Table 1. Summary of the primer pairs used to generate the 16S rRNA gene fragment fragments and the characteristics of each region.

% latex table generated in R 3.2.2 by xtable 1.8-0 package % Wed Feb 3 14:51:18 2016

	Forward	Reverse	coordinates	length
V1-V9	AGRGTTTGATYMTGGCTCAG	GGYTACCTTGTTACGACTT	8-1510	1464.00
V1-V6	AGRGTTTGATYMTGGCTCAG	ACRACACGAGCTGACGAC	8-1078	1033.00
V1-V5	AGRGTTTGATYMTGGCTCAG	CCCGTCAATTCMTTTRAGT	8-927	881.00
V1-V3	AGRGTTTGATYMTGGCTCAG	ATTACCGCGGCTGCTGG	8-534	490.00
V3-V5	CCTACGGGAGGCAGCAG	CCCGTCAATTCMTTTRAGT	341-927	551.00
V4	GTGCCAGCMGCCGCGGTAA	GGACTACHVGGGTWTCTAAT	515-806	253.00

[a] The coordinates where the start and end of the forward and reverse primers anneal, respectively.

[b] The number of bases between the primers.