SUPPLEMENTARY MATERIAL

Genetic differences in floc formation among three closely related *Competibacteraceae* clades at a full-scale activated sludge wastewater treatment plant and putative linkages to process performance

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Supplementary Tables

Table S1- Average Nucleotide Identity (ANI) values for selected Competibacter-lineage genomes. All groups listed are '*Candidatus.*'

	CPB_ P15 CA14.1	CPB_ M38 CA23.2	CA23.1	C. odensis Run BJ11	Conten-dobacter sp. UBA 2788	Compet-ibacter sp. UBA 3908	Compet-ibacter sp. UBA 2792	Compet-ibacter sp.1 UBA 2368	C. denit-rificans Run AD11	UBA 2383 UBA 2383
CPB_P15 CA14.1	1									
CPB_M38 CA23.2	0.76	1								
CA23.1	0.77	0.78	1							
Contendobacter odensis RunBJ11	0.77	0.77	0.76	1						
Contendobacter sp UBA2788	0.77	0.78	0.77	0.86	1					
Competibacter sp UBA3908	0.77	0.79	0.78	0.79	0.80	1				
Competibacter sp UBA2792	0.75	0.77	0.75	0.76	0.77	0.81	1			
Competibacter sp1 UBA2368	0.75	0.77	0.76	0.76	0.77	0.79	0.77	1		
Competibacter denitrificans RunAD11	0.74	0.75	0.75	0.75	0.75	0.77	0.75	0.77	1	
UBA2383 UBA2383	0.75	0.75	0.75	0.75	0.75	0.76	0.74	0.74	0.73	1

ANI values calculated using pyani (https://github.com/widdowquinn/pyani) using the BLAST method

Table S2- Summary of Plant Data for 2014-2015

Parameter	n	Range[a]	Average	Standard deviation
Primary TSS, mg/L	407	110-2000	404.3	172.0
Secondary TSS, mg/L	730	60-564	147.1	46.5
Mixed Liquor TSS, mg/L	730	1179-3907	2257	495
Waste Return Activated Sludge TSS, mg/L	730	3618-13860	7402	1929
Effluent TSS, mg/L	425	5-44	14.6	6.7
Secondary Influent Flow, MGD	730	43-170	58.1	16.8
Recycle Rate	425	0.15-1.00	0.42	0.12
Solids Retention Time, d	730	0.7-3.5	1.54	0.42
Mixed Liquor Volatile Suspended Solids, mg/L	206	600-4300	2024	621
pH	612	6.4-7.0	6.8	0.1
Influent cBOD, mg/L	406	50-273	160.4	37.8
Effluent cBOD, mg/L	418	3-36	9.8	4.0
Dispersed large coccoid cells, abundance[b]	233	0.5-6	2.79	1.30

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[a] Range represents minimum and maximum values for full time period

[b] Abundance rated per Jenkins method (1)

