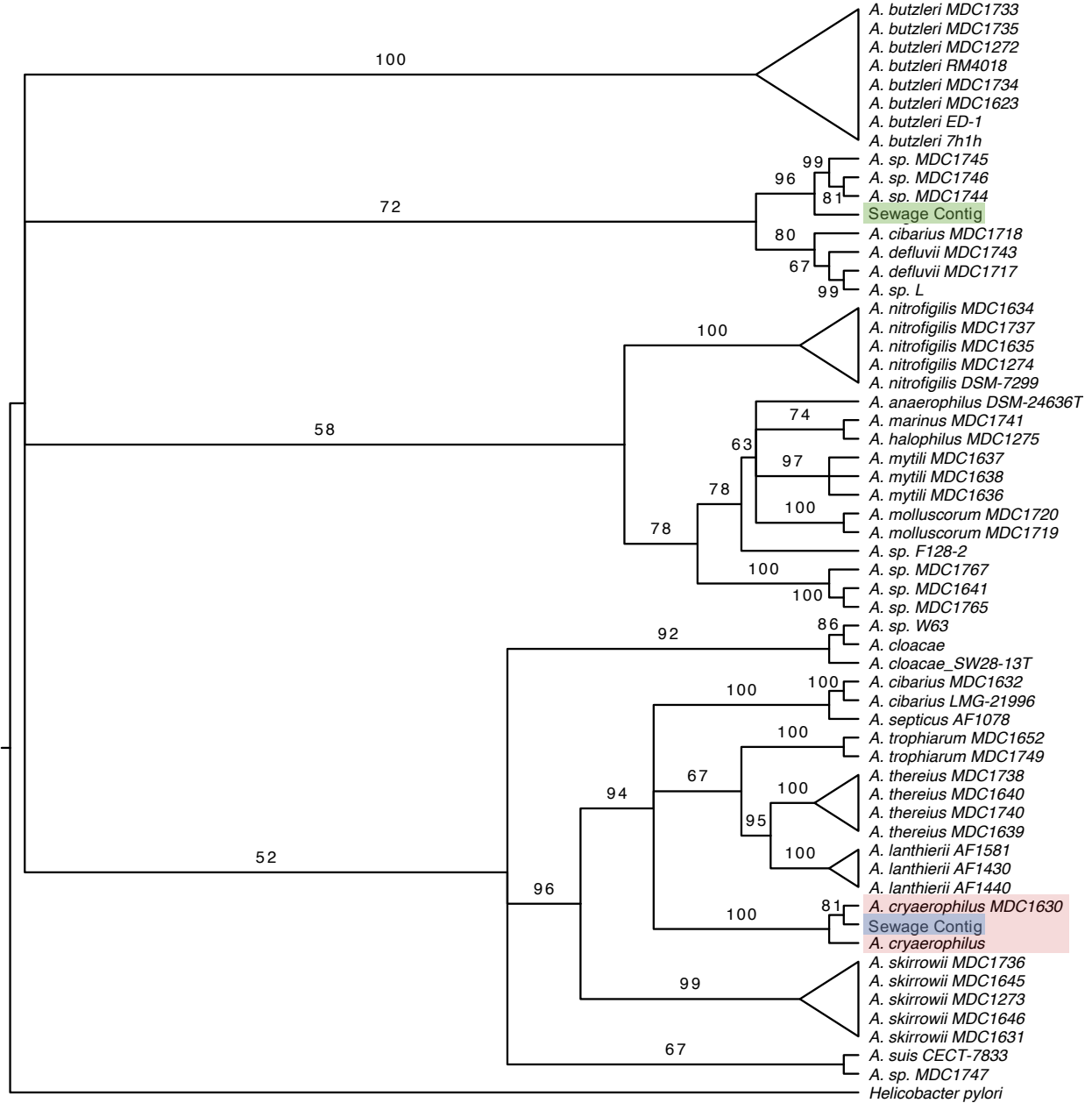
