

Table S2. Single amplified genomes (SAGs) comprising Marine Group I (MGI) Thaumarchaeota SSU rRNA phylotypes. Phylotypes are defined as sequences having $\geq 99\%$ similarity.

Phylotype	Station¹	SAG sequence²	Accession no.	
Phylotype-1	SA	AAA007-J08	HQ675763	
Phylotype-2	SA	AAA001-B06	HQ675728	
		AAA001-C02	HQ675732	
		AAA001-D14	HQ675733	
		AAA001-I14	HQ675738	
		AAA001-J17	HQ675740	
		AAA003-E14	HQ675744	
		AAA008-E23	HQ675781	
		AAA003-G07	HQ675746	
		AAA008-J11	HQ675785	
	AAA008-M21	HQ675791		
	AAA008-N10	HQ675794		
	HOT	AAA288-B04	HQ675806	
		AAA288-E04	HQ675823	
		AAA288-G03	HQ675830	
		AAA288-G06	HQ675832	
		AAA288-G14	HQ675833	
		AAA288-G19	HQ675834	
		AAA288-J20	HQ675840	
		AAA288-K02	HQ675841	
Phylotype-3		SA	AAA003-D11	HQ675743
			AAA003-P19	HQ675756
	AAA007-C21		HQ675759	
	AAA007-M20		HQ675767	
	HOT	AAA288-A08	HQ675803	
		AAA288-D03	HQ675814	
		AAA288-N06	HQ675847	
		AAA288-P02	HQ675854	
Phylotype-4	SA	AAA001-L13	HQ675742	
		AAA007-G17	HQ675762	
		AAA008-A20	HQ675774	
	HOT	AAA008-I15	HQ675784	
		AAA288-A16	HQ675805	
		AAA288-D06	HQ675816	
		AAA288-K05	HQ675842	
AAA288-K20	HQ675844			
Phylotype-5	SA	AAA001-D19	HQ675734	
		AAA003-J13	HQ675753	
		AAA003-O17	HQ675755	

	AAA008-K15	HQ675788
	AAA008-N14	HQ675795
	AAA008-P23	HQ675800
HOT	AAA240-K17	HQ675801
	AAA288-A10	HQ675804
	AAA288-B11	HQ675808
	AAA288-C11	HQ675810
	AAA288-C17	HQ675812
	AAA288-D04	HQ675815
	AAA288-I17	HQ675836
	AAA288-N08	HQ675848
	AAA288-O22	HQ675853
	AAA288-P18	HQ675855

Phylotype-6	SA	AAA008-L08	HQ675790
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Phylotype-7	SA	AAA001-A19	HQ675727
		AAA001-B14	HQ675729
		AAA001-B20	HQ675730
		AAA001-E03	HQ675735
		AAA001-E10	HQ675736
		AAA001-G21	HQ675737
		AAA001-I18	HQ675739
		AAA001-J20	HQ675741
		AAA003-E23	HQ675745
		AAA003-G11	HQ675747
		AAA003-G15	HQ675748
		AAA003-I10	HQ675750
		AAA003-I22	HQ675751
		AAA003-J10	HQ675752
		AAA003-O08	HQ675754
		AAA007-C17	HQ675758
		AAA007-E15	HQ675760
		AAA007-E18	HQ675761
		AAA007-L04	HQ675765
		AAA007-N15	HQ675768
		AAA007-N19	HQ675769
		AAA007-N23	HQ675770
		AAA007-O23	HQ675772
		AAA008-A08	HQ675773
		AAA008-B15	HQ675775
		AAA008-C15	HQ675776
		AAA008-E02	HQ675777
		AAA008-E15	HQ675859
		AAA008-E18	HQ675780

		AAA008-G03	HQ675782
		AAA008-K07	HQ675786
		AAA008-K16	HQ675789
		AAA008-M23	HQ675792
		AAA008-N07	HQ675793
		AAA008-O05	HQ675796
		AAA008-O18	HQ675797
		AAA008-P02	HQ675798
		AAA008-P03	HQ675799
HOT		AAA240-O10	HQ675802
		AAA288-B07	HQ675807
		AAA288-C14	HQ675811
		AAA288-D10	HQ675817
		AAA288-D18	HQ675820
		AAA288-D22	HQ675821
		AAA288-E03	HQ675822
		AAA288-E09	HQ675824
		AAA288-E15	HQ675825
		AAA288-F11	HQ675827
		AAA288-G02	HQ675829
		AAA288-G05	HQ675831
		AAA288-I14	HQ675835
		AAA288-J07	HQ675837
		AAA288-J11	HQ675838
		AAA288-J14	HQ675839
		AAA288-K09	HQ675843
		AAA288-M04	HQ675845
		AAA288-M23	HQ675846
		AAA288-N15	HQ675849
		AAA288-N23	HQ675850
		AAA288-O07	HQ675851
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Phylotype-8	SA	AAA008-E17	HQ675779
	HOT	AAA288-C05	HQ675809
		AAA288-D11	HQ675818
		AAA288-F20	HQ675828
		AAA288-O17	HQ675852
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Phylotype-9	SA	AAA008-G11	HQ675783

¹HOT, North Pacific station ALOHA; SA, South Atlantic.

²Sequences in bold were chosen as the representative sequence(s) in the SSU rRNA tree.