

Supporting Information

Table S1. List of proteins on the *pI* 4-7 gel identified by MALDI-MS and MS/MS analysis. The scores greater than 53 are significant ($p < 0.05$).

Table S2. List of proteins on the *pI* 6-11 gel identified by MALDI-MS and MS/MS analysis. The scores greater than 53 are significant ($p < 0.05$).

Table S3. Totally identified membrane proteins, and proteins are assigned to functional categories. Besides their function also physico-chemical properties as their gene, GRAVY indices and number of transmembrane domains (#TMDs) are given. A cross indicates by which of the two approaches (2DE-MALDI-TOF-MS/MS and 1DE-LC-MS/MS) a protein was identified.

Figure S1. Images of all of the gels, wild type *C. acetobutylicum* DSM 1731 and mutant strain *C. acetobutylicum* Rh8 during acidogenesis; a, b and c are experimental triplicate of each strain.

Figure S2. Images of all of the gels, wild type *C. acetobutylicum* DSM 1731 and mutant strain *C. acetobutylicum* Rh8 during solventogenesis; a, b and c are experimental triplicate of each strain.

Table S1. List of proteins on the *pI* 4-7 gel identified by MALDI-MS and MS/MS analysis. The scores greater than 53 are significant ($p < 0.05$).

Spot Id ^{a)}	ID	protein	MW	pI	Gene locus	Gene	Score	coverage	Peptides matched/unmatched	No. of identified peptides by MS/MS ^{b)}	Expect ^{c)}
11	gi 15895497	Pyruvate:ferredoxin oxidoreductase	129740	5.88	CAC2229		381	31	46/18	7	8.10E-35
12	gi 15895497	Pyruvate:ferredoxin oxidoreductase	129740	5.88	CAC2229		56	10	17/18	2	2.30E-02
15	gi 15895497	Pyruvate:ferredoxin oxidoreductase	129740	5.88	CAC2229		175	22	33/23	4	3.20E-14
16	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		61	39	27/46	–	8.40E-03
30	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		61	16	9/4	–	8.80E-03
32	gi 15895623	Phenylalanyl-tRNA synthetase (beta subunit)	89238	5.13	CAC2356	<i>pheT</i>	230	23	25/11	5	1.00E-19
36	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		59	30	24/41	–	1.30E-02
40	gi 15894879	Methyl-accepting chemotaxis-like protein (chemotaxis sensory transducer)	30535	4.86	CAC1601		57	22	7/13	–	2.30E-02
43	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	56	13	8/13	2	2.80E-02
48	gi 15894879	Methyl-accepting chemotaxis-like protein	30535	4.86	CAC1601		53	26	14/31	–	4.60E-02
52	gi 15895916	Glutamine synthetase type III	77036	5.56	CAC2658	<i>glnA</i>	58	11	8/36	1	1.80E-02
57	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		61	36	28/44	–	8.30E-03
60	gi 15895916	Glutamine synthetase type III	77036	5.56	CAC2658	<i>glnA</i>	224	19	17/15	6	4.00E-19
63	gi 15895916	Glutamine synthetase type III	77036	5.56	CAC2658	<i>glnA</i>	508	31	29/30	8	1.60E-47
69	gi 15894267	Pyruvate-formate lyase	84406	6.24	CAC0980	<i>pflB</i>	154	25	25/17	3	4.00E-12
71	gi 15895916	Glutamine synthetase type III	77036	5.56	CAC2658	<i>glnA</i>	172	21	17/16	5	6.40E-14
83	gi 15895459	Spore coat polysaccharide biosynthesis protein F	29341	5.61	CAC2190	<i>spsF</i>	61	25	6/12	–	7.70E-03
97	gi 15895634	Uncharacterized protein containing predicted cell adhesion domain and ChW-repeats	80439	5.72	CAC2367		394	19	17/43	5	4.00E-36
101	gi 15894231	Transketolase	72776	5.21	CAC0944	<i>tkt</i>	198	23	23/73	3	1.60E-16
110	gi 15894564	Molecular chaperone DnaK, HSP70 family	65723	4.80	CAC1282	<i>dnaK</i>	204	25	23/39	5	4.00E-17
111	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	151	39	28/45	3	8.10E-12
113	gi 15894564	Molecular chaperone DnaK, HSP70 family	65723	4.80	CAC1282	<i>dnaK</i>	228	20	14/19	5	1.60E-19
114	gi 15896558	Molecular chaperone, HSP90 family	72590	5.09	CAC3315	<i>htpG</i>	189	19	18/28	4	1.3e-015
115	gi 15896558	Molecular chaperone, HSP90 family	72590	5.09	CAC3315	<i>htpG</i>	61	4	5/17	2	8.40E-03
116	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		55	23	17/18	–	3.40E-02
124	gi 15896145	CTP synthase (UTP-ammonia lyase)	60555	5.42	CAC2892	<i>ctrA</i>	149	17	15/25	4	1.30E-11
130	gi 15896145	CTP synthase (UTP-ammonia lyase)	60555	5.42	CAC2892	<i>ctrA</i>	66	8	8/8	2	2.90E-03
134	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	222	30	20/16	5	6.40E-19
137	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	86	17	10/17	1	2.50E-05
142	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	123	12	10/10	4	5.10E-09
143	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	445	42	29/29	7	3.20E-41

145	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	317	35	23/8	8	2.00E-28
151	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	398	27	18/8	7	1.60E-36
152	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	416	52	38/27	6	2.60E-38
155	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	67	13	11/14	2	2.20E-03
159	gi 15895899	FKBP-type peptidyl-prolyl cis-transisomerase (trigger factor)	49565	4.68	CAC2641	<i>tig</i>	270	45	28/35	5	1.00E-23
163	gi 15895899	FKBP-type peptidyl-prolyl cis-transisomerase (trigger factor)	49565	4.68	CAC2641	<i>tig</i>	91	10	9/11	2	7.70E+00
168	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	94	21	17/8	4	4.30E-06
172	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	444	39	29/43	7	4.00E-41
174	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	82	18	12/18	3	6.10E-05
176	gi 15896444	Lysyl-tRNA synthetase	59795	5.41	CAC3197	<i>lysS</i>	142	13	12/7	6	6.40E-11
181	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	324	34	28/48	4	4.00E-29
188	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	452	38	28/45	4	6.40E-42
189	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	205	17	13/41	3	3.20E-17
192	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	97	12	10/6	4	1.90E-06
193	gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	63074	6.04	CAC3632	<i>oppA</i>	75	31	19/40	2	2.90E-04
196	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	212	48	21/22	3	6.40E-18
202	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	160	43	26/48	5	1.00E-12
205	gi 15894277	Glutamyl-tRNA synthetase	55721	5.41	CAC0990	<i>gltX</i>	70	15	9/21	1	9.90E-04
207	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	264	38	29/18	5	4.00E-23
212	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	65	17	10/29	2	3.10E-03
215	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	450	41	34/39	5	1.00E-41
217	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	203	47	30/41	3	5.10E-17
218	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	109	15	11/18	3	1.30E-07
226	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	88	30	18/24	3	1.80E-05
230	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	73	12	9/14	2	5.70E-04
231	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	101	25	14/56	2	8.10E-07
232	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		53	24	14/22	–	4.90E-02
236	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	152	27	17/54	3	6.40E-12
239	gi 15896420	3-isopropylmalate dehydratase, small subunit	18355	5.74	CAC3172	<i>leuD</i>	56	38	8/22	–	2.40E-02
242	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	75	24	18/40	2	3.20E-04
244	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	305	51	36/35	4	3.20E-27
246	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	55	26	16/24		3.20E-02
247	gi 15895927	Glu-tRNAGln amidotransferase subunit B	54377	5.74	CAC2669		70	31	15/34	1	9.50E-04
249	gi 15894810	Protein containing ChW-repeats	53593	5.03	CAC1532		380	36	22/17	5	1.00E-34
250	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		63	41	27/44	–	5.30E-03
269	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	300	20	15/7	5	1.00E-26

270	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		65	35	28/42	–	3.10E-03
275	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	56	11	7/22	1	2.60E-02
277	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	143	18	11/12	2	5.10E-11
278	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	135	33	19/43	2	3.20E-10
280	gi 15893775	Phosphomannomutase	49173	5.50	CAC0484		110	16	14/7	2	1.00E-07
281	gi 15895844	Protein containing ChW-repeats	52908	5.19	CAC2584		541	33	21/52	4	8.10E-51
284	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	79	8	8/5	3	1.40E-04
293	gi 15895844	Protein containing ChW-repeats	52908	5.19	CAC2584		104	24	14/14	2	4.00E-07
294	gi 15894323	Pyruvate kinase	51579	6.18	CAC1036	<i>pykA</i>	130	10	9/11	3	1.00E-09
298	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	57	12	10/19	2	2.10E-02
303	gi 15896469	UDP-N-acetylglucosamine pyrophosphorylase	50231	6.01	CAC3222	<i>g</i>	81	27	16/57	2	7.40E-05
307	gi 15896827	Adenylosuccinate synthase	47338	5.49	CAC3593	<i>purA</i>	128	22	19/18	3	1.60E-09
313	gi 15895423	Flagellar hook protein FlgE.	43999	4.71	CAC2154	<i>flgE</i>	411	33	25/38	4	8.10E-38
315	gi 15896472	UDP-N-acetylmuramate-alanine ligase	50553	5.85	CAC3225	<i>murC</i>	294	33	14/19	4	4.00E-26
320	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	887	67	35/36	6	2.00E-85
324	gi 15895938	glucose-6-phosphate isomerase	49930	5.37	CAC2680	<i>pgi</i>	139	14	9/18	3	1.30E-10
326	gi 15895938	glucose-6-phosphate isomerase	49930	5.37	CAC2680	<i>pgi</i>	66	9	5/17	2	2.60E-03
329	gi 15893519	Predicted permease	73110	9.55	CAC0227		55	23	19/36	–	3.00E-02
330	gi 15895938	Glucose-6-phosphate isomerase	49930	5.37	CAC2680	<i>pgi</i>	136	12	6/41	2	2.60E-10
336	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	871	66	35/35	6	8.10E-84
341	gi 15895507	Glycogen synthase, glgA	55263	5.96	CAC2239	<i>glgA</i>	137	17	10/14	3	2.00E-10
342	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	946	62	36/35	6	2.60E-91
346	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	751	56	34/37	6	8.10E-72
347	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	115	38	17/13	1	3.20E-08
355	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		57	37	22/43	–	2.00E-02
356	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		55	24	16/18	–	3.00E-02
358	gi 15895698	HtrA-like serine protease (with PDZ domain)	45613	6.02	CAC2433		589	41	22/24	5	1.30E-55
360	gi 15896386	Elongation Factor Tu (Ef-Tu)	43482	5.04	CAC3136	<i>tufA</i>	453	43	20/18	5	5.10E-42
361	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	181	38	20/26	4	8.10E-15
372	gi 15893319	Seryl-tRNA synthetase	48587	5.75	CAC0021	<i>serS</i>	196	33	25/49	4	2.60E-16
373	gi 15895698	HtrA-like serine protease (with PDZ domain)	45613	6.02	CAC2433		320	42	22/42	5	1.00E-28
375	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	80	25	10/18	2	9.30E-05
376	gi 15893896	putative aminopeptidase 2	48648	5.49	CAC0607		97	26	12/19	1	2.00E-06
391	gi 15895595	Polysaccharide ABC transporter, ATPase component	48565	6.22	CAC2328		269	54	30/41	4	1.30E-23
392	gi 15895960	Chaperonin GroEL, HSP60 family	58152	4.89	CAC2703	<i>groEL</i>	128	28	17/42	2	1.60E-09
393	gi 15894314	Flavoprotein	44804	5.23	CAC1027		229	60	32/39	2	1.30E-19
402	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		56	38	26/45	–	2.60E-02
407	gi 15895471	Possible hook-associated protein, flagellin family	29503	5.78	CAC2203	<i>hag</i>	85	22	9/51	2	3.60E-05

