Supplementary information

Rapid identification of haloarchaea and methanoarchaea using the matrix assisted laser desorption/ionization time-of-flight mass spectrometry

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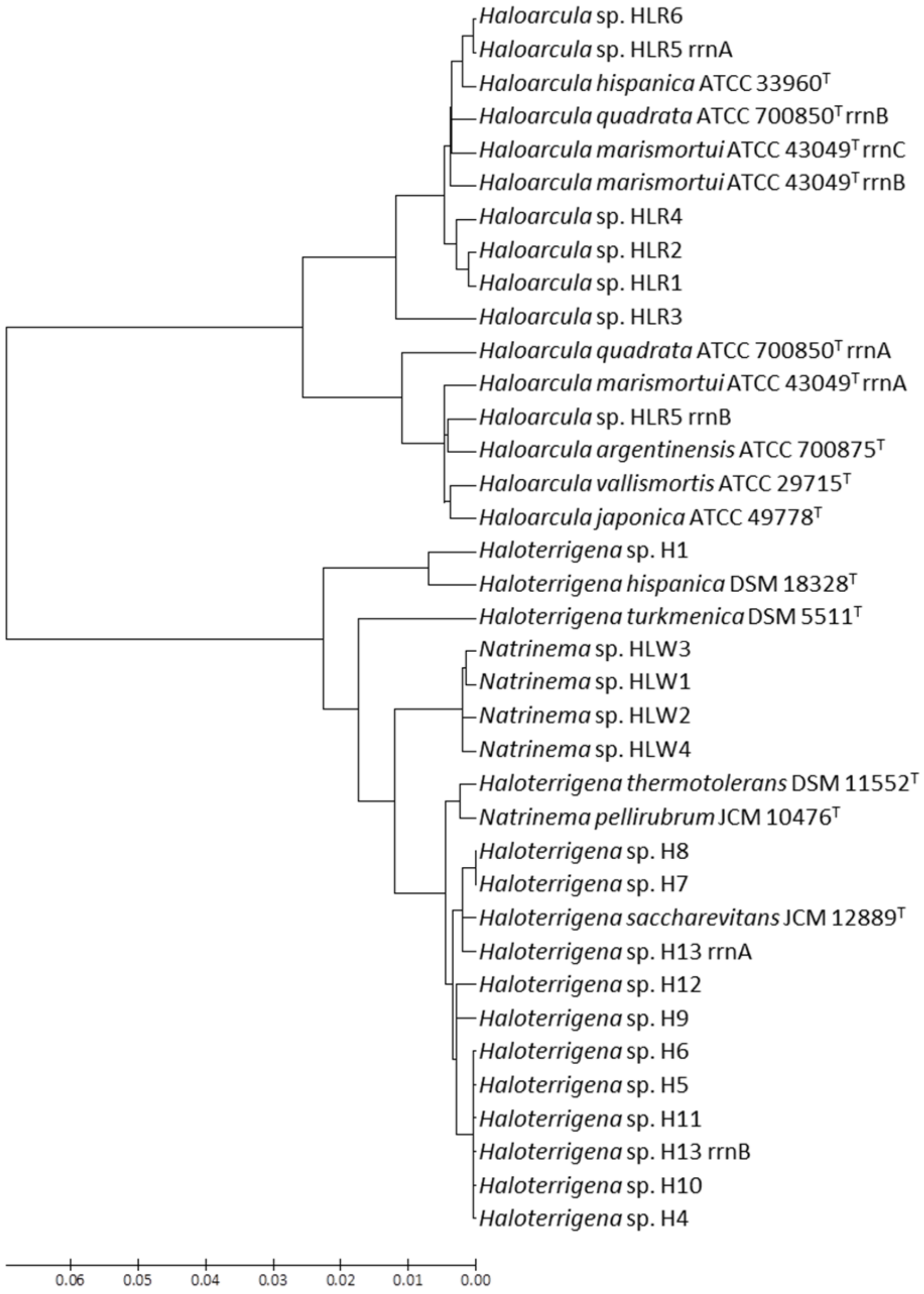

Fig. S1. Phylogenetic tree of total 37 haloarchaea 16S rRNA sequences included the different copies from one strains. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.31769326 is shown. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. The analysis involved 37 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1312 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

