**Figure S1**

**C. coli**

**flaB**

\[AAGCUUAAACCUUUUCUAA - G5']

\[GAGCAAUAAUUGAAAGGAUUAA AUG\]

\[cj0243\]

\[AAGCUUAAAACUUUCUAA - G5']

\[AAACUGCAUAAUUGAAAGGAUUAA AUG\]

\[cj0428\]

\[AAGCUUAAAACUUUCUAA - G5']

\[UUUUUGCA-UAAUUGAAAGGAAGCU AUG\]

**flaD**

\[AAGCUUAAACCUUUUCUAA - G5']

\[AGCAUGUUG-GAAAAGAU<18> AUG\]

\[flgP\]

\[AAGCUUAAAACUUUCUAA - G5']

\[U<\text{N7}>UAAUUGAAUUGAAAGGA UAAUG\]

\[cj1650\]

\[AAGCUUAAAACUUUCUAA - G5']

\[CUUUACGAUAAUUGAAAGGAUG\]

\[flgE2\]

\[AAGCUUAAAACUUUCUAA - G5']

\[U<\text{N41}>AAGCAUAAUUGAAAGGAUG\]

**C. upsaliensis**

**flaB**

\[AAGCUUAAACCUUUUCUAA - G5']

\[GAGCAAUAAUUGAAAGGAUUAA AUG\]

\[cj0243\]

\[AAGCUUAAAACUUUCUAA - G5']

\[AAGCAAUAAUUGAAAGGAUCA AUG\]

\[no cj0428 ortholog\]

**flaD**

\[AAGCUUAAACCUUUUCUAA - G5']

\[AGCAUAAUUG-GAAAAGAU<12> AUG\]

\[flgP\]

\[AAGCUUAAAACUUUCUAA - G5']

\[UAUUACGAUAAUUGAAAGGAU AUG\]

\[cj1650\]

\[AAGCUUAAAACUUUCUAA - G5']

\[AGCAUAAUUG-GAAGGAAGCAU AUG\]

\[flgE2\]

\[AAGCUUAAAACUUUCUAA - G5']

\[G<\text{N8}>AAGCAUAAUUGAAAGGAUCA AUG\]

**C. lari (C. lari group)**

**flaB**

\[UUCGUUAAAACUUUUUCUAA - G5']

\[UAAGCAUAAUUGAAAGGAUUAA AUG\]

\[cj0243\]

\[UUCGUUAAAACUUUUUCUAA - G5']

\[AAGCAUAAUUGAAAGGAU AUG\]

\[no cj0428 ortholog\]

**flaD**

\[UUCGUUAAAACUUUUUCUAA - G5']

\[UAUUAAUAAUUGAGAGAAAUG\]

\[flgP\]

\[UUCGUUAAAACUUUUUCUAA - G5']

\[UUAAUCAUUGGUUAAGGAUG\]

\[cj1650\]

\[UUCGUUAAAACUUUUUCUAA - G5']

\[AGCAUAAUUGAGAGAAAUG\]

\[flgE2\]

\[UUCGUUAAAACUUUUUCUAA - G5']

\[A<\text{N27}>AAGCAUAAUUGAAAGGAUG\]
C. volucris (C. lari group)

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<td>UUCGUAUAAAAACUUUUCUAAG-5'</td>
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<tr>
<td>cj0428</td>
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C. insulaenigrae (C. lari group)

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C. subantarcticus (C. lari group)

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<tr>
<td>cj0428</td>
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Figure S1. Alignment of CjNC1/CjNC4 orthologs from thermophilic Campylobacter species with the predicted σ54-dependent target 5' UTRs. Sequences are shown as RNA, lines depict identities, semicolons indicate U:G basepairs. Red residues indicate the predicted ribosome binding site, blue residues the conserved ncRNA part, bold and underlined the predicted AUG startcodon. The +1 of the 5' UTR sequence depicted is based on the distance from the σ54 promoter.