413	gi 15896807	3-oxoacyl-(acyl-carrier-protein) synthase II	44195	5.49	CAC3573	<i>fabF</i>	192	36	14/20	3	6.40E-16
424	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	72	23	11/13	2	6.00E-04
425	gi 15896386	Elongation Factor Tu (Ef-Tu)	43482	5.04	CAC3136	<i>tufA</i>	74	35	14/57	1	4.50E-04
428	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		56	34	25/42	–	2.70E-02
429	gi 15896384	Enolase	46830	4.59	CAC3134	<i>eno</i>	294	25	15/10	5	4.00E-26
444	gi 15896386	Elongation Factor Tu (Ef-Tu)	43482	5.04	CAC3136	<i>tufA</i>	71	24	10/25	1	7.50E-04
445	gi 15896775	UDP-N-acetylglucosamine enolpyruvyl transferase	44641	5.72	CAC3539	<i>murA</i>	61	21	10/61	2	7.50E-03
447	gi 15896386	Elongation Factor Tu (Ef-Tu)	43482	5.04	CAC3136	<i>tufA</i>	562	58	28/34	4	6.40E-53
453	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	113	32	15/56	1	5.10E-08
456	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	135	35	21/50	4	3.20E-10
457	gi 15894566	ribosomal protein L11 methyltransferase	35006	4.81	CAC1284	<i>prmA</i>	71	54	18/21	–	8.40E-04
461	gi 15894970	Cell division GTPase FtsZ	39422	4.87	CAC1693	<i>ftsZ</i>	144	21	9/14	3	4.00E-11
462	gi 15893998	3-phosphoglycerate kinase	42585	5.62	CAC0710	<i>pgk</i>	85	38	16/57	1	3.20E-05
470	gi 15894408	hypothetical protein CAC1124	39380	4.66	CAC1124		295	38	15/24	4	3.20E-26
472	gi 15896355	DNA-dependent RNA polymerase alpha subunit	35564	4.96	CAC3104	<i>rpoA</i>	182	35	15/10	5	6.40E-15
475	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	132	28	15/14	5	6.40E-10
480	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		57	28	17/29	–	2.20E-02
482	gi 15894879	Methyl-accepting chemotaxis-like protein (chemotaxis sensory transducer)	30535	4.86	CAC1601		55	27	9/30	–	7.00E-02
483	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	111	38	20/24	2	8.10E-08
485	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	61	33	16/55	2	8.40E-03
489	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	76	20	11/2	1	2.30E-04
491	gi 15894690	Similar to toxic anion resistance protein terA, ortholog of YCEH B.subtilis	42639	5.62	CAC1411		78	38	20/51	1	1.50E-04
495	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	333	48	26/20	6	5.10E-30
497	gi 15895080	Exopolyphosphatase family protein	35853	4.97	CAC1804		100	23	6/45	1	1.10E-06
501	gi 15895968	Butyryl-CoA dehydrogenase	41474	5.98	CAC2711	<i>bcd</i>	288	36	16/55	4	1.60E-25
511	gi 15893519	Predicted permease	73110	9.55	CAC0227		56	25	22/43	–	2.60E-02
512	gi 15893467	Response regulator, CheY-like receiver domain and HTH DNA-binding domain	23903	5.01	CAC0174		54	51	12/57	–	4.30E-02
513	gi 15895968	Butyryl-CoA dehydrogenase	41474	5.98	CAC2711	<i>bcd</i>	55	22	12/40	2	3.20E-02
515	gi 15895941	Related to spore coat protein F	10783	5.40	CAC2683	<i>cotF</i>	72	47	10/16	–	6.60E-04
518	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		55	29	18/45	–	3.40E-02
537	gi 15893997	Glyceraldehyde 3-phosphate dehydrogenase, gene gapC	35999	5.93	CAC0709	<i>gapC</i>	175	38	12/59	1	3.20E-14
541	gi 15896542	NADH-dependent butanol dehydrogenase B (BDH II)	43487	5.75	CAC3298	<i>bdhB</i>	95	21	14/59	2	3.10E-06

546	gi 15893997	Glyceraldehyde 3-phosphate dehydrogenase, gene gapC	35999	5.93	CAC0709	<i>gapC</i>	341	44	21/49	4	8.10E-31
547	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		64	39	25/46	–	3.70E-03
553	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		61	39	27/46	–	0.0088
560	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		64	37	24/45	–	4.00E-03
566	gi 15896326	Butyrate kinase, BUK	39146	5.98	CAC3075	<i>buk</i>	327	38	15/18	4	2.00E-29
567	gi 15895599	DTDP-D-glucose 4,6-dehydratase	40812	5.50	CAC2332	<i>spsJ</i>	112	40	13/32	2	6.40E-08
569	gi 15894164	Cyclopropane fatty acid synthase	45684	6.39	CAC0877	<i>cfa</i>	72	24	12/19	1	6.90E-04
570	gi 15895064	Translation elongation factor Ts	33800	5.29	CAC1788	<i>tsf</i>	240	48	16/25	5	1.00E-20
571	gi 15894164	Cyclopropane fatty acid synthase	45684	6.39	CAC0877	<i>cfa</i>	291	52	29/37	5	8.10E-26
587	gi 15895471	Possible hook-associated protein, flagellin family	29503	5.78	CAC2203	<i>hag</i>	237	46	17/18	3	2.00E-20
598	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	68	27	12/59	1	1.50E-03
599	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		61	33	27/44	–	8.10E-03
600	gi 15894525	Mixture: mreB + Electron transfer flavoprotein alpha-subunit	35785	5.55	CAC1242	<i>mreB</i>	192	35	16/55	2	6.40E-16
	gi 15895966		36170	5.55	CAC2709	<i>etfA</i>	166	41	17/54	3	2.60E-13
607	gi 15896112	Shape-determining protein envB (HSP70 family charepones)	36661	6.08	CAC2858	<i>mreV</i>	58	34	19/52	2	1.70E-02
618	gi 15894040	PolyA polymerase related protein (HD hydrolase) and P-loop ATP-ase domain	43360	9.44	CAC0753		60	45	21/50	–	1.10E-02
622	gi 15894758	Branched-chain-amino-acid transaminase (ilvE)	37830	5.94	CAC1479	<i>ilvE</i>	72	35	14/57	2	6.00E-04
623	gi 15895471	Possible hook-associated protein, flagellin family	29503	5.78	CAC2203	<i>hag</i>	389	67	22/49	3	1.30E-35
631	gi 15893442	ABC transporter, ATP-binding protein	35632	5.99	CAC0147		401	54	29/43	5	8.10E-37
633	gi 15895471	Possible hook-associated protein, flagellin family	29503	5.78	CAC2203	<i>hag</i>	401	52	18/33	4	8.10E-37
639	gi 15893442	ABC transporter, ATP-binding protein	35632	5.99	CAC0147		74	33	11/21	1	4.40E-04
668	gi 15893844	Autolytic lysozyme (1,4-beta-N-acetylmuramidase), family 25 of glycosyl hydrolases	35127	4.43	CAC0554	<i>lyc</i>	89	32	12/28	2	1.40E-05
671	gi 15893442	ABC transporter, ATP-binding protein	35632	5.99	CAC0147		147	48	23/48	4	2.00E-11
675	gi 15893354	hypothetical protein CAC0057	31249	4.67	CAC0057		87	26	7/48	2	2.20E-05
679	gi 15004770	Mannose-specific phosphotransferase system component IIAB	35282	5.81	CAP0066	<i>ptna</i>	67	46	16/34	1	2.00E-03
694	gi 15004770	Mannose-specific phosphotransferase system component IIAB	35282	5.81	CAP0066	<i>ptna</i>	468	47	25/29	5	1.60E-43
702	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		66	37	29/42	–	2.70E-03
706	gi 15895698	HtrA-like serine protease (with PDZ domain)	45613	6.02	CAC2433		72	21	11/40	3	0.00061
713	gi 15896449	ATP-dependent Zn protease, FTSH	66226	5.40	CAC3202	<i>ftsH</i>	54	29	25/46	–	4.50E-02
719	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		59	31	27/44		1.20E-02
720	gi 15895503	Cysteine synthase/cystathionine beta-synthase, CysK	32918	5.54	CAC2235	<i>cysK</i>	74	22	11/13	3	3.90E-04
722	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		65	35	28/41	–	0.0036

734	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	55	13	10/29	2	3.10E-02
747	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		57	38	25/48	–	0.0210
761	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		58	39	23/42	–	1.70E-02
766	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	93	27	14/57	1	5.60E-06
767	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		65	35	30/41	–	0.0029
769	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		58	32	22/39	–	1.60E-02
774	gi 15896233	Mannose-1-phosphate guanyltransferase	92856	5.62	CAC2981		55	16	10/10	–	3.60E-02
775	gi 15895844	Protein containing ChW-repeats	52908	5.19	CAC2584		387	23	17/55	3	2.00E-35
776	gi 15893354	hypothetical protein CAC0057	31249	4.67	CAC0057		99	19	9/30	4	1.40E-06
777	gi 15895884	Possible 3-ketoacyl-acyl carrier protein reductase	27040	4.89	CAC2626	<i>fabG</i>	55	29	9/19	–	3.00E-02
782	gi 15893354	hypothetical protein CAC0057	31249	4.67	CAC0057		420	50	15/27	4	1.00E-38
787	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		59	39	23/48	–	1.20E-02
802	gi 15894879	Methyl-accepting chemotaxis-like protein	30535	4.86	CAC1601		53	30	10/30	–	4.60E-02
808	gi 15894879	Methyl-accepting chemotaxis-like protein	30535	4.86	CAC1601		55	26	9/21	–	3.10E-02
813	gi 15895341	Spo0A protein, (CheY-like receiver domain and HTH-type DNA binding domain)	31568	6.36	CAC2071	<i>spo0A</i>	194	39	19/54	3	4.00E-16
814	gi 15896425	cysteinyl-tRNA synthetase	53545	5.28	CAC3177	<i>cysS</i>	60	28	19/52	–	1.10E-02
829	gi 15894532	Septum site-determining protein MinD, ATPase	28865	5.45	CAC1249	<i>minD</i>	63	32	10/31	2	0.0053
848	gi 15894114	Fructose-bisphosphate aldolase	30482	5.49	CAC0827		195	33	23/48	4	3.20E-16
853	gi 15896425	Cysteinyl-tRNA synthetase	53545	5.28	CAC3177	<i>cysS</i>	55	26	13/40	–	3.20E-02
860	gi 15896802	Acetyl-CoA carboxylase alpha subunit	30244	4.98	CAC3568	<i>ac</i>	74	17	13/6	2	0.00044
866	gi 15894670	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase	27055	5.48	CAC1391	<i>purC</i>	73	35	13/7	–	4.90E-04
873	gi 15893560	ABC transporter ATP-binding protein	29154	5.55	CAC0268		110	17	9/6	3	1.00E-07
878	gi 15895063	Ribosomal protein S2	26178	6.37	CAC1787	<i>rpsB</i>	153	30	15/36	4	5.10E-12
891	gi 15895969	Crotonase (3-hydroxybutyryl-CoA dehydratase)	28400	5.39	CAC2712	<i>crt</i>	89	31	12/46	2	1.20E-05
898	gi 15004868	acetoacetate decarboxylase	27703	5.81	CAP0165	<i>adc</i>	100	22	9/13	3	1.00E-06
910	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		68	29	19/21	–	0.0017
914	gi 15895647	Tetrahydrodipicolinate N-succinyltransferase	25274	5.22	CAC2381	<i>dapD</i>	123	26	4/25	1	5.10E-09
916	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		152	70	28/43	2	6.40E-12
927	gi 15894855	Ncharacterized conserved protein	25628	7.97	CAC1577		55	40	11/31	–	3.30E-02
929	gi 15893558	ABC transporter, ATP-binding protein	26554	5.30	CAC0266		59	31	12/14	2	1.30E-02
930	gi 15893999	Triosephosphate isomerase	26698	5.78	CAC0711	<i>tpi</i>	94	33	9/15	2	3.70E-06
931	gi 15893999	Triosephosphate isomerase	26698	5.78	CAC0711	<i>tpi</i>	80	33	10/14	2	9.30E-05
935	gi 15893999	Triosephosphate isomerase	26698	5.78	CAC0711	<i>tpi</i>	132	71	18/13	–	6.40E-10
938	gi 15895825	NifU-related domain containing protein	24966	5.49	CAC2565		61	33	15/38	3	7.50E-03
939	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		327	63	27/33	5	2.00E-29
943	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		95	32	10/16	1	3.10E-06
945	gi 15893408	Glutamine ABC transporter (ATP-binding protein)	27393	5.28	CAC0112	<i>glnQ</i>	76	36	11/25	3	2.60E-04

