

Table S1. Primers, oligonucleotide probes, and LNAzymes used in this study.

Oligonucleotide	Sequence (5'-3')
Probes used for FISH	
Ntspa1431 (6)	TTG GCT TGG GCG ACT TC
EUB338 (1)	GCT GCC TCC CGT AGG AGT
EUB338-II (2)	GCA GCC ACC CGT AGG TGT
EUB338-III (2)	GCT GCC ACC CGT AGG TGT
PCR Primers	
1492R (5)	GGY TAC CTT GTT ACG ACT T
8F (modified) (3, 4)	AGA GTT TGA TYM TGG CTC
T3-8F (7)	AAT TAA CCC TCA CTA AAG GG AGA GTT TGA TYM TGG CTC
907R (5)	CCG TCA ATT CMT TTG AGT TT
LNAzymes	
Ntspa668 (this study) ¹	CTA <u>CAC</u> CGG <u>GAA</u> GGC TAG CTA CAA CGA TCC <u>GCG</u> CTC C
Ntspa665 (this study) ¹	<u>CCG</u> CTA CAC <u>CGG</u> GAA GGC TAG CTA CAA CGA TCC <u>GCG</u> CTC CTC <u>TCC</u>
Nso215 (this study) ¹	AAC <u>TAG</u> CTA <u>ATC</u> AGA GGC TAG CTA CAA CGA ATC <u>GGC</u> <u>CRC</u> TCC
Helper probes	
Ntspa630help (this study)	CCT CTA GCC KRG CAG TMC CCT CYG CRC TTT CC
Ntspa700help (this study)	GCC ACC GGC CTT CCT CCC GAT CTC TAC GC

¹ LNA nucleotides are underlined and substrate-binding arms are in boldface.

References

1. **Amann, R. I., B. J. Binder, R. J. Olson, S. W. Chisholm, R. Devereux, and D. A. Stahl.** 1990. Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. *Appl. Environ. Microbiol.* **56**:1919-1925.

2. **Daims, H., A. Brühl, R. Amann, K.-H. Schleifer, and M. Wagner.** 1999. The domain-specific probe EUB338 is insufficient for the detection of all *Bacteria*: Development and evaluation of a more comprehensive probe set. *System. Appl. Microbiol.* **22**:434-444.
3. **Hicks, R. E., R. I. Amann, and D. A. Stahl.** 1992. Dual staining of natural bacterioplankton with 4',6-diamidino-2-phenylindole and fluorescent oligonucleotide probes targeting kingdom-level 16S rRNA sequences. *Appl. Environ. Microbiol.* **58**:2158-2163.
4. **Juretschko, S., G. Timmermann, M. Schmid, K.-H. Schleifer, A. Pommerening-Röser, H.-P. Koops, and M. Wagner.** 1998. Combined molecular and conventional analyses of nitrifying bacterium diversity in activated sludge: *Nitrosococcus mobilis* and *Nitrospira*-like bacteria as dominant populations. *Appl. Environ. Microbiol.* **64**:3042-3051.
5. **Lane, D. J.** 1991. 16S/23S rRNA sequencing, p. 115-175. *In* E. Stackebrandt and M. Goodfellow (ed.), *Nucleic acid techniques in bacterial systematics*. John Wiley & Sons, Inc., New York.
6. **Maixner, F., D. R. Noguera, B. Anneser, K. Stoecker, G. Wegl, M. Wagner, and H. Daims.** 2006. Nitrite concentration influences the population structure of *Nitrospira*-like bacteria. *Environ. Microbiol.* **8**:1487-1495.
7. **Steger, D., D. Berry, S. Haider, M. Horn, M. Wagner, R. Stocker, and A. Loy.** 2011. Systematic spatial bias in DNA microarray hybridization is caused by probe spot position-dependent variability in lateral diffusion. *PLoS ONE* **6**:e23727.