Gammapr oteobacteri a	Burkholderial es	Sutterellaceae	Parasutterella
raber- 2020- dss_ ASV4 16	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA

raher- 2020- dss_ ASV4 17	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV4 18	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	Enterorhabdus
raher- 2020- dss_ ASV4 19	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV4 20	Bact eria	Firmicu tes	NA	NA	NA	NA
raher- 2020- dss_ ASV4 21	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-001
raher- 2020- dss_ ASV4 25	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV4 26	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _FCS020_group
raher- 2020- dss_ ASV4 27	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA

raber- 2020- dss_ ASV4 29	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 30	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 31	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV4 32	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 33	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809
raber- 2020- dss_ ASV4 34	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 35	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raber- 2020- dss_ ASV4 36	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809

raher- 2020- dss_ ASV4 37	Bact eria	Firmicu tes	Clostridia	Peptostreptococcales- Tissierellales	Anaerovoracaceae	Family_XIII_AD 3011_group
raher- 2020- dss_ ASV4 38	Bact eria	Firmicu tes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raher- 2020- dss_ ASV4 39	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raher- 2020- dss_ ASV4 40	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	Acetatifactor
raher- 2020- dss_ ASV4 41	Bact eria	Firmicu tes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raher- 2020- dss_ ASV4 42	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raher- 2020- dss_ ASV4 43	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raher- 2020- dss_ ASV4 44	Bact eria	Firmicu tes	Clostridia	Oscillospirales	Ruminococcaceae	Incertae_Sedis

raber- 2020- dss_ ASV4 45	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV4 46	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV4 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _NK4A136_grou p
raber- 2020- dss_ ASV4 48	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 49	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV4 51	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV4 52	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV4 53	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raher- 2020- dss_ ASV4 54	Bact eria	Firmicu tes	Clostridia	Peptostreptococcales- Tissierellales	Anaerovoracaceae	Family_XIII_UC G-001
raher- 2020- dss_ ASV4 55	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnoclostridium
raher- 2020- dss_ ASV4 56	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	Acetatifactor
raher- 2020- dss_ ASV4 57	Bact eria	Bacteroidota	Bacteroidia	Bacteroidales	Muribaculaceae	NA
raher- 2020- dss_ ASV4 58	Bact eria	Firmicu tes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raher- 2020- dss_ ASV4 59	Bact eria	Firmicu tes	Clostridia	Oscillospirales	Ruminococcaceae	NA
raher- 2020- dss_ ASV4 60	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_UCG-006
raher- 2020- dss_ ASV4 61	Bact eria	Bacteroidota	Bacteroidia	Bacteroidales	Muribaculaceae	NA

raher- 2020- dss_ ASV4 62	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV4 63	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raher- 2020- dss_ ASV4 64	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV4 65	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raher- 2020- dss_ ASV4 66	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Tuzzerella
raher- 2020- dss_ ASV4 67	Bact eria	Desulfo bacterot a	Desulfovib rionia	Desulfovibrio nales	Desulfovibrion aceae	Desulfovibrio
raher- 2020- dss_ ASV4 68	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raher- 2020- dss_ ASV4 69	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	NA

raber- 2020- dss_ ASV4 70	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raber- 2020- dss_ ASV4 71	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	NA
raber- 2020- dss_ ASV4 72	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV4 73	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV4 74	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	UCG-003
raber- 2020- dss_ ASV4 75	Bact eria	Firmicu tes	Clostridia	Peptococcales	Peptococcaceae	NA
raber- 2020- dss_ ASV4 78	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raber- 2020- dss_ ASV4 80	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA

raber- 2020- dss_ ASV4 81	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Harryflintia
raber- 2020- dss_ ASV4 82	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV4 83	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiraceae	Colidextribacter
raber- 2020- dss_ ASV4 84	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiraceae	NA
raber- 2020- dss_ ASV4 85	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnospiraceae _FCS020_group
raber- 2020- dss_ ASV4 88	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculaceae	NA
raber- 2020- dss_ ASV4 89	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Roseburia
raber- 2020- dss_ ASV4 90	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiraceae	Intestinimonas

raher- 2020- dss_ ASV4 91	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV4 92	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV4 93	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV4 95	Bact eria	Firmicu tes	Clostridia	Clostridia_UC G-014	NA	NA
raher- 2020- dss_ ASV4 96	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-010
raher- 2020- dss_ ASV4 97	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV4 98	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia
raher- 2020- dss_ ASV5 00	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m

