

Supplementary Material

Pheno- And Genotyping Of Hopanoid Production In Acidobacteria

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1 Supplementary Figure

2 Supplementary Tables

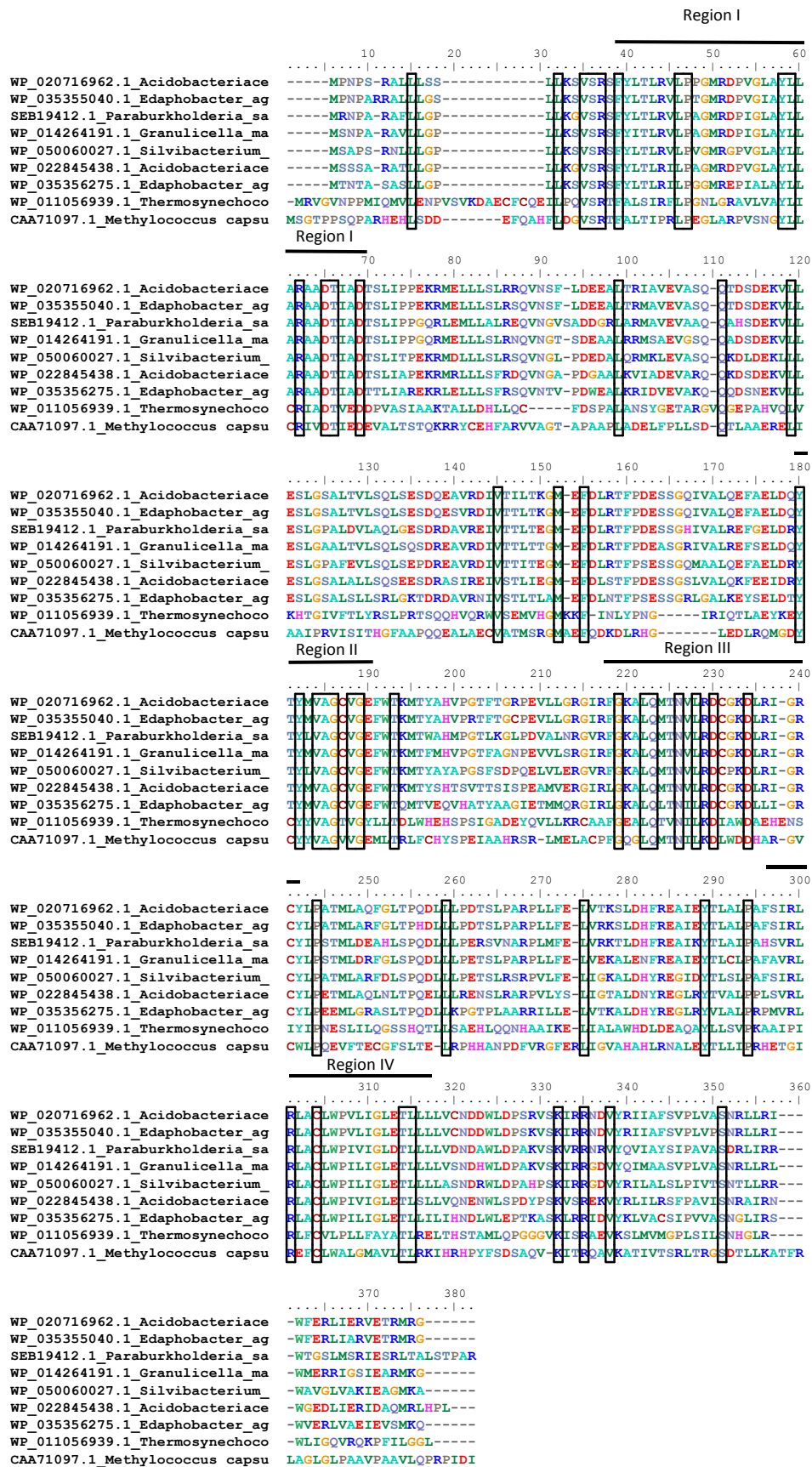


Figure S1: Amino acid sequence alignments for FdtP for *Silvibacterium bohemicum* S15 (WP_050060027.1), Acidobacteriaceae bacterium KBS 89 (WP_020716962.1), *Edaphobacter aggregans* Wbg-1 (WP_035355040.1, WP_035356275.1), *Granulicella mallensis* MP5ACTX8 (WP_014264191.1), Acidobacteriaceae bacterium TAA166 (WP_022845438.1), *Paraburkholderia sartolii* (SEB19412.1) in comparison to those of *Thermosynechococcus elongates* BP-1 (WP_011056939) (Lee and Poulter, 2008) and *Methylococcus capsulatus* ATCC 33009 (CAA71097.1). Dashes indicate gaps that were introduced to maximize the alignments. The conserved regions I-IV, previously identified on basis of comparison with eukaryotic squalene synthases ((Lee and Poulter, 2008) are indicated.

Table S1: Genes involved in the biosynthesis of BHPs and some other unknown genes often closely located to these genes in genomes of *Acidobacteria*.

