Table S1. Quantity and quality of DNA extracted from samples of activated sludge (S1–S8). DNA concentration was analysed with a Qubit Fluorometer and a NanoDrop Spectrophotometer. DNA quality was measured by calculating the ratio of absorbance at 260 and to absorbance at 280 nm.

Kit	Sample	Qubit DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	Nanodrop DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	A260 nm/ A280 nm
FASTD	S1	183	0,73	318	1,27	1,92
	S2	246	0,98	386	1,54	1,87
	S3	233	0,93	414	1,66	1,87
	S4	219	0,88	383	1,53	1,91
	S5	262	1,05	386	1,54	1,9
	S6	127	0,51	290	1,16	1,92
	S7	200	0,80	348	1,39	1,96
	S8	207	0,83	313	1,25	1,93
	Mean (SD)	**209,63 (±41.97)**	**0,84 (±0.17)**	**354,75 (±44.06)**	**1,42 (±0,17)**	**1,91 (±0.03)**
PUREL	S1	74	0,37	99	0,495	1,92
	S2	81	0,405	102	0,51	1,94
	S3	84	0,42	111	0,555	1,93
	S4	90	0,45	117	0,585	1,94
	S5	88	0,44	118	0,59	1,98
	S6	80	0,4	105	0,525	1,85
	S7	81	0,405	108	0,54	1,86
	S8	81	0,405	109	0,545	1,88
	Mean (SD)	**82,38 (±4.98)**	**0,41 (±0.02)**	**108,63 (±6.69)**	**0,54 (±0.03)**	**1,91 (±0.04)**
FAVOR	S1	19,6	0,0784	721	2,884	2,05
	S2	31,5	0,126	714	2,856	2,03
	S3	33,4	0,1336	439	1,756	2,06
	S4	28,2	0,1128	801	3,204	2,14
	S5	34,9	0,1396	646	2,584	2,13
	S6	19,5	0,078	304	1,216	2,09
	S7	31	0,124	554	2,216	2,1
	S8	31,2	0,1248	509	2,036	2,09
	Mean (SD)	**28,66 (±5.94)**	**0,11 (±0.02)**	**586,00 (±165.8)**	**2,34 (±0.66)**	**2,09 (±0.04)**

Table S2. Quantity and quality of DNA extracted form samples of biofilm (S11–S18). DNA concentration was analyzed with a Qubit Fluorometer and a NanoDrop Spectrophotometer. DNA quality was measured by calculating the ratio of absorbance at 260 and to absorbance at 280 nm.

Kit	Sample	Qubit DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	Nanodrop DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	A260 nm /A280 nm
FASTD	S11	101	0,40	154	0,62	1,97
	S12	30	0,12	80	0,32	2,04
	S13	75	0,30	147	0,59	2,05
	S14	60	0,24	86	0,35	2,01
	S15	124	0,50	190	0,76	1,99
	S16	137	0,55	157	0,63	1,9
	S17	95	0,38	135	0,54	1,93
	S18	134	0,54	194	0,78	1,96
	Mean (SD)	**94,43 (±37.81)**	**0,38 (±0.15)**	**143,00 (±42.13)**	**0,57 (±0.16)**	**1,98 (±0.05)**
PUREL	S11	26	0,13	26	0,13	1,72
	S12	12	0,06	16	0,08	1,79
	S13	23	0,12	26	0,13	1,78
	S14	46	0,23	44	0,22	1,85
	S15	44	0,22	45	0,23	1,95
	S16	34	0,17	46	0,23	1,84
	S17	19	0,09	27	0,13	1,89
	S18	19	0,10	26	0,13	1,85
	Mean (SD)	**27,96 (±12.32)**	**0,14 (±0.06)**	**32,08 (±11.32)**	**0,16 (±0.06)**	**1,83 (±0.07)**
FAVOR	S11	35	0,14	2 320	9,28	2,07
	S12	17	0,07	1 330	5,32	2,25
	S13	24	0,10	174	0,70	2,2
	S14	43	0,17	681	2,72	2,06
	S15	43	0,17	75	0,30	2,06
	S16	58	0,23	1 078	4,31	2,1
	S17	21	0,08	1 670	6,68	2,19
	S18	24	0,10	3 418	13,67	2,04
	Mean (SD)	**32,94 (±14.09)**	**0,13 (±0.05)**	**1343,25 (±1124.4)**	**5,37 (±4.49)**	**2,12 (±0.08)**

Table S3. Quantity and quality of DNA extracted form samples of digestate (S21–S28). DNA concentration was analyzed Qubit Fluorometer and NanoDrop Spectrophotometer. DNA quality was measured by calculating the ratio of absorbance at 260 and to absorbance at 280 nm.

