Supporting Information for

Ocean acidification regulates the activity, community structure and functional potential of heterotrophic bacterioplankton in an oligotrophic gyre

Xiaomin Xia[1], Yu Wang[2,3], Yunlan Yang[2,3], Tingwei Luo[2,3], Joy D. Van Nostrand[4], Jizhong Zhou[4,5,6], Nianzhi Jiao*[2,3], Rui Zhang*[2,3]

[1]Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences

[2]State Key Laboratory of Marine Environmental Science, Xiamen University

[3]Institute of Marine Microbes and Ecospheres, Xiamen University

[4]Institute for Environmental Genomics, Department of Microbiology and Plant Biology, and School of Civil Engineering and Environmental Sciences, University of Oklahoma, 101 David L. Boren Boulevard, Norman, OK 73072, USA

[5]State Key Joint Laboratory of Environment Simulation and Pollution Control, School of Environment, Tsinghua University, Beijing, China;

[6]Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, Berkeley, California, USA

Contents of this file

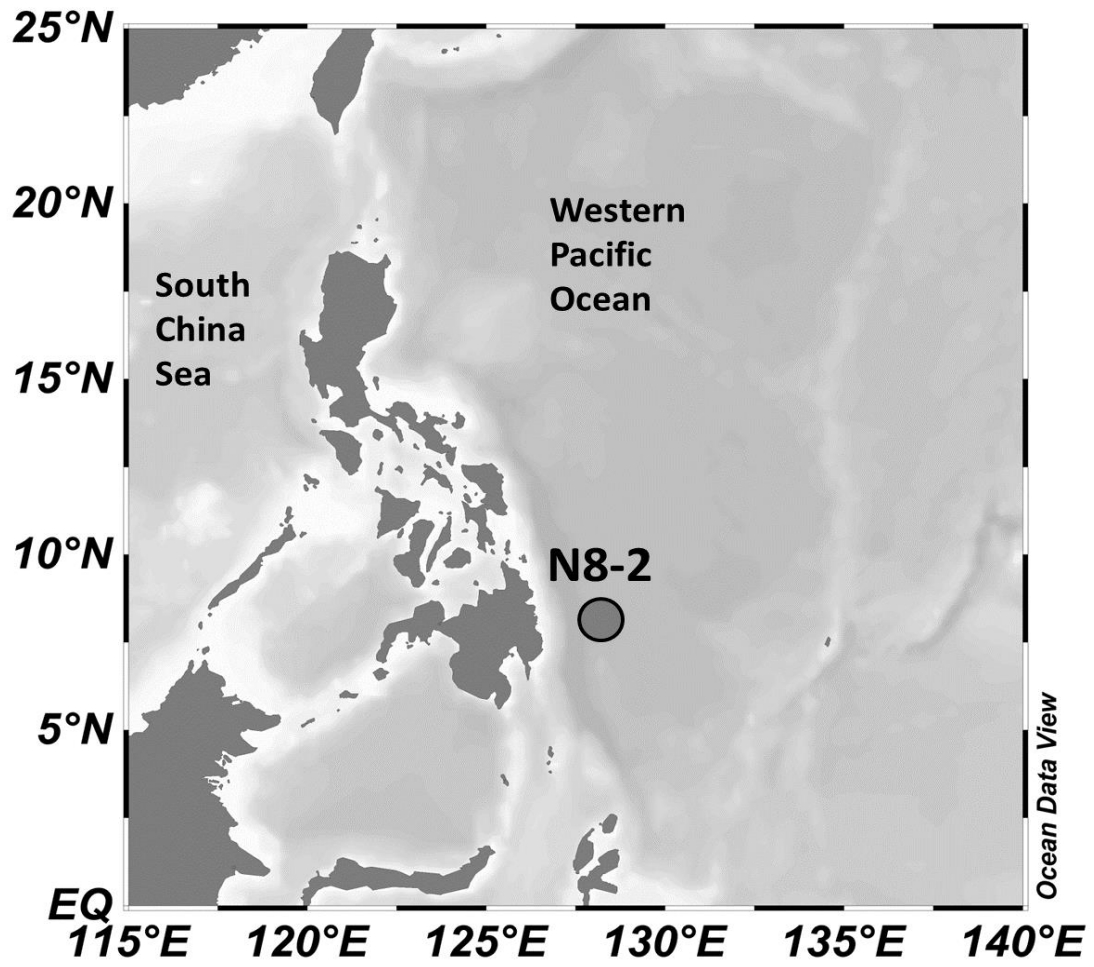**Additional Supporting Information (Files uploaded separately)**