raber- 2020- dss_ ASV5 01	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raber- 2020- dss_ ASV5 03	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV5 04	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 05	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 06	Bact eria	Firmicu tes	Clostridia	Peptostreptococcales- Tissierellales	Anaerovoracaceae	NA
raber- 2020- dss_ ASV5 07	Bact eria	Firmicu tes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus
raber- 2020- dss_ ASV5 09	Bact eria	Firmicu tes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	NA
raber- 2020- dss_ ASV5 10	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Roseburia

raber-2020-dss_ASV511	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raber-2020-dss_ASV513	Bacteria	Firmicutes	Clostridia	Clostridia_vadinBB60_group	NA	NA
raber-2020-dss_ASV515	Bacteria	Firmicutes	Clostridia	Monoglobales	Monoglobaceae	Monoglobus
raber-2020-dss_ASV516	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	Oscillospira
raber-2020-dss_ASV518	Bacteria	Firmicutes	Clostridia	Oscillospirales	Ruminococcaceae	NA
raber-2020-dss_ASV520	Bacteria	Firmicutes	Clostridia	Oscillospirales	Oscillospiraceae	UCG-003
raber-2020-dss_ASV523	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	Lachnospiraceae_FCS020_group
raber-2020-dss_ASV524	Bacteria	Actinobacteriota	Coriobacteriia	Coriobacteriales	Coriobacteriales_Incertae_Sedimentis	NA

raber- 2020- dss_ ASV5 25	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 27	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 28	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 29	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 30	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Leuconostocac eae	Weissella
raber- 2020- dss_ ASV5 31	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Atopobiaceae	Olsenella
raber- 2020- dss_ ASV5 33	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raber- 2020- dss_ ASV5 36	Bact eria	Firmicu tes	Clostridia	Clostridiales	Clostridiaceae	Candidatus_Art hromitus

raber- 2020- dss_ ASV5 37	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raber- 2020- dss_ ASV5 39	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raber- 2020- dss_ ASV5 43	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 44	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	Enterorhabdus
raber- 2020- dss_ ASV5 47	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	NA
raber- 2020- dss_ ASV5 49	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raber- 2020- dss_ ASV5 50	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 54	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA

raber- 2020- dss_ ASV5 61	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 62	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter
raber- 2020- dss_ ASV5 63	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raber- 2020- dss_ ASV5 64	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnoclostridiu m
raber- 2020- dss_ ASV5 66	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 69	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 70	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV5 73	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA

raber- 2020- dss_ ASV5 74	Bact eria	Proteob acteria	Gammapr oteobacteri a	Burkholderial es	Sutterellaceae	Parasutterella
raber- 2020- dss_ ASV5 83	Bact eria	Actinob acteriota	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809
raber- 2020- dss_ ASV5 84	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Lachnospiraceae _UCG-004
raber- 2020- dss_ ASV5 86	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Tuzzerella
raber- 2020- dss_ ASV5 87	Bact eria	Firmicu tes	Clostridia	Christensenell ales	Christensenella ceae	Christensenellac eae_R-7_group
raber- 2020- dss_ ASV5 88	Bact eria	Firmicu tes	Clostridia	Clostridia_va dinBB60_grou p	NA	NA
raber- 2020- dss_ ASV5 89	Bact eria	Patescib acteria	Saccharim onadia	Saccharimona dales	Saccharimonad aceae	Candidatus_Sacc harimonas
raber- 2020- dss_ ASV5 91	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber- 2020- dss_ ASV5 92	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 93	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raber- 2020- dss_ ASV5 94	Bact eria	Proteob acteria	Gammapr oteobacteri a	Pseudomona dales	Pseudomonada ceae	Pseudomonas
raber- 2020- dss_ ASV5 95	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV5 97	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	Enterorhabdus
raber- 2020- dss_ ASV6 01	Bact eria	Firmicu tes	Clostridia	NA	NA	NA
raber- 2020- dss_ ASV6 02	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelatoclos tridiaceae	NA
raber- 2020- dss_ ASV6 05	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV6 09	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809
raber- 2020- dss_ ASV6 10	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV6 13	Bact eria	Actinob acteriot a	Coriobacte riia	Coriobacterial es	Eggerthellacea e	DNF00809
raber- 2020- dss_ ASV6 22	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV6 25	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV6 26	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 27	Bact eria	Firmicu tes	Bacilli	Erysipelotrich ales	Erysipelotricha ceae	Turicibacter
raber- 2020- dss_ ASV6 32	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber- 2020- dss_ ASV6 33	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 36	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	Alistipes
raber- 2020- dss_ ASV6 37	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 38	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV6 40	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 41	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV6 42	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	CAG-873
raber- 2020- dss_ ASV6 43	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Colidextribacter

