

Supplementary Online Material

(SOM)

Improved 16S rRNA-Targeted Probe Set for Analysis of Sulfate-Reducing
Bacteria by Fluorescence In Situ Hybridization

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SOM-Table 1. Previously published 16S rRNA-targeted oligonucleotide probes for the detection of different taxa of SRMs (and related organisms) by FISH. Probes are roughly ordered according to the taxonomy of the intended target organisms; higher taxa are listed first. See probeBase at <http://www.microbial-ecology.net/probebase/> for further probe details (Loy et al., 2007). This table is a considerably up-dated and extended version of a table published by Stahl et al., 2007.

probeBase accession number	Probe name	FA [%] for standard FISH ^a	FA [%] for CARD-FISH ^a	Specificity ^b	Sequence 5'-3'	Probe evaluation with RDP II probe match ^c							
						RDP II target taxon	Coverage of target taxon ^d	Hits in target taxon ^e	Total non-target hits ^f	Major non-target taxa	Coverage of non-target taxon ^d	Hits in non-target taxon ^e	Reference
pB-00300	SRB385 (SRB)	35	N. D.	Most <i>Desulfovibrionales</i> and other Bacteria	CGGCGTCGCTGCGTCAGG	class <i>Deltaproteobacteria</i>	33.1%	1991	4135	phylum <i>Nitrospira</i>	42.8%	270	Amann et al., 1990; Manz et al., 1998
						order <i>Desulfovibrionales</i>	73.3%	995	5131	phylum <i>Firmicutes</i>	0.9%	455	
						order <i>Desulfobacterales</i>	40.6%	615	5511	phylum <i>Actinobacteria</i>	9.5%	2070	
						order <i>Bdellovibrionales</i>	8.9%	16	6110	phylum <i>Acidobacteria</i>	2.0%	39	
						order <i>Myxococcales</i>	16.9%	154	5972	phylum <i>Gemmatimonadetes</i>	19.2%	85	
						unclassified <i>Deltaproteobacteria</i>	20.5%	191	5935	phylum <i>Genera incertae sedis_OP10</i>	21.3%	19	
pB-00301	SRB385Db	30	N. D.	<i>Desulfobacterales</i> , <i>Desulfuromonales</i> , <i>Syntrophobacterales</i> , <i>Myxococcales</i> , and other Bacteria	CGGCGTTGCTGCGTCAGG	class <i>Deltaproteobacteria</i>	37.5%	2256	4484	class <i>Epsilonproteobacteria</i>	6.5%	152	Rabus et al., 1996
						order <i>Desulfovibrionales</i>	6.4%	87	6653	order <i>Campylobacteriales</i>	6.7%	151	
						order <i>Desulfobacterales</i>	49.0%	743	5997	phylum <i>Chloroflexi</i>	4.2%	56	
						order <i>Desulfuromonales</i>	69.2%	413	6327	phylum <i>Nitrospira</i>	18.4%	116	
						order <i>Syntrophobacterales</i>	57.3%	283	6457	phylum <i>Chlorobi</i>	78.5%	161	
						order <i>Bdellovibrionales</i>	17.3%	31	6709	phylum <i>Firmicutes</i>	1.8%	930	
						order <i>Myxococcales</i>	43.1%	392	6348	phylum <i>Actinobacteria</i>	3.7%	815	
						unclassified <i>Deltaproteobacteria</i>	32.9%	307	6433	phylum <i>Acidobacteria</i>	69.8%	1379	
pB-00084	DSS658	60	80	<i>Desulfobacteraceae</i> and other Bacteria	TCCACTTCCTCTCCCAT	family <i>Desulfobacteraceae</i>	55.6%	606	108				Manz et al., 1998; Musmann et al., 2005
						genus <i>Desulfatibacillum</i>	66.7%	10	704				
						genus <i>Desulfococcus</i>	77.8%	7	707				
						genus <i>Desulfofaba</i>	82.4%	14	700				
						genus <i>Desulfofrigus</i>	100.0%	14	700				
						genus <i>Desulfonema</i>	30.9%	17	697				
						genus <i>Desulfosarcina</i>	91.5%	75	639				
						unclassified <i>Desulfobacteraceae</i>	65.2%	468	246				
						pB-00009	804 (Dsb804)	10	N. D.	Some <i>Desulfobacteraceae</i>	CAACGTTTACTGCGTGGA	family <i>Desulfobacteraceae</i>	
genus <i>Desulfobacter</i>	88.2%	30	335										
genus <i>Desulfatibacillum</i>	60.0%	9	356										
genus <i>Desulfobacterium</i>	18.3%	15	350										
genus <i>Desulfobotulus</i>	100.0%	1	364										
genus <i>Desulfocella</i>	60.0%	3	362										
genus <i>Desulfococcus</i>	62.5%	5	360										
genus <i>Desulfofaba</i>	58.8%	10	355										
genus <i>Desulfofrigus</i>	92.9%	13	352										
genus <i>Desulfonema</i>	30.9%	17	348										
genus <i>Desulforegula</i>	100.0%	2	363										
genus <i>Desulfosarcina</i>	89.6%	69	296										

pB-00075	DSB985	20	N. D.	<i>Desulfobacter</i> , <i>Desulfobacula</i> , <i>Desulfospira</i> , and <i>Desulfotignum</i>	CACAGGATGTCAAACCCAG	unclassified_ <i>Desulfobacteraceae</i> family <i>Desulfobacteraceae</i> genus <i>Desulfobacter</i> genus <i>Desulfobacula</i> genus <i>Desulfospira</i> genus <i>Desulfotignum</i>	25.2% 14.3% 100.0% 81.1% 75.0% 100.0%	177 101 22 43 6 8	188 4 83 62 99 97	Manz et al., 1998
pB-00073	129 (DSB129)	15	N. D.	Most <i>Desulfobacter</i>	CAGGCTTGAAGGCAGATT	family <i>Desulfobacteraceae</i> genus <i>Desulfobacter</i>	2.6% 69.6%	16 16	1 1	Devereux et al., 1992; Ramsing et al., 1996
pB-00069	Dsb220 (desulfobacter)	N. D.	N. D.	Most <i>Desulfobacter</i>	TMCGCARACTCATCCCCAAA	family <i>Desulfobacteraceae</i> genus <i>Desulfobacter</i>	2.6% 69.6%	17 16	0 1	Amann et al., 1990
pB-00062	221 (DBM221)	35	N. D.	<i>Desulfobacterium vacuolatum</i> , <i>D. niacini</i> , <i>D. autotrophicum</i>	TGCGCGGACTCATCTTCAAA	family <i>Desulfobacteraceae</i> genus <i>Desulfobacterium</i>	0.9% 9.6%	6 5	0 1	Devereux et al., 1992; Manz et al., 1998
pB-00083	DSS225	40	80	<i>Desulfosarcina</i> and many other <i>Desulfobacteraceae</i>	TGGTACGCGGGCTCATCT	family <i>Desulfobacteraceae</i> genus <i>Desulfonema</i> genus <i>Desulfosarcina</i> unclassified_ <i>Desulfobacteraceae</i>	27.4% 25.5% 77.4% 33.8%	180 13 24 142	15 182 171 53	Mussmann et al., 2005; Ravenschlag et al., 2000
pB-00010	814 (Dscoc814)	10	N. D.	Few <i>Desulfobacteraceae</i>	ACCTAGTGATCAACGTTT	family <i>Desulfobacteraceae</i> genus <i>Desulfatibacillum</i> genus <i>Desulfobotulus</i> genus <i>Desulfococcus</i> genus <i>Desulfonema</i> genus <i>Desulfosarcina</i>	9.2% 60.0% 100.0% 62.5% 23.6% 26.7%	96 9 1 5 13 20	4 91 99 95 87 80	Devereux et al., 1992; Ramsing et al., 1996; Icgen et al., 2006
pB-00051	cl81-644	25	55	Few <i>Desulfobacteraceae</i>	CCCATACTCAAGTCCCTT	family <i>Desulfobacteraceae</i> genus <i>Desulfonema</i> unclassified_ <i>Desulfobacteraceae</i>	7.3% 7.3% 10.4%	80 4 75	1 77 6	Mussmann et al., 2005; Ravenschlag et al., 2000
pB-01307	DSS449	N. D.	45	Some <i>Desulfosarcina</i>	TTAGCATACTGCAGGTTC	genus <i>Desulfosarcina</i>	35.6%	31	1	Mussmann et al., 2005
pB-01308	DSS138	N. D.	50	Few <i>Desulfobacteraceae</i>	CGGGTTATCCCGATTCCG	family <i>Desulfobacteraceae</i> genus <i>Desulfonema</i> unclassified_ <i>Desulfobacteraceae</i>	2.4% 4.0% 3.3%	15 2 13	0 13 2	Mussmann et al., 2005
pB-00078	DSC193	35	N. D.	<i>Desulfosarcina variabilis</i>	AGGCCACCCTTGATCCAA	genus <i>Desulfosarcina</i>	74.2%	23	0	Ravenschlag et al., 2000
pB-00080	DSF672	45	70	<i>Desulfofrigus</i> , <i>Desulfofaba gelida</i> , <i>Desulfomusa hansenii</i>	CCTCTACACCTGGAATTCC	family <i>Desulfobacteraceae</i>	1.8%	20	32	Mussmann et al., 2005; Ravenschlag et al., 2000
pB-00063	DCC209	25	N. D.	<i>Desulfococcus multivorans</i>	CCCAAACGGTAGCTTCCT	genus <i>Desulfococcus</i>	66.7%	4	0	Ravenschlag et al., 2000
pB-00071	DNMA657	30	N. D.	Some <i>Desulfonema</i>	TTCCGCTTCCCTCTCCCATA	family <i>Desulfobacteraceae</i> genus <i>Desulfonema</i> unclassified_ <i>Desulfobacteraceae</i>	7.0% 41.8% 7.3%	76 23 52	26 79 50	Fukui et al., 1999
pB-00899	OalgDEL136	N. D.	N. D.	Deltaproteobacterial symbiont of <i>Olavius</i>	GTTATCCCCGACTCGGGG	family <i>Desulfobacteraceae</i> genus <i>Desulfonema</i>	0.3% 2.0%	2 1	0 1	Dubilier et al., 2001

