

**Table S2.** 16/18S pyrosequencing primers.

<b>Primer Name<sup>a</sup></b>	<b>Sequence 5'-3'</b>
<b><i>Bacteria 16S</i></b>	
A1-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGAGTGCGT•ACGCGHNRAACCTTACC
A2-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGCTCGACA•ACGCGHNRAACCTTACC
A3-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGACGCACTC•ACGCGHNRAACCTTACC
A4-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGCACTGTAG•ACGCGHNRAACCTTACC
A5-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATCAGACACG•ACGCGHNRAACCTTACC
A6-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATATCGCGAG•ACGCGHNRAACCTTACC
A7-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CGTGTCTCTA•ACGCGHNRAACCTTACC
A8-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CTCGCGTGTC•ACGCGHNRAACCTTACC
A9-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TAGTATCAGC•ACGCGHNRAACCTTACC
A10-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TCTCTATGCG•ACGCGHNRAACCTTACC
A12-B969F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TACTGAGCTA•ACGCGHNRAACCTTACC
B-BA1406R	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG•ACGGGCRGTGWGTRCAA
<b><i>Archaea 16S</i></b>	
A1-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGAGTGCGT•TYAATYGGANTCAACRCC
A2-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGCTCGACA•TYAATYGGANTCAACRCC
A3-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGACGCACTC•TYAATYGGANTCAACRCC
A4-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGCACTGTAG•TYAATYGGANTCAACRCC
A5-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATCAGACACG•TYAATYGGANTCAACRCC
A6-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATATCGCGAG•TYAATYGGANTCAACRCC
A7-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CGTGTCTCTA•TYAATYGGANTCAACRCC
A8-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CTCGCGTGTC•TYAATYGGANTCAACRCC
A9-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TAGTATCAGC•TYAATYGGANTCAACRCC
A10-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TCTCTATGCG•TYAATYGGANTCAACRCC
A12-A956F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TACTGAGCTA•TYAATYGGANTCAACRCC
B-A1401R	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG•CRGTGWGTRCAAGGRGCA

**Table S2 continued...**

<b>Primer Name<sup>a</sup></b>	<b>Sequence 5'-3'</b>
<b><i>Eukarya 18S</i></b>	
A1-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGAGTGCGT•CYGCGGTAATTCCAGCTC
A2-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ACGCTCGACA•CYGCGGTAATTCCAGCTC
A3-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGACGCACTC•CYGCGGTAATTCCAGCTC
A4-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•AGCACTGTAG•CYGCGGTAATTCCAGCTC
A5-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATCAGACACG•CYGCGGTAATTCCAGCTC
A6-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•ATATCGCGAG•CYGCGGTAATTCCAGCTC
A7-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CGTGTCTCTA•CYGCGGTAATTCCAGCTC
A8-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•CTCGCGTGTC•CYGCGGTAATTCCAGCTC
A9-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TAGTATCAGC•CYGCGGTAATTCCAGCTC
A10-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TCTCTATGCG•CYGCGGTAATTCCAGCTC
A12-E572F	CCATCTCATCCCTGCGTGTCTCCGACTCAG•TACTGAGCTA•CYGCGGTAATTCCAGCTC
B-E1009R	CCTATCCCCTGTGTGCCTTGGCAGTCTCAG•AYGGTATCTRATCRTCTTYG

<sup>a</sup> Bar-code #11 was skipped and the 11<sup>th</sup> sample used Roche MID #12 (i.e.: A12-B969F).

Primers are constituted of 30 bp Roche 454 adaptors (A for forward, B for reverse), 10 bp Roche MID bar-codes (shown between dots for clarity; absent from reverse primers), and the 17-20 bp rDNA-specific sequences detailed in **Table S1**.