

Supplementary Table I. Location and sequences of primers used for extracting data on each hypervariable region (HVR) and combinations of adjacent HVRS

HVR	Location of the forward primer	Sequence of the forward primer	Location of the reverse primer	Sequence of the reverse primer	Reference
V2	119	AGYGGCGNACGGGTGAGTAA	338	TGCTGCCTCCCGTAGGAGT	1
V3	341	CCTACGGGAGGCAGCAG	534	ATTACCGCGGCTGCTGG	2
V4	577	AYTGGGYDTAAAGNG	785	TACNVGGGTATCTAATCC	3,4
V5	784	AGGATTAGATACCCT	907	CCGTCAATTCCTTTGAGTTT	5,6
V6	961	TCGAtGCAACGCGAAGAA	1085	ACATtTCACaACACGAGCTGACGA	7
V7	1099	GYAACGAGCGCAACCC	1238	GTAGCRCGTGTGTMGCCC	8,9
V8	1050	ATGGCTGTCTCAGCT	1385	ACGGGCGGTGTGTAC	10
V2+V3	119	AGYGGCGNACGGGTGAGTAA	518	ATTACCGCGGCTGCTGG	1,2
V3+V4	341	CCTACGGGRSGCAGCAG	798	GGGGTATCTAATCCC	2,11
V4+V5	577	AYTGGGYDTAAAGNG	907	CCGTCAATTYTTRAGTTT	3,5,6
V5+V6	805	GACTACCAGGGTATCTAATCC	1065	AGGTGCTGCATGGCTGT	9
V6+V7	967	CAACGCGAAGAACCTTACC	1238	GTAGCRCGTGTGTMGCCC	9
V7+V8	1046	ACAGCCATGCAGCACCT	1406	GACGGGCGGTGWTRCA	9
N, any nucleotide; Y, C or T; D, not C; V, not T; R, A or G; M, A or C; lowercase nucleotide, low confidence base					

References

1. Hsiao WW, Li KL, Liu Z, Jones C, Fraser-Liggett CM, Fouad AF. Microbial transformation from normal oral microbiota to acute endodontic infections. *BMC Genomics* 2012; 13 : 345.
2. He S, Gall DL, McMahon KD. "Candidatus Accumulibacter" population structure in enhanced biological phosphorus removal sludges as revealed by polyphosphate kinase genes. *Appl Environ Microbiol* 2007; 73 : 5865-74.
3. Reddy BV, Kallifidas D, Kim JH, Charlop-Powers Z, Feng Z, Brady SF. Natural product biosynthetic gene diversity in geographically distinct soil microbiomes. *Appl Environ Microbiol* 2012; 78 : 3744-52.
4. Rodrigues JL, Pellizari VH, Mueller R, Baek K, Jesus Eda C, Paula FS, *et al.* Conversion of the Amazon rainforest to agriculture results in biotic homogenization of soil bacterial communities. *Proc Natl Acad Sci U S A* 2013; 110 : 988-93.
5. Sridevi G, Minocha R, Turlapati SA, Goldfarb KC, Brodie EL, Tisa LS, *et al.* Soil bacterial communities of a calcium-supplemented and a reference watershed at the Hubbard Brook Experimental Forest (HBEF), New Hampshire, USA. *FEMS Microbiol Ecol* 2012; 79 : 728-40.
6. Nossa CW, Oberdorf WE, Yang L, Aas JA, Paster BJ, Desantis TZ, *et al.* Design of 16S rRNA gene primers for 454 pyrosequencing of the human foregut microbiome. *World J Gastroenterol* 2010; 16 : 4135-44.
7. Chakravorty S, Helb D, Burday M, Connell N, Alland D. A detailed analysis of 16S ribosomal RNA gene segments for the diagnosis of pathogenic bacteria. *J Microbiol*

Methods 2007; 69 : 330-9.

8. Mizrahi-Man O, Davenport ER, Gilad Y. Taxonomic classification of bacterial 16S rRNA genes using short sequencing reads: evaluation of effective study designs. *PLoS One* 2013; 8 : e53608.
9. Youssef N, Sheik CS, Krumholz LR, Najjar FZ, Roe BA, Elshahed MS. Comparison of species richness estimates obtained using nearly complete fragments and simulated pyrosequencing-generated fragments in 16S rRNA gene-based environmental surveys. *Appl Environ Microbiol* 2009; 75 : 5227-36.
10. Huws SA, Edwards JE, Kim EJ, Scollan ND. Specificity and sensitivity of eubacterial primers utilized for molecular profiling of bacteria within complex microbial ecosystems. *J Microbiol Methods* 2007; 70 : 565-9.
11. Liu Z, Lozupone C, Hamady M, Bushman FD, Knight R. Short pyrosequencing reads suffice for accurate microbial community analysis. *Nucleic Acids Res* 2007; 35 : e120.