

# Supplementary Material

**Table S1.** DNA sequencing results of the phototrophic mixed cultures operated with synthetic acetate.

	S1	S2	S3	S4	S5
	%				
<i>p_Acidobacteria/c_Chloracidobacteria</i>	0.00	0.04	0.00	0.00	0.00
<i>p_Actinobacteria</i>	0.00	2.10	0.00	0.06	1.80
<i>o_Actinomycetales</i>	0.00	2.10	0.00	0.06	1.80
<i>p_Bacteroidetes</i>	5.80	0.08	0.20	0.14	7.36
<i>c_Bacteroidia/o_Bacteroidales</i>	3.60	0.00	0.10	0.06	7.08
<i>c_Shingobacteriia/o_Saprospirales/f_Saprospiraceae</i>	0.00	0.06	0.00	0.00	0.00
<i>c_Cytophagales/ f_WCHB1-69_OTU_43;17;</i>	2.20	0.00	0.10	0.00	0.00
<i>p_Chlorobi</i>	0.10	0.00	0.60	0.76	0.00
<i>p_Chloroflexi</i>	2.20	0.06	0.40	0.10	0.00
<i>c_Anaerolineae</i>	2.20	0.04	0.10	0.10	0.00
<i>c_Thermomicrobia</i>	0.00	0.02	0.00	0.00	0.00
<i>c_Ktedonobacteria_OTU_24</i>	0.00	0.00	0.30	0.00	0.00
<i>p_Cyanobacteria/c_Chloroplast</i>	5.10	4.62	6.60	1.70	0.36
<i>p_Firmicutes</i>	0.00	0.04	0.00	0.00	0.12
<i>c_Bacilli</i>	0.00	0.04	0.00	0.00	0.00
<i>c_Clostridia</i>	0.00	0.00	0.00	0.00	0.12
<i>p_Proteobacteria</i>	80.60	91.22	88.00	90.52	85.58
<i>c_Alphaproteobacteria</i>	77.70	80.96	87.10	84.32	59.46
<i>o_Rhizobiales</i>	68.60	68.58	86.80	81.92	59.08
<i>f_Bradyrhizobiaceae</i>	37.50	6.54	1.60	5.08	58.64
<i>f_Methylocystaceae</i>	0.10	0.54	0.00	0.10	0.12
<i>f_Phyllobacteriaceae</i>	0.00	1.00	0.00	1.98	0.00
<i>f_Rhizobiaceae</i>	0.10	0.52	72.50	0.02	0.12
<i>f_Hyphomicrobiaceae/g_Blastochloris</i>	30.90	59.98	12.70	74.74	0.20
<i>o_Rhodobacterales/f_Rhodobacteraceae</i>	7.70	5.24	0.20	0.22	0.00
<i>g_Pannonibacter</i>	1.40	0.00	0.10	0.00	0.00
<i>o_Rhodospirillales/f_Rhodopirillaceae/g_Telmatospirillum</i>	0.00	0.00	0.00	0.00	0.06
<i>o_Rickettsiales</i>	0.00	2.74	0.00	0.26	0.00
<i>o_Sphingomonadales/f_Sphingomonadaceae/g_Sphingopyxis</i>	0.00	0.04	0.00	0.20	0.00
<i>c_Betaproteobacteria</i>	0.60	0.08	0.10	0.00	0.04
<i>o_Burkholderiales/f_Comamonadaceae/g_Comamonas</i>	0.00	0.06	0.00	0.00	0.00
<i>o_Burkholderiales/f_Comamonadaceae/g_Acidovorax</i>	0.60	0.00	0.10	0.00	0.00
<i>o_Rhodocyclales/f_Rhodocyclaceae</i>	0.00	0.02	0.00	0.10	0.04
<i>c_Gammaproteobacteria</i>	2.30	10.18	0.80	6.20	26.06
<i>o_Chromatiales/f_Chromatiaceae</i>	2.20	0.00	0.30	5.12	26.02
<i>o_Xanthomonadales/f_Xanthomonadaceae</i>	0.00	10.12	0.50	0.64	0.02
<i>p_Verrucomicrobia/c_/o_/f_/g_Luteolibacter</i>	0.00	0.00	0.00	0.04	0.00
<i>p_Tenericutes/c_/o_/f_/g_Acholeplasma</i>	3.40	0.00	0.00	0.00	0.00
Total	97.20	98.16	95.80	93.32	95.22

**Table S2.** DNA sequencing results of the phototrophic mixed cultures operated with fermented wastewaters with molasses.