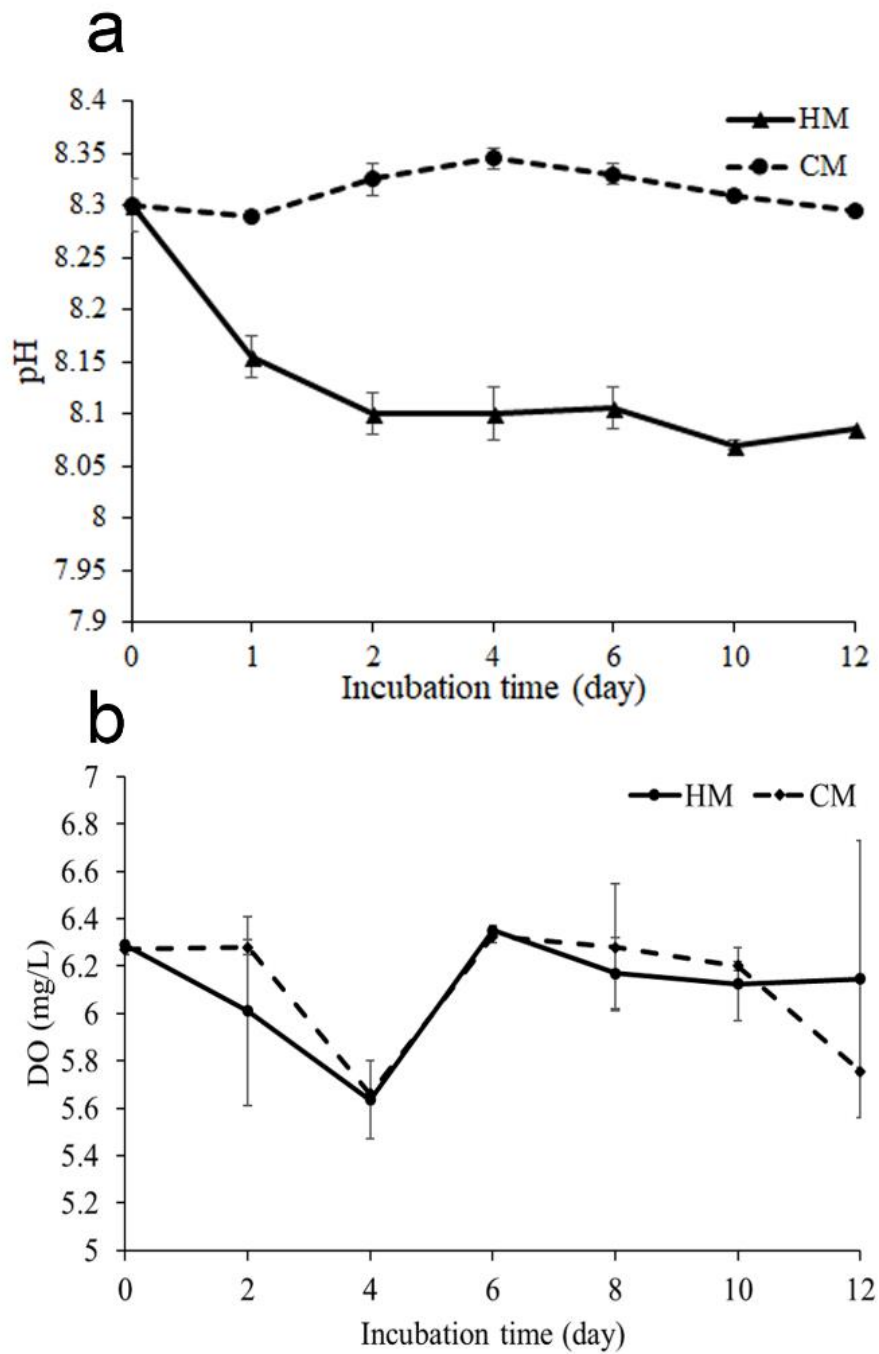Figure S1. Map showing the location of experiment station N8-2.