raber- 2020- dss_ ASV6 44	Bact eria	Proteob acteria	Alphaprot eobacteria	Rickettsiales	Mitochondria	NA
raber- 2020- dss_ ASV6 46	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	Incertae_Sedis
raber- 2020- dss_ ASV6 50	Bact eria	Patescib acteria	Saccharim onadia	Saccharimona dales	Saccharimonad aceae	Candidatus_Sacc harimonas
raber- 2020- dss_ ASV6 51	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 52	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV6 53	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV6 58	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 59	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV6 61	Bact eria	Firmicu tes	NA	NA	NA	NA
raber- 2020- dss_ ASV6 62	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 64	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Lactobacillacea e	Lactobacillus
raber- 2020- dss_ ASV6 65	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV6 66	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	ASF356
raber- 2020- dss_ ASV6 67	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV6 68	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV6 71	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA

raber- 2020- dss_ ASV6 72	Bact eria	Firmicu tes	Clostridia	Christensenell ales	Christensenella ceae	NA
raber- 2020- dss_ ASV6 73	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV6 74	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV6 75	Bact eria	Firmicu tes	Clostridia	Peptostreptococcales- Tissierellales	Anaerovoracaceae	NA
raber- 2020- dss_ ASV6 76	Bact eria	Firmicu tes	Clostridia	Oscillospirales	Ruminococcaceae	Phoceae
raber- 2020- dss_ ASV6 77	Bact eria	Firmicu tes	Clostridia	Lachnospirales	Lachnospiraceae	ASF356
raber- 2020- dss_ ASV6 78	Bact eria	Firmicu tes	Clostridia	NA	NA	NA
raber- 2020- dss_ ASV6 79	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA

raiber-2020-dss_	ASV6	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Marinifilaceae	Odoribacter
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Bacilli	Erysipelotrichales	Erysipelotrichaceae	Faecalibaculum
raiber-2020-dss_	ASV6	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Muribaculaceae	NA
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Clostridia	Oscillospirales	Butyricicoccaceae	NA
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Bacilli	Acholeplasmales	Acholeplasmataceae	Anaeroplasmataceae
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA
raiber-2020-dss_	ASV6	Bacteria	Firmicutes	Clostridia	Lachnospirales	Lachnospiraceae	NA

raber- 2020- dss_ ASV6 90	Bact eria	Firmicu tes	Bacilli	Lactobacillale s	Leuconostocac eae	Leuconostoc
raber- 2020- dss_ ASV6 94	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Sporobacter
raber- 2020- dss_ ASV6 95	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 96	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV6 97	Bact eria	Firmicu tes	Clostridia	NA	NA	NA
raber- 2020- dss_ ASV6 98	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV7 00	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV7 01	Bact eria	Patescib acteria	Saccharim onadia	Saccharimona dales	Saccharimonad aceae	Candidatus_Sacc harimonas

raher- 2020- dss_ ASV7 02	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV7 03	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV7 04	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raher- 2020- dss_ ASV7 06	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raher- 2020- dss_ ASV7 07	Bact eria	Actinob acteriot a	Actinobact eria	Micrococcales	Micrococcaceae	Pseudarthrobact er
raher- 2020- dss_ ASV7 10	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV7 14	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Sporobacter
raher- 2020- dss_ ASV7 15	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV7 16	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV7 17	Bact eria	Patescib acteria	Saccharim onadia	Saccharimona dales	Saccharimonad aceae	Candidatus_Sacc harimonas
raber- 2020- dss_ ASV7 18	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Oscillibacter
raber- 2020- dss_ ASV7 21	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	A2
raber- 2020- dss_ ASV7 23	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV7 30	Bact eria	Firmicu tes	Bacilli	NA	NA	NA
raber- 2020- dss_ ASV7 31	Bact eria	Firmicu tes	Clostridia	NA	NA	NA
raber- 2020- dss_ ASV7 32	Bact eria	Firmicu tes	Bacilli	NA	NA	NA

