OTU	*Cephalotrix simula*			*Tubulanus punctatus*			*Parahubrechtia sp.*			*Hubrechtella juliae*			*Cerebratulus cf. marginatus*			*Micrura cf. bella*			*Kulkovia albarostrata*			*Quasitetrastemma stimpsoni*			Sequence	Taxonomy						
	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3	Sample 1	Sample 2	Sample 3		Kingdom	Phylum	Class	Order	Family	Genus	Species
OTU_NEM_1	0	0	0	0	0	52	0	0	0	0	4	0	0	0	0	151	0	41	0	174	86	3125	0	0	CCTACGGGGGGCTCAGTGAGGGGATATTTCGGCAATGGGGGAAACCCTGACCGAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ruminococcus	s__
OTU_NEM_2	0	8	0	0	0	8	0	0	0	0	0	0	0	0	0	267	0	9	2280	130	2638	9029	7443	533	CCTACGGGGGGCAGCAGTGGGGAATATTTGCACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Pseudoalteromonadaceae	g__Pseudoalteromonas	s__
OTU_NEM_3	0	0	0	0	1448	0	0	0	285	5645	30	680	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiohalorhabdales	f__	g__	s__
OTU_NEM_4	0	32	0	0	0	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGTGGCTGCAGTGGGGAATATCGCACAATGGGGGCAACCCTGATCTGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__Glaciecola	s__
OTU_NEM_5	0	0	0	0	0	0	0	0	573	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCTGCAGTAGGGGAATATTGGACAATGGGGCAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__	g__	s__
OTU_NEM_6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80	0	0	CCTACGGGGCGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__	s__
OTU_NEM_7	0	0	0	0	0	0	49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCTGCAGTGGGGAATATTTTGCAATGCCGCGAAAGGGTGACAATGCGACGGCCGCGTG	k__Bacteria	p__OP3	c__BD4-9	o__	f__	g__	s__
OTU_NEM_8	0	0	0	0	0	0	503	0	0	0	0	0	0	0	0	69	0	0	232	16	131	409	1461	96	CCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Pseudoalteromonadaceae	g__Pseudoalteromonas	s__
OTU_NEM_9	0	0	0	0	0	0	42	58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGGGAAACCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Piscirickettsiaceae	g__	s__
OTU_NEM_10	0	0	0	0	0	13	342	0	0	0	0	0	0	0	0	0	0	0	0	30	5	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGCGCAATGGGGGCAACCCTGACGCGAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pasteurellales	f__Pasteurellaceae	g__Haemophilus	s__parainfluenzae
OTU_NEM_11	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGCGCAATGGGCGCAAGCCTGACGCGACGCCGCGTG	k__Bacteria	p__Acidobacteria	c__DA052	o__Ellin6513	f__	g__	s__
OTU_NEM_12	0	0	0	0	0	0	0	0	206	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCGCAATGGGGGAAACCCTGACGCAGTGACGCCGTGTG	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Syntrophobacterales	f__	g__	s__
OTU_NEM_13	0	0	0	0	0	0	0	802	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Dermatophilaceae	g__Pisciccoccus	s__intestinalis
OTU_NEM_14	0	0	181	0	0	26	0	202	1	0	188	45	0	58	0	21	0	98	0	5	0	125	0	0	CCTACGGGGGCAGCAGTAAGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Bacteroidetes	c__[Saprospirae]	o__[Saprospirales]	f__Chitinophagaceae	g__Sediminibacterium	s__
OTU_NEM_15	0	0	0	0	0	0	0	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Rhizobiaceae	g__	s__
OTU_NEM_16	0	0	222	0	0	0	0	1164	0	33	0	0	0	0	0	481	30	0	0	0	213	457	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Sphingomonadaceae	g__Sphingomonas	s__
OTU_NEM_17	0	0	0	0	0	0	0	0	653	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGTGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATACCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Xanthomonadales	f__Xanthomonadaceae	g__	s__
OTU_NEM_18	0	0	0	0	0	0	0	770	997	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGAGGCTGCAGTGGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__	f__	g__	s__
OTU_NEM_19	0	0	0	0	0	46	0	0	0	0	1836	263	0	0	0	0	0	0	193	39	13	1261	1908	271	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGAGGAAACTCTGATGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Psychromonadaceae	g__Psychromonas	s__
