

Supplementary materials

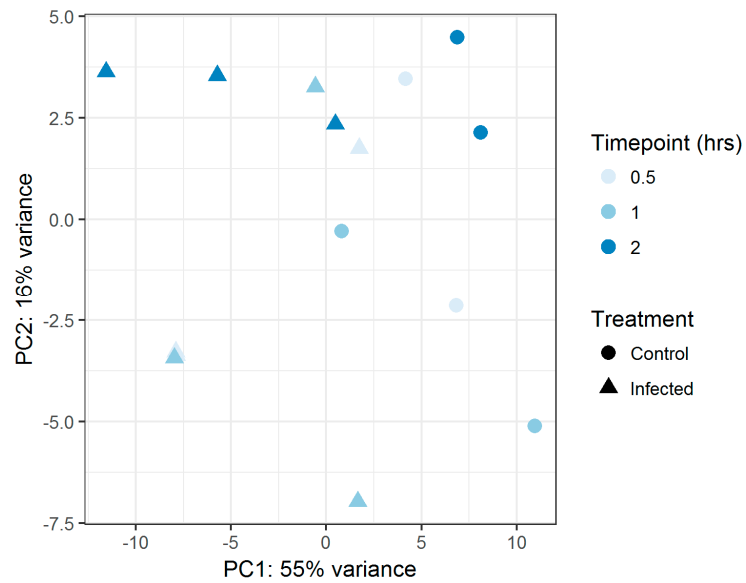


Figure S1. PCA plot for infected vs. uninfected controls at each time point post NCTC 12673 phage infection of *C. jejuni* NCTC 11168 cells. Plots were generated using the data from the 500 genes with the greatest variation in expression across samples.

Table S1. RNA-seq read statistics.

Sample Barcode	Replicate Number	Group	Sampling Timepoint (h)	Total Reads	Reads Aligning to NCTC 11168	Reads aligning to NCTC 12673
BC01	1	Infected	0.5	4675121	3624270	497744
BC02	1	Infected	1	4158337	3481256	254092
BC03	1	Infected	2	6029137	5401531	369292
BC04	2	Infected	0.5	7329874	6525606	465763
BC05	2	Infected	1	6627184	5896267	403863
BC06	2	Infected	2	6446221	5803434	361905
BC07	2	Control	0.5	8711385	8649245	41
BC08	2	Control	1	6454979	6405427	330
BC09	2	Control	2	7161982	7111778	6
BC10	3	Infected	0.5	7173169	6580235	360334
BC11	3	Infected	1	6510986	6113184	236263
BC12	3	Infected	2	5850072	5354073	320383
BC13	3	Control	0.5	7241333	7183906	65
BC14	3	Control	1	8448990	8381159	27
BC15	3	Control	2	6872600	6819512	28

Table S2. Relative transcription of NCTC 12673 phage genes during *C. jejuni* NCTC 11168 infection.

Locus Tag	Annotation	% AA coverage^a (Kropinski <i>et al.</i> 2011)	Relative transcription (log₁₀(RPKM))^b
<i>ncR001^d</i>	Novel non-coding RNA	N/A	5.81
<i>gp074</i>	Gp23 major capsid protein	43	5.23
<i>gp089</i>	Hypothetical protein	21.3	4.89
<i>gp060</i>	Gp18 tail sheath protein	0	4.66
<i>gp068</i>	Conserved hypothetical protein	7.6	4.40
<i>gp075</i>	Hypothetical protein	0	4.66
<i>gp087</i>	Conserved hypothetical protein	0	4.45
<i>gp069</i>	Hypothetical protein	7.3	4.65
<i>gp112</i>	Conserved hypothetical protein	0	4.40
<i>gp153</i>	Hypothetical protein	13.2	4.38
<i>gp051</i>	Gp32 ssDNA binding protein	0	4.41
<i>gp079</i>	Conserved hypothetical protein	4.7	4.49
<i>gp036</i>	Gp19 tail tube protein	6.9	4.36
<i>gp038</i>	Conserved hypothetical protein	0	4.48
<i>gp076</i>	Gp21 prohead core scaffold and protease	0	4.35
<i>gp119</i>	Hypothetical protein	16.8	4.12
<i>gp117</i>	Conserved hypothetical protein	2.5	4.37
<i>gp111</i>	Conserved hypothetical protein	0	3.94
<i>gp001</i>	Hypothetical protein	7.3	4.18
<i>gp122</i>	Gp23 major head protein II	25.3	4.24
<i>gp080</i>	Gp13 neck protein	6.6	4.18
<i>gp088</i>	Hypothetical protein	8.5	4.08
<i>gp085</i>	Phosphatidylserine decarboxylase	5.1	4.13
<i>gp086</i>	Co-chaperonin GroES	0	4.16
<i>gp019</i>	Hypothetical protein	22.7	4.13
<i>gp037</i>	Gp19 tail tube protein II	0	4.07
<i>gp044</i>	Amidinotransferase	20.8	4.14
<i>gp108</i>	Conserved hypothetical protein	18.3	4.08
<i>gp123</i>	Gp14 head completion protein	0	3.98
<i>gp160</i>	Hypothetical protein	0	3.19
<i>gp138</i>	Putative exonuclease	9.5	3.87
<i>gp163</i>	Ribonucleotide reductase, small subunit	0	3.57
<i>gp116</i>	Conserved hypothetical protein	2.7	3.78
<i>gp043</i>	Gp45 sliding clamp protein	0	3.88
<i>gp115</i>	Hypothetical protein	0	3.59
<i>gp062</i>	Conserved hypothetical protein	0	3.88
<i>gp170</i>	Hypothetical protein	0	3.70
<i>gp077</i>	Phage hypothetical protein	0	3.44
<i>gp168</i>	RecA	0	3.79
<i>gp094</i>	Conserved hypothetical protein	2.4	3.54
<i>gp083</i>	Gp19 tail tube protein III	7.8	3.81