Kit	Sample	Qubit DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	Nanodrop DNA concentration (ng/µl)	DNA yield (ng of DNA/mg of biomass)	A260 nm/ A280 nm
FASTD	S21	64	0,25	220	0,88	1,95
	S22	31	0,12	349	1,40	1,8
	S23	50	0,20	206	0,82	1,96
	S24	17	0,07	231	0,93	2,0
	S25	74	0,29	217	0,87	2,0
	S26	49	0,19	132	0,53	1,87
	S27	59	0,24	153	0,61	1,94
	S28	49	0,20	139	0,56	1,89
	Mean (SD)	**49,03 (18.12)**	**0,20 (0.07)**	**205,76 (69.86)**	**0,82 (0.28)**	**1,93 (0.07)**
PUREL	S21	18	0,09	42	0,21	1,88
	S22	14	0,07	34	0,17	1,9
	S23	12	0,06	32	0,16	1,99
	S24	15	0,08	38	0,19	1,81
	S25	14	0,07	33	0,17	1,85
	S26	12	0,06	20	0,10	1,71
	S27	11	0,05	28	0,14	1,65
	S28	11	0,05	23	0,11	1,7
	Mean (SD)	**13,30 (2.38)**	**0,07 (0.01)**	**31,27 (7.34)**	**0,16 (0.04)**	**1,81 (0.11)**
FAVOR	S21	9	0,04	33	0,13	2,18
	S22	15	0,06	183	0,73	2,03
	S23	13	0,05	87	0,35	2,13
	S24	15	0,06	125	0,50	2,1
	S25	12	0,05	104	0,42	2,11
	S26	13	0,05	126	0,50	2,02
	S27	13	0,05	82	0,33	1,96
	S28	10	0,04	113	0,45	2,06
	Mean (SD)	**12,26 (2.13)**	**0,05 (0.01)**	**106,65 (43.10)**	**0,43 (0.17)**	**2,07 (0.07)**

