

SUPPORTING INFORMATION of “Combusted-diesel additives containing CeO₂ nanomaterials shape methanogenic pathways during sludge digestion and enhance biogas production”

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Feature volatility analysis: dynamic view of important features: For a dynamic visualization of the feature volatility analysis, open the <https://view.qiime2.org/> and drag the volatility_plot.qzv file into the frame. Select group column “treatment” and the ASV number in the metric column menu.

Figure S 1. Aerobic wastewater treatment operating parameters: (A) Evolution of VSS, (B) COD removal, (C) Nitrogen removal, (D) Phosphorus removal, (E) ATP production, (F) pH evolution.

Figure S 2. Microbial community structure of the aerobic sludge. PCA based on Weighted UniFrac distance Abundance & Phylogeny.

Figure S 3. Aerobic sludge response following combusted CeO₂ NMs dosing. (A, B) Specific hydrolytic enzyme activities (Protease and α -glucosidase), (C, D) Polysaccharides of extracellular polymeric substances secretion during the aerobic sludge culture. *Represents data that are statistically significant (p-value<0.05). Values are average \pm standard deviation.

Figure S 4. Distribution and speciation of Ce during the anaerobic sludge production. (Left) Total and dissolved (<3 KDa) Ce concentrations remaining in the liquid phase after separation by centrifugation of the anaerobic sludge (Black symbols). Blue squares represent the total concentration of combusted CeO₂ NMs (in mg CeO₂.L⁻¹) injected in the digestors during 40 days. Red circles represent the Ce concentration in the liquid phase of control digestors at the end of the experiment. Values are means of three repetitions \pm standard deviation. (Right) Experimental HERFD-XANES spectra at the Ce L₃-edge in the anaerobic sludge fed with contaminated aerobic sludge. Experimental XANES spectrum is compared to Ce (III)-phosphate and initial combusted EnviroxTM reference compounds.

Figure S 5. Anaerobic digestion operating parameters. (A). Time course of volatile suspended solids, (B). ATP production, (C). Culture pH. Opened symbols correspond to control culture and filled symbols to reactor spiked with comb-CeO₂ NMs.

Figure S 6. Microbiome composition in the control and comb-CeO₂ contaminated AD. Stacked bar plots showing the relative abundance and distribution of the total microbial community at class level at day (D) 1, 11, 19, 22 and 29.

Figure S 7. Feature volatility analysis: abundance (\pm error bars) of the two most discriminatory ASV over time between the control (orange) and the comb-CeO₂ AD.

Figure S 8. Main physico-chemical and structural and characteristics adapted from Auffan et al. (2017).

Table S 1. Feature volatility analysis is used to determine how microbial communities change over time on the ASV level. Feature importance, and descriptive statistics (global mean and global standard deviation) help guiding an exploratory investigation to identify relevant features for subsequent investigation ⁵⁰.

Table S ⁴⁶. Differentially abundant taxa between the control and comb-CeO₂ contaminated AD. Linear Discriminant Analysis Effect Size (LEfSe): all linear discriminant analysis [LDA] scores, >3). Taxonomy levels: (p), phylum; (c), class; (o), order; (f), family; (g), genus. Relative abundances of taxa that are increased in the control (green) and comb-CeO₂ contaminated (red) AD.

