

	Region 1 (ASF1)	Region 2 (ASF2)	Region 3 (ASR1)	Region 4 (ASR2)
ASS1 (MW364375)	C---AATA-G-----GTATGCTTAGGGAG-GAG	TAGGGAAG-AAT-----AAATGATGAAAA	TAAACGTTGGGT---A---AAAC---CAGTG	ACACAGTGGAG---GTTATCAGTTGC
SPLDaP1 (OP020448)
SPLDaP2 (OP020449)
SPLDaP3 (OP020450)
SPLDaP4 (ON921300)
SPLDaP5 (ON921301)
SPLDaP6 (ON921302)
SPLDaP7 (ON921303)
SPLDaP8 (ON921304)
SPLDaP9 (ON921305)
16SrI-A (AY389828)	T.....
16SrI-C (HQ530150)
16SrI-D (AY265206)
16SrI-E (AY265213)A..
16SrI-F (AY265211)
16SrI-H (AY265288)	T.....
16SrI-K (U96616)
16SrI-L (GU223210)
16SrI-M (AY265209)	T.....
16SrI-N (AY265205)
16SrI-O (AF268405)
16SrI-P (EU333397)	T.....
16SrI-Q (AY034089)
16SrI-R (KP662136)
16SrI-S (KX691443)
16SrI-T (FJ914639)
16SrI-U (FJ914650)
16SrI-V (JX857822)
16SrII-A (JX403944)	TTA.TA.....TA.....G.	CGA.....A.....GCAA.....CG.	..GT..C.....T.T.....G..A	T.TC.....C.....GAAA
16SrIII-A (JN903385)	TTTGAA.....A.....G.	..A.....A.....GA.....	..GT..C.....A.....CT.....G..A	T.T.A.....C.....GGAA
16SrIV-A (KX982668)	TTTCGGA.....A.....G.	..GAA.....AC.....AG.....	..GT..C.....G..T.....CT.....G..A	T.T.....GGAT
16SrV-A (AY197658)	TTTCGGAG.....AA.....G.	..GAA.....A.....A.....	..GT..C.....G.....CT.....G..A	T.T.....GG.A
16SrVI-A (AF409070)	TTACGA.....AA.....G.	..GAA.....A.....G.A.....	..GT..C.....G..TA.....CT.....G..A	T.T.....GG.A
16SrVII-A (AF105317)	TTTCGAA.....AA.T.....	..GAA.....A.....A.....	..GT..C.....A..TA.....CT.....G..A	T.T.....GG.A
16SrVIII-A (AF248956)	TAA..AA.....AA.....G.	..GAA.....A.....A.....	..GT..CA..G..TA.....CT.....TG..A	T.T.A.....GG.A
16SrIX-A (KJ817873)	TTTCG.A.....A.....G.	..GAAA.....A.....A.....	..GT..C.....TTC..G.CT.....G..A	T.T.A.A.....GAAT
16SrX-A (AF248958)	A...AG.....AA.A.T..G.	..AA.....A.....A.....	..GT.....T.....C.....G	T.T.....GG.A
16SrXI-A (AB052873)	TTTCGAA.....A.....G.	..GAA.....A.....A.....	..GT..C.....G.....CT.....G..A	T.T.....GG.A
16SrXII (AY739654)A.....G.	..A.....A.....T.....	..GT.....A.....	T.....GAAG
16SrXIII-A (AF248960)A.....G.	..A.....A.....G.....	..G.....T.....	T.....GTTG
16SrXIV-A (AJ550984)	TTTCG.A.....A.....G.	..GAA.....A.....A.....	..GT..C.....G.....CT.....G..A	T.T.....GG.A
16SrXV-A (AF147708)	TTTCGGA.....AA.....G.	..GAA.....A.....A.TA.....	..GT..C.....G..TT.....CT.....G..A	T.T.....GG.A
16SrXVI-A (AY725228)	TTTCGGAG.....AA.....G.	C.AA.....A.....GCAA.....CG.	..GT..C.....TC.....G..A	T.TC.....GAAA
16SrXVII-A (AY725234)	T.A.T.....GT.A.....G.	..A.....A.....GA.....	..GT.....A.....	T.....GAAG
16SrXVIII-A (DQ174122)ATG.....A.....	..A.....A.....G..G..AA.T	..GT.....A.....	T.....GAAG
16SrXIX-A (AB054986)AAC.A.....	..A.....A.....G.....	..GT..C.....TTC..GGCT.....G..A	T.T.A.A.....GAAT
16SrXX-A (KP851770)	T.AG.T.....TT..G.....	..GAAA.....A.....A.....	..GT.....T.....C.....C	T.T.....GTTG
