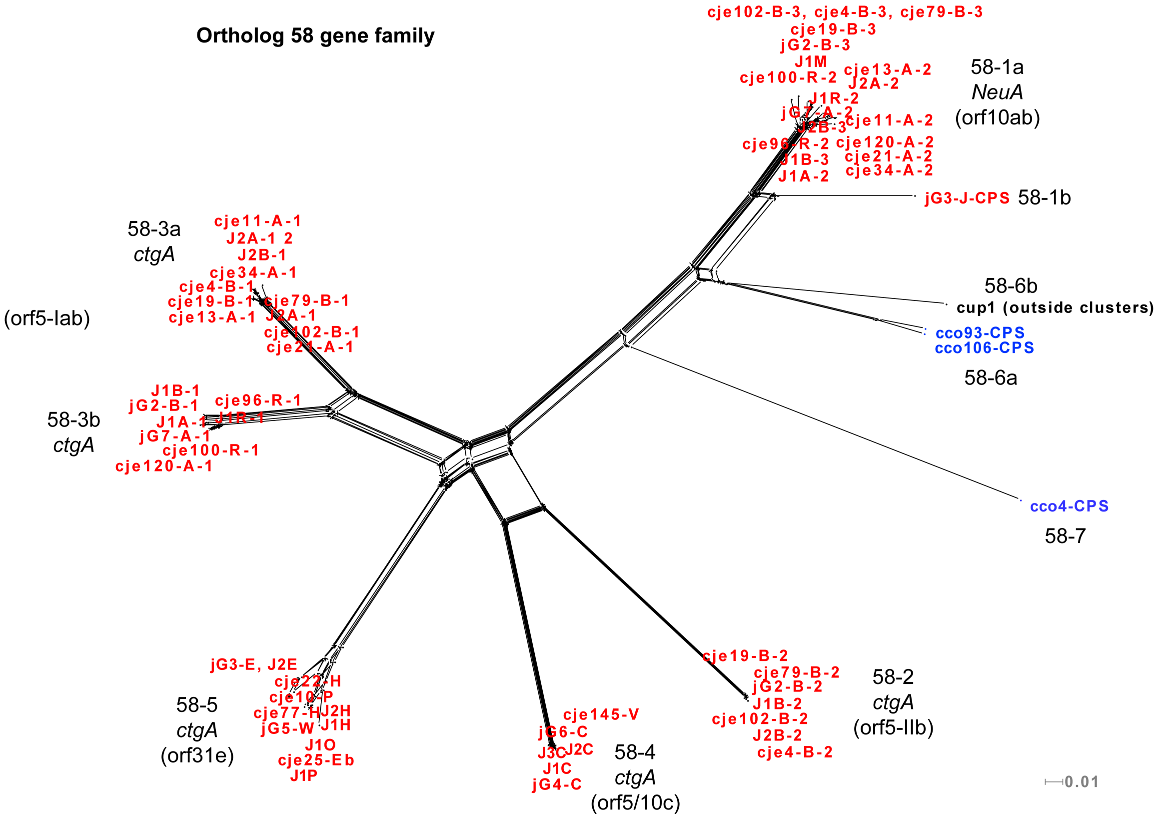

Fig. S1. Split network based on nucleotide sequences showing relationship among different CDS representing ortholog 58. *C. jejuni* subsp. *jejuni* strains are shown in red and *C. coli* strains are shown in blue. Class IDs are shown in upper case after strain IDs (see Table 1 for additional strain information). Number following class IDs A, B, and C indicates the order in which the particular ortholog copy occurred in the class. For reference, gene IDs used by Godschalk et al. (2004) are shown in parentheses.