<i>gp171</i>	Hypothetical protein	0	3.20
<i>gp152</i>	Gp4 head completion protein	0	3.68
<i>gp035</i>	Hypothetical protein	0	3.78
<i>gp104</i>	Conserved hypothetical protein	0	3.76
<i>gp017</i>	Hypothetical protein	0	3.79
<i>gp078</i>	Gp20 portal vertex protein	16.9	3.76
<i>gp110</i>	Conserved hypothetical protein	0	3.26
<i>gp066</i>	Conserved hypothetical protein	0	3.80
<i>gp082</i>	Hypothetical protein	0	3.25
<i>gp026</i>	Hypothetical protein	0	3.68
<i>gp158</i>	Hypothetical protein	0	3.80
<i>gp048</i>	Putative RNase H	0	3.55
<i>gp020</i>	Conserved hypothetical protein	0	3.62
<i>gp166</i>	Hypothetical protein	0	3.63
<i>gp041</i>	Gp6 baseplate wedge subunit	0	3.55
<i>gp098</i>	Hypothetical protein	0	3.47
<i>gp050</i>	Gp62 clamp loader subunit	0	3.46
<i>gp064</i>	Hypothetical protein	0	3.71
<i>gp154</i>	Hypothetical protein	0	3.13
<i>gp126</i>	Gp15 tail sheath stabilizer and completion protein	0	3.57
<i>gp049</i>	Hypothetical protein	0	3.32
<i>gp030</i>	Gp5 baseplate hub subunit and tail lysozyme	0	3.43
<i>gp061</i>	Hypothetical protein	0	3.30
<i>gp093</i>	Hypothetical protein	16.2	3.44
<i>gp159</i>	Hypothetical protein	0	3.16
<i>gp162</i>	Ribonucleotide reductase, large subunit	0	3.54
<i>gp099</i>	Hypothetical protein	0	3.39
<i>gp067</i>	Hypothetical protein	0	3.58
<i>gp155</i>	RnlA; RNA ligase	0	3.15
<i>gp165</i>	Conserved hypothetical protein	0	3.41
<i>gp063</i>	Gp30 DNA ligase	0	3.49
<i>gp102</i>	Putative methyltransferase	0	3.45
<i>gp148</i>	Conserved hypothetical protein	0	3.35
<i>gp105</i>	Thymidine kinase	0	3.22
<i>gp140</i>	Hypothetical protein	0	3.46
<i>gp006</i>	Potential dUTP pyrophosphatase	0	3.11
<i>gp149</i>	Hypothetical protein	10.1	2.86
<i>gp012</i>	Conserved hypothetical protein	0	3.33
<i>gp025</i>	Hypothetical protein	0	3.36
<i>gp142</i>	Conserved hypothetical protein	0	3.32
<i>gp109</i>	Gp3 tail completion and sheath stabilizer protein	0	3.33
<i>gp032</i>	Probable Gp5.4 conserved hypothetical protein	0	3.46
<i>gp007</i>	Hypothetical protein	0	3.39

<i>gp151</i>	Hypothetical protein	0	3.22
<i>gp016</i>	Conserved hypothetical protein	0	3.32
<i>gp156</i>	Conserved hypothetical protein	0	2.94
<i>gp114</i>	Conserved hypothetical protein	0	3.42
<i>gp027</i>	Hypothetical protein	0	3.44
<i>gp132</i>	Hypothetical protein	0	3.18
<i>gp169</i>	Hypothetical protein	0	3.40
<i>gp005</i>	Hypothetical protein	0	3.33
<i>gp003</i>	Gp44 sliding clamp loader subunit (DNA polymerase accessory protein)	0	3.28
<i>gp065</i>	Hypothetical protein	0	3.31
<i>gp107</i>	Gp61 DNA primase subunit	0	3.08
<i>gp084</i>	Hef85 homing endonuclease	0	3.32
<i>gp092</i>	Putative repair and recombination protein	0	2.97
<i>gp015</i>	Gp39; topoisomerase II large subunit	0	3.27
<i>gp042</i>	Gp25 baseplate wedge subunit	0	3.27
<i>gp028</i>	Hypothetical protein	0	2.91
<i>gp008</i>	Potential NAD(FAD)-utilizing dehydrogenase	0	3.29
<i>gp164</i>	Hypothetical protein	0	3.26
<i>gp141</i>	Conserved hypothetical protein	0	3.05
<i>gp103</i>	Hypothetical protein	0	3.02
<i>gp039</i>	Hypothetical protein	0	3.34
<i>gp029</i>	Conserved hypothetical protein	0	3.20
<i>gp118</i>	Gp46 recombination endonuclease	0	3.05
<i>gp139</i>	Conserved hypothetical protein	0	3.11
<i>gp045</i>	Gp41 DNA primase-helicase subunit	0	3.20
<i>gp033</i>	Hef34 homing endonuclease	0	3.11
<i>gp021</i>	Hypothetical protein	0	3.13
<i>gp127</i>	Conserved hypothetical protein	0	3.06
<i>gp135</i>	Hypothetical protein	0	3.30
<i>gp128</i>	Hypothetical protein	0	2.95
<i>gp134</i>	Hypothetical protein	0	3.37
<i>gp009</i>	Hypothetical protein	0	3.19
<i>gp024</i>	Putative peptidase	0	3.14
<i>gp040</i>	Conserved hypothetical protein	0	3.14
<i>gp056</i>	Thymidylate synthetase	0	3.19
<i>gp002</i>	Hypothetical protein	17.9	3.08
<i>gp047</i>	Conserved hypothetical protein; flagellar glycan binding protein ^c	0	3.11
<i>gp091</i>	DNA helicase UvsW	0	3.08
<i>gp146</i>	Conserved hypothetical protein	0	2.70
<i>gp143</i>	Hypothetical protein	0	2.82
<i>gp053</i>	Gp2 DNA end protector protein	0	2.96
<i>gp147</i>	Conserved hypothetical protein	0	3.03
<i>gp034</i>	Hypothetical protein	0	2.63

gp133	Conserved hypothetical protein	0	2.75
gp144	Conserved hypothetical protein	0	2.75
gp070	Hef71 homing endonuclease	0	2.98
gp101	Gp43 DNA polymerase	0	2.95
gp096	Possible methylase	0	2.80
gp121	Gp55 sigma factor for T4 late transcription	0	2.76
gp095	Conserved hypothetical protein	6.5	2.79
gp120	Gp47 recombination endonuclease	0	2.93
gp161	Putative poly A polymerase	0	2.93
gp018	Hypothetical protein	0	2.55
gp023	Hypothetical protein	0	2.57
gp136	Conserved hypothetical protein	0	2.92
gp145	Hypothetical protein	0	2.75
gp052	Hef53 homing endonuclease	0	2.84
gp097	Putative RecB family exonuclease	0	2.62
gp073	Hef74 homing endonuclease	0	2.94
gp022	Hypothetical protein	0	2.73
gp129	Hypothetical protein	0	2.33
gp150	Hypothetical protein	0	2.52
gp004	Hypothetical protein	0	2.83
gp055	Conserved hypothetical protein	0	2.58
gp157	Hypothetical protein	0	2.70
gp014	Hef15 homing endonuclease	0	2.88
gp137	Hypothetical protein	0	2.64
gp100	Hypothetical protein	0	2.89
gp167	Hef168 homing endonuclease	0	2.64
gp010	Hypothetical protein	0	2.66
gp113	Conserved hypothetical protein	0	2.64
gp106	Hypothetical protein	0	2.67
gp011	Hypothetical protein	0	2.54
gp057	Hef58 homing endonuclease	0	2.70
gp131	Conserved hypothetical protein	0	2.54
gp046	Hypothetical protein	0	2.09
gp090	Putative DEAD/DEAH box helicase	0	2.45
gp072	Hef73 homing endonuclease	0	2.48
gp059	Hef60 homing endonuclease	0	2.59
gp031	Hypothetical protein	0	2.04
gp058	Hef59 homing endonuclease	0	2.33
gp130	Hypothetical protein	0	1.04

