

1 **Supplementary information**

2 Table S1. Genome accession numbers and sequence types of *Campylobacter jejuni* isolates
3 sequenced in this study. Sequence types novel to the PubMLST database are indicated in
4 boldface.

5 Figure S1. Phylogenomic tree based on the core genome alignment (942 core genes) of 1261 *C.*
6 *jejuni* genomes listed in Supplementary Dataset S1.

7 Figure S2. Neighbor-joining tree representing the alignment of nucleotide sequences of the beta-
8 lactamase (*bla-OXA*) gene. Sequence accession number, *Campylobacter* sp., and strain number
9 are indicated for each sequence and with allele number when available. Strains from this study
10 are indicated in boldface and with CB for western jackdaw, SO or SS for mallard duck, and FA
11 for pheasant in the strain name.

12 Figure S3. goeBURST full Minimum spanning tree (MST) of MLST allelic profiles of *C. jejuni*
13 STs detected from different hosts (2, 5, 7, 16, 18, 19, 29). Mallard duck (brown) and barnacle
14 geese (purple) STs are mostly located in their own clade. STs from western jackdaw also form a
15 separate clade. The most common clonal complexes (CCs) associated with domestic animals and
16 human patients are indicated. Also, the most frequent STs among western jackdaws (ST-1282
17 and ST-6460), mallard ducks (ST-2314), and pheasants (ST-19) are indicated with arrows.

18 **References**

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BioSample	Accession	Organism	Strain	Source	Sequence type (ST)	Clonal complex (CC)
SAMN08398758	PRCT000000000	<i>Campylobacter jejuni</i>	CB286	<i>Corvus monedula</i>	6460	UA
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SAMN08398760	PRCR000000000	<i>Campylobacter jejuni</i>	CB288	<i>Corvus monedula</i>	1282	UA
SAMN08398761	PRCQ000000000	<i>Campylobacter jejuni</i>	CB289	<i>Corvus monedula</i>	7804	UA
SAMN08398762	PRCP000000000	<i>Campylobacter jejuni</i>	CB290	<i>Corvus monedula</i>	7805	UA
SAMN08398763	PRCO000000000	<i>Campylobacter jejuni</i>	CB291	<i>Corvus monedula</i>	7806	UA
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