SUPPLEMENTARY INFORMATION FIGURES

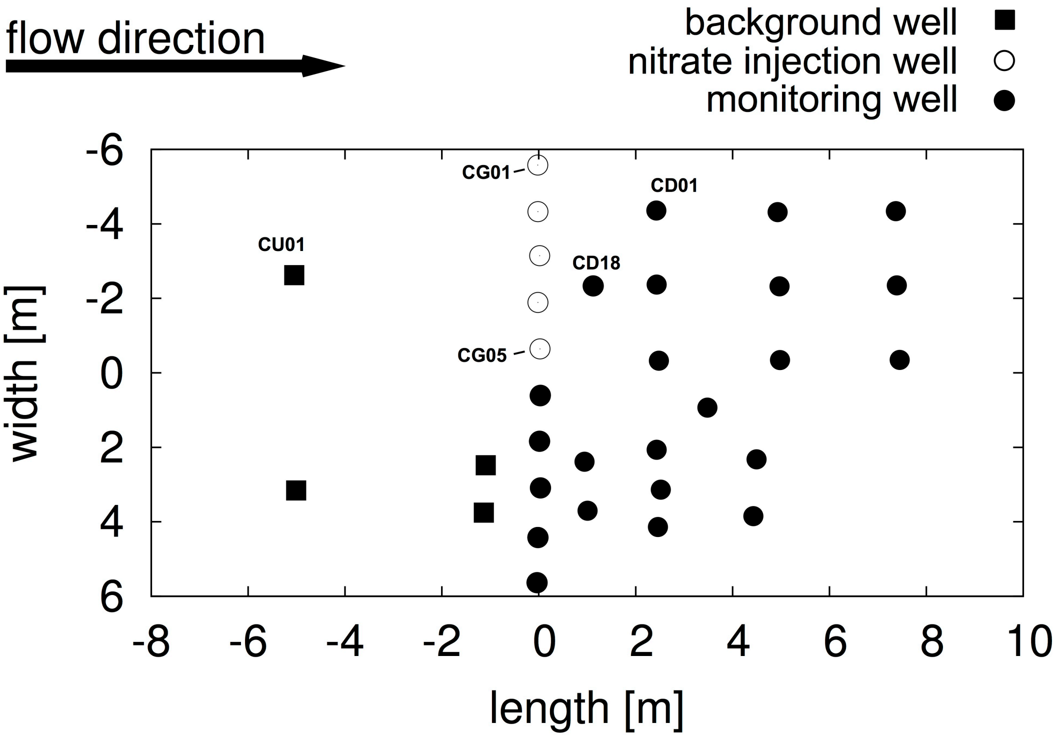

Figure S1. Flow cell layout of Rifle-site nitrate injection wells, sampling well (CD01), and background well used in this study. Predominant groundwater flow direction is indicated.

