

Table S1. The 16S rRNA gene sequences content and similarity for the strains *P. distincta* 16-SW-7, *P. distincta* ATCC 700518^T, *P. distincta* KMM 3548^T, and *P. arctica* A 37-1-2^T (from the alignment on query gene of the strain 16-SW-7 under the locus_tag FFU37_04590)

Genome Name	NCBI Homolog 16S rRNA (Locus_tag)	Identity %	Genome ID	Chromosome (Contig)/ Length	Coordinates
<i>Pseudoalteromonas distincta</i> 16-SW-7	FFU37_04590	100.00	CP040558	L1/3735685	1023946..1025481
	FFU37_00210	100.00	CP040558	L1/ 3735685	48439..49974
	FFU37_18380	99.94	CP040559	S1/795760	375599..377134
	FFU37_15325	99.94	CP040558	L1/3735685	3416198..3417733
	FFU37_14755	99.94	CP040558	L1/3735685	3277653..3279188
	FFU37_15610	99.87	CP040558	L1/3735685	3477632..3479167
	FFU37_14215	99.87	CP040558	L1/3735685	3172769..3174304
	FFU37_00060	99.87	CP040558	L1/3735685	16934..18469
<i>Pseudoalteromonas arctica</i> A 37-1-2 ^T	PARC_bR026	100.00	CP011026	Chr II/ 783876	192599..194122
	PARC_aR001	99.61	CP011025	Chr I/ 3840834	36983..38506
	PARC_aR004	99.67	CP011025	Chr I/ 3840834	313581..315104
	PARC_aR007	99.28	CP011025	Chr I/ 3840834	345719..347242
	PARC_aR012	99.34	CP011025	Chr I/ 3840834	2483422..2484945
	PARC_aR016	99.67	CP011025	Chr I/ 3840834	3068857..3070380
	PARC_aR019	99.28	CP011025	Chr I/ 3840834	3589860..3591383
	PARC_aR022	99.67	CP011025	Chr I/ 3840834	3690377..3691900
	PARC_aR025	99.67	CP011025	Chr I/ 3840834	3815090..3816613
<i>Pseudoalteromonas distincta</i> KMM 3548 (= <i>P. paragorgicola</i>)	PPAR_aR004	99.87	AQHE01000014	14/ 767276	187495..189018
	PPAR_aR007	100.00	AQHE01000021	21/ 300025	298305..299828
<i>Pseudoalteromonas distincta</i> 2-2A-13	NQU47_RS19790	100.00	JANIHL010000061	Contig 61/1771	192..1727
<i>Pseudoalteromonas distincta</i> ATCC 700518 ^T	QT16_19995	99.94	JWIG01000030	C30/ 180150	175393..176935