TABLE 3. Archaeal and bacterial 16S rRNA gene clones generated in this study, in addition to previously published LCMS and marine group I clones[a]

Domain	Clone	GenBank accession no.	Phylogenetic group	Fragment size (bp)		
				HaeIII	MspI	BstuI
Archaea	LC1022A-1	AY299516	LCMS	219	130	340
	LC1149A-56	AY299515	LCMS	219*	130*	340*
	LC1133A-9	AY760632	ANME-1	236*	96*	196*
	LC1133A-17	DQ270605	ANME-1	235	96	197
	FS197A-23	DQ270592	*Thermococcales*	154*	78	73
	FS197A-30	DQ270593	*Thermococcales*	154	78	73
	FS209A-41	DQ270596	*Thermococcales*	154	78	73
	FS243A-6	DQ270598	Unc. Eury.	22	81	93
	FS243A-60	DQ270602	Unc. Cren.	152	124	331
	FS209A-10	DQ270595	Unc. Cren.	165	68	82
Bacteria	LC1228B-35	DQ270650	*Actinobacteria*	187	426	184
	LC1022B-39	DQ228573	*Actinobacteria*	191	105	472
	LC1022B-1	DQ228574	*Actinobacteria*	309	455	96
	LC1022B-27	DQ228572	*Actinobacteria*	ND	ND	ND
	LC1133B-64	DQ270644	Alpha-proteobacteria	188	399	58
	LC1133B-90	DQ270648	Alpha-proteobacteria	188	400	58
	LC1133B-8	DQ270640	Alpha-proteobacteria	188	400	58
	LC1133B-74	DQ270646	Alpha-proteobacteria	183	429	72
	LC1133B-45	DQ270642	Alpha-proteobacteria	163	410	167
	LC1231B-170	DQ228567	Alpha-proteobacteria	188	400	58
	LC1022B-48	DQ228566	Alpha-proteobacteria	188	399	58
	LC1133B-23	DQ270615	Animal	152	288	26
	LC1228B-46	DQ270625	Animal	151	286	26
	LC1133B-24	DQ270616	Animal	155	107	358
	LC1524B-50	DQ270636	Beta-proteobacteria	165	395	354
	LC1537B-16	DQ270638	Beta-proteobacteria	165	440	354
	LC1022B-30	DQ228559	Beta-proteobacteria	165	455	354
	LC1537B-77	DQ272585	*Chloroflexus*	181	174	361
	LC1231B-173	DQ228575	*Chloroflexus*	179	256	202
	LC1408B-77	DQ270634	CFB	361	442	65
	LC1446B-1	DQ270658	CFB	362	161	68
	LC1524B-89	DQ270637	CFB	376	458	351
	LC1228B-138	DQ270654	CFB	243	50	70
	LC1133B-32	DQ270641	CFB	368	50	70
	LC1022B-31	DQ228583	CFB	235	441	57
	LC1228B-98	DQ270651	*Desulfotomaculum*	270	131*	77*
	LC1537B-22	DQ270639	*Desulfotomaculum*	225	130	26
	LC1404B-6	DQ270655	Epsilon-proteobacteria	769	431	355
	LC1133B-68	DQ270645	Epsilon-proteobacteria	767	431	355
	LC1228B-116	DQ270653	Epsilon-proteobacteria	767	431	355
	LC1133B-58	DQ270643	Epsilon-proteobacteria	246	431	455
	LC1408B-26	DQ270633	Epsilon-proteobacteria	855	431	355
	LC1149B-14	DQ228557	Epsilon-proteobacteria	270	127	340
	LC1149B-70	DQ228579	Epsilon-proteobacteria	1,133	162	349
	LC1149B-104	DQ228555	Epsilon-proteobacteria	1,419	125	335
	LC1231B-176	DQ228582	Epsilon-proteobacteria	ND	436	360
	LC1149B-9	DQ228581	Epsilon-proteobacteria	ND	ND	353
	LC1149B-130	DQ228580	Epsilon-proteobacteria	ND	162	349
	LC1149B-115	DQ228556	Epsilon-proteobacteria	ND	124	264
	LC1408B-88	DQ270635	*Firmicutes*	267*	435ˆ	76*
	LC1022B-45	DQ228570	*Firmicutes*	270	515	196
	FS209A-1	DQ270594	Unc. Cren.	192	124	332
	FS197A-14	DQ270591	Marine group I	214*	284*	460
	FS243A-39	DQ270601	Marine group I	214	284	460
	FS243A-7	DQ270590	Marine group I	214*	285*	461ˆ
	FS243A-90	DQ270604	Marine group I	214	284	460
	LC1231A-51	AY505046	Marine group I	214	284	460
	FS243A-20	DQ270599	Marine group II	208	191	260
	FS243A-33	DQ270600	Marine group II	208	191	59
	FS243A-89	DQ270603	Marine group II	315	191	130
	FS243A-3	DQ270597	Marine group III	216	75	131
	LC1022B-35	DQ228568	*Firmicutes*	236	28	196
	LC1149B-139	DQ228571	*Firmicutes*	268	434	76
	LC1022B-12	DQ228569	*Firmicutes*	269	114	195

