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Table S1
List of 8nt barcodes for 454 pyrosequencing.

Barcode sequence	Sample	Extraction Library
CACAACTG	A	Maxwell
CACAACAC	A	PowerBiofilm
CAAGTGGA	A	QuickGene
CACACACA	B	Maxwell
CACAAGTC	B	PowerBiofilm
CACAAGAG	B	QuickGene
CACACTGA	C	Maxwell
CACACTCT	C	PowerBiofilm
CACACAGT	C	QuickGene
CAAGGAAC	A	Maxwell replicate #1
CAAGGATG	A	Maxwell replicate #2
CAAGGTAG	A	Maxwell replicate #3
CAAGGTTC	A	PowerBiofilm replicate #1
CAAGTCCA	A	PowerBiofilm replicate #2
CAAGTCGT	A	PowerBiofilm replicate #3

Table S2
Measures of alpha diversity for each library.[a]

Sample A library	% Library coverage[b]	OTUs[c]	Chao[d]	ACE[e]	H^[f]	Simpson (D)[g]
Maxwell#1	0.964	122	308 (215,495)	455 (371,567)	2.76	0.157 (0.145,0.168)
Maxwell#2	0.972	102	191 (145,286)	305 (248,384)	2.20	0.310 (0.289, 0.331)
Maxwell#3	0.976	107	150 (128,197)	218 (182,273)	2.28	0.297 (0.276, 0.317)
Powerbiofilm#1	0.972	103	187 (144,275)	198 (153,282)	2.67	0.162 (0.150, 0.175)
Powerbiofilm#2	0.966	118	276 (197,434)	387 (316,482)	2.83	0.132 (0.123, 0.142)
Powerbiofilm#3	0.967	114	253 (184,390)	361 (289,463)	2.69	0.174 (0.161, 0.188)

[a]Based on a random subsampling of 1958 sequences.
[b]Good's coverage for an OTU definition.
[c]OTU: operational taxonomic units
[d]Chao richness estimator, mean value (95% low and high confidence intervals).
[e]Abundance based coverage estimator (ACE), mean value (95% low and high confidence intervals).
[f]Non-parametric estimate of the classical Shannon diversity index (H^).
[g]Simpson index, mean value (95% low and high confidence intervals).