Fig. S2. The pH (a) and DO (b) of the mesocosms during 12 days incubation. HM: high CO2 microcosm. CM: control microcosm. Errors bars represent SD of replicate samples.
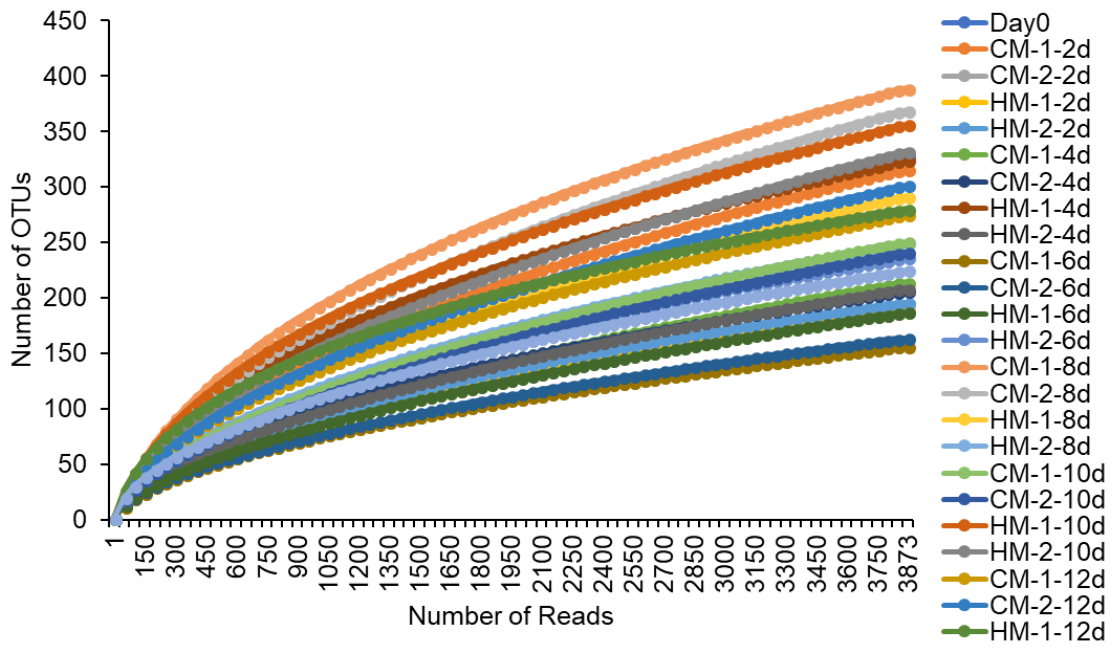
Fig. S3, Rarefaction curves of the samples. OTU, Operational Taxonomic Unit (97% similarity threshold).
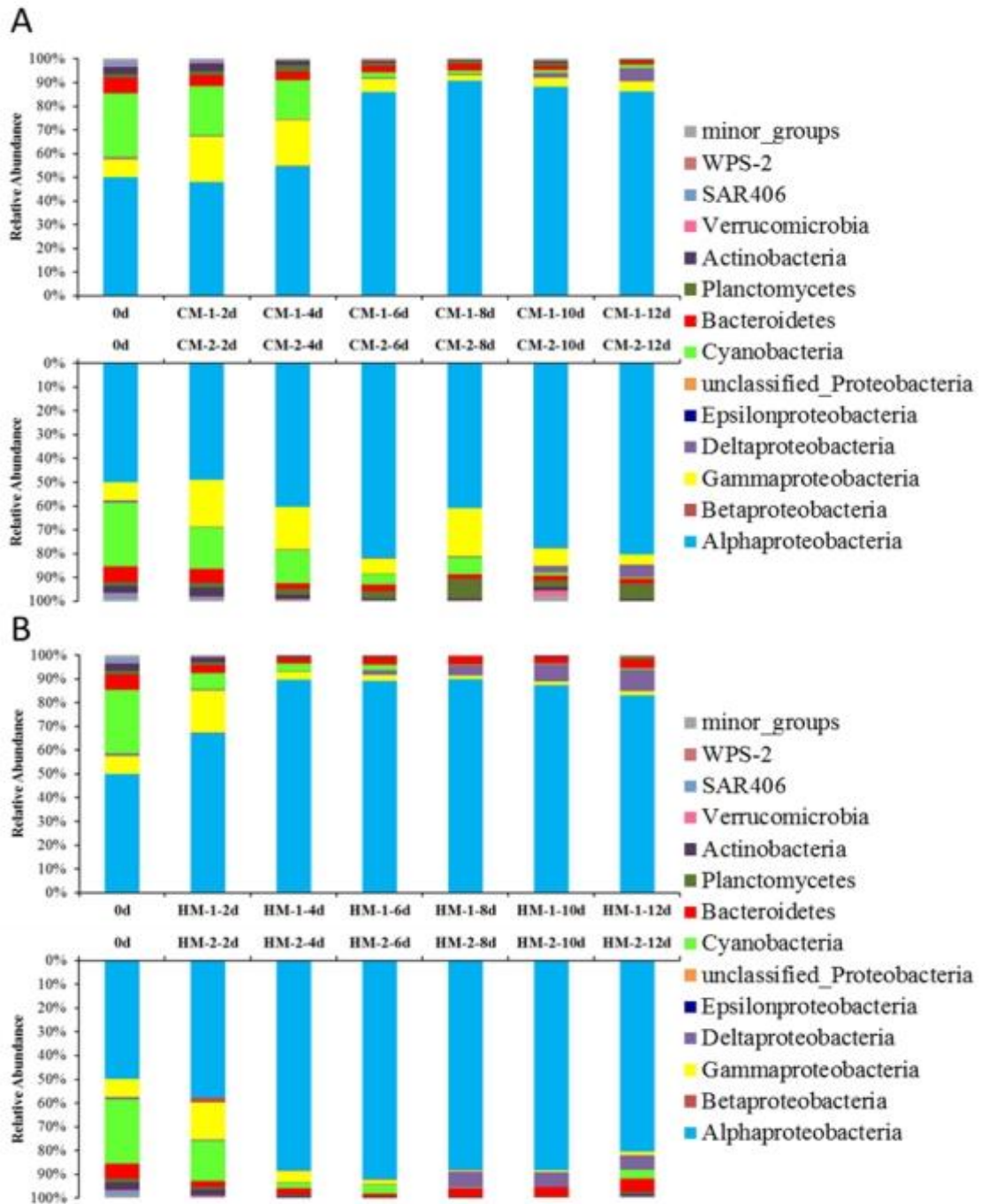