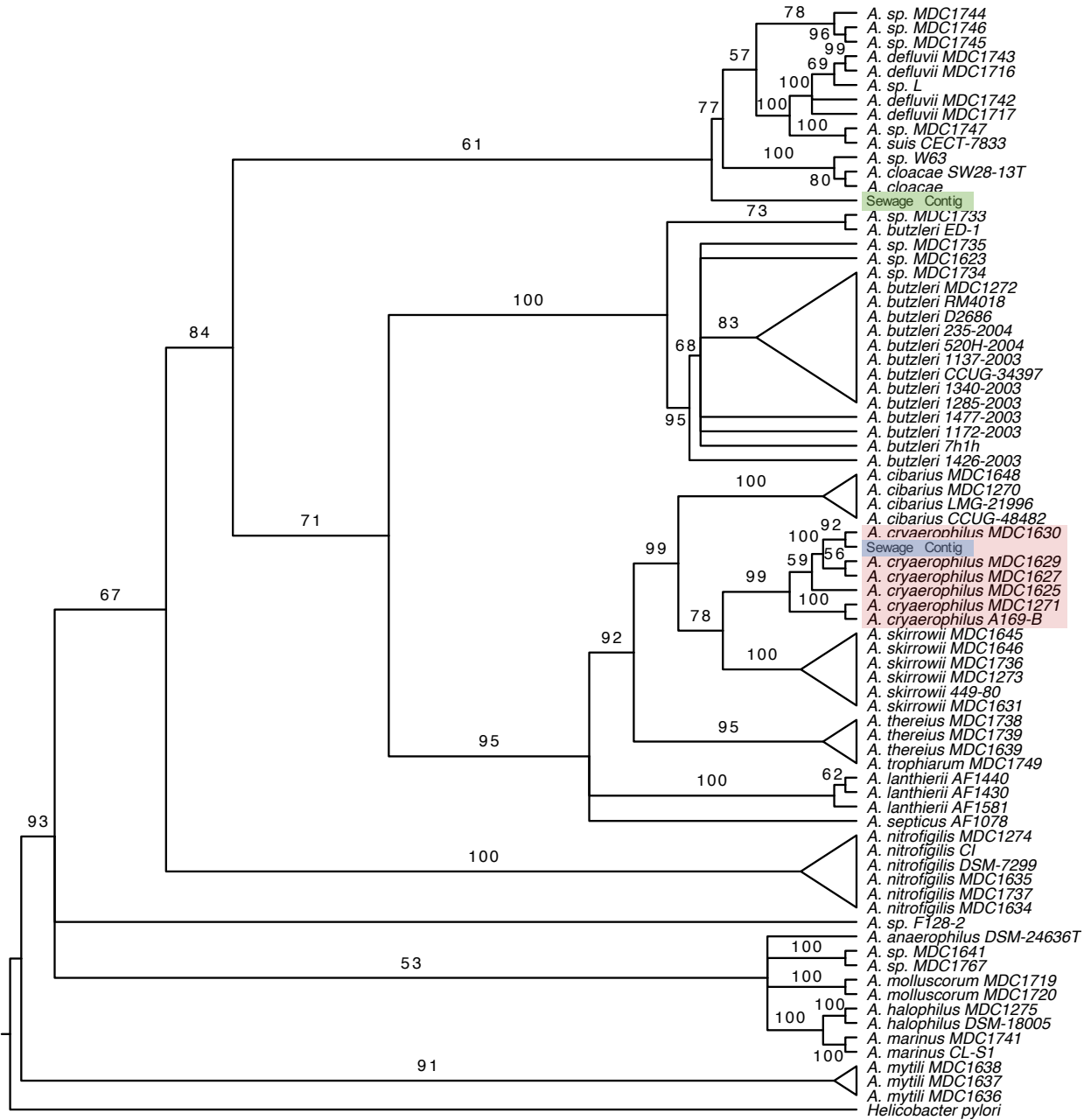


