Supporting Information

Palovaara et al. 10.1073/pnas.1402617111



Fig. S1. Taxon-specific dynamics in gene expression patterns in the Pacific off Monterey Bay. Dynamics in SAR11 (*A* and *B*) and SAR86 (*C* and *D*) clade-specific relative expression levels of the genes encoding proteorhodopsin and RecA compared with light intensity (*A* and *C*) and the genes encoding isocitrate lyase and malate synthase (*B* and *D*). Figure based on gene-specific analyses of metatranscriptome data over a 48-h period in natural seawater at 23 m depth reported by Ottesen et al. (1), who showed SAR11 and SAR86 were the dominant heterotrophic bacteria clades in the studied seawater samples. Percent transcripts in total bacterioplankton community were obtained by BLASTX against RefSeq.

1. Ottesen EA, et al. (2013) Pattern and synchrony of gene expression among sympatric marine microbial populations. Proc Natl Acad Sci USA 110(6):E488-E497.



Fig. 52. Proposed alterations in metabolic pathways in *Dokdonia* sp. MED134 during growth in seawater with yeast extract and peptone (YEP) or alanine (Ala) in the absence (A) or presence (B) of light. In the dark, MED134 behaves like a standard chemoheterotrophic bacterium (A). Oxidation of a major portion of available organic matter for aerobic respiration is needed to generate the proton motive force that provides energy for growth. Only the remaining carbon can be used for biomass production. The much lower growth yield with Ala compared with YEP in dark cultures (Fig. 1) is consistent with the general notion that growth of bacteria on single carbon compounds imposes important metabolic challenges compared with growth with rich mixed carbon sources (the degree of difference depending on organism and the substrates compared). A shows part of this difference by indicating regular glycolysis and tricaboxylic acid (TCA) cycle functioning in the case of YEP, but emphasizing gluconeogenesis in the case of Ala. Interesting metabolic shifts occur when the cells are exposed to light (B). Thanks to proteorhodopsin (PR) proton pumping, and mediated by strongly increased expression of the PR gene, light energy can be used to generate a significant portion of the proton motive force and/or ATP for growth. Thus, a lower fraction of available dissolved organic carbon (DOC) needs to be oxidized to supply energy for cell metabolism. Consequently, a larger fraction of the carbon can be used for biosynthesis. This shift in metabolism is not the only significant change however. Further shifts in metabolism are illustrated in *B* by highlighting that PR phototrophy induces carbon dioxide transport into the cell through BicA, the concentration/interconversion of carbon dioxide to bicarbonate by carbonic anhydrase, and its subsequent anaplerotic fixation by ATP dependent pyruvate carboxylase. In YEP, the metabolism is mainly directed through the standard TCA cycle, whereas in Ala it goes through the glyoxylate shunt to thereby

