

TABLE 2. Archaeal and bacterial phylotypes recovered in 16S rRNA gene clone libraries and OTUs resolved by T-RFLP analysis of carbonate chimney and fluid samples^a

Sample	Archaeal phylotype (no. of clones)	Archaeal OTUs (no. identified) (HaeIII-MspI-BstUI)	Bacterial phylotype (no. of clones)	Bacterial OTUs (no. identified) (HaeIII-MspI-BstUI)
3864-1524	ND	ND	7 (27)	12 (4)-15 (5)-15 (4)
3864-1537	ND	5 (1)-7 (2)-4 (1)	15 (46)	12 (8)-16 (11)-15 (6)
3881-1408	1 (29)	5 (1)-6 (2)-4 (2)	37 (55)	13 (6)-ND-13 (7)
FS242	ND	10 (4)-9 (1)-13 (2)	ND	20 (14)-24 (13)-19 (9)
3881-1228	2 (3)	7 (2)-4 (3)-4 (3)	24 (32)	ND
FS243	16 (57)	9 (3)-8 (1)-11 (3)	ND	24 (10)-22 (11)-23 (10)
3869-1404	1 (3)	4 (1)-3 (1)-4 (1)	3 (3)	23 (12)-26 (10)-18 (7)
3869-1443	ND	7 (2)-7 (3)-5 (4)	8 (9)	27 (14)-37 (15)-20 (9)
3869-1446	ND	10 (3)-7 (4)-9 (2)	40 (72)	ND
FS221	ND	ND	ND	8 (6)-9 (4)-7 (2)
3876-1133	1 (2)	4 (2)-4 (2)-4 (2)	30 (54)	23 (12)-ND-22 (6)
3880-1557	1 (2)	2 (1)-3 (2)-4 (1)	ND	21 (10)-24 (7)-20 (8)
FS222	ND	9 (2)-8 (1)-11 (1)	ND	15 (7)-24 (13)-17 (5)
FS197	2 (3)	12 (3)-12 (2)-15 (2)	ND	24 (9)-16 (3)-17 (8)
FS209	12 (50)	ND	ND	11 (4)-7 (4)-11 (5)

^a Archaeal and bacterial phylotypes are defined as 97% DNA sequence similarity. The total number of clones in the library and the number of OTUs that were identified as corresponding to a terminal restriction fragment of a clone in Table 3 are shown in parentheses. Samples for which a clone library or T-RFLP analysis was not attained are indicated by "ND."