Name	Annotation	Function of protein	Reference
<i>dxs</i>	1-deoxy-D-xylulose-5-phosphate synthase	Catalyzes the condensation of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP)	Zhao et al. (2013)
<i>dxr</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Catalyzes the NADP-dependent rearrangement and reduction of DXP to 2-C-methyl-D-erythritol 4-phosphate (MEP)	Zhao et al. (2013)
<i>ispD</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	Catalyzes the formation of 4-diphosphocytidyl-2-C-methyl-D-erythritol from CTP and ME.	Zhao et al. (2013)
<i>ispE</i>	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2-C-methyl-D-erythritol	Zhao et al. (2013)
<i>ispF</i>	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Catalyzes the conversion of 4-diphosphocytidyl-2-C-methyl-D-erythritol 2-phosphate (CDP-ME2P) to 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-CPP)	Zhao et al. (2013)
<i>ispG</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Converts 2-C-methyl-D-erythritol 2,4-cyclodiphosphate (ME-2,4cPP) into 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate, using flavodoxin as the reducing agent	Zhao et al. (2013)
<i>ispH</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP)	Zhao et al. (2013)
<i>orfD</i>	Isopentenyl-diphosphate delta-isomerase type II	Catalyzes the 1,3-allylic rearrangement of IPP to DMAPP	Kaneda et al. (2001) PNAS 98(3): 932–937
<i>hmgcR</i>	3-hydroxy-3-methyl-glutaryl-coenzyme A reductase	Catalyzes the conversion of 3-hydroxy-3-methyl-glutaryl-coenzyme A to mevalonic acid in the mevalonate pathway	Miziorki (2011)
<i>mvK</i>	Mevalonate kinase	Catalyzes the conversion of mevalonic acid in mevalonate-5-phosphate	Miziorki (2011)
<i>mvD</i>	Mevalonate diphosphate decarboxylase	Catalyzes the conversion of mevalonate pyrophosphate into isopentenyl pyrophosphate	Miziorki (2011)
<i>ispA</i>	Farnesyl diphosphate synthase	Production of farnesyl diphosphate from IPP and DMAPP	
<i>hpnD</i>	Squalene/phytoene synthase	Production of presqualene diphosphate from farnesyl diphosphate	Pan et al. (2015)
<i>hpnC</i>	Squalene/phytoene synthase	Conversion of presqualene diphosphate into hydroxysqualene	Pan et al. (2015)
<i>hpnE</i>	Amine oxidoreductase	Reduction of hydroxysqualene	Pan et al. (2015)
<i>fdFT</i>	Farnesyl diphosphate farnesyl transferase	Putative enzyme for producing squalene from farnesyl diphosphate	
<i>shc</i>	Squalene hopene cyclase	Formation of diploptene from cyclization of squalene	Reipen et al. (1995)
<i>hpnH</i>	Hopanoid-associated radical SAM superfamily protein	Addition of adenosine to hopane skeleton	Bradley et al. (2010); Welander et al. (2012); Schmerk et al. (2015)
<i>hpnG</i>	Hopanoid-associated nucleosidase	Removal of adenine from adenosylhopane	Bradley et al. (2010); Welander et al. (2012); Schmerk et al. (2015)
<i>hpnI</i>	Hopanoid-associated glycosyl transferase	Transfer of acetylglucosamine from UDP-acetylglucosamine to BHT	Schmerk et al. (2015)
<i>hpnK</i>	Hopanoid biosynthesis associated protein	Deacetylation of BHT acetylglucosamine	Schmerk et al. (2015)
<i>hpnJ</i>	Hopanoid-associated radical SAM superfamily protein	Ring contraction to generate BHT cyclitol ether	Schmerk et al. (2015)
<i>hpnO</i>	Aminotransferase	Introduces the amino group to produce aminobacteriohopanetriol	Welander et al. (2012)
<i>hpnP</i>	Hopanoid C-2 methylase HpnR	Introduces a methyl group at position C-2 in a BHP or C ₃₀ hopanoid	Welander et al. (2010)
<i>hpnR</i>	Hopanoid C-3 methylase HpnR	Introduces a methyl group at position C-3 in a BHP or C ₃₀ hopanoid	Welander and Summons (2012)

<i>hpnA</i>	Hopanoid-associated sugar epimerase	Not established	
<i>hpnB</i>	Hopanoid-associated glycosyl transferase	Not established	
<i>ug1</i>	Zn-dependent alcohol dehydrogenase (ca. 370 AA)	Not established	
<i>ug2</i>	Zn-binding alcohol dehydrogenase (ca. 350 AA)	Not established	
<i>ug3</i>	Hypothetical protein (ca. 150 AA)	Not established	
<i>ug4</i>	Hypothetical protein (ca. 130 AA)	Not established	
<i>ug5</i>	Transporter (ca. 140 AA)	Not established	

Table S2: Presence of the *ispA* gene encoding farnesyl diphosphate synthase in genomes of cultivated *Acidobacteria* and environmental genomes based on BLAST searches of the protein sequence in the NCBI database.

Acidobacterial genome	SD	<i>ispA</i>	SI (%)	AC
Cultures				
<i>Acidobacterium capsulatum</i> 161	1	✓	100	WP_015896781.1
<i>Acidobacterium ailaui</i> PMMR2	1	✓	81	WP_026443680.1
<i>Silvibacterium bohemicum</i> S15	1	✓	79	WP_050058068.1
<i>Acidobacteriaceae</i> bacterium KBS 83	1	✓	70	WP_026335820.1
<i>Acidobacteriaceae</i> bacterium KBS 89	1	✓	59	WP_020712160.1
<i>Terracidiphilus gabretensis</i> S55	1	✓	70	WP_058189358.1
<i>Edaphobacter aggregans</i> Wbg-1	1	✓	66	WP_035351326.1
<i>Acidobacteriaceae</i> bacterium URHE0068	1	✓	77	WP_026444623.1
<i>Acidobacteria</i> bacterium KBS 146	1	✓	66	WP_026386959.1
<i>Terriglobus saanensis</i> SPIPR4	1	✓	68	WP_013569474.1
<i>Granulicella mallensis</i> MP5ACTX8	1	✓	64	WP_014267017.1
<i>Granulicella tundricola</i> MP5ACTX9	1	✓	63	WP_013579430.1
<i>Granulicella pectinivorans</i> TPB6011	1	✓	62	SFS13509.1
<i>Bryocella elongata</i> SN10	1	✓	60	SEG01803.1
<i>Terriglobus roseus</i> DSM 18391	1	✓	65	WP_014787013.1
<i>Terriglobus</i> sp. TAA 43	1	✓	67	WP_047498047.1
<i>Terriglobus roseus</i> GAS232	1	-		
<i>Terriglobus roseus</i> AB35.6	1	✓	65	SEC27148.1
<i>Acidobacteriaceae</i> bacterium TAA166	1	✓	66	WP_022844472.1
' <i>Ca. Koribacter versatilis</i> Ellin345'	1	✓	62	ABF42433.1
<i>Acidobacteriaceae</i> bacterium KBS 96	3	✓	53	WP_020721398.1
' <i>Ca. Solibacter usitatus</i> Ellin6076'	3	✓	54	ABJ82108.1
<i>Bryobacter aggregatus</i> MPL3	3	✓	51	WP_031499979.1
<i>Chloracidobacterium thermophilum</i> B	4	✓	50	WP_014100740.1
<i>Chloracidobacterium thermophilum</i> OC1	4	✓	50	WP_058867867.1
<i>Pyrinomonas methylaliphatoles</i> K22	4	✓	44	WP_060635749.1
<i>Luteitalea pratensis</i> HEG_-6_39	6	✓	42	AMY09642.1
<i>Holophaga foetida</i> TMBS4	8	✓	43	WP_005036318.1
<i>Geothrix fermentans</i> H-5	8	✓	45	WP_026852490.1
<i>Thermotomaculum hydrothermale</i> AC55	10	✓	nd	ORF TTHT_0896
<i>Thermoanaerobaculum aquaticum</i> MP-01	23	✓	46	WP_038049832.1
Environmental genomes				
<i>Acidobacteriales</i> bacterium 59-55	1	✓	64	OJV41243.1
<i>Acidobacteriales</i> bacterium 13_1_20CM_4_56_7	1	-		
<i>Acidobacteriales</i> bacterium 13_1_40CM_3_55_5	1	✓	61	OLD16780.1
<i>Acidobacteriales</i> bacterium 13_2_20CM_2_55_5	1	✓	61	OLB88925.1
<i>Acidobacteriales</i> bacterium 13_2_20CM_55_8	1	✓	62	OLB23326.1
<i>Acidobacteria</i> bacterium 13_1_20CM_2_60_10	2	✓	53	OLE84963.1
<i>Acidobacteria</i> bacterium 13_1_20CM_3_58_11	2	✓	54	OLE48756.1