| Table S1 | I. Statistic | al analysis o | f changes in relativ | 'e gene exp | ression leve | ls between ti | ime points withi | n light treatme | ent or darknes | s in YEP and A | la cultures, as dete | ermined by | Fisher's |
|-----------|--------------------|---------------|----------------------|------------------|-----------------------|-------------------------|-------------------------|-------------------------|------------------------|--------------------|---|---------------------|--------------------|
| least sig | anificant dif | iference test | following repeate | d-measures | S ANOVA | | 2-Oxoglutarate | | | | Malate dehydro- | | |
| Media | Light condition | Time (h) | Proteorhodopsin | BicA | Carbonic anhydrase | lsocitrate dehydrase | dehydro- genase (E1) | Pyruvate carboxylase | PEP carboxy- kinase | PEP carboxylase | genase (NADP ⁺ , decarboxylating) | lsocitrate lyase | Malate synthase |
| ΥEP | Light | 19 vs. 36 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 19 vs. 46 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | P < 0.05 |
| | | 19 vs. 67 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.05 |
| | | 19 vs. 114 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.05 |
| | | 36 vs. 46 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | P < 0.01 |
| | | 36 vs. 67 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.01 |
| | | 36 vs. 114 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 46 vs. 67 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 46 vs. 116 | <i>P</i> < 0.01 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 |
| | | 67 vs. 116 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | P < 0.01 |
| | Dark | 19 vs. 36 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 19 vs. 46 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | P < 0.05 |
| | | 19 vs. 67 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.05 |
| | | 19 vs. 114 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> > 0.05 |
| | | 36 vs. 46 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 |
| | | 36 vs. 67 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> < 0.05 |
| | | 36 vs. 114 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 46 vs. 67 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> > 0.05 |
| | | 46 vs. 116 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P < 0.05 |
| | | 67 vs. 116 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 |
| Ala | Light | 24 vs. 51 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | P > 0.05 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.001 | P < 0.001 |
| | | 24 vs. 72 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 |
| | | 24 vs. 94 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | P < 0.001 |
| | | 24 vs. 141 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | P < 0.001 |
| | | 51 vs. 72 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 51 vs. 94 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | P < 0.05 |
| | | 51 vs. 141 | <i>P</i> < 0.001 | P < 0.001 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | P < 0.001 |
| | | 72 vs. 94 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | P < 0.05 |
| | | 72 vs. 141 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 |

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| | | | | | | | 2-Oxoglutarate | | | | Malate dehydro- | | |
|-------|--------------------|------------|--------------------------|------------------|-----------------------|-------------------------|-------------------------|-------------------------|------------------------|--------------------|---|---------------------|--------------------|
| Media | Light condition | Time (h) | Proteorhodo <i>p</i> sin | BicA | Carbonic anhydrase | lsocitrate dehydrase | dehydro- genase (E1) | Pyruvate carboxylase | PEP carboxy- kinase | PEP carboxylase | genase (NADP ⁺ , decarboxylating) | lsocitrate lyase | Malate synthase |
| | | 94 vs. 141 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | <i>P</i> < 0.01 | P > 0.05 | P > 0.05 | <i>P</i> < 0.05 | P > 0.05 | <i>P</i> < 0.01 | P > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 |
| | Dark | 24 vs. 51 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 24 vs. 72 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 24 vs. 94 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 24 vs. 141 | <i>P</i> < 0.001 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> < 0.001 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.01 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 51 vs. 72 | P > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 51 vs. 94 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 51 vs. 141 | <i>P</i> < 0.001 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 72 vs. 94 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 72 vs. 141 | <i>P</i> < 0.01 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 |
| | | 94 vs. 141 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> < 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | <i>P</i> > 0.05 | P > 0.05 |
| | | | | | | | | | | | 1 | | |

Statistical significance levels are indicated by different types of shading: dark blue, P < 0.001; medium blue, P < 0.01; pale blue, P < 0.05; white, not significant (P > 0.05).

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| Table S2. | Abundance of the genes encoding PR, isocitrate lyase (AceA), malate synthase (AceB), and recombinase A (RecA) in samples |
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| from the g | Jobal ocean survey |

