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## Hydrogen consumption and methanogenic community evolution in anodophilic biofilms

## in single chamber microbial electrolysis cells under different startup modes

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Reactors	#1	#2	#3	#4	#5	#6
#1	86(6.4%)	784(41.7%)	847(42.0%)	1039(47.6%)	1164(34.6%)	1028(32.4%)
#2		112(8.5%)	850(42.9%)	1004(45.9%)	1086(31.8%)	998(31.4%)
#3			158(10.4%)	1128(49.9%)	1258(36.6%)	1193(37.5%)
#4				125(6.7%)	1628(47.4%)	1402(42.1%)
#5					778(24.4%)	1950(47.6%)
#6						738(25.8%)
No. of						
genes	1347	1316	1515	1875	3185	2858
detected						
Shannon	6.0	6.0	7.0	7 2	7 8	77
Diversity	0.9	0.7	1.0	1.2	1.0	1.1

Table S1. Gene overlap (unshaded number and percentages), gene uniqueness (shaded gene number and percentages), and diversity indices for each sample.



Figure S1 Experimental single chamber microbial electrolysis cells



**Figure S2** Current produced by reactors during enrichment: #1 and #2, closed circuit operation (1000  $\Omega$ ); #3, open circuit MFC (control); #6, open circuit MEC (control).



**Figure S**<sup>3</sup> Current produced by MECs at applied voltages of 0.3 V (#4) or 0.7 V (#5) and compared to those switched from MFC mode to MEC, at applied voltages of 0.3 V (#1, #3) and 0.7 V (#2, #4)