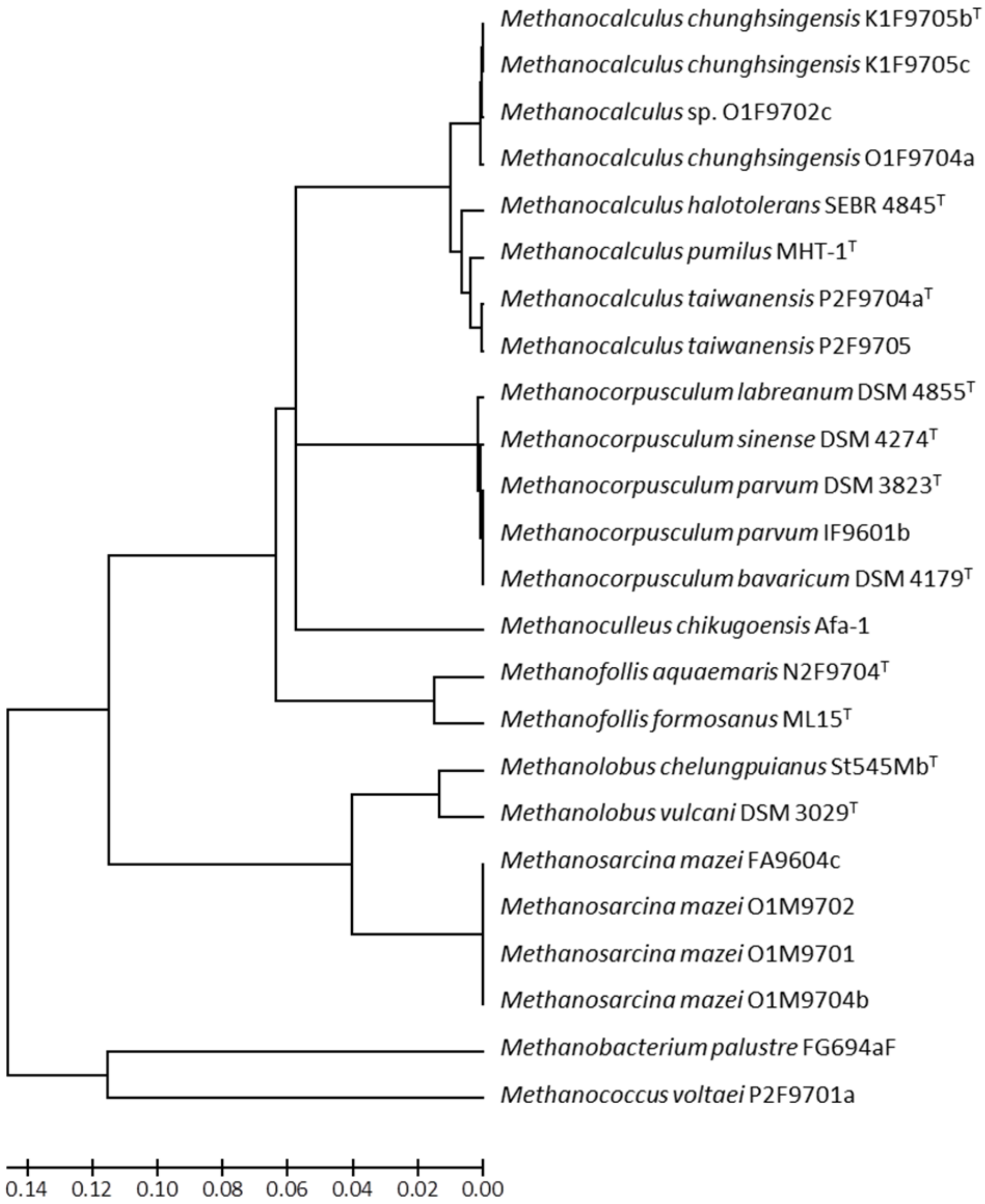

Fig. S2. Phylogenetic tree of 24 halotorelent and non-halophilic methanogens 16S rRNA sequences. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.77133833 is shown. The analysis involved 24 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1097 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