<i>Acidobacteria</i> bacterium 13_1_20CM_58_21	2	✓	54	OLD79709.1
<i>Acidobacteria</i> bacterium 13_1_20CM_4_57_6	2	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_58_4	2	✓	53	OLC90121.1
<i>Acidobacteria</i> bacterium 13_1_40CM_4_61_5	2	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_2_57_6	2	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_17	2	✓	54	OLB40006.1
<i>Acidobacteria</i> bacterium 13_2_20CM_57_7	2	✓	52	OLB17076.1
<i>Acidobacteria</i> bacterium 13_2_20CM_58_27	2	✓	53	OLB25819.1
<i>Acidobacteria</i> bacterium 13_1_20CM_56_16	2'	✓	44	OLC30141.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_59_13	1/3	✓	49	OFW23766.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_61_28	1/3	✓	48	OFW00007.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_54_10	1/3	✓	48	OFV99601.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_11	1/3	✓	48	OFW07476.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_60_22	1/3	✓	52	OFW38722.1
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_02_FULL_67_57	3/4	✓	53	OFV84683.1
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_12_FULL_67_30	3/4	✓	52	OFV88534.1
<i>Acidobacteria</i> bacterium OLB17	4	✓	46	KXK04241.1
<i>Acidobacteria</i> bacterium 13_1_20CM_3_53_8	4	✓	47	OLE51688.1
<i>Acidobacteria</i> bacterium RBG_16_70_10	4'	✓	47	OFV86782.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_64_15	6	✓	40	OFV94460.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_65_29	6	✓	40	OFW19478.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_36	6	✓	44	OFW06494.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_21	6	✓	41	OFW14569.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_68_18	6	✓	40	OFW01586.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_67_14b	6	✓	41	OFW43465.1
<i>Acidobacteria</i> bacterium 13_1_20CM_2_65_9	6	✓	42	OLE82011.1
<i>Acidobacteria</i> bacterium 13_1_40CM_2_64_6	6	✓	42	OLD54426.1
<i>Acidobacteria</i> bacterium 13_1_40CM_65_14	6	✓	42	OLC51735.1
<i>Acidobacteria</i> bacterium SCN 69-37	6	✓	39	ODS51911.1
<i>Acidobacteria</i> bacterium Mor-1	22	✓	47	ANM28771.1
<i>Acidobacteria</i> bacterium RBG_13_68_16	23	✓	45	OFV82917.1
<i>Acidobacteria</i> bacterium 13_1_20CM_2_68_14	U	✓	51	OLE65119.1
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_10	U	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_5	U	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_69_4	U	✓	48	OLC54462.1

Key: SD = subdivision, ✓ = present, - = absent, SI = similarity (%) as blasted against the corresponding gene of *A. capsulatum* ATCC 51196, AC = Accession number in NCBI database, U = unknown

Table S3: Presence of the *hpnC*, *hpnD*, *hpnE* and putative *fdpT* genes encoding enzymes for the synthesis of squalene in *Acidobacterial* genomes of cultures and environmental metagenomes based on BLAST searches of the protein sequence in the NCBI database.