pB-01317	OcraDEL1	20	N. D.	<i>algarvensis</i> Deltaproteobacterial symbiont 1 of <i>Olavius crassitunicatus</i>	CGTCAGCACCTGGTGATA	unclassified_ <i>Desulfobacteraceae</i> unclassified_ <i>Desulfobacteraceae</i>	0.2% 0.1%	1 1	1 0	Blazejak et al., 2005
pB-01318	OcraDEL2	20	N. D.	Deltaproteobacterial symbiont 2 of <i>Olavius crassitunicatus</i>	CATGCAGATTCTTCCCAC	unclassified_ <i>Desulfobacteraceae</i>	0.1%	1	0	Blazejak et al., 2005
pB-00081	DSMA488	60	N. D.	<i>Desulfarculus baarsii</i> , <i>Desulfomonile tiedjei</i> , and <i>Syntrophus</i>	GCCGGTGCTTCCTTTGGCGG	genus <i>Desulfarculus</i> genus <i>Syntrophus</i> genus <i>Desulfomonile</i>	33.3% 58.5% 14.0%	2 31 6	47 18 43	Manz et al., 1998
pB-01116	DsmA455	20	N. D.	<i>Desulfomonile</i> -related Lake Cadagno clones 618, 624, 626, and 651	AGTTCYCTGAGCTATTTACTCA AAGA	genus <i>Desulfomonile</i>	11.6%	5	0	Tonolla et al., 2005
pB-01117	DsmB455	20	N. D.	<i>Desulfomonile</i> -related Lake Cadagno clone 650	AGATCCCTGAGCTATTTACTCA AGGA	genus <i>Desulfomonile</i>	2.3%	1	0	Tonolla et al., 2005
pB-01333	DSBA1017	30	N. D.	<i>Desulfobacca acetoxidans</i>	GTTGCCAGGCACCCCAT	genus <i>Desulfobacca</i>	6.7%	2	0	Dar et al., 2007
pB-00082	DSR651	35	70	Some <i>Desulfobulbaceae</i>	CCCCCTCCAGTACTCAAG	family <i>Desulfobulbaceae</i> genus <i>Desulfocapsa</i> genus <i>Desulfofustis</i> genus <i>Desulforhopalus</i> genus <i>Desulfotalea</i> unclassified_ <i>Desulfobulbaceae</i>	39.0% 43.0% 80.0% 70.9% 28.6% 45.3%	297 37 4 83 8 165	11 271 304 225 300 143	Manz et al., 1998; Musmann et al., 2005
pB-00306	Sval428	25	N. D.	Some <i>Desulfobulbaceae</i> (excluding most <i>Desulfobulbus</i>)	CCATCTGACAGGATTTTAC	family <i>Desulfobulbaceae</i> genus <i>Desulfocapsa</i> genus <i>Desulfofustis</i> genus <i>Desulforhopalus</i> genus <i>Desulfotalea</i> unclassified_ <i>Desulfobulbaceae</i>	43.8% 32.9% 100.0% 83.6% 96.4% 49.4%	324 27 6 92 27 172	4 301 322 236 301 156	Musmann et al., 2005; Sahm et al., 1999
pB-00061	660 (DBB660)	60	N. D.	Some <i>Desulfobulbus</i>	GAATTCACCTTCCCCTCTG	family <i>Desulfobulbaceae</i> genus <i>Desulfobulbus</i>	12.8% 59.6%	97 96	11 12	Devereux et al., 1992; Manz et al., 1998
pB-01309	DSR1256	N. D.	10	Few <i>Desulfobulbaceae</i>	ACAGGTCGCCCTGTCGCT	family <i>Desulfobulbaceae</i> genus <i>Desulfotalea</i> unclassified_ <i>Desulfobulbaceae</i>	4.0% 20.0% 7.5%	15 4 11	24 35 28	Musmann et al., 2005
pB-01310	Dblb1243	10	N. D.	<i>Desulfobacterium catecholicum</i> -related strains LacK1, LacK4 and LacK9	GCGTGCCCTGTCTATG	- ¹	-	-	-	Musmann et al., 2005
pB-01311	Dcap1031	10	N. D.	Few <i>Desulfocapsa</i> including strain LacK10	TGTCACCAAGCTCCTCTA	family <i>Desulfobulbaceae</i> genus <i>Desulfocapsa</i>	1.8% 9.1%	8 7	0 1	Musmann et al., 2005
pB-01312	Dblb1032	10	N. D.	<i>Desulfobacterium catecholicum</i> and related strains LacK1 and LacK9	ACCTGTCCACCGAGCTCCT	family <i>Desulfobulbaceae</i>	1.2%	5	6	Musmann et al., 2005
pB-01313	DSR186	N. D.	50	<i>Desulfobacterium catecholicum</i> and related strains LacK1 and LacK9	GCCACCTTTCCTGATAAA	family <i>Desulfobulbaceae</i>	5.5%	34	4	Musmann et al., 2005

pB-01111	DSC213	30	N. D.	<i>Desulfocapsa thiozymogenes</i>	CCTCCCTGTACGATAGCT	family <i>Desulfobulbaceae</i> genus <i>Desulfocapsa</i>	4.1% 35.1%	26 26	1 1						Tonolla et al., 2000
pB-01112	DSC441	30	N. D.	Few <i>Desulfocapsa</i>	ATTACACTTCTTCCCATCC	family <i>Desulfobulbaceae</i> genus <i>Desulfocapsa</i>	1.2% 11.0%	9 9	0 0						Tonolla et al., 2000
pB-01115	SRB441	5	N. D.	Few <i>Desulfobulbaceae</i>	CATGCACTTCTTCCACTT	family <i>Desulfobulbaceae</i>	0.5%	4	0						Tonolla et al., 2000
pB-01319	OcraDEL3	20	N. D.	Deltaproteobacterial symbiont 3 of <i>Olavius crassitunicatus</i>	TTTCATAGAGCTTCCCGG	family <i>Desulfobulbaceae</i>	0.2%	2	0						Blazejak et al., 2005
pB-00090	687 (DSV687)	15	N. D.	Most <i>Desulfovibrionales</i> (excluding <i>Lawsonia</i>) and many <i>Desulfuromonales</i>	TACGGATTTCACTCCT	class <i>Deltaproteobacteria</i> order <i>Desulfovibrionales</i> family <i>Desulfovibrionaceae</i> family <i>Desulfomicrobiaceae</i> family <i>Desulfohalobiaceae</i> family <i>Desulfonatronumaceae</i> unclassified_ <i>Desulfovibrionales</i> order <i>Desulfuromonales</i> family <i>Desulfuromonaceae</i> family <i>Geobacteraceae</i> unclassified_ <i>Desulfuromonales</i>	25.1% 90.1% 93.0% 90.1% 58.5% 85.7% 45.8% 54.8% 17.2% 89.3% 54.0%	1585 1270 1109 109 24 6 22 301 41 233 27	245 560 721 1721 1806 1824 1808 1529 1789 1597 1803	phylum Genera_incertae_sedis_TM7	79.0%	229		Devereux et al., 1992; Ramsing et al., 1996	
pB-01043	DSV (DSV321)	N. D.	N. D.	Some <i>Desulfovibrionaceae</i> , <i>Desulfomicrobiaceae</i> , <i>Desulfohalobiaceae</i> , and other <i>Bacteria</i>	TGGGCCGTGTTNCAGT	class <i>Deltaproteobacteria</i> order <i>Desulfovibrionales</i> order <i>Desulfarcales</i>	6.4% 25.4% 50.0%	356 318 4	247 285 599	phylum <i>Chloroflexi</i>	1.2%	15			Küsel et al., 1999
pB-00091	DSV698 [§]	35	40	Some <i>Desulfovibrio</i> , <i>Bilophila wadsworthia</i> , and <i>Lawsonia intracellularis</i>	GTTCTCCAGATATCTACGG	class <i>Deltaproteobacteria</i> order <i>Desulfovibrionales</i> family <i>Desulfovibrionaceae</i> genus <i>Desulfovibrio</i> genus <i>Lawsonia</i> unclassified_ <i>Desulfovibrionaceae</i> family <i>Desulfohalobiaceae</i> genus <i>Desulfohalobium</i>	13.5% 60.8% 71.2% 48.9% 92.3% 49.1% 9.5% 33.3%	856 856 849 257 566 26 4 1	7 7 14 606 297 837 859 862						Manz et al., 1998; Mussmann et al., 2005
pB-00086	DSV1292	35	N. D.	Some <i>Desulfovibrio</i> and <i>Bilophila wadsworthia</i>	CAATCCGGACTGGGACGC	class <i>Deltaproteobacteria</i> order <i>Desulfovibrionales</i> family <i>Desulfovibrionaceae</i> genus <i>Desulfovibrio</i> unclassified_ <i>Desulfovibrionaceae</i>	3.1% 10.6% 11.8% 24.7% 55.1%	126 126 124 97 27	1 1 3 30 100						Manz et al., 1998
pB-00088	DSV407	50	N. D.	Few <i>Desulfovibrionaceae</i> , <i>Desulfohalobiaceae</i> , and <i>Desulfonatronumaceae</i>	CCGAAGGCCTTCTTCCCT	order <i>Desulfovibrionales</i> family <i>Desulfovibrionaceae</i> genus <i>Desulfovibrio</i> family <i>Desulfohalobiaceae</i> genus <i>Desulfohalobium</i> genus <i>Desulfonauticus</i> genus <i>Desulfothermus</i> unclassified_ <i>Desulfohalobiaceae</i> family <i>Desulfonatronumaceae</i> genus <i>Desulfonatronum</i>	4.8% 4.6% 10.7% 18.2% 33.3% 100.0% 50.0% 18.8% 62.5% 62.5%	67 55 55 6 1 1 1 3 5 5	293 305 305 354 359 359 359 357 355 355					Manz et al., 1998	