OTU_NEM_20	0	0	0	0	0	0	1	0	55	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	CCTACGGGTGGCAGCAGTGGGGAATATTGGACAATGGGGGAAACCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Sphingomonadaceae		s__
OTU_NEM_21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	181	0	0	0	0	0	0	0	0	CCTACGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Oceanospirillaceae	g__Marinomonas	s__
OTU_NEM_22	50	320	0	0	0	35	0	0	0	0	0	0	0	0	0	317	0	0	0	0	0	1488	0	0	CCTACGGGAGGCAGCAGTGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Oscillospira	s__
OTU_NEM_23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1015	0	41	CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Phyllobacteriaceae	g__Mesorhizobium	s__
OTU_NEM_24	52	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCTATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rickettsiales	f__	g__	s__
OTU_NEM_25	0	0	0	0	0	0	511	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGCTGCAGTGAGGGAATATTGTCAATGTACGAAACTATGTGAACGCGCGCGTGTG	k__Bacteria	p__Verrucomicrobia	c__Verruco-5	o__MSB1.3	f__	g__	s__
OTU_NEM_26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	120	CCTACGGGGGGCTGCAGTGGGGGAATATTCTAGACAATGGGGGAAACCCTGATCTAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Paracoccus	s__
OTU_NEM_27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTAGGGGAATCTTGCGCAATGGGCGAAAGCCTGACGCGAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__EB1017	g__	s__
OTU_NEM_28	0	0	0	0	0	0	0	226	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGCAGCAGTGAGGGAATATTGGTCAATGGAGGGAAACTCTGAACACGCCATGCCGCGTG	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Cryomorphaceae	g__Crocinitomix	s__
OTU_NEM_29	0	0	0	0	0	0	581	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGCTGCAGTGGGGAATTTTGCGCAATGGGCGAAAGCCTGACGCAGCAATACCGCGTG	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Desulfuromonadales	f__Desulfuromonadaceae	g__	s__
OTU_NEM_30	0	0	0	0	0	0	187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGTGGCAGCAGTCGAGAATCATTCGCAATGGGGGAAACCCTGACGGTGCGACGCCGCGTG	k__Bacteria	p__Verrucomicrobia	c__Verrucomicrobiae	o__Verrucomicrobiales	f__Verrucomicrobiaceae	g__	s__
OTU_NEM_31	0	0	0	0	0	0	68	0	9	12	0	3718	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGCTGCAGTCGAGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAATGCCGCGTG	k__Bacteria	p__Lentisphaerae	c__[Lentisphaeria]	o__Victivallales	f__Victivallaceae	g__	s__
OTU_NEM_32	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	CCTACGGAGCAGCAGTCGAGAATTTTCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Verrucomicrobia	c__[Pedosphaerae]	o__[Pedosphaerales]	f__Ellin515	g__	s__
OTU_NEM_33	0	0	0	0	0	0	0	0	337	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCTGCAGTCAAGGAATCTTCCCCAATGCGCGAAAGCGTGAGGGAGCGACGCCGCGTG	k__Bacteria	p__OD1	c__ABY1	o__	f__	g__	s__
OTU_NEM_34	0	0	20	23	23	2	0	495	0	50	0	30	0	176	115	0	0	0	28	0	18	0	0	1	CCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCAACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Propionibacteriaceae	g__Propionibacterium	s__acnes
OTU_NEM_35	0	0	0	0	0	0	0	0	311	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGTGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Alteromonadaceae	g__BD2-13	s__
OTU_NEM_36	0	0	0	0	0	0	0	28	0	0	0	0	0	0	0	0	0	0	45	12	15	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Pseudomonadaceae	g__Pseudomonas	s__
OTU_NEM_37	0	0	0	0	0	0	1	309	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCTGCAGTGGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAACGCCGCGTG	k__Bacteria	p__Acidobacteria	c__Sva0725	o__Sva0725	f__	g__	s__
