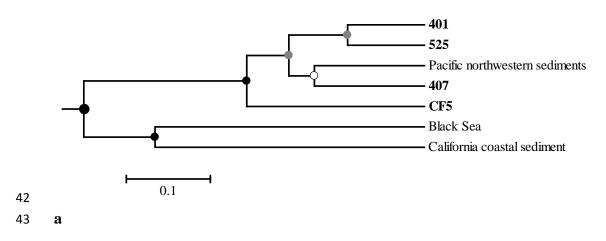
1 2	Supplementary materials
3	Diversity, Abundance and Distribution of NO-forming Nitrite
4	Reductase-encoding Genes in Deep-Sea Subsurface Sediments of the
5	South China Sea
6	
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26 27	
28	Figure S1 Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea
29	deep-ocean subseafloor sediments nirK protein sequences and representative data from
30	Pacific northwestern sediments, Black Sea suboxic zone and California coastal sediments.

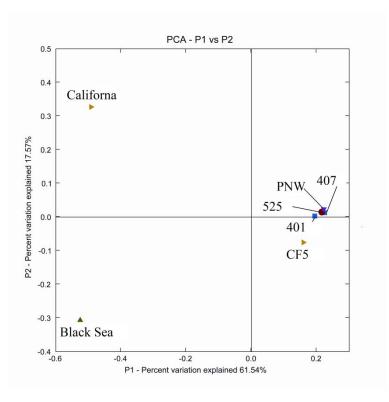
Operational taxonomic units were defined by the DOTUR software using a 5% cut-off with protein sequence data; Black circle: >99.9%, grey circle: 90%-99.9%, and white circle: 70%-90% (The same as below).

34

* 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).









47 Figure S2 Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea
48 deep-ocean subseafloor sediments *nirS* protein sequences and representative data from
49 Pacific northwestern sediments, Black Sea suboxic zone, Peruvian OMZ, Arabian OMZ, and
50 Baltic Sea.

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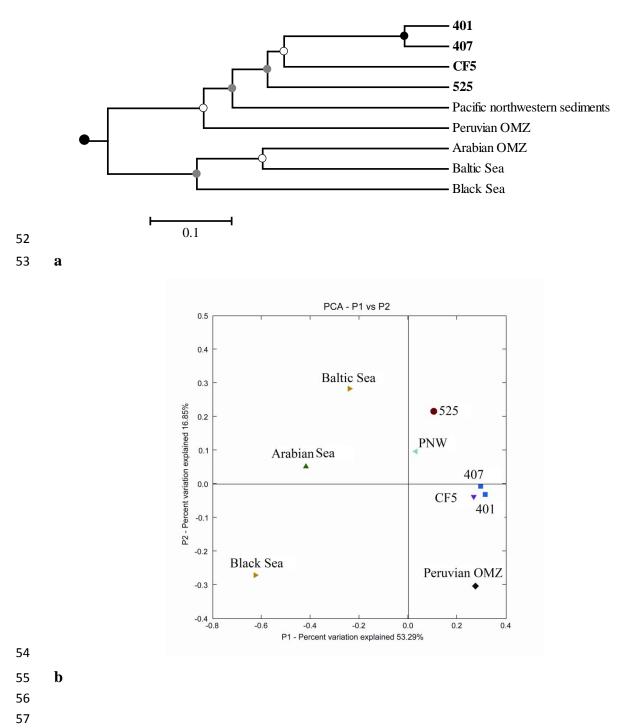
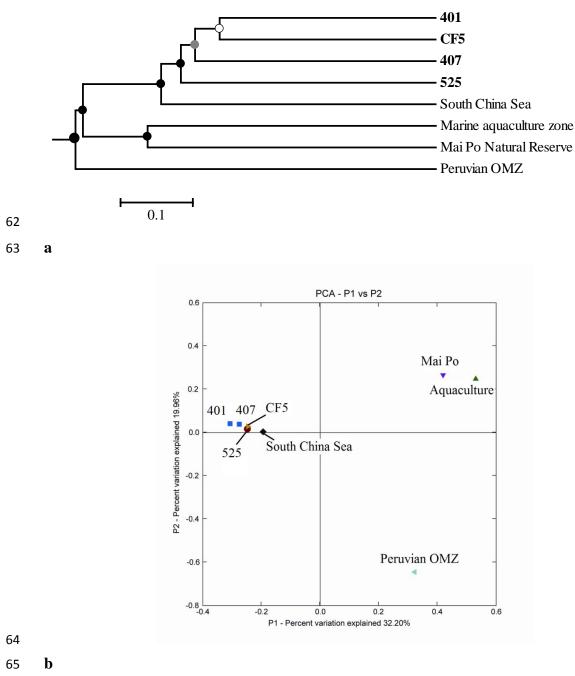


Figure S3 Jackknife Environmental Clusters (a) and PCoA (b) for the South China Sea
deep-ocean subseafloor sediments Scalindua-*nirS* protein sequences and representative data
from Peruvian OMZ, Marine aquaculture zone, Mai Po Natural Reserve.





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