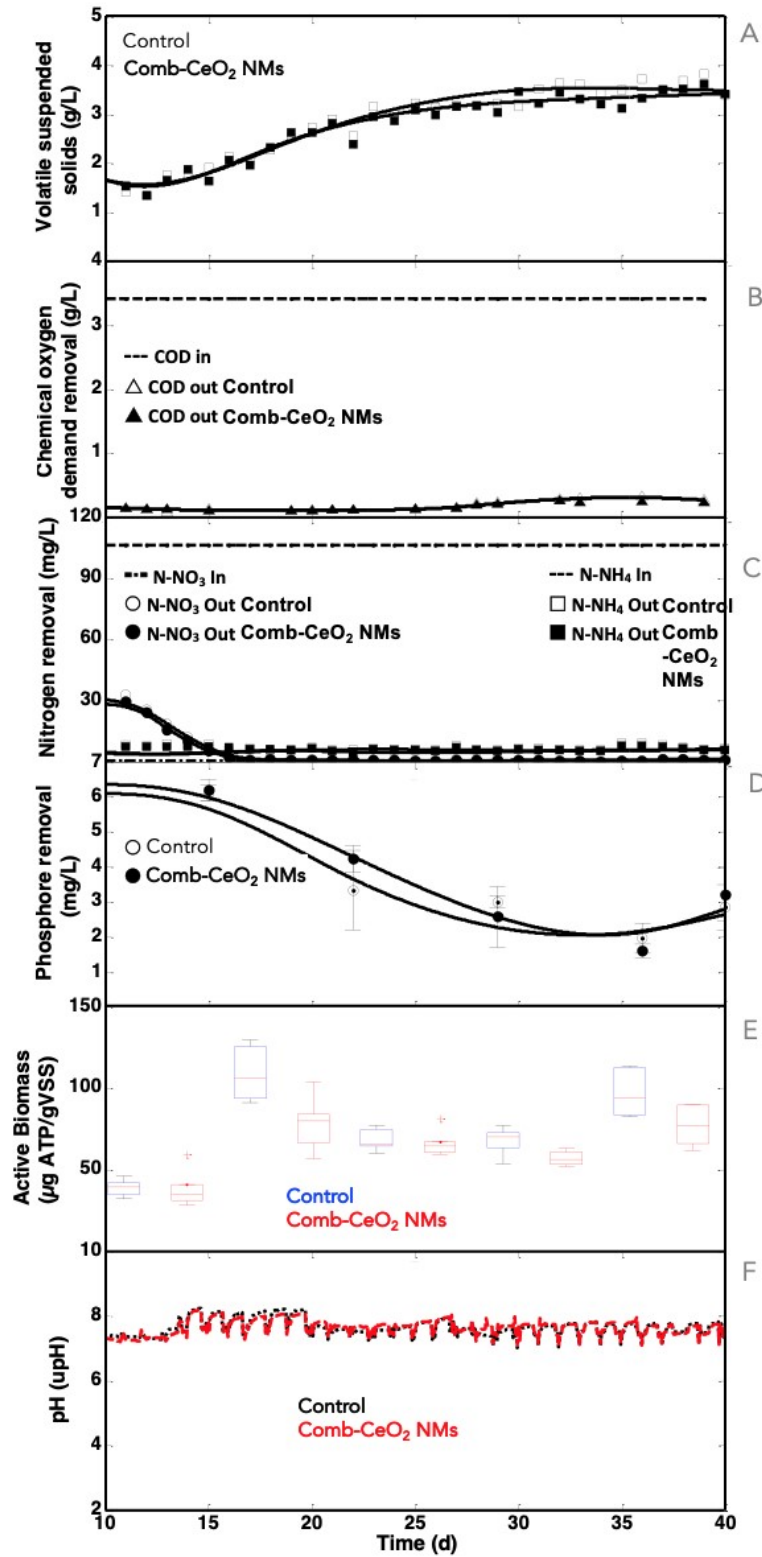


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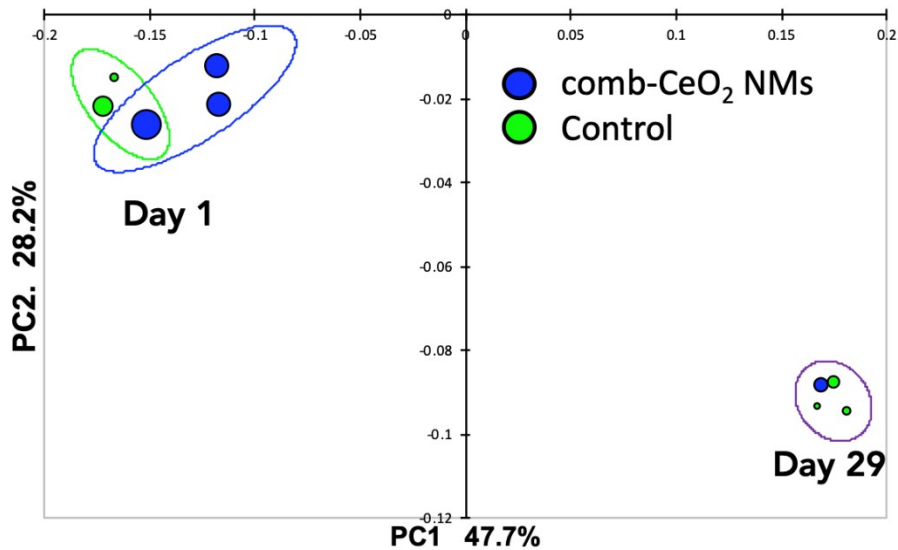


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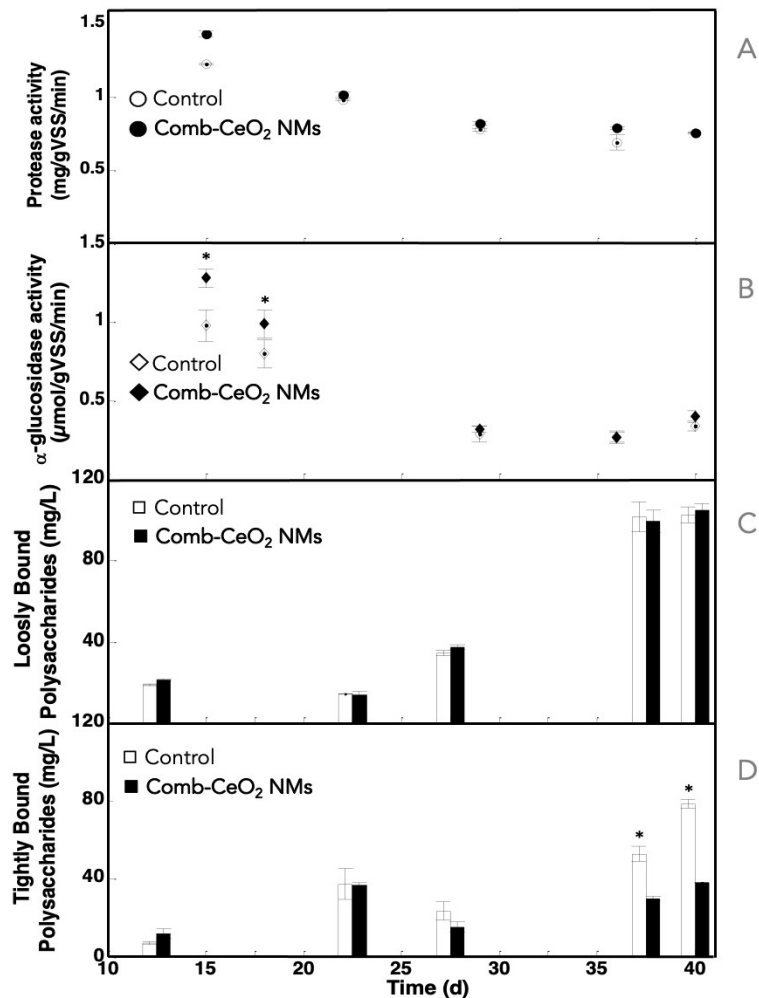