FIG S1. *Arcobacter* housekeeping gene trees. Bayesian phylogenetic trees for nucleotide sequences of *Arcobacter* housekeeping genes **(A)** *atpA* (618nt) **(B)** *gyrA* (684nt) **(C)** *hsp60* (285nt) and **(D)** *rpoB* (618nt) to identify sewage contigs belonging to *A. cryaerophilus* (in blue).

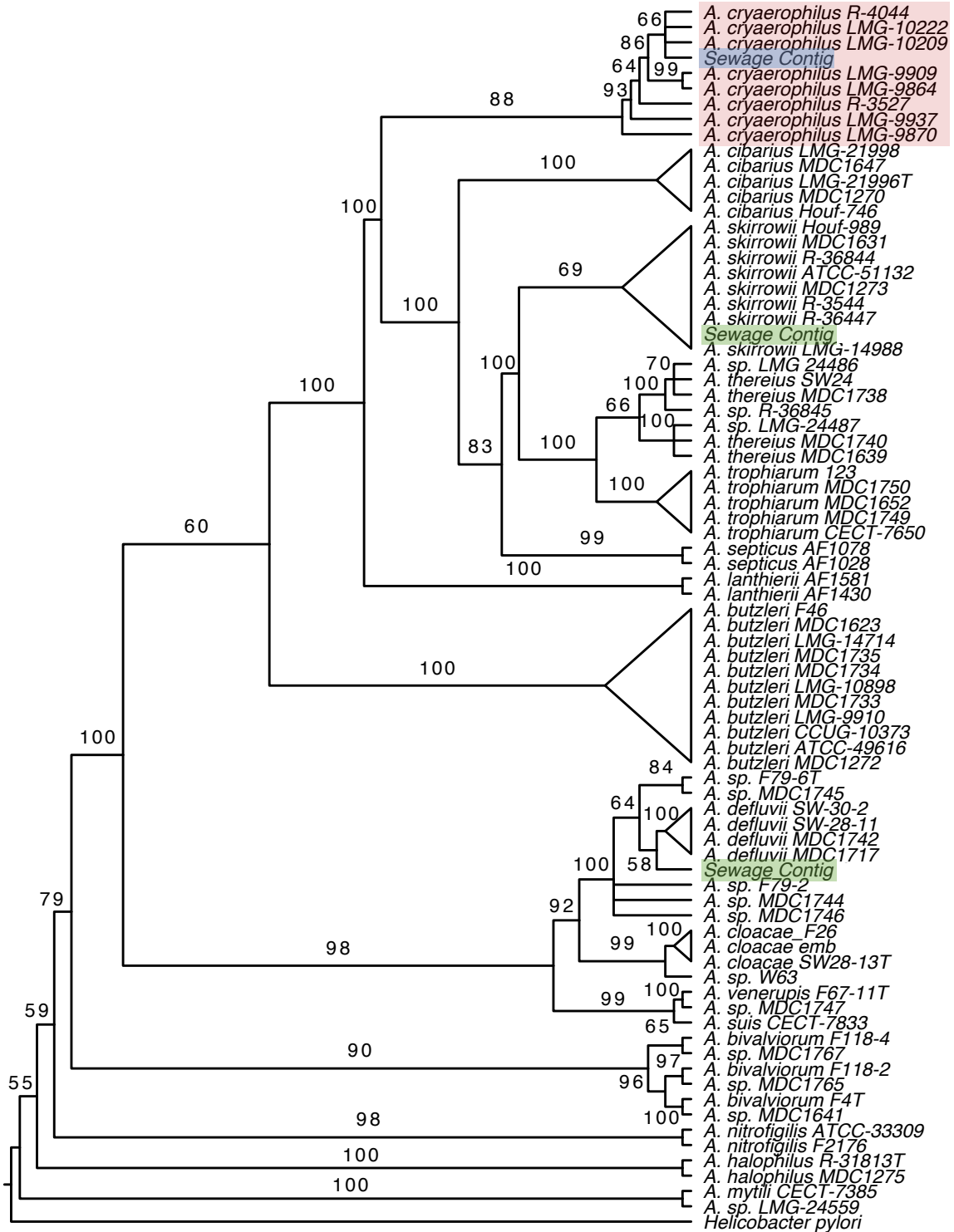
A



