Supplemental figures

Fig. S4 Heatmap comparison of relative abundance (within studies) of bacterial groups present in the current study and those detected by Dahle et al. (2008), Grabowski et al. (2005), Li et al. (2006), Oliveira et al. (2008), Orphan et al. (2000), Pham et al. (2009), Sette et al. (2007), Voordouw et al. (1996) and Yamane et al. (2008). W indicates formation water. Identities of taxa are described in Table S3. The dendrogram represents the hierarchical cluster analysis of relatedness. Well-supported branches on the dendrogram include p-values. Dashed branches indicate a lack a statistical support for the placement of that branch.

Fig. S5 Heatmap comparison of relative abundance (within studies) archaeal groups present in the current study and those detected by Dahle et al. (2008), Grabowski et al. (2005), Orphan et al. (2000), Pham et al. (2009) and Yamane et al. (2008). W indicates formation water. Identities of taxa are described in Table S3. The dendrogram represents the hierarchical cluster analysis of relatedness. Well-supported branches on the dendrogram include p-values.

Fig. S6 Hierarchical clustering of the PCR primer pairs compared in this study, based on their percentage match to all species within each genus examined. The figure indicated the clusters of primers used to amplify Archaea (A) and Bacteria (B). Inside Fig. 3A, the primer pairs clustered into the same cluster were represented with the same colour bars next to them. For example, primer pairs A21F/A976R and A21F/A1401R are related primers and clustered into the same group, red bar was applied to them. Corresponding to it, in Fig. 5, the red line represents the two pair of primers. It is the same for Fig. 3b, but the colours used within are linked to Fig. 4. The clustering for Bacteria and Archaea indicated the presence of five and six clusters among the bacterial (Fig. 3B) and archaeal primers (Fig 3A), respectively. Although the cluster of the primer pairs were based on their relatedness, please note that primer pairs of 27F/1525R and EUB338F/UNIV907R was clustered together was more likely due to both the poor matching of the primer pairs to the known 16S rRNA gene.
Fig. S7 Percentage of taxa within a genus that match the primers used to amplify Bacteria. A representative example from each cluster in Fig. 3B, (except for the 27F/1525R and EUB338F/UNIV907R primer pairs) was plotted using Matlab. The lines were smoothed as described to improve legibility. The line colour is correlated to the cluster colour in Fig. 3B. The phyla and classes are indicated in the bottom of the X-axis. The cluster of 27F/1525R and EUB338F/UNIV907R, used by Voordouw et al. (1996) and Dahle et al. (2008), respectively were particularly poor by this analysis, with generally low matching (< 10% of most genera) across the entire bacterial domain, thus the matching of those primers were excluded from the figure. In contrast, the bacterial primers used by Yamane et al (2008), 63F/1387R had relatively good matches to taxa in the Bacteroidetes, Alpha- and Gammaproteobacteria, to the exclusion of most other microbial groups. The remaining clusters, represented by U968F/L1401R, 27F/Univ519R and 27F/1492R, were relatively consistent across the bacterial spectrum, albeit with varying degrees of coverage.

Fig. S8 Percentage taxa within a genus that match the primers used to amplify Archaea. A representative example from each cluster (Fig. 3A) was plotted using Matlab. The lines were smoothed as described to improve legibility. The line colour correlated to the cluster colour in Fig. 3A. The phyla and orders from the archaeal domain are indicated at the bottom of the X-axis. Of those primers targeted to Archaea some broad patterns were apparent. The six clusters had similarly structured bias, with generally fewer matches to some Desulfurococcales, Thermoproteales, Halobacteriales along with some members of the methanogenic orders Methanobacteriales and Methanomicrobiales.