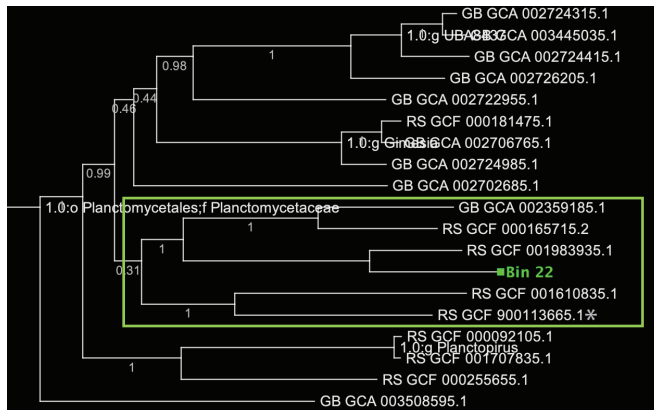


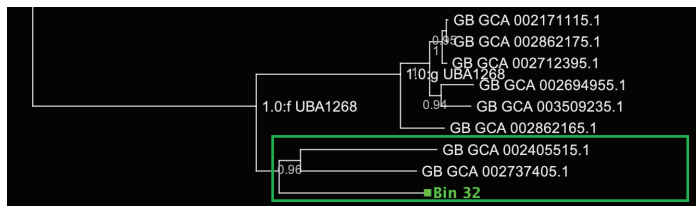
nGOM_Bacteria_50

Latescibacterota

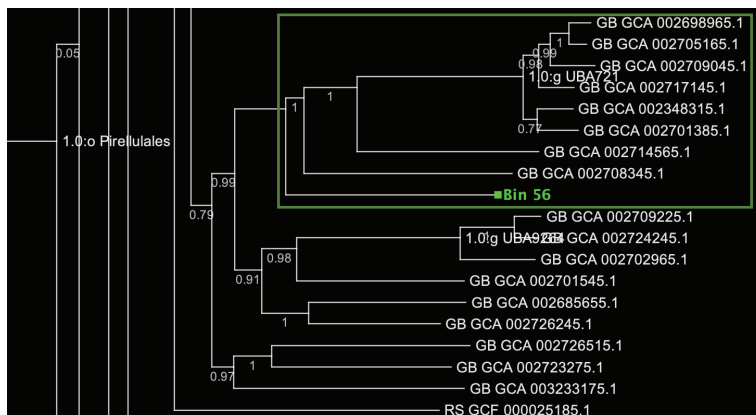


nGOM_Plancto_22

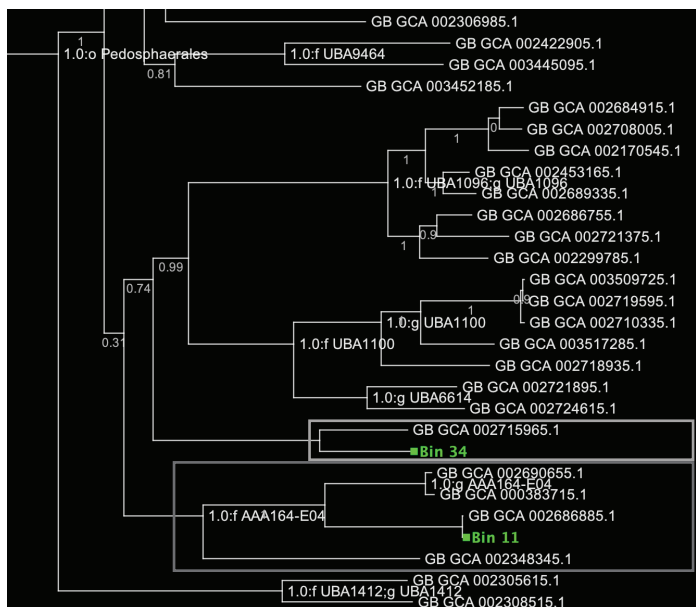
Planctomycetota



nGOM_Plancto_32



nGOM_Plancto_56



nGOM_Verruco_34

nGOM_Verruco_11

Verrucomicrobiota

Supplemental Figure 2.

Ribosomal protein phylogenetic tree from GTDB showing only relevant microbes, not all 46,926 nodes in the original tree, with boxes denoting close relatives of the nGOM MAGs. The asterisk indicates a microbe that was a close relative to nGOM MAGs, but its genomic data was restricted, so it was not included in any analyses. The four canonical methanotrophs included in our analyses were not closely related to the nGOM MAGs, so are not shown in this figure.

Supplemental Figure 2. Ribosomal protein phylogenetic tree with boxes denoting close relatives of the nGOM MAGs used in downstream analysis. The asterisk indicates a microbe that was a close relative to nGOM MAGs, but its genomic data was restricted, so it was not included in any analyses. The four canonical methanotrophs included in our analyses were not closely related to the nGOM MAGs, so are not shown in this figure.