

Supplementary Tables

Table S1. *C. jejuni* 11168H genes up-regulated after 6 h of co-culturing with Caco-2 IECs in the VDC with microaerobic conditions in the apical compartment.

ORF number	Fold change	Re-annotation
<i>Cj1511c</i>	2.3	<i>fdhA</i> putative formate dehydrogenase large subunit
<i>Cj1705c</i>	2.0	binds third domain of 23S rRNA and protein L29; part of exit tunnel
<i>Cj1186c</i>	2.0	<i>petA</i> putative ubiquinol-cytochrome C reductase iron-sulfur subunit
<i>Cj1325</i>	1.9	putative methyltransferase
<i>Cj0347</i>	1.9	<i>rpF</i> N-(5'-phosphoribosyl) anthranilate isomerase
<i>Cj0414</i>	1.8	putative oxidoreductase subunit
<i>Cj0473</i>	1.7	<i>nusG</i> transcription antitermination protein NusG
<i>Cj0207</i>	1.6	translation initiation factor IF-3
<i>Cj1591</i>	1.6	50S ribosomal protein L36
<i>Cj0330c</i>	1.6	50S ribosomal protein L32
<i>Cj1439c</i>	1.6	<i>glf</i> UDP-galactopyranose mutase part of the capsule locus
<i>Cj0859c</i>	1.6	hypothetical protein
<i>Cj1267c</i>	1.6	<i>hydA</i> Ni/Fe-hydrogenase small chain
<i>Cj0581</i>	1.5	dinucleoside polyphosphate hydrolase
<i>Cj0329c</i>	1.5	putative glycerol-3-phosphate acyltransferase PlsX
<i>Cj1027c</i>	1.5	<i>gyrA</i> DNA gyrase subunit A
<i>Cj0007</i>	1.5	<i>gltB</i> glutamate synthase large subunit
<i>Cj1028c</i>	1.5	putative purine/pyrimidine phosphoribosyltransferase
<i>Cj0397c</i>	1.5	hypothetical protein
<i>Cj0519</i>	1.5	putative rhodanese-like domain protein
<i>Cj0995c</i>	1.5	<i>hemB</i> delta-aminolevulinic acid dehydratase
<i>Cj0802</i>	1.5	cysteinyI-tRNA synthetase
<i>Cj0315</i>	1.5	putative HAD-superfamily hydrolase
<i>Cj0398</i>	1.4	<i>gatC</i> aspartyl/glutamyl-tRNA amidotransferase subunit C
<i>Cj0462</i>	1.4	hypothetical protein
<i>Cj1223c</i>	1.4	<i>dccR</i> two-component response regulator
<i>Cj1172c</i>	1.4	hypothetical protein
<i>Cj0953c</i>	1.4	<i>urH</i> de novo purine biosynthesis
<i>Cj0961c</i>	1.4	50S ribosomal protein L34
<i>Cj0092</i>	1.4	putative periplasmic protein
<i>Cj0789</i>	1.4	<i>cca</i> putative multifunctional Cca protein RNA synthesis
<i>Cj1621</i>	1.3	putative periplasmic protein
<i>Cj0271</i>	1.3	bacterioferritin comigratory protein homolog
<i>Cj0348</i>	1.3	<i>trpB</i> tryptophan synthase subunit beta

<i>Cj0320</i>	1.3	<i>fliH</i> flagellar assembly protein H
<i>Cj0146c</i>	1.3	<i>trxB</i> thioredoxin reductase
<i>Cj0498</i>	1.3	<i>trpC</i> indole-3-glycerol-phosphate synthase
<i>Cj0237</i>	1.3	<i>cynT</i> carbonic anhydrase
<i>Cj0976</i>	1.3	putative methyltransferase
<i>Cj0891c</i>	1.2	<i>serA</i> D-3-phosphoglycerate dehydrogenase
<i>Cj0934c</i>	1.2	putative sodium:amino-acid symporter family protein
<i>Cj0055c</i>	1.2	hypothetical protein
<i>Cj0552</i>	1.2	hydrophobic protein

Table S2. *C. jejuni* 11168H genes down-regulated after 6 h of co-culturing with Caco-2 IECs in the VDC with microaerobic conditions in the apical compartment.