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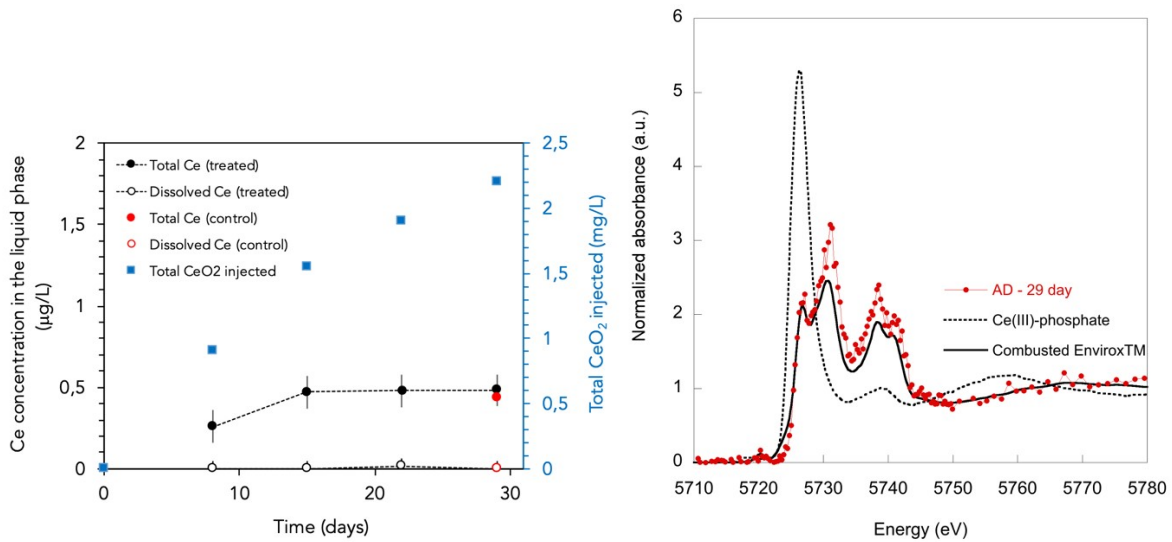


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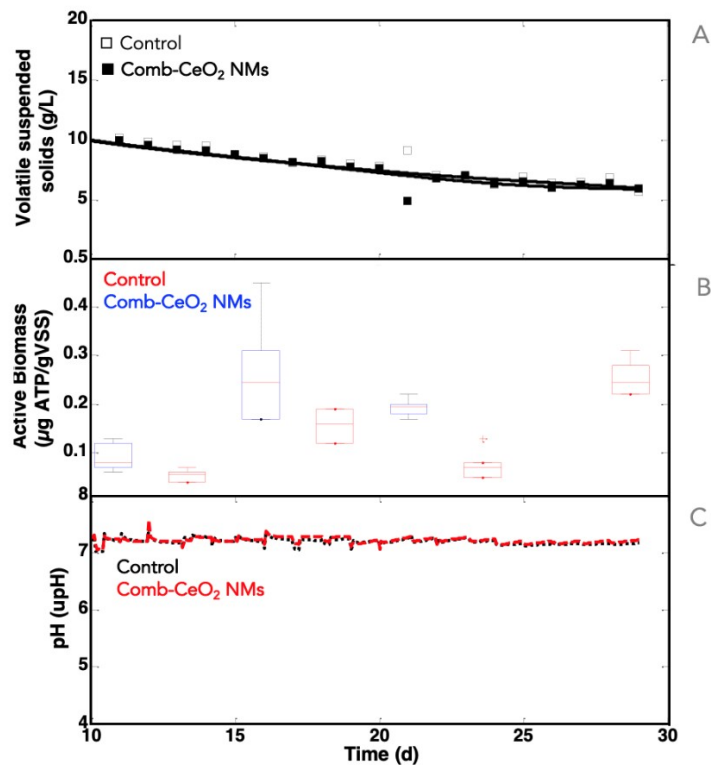


