

Non-specific amplification of human DNA is a major challenge for 16S rRNA gene sequence analysis

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Supplementary Table 1:

Family	P Value	Adjusted P value
actinomycetaceae	0.799846105662473	1
actinomycetales_unclassified	0.932646638965876	1
aerococcaceae	0.799846105662473	1
alcanivoracaceae	1	1
bacillaceae_1	0.855132140584706	1
bacillales_incertae_sedis_x	1	1
bacillales_incertae_sedis_xi	0.932646638965876	1
bacillales_incertae_sedis_xii	1	1
bacillales_unclassified	0.371093369522698	0.866490052
bacilli_unclassified	1	1
bacteria_unclassified	0.0390625	0.355902778
bacteroidales_unclassified	1	1
bacteroidetes_unclassified	1	1
betaproteobacteria_unclassified	0.371093369522698	0.866490052
bifidobacteriaceae	0.833935414088552	1
bradyrhizobiaceae	1	1
brevibacteriaceae	0.0346105575157073	0.355902778
burkholderiaceae	0.422678074170635	0.866490052
burkholderiales_incertae_sedis	0.789268026134281	1
campylobacteraceae	0.18144920772142	0.826601946
candidatus_saccharibacteria_unclassified	1	1
cardiobacteriaceae	1	1
carnobacteriaceae	0.29450739368011	0.866490052
caulobacteraceae	1	1
chitinophagaceae	1	1
clostridiales_incertae_sedis_xi	0.208412803684149	0.854492495
clostridiales_unclassified	0.787406490666269	1
comamonadaceae	0.41849223344682	0.866490052
coriobacteriaceae	0.371093369522698	0.866490052
corynebacteriaceae	0.0078125	0.3203125
dermabacteraceae	0.18144920772142	0.826601946
dermacoccaceae	1	1
dermatophilaceae	1	1
enterobacteriaceae	0.142213241936393	0.826601946
enterococcaceae	0.422678074170635	0.866490052
erysipelotrichaceae	0.371093369522698	0.866490052
eubacteriaceae	1	1
firmicutes_unclassified	1	1
flavobacteriaceae	0.352542137499713	0.866490052
fusobacteriaceae	0.799846105662473	1
fusobacteriales_unclassified	0.371093369522698	0.866490052
gammaproteobacteria_unclassified	0.371093369522698	0.866490052
halomonadaceae	0.583882420770365	1

intrasporangiaceae	0.855132140584706	1
lachnospiraceae	0.787406490666269	1
lactobacillaceae	0.18144920772142	0.826601946
leptotrichiaceae	0.401678166469773	0.866490052
leuconostocaceae	1	1
listeriaceae	1	1
methylobacteriaceae	0.015625	0.3203125
microbacteriaceae	0.18144920772142	0.826601946
micrococcaceae	0.0390625	0.355902778
moraxellaceae	0.7421875	1
neisseriaceae	1	1
nitrospiraceae	1	1
nocardiaceae	1	1
pasteurellaceae	0.204893893816379	0.854492495
peptostreptococcaceae	0.371093369522698	0.866490052
phyllobacteriaceae	0.0759269629825577	0.622601096
porphyromonadaceae	0.100348246462291	0.740182435
prevotellaceae	0.0360316862182336	0.355902778
promicromonosporaceae	0.422678074170635	0.866490052
propionibacteriaceae	0.0224942712224497	0.355902778
proteobacteria_unclassified	1	1
pseudomonadaceae	0.371093369522698	0.866490052
rhizobiaceae	1	1
rhizobiales_unclassified	0.18144920772142	0.826601946
rhodobacteraceae	0.280712665268496	0.866490052
rhodocyclaceae	1	1
ruminococcaceae	1	1
sphingobacteriaceae	1	1
sphingomonadaceae	0.280712665268496	0.866490052
spirochaetaceae	1	1
sporolactobacillaceae	1	1
sr1_unclassified	1	1
staphylococcaceae	0.015625	0.3203125
streptococcaceae	0.108319380730004	0.740182435
streptophyta	0.271898710819648	0.866490052
thermaceae	0.371093369522698	0.866490052
unknown_unclassified	0.0078125	0.3203125
veillonellaceae	0.280712665268496	0.866490052
xanthomonadaceae	1	1

Supplementary Table 1: Differentially enriched bacterial families between V1-V2 and V3-V4 primer sites. Significance calculated using Wilcoxon signed-rank test. Once p-values are corrected for multiple testing using FDR method, no families are significantly elevated between primer pairs.