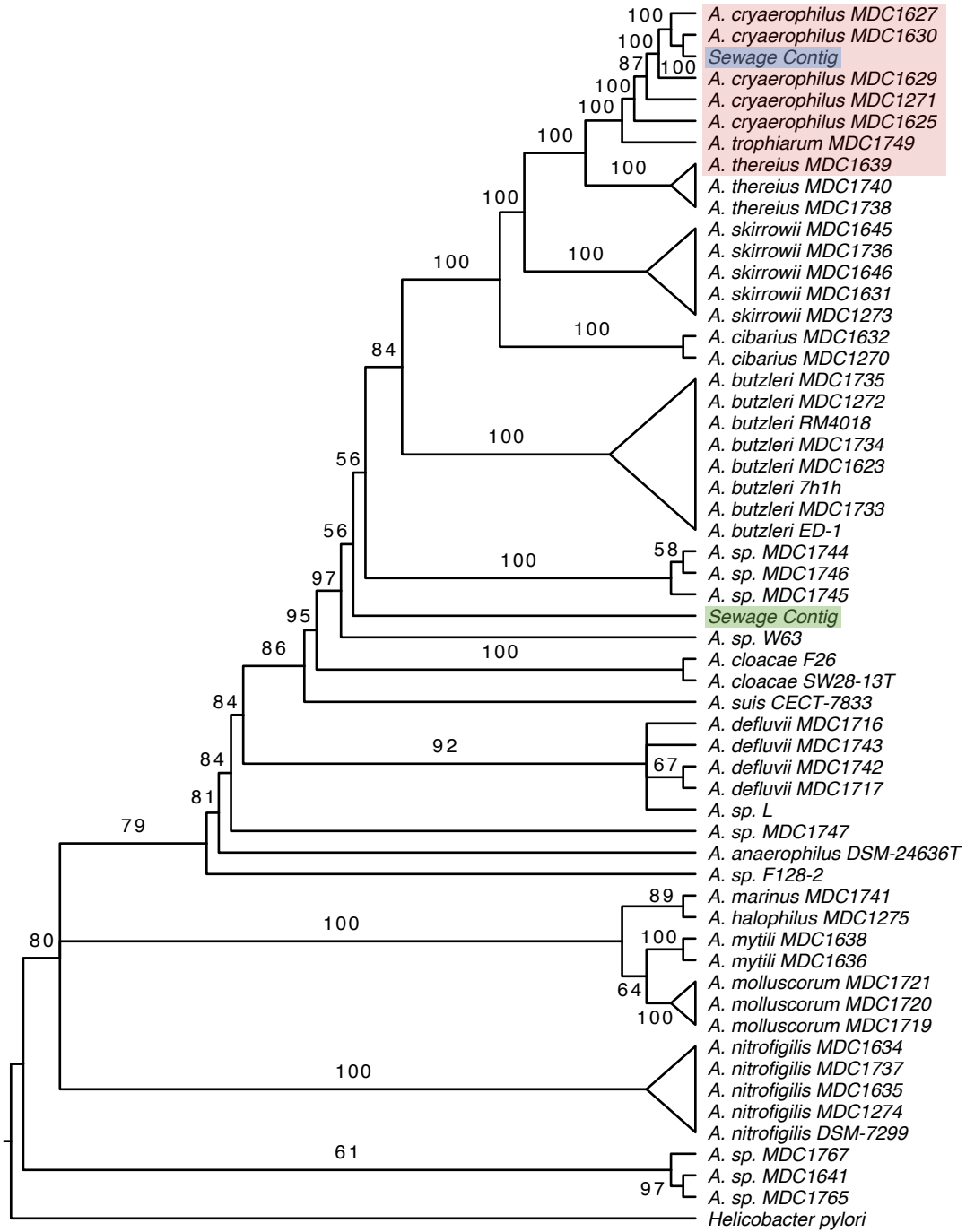
B



C



D



0.2

FIG S2. Genome bins found in initial clustering using Albertsen et al. 2013 differential coverage binning procedure for metagenomic data. The top right cluster with ~200x coverage contained all *A. cryaerophilus* housekeeping genes (Fig. S1) and was selected for secondary refinement and finishing.

