

Table S1. Summary of microbial community composition detected in Deer Lake (DL-M) bioreactors on day 58, 85, 98 and 128 using 16S rRNA gene sequencing. Day 0 microbial mat sample is taken from the initial inoculation. Numbers indicate proportion of reads with a > 1% average relative abundance in an OTU compared to all OTUs listed on a per sample basis. Closest cultured relative as determined by BLAST search is shown.

OTU Number	% total DL-M OTUs	Relative % abundance in duplicate DL-M bioreactors at time point (day)										Phylum	Genus	Accession No.	% Identity
		0	58		85		98		128						
			BR1	BR2	BR1	BR2	BR1	BR2	BR1	BR2					
2	18.43	1.01	3.02	3.57	16.61	24.10	20.98	31.59	40.82	33.36	<i>Proteobacteria</i>	<i>Wenzhouxiangella</i>	CP012154.1	98	
1	17.15	2.04	45.11	39.81	37.48	26.76	0.40	0.80	0.06	0.11	<i>Bacillariophyta</i>	<i>Dickieia</i>	FJ002229.1	99	
5	8.37	2.42	3.11	3.94	5.82	4.88	14.34	11.88	14.19	22.39	<i>Proteobacteria</i>	<i>Rhodobaca</i>	EU908048.1	100	
3	6.37	0.02	2.07	9.71	14.34	19.12	10.48	0.48	2.04	0.56	<i>Cyanobacteria</i>	<i>Phormidium</i>	JN166666.1	100	
7	5.94	0.68	2.13	3.21	4.59	2.60	13.08	13.27	3.85	3.21	<i>Bacteroidetes</i>	<i>Lewinella</i>	NR_115013.1	89	
6	4.35	1.18	0.41	0.68	1.98	4.15	10.04	9.69	3.85	4.86	<i>Proteobacteria</i>	<i>Chelatococcus</i>	NR_025428.1	98	
4	4.16	0.51	28.18	7.49	4.64	2.30	0.40	0.14	0.09	0.09	<i>Bacillariophyta</i>	<i>Nitzschia</i>	FJ002224.1	99	
245	3.01	0.22	4.19	3.90	1.14	1.81	3.50	5.70	2.41	4.39	<i>Bacteroidetes</i>	<i>Lewinella</i>	KF228160.1	89	
8	2.27	1.30	0.17	0.71	1.48	1.77	4.03	3.48	6.05	3.23	<i>Proteobacteria</i>	<i>Rhodobaculum</i>	KM077018.1	99	
40	1.31	2.68	0.12	0.09	1.42	1.46	0.94	1.45	1.72	0.67	<i>Proteobacteria</i>	<i>Halomonas</i>	GU113002.1	99	