pB-00079	DSD131	20	N. D.	" <i>Desulfovibrio aestuarii</i> "	CCCGATCGTCTGGGCAGG	genus <i>Desulfovibrio</i>	0.2%	1	0	Manz et al., 1998
pB-01314	DSV185	10	N. D.	<i>Desulfovibrio acrylicus</i>	GCCCCCTTTCCCGTTTCC	genus <i>Desulfovibrio</i>	3.5%	14	0	Mussmann et al., 2005
pB-01315	DSV445	10	N. D.	<i>Desulfovibrio</i> strain EtOHK3	GAACCACAGTTTCTTCC	- ¹	-	-	-	Mussmann et al., 2005
pB-01316	DSV64	10	N. D.	<i>Desulfovibrio</i> strain EtOHK2	AAGAGGCCGTTCTCGCTC	genus <i>Desulfovibrio</i>	1.1%	7	0	Mussmann et al., 2005
pB-01332	DSV827	30	N. D.	Few <i>Desulfovibrio</i>	GGTCGCCCCCGACACCT	genus <i>Desulfovibrio</i>	3.2%	18	0	Dar et al., 2007
pB-00077	DSBO224	60	N. D.	<i>Desulfobotulus saporans</i> , <i>Desulfovibrio fairfieldensis</i> , and other <i>Deltaproteobacteria</i>	GGGACGCGGACTCATCCTC	family <i>Desulfovibrionaceae</i> family <i>Desulfobacteraceae</i>	0.8% 0.3%	9 2	9 16	Manz et al., 1998
pB-00087	DSV214	10	N. D.	Most <i>Desulfomicrobium</i>	CATCCTCGGACGAATGC	genus <i>Desulfomicrobium</i>	85.1%	63	0	Manz et al., 1998
pB-00097	Dtm229	15	N. D.	<i>Desulfotomaculum</i> cluster I and other <i>Firmicutes</i>	AATGGGACGCGGAYCCAT	phylum <i>Firmicutes</i> family <i>Peptococcaceae</i> genus <i>Desulfotomaculum</i> genus <i>Pelotomaculum</i> genus <i>Cryptanaerobacter</i> unclassified_ <i>Peptococcaceae</i> family <i>Thermoanaerobacteriaceae</i> genus <i>Sporotomaculum</i> genus <i>Thermacetogenium</i>	0.5% 45.4% 88.6% 70.0% 91.9% 50.0% 5.6% 83.3% 71.4%	259 161 62 7 68 24 12 5 5	17 115 214 269 208 252 264 271 271	Hristova et al., 2000
pB-00093	Dtm(bcd)230	10	N. D.	Many <i>Desulfotomaculum</i> cluster I and other <i>Firmicutes</i>	TAATGGGACGCGGACCCA	phylum <i>Firmicutes</i> family <i>Peptococcaceae</i> genus <i>Desulfotomaculum</i> genus <i>Pelotomaculum</i> genus <i>Cryptanaerobacter</i> unclassified_ <i>Peptococcaceae</i> family <i>Thermoanaerobacteriaceae</i> genus <i>Sporotomaculum</i> genus <i>Thermacetogenium</i>	0.4% 35.5% 54.3% 70.0% 89.2% 31.3% 5.1% 83.3% 57.1%	220 126 38 7 66 15 11 5 4	18 112 200 231 172 223 227 233 234	Hristova et al., 2000
pB-00067	DEM1164r	10	N. D.	<i>Desulfotomaculum</i> cluster I and other <i>Firmicutes</i>	CCTTCCTCCGTTTTGTCA	phylum <i>Firmicutes</i> class <i>Clostridia</i> order <i>Clostridiales</i> family <i>Clostridiaceae</i> genus <i>Anaerotruncus</i> genus <i>Faecalibacterium</i> genus <i>Sporobacter</i> genus <i>Acetanaerobacterium</i> genus <i>Subdoligranulum</i> unclassified_ <i>Clostridiaceae</i> family <i>Lachnospiraceae</i> genus <i>Anaerofilum</i> genus <i>Ruminococcus</i>	11.9% 20.3% 21.2% 37.4% 93.5% 98.3% 94.6% 86.2% 99.2% 32.1% 3.5% 73.3% 9.8%	4149 4149 4127 2677 187 1784 87 25 243 330 177 11 166	224 224 246 1696 4186 2589 4286 4348 4130 4043 4196 4362 4207	Imachi et al., 2006; Stubner and Meuser, 2000

						family <i>Peptococcaceae</i>	42.1%	126	4247	
						genus <i>Desulfotomaculum</i>	95.5%	64	4309	
						genus <i>Pelotomaculum</i>	50.0%	3	4370	
						genus <i>Cryptanaerobacter</i>	88.1%	37	4336	
						unclassified_ <i>Peptococcaceae</i>	35.5%	22	4351	
						family <i>Acidaminococcaceae</i>	30.7%	553	3820	
						genus <i>Papillibacter</i>	97.9%	553	3820	
						unclassified_ <i>Clostridiales</i>	15.2%	592	3781	
						order <i>Thermoanaerobacteriales</i>	2.4%	5	4368	
						family <i>Thermoanaerobacteriaceae</i>	2.5%	5	4368	
						genus <i>Sporotomaculum</i>	100.0%	5	4368	
pB-01179	Ih820 ^h	20	N. D.	<i>Desulfotomaculum</i> subcluster Ih (<i>Pelotomaculum</i> and <i>Cryptanaerobacter</i>)	ACCTCCTACACCTAGCAC	family <i>Peptococcaceae</i>	22.3%	85	11	Imachi et al., 2006
						genus <i>Pelotomaculum</i>	75.0%	9	87	
						genus <i>Cryptanaerobacter</i>	84.3%	59	37	
						unclassified_ <i>Peptococcaceae</i>	23.9%	17	79	
pB-00739	TGP690	15	N. D.	<i>Pelotomaculum</i> <i>thermopropionicum</i>	CTCAAGTCCCTCAGTTTCAA	genus <i>Pelotomaculum</i>	41.7%	5	8	Imachi et al., 2000
pB-00533	Tdesulfo848	20 – 30	N. D.	Most <i>Thermodesulfovibrio</i> and some <i>Magnetobacterium</i>	TTTCCCTTCGGCACAGAG	family <i>Nitrospiraceae</i>	13.5%	77	0	Daims et al., 2000
						genus <i>Magnetobacterium</i>	35.0%	63	14	
						genus <i>Thermodesulfovibrio</i>	53.8%	14	63	

^a FA [%]: formamide concentration in the hybridization buffer; N. D., not determined.

^b The intended specificity of the probe.

^c RDP II probe match was performed with database release 9.44 (Oct 31, 2006) containing 273,300 bacterial 16S rRNA sequences. The search for each probe was restricted to sequences of good quality with data in the respective probe binding region.

^d The percentage of sequences within the RDP II (non-)target taxon that show a full match to the probe sequence.