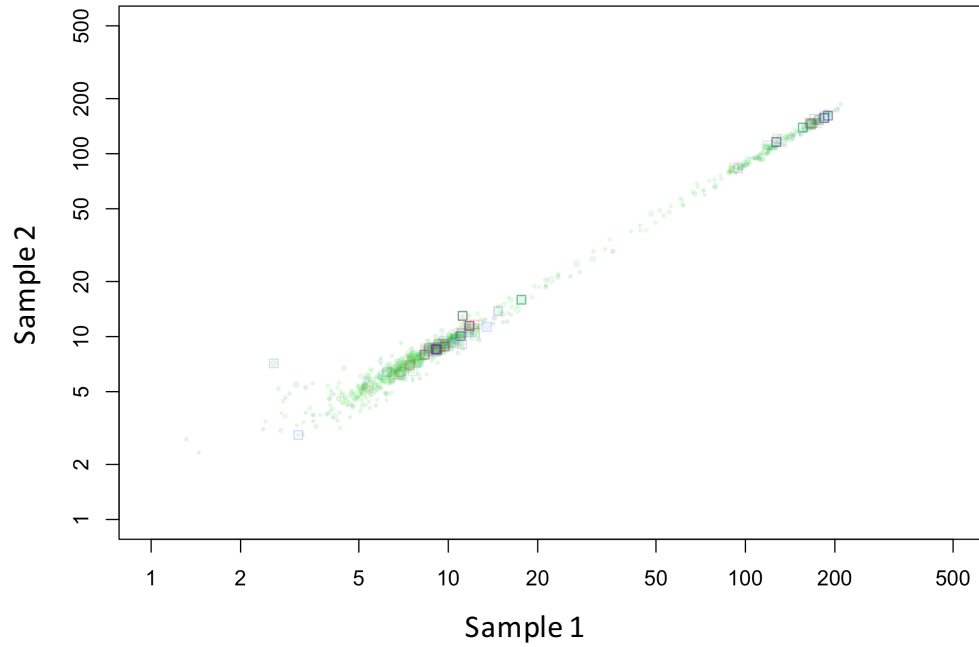
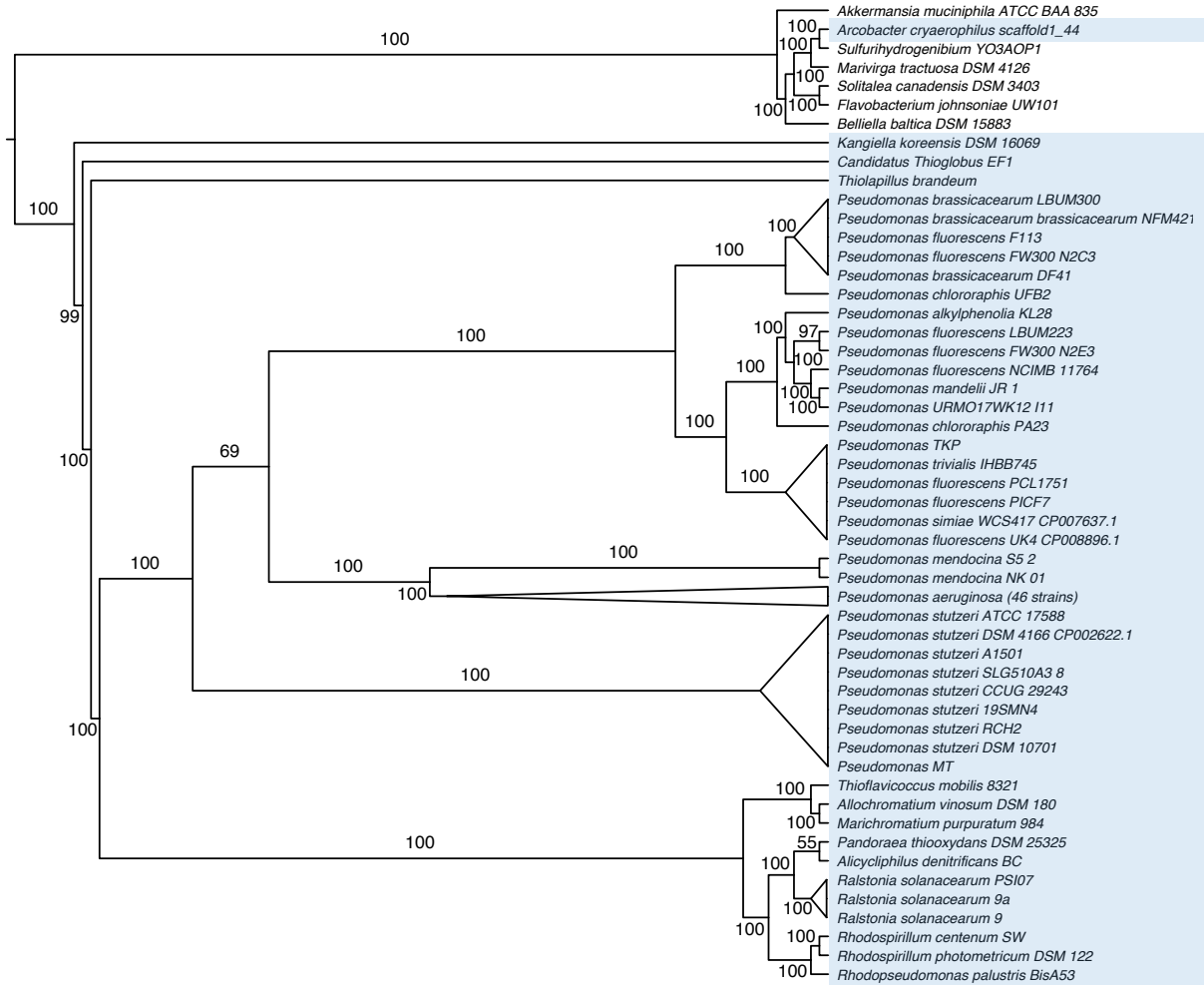