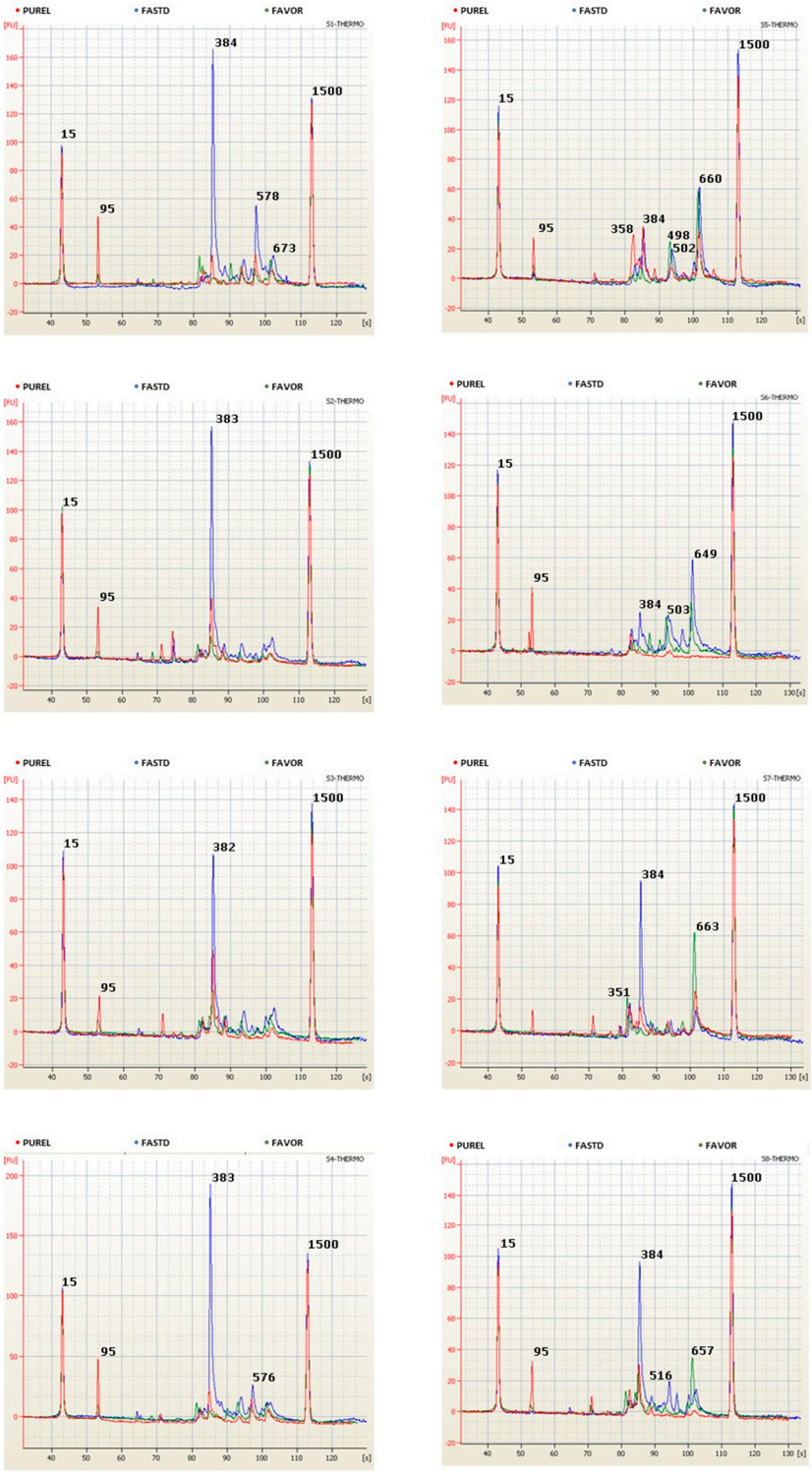

Figure S1. Automated Ribosomal Intergenic Spacer Analysis profiles from activated sludge samples (S1-S8). DNA was extracted with three kits: blue peaks – FASTD, red peaks – PUREL, green peaks – FAVOR.

