

Table S1. Numerically dominant *Alphaproteobacteria nifH* OTUs₉₅

OTU ₉₅	Source (# sequences)	Top blastp hits / % similarity
1	NCD (22); TNO (9); WIR (6)	<i>Azospirillum amazonense</i> (WP_004274319), <i>Bradyrhizobium</i> sp. BTAi1 (YP_001241772), <i>Bradyrhizobium</i> sp. ORS 278 (YP_001207334) / 97-99%
2	NCD (15); TNO (9); WIR (6)	<i>Hyphomicrobium</i> sp. MC1 (YP_004677463), <i>Methylocystis</i> sp. SC2 (YP_006592725) / 97-98%
3	WIR (24)	<i>Azospirillum brasilense</i> Sp245 (YP_005030951), <i>Gluconacetobacter diazotrophicus</i> PAI 5 (YP_001600720), <i>Zymomonas mobilis</i> subsp. <i>mobilis</i> ZM4 (YP_163558) / 93-96%
4	NCD (1); TNO (7); WIR (7)	<i>Bradyrhizobium diazoefficiens</i> USDA 110 (NP_768409), <i>Xanthobacter autotrophicus</i> Py2 (YP_001415004) / 95-96%

Figure S1 Collector's curves for *NifH* sequences at different OTU cutoff values

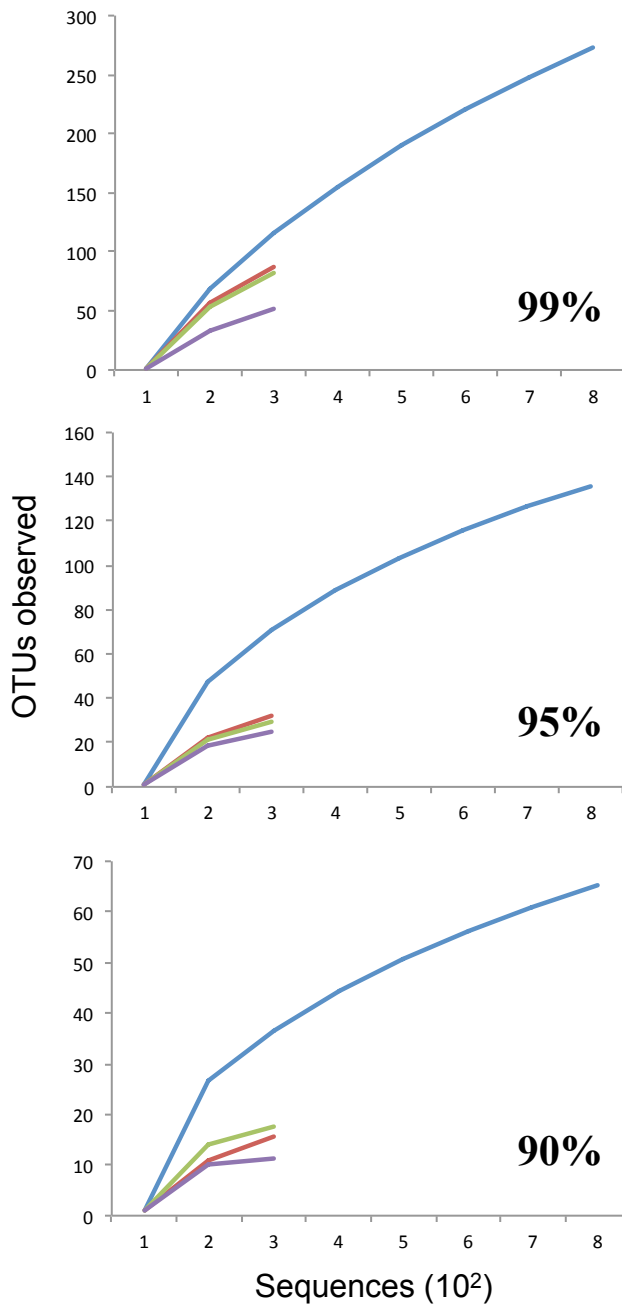


Figure S1. Collector's curves for translated *nifH* sequences at different OTU cutoff values. Sequences were pooled by site, from both ambient and elevated CO₂ plots (MDE, blue, 5 ambient and 5 elevated plots; NCD, red, 3 ambient and 3 elevated plots; TNO, green, 2 ambient and 2 elevated plots; WIR, purple, 3 ambient and 3 elevated plots).

