

Supplementary information S2 (box)

This supplementary information provides a brief description of the methods used for the metagenomic analyses presented in Box 2. Percent of genomes were calculated using *recA* recovery and gene length correction¹. Tblastx was used with *hipA*, *hipB*, *relE*, *relB*, *mazE*, *mazF*, *yafQ*, and *dinJ*, sequences from the *E. coli* K-12 genome accessed using <http://ecogene.org/> and the *RpfC* sequence from the *M. tuberculosis* H37Rv genome accessed with NCBI entrez. Metagenome matches to the above query sequences were reverse-blasted against NCBI's non-redundant protein sequences (nr) using blastx for quality control.

Reference

- 1 Mou, X., Sun, S., Edwards, R. A., Hodson, R. E. & Moran, M. A. Bacterial carbon processing by generalist species in the coastal ocean. *Nature* **451**, 708-711 (2008).