



Supplementary Material

Table S1. pH and Temperature values at different sampling points. (n=50).

Parameter	P1	P3	P5
pH (50)	7.16±0.71	7.10±0.36	7.67±0.39
Temperature °C (50)	24.8±4.1	24.7±2.9	24.7±2.8
Redox potential mV (50)	-28.04±218.74	-302.63±39.12	-260.24±53.10

Table S2. Number of OTUs and % distribution among the 6 biomass samples. Microbial genera are divided into three groups based on functional pathway.

Group	Genus	C-AnC		C-G2		C-Soil		C-Slag		CW-In		CW-Out	
Hydrolysis, fermentation, syntrophy, and acetogenesis	<i>Acinetobacter</i>	12	0.03%	13	0.71%	13	0.38%	13	0.35%	12	0.23%	9	0.15%
	<i>Aminiphilus</i>	5	0.01%	4	0.22%	3	0.09%	3	0.08%	4	0.08%	3	0.05%
	<i>Aminivibrio</i>	6	0.02%	6	0.33%	5	0.15%	6	0.16%	6	0.12%	5	0.08%
	<i>Aminomonas</i>	6	0.02%	5	0.27%	3	0.09%	3	0.08%	5	0.10%	6	0.10%
	<i>Bacteroides</i>	9	0.02%	39	2.14%	10	0.29%	35	0.93%	10	0.20%	1	0.02%
	<i>Christensenellaceae_R-7_group</i>	42	0.11%	31	1.70%	16	0.47%	42	1.12%	16	0.31%	28	0.47%
	<i>Cloacibacillus</i>	9	0.02%	9	0.49%	5	0.15%	6	0.16%	9	0.18%	9	0.15%
	<i>Faecalibacterium</i>	2	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	1	0.02%
	<i>Lactivibrio</i>	3	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	3	0.05%
	<i>Microbacterium</i>	3	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	3	0.05%
	<i>Paenisporsarcina</i>	1	0.00%	1	0.05%	2	0.06%	2	0.05%	3	0.06%	3	0.05%
	<i>Prevotella_9</i>	0	0.00%	1	0.05%	1	0.03%	0	0.00%	1	0.02%	0	0.00%
	<i>Rhodopseudomonas</i>	10	0.03%	6	0.33%	3	0.09%	5	0.13%	7	0.14%	9	0.15%
	<i>Roseburia</i>	3	0.01%	9	0.49%	2	0.06%	7	0.19%	3	0.06%	0	0.00%
	<i>Ruminococcaceae_UCG-002</i>	4	0.01%	9	0.49%	3	0.09%	6	0.16%	3	0.06%	4	0.07%
	<i>Sediminibacterium</i>	0	0.00%	2	0.11%	3	0.09%	1	0.03%	2	0.04%	1	0.02%
	<i>Syntrophus</i>	11	0.03%	15	0.82%	15	0.44%	12	0.32%	17	0.33%	14	0.23%
	<i>Thermovirga</i>	5	0.01%	6	0.33%	1	0.03%	6	0.16%	1	0.02%	7	0.12%
Methanogenesis	<i>unidentified_Synergistaceae</i>	15	0.04%	13	0.71%	10	0.29%	15	0.40%	13	0.25%	16	0.27%
	<i>vadinBC27_wastewater-sludge_group</i>	10	0.03%	8	0.44%	4	0.12%	9	0.24%	6	0.12%	9	0.15%
	<i>Methanobacterium</i>	11	0.03%	11	0.60%	4	0.12%	11	0.29%	10	0.20%	12	0.20%
	<i>Methanobrevibacter</i>	3	0.01%	3	0.16%	1	0.03%	3	0.08%	3	0.06%	2	0.03%
	<i>Methanomethylovorans</i>	3	0.01%	3	0.16%	1	0.03%	3	0.08%	3	0.06%	2	0.03%