946	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		58	38	17/54	1	1.50E-02
947	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		142	59	23/15	1	6.40E-11
949	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		150	65	25/34	3	1.00E-11
950	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		77	44	16/8	–	1.90E-04
960	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		68	65	13/58	–	1.80E-03
964	gi 15895825	NifU-related domain containing protein	24966	5.49	CAC2565		91	46	12/24	2	9.10E-06
969	gi 15894626	putative translaldolase	23388	5.45	CAC1347		92	21	6/32	3	6.40E-06
970	gi 15004832	Glycogen-binding regulatory subunit of S/T protein phosphatase I	28066	6.08	CAP0129		209	37	9/60	3	1.30E-17
971	gi 15893605	Phage shock protein A	25021	5.35	CAC0313		67	45	13/45	2	2.20E-03
974	gi 15893999	Triosephosphate isomerase	26698	5.78	CAC0711	<i>tpi</i>	47	99	18/52	1	1.30E-06
981	gi 15893501	Predicted membrane protein; CF-20 family	23812	6.48	CAC0208		331	31	9/28	2	8.10E-30
983	gi 15895461	Ucharacterize dprotein, CGEBhomolog	62815	6.47	CAC2193		55	32	17/33	–	3.10E-02
990	gi 15895364	Translation elongation factor P	21120	4.98	CAC2094	<i>efp</i>	162	32	12/26	4	6.40E-13
1007	gi 15894160	Xanthine phosphoribosyltransferase	21402	6.19	CAC0873	<i>xpt</i>	57	35	10/10	–	2.10E-02
1010	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	57	20	14/39	1	1.80E-02
1011	gi 15896387	Translation elongation factor EF-G	76526	4.96	CAC3138	<i>fus</i>	802	62	48/22	6	6.40E-77
1012	gi 15895898	Protease subunits of ATP-dependent protease, ClpP	21467	5.03	CAC2640	<i>clpP</i>	62	10	4/10	1	0.007
1019	gi 15896397	Transcription antiterminator NusG	19647	6.00	CAC3149	<i>nusG</i>	54	35	12/10	–	4.50E-02
1028	gi 15896832	Rubrerhythrin	20479	5.50	CAC3598		74	28	9/21	2	0.0004
1033	gi 15894879	Methyl-accepting chemotaxis-like protein	30535	4.86	CAC1601		55	27	10/39	–	3.40E-02
1043	gi 15896945	Molecular chaperone (small heat shock protein), HSP18	17734	5.27	CAC3714		66	36	16/55	2	2.90E-03
1045	gi 15894415	hypothetical protein CAC1131	16192	4.59	CAC1131		61	36	6/13	1	9.10E-03
1050	gi 15896123	FoF1-type ATP synthase B subunit	18234	5.30	CAC2869	<i>atpF</i>	226	40	15/31	4	2.60E-19
1051	gi 15896123	FoF1-type ATP synthase B subunit	18234	5.30	CAC2869	<i>atpF</i>	54	47	14/49	1	4.00E-02
1054	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	100	22	10/61	1	1.00E-06
1055	gi 15896119	FoF1-type ATP synthase beta subunit	51119	4.87	CAC2865	<i>atpD</i>	83	16	7/45	1	5.70E-05
1065	gi 15896118	FoF1-type ATP synthase epsilon subunit	14913	5.33	CAC2864	<i>atpC</i>	59	27	6/64	1	1.30E-02
1076	gi 15893882	Riboflavin synthase beta-chain	16647	6.14	CAC0593	<i>ribH</i>	149	40	9/13	3	1.30E-11
1094	gi 15896470	Stage V sporulation protein G	10802	5.25	CAC3223	<i>spoVG</i>	80	41	9/11	2	9.50E-05
1106	gi 15896121	FoF1-type ATP synthase alpha subunit	55369	5.21	CAC2867	<i>atpA</i>	370	41	29/31	4	1.00E-33

Note: ^{a)} Numbers refer to spot numbers as given in Figure 2A, protein identified by IPG 4-7; ^{b)} Protein identified by peptide mass fingerprint (PMF) and MS/MS; –) Protein identified by peptide mass fingerprint (PMF). ^{c)} In MALDI-TOF mass spectrometry analysis, peptide mixtures that yielded statistically significant search scores (> 95% C.I., equivalent to MASCOT expected value < 0.05) and accounted for the majority of ions present in the mass spectra were defined as positive identifications

Table S2. List of proteins on the *pI* 6-11 gel identified by MALDI-MS and MS/MS analysis. The scores greater than 53 are significant ($p < 0.05$).

Spot Id ^{c)}	protein	ID	MW	pI	Gene locus	Gene	Score	coverage	Peptides matched/unmatched	No. of identified peptides by MS/MS ^{d)}	Expect _{c)}
12	gi 15896387	Translation elongation factor EF-G	76526	4.96	CAC3138	<i>fus</i>	82	35	25/31	–	6.60E-05
36	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		67	41	27/44	–	2.30E-03
40	gi 15893326	Hydrogene dehydrogenase	65578	7.41	CAC0028	<i>hydA</i>	96	41	32/39	–	2.80E-06
42	gi 15893326	Hydrogene dehydrogenase	65578	7.41	CAC0028	<i>hydA</i>	78	35	28/43	–	1.60E-04
63	gi 15896448	Formate--tetrahydrofolate ligase	61096	6.5	CAC3201		71	40	24/47	–	8.40E-04
65	gi 15896448	Formate--tetrahydrofolate ligase	61096	6.5	CAC3201		66	41	22/49	–	2.70E-03
71	gi 15893991	Sugar ABC-transporter, ATP-ase component	56707	8.48	CAC0703		138	44	33/38	3	1.60E-10
76	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		59	37	24/47	–	1.40E-02
78	gi 15895018	Uncharacterized conserved protein, YLBM <i>B. subtilis</i> ortholog	46173	8.69	CAC1741		54	38	13/39	–	4.30E-02
90	gi 15895958	IMP dehydrogenase	52497	7.05	CAC2701	<i>guaB</i>	81	40	27/44	–	8.40E-05
94	gi 15895958	IMP dehydrogenase	52497	7.05	CAC2701	<i>guaB</i>	64	39	20/51	–	3.80E-03
95	gi 15895097	Adenylosuccinate lyase	54690	6.82	CAC1821	<i>purB</i>	67	45	25/46	–	2.30E-03
99	gi 15895958	IMP dehydrogenase	52497	7.05	CAC2701	<i>guaB</i>	65	41	25/46	–	3.40E-03
108	gi 15894191	ATPase with chaperon activity, two ATP-binding domains, ClpC orthologs	85216	5.69	CAC0904		56	26	25/46	–	2.60E-02
109	gi 15896244	Predicted short-chain dehydrogenase	28951	9.53	CAC2992		55	48	12/43	–	3.50E-02
110	gi 15895532	Glycine hydroxymethyltransferase	45925	6.16	CAC2264	<i>glyA</i>	65	45	22/49	–	3.40E-03
127	gi 15896499	Gamma-glutamyl phosphate reductase	46107	6.63	CAC3254	<i>proA</i>	86	44	25/46	–	2.70E-05
130	gi 15896881	Acetyltransferase (with duplicated domains), possibly RIMI-like protein	34218	5.63	CAC3648		56	46	14/52	–	2.30E-02
134	gi 15896224	Thiamine biosynthesis enzyme, THII	43799	8.29	CAC2971	<i>thil</i>	57	13	8/15	4	2.00E-02
138	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		73	44	26/45	–	4.60E-04
139	gi 15893858	Aspartate semialdehyde dehydrogenase	40643	6.43	CAC0568	<i>asd</i>	54	44	13/58	–	4.00E-02
140	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		58	38	22/43	–	1.70E-02
143	gi 15894106	Phosphoribosylpyrophosphate synthetase	43010	6.73	CAC0819		113	55	34/37	1	5.10E-08
145	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		53	39	23/48	–	4.80E-02
150	gi 15895710	AICAR transformylase domain of PurH-like protein	43806	8.92	CAC2445		78	48	21/50	–	1.80E-04
155	gi 15896127	Acetyl-CoA acetyltransferase (thiolase A)	41443	6.92	CAC2873		118	47	18/47	3	1.60E-08
156	gi 15896127	Acetyl-CoA acetyltransferase (thiolase A)	41443	6.92	CAC2873		92	19	9/13	3	6.10E-06
157	gi 15896127	Acetyl-CoA acetyltransferase (thiolase A)	41443	6.92	CAC2873		91	11	3/37	1	7.40E-06
158	gi 15896127	Acetyl-CoA acetyltransferase (thiolase A)	41443	6.92	CAC2873		329	53	20/47	4	3.20E-13
164	gi 15896315	UDP-N-acetylglucosamine 2-epimerase	43242	8.63	CAC3064		59	34	14/21	–	1.20E-02

165	gi 15896127	Acetyl-CoA acetyltransferase (thiolase A)	41443	6.92	CAC2873		66	21	9/19	2	2.70E-03
170	gi 15895624	Phenylalanyl-tRNA synthetase (alpha subunit)	38826	6.69	CAC2357	<i>pheS</i>	82	58	25/46	–	6.90E-05
171	gi 15894164	Cyclopropane fatty acid synthase	45684	6.39	CAC0877	<i>cfa</i>	207	27	13/16	4	2.00E-17
174	gi 15895624	Phenylalanyl-tRNA synthetase (alpha subunit)	38826	6.69	CAC2357	<i>pheS</i>	80	55	26/45	–	1.10E-04
181	gi 15895824	hypothetical protein CAC2564	35733	6.46	CAC2564		272	37	19/36	5	6.40E-24
183	gi 15895824	hypothetical protein CAC2564	35733	6.46	CAC2564		69	34	21/49	–	1.30E-03
190	gi 15895824	hypothetical protein CAC2564	35733	6.46	CAC2564		58	25	14/42	2	1.60E-02
192	gi 15896462	Foldase protein prsA precursor	37713	9.08	CAC3215	<i>prsA</i>	75	43	22/49	–	3.50E-04
195	gi 15895824	hypothetical protein CAC2564	35733	6.46	CAC2564		573	59	35/6	6	5.10E-54
198	gi 15895111	DNA mismatch repair enzyme, MutL	71249	5.8	CAC1836	<i>mutL</i>	56	29	17/48	–	2.60E-02
202	gi 15896863	Oligopeptide ABC transporter, ATPase component	37724	6.52	CAC3629	<i>oppD</i>	76	28	11/11	3	2.90E-04
214	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		64	43	24/47	–	4.00E-03
217	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		56	37	20/45	–	2.60E-02
225	gi 15895912	Aspartate carbamoyltransferase catalytic subunit	35245	7.02	CAC2654		90	41	19/52	2	9.70E-06
239	gi 15896862	Oligopeptide ABC transporter, ATPase component	36421	8.49	CAC3628	<i>oppF</i>	110	39	16/36	1	1.00E-07
245	gi 15893990	Predicted lipoprotein, Med/BMP family	38444	8.85	CAC0702		84	48	26/45	–	3.90E-05
248	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		75	44	25/46	–	3.50E-04
251	gi 15894271	ABC transporter, ATP-binding protein	35696	6.97	CAC0984		55	35	16/32	–	3.40E-02
254	gi 15893808	6-phosphofructokinase	34343	6.92	CAC0517	<i>pfk</i>	101	27	10/33	3	8.10E-07
260	gi 15893808	6-phosphofructokinase	34343	6.92	CAC0517	<i>pfk</i>	167	35	14/27	3	2.00E-13
276	gi 15896327	Phosphate butyryltransferase	32321	6.34	CAC3076	<i>ptb</i>	494	65	31/40	5	4.00E-46
278	gi 15896327	Phosphate butyryltransferase	32321	6.34	CAC3076	<i>ptb</i>	201	48	18/32	5	8.10E-17
280	gi 15896120	FoF1-type ATP synthase gamma subunit	31175	9.19	CAC2866	<i>atpG</i>	124	21	7/12	3	4.00E-09
282	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		63	37	27/44	–	4.60E-03
284	gi 15893750	NtrC family transcriptional regulator (PAS and AAA domains)	71095	9.04	CAC0459		68	32	18/40	–	1.70E-03
300	gi 15896952	Hypothetical secreted protein	31633	9.13	CAC3721		145	34	12/37	3	3.20E-11
301	gi 15894801	Fructokinase	31967	6.96	CAC1523		76	58	22/49	–	2.60E-04
305	gi 15894801	Fructokinase	31967	6.96	CAC1523		75	32	8/37	2	3.30E-04
313	gi 15894273	Lipoprotein, attached to the cytoplasmic membrane, NLPA family	30037	5.69	CAC0986		109	31	22/49	1	1.30E-07
338	gi 15896395	50S ribosomal protein L1	24445	9.43	CAC3147	<i>rplA</i>	214	31	11/55	3	4.00E-18
339	gi 15894167	Periplasmic amino acid binding protein	30333	9.13	CAC0880		83	68	25/46	–	5.10E-05
342	gi 15893788	Cell division ATP-binding protein	25428	8.87	CAC0497	<i>ftsE</i>	112	64	32/39	–	6.40E-08
344	gi 15896014	Uncharacterized protein, YPUA B.subtilis ortholog	31706	9.06	CAC2758		102	56	22/47	–	6.40E-07

