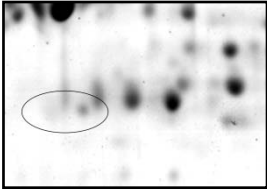
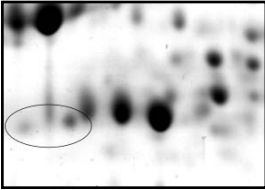
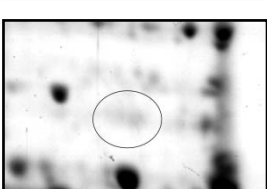
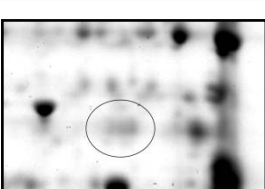
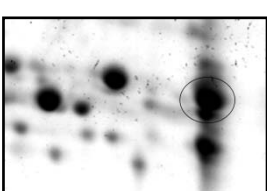
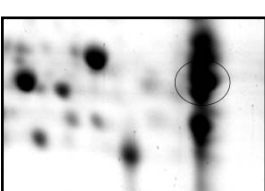
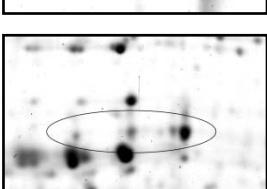
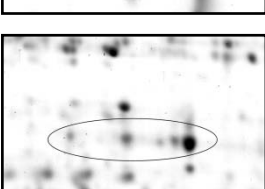
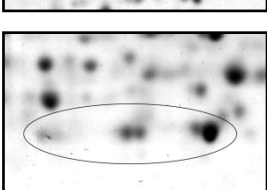
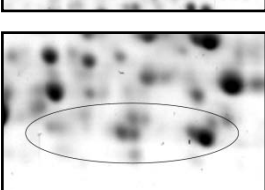
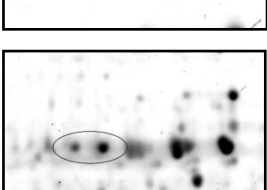
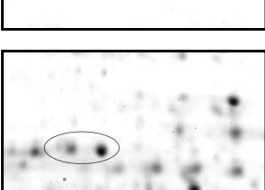
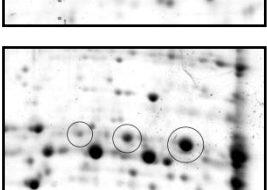
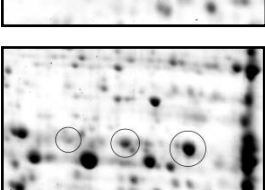
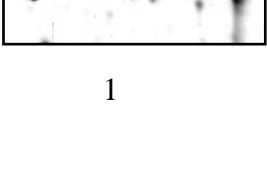
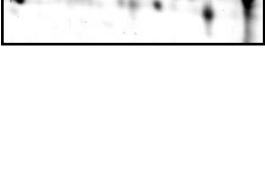


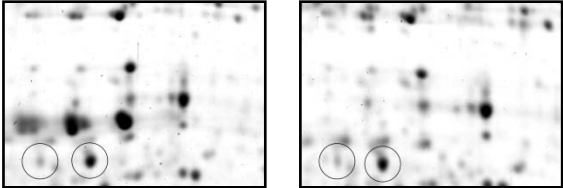
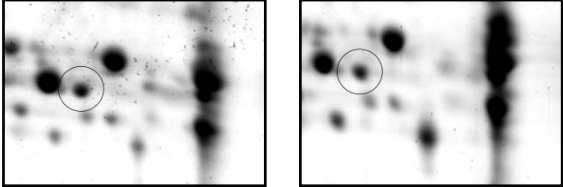