raiber- 2020- dss_ ASV7 33	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	Muribaculum
raiber- 2020- dss_ ASV7 34	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raiber- 2020- dss_ ASV7 35	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Sporobacter
raiber- 2020- dss_ ASV7 36	Bact eria	Actinob acteriot a	Actinobact eria	Micrococcales	Microbacteriac eae	Curtobacterium
raiber- 2020- dss_ ASV7 37	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raiber- 2020- dss_ ASV7 42	Bact eria	Firmicu tes	Clostridia	Peptostreptoc occales- Tissierellales	Anaerovoracac eae	NA
raiber- 2020- dss_ ASV7 43	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raiber- 2020- dss_ ASV7 44	Bact eria	Firmicu tes	Clostridia	NA	NA	NA

raber- 2020- dss_ ASV7 45	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV7 46	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV7 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV7 50	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV7 67	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV7 69	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	NA
raber- 2020- dss_ ASV7 70	Bact eria	Firmicu tes	Bacilli	RF39	NA	NA
raber- 2020- dss_ ASV7 71	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiraceae	Lachnospiraceae _NK4A136_group

raber- 2020- dss_ ASV7 72	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV7 73	Bact eria	NA	NA	NA	NA	NA
raber- 2020- dss_ ASV7 74	Bact eria	Bacteroi dota	Bacteroidi a	NA	NA	NA
raber- 2020- dss_ ASV7 75	Bact eria	Firmicu tes	NA	NA	NA	NA
raber- 2020- dss_ ASV7 76	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV7 78	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV7 79	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	NA
raber- 2020- dss_ ASV7 80	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Bacteroidaceae	Bacteroides

raiber- 2020- dss_ ASV7 81	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	NA	NA
raiber- 2020- dss_ ASV7 82	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raiber- 2020- dss_ ASV7 83	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raiber- 2020- dss_ ASV7 84	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	Acetatifactor
raiber- 2020- dss_ ASV7 85	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raiber- 2020- dss_ ASV7 86	Bact eria	Firmicu tes	Bacilli	Staphylococca les	Staphylococcac eae	NA
raiber- 2020- dss_ ASV7 87	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raiber- 2020- dss_ ASV7 88	Bact eria	Firmicu tes	Clostridia	NA	NA	NA

raher- 2020- dss_ ASV7 90	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV7 91	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV7 92	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	CAG-873
raher- 2020- dss_ ASV7 93	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Pseudoflavonifra ctor
raher- 2020- dss_ ASV7 94	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raher- 2020- dss_ ASV7 96	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	NA	NA
raher- 2020- dss_ ASV8 24	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raher- 2020- dss_ ASV8 25	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA

raber- 2020- dss_ ASV8 26	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	CAG-873
raber- 2020- dss_ ASV8 27	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Ruminococcace ae	NA
raber- 2020- dss_ ASV8 28	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 29	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV8 30	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV8 31	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Bacteroidaceae	Bacteroides
raber- 2020- dss_ ASV8 33	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Rikenellaceae	NA
raber- 2020- dss_ ASV8 34	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber- 2020- dss_ ASV8 35	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 36	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	NA	NA
raber- 2020- dss_ ASV8 38	Bact eria	Firmicu tes	NA	NA	NA	NA
raber- 2020- dss_ ASV8 39	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 40	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV8 41	Bact eria	Firmicu tes	NA	NA	NA	NA
raber- 2020- dss_ ASV8 42	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 43	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA

raber- 2020- dss_ ASV8 44	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	Muribaculacea e	NA
raber- 2020- dss_ ASV8 45	Bact eria	Firmicu tes	Clostridia	NA	NA	NA
raber- 2020- dss_ ASV8 46	Bact eria	Patescib acteria	Saccharim onadia	Saccharimona dales	Saccharimonad aceae	Candidatus_Sacc harimonas
raber- 2020- dss_ ASV8 47	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 50	Bact eria	Bacteroi dota	Bacteroidi a	Bacteroidales	NA	NA
raber- 2020- dss_ ASV8 52	Bact eria	Firmicu tes	NA	NA	NA	NA
raber- 2020- dss_ ASV8 53	Bact eria	Firmicu tes	Clostridia	Lachnospirale s	Lachnospiracea e	NA
raber- 2020- dss_ ASV8 54	Bact eria	Firmicu tes	Clostridia	Oscillospirale s	Oscillospiracea e	Pseudoflavonifra ctor

raber-
 2020-
 dss_

ASV8 Bact Firmicu Lachnospirale Lachnospiraceae
 55 eria tes Clostridia s e NA

raber-
 2020-
 dss_

ASV8 Bact Firmicu Oscillospirale Butyricicoccace
 59 eria tes Clostridia s ae UCG-008