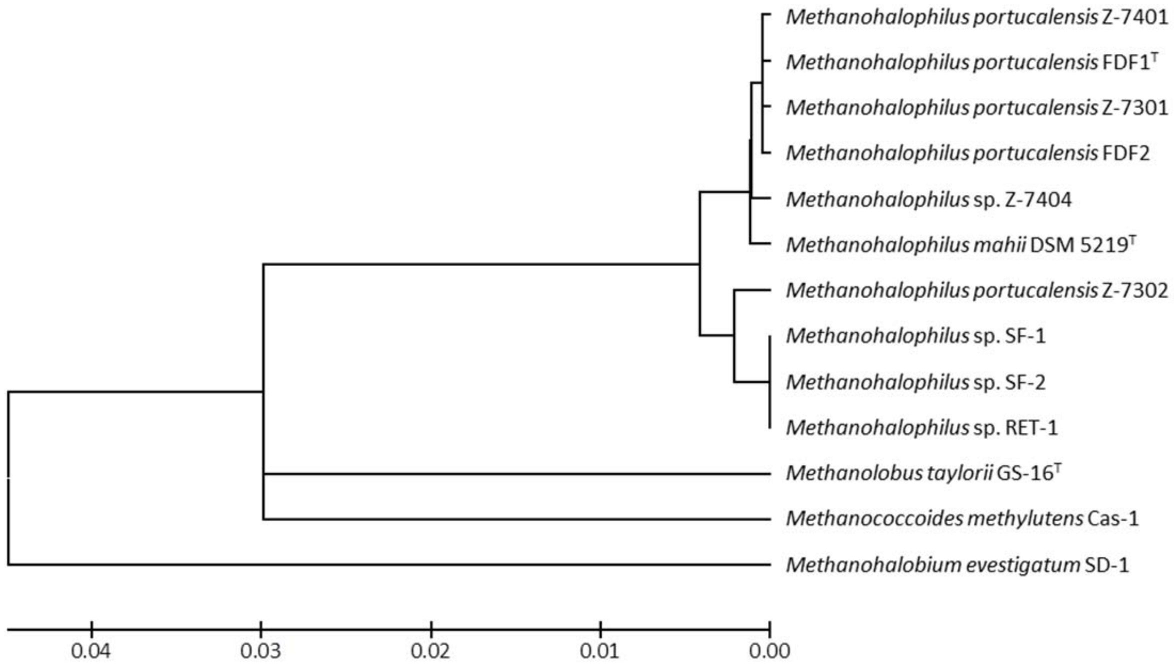

Fig. S3. Phylogenetic tree of 13 halophilic methanogens 16S rRNA sequences. The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.15665621 is shown. The analysis involved 13 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 1205 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