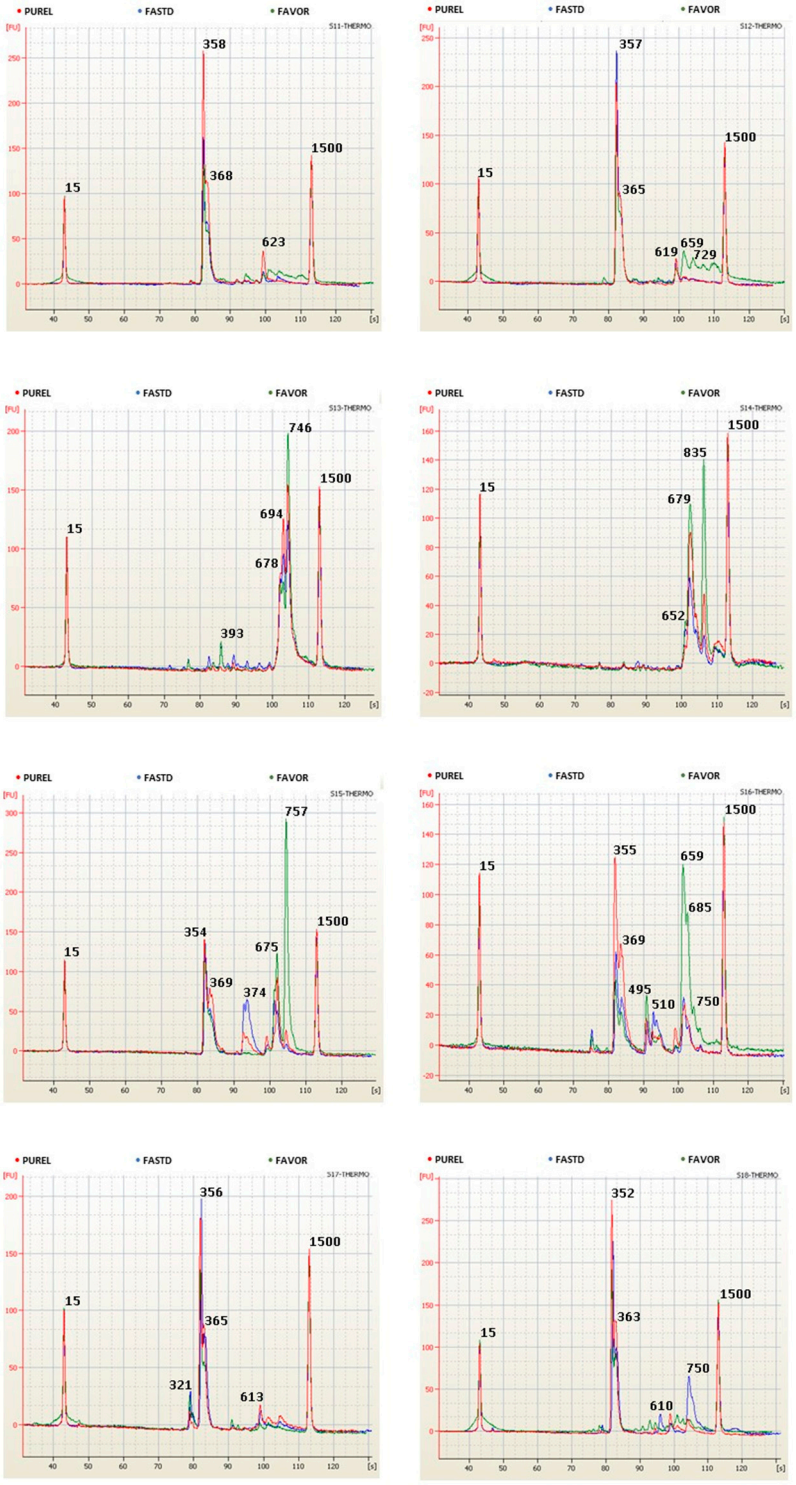

Figure S2. Automated Ribosomal Intergenic Spacer Analysis profiles from biofilm samples (S11-S18). DNA was extracted with three kits: blue peaks – FASTD, red peaks – PUREL, green peaks – FAVOR.