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ASV9 Bact Firmicu Lachnospirale Lachnospiraceae
 05 eria tes Clostridia s e NA

Table S4. DSS metadata.

Sample ID	SID	Sex	Geno	DSS	Timepoint		OF1. TotD	OF1. Weeist	NO1. SOT	SO. total.d	NO2. DO.T	NO2. D	NO2. Y.Maze	TotY.Maze	P.Delta	FallScore	ReachScore	Grip.Strength	Grip.Wk3.weight	Grip.Ratio	FST.S	Context	FC. Context	FC. Context
					int.k	move.m	CentDur	tDistcm	Move.ys	all.3.dat	DistMov	O.Pct	ODO.D	al.Arm.Ent	ct.Spont						rotorod	corin	ContTotPct	CuedTone
594wk4-1	1	M	WT	0%	4	878.29	0	2016.81	460.674	1502.48	32.3272322	0.3534554	19	52.9411765	10.7	9	0	126	27.6	4.5652233331739	3333	69.22	41.17	
594wk4-2	2	M	Het	0%	4	1471.63	8.40838	2631.61	1069.604	1908.24	64.5885105	0.29177021	28	53.8461539	-14.1	6	0	67.2	25.2	2.6666116666667	3333	50.57	8.24	
594wk4-3	3	M	Het	3%	4	1164.23	12.4791	1669.15	747.047	1448.41	40.0000245	0.1999995	15	46.1538462	1.7	9	0	112.5	30.6	3.6764333337059	3333	84.73	13.81	
594wk4-4	4	F	WT	3%	4	2070.77	15.9492	2822.02	912.59	2013.67	36.5759712	0.2684806	36	52.9411765	-16.6	9	0	92	19	4.84210526	0	74.19	1.56	
594wk4-5	5	F	WT	0%	4	2105.13	9.00898	2567.65	510.08	2575.4	68.4101133	0.36820227	20	33.3333333	29	6	3	97.2	24.1	4.0331666669502	6667	48.94	1.44	
594wk4-6	6	F	Het	3%	4	1480.37	0	2230.5	516.074	1954.17	19.0476318	0.6190474	15	23.0769231	0.6	5	0	128.2	22.3	5.7488833337892	3333	39.88	14.57	
594wk4-7	7	F	Het	0%	4	1458.68	17.017	2088.3	206.4	1173.14	72.493564	0.44987128	13	54.5454546	13.3	8	0	83.5	22.6	3.6946366669027	6667	85.04	73.52	
594wk4-8	8	M	WT	3%	4	1233.78	34.1674	1404.63	552.637	1359.87	73.8128399	0.4762568	18	87.5	5.4	8	0	100.5	25.9	3.8803366660888	6667	54.86	25.2	
594wk4-9	9	M	WT	0%	4	1281.82	10.0767	1491.28	458.501	1488.18	NA	NA	20	44.4444444	22	9	0	107.5	25.6	4.1992233331875	3333	77.24	26.57	
594wk4-10	10	M	Het	3%	4	1244.53	18.0847	1674.94	918.556	837.252	NA	NA	14	58.3333333	15.8	5	0	120.5	24.4	4.9385116662459	6667	81.24	10.7	
594wk4-11	11	M	Het	0%	4	1986.11	16.6166	3515.36	720.97	2420.52	81.2976789	0.62595358	22	55	1.8	4	1	117	21.7	5.39170507	15	36.81	33.28	
594wk4-12	12	F	WT	3%	4	2124.24	22.6226	2199.28	1334.148	2747.43	58.6583194	0.17316639	25	39.1304348	6.1	7	0	96	23.5	4.08510638	25	70.24	35.91	
594wk4-13	13	F	WT	0%	4	1311.7	0	1821.92	386.581	1468.84	83.1695231	0.66339046	15	23.0769231	13.3	5	2	80.7	20.9	3.8612166664402	6667	72.99	33.61	
594wk4-14	14	F	WT	3%	4	1306.84	10.6106	2511.31	675.51	1326.12	37.7358527	0.2452829	14	25	20.3	5	1	96	23.2	4.1379433333103	3333	73.1	8.17	
594wk4-15	15	F	Het	0%	4	3276.91	28.2949	3714.74	1809.34	3488.76	47.6662018	0.046676	21	52.631579	6.8	9	2	108	24.2	4.4628233330992	3333	40.74	9.43	
594wk4-16	16	M	Het	0%	4	1704.38	25.759	3321.37	943.376	2647.62	55.9386973	0.11877395	17	73.3333333	17	4	3	150.5	27.8	5.4136283336907	3333	81.17	20.96	
594wk4-17	17	M	Het	3%	4	812.729	10.8775	1311.05	350.516	1353.81	60.0733111	0.20146622	13	54.5454546	5.1	6	0	125.5	28.8	4.35763889	30	73.43	52.28	
594wk4-18	18	F	Het	3%	4	1690.28	14.014	3854.12	971.119	4180.94	51.7112047	0.0342241	28	34.6153846	-1.1	7	0	126	24.8	5.08064516	40	75.77	24.3	
594wk4-19	19	F	Het	0%	4	1228.12	12.0787	2314.5	304.877	1360.32	61.5176506	0.23035301	14	58.3333333	-4.3	8	0	107.5	25.5	4.21568628	5	64.33	36.83	

