S1 File. Quantification limit was 0.5%. When 0.2% is indicated, it indicates that they were present but below 0.5%. 0 means none were found. Average values are from Nielsen et al., 2010. ND: Not Determined.

Functional group	Probe name	Target	Phylum	Class	Reference	Aalborg West	Average Value (%)	Range (%)
AOB	Nso190	Betaproteobacterial AOB*	Proteobacteria	Betaproteobacteria	Mobarry et al., 1996	2.5	3.8	1.2-8.2
	Nsv443	*Nitrosospira* spp.			Mobarry et al., 1996	0	1.4	0.2-3.2
	Nsm156	*Nitrosomonas* spp., *Nitrosococcus mobilis*			Mobarry et al., 1996	1.2	1.6	0.2-3.8
NOB	Ntspa662	Genus *Nitrospira**	Nitrospirae	Nitrospira	Daims et al., 2001	3.4	3.1	0.2-5.7
	Ntspa1431	Sublineage I of the genus *Nitrospira*			Maixner et al., 2006	0.3	1.6	0.2-2.5
	Ntspa1151	Sublineage II of the genus *Nitrospira*			Maixner et al., 2006	0.3	1.4	0.2-3.9
Denitrifiers	Curvi997 (Aqs997)	*Curvibacter* (former *Aquaspririllum*)*	Proteobacteria	Betaproteobacteria	Thomsen et al., 2004	5.3	7.1	1.5-14.1
	ZRA23a (ZRA, ZOGLO647)	Most members of *Zoogloea* lineage, not *Z. Resiniphila**			Rossello-Mora et al., 1995	0.5	2.1	0.2-5.2
	Azo644 (AZA645)	Most members of the *Azoarcus* cluster*			Hess et al., 1997	3.2	3.1	0.8-9.3
	Thau646	*Thauera**			Lanjoie et al., 2000	3.8	3.1	0.2-6.2
	G Rb	*Rhodobacter, Roseobacter**		Alphaproteobacteria	Giuliano et al., 1999	2.2	1.2	0.2-3.4
PAO/Denitrifiers	PAOmix (PAO462, PAO651, PAO846)	Most Accumulibacter*		Betaproteobacteria	Crocetti et al., 2000	1.6	3.6	1.0-10.8
	Acc-I-444	Accumulibacter – clade IA and others			Flowers et al., 2008	ND	1.5	0.2-4.6
PAO	Acc-II-444	Accumulibacter – clade IIA, IIC, IID		Betaproteobacteria	Flowers et al., 2008	ND	1.1	0.2-3.2
	Actino-221	Some *Tetrasphaera*	Actinobacteria	Actinobacteria	Kong et al., 2005	ND	4.3	0.8-9.9
	Actino-658	Some *Tetrasphaera*			Kong et al., 2005	ND	4.1	1.0-10.8
	Tet1-266	*Tetrasphaera* clade I*			Nguyen et al., 2011	8.5	ND	ND
	Tet2-892, Tet2-174	*Tetrasphaera* clade 2*			Nguyen et al., 2011	5.8	ND	ND
	Tet3-654	*Tetrasphaera* clade 3*			Nguyen et al., 2011	3.9	ND	ND
GAO	GBmix	Most *Competibacter**	Proteobacteria	Gammaproteobacteria	Kong et al., 2002	0.3	1	0-8.0
Protein hydrolysers	SAP-309	Saprospiraceae*	Bacteroidetes	Sphingobacteria	Schauer and Hahn 2005	3.5	6.1	1.2-12.2
Fermenters	Str	*Streptococcus* spp.*	Firmicutes	Bacilli	Trebesius et al., 2000	1.3	2.3	0.2-6.7
Filamentous bacteria	G123 T	*Thiothrix eikelboomii, T. nivea, T. unzii, T. fructosivorans, T. defluvii, T. Eikelbloom* Type 021N group I, II, III*	Proteobacteria	Gammaproteobacteria	Kanagawa et al., 2000	0.3	0.9	0.2-4.5
	MPAmix	*Candidatus* Microthrix parvicella, *Candidatus* Microthrix calida*	Actinobacteria	Actinobacteria	Erhart et al., 1997; Levantesi et al., 2006	4.2	5.6	0.2-15.4
	CFXmix (GNSB941, CFX1223)	Phylum Chloroflexi*	Chloroflexi		Gieseke et al., 2001	10.0	10.2	2.4-22.3
	TM7905	Candidate division TM7*	Candidate division TM7		Hugenholtz et al., 2001	3.6	4.9	0.9-12.3
	HHY-654	Several *Haliscomenobacter* species among others the type strain	Bacteroidetes	Sphingobacteria	Kragelund et al., 2008	2.2	1.9	0.2-6.3

* Data used for calculating summed abundance. Data without an asterisk is covered by a broader probe.

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