Supplementary Figures

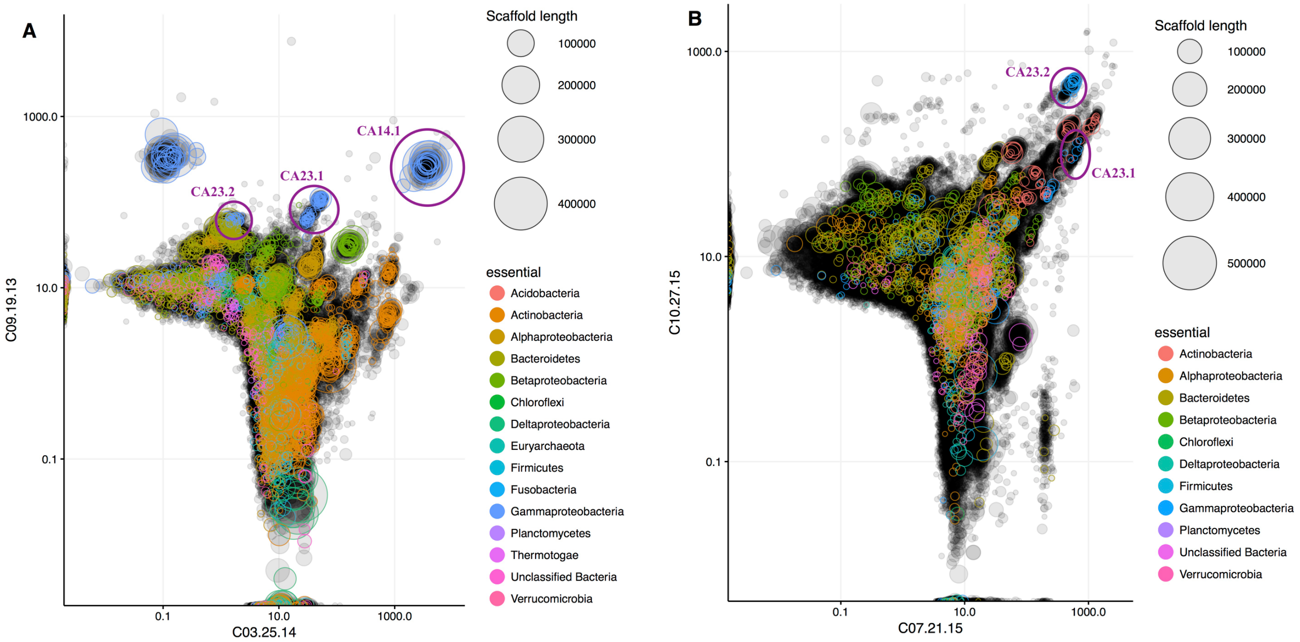

Figure S1- Contigs in metagenome samples from the Northern California plant. Coverage plots for (A) samples 2014-03-25 and 2013-09-19, and (B) samples 2015-07-21 and 2015-10-27. Extracted bins are marked. Contigs are colored by phyla based on predicted essential genes using the ‘mmgenome’ workflow (2).