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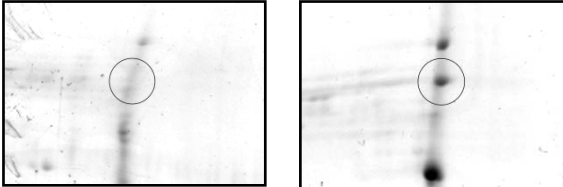
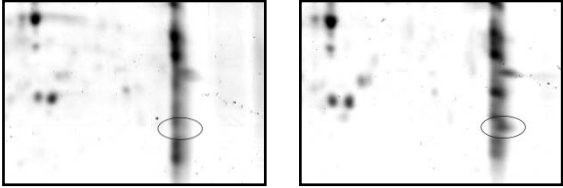
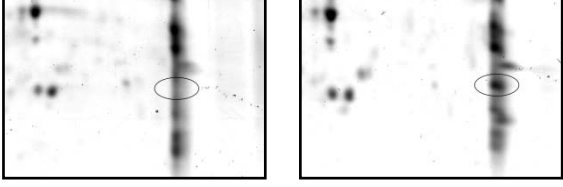
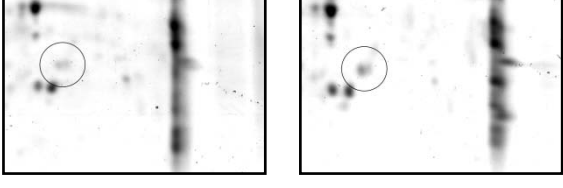
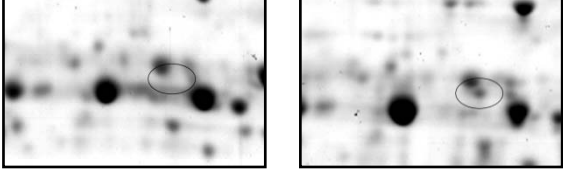
2 **Supplementary Table S1:** Listed proteins are classified with regard to their function. Proteins with a factor3 > 1.0 (significant: factor ≥ 2.0) showed increased abundance in the acidogenesis (pH 5.7). Proteins with factor4 < 1.0 (significant: factor ≤ 0.5) showed increased abundance in the solventogenesis (pH 4.5).

5

ORF	Protein name ^a	Spot # ^b	pH 5.7	pH 4.5	Ratio ^{c,d}
<u>formation of acids</u>					
CAC1742 (<i>pta</i>)	Phosphate acetyl- transferase	A 220 S 320, 321			~ 0.6
					
CAC1743 (<i>ack</i>)	Acetate kinase	A 179 S 206			~ 0.9
					
CAC2873 (<i>thl</i>)	Acetyl-CoA acetyl- transferase	A 275 S 227			~1.3
					
CAC2708 (<i>hbd</i>)	3-hydroxy-butyryl- CoA dehydrogenase	A 272, 324, 345 S 249, 251, 322			~1.2
					
CAC2709 (<i>etfA</i>)	Electron transfer flavoprotein alpha- subunit	A 219, 223, 285 S 229, 387			~1.2
CAC2710 (<i>etfB</i>)	Electron transfer flavoprotein beta- subunit	A 335, 336 S 324, 325			~ 2.1
CAC2711 (<i>bcd</i>)	Butyryl-CoA dehydrogenase	A 194, 195, 197 S 220, 362, 365			~1.3

CAC2712 (<i>crt</i>)	Enoyl-CoA hydratase	A 338, 339 S 264, 265		~1.1
CAC3075 (<i>buk</i>)	Butyrate kinase	A 206 S 224		~1.2

formation of solvents

CA_P0162 (<i>adhe1</i>)	Aldehyde dehydrogenase (NAD ⁺)	S 45		∞
CA_P0163 (<i>ctfA</i>)	Butyrate- acetoacetate CoA- transferase subunit A	S 344		∞
CA_P0164 (<i>ctfB</i>)	Butyrate- acetoacetate CoA- transferase subunit B	S 278		∞
CA_P0165 (<i>adc</i>)	Acetoacetate decarboxylase	A 263 S 268		~0.8
CAC3298 (<i>bdhB</i>)	NADH-dependent butanol dehydrogenase B	S 369		∞

1 ^a: Protein names according to NÖLLING et al. (2001).

2 ^b: The spot number indicated the proteins of the proteome map for the acidogenesis (A) at pH 5.7 (Fig. S1) or
3 solventogenesis (S) at pH 4.5 (Fig. S2).

4 ^c: If more than one protein spot was detected, the average of all protein spots is shown (SD4).

1 ^d: The sign for nonterminating (⊖) indicates that the protein was not detectable under acidogenic conditions at
 2 pH 5.7.

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5 **Supplementary Table S2: Classification of genes with regard to their function.** Genes with an average fold
 6 regulation > 1.0 (significant: average ≥ 3.0 and the values in at least in three out of four microarrays ≥ 2.0)
 7 showed elevated transcript levels in acidogenesis (pH 5.7) or repressed transcript levels in the solventogenesis,
 8 respectively. Genes with fold regulation < 1.0 (significant: average ≤ 0.33 and the values in at least three out of
 9 four microarrays ≤ 0.5) showed elevated transcript levels in the solventogenesis (pH 4.5) or repressed transcript
 10 levels in the acidogenesis (pH 5.7), respectively.

