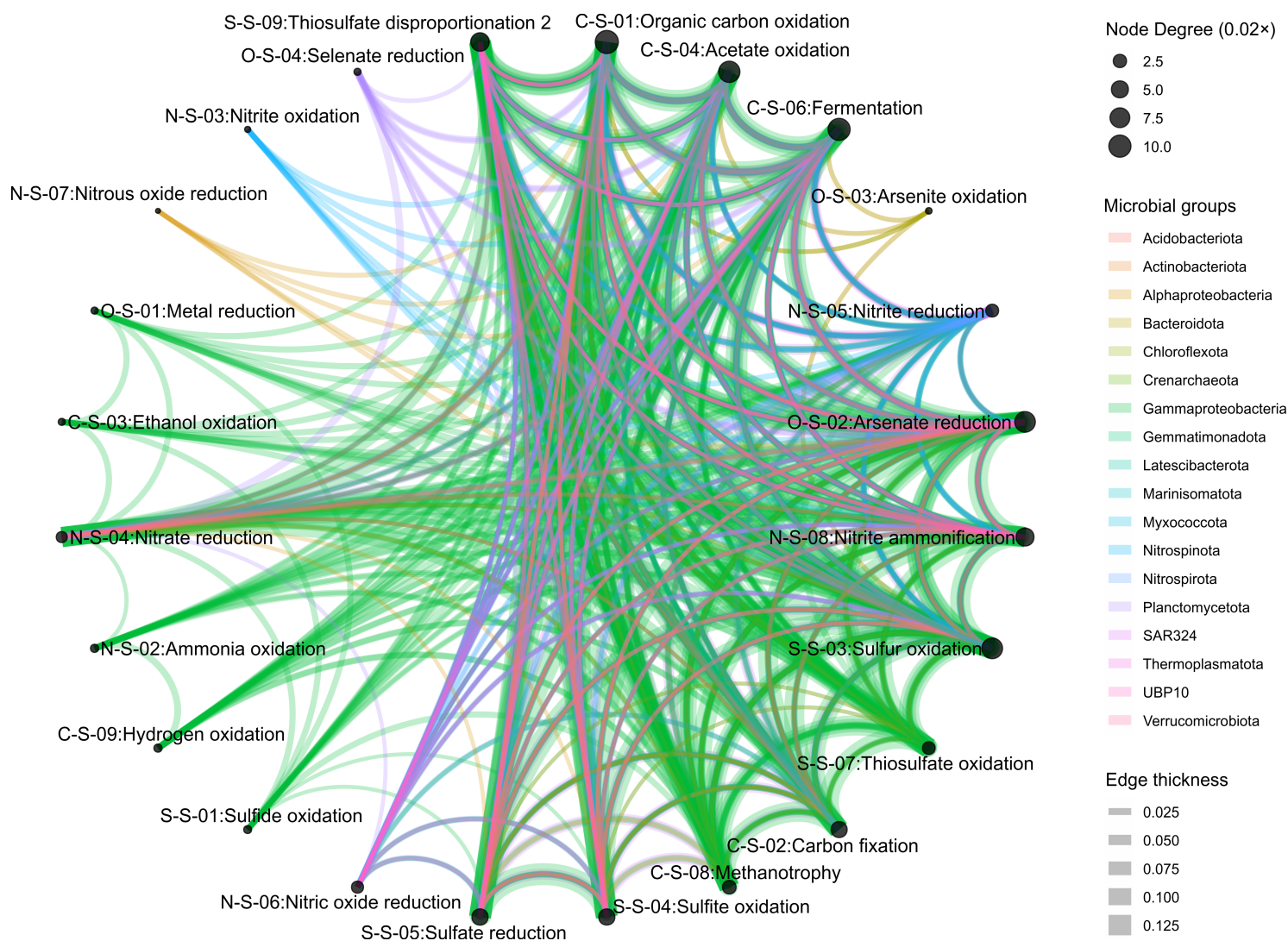




Supplementary Figure S2. Functional network diagram based on the transcriptomic dataset from a hydrothermal vent sample. The nodes represent biogeochemical cycling steps, and edges connecting two given nodes represent the functional connections between them. The size of the node was depicted according to the degree (number of connections to each node). The thickness of the edge was depicted according to the average of the gene expression values of the connected two biogeochemical cycling steps, which were calculated by the transcriptomic dataset from the Guaymas Basin hydrothermal vent sample. The color of the edge was assigned based on the taxonomic group of the represented genome.