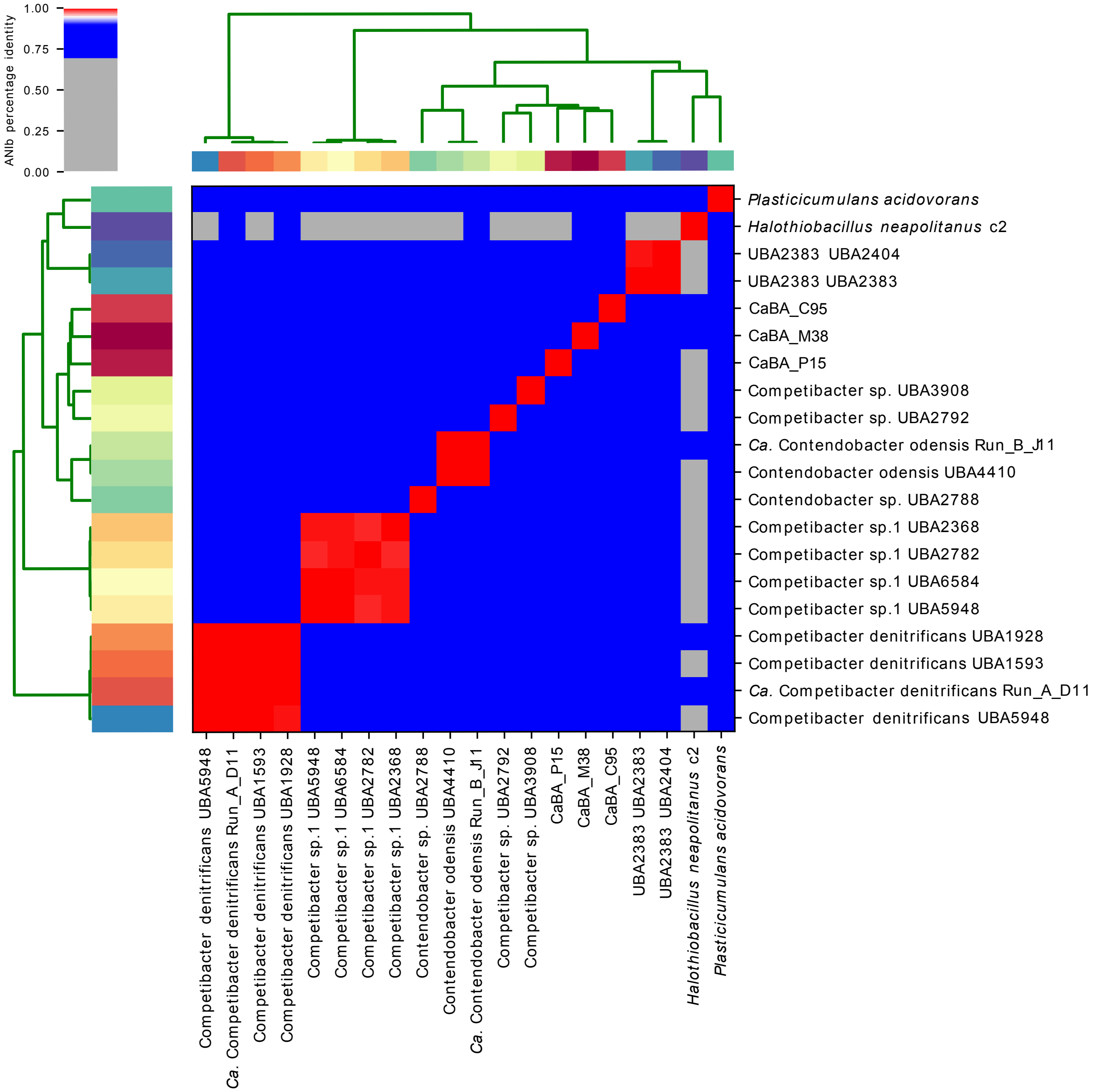

Figure S2- Average Nucleotide Identity plot of all available *Competibacteraceae* genomes (as of June 2018). Plot produced with pyani (https://github.com/widdowquinn/pyani) using the BLAST method.

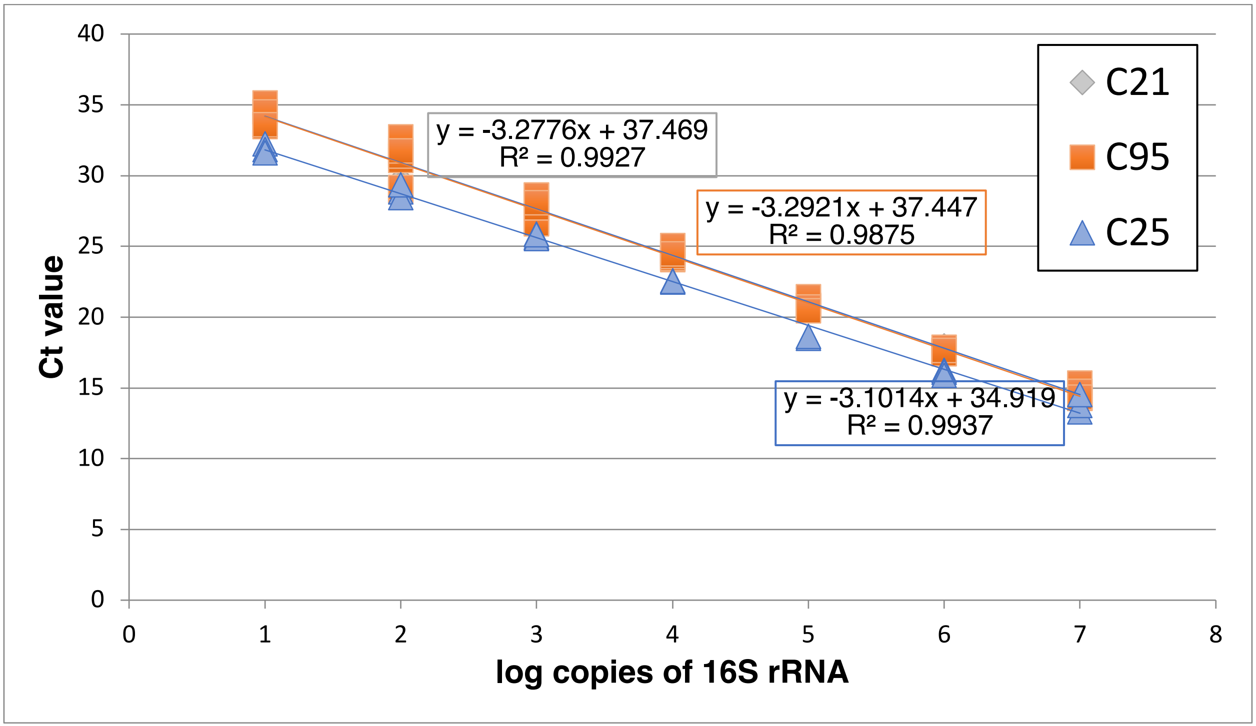

Figure S3- Standard curves for qPCR Assay. CaBA clone C21- CPB_M38; CaBA clone C95-CPB_C95; CaBA clone C25- CPB_P15.

REFERENCES

1. Jenkins D, Richard MG, Daigger GT. 2004. Manual on the causes and control of activated sludge bulking, foaming, and other solids separation problems. Lewis Publishers.
2. Karst SM, Kirkegaard RH, Albertsen M. 2016. mmgenome: a toolbox for reproducible genome extraction from metagenomes. bioRxiv 059121.