OTU_NEM_38	0	0	0	0	0	0	248	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGAGGGAATATTGGACAATGGGCGAGAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Bacteroidetes	c__Flavobacteriia	o__Flavobacteriales	f__Flavobacteriaceae	g__Ulvibacter	s__
OTU_NEM_39	0	0	0	0	0	0	0	0	6	0	0	2	0	65	0	0	0	0	0	0	0	0	0	0	CCGGGCGGCAGCAGTGAGGGAATATTGGTCAATGGAGGAGAGTCTGAACCAGCCAAGTAGCGTG	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__	g__	s__
OTU_NEM_40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	CCTACGGGGGGCAGCAGTAGGGGAATTTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG	k__Bacteria	p__TM7	c__TM7-1	o__	f__	g__	s__
OTU_NEM_41	0	0	0	0	0	0	34	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGAGGGAATATTTGCGCAATGGGGGAAACCCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria				
OTU_NEM_42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	CCTACGGGTGGCTGCAGTGAGGGAATTTTCCGCAATGGTCGCAAGACTGACGGAGCAACGCCGCGTG	k__Bacteria	p__Chloroflexi	c__Ktedonobacteria	o__Thermogemmatisporales	f__Thermogemmatisporaceae	g__	s__
OTU_NEM_43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Bacteroidetes	c__[Saprospirae]	o__[Saprospirales]	f__	g__	s__
OTU_NEM_44	0	0	0	0	0	0	0	0	0	0	0	0	0	109	0	0	0	0	0	0	0	0	0	49	CCTACGGGTGGCAGCAGTAGGGGAATCTTCGGCAATGGGCGAAAGCCTGACCGAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Bacilli	o__Bacillales	f__[Thermicanaceae]	g__Thermicanus	s__
OTU_NEM_45	0	0	4	0	0	2	0	57	0	0	32	0	0	0	0	0	0	0	44	1	6	84	117	20	CCTACGGGGGGCAGCAGTGAGGGAATATTGGTCAATGGGGGCAACTCTGAACCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Vibrionales	f__Vibrionaceae	g__Listonella	s__anguillarum
OTU_NEM_46	1	0	0	0	0	0	284	736	0	0	0	0	0	0	0	0	0	0	0	0	18	1	8	39	CCTACGGGAGCAGCAGTGGGGAATATTCTAGACAATGGGGGCAACCCTGATCTAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Paracoccus	s__
OTU_NEM_47	0	0	0	209	0	0	0	78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG	k__Bacteria	p__Cyanobacteria	c__Synechococcophycideae	o__Synechococcales	f__Synechococcaceae	g__Synechococcus	s__
OTU_NEM_48	0	0	0	0	0	0	0	0	0	0	0	0	0	24	0	0	0	0	0	0	0	0	0	0	CCTACGGGAGGCAGCAGTAGGGGAATCTTCCGCAATGAGCGCAAGTCTGACGGAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Bacilli	o__Lactobacillales	f__Carnobacteriaceae	g__Granulicatella	s__
OTU_NEM_49	1	0	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	CCTACGGGTGGCTGCAGTAGGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Bacilli	o__Bacillales	f__Staphylococcaceae	g__Staphylococcus	s__
OTU_NEM_50	0	0	0	0	0	0	0	892	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCTGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCAACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__[Marinicellales]	f__[Marinicellaceae]	g__	s__
OTU_NEM_51	0	0	0	0	0	0	872	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTAGGGGAATCTTCGGCAATGGAGCGAAAGTCTGACCGAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Bacilli	o__Lactobacillales	f__Streptococcaceae	g__Lactococcus	s__
OTU_NEM_52	0	0	0	0	0	0	720	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGAGGGAATATTGGTCAATGGAGCGAAGTCTGAACCAGCCAAGTAGCGTG	k__Bacteria	p__Bacteroidetes	c__Bacteroidia	o__Bacteroidales	f__Prevotellaceae	g__Prevotella	s__melaninogenica
OTU_NEM_53	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGCGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Micrococcaceae	g__Kocuria	s__
OTU_NEM_54	0	16	321	0	0	0	0	0	764	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATACCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Xanthomonadales	f__Xanthomonadaceae	g__Stenotrophomonas	s__
OTU_NEM_55	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGTGGCAGCAGTGGGGAATTTTGCGCAATGGGCGAAAGCCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Acidobacteria	c__BPC102	o__MVS-40	f__	g__	s__