16SrXXI-A (AJ310849)	TTTCG.A.....AA.....G.	..GAA.....A.....G..G.....TTTG	..GT..C.....G..TTA.....CT.....G..A	T.T.....GG.A
16SrXXII-A (KF751387)	TTTCGGA.....AA.....G.	..GAA.....A.....G..G.....	..GT.....T.....	T.....GTTG
16SrXXIII (AY083605)	TTTG.A.....AA.....G.	..GAA.....A.....CA.....	..GT..C.....AG.....C.....TT.....G..A	T.T.C.....GG.A
16SrXXIV-A (AF509322)	TTTCG.A.....AA.A.A..G.	..GAA.....A.....GA.....	..GT..C.....GTTA.....GCT.....G..A	T.T.A.....AAAT
16SrXXV-A (AF521672)	TTT.T.....A.....G.	..A.....A.....TA.....	..GT..CA.....TC.....T..A	T.T.A.C.....C.C..GAAA
16SrXXVI-A (AJ539179)	TTT.T.....A.....G.	..A.....A.....TTG.....	..GT.....T.....C.....	T.....GA.T
16SrXXIX-A (EF666051)	A.A.....AA.A.T..G.	..GAA.....A.....TA.....	..GT..C.....G..TT.....CT.....G..A	T.T.....C.G..G.A
16SrXXX-A (FJ432664)	TTTCGGA.....AA.....G.	..AA.....A.....	..GT.....T.....	T.T.....GCT.....GG.A
16SrXXXI-A (HQ225630)	TTTCGGA.....AA.....G.	C.T.....A.CG.CTTGTG.GAG.A.ACTG	..GGT.....A..GGTTTCGAT..C.....CTTG.....	T.GG.CTTTC..CTTCGGGACAGGG.A
16SrXXXII-A (EU371934)	TGA.TTT.TTCAGGGCTGTCA.....TG..T..GA	CT.T.....A.CA.AGCCTGTGAG..AA.G	..GGT.....GGGTAC..C.C.....CT.....	T.G...TTCC..CTTCGGGGCAGCG.T
16SrXXXIII-A (AY135523)	.GCT.....TCA..GTCA..T..GA	CT.T.....A.CA.AGTGTG.GAAGA.AACG	..GGT.....GGGTAC..C.C.....CT.....	T.GTCCCTCC..CTTCGGGGCAGCG.T
NSQ1	GGA.....TCA.....A..GT	A...A.C.A.A.....	..GGT..G..TCTCAAC..C..GAGAT.C.C.	T.G.T.TCC..TTTCGGGT..CGTA
NSQ2	GGA.....TCA.....A..GT	A...A.C.A.A.....	..GGT..A..AGGTATCGACCC..TT.T...	TGGTTCCTCTTC.TTCGGAAGCCAGAA
NSQ3	.TACATGTAA.....GC..TCA..GAA.A..G.	C.T.....C.AA.GGCCTCTTCGCAATAGTG	..GGT.....GGGTAC..C.C.....CT.....	TGAGCCTTCC.C.TTCGGGGCAGCG.T
NSQ4	.GCT.....CCG..GTTC..T..GA	C.T.....A.CA.AGCCTGTGAG..AA.G	..GGT.....GGGTAC..C.C.....CT.....	T.G..CTTTC.C.TTCGGGGCAGCG.T
NSQ5	.GCA.T.....CTGTCA.....T..GA	CT.T.....A.CA.AGTGTG.GAAGA.AATG	..GGT..G..TCTCAAC..C..GAGAT.C.C.	TG.G...TCC..TTTCGGGT..CGTA
NSQ6	.GCT.....TCA..GTTA..T..GA	CT.T..C.A..C.AGTGCGTGAG..AA.G	..GGT.....GGGTAC..C.C.....CT.....	T.G...TCC..TTTCGGGT..CGTA
NSQ7	.GCC.....TCA..GTTA..T..GA	CT.T..C.A.CA.AGCCTGTGAG.AAAATG	..GGT.....GGGTAC..C.C.....CT.....	T.G...TTCC.C.TTCGGGGCAGCG.T
NSQ8	.GCC.....TCA--GTCA..T..GA			
NSQ9				
NSQ10				
NSQ11				

Figure S1. Alignment of 16S rRNA gene nucleotide sequences from 10 SPLDaP (16SrI-B) (ASS1, SPLDaP1 to SPLDaP9), 18 subgroups of 16SrI (-A,-C to -V), 30 representative 16Sr groups (16SrII to 16SrXXXIII), as well as 11 non-target bacterial species (NSQ1- NSQ11) amplified from the sisal in the 5'-to-3' direction, and four regions (1-4) of sequence polymorphism were trimmed. The primers ASR1 and ASR2 is the reverse compliment to the region (3, 4) highlighted in Figure S1. '----' represented spacer sequence, '...' represented same sequence as target primer.