

Table S1. Taxonomic composition of the enrichment stock culture used to initiate disturbance experiments, summarized at the genus level. Relative abundances of 15 dominant heterotrophic genera are shown at two different collection dates, along with the most resolved Greengenes annotation available. The phosphate concentration was high when the sample was collected in August (> 10 μM) and low when the sample was collected in November (< 1 μM). The genera containing het1, het2, and het3 OTUs are highlighted in bold; the het1, het2 and het3 OTUs each accounted for >99% of the reads in their respective genus.

	Aug. 2013 (high PO_4^{3-})	Nov. 2013 (low PO_4^{3-})
het1 genus (<i>Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>)	0.127 ± 0.034	0.000 ± 0.000
het2 genus (<i>Alphaproteobacteria, Sphingomonadales, Erythrobacteraceae</i>)	0.066 ± 0.006	0.440 ± 0.015
<i>Polaromonas</i> (<i>Betaproteobacteria, Burkholderiales, Comamonadaceae</i>)	0.119 ± 0.010	0.084 ± 0.016
<i>Flavobacterium</i> (<i>Bacteroidetes, Flavobacteriales, Flavobacteraceae</i>)	0.082 ± 0.018	0.100 ± 0.024
<i>Chitinophagaceae</i> genus (<i>Bacteroidetes, Sphingobacteriales</i>)	0.054 ± 0.020	0.061 ± 0.012
<i>Caulobacteraceae</i> genus (<i>Alphaproteobacteria, Caulobacterales</i>)	0.033 ± 0.012	0.043 ± 0.023
<i>Sphingomonadales</i> genus (<i>Alphaproteobacteria</i>)	0.047 ± 0.012	0.016 ± 0.005
<i>Mycoplana</i> (<i>Alphaproteobacteria, Rhizobiales, Brucellaceae</i>)	0.047 ± 0.011	0.015 ± 0.007
<i>Bradyrhizobiaceae</i> genus (<i>Alphaproteobacteria, Rhizobiales</i>)	0.010 ± 0.008	0.047 ± 0.010
<i>Rhizobiales</i> genus (<i>Alphaproteobacteria</i>)	0.018 ± 0.004	0.023 ± 0.006
<i>Sphingomonadaceae</i> genus (<i>Alphaproteobacteria, Sphingomonadales</i>)	0.020 ± 0.015	0.015 ± 0.007
<i>Hyphomonadaceae</i> genus (<i>Alphaproteobacteria, Rhodobacterales</i>)	0.000 ± 0.000	0.029 ± 0.007
het3 genus (<i>Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae</i>)	0.017 ± 0.010	0.005 ± 0.006
<i>Rhodobacter</i> (<i>Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae</i>)	0.012 ± 0.002	0.010 ± 0.005
<i>Bradyrhizobium</i> (<i>Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae</i>)	0.006 ± 0.006	0.012 ± 0.001