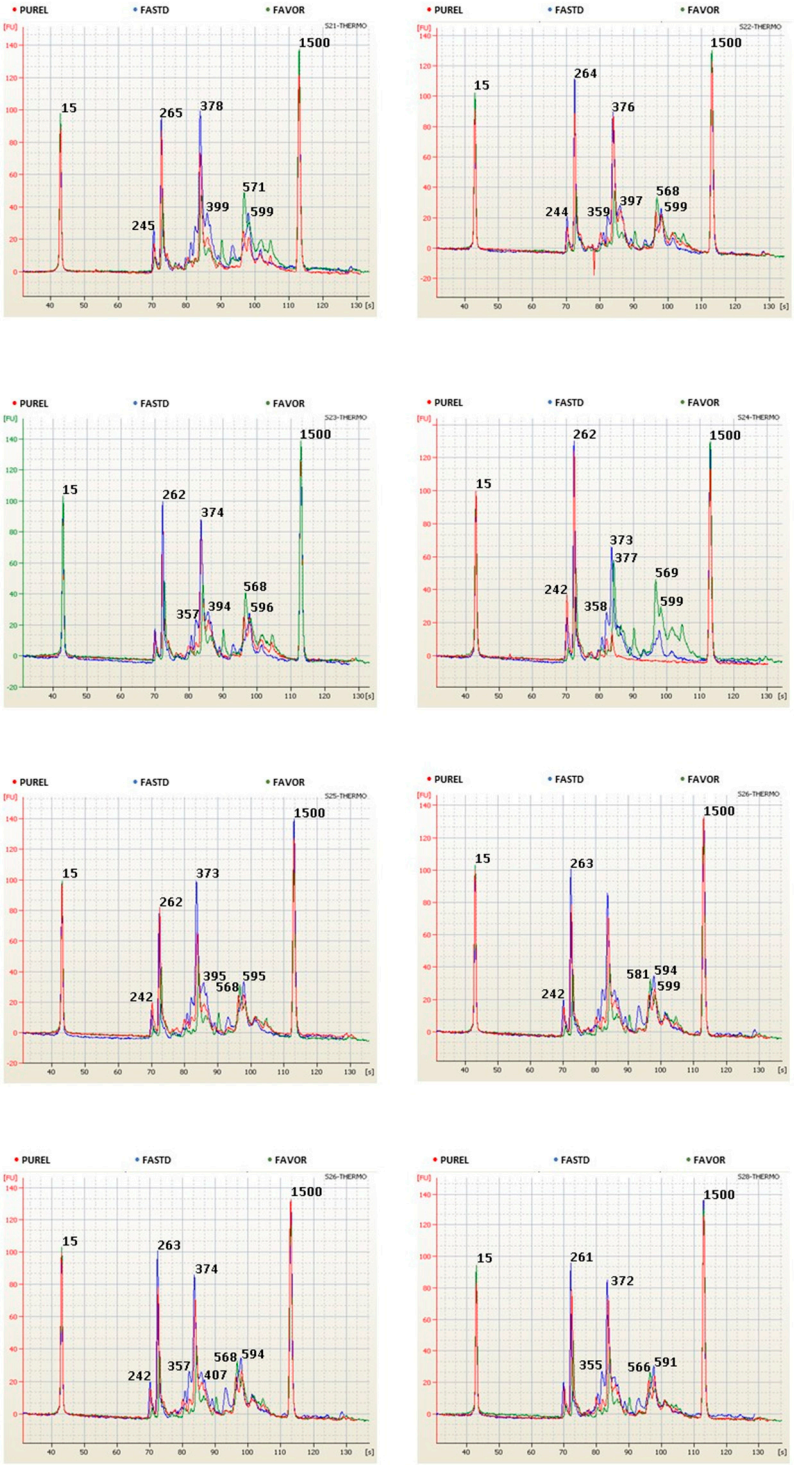

Figure S3. Automated Ribosomal Intergenic Spacer Analysis profiles from digestate samples (S21-S28). DNA was extracted with three kits: blue peaks – FASTD, red peaks – PUREL, green peaks – FAVOR.

