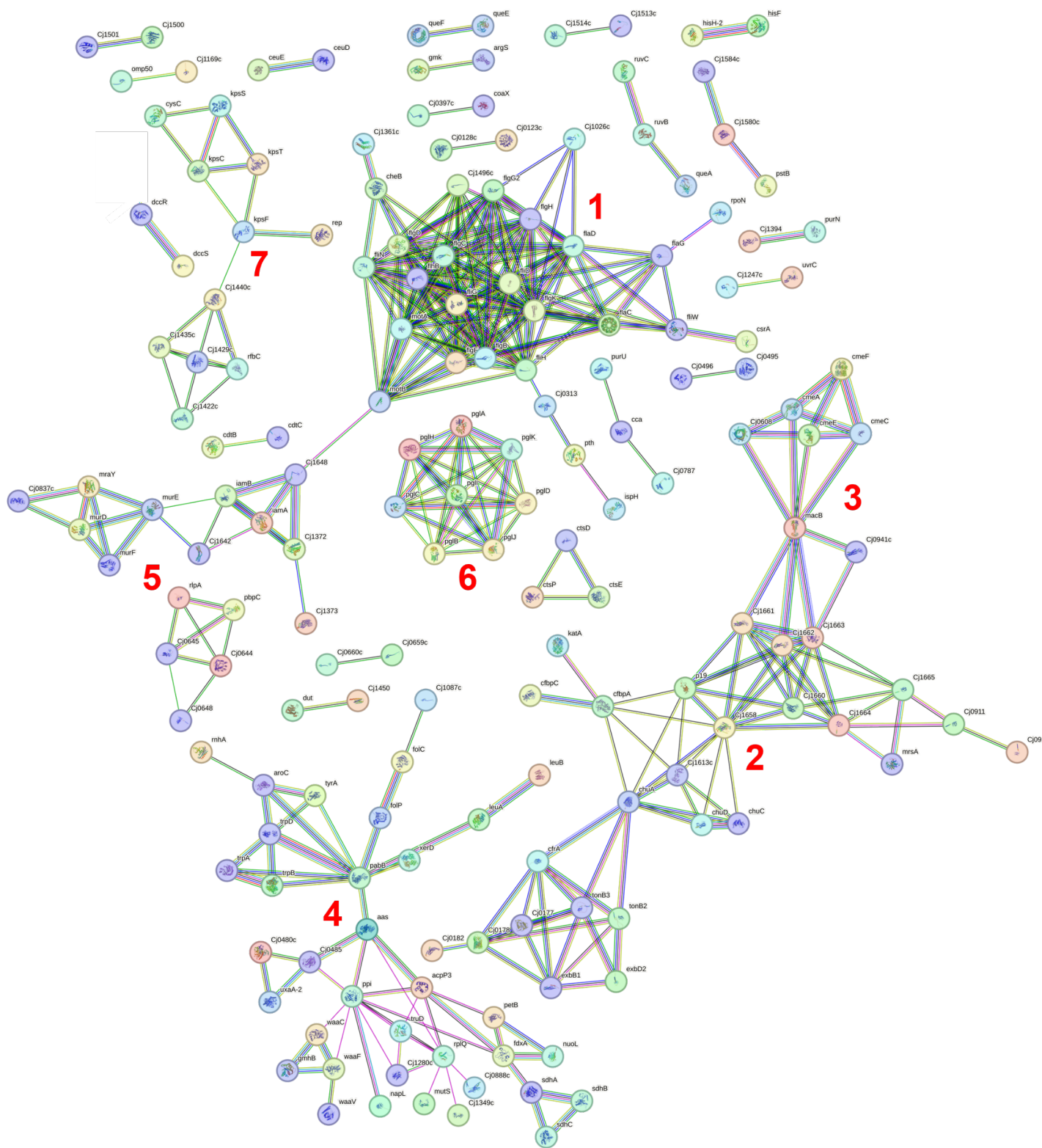