	R0	R1	R2	R3	R4	R5	R6
	%						
<b><i>p_Acidobacteria/c_Chloracidobacteria</i></b>	0.0	0.0	0.1	0.0	0.0	0.0	0.1
<b><i>p_Actinobacteria</i></b>	19.7	0.2	56.5	0.3	1.3	12.1	2.6
<i>o_Actinomycetales</i>	0.5	0.0	55.2	0.1	0.0	0.2	0.2
<i>f_Actinomycetaceae</i>	0.5	0.0	55.2	0.1	0.0	0.2	0.1
<i>g_Actinomyces</i>	0.2	0.0	55.2	0.1	0.0	0.1	0.1
<i>f_Corynebacteriaceae</i>	0.1	0.0	0.0	0.0	0.0	0.0	0.0
<i>f_Nocardiaceae</i>	0.2	0.0	0.0	0.0	0.0	0.0	0.0
<i>o_Coriobacteriales</i>	0.1	0.1	0.1	0.0	0.0	0.0	0.8
<i>o_Corynebacteriales</i>	4.3	0.0	0.0	0.0	0.2	0.0	0.0
<i>o_Mycobacteriales</i>	0.2	0.0	0.0	0.0	0.0	0.0	0.0
<i>o_Propionibacteriales</i>	0.6	0.1	0.9	0.2	0.3	11.5	0.8
<i>f_Propionibacteriaceae / g_Propionimonas</i>	0.0	0.0	0.8	0.2	0.1	11.1	0.4
<i>o_Micrococcales</i>	2.1	0.0	0.1	0.0	0.6	0.3	0.9
<i>o_PeM15</i>	10.9	0.0	0.0	0.0	0.1	0.1	0.0
<b><i>p_Bacteroidetes</i></b>	0.6	0.2	1.5	0.1	1.1	1.0	0.9
<i>c_Bacteroidia/o_Bacteroidales</i>	0.0	0.0	0.8	0.1	0.0	0.0	0.1
<i>f_Prevotellaceae / g_Prevotella</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.1
<i>c_Flavobacteriia</i>	0.4	0.1	0.5	0.0	0.4	0.0	0.5
<i>c_Cytophagales</i>	0.0	0.0	0.0	0.0	0.4	0.5	0.0
<b><i>p_Chlorobi / c_Chlorobia / o_Chlorobiales / f_Chlorobiaceae</i></b>	0.0	0.0	0.0	0.0	0.0	0.0	1.3
<b><i>p_Chloroflexi</i></b>	13.7	0.3	1.1	0.0	1.0	0.6	0.1
<i>c_Anaerolineae</i>	0.3	0.2	0.1	0.0	0.1	0.2	0.0
<i>c_Caldilineae / o_Caldilineales</i>	11.7	0.0	0.0	0.0	0.8	0.3	0.0
<b><i>p_Cyanobacteria/c_Chloroplast</i></b>	0.3	0.0	0.4	1.0	0.4	1.4	2.4
<b><i>p_Firmicutes</i></b>	10.8	83.6	19.7	0.5	1.7	0.4	2.4
<i>c_Bacilli</i>	1.3	72.0	12.1	0.3	0.9	0.2	0.3
<i>o_Lactobacillales</i>	1.2	71.5	11.6	0.3	0.1	0.2	0.3
<i>f_Carnobacteriaceae/g_Trichococcus</i>	0.6	68.8	3.5	0.0	0.0	0.0	0.0
<i>f_Lactobacillaceae/g_Leuconostoc</i>	0.0	0.9	0.0	0.0	0.0	0.0	0.0
<i>c_Clostridia</i>	9.1	11.8	7.0	0.1	0.7	0.2	2.0
<i>o_Clostridiales</i>	9.1	11.8	7.0	0.1	0.7	0.2	2.0
<i>f_Clostridiaceae / g_Clostridium</i>	2.0	0.3	1.2	0.0	0.3	0.1	0.0
<i>f_Veillonellaceae</i>	0.0	0.0	0.6	0.0	0.0	0.0	0.1
<i>f_Peptostreptococcaceae</i>	6.7	10.0	2.0	0.0	0.3	0.1	0.0
<i>f_Ruminococcaceae</i>	0.0	0.0	0.4	0.0	0.0	0.0	0.3
<i>c_Negativicutes / o_Selenomonadales / f_Acidaminococcaceae_OTU_21</i>	0.0	0.0	0.6	0.0	0.0	0.0	0.1

