Supplementary Information

Reference strains. The *Epsilonproteobacteria* used as reference strains in this study were: *Caminibacter mediatlanticus* DSM 16658 (Voordeckers *et al*, 2005), *Caminibacter* sp. strain TB-1 (Voordeckers *et al*, 2005), *Nautilia* spp. strains MT3, MT4, and MT5 (Voordeckers *et al*, 2008), *Nautilia nitratireducens* DSM 22087 (Perez-Rodriguez *et al*, 2010), *Caminibacter hydrogeniphilus* DSM 14510 (Alain *et al*, 2002), *Caminibacter profundus* DSM 15016 (Miroshnichenko *et al*, 2004), *Hydrogenimonas thermophila* JCM 11971 (Takai *et al*, 2004)*, Thioreductor micantisoli* DSM 16661 (Nakagawa *et al*, 2005a)*, Nitratiruptor tergarcus* (Nakagawa *et al*, 2005b), *Nitratifractor salsuginis* (Nakagawa *et al*, 2005b), *Sulfurimonas paralvinellae* DSM 17229 (Takai *et al*, 2006) and *Sulfurovum lithotrophicum* (Inagaki *et al*, 2004).

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Legend to Supplementary Figures

Figure S1. Total RNA from cultures of *Caminibacter* spp. grown under nitrate-reducing conditions (A). Lane 1: *C. mediatlanticus*; lane 2: *C. profundus*. Detection of *napA* transcripts by RT-PCR (B): lane 1: 100 bp ladder; lane 2: negative control (no RT); lane 3: *napA* reverse transcript from *C. mediatlanticus*; lane 4: *napA* reverse transcript from *C. profundus*.

Figure S2. Rarefaction curves of the *napA* libraries from the four sampling sites. The curves were generated using Analytic Rarefaction 1.3, kindly provided by Steven M. Holland (http://www.uga.edu/%7Estrata/software/Software.html).