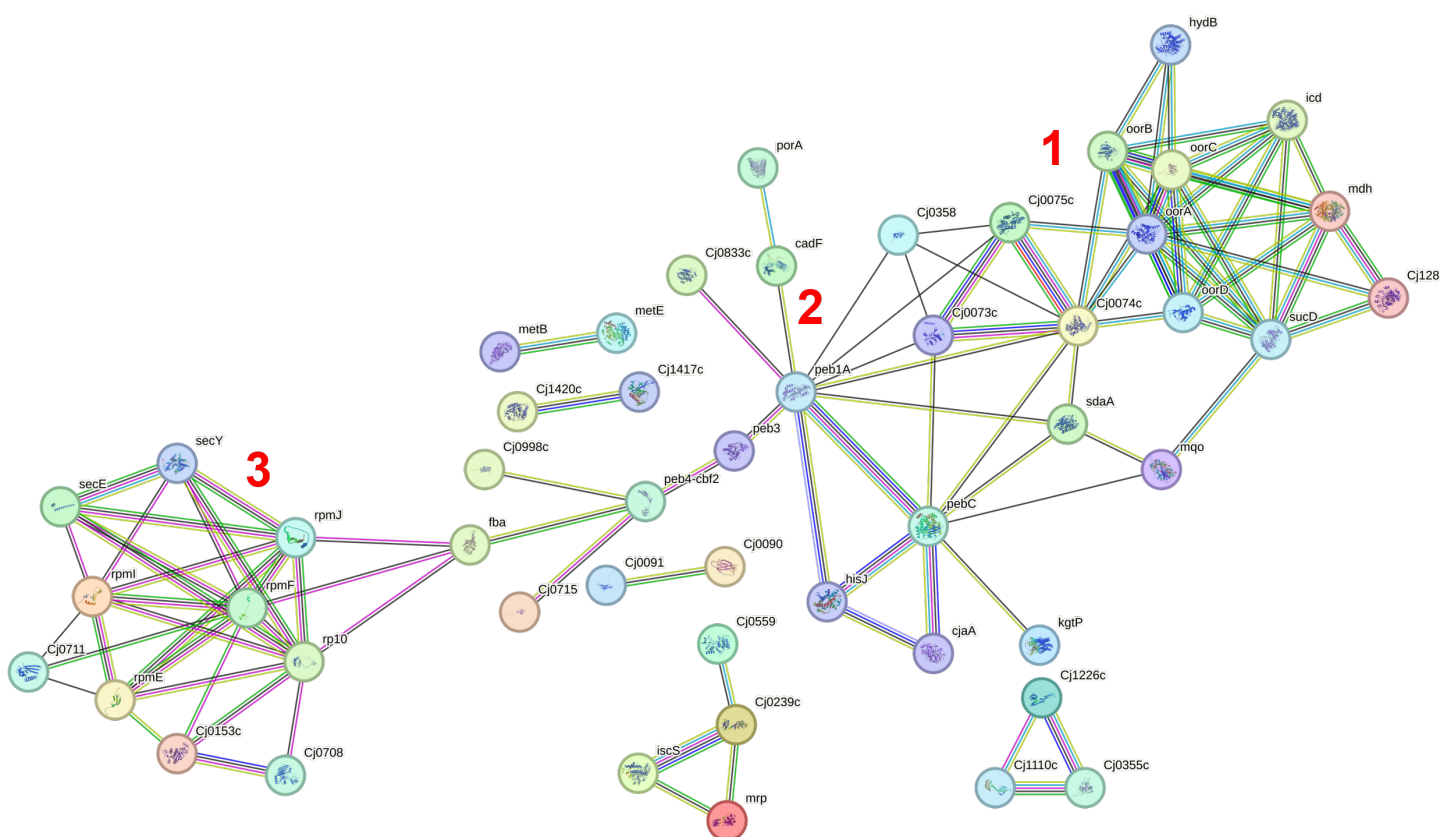