345	gi 15893771	Oxygen-sensitive ribonucleoside-triphosphate reductase <i>nrdD</i>	80123	6.22	CAC0480	<i>nrdD</i>	55	26	17/31	–	3.10E-02
351	gi 15896787	Na ⁺ ABC transporter (ATP-binding protein), NATA	26659	6.56	CAC3551	<i>natA</i>	105	32	6/20	2	3.20E-07
361	gi 15896383	50S ribosomal protein L3	22599	10	CAC3133	<i>rplC</i>	182	22	7/21	3	6.40E-15
378	gi 15896133	Uracil phosphoribosyltransferase	23223	6.45	CAC2879	<i>upp</i>	68	19	7/15	2	1.50E-03
379	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		55	37	28/43	–	3.60E-02
389	gi 15894690	Similar to toxic anion resistance protein <i>terA</i> , ortholog of YCEH B.subtilis	42639	5.62	CAC1411		56	48	15/50	–	2.70E-02
394	gi 15895824	hypothetical protein CAC2564	35733	6.46	CAC2564		86	48	26/45	–	2.40E-05
400	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		54	33	18/35	–	4.10E-02
404	gi 15896584	Multimeric flavodoxin WrbA family protein	22849	8.47	CAC3341		74	54	15/47	–	4.40E-04
409	gi 15896226	2-keto-3-deoxy-6-phosphogluconate aldolase, <i>eda/kdgA</i>	22732	7.68	CAC2973	<i>kdgA</i>	58	72	13/58	–	1.70E-02
415	gi 15896341	Fumarate hydratase, subunit B (C-terminal domain of FumA E.coli) class I	20318	9.4	CAC3090		66	70	15/56	–	2.70E-03
417	gi 15896122	FoF1-type ATP synthase delta subunit	20781	7.82	CAC2868	<i>atpH</i>	106	60	25/46	–	2.60E-07
421	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		54	37	22/49	–	4.20E-02
422	gi 15896122	FoF1-type ATP synthase delta subunit	20781	7.82	CAC2868	<i>atpH</i>	62	54	20/51	–	5.80E-03
423	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		66	42	26/45	–	2.50E-03
429	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		57	40	24/46	–	1.80E-02
448	gi 15896349	50S ribosomal protein L13	16431	9.76	CAC3098	<i>rplM</i>	255	61	18/53	4	3.20E-22
451	gi 15896366	30S ribosomal protein S5	17425	9.57	CAC3116	<i>rpsE</i>	72	76	19/52	–	6.60E-04
458	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		58	37	25/46	–	1.60E-02
473	gi 15896354	50S ribosomal protein L17	13001	10.35	CAC3103	<i>rplQ</i>	83	49	13/39	2	5.20E-05
476	gi 15896396	50S ribosomal protein L11	14737	9.75	CAC3148	<i>rplK</i>	118	28	7/42	2	1.60E-08
484	gi 15895461	Ucharacterized protein, CGEB homolog	62815	6.47	CAC2193		72	36	29/42	–	6.10E-04
491	gi 15896378	50S ribosomal protein L22	12365	10.1	CAC3128	<i>rplV</i>	331	50	13/41	5	8.10E-30
495	gi 15896384	30S ribosomal protein S10	11474	9.64	CAC3134	<i>rpsJ</i>	72	64	12/38	–	7.00E-04
497	gi 15896120	FoF1-type ATP synthase gamma subunit	31175	9.19	CAC2866	<i>atpG</i>	86	65	18/53	–	2.70E-05

Note: ^{c)} Numbers refer to spot numbers as given in Figure 2B, protein identified by IPG 6-11; ^{d)} Protein identified by peptide mass fingerprint (PMF) and MS/MS; –) Protein identified by peptide mass fingerprint (PMF). ^{e)} In MALDI-TOF mass spectrometry analysis, peptide mixtures that yielded statistically significant search scores (> 95% C.I., equivalent to MASCOT expected value < 0.05) and accounted for the majority of ions present in the mass spectra were defined as positive identifications

Table S3. Totally identified membrane proteins, and proteins are assigned to functional categories. Besides their function also physico-chemical properties as their gene, GRAVY indices and number of transmembrane domains (#TMDs) are given. A cross indicates by which of the two approaches (2DE-MALDI-TOF-MS/MS and 1DE-LC-MS/MS) a protein was identified.

NCBI accession number # function	Protein Description	Gene locus	Gene	GRAVY	2DE-M ALDI-TOF-MS/MS	1D-gel-LC-MS/MS	No. of TMHs ^{b)}
1. Transport							
gi 15894532	Septum site-determining protein MinD, ATPase	CAC1249	<i>minD</i>	-0.0821	+		0
gi 15895595	Polysaccharide ABC transporter, ATPase component	CAC2328		-0.4291	+		0
gi 15896787	Na ⁺ ABC transporter (ATP-binding protein), NATA	CAC3551	<i>natA</i>	-0.2630	+		0
gi 15894159	Xanthine permease	CAC0872		0.9756		+	12
gi 15895381	Uracil permease UraA/PyrP	CAC2112	<i>uraA</i>	0.9279		+	11
gi 15893991	Sugar ABC-transporter, ATPase component	CAC0703		-0.2356	+	+	0
gi 15893526	PTS system, fructoso-specific IIBC component	CAC0234		0.6747		+	8
gi 15893860	PTS enzyme II, ABC component	CAC0570		0.4059		+	9
gi 15896104	Proline/glycine betaine ABC-type transport system, ATPase component	CAC2850		-0.2414		+	0
gi 15896351	Predicted permease (Cobalt permease subfamily)	CAC3100		0.6330		+	4
gi 15894632	Phosphotransferase system IIC component	CAC1353		0.5184		+	11
gi 15896338	Phosphoenolpyruvate-protein kinase (PTS system enzyme I)	CAC3087		-0.2512		+	0
gi 15893671	Periplasmic amino acid-binding protein	CAC0380		-0.4022		+	0
gi 15896568	Periplasmic amino acid binding protein	CAC3325		-0.3721		+	1
gi 15894167	Periplasmic amino acid binding protein	CAC0880		-0.5239	+	+	0
gi 15896872	Oligopeptide ABC transporter, permease component	CAC3638		0.6683		+	6
gi 15896877	Oligopeptide ABC transporter, permease component	CAC3644		0.6291		+	6
gi 15896866	Oligopeptide ABC transporter, periplasmic substrate-binding component	CAC3632	<i>oppA</i>	-0.4261	+	+	0

gi 15896868	Oligopeptide ABC transporter, periplasmic substrate-binding component	CAC3634		-0.5456		+	0
gi 15893473	Oligopeptide ABC transporter, ATP-binding protein	CAC0180	<i>appF</i>	-0.1788		+	0
gi 15896862	Oligopeptide ABC transporter, ATPase component	CAC3628	<i>oppF</i>	-0.3000	+	+	0
gi 15896863	Oligopeptide ABC transporter, ATPase component	CAC3629	<i>oppD</i>	-0.1938	+	+	0
gi 15896483	Multiple sugar-binding ABC-transporter, MSMX ATP-binding protein	CAC3237	<i>msmX</i>	-0.2301		+	0
gi 15894271	Methionine import ATP-binding protein metN	CAC0984	<i>metN</i>	-0.0500	+	+	0
gi 15004770	Mannose-specific phosphotransferase system component IIAB	CAP0066	<i>ptna</i>	-0.2791	+	+	0
gi 15894273	Lipoprotein, attached to the cytoplasmic membrane, NLPA family	CAC0986		-0.3364	+	+	0
gi 15896534	Iron-regulated ABC-type transporter membrane component (SufB)	CAC3289		-0.3391		+	0
gi 15893407	Glutamine-binding periplasmic protein fused to glutamine permease	CAC0111		0.1346		+	5
gi 15893669	Glutamine ABC transporter, ATP-binding protein	CAC0378	<i>glnQ</i>	-0.2176		+	0
gi 15893408	Glutamine ABC transporter (ATP-binding protein)	CAC0112	<i>glnQ</i>	-0.2176	+	+	0
gi 15893739	Ferrous iron transport protein B (feoB-2)	CAC0448	<i>feoB</i>	0.4639		+	8
gi 15895966	Electron transfer flavoprotein subunit alpha (Alpha-ETF)	CAC2709	<i>etfA</i>	-0.0074	+	+	0
gi 15896353	Cobalt import ATP-binding protein <i>cbiO</i> 2	CAC3102	<i>cbiO2</i>	-0.3064		+	0
gi 15896352	Cobalt import ATP-binding protein <i>cbiO</i> 1	CAC3101	<i>cbiO1</i>	-0.2231		+	0
gi 15893564	Amino acid transporter	CAC0272		0.6371		+	13
gi 15896433	Membrane-associated protein containing a homolog of PilT-like ATPase	CAC3185		0.3446		+	4
gi 15894014	Amino acid permease, gene <i>yifK</i>	CAC0727	<i>yifK</i>	0.7678		+	12
gi 15894166	ABC-type polar amino acid transport system, ATPase component	CAC0879		-0.1975		+	0
gi 15896527	ABC-type multidrug/protein/lipid transport system, ATPase component	CAC3282		0.1812		+	6

gi 15896526	ABC-type multidrug/protein/lipid transport system, ATPase component	CAC3281		-0.0721		+	4
gi 15894679	ABC transporter, periplasmic binding component	CAC1400		-0.3898		+	0
gi 15893442	ABC transporter, ATP-binding protein	CAC0147		-0.3248	+	+	0
gi 15893558	ABC transporter, ATP-binding protein	CAC0266		-0.2615	+	+	0
gi 15893433	ABC transporter, ATP-binding component	CAC0138		-0.2375		+	0
gi 15893818	ABC transporter, ATPase component (two ATPase domains)	CAC0528		-0.5043		+	0
gi 15893560	ABC transporter ATP-binding protein	CAC0268		-0.2775	+	+	0
gi 15893441	Related to ABC transporter permease component	CAC0146		0.3524		+	6
gi 15896433	Membrane-associated protein containing a homolog of PilT-like ATPase N	CAC3185		0.3446		+	4
2. Synthesis and turnover of cellular membrane/ wall and cell division							
gi 15896470	Stage V sporulation protein G	CAC3223	<i>spoVG</i>	-0.5674	+		0
gi 15896960	Stage 0 sporulation J, ParB family of DNA-binding proteins	CAC3729	<i>spo0J</i>	-0.5389	+		0
gi 15895899	FKBP-type peptidyl-prolyl cis-transisomerase (trigger factor)	CAC2641	<i>tig</i>	-0.7169	+		0
gi 15895879	Cell wall hydrolase (autolysin), family 25 of glycosyl hydrolase; peptidoglycan-binding domain	CA_C2621		-0.2609	+		0
gi 15894970	Cell division GTPase FtsZ	CAC1693	<i>ftsZ</i>	-0.0839	+		0
gi 15893844	Autolytic lysozyme (1,4-beta-N-acetylmuramidase), family 25 of glycosyl hydrolases	CAC0554	<i>lyc</i>	-0.2034	+		0
gi 15896156	LysM domain containing membrane protein	CAC2903		-0.2627	+		0
gi 15896775	UDP-N-acetylglucosamine enolpyruvyl transferase	CAC3539	<i>murA</i>	0.1163	+		0
gi 15895499	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)	CAC2231	<i>murG</i>	-0.0627		+	0
gi 15896472	UDP-N-acetylmuramate-alanine ligase	CAC3225	<i>murC</i>	-0.1096	+		0
gi 15893621	Sporulation specific penicillin-binding protein	CAC0329	<i>spoVD</i>	-0.2741		+	1
gi 15896112	Shape-determining protein envB (HSP70 family chaperones)	CAC2858	<i>mreV</i>	0.0097	+	+	0
gi 15895396	Phospho-N-acetylmuramoyl-pentapeptide-transferase	CAC2127	<i>mraY</i>	0.9498		+	9

gi 15893797	Penicillin-binding protein	CAC0506		-0.2297		+	1
gi 15894525	mreB	CAC1242	<i>mreB</i>	0.0922	+	+	0
gi 15895568	Membrane carboxypeptidase mrcB	CAC2301	<i>mrcB</i>	-0.6068		+	1
gi 15896541	D-alanyl-D-alanine carboxypeptidase family hydrolase, YODJ <i>B.subtilis</i>	CAC3297		-0.6407		+	1
gi 15894280	D-alanyl-D-alanine carboxypeptidase (penicilin binding protein)	CAC0993	<i>dacF</i>	-0.3014		+	1
gi 15896148	D-alanine--D-alanine ligase (D-alanylalanine synthetase)	CAC2895	<i>ddl/ddlA</i>	-0.2755		+	0
gi 15893597	Chemotaxis motility protein B, gene motB	CAC0305	<i>motB</i>	-0.4914		+	1
gi 15893789	Cell division protein (ftsX)	CAC0498	<i>ftsX</i>	0.4688		+	4
gi 15893788	Cell division ATP-binding protein	CAC0497	<i>ftsE</i>	-0.1768	+	+	0
gi 15894946	Carbon starvation protein	CAC1669	<i>CstA</i>	0.8380		+	15
3. Surface coat and flagellar proteins							
gi 15895941	Related to spore coat protein F	CAC2683	<i>cotF</i>	-0.8097	+		0
gi 15895428	Flagellar-Type ATPase	CAC2159	<i>fliL</i>	-0.2573			0
gi 15896091	Zn-binding lipoprotein related (surface adhesin A), ADHS	CAC2836		-0.5101		+	0
gi 15896518	Possible surface protein, responsible for cell interaction; contains cell adhesion domain and ChW-repeats	CAC3273		-0.1896	+		0
gi 15896520	Possible surface protein, responsible for cell interaction; contains cell adhesion domain and ChW-repeats	CAC3275		-0.2720		+	0
gi 15896524	Possible surface protein, responsible for cell interaction; contains cell adhesion domain and ChW-repeats	CAC3279		-0.2785	+	+	0
gi 15896525	Possible surface protein, responsible for cell interaction; contains cell adhesion domain and ChW-repeats	CAC3280		-0.2694		+	0
gi 15896519	Possible surface protein, responsible for cell interaction; contains cell adhesion domain and ChW-repeats	CAC3274		-0.2344		+	0
gi 15895634	Uncharacterized protein containing predicted cell adhesion domain and ChW-repeats	CAC2367		-0.1545	+	+	0
gi 15895471	Possible hook-associated protein, flagellin family	CAC2203	<i>hag</i>	-0.4066	+		0
gi 15895421	Flagellar protein FliL	CAC2152	<i>fliL</i>	-0.2573		+	1
gi 15896523	Uncharacterized protein, containing cell adhesion domain and ChW-repeats	CAC3278		-0.4197	+	+	0