^aPercent amino acid (AA) coverage following mass spectrometry of purified virions as determined by Kropinski *et al.* (2011); "0" indicates no peptides mapping to predicted AA sequence were detected

^bRPKM (reads per kilobase million) values for each gene

^cAnnotation updated according to Javed *et al.* (2015)

^dNon-coding RNA

Table S3. Number and percentage of *C. jejuni* NCTC 11168 genes differentially expressed (DE) at each time point post NCTC 12673 phage infection.

Differentially expressed host genes ^a	30 min p.i.		60 min p.i.		120 min p.i.	
	Number	% of total	Number	% of total	Number	% of total
Upregulated	61	3.7 %	32	1.9 %	212	12.7 %
Downregulated	1	0.06 %	8	0.5 %	78	4.7 %
Total DE	62	3.7 %	40	2.4 %	290	17.4 %

^aGenes were considered DE if they underwent a fold change of >1.5 or <-1.5 with a false discovery rate (FDR)-adjusted p-value of <0.05.

CAAGGTTATGGTAAGCTTATTATGTAAATTTTCTCTTTACTTCTAAAGAGACCAT
AGCCTGAGTAATAAAATAGAACACATAAGGTTAATACGCAGACCTAAAATAA
GGTCCCTCCTTTCAATCTTCAGATACTCTTAACCTGGTGTCTCTAAACAT

Figure S2. Nucleotide sequence of the novel 158-bp non-coding RNA (ncRNA) identified between *gp012* and *gp013* (nucleotides 7110-7267) on the phage genome.

Table S4. KEGG pathways for *C. jejuni* NCTC 11168 genes statistically significantly downregulated at 30, 60 and 120 min post NCTC 12673 phage infection.

Significantly downregulated pathways ^a	Significance value (<i>p</i> -value) ^b		
	30 min	60 min	120 min
cje00010 Glycolysis /gluconeogenesis	0.02	<0.01	0.01
cje00020 Citrate cycle (TCA cycle)	0.00	<0.01	<0.01
cje00190 Oxidative phosphorylation			0.02
cje00250 Alanine, aspartate and glutamate metabolism	0.03	0.01	
cje00520 Amino sugar and nucleotide sugar metabolism	0.03		0.03
cje00620 Pyruvate metabolism	0.03	<0.01	0.01
cje00640 Propanoate metabolism	0.04	<0.01	0.01
cje00650 Butanoate metabolism	0.04	0.03	0.01
cje00680 Methane metabolism	0.04		
cje00970 Aminoacyl-tRNA biosynthesis		0.02	
cje01100 Metabolic pathways	<0.01	<0.01	<0.01
cje01110 Biosynthesis of secondary metabolites	0.02	<0.01	
cje01120 Microbial metabolism in diverse environments	<0.01	<0.01	<0.01
cje01130 Biosynthesis of antibiotics	<0.01	<0.01	0.01
cje01200 Carbon metabolism	<0.01	<0.01	<0.01
cje01230 Biosynthesis of amino acids		<0.01	
cje02020 Two-component system		0.02	0.03
cje02030 Bacterial chemotaxis		0.03	0.03
cje02040 Flagellar assembly		0.03	

^aDifferentially expressed host genes for each condition were subjected to gene set enrichment analysis (GSEA) on annotated Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways using GAGE with an FDR cutoff of <0.1. KEGG pathways along with their significance values at each time point are listed in Table 5.

^bNumerical values correspond to FDR-adjusted p-values (<0.05 was considered to be significant). A blank space indicates that the corresponding category was not statistically significantly downregulated.

Table S5. Differentially expressed *C. jejuni* NCTC 11168 genes upon NCTC 12673 phage infection according to COG categories.

Gene and annotation according to COG category ^a		Fold change (p-value) ^b		
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
Amino acid transport and metabolism				
<i>argB</i>	acetylglutamate kinase			3.3 (<0.01)
<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase			2.72 (<0.01)
<i>argD</i>	putative acetylmethionine/succinylmethionine aminotransferase			3.18 (<0.01)
<i>aroQ</i>	3-dehydroquinate dehydratase			-1.72 (0.04)
<i>aspB</i>	aspartate aminotransferase			-2.04 (0.01)
<i>cj0731</i>	putative ABC transport system permease			3.08 (0.02)
<i>cj0732</i>	ABC transport system ATP-binding protein			3.29 (<0.01)
<i>cj0919c</i>	putative ABC-type amino-acid transporter permease protein			-1.63 (0.03)
<i>cj0920c</i>	putative ABC-type amino-acid transporter permease protein			-2.3 (<0.01)
<i>cj0980</i>	putative peptidase			-1.72 (0.03)
<i>cj1111c</i>	putative MarC family integral membrane protein			-1.97 (0.04)
<i>cj1581c</i>	putative peptide ABC-transport system ATP-binding protein	5.38 (<0.01)	4.4 (<0.01)	4.82 (<0.01)
<i>cj1583c</i>	putative peptide ABC-transport system permease protein	2.13 (<0.01)		4.82 (<0.01)
<i>ilvD</i>	dihydroxy-acid dehydratase		-1.82 (0.02)	4.82 (<0.01)
<i>leuA</i>	2-isopropylmalate synthase			2.62 (<0.01)
<i>leuC</i>	3-isopropylmalate dehydratase large subunit			2.37 (<0.01)
<i>leuD</i>	3-isopropylmalate dehydratase small subunit			2.43 (<0.01)
<i>livF</i>	branched-chain amino-acid ABC transport system ATP binding protein			1.89 (0.02)
<i>livH</i>	branched-chain amino-acid ABC transport system permease protein			1.69 (0.04)
<i>livJ</i>	branched-chain amino-acid ABC transport system periplasmic binding protein			1.47 (0.05)

