APPENDIX 1

Composition of Media

**Reasonar’s 2 agar** (R2A): Casein acid hydrolysate 0.5 g/l, Yeast extract 0.5g/l, Biopeptone 0.5g/l, Dextrose 0.5g/l, Starch soluble 0.5g/l, Dipotassium phosphate 0.3g/l, Magnesium sulfate 0.024g/l, Sodium pyruvate 0.3g/l, Agar 15 g/l.

**Luria agar:** Casein enzyme hydrolysate 10g/l, Yeast extract 5g/l, Sodium chloride 5g/l, Agar 15g/l.

**Nutrient Agar:** Peptic digest of animal tissue 5g/l, Beef extract 1.5g/l, Yeast extract 1.5g/l, Sodium chloride 5g/l, Agar 3g/l.

**Zobell Marine Agar:** Peptic digest of animal tissue 5g/l, Yeast extract 1g/l, Ferric citrate0.01g/l, Sodium chloride 8.8g/l, Sodium sulphate 3.24g/l, calcium chloride1.8g/l, potassium chloride0.55g/l, sodium carbonate0.16g/l, potassium bromide0.08g/l, strontium bromide0.034g/l, boric acid0.022g/l, sodium silicate0.004g/l, sodium fluoride0.0024g/l, ammonium nitrate0.0016g/l, disodium phosphate0.008, agar15g/l.

**25% MS salts:** Sodium Bromide 0.128g/l, Sodium carbonate 0.14g/l, Potassium chloride 0.95g/l, Calcium chloride 3.32g/l, Sodium chloride 234g/l, Agar 15g/l

**Plate Count Agar:** Casein enzymic hydrolysate 5g/l , Yeast extract 2.5 g/l, Dextrose 1g/l, Agar 15g/l

**A1 Agar:** Casein enzymic hydrolysate 20g/l, Lactose 5g/l, Sodium chloride 5g/l, Salicin 0.50 g/l, Polyethylene glycol pisoctylphenylether (Triton 100) 1.00 ml/l, Agar 15g/l

**Pikovskayas Agar:** Yeast extract 0.500 g/L, Dextrose 10g/L, Calcium phosphate 5g/l, Ammonium sulphate 0.500 g/l, Potassium chloride 0.200 g/l, Magnesium sulphate 0.100 g/l, Manganese sulphate 0.0001 g/l, Ferrous sulphate 0.0001 g/l, Agar 15g/l.

**Sea water Agar:** Sea water from AlangSosiya ship breaking yard 1l, Agar 15g/l.

**Glycerol Agar:** Peptone 5.0g/l, Beef extract 3.0 g/l Glycerol 70ml/l, Soil extract 250ml/l, Tap water 750ml/l, Agar 15g/l.

**Marine Methylotroph Medium:** Potassium dihydrogen phosphate 0.14g/l, Bis Tris 2g/l, Ferric ammonium citrate 0.06g/l, Sea water 1l, Agar 15 g/l.

**Bushnell Hass Medium:** Magnesium sulfate 0.2g/l, Calcium chloride 0.02g/l, Monopotassium phosphate 1g/l, Dipotassium phosphate 1g/l, Ammonium nitrate 1g/l, Ferric chloride 0.050g/l, Agar 15g/l.
## APPENDIX 2

### Accession number of clones

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<th>Season</th>
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APPENDIX 3

Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from seven sediment samples:

**Figure A3.1.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASD_J (Monsoon season of ASSBY).

**Figure A3.2.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSD_J (Monsoon season of ASSBY).

**Figure A3.3.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASD_D (winter season of ASSBY).

**Figure A3.4.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSD_D (Winter season of ASSBY).

**Figure A3.5.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASD_M (summer season of ASSBY).

**Figure A3.6.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSD_M (summer season of ASSBY).

**Figure A3.7.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVPsd (Pristine).

**Note:** In each case the trees were constructed based on partial sequences (1200 bp) of 16S rRNA genes retrieved 16S rRNA gene clone libraries and neighbouring RDP sequences. The trees were constructed using the neighbor joining algorithm with Kimura 2 parameter distances in MEGA 4.0 software. Numbers at nodes indicate percent bootstrap values above 50 supported by 1000 replicates. Bar indicates JukeseCantor evolutionary distance. Numbers in parentheses indicate RDPID numbers of neighbouring sequences downloaded from the Ribosomal Database Project (RDPII).
Fig. A3.4
APPENDIX 4

Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from seven coastal water samples:

**Figure A4.1.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASW_J (monsoon season of ASSBY).

**Figure A4.2.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSW_J (monsoon season of ASSBY).

**Figure A4.3.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASW_D (winter season of ASSBY).

**Figure A4.4.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSW_D (winter season of ASSBY).

**Figure A4.5.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVASW_M (summer season of ASSBY).

**Figure A4.6.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVBSW_M (summer season of ASSBY).

**Figure A4.7.** Phylogenetic trees depicting unique OTUs obtained within different bacterial phyla recovered from DVPSW (pristine coastal water).

**Note:** In each case the trees were constructed based on partial sequences (1000 bp) of 16S rRNA genes retrieved 16S rRNA gene clone libraries and neighbouring RDP sequences. The trees were constructed using the neighbor joining algorithm with Kimura 2 parameter distances in MEGA 4.0 software. Numbers at nodes indicate percent bootstrap values above 50 supported by 1000 replicates. Bar indicates Jukes-Cantor evolutionary distance. Numbers in parentheses indicate RDP-ID numbers of neighbouring sequences downloaded from the Ribosomal Database Project (RDP-II).
Fig. A4.1
Fig. A4.2
Fig. A4.3