^e The number of sequences within the RDP II (non-)target taxon that show a full match to the probe sequence.

^f The total number of sequences outside the respective RDP II target taxon that show a full match to the probe sequence.

^g Competitor probe for DSV698 (5'-GTT CCT CCA GAT ATC TAC GC-3').

^h Competitor probe for Ih820 (5'-ACC TCC TAC ACC TAG TAC-3').

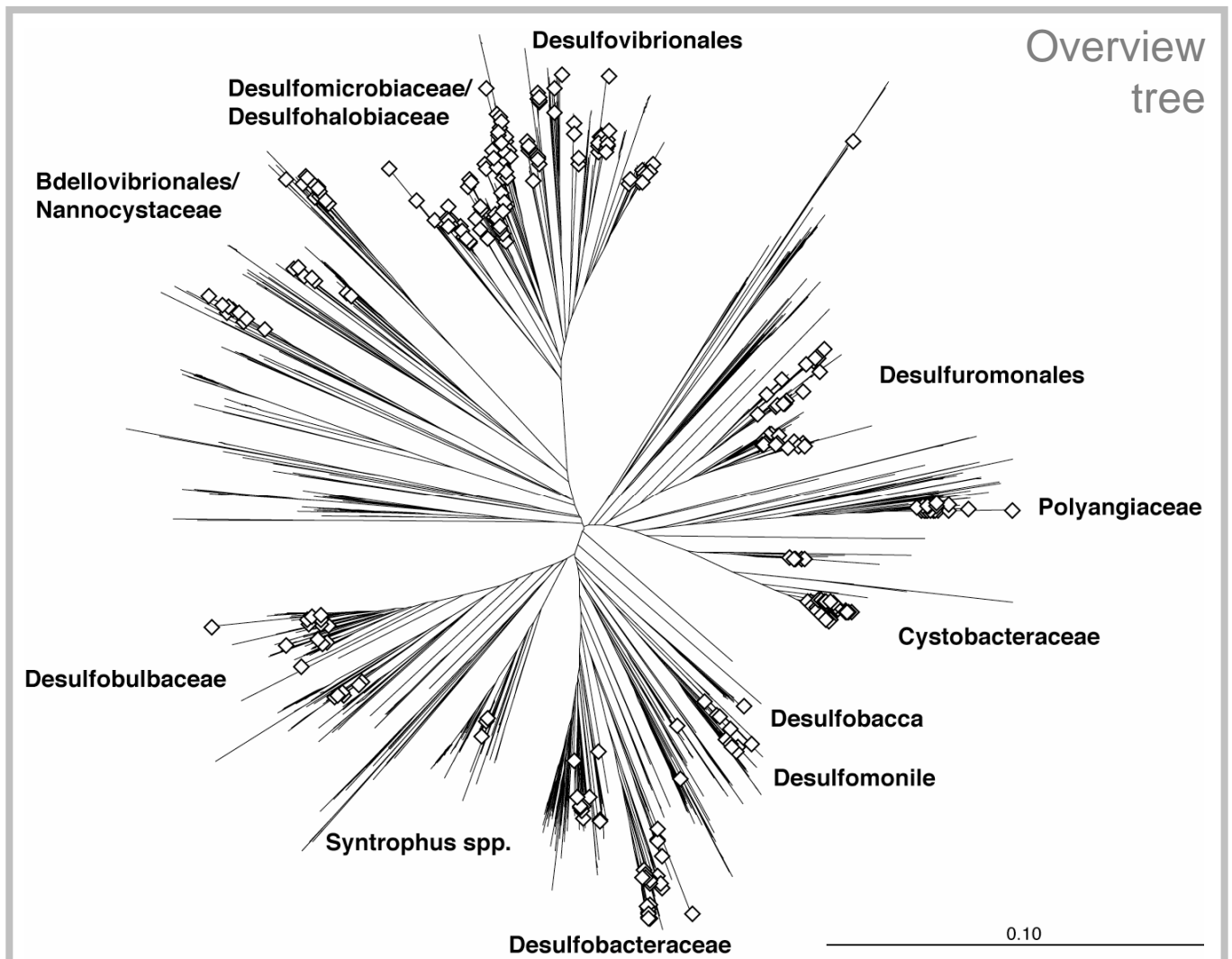
ⁱ Target sequence(s) not listed in RDP II.

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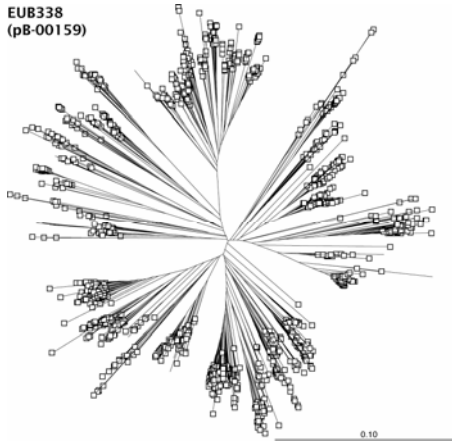
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SOM Figure 1. In silico coverage of deltaproteobacterial FISH probes as evaluated against a curated Greengenes-based ARB database for *Deltaproteobacteria*. The neighbor joining tree was constructed with 1633 deltaproteobacterial 16S rRNA sequences applying a 50% maximum frequency filter. The bar indicates 10% estimated sequence divergence. Putative chimeric sequences and sequences without complete, unambiguous target-regions for the probes tested were removed from the dataset. The box shows an overview tree with diamonds marking named species and isolates identified to genus level (527 of 1633 sequences). Unmarked branches in the overview tree represent environmental clones. In each small tree, squares indicate sequences that perfectly match the respective probe. Trees are ordered according to Table 1 and SOM Table 1. Probes with no perfectly-matched sequences in the curated deltaproteobacterial database are not shown.



