

Title: Identification and Characterization of a Dominant Sulfolane-Degrading *Rhodoferrax* sp.
via Stable Isotope Probing Combined with Metagenomics

Running Title: Sulfolane Stable Isotope Probing and Metagenomics

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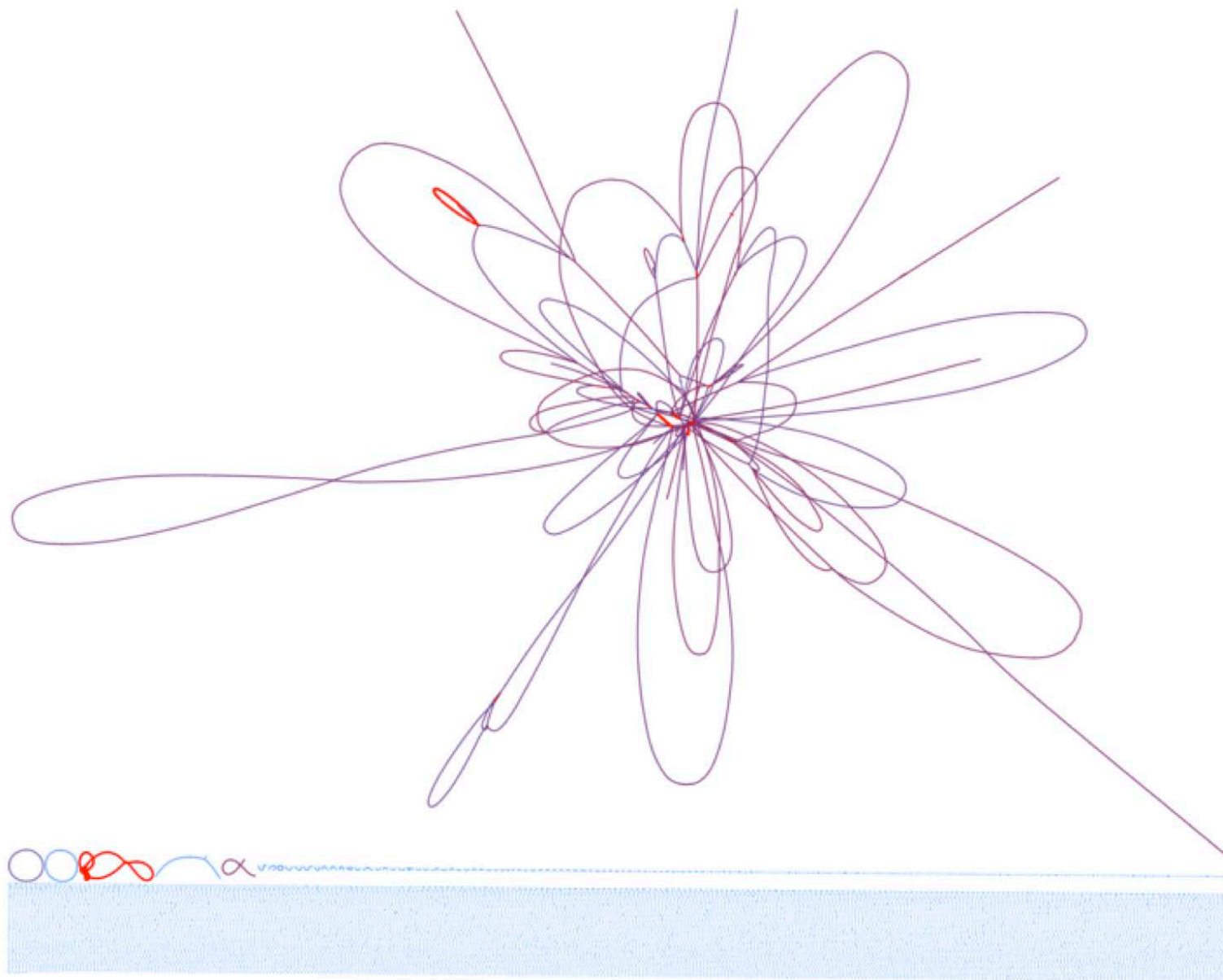