OTU_NEM_56	0	0	0	0	0	0	842	71	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCAGCAGTGAGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCAACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Epsilonproteobacteria	o__Campylobacterales	f__Helicobacteraceae	g__Sulfurimonas	s__
OTU_NEM_57	0	0	0	0	0	0	0	0	0	0	0	0	0	362	0	0	0	0	1	0	0	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCTATCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__Halomonadaceae	g__Candidatus Portiera	s__
OTU_NEM_58	0	0	0	0	0	0	0	107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCAATACCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Thiotrichaceae	g__	s__
OTU_NEM_59	0	0	0	2	0	0	669	0	0	0	21	0	0	139	0	0	0	0	8	0	0	0	0	0	CCTACGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Micrococcaceae	g__Micrococcus	s__
OTU_NEM_60	0	0	0	0	0	0	0	1563	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__OM60	g__	s__
OTU_NEM_61	0	0	0	6	4	0	0	364	0	0	0	0	56	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGAGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Methylophilales	f__Methylophilaceae		s__
OTU_NEM_62	0	0	0	473	0	0	0	974	0	18	0	4	0	0	0	0	0	0	0	0	0	0	0	100	CCTACGGGTGGCTGCAGTCGAGAATCTTCGGCAATGGGCGAAAGCCTGACCGAGCAATGCCGCGTG	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae		s__
OTU_NEM_63	0	0	0	0	0	0	0	716	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTAGGGGAATATTGGTCAATGGGCGCAAGCCTGAACCAGCCAAGTAGCGTG	k__Bacteria	p__Bacteroidetes	c__Cytophagia	o__Cytophagales	f__Flammeovirgaceae	g__	s__
OTU_NEM_64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGCGCTGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCAACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Propionibacteriaceae	g__Propionibacterium	s__
OTU_NEM_65	0	0	0	0	0	0	0	224	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Thiotrichales	f__Thiotrichaceae	g__Cocleimonas	s__
OTU_NEM_66	0	0	0	0	0	0	0	378	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales			
OTU_NEM_67	0	0	0	0	0	34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGAGGCAGCAGTGGGGAATTTTGCACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__[Tissierellaceae]	g__Anaerococcus	s__
OTU_NEM_68	0	0	0	0	0	0	0	39	0	0	0	0	0	0	0	0	0	0	30	0	30	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATCCAGCCATGCCGC

OTU_NEM_314	0	7	0	33	239	16	0	0	0	0	0	0	0	0	0	2	0	0	33	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Blautia	
OTU_NEM_315	0	89	0	222	220	48	0	0	0	215	8	0	0	0	0	177	15	92	26	99	237	0	0	0	33	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__[Ruminococcus]	s__
OTU_NEM_316	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Lachnospiraceae	g__Coprococcus	s__eutactus
OTU_NEM_317	0	0	0	2957	53	1992	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	CCTACGGGGGGCAGCAGTGGGGAATATTGCGCAATGGGCGAAAGCCTGACGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Kiloniellales	f__	g__	s__
OTU_NEM_318	0	0	0	0	50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGACGCAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Geodermatophilaceae	g__Blastococcus	s__aggregatus
OTU_NEM_319	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGACGCAGCGACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Actinobacteria	o__Actinomycetales	f__Pseudonocardiaceae	g__Pseudonocardia	
OTU_NEM_320	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGACGAAAAGTCTGATCCAGCAATTCTGTGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Alteromonadales	f__Shewanellaceae	g__Shewanella	
OTU_NEM_321	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGACGAAAAGTCTGATCCAGCAATTCTGTGTG	k__Bacteria	p__Fusobacteria	c__Fusobacteria	o__Fusobacteriales	f__Fusobacteriaceae	g__Fusobacterium	s__