| Samplo | Total | PR (no. | AceA (no. | AceB (no. | RecA (no. | PR:RecA | AceA:RecA | AceB:RecA |
|---------------------------------------|-----------|-----------|-----------|-------------|-----------|--------------|--------------|--------------|
| | peptides | 011113) | 01 mits) | of filts) | of filts) | (70) | (70) | (70) |
| GS000a—Sargasso Sea | 1,002,506 | 179 | 329 | 502 | 303 | 59.1 | 108.6 | 165.7 |
| GS000b—Sargasso Sea | 492,305 | 262 | 230 | 430 | 339 | //.3 | 67.8 6F.0 | 126.8 |
| GS000d Sargasso Sea | 517 2/10 | 200 | 214 | 540 //22 | 329 | 77.0 66.6 | 55 C | 105.5 |
| GS001c—Hydrostation S | 138 631 | 96 | 63 | 108 | 141 | 68.1 | 44 7 | 76.6 |
| GS002—Gulf of Maine | 195,047 | 93 | 68 | 100 | 159 | 58.5 | 42.8 | 79.2 |
| GS003—Browns Bank Gulf of Maine | 100,992 | 43 | 37 | 43 | 59 | 72.9 | 62.7 | 72.9 |
| GS004—Outside Halifax Nova Scotia | 86,213 | 39 | 50 | 54 | 63 | 61.9 | 79.4 | 85.7 |
| GS005—Bedford Basin Nova Scotia | 100,367 | 38 | 22 | 24 | 97 | 39.2 | 22.7 | 24.7 |
| GS006—Bay of Fundy Nova Scotia | 96,567 | 65 | 47 | 59 | 97 | 67.0 | 48.5 | 60.8 |
| GS007—Northern Gulf of Maine | 84,286 | 43 | 33 | 27 | 78 | 55.1 | 42.3 | 34.6 |
| GS008—Newport Harbor RI | 211,453 | 89 | 31 | 106 | 126 | 70.6 | 24.6 | 84.1 |
| GS009—Block Island NY | 120,589 | 53 | 49 | 93 | 76 | 69.7 | 64.5 | 122.4 |
| GS010—Cape May NJ | 124,769 | 63 | 50 | 84 | 87 | 72.4 | 57.5 | 96.6 |
| GS011—Delaware Bay NJ | 202,844 | 76 | 35 | 104 | 125 | 60.8 | 28.0 | 83.2 |
| GS012—Chesapeake Bay MD | 205,465 | /5 | 3/ | 8/ | 160 | 46.9 | 23.1 | 54.4 |
| GS013—Off Nags Head NC | 226,967 | 63 116 | 5/ | 101 | 100 | 54.3 | 49.1 | 87.1 |
| GS014—South of Charleston SC | 207,360 | 0/1 | 98 | 147 | 188 | 64.8 | 52.1 | 78.2 73.1 |
| GS016—Gulf of Mexico | 203,933 | 94 | 68 | 100 | 145 | 61.2 | 44.8 | 69.7 |
| GS017—Yucatan Channel | 415 844 | 180 | 128 | 242 | 372 | 48.4 | 34.4 | 65.1 |
| GS018—Rosario Bank | 230,700 | 85 | 88 | 141 | 223 | 38.1 | 39.5 | 63.2 |
| GS019—Northeast of Colon | 218,170 | 104 | 49 | 102 | 232 | 44.8 | 21.1 | 44.0 |
| GS020—Lake Gatun | 471,840 | 149 | 76 | 66 | 537 | 27.7 | 14.2 | 12.3 |
| GS021—Gulf of Panama | 212,561 | 88 | 73 | 140 | 201 | 43.8 | 36.3 | 69.7 |
| GS022—250 miles from Panama City | 193,148 | 73 | 63 | 120 | 157 | 46.5 | 40.1 | 76.4 |
| GS023—30 miles from Cocos Island | 212,713 | 83 | 70 | 148 | 218 | 38.1 | 32.1 | 67.9 |
| GS025—Dirty Rock Cocos Island | 201,505 | 15 | 9 | 7 | 140 | 10.7 | 6.4 | 5.0 |
| GS026—134 miles NE of Galapagos | 164,342 | 62 | 61 | 127 | 152 | 40.8 | 40.1 | 83.6 |