gi 15894668	Protein containing ChW-repeats and cell-adhesion domain	CA_C1389		-0.1442		+	0
gi 15896523	Uncharacterized protein, containing cell adhesion domain and ChW-repeats	CAC3278		-0.4197	+	+	0
gi 15895431	flagellar MS-ring protein	CAC2162	<i>fliF</i>	-0.5800		+	2
gi 15895423	Flagellar hook protein FlgE	CAC2154	<i>flgE</i>	-0.3182	+	+	0
gi 15894001	Enolase	CAC0713	<i>eno</i>	-0.1381	+	+	0
4. Respiratory chain and energy metabolism							
gi 15896122	FoF1-type ATP synthase delta subunit	CAC2868	<i>atpH</i>	-0.2737	+		0
gi 15895407	Probable manganese-dependent inorganic pyrophosphatase	CAC2138	<i>ppaC</i>	-0.2468		+	0
gi 15896119	ATP synthase subunit beta (ATPase subunit beta)	CAC2865	<i>atpD</i>	-0.1730	+	+	0
gi 15896121	ATP synthase subunit alpha (ATPase subunit alpha)	CAC2867	<i>atpA</i>	-0.1160	+	+	0
gi 15896120	ATP synthase gamma chain (ATP synthase F1 sector gamma subunit)	CAC2866	<i>atpG</i>	-0.2734	+	+	0
gi 15896123	ATP synthase B chain membrane protein, YUEB	CAC2869	<i>atpF</i>	-0.4157	+	+	0
gi 15896118	ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit)	CAC2864	<i>atpC</i>	-0.3805	+	+	0
5. Protein synthesis, processing, stability, and degradation							
gi 15894564	Molecular chaperone DnaK, HSP70 family	CAC1282	<i>dnaK</i>	-0.4194	+		0
gi 15894191	ATPase with chaperon activity, two ATP-binding domains, ClpC orthologs	CAC0904		-0.4086	+		0
gi 15895904	Signal peptidase I	CAC2646	<i>sipS</i>	-0.0897		+	1
gi 15896101	Protein translocase subunit secA	CAC2846	<i>secA</i>	-0.5628		+	0
gi 15893896	Probable M18 family aminopeptidase 2	CAC0607	<i>apeB</i>	-0.2351	+	+	0
gi 15896363	preprotein translocase subunit SecY	CAC3113	<i>secY</i>	0.5534		+	10
gi 15895546	preprotein translocase subunit SecD	CAC2278	<i>secD</i>	0.4405		+	6
gi 15893936	Molecular chaperone, DnaJ family (contain C-term. Zn finger domain)	CAC0648		-1.0133		+	0
gi 15896967	Membrane protein oxaAI	CAC3736	<i>oxaA</i>	0.1130		+	4

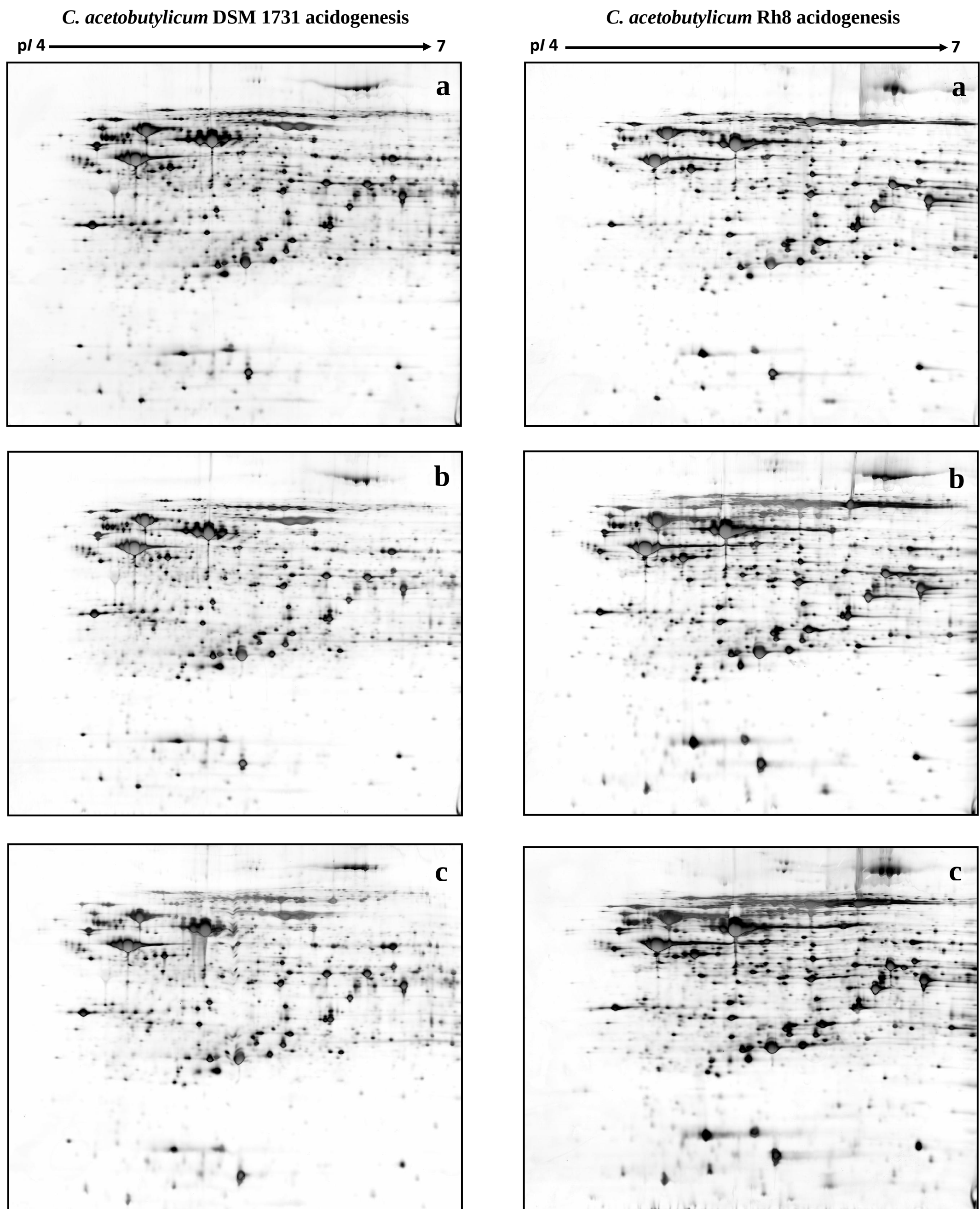
gi 15895698	HtrA-like serine protease (with PDZ domain)	CAC2433		-0.2679	+	+	1
gi 15896558	Molecular chaperone, HSP90 family	CAC3315	<i>htpG</i>	-0.6218	+	+	0
gi 15894246	Chaperone protein clpB	CAC0959	<i>clpB</i>	-0.4467		+	0
gi 15893790	Carboxyl-terminal protease	CAC0499		-0.3682		+	1
gi 15896449	ATP-dependent Zn protease, FTSH	CAC3202	<i>ftsH</i>	-0.2467	+	+	2
gi 15895898	ATP-dependent Clp protease proteolytic subunit	CAC2640	<i>clpP</i>	-0.1591	+	+	0
gi 15893891	ATP-dependent zinc metalloproteinase FtsH (cell division protein)	CAC0602	<i>ftsH</i>	-0.2467		+	2
gi 15895001	Predicted metal-dependent peptidase	CAC1724		0.4793		+	3
gi 15896437	ATPase with chaperone activity clpC, two ATP-binding domain	CAC3189	<i>clpC</i>	-0.4754		+	0
gi 15895960	Chaperonin GroEL, HSP60 family	CAC2703	<i>groEL</i>	-0.1446	+	+	0
gi 15896945	18 kDa heat shock protein (HSP 18)	CAC3714	<i>hsp18</i>	-0.8662	+	+	0
6. Signal Transduction							
gi 15893467	Response regulator, CheY-like receiver domain and HTH DNA-binding domain	CAC0174		0.0197	+		0
gi 15896515	Permease, predicted cation efflux pump	CAC3270		-0.4972	+		0
gi 15893750	NtrC family transcriptional regulator (PAS and AAA domains)	CAC0459		-0.2077	+		0
gi 15894879	Methyl-accepting chemotaxis-like protein	CAC1601		-0.1928	+		0
gi 15895341	Stage 0 sporulation protein A homologue	CAC2071	<i>spo0A</i>	-0.1929	+	+	0
gi 15895356	Stage III sporulation protein AH, SpoIIAH	CAC2086		-0.5904		+	1
gi 15895027	SpoVS-related protein	CAC1750		0.4244		+	0
gi 15004714	Response regulator (CheY + HTH domains)	CAP0009		-0.2708		+	0
gi 15894878	Methyl-accepting chemotaxis-like protein	CAC1600		-0.1525		+	2
gi 15894196	Methyl-accepting chemotaxis protein, contain HAMP domain	CAC0909		-0.2928		+	2
gi 15894092	Methyl-accepting chemotaxis protein	CAC0805		-0.2278		+	2
gi 15893724	Methyl-accepting chemotaxis protein	CAC0433		-0.0175		+	2

gi 15896595	Membrane associated methyl-accepting chemotaxis protein with HAMP doma	CAC3352		-0.2664		+	2
gi 15896747	Membrane associated methyl-accepting chemotaxis protein (with HAMP dom	CAC3510		-0.1894		+	2
gi 15896058	Membrane associated methyl-accepting chemotaxis protein	CAC2803		-0.2296		+	2
gi 15896488	Membrane associated methyl-accepting chemotaxis protein	CAC3243		-0.2227		+	2
gi 15894666	Membrane associated chemotaxis sensory transducer protein	CAC1387		-0.2475		+	2
gi 15896584	Multimeric flavodoxin WrbA family protein	CAC3341		-0.1808	+	+	0
gi 15893605	Phage shock protein A	CAC0313		-1.0335	+	+	0
gi 15896723	Multimeric flavodoxin WrbA family protein	CAC3486		-0.3256		+	0
gi 15896297	Transcriptional regulator, LytR family	CAC3046		-0.3669		+	1
gi 15896314	Transcriptional regulator, LytR family	CAC3063		-0.3537		+	1
gi 15894810	Protein containing ChW-repeats	CAC1532		-0.6633	+	+	0
gi 15895844	Protein containing ChW-repeats	CAC2584		-0.5615	+	+	1
gi 15895796	Protein containing ChW-repeats	CAC2533		-0.2197	+	+	0
7. Miscellaneous							
gi 15896469	UDP-N-acetylglucosamine pyrophosphorylase	CAC3222	<i>gcaD</i>	-0.2195	+		0
gi 15895459	Spore coat polysaccharide biosynthesis protein F	CAC2190	<i>spsF</i>	-0.3885	+		0
gi 15895884	Possible 3-ketoacyl-acyl carrier protein reductase	CAC2626	<i>fabG</i>	0.0214	+		0
gi 15895602	UTP-glucose-1-phosphate uridylyltransferase	CAC2335		-0.3436		+	0
gi 15895597	Sugar transferase involved in lipopolysaccharide synthesis	CAC2330		0.2386		+	5
gi 15894526	Shape-determining protein mreC	CAC1243	<i>mreC</i>	-0.2314		+	1
gi 15893622	Prolipoprotein diacylglycerol transferaseX	CAC0330	<i>lgt</i>	0.5699		+	6
gi 15894690	Similar to toxic anion resistance protein terA, ortholog of YCEH <i>B.subtilis</i>	CAC1411		-0.5987	+		0
gi 15894034	Secreted protein containing uncharacterized conserved protein of ErfK	CAC0747		-0.5867		+	1
gi 15004832	Glycogen-binding regulatory subunit of S/T protein phosphatase I	CAP0129		-0.5126	+		1
gi 15894339	Membrane protease subunit, stomatin/prohibitin homolog	CAC1052		-0.0547		+	1

