clade relative abundance (%)

Biome 3

Fig. S3 Relative abundance of *nirS* clades in metagenomes from various biomes. Basal branches indicate the best placement for a read occurred in regions of the phylogeny not belonging to a specific clade. Unknown indicates best placements was distributed across multiple clades. Remaining clades follow Fig. 2. Boxplots show median and quartiles, and whiskers show 95 percentiles, and values outside 95 percentiles are shown as points. Please note differences in y-axis scale across plots.