Processing amoA amplicons from sequencing data

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16S rRNA gene amplicon sequences were trimmed with TrimGalore ([Krueger et al. 2021](#ref-krueger2021)), a wrapper using CutAdapt ([Martin 2011](#ref-EJ200)) for trimming of sequencing primers and adapters and FastQC ([Andrews et al. 2012](#ref-andrews2012)) for quality control. Trimmed reads were merged and assigned to amplicon sequence variants (ASVs) using dada2([Callahan et al. 2016](#ref-callahan2016)), with quality filtering and chimera removal using the default settings (Table S7). Taxonomy was assigned to ASVs in dada2 using the Silva rRNA database (SSU Ref NR 99 v138.1)[quast\_silva\_2012]. Community diversity (Table S8) and relative abundance (Table S9) of all sample replicates and fractions were calculated using phyloseq([McMurdie and Holmes 2013](#ref-mcmurdie_phyloseq_2013)).

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