Supplementary Figure S1A. STRINGdb analysis of proteins significantly elevated in abundance in *C. jejuni* grown in MH medium with 5% CE compared with MH only control. Enriched functions included (1) flagellar motility, (2) iron uptake and antioxidants, (3) antibiotic resistance, (4) the *pgl*-encoded protein glycosylation system and (5) nutrient transporters and metabolism. Minimum required interaction score was set to confidence 0.700, cut-off for inclusion was >+1.5 fold-change; 181 edges observed, 74 expected with PPI enrichment *p*-value <1.0e-16.

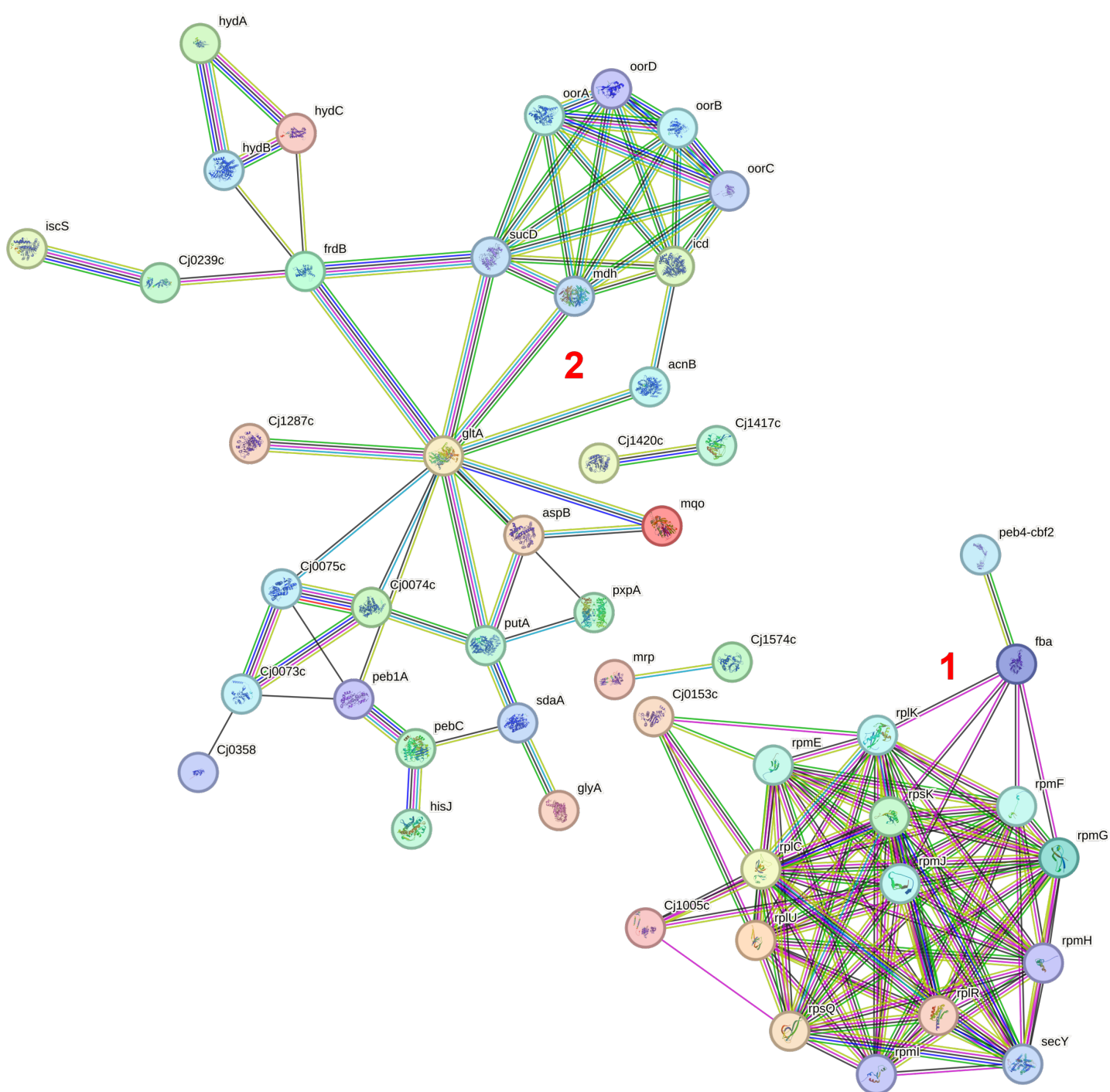


Supplementary Figure S1B. STRINGdb analysis of proteins significantly elevated in abundance in *C. jejuni* grown in 100% CE compared with MH only control.