Figure S4. Bacteria community composition in the control (A) and treatment microcosms (B) at the phylum/class level. HM: high CO_2 microcosm. CM: control microcosm. Number following CM or HM indicates microcosm replicate (1 or 2).
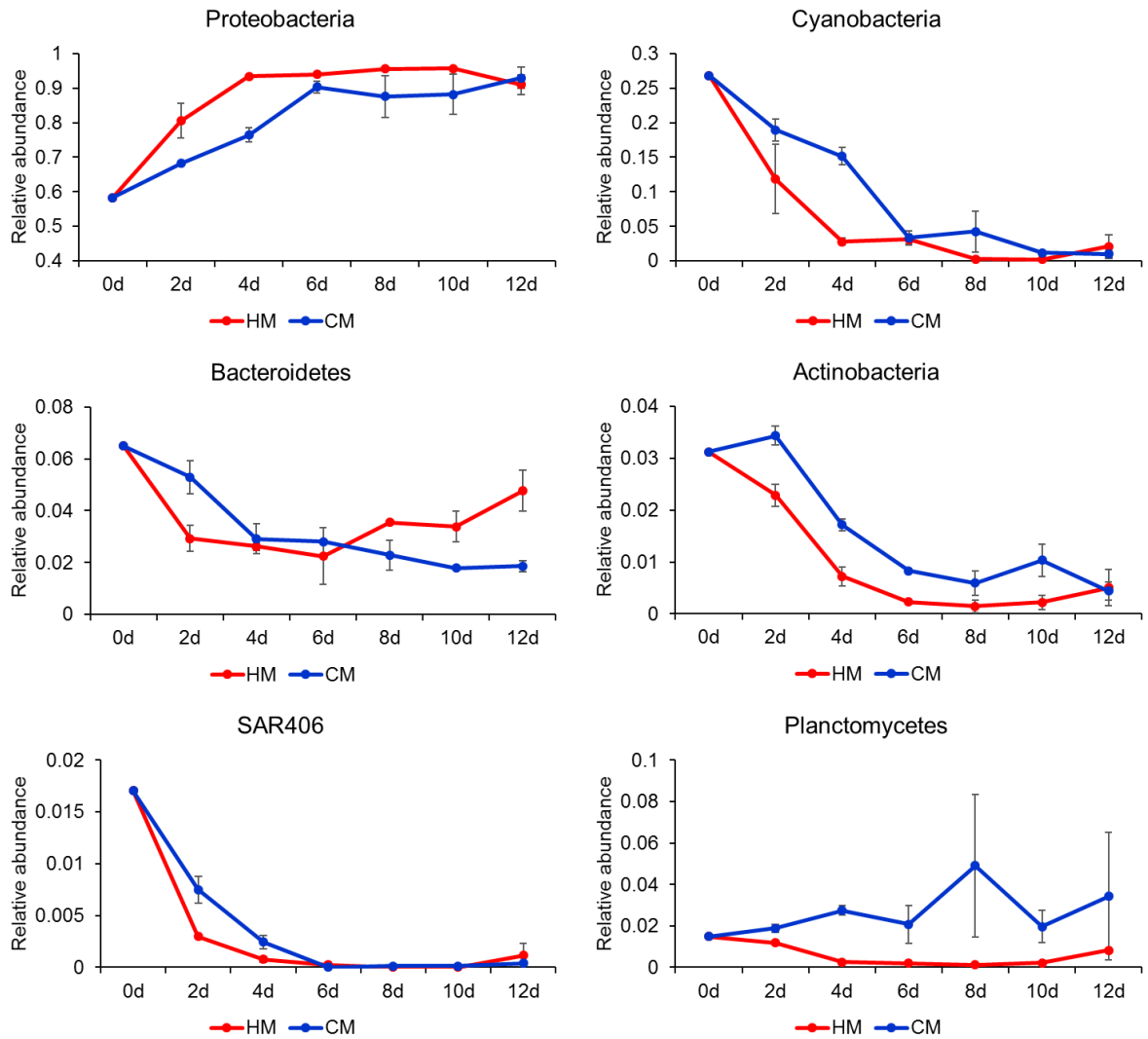
Figure S5. Relative abundance of the top six abundant bacterial phyla over time. HM: high CO2 microcosm. CM: control microcosm. Error bars represent SD of replicate samples.