Group	Genus	C-AnC		C-G2		C-Soil		C-Slag		CW-In		CW-Out	
	<i>Methanosaeta</i>	8	0.02%	16	0.88%	6	0.17%	12	0.32%	15	0.29%	11	0.18%
	<i>Methanosarcina</i>	3	0.01%	3	0.16%	1	0.03%	2	0.05%	2	0.04%	2	0.03%
	<i>Methanospirillum</i>	11	0.03%	11	0.60%	5	0.15%	9	0.24%	8	0.16%	11	0.18%
Surfactants degraders (related to anaerobic degradation of aromatic compounds)	<i>Acinetobacter lwoffii</i>	85	0.23%	92	5.04%	6	0.17%	156	4.17%	4	0.08%	9	0.15%
	<i>Acinetobacter schindleri</i>	6	0.02%	69	3.78%	1989	57.97%	234	6.25%	137	2.68%	121	2.02%
	<i>Acinetobacter townneri</i>	7	0.02%	2	0.11%	3	0.09%	7	0.19%	2	0.04%	0	0.00%
	<i>Acinetobacter ursingii</i>	34	0.09%	61	3.34%	472	13.76%	104	2.78%	71	1.39%	26	0.43%
	<i>Dechloromonas agitata</i>	0	0.00%	3	0.16%	31	0.90%	3	0.08%	4	0.08%	0	0.00%
	<i>Geobacter lovleyi</i>	70	0.19%	112	6.13%	124	3.61%	463	12.36%	86	1.68%	29	0.48%
	<i>Geobacter pickeringii</i>	0	0.00%	0	0.00%	9	0.26%	0	0.00%	0	0.00%	1	0.02%
	<i>Geobacter</i> sp. AOG5	72	0.20%	56	3.07%	125	3.64%	309	8.25%	85	1.66%	189	3.16%
	<i>Geobacter</i> sp. OR-1	0	0.00%	1	0.05%	5	0.15%	2	0.05%	0	0.00%	8	0.13%
	<i>Pseudomonas alcaligenes</i>	0	0.00%	20	1.10%	2	0.06%	44	1.17%	4	0.08%	1	0.02%
	<i>Pseudomonas caeni</i>	0	0.00%	20	1.10%	0	0.00%	23	0.61%	0	0.00%	0	0.00%
	<i>Pseudomonas japonica</i>	6	0.02%	8	0.44%	164	4.78%	20	0.53%	10	0.20%	11	0.18%
	<i>Pseudomonas psychrotolerans</i>	5	0.01%	13	0.71%	40	1.17%	16	0.43%	13	0.25%	7	0.12%
	<i>Pseudoxanthomonas mexicana</i>	14	0.04%	17	0.93%	178	5.19%	77	2.06%	36	0.70%	107	1.79%
	<i>Rhodopseudomonas palustris</i>	35905	98.29%	980	53.67%	26	0.76%	1933	51.62%	4365	85.25%	5149	86.10%
	<i>Desulfitobacterium</i>	1	0.00%	2	0.11%	1	0.03%	3	0.08%	3	0.06%	1	0.02%
	<i>Desulfobacca</i>	0	0.00%	1	0.05%	2	0.06%	0	0.00%	0	0.00%	1	0.02%
	<i>Desulfomicrobium</i>	6	0.02%	6	0.33%	5	0.15%	6	0.16%	6	0.12%	6	0.10%
	<i>Desulfomonile</i>	18	0.05%	18	0.99%	18	0.52%	20	0.53%	21	0.41%	27	0.45%
	<i>Desulforegula</i>	3	0.01%	6	0.33%	4	0.12%	6	0.16%	6	0.12%	4	0.07%
	<i>Desulforhabdus</i>	3	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	3	0.05%

Group	Genus	C-AnC		C-G2		C-Soil		C-Slag		CW-In		CW-Out		
Sulphate Reducing Bacteria	<i>Desulfovibrio</i>	66	0.18%	73	4.00%	62	1.81%	67	1.79%	61	1.19%	71	1.19%	
	<i>Desulfovirga</i>	4	0.01%	2	0.11%	6	0.17%	1	0.03%	5	0.10%	5	0.08%	
	<i>Smithella</i>	3	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	3	0.05%	
	<i>Syntrophobacter</i>	2	0.01%	3	0.16%	3	0.09%	3	0.08%	3	0.06%	2	0.03%	
	<i>Rhodoblastus</i>	12	0.03%	10	0.55%	10	0.29%	12	0.32%	10	0.20%	10	0.17%	
	<i>Roseobacter_clade_CHAB-I-5_lineage</i>	5	0.01%	7	0.38%	6	0.17%	5	0.13%	5	0.10%	9	0.15%	
	<i>Sulphuricurvum</i>	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	
	<i>Thiobacillus</i>	9	0.02%	5	0.27%	8	0.23%	5	0.13%	9	0.18%	9	0.15%	
Number of OTU		36531		1	1826	1	3431	1	3745	1	5120	1	5980	1