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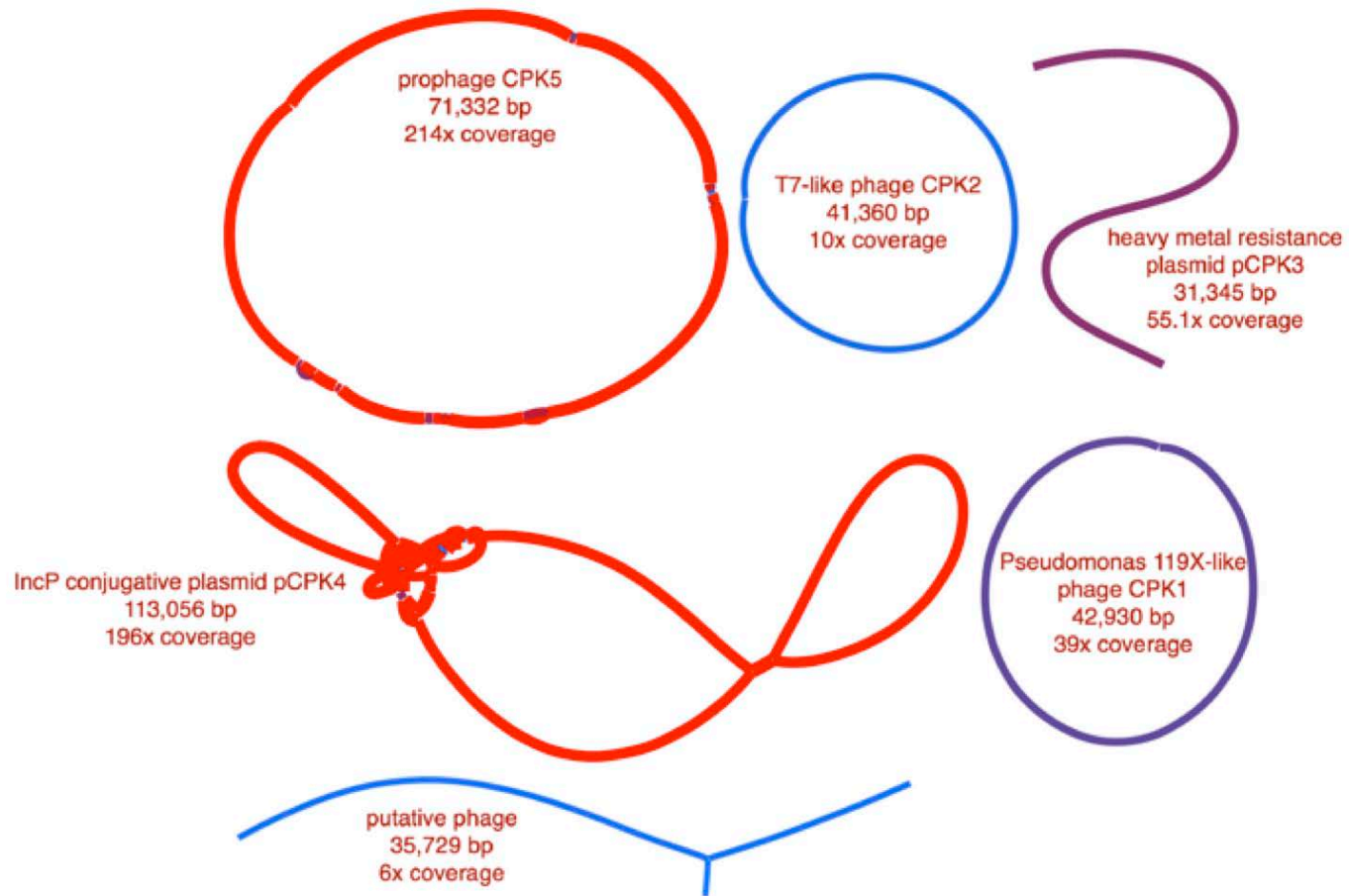
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All authors declare there are no competing interests in relation to the work described.