<i>metE</i>	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase			1.8 (0.01)
<i>peb1A</i>	aspartate/glutamate-binding ABC transporter protein			-2.51 (0.01)
<i>proA</i>	gamma-glutamyl phosphate reductase			-1.88 (0.02)
<i>putP</i>	putative sodium/proline symporter			-1.96 (0.02)
<i>sdaA</i>	L-serine dehydratase			-1.82 (0.03)
<i>sdaC</i>	amino acid transporter			-1.76 (<0.01)
<i>thrB</i>	putative homoserine kinase			1.92 (<0.01)
<i>trpD</i>	anthranilate synthase component II			1.86 (0.02)

Carbohydrate transport and metabolism

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0035c</i>	putative efflux protein	2.08 (0.04)		3.05 (<0.01)
<i>cj1241</i>	putative MFS (Major Facilitator Superfamily) transporter protein			2.64 (0.02)
<i>cj1548c</i>	putative NADP-dependent alcohol dehydrogenase		-1.7 (0.04)	2.64 (0.02)
<i>dcuA</i>	anaerobic C4-dicarboxylate transporter			2.64 (0.02)
<i>kgtp</i>	alpha-ketoglutarate permease			-2.26 (0.04)
<i>pyk</i>	pyruvate kinase			-1.81 (0.03)

Cell cycle control, cell division, chromosome partitioning

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>pbpC</i>	penicillin-binding protein			1.68 (0.04)

Cell motility

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj1506c</i>	putative MCP-type signal transduction protein			-1.53 (0.03)
<i>fliR</i>	flagellar biosynthetic protein			2.7 (<0.01)

Cell wall/membrane/envelope biogenesis

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cadF</i>	outer membrane fibronectin-binding protein			-1.52 (0.04)
<i>cj0313</i>	putative integral membrane protein			2.12 (0.02)
<i>cj0505c</i>	putative aminotransferase (DegT family)			2.11 (<0.01)
<i>cj0646</i>	putative lipoprotein			1.74 (<0.01)
<i>cj0826</i>	putative integral membrane protein	3.07 (<0.01)		3.46 (<0.01)
<i>cj0958c</i>	putative membrane protein			1.79 (<0.01)

<i>Int</i>	putative apolipoprotein N-acyltransferase	2.37 (0.02)		2.71 (0.01)
<i>cj1180c</i>	putative ABC transporter ATP-binding protein			3.41 (<0.01)
<i>cj1434c</i>	putative sugar transferase		1.89 (0.02)	3.41 (<0.01)
<i>cj1442c</i>	putative sugar transferase		2.04 (0.03)	3.41 (<0.01)
<i>cj1661</i>	possible ABC transport system permease	2.54 (<0.01)		2.27 (0.03)
<i>cj1662</i>	putative integral membrane protein			2.82 (<0.01)
<i>iamB</i>	putative ABC transport system permease			1.7 (0.03)
<i>lpxC</i>	UDP-3-O-[3-hydroxymyristoyl] n-acetylglucosamine deacetylase			-1.76 (<0.01)
<i>murD</i>	UDP-N-acetylmuramoylalanine--D-glutamate ligase			1.69 (0.03)
<i>tonB1</i>	TonB transport protein	2.53 (0.03)		3 (0.01)
<i>tonB2</i>	putative TonB transport protein	3.92 (<0.01)	2.67 (0.02)	3.13 (0.01)

Coenzyme transport and metabolism

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>bioB</i>	putative biotin synthase			1.73 (0.04)
<i>birA</i>	putative biotin--[acetyl-CoA-carboxylase] synthetase			2.19 (0.03)
<i>chuC</i>	putative haemin uptake system ATP-binding protein			2.49 (0.05)
<i>cj0230c</i>	putative transferase protein			1.68 (0.03)
<i>hemN</i>	putative oxygen-independent coproporphyrinogen III oxidase	1.84 (<0.01)		2.43 (<0.01)
<i>cj0541</i>	polyprenyl synthetase		2.11 (0.02)	1.8 (0.02)
<i>cj1420c</i>	putative methyltransferase		-1.73 (0.03)	1.8 (0.02)
<i>hemA</i>	glutamyl-tRNA reductase			1.65 (0.02)
<i>hemC</i>	porphobilinogen deaminase			1.63 (0.03)
<i>hemH</i>	putative ferrochelatase			2.27 (<0.01)
<i>cj0725c</i>	molybdopterin biosynthesis protein			-1.87 (0.04)
<i>ribD</i>	riboflavin-specific deaminase/reductase			3.24 (<0.01)

Defense mechanisms

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0140</i>	hypothetical protein Cj0140			1.75 (0.03)
<i>cj0424</i>	putative acidic periplasmic protein	9.95 (<0.01)	10.51 (<0.01)	12.75 (<0.01)
<i>cj1174</i>	putative efflux protein (multidrug resistance protein)			2.45 (0.03)
<i>cj1298</i>	putative N-acetyltransferase		2.5 (0.02)	2.45 (0.03)

Energy production and conversion

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>ackA</i>	acetate kinase			-2.42 (<0.01)
<i>acnB</i>	aconitate hydratase			-2.16 (0.03)
<i>cj0037c</i>	putative cytochrome C	2.51 (0.01)		-2.16 (0.03)
<i>cj0073c</i>	conserved hypothetical protein Cj0073c			-2.38 (0.01)
<i>cj0074c</i>	putative iron-sulfur protein			-2.32 (0.02)
<i>cj0604</i>	putative polyphosphate kinase			-2.72 (<0.01)
<i>cj0833c</i>	putative oxidoreductase			-1.86 (0.03)
<i>cydA</i>	cytochrome bd oxidase subunit I			2.33 (0.01)
<i>cydB</i>	cytochrome bd oxidase subunit II			2.54 (<0.01)
<i>gltA</i>	citrate synthase			-2.55 (0.01)
<i>hydB</i>	Ni/Fe-hydrogenase large subunit			-1.77 (0.05)
<i>hydC</i>	Ni/Fe-hydrogenase B-type cytochrome subunit			-1.95 (<0.01)
<i>icd</i>	isocitrate dehydrogenase		-1.87 (0.04)	-2.03 (0.04)
<i>lctP</i>	L-lactate permease			-2.28 (<0.01)
<i>oorB</i>	OORB subunit of 2-oxoglutarate:acceptor oxidoreductase			-1.87 (0.03)
<i>pta</i>	putative phosphate acetyltransferase			-2.25 (0.02)
<i>putA</i>	putative proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase			-2.22 (<0.01)
<i>sucC</i>	succinyl-coA synthetase beta chain			-2.09 (0.03)
<i>sucD</i>	succinyl-coA synthetase alpha chain			-1.9 (0.05)
<i>icd</i>	isocitrate dehydrogenase		-1.87 (0.04)	-1.9 (0.05)

