LIST OF TABLES

Table 3-3: Rates of Fe(II) oxidation by cell suspensions of TIE-1 and SW2. The rate of Fe(II) oxidation for the TIE-1 + H_2/CO_2 + 1 mM NaHCO₃ + 0.5 mM Fe(II)Cl₂·H₂O assay was calculated using the first four time points, all others were calculated using the first three time points. The rate of Fe(II) oxidation for the SW2 + H_2/CO_2 + 1 mM NaHCO₃ + 0.5 mM FeCl₂·H₂O assay was calculated using the first five time points, all others were calculated using the first five 500 solution for the SW2 + H_2/CO_2 + 1 mM NaHCO₃ + 0.5 mM FeCl₂·H₂O assay was calculated using the first five time points, all others were calculated using the first five 500 solution for the SW2 + H_2/CO_2 + 1 mM NaHCO₃ + 0.5 mM FeCl₂·H₂O assay was calculated using the first five time points, all others were calculated using the first three time points.

Table 4-1: Fe isotope compositions of the experimental reagents and enrichment culture inoculums. In the analyses column, up to triplicate mass spectrometry runs of a sample conducted on different days are reported; the errors are 2-SE from in-run statistics and reflect machine uncertainties and/or processing errors. The Mass Spec Average is the average of up to three analyses of a single sample, 1-SD is one standard deviation external; note that if there is only one mass spectrometry analysis, the error is 2-SE. The Average of Replicate is the average of processing replicates of a sample throughout the entire analytical procedure; the best estimate of external reproducibility. ¹Inoculum refers to the cells and small amount of Fe(III) precipitates (~1.2 millimoles) transferred from a grown culture of the enrichments to the fresh filtered Fe(II) medium used for these experiments. Inoculum cultures where the Fe(II) substrate initially provided was oxidized to completion were used to minimize Fe carryover. ²Yellow crystals among the bulk of the green crystals of the solid $FeCl_2 H_2O$ used for the isotopic experiments indicate slight oxidation of the reagent. The isotopic composition of the solid FeCl₂·H₂O reagent is heterogeneous ³1M FeCl₂·H₂O stock solution used for on the 100 mg scale. enrichment medium preparation. ⁴10 mM FeCl₂·H₂O was added to 25 The resulting ferrous minerals were allowed to mls of medium. precipitate to completion. Under an aerobic atmosphere, the medium was mixed well and 1 ml was extracted with a syringe and transferred to a microcentrifuge tube. The precipitate and soluble phases were

Table 4-2: Fe isotope compositions of enrichments 1 and 2 and the All cultures started at 25 ml total volume. uninoculated control. Sampling volumes were always 1 ml, and were split into two 0.5 ml subvolumes to obtain duplicate soluble and precipitate fractions for that time point. Start volume is the volume of the culture on the day the sample was taken. Mmol Fe(III) is calculated by mass balance using the Ferrozine measurements for Fe(II). In the analyses column, up to triplicate mass spectrometry runs of a sample conducted on different days are reported; the errors are 2-SE from in-run statistics and reflect machine uncertainties and/or processing errors. The Mass Spec Average is the average of up to three analyses of a single sample, 1-SD is one standard deviation external; note that if there is only one mass spectrometry analysis, the error is 2-SE. The Average of Replicate is the average of processing replicates of a sample throughout the entire analytical procedure; the best estimate of external reproducibility. ¹per 0.5 ml split......76

 Table 4-3:
 Fe isotope compositions of the pure culture, F4, incubated
 at 40. 80 and 120 cm from the light and the uninoculated and dark controls. All cultures started at 25 ml total volume. Sampling volumes were always 1 ml, and were split into two 0.5 ml sub-volumes to obtain duplicate soluble and precipitate fractions for that time point. Start volume is the volume of the culture on the day the sample was taken. Mmol Fe(III) is calculated by mass balance using the Ferrozine measurements for Fe(II). In the analyses column, up to triplicate mass spectrometry runs of a sample conducted on different days are reported; the errors are 2-SE from in-run statistics and reflect machine uncertainties and/or processing errors. The Mass Spec Average is the average of up to three analyses of a single sample, 1-SD is one standard deviation external; note that if there is only one mass spectrometry analysis, the error is 2-SE. The Average of Replicate is the average of processing replicates of a sample throughout the entire analytical procedure; the best estimate of external reproducibility. ¹per

Table 4-4: Summary of fractionation factors using initial precipitates.Errors for individual experiments based on 1-standard deviation of theduplicate aliquots.Error for the Grand Average is based on the square

Table 5-1: Bacterial strains and plasmids used in this study......131

 Table 5-2:
 Summary of ORF finder, BlastP and Conserved Domain
 Database search results from the p9E12 insert sequence. The top BlastP matches to predicted ORFs in the pP1, pP2, pP3, pP4, pP5, pP6, pP7 pH5 and pH6 insert sequences are listed, as are conserved domains within the predicted ORF when they are present. When the top match is not a *Rhodobacter* species, the highest *Rhodobacter* or related purple non-sulfur bacterium match, when it exists, is also listed. ¹The number of amino acid residues that encode the predicted ORF. ^{2,3}Amino acid identity and similarity between the predicted ORF translation and the proteins in the database that showed the best BlastP matches. ⁴The expectation value; the lower the E value, the more significant the score. ⁵Translated fragments of the same ORF detected in different reading frames, likely due to mistakes in the sequence that result in a frame shift mutation. ⁶The ORF of this predicted ABC transporter ATP-binding protein lies within that of this