gi 15896233	Mannose-1-phosphate guanyltransferase	CAC2981		-0.1166	+		0
gi 15004771	Mannose/fructose-specific phosphotransferase system component IIC	CAP0067	<i>manY/levF</i>	1.0989		+	7
gi 15894340	LPS glycosyltransferase	CAC1053		-0.3755		+	0
gi 15893487	Glycosyltransferase involved in cell wall biogenesis	CAC0194		-0.0172		+	2
gi 15895594	Glycosyltransferase domain containing protein	CAC2327		-0.4472		+	0
gi 15895591	Glycosyltransferase	CAC2324		-0.0848		+	2
gi 15896462	Foldase protein prsA precursorg protein	CAC3215	<i>prsA</i>	-0.7603	+	+	1
gi 15895593	Diverged glycosyltransferase domain containing protein	CAC2326		-0.2906		+	0
gi 15896301	AMSJ/WSAK related protein, possibly involved in exopolysaccharide bios	CAC3050		-0.1902		+	0
gi 15895465	Aminoglycoside N3'-acetyltransferase	CAC2197		-0.1773		+	0
gi 15894385	Secreted protein, similar to catalytic domain of murein transglycosyla	CAC1100		-0.3421		+	1
8. Unknown function							
gi 15893519	Predicted permease	CAC0227		0.3491	+		10
gi 15893990	Predicted lipoprotein, Med/BMP family	CAC0702		-0.3333	+	+	1
gi 15895388	Predicted integral membrane protein, YggT family	CAC2119		1.1954		+	2
gi 15895588	Predicted glycosyltransferase	CAC2321		-0.1191		+	1
gi 15893501	Predicted membrane protein; CF-20 family	CAC0208		-0.4474	+	+	1
gi 15893900	Predicted membrane protein, YohK family	CAC0611		0.9658		+	6
gi 15893697	Predicted membrane protein, containing FHA domain	CAC0406		-0.2806		+	2
gi 15895021	Predicted Zn-finger-like protein, possible nucleic acid binding	CAC1744		-0.2229	+		0
gi 15894855	Ncharacterized conserved protein	CAC1577		-0.8909	+		0
gi 15896509	Uncharacterized conserved protein, YTFJ <i>B.subtilis</i> ortholog	CAC3264		-0.2737		+	0
gi 15894026	Predicted membrane protein	CAC0739		-0.4948		+	2
gi 15893956	Predicted membrane protein	CAC0668		0.0970		+	4
gi 15895633	Predicted membrane protein	CAC2366		1.0674		+	4
gi 15895883	Predicted membrane protein	CAC2625		-0.0667		+	2
gi 15894820	Predicted membrane protein	CAC1542		0.6147		+	2
gi 15895669	Predicted membrane protein	CAC2403		-0.1714		+	12
gi 15895184	Predicted membrane protein	CAC1910		-0.1502		+	2
gi 15895461	Ucharacterized protein, CGEB homolog	CAC2193		-0.4154	+		0
gi 15896941	Uncharacterized protein CAC3710	CAC3710		-0.3226		+	1
gi 15895913	Uncharacterized membrane-associated protein, DedA family	CAC2655		0.7068		+	4

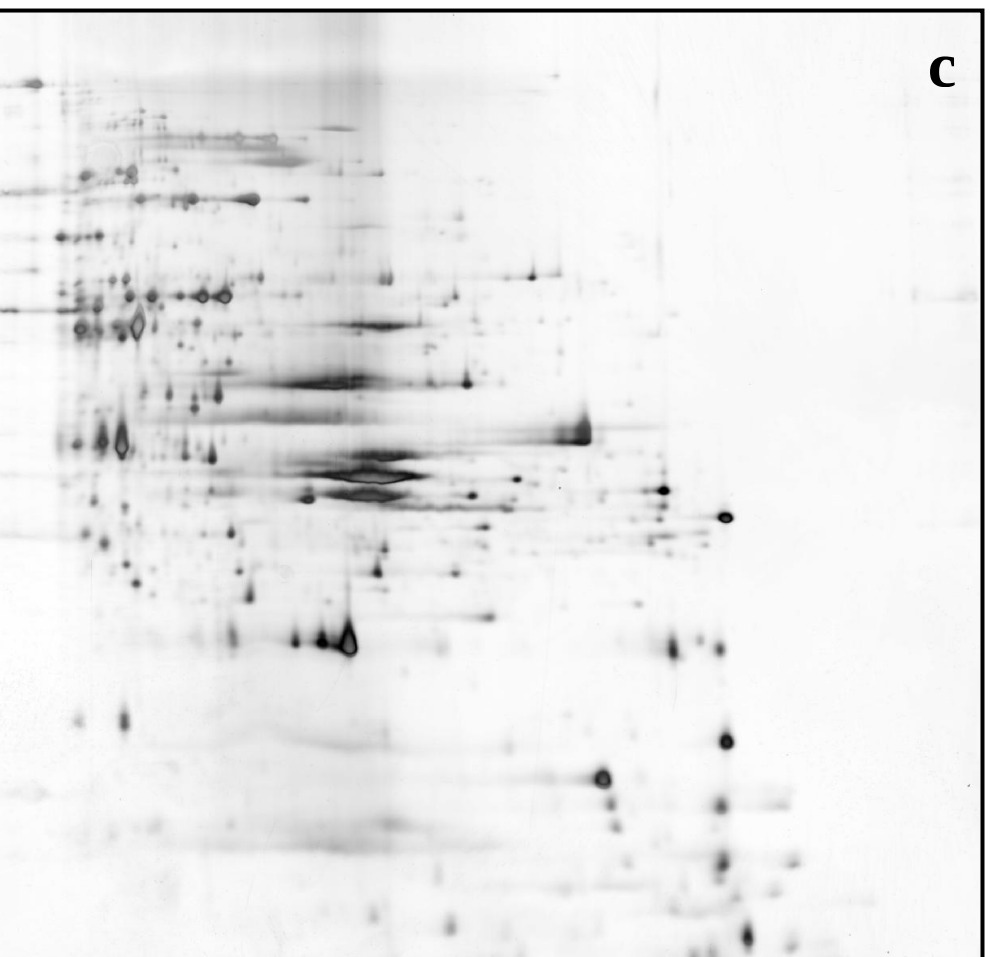
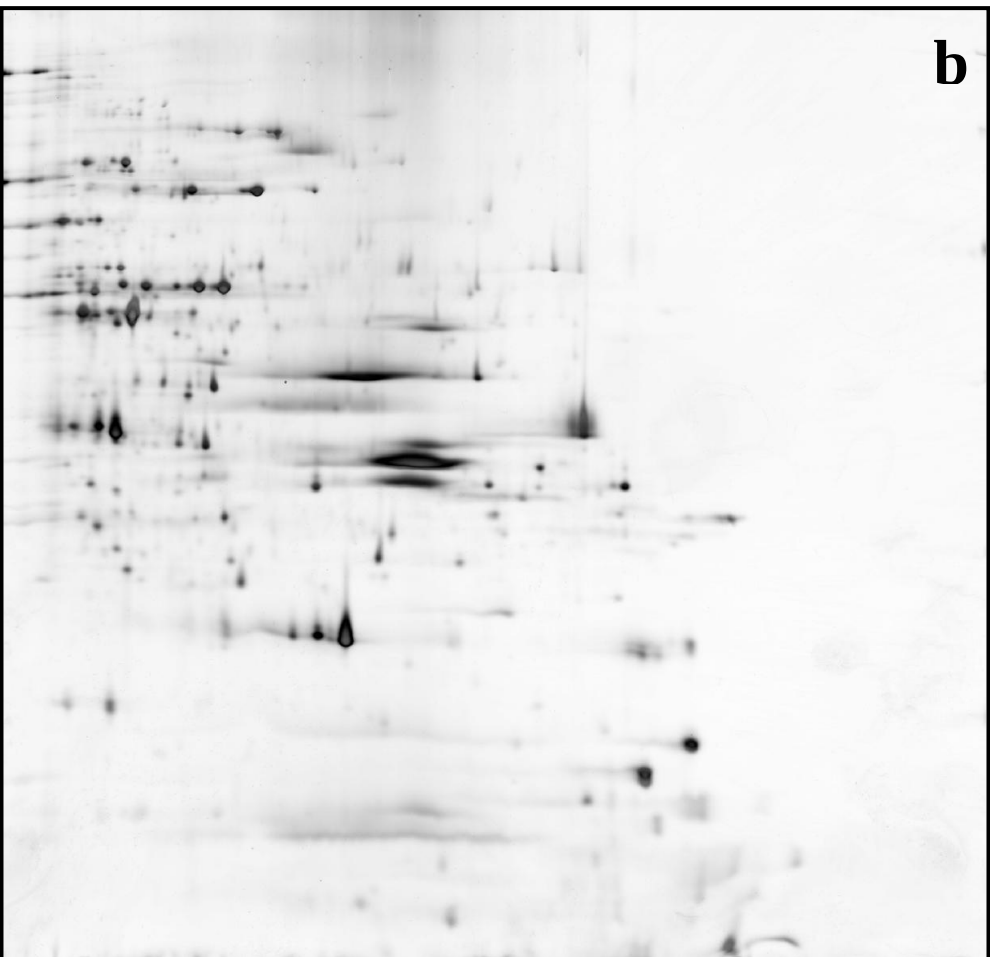
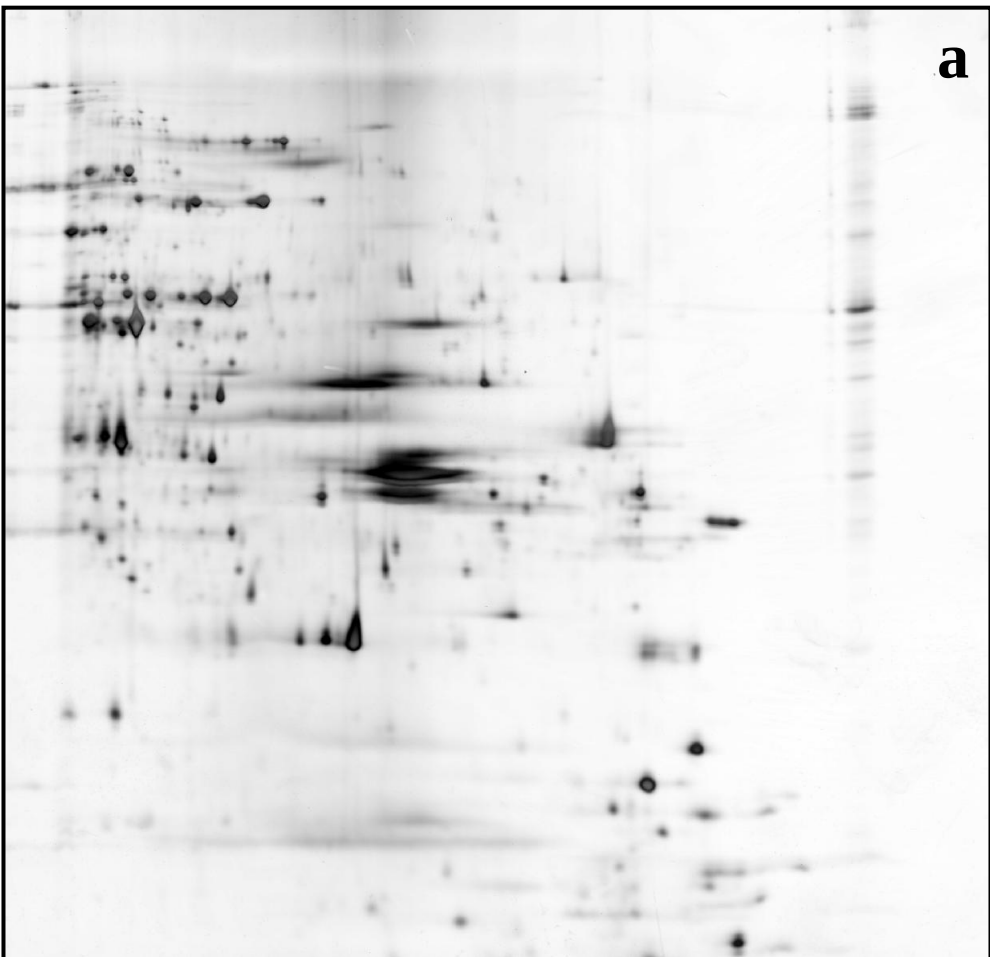
gi 15895186	Uncharacterized phage related protein	CAC1912		-0.4829		+	0
gi 15893795	FHA-domain containing secreted protein	CAC0504		0.0038		+	1
gi 15893732	Uncharacterized conserved membrane protein of SANA family	CAC0441		0.1208		+	3
gi 15896014	Uncharacterized protein, YPUA <i>B. subtilis</i> ortholog	CAC2758		-0.328819	+	+	1
gi 15895143	Uncharacterized secreted protein, homolog YXKC <i>B. subtilis</i>	CAC1868		-0.426733		+	1
gi 15895154	Uncharacterized, phage-related protein	CAC1879		-0.373058		+	0
gi 15895018	Uncharacterized conserved protein, YLBM <i>B. subtilis</i> ortholog	CAC1741		-0.243035	+		0
gi 15896952	Hypothetical secreted protein	CAC3721		-0.8403	+	+	0
gi 15896959	hypothetical protein CAC3728	CAC3728		-0.2669		+	1
gi 15896701	hypothetical protein CAC3461	CAC3461		-0.9820		+	0
gi 15896493	hypothetical protein CAC3248	CAC3248		-0.4535		+	0
gi 15896413	hypothetical protein CAC3165	CAC3165		-0.5256		+	1
gi 15896236	hypothetical protein CAC2984	CAC2984		-0.3661		+	1
gi 15896235	hypothetical protein CAC2983	CAC2983		-0.4782		+	1
gi 15895995	hypothetical protein CAC2738	CAC2738		0.0440		+	0
gi 15895907	hypothetical protein CAC2649	CAC2649		0.7978		+	6
gi 15895901	hypothetical protein CAC2643	CAC2643		-0.4837		+	1
gi 15895824	hypothetical protein CAC2564	CAC2564		-0.0823	+	+	0
gi 15895820	hypothetical protein CAC2558	CAC2558		-0.4378		+	0
gi 15895405	hypothetical protein CAC2136	CAC2136		-0.4273		+	0
gi 15895227	hypothetical protein CAC1954	CAC1954		-0.3536		+	1
gi 15894598	hypothetical protein CAC1318	CAC1318		-0.6165		+	1
gi 15894430	hypothetical protein CAC1147	CAC1147		-0.8420		+	0
gi 15894414	hypothetical protein CAC1130	CAC1130		-0.2407		+	0
gi 15894401	hypothetical protein CAC1116	CAC1116		-0.4843		+	0
gi 15894093	hypothetical protein CAC0806	CAC0806		-0.3727		+	0
gi 15893604	hypothetical protein CAC0312	CAC0312		-0.5032		+	0
gi 15893520	hypothetical protein CAC0228	CAC0228		-0.2870		+	0
gi 15893512	hypothetical protein CAC0220	CAC0220		-0.6057		+	0
gi 15893355	hypothetical protein CAC0058	CAC0058		-0.5164		+	0
gi 15893354	hypothetical protein CAC0057	CAC0057		-0.0662	+	+	0
gi 15893332	hypothetical protein CAC0034	CAC0034		-0.5257		+	0
gi 15894408	hypothetical protein CAC1124	CAC1124		-0.2422	+		0
gi 15894415	hypothetical protein CAC1131	CAC1131		-0.3531	+		0