Function unknown

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0014c</i>	putative integral membrane protein			-1.69 (0.04)
<i>cj0177</i>	putative iron transport protein			3.84 (<0.01)
<i>cj0189c</i>	conserved hypothetical protein Cj0189c			1.7 (0.03)
<i>cj0341c</i>	putative integral membrane protein			2.18 (0.04)
<i>cj0449c</i>	conserved hypothetical protein Cj0449c			-2.43 (0.02)
<i>cj0602c</i>	MOSC-domain containing protein			-2.2 (0.03)
<i>cj0728</i>	putative periplasmic protein			3.37 (<0.01)
<i>cj1384c</i>	hypothetical protein Cj1384c			3.64 (<0.01)
<i>cj1660</i>	putative integral membrane protein			2.85 (<0.01)

General function prediction only

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0145</i>	putative TAT (Twin-Arginine Translocation) pathway signal sequence domain protein	2.5 (0.02)		3.55 (<0.01)
<i>cj0184c</i>	putative serine/threonine protein phosphatase			2.37 (<0.01)
<i>cj0504c</i>	putative oxidoreductase			2.31 (0.01)
<i>cj0605</i>	putative amidohydrolase			-2.2 (<0.01)
<i>cj0620</i>	conserved hypothetical protein Cj0620		2.71 (0.02)	-2.2 (<0.01)
<i>cj0711</i>	hypothetical protein Cj0711		2.41 (0.02)	2.45 (0.03)
<i>cj0730</i>	putative ABC transport system permease			2.76 (0.03)
<i>cj0937</i>	putative integral membrane protein	7.19 (<0.01)	4.54 (<0.01)	10.14 (<0.01)
<i>cj1028c</i>	putative purine/pyrimidine phosphoribosyltransferase	2.36 (0.02)		2.7 (<0.01)
<i>cj1225</i>	conserved hypothetical protein Cj1225			-1.88 (<0.01)
<i>cj1373</i>	putative ntegral membrane protein			1.89 (0.02)
<i>cj1500</i>	putative integral membrane protein			4.26 (<0.01)
<i>cj1164c</i>	hypothetical protein Cj1164c	-2.13 (0.03)		4.26 (<0.01)

Inorganic ion transport and metabolism

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>arsB</i>	arsenical pump membrane protein			2.14 (0.03)
<i>ceuB</i>	enterochelin uptake permease			3.36 (<0.01)
<i>cfrA</i>	ferric enterobactin uptake receptor			2.33 (0.03)
<i>cft</i>	ferritin			-2.05 (0.02)
<i>chuA</i>	haemin uptake system outer membrane receptor	7.73 (<0.01)	4.9 (<0.01)	6.84 (<0.01)
<i>chuD</i>	putative haemin uptake system periplasmic haemin-binding protein	3.9 (<0.01)	2.73 (0.02)	3.31 (<0.01)
<i>cj0167c</i>	putative integral membrane protein	3.35 (<0.01)	2.71 (0.01)	5.35 (<0.01)
<i>cj0178</i>	putative TonB-dependent outer membrane receptor	4.5 (<0.01)		4.86 (<0.01)
<i>cj0186c</i>	putative TerC family integral membrane protein			2.27 (<0.01)
<i>cj0727</i>	putative periplasmic solute-binding protein			2.5 (0.02)
<i>cj0909</i>	putative periplasmic protein			-2.73 (<0.01)
<i>cj1609</i>	putative sulfate adenyltransferase			-1.7 (0.02)
<i>cj1613c</i>	putative pyridoxamine 5'-phosphate oxidase	3.34 (<0.01)	3.25 (<0.01)	2.47 (<0.01)
<i>cj1658</i>	putative iron permease	2.4 (0.01)		2.93 (<0.01)
<i>feoB</i>	ferrous iron transport protein			-1.64 (0.04)
<i>kata</i>	catalase	3.1 (<0.01)		3.42 (<0.01)
<i>kdpB</i>	potassium-transporting ATPase B chain			3.61 (<0.01)
<i>ktrA</i>	putative K ⁺ uptake protein	4.08 (<0.01)	2.78 (<0.01)	6.99 (<0.01)

<i>ktrB</i>	putative K ⁺ uptake protein	3.63 (<0.01)	2.4 (0.01)	5.8 (<0.01)
<i>ppk</i>	polyphosphate kinase			-1.9 (0.03)
<i>pstS</i>	putative periplasmic phosphate binding protein			1.8 (0.02)
<i>chuB</i>	putative haemin uptake system permease protein	3.02 (<0.01)		1.8 (0.02)
Intracellular trafficking, secretion, and vesicular transport				
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0975</i>	putative outer-membrane protein	2.77 (0.01)	2.43 (0.05)	3.13 (<0.01)
<i>exbB1</i>	biopolymer transport protein			3.76 (<0.01)
<i>exbD3</i>	putative ExbD/TolR family transport protein			1.84 (0.04)
<i>ffh</i>	signal recognition particle protein			1.64 (0.05)
<i>secY</i>	preprotein translocase subunit			2.49 (<0.01)
Lipid transport and metabolism				
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>acs</i>	acetyl-coenzyme A synthetase		-2.53 (<0.01)	-2.03 (0.02)
<i>cj0807</i>	putative oxidoreductase			-1.69 (0.03)
<i>fabH</i>	3-oxoacyl-[acyl-carrier-protein] synthase			1.56 (0.02)
<i>p19</i>	periplasmic protein p19			2.23 (0.01)
<i>plsC</i>	putative 1-acyl-SN-glycerol-3-phosphate acyltransferase			1.77 (0.02)
<i>pycA</i>	pyruvate carboxylase A subunit			-2.04 (<0.01)
Nucleotide transport and metabolism				
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>nrdA</i>	ribonucleoside-diphosphate reductase alpha chain			1.93 (0.01)
<i>oorD</i>	OORD subunit of 2-oxoglutarate:acceptor oxidoreductase			-1.76 (0.04)
<i>purB</i>	adenylosuccinate lyase			2.15 (0.02)
<i>purH</i>	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase			2.64 (<0.01)
<i>purL</i>	phosphoribosylformylglycinamide synthase			2.2 (<0.01)
<i>purE</i>	phosphoribosylaminoimidazole carboxylase catalytic subunit		-1.95 (<0.01)	2.2 (<0.01)
Posttranslational modification, protein turnover, chaperones				
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0190c</i>	conserved hypothetical protein Cj0190c			1.95 (<0.01)