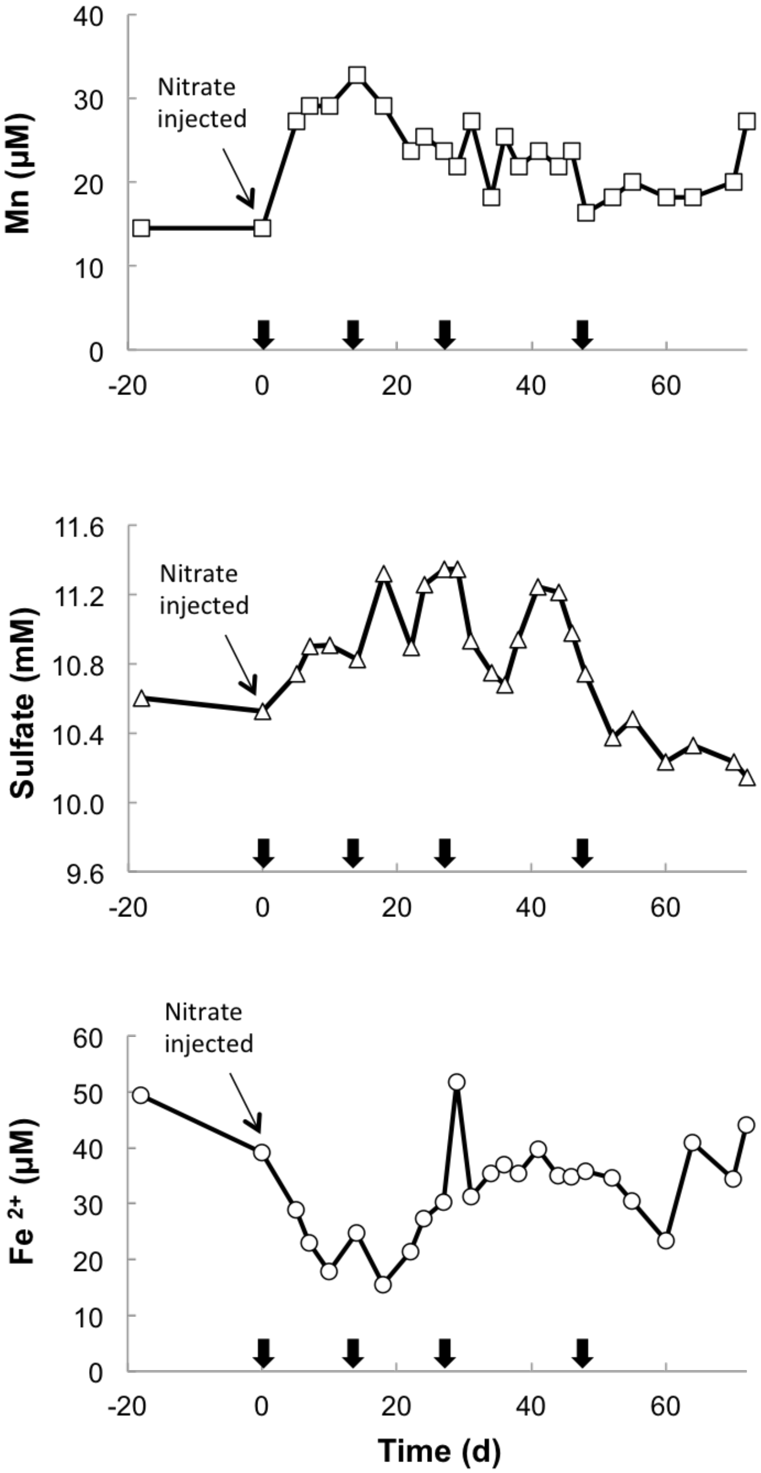

Figure S2. Concentrations in groundwater (well CD01) of dissolved Mn, sulfate, and dissolved Fe^{2+}. The time that nitrate injection began is indicated, and black arrows represent the time of collection for metagenomic / metatranscriptomic samples.

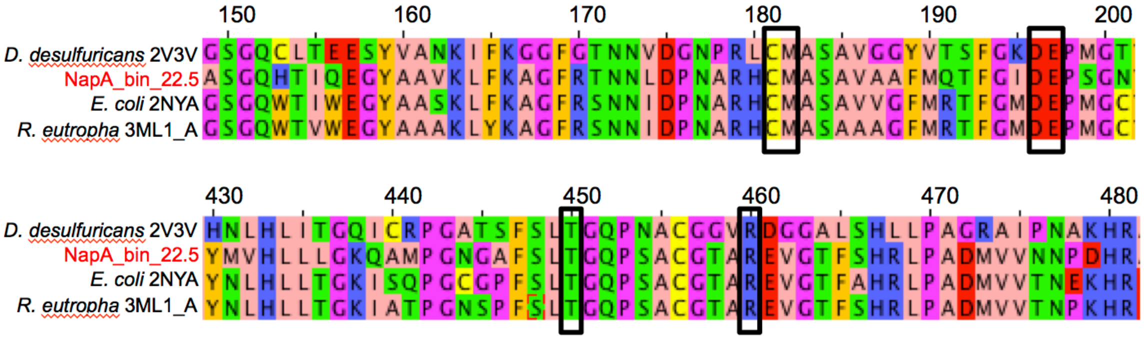

Figure S3. Partial alignment of NapA from Gallionellaceae bin 22.5 (scaffold-1168_1169_1) versus NapA copies from other bacteria (*Desulfovibrio desulfuricans Escherichia coli*, and *Ralstonia eutropha*). PDB (Protein Data Bank) accession numbers for the bacterial NapA versions (other than for bin 22.5) are shown. The black boxes highlight all six active-site conserved residues documented for NapA (Moura et al. 2004).