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Supplementary Material

2 **Table S1. Breakpoints used for susceptibility testing of *Campylobacter* species**

Class	Agent	Species	Range (mg/L)	ECOFF ^a
Aminoglycosides	Gentamicin	All	0.12 - 32	2
Ketolides	Telithromycin	All ^b	0.015 - 8	4
Lincosamide	Clindamycin	<i>C. coli</i>	0.03 - 16	1
		<i>C. jejuni</i>	0.03 - 16	0.5
Macrolides	Azithromycin	<i>C. coli</i>	0.015 - 64	0.5
		<i>C. jejuni</i>	0.015 - 64	0.25
	Erythromycin	<i>C. coli</i>	0.03 - 64	8
		<i>C. jejuni</i>	0.03 - 64	4
Phenicols	Florfenicol	All	0.03 - 64	4
Quinolones	Ciprofloxacin	All	0.015 - 64	0.5
	Nalidixic acid	All	4 - 64	16
Tetracyclines	Tetracycline	<i>C. coli</i>	0.06 - 64	2
		<i>C. jejuni</i>	0.06 - 64	1

3 ^a EUCAST epidemiological cut-off values (ECOFF) (mg/L)

4 ^b *C. coli* ECOFF derived from National Antimicrobial Resistance Monitoring System
5 (NARMS) programme, Centre for Disease Control and Prevention (CDC)

6 **Table S2. Distribution of minimum inhibitory concentrations for *Campylobacter jejuni* (n=108) isolated from Australian**
 7 **meat chickens.**

Antimicrobial	Minimum inhibitory concentration (mg/L)														% Resistant (95% CI)	
	0.016	0.03	0.06	0.13	0.25	0.5	1	2	4	8	16	32	64	128		
Azithromycin	56.5	38.0	4.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.9 (0.0 – 5.1)
Ciprofloxacin	0.0	4.6	44.4	30.6	5.6	0.0	0.0	0.0	0.9	7.4	6.5	0.0	0.0	0.0	14.8 (8.7 – 22.9)	
Clindamycin	0.0	17.6	43.5	34.3	3.7	0.0	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.0	0.9 (0.0 – 5.1)	
Erythromycin	0.0	0.9	9.3	24.1	53.7	11.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.9	0.9 (0.0 – 5.1)	
Florfenicol	0.0	0.0	0.0	0.9	8.3	50.0	40.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 (0.0 – 3.4)	
Gentamicin	0.0	0.0	0.0	7.4	50.9	41.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 (0.0 – 3.4)	
Nalidixic acid	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	65.7	19.4	0.0	0.0	2.8	12.0	14.8 (8.7 – 22.9)	
Telithromycin	0.0	0.0	4.6	13.9	23.1	49.1	8.3	0.0	0.0	0.0	0.9	0.0	0.0	0.0	0.9 (0.0 – 5.1)	
Tetracycline	0.0	0.0	20.4	33.3	18.5	4.6	0.9	2.8	0.0	0.9	10.2	6.5	0.9	0.9	22.2 (14.7 – 31.2)	

8 % Resistant: Percentage of isolates classified as non-wild type by EUCAST, and corresponding 95% confidence limits.

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10 **Table S3. Distribution of minimum inhibitory concentrations for *Campylobacter coli* (n=96) isolated from Australian meat**
 11 **chickens.**

Antimicrobial	Minimum inhibitory concentration (mg/L)														% Resistant (95% CI)	
	0.016	0.03	0.06	0.13	0.25	0.5	1	2	4	8	16	32	64	128		
Azithromycin	7.3	42.7	36.5	8.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.2	5.2 (1.7 – 11.7)
Ciprofloxacin	0.0	4.2	39.6	42.7	8.3	0.0	0.0	0.0	2.1	3.1	0.0	0.0	0.0	0.0	0.0	5.2 (1.7 – 11.7)
Clindamycin	0.0	0.0	11.5	49.0	32.3	2.1	0.0	2.1	2.1	1.0	0.0	0.0	0.0	0.0	0.0	5.2 (1.7 – 11.7)
Erythromycin	0.0	0.0	0.0	9.4	42.7	28.1	10.4	4.2	0.0	0.0	0.0	0.0	0.0	0.0	5.2	5.2 (1.7 – 11.7)
Florfenicol	0.0	0.0	0.0	0.0	6.3	43.8	45.8	4.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 (0.0 – 3.8)
Gentamicin	0.0	0.0	0.0	4.2	26.0	68.8	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0 (0.0 – 3.8)
Nalidixic acid	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	55.2	39.6	0.0	0.0	2.1	3.1	5.2 (1.7 – 11.7)	
Telithromycin	0.0	0.0	0.0	11.5	24.0	33.3	15.6	7.3	4.2	0.0	4.2	0.0	0.0	0.0	4.2	4.2 (1.1 – 10.3)
Tetracycline	0.0	0.0	15.6	43.8	29.2	6.3	2.1	0.0	0.0	0.0	2.1	0.0	0.0	1.0	3.1	3.1 (0.6 – 8.9)

12 % Resistant: Percentage of isolates classified as non-wild type by EUCAST, and corresponding 95% confidence limits.

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16 **Table S4. MLST and resistance profile of *Campylobacter jejuni* isolates (n=107)**

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Clonal Complex	MLST	Number of isolates	QRDR mutation	Ciprofloxacin (S/R)
N/a	7323	9	yes	R
N/a	2083	8	yes	R
48	2343	1	yes	R
460	535	7		S
353	4896	7		S
N/a	9432	7		S
45	45	5		S
354	528	5		S
48	48	4		S
21	50	4		S
52	161	3		S
257	257	3		S
354	354	3		S
45	6722	3		S
22	7888	3		S
N/a	9422	3		S
N/a	449	2		S
45	583	2		S
257	7572	2		S
21	8470	2		S
N/a	9425	2		S
N/a	9426	2		S
N/a	9429	2		S
42	42	1		S
206	46	1		S
21	190	1		S
45	233	1		S
607	525	1		S
22	567	1		S
N/a	791	1		S
	996	1		S
692	3804	1		S
692	4378	1		S
1332	6788	1		S
N/a	7013	1		S
443	7208	1		S
45	8559	1		S
N/a	9424	1		S
N/a	9427	1		S
N/a	9428	1		S
N/a	9431	1		S

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19 Isolates grouped by MLST with resistant isolates above the line. Gaps represent no presence.
 20 S-sensitive; R-resistant. QRDR; quinolone resistance-determining region.