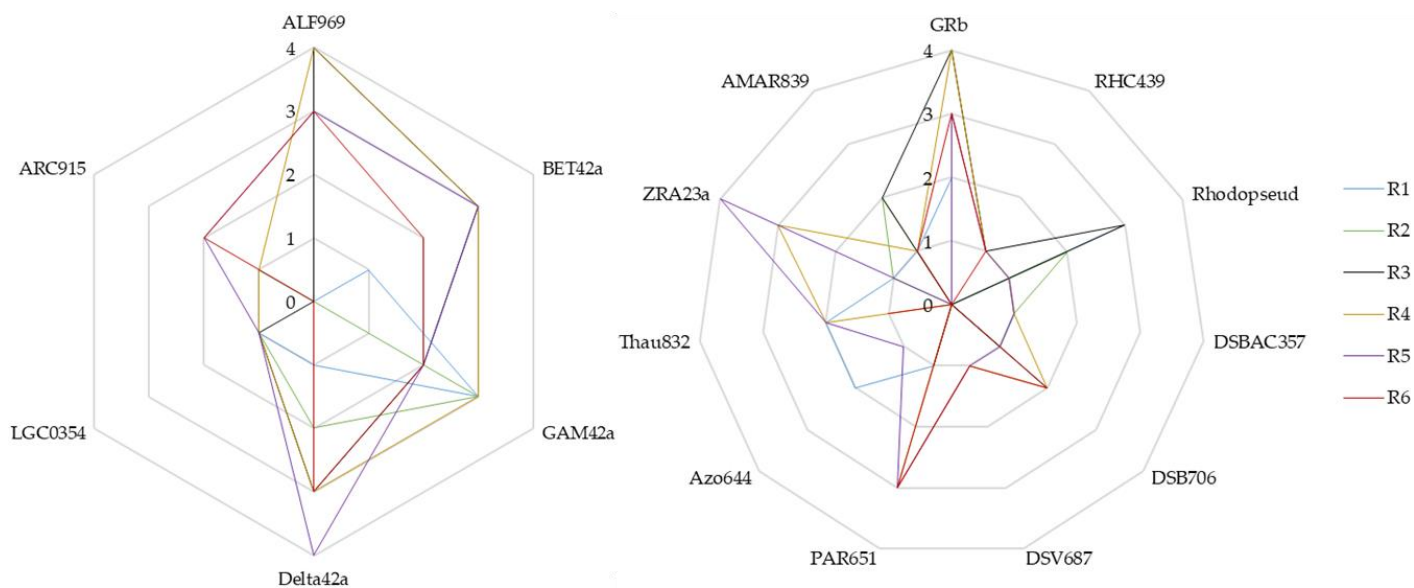
Table S2. Cont.