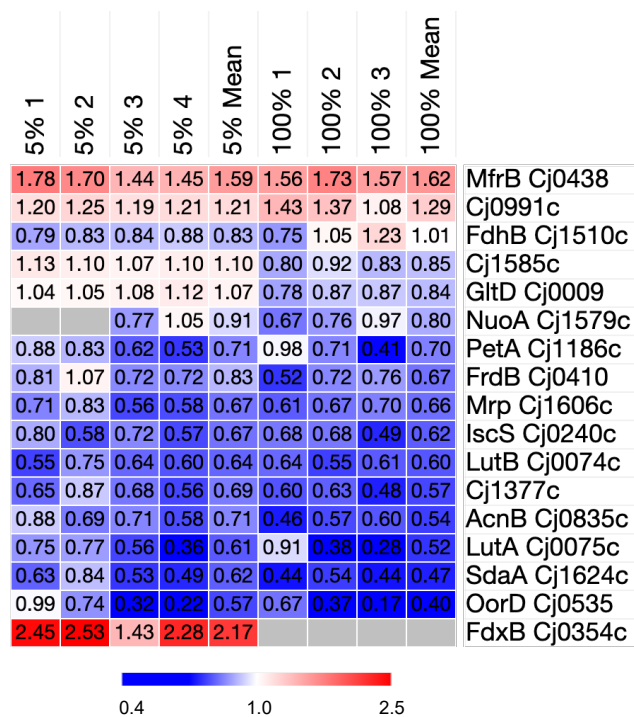
Enriched functions included (1) flagellar motility, (2) iron uptake and antioxidants, (3) antibiotic resistance, (4) nutrient transport and metabolism, (5) peptidoglycan structure and cell shape, (6) the *pgl*-encoded protein glycosylation system and (7) lipooligosaccharide. Minimum required interaction score was set to confidence 0.700, cut-off for inclusion was $>+1.5$ fold-change; 381 edges observed, 182 expected with PPI enrichment p -value $<1.0e-16$.