ORF number	Fold change	Re-annotation
<i>Cj0304c</i>	1.3	<i>bioC</i> putative biotin synthesis protein
<i>Cj0522</i>	1.3	putative Na ⁺ /Pi cotransporter protein
<i>Cj1634c</i>	1.3	chorismate synthase
<i>Cj0410</i>	1.4	fumarate reductase iron-sulfur protein
<i>Cj0486</i>	1.4	possible L-fucose symporter
<i>Cj0303c</i>	1.4	<i>modA</i> putative molybdate-binding lipoprotein
<i>Cj1666c</i>	1.4	putative periplasmic protein
<i>Cj0988c</i>	1.5	very hypothetical protein
<i>Cj1079</i>	1.5	putative periplasmic protein
<i>Cj1134</i>	1.5	<i>htrB</i> lipid A biosynthesis lauroyl acyltransferase
<i>Cj0728</i>	1.6	putative periplasmic protein
<i>Cj0590</i>	1.6	putative SAM-dependent methyltransferase
<i>Cj0737</i>	1.6	putative hemagglutination activity domain-containing protein
<i>Cj0560</i>	1.7	putative MATE family transport protein
<i>Cj1521c</i>	1.7	putative CRISPR-associated protein
<i>Cj0290c</i>	1.8	pseudogene (partial <i>glpT</i>)
<i>Cj1581c</i>	1.9	putative peptide ABC transporter ATP-binding protein
<i>Cj0302c</i>	2.0	putative molybdenum-pterin binding protein
<i>Cj0141c</i>	2.0	putative ABC transporter integral membrane protein
<i>Cj0422c</i>	2.0	putative H-T-H containing protein
<i>Cj1378</i>	2.2	<i>selA</i> selenocysteine synthase
<i>Cj1352</i>	2.3	<i>ceuB</i> enterochelin uptake permease
<i>Cj1629</i>	2.5	<i>exbD2</i> putative <i>exbD</i> /toIR family transport protein
<i>Cj1393</i>	2.6	<i>metC'</i> putative cystathionine beta-lyase

Table S3. *C. jejuni* 11168H genes upregulated after 24 h of co-culturing with Caco-2 IECs in the VDC with microaerobic conditions in the apical compartment.

ORF number	Fold change	Re-annotation
<i>Cj1325</i>	2.8	putative methyltransferase
<i>Cj1176c</i>	2.2	<i>tatA</i> Sec-independent protein translocase
<i>Cj0985c</i>	2.1	<i>hipO</i> hippurate hydrolase
<i>Cj0073c</i>	2.1	hypothetical protein
<i>Cj0922c</i>	2.1	<i>pebC</i> amino-acid ABC transporter ATP-binding protein
<i>Cj1326</i>	2.0	hypothetical protein
<i>Cj0347</i>	2.0	<i>trpF</i> N-(5'-phosphoribosyl)anthranilate isomerase
<i>Cj0592c</i>	1.9	putative periplasmic protein
<i>Cj0920c</i>	1.9	putative ABC-type amino-acid transporter permease
<i>Cj0628</i>	1.8	putative lipoprotein
<i>Cj0127c</i>	1.8	<i>accD</i> acetyl-CoA carboxylase subunit beta
<i>Cj1558</i>	1.8	hypothetical protein
<i>Cj1273c</i>	1.8	<i>rpoZ</i> DNA-directed RNA polymerase subunit omega
<i>Cj0346</i>	1.6	<i>trpD</i> anthranilate synthase component II
<i>Cj1172c</i>	1.6	hypothetical protein
<i>Cj1668c</i>	1.6	putative periplasmic protein
<i>Cj1560</i>	1.6	pseudogene
<i>Cj0802</i>	1.6	<i>cysS</i> cysteinyl-tRNA synthetase
<i>Cj0813</i>	1.6	<i>kdsB</i> 3-deoxy-manno-octulosonate cytidyltransferase
<i>Cj0459c</i>	1.6	hypothetical protein
<i>Cj0029</i>	1.6	<i>ansA</i> cytoplasmic L-asparaginase
<i>Cj1321</i>	1.6	putative transferase LSO
<i>Cj1193c</i>	1.6	putative periplasmic protein
<i>Cj0152c</i>	1.6	hypothetical protein
<i>Cj1345c</i>	1.5	putative periplasmic protein
<i>Cj0244</i>	1.5	<i>rpmI</i> 50S ribosomal protein L35
<i>Cj1186c</i>	1.5	<i>petA</i> putative ubiquinol-cytochrome C reductase iron-sulfur subunit
<i>Cj1639</i>	1.5	NifU protein
<i>Cj1503c</i>	1.5	<i>putA</i> putative /Δ-1-pyrroline-5-carboxylate dehydrogenase
<i>Cj1705c</i>	1.5	50S ribosomal protein L23
<i>Cj0960c</i>	1.5	putative ribonuclease P protein component
<i>Cj0330c</i>	1.5	50S ribosomal protein L32
<i>Cj0898</i>	1.5	putative histidine triad (HIT) family protein

