Table S2. 16S rRNA sequences retrieved from clone libraries that were established from the *Ca.* Nitrospira deluvii enrichment with preceding treatment by LNAzymes targeting *Ca*. N. defluvii.

Next cultured relative (identity)	Next uncultured relative, GenBank accession no. (identity)	Sequences from 8F - 907R RNA library	Sequences from 8F - 1492R RNA library	Sequences from 8F - 907R DNA library
Betaproteobacteria				
Methyloversatilis universalis (99.1 %)	denitrifying sequencing batch reactor clone, HQ703525 (99.9 %)		2	
Methyloversatilis universalis (98.6 %)	denitrifying fluidized bed reactor clone, DQ202141 (99.7 %)	1		1
Rubrivivax gelatinosus (96.5 %)	activated sludge clone, EU283352 (98.7 %)		1	
Denitratisoma oestradiolicum (91.9 %)	denitrifying bioreactor clone, FJ167494 (99.7 %)		1	
Variovorax paradoxus (99.8 %)	biofilm on oxygen-transfer membrane clone, AY444994 (99.8 %)			1
Alphaproteobacteria				
Meganema perideroedes (90.8 %)	soil clone, GQ169020 (98.2 %)	1	1	2
Caedibacter caryophilus *(* 88.0 %)	autotrophic nitrifying biofilm reactor clone, FJ529966 (94.9 %)	1		
Geminicoccus roseus (85.5 %)	activated sludge clone, HQ385549 (98.8 %)	1		
Rhodobacter litoralis (95.4 %)	autotrophic nitrifying biofilm reactor clone, FJ529978 (98.4 %)		2	
Pelagibius litoralis (93.1 %)	soil clone, HQ727620 (96.13 %)		1	
Afipia birgiae (99.6 %)	clean room clone, EU071489 (99.9 %)			1
Bacteroidetes				
Terrimonas lutea (95.0 %)	activated sludge clone, FJ536929 (99.3 %)	2		2
Flexibacter flexilis (83.8 %)	Hanford site subsurface clone, HM186924 (91.8 %)	4	5	4
Chlorobi				
N.A.	iron snow from acidic coal clone, FR667812 (92.9 %)	2		
Gemmatimonadetes				
Gemmatimonas aurantiaca (90.1 %)	oil seep clone, EF157193 (96.6 %)		1	
Actinobacteria				
Mycobacterium austroafricanum (99.8 %)	indoor dust clone, AM697434 (98.8 %)	2		
Cyanobacteria				
Gloeobacter violaceus (82.7 %)	human skin clone, JF219539 (100 %)	2		
Deinococcus-Thermus				
Meiothermus ruber (90.7 %)	compost clone, FN667273 (90.4 %)			2