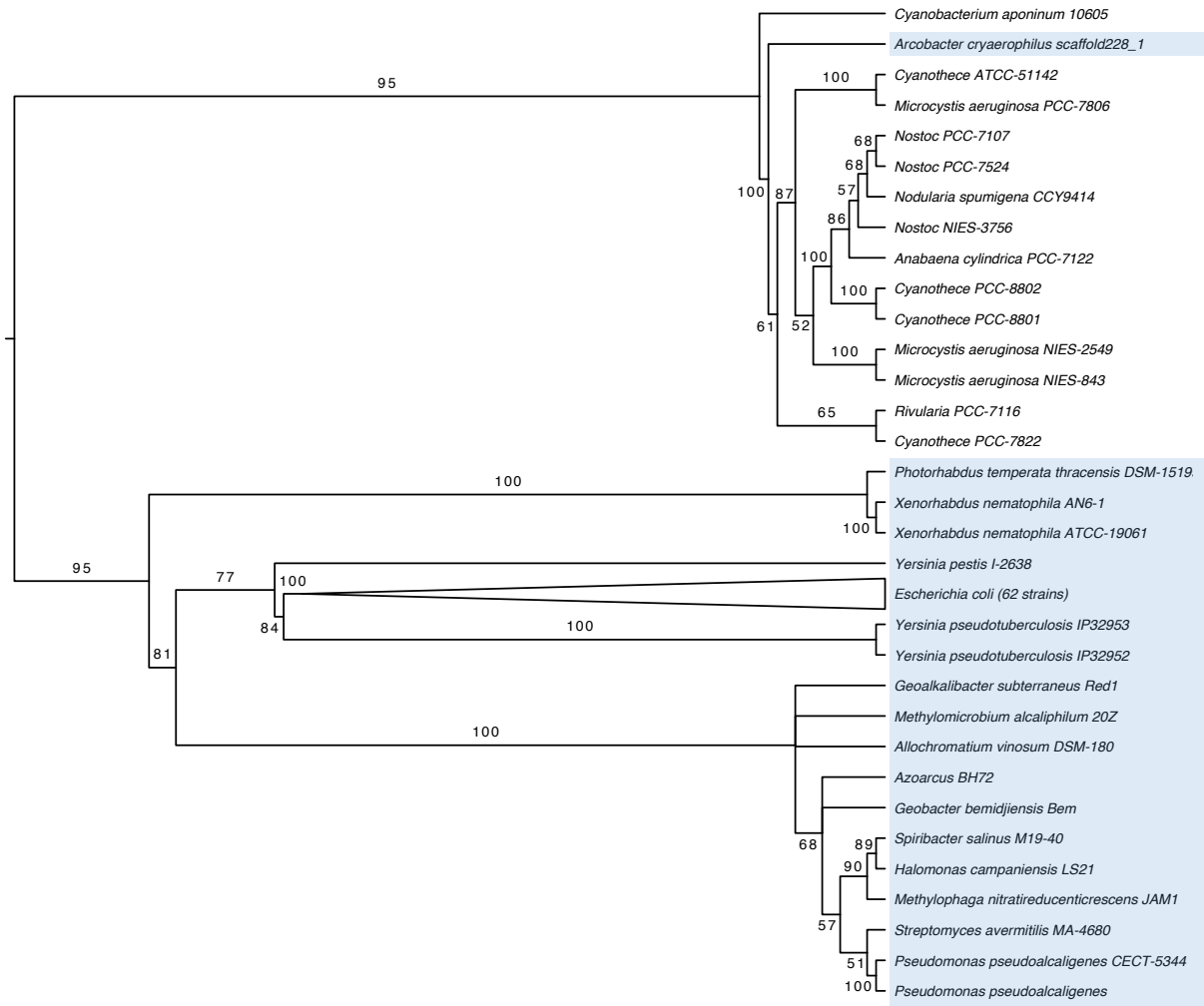
FIG S3. Phylogenetic trees to validate HGTector data. Bayesian trees of *Arcobacter cryaerophilus* ORFs **(A)** scaffold1_44 (tetracycline resistance ribosomal protection protein, 2151nt) and **(B)** scaffold228_1 (chloramphenicol phosphotransferase, 258nt) that place the ORFs outside of the phylum Proteobacteria (in blue).

A



0.2

B



0.2

FIG S4. Genome alignment of *Arcobacter butzleri* (top) and *Arcobacter cryaerophilus* (bottom). Homologous “locally collinear blocks” are identified using Mauve and connected with lines of the same color to show genome rearrangements.