	R0	R1	R2	R3	R4	R5	R6
	%						
<i>p_Proteobacteria</i>	50.8	15.4	19.6	98.0	93.5	84.3	88.4
<i>c_Alphaproteobacteria</i>	42.3	10.1	12.8	97.6	79.5	20.8	81.9
<i>o_Rhizobiales</i>	21.1	2.9	9.7	95.9	7.6	6.5	73.7
<i>f_Bradyrhizobiaceae</i>	7.2	2.7	8.7	84.4	1.2	1.2	10.9
<i>g_Rhodopseudomonas</i>	5.7	2.7	8.7	83.9	0.7	0.7	10.5
<i>f_Rhizobiaceae</i>	0.6	0.0	0.0	11.2	1.0	1.9	32.9
<i>g_Rhizobium</i>	0.5	0.0	0.0	11.2	0.6	1.7	32.8
<i>f_Hyphomicrobiaceae</i>	3.0	0.1	0.8	0.1	1.8	0.5	22.5
<i>g_Blastochloris</i>	0.1	0.0	0.3	0.0	0.0	0.0	0.3
<i>o_Rhodobacterales</i>	18.4	6.8	1.6	1.3	70.6	10.0	6.3
<i>f_Rhodobacteraceae</i>	18.4	6.8	1.6	1.3	70.6	10.0	6.3
<i>g_Rhodobacter</i>	6.5	6.7	1.5	1.3	15.4	0.5	5.7
<i>g_Paracoccus</i>	0.5	0.0	0.1	0.0	53.7	9.5	0.7
<i>g_Amaricoccus</i>	0.0	0.0	0.0	0.0	0.1	0.0	0.0
<i>o_Rhodospirillales</i>	0.5	0.1	1.4	0.3	0.3	0.6	1.8
<i>f_Rhodospirillaceae</i>	0.1	0.0	0.1	0.2	0.1	0.2	0.1
<i>o_Caulobacterales</i>	0.8	0.4	0.0	0.0	1.0	3.7	0.0
<i>c_Betaproteobacteria</i>	5.3	0.1	0.2	0.4	5.0	63.0	1.9
<i>o_Burkholderiales</i>	3.7	0.0	0.1	0.3	0.5	0.2	1.8
<i>f_Comamonadaceae</i>	3.6	0.0	0.0	0.3	0.5	0.2	0.1
<i>o_Rhodocyclales/f_Rhodocyclaceae</i>	1.6	0.0	0.1	0.1	4.4	62.9	0.1
<i>g_OTU-10</i>	0.0	0.0	0.0	0.0	4.3	58.1	0.0
<i>c_Gammaproteobacteria</i>	2.7	5.2	6.7	0.0	8.9	0.5	4.4
<i>o_Chromatiales/f_Chromatiaceae</i>	0.4	5.0	2.1	0.0	2.9	0.1	3.9
<i>o_Xanthomonadales</i>	1.7	0.1	0.0	0.0	5.9	0.3	0.5
<i>p_Saccharibacteria</i>	2.0	0.0	0.4	0.0	0.0	0.0	0.8
<i>p_Planctomycetes / c_Planctomycetacia</i>	1.4	0.0	0.0	0.0	0.7	0.0	0.0
<i>p_Synergistetes</i>	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Total	99.4	99.7	99.3	99.9	99.7	99.8	99.0

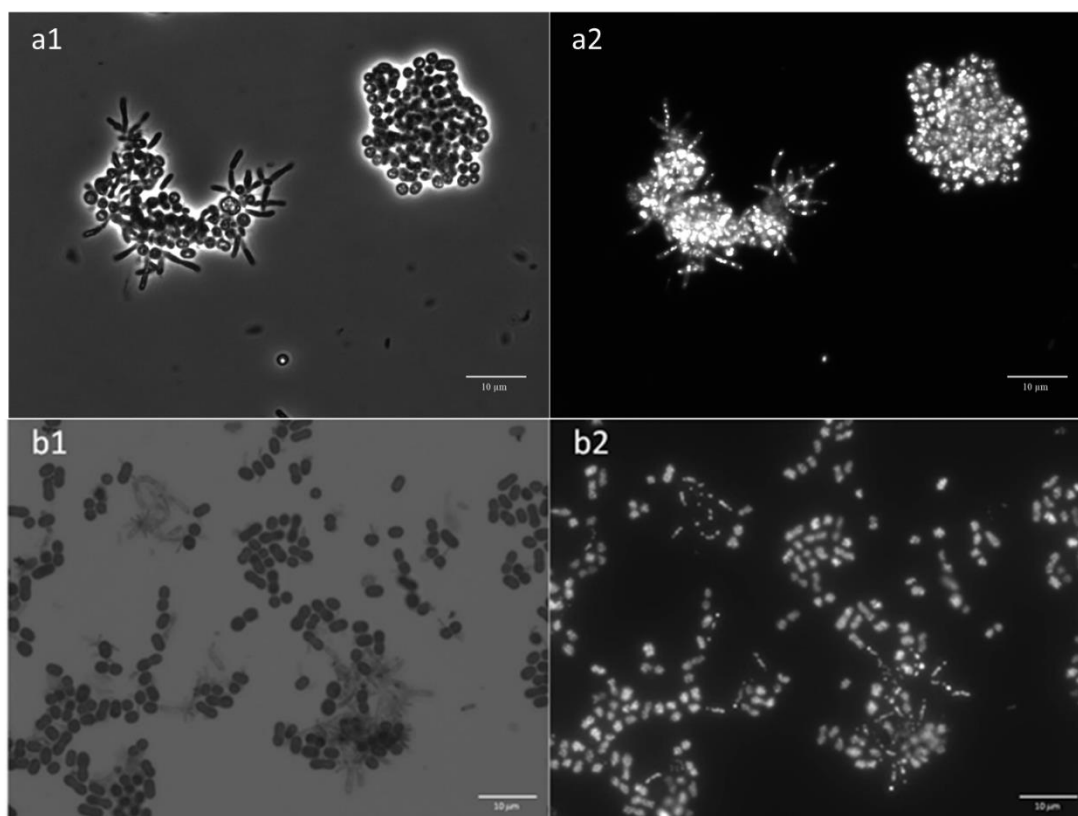
**Table S3.** FISH results for GAOmix and PAOmixon probes for the PMC fed with acetate synthetic medium (S1 to S5) and PMC fed with a fermented wastewater (R1 to R6).

