

Table S1. Operational taxonomic units (OTU) identified as discriminatory according to oxytetracycline exposure by Metastats and LEfSe algorithms in Mothur.

Day	Phylotype			<i>p</i> value	
	OTU	Phylum	Genus	Metastats	LEfSe
8	Otu0140	Actinobacteria	<i>Kineosporiaceae_unclassified</i>	0.040	-
	Otu0237	Actinobacteria	<i>uncultured_ge</i>	0.027	-
	Otu0321	Actinobacteria	<i>Iamia</i>	0.049	-
	Otu0359	Actinobacteria	<i>Microtrichales_unclassified</i>	0.028	-
	Otu0802	Actinobacteria	<i>Microtrichales_unclassified</i>	0.046	-
	Otu0008	Bacteroidetes	<i>uncultured</i>	0.019	-
	Otu0308	Planctomycetes	<i>uncultured</i>	0.041	-
	Otu0004	Proteobacteria	<i>Plesiomonas</i>	0.007	0.022
	Otu0006	Proteobacteria	<i>Reyranella</i>	0.029	-
	Otu0059	Proteobacteria	<i>Pseudomonas</i>	0.027	-
	Otu0163	Proteobacteria	<i>Uncultured</i>	0.032	-
	Otu0005	Proteobacteria	<i>Aeromonas</i>	-	0.030
	Otu0017	Proteobacteria	<i>Deefgea</i>	-	0.008
	Otu0155	Proteobacteria	<i>Pedomicrobium</i>	-	0.042
	Otu0208	Proteobacteria	<i>Reyranella</i>	-	0.044
15	Otu0065	Acidobacteria	<i>DS-100_ge</i>	0.039	-
	Otu0010	Actinobacteria	<i>Nocardioides</i>	0.044	-
	Otu0053	Actinobacteria	<i>Mycobacterium</i>	0.037	-
	Otu0609	Actinobacteria	<i>Corynebacterium</i>	0.026	-
	Otu0028	Bacteroidetes	<i>Flavobacterium</i>	-	0.010
	Otu0062	Chloroflexi	<i>RBG-13-54-9_ge</i>	0.031	-
	Otu0219	Chloroflexi	<i>KD4-96_ge</i>	0.022	-
	Otu0434	Chloroflexi	<i>S085_ge</i>	0.046	-
	Otu0945	Chloroflexi	<i>JG30-KF-CM45_ge</i>	0.034	-
	Otu0750	Firmicutes	<i>Lactobacillales_unclassified</i>	0.028	-
	Otu2501	Firmicutes	<i>Bacillales_unclassified</i>	0.024	-
	Otu0018	Proteobacteria	<i>Desulfovibrionaceae_unclassified</i>	0.028	-
	Otu0024	Proteobacteria	<i>Hyphomicrobium</i>	0.030	-
	Otu0044	Proteobacteria	<i>Aquicella</i>	0.013	-
	Otu0051	Proteobacteria	<i>Rhodobacteraceae_unclassified</i>	0.006	-
	Otu0098	Proteobacteria	<i>Rhizobiales_unclassified</i>	0.014	-
	Otu0113	Proteobacteria	<i>Methylobacteriaceae_unclassified</i>	0.048	-
	Otu0116	Proteobacteria	<i>Rhizobiales_unclassified</i>	0.004	-
	Otu0136	Proteobacteria	<i>Sphingomonadaceae_unclassified</i>	-	0.032
	Otu0169	Proteobacteria	<i>Pseudorhodoplanes</i>	0.020	-
	Otu0187	Proteobacteria	<i>Stenotrophomonas</i>	0.028	-
	Otu0196	Proteobacteria	<i>Rhodobacteraceae_unclassified</i>	0.016	-
	Otu0246	Proteobacteria	<i>Alphaproteobacteria_unclassified</i>	0.037	-