<i>Acidobacterial</i> genome	SD	<i>hpnC</i>	SI ^b	AN	<i>hpnD</i>	SI ^b	AN	<i>hpnE</i>	SI ^b	AN	<i>fdpT</i>	SI ^b	AN
Culture													
<i>Acidobacterium capsulatum</i> 161	1	✓		WP_015895982.1	✓		WP_015895981.1	✓		WP_015895980.1	-		
<i>Acidobacterium ailaui</i> PMMR2	1	✓	78	WP_026441648.1	✓	69	WP_026441649.1	✓	60	WP_026441650.1	-		
<i>Silvibacterium bohemicum</i> S15	1	-			✓	68	WP_050062226.1	-			✓	100	WP_050060027.1
<i>Acidobacteriaceae</i> bacterium KBS 83	1	✓	69	WP_020710815.1	✓	59	WP_020710814.1	✓	61	WP_020710813.1	-		
<i>Acidobacteriaceae</i> bacterium KBS 89	1	✓	55	WP_020713414.1	✓	60	WP_020713415.1	✓			✓	75	WP_020716962.1
<i>Terracidiphilus gabretensis</i> S55	1	✓	70	WP_058185580.1	✓	63	WP_058185519.1	✓	52	WP_058185520.1	-		
<i>Edaphobacter aggregans</i> Wbg-1	1	✓	53	WP_035350376.1	✓	58	WP_035350375.1	✓	50	WP_035350374.1	✓	75 64	WP_035355040.1 WP_035356275.1
<i>Acidobacteriaceae</i> bacterium URHE0068	1	✓	71	WP_051566372.1	✓	62	WP_026448080.1	✓	53	WP_051566374.1	-		
<i>Acidobacteria</i> bacterium KBS 146	1	✓	51	WP_026386235.1	✓	61	WP_026386234.1	✓	50	WP_026386233.1	-		
<i>Terriglobus saanensis</i> SP1PR4	1	✓	55	WP_013568394.1	✓	53	WP_013568395.1	✓	46	WP_013568396.1	-		
<i>Granulicella mallensis</i> MP5ACTX8	1	-			✓	51	WP_014265798.1	-			✓	74	WP_014264191.1
<i>Granulicella tundricola</i> MP5ACTX9	1	✓	55	WP_013580011.1	✓	56	WP_013580012.1	✓	47	WP_013580013.1	-		
<i>Granulicella pectinivorans</i> TPB6011	1	✓	53	SFS16941.1	✓	55	SFS16936.1	✓	48	SFS16932.1	-		
<i>Bryocella elongata</i> SN10	1	✓	50	SEF64291.1	✓	54	SEF64330.1	✓	47	SEF64359.1	-		
<i>Terriglobus roseus</i> DSM 18391	1	✓	51	WP_014785728.1	✓	50	WP_014785729.1	✓	48	WP_014785730.1	-		
<i>Terriglobus</i> sp. TAA 43	1	✓	54	WP_047487867.1	✓	47	WP_047487864.1	✓	49	WP_047487859.1	-		
<i>Terriglobus roseus</i> GAS232	1	✓	54	SDF10618.1	✓	47	SDF10652.1	✓	49	SDF10676.1	-		
<i>Terriglobus roseus</i> AB35.6	1	✓	50	SEB36906.1	✓	52	SEB36915.1	✓	48	SEB36925.1	-		
<i>Acidobacteriaceae</i> bacterium TAA166	1	-			✓	62	WP_026392933.1	-			✓	67	WP_022845438.1
' <i>Ca. Koribacter versatilis</i> Ellin345'	1	✓	64	WP_011522548.1	✓	51	WP_011522549.1	✓	55	WP_011522550.1	-		
<i>Acidobacteriaceae</i> bacterium KBS 96	3	✓	52	WP_020719488.1	✓	44	WP_020719487.1	✓	49	WP_020719725.1	-		
' <i>Ca. Solibacter usitatus</i> Ellin6076'	3	✓	53	WP_011683035.1	✓	44	WP_011683036.1	✓	48	WP_011685297.1	-		
<i>Bryobacter aggregatus</i> MPL3	3	-			✓	41	WP_035957817.1	✓	44	WP_035957682.1	-		
<i>Chloracidobacterium thermophilum</i> B	4	✓	44	AEP13731.1	✓	38 40	WP_014101470.1 WP_014099727.1	✓	28	WP_014100595.1	-		
<i>Chloracidobacterium thermophilum</i> OC1	4	✓ ^b			✓	38 40	WP_058865892.1 WP_058867469.1	✓	27	WP_058867994.1	-		
<i>Pyrinomonas methylaliphatogenes</i> K22	4	-			-			-			-		
<i>Luteitalea pratensis</i> HEG_-6_39	6	✓	35	AMY12733.1	✓	38	AMY12732.1	✓	32	AMY12731.1	-		
<i>Holophaga foetida</i> TMBS4	8	-			-			-			-		
<i>Geothrix fermentans</i> H-5	8	-			-			-			-		
<i>Thermotomaculum hydrothermale</i> AC55	10	-			-			-			-		
<i>Thermoanaerobaculum aquaticum</i> MP-01	23	-			-			-			-		
Environmental genomes													
<i>Acidobacteria</i> bacterium 59-55	1	✓	52	OJV42131.1	✓	57	OJV41583.1	✓	47	OJV41582.1	-		
<i>Acidobacteriales</i> bacterium 13_1_20CM_4_56_7	1	-			-			-			-		

<i>Acidobacteriales</i> bacterium 13_1_40CM_3_55_5	1	✓	62	OLD18787.1	✓	56	OLD18773.1	✓	55	OLD18774.1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_2_55_5	1	✓	62	OLB87678.1	✓	55	OLB87673.1	✓	57	OLB87672.1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_55_8	1	✓	63	OLB22764.1	✓	56	OLB22763.1	✓	58	OLB22762.1	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_60_10	2	✓ ^a	53	OLE83119.1	✓ ^a	41	OLE83119.1	✓	43	OLE83120.1	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_3_58_11	2	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_58_21	2	✓ ^a	52	OLB40690.1	✓ ^a	40	OLB40690.1	✓	43	OLD83138.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_57_6	2	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_58_4	2	✓ ^a	50	OLC96287.1	✓ ^a	41 46	OLC96287.1 OLC90952.1	✓	41	OLC96288.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_61_5	2	✓ ^a	53	OLC88152.1	✓ ^a	39	OLC88152.1	✓	43	OLC88151.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_2_57_6	2	✓ ^a	52	OLB88656.1	✓ ^a	39	OLB88656.1	✓	39	OLB88667.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_17	2	✓ ^a	52	OLB40690.1	✓ ^a	39	OLB40690.1	✓	43	OLB40689.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_7	2	✓ ^a	53	OLB21794.1	✓ ^{ab}			-			-		
<i>Acidobacteria</i> bacterium 13_2_20CM_58_27	2	✓ ^a	52	OLB28866.1	✓ ^a	40	OLB28866.1	✓	43	OLB28865.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_56_16	2 [*]	✓	53	OLC39076.1	✓	42	OLC39075.1	✓	41	OLC39074.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_59_13	1/3	✓	55	OFW14230.1	✓	40	OFW14228.1				-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_61_28	1/3	✓ ^b			✓	41	OFV94765.1	✓	43	OFV94773.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_54_10	1/3	-			-			✓	41	OFV96917.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_11	1/3	-			-						-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_60_22	1/3	✓	60	OFW33133.1	✓	43	OFW33134.1	✓	44	OFW33135.1	-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_02_FULL_67_57	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_12_FULL_67_30	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium OLB17	4	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_3_53_8	4	-			-			-			-		
<i>Acidobacteria</i> bacterium RBG_16_70_10	4 [*]	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_64_15	6	✓	35	OFV91905.1	✓	36	OFV91717.1	-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_65_29	6	✓	39	OFW27858.1	✓	34	OFW27845.1	✓	33	OFW27859.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_36	6	✓	40	OFW11518.1	✓	38	OFW11459.1	✓	34	OFW11460.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_21	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_68_18	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_67_14b	6	✓	39	OFW46408.1	✓	37	OFW46352.1	✓	32	OFW46351.1	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_65_9	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_64_6	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_65_14	6	✓	34	OLC40177.1	✓	36	OLC40174.1	✓	32	OLC40173.1	-		
<i>Acidobacteria</i> bacterium SCN 69-37	6	✓	42	ODS52724.1	✓	35	ODS52560.1	✓	31	ODS52559.1	-		
<i>Acidobacteria</i> bacterium Mor-1	22	-			-			-			✓		ANM31419.1
<i>Acidobacteria</i> bacterium RBG_13_68_16	23	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_68_14	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_10	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_5	U	✓	44	OLD62390.1	✓	38	OLD62389.1	✓ ^b		OLD62377.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_69_4	U	-			-			-			-		