<b>Samples</b>	<b>GAOmixon (GBG2 + GAOQ989)</b>	<b>PAOmixon (PAO462 + PAO651 + PAO846)</b>
<b>S1</b>	n.a	n.a
<b>S2</b>	(-)	(-)
<b>S3</b>	(-)	n.a
<b>S4</b>	n.a	n.a
<b>S5</b>	n.a	n.a
<b>R1</b>	(-)	(-)
<b>R2</b>	(-)	(-)
<b>R3</b>	(-)	(-)
<b>R4</b>	(-)	(-)
<b>R5</b>	(-)	(-)
<b>R6</b>	(-)	(-)

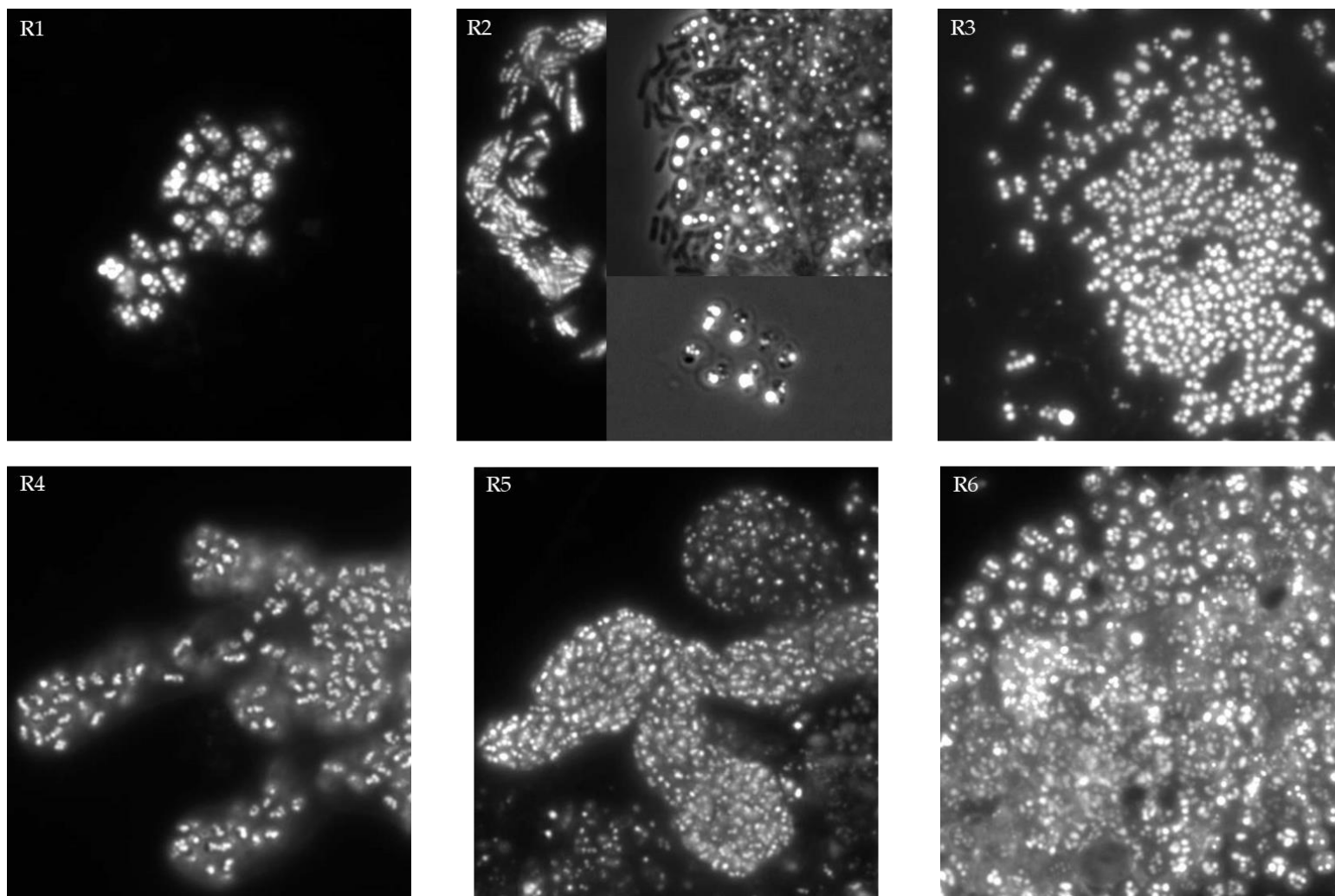
Non-present (-); n.a. – not analyzed



**Figure S1:** FISH results for the PMC fed with a fermented mixture of domestic wastewater supplemented with molasses (R1 to R6) presented in a radar chart. The relative abundances correspond to 4 - Extremely abundant (+++), 3 - Abundant (++), 2 - Present (+), 1 - Almost non-existent ( $\pm$ ) and 0 - Not detected, not analysed or inconclusive.



**Figure S2.