OTU_NEM_322	0	0	0	0	0	0	0	0	0	0	1148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGAAGCTGTGATCCAGCAATTCTGTGTG	k__Bacteria	p__Fusobacteria	c__Fusobacteria	o__Fusobacteriales	f__Fusobacteriaceae	g__Propionigenium	s__
OTU_NEM_323	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Sphingomonadaceae	g__Sphingopyxis	s__alaskensis
OTU_NEM_324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__Sphingomonadaceae	g__Sphingomonas	s__wittichii
OTU_NEM_325	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	42	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Sphingomonadales	f__	g__	s__
OTU_NEM_326	0	0	14424	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	710	7091	0	0	0	74	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCATACCGCATG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rickettsiales	f__Anaplasmataceae	g__Neorickettsia	s__
OTU_NEM_327	1	83	125	13	0	0	0	302	317	0	0	0	123	0	0	0	93	0	17	4384	139	1260	1030	105	1	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Moraxellaceae	g__Acinetobacter	s__johnsonii
OTU_NEM_328	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAATCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Xanthomonadales	f__Xanthomonadaceae	g__Pseudoxanthomonas	s__taiwanensis
OTU_NEM_329	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	27	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Chromatiales	f__Chromatiaceae	g__	s__
OTU_NEM_330	0	0	38	0	0	0	0	0	0	0	0	0	0	0	0	170	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Acetobacteraceae	g__	s__
OTU_NEM_331	0	0	0	0	0	0	0	0	0	0	0	86	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Brucellaceae	g__Ochrobactrum	s__
OTU_NEM_332	34	0	673	72	0	19	164	850	239	0	0	124	223	0	0	4	0	7	54	50	0	463	0	12	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Bradyrhizobiaceae	g__	s__
OTU_NEM_333	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	CCTACGGGCGTGTACAAGACCTGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Beijerinckiaceae	g__	s__
OTU_NEM_334	0	0	158	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Bartonellaceae	g__	s__
OTU_NEM_335	0	0	1847	0	0	0	0	0	0	0	0	0	59	0	207	0	0	0	0	0	0	204	0	21	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylobacteriaceae	g__Methylobacterium	s__
OTU_NEM_336	0	72	2470	0	0	1	0	228	0	0	0	0	191	0	0	0	0	0	39	0	12	643	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylobacteriaceae	g__	s__
OTU_NEM_337	0	0	0	2	0	0	0	0	0	0	0	122	0	0	0	0	0	0	0	0	0	0	0	17	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGGGAAACCCTGATCCAGCGACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Xanthomonadales	f__Sinobacteraceae	g__	s__
OTU_NEM_338	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	263	0	0	0	0	0	0	0	0	0	CCTACGGGCGCAGCAGTGGGGAATATTGGACAATGGGGGCAAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhizobiales	f__Methylocystaceae	g__Pleomorphomonas	s__oryzae
OTU_NEM_339	0	0	0	0	0	0	0	0	0	0	0	114	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGGGCAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Moraxellaceae	g__Psychrobacter	s__celer
OTU_NEM_340	0	0	0	0	11	81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9167	0	0	0	0	CCTACGGCGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rickettsiales	f__	g__	s__
OTU_NEM_341	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	199	0	37	0	0	23	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGGGAAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Pseudomonadales	f__Moraxellaceae	g__Psychrobacter	s__pacificensis
OTU_NEM_342	0	0	0	0	0	0	0	0	0	0	0	463	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGGCAATGGACGAAGTCTGACCCAGACAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Oscillospira	s__guilliermondii
OTU_NEM_343	147	0	0	0	207	9	591	0	1026	0	0	1195	0	1013	0	0	0	65	0	0	86	2180	2785	0	0	CCTACGGGCGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__	s__