Figure S1. Images of all of the gels, wild type *C. acetobutylicum* DSM 1731 and mutant strain *C. acetobutylicum* Rh8 during acidogenesis; a, b and c are experimental triplicate of each strain.



C. acetobutylicum DSM 1731 acidogenesis

pI 6 → 11



C. acetobutylicum Rh8 acidogenesis

pI 6 → 11

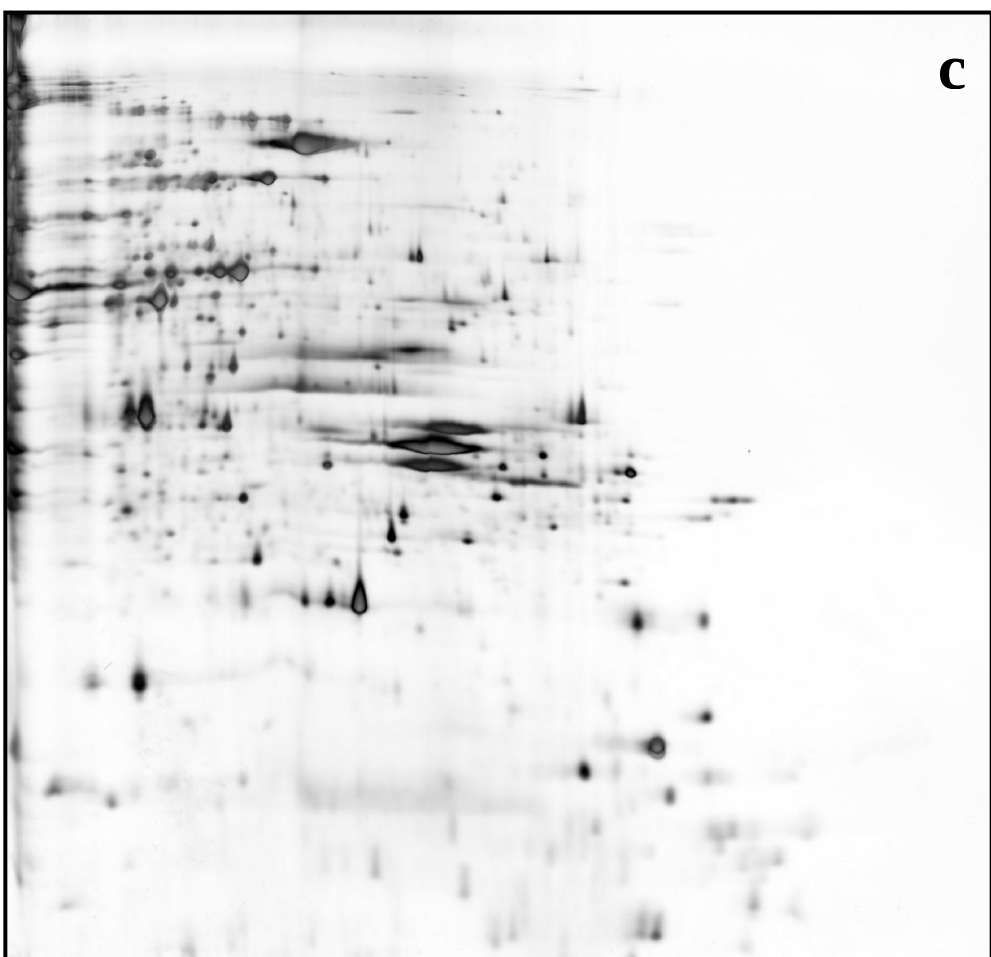
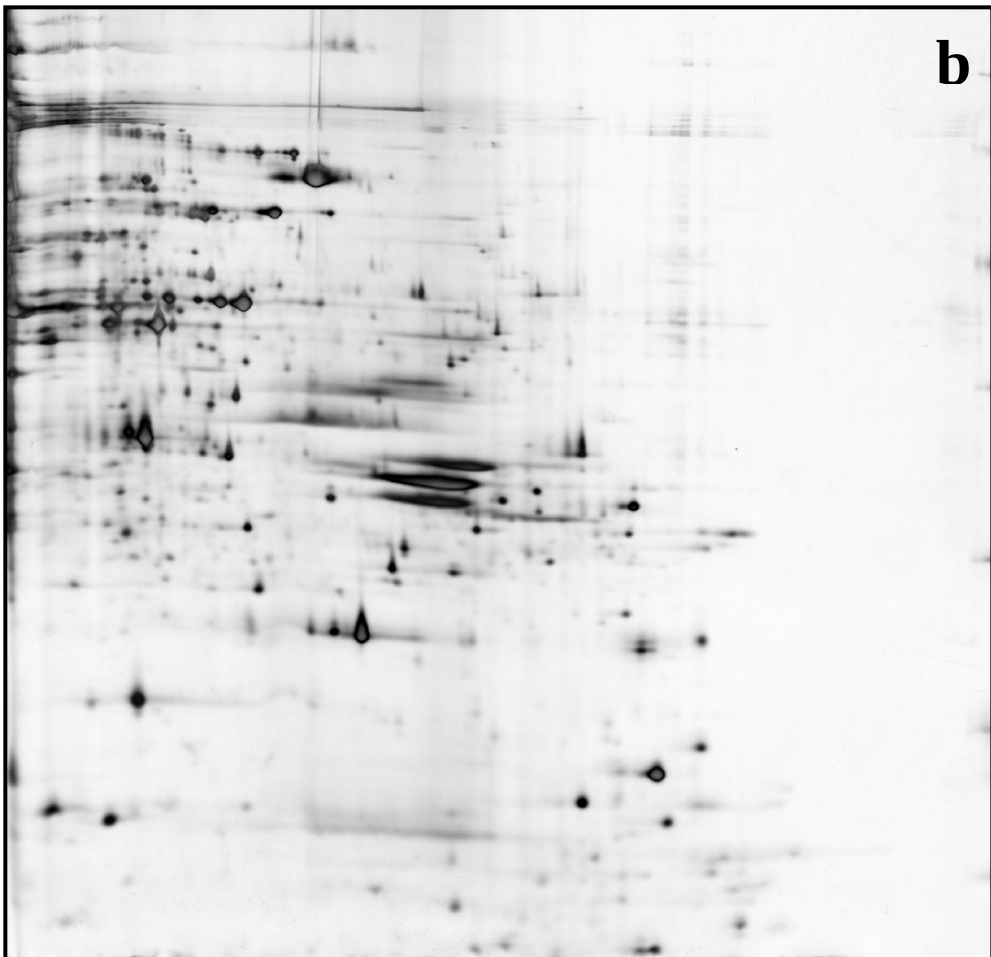
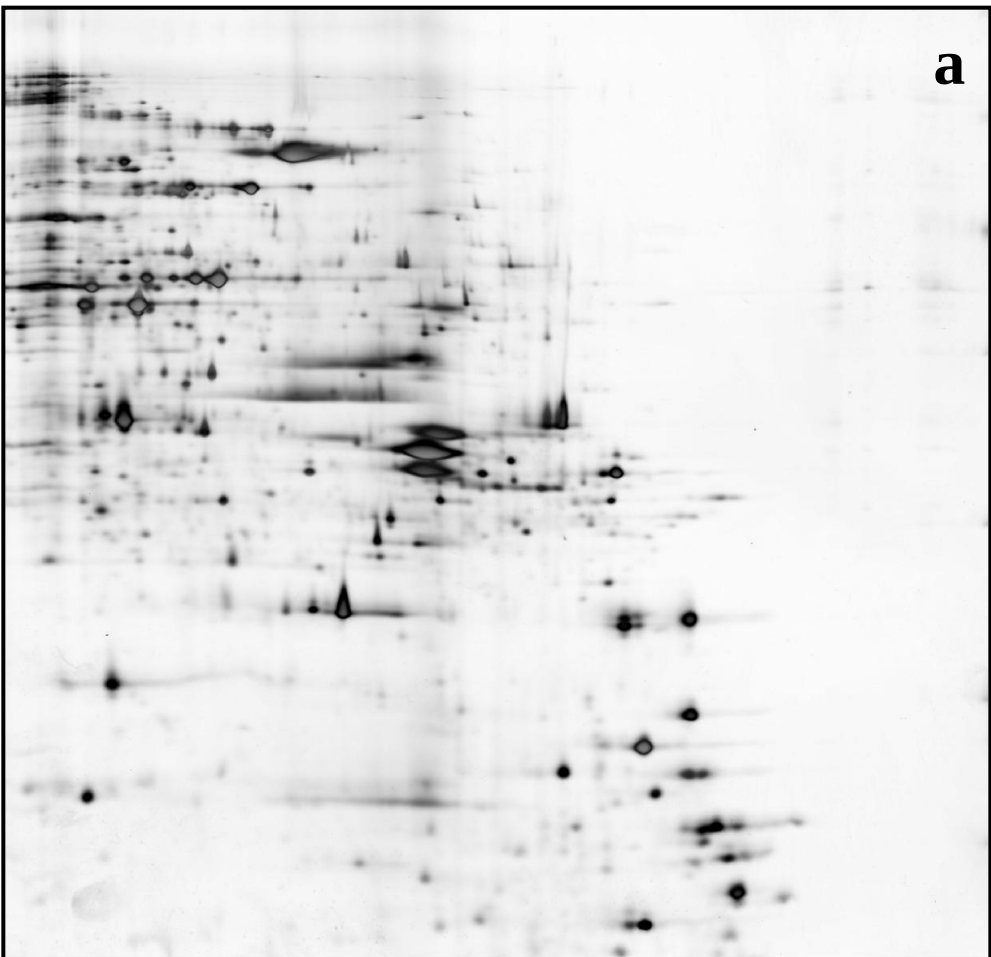
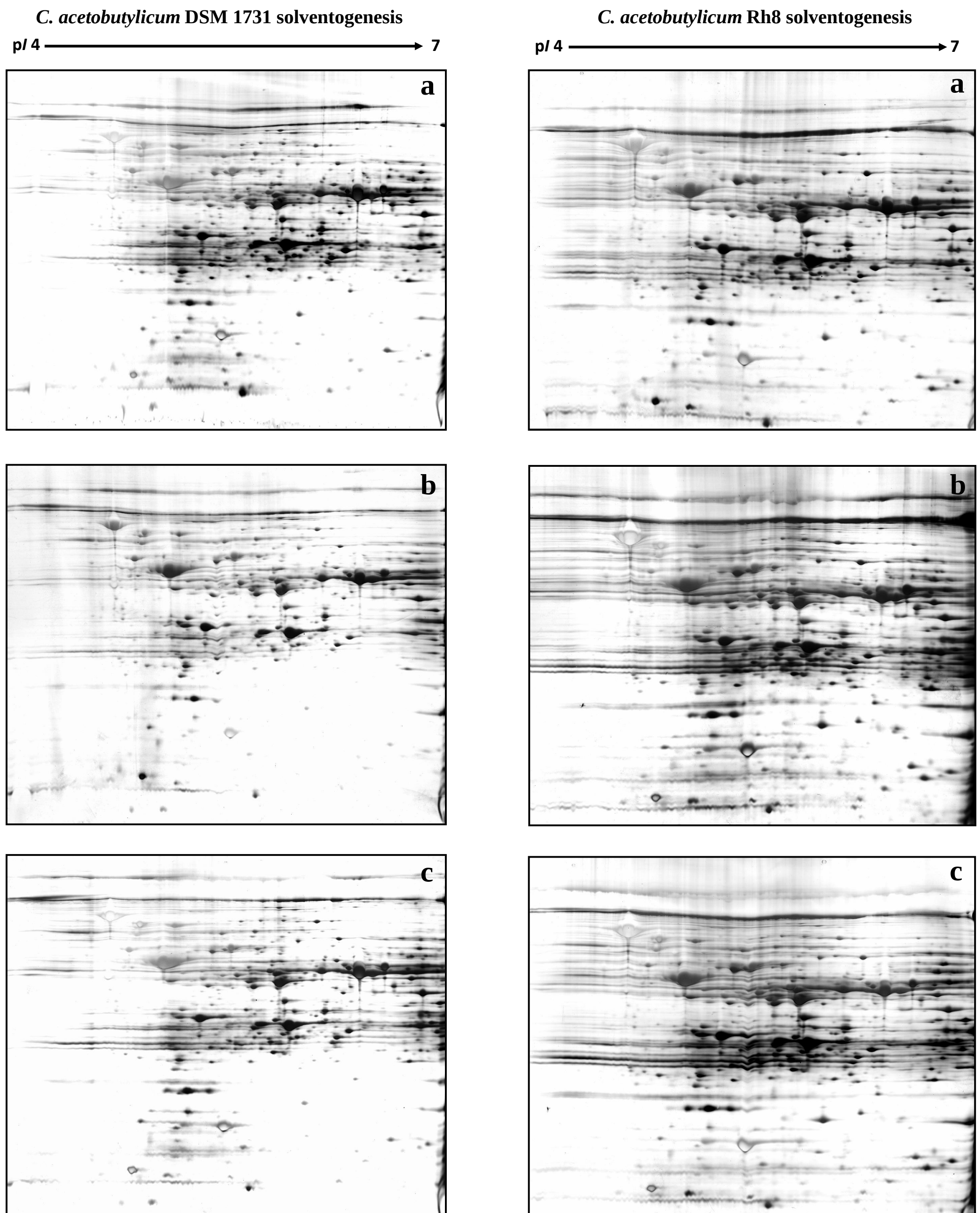
