

Supplementary Figure Legends

Fig. S1. Rarefaction curves for the 12 gene libraries from the Peru Margin site 1229 shown in Fig. 2a plotted for three levels of similarity, which represent approximately the subspecies (99% similarity; ●), species (97%; △) and genus (95%; ○) level of phylotype differentiation (Schloss and Handelsman, 2004). Columns are labelled (A) *Archaea* 16S rRNA genes, (B) *Bacteria* 16S rRNA genes and (C) *mcrA* genes, the depths at which each library was obtained are indicated above each row.

Fig. S2. Phylogenetic tree of representative bacterial 16S rRNA gene sequences from Peru Margin site 1229 clone libraries presented in Fig. 2a. Minimum evolution tree derived from LogDet/Paralinear distances of variable sites (estimated value of proportion of invariable sites = 0.2532). The tree is based on 545 bases of aligned 16S rRNA gene sequences. Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences were chosen for comparison with the example clone sequences from this study by selecting closely related environmental clone sequences, primarily from deep marine sediments, and the most closely related pure cultures from within the phyla and from other neighbouring phyla. Sequences of *Deinococcus-Thermus* were used as outgroups, *Thermus aquaticus* (L09663), *Meiothermus ruber* (C09672), and *Deinococcus radiodurans* (M21413). The novel group NT-B2 corresponds to the cluster designation described in Reed *et al.* (2002). The new sequences in bold have been submitted to the database under accession numbers AJ867585-AJ867605.

Fig. S3. Phylogenetic trees showing representative archaeal 16S rRNA gene sequence from Peru Margin site 1229 clone libraries presented in Fig. 2a in the *Crenarchaeota* (A) and *Euryarchaeota* (B). Minimum evolution trees derived from LogDet/Paralinear distances of variable sites (estimated value of proportion of invariable sites = 0.3656 (A) and 0.4304 (B)). The trees were constructed from 769 (A) and 678 (B) bases of aligned 16S rRNA gene sequences. Bootstrap support values over 50% (1000 replicates) are shown. Representative sequences were chosen for comparison as described in Fig. S2. Sequences of the *Korarchaeota* were used as outgroups, *Korarchaeote* clone pBA5 (AF176347), *Korarchaeote* clone pJP27 (L25852), and *Korarchaeote* clone SRI-306 (AF255604). The new sequences in bold have been submitted to the database under accession numbers AJ867778-AJ867808.

Fig. S4. Phylogenetic tree of representative *mcrA* gene sequences from Peru Margin site 1229 clone libraries presented in Fig. 2a. The tree was constructed by neighbour-joining and Paralinear distances using 410 aligned nucleotides with *Methanopyrus kandleri* (U57340) as the outgroup. Representative sequences were chosen for comparison as described in Fig. S2. Bootstrap support values over 50% (1000 replicates) are shown. The new sequences in bold have been submitted to the database under accession numbers AJ867759-AJ867766.

Supplementary References

Reed, D.W., Fujita, Y., Delwiche, M.E., Blackwelder, D.B., Sheridan, P.P., Uchida, T. and Colwell, F.S. (2002) Microbial communities from methane hydrate-bearing deep marine sediments in a forearc basin. *Appl. Environ. Microbiol.* 68, 3759-3770.

Schloss, P.D. and Handelsman, J. (2004) Status of the microbial census. *Microbiol. Molec. Biol. Rev.* 68, 686-691.