Key: SD = subdivision, ✓ = present, - = absent, SI = similarity (%) as blasted against the corresponding gene of *A. capsulatum* ATCC 51196 or *S. bohemicum* S15 (in case of the putative *fdpT*), AC = Accession number in NCBI database, U = unknown

^a in these cases *hpnC* and *hpnD* are fused (see text); ^b partial gene

Table S4: Presence of the *shc*, *hpnH*, *hpnG*, and *hpnA* genes encoding enzymes in BHP synthesis in genomes of cultivated *Acidobacteria* based on BLAST searches of the protein sequence in the NCBI database.

<i>Acidobacterial genome</i>	SD	<i>shc</i>	SI ^a (%)	AC	<i>hpnH</i>	SI ^b (%)	AC	<i>hpnG</i>	SI ^b	AC	<i>hpnA</i>	SI ^b	AC
Cultures													
<i>Acidobacterium capsulatum</i> 161	1	✓	100	WP_015898362.1	✓	100	WP_015898363.1	✓	100	WP_015895985.1	✓	100	WP_015895986.1
<i>Acidobacterium ailaui</i> PMMR2	1	✓	85	WP_026443152.1	-	-	-	✓	49	WP_026441645.1	✓	76	WP_026441644.1
<i>Silvibacterium bohemicum</i> S15	1	✓	82	WP_050061632.1	✓	92	WP_050061630.1	✓	54	WP_050062229.1	✓	81	WP_050062230.1
<i>Acidobacteriaceae</i> bacterium KBS 83	1	✓	81	WP_035222935.1	✓	82	WP_020710821.1	✓	39	WP_020710818.1	✓	76	WP_020710819.1
<i>Acidobacteriaceae</i> bacterium KBS 89	1	✓	78	WP_020713669.1	✓	81	WP_020713668.1	✓	39	WP_020713665.1	✓	74	WP_020713666.1
<i>Terracidiphilus gabretensis</i> S55	1	✓	78	WP_058185512.1	✓	71	WP_058185513.1	✓	40	WP_058185516.1	✓	71	WP_058185515.1
<i>Edaphobacter aggregans</i> Wbg-1	1	✓	76	WP_035349256.1	✓	87	WP_035349255.1	✓	45	WP_051978543.1	✓	76	WP_035349251.1
<i>Acidobacteriaceae</i> bacterium URHE0068	1	✓	78	WP_026448065.1	✓	70	WP_026448064.1	✓	40	WP_051566259.1	✓	71	WP_026448074.1
<i>Acidobacteria</i> bacterium KBS 146	1	✓	76	WP_026385916.1	✓	90	WP_026385917.1	✓	47	WP_051627860.1	✓	73	WP_026385919.1
<i>Terriglobus saanensis</i> SP1PR4	1	✓	75	WP_013568531.1	✓	82	WP_013568529.1	✓	37	WP_013568523.1	✓	74	WP_013568525.1
<i>Granulicella mallensis</i> MP5ACTX8	1	✓	74	WP_014264569.1	✓	86	WP_014264570.1	✓	39	WP_014264573.1	✓	74	WP_014264572.1
<i>Granulicella tundricola</i> MP5ACTX9	1	✓	71	WP_013579964.1	✓	82	WP_013579965.1	✓	40	WP_013579968.1	✓	75	WP_013579967.1
<i>Granulicella pectinivorans</i> TPB6011	1	✓	70 44	SFS15998.1 SFS15307.1	✓	86	SFS16003.1	✓	36	SFS16018.1	✓	74	SFS16012.1
<i>Bryocella elongata</i> SN10	1	✓	70	SEF69162.1	✓	85	SEF69136.1	✓	38	SEF69052.1	✓	69	SEF69081.1
<i>Terriglobus roseus</i> DSM 18391	1	✓	74	WP_014785831.1	✓	80	WP_014785830.1	✓	40	WP_014785827.1	✓	72	WP_014785828.1
<i>Terriglobus</i> sp. TAA 43	1	✓	70	WP_047488088.1	✓	81	WP_047488086.1	✓	40	WP_052200307.1	✓	71	WP_047488072.1
<i>Terriglobus roseus</i> GAS232	1	✓	71	SDF08232.1	✓	81	SDF08278.1	✓	38	SDF08494.1	✓	70	SDF08455.1
<i>Terriglobus roseus</i> AB35.6	1	✓	74	SEB38205.1	✓	80	SEB38193.1	✓	38	SEB38159.1	✓	72	SEB38171.1
<i>Acidobacteriaceae</i> bacterium TAA166	1	✓	71	WP_022845288.1	✓	88	WP_022845289.1	✓	45	WP_022845292.1	✓	71	WP_022845291.1
' <i>Ca. Koribacter versatilis</i> Ellin345'	1	✓	68	ABF40741.1	✓	71	WP_011521820.1	✓	31	WP_011522545.1	✓	62	WP_011522544.1
<i>Acidobacteriaceae</i> bacterium KBS 96	3	✓	47	WP_020719493.1	✓	73	WP_020719381.1	✓	27	WP_020719491.1	✓	51	WP_020719492.1
' <i>Ca. Solibacter usitatus</i> Ellin6076'	3	✓	44 46	WP_011683030.1 WP_011682956.1	✓	69	WP_011685281.1	✓	36	WP_011683032.1	✓	54	WP_011683031.1
<i>Bryobacter aggregatus</i> MPL3	3	✓	44	WP_035957816.1	✓	44	WP_051670105.1	✓	44	WP_031498836.1	✓	51	WP_031498835.1
<i>Chloracidobacterium thermophilum</i> B	4	✓	43	WP_014100779.1	✓	39	WP_014100993.1	✓	33	WP_014101332.1	✓	50	WP_014101352.1
<i>Chloracidobacterium thermophilum</i> OC10	4	✓	43	WP_058866228.1	✓	39	WP_058866121.1	✓	30	WP_058868517.1	✓	50	WP_058868498.1
<i>Pyrinomonas methylaliphatogenes</i> K22	4	-			-			-			-		
<i>Luteitalea pratensis</i> HEG -6_39	6	-			-			-			-		
<i>Holophaga foetida</i> TMBS4	8	-			-			-			-		
<i>Geothrix fermentans</i> H-5	8	-			-			-			-		
<i>Thermotomaculum hydrothermale</i> AC55	10	-			-			-			-		
<i>Thermoanaerobaculum aquaticum</i> MP-01	23	-			-			-			-		
Environmental genomes													
<i>Acidobacteriales</i> bacterium 59-55	1	✓	76	OJV41826.1	✓	80	OJV41825.1	-			✓	80	OJV41823.1
<i>Acidobacteriales</i> bacterium 13_1_20CM_4_56_7	1	✓	68	OLE14569.1	✓	65	OLE14570.1	-			-		
<i>Acidobacteriales</i> bacterium 13_1_40CM_3_55_5	1	✓	68	OLD19462.1	-			✓	31	OLD19458.1	✓	64	OLD19459.1