ORF	Gene	Protein function ^a	1. array	2. array	3. array	4. array	Average fold reg.	SD
<u>glycolysis</u>								
CAC2680	<i>pgi</i>	Glucose-6-phosphate isomerase	1.2	1.1	4.4	2.8	2.4	1.5
CAC0517	<i>pfkA</i>	6-phosphofructokinase	1.1	1.0	1.7	1.1	1.2	0.3
CAC0827		Fructose-bisphosphate aldolase	1.1	1.0	1.8	1.6	1.4	0.4
CAC3657		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	0.6	0.5	1.3	0.7	0.8	0.3
CAC0709	<i>gapC</i>	Glyceraldehyde 3-phosphate dehydrogenase	1.0	0.9	1.9	1.9	1.4	0.5
CAC0710	<i>pgk</i>	Phosphoglycerate kinase	1.5	1.4	2.5	1.8	1.8	0.5
CAC0711	<i>tpi</i>	Triosephosphate isomerase	1.2	0.8	3.4	1.7	1.8	1.1
CAC0712	<i>pgm</i>	Phosphoglyceromutase	0.7	0.7	2.9	1.7	1.5	1.1
CAC0713	<i>eno</i>	Phosphopyruvate hydratase	0.9	0.8	2.8	1.6	1.5	0.9
CAC0518	<i>pykA</i>	Pyruvate kinase	1.8	1.1	4.4	1.8	2.3	1.5
CAC1036	<i>pykA</i>	Pyruvate kinase	1.6	1.3	3.4	1.8	2.0	0.9
CAC0028	<i>hydA</i>	Hydrogene dehydrogenase	1.6	1.4	2.2	1.7	1.7	0.4
<u>formation of acids</u>								
CAC1742	<i>pta</i>	Phosphate acetyltransferase	0.8	0.8	1.2	1.0	0.9	0.2
CAC1743	<i>ack</i>	Acetate kinase	0.9	0.8	1.0	0.9	0.9	0.1
CAC2873	<i>thlA</i>	Acetyl-CoA acetyltransferase	2.3	1.7	8.1	3.5	3.9	2.9
CAC2708	<i>hbd</i>	3-hydroxybutyryl-CoA dehydrogenase	1.9	1.5	3.3	3.3	2.5	0.9

CAC2709	<i>etfA</i>	Electron transfer flavoprotein alpha-subunit	2.3	2.0	5.4	2.4	3.0	1.6
CAC2710	<i>etfB</i>	Electron transfer flavoprotein beta-subunit	1.9	1.6	6.6	2.4	3.1*	2.4
CAC2711	<i>bcd</i>	Butyryl-CoA dehydrogenase	2.0	1.8	6.1	2.4	3.1	2.0
CAC2712	<i>crt</i>	Enoyl-CoA hydratase	2.1	1.8	7.2	2.9	3.5	2.5
CAC3075	<i>buk</i>	Butyrate kinase	4.0	2.8	8.1	5.7	5.1	2.3
CAC3076	<i>ptb</i>	Phosphate butyryltransferase	3.4	2.5	9.5	5.4	5.2	3.1

formation of solvents

CA_P0162	<i>adhe1</i>	Aldehyde dehydrogenase (NAD ⁺)	0.012	0.009	0.008	0.004	0.008	0.003
CA_P0163	<i>ctfA</i>	Butyrate-acetoacetate CoA-transferase subunit A	0.009	0.010	0.009	0.004	0.008	0.003
CA_P0164	<i>ctfB</i>	Butyrate-acetoacetate CoA-transferase subunit B	0.014	0.010	0.007	0.004	0.008	0.004
CA_P0165	<i>adc</i>	Acetoacetate decarboxylase	0.4	0.4	0.5	0.4	0.4	0.1
CAC3298	<i>bdhB</i>	NADH-dependent butanol dehydrogenase B	0.5	0.5	1.0	0.6	0.6	0.2
CAC3299	<i>bdhA</i>	NADH-dependent butanol dehydrogenase A	1.2	1.1	2.3	2.2	1.7	0.6
CA_P0035	<i>adhe2</i>	Aldehyde-alcohol dehydrogenase	2.9	3.4	2.9	2.3	2.9	0.4
CA_P0059		Alcohol dehydrogenase	1.0	0.9	0.9	1.0	1.0	0.1
CAC3392		NADH-dependent butanol dehydrogenase	1.2	0.9	2.2	1.1	1.4	0.6

