**Supplementary Figure 1**

Community composition of major taxonomic groups of (**A**) *Bacteria* and (**B**) *Archaea* from 16S rRNA gene libraries at various sites and sediment depths from different provinces of the seafloor (0-2 m) and deep subseafloor biosphere (below 2 m). Each bar represents the relative distribution of major bacterial groups reported within each library. The site details and sediment depths (metres below sea floor, mbsf) for each gene library are given to the left of the bars followed by (number of clones in each library) and [the citation]. The citation codes are: 1, Arakawa et al. (2006); 2, Biddle et al. (2006); 3, Breuker et al. (2013); 4, Dang et al. (2009); 5, Durbin & Teske (2011); 6, Fang et al. (2006); 7, Forschner et al. (2009); 8, Hoshino et al. (2011); 9a, Inagaki et al. (2002); 9, Inagaki et al. (2003); 10, Inagaki et al. (2004); 11, Inagaki et al. (2006); 12, Jiang et al. (2007); 13, Jorgensen et al. (2012); 14, Kormas et al. (2003); 15, Li et al. (1999); 16, Li et al. (2008); 17, Marchesi et al. (2001); 18, Newberry et al. (2004); 19, Nunoura et al. (2008); 20, Nunoura et al. (2009); 21, Orcutt et al. (2010); 22, Parkes et al. (2005); 23, Reed et al. (2002); 24, Roussel et al. (2008); 25, Roussel et al. (2009); 26, Sørensen et al. (2004); 27, Sørensen & Teske (2006); 28, Teske (2006); 29, Webster et al. (2006); 30, Webster et al. (unpublished data); 31, Zhang et al. (2012). Accepted names are used for the taxonomic bacterial groups (namely Classes for *Proteobacteria*, Phyla and Candidate Divisions, e.g. JS1); NT-B2 and NT-B6 are novel groups first named by Reed et al. (2002). Names used for uncultivated taxonomic archaeal groups are based on their first reported use: MG1, Marine Group I (*Thaumarchaeota*); MBG-B/DSAG, Marine Benthic Group-B/Deep Sea Archaeal Group, MBG-A, Marine Benthic Group-A, MCG, Miscellaneous Crenarchaeotal Group, MHVG, Marine Hydrothermal Vent Group (*Crenarchaeota*); MBG-D/*Thermoplasmatales* affiliated, Marine Benthic Group-D/*Thermoplasmatales* affiliated (includes MGII, MGIII and MGV; Durbin & Teske, 2011), SAGMEG, South African Gold Mine Euryarchaeotal Group, TMEG, Terrestrial Miscellaneous Euryarchaeotal Group, DSEGs, Deep-Sea Euryarchaeotal Groups, DHVEGs, Deep-sea Hydrothermal Vent Euryarchaeotal Groups (*Euryarchaeota*). Others, all sequences belonging to minority groups and unidentified sequences.

**Supplementary Figure 2**

Community composition of major taxonomic groups of (**A**) *Bacteria* and (**B**) *Archaea* from PCR-DGGE analysis of 16S rRNA genes at various sites and depths from marine subsurface sediments. Each bar represents the relative distribution of major bacterial groups reported within each library. The site details and sediment depths (metres below sea floor, mbsf) for each gene library are given to the left of the bars followed by (number of clones in each library) and [the citation]. The citation codes are: 1, Ciobanu et al. (2012); 2, Coolen et al. (2002); 3, Rochelle et al. (1994); 4, Webster et al. (2006); 5, Webster et al. (2009); 6, Webster et al. (unpublished data). Accepted names are used for the taxonomic bacterial groups (namely Classes for *Proteobacteria*, Phyla and Candidate Divisions, e.g. JS1); NT-B2 and NT-B6 are novel groups first named by Reed et al. (2002). Names used for uncultivated taxonomic archaeal groups are based on their first reported use: MG1, Marine Group I (*Thaumarchaeota*); MBG-B/DSAG, Marine Benthic Group-B/Deep Sea Archaeal Group, MCG, Miscellaneous Crenarchaeotal Group (*Crenarchaeota*); MBG-D/*Thermoplasmatales* affiliated, Marine Benthic Group-D/ *Thermoplasmatales* affiliated, SAGMEG, South African Gold Mine Euryarchaeotal Group (*Euryarchaeota*). Others, all unsequenced DGGE bands and unidentified sequences. Note, the study by Rochelle et al. (1994) is included here since 16S rRNA genes retrieved in this study were too few to be included in Supplementary Figure 1.

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