<i>Acidobacteriales</i> bacterium 13_2_20CM_2_55_5	1	✓	68	OLB88617.1	✓	73	OLB88618.1	✓	31	OLB87675.1	✓	65	OLB87680.1
<i>Acidobacteriales</i> bacterium 13_2_20CM_55_8	1	✓	69	OLB21625.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_60_10	2	✓	44	OLE83115.1	-			✓	25	OLE83117.1	✓	51	OLE83116.1
<i>Acidobacteria</i> bacterium 13_1_20CM_3_58_11	2	✓	44	OLE45836.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_58_21	2	-			✓	74	OLD79942.1	✓	28	OLD83135.1	✓	52	OLD83134.1
<i>Acidobacteria</i> bacterium 13_1_40CM_4_57_6	2		45	OLC82649.1	-			-			✓	50	OLC82648.1
<i>Acidobacteria</i> bacterium 13_1_40CM_4_58_4	2	✓	45 43	OLC90948.1 OLC96281.1	✓	73 40	OLC89682.1 OLC90949.1	✓	24 24	OLC90951.1 OLC96285.1	✓	51 50	OLC96284.1 OLC90950.1
<i>Acidobacteria</i> bacterium 13_1_40CM_4_61_5	2	-			✓	75	OLC88768.1	✓	25	OLC88154.1	✓	50	OLC88155.1
<i>Acidobacteria</i> bacterium 13_2_20CM_2_57_6	2	✓	45	OLB87282.1	✓	74	OLB82578.1	✓	26	OLB88654.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_17	2	✓	45	OLB40694.1	✓	74	OLB40168.1	✓	26	OLB40691.1	✓	50	OLB40692.1
<i>Acidobacteria</i> bacterium 13_2_20CM_57_7	2	✓	45	OLB21789.1	✓	74	OLB18125.1	✓	26	OLB21792.1	✓	50	OLB21791.1
<i>Acidobacteria</i> bacterium 13_2_20CM_58_27	2	✓	45	OLB28953.1	✓	73	OLB28086.1	✓	27	OLB28868.1	✓	50	OLB28869.1
<i>Acidobacteria</i> bacterium 13_1_40CM_56_16	2'	✓	44	OLC39085.1	✓	40	OLC39079.1	✓	23	OLC39077.1	✓	50	OLC39078.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_59_13	1/3	-			-			✓	29	OFW14227.1	✓	53	OFW14226.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_61_28	1/3	✓	51	OFV92199.1	✓	41	OFV92200.1	✓	32	OFV92202.1	✓	54	OFV92201.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_54_10	1/3	-			✓	43	OFV98826.1	-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_11	1/3	✓	47	OFW00329.1	✓	43	OFW00328.1	✓	28	OFW00326.1	✓	54	OFW00327.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_60_22	1/3	-			-			✓	19	OFW36620.1	-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_02_FULL_67_57	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_12_FULL_67_30	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium OLB17	4	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_3_53_8	4	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_3_55_6	4	-			-			-			-		
<i>Acidobacteria</i> bacterium RBG_16_70_10	4'	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_64_15	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_65_29	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_36	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_21	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_68_18	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_67_14b	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_65_9	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_64_6	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_65_14	6	-			-			-			-		
<i>Acidobacteria</i> bacterium SCN 69-37	6	-			-			-			-		
<i>Acidobacteria</i> bacterium Mor-1	22	✓	47	ANM31425.1	✓	39	ANM31424.1	-			?	28	ANM30436.1
<i>Acidobacteria</i> bacterium RBG_13_68_16	23	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_68_14	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_10	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_5	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_69_4	U	-			-			-			-		

Key: SD = subdivision, ✓ = present, - = absent, SI = similarity (%) as blasted against the corresponding gene of *A. capsulatum* ATCC 51196, AC = Accession number in NCBI database, U = unknown

Table S5: Presence of the *hpnB*, *hpnI*, *hpnJ* and *hpnK* genes encoding enzymes in BHP synthesis in genomes of cultivated *Acidobacteria* and *Acidobacterial* metagenomes based on BLAST searches of the protein sequence in the NCBI database.