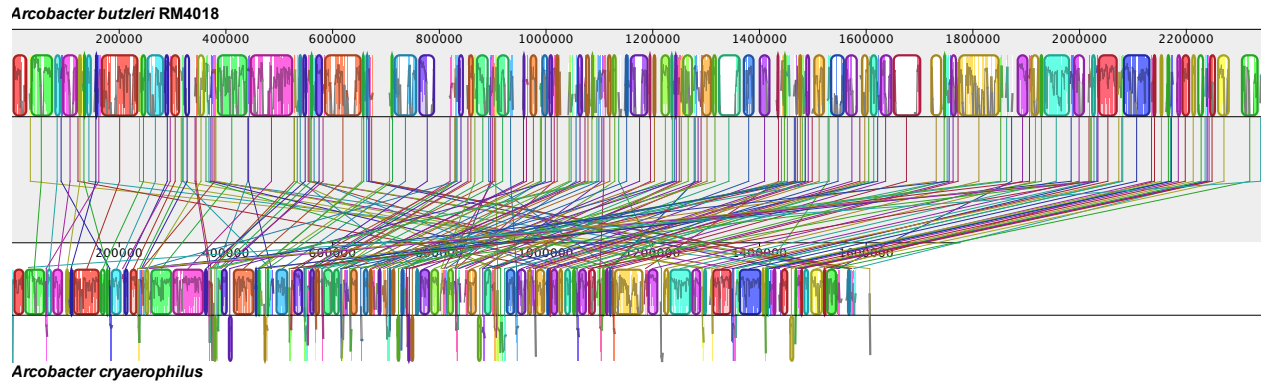


TABLE S1. DNA/RNA Reads and Assembly Totals

Reads		Sample 1	Sample 2	Sample 3
DNA	Raw	27,149,400	56,951,058	69,948,228
	Cleaned	17,632,699	37,306,119	46,473,784
	Sub Sample	17,000,000	17,000,000	17,000,000
	Mapped to Sewage Contigs	7,703,851	10,257,818	11,710,891
	Mapped to <i>Arcobacter</i> Contigs	6,947,969	9,192,258	10,294,926
RNA	Raw	142,205,531	91,010,362	58,196,397
	Cleaned	125,234,635	84,879,463	54,872,132
	Sub Sample	50,000,000	50,000,000	50,000,000
	Mapped to Sewage Contigs	8,641,383	6,985,173	7,355,494
	Mapped to <i>Arcobacter</i> Contigs	8,122,362	6,409,562	6,756,931
Contigs	Raw	6,522	15,910	17,210
	Sub Sample	6,000	6,000	6,000
	Average Length	1,189	1,145	1,087
	Length Range	300 - 27,864	300 - 27,810	300 - 18,778
	Phylum Annotated	2,866	3,433	3,264

TABLE S2. Comparison of annotated categories in *Arcobacter*.

Category	Ac ^a	Ab ^b	Category	Ac	Ab
Virulence Factors			Antibiotic Resistance		
Acid resistance	1	1	Aminocoumarin	17	15
Adhesion	18	20	Aminoglycosides	8	23
Anti-apoptosis	1	1	Bacitracin	4	5
Biofilm	1	1	Beta Lactams	11	16
Capsule	1	1	Bicyclomycin	0	2
Cell surface and memb. prot.	5	6	Chloramphenicol	4	4
Cell-to-cell spread	1	1	Ciprofloxacin	4	4
Cellular metabolism	22	12	Elfamycin	0	2
Chaperone	3	1	Erythromycin	3	2
Cording	2	1	Fluoroquinolones	18	21
Defense agnst. host imm. resp.	3	3	Fosfomycin	2	1
Intracellular survival and repl.	30	20	Fosmidomycin	1	2
Invasion	11	14	Glycylcycline	1	0
Iron uptake	4	14	Isoniazid	0	1
Mitogenic	3	1	Kanamycin	0	2
Modulate host immune resp.	3	9	Lincosamide	5	6
Phosphate uptake	3	0	Macrolide	26	25
Regulation of gene expression	4	5	Mupirocin	4	1
Secretion	4	3	Norfloxacin	2	3
Stress	5	3	Penicillin	2	6
Two-component system	6	2	Polymyxin	9	9
Type III secretion	4	1	Roxithromycin	1	0
Type VII secretion	0	1	Streptogramin	9	9
Virulence	153	114	Streptomycin	0	4
Zinc uptake	2	1	Sulfonamide	1	1
			Teicoplanin	0	3
Transposases			Tetracycline	12	24
IS1	26	34	Thiostrepton	1	1
IS110	4	0	Tigecycline	2	6
IS116	0	3	Triclosan	2	3
IS21	4	1	Vancomycin	13	27
IS3	6	4			
IS4-5	0	5	Prophage genes	290	320
IS408	4	0			
IS4like	13	2	Single copy genes	100	106
IS66	4	8			

^a*A. cryaerophilus*, ^b*A. butzleri*

TABLE S3. Number and expression of antibiotic resistance categories annotated in *A. cryaerophilus*.

Antibiotic Resistance Category	Average Total ORFs	Average Expressed ORFs
Aminocoumarin	17	17.0
Aminoglycosides	8	8.0
Bacitracin	4	4.0
Beta Lactams	11	11.0
Chloramphenicol	4	4.0
Ciprofloxacin	4	4.0
Erythromycin	3	3.0
Fluoroquinolones	18	18.0
Fosfomycin	2	1.7
Fosmidomycin	1	1.0
Glycylcycline	1	1.0
Lincosamide	5	5.0
Macrolide	26	25.7
Mupirocin	4	3.7
Norfloxacin	2	2.0
Penicillin	2	2.0
Polymyxin	9	9.0
Streptogramin	9	9.0
Sulfonamide	1	1.0
Tetracycline	12	12.0
Thiostrepton	1	1.0
Tigecycline	2	2.0
Triclosan	2	2.0
Vancomycin	13	12.7

TABLE S4. Number and expression of antibiotic resistance categories annotated in whole sewage sample.