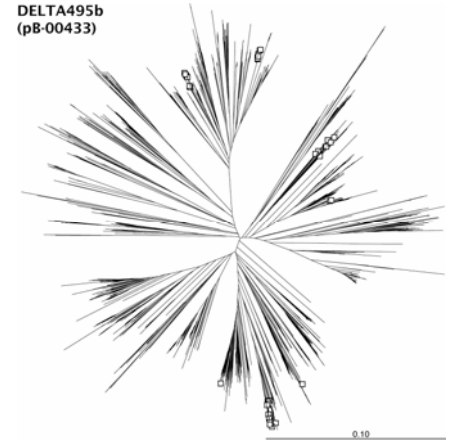
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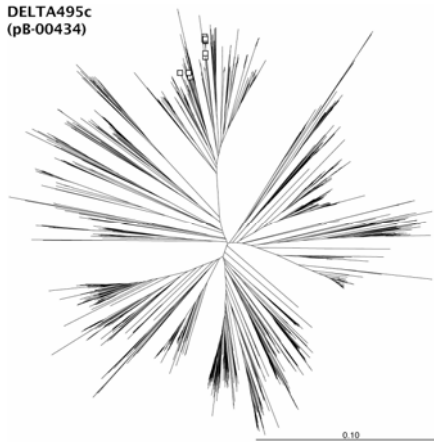
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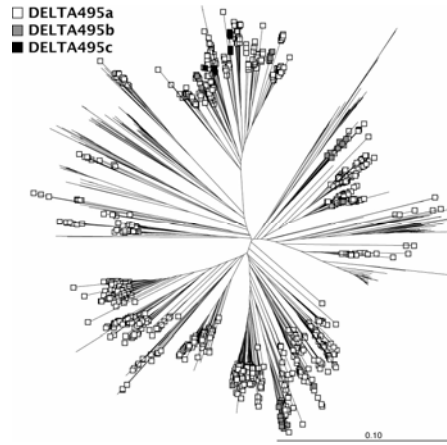
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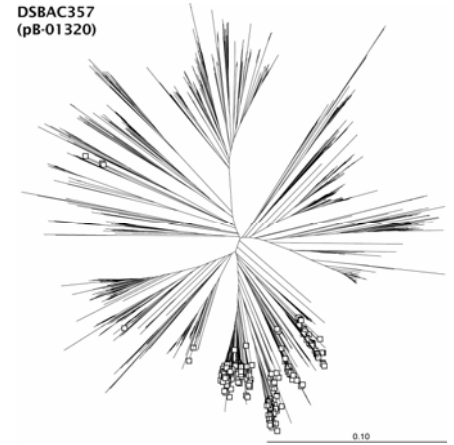
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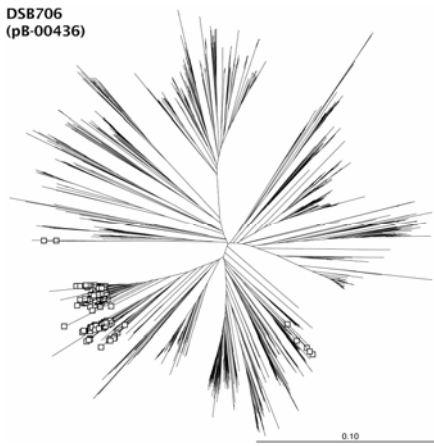
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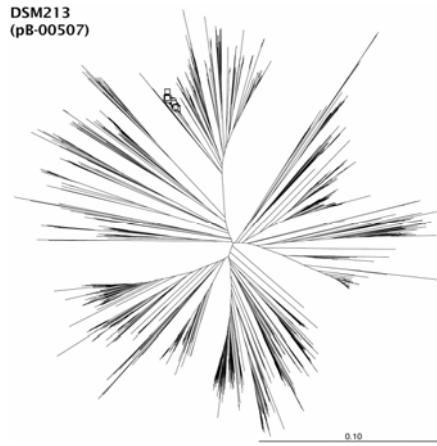
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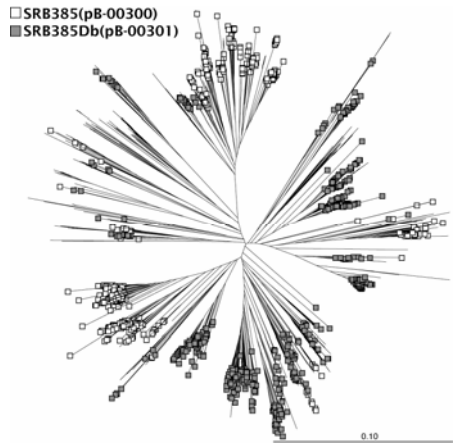
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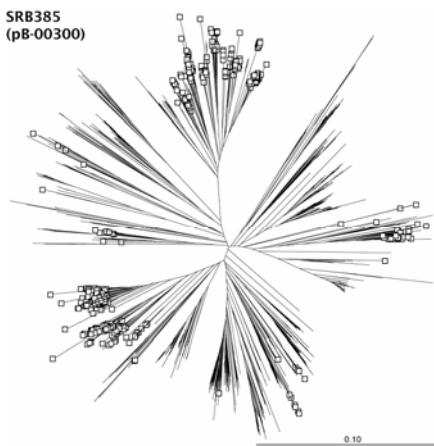
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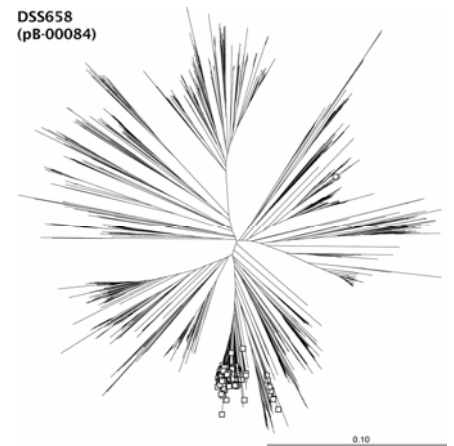
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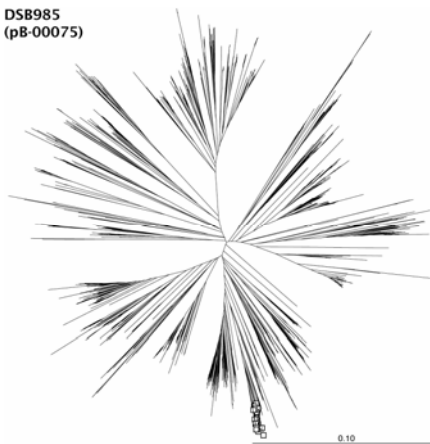
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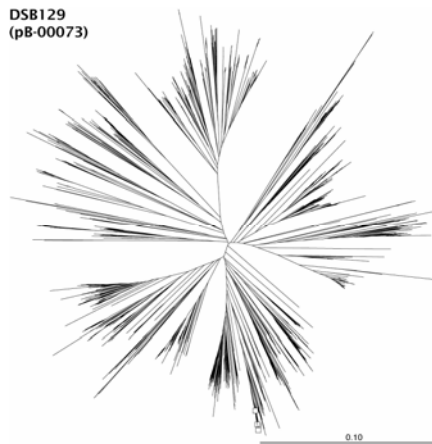
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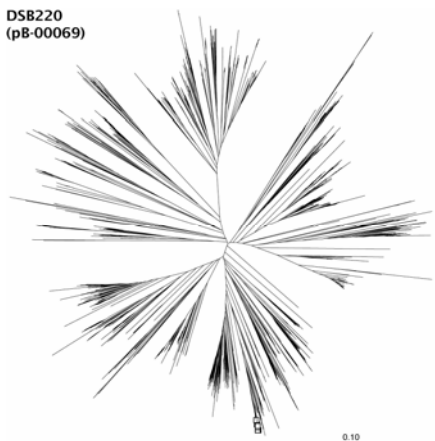
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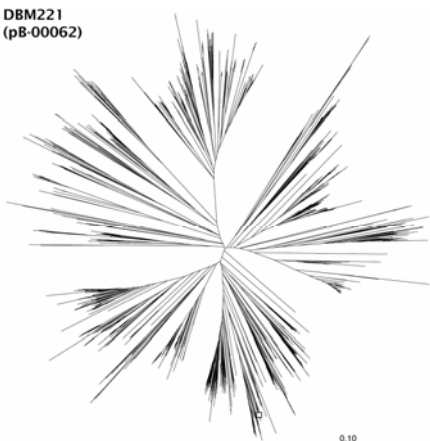
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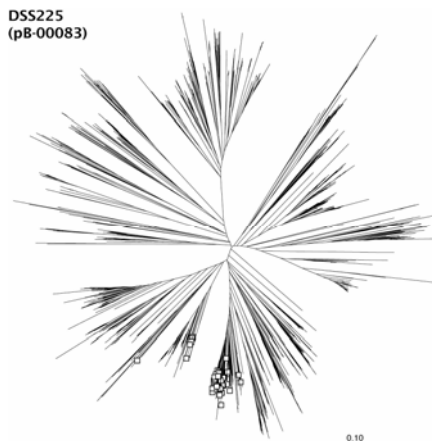
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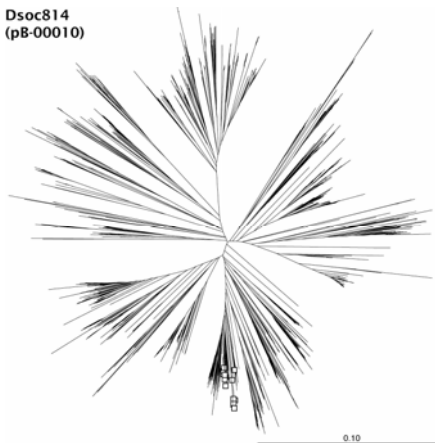
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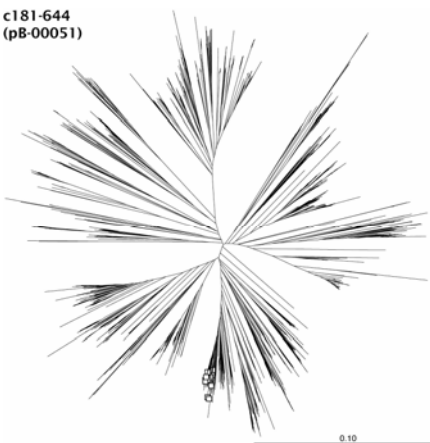