| GS027—Devil's Crown Floreana Island | 353,225 | 183 | 146 | 258 | 292 | 62.7 | 50.0 | 88.4 |
| GS028—Coastal Floreana | 301,799 | 164 | 93 | 213 | 253 | 64.8 | 36.8 | 84.2 |
| GS029—North James Bay Santigo Island | 208,795 | 112 | 66 220 | 13/ | 184 | 60.9 | 35.9 | /4.5 |
| GS030—Warm seep Roca Redonda | 492,926 | 243 | 238 | 414 E20 | 410 | 59.3 | 58.0 | 101.0 |
| GS031—Opwening Fernandina Island | 222.062 | 202 | 549 | 220 | 116 | 04.1 28.4 | 64.7 | 95.2 70.7 |
| GS032—Hypersaline Lagoon | 1 083 /85 | 210 | 216 | 37/ | 533 | 20.4 | 40.5 | 70.7 |
| GS034—North Seamore Island | 215 123 | 84 | 59 | 109 | 182 | 46.2 | 32.4 | 59.9 |
| GS035—Wolf Island | 225.307 | 119 | 87 | 129 | 170 | 70.0 | 51.2 | 75.9 |
| GS036—Cabo Marshall Isabella Island | 124,562 | 41 | 57 | 64 | 117 | 35.0 | 48.7 | 54.7 |
| GS037—Equatorial Pacific TAO Buoy | 101,325 | 45 | 32 | 78 | 83 | 54.2 | 38.6 | 94.0 |
| GS047—201 miles from F, Polynesia | 102,474 | 48 | 28 | 64 | 84 | 57.1 | 33.3 | 76.2 |
| GS048a—Moorea Cooks Bay | 142,956 | 56 | 45 | 89 | 96 | 58.3 | 46.9 | 92.7 |
| GS049—Moorea Outside Cooks Bay | 145,765 | 62 | 38 | 116 | 117 | 53.0 | 32.5 | 99.1 |
| GS051—Rangirora Atoll | 205,339 | 93 | 86 | 110 | 202 | 46.0 | 42.6 | 54.5 |
| GS108—Lagoon Reef | 1,543,979 | 594 | 531 | 1142 | 1549 | 38.3 | 34.3 | 73.7 |
| GS108a—Coccos Keeling Inside Lagoon | 81,323 | 16 | 21 | 48 | 52 | 30.8 | 40.4 | 92.3 |
| GS109—Indian Ocean | 94,829 | 31 | 12 | 58 | 72 | 43.1 | 16.7 | 80.6 |
| GS110a—Indian Ocean | 157,847 | 67 | 49 | 86 | 145 | 46.2 | 33.8 | 59.3 |
| GS111—Indian Ocean | 93,629 | 39 | 36 | 61 | 6/ | 58.2 | 53.7 | 91.0 |
| GS112—Indian Ocean | 1,217,028 | 400 | 529 | /83 77 | 1219 | 32.8 57.0 | 27.0 | 64.Z |
| GS112 Indian Ocean | 136,363 | 82 | 55 | 103 | 121 | 56.9 | 45.8 | 05.0 71.5 |
| GS114—500 Miles west Sevenelles | 536 593 | 214 | 175 | 315 | 443 | 48.3 | 39.5 | 71.5 |
| GS115—Indian Ocean | 96.414 | 48 | 27 | 52 | 73 | 65.8 | 37.0 | 71.2 |
| GS116—Outside Sevchelles Indian Ocean | 96.918 | 49 | 2, | 67 | 76 | 64.5 | 31.6 | 88.2 |
| GS117a—St, Anne Island Sevchelles | 530,775 | 255 | 199 | 333 | 397 | 64.2 | 50.1 | 83.9 |
| GS119—Off Reunion Island | 97,846 | 43 | 26 | 70 | 87 | 49.4 | 29.9 | 80.5 |
| GS120—Madagascar Waters | 72,241 | 35 | 19 | 45 | 59 | 59.3 | 32.2 | 76.3 |
| GS121—Indian Ocean off South Africa | 177,501 | 70 | 42 | 122 | 125 | 56.0 | 33.6 | 97.6 |
| GS122a—Indian Ocean off South Africa | 164,110 | 66 | 58 | 90 | 116 | 56.9 | 50.0 | 77.6 |
| GS123—Indian Ocean off South Africa | 173,644 | 87 | 75 | 103 | 105 | 82.9 | 71.4 | 98.1 |

