Supporting Information

Table S1 Phylogenetic relation of the OTUs retrieved from valerate-hydrolysate enriched culture and valerate-hydrolysate enriched culture

mixed culture	OUT number	number of clones	length/bp	closest strain	identity/%
valerate-hydrolysate enriched culture	1	80	1446	*Brevundimonas vesicularis* strain NBRC 12165 (NR_113586.1)	98
	2	8	1489	*Sphingobacterium psychroaquaticum* strain MOL-1 (NR_108297.1)	97
	3	5	1492	*Achromobacter xylosoxidans* strain IHB B 6801 (KF668455.1)	99
	4	2	1446	*Nitratireductor lucknowense* strain IITR-21 (NR_118014.1)	95
	5	1	1490	*Aquamicrobium lusatiense* strain S1 (NR_025312.1)	99
	6	1	1450	*Nitrobacter hamburgensis* strain X14 (NR_074313.1)	97
	7	1	1492	*Achromobacter xylosoxidans* A8 strain (NR_074754.1)	98
	8	1	1473	*Mesorhizobium sp.* enrichment culture clone SA_NR7_4 (GU726975)	94
	9	1	1422	*Brevundimonas naejangsanensis* strain BIO-TAS2-2 (NR_116722.1)	95
acetate-hydrolysate enriched culture	1	70	1446	*Brevundimonas vesicularis* strain NBRC 12165 (NR_113586.1)	98
	2	14	1492	*Achromobacter xylosoxidans* strain IHB B 6801 (KF668455.1)	99
	3	5	1490	*Aquamicrobium lusatiense* strain S1 (NR_025312.1)	99
	4	4	1489	*Sphingobacterium psychroaquaticum* strain MOL-1 (NR_108297.1)	97
	5	2	1448	*Bacillus cereus* strain CCM 2010 (NR_115714.1)	99
	6	1	1447	*Sphingobacterium alimentarium* strain WCC 4521 (NR_108489.1)	96
	7	1	1514	*Aquamicrobium defluvii* strain DSM 11603 (NR_026443.1)	96
	8	1	1499	*Brevundimonas abyssalis* strain TAR-001 (NR_114308.1)	94
	9	1	1516	*Alcaligenes faecalis* strain NBRC 13111 (NR_113606.1)	92

	10	1	1509	*Stenotrophomonas rhizophila* strain e-p10 (NR_121739.1)	99

Table S2 Comparisons of PHAs production by acetate-hydrolysate enriched culture and valerate-hydrolysate enriched culture with acetate-hydrolysate as substrate

mixed culture	PHA_{max} /($g \cdot L^{-1}$)	X_{max} /($g \cdot L^{-1}$)	3HB/3HV/3H2MV /mol%
acetate-hydrolysate enriched culture	0.59	0.79	91.21/7.11/1.67
valerate-hydrolysate enriched culture	0.78	1.13	78.04/14.02/7.94