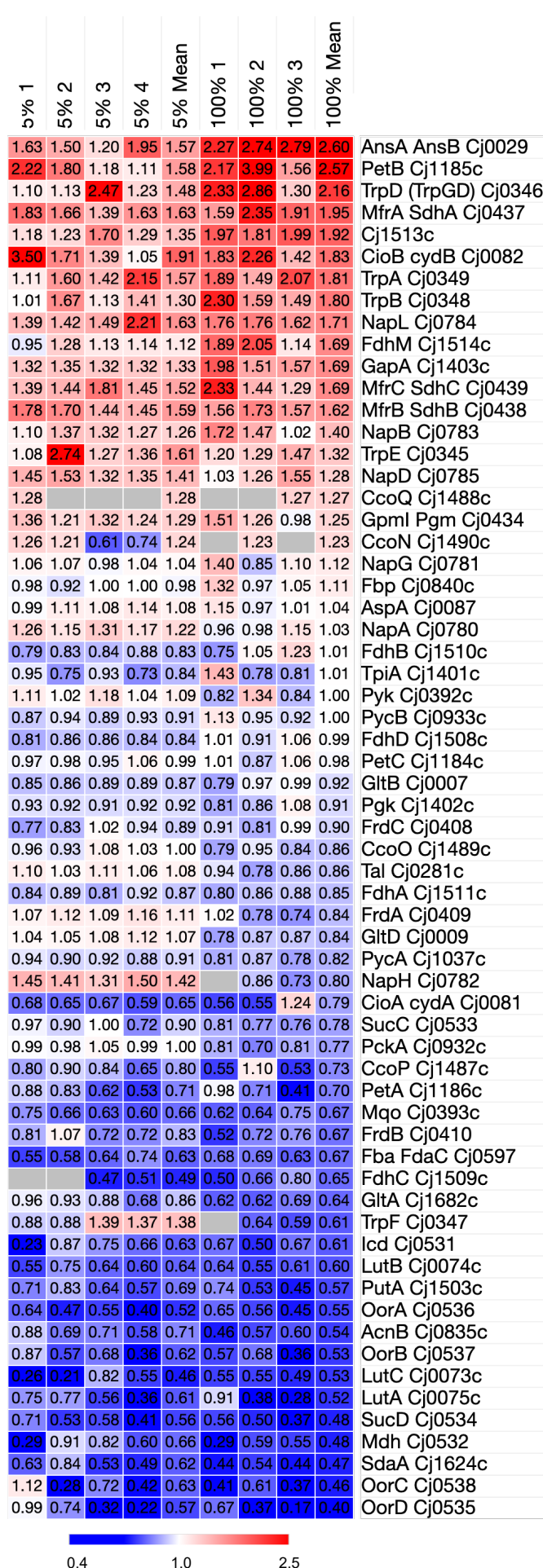
Supplementary Figure S1C. STRINGdb analysis of proteins significantly reduced in abundance in *C. jejuni* grown in MH medium with 5% CE compared with MH only control. Enriched functions included (1) metabolism, (2) virulence and antigenicity and (3) translation and protein secretion. Minimum required interaction score was set to confidence 0.700, cut-off for inclusion was <-1.5 fold-change (<0.67-fold); 104 edges observed, 52 expected with PPI enrichment p -value = 8.9×10^{-11} .



