Ecology

Large-scale amplicon analysis

Identification of MAG relatives (n≈52,000)

Taxonomy

Closest relatives based on 16S rRNA

Closest relatives based on genome

User provided
Genome
16S rRNA

16S rRNA

Genome

Output
-16S tree
-Genome tree
-GC (%) difference
-ANI to closest relatives
-POCP to closest relatives
-CAZy profile

-16S rRNA identity to closest relatives
-KEGG based; urease, oxidase, sulfide utilisation, ammonia utilisation, sulfate reduction, nitrogen fixation, flagella, vitamin biosynthesis, carbon source utilisation

Functional

Carbohydrate degrading potential

Pathway analysis