<i>Acidobacterial</i> (meta)genome	SD	<i>hpnB</i>	SI (%) ^b	AC	<i>hpnI</i>	SI (%) ^b	AC	<i>hpnJ</i>	SI (%) ^b	AC	<i>hpnK</i>	SI ^b	AC
Cultures													
<i>Acidobacterium capsulatum</i> ATCC 51196	1	-			✓	100	WP_015897110.1	✓	100	WP_015898078.1	-		
<i>Acidobacterium ailaui</i> PMMR2	1	-			✓	60	WP_026442134.1	✓	91	WP_026441760.1	-		
<i>Silvibacterium bohemicum</i> S15	1	-			✓	59	WP_050060510.1	✓	90	WP_050062222.1	-		
<i>Acidobacteriaceae</i> bacterium KBS 83	1	-			✓	58	WP_035223311.1	✓	86	WP_020710808.1	-		
<i>Acidobacteriaceae</i> bacterium KBS 89	1	-			✓	57	WP_020715618.1	✓	84	WP_020713421.1	-		
<i>Terracidiphilus gabretensis</i> S55	1	-			✓	56	WP_058187425.1	✓	83	WP_058185522.1	-		
<i>Edaphobacter aggregans</i> DSM 19364	1	✓	90	WP_035352220.1	✓	56	WP_064742595.1	✓	87	WP_035350369.1	-		
<i>Acidobacteriaceae</i> bacterium URHE0068	1	✓	57	WP_026446012.1	✓	55	WP_026448633.1	✓	83	WP_026448084.1	-		
<i>Acidobacteria</i> bacterium KBS 146	1	-			✓	56	WP_035176462.1	✓	87	WP_026386227.1	-		
<i>Terriglobus saanensis</i> SP1PR4	1	-			✓	54	WP_049781167.1	✓	85	WP_013568400.1	-		
<i>Granulicella mallensis</i> MP5ACTX8	1	✓	100	WP_014265833.1	✓	55	WP_014263407.1	✓	84	WP_014265795.1	-		
<i>Granulicella tundricola</i> MP5ACTX9	1	-			✓	54	WP_013578476.1	✓	82	WP_013580018.1	-		
<i>Granulicella pectinivorans</i> DSM 21001	1	-			✓	55	SFS03073.1	✓	85	SFS16903.1	-		
<i>Bryocella elongata</i> DSM 22489	1	-			✓	54	SEG20810.1	✓	85	SEF64546.1	-		
<i>Terriglobus roseus</i> DSM 18391	1	-			✓	52	WP_014784111.1	✓	81	WP_014785733.1	-		
<i>Terriglobus</i> sp. TAA 43	1	✓	57	WP_047494619.1	✓	50	WP_047492068.1	✓	83	WP_047487014.1	-		
<i>Terriglobus roseus</i> GAS232	1	✓	56	SDF88027.1	✓	51	SDF78336.1	✓	83	SDF24644.1	-		
<i>Terriglobus roseus</i> AB35.6	1	-			✓	54	SEB85419.1	✓	82	SEB36957.1	-		
<i>Acidobacteriaceae</i> bacterium TAA166	1	-			✓	54	WP_022843429.1	✓	85	WP_022844919.1	-		
'Ca. Koribacter versatilis Ellin345'	1	-			✓	49	WP_011521530.1	✓	76	WP_011523121.1	-		
<i>Acidobacteriaceae</i> bacterium KBS 96	3	✓	46	WP_020722380.1	✓	38	WP_020720612.1	✓	65	WP_020720609.1	-		
'Ca. Solibacter usitatus Ellin6076'	3	✓	44	WP_011685564.1	✓	40	WP_049873324.1	✓	68	WP_011689127.1	-		
<i>Bryobacter aggregatus</i> MPL3	3	-			✓	39	WP_051669583.1	✓	63	WP_031496923.1	-		
<i>Chloracidobacterium thermophilum</i> B	4	-			✓	39	WP_014100987.1	✓	64	WP_014100991.1	✓	100	WP_014100990.1
<i>Chloracidobacterium thermophilum</i>	4	-			✓	42	WP_058866115.1	✓	64	WP_058866119.1	✓	98	WP_058866118.1
<i>Pyrinomonas methylaliphatogenes</i> K22	4	-			-			-			-		
<i>Luteitalea pratensis</i> HEG -6 39	6	-			-			-			-		
<i>Holophaga foetida</i> DSM 6591	8	-			-			-			-		
<i>Geothrix fermentans</i> DSM 14018	8	-			-			-			-		
<i>Thermotomaculum hydrothermale</i> AC55	10	-			-			-			-		
<i>Thermoanaerobaculum aquaticum</i> MP-01	23	-			-			-			-		
Environmental genomes													
<i>Acidobacteria</i> bacterium 59-55	1	-			✓	56	OJV44113.1	✓	82	OJV41462.1	-		
<i>Acidobacteriales</i> bacterium 13_1_20CM_4_56_7	1	-			-			-			-		
<i>Acidobacteriales</i> bacterium 13_1_40CM_3_55_5	1	✓	42	OLD15195.1	-			✓	76	OLD18777.1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_2_55_5	1	-			✓	48	OLB84463.1	✓	73	OLB87669.1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_55_8	1	-			✓	49	OLB20242.1	✓	77	OLB22759.1	-		

<i>Acidobacteria</i> bacterium 13_1_20CM_2_60_10	2	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_3_58_11	2	✓	37	OLE47118.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_58_21	2	✓	38	OLD82715.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_57_6	2	✓	40	OLC84446.1	✓	39 34	OLC83552.1 OLC83269.1	✓	64	OLC83549.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_58_4	2	✓	39	OLC96924.1	✓	40	OLC91614.1	✓	62	OLC91617.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_61_5	2	✓	43	OLC88360.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_2_20CM_2_57_6	2	✓	42	OLB84357.1	-			-			-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_17	2	✓	40	OLB34865.1	✓	39	OLB34984.1	✓	63	OLB34980.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_7	2	-			✓	40	OLB18610.1	✓	63	OLB18614.1	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_58_27	2	✓	39	OLB32266.1	✓	40	OLB30651.1	✓	65	OLB30648.1	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_56_16	2'	-			✓	44 40 34	OLC31961.1 OLC29808.1 OLC37113.1	✓	62	OLC31958.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_13	1/3	-			✓	40	OFW16935.1	✓	66	OFW16931.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_61_28	1/3	-			✓	38 35	OFV99257.1 OFV98740.1	✓	63	OFV99253.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_54_10	1/3	-			-			✓	65	OFV93540.1	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_11	1/3	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_60_22	1/3	-			✓	34	OFW35345.1	-			-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_02_FULL_67_57	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_12_FULL_67_30	3/4	-			-			-			-		
<i>Acidobacteria</i> bacterium OLB17	4	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_3_53_8	4	-			-			-			-		
<i>Acidobacteria</i> bacterium RBG_16_70_10	4'	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_64_15	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_65_29	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_36	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_21	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_68_18	6	-			-			-			-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_67_14b	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_65_9	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_64_6	6	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_65_14	6	-			-			-			-		
<i>Acidobacteria</i> bacterium SCN 69-37	6	-			-			-			-		
<i>Acidobacteria</i> bacterium Mor-1	22	✓	39	ANM31838.1	-			-			-		
<i>Acidobacteria</i> bacterium RBG_13_68_16	23	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_68_14	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_10	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_5	U	-			-			-			-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_69_4	U	-			-			-			-		

Key: SD = subdivision, ✓ = present, - = absent, SI = similarity (%) as blasted against the corresponding gene of *A. capsulatum* ATCC 51196, *G. mallensis* MP5ACTX8 or *C. thermophilum* B, AC = Accession number in NCBI database, U = unknown

Table S6: Presence of the *hpnO* gene encoding an enzyme in BHP synthesis in genomes of cultivated *Acidobacteria* and *Acidobacterial* metagenomes based on BLAST searches of the protein sequence in the NCBI database.