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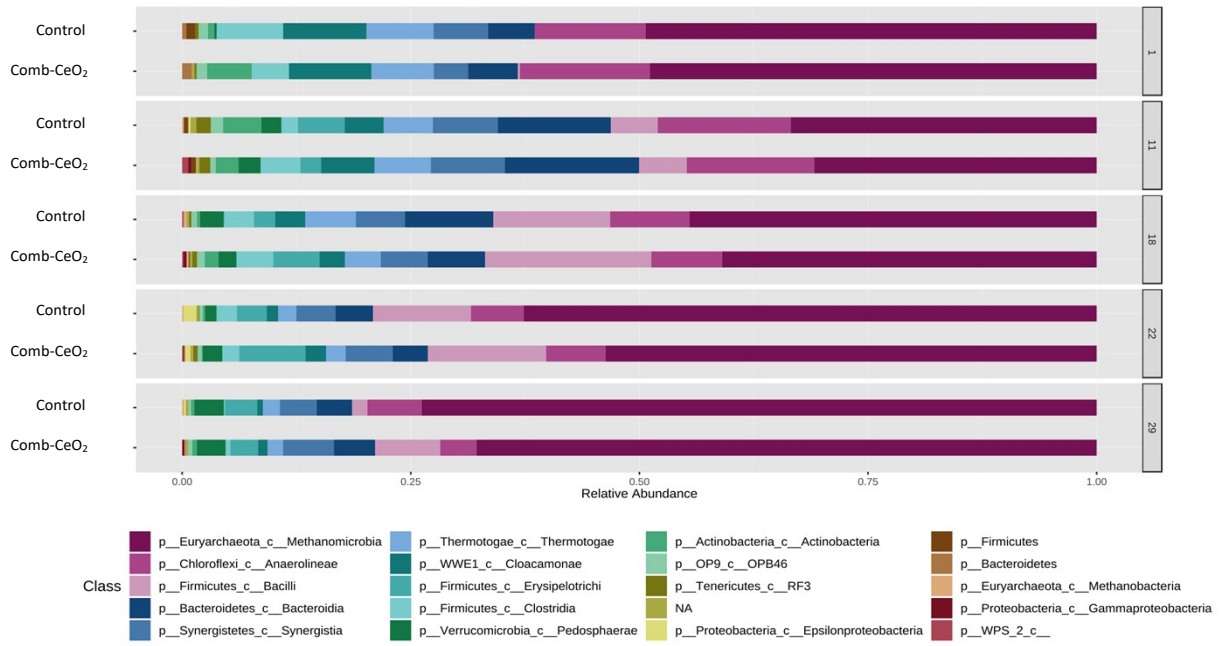


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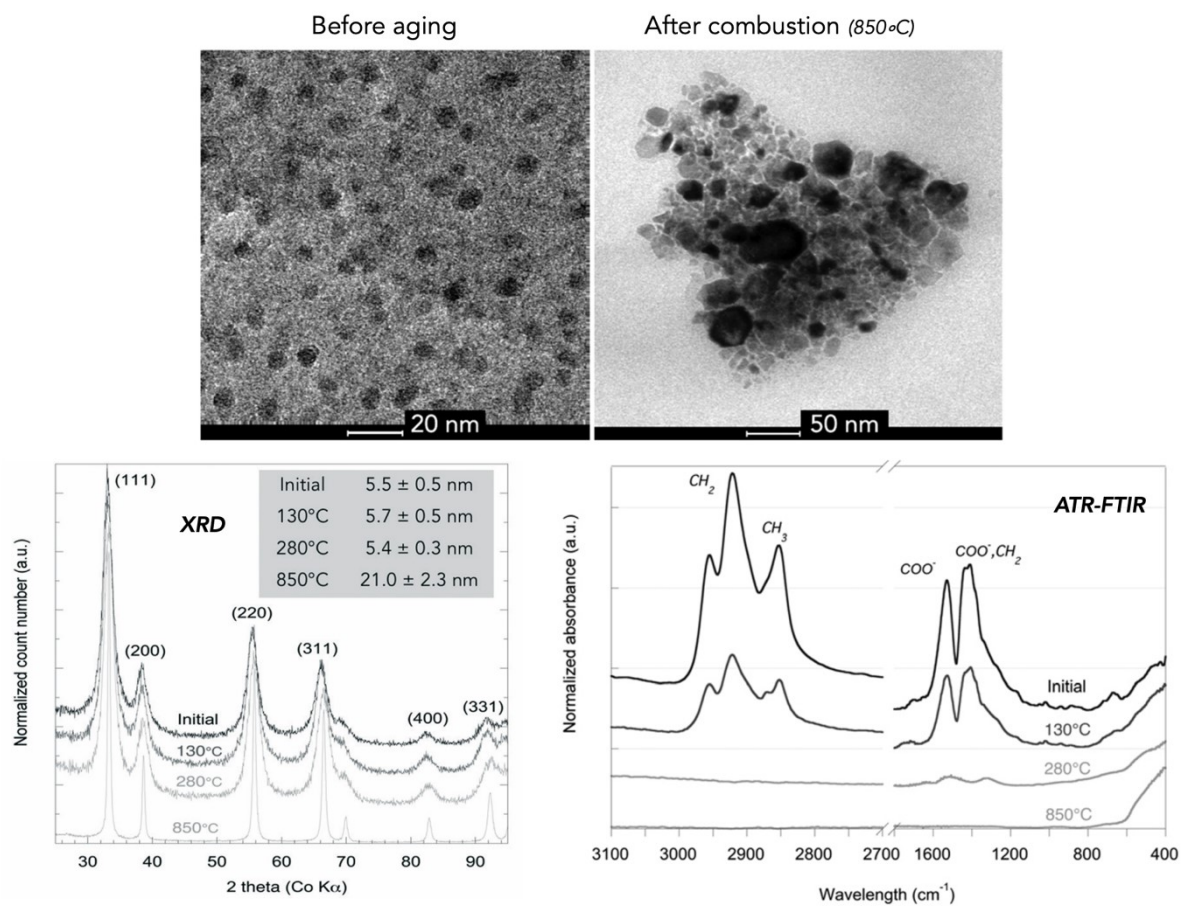


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Table S 1. Feature volatility analysis is used to determine how microbial communities change over time on the ASV level. Feature importance, and descriptive statistics (global mean and global standard deviation) help guiding an exploratory investigation to identify relevant features for subsequent investigation⁵⁰.