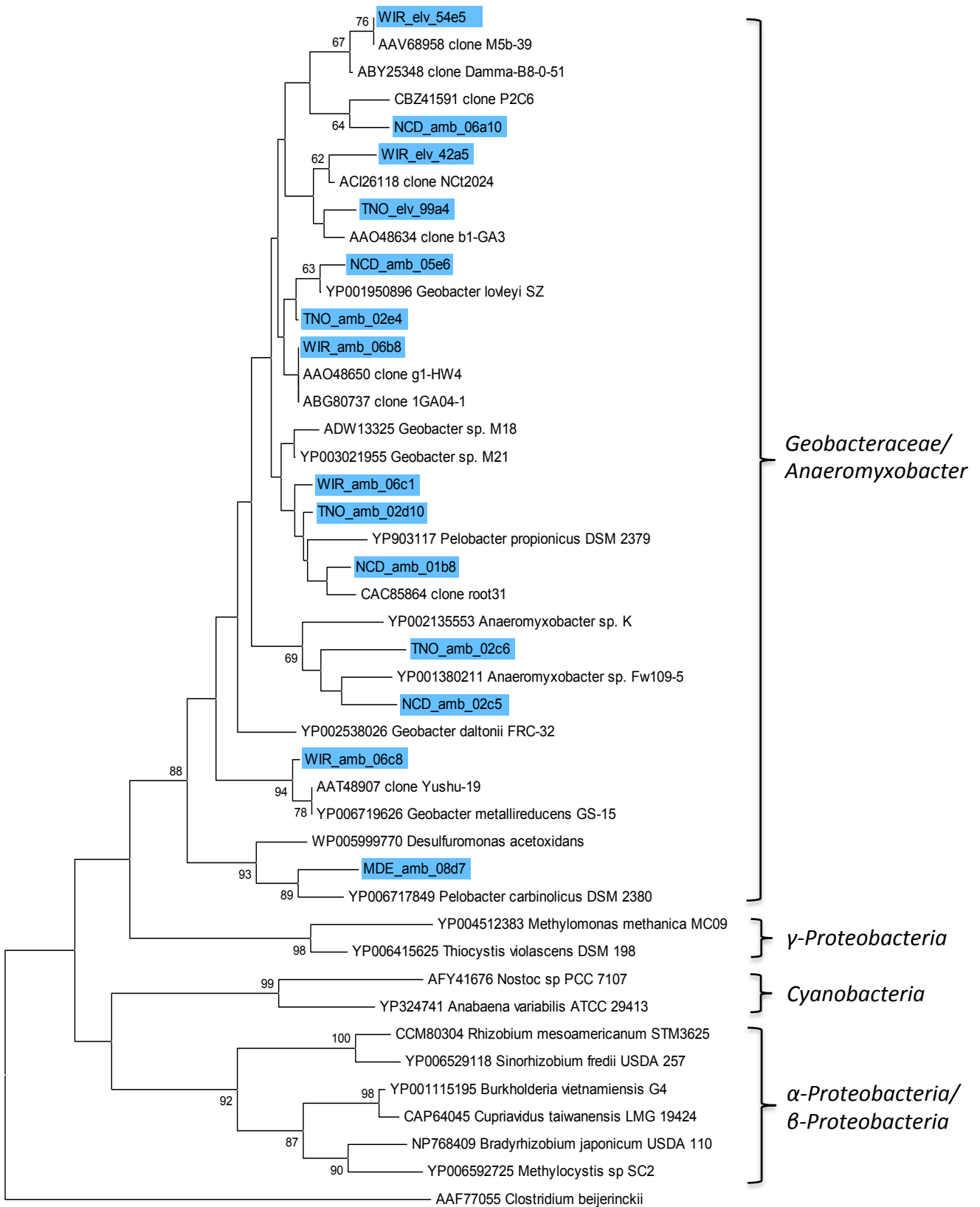


Figure S2. Phylogenetic depiction of *Geobacteraceae nifH* sequence diversity. The Neighbor-Joining tree was generated from translated *nifH* sequences (161 amino acids), evolutionary distances were computed using t p-distance method, and ambiguous positions were removed for each pairwise comparison. Sequences from this study are highlighted in blue and designated by site (NCD, TNO, WIR or MDE) and CO₂ treatment (elevated, elv; ambient, amb).