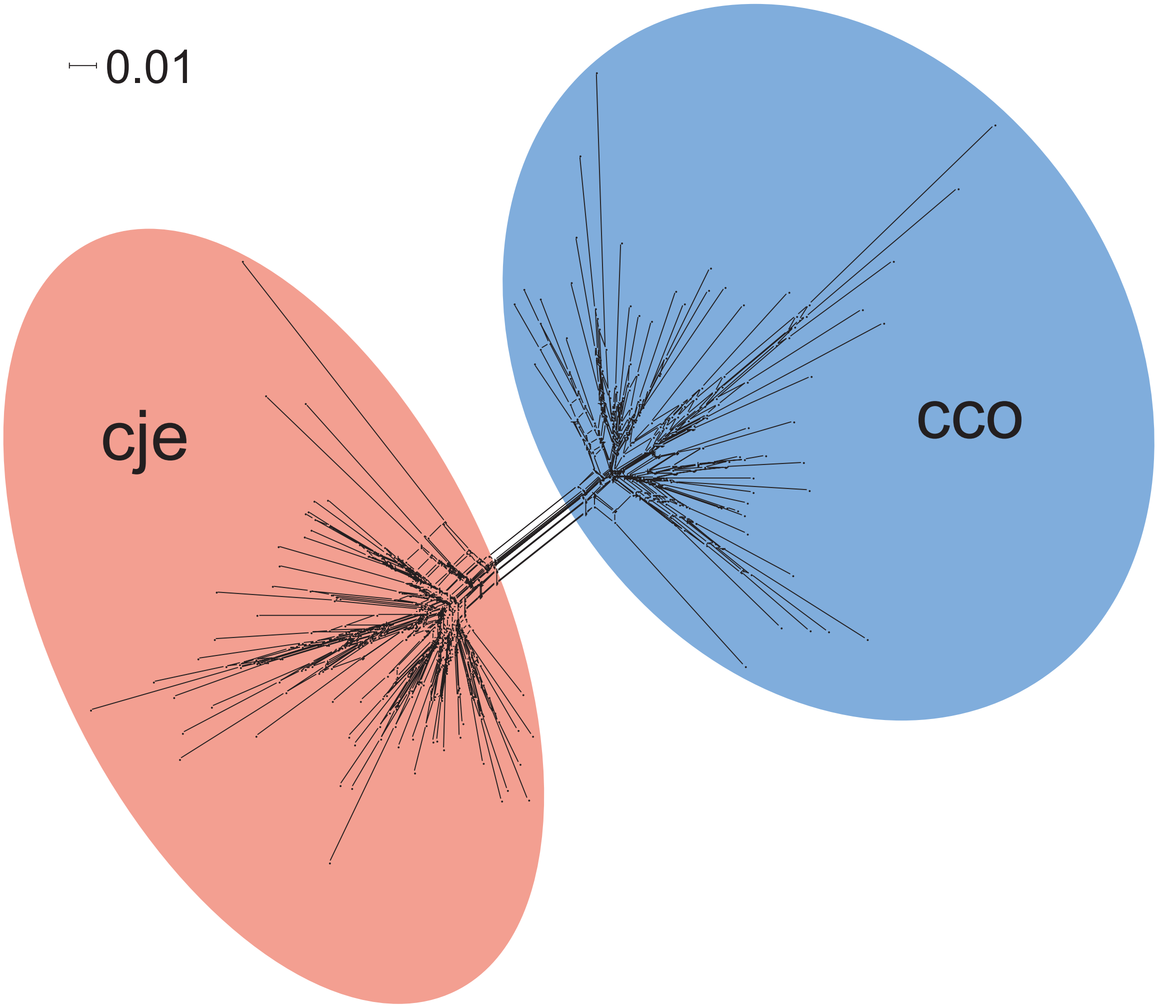

Fig. S2. Split network utilizing genomic data (gene content) for *C. coli* (cco, blue) and *C. jejuni* subsp. *jejuni* (cje, red). Network was based on the collective dispensable genome (i.e. presence/absence of 2901 orthologs not shared among all strains analyzed).