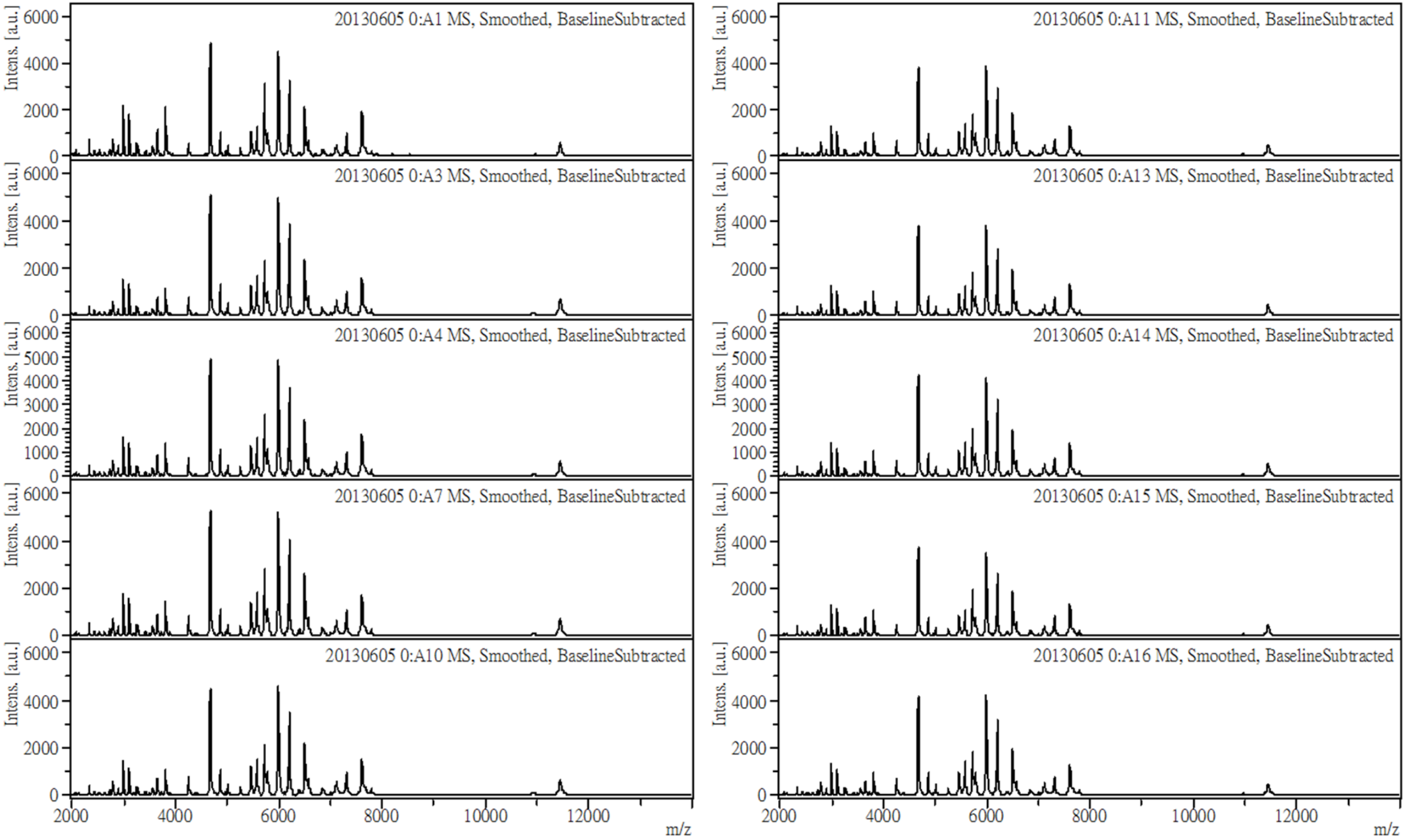

Fig. S4. MALDI-TOF mass spectra of *Methanohalophilus portucalensis* FDF1^T were selected to establish the database.