<i>cj0911</i>	putative periplasmic protein			-2.17 (0.02)
<i>cj0954c</i>	putative DnaJ-like protein			2.31 (0.01)
<i>cj1501</i>	conserved hypothetical protein Cj1501			4.14 (<0.01)
<i>dnaK</i>	heat shock protein DnaK			1.59 (0.05)
<i>dsbD</i>	putative thiol:disulphide interchange protein			-2.1 (0.03)
<i>htpG</i>	hsp90 family heat shock protein			1.58 (0.04)

Replication, recombination and repair

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0208</i>	putative DNA modification methylase (adenine-specific methyltransferase)			2.93 (<0.01)
<i>cj0777</i>	putative ATP-dependent DNA helicase			1.88 (0.02)
<i>cj1254</i>	hypothetical protein Cj1254			2.63 (<0.01)
<i>ruvC</i>	crossover junction endodeoxyribonuclease			3.51 (<0.01)
<i>ssb</i>	single-strand DNA binding protein			2.5 (0.01)
<i>topA</i>	DNA topoisomerase I			1.53 (0.04)
<i>xseA</i>	exodeoxyribonuclease VII large subunit			1.85 (0.03)

Secondary metabolites biosynthesis, transport and catabolism

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0021c</i>	putative fumarylacetoacetate (FAA) hydrolase family protein			-2.26 (0.02)
<i>cj1199</i>	putative iron/ascorbate-dependent oxidoreductase	2.31 (0.03)		-2.26 (0.02)

Signal transduction mechanisms

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0241c</i>	putative iron-binding protein	2.69 (<0.01)		3.54 (<0.01)
<i>cj1224</i>	putative iron-binding protein			-1.98 (0.02)
<i>cj1258</i>	putative phosphotyrosine protein phosphatase			-2.53 (<0.01)
<i>cstA</i>	putative integral membrane protein (CstA homolog)		-1.82 (0.03)	-2.53 (<0.01)
<i>typA</i>	GTP-binding protein TypA homolog			-2.53 (<0.01)

Transcription

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj1556</i>	putative transcriptional regulator			1.83 (0.05)
<i>hrcA</i>	putative heat shock regulator			2.01 (<0.01)
<i>rpoA</i>	DNA-directed RNA polymerase alpha chain			1.87 (<0.01)

<i>rpoC</i>	DNA-directed RNA polymerase beta chain			1.55 (0.05)
Translation, ribosomal structure and biogenesis				
Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>cj0123c</i>	putative tRNA-dihydrouridine synthase			2.24 (<0.01)
<i>cj0154c</i>	putative tetrapyrrole methylase family protein			2.18 (0.01)
<i>cj0225</i>	putative acetyltransferase			3.27 (<0.01)
<i>rplY</i>	putative 50S ribosomal protein L25 (general stress protein Ctc)			1.64 (0.04)
<i>cj0495</i>	putative methyltransferase domain protein			2.86 (<0.01)
<i>cj0636</i>	NOL1/NOP2/sun family protein			2.14 (0.02)
<i>cj1172c</i>	conserved hypothetical protein Cj1172c			1.63 (0.05)
<i>cj1709c</i>	putative ribosomal pseudouridine synthase			1.85 (0.03)
<i>cj1713</i>	putative radical SAM domain protein			2.28 (0.02)
<i>fnt</i>	methionyl-tRNA formyltransferase			2.16 (<0.01)
<i>prfA</i>	peptide chain release factor 1			2.65 (<0.01)
<i>pth</i>	peptidyl-tRNA hydrolase			1.77 (0.02)
<i>rimM</i>	putative 16S rRNA processing protein			2.02 (<0.01)
<i>rplD</i>	50S ribosomal protein L4			1.59 (0.03)
<i>rplF</i>	50S ribosomal protein L6			1.91 (<0.01)
<i>rplJ</i>	50S ribosomal protein L10			1.94 (<0.01)
<i>rplK</i>	50S ribosomal protein L11			1.85 (0.03)
<i>rplM</i>	50S ribosomal protein L13			1.8 (0.01)
<i>rplT</i>	50S ribosomal protein L20			1.7 (<0.01)
<i>rplW</i>	50S ribosomal protein L23			2.17 (<0.01)
<i>rpmC</i>	50S ribosomal protein L29			1.77 (0.04)
<i>rpmE</i>	50S ribosomal protein L31			2.51 (<0.01)
<i>rpsB</i>	30S ribosomal protein S2			1.87 (<0.01)
<i>rpsC</i>	30S ribosomal protein S3			1.57 (0.02)
<i>rpsD</i>	30S ribosomal protein S4			1.71 (0.02)
<i>rpsE</i>	30S ribosomal protein S5			1.69 (0.02)
<i>rpsF</i>	30S ribosomal protein S6			1.63 (0.03)
<i>rpsH</i>	30S ribosomal protein S8			1.86 (0.01)
<i>rpsI</i>	30S ribosomal protein S9			2.46 (<0.01)
<i>rpsK</i>	30S ribosomal protein S11			2.31 (<0.01)
<i>rpsM</i>	30S ribosomal protein S13			1.57 (0.05)

<i>rpsQ</i>	30S ribosomal protein S17			2.05 (0.02)
<i>rpsR</i>	30S ribosomal protein S18			2.12 (<0.01)
<i>rpsS</i>	30S ribosomal protein S19			1.73 (0.04)
<i>rpsT</i>	30S ribosomal protein S20			1.74 (0.04)
<i>serS</i>	seryl-tRNA synthetase			-1.64 (0.04)
<i>tlyA</i>	putative haemolysin			2.37 (<0.01)
<i>trmD</i>	tRNA (guanine-N1)-methyltransferase	2.22 (0.03)		2.68 (<0.01)
<i>tsf</i>	elongation factor TS			2.04 (<0.01)