** Microscopic images of the synthetically fed cultures S3 and S4 operated under a feast and famine (FF) regime. **a1** – Phase contrast of culture S4; **b1** – Bright field of culture S3; **a2 and b2** – Fluorescence images of Nile blue staining indicating PHA granules in culture S4 and S3, respectively. In the two cultures, both rods and cocci bacteria present PHA granules.

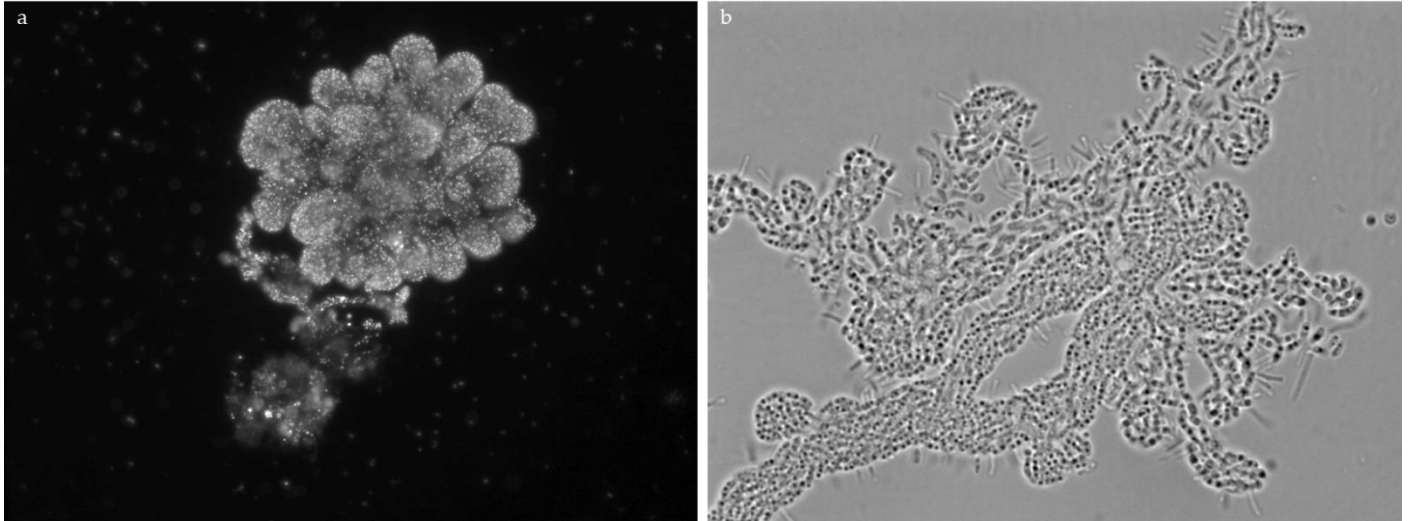


**Figure S3.** Fluorescence images of Nile blue staining indicating polyhydroxyalkanoates granules in R1 to R6 cultures. Magnification of 100x.

1

2

3



**Figure S4.** Microscopic pictures of swarm shaped aggregation observed in culture R5. **a** – Fruitig body development observation with Nile blue staining, magnification 100x; **b** – Bright field observation of swarm aggregated bacteria identified by FISH as Deltaproteobacteria, magnification 100x.