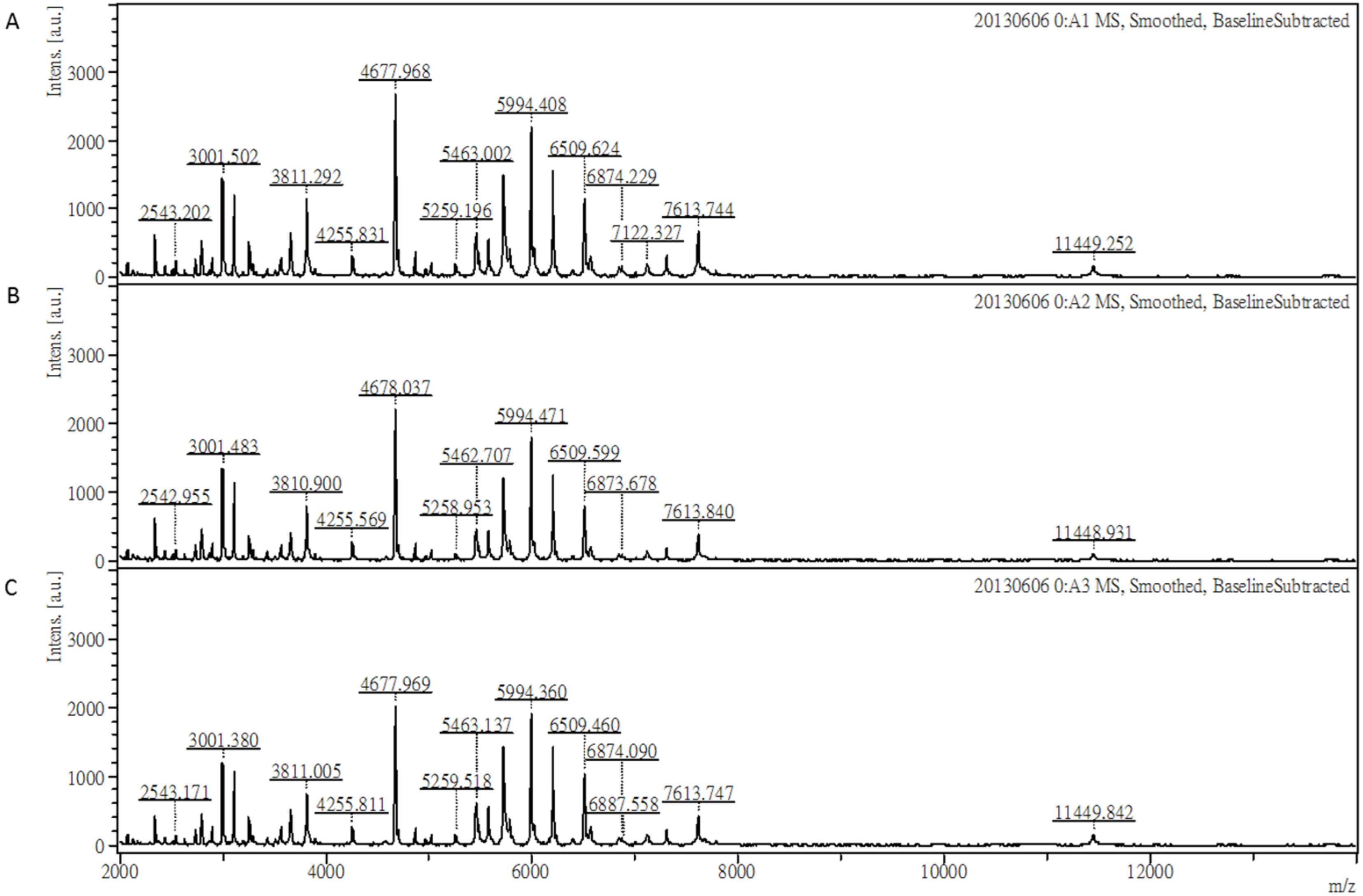

Fig. S5. MALDI-TOF mass spectra of subculturing *Methanohalophilus portucalensis* FDF1^T were used to against the database. The identified score values of the triplicated spectra were A) 2.674, B) 2.696 and C) 2.659.

Table S1. Similarity matrix of 13 halophilic methanoarchaea 16S rRNA sequences (%)

		1	2	3	4	5	6	7	8	9	10	11	12	13
1	*Methanohalophilus portucalensis* FDF1^{T}		0.25	0.08	0.08	0.25	0.25	0.85	0.76	0.76	0.76	5.89	5.91	8.95
2	*Methanohalophilus portucalensis* Z-7401	99.75		0.17	0.17	0.34	0.34	0.93	0.85	0.85	0.85	5.98	6.00	9.04
3	*Methanohalophilus portucalensis* Z-7301	99.92	99.83		0.00	0.17	0.17	0.76	0.68	0.68	0.68	5.80	5.81	8.85
4	*Methanohalophilus portucalensis* FDF2	99.92	99.83	100.00		0.17	0.17	0.76	0.68	0.68	0.68	5.80	5.81	8.85
5	*Methanohalophilus mahii* DSM 5219^{T}	99.75	99.66	99.83	99.83		0.25	0.76	0.68	0.68	0.68	5.71	5.82	8.84
6	*Methanohalophilus* sp. Z-7404	99.75	99.66	99.83	99.83	99.75		0.85	0.76	0.76	0.76	5.62	5.82	8.94
7	*Methanohalophilus porucalensis* Z-7302	99.15	99.07	99.24	99.24	99.24	99.15		0.34	0.34	0.34	6.35	6.27	9.32
8	*Methanohalophilus* sp. SF-1	99.24	99.15	99.32	99.32	99.32	99.24	99.66		0.00	0.00	6.26	6.27	9.23
9	*Methanohalophilus* sp. SF-2	99.24	99.15	99.32	99.32	99.32	99.24	99.66	100.00		0.00	6.26	6.27	9.23
10	*Methanohalophilus* sp. RET-1	99.24	99.15	99.32	99.32	99.32	99.24	99.66	100.00	100.00		6.26	6.27	9.23
11	*Methanococcoides methylutens* MM1	94.11	94.02	94.20	94.20	94.29	94.38	93.65	93.74	93.74	93.74		6.29	7.69
12	*Methanohalophilus taylorii* GS-16^{T}	94.09	94.00	94.19	94.19	94.18	94.18	93.73	93.73	93.73	93.73	93.71		8.16
13	*Methanohalobium evestigatum* SD-1	91.05	90.96	91.15	91.15	91.16	91.06	90.68	90.77	90.77	90.77	92.31	91.84	