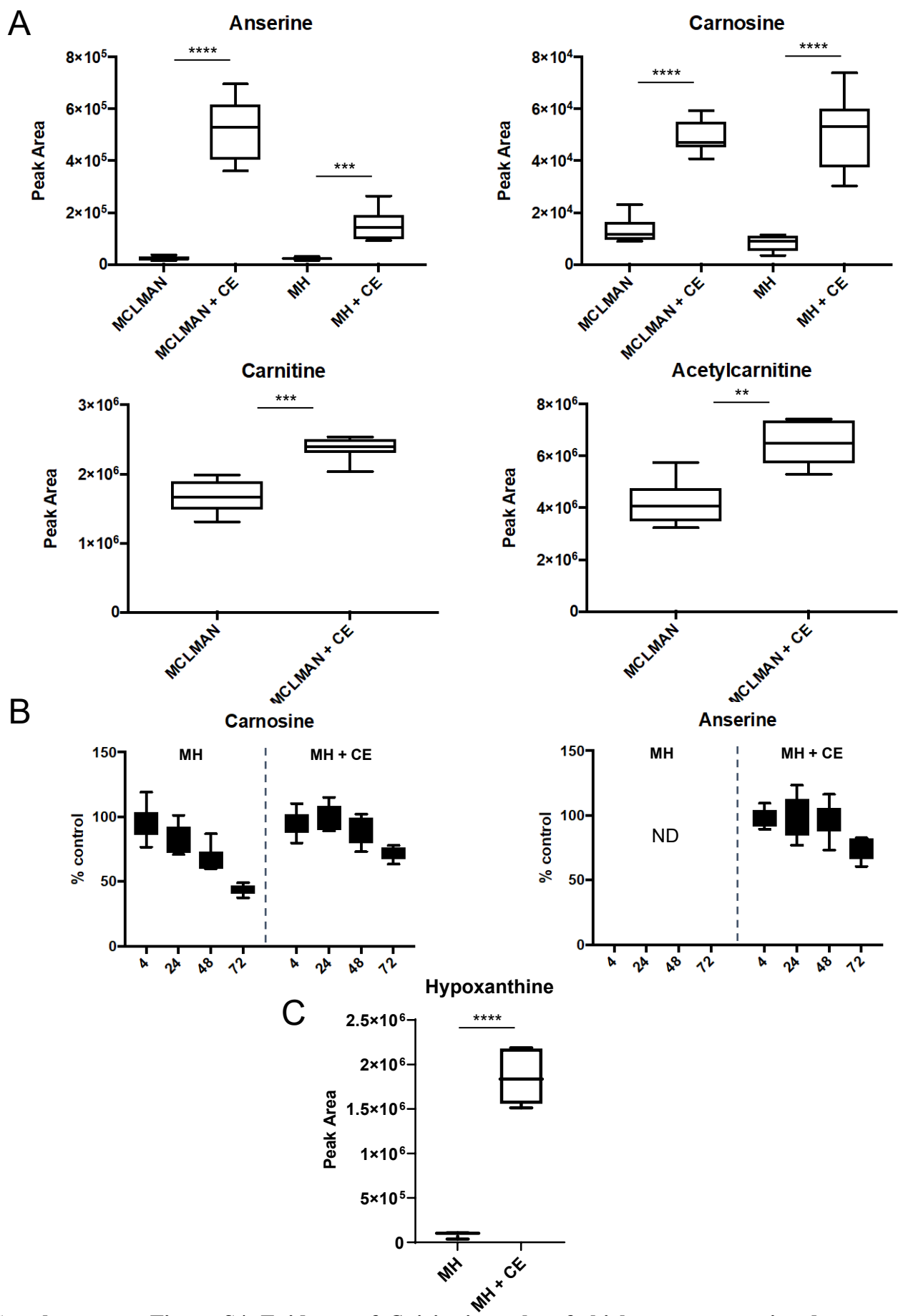
Supplementary Figure S1D. STRINGdb analysis of proteins significantly reduced in abundance in *C. jejuni* grown in 100% CE compared with MH only control. Enriched functions included (1) translation and (2) metabolism. Minimum required interaction score was set to confidence 0.700, cut-off for inclusion was <-1.5 fold-change (<0.67 -fold); 150 edges observed, 96 expected with PPI enrichment p -value $=2.7e-7$.



