

Supplemental Table 1. Relative abundances of sequences assigned to different outgroups on a reference phylogenetic tree by AMPHORA for metagenomic sequences collected along an oceanic depth gradient at the HOT ALOHA site. Outgroups represent the reference sequence most closely related to each metagenomic sequence based on a phylogenetic placement of each sequence on a phylogeny based on 31 gene families from 571 fully sequenced bacterial genomes.

Outgroup	10m	70m	130m	200m	500m	770m	4000m
Acetobacteraceae	0.00	0.00	0.00	0.00	0.01	0.01	0.00
Acholeplasmataceae	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Acidobacteria	0.00	0.04	0.00	0.00	0.01	0.03	0.01
Acidobacteria bacterium Ellin345	0.00	0.00	0.00	0.02	0.00	0.01	0.01
Actinobacteria	0.01	0.00	0.00	0.00	0.00	0.01	0.00
Actinobacteridae	0.02	0.00	0.05	0.02	0.05	0.07	0.00
Actinomycetales	0.00	0.00	0.00	0.00	0.01	0.01	0.01
Alcanivorax borkumensis SK2	0.03	0.02	0.00	0.00	0.03	0.00	0.01
Alkalilimnicola ehrlichei MLHE-1	0.00	0.00	0.05	0.00	0.00	0.00	0.00
Alphaproteobacteria	0.02	0.06	0.00	0.04	0.06	0.02	0.04
Aquifex aeolicus VF5	0.02	0.00	0.00	0.00	0.00	0.03	0.00
Bacteria	0.02	0.04	0.12	0.09	0.07	0.13	0.10
Bacteroidetes/Chlorobi group	0.00	0.00	0.05	0.09	0.01	0.04	0.00
Bdellovibrio bacteriovorus HD100	0.00	0.00	0.00	0.07	0.01	0.01	0.00
Betaproteobacteria	0.00	0.00	0.00	0.02	0.00	0.01	0.00
Borrelia burgdorferi group	0.00	0.00	0.00	0.00	0.02	0.03	0.00
Burkholderiales	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Candidatus Pelagibacter ubique HTCC1062	0.02	0.06	0.02	0.04	0.00	0.00	0.01
Candidatus Phytoplasma asteris	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Candidatus Sulcia muelleri GWSS canis group	0.01	0.00	0.02	0.00	0.00	0.00	0.01
Caulobacteraceae	0.01	0.02	0.00	0.00	0.00	0.00	0.00
Chlamydiales	0.00	0.00	0.00	0.07	0.01	0.00	0.00
Chlorobiaceae	0.00	0.04	0.02	0.02	0.00	0.02	0.00
Chloroflexaceae	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Chloroflexi	0.03	0.00	0.07	0.02	0.01	0.02	0.09
Chromohalobacter salexigens DSM 3043	0.01	0.06	0.00	0.00	0.00	0.00	0.00
Clostridiaceae	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Clostridium phytofermentans ISDg	0.00	0.00	0.00	0.02	0.00	0.00	0.00
Clostridium thermocellum ATCC 27405	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Coxiella burnetii	0.01	0.04	0.00	0.00	0.00	0.01	0.00
Cyanobacteria	0.00	0.02	0.00	0.00	0.01	0.00	0.03
Cytophaga hutchinsonii ATCC 33406	0.00	0.02	0.00	0.00	0.00	0.01	0.00
Dehalococcoides	0.00	0.00	0.00	0.07	0.05	0.01	0.18
Deltaproteobacteria	0.00	0.00	0.00	0.04	0.00	0.02	0.00
Desulfobacterium hafniense Y51	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Desulfococcus oleovorans Hxd3	0.00	0.02	0.00	0.00	0.00	0.01	0.00
Desulfotalea psychrophila LSV54	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Desulfovibrionaceae	0.00	0.00	0.00	0.00	0.02	0.03	0.00
Dichelobacter nodosus VCS1703A	0.00	0.04	0.00	0.00	0.00	0.06	0.00
Epsilonproteobacteria	0.01	0.02	0.00	0.00	0.02	0.01	0.00
Flavobacteriaceae	0.00	0.02	0.00	0.02	0.00	0.00	0.00
Flavobacteriales	0.05	0.00	0.00	0.00	0.00	0.00	0.00
Francisella tularensis	0.03	0.00	0.00	0.00	0.01	0.00	0.00
Gammaproteobacteria	0.01	0.11	0.00	0.00	0.08	0.00	0.09
Geobacter	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Hahella chejuensis KCTC 2396	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Halorhodospira halophila SL1	0.00	0.00	0.00	0.00	0.02	0.00	0.00
Herpetosiphon aurantiacus ATCC 23779	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Hyphomonas neptunium ATCC 15444	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Lactobacillus reuteri F275	0.00	0.00	0.00	0.00	0.00	0.00	0.01
Leptospira	0.00	0.06	0.00	0.00	0.06	0.01	0.00
Magnetospirillum magneticum AMB-1	0.00	0.02	0.00	0.00	0.00	0.00	0.01
Marinobacter aquaeolei VT8	0.00	0.00	0.00	0.00	0.00	0.01	0.03
Marinomonas sp. MWYL1	0.01	0.04	0.00	0.00	0.00	0.01	0.01
Mesorhizobium loti MAFF303099	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Microbacteriaceae	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Micrococcaceae	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Mollicutes	0.00	0.00	0.00	0.04	0.00	0.02	0.00
Mycoplasma	0.02	0.00	0.00	0.07	0.00	0.02	0.00
Mycoplasma gallisepticum R	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Mycoplasma mobile 163K	0.00	0.00	0.00	0.02	0.00	0.00	0.00
Myxococcaceae	0.01	0.02	0.05	0.00	0.00	0.00	0.00
Myxococcales	0.01	0.00	0.05	0.00	0.01	0.00	0.00
Neorickettsia sennetsu str. Miyayama	0.01	0.02	0.07	0.00	0.00	0.00	0.00
Nitrosococcus oceani ATCC 19707	0.00	0.00	0.00	0.00	0.02	0.00	0.04
Oceanospirillales	0.00	0.02	0.00	0.00	0.00	0.00	0.01
Orientia tsutsugamushi Boryong	0.01	0.00	0.00	0.00	0.00	0.00	0.01
Parvibaculum lavamentivorans DS-1	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Pasteurellaceae	0.00	0.00	0.02	0.00	0.00	0.00	0.00
Petrogona mobilis SJ95	0.00	0.00	0.02	0.00	0.00	0.01	0.01
Prochlorococcus marinus	0.15	0.06	0.15	0.04	0.00	0.02	0.00
Prochlorococcus marinus str. MIT 9301	0.01	0.00	0.00	0.00	0.00	0.00	0.00
Propionibacterium acnes KPA171202	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Proteobacteria	0.00	0.00	0.02	0.00	0.02	0.06	0.01
Pseudoalteromonas atlantica T6c	0.00	0.00	0.00	0.00	0.00	0.02	0.00
Psychrobacter	0.00	0.00	0.00	0.00	0.01	0.00	0.00
Rhizobiales	0.02	0.00	0.00	0.00	0.00	0.00	0.00
Rhodobacteraceae	0.02	0.00	0.00	0.00	0.06	0.02	0.01
Rhodiferax ferrireducens T118	0.00	0.00	0.05	0.00	0.00	0.00	0.00
Rhodopirellula baltica SH 1	0.00	0.02	0.02	0.02	0.03	0.01	0.01
Rhodospirillaceae	0.01	0.00	0.00	0.00	0.00	0.00	0.00