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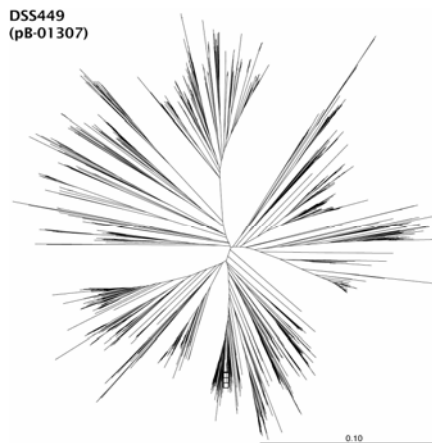
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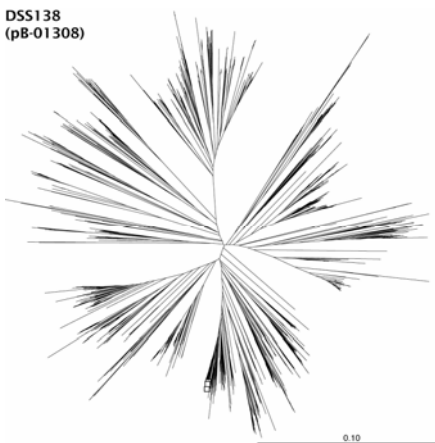
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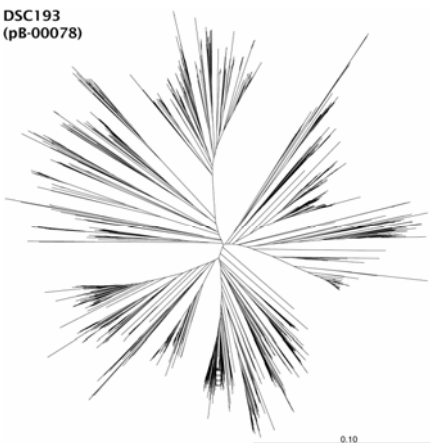
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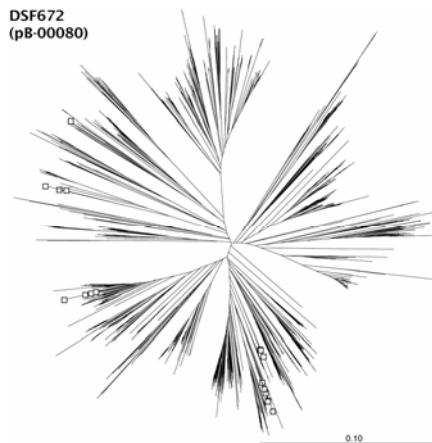
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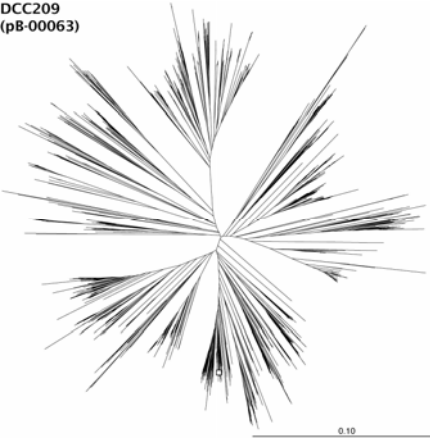
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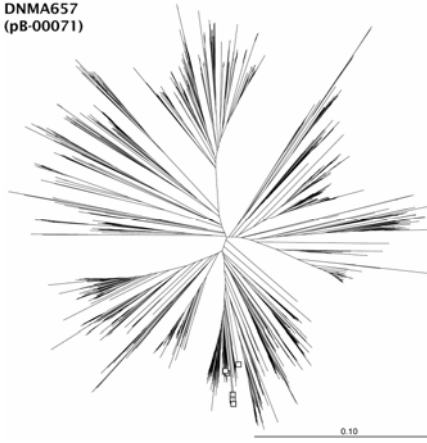
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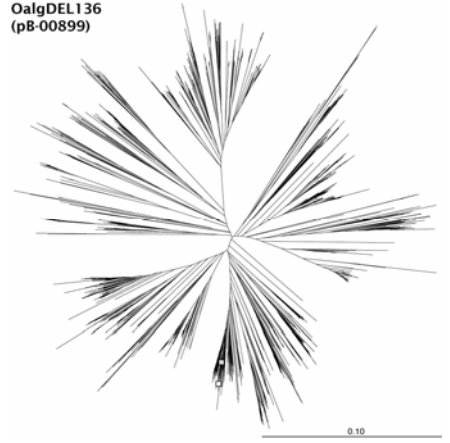
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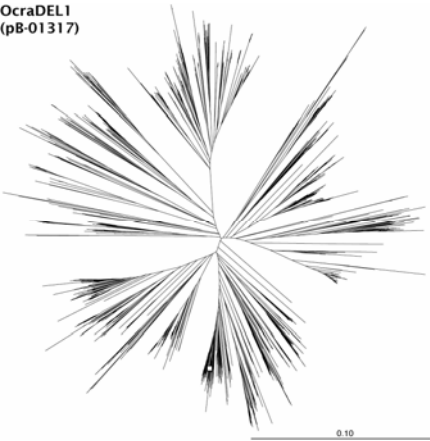
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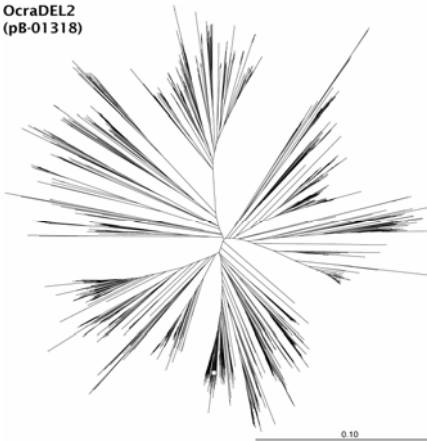
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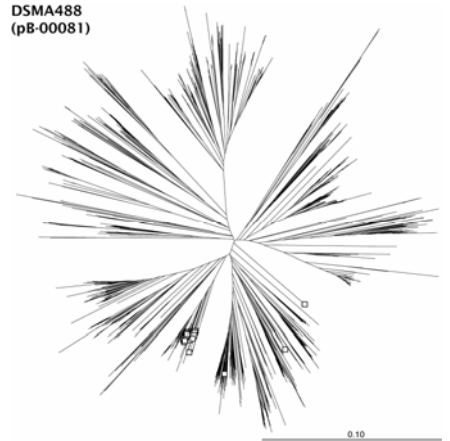
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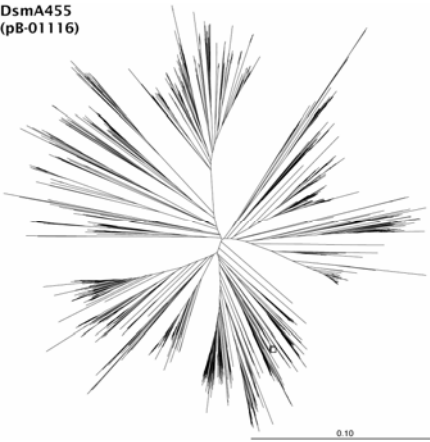
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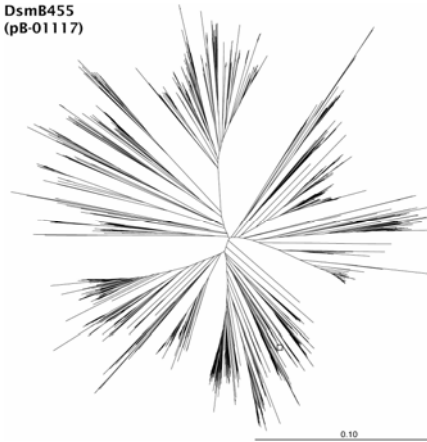
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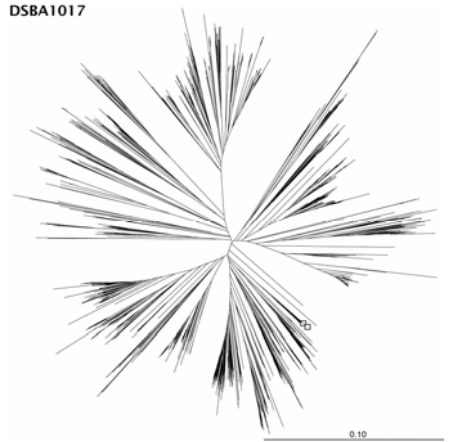
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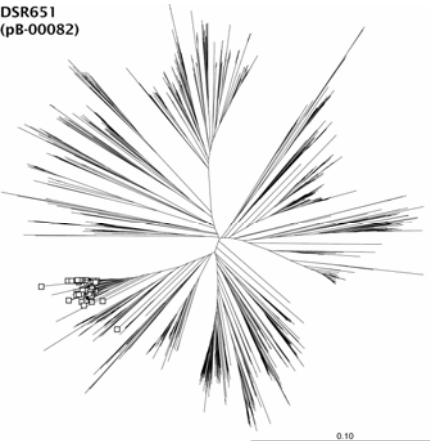
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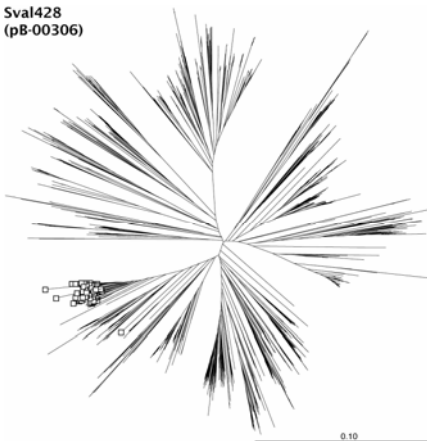
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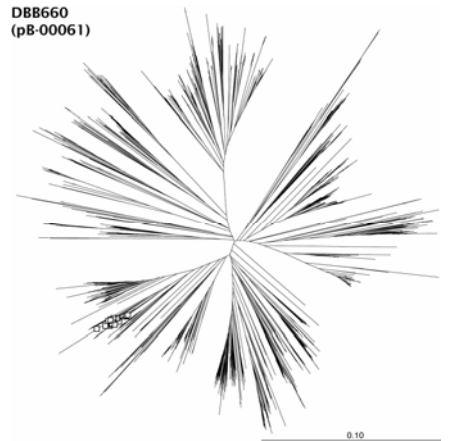