Supplementary Figure S2. Elevated abundances of iron acquisition proteins correlate with reduced abundances of proteins containing Fe-S clusters. Heat map showing replicate (MH+5% CE [left; $n=4$] and 100% CE [right; $n=3$] compared with MH only control) and mean n -fold data for proteins containing Fe-S clusters.



Supplementary Figure S3. Growth in CE alters *C. jejuni* proteins associated with metabolism. Heat maps showing replicate (MH+5% CE [left; $n=4$] and 100% CE [right; $n=3$] compared with MH only control) and mean n -fold data for proteins involved in metabolism.



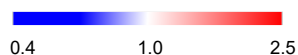
Supplementary Figure S4. Evidence of *C. jejuni* uptake of chicken meat-associated compounds carnosine and anserine. (A) Intracellular metabolite abundances as determined by targeted LC-MS/MS. (B) Culture supernatant levels as determined by targeted LC-MS/MS, box and whisker plots based on peak area values determined as a % of the corresponding non-inoculated control (MH and MH+5%CE) at each time-point. (C) Intracellular abundance of hypoxanthine. **, $p < 0.01$; *, $p < 0.001$; ****, $p < 0.0001$; ND, not detected.**

A

5% 1	5% 2	5% 3	5% 4	5% Mean	100% 1	100% 2	100% 3	100% Mean	
1.17	1.72	1.50	1.64	1.51	1.71	1.76	2.06	1.84	CheB ⁺ Cj0924c
1.19	1.14	1.23	1.29	1.21	1.80	1.08	1.06	1.31	Tlp6 Cj0448c
0.97	0.97	1.05	1.02	1.00	1.19	0.97	0.95	1.04	CheR Cj0923c
0.71	0.79	0.75	0.82	0.77	1.28	0.90	0.77	0.98	Tlp10 Cj0019c
0.86	0.86	0.86	0.89	0.87	0.82	0.94	1.13	0.96	Tlp2 Cj0144
1.08	1.01	1.13	0.95	1.04	0.86	1.35	0.64	0.95	CheY Cj1118c
1.06	1.11	1.11	1.13	1.10	1.19	0.74	0.87	0.93	Cj0700
0.68	0.73	0.74	0.74	0.73	0.86	0.87	1.05	0.93	Tlp4 Cj0262c
1.08	1.02	1.12	1.03	1.06	0.87	1.15	0.73	0.92	CheA Cj0284c
1.17	1.14	1.16	1.12	1.15	0.91	0.98	0.82	0.91	CheV Cj0285c
1.13	1.06	1.10	1.01	1.08	0.99	1.00	0.72	0.90	CheW Cj0283c
0.95	0.78	0.91	0.84	0.87	0.85	0.78	0.98	0.87	Aer1 CetC Cj1191c
0.82	0.86	0.78	0.86	0.83	0.83	0.96	0.75	0.84	Tlp1 CcaA Cj1506c
0.65	0.72	0.66	0.63	0.66	0.88	0.74	0.68	0.77	Tlp9 CetA Cj1190c
0.77	0.80	0.81	0.67	0.76	0.66	0.83	0.71	0.73	Tlp3 CcmL Cj1564
0.75	0.71	0.76	0.71	0.73	0.73	0.69	0.71	0.71	Aer2 CetB Cj1189c
0.31	0.71	0.73	0.48	0.56	0.59	0.67	0.53	0.60	Tlp8 CetZ Cj1110c

