Table S1. Output of SIMPER analysis showing OTUs responsible for approximately 25% of the overall average dissimilarity (~54%) observed between the bacterial communities in the CAS bioreactors[a]

TRF (bp)[b]	Cum %[c]	Mean abundance[d]		Restriction enzyme			Putative Phylogeny[e]
		HC	LC	*Hae*III	*Rsa*I	*Msp*I	
242	1.40	0.73	**2.86**	X			*Bacteroidetes, Firmicutes*
245	2.67	1.77	**2.37**		X		*Deltaproteobacteria*
230	3.82	0.00	**2.44**			X	*Firmicutes*
486	4.86	**3.04**	1.14			X	Various groups
239	5.83	0.87	**1.69**		X		*Alphaproteobacteria*
240	6.78	**1.54**	1.36	X			*Firmicutes*
494	7.59	**1.58**	1.33			X	*Cyanobacteria, Gammaproteobacteria*
233	8.36	**1.70**	0.17	X			*Firmicutes*
63	9.10	**1.50**	1.33		X		*Bacteroidetes*
470	9.84	**3.67**	3.08		X		Various groups
477	10.55	**2.27**	1.46		X		Various groups
225	11.26	0.85	**1.36**			X	*Deltaproteobacteria*, *Firmicutes*
251	11.97	0.68	**1.51**		X		*Deltaproteobacteria*
68	12.67	0.84	**1.32**	X			*Actinobacteria*
539	13.37	**1.66**	0.87			X	*Bacteroidetes, Firmicutes*
237	14.05	**1.18**	0.65	X			*Firmicutes*
245	14.73	**0.94**	0.89			X	*Alphaproteobacteria*
491	15.40	**2.09**	1.48			X	*Betaproteobacteria*
545	16.06	2.34	**2.52**			X	*Bacteroidetes, Firmicutes*
68	16.71	0.46	**1.56**		X		*Gammaproteobacteria*
60	17.35	0.75	**1.35**	X			*Gammaproteobacteria*
110	17.97	1.08	**1.50**		X		*Alphaproteobacteria*
227	18.57	**1.74**	1.10	X			*Actinobacteria*
64	19.14	**1.20**	0.72			X	*Firmicutes*
198	19.70	**1.18**	0.96	X			*Betaproteobacteria*
308	20.25	1.01	**1.24**	X			*Firmicutes*
500	20.79	**1.47**	1.46			X	*Alphaproteobacteria*
64	21.33	**1.13**	0.30	X			*Actinobacteria, Alphaproteobacteria*
597	21.87	**1.19**	0.16			X	Various groups
426	22.41	0.56	**1.24**		X		*Cyanobacteria, Deltaproteobacteria*
457	22.94	0.67	**1.02**		X		*Actinobacteria, Firmicutes*
175	23.46	**0.82**	0.42		X		*Bacteroidetes, Firmicutes*
257	23.98	**1.10**	0.70	X			*Gammaproteobacteria, Actinobacteria*
218	24.49	**1.56**	1.45	X			Various groups
71	24.99	0.35	**1.13**			X	Various groups

[a] SIMPER: Similarity Percent; OTU: Operational Taxonomic Unit; CAS: Conventional Activated Sludge

[b] TRF (bp): Terminal Restriction Fragments identified by their size in base pairs

[c] Cum %: Cumulative percent of contribution to the overall dissimilarity between groups

[d] Values in bold show in which CAS bioreactor that taxa (population) was more abundant

[e] Putative phylogeny determined with the Phylogenetic Assigment Tool (PAT+); Various Groups: 3 or more phylogenetic groups (Phyla) were associated to this TRF