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TABLE 3—*Continued*

Domain	Clone	GenBank accession no.	Phylogenetic group	Fragment size (bp)		
				HaeIII	MspI	BstuI
	LC1022B-45	DQ228570	*Firmicutes*	270	515	196
	LC1537B-86	DQ270611	*Marinomonas*	212	449	69
	LC1228B-136	DQ270627	*Methylobacter*	365	451	350
	LC1133B-145	DQ270623	*Methylobacter*	367	453	477
	LC1133B-37	DQ270617	*Methylobacter*	163	452	168
	LC1446B-16	DQ270628	*Methylobacter*	289	459	176
	LC1133B-99	DQ270621	*Methylobacter*	230	465	70
	LC1446B-37	DQ270629	*Methylobacter*	279	449	70
	LC1133B-5	DQ270612	*Methylobacter*	282	453	168
	LC1133B-61	DQ270619	*Methylobacter*	214	451	70
	LC1133B-86	DQ270620	*Methylobacter*	161	451	70
	LC1231B-184	DQ228565	*Methylobacter*	215	452	70
	LC1408B-19	DQ270606	*Methylophaga*	182	451	352
	LC1446B-88	DQ270631	*Methylophaga*	282	453	352
	LC1231B-11	DQ228564	*Methylophaga*	208	426	26
	LC1443B-4	DQ270657	*Nitrospira*	357*	408*	520^
	LC1228B-113	DQ270652	*Nitrospira*	355	406	518
	LC1404B-28	DQ270656	*Nitrospira*	357*	408*	520^
	LC1446B-146	DQ270662	*Planctomycetes*	247	88	74
	LC1446B-77	DQ270660	*Planctomycetes*	217	150	84
	LC1231B-20	DQ228576	*Planctomycetes*	173	103	20
	LC1231B-166	DQ228578	*Planctomycetes*	220	438	217
	LC1231B-5	DQ228577	*Planctomycetes*	245	134	112
	LC1228B-91	DQ270626	Seep/hydrate	152	455	26
	LC1133B-18	DQ270614	Seep/hydrate	216	104	72
	LC1446B-28	DQ270659	Subsurface firm	297	157	40
	LC1133B-75	DQ270647	Subsurface firm	297	157	40
	LC1133B-108	DQ270649	Subsurface firm	171	151	211
	LC1446B-39	DQ270630	*Thiomicrospira*	85	355	89
	LC1537B-12	DQ270608	*Thiomicrospira*	184	455	72
	LC1408B-58	DQ270607	*Thiomicrospira*	220	457	481
	LC1537B-49	DQ270609	*Thiomicrospira*	184	454	170
	LC1133B-148	DQ270624	*Thiomicrospira*	186	432	74
	LC1133B-127	DQ270622	*Thiomicrospira*	185	455	73
	LC1149B-99	DQ228561	*Thiomicrospira*	184	455	72
	LC1022B-40	DQ228560	*Thiomicrospira*	297	255	86
	LC1537B-81	DQ270610	*Vibrio*	174	464	181

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[a] See reference 65. The predicted terminal restriction fragment size for each restriction enzyme is generated by identifying the first restriction site for each enzyme 3′ to the fluorescently tagged forward primer. Fragment sizes were experimentally verified within ±2 bp (*) or ±4 bp (^). The absence of a restriction site present in the portion of the clone that was sequenced is indicated by "ND." Unc. Eury., uncultured *Euryarchaeota*; Unc. Cren, uncultured *Crenarchaeota*; CFB, *Cytophaga-Flavobacterium-Bacteroides*.