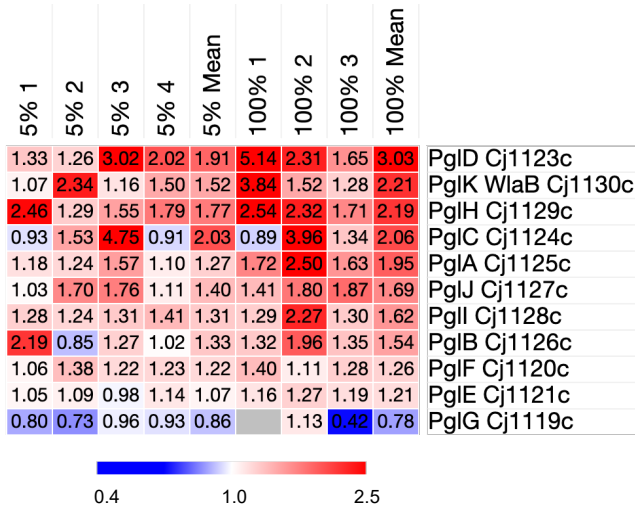
B

5% 1	5% 2	5% 3	5% 4	5% Mean	100% 1	100% 2	100% 3	100% Mean	
0.90	1.78	1.00	1.87	1.39	1.53	2.87	2.58	2.32	MurF Cj0795c
1.70	1.74	1.17	1.48	1.52	2.59	2.03	1.54	2.05	MurE Cj1641
1.35	1.38	1.82	2.03	1.65	2.29	1.58	2.02	1.96	MurD Cj0432c
						1.80		1.80	MltD Cj0645
1.52	1.05	1.19	1.45	1.30	1.86	1.45	1.97	1.76	MltG Cj0529c
1.03	1.43	1.51	1.95	1.48	1.51	1.34	2.18	1.68	CslT Cj0843c
1.32	1.76	1.24	1.87	1.55	1.74	1.29	1.97	1.67	PatA Cj0610c
1.37	1.38	1.36	1.57	1.42	2.12	1.56	1.27	1.65	RlpA Cj0646
		0.90	1.09	1.00		1.59	1.65	1.62	MraY Cj0433c
1.80	1.27	1.02	1.16	1.31	1.89	1.46	1.50	1.61	Csd1 Cj1087c
1.49	1.65	1.14	1.45	1.44	1.82	1.30	1.44	1.52	PbpC Cj0652
1.14	1.83	1.01	1.25	1.31	1.38	1.20	1.43	1.34	PbpB Cj0525c
1.36	1.27	1.31	1.18	1.28	1.43	1.18	1.24	1.29	MurC Cj1054c
1.19	1.18	1.35	1.34	1.27	1.27	1.27	1.09	1.21	MurI Cj1652c
0.99	1.02	0.95	0.98	0.99	1.91	0.77	0.86	1.18	DdlA Cj0798c
1.00	0.91	0.85	0.86	0.91	1.79	0.87	0.67	1.11	CcmA Cj1086c
0.85	0.82	0.90	0.92	0.87	1.40	1.12	0.77	1.10	MreC Cj0277
0.91	0.81	0.79	0.88	0.85	0.88	1.00	1.31	1.06	UppS Cj0824
1.10	0.97	1.15	1.06	1.07	0.81	1.33	1.03	1.06	MurG Cj1039
0.79	0.90	0.80	0.92	0.85	0.83	1.06	1.27	1.05	AmiA Cj1269c
0.96	1.01	1.00	1.03	1.00	0.95	0.99	1.11	1.02	MurA Cj0858c
0.82	0.82	0.99	0.88	0.88	0.94	0.94	1.15	1.01	MurB Cj1676
1.00	1.03	1.07	1.08	1.04	1.52	0.77	0.69	0.99	MreB Cj0276
0.61	0.72	0.71	0.78	0.70	1.05	1.23	0.68	0.99	Csd3 Cj1215
0.65	0.70	0.66	0.74	0.69	0.99	0.94	0.97	0.97	Cj0131
0.87	0.88	0.87	0.88	0.88	0.76	1.25	0.79	0.93	PbpA Cj0508
0.96	0.92	0.96	0.99	0.96	0.68	0.98	1.15	0.93	Cj1275c
0.88	0.89	0.86	0.99	0.90	0.70	0.94	0.91	0.85	Ape1 Cj0609c
0.71	0.76	0.75	0.79	0.75	0.71	0.90	0.88	0.83	Pgp2 Cj0906c
0.74	0.77	0.68	0.80	0.75	1.08	0.81	0.52	0.80	Pgp3 Cj1235

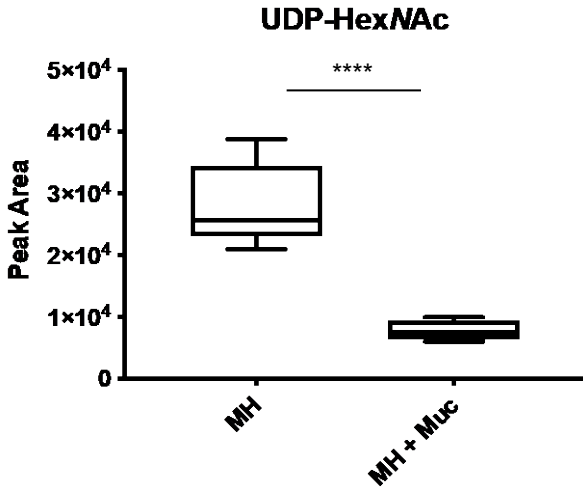


Supplementary Figure S5. Growth in CE results in changes to abundances of proteins involved in chemotaxis and peptidoglycan (PGN) biosynthesis, modification and cell shape. Heat map showing replicate (MH+5% CE [left; $n=4$] and 100% CE [right; $n=3$] compared with MH only control) and mean n -fold data for proteins involved in (A) chemotaxis and (B) PGN biosynthesis, modification and cell shape.

A



C



Supplementary Figure S6. Growth in CE results in increased abundances of proteins associated with the Pgl *N*-linked glycosylation system. Heat maps showing replicate (MH+5% CE [left; *n*=4] and 100% CE [right; *n*=3] compared with MH only control) and mean *n*-fold data for proteins involved in (A) biosynthesis and attachment of *N*-linked glycans to proteins (Pgl cluster); (B) known targets of *N*-linked glycosylation; (C) intracellular levels of UDP-HexNAc as determined by targeted intracellular metabolomics, ****, *p* < 0.0001.

B

