

Table S1. Average fluorescence intensity of the 20 dominant bacteria in the MBfR (30 days).

<i>class_tax</i>	<i>order_tax</i>	<i>family_tax</i>	<i>rep_prokMSAname</i>	<i>Average fluorescence intensity</i>
<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Dyemonas todaii</i> str. XD10	6743
<i>Betaproteobacteria</i>	<i>Nitrosomonadales</i>	<i>Nitrosomonadaceae</i>		5819
<i>Gammaproteobacteria</i>	<i>Legionellales</i>	<i>Unclassified</i>	<i>uranium mining waste pile clone JG37-AG-14 proteobacterium</i>	5730
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Hydrogenophaga taeniospiralis</i> str. ATCC 49743	5552
<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Sphingopyxis flavimaris</i> str. SW-151	5519
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Variovorax paradoxus</i> TG27	5437
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Comamonas testosteroni</i> str. SMCC B329	5419
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>	<i>Massilia timonae timone</i>	5353
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>travertine hot spring clone SM1E01</i>	5352
<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Waste-gas biofilter clone BIyi3</i>	5331
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Lampropedia hyalina</i> str. DSM 15336	5183
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Aquaspirillum metamorphum</i> str. DSM 1837	5127
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Acidovorax facilis</i> str. CCUG 2113	5123
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>naphthalene-contaminated sediment clone 76</i>	4945
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>strain isolate str. rJ10</i>	4923
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>hydrocarbon-degrading consortium clone AF1-8</i>	4906
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Delftia tsuruhatensis</i> str. AD9	4855
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>strain isolate str. rM4</i>	4849
<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Acidovorax defluvii</i> str. BSB411	4846
<i>Alphaproteobacteria</i>	<i>Rickettsiales</i>	<i>Unclassified</i>	<i>termite gut homogenate clone Rs-M62 proteobacterium</i>	4820

Table S2. Average fluorescence intensity of the 20 dominant bacteria in the MBfR (60 days).

phylum_tax	class_tax	order_tax	family_tax	rep_prokMSAname	Average fluorescence intensity
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Dyemonas todaii</i> str. XD10	3789
Firmicutes	Clostridia	Unclassified	Unclassified		3756
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Beijerinck/Rhodoplan/Methylocyst	<i>Beijerinckia indica</i>	3658
Proteobacteria	Gammaproteobacteria	Legionellales	Unclassified	uranium mining waste pile clone JG37-AG-14 proteobacterium	3561
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	<i>Rhodobacter sphaeroides</i> str. 2.4.1	3553
Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae		3491
Firmicutes	Clostridia	Clostridiales	Peptococc/Acidaminococc	anoxic bulk soil flooded rice microcosm clone BSV43 clone	3481
Acidobacteria	Acidobacteria	Acidobacteriales	Acidobacteriaceae		3464
Proteobacteria	Gammaproteobacteria	Methylococcales	Unclassified	<i>Methylobacter marinus</i> str. A45	3443
Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	termite gut homogenate clone Rs-Q18 bacterium	3372
Proteobacteria	Gammaproteobacteria	Symbionts	Unclassified	<i>Seepiophila jonesi</i> symbiont	3343
Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	<i>Paucimonas lemoignei</i> str. ATCC 17989T	3340
Chloroflexi	Anaerolineae	Unclassified	Unclassified	DCP-dechlorinating consortium clone SHA-36	3332
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Hyphomicrobiaceae	<i>Hyphomicrobium aestuarii</i> str. DSM 1564	3328
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	<i>Clostridium acetobutylicum</i> str. ATCC 824	3308
Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	<i>Brevundimonas diminuta</i> str. IAM 12691T	3280
Proteobacteria	Alphaproteobacteria	Bradyrhizobiales	Methylobacteriaceae	<i>Methylobacterium thiocyanatum</i> str. ALL/SCN-P	3269
Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified		3249
Proteobacteria	Gammaproteobacteria	Unclassified	Unclassified		3245
Firmicutes	Mollicutes	Anaeroplasmatales	Erysipelotrichaceae		3238