Reduced diversity and changed bacterioplankton community composition do not affect utilization of dissolved organic matter in the Adriatic Sea

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Supplement. Additional Figs. S1 to S4

Fig. S1. Bacterial community dynamics over time in Stress 3 as analyzed by denaturing gradient gel electrophoresis (DGGE). A denaturing gradient of 26 to 52% was applied
Fig. S2. Phylogenetic tree based on (I) 121 OTUs representing >100 sequences, (II) 49 reference sequences from other studies and (III) 1 outgroup sequence from the *Aquifex* genus. The tree was calculated by the aid of RAxML using GTRGAMMA as a substitution model. Tree branches are coloured according to phylum or class. Note that taxonomic assignments were made with the aid of the Greengenes classification module, and therefore, some taxa are not placed in expected clades. The number of sequences in each OTU was normalized by dividing with the total number of sequences in the sample and then multiplying by the number of sequences in the inoculum. In: inoculum; C: Control (24°C); S1: Stress 1 (16°C); S2: Stress 2 (16°C and elevated phosphate); S3: Stress 3 (16°C, elevated phosphate and lowered oxygen level).
Fig. S3. Rarefaction curves constructed from 15,000 random resampled sequences from each sample. Control (24°C); Stress 1 (16°C); Stress 2 (16°C and elevated phosphate); Stress 3 (16°C, elevated phosphate and lowered oxygen level)

Fig. S4. (A) Distribution of major taxonomic groups based on 454-pyrosequencing. (B) Distribution of major families within *Gammaproteobacteria* determined by 454-pyrosequencing. Control (24°C); Stress 1 (16°C); Stress 2 (16°C and elevated phosphate); Stress 3 (16°C, elevated phosphate and lowered oxygen level)