

Figure S4 Phylogenetic tree with SAR11 MAGs that have >50% completeness and <5% contamination described in this study with previously published SAR11 single amplified genomes (SAGs) (Haro-Moreno JM, Rodriguez-Valera F, Rosselli R, Martinez-Hernandez F, Roda-Garcia JJ, Gomez ML, Fornas O, Martinez-Garcia M, López-Pérez M. 2020. Environmental Microbiology 22:1748–1763) and SAR11 isolates (Delmont TO, Kiefl E, Kilinc O, Esen OC, Uysal I, Rappe MS, Giovannoni S, Eren AM. 2019. eLife 8:e46497). Colours according to clade assignment (indicated in outer ring) according to the literature (see above).