Supporting Table S2. Summary of metagenomic sequencing libraries used in this study. Average read length is shown \pm standard deviation.

Library name	Retention Filter	Collection Date	Library type	Sequencing platform	Number of reads	Avg. read length
ABM	0.8 μm	1/23/2007	8-10 kb plasmid	Sanger	81,197	776 ± 157
ABL	0.8 μm	1/23/2007	40 kb fosmid	Sanger	43,490	599 ± 230
CBM	0.8 μm	1/25/2007	8-10 kb plasmid	Sanger	81,032	781 ± 155
CBL	0.8 µm	1/25/2007	40 kb fosmid	Sanger	33,029	678 ± 191
AAM	0.1 μm	1/23/2007	8-10 kb plasmid	Sanger	95,988	699 ± 198
CAM	0.1 μm	1/25/2007	8-10 kb plasmid	Sanger	92,242	747 ± 179
Sanger Total					426,978	727 ± 180

ABT	0.8 µm	1/23/2007	-	454 Titanium	994,337	362 ± 96
CAT	0.1 μm	1/25/2007	-	454 Titanium	205,925	401 ± 119
454 total					1,200,262	368 ± 100