Uncategorized

Gene	Annotation	30 min (P)	60 min (P)	120 min (P)
<i>bioC</i>	putative biotin synthesis protein	2.39 (0.04)		2.95 (0.02)
<i>cca</i>	putative multifunctional Cca protein			2.13 (<0.01)
<i>cdtA</i>	cytolethal distending toxin A			-1.76 (0.03)
<i>cgb</i>	single domain haemoglobin			2.56 (0.02)
<i>cj0011c</i>	putative non-specific DNA binding protein			-2.12 (<0.01)
<i>cj0030</i>	hypothetical protein Cj0030	2.13 (0.04)	2.41 (<0.01)	2.49 (<0.01)
<i>cj0038c</i>	putative poly(A) polymerase family protein			3.33 (<0.01)
<i>cj0069</i>	hypothetical protein Cj0069			-2.03 (0.04)
<i>cj0075c</i>	putative oxidoreductase iron-sulfur subunit			-2.52 (<0.01)
<i>cj0080</i>	putative membrane protein			3.14 (0.01)
<i>cj0093</i>	putative periplasmic protein			1.64 (0.02)
<i>cj0111</i>	putative periplasmic protein			1.98 (<0.01)
<i>cj0120</i>	hypothetical protein Cj0120			2.19 (0.03)
<i>cj0124c</i>	putative membrane protein			2.2 (<0.01)
<i>cj0223</i>	pseudogene (putative IgA protease family protein)			1.72 (0.05)
<i>cj0254</i>	hypothetical protein Cj0254			-1.54 (0.04)
<i>cj0260c</i>	small hydrophobic protein		2.13 (0.02)	2.56 (0.02)
<i>cj0267c</i>	putative integral membrane protein			2.53 (0.02)
<i>cj0295</i>	putative acetyltransferase			2.4 (0.02)
<i>cj0323</i>	hypothetical protein Cj0323			1.82 (0.05)
<i>cj0344</i>	hypothetical protein Cj0344			-2.17 (0.01)
<i>cj0350</i>	hypothetical protein Cj0350			-1.77 (0.02)
<i>cj0391c</i>	hypothetical protein Cj0391c	1.64 (0.03)		-1.77 (0.02)
<i>cj0406c</i>	putative lipoprotein			-1.66 (0.05)
<i>cj0414</i>	putative oxidoreductase subunit			2.15 (0.04)

<i>cj0421c</i>	putative integral membrane protein	2.59 (0.03)		6.38 (<0.01)
<i>cj0423</i>	putative integral membrane protein	5.73 (<0.01)	3.36 (<0.01)	16.14 (<0.01)
<i>cj0425</i>	putative periplasmic protein	9.01 (<0.01)	9.1 (<0.01)	10.39 (<0.01)
<i>cj0427</i>	hypothetical protein Cj0427			-2.11 (0.02)
<i>cj0444</i>	pseudogene (putative TonB-dependent outer membrane receptor)	2.04 (0.04)	2.12 (0.04)	2.29 (<0.01)
<i>cj0448c</i>	putative MCP-type signal transduction protein			-2.17 (0.05)
<i>cj0494</i>	putative exporting protein			2.57 (<0.01)
<i>cj0515</i>	putative periplasmic protein			1.82 (0.02)
<i>cj0520</i>	putative membrane protein			2.2 (<0.01)
<i>cj0522</i>	putative Na ⁺ /Pi cotransporter protein			2.68 (<0.01)
<i>cj0544</i>	putative integral membrane protein			2.3 (<0.01)
<i>cj0566</i>	hypothetical protein Cj0566	7.23 (<0.01)	3.99 (<0.01)	2.3 (<0.01)
<i>cj0584</i>	hypothetical protein Cj0584			1.94 (0.03)
<i>cj0590</i>	putative SAM-dependent methyltransferase			1.86 (0.03)
<i>cj0648</i>	putative membrane protein			2.22 (0.01)
<i>cj0651</i>	putative integral membrane protein		2.8 (<0.01)	2.22 (0.01)
<i>cj0694</i>	putative periplasmic protein			1.57 (0.03)
<i>cj0700</i>	hypothetical protein Cj0700			-1.82 (0.04)
<i>cj0729</i>	putative type I phosphodiesterase/nucleotide	2.77 (0.02)	2.57 (0.02)	4.25 (<0.01)
<i>cj0735</i>	putative periplasmic protein	2.58 (<0.01)		4.25 (<0.01)
<i>cj0736</i>	hypothetical protein Cj0736	5.35 (<0.01)	2.49 (0.04)	4.25 (<0.01)
<i>cj0742</i>	pseudogene (putative outer membrane protein)	4.71 (<0.01)	4.07 (<0.01)	3.91 (<0.01)
<i>cj0752</i>	pseudogene (IS element transposase)	2.72 (0.02)	2.68 (0.02)	3.54 (<0.01)
<i>cj0794</i>	hypothetical protein Cj0794	3.22 (<0.01)		2.6 (0.02)
<i>cj0834c</i>	ankyrin repeat-containing putative periplasmic protein			-1.82 (0.04)
<i>cj0873c</i>	hypothetical protein Cj0873c			-2.14 (0.01)
<i>cj0910</i>	putative periplasmic protein			-2.21 (<0.01)
<i>cj0944c</i>	putative periplasmic protein		-1.88 (0.03)	-2.21 (<0.01)
<i>cj0951c</i>	putative MCP-domain signal transduction protein			-1.8 (0.04)
<i>cj0967</i>	putative periplasmic protein	4.42 (<0.01)		3.8 (<0.01)
<i>cj1012c</i>	putative membrane protein			2.3 (0.01)
<i>cj1041c</i>	putative periplasmic ATP/GTP-binding protein	2.68 (<0.01)		1.95 (0.04)
<i>cj1078</i>	putative periplasmic protein	2.49 (0.05)		1.95 (0.04)
<i>cj1159c</i>	small hydrophobic protein	2.62 (0.03)		2.65 (0.04)
<i>cj1162c</i>	putative heavy-metal-associated domain protein	3.35 (<0.01)		3.31 (<0.01)
<i>cj1169c</i>	putative periplasmic protein			2.21 (0.02)

