



**Figure S1.** Phylogenomic placement of ANME MAGs based on concatenated partial amino acid sequences of 122 archaeal single copy conserved marker genes with taxonomic designations according to the GTDB. The tree was built using the IQ-TREE 2 program [Minh et al., 2020] with fast model selection via ModelFinder [Kalyanamoorthy et al., 2017] and ultrafast bootstrap approximation [Minh et al., 2013], as well as an approximate likelihood-ratio test for branches [Anisimova and Gascuel, 2006]. Bootstrap consensus tree is shown with values placed at the nodes. Bar, 0.1 changes per position.

## References

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