<i>Cj1603</i>	1.5	<i>hisF</i> imidazole glycerol phosphate synthase subunit HisF
<i>Cj1681c</i>	1.5	<i>cysQ</i> CysQ protein
<i>Cj0685c</i>	1.5	<i>cipA</i> invasion protein CipA
<i>Cj0092</i>	1.4	putative periplasmic protein
<i>Cj1616</i>	1.4	<i>chuC</i> putative hemin uptake system ATP-binding protein
<i>Cj0912c</i>	1.4	<i>cysM</i> cysteine synthase
<i>Cj1207c</i>	1.4	putative lipoprotein thioredoxin
<i>Cj0771c</i>	1.4	putative NLPA family lipoprotein
<i>Cj0129c</i>	1.4	outer membrane protein
<i>Cj0070c</i>	1.4	hypothetical protein
<i>Cj1719c</i>	1.4	<i>eua</i> 2-isopropylmalate synthase
<i>Cj0371</i>	1.4	hypothetical protein
<i>Cj0234c</i>	1.4	<i>frr</i> ribosome recycling factor
<i>Cj0507</i>	1.4	<i>maf</i> Maf-like protein
<i>Cj1541</i>	1.4	LamB/YcsF family protein
<i>Cj0979c</i>	1.4	putative secreted nuclease
<i>Cj0362</i>	1.3	putative integral membrane protein
<i>Cj0914c</i>	1.3	CiaB protein
<i>Cj0089</i>	1.3	putative lipoprotein
<i>Cj1537c</i>	1.3	<i>acs</i> acetyl-CoA synthetase
<i>Cj0407</i>	1.3	<i>lgt</i> prolipoprotein diacylglyceryl transferase
<i>Cj0290c</i>	1.3	pseudogene
<i>Cj0489</i>	1.3	<i>ald'</i> putative aldehyde dehydrogenase N-terminus
<i>Cj0424</i>	1.3	putative acidic periplasmic protein
<i>Cj1508c</i>	1.3	<i>fdhD</i> formate dehydrogenase accessory protein
<i>Cj1543</i>	1.3	putative allophanate hydrolase subunit 2
<i>Cj0854c</i>	1.3	putative periplasmic protein
<i>Cj0466</i>	1.3	<i>nssR</i> transcriptional regulator
<i>Cj0473</i>	1.3	<i>nusG</i> transcription antitermination protein NusG
<i>Cj0682</i>	1.2	hypothetical protein
<i>Cj1115c</i>	1.2	putative phosphatidylserine decarboxylase-related protein
<i>Cj0068</i>	1.2	<i>pspA</i> protease
<i>Cj1254</i>	1.2	hypothetical protein
<i>Cj0099</i>	1.2	<i>birA</i> biotin--protein ligase
<i>Cj0808c</i>	1.2	hypothetical protein
<i>Cj0408</i>	1.2	<i>frdC</i> fumarate reductase cytochrome b-556 subunit
<i>Cj0460</i>	1.2	<i>nusA</i> transcription elongation factor NusA
<i>Cj1504c</i>	1.2	<i>selD</i> putative selenide,water dikinase
<i>Cj0734c</i>	1.1	<i>hisJ</i> histidine-binding protein precursor

<i>Cj0306c</i>	1.1	<i>bioF</i> 8-amino-7-oxononanoate synthase
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Table S4. *C. jejuni* 11168H genes down-regulated after 24 h of co-culturing with Caco-2 IECs in the VDC with microaerobic conditions in the apical compartment.