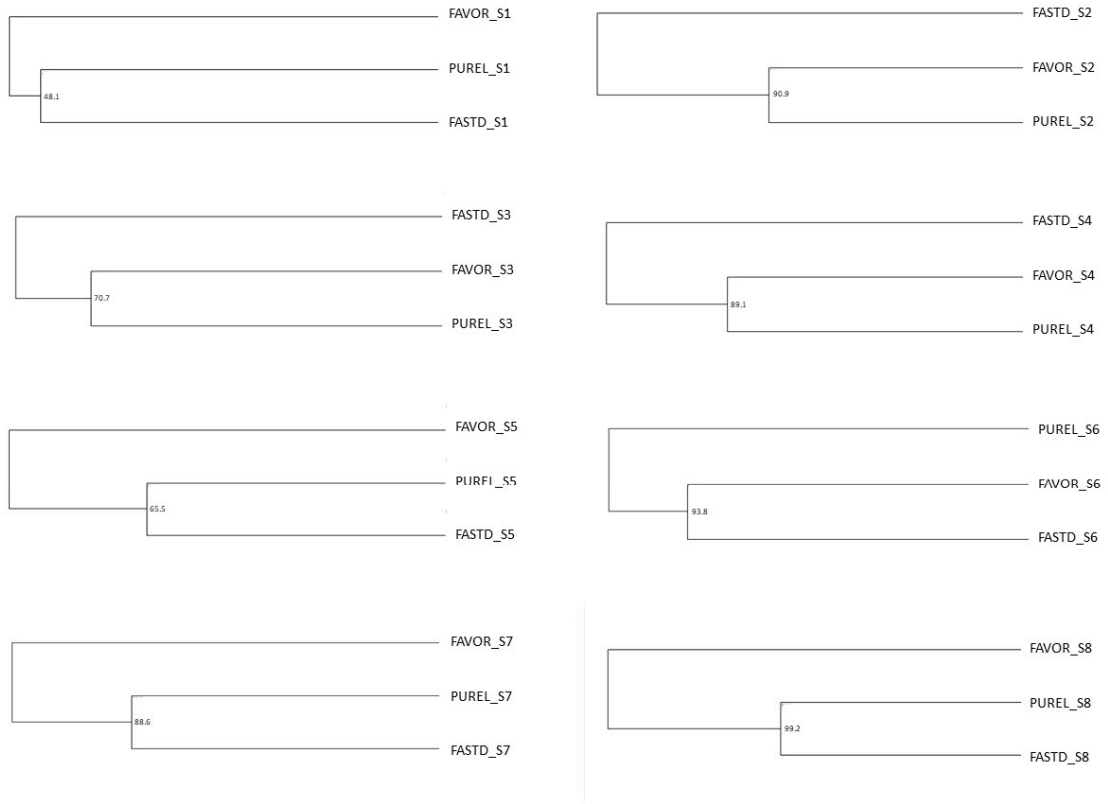

Figure S4. Phylogenetic trees showing genetic distance between samples of activated sludge (S1-S8) based on DNA extracted using three kits (FASTD, PUREL, and FAVOR). Bootstrap values are given at nodes.