ASV id	Taxonomy	Importance	Global Mean	Global Standard Deviation
b25e1bee18677eb0898c7f6fc3aa5204	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanoregularae; g__Methanosphaera; s__	0.23092847	0.010925007	0.008577815
69a67a19729a3c18cd9279f5e288778e	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanoregularae; g__Methanosphaera; s__	0.12050728	0.010880877	0.008045194
7afe23990e04de1c9f43a641f7b6fd9	k__Bacteria; p__Firmicutes; c__Erysipelotrichi; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Clostridium	0.08310119	0.006762499	0.006581115
07300b6d32de20a6780fee670ef7848	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.08013636	0.007543341	0.007733178
5d62e652303e12b3688e6dd8a655c97	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.07594373	0.073510722	0.029663486
fa432c2a8dd82599b6149bdebea0c5cc	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.04820452	0.087228068	0.035224222
016e4569ff3c443c63836c121e6b48	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.03976716	0.079744692	0.03191055
7ed38c44cfc94f855a421bc77e0554	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.02521171	0.003866683	0.006750624
bd0b0379d263c2b64ca733677d44745a	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.02474832	0.068180223	0.02640936
18b65b953a2d2e7644a4a0820c236b4	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.02443555	0.007232002	0.004803437
c795b44d8d52497644a0c39d2fd1	k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__HA73; s__	0.01916828	0.00214778	0.00326215
1c4449e9b325b09240694db4b497f1	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.01734321	0.003933945	0.00512809
82396f2ab90f1d583a5e42e2a1198	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.01708814	0.014172222	0.015363745
457a4019d9525ec1abb55e91342f6f	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Lutispora; s__	0.01587157	0.00125333	0.002817788
be9d945e7e21b9625e7d754c5c0c76	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.01487859	0.005727205	0.00681843
4d53af2498f70adbbd0ca35eb8e48a2	k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__HA73; s__	0.01243279	0.004318722	0.005134768
b94996aa83b530cc9954db84537165	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.01140165	0.015195941	0.016170305
7aca67a8d70252ba4d5a60c7ea210e	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Marinifilabacterae; g__	0.0093195	0.006953402	0.007588195
e73b7a0ad7ccc3b9eb91755deb4583c	k__Bacteria; p__OP8; o__OP8_1; o__OP95; f__	0.00884474	0.000882169	0.002210582
31b774be9385116bc9e55ea1ae2da1	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00832951	0.005219208	0.005176873
7e4a158ab22a1fc3521d2974c11d71	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	0.00831132	0.004532963	0.005370767
e9034d5606226a6f7bceae755967d5	k__Bacteria; p__WWE1; c__Cloacamonae; o__Cloacamonales; f__Cloacamonaceae; g__W5; s__	0.00759834	0.004583006	0.006410354
e95d0ff43acbc59798914446bc4a0083	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Paludibacter; s__	0.00731582	0.004262497	0.005084272
ee05394c1f83aa3947458c2393c7f	k__Archaea; p__Euryarchaeota; c__Methanobacteriales; f__WSA2; g__	0.00687637	0.00094014	0.002126499
3a81c9f645bc328495012327abc0f7	k__Bacteria; p__Firmicutes; c__Erysipelotrichi; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Clostridium	0.00659725	0.006918149	0.007352384
d2ce3456f82292e79e34b9e2d715	k__Bacteria; p__WWE1; c__Cloacamonae; o__Cloacamonales; f__Cloacamonaceae; g__W5; s__	0.00586529	0.00353668	0.004541319
1b1bc30b8e3fae3899a6e7af8c5269	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00539825	0.005391113	0.006485766
15382277400c7f78118b35ea0860c	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales	0.00473687	0.013208162	0.009044988
340c0e7f7f932a2e024db2156a6c5b	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Paludibacter; s__	0.00411639	0.004132441	0.006039238
0e259dc3f35a8a3d137ca6c8efb100b	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__	0.00349114	0.000901942	0.002848567
37e74e8e8045d9128cd1a5a2e17b006	k__Bacteria; p__Verrucomicrobia; c__Pedosphaerae; f__Pedosphaerales; f__R4-41B; g__	0.00344443	0.003140521	0.003722265
1a8e569daab17f8ac0866603260c40	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Paludibacter; s__	0.00314717	0.002954485	0.004714843
18777b7bc5ec4f55d2c3140cac7e4e	k__Bacteria; p__Firmicutes; c__Erysipelotrichi; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Clostridium	0.00313986	0.009868156	0.007166936
fa92c1a82d324034bac63bd2a181c	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__HOC36; f__	0.00269621	6.33E-05	0.000251113
daa6048e0f7d2ec1ade44d130a21	k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Dethiosulfovibrionaceae; g__HA73; s__	0.00269271	9.29E-05	0.000353433
100e04e9925325550702ea16c4519a	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00263168	0.007947818	0.004657548
924f93b61584e812e9f73a5c214d6e	k__Bacteria; p__Thermotogae; c__Thermotogae; o__Thermotogales; f__Thermotogaceae; g__Kosmotoga; s__mrj	0.00241075	0.004462647	0.006253501
c9186cb86211857b2d4fd4f686f6a3	k__Bacteria; p__Verrucomicrobia; c__Thermotogae; o__Limnisphearae; f__Limnisphearae; g__	0.00216657	0.000926241	0.005133123
1a1acec9969c0c502af1f7a5e771c	k__Bacteria; p__Firmicutes; c__Clostridia; o__SHA-98; f__	0.00203682	0.000370014	0.001569175
164078135a4d12642851d2309177ad7	k__Bacteria; p__WWE1; c__Cloacamonae; o__Cloacamonales; f__Cloacamonaceae; g__BHB21; s__	0.00192308	0.001175615	0.00319054
003dea16a248b965c396839360571c	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Clostridiaceae; g__Clostridium; s__calatum	0.00189937	0.000474282	0.001188712
dfaf4f6b1d2137a5c18fbc0f937900	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__SHA-20; f__	0.00171931	0.00014706	0.000809642
fd8ae426805e27be1944109d97f2	k__Bacteria; p__WWE1; c__Cloacamonae; o__Cloacamonales; f__Cloacamonaceae; g__W5; s__	0.00158044	0.004411748	0.006424281
dc9fb0a0de0e05ab4d29c9e795a24ef	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanosarcina	0.00148654	0.003308502	0.000579936
e076ad1e04e3d3e3671e2fdeab8aa	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	0.00145262	0.002882965	0.004854244
0c5738909b7b0da0c5289b842c78b0	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__BA08; g__	0.00127368	0.001128862	0.001933484