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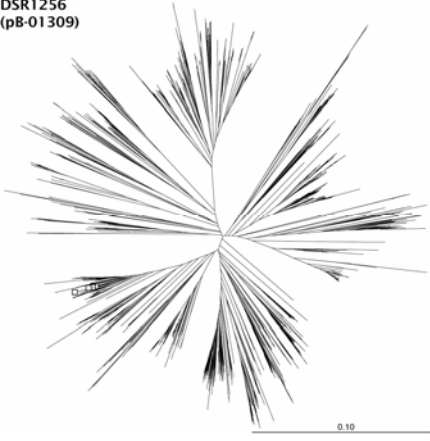
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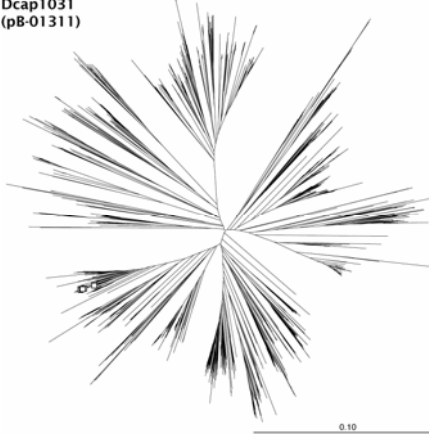
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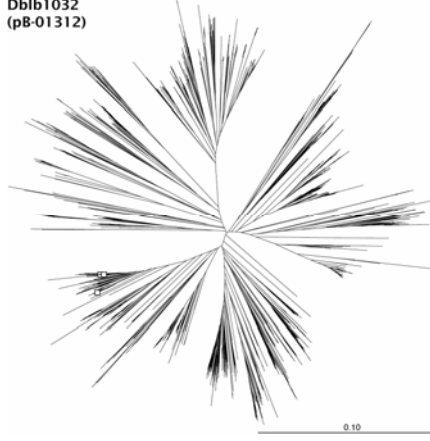
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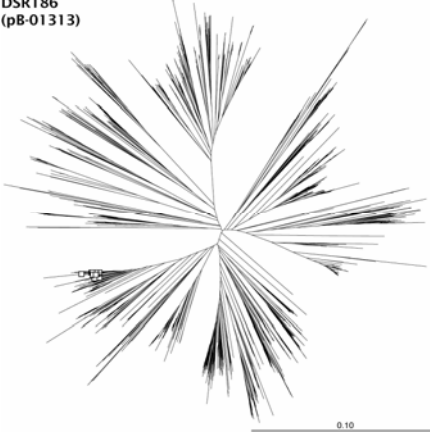
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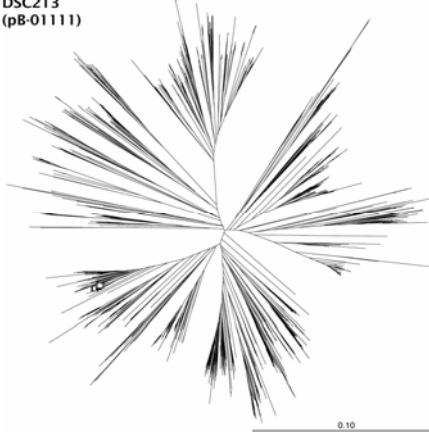
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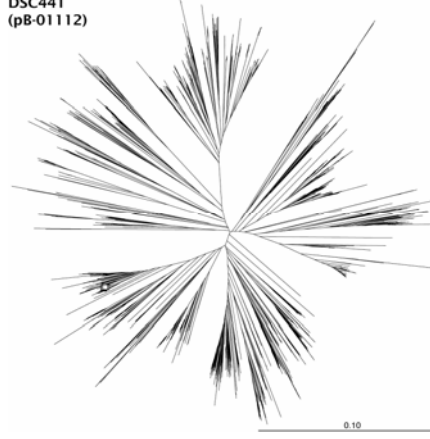
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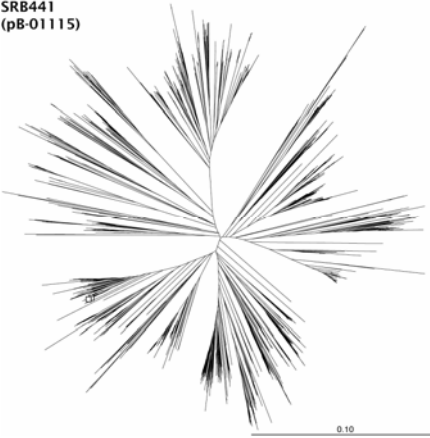
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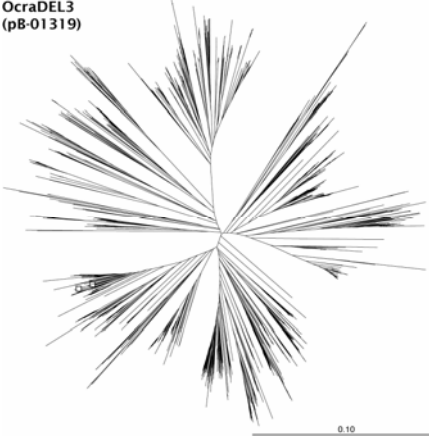
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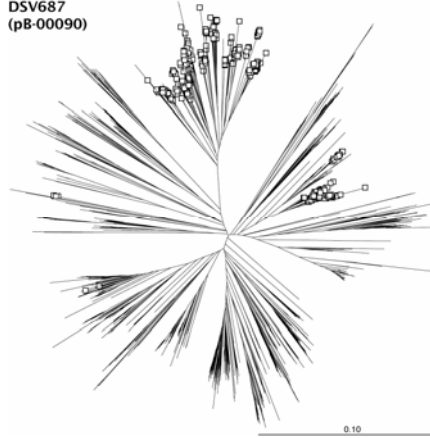
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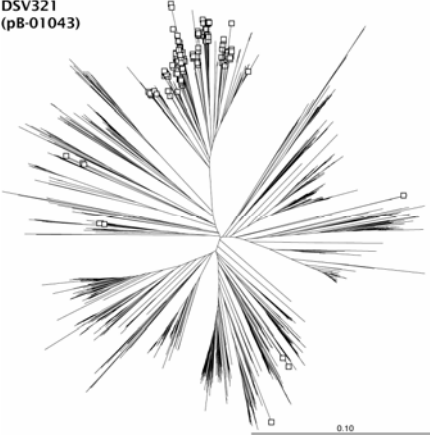
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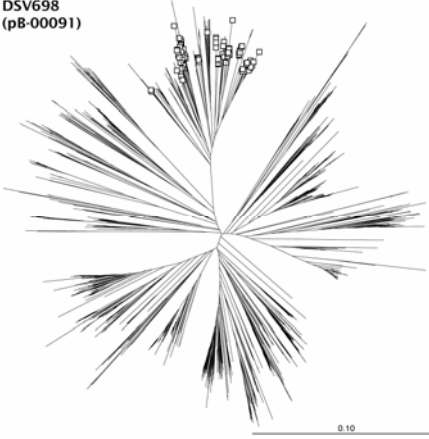
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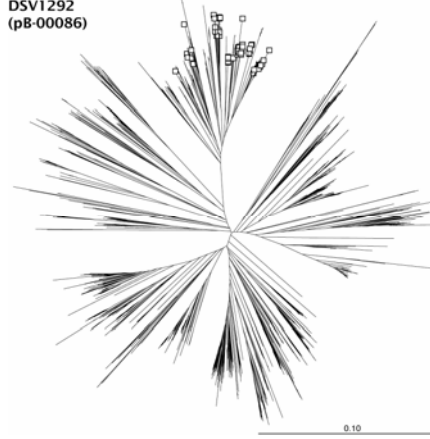
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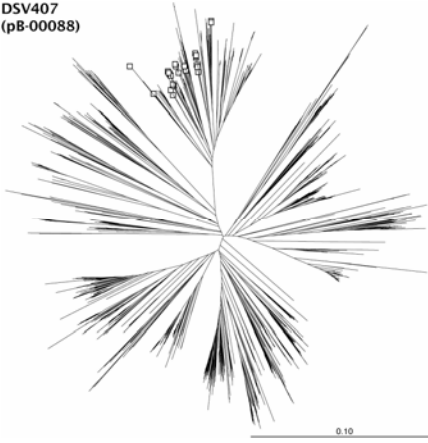
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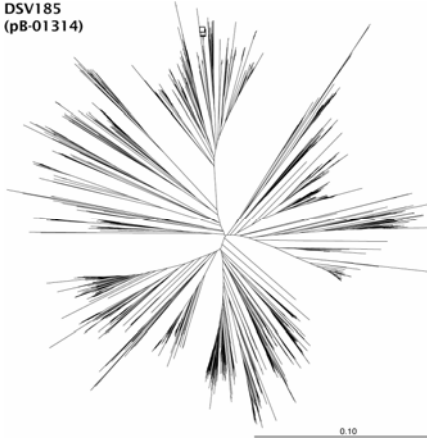
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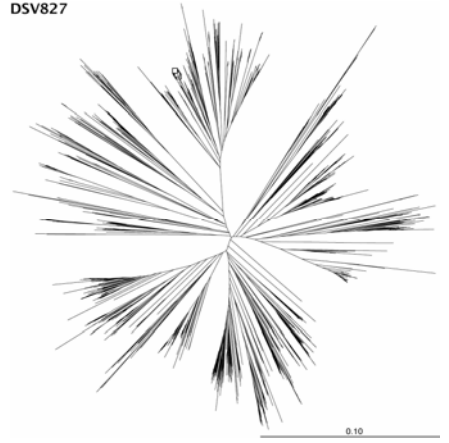
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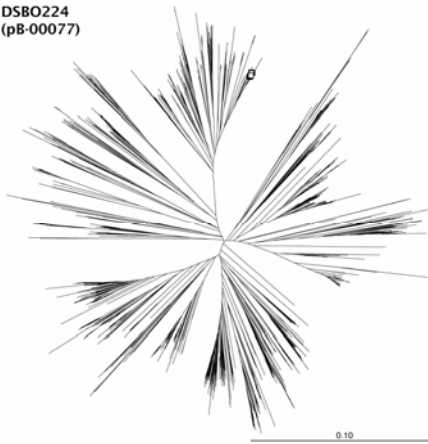