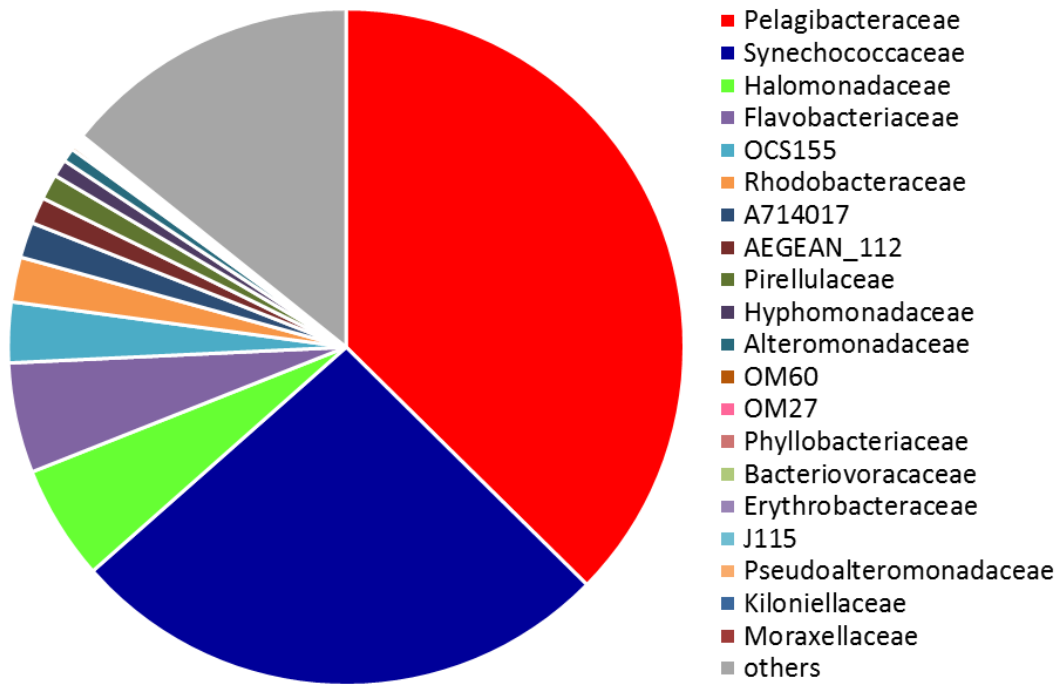
Figure S6. Bacterial community composition in the WPWP at the family level.
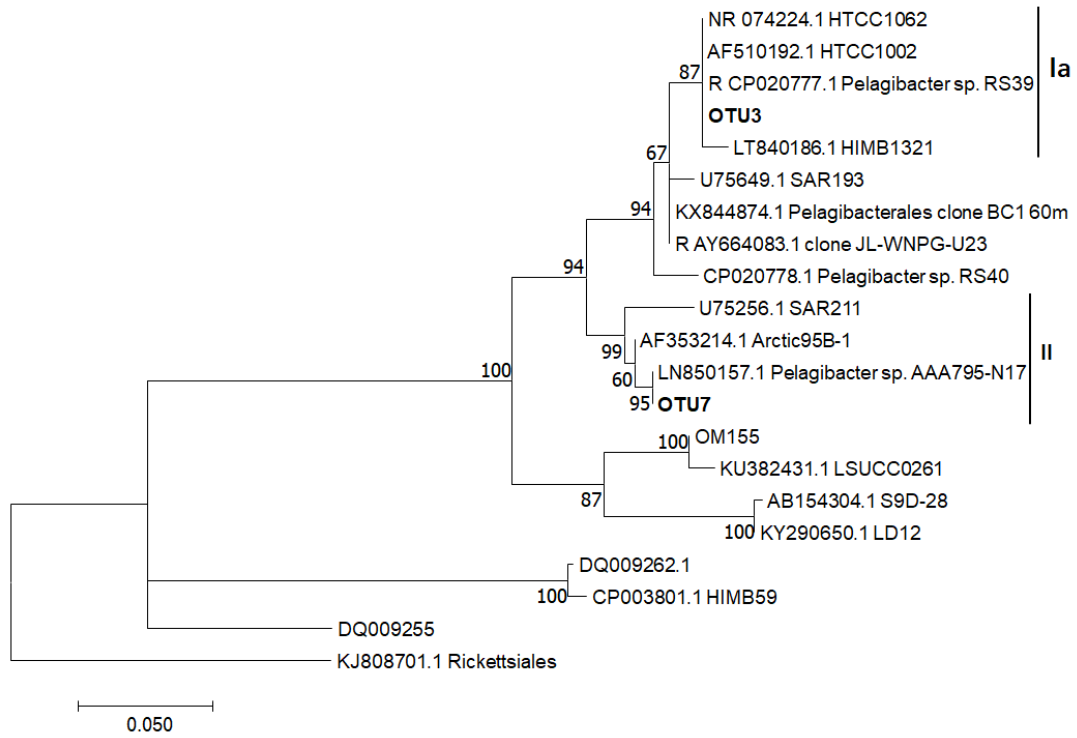
Figure S7. Maximum-likelihood phylogenetic tree of Pelagibacteraceae OTUs detected in the WPWP. Numbers in tree indicate the bootstrap values. Ia and II correspond to different clades of SAR11 which were defined by (Grote *et al.*, 2012).