594wk 4-20	20	F	WT	0%	4	1137.5	7.0069 8	1794.9	485.61	1641.04	69.2307 536	0.3846 1507	24	40.90909 09	8.3	6	1	96	21.2	4.5283 0189	50	82.76	4.19
594wk 4-21	21	F	Het	3%	4	3016.85	19.486 1	7341.13	302.82	6048.21	58.1594 325	0.1631 8865	28	38.46153 85	14.6	8	1	87.5	26.6	3.289438.333 7368 3333	75.03	17.91	
594wk 4-22	22	F	Het	0%	4	753.011	2.002	1020.49	57.179	945.582	NA	NA	9	71.42857 14	41.8	8	0	90.5	23.1	3.917713.333 4892 3333	72.36	53.22	
594wk 4-23	23	M	Het	3%	4	1049.81	6.8735 2	1794.37	431.151	1414.57	57.6922 634	0.1538 4527	19	35.29411 77	-5.1	0	0	71.2	24.9	2.8594 3775	25	53.96	8.2
594wk 4-24	24	M	Het	0%	4	1912.33	12.078 7	4622.27	-79.02	4044.95	62.8016 405	0.2560 3281	29	55.55555 56	50.3	8	0	106.2	23.3	4.5579 3991	20	22.49	1.89
594wk 4-25	25	M	Het	3%	4	1392.18	32.165 4	2064.98	656.569	1702.97	68.6411 337	0.3728 2267	24	50	28.1	7	0	83	25.3	3.280661.666 3241 6667	69.02	29.44	
594wk 4-26- kit	26	M	WT	3%	4	1338.4	4.8715 2	1871.72	724.87	1820.9	34.0886 012	- 0.3182 28	17	40	-12.7	9	1	97.2	23	4.2260 8696	50	88.04	47.96
594wk 4-27	27	M	WT	0%	4	1590.97	41.174 4	2445.91	769.717	1044.56	34.9206 33	- 0.3015 873	21	47.36842 11	2.3	8	2	114.2	24.1	4.7385 8921	50	49.38	23.22
594wk 4-28	28	M	Het	0%	4	882.171	45.378 6	2069.9	-194.899	2149.78	72.3756 325	0.4475 1265	18	62.5	26.6	10	0	110.2	23.4	4.7094 0171	0	55.72	43.3
594wk 4-29	29	F	Het	0%	4	1734.62	14.748	1869.07	794.353	1773.11	39.2618 413	0.2147 632	29	70.37037 04	23.7	10	0	99	21.5	4.604638.333 5116 3333	46.12	3.19	
594wk 4-30	30	F	Het	3%	4	1547.28	12.145 4	1636.1	906.188	1316.04	68.5714 775	0.3714 2955	14	58.33333 33	-0.5	6	1	82	21	3.9047 6191	10	54.27	31.11