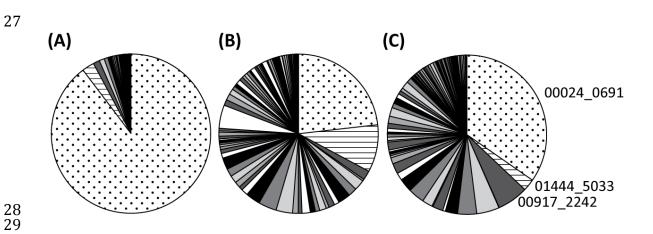
| 1 | 1 Supplemental Files for: | | | |
|----|---|--|--|--|
| 2 | | | | |
| 3 | Why orange Guaymas Basin Beggiatoa (Maribeggiatoa) are orange: | | | |
| 4 | Single-filament genome-enabled identification of an abundant octaheme cytochrome | | | |
| 5 | with hydroxylamine oxidase, hydrazine oxidase, and nitrite reductase activities | | | |
| 6 | | | | |
| 7 | Barbara J. MacGregor, Jennifer F. Biddle, Jason R. Siebert, Eric Staunton, Eric L. Hegg, | | | |
| 8 | Ann G. Matthysse, and Andreas Teske | | | |
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| 19 | ⁵ Department of Biology, University of North Carolina - Chapel Hill, Chapel Hill NC | | | |
| 20 | 27599 | | | |
| 21 | | | | |
| 22 | #To whom correspondence should be addressed: bmacgreg@unc.edu | | | |



Sum of total ion currents per identified ORF (0.2% not assigned). (**B**) Average of total ion currents for fragments assigned to each identified ORF (0.8% not assigned). (**C**) Number of MS/MS spectra attributed to each identified ORF (total 1272, with 29 not

Figure S1. Identification of ORF encoding the orange protein by μ LC/MS/MS. (A)

assigned)

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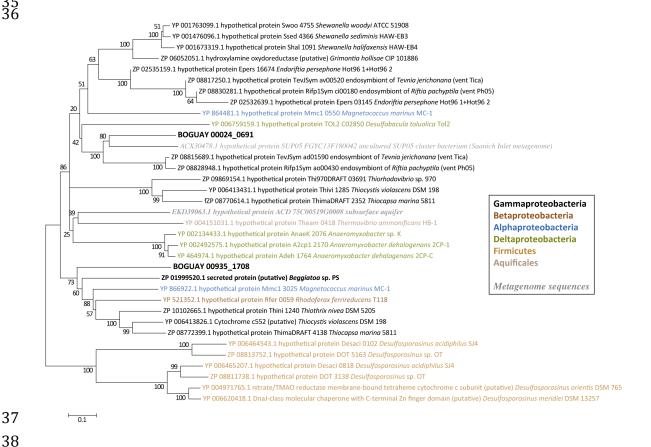


Figure S2. Phylogenetic tree of inferred amino acid sequences of BOGUAY **00024 0691 and BOGUAY 00935 1708.** The first 100 BLASTP/nr hits for each sequence (all but two of which were identical) were used to construct an initial tree, which was then trimmed to show only closest relatives. Evolutionary analyses were conducted in MEGA5 (4) with sequences aligned by MUSCLE (1). The evolutionary history was inferred using the Neighbor-Joining method (3). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches (2). The evolutionary distances were computed using the Poisson correction method (5) and are in units of amino acid substitutions per site. All ambiguous positions were removed for each sequence pair. The analysis involved 35 amino acid sequences, and 1132 positions were included in the final analysis.

Table S1. NADPH-quinone oxidoreductase genes.

| Gene product | Complex | Contig_ORF |
|--------------|------------------|------------------------|
| NuoA | Membrane complex | 00285_1243 |
| NuoB | FeS protein | 00285_1242, 00322_3116 |
| NuoC | FeS protein | 00285_1236, 00322_3117 |
| NuoD | FeS protein | 00285_1234, 00322_3119 |
| NuoE | FMN | 00285_1225 |
| NuoF | FMN | 00552_2594, 01153_1100 |
| NuoG | FMN | 00432_3220 |
| NuoH | Membrane complex | 00432_3219, 00362_1731 |
| Nuol | FeS protein | 00432_3218 |
| NuoJ | Membrane complex | 00432_3216 |
| NuoK | Membrane complex | 00432_3215 |
| NuoL | Membrane complex | 00543_4484 |
| NuoM | Membrane complex | 01191_1496 |
| NuoN | Membrane complex | 00024_0688 |

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SUPPLEMENTAL REFERENCES

- 58 1. **Edgar, R. C.** 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research **32:**1792-1797.
- Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39:783-791.
- Saitou, N., and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution
 4:406-425.
- Tamura, K., D. Peterson, N. Peterson, G. Stecher, M. Nei, and S. Kumar.
 2011. MEGA5: Molecular Evolutionary Genetics Analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.
 Molecular Biology and Evolution 28:2731-2739.
- Zuckerkandl, E., and L. Pauling. 1965. Evolutionary convergence and divergence in proteins, p. 97-166. *In* V. Bryson and H. J. Vogel (ed.), Evolving Genes and Proteins. Academic Press, New York.