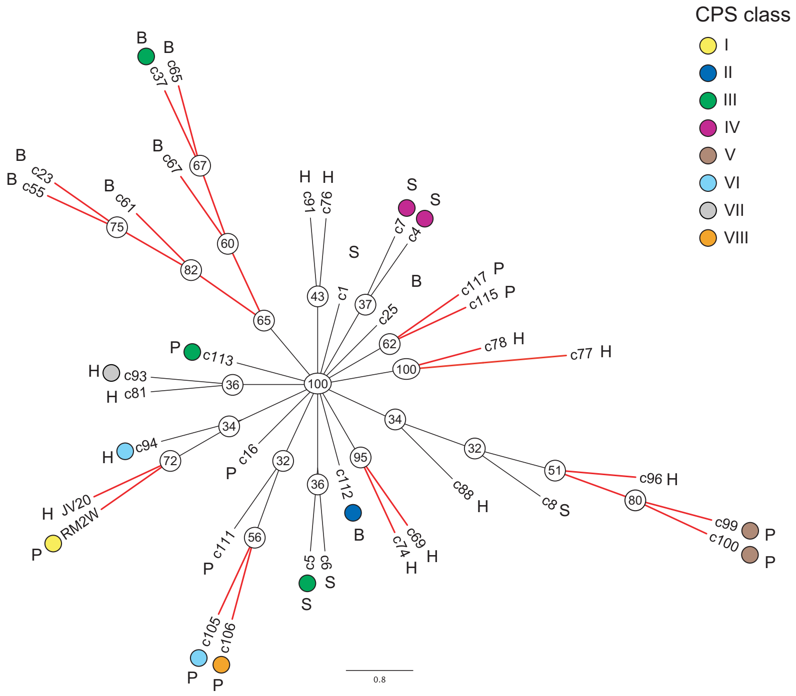

Fig. S3. Phylogeny showing the consensus of 399 gene-trees for *C. coli.* Numbers in circles show the proportion of gene-trees that supported a particular grouping. Branches for groupings with greater than 50% support are shown in red. Colored circles identify the different CPS classes. Strain isolation source is shown with a single letter code (H=human, B=bovine, S=swine, and P=poultry).

Table S3-A (A-G). Number of homopolymeric tracts for each gene cluster

	C. jejuni subsp. *jejuni*							
	LOS n=22				CPS n=12			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	2044	3	20	1235	1973	5	70	1367
6	1155		3	461	938		11	492
7	442		4	201	348		2	230
8	109		18	39	87		0	38
9	2		3	18	24		29	10
10							6	

Table S3-B

	C. coli							
	LOS n=8				CPS n=8			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	997		14	626	1334	6	28	955
6	520		4	208	614		5	385
7	166			100	250		2	183
8	57			5	102		0	29
9	7				12		8	5
10								

Table S3-C

	C. jejuni subsp. *doylei*							
	LOS n=1				CPS n=1			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	60			38	87		7	69
6	34			13	45		2	21
7	11			10	18			9
8	3			2	3			

Table S3-D

	C. lari							
	LOS n=1				CPS n=1			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	144		2	79	158		6	121
6	65			20	71			30
7	36			13	34			25
8	14			3	7			7
9					5			2

Table S3-E

	C. upsaliensis				*C. fetus* subsp. *fetus*			
	LOS n=1				LOS n=1			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	161	5	7	104	72			40
6	56		2	46	37			22
7	27			13	10			4
8	3				3			

Table S3-F

	C. rectus				*C. showae*			
	LOS n=1				LOS n=1			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	68		3	53	76		2	61
6	24			14	21			11
7	8			3	10			3
8								

Table S3-G

	C. curvus				*C. concisus*			
	LOS n=1				LOS n=1			
bp	**A**	**C**	**G**	**T**	**A**	**C**	**G**	**T**
5	45		2	34	59			23
6	20			16	24			11
7	8			2	3			
8				2	2			

Where applicable, single representative strains for each class were analyzed (n = number of classes).