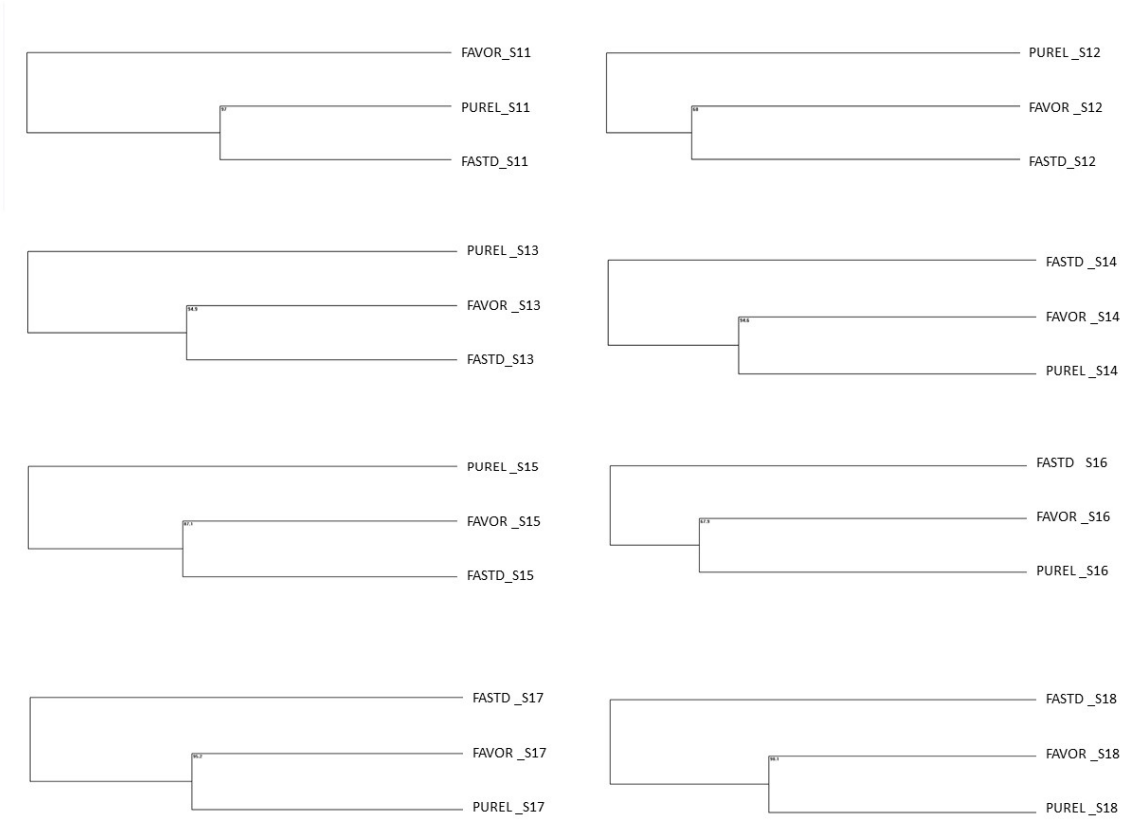

Figure S5. Phylogenetic trees showing genetic distance between samples of biofilm (S11-S18) based on DNA extracted using three kits (FASTD, PUREL, and FAVOR). Bootstrap values are given at nodes.

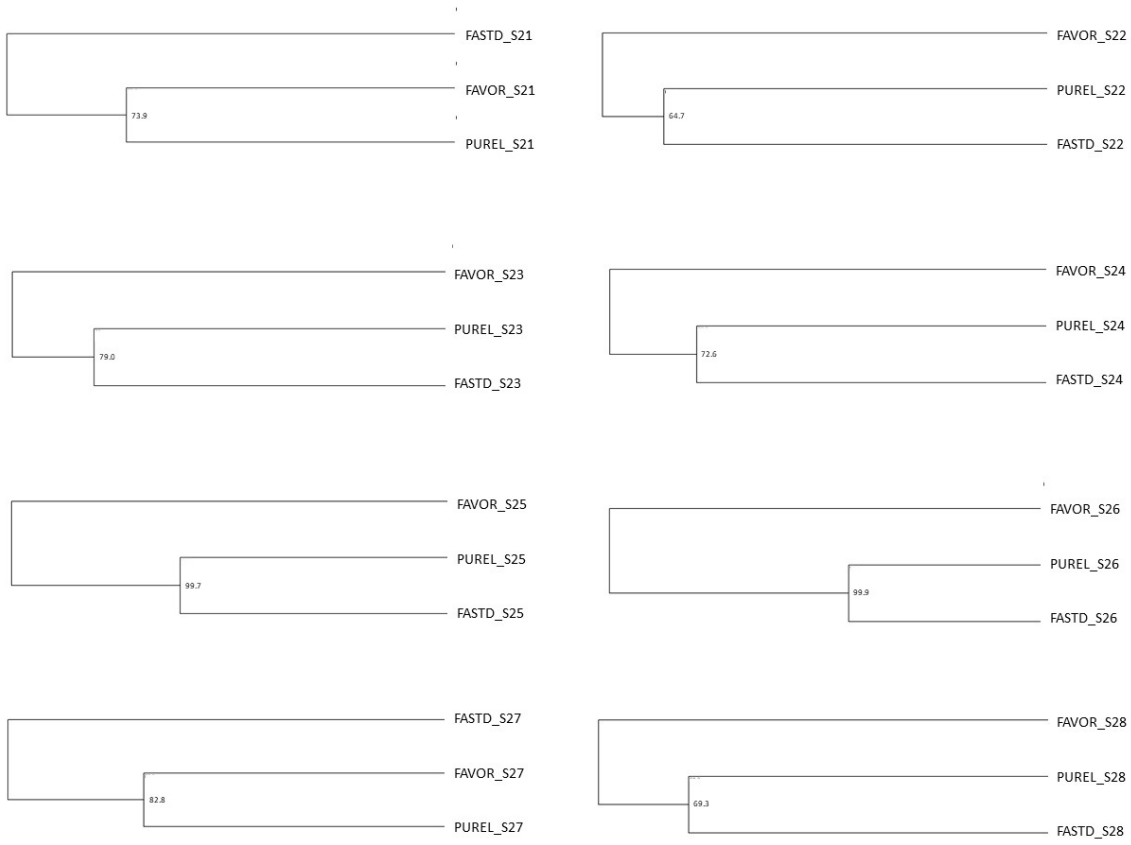

Figure S6. Phylogenetic trees showing genetic distance between samples of digestate (S21-S28) based on DNA extracted using three kits (FASTD, PUREL, and FAVOR). Bootstrap values are given at nodes.