fae185507dc6477376509ad23e1e64a	k__Bacteria; p__Actinobacteria; c__Actinobacteria; o__Actinomycetales; f__Mycobacteriaceae; g__Mycobacterium	0.00119538	0.003298485	0.006485537
4ff4d5b6ca3155aeb640d5866a4ace7	k__Bacteria; p__WWE1; c__Cloacamonae; o__Cloacamonales; f__Cloacamonaceae; g__BHB21; s__	0.00107646	0.005433821	0.006559024
0ee1f6bd0d325b91de28ca186e69b6e	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Porphyromonadaceae; g__Paludibacter; s__	0.00100398	0.000982433	0.001893398
d0f01b515504b09960ed27ad306084a	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00097653	0.004219963	0.003735722
0f0d51c640774ef5e01520881c850655	k__Bacteria; p__Firmicutes; c__Clostridia; o__SHA-98; f__	0.00095082	0.000771151	0.000232824
3516b33b0e5c1f18a8e462c051f141b	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Acrobacter; s__cryaerophilus	0.00091637	0.00191792	0.000395195
ee20e6bc40167847b4946e6a6c9950	k__Bacteria; p__Thermotogae; c__Thermotogae; o__Thermotogales; f__Thermotogaceae; g__Kosmotoga; s__mrj	0.00090712	0.007265767	0.005755426
e2bc572632e1414b6960b3fec430f0f	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__DRC31; f__	0.00086326	0.00074654	0.003114053
ae37a52e042a90525385a968ba6506	k__Bacteria; p__Bacteroidetes	0.00082182	0.000802736	0.001844055
e3ff1d12b164cf0f2e3e7ceac32cae7	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__SBR1031; f__A4b; g__	0.00080778	2.24E-05	0.000122753
4aa09e866125c1839a3f3ca8e5c1b	k__Bacteria; p__Chloroflexi; c__Thermotogae; o__Thermotogales; f__Thermotogaceae; g__Kosmotoga; s__mrj	0.00076362	0.000447789	0.001246313
59e8940c3f17931f2f4b4e479f6f	k__Bacteria; p__Thermotogae; c__Thermotogae; o__Thermotogales; f__Thermotogaceae; g__Kosmotoga; s__mrj	0.00075587	0.00087668	0.000279961
0c38a56bd2609e5283c152ea15a0053	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae; g__Dokdonella; s__	0.00066447	9.71E-05	0.000531928
148ae43b49bd18bc9ca73fbc18db4	k__Bacteria; p__Chloroflexi; c__Chloroflexi; o__Roseiflexales; f__Koulothraxaceae; g__	0.00060662	3.98E-05	0.00021798
8adea10902b6443b75e724402e47c	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Lachnospiraceae	0.00059201	0.0024889	0.004677789
efec3d80e500decbb2e643c0de14a	k__Bacteria; p__Proteobacteria; c__Deltaproteobacteria; o__Syntrophobacterales; f__Syntrophobacterales; g__	0.00045399	6.37E-05	0.000394909
b1f9fb2f0c829b9528a75d7236e6d3	k__Bacteria; p__Firmicutes; c__Clostridia; o__OPB54; f__	0.00045339	0.000464838	0.0003719592
9f857aad6d33b8b93843229b3562611	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanocorpusculum; s__	0.00044247	0.002831814	0.004608879
06bc973407a92d681af5496290c	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__	0.00041608	0.001087542	0.00209334
fae9d71d060c3be71805ec2c8683005	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00029097	0.003424254	0.005912625
60ef4d2804f1ace93b95f7e6e5a545	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__Anaerolineales; f__Anaerolineaceae; g__T78; s__	0.00028445	0.009619875	0.005372838
fb06b629b72b328f67171b6959c8a0b	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Acrobacter; s__cryaerophilus	0.00024911	0.00144479	0.003285478
fd2043bfaa75060dbec3a3d51703454	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanocorpusculae; g__Methanosarcina; s__mazel	0.00019053	0.002970585	0.004531108
18e93e5a4902529c9f7fc3b1d2b71	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__GCA004; f__	0.00018605	0.000613569	0.000500729
23b1ceda51870533e4522d05913610	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Tissierellaceae; g__Sedimentibacter; s__	0.00017894	0.000631331	0.001353006
edc9f3b681181488510f7ba1b8c25	k__Bacteria; p__Verrucomicrobia; c__Pedosphaerae; f__Pedosphaerales; f__R4-41B; g__	0.00017812	0.002716979	0.003502748
1613e04d58517632bc8139209b7d7a7	k__Bacteria; p__Planctomycetes; c__Planctomycetia; o__Planctomycetales; f__Planctomycetaceae; g__Planctomycetes; s__	0.00016114	1.23E-05	6.71E-05
ded64b574c09badc1509404654073	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__BA08; g__	9.24E-05	0.000380536	0.001253673
0a32c8a8c9d042579418219166903	k__Bacteria; p__WPS-2; c__	8.20E-05	0.000122775	0.000672465
0e049912b2c287528c96739063a507	k__Bacteria; p__Armatimonadetes; c__SJA-176; o__RB046; f__	0	0.000123158	0.000485647
0e71d2ab88063c4e4484849036b4334	k__Bacteria; p__WS1; c__	0	2.80E-05	0.000153327
0e8f3b3ae8b19e8a045a222bd2466a7	k__Bacteria; p__Firmicutes; c__Clostridia	0	0.000598336	0.001596128
0e939130fd103711b1bd8b1bb1432bf	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__	0	3.16E-05	0.00017308
0ed716825d213b3aca0e1efa230ad6	k__Bacteria; p__Armatimonadetes; c__SJA-176; o__RB046; f__	0	0.000439843	0.002409119
116638569a765a49e6676a7ca039c0	k__Bacteria; p__Firmicutes; c__Clostridia; o__Thermoanaerobacterales; f__	0	2.84E-05	0.00011557
05f105e4d01361dae8c46f5deb3e9	k__Archaea; p__Euryarchaeota; c__Methanomicrobiales; f__Methanosarcinaceae; g__Methanosarcina; s__	0	0.000230234	0.000710694
0295224e9bd4c46d9f8c971549af2	k__Archaea; p__Euryarchaeota; c__Methanobacteriales; f__Methanobacteriales; g__Methanobacterium; s__	0	0.000951817	0.002041983
0684014c4d54892c4f0c068b5e4d4e	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__SB-1; g__	0	3.97E-05	0.000217609
0fd24ffe6e3af5b614c2dbde463af2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Syntrophomonadaceae; g__Syntrophomonas; s__	0	0.000898991	0.001684713
0f78f0c0be15f7b3b8c00ec906d14	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Sinobacteraceae; g__	0	4.74E-05	0.000259661
0c12a82b5bd52834f8ac998b8e3d04	k__Bacteria	0	2.00E-05	0.000190539
104d10c98856b164ec0004f272525d9	k__Bacteria; p__Firmicutes; c__Clostridia; o__MBA08; f__	0	0.000181238	0.00075878
10cded4995b9114c4bca6b5fbdca3a	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	0	6.46E-05	0.000176936
175ec29f5320544a571dc6b884c4f62	k__Bacteria; p__Chloroflexi; c__Anaerolineae; o__SHA-20; f__	0	0.000546668	0.001724775
108280bb4474fa4cfd5da5a5b56	k__Bacteria; p__Chloroflexi; c__Chloroflexi; o__Roseiflexales; f__Koulothraxaceae; g__Koulothrax; s__	0	0.000179292	0.000982022
0d526e8aebad1f014d38b724ee6788	k__Bacteria; p__Verrucomicrobia; c__Verruco-5; o__WCHB1-41; f__RFP12; g__	0	0.0001431	0.00078379
175ea5410495d30f1514081755f543	k__Bacteria; p__Spirochaetes; c__Spirochaetes; o__Spirochaetales; f__Spirochaetaceae; g__Treponema; s__	0	0.00021799	0.000841807
0				

