Supplementary materials

Diversity, Abundance and Distribution of NO-forming Nitrite Reductase-encoding Genes in Deep-Sea Subsurface Sediments of the South China Sea

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Figure S1 Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea deep-ocean subseafloor sediments nirK protein sequences and representative data from Pacific northwestern sediments, Black Sea suboxic zone and California coastal sediments.
Operational taxonomic units were defined by the DOTUR software using a 5% cut-off with protein sequence data; Black circle: >99.9%, grey circle: 90%-99.9%, and white circle: 70%-90% (The same as below).

* Sequences were downloaded from NCBI database, and sequence numbers were following:
  California coastal sediments (AAZ83786 to AAZ83974), Pacific Northwestern sediments (CAB76764 to CAB76818) Black Sea (ABG36123 to ABG36515) Peruvian OMZ (ACR07874 to ACR07917), Arabian OMZ (AAP91545 to AAP91545), Baltic Sea (AAY87336 to AAY87401), Marine aquaculture zones (HQ265346 to HQ265363) and Mai Po Natural Reserve (HQ265325 to HQ265345).
Figure S2 Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea deep-ocean subseafloor sediments nirS protein sequences and representative data from Pacific northwestern sediments, Black Sea suboxic zone, Peruvian OMZ, Arabian OMZ, and Baltic Sea.
**Figure S3** Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea deep-ocean subseafloor sediments Scalindua-*nirS* protein sequences and representative data from Peruvian OMZ, Marine aquaculture zone, Mai Po Natural Reserve.