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Table S2. Cont.

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| Sample | Total peptides | PR (no. of hits) | AceA (no. of hits) | AceB (no. of hits) | RecA (no. of hits) | PR:RecA (%) | AceA:RecA (%) | AceB:RecA (%) |
|--|--------------------|---------------------|-----------------------|-----------------------|-----------------------|---------------------------|----------------------|---------------------------|
| GS148—East coast Zanzibar, off Paje lagoon | 168,982 | 81 | 67 | 100 | 115 | 70.4 | 58.3 | 87.0 |
| GS149—West coast Zanzibar, harbor region | 172,203 | 82 | 67 | 124 | 143 | 57.3 | 46.9 | 86.7 |
| Summary | 17×10^{6} | 7,087* | 5,881* | 10,727* | 13,928* | $54.6 \pm 13.9^{\dagger}$ | $43.5 \pm 16.5^{++}$ | $77.7 \pm 24.9^{\dagger}$ |

*Total number of hits in the investigated samples. [†]Mean values \pm SD of frequencies of PR, AceA, and AceB abundances normalized to RecA across the investigated samples (n = 63).

Table S3. Genes and primer sets used for quantitative PCR

| Gene product | ORFs* | Primer pair (forward/reverse) | Product size (bp) |
|---|--------------|---|-------------------|
| Proteorhodopsin | MED134_07119 | AACCGGATACATAGGCGAAG/ACAGCTCCACCTGCCCTTAC | 141 |
| BicA | MED134_10061 | GGCTACGGCAACAAGAGGT/GGATGGAGAAAACACCCTGTC | 169 |
| Carbonic anhydrase | MED134_10056 | ACGAGTTTTGACCCAGCAAC/TGTATCGACTCTCGCGTACCT | 146 |
| Pyruvate carboxylase | MED134_06244 | CAGGAGGAATAGCCGAAGGT/ATGTGCCCCAGCATTTTCTA | 122 |
| PEP carboxykinase | MED134_10331 | TGGGTAAAACCGCATCATCT/GCAAACGCCTCTTCTTCAAA | 154 |
| PEP carboxylase | MED134_06089 | CGCTCACCATTTTCATCTTG/CGGAGGGTTATCTCGCTTTA | 157 |
| Malate dehydrogenase (NADP ⁺ , decarboxylating) [†] | MED134_11446 | CGTGTTTTTAGGTCTCTCTGTGG/CCTTCCCGTTGCCATTATT | 160 |
| Isocitrate dehydrogenase | MED134_14141 | AGTATGGGTGCTTGGAGTGC/CGTATGTTGCCTGCCTCTTT | 110 |
| 2-Oxoglutarate dehydrogenase (E1) | MED134_07711 | CCGCACATACCGCTTACTTT/CCACAGTCTCTCCCCCTACA | 153 |
| Isocitrate lyase | MED134_01780 | GGCACCAAGATGGAAAGGTA/AGTAAGACCAGCCCCCTCA | 140 |
| Malate synthase | MED134_01770 | TGCTACAGCCGAAATCTCAA/ATCTTATCTGCCCCCACCTC | 153 |
| RpoD [‡] | MED134_12871 | CACGGTCAGGGTTAGGTGAT/TGCAAAGGAGCTGGATATGA | 152 |
| RecA [‡] | MED134_08916 | ACTCAAAAATGGGGCTTCAC/CCCGTAGTAGTCTCTGGGTTTC | 151 |

*The ORFs of Dokdonia sp. MED134 can be accessed using GeneBank accession no. AAMZ00000000.

[†]This enzyme (EC:1.1.1.40) has traditionally been referred to as malic enzyme, but is currently denoted malate dehydrogenase (oxaloacetate-decarboxylating) (NADP⁺) or malate dehydrogenase (NADP⁺, decarboxylating) as used here.

[‡]Reference genes used for normalization.

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