Antibiotic Resistance Category	Average Total ORFs	Average Expressed ORFs
Acriflavine	29	25.0
Aminocoumarin	275	210.3
Aminoglycosides	184	137.7
Bacitracin	140	90.0
Beta Lactams	323	249.7
Bicyclomycin	13	10.3
Chloramphenicol	148	115.3
Ciprofloxacin	113	77.7
Deoxycholate	2	0.0
Doxorubicin	1	1.0
Elfamycin	52	48.7
Enoxacin	8	1.3
Erythromycin	33	29.7
Fluoramphenicol	3	1.0
Fluoroquinolones	471	346.7
Fosfomycin	22	17.0
Fosmidomycin	19	13.0
Glycylcycline	17	16.0
Isoniazid	20	19.0
Kanamycin	14	6.0
Lincomycin	6	2.7
Lincosamide	168	130.3
Macrolide	682	485.3
Mupirocin	57	51.7
Norfloxacin	44	28.3
Penicillin	54	47.7
Polymyxin	134	108.0
Puromycin	6	4.0
Rifampin	27	18.7
Roxithromycin	4	4.0
Streptogramin	144	112.3
Streptomycin	35	27.7
Sulfonamide	23	15.3
Teicoplanin	88	54.3
Tetracenomycin C	2	1.3
Tetracycline	392	317.3
Tetraphenylarsonium Chloride	6	4.0
Thiostrepton	21	15.3
Tigecycline	55	40.7
Triclosan	43	38.3
Trimethoprim	35	24.0
Vancomycin	244	162.7

TABLE S5. Number and expression of virulence factor categories annotated in *A. cryaerophilus*.

Virulence Factor Category	Average Total ORFs	Average Expressed ORFs
Acid resistance	1	1.0
Adhesion	18	17.7
Anti-apoptosis	1	1.0
Biofilm	1	1.0
Capsule	1	1.0
Cell surface and memb. proteins	5	5.0
Cell-to-cell spread	1	1.0
Cellular metabolism	22	22.0
Chaperone	3	3.0
Cording	2	2.0
Defense against host imm. resp.	3	3.0
Intracell. survival and replication	30	30.0
Invasion	11	11.0
Iron uptake	4	3.7
Mitogenic	3	3.0
Modulate host immune response	3	3.0
Phosphate uptake	3	3.0
Regulation of gene expression	4	4.0
Secretion	4	4.0
Stress	5	5.0
Two-component system	6	6.0
Type III secretion	4	4.0
Virulence	153	151.0
Zinc uptake	2	1.7

TABLE S6. Number and expression of virulence factor categories annotated in whole sewage sample.

Virulence Factor Category	Average Total ORFs	Average Expressed ORFs
Acid resistance	33	28.0
Acquisition of nutrients	2	1.0
Actin-based motility	7	3.0
Adhesion	248	207.3
Anti-apoptosis	19	17.0
Apoptosis	1	1.0
Avoidance of host defense	1	0.0
Bile resistance	1	1.0
Biofilm	16	15.3
Capsule	43	38.7
Cell surface and memb. proteins	82	75.0
Cell wall	1	1.0
Cell-to-cell spread	13	11.0
Cellular metabolism	233	191.0
Chaperone	41	35.3
Cording	45	36.7
Defense against host imm. resp.	90	74.0
Drug efflux system	6	4.7
Escape from the phagosome	8	4.7
Excretion	1	0.0
Heme uptake	5	3.0
Intracell. survival and replication	635	502.3
Invasion	347	291.3
Iron uptake	81	54.0
LPS (Lipopolysaccharide)	4	3.7
Mitogenic	29	29.0
Modulate host immune response	78	60.0
Molecular mimicry	10	8.0
Protease	5	3.0
Regulation of gene expression	46	35.7
Secretion	93	81.3
Stress	67	50.0
Toxin	18	10.7
Two-component system	83	57.7
Type III secretion	53	51.3
Type VII secretion	13	8.7
Virulence	2965	2294.7

DATA SET S1. Expression of ORFs mapped to antibiotic resistance categories

DATA SET S2. Comparison of overlapping genes and annotations in *Arcobacter*

DATA SET S3. Comparison of *Arcobacter* in RAST

DATA SET S4. Expression of ORFs mapped to virulence factors

DATA SET S5. Descriptive statistics of *A. cryaerophilus* contigs