

**Table S2** - Potential ecological roles of full-length clones for which obvious metabolisms can be inferred. Data is pooled from all samples, therefore multiple clones are represented per lineage listed. The % Clones in Dataset is for the entire dataset (n=452). Taxa are designated by Class: Order: Family: Genus. The highest level at which an ecological role can be assigned per group of tags is given.

| Potential Ecological Role               | Taxa   | # Clones | % Clones in Dataset |
|---|--|----------|---------------------|
| S-oxidation                             | $\gamma$ -proteobacteria: Chromatiales   | 82       | 18.14               |
|   | $\gamma$ -proteobacteria: Chromatiales: Ectothiorhodospiraceae                       | 21       | 4.65                |
|   | $\gamma$ -proteobacteria: Chromatiales: Sinobacteraceae                              | 2        | 0.442               |
|   | $\gamma$ -proteobacteria: Chromatiales: Halothiobacillaceae; Halothiobacillus        | 1        | 0.221               |
|   | Chlorobi; Ignavibacteria; Ignavibacteriales; Ignavibacteriaceae                      | 1        | 0.221               |
|   | $\epsilon$ -proteobacteria; Campylobacterales; Sulfurovum                            | 10       | 2.21                |
|   | $\epsilon$ -proteobacteria; Campylobacterales; Helicobacteraceae; Sulfurimonas       | 19       | 4.20                |
| SO <sub>4</sub> <sup>2-</sup> reduction | $\delta$ -proteobacteria: Desulfobacterales: Desulfobulbaceae                        | 49       | 10.84               |
|   | $\delta$ -proteobacteria: Desulfuromonadales: Desulfuromonadaceae                    | 7        | 1.54                |
|   | $\delta$ -proteobacteria: Syntrophobacteriales: Desulfobacteraceae; Desulfobacterium | 5        | 1.11                |
|   | <i>sum of S-oxidation and SO<sub>4</sub><sup>2-</sup> reduction</i>                  |          | <i>43.57</i>        |
| nitrite oxidation                       | Nitrospira; Nitrospirales  | 7        | 1.54                |
| nitrification                           | $\beta$ -proteobacteria: Nitrosomonadales: Nitrosomonadaceae                         | 14       | 3.10                |
| N-fixation                              | $\alpha$ -proteobacteria: Rhizobiales  | 3        | 0.664               |
|   | $\alpha$ -proteobacteria: Rhizobiales; Hyphomicrobiaceae; Devosia                    | 3        | 0.664               |
|   | $\alpha$ -proteobacteria: Rhizobiales; Brucellaceae; Ochrobactrum                    | 1        | 0.221               |
|   | $\alpha$ -proteobacteria: Rhizobiales; Phyllobacteriaceae                            | 5        | 1.11                |
|   | <i>sum of nitrite oxidation, nitrification and N-fixation</i>                        |          | <i>7.30</i>         |
| Fe-oxidation                            | $\beta$ -proteobacteria: Nitrosomonadales: Gallionellaceae                           | 1        | 0.221               |
| CH <sub>4</sub> oxidation               | $\gamma$ -proteobacteria: Methylococcales  | 2        | 0.442               |
|   | <b>Total Sum</b>   |          | <b>51.53</b>        |