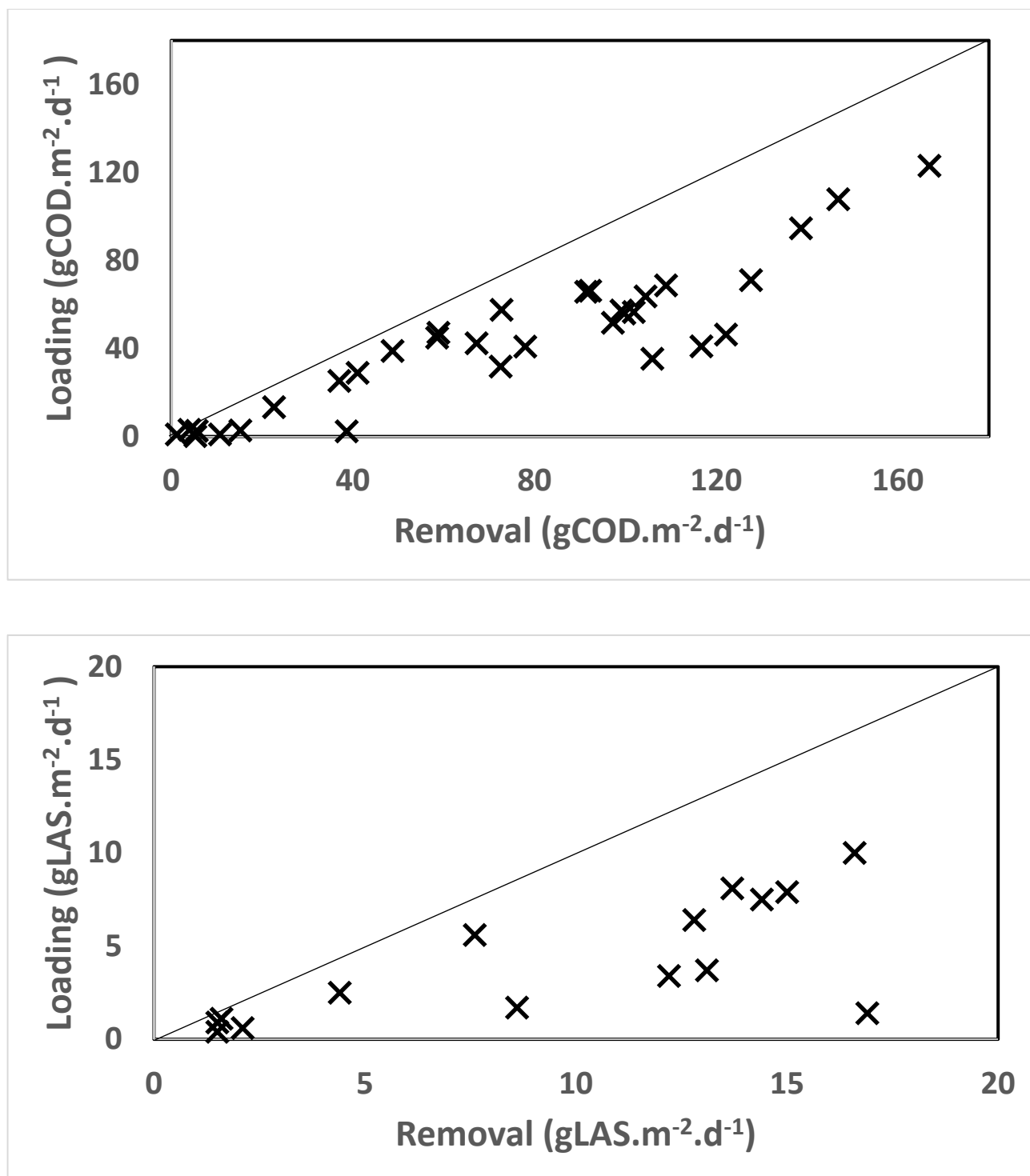


Figure S1. Top: Correlation between loading and removal in the EvaTAC system. Top: organic load applied (loading) and removed (removal) for chemical oxygen demand (COD). Bottom: LAS load applied (loading) and removed (removal) for linear alkyl benzene sulfonate (LAS).