OTU_NEM_344	0	0	0	0	0	0	0	19604	322	0	10	987	0	0	0	469	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTTACAATTTTTCTCCCTCCTTTCTCCCTTCCTTTCCCTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Oceanospirillales	f__	g__	s__
OTU_NEM_345	0	151	2911	0	0	6	75	62	85	0	0	0	153	0	116	0	0	0	0	24	0	157	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTCCCCCTTTTCTCCCTCCTTCCCCCGCAATGCCGCGCTGGG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodospirillales	f__Acetobacteraceae	g__Roseomonas	s__mucosa
OTU_NEM_346	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50	CCTACGGGGGGCAGCAGTGGGGAATATTAGACAATGGGGGAAACCCTGATCTAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Rhodobacter	s__
OTU_NEM_347	0	0	0	0	0	0	0	0	0	30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGCAGCAGTGGGGAATATTCCCGCAATGGGCGAAAGCTCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Veillonellaceae	g__Veillonella	s__dispar
OTU_NEM_348	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	25	CCTACGGGGGGCAGCAGTGGGGAATCTTGCGCAATGGGCGAAAGCCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Acidimicrobiia	o__Acidimicrobiales	f__	g__	s__
OTU_NEM_349	0	0	0	0	0	0	93	0	0	0	0	0	0	0	0	0	16	0	0	0	0	24	0	57	CCTACGGGGGGCAGCAGTGGGGAATATTGCGCAATGGGCGAAAGCCTGACGCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Caulobacterales	f__Caulobacteraceae	g__	s__
OTU_NEM_350	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	115	0	0	0	0	0	0	0	CCTACGGGGGCAGCAGTGGGGAATCTTGCGCAATGGGCGCAAGCCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Actinobacteria	c__Thermoleophilia	o__Gaiellales	f__	g__	s__
OTU_NEM_351	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	CCTACGGGGGGCAGCAGTGGGGAATCTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Hyphomonadaceae	g__	s__
OTU_NEM_352	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	271	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Phaeobacter	s__
OTU_NEM_353	0	0	0	0	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATCTTGGACAATGGGGGAAACCCTGATCCAGCGATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Gammaproteobacteria	o__Legionellales	f__Coxiellaceae	g__Rickettsiella	s__
OTU_NEM_354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1156	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Rhodobacterales	f__Rhodobacteraceae	g__Amaricoccus	s__
OTU_NEM_355	0	0	0	0	0	0	0	0	0	7803	352	17289	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGCGCAATGGACGAAAGTCTGACGCAGCAACGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Deltaproteobacteria	o__Syntrophobacterales	f__Syntrophobacteraceae	g__JTB36	s__
OTU_NEM_356	0	0	0	0	0	0	0	0	6	0	0	0	0	0	0	0	18	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATTTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Oxalobacteraceae	g__Janthinobacterium	
OTU_NEM_357	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65	0	22	0	29	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Comamonadaceae	g__Comamonas	s__
OTU_NEM_358	70	10	282	81	83	11	522	1757	71	0	0	162	49	251	154	9	39	9	329	59	53	511	41	18	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCTAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Comamonadaceae	g__	s__
OTU_NEM_359	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Rhodocyclales	f__Rhodocyclaceae	g__Zoogloea	s__
OTU_NEM_360	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Methylophilales	f__Methylophilaceae	g__	s__
OTU_NEM_361	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Comamonadaceae	g__Acidovorax	s__
OTU_NEM_362	0	0	0	0	0	0	0	0	0	0	0	144	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCCAGCGACGCCGCGTG	k__Bacteria	p__Gemmatimonadetes	c__Gemm-6	o__	f__	g__	s__