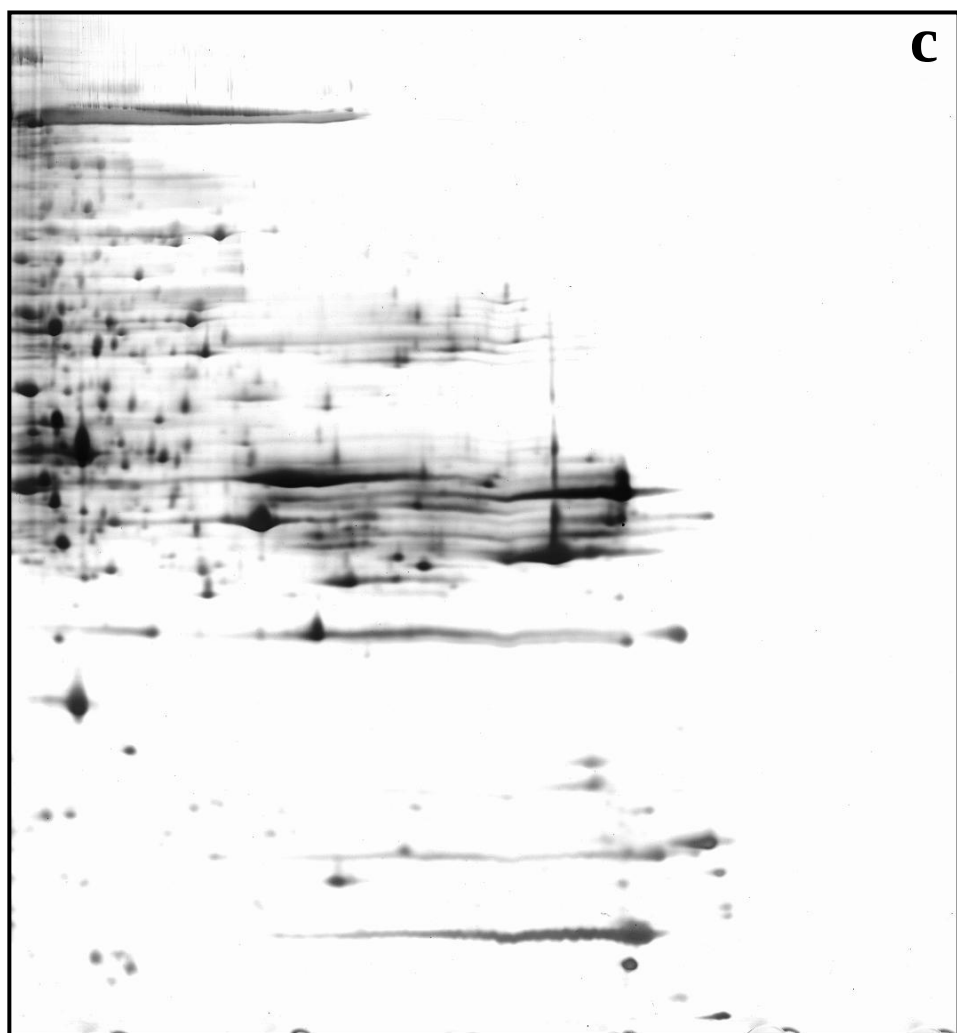
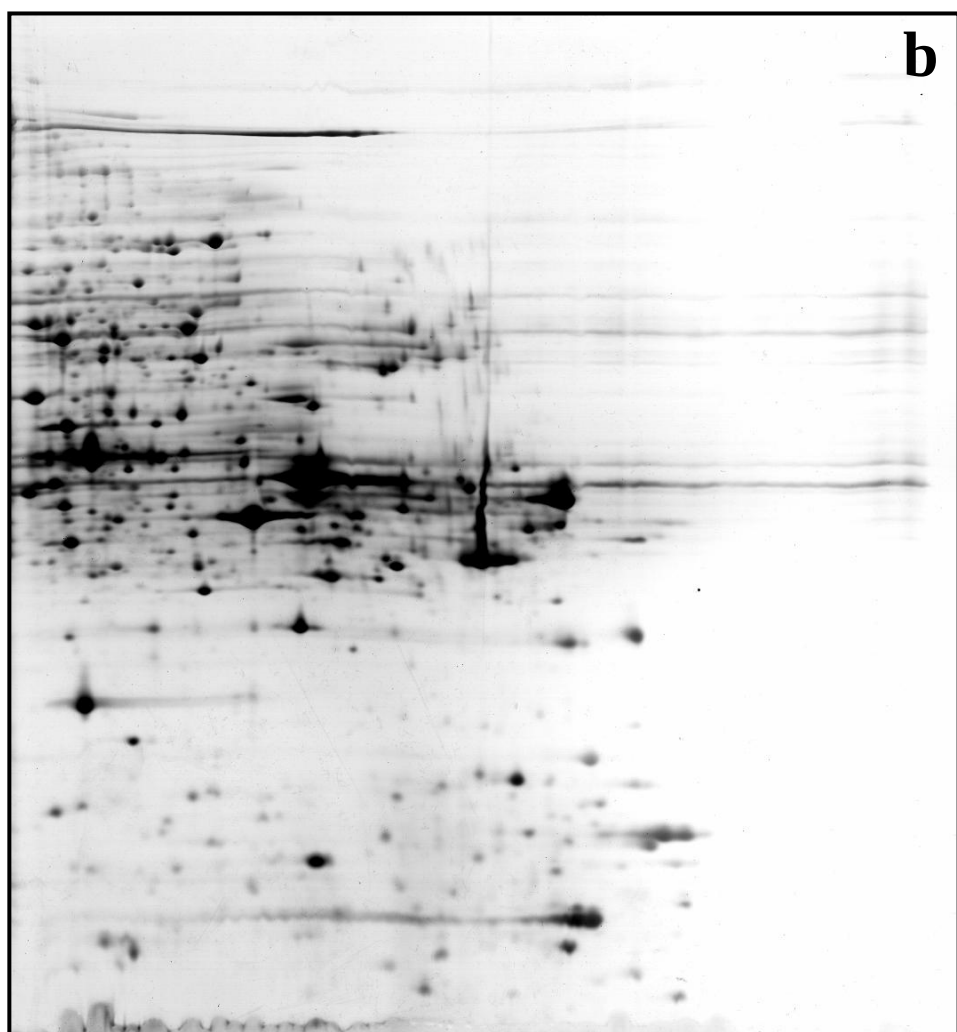
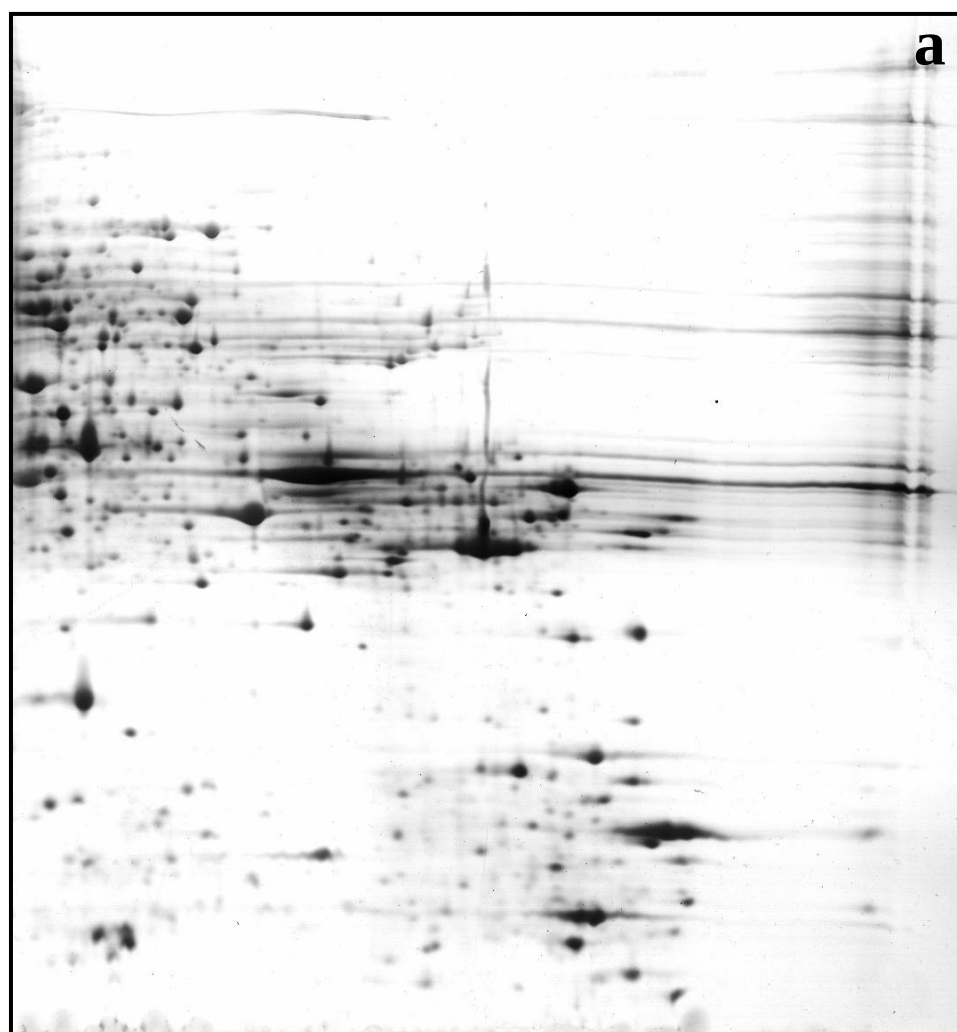


Figure S2. Images of all of the gels, wild type *C. acetobutylicum* DSM 1731 and mutant strain *C. acetobutylicum* Rh8 during solventogenesis; a, b and c are experimental triplicate of each strain.



C. acetobutylicum DSM 1731 solventogenesis

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C. acetobutylicum Rh8 solventogenesis

pI 6 → 11