<i>cj1307</i>	putative amino acid activating enzyme			-1.67 (0.02)
<i>cj1322</i>	hypothetical protein Cj1322	3.48 (<0.01)		2.42 (0.05)
<i>cj1383c</i>	hypothetical protein Cj1383c	2.39 (0.04)		2.42 (0.05)
<i>cj1389</i>	pseudogene (putative C4-dicarboxylate anaerobic carrier)	2.11 (<0.01)		2.42 (0.05)
<i>cj1395</i>	pseudogene (putative MmgE/PrpD family protein)	2.82 (0.02)		2.42 (0.05)
<i>cj1422c</i>	putative sugar transferase			2.42 (0.05)
<i>cj1459</i>	hypothetical protein Cj1459			2.42 (0.05)
<i>cj1664</i>	putative periplasmic thioredoxin	2.66 (<0.01)		2.42 (0.05)
<i>cj1665</i>	putative lipoprotein thioredoxin			2.42 (0.05)
<i>cj1677</i>	putative lipoprotein	5.48 (<0.01)	2.99 (<0.01)	2.42 (0.05)
<i>cj1712</i>	hypothetical protein Cj1712			2.42 (0.05)
<i>cetB</i>	bipartate energy taxis response protein <i>cetB</i>	2.21 (0.03)		2.42 (0.05)
<i>cmeA</i>	periplasmic fusion protein CmeA (multidrug efflux system CmeABC)	2.6 (<0.01)		1.99 (<0.01)
<i>cmeB</i>	inner membrane efflux transporter CmeB (multidrug efflux system CmeABC)	2.09 (<0.01)		2.14 (<0.01)
<i>cmeC</i>	outer membrane channel protein CmeC (multidrug efflux system CmeABC)	2.04 (<0.01)		2.02 (<0.01)
<i>ctsP</i>	putative ATP/GTP-binding protein	2.8 (<0.01)	2.55 (<0.01)	2.47 (0.01)
<i>dba</i>	disulphide bond formation protein	2.44 (0.04)		3.32 (<0.01)
<i>dccR</i>	two-component regulator			-1.93 (0.02)
<i>dprA</i>	DNA processing protein A			1.91 (0.02)
<i>dsbI</i>	disulphide bond formation protein	2.33 (0.03)		4.15 (<0.01)
<i>exoA</i>	exodeoxyribonuclease			1.97 (0.03)
<i>fdxA</i>	ferredoxin			-1.89 (0.05)
<i>flaC</i>	flagellin			-2.1 (0.03)
<i>glpT</i>	pseudogene (putative glycerol-3-phosphate transporter)			-2.12 (0.05)
<i>hldD</i>	ADP-glyceromanno-heptose 6-epimerase			-1.57 (0.03)
<i>kdpA</i>	pseudogene (potassium-transporting ATPase A chain)	2.76 (<0.01)	2.62 (<0.01)	2.27 (<0.01)
<i>kpsC</i>	capsule polysaccharide modification protein			1.6 (0.04)
<i>lola</i>	putative outer-membrane lipoprotein carrier protein precursor			-1.89 (0.03)
<i>mreC</i>	homolog of <i>E. coli</i> rod shape-determining protein			1.72 (0.04)
<i>nrdB</i>	ribonucleoside-diphosphate reductase beta chain			1.66 (0.04)
<i>cj0096</i>	GTP-binding protein			2.25 (<0.01)
<i>omp50</i>	50 kDa outer membrane protein precursor	2.43 (0.05)		3.89 (<0.01)
<i>pglA</i>	GalNAc transferase			1.99 (0.04)

<i>pseI</i>	Pse synthetase	-1.67 (0.03)
<i>rpmJ</i>	50S ribosomal protein L36	1.73 (0.04)
<i>rpoB</i>	DNA-directed RNA polymerase beta chain	1.96 (0.01)
<i>trmE</i>	putative tRNA modification GTPase	2.16 (<0.01)
<i>ubiD</i>	putative 3-octaprenyl-4-hydroxybenzoate carboxylase	1.61 (0.03)

^aHost genes found to be differentially expressed between infected and control samples for at least one time point were assigned to one of 25 functional categories based on clusters of orthologous groups (COG) classification. Genes were assigned according to the COG function list for *C. jejuni jejuni* NCTC 11168 according to the Integrated Microbial Genomes and Microbiomes (IMG/M) database (<https://img.jgi.doe.gov>). Gene annotations were obtained from NCBI. ^bFor each gene, fold change in expression post NCTC 12673 phage infection is listed followed by the adjusted *P*-value (*P*) in brackets. Fold change values for genes whose transcripts were not significantly differentially expressed are not shown.

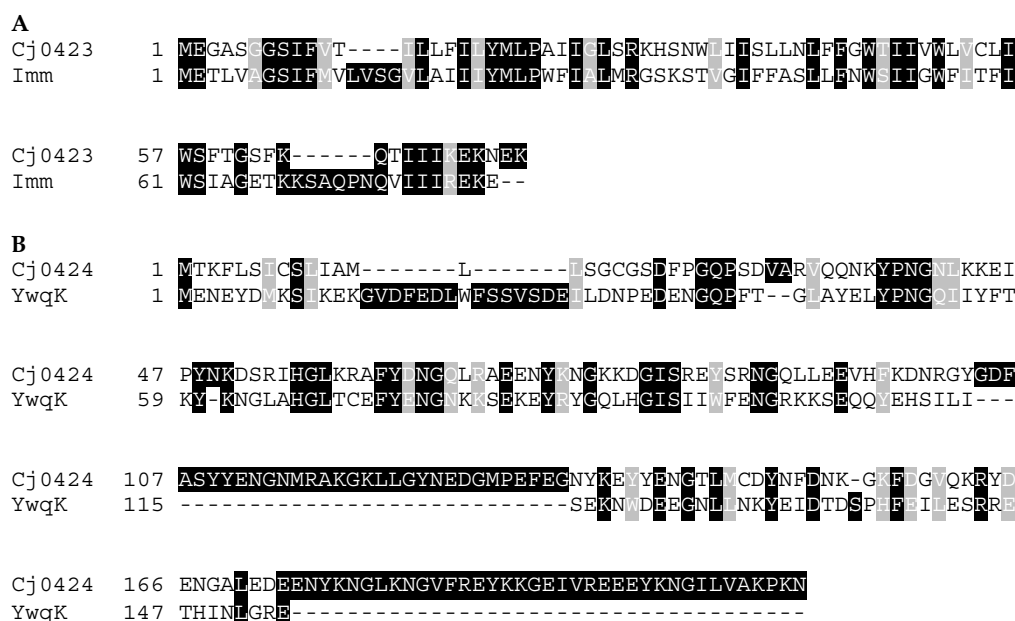


Figure S3. BLASTp alignment between *C. jejuni* NCTC 11168 protein Cj0423 and T4 phage protein Imm (**A**) and between *C. jejuni* NCTC 11168 protein Cj0424 and *Bacillus subtilis* strain 168 antitoxin protein YwqK (**B**). Alignments were generated using T-Coffee [2] and Boxshade (<http://sourceforge.net/projects/boxshade/>). Black shading indicates the consensus sequence, grey shading indicates similar residues.