OTU_NEM_363	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	404	0	0	0	0	0	0	0	7	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Comamonadaceae	g__Tepidimonas	s__
OTU_NEM_364	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	17	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGCAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__	g__	s__
OTU_NEM_365	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGCAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Comamonadaceae	g__Acidovorax	s__
OTU_NEM_366	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	208	107	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCTATTCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Alcaligenaceae	g__Sutterella	s__
OTU_NEM_367	0	0	0	0	0	0	168	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Neisseriales	f__Neisseriaceae	g__	s__
OTU_NEM_368	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Oxalobacteraceae	g__Ralstonia	s__
OTU_NEM_369	0	0	0	0	19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAAGCCTGATCCAGCAATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Burkholderiales	f__Oxalobacteraceae	g__	s__
OTU_NEM_370	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	381	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Rhodocyclales	f__Rhodocyclaceae		
OTU_NEM_371	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAACCCTGATCCAGCCATTCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Rhodocyclales	f__Rhodocyclaceae	g__Methyloversatilis	s__
OTU_NEM_372	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAACCCTGATCCAGCCATTCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__	f__	g__	s__
OTU_NEM_373	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	CCTACGGGGGGCAGCAGTGGGGAATATTTGGACAATGGGCGAAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Betaproteobacteria	o__Procabacteriales	f__Procabacteriaceae	g__Procabacter	s__
OTU_NEM_374	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	163	0	0	0	0	0	0	0	204	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGAGCGAAACTCTGATGCAGCGACGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Ethanoligenens	s__
OTU_NEM_375	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	47	CCTACGGGGGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATCCAGCGATGCCGCGTG	k__Bacteria	p__Firmicutes	c__Clostridia	o__Clostridiales	f__Ruminococcaceae	g__Clostridium	s__islandicum
OTU_NEM_376	25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCAGCAGTTAGGAATATTCCCGCAATGGACGGAAGTCTGACGGAGCGACGCCGCTTG	k__Bacteria	p__[Thermi]	c__Deinococci	o__Thermales	f__Thermaceae	g__Thermus	s__
OTU_NEM_377	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	27	CCTACGGGGGGCAGCAGTTGGGAATCTTGGACAATGGGGGAAACCCTGATCCAGCCATGCCGCGTG	k__Bacteria	p__Proteobacteria	c__Alphaproteobacteria	o__Ellin329	f__	g__	s__
OTU_NEM_378	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	43	CCTACGGGGGGCTGCAGTAACGAATCTTCCGCAATGCACGAAAGTGTGACGGAGCGACGCCGCGTG	k__Bacteria	p__Planctomycetes	c__Phycisphaerae	o__WD2101	f__	g__	s__
OTU_NEM_379	104	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGCGCAGCAGTGGGGAATATTCACAATGGACGAAAGTCTGATGGTGCAGCAGCCGCGTG	k__Bacteria	p__Firmicutes	c__Bacilli	o__Lactobacillales	f__Leuconostocaceae	g__	s__
OTU_NEM_380	0	0	36	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	58	CCTACGGGGGGCTGCAGTCGAGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCGACGCCGCGTG	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Planctomycetales	f__Planctomycetaceae	g__Planctomyces	s__
OTU_NEM_381	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	CCTACGGGGGGCTGCAGTCGAGAATCTTCCGCAATGGACGAAAGTCTGACCGAGCGACGCCGCGTG	k__Bacteria	p__Planctomycetes	c__Planctomycetia	o__Pirellulales	f__Pirellulaceae	g__	s__
OTU_NEM_382	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0