SUPPLEMENTARY INFORMATION

ARISA assays 120 DNA extracts (40 samples in triplicate) were titrated to a standard working concentration range of 5-10 ng µl^{-1}. The technical replicates were analysed with automated ribosomal intergenic spacer analysis (ARISA) to evaluate inter/intra sample similarity according van Dorst *et al* (2014) Community fingerprinting in a sequencing world FEMS Microbiol. Ecol. DOI:10.1111/1574-6941.12308. Inter-sample replication was evaluated with analysis of similarity (ANOSIM) in PRIMER v6. After inter-sample similarity was confirmed, the extracted genomic DNA from three randomly selected replicates within each fuel category was used as a template for barcoded tag pyrosequencing. Examples for P2 have been provided in Table S1 and Figure S1.

Table S1. Analysis of similarity (ANOSIM) results testing for significant differences between fuel categories based on the ARISA and pyrosequencing results.

Differences between fuel groups	**Global R**	***p* value**
ARISA	0.397	0.001
Pyrosequencing	0.691	0.004

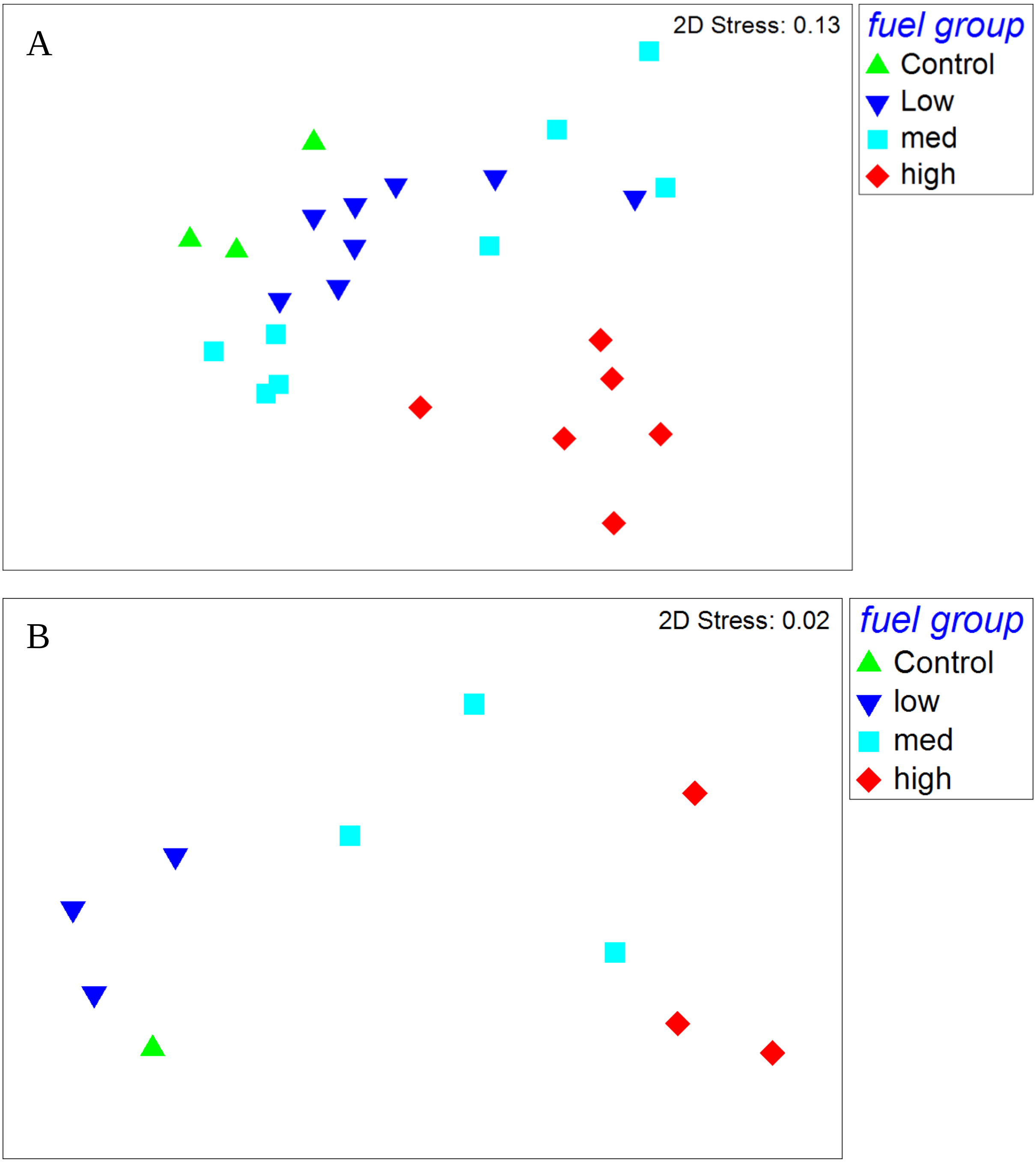

Figure S1. Ordination plots of samples from P2 based on ARISA fragments (S1A) and pyrosequencing data (S1B). After Analysis of similarity (ANOSIM) testing of the ARISA results in S1A, three replicates from each fuel group were randomly selected for pyrosequencing, S1B.

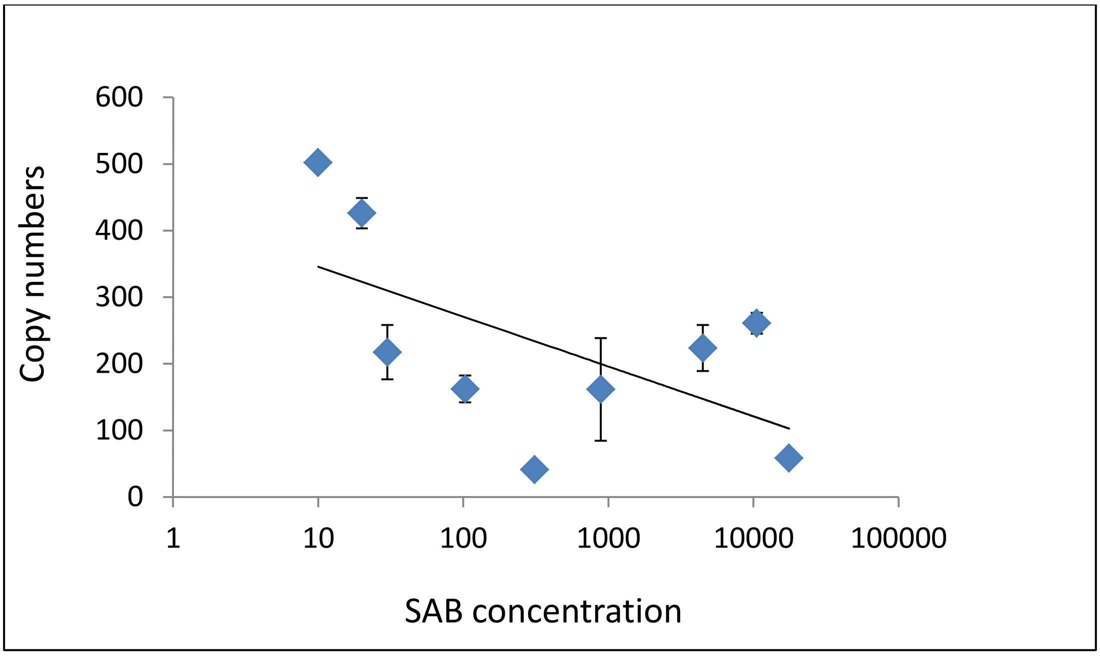

Figure S2. Abundance of the Archaeal *amoA* gene in P2. Abundances decline with increasing SAB concentration. Copy numbers range from 5.02 x 10^2 to 4.07 x 10^1.