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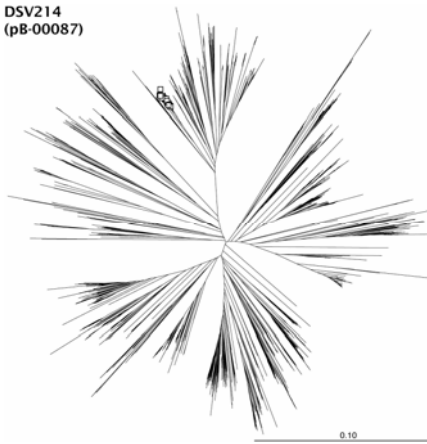
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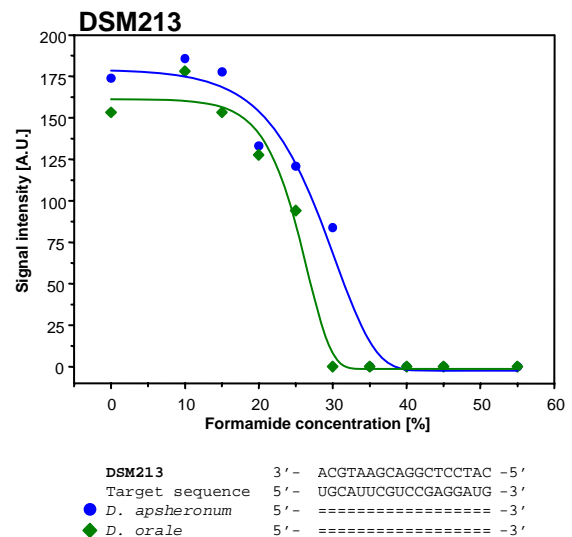
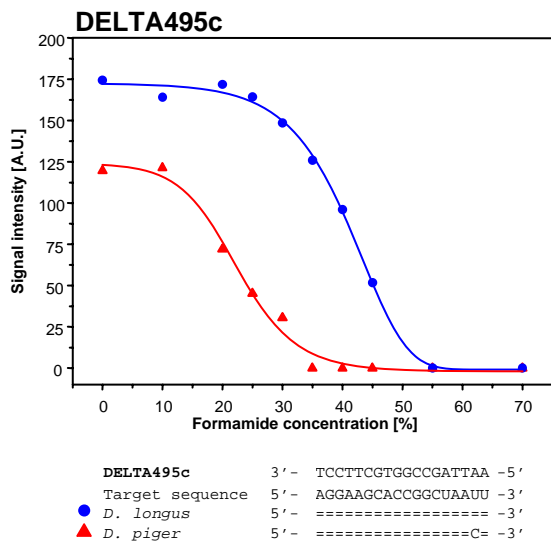
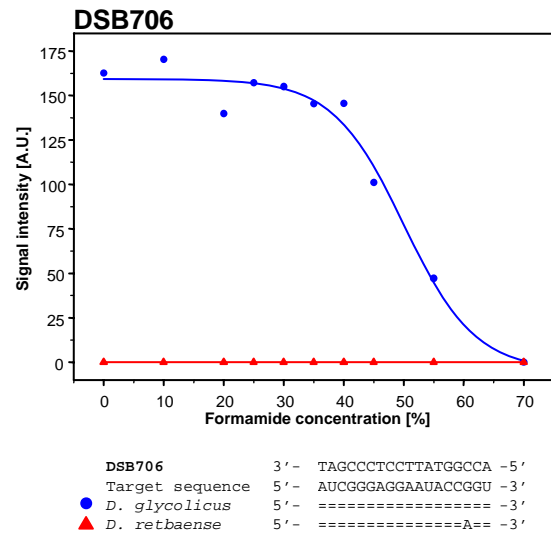
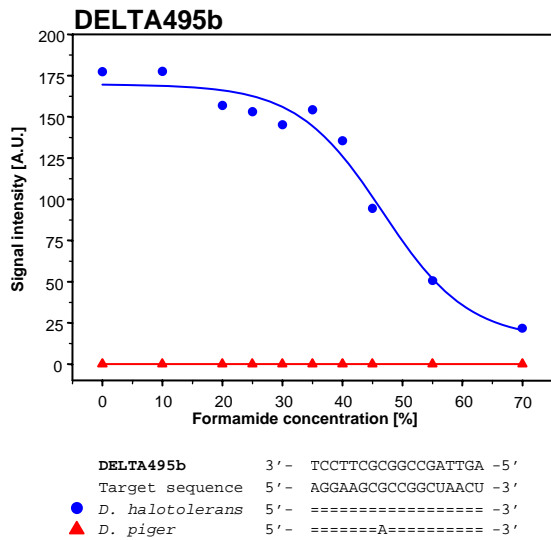
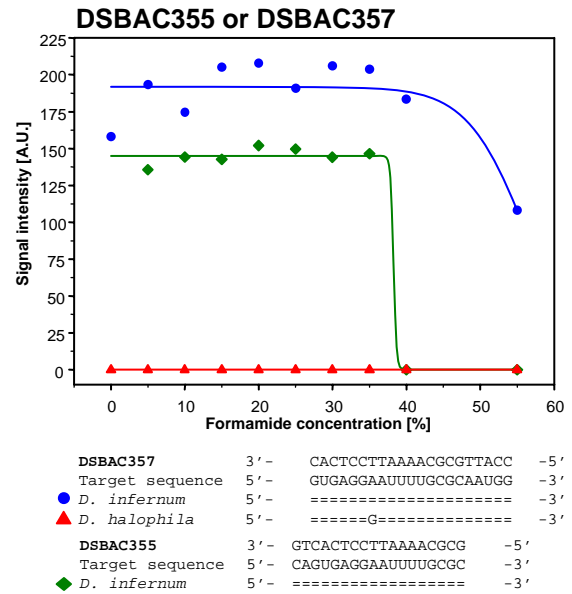
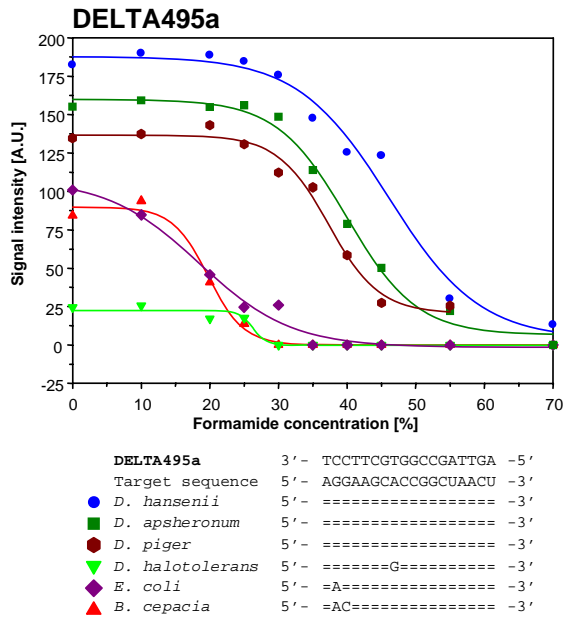
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DSV214
(pB-00087)



SOM Figure 2. Dissociation profiles of 16S rRNA-targeted FISH probes with perfectly-matching and mismatching reference organisms. Difference alignments of probes and target sites are shown for all reference organisms. Melting profiles of probe DSM213 were not recorded for microorganisms not belonging to the genus *Desulfomicrobium* because they had at least three strongly mismatching bases in the probe target site (tested with ARB database ssu_jan04_corr_opt.arb). A.U., arbitrary units.



SOM Figure 3. Simultaneous hybridization of an anaerobic digester sludge sample with the EUB338 (Cy5 in blue), DELTA495 (Cy3 in red), and SRB385 probe mixtures (FLUOS in green). Two microscopic fields, A and B, are shown. At least three microbial consortia are visible in the overlay images and are indicated with arrows. Consortium I in magenta hybridized only with the EUB338 and the DELTA495 mixes, consortium II in cyan blue hybridized only with the EUB338 and the SRB385 probe mixes, and consortium III in white and/or pinkish hybridized with all probes).