Table S1. Continued

Day	Phylotype			<i>p</i> value	
	OTU	Phylum	Genus	Metastats	LEfSe
22	Otu0065	Acidobacteria	<i>DS-100_ge</i>	0.028	-
	Otu0063	Actinobacteria	<i>Smaragdicoccus</i>	0.014	-
	Otu0217	Actinobacteria	<i>uncultured_ge</i>	0.042	-
	Otu0582	Actinobacteria	<i>Corynebacterium_1</i>	0.038	-
	Otu0685	Actinobacteria	<i>Nocardioides</i>	0.044	-
	Otu1031	Actinobacteria	<i>Mycobacterium</i>	0.024	-
	Otu0132	Bacteria_unclassified	<i>Bacteria_unclassified</i>	0.033	-
	Otu0505	Bacteria_unclassified	<i>Bacteria_unclassified</i>	0.029	-
	Otu0782	Bacteria_unclassified	<i>Bacteria_unclassified</i>	0.030	-
	Otu1130	Bacteria_unclassified	<i>Bacteria_unclassified</i>	0.030	-
	Otu0020	Bacteroidetes	<i>Macellibacteroides</i>	0.024	-
	Otu0435	Chlamydiae	<i>Chlamydiales_unclassified</i>	0.013	-
	Otu0544	Chlamydiae	<i>Chlamydia</i>	0.017	-
	Otu1093	Chlamydiae	<i>Parachlamydiaceae_unclassified</i>	0.040	-
	Otu0012	Chloroflexi	<i>uncultured</i>	0.029	-
	Otu0058	Chloroflexi	<i>JG30-KF-CM45_ge</i>	0.021	-
	Otu0219	Chloroflexi	<i>KD4-96_ge</i>	0.044	-
	Otu0976	Cyanobacteria	<i>Obscuribacterales_ge</i>	0.021	-
	Otu0002	Fusobacteria	<i>Cetobacterium</i>	0.004	-
	Otu0073	Planctomycetes	<i>Planctopirus</i>	0.018	-
	Otu0080	Planctomycetes	<i>uncultured</i>	0.006	-
	Otu0121	Planctomycetes	<i>Gemmataceae_unclassified</i>	0.027	-
	Otu0221	Planctomycetes	<i>uncultured</i>	0.004	-
	Otu0238	Planctomycetes	<i>uncultured</i>	0.035	-
	Otu0262	Planctomycetes	<i>Gemmata</i>	0.011	-
	Otu0478	Planctomycetes	<i>Pirellulaceae_unclassified</i>	0.011	-
	Otu0574	Planctomycetes	<i>uncultured</i>	0.003	-
	Otu0588	Planctomycetes	<i>Gemmata</i>	0.002	-
	Otu0626	Planctomycetes	<i>uncultured</i>	0.007	-
	Otu0005	Proteobacteria	<i>Aeromonas</i>	0.006	-
	Otu0006	Proteobacteria	<i>Reyranella</i>	0.013	-
	Otu0024	Proteobacteria	<i>Hyphomicrobium</i>	0.005	-
	Otu0034	Proteobacteria	<i>Novosphingobium</i>	0.045	-
	Otu0036	Proteobacteria	<i>Bradyrhizobium</i>	0.045	-
	Otu0046	Proteobacteria	<i>Proteobacteria_unclassified</i>	0.013	-
	Otu0048	Proteobacteria	<i>Rhodobacteraceae_unclassified</i>	0.043	-
	Otu0051	Proteobacteria	<i>Rhodobacteraceae_unclassified</i>	0.047	-
	Otu0116	Proteobacteria	<i>Rhizobiales_unclassified</i>	0.019	-
	Otu0150	Proteobacteria	<i>uncultured</i>	0.049	-
	Otu0189	Proteobacteria	<i>Xanthobacteraceae_unclassified</i>	0.009	-
	Otu0201	Proteobacteria	<i>Hyphomicrobiaceae_unclassified</i>	0.036	-
	Otu0204	Proteobacteria	<i>Hyphomicrobium</i>	0.042	-
	Otu0206	Proteobacteria	<i>Enterobacteriaceae_unclassified</i>	0.046	-
	Otu0229	Proteobacteria	<i>uncultured</i>	0.041	-
	Otu0258	Proteobacteria	<i>Arenimonas</i>	0.048	-
	Otu0271	Proteobacteria	<i>Deltaproteobacteria_unclassified</i>	0.011	-

Otu0314	Proteobacteria	<i>Xanthobacteraceae_unclassified</i>	0.009	-
Otu0324	Proteobacteria	<i>Reyranella</i>	0.001	-
Otu0332	Proteobacteria	<i>Pedomicrobium</i>	0.022	-
Otu0334	Proteobacteria	<i>Phreatobacter</i>	0.033	-
Otu0412	Proteobacteria	<i>Gammaproteobacteria_unclassified</i>	0.019	-
Otu0503	Proteobacteria	<i>Pedomicrobium</i>	0.030	-
Otu0594	Proteobacteria	<i>Rickettsiaceae_unclassified</i>	0.010	-
Otu0679	Proteobacteria	<i>Dechloromonas</i>	0.038	-
Otu1564	Proteobacteria	<i>Deltaproteobacteria_unclassified</i>	0.030	-
Otu0425	Verrucomicrobia	<i>Verrucomicrobiaceae_unclassified</i>	0.012	-