Table S1. Sequencing information for the samples.

	Raw Sequences	Clean Sequences	Sequences after removed singleton	Subsampled sequences	No. of OTUs	Coverage
Day0	17044	10926	10646	3873	347	0.95
CM-1-2d	9492	5442	5248	3873	388	0.95
CM-2-2d	40635	23745	23213	3873	414	0.95
HM-1-2d	9196	5350	5221	3873	316	0.96
HM-2-2d	16141	9812	9587	3873	352	0.96
CM-1-4d	16241	9109	8845	3873	370	0.95
CM-2-4d	30352	17821	17449	3873	337	0.96
HM-1-4d	9488	5882	5809	3873	198	0.97
HM-2-4d	12754	7890	7773	3873	220	0.97
CM-1-6d	14720	8916	8692	3873	292	0.96
CM-2-6d	12604	7155	7029	3873	268	0.97
HM-1-6d	13108	8354	8214	3873	205	0.97
HM-2-6d	11197	6531	6460	3873	157	0.98
CM-1-8d	11646	7145	6974	3873	265	0.96
CM-2-8d	16794	9859	9670	3873	319	0.95
HM-1-8d	4125	3990	3873	3873	196	0.97
HM-2-8d	25749	6854	6672	3873	162	0.98
CM-1-10d	11641	6779	6658	3873	245	0.97
CM-2-10d	11023	6600	6436	3873	276	0.97
HM-1-10d	7502	7185	6958	3873	220	0.97
HM-2-10d	8097	7928	7699	3873	188	0.97
CM-1-12d	9712	7655	7530	3873	258	0.96
CM-2-12d	13047	5780	5653	3873	232	0.97
HM-1-12d	13209	7422	7262	3873	206	0.97
HM-2-12d	11893	6859	6731	3873	227	0.97