<i>Acidobacterial</i> genomes	SD	<i>hpnO</i>	SI (%) ^b	AC
Cultures				
<i>Acidobacterium capsulatum</i> 161	1	✓	100	WP_015897314.1
<i>Acidobacterium ailaui</i> PMMR2	1	✓	79	WP_044933846.1
<i>Silvibacterium bohemicum</i> S15	1	✓	82	WP_050058300.1
<i>Acidobacteriaceae</i> bacterium KBS 83	1	✓	82	WP_020707688.1
<i>Acidobacteriaceae</i> bacterium KBS 89	1	✓	77	WP_051098220.1
<i>Terracidiphilus gabretensis</i> S55	1	✓	75	WP_058188695.1
<i>Edaphobacter aggregans</i> Wbg-1	1	✓	78	
<i>Acidobacteriaceae</i> bacterium URHE0068	1	✓	79	WP_035237387.1
<i>Acidobacteria</i> bacterium KBS 146	1	✓	77	WP_026387216.1
<i>Terriglobus saanensis</i> SP1PR4	1	-		
<i>Granulicella mallensis</i> MP5ACTX8	1	✓	77	WP_044178275.1
<i>Granulicella tundricola</i> MP5ACTX9	1	-		
<i>Granulicella pectinivorans</i> TPB6011	1	-		
<i>Bryocella elongata</i> SN10	1	-		
<i>Terriglobus roseus</i> DSM 18391	1	-		
<i>Terriglobus</i> sp. TAA 43	1	-		
<i>Terriglobus roseus</i> GAS232	1	-		
<i>Terriglobus roseus</i> AB35.6	1	-		
<i>Acidobacteriaceae</i> bacterium TAA166	1	-		
'Ca. Koribacter versatilis Ellin345'	1	✓	72	WP_011524788.1
<i>Acidobacteriaceae</i> bacterium KBS 96	3	✓	60	WP_044952283.1
'Ca. Solibacter usitatus Ellin6076'	3	✓	56	WP_011684194.1
<i>Bryobacter aggregatus</i> MPL3	3	✓	54	WP_035957839.1
<i>Chloracidobacterium thermophilum</i> B	4	✓	53	WP_014098758.1
<i>Chloracidobacterium thermophilum</i> OC1	4	-		
<i>Pyrinomonas methylaliphatogenes</i> K22	4	✓	58	WP_041978156.1
<i>Luteitalea pratensis</i> HEG_-6_39	6	✓	57	AMY11128.1
<i>Holophaga foetida</i> TMBS4	8	-		
<i>Geothrix fermentans</i> H-5	8	-		
<i>Thermotomaculum hydrothermale</i> AC55	10	-		
<i>Thermoanaerobaculum aquaticum</i> MP-01	23	-		
Environmental genomes				
<i>Acidobacteriales</i> bacterium 59-55	1	-		
<i>Acidobacteriales</i> bacterium 13_1_20CM_4_56_7	1	✓	72	OLE11736.1
<i>Acidobacteriales</i> bacterium 13_1_40CM_3_55_5	1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_2_55_5	1	-		
<i>Acidobacteriales</i> bacterium 13_2_20CM_55_8	1	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_60_10	2	✓	61	OLE86312.1

<i>Acidobacteria</i> bacterium 13_1_20CM_3_58_11	2	✓	58	OLE46603.1
<i>Acidobacteria</i> bacterium 13_1_20CM_58_21	2	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_4_57_6	2	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_58_4	2	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_4_61_5	2	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_2_57_6	2	-	59	OLB88366.1
<i>Acidobacteria</i> bacterium 13_2_20CM_57_17	2	-		
<i>Acidobacteria</i> bacterium 13_2_20CM_57_7	2	✓	59	OLB17291.1
<i>Acidobacteria</i> bacterium 13_2_20CM_58_27	2	✓	56	OLB27672.1
<i>Acidobacteria</i> bacterium 13_1_20CM_56_16	2'	✓	56	OLC29154.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_59_13	1/3	✓	57	OFW10540.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_61_28	1/3	✓	60	OFV98128.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_54_10	1/3	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_59_11	1/3	✓	60	OFW06698.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_60_22	1/3	✓	57	OFW10540.1
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_02_FULL_67_57	3/4	-		
<i>Acidobacteria</i> bacterium RIFCSPHIGHO2_12_FULL_67_30	3/4	-		
<i>Acidobacteria</i> bacterium OLB17	4	✓	49	KXK05977.1
<i>Acidobacteria</i> bacterium 13_1_20CM_3_53_8	4	✓	55	OLE53531.1
<i>Acidobacteria</i> bacterium RBG_16_70_10	4'	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_64_15	6	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_65_29	6	✓	56	OFW28539.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_36	6	✓	56	OFW09896.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_67_21	6	✓	57	OFW14803.1
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_02_FULL_68_18	6	-		
<i>Acidobacteria</i> bacterium RIFCSPLOWO2_12_FULL_67_14b	6	✓	53	OFW42207.1
<i>Acidobacteria</i> bacterium 13_1_20CM_2_65_9	6	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_64_6	6	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_65_14	6	-		
<i>Acidobacteria</i> bacterium SCN 69-37	6	-		
<i>Acidobacteria</i> bacterium Mor-1	22	-		
<i>Acidobacteria</i> bacterium RBG_13_68_16	23	-		
<i>Acidobacteria</i> bacterium 13_1_20CM_2_68_14	U	-		
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_10	U	✓	50	OLD67358.1
<i>Acidobacteria</i> bacterium 13_1_40CM_2_68_5	U	✓	50	OLD62359.1
<i>Acidobacteria</i> bacterium 13_1_40CM_4_69_4	U	-		

Key: SD = subdivision, ✓ = present, - = absent, SI = similarity (%) as blasted against the corresponding gene of *A. capsulatum* ATCC 51196, AC = Accession number in NCBI database, U = unknown