Table S 2. Differentially abundant taxa between the control and comb-CeO₂ contaminated AD. Linear Discriminant Analysis Effect Size (LEfSe): all linear discriminant analysis [LDA] scores, >3). Taxonomy levels: (p), phylum; (c), class; (o), order; (f), family; (g), genus. Relative abundances of taxa that are increased in the control (green) and comb-CeO₂ contaminated (red) AD.

LDA Score	Taxa	Potential function
3.4	Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales	The hydrogenotrophic order <i>Methanomicrobiales</i> includes <i>Methanoculleus spp.</i> , <i>Methanocorpusculum sp.</i> , and unclassified <i>Methanoregulaceae</i> (Ziganshin 2016)
4.3	<i>Bacteria</i>	
3.7	Bacteria; Bacteroidetes	Macromolecules degradation, volatil fatty acid (VFA) and alcohol production. Higher population of <i>Bacteroidetes</i> phyla are associated with high hydrolytic activity in full-scale anaerobic digesters (Khan 2021)
3.7	<i>Bacteria; Bacteroidetes; Bacteroidia</i>	
3.6	Bacteria; Chloroflexi; Anaerolineae; GCA004	Cellulose hydrolysis (Xia 2016), important for the granulation of sludge (Yamada and Sekiguchi 2009)
4.3	<i>Bacteria; Firmicutes</i>	Macromolecules degradation, VFA and alcohol. Higher population of <i>Bacteroidetes</i> phyla can be associated with high hydrolytic activity in full-scale anaerobic digesters (Khan 2021)
4.3	<i>Bacteria; Firmicutes; Bacilli</i>	
4.3	<i>Bacteria; Firmicutes; Bacilli; Lactobacillales</i>	
4.4	Bacteria; Firmicutes; Bacilli; Lactobacillales; Carnobacteriaceae; Trichococcus	Fermentative bacteria, detected in mesophilic hydrogen-producing consortia as bacteria that accompany hydrogen producers (Sikora 2013)
4.1	<i>Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminobacteraceae</i>	Potential syntrophic oxidizing bacteria (SAO) (Dyksma 2020, Lim 2020)
3.3	<i>Bacteria; Firmicutes; Clostridia; Clostridiales; Tissierellaceae</i>	Potential syntrophic oxidizing bacteria (Dyksma 2020, Lim 2020)
3.4	Bacteria; Firmicutes; Clostridia; Clostridiales; Tissierellaceae; Sedimentibacter	Potential syntrophic oxidizing bacteria (Dyksma 2020, Lim 2020)
3.4	Bacteria; Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; Clostridium	Syntrophic butyrate producer (Vital 2014)
3.3	<i>Bacteria; Proteobacteria; Gammaproteobacteria</i>	Macromolecules degradation, VFA and alcohol (Khan 2021)
3.5	<i>Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales</i>	
3.4	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae	
3.3	Bacteria; Synergistetes; Synergistia; Synergistales; Thermovirgaceae	The increase in the relative abundance of <i>Synergistales</i> was found to be highly correlated with the increased rate of methane production from oil via hydrogenotrophic <i>archaea</i> (Nakasaki 2019)
3.5	<i>Bacteria; WWE1</i>	
3.6	<i>Bacteria; WWE1; Cloacamonae</i>	
3.6	<i>Bacteria; WWE1; Cloacamonae; Cloacamonales</i>	
3.6	<i>Bacteria; WWE1; Cloacamonae; Cloacamonales; Cloacamonaceae</i>	
3.4	Bacteria; WWE1; Cloacamonae; Cloacamonales; Cloacamonaceae; W22	Syntrophic fatty-acid bacteria (Esquivel-Elizondo 2016) that have metabolic capabilities for butyrate and propionate fermentation, as well as for reverse acetogenesis (acetate catabolism by methanogens)
4.6	<i>Archaea</i>	
4.4	<i>Archaea; Euryarchaeota</i>	
3.6	<i>Archaea; Euryarchaeota; Methanobacteria</i>	