stress response

CAC1280	<i>hrcA</i>	Heat-inducible transcription repressor	0.7	0.5	1.4	0.7	0.8	0.4
CAC1281	<i>grpE</i>	Molecular chaperone GrpE	0.8	0.7	1.9	0.6	1.0	0.6
CAC1282	<i>dnaK</i>	Molecular chaperone DnaK	0.7	0.6	2.2	0.8	1.1	0.8
CAC1283	<i>dnaJ</i>	Molecular chaperones DnaJ (HSP40 family)	0.6	0.6	1.8	0.8	0.9	0.6
CAC0456	<i>lonA</i>	ATP-dependent protease	0.7	0.7	0.5	0.6	0.6	0.1
CAC2637	<i>lonA</i>	ATP-dependent Lon protease	1.2	1.1	1.7	1.0	1.3	0.3
CAC2703	<i>groEL</i>	Chaperonin GroEL	0.6	0.5	2.0	1.5	1.2	0.7
CAC2704	<i>groES</i>	Co-chaperonin GroES (HSP10 family)	0.7	0.4	3.5	1.0	1.4	1.4
CAC3189	<i>clpC</i>	ATPase with chaperone activity	1.3	1.1	3.0	1.8	1.8	0.9
CAC3190		ATP guanido phosphotransferase	1.7	1.5	2.9	1.2	1.8	0.7
CAC3191	<i>yacH</i>	Uncharacterized conserved protein	1.7	1.4	2.4	1.2	1.7	0.6
CAC3192	<i>ctsR</i>	Transcriptional regulator	1.7	1.5	1.8	1.4	1.6	0.2

CAC0648		Molecular chaperone, DnaJ family	0.8	1.2	0.5	0.8	0.8	0.3
CAC1412	<i>cdrC</i>	Methyl methane sulfonate/mytomycin C/UV resistance protein	2.5	2.5	2.2	1.5	2.2	0.5
CAC1415		TerC family protein, ortholog of stress response protein	1.7	2.0	0.9	1.2	1.5	0.5
CAC1716		Uncharacterized stress-induced protein, YicC family	1.1	1.0	3.3	1.3	1.7	1.1
CAC3315	<i>htpG</i>	Heat shock protein 90	1.3	1.0	5.7	2.4	2.6	2.1
CAC3714		Molecular chaperone (small heat shock protein) HSP18	0.5	0.4	0.6	0.6	0.5	0.1
<u>formation of branched chain amino acids</u>								
CAC0091	<i>ilvC</i>	Ketol-acid reductoisomerase	0.4	0.3	1.4	0.9	0.7	0.5
CAC1479	<i>ilvE</i>	Branched-chain amino acid aminotransferase	0.8	0.8	1.3	1.1	1.0	0.2
CAC3169	<i>ilvB</i>	Acetolactate synthase large subunit	0.6	0.7	0.7	0.5	0.6	0.1
CAC3170	<i>ilvD</i>	Dihydroxy-acid dehydratase	0.5	0.6	0.7	0.5	0.6	0.1
CAC3171	<i>leuB</i>	Isopropylmalate dehydrogenase	0.5	0.6	0.6	0.6	0.6	0.02
CAC3172	<i>leuD</i>	3-isopropylmalate dehydratase, small subunit	0.5	0.5	0.7	0.6	0.6	0.1
CAC3173	<i>leuC</i>	3-isopropylmalate dehydratase	0.5	0.5	0.8	0.6	0.6	0.1
CAC3174	<i>leuA</i>	2-isopropylmalate synthase	0.6	0.5	1.2	0.8	0.8	0.3
CAC3175		Hypothetical protein	0.6	0.5	0.6	0.4	0.5	0.1
CAC3176	<i>ilvN</i>	Acetolactate synthase. small subunit	0.4	0.3	0.7	0.4	0.4	0.2

1 ^a: Protein names according to NÖLLING et al. (2001).

2 *: The average of the fold regulation was higher than three, but three of four microarrays were not 2-fold
3 upregulated. That means these genes were not significant upregulated in the acidogenesis.

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