Supplemental Table 2

Relative abundances of all bacterial phyla sequenced with the tested forward primers.

	A. constructor						*L. dispar*							
	799F/1392R	799F-tags/1392R	799F-mod2/1392R	799F-mod3/1392R	799F-mod6/1392R	799F-mod7/1392R	799F/1392R	799F-tags/1392R	799F-thio/1392R	799F-mod2/1392R	799F-mod3/1392R	799F-mod6/1392R	799F-mod7/1392R	799F-mod7thio/1392R
Acidobacteria	0	0	0	0	0.1	0	0	0	1.6	0	0	0	0.3	0
Actinobacteria	38.1	36.4	33.1	39.9	32.7	27.0	6.0	5.4	6.7	6.4	16.1	4.6	3.1	6.9
Bacteroidetes	1.6	2.8	2.2	2.8	4.3	1.9	0.3	0.5	0	5.4	3.4	2.6	0.2	0.6
Chlamydiae	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0
Chloroflexi	0	0	0.01	0	0.01	0	0	0	0	0	0	0	0	0
Cyanobacteria	0.4	2.0	0.02	0	0	0	0.4	6.9	0	0.1	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0.6	0	0	0	0
Firmicutes	3.3	2.0	3.1	2.1	2.6	2.9	1.2	1.7	1.6	1.9	1.0	0.6	2.2	2.8
Planctomycetes	0	0.1	0.02	0	0.01	0	0	0	0	0	0	0	0	0
Proteobacteria	56.4	56.6	61.2	55.3	60.0	68.1	92.1	85.6	89.8	85.6	78.9	90.5	94.2	89.6
Verrucomicrobia	0.01	0	0	0	0	0.06	0	0	0	0	0	0	0	0
unclassified	0.3	0	0.2	0	0.2	0	0	0	0	0	0.5	1.5	0	0