Table S5. The percentage of nucleotides overlap (upper triangle) and average nucleotide identity (ANI, lower triangle) between pairs of genomes, including our SAGs (in bold), the related *Ca.* Nitromaritima SAGs and fosmids (in red and green respectively), and canonical NOBs.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. SCGC AAA799-A02	---	43.4	12.6	13.1	13.9	47.2	25.4	17.9	42.1	10.6	0.6	0.7	1.8	1.3	1.0
2. SCGC AAA799-C22	99.2	---	16.1	20.1	19.9	54.0	57.9	32.0	46.8	14.3	1.1	0.9	1.1	1.9	1.2
3. SCG AB629-B06	68.6	68.4	---	67.1	54.7	33.6	77.3	19.7	22.5	22.8	0.7	0.6	0.3	1.1	1.2
4. SCGC AB629-B18	68.6	68.6	85.3	---	66.5	87.7	89.3	37.3	38.1	15.3	1.0	0.8	0.7	2.0	1.8
5. SCGC AAA288-L16	68.4	68.3	84.7	92.5	---	98.6	94.4	35.6	46.7	13.4	0.9	0.6	0.5	1.6	1.6
6. HF0770_08F21 (Fosmid)	76.7	75.1	85.6	91.9	90.8	---	38.7	18.5	42.2	0.5	0.1	0.1	0.1	0.1	0.2
7. 4050020-J15 (Fosmid)	81.7	72.0	81.6	89.5	90.1	89.3	---	15.2	27.2	0.5	0.1	0.2	0.1	0.1	0.1
8. EB080L20_F04 (Fosmid)	75.8	71.1	69.3	68.4	69.1	75.0	75.6	---	54.5	0.9	0.1	0.2	0.1	0.1	0.2
9. HF0200_07G10 (Fosmid)	72.5	72.1	67.6	73.6	72.3	72.9	76.7	84.7	---	0.6	0.1	0.1	0.1	0.1	0.1
10. *Nitrospina gracilis*	66.5	66.8	63.2	63.3	63.2	71.5	70.7	67.8	70.6	---	2.9	2.6	3.0	4.9	1.8
11. *Nitrococcus mobilis*	63.0	61.5	60.2	60.7	60.8	77.1	77.4	79.1	79.6	62.4	---	2.3	5.4	2.7	0.9
12. *Nitrolancetus hollandicus*	63.4	63.3	59.4	60.8	61.0	70.6	69.8	67.4	70.5	62.7	62.5	---	2.7	2.1	0.8
13. *Nitrobacter winogradskyi*	64.2	63.5	61.6	60.0	61.2	78.4	78.3	77.9	78.8	63.9	63.9	63.7	---	2.7	0.7
14. "Nitrospira defluvii"	63.0	62.6	60.1	60.9	60.6	71.4	71.2	76.2	71.0	62.9	62.3	62.7	63.3	---	1.6
15. "Kuenenia stuttgartiensis"	62.0	61.4	60.2	60.7	60.6	65.5	65.8	65.2	68.6	60.0	60.7	61.1	60.9	61.0	---

The color codes denote *Nitrospina*-like genome clusters that are phylogenetically related at the rRNA gene level as indicated in Figure 1.