3.5	<i>Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales</i>	Hydrogenotrophic methanogens (Ziganshin 2016)
3.5	<i>Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae</i>	Hydrogenotrophic methanogens (Ziganshin 2016)
3.5	<i>Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanobacterium</i>	Hydrogenotrophic methanogens (Ziganshin 2016)
4.6	<i>Archaea; Euryarchaeota; Methanomicrobia</i>	
4.1	<i>Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales; Methanocorpusculaceae</i>	Hydrogenotrophic methanogens (Ziganshin 2016)
4.2	<i>Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales; Methanocorpusculaceae; Methanocorpusculum</i>	Hydrogenotrophic methanogens (Ziganshin 2016)
4.1	<i>Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales</i>	Acetoclastic methanogens (Ziganshin 2016)
4.2	<i>Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae</i>	Acetoclastic methanogens (Ziganshin 2016)
4.4	<i>Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina</i>	Acetoclastic methanogens (Ziganshin 2016)
3.3	<i>Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales; Marinilabiaceae</i>	Saccharolytic bacteria (Hanreich 2013)
3.9	<i>Bacteria; Chloroflexi</i>	
3.7	<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales</i>	
3.6	<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolinaceae</i>	
3.7	<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolinaceae; T78</i>	Hydrolytic or fermentative bacteria (Yamada 2005)
3.3	<i>Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae</i>	Syntrophic acetogenic bacteria (Gagen 2015)
3.8	<i>Bacteria; Firmicutes; Erysipelotrichi; Erysipelotrichales; Erysipelotrichaceae; RFN20</i>	
3.5	<i>Bacteria; Spirochaetes; Spirochaetes</i>	
3.5	<i>Bacteria; Spirochaetes; Spirochaetes; Spirochaetales</i>	
3.5	<i>Bacteria; Spirochaetes; Spirochaetes; Spirochaetales; Spirochaetaceae</i>	
3.5	<i>Bacteria; Spirochaetes; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema</i>	Homoacetogens, which consume H ₂ and CO ₂ to produce acetate. Alternative hydrogenotrophs (Li 2016)
3.5	<i>Bacteria; Synergistetes; Synergistia; Synergistales; Dethiosulfovibrionaceae; Aminobacterium</i>	Syntrophic acetogenic bacteria on aminoacids (Morris 2013)