ORF number	Fold change	Re-annotation
<i>Cj1680c</i>	1.1	putative periplasmic protein
<i>Cj1447c</i>	1.1	<i>kpsT</i> capsule polysaccharide export ATP-binding protein
<i>Cj0642</i>	1.2	<i>recN</i> putative DNA repair protein
<i>Cj0843c</i>	1.1	putative secreted transglycosylase
<i>Cj1234</i>	1.1	<i>glyS</i> glycyl-tRNA synthetase subunit bet
<i>Cj0847</i>	1.1	<i>psd</i> phosphatidylserine decarboxylase
<i>Cj1241</i>	1.1	putative MFS transport protein arabinose efflux
<i>Cj1040c</i>	1.2	putative MFS transport protein cyanate transport
<i>Cj1484c</i>	1.2	putative membrane protein
<i>Cj1600</i>	1.2	<i>hisH</i> imidazole glycerol phosphate synthase subunit HisH
<i>Cj0272</i>	1.2	hypothetical protein
<i>Cj0343c</i>	1.2	putative integral membrane protein
<i>Cj0238</i>	1.2	putative mechanosensitive ion channel family protein
<i>Cj0652</i>	1.2	<i>pbpC</i> penicillin-binding protein
<i>Cj0574</i>	1.2	<i>ilvI</i> acetolactate synthase 3 catalytic subunit
<i>Cj0319</i>	1.2	<i>fliG</i> flagellar motor switch protein G
<i>Cj1655c</i>	1.2	<i>nhaA1</i> Na(+)/H(+) antiporter
<i>Cj0720c</i>	1.2	<i>flaC</i> flagellin
<i>Cj0850c</i>	1.3	putative MFS transport protein Sugar transporter
<i>Cj0265c</i>	1.3	putative cytochrome C-type haem-binding periplasmic protein
<i>Cj0849c</i>	1.3	hypothetical protein
<i>Cj0549</i>	1.3	<i>fliS</i> flagellar protein FliS
<i>Cj1294</i>	1.3	<i>pseC</i> C4 aminotransferase
<i>Cj0453</i>	1.3	<i>thiC</i> thiamine biosynthesis protein ThiC
<i>Cj0931c</i>	1.3	<i>argH</i> argininosuccinate lyase
<i>Cj0174c</i>	1.3	<i>cfbpB</i> putative iron-uptake ABC transporter permease
<i>Cj0241c</i>	1.3	putative iron-binding protein
<i>Cj1440c</i>	1.3	putative sugar transferase capsule locus
<i>Cj0846</i>	1.3	putative metallophosphoesterase
<i>Cj0293</i>	1.3	<i>surE</i> stationary phase survival protein SurE
<i>Cj1685c</i>	1.4	<i>bioB</i> biotin synthase
<i>Cj1669c</i>	1.4	DNA ligase
<i>Cj1686c</i>	1.4	<i>topA</i> DNA topoisomerase I
<i>Cj1277c</i>	1.4	putative ABC transporter ATP-binding protein

<i>Cj1555c</i>	1.4	hypothetical protein
<i>Cj0263</i>	1.4	<i>zupT</i> zinc transporter ZupT
<i>Cj0053c</i>	1.4	<i>mnmA</i> tRNA-specific 2-thiouridylase MnmA
<i>Cj1425c</i>	1.5	<i>hddA</i> putative D-glycero-D-manno-heptose 7-phosphate kinase capsule locus
<i>Cj0081</i>	1.5	<i>cydA</i> cytochrome bd oxidase subunit I
<i>Cj1119c</i>	1.5	<i>pglG</i> putative integral membrane protein
<i>Cj0316</i>	1.5	<i>pheA</i> chorismate mutase/prephenate dehydratase
<i>Cj1085c</i>	1.6	<i>mfd</i> transcription-repair coupling factor
<i>Cj1224</i>	1.6	putative iron-binding protein
<i>Cj0303c</i>	1.6	<i>modA</i> putative molybdate-binding lipoprotein
<i>Cj0456c</i>	1.6	hypothetical protein
<i>Cj1138</i>	1.6	putative glycosyltransferase LOS
<i>Cj0439</i>	1.6	<i>dhC</i> putative succinate dehydrogenase subunit C
<i>Cj1098</i>	1.7	<i>pyrB</i> aspartate carbamoyltransferase catalytic subunit
<i>Cj0111</i>	1.7	periplasmic protein
<i>Cj1529c</i>	1.7	<i>purM</i> phosphoribosylaminoimidazole synthetase
<i>Cj0082</i>	1.7	<i>cydB</i> cytochrome bd oxidase subunit II
<i>Cj0480c</i>	1.7	H-T-H motif
<i>Cj0437</i>	1.7	<i>sdhA</i> succinate dehydrogenase flavoprotein subunit
<i>Cj0198c</i>	1.7	recombination factor protein RarA
<i>Cj0501</i>	1.8	pseudo
<i>Cj0032</i>	1.9	putative type IIS restriction /modification enzyme, C-terminal half
<i>Cj1170c</i>	2.1	omp50 50 kda outer membrane protein precursor
<i>Cj0017c</i>	2.4	<i>dsbI</i> disulphide bond formation protein
<i>Cj0799c</i>	2.9	<i>ruvA</i> Holliday junction DNA helicase RuvA