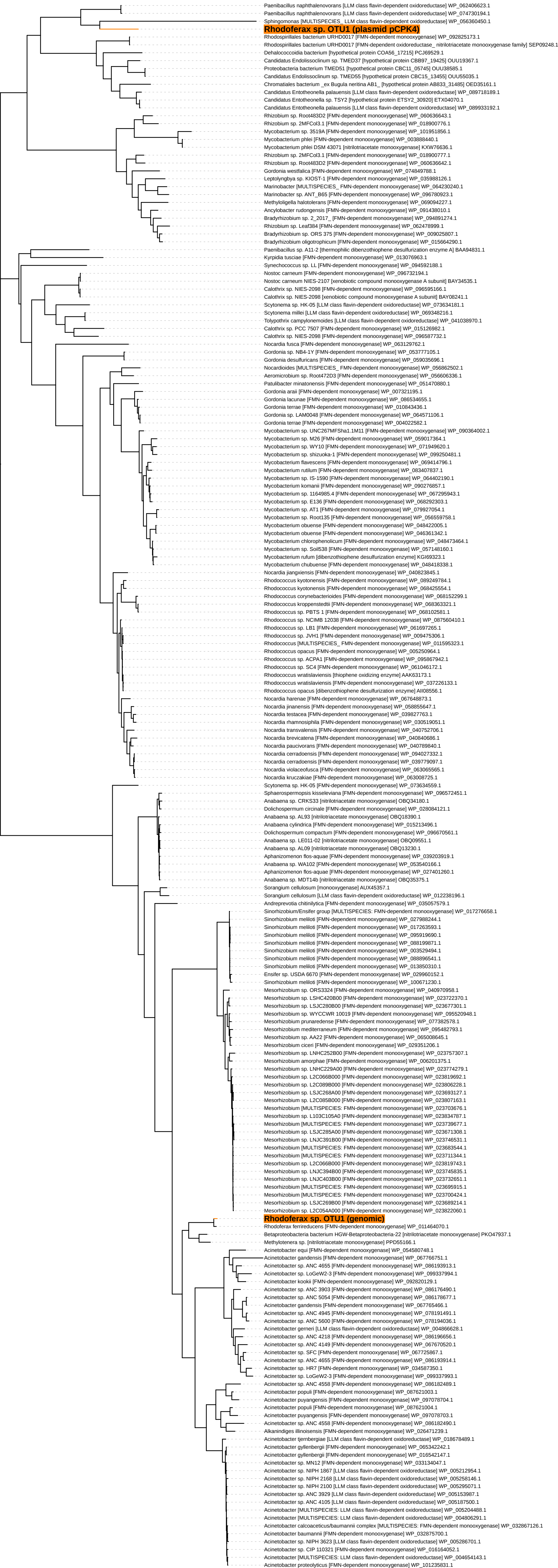


Supplementary Figure 1: Metagenome co-assembly de Bruijn graph from SPAdes visualized with Bandage. Sequencing depth is scaled to color, from blue (0x) to red (100x). The mean depth of the large connected component is 53.1x.



Supplementary Figure 2: Extrachromosomal elements from metagenome co-assembly de Bruijn graph visualized with Bandage. Sequencing depth is scaled to color, from blue (0x) to red (100x). Phage and plasmid genes were identified with PHASTER.

Supplementary Figure 3. A maximum likelihood phylogenetic tree of amino acid sequences homologous to *dszA*. Tree was constructed using PhyML in SeaView after alignment in MUSCLE.





Supplementary Figure 4. IncP conjugative plasmid pCPK4 from the metagenome co-assembly de Bruijn graph visualized with Bandage. Sequencing depth is scaled to node width (max depth 894x). pCPK4 is highly similar (99%) over large regions (>40%; purple) to an IncP plasmid from *Pseudomonas* spp. and other soil microorganisms. The orange segment is a putative flavin-using monooxygenase homologous to *dszA*, which is only distantly related to the chromosomal *dszA*-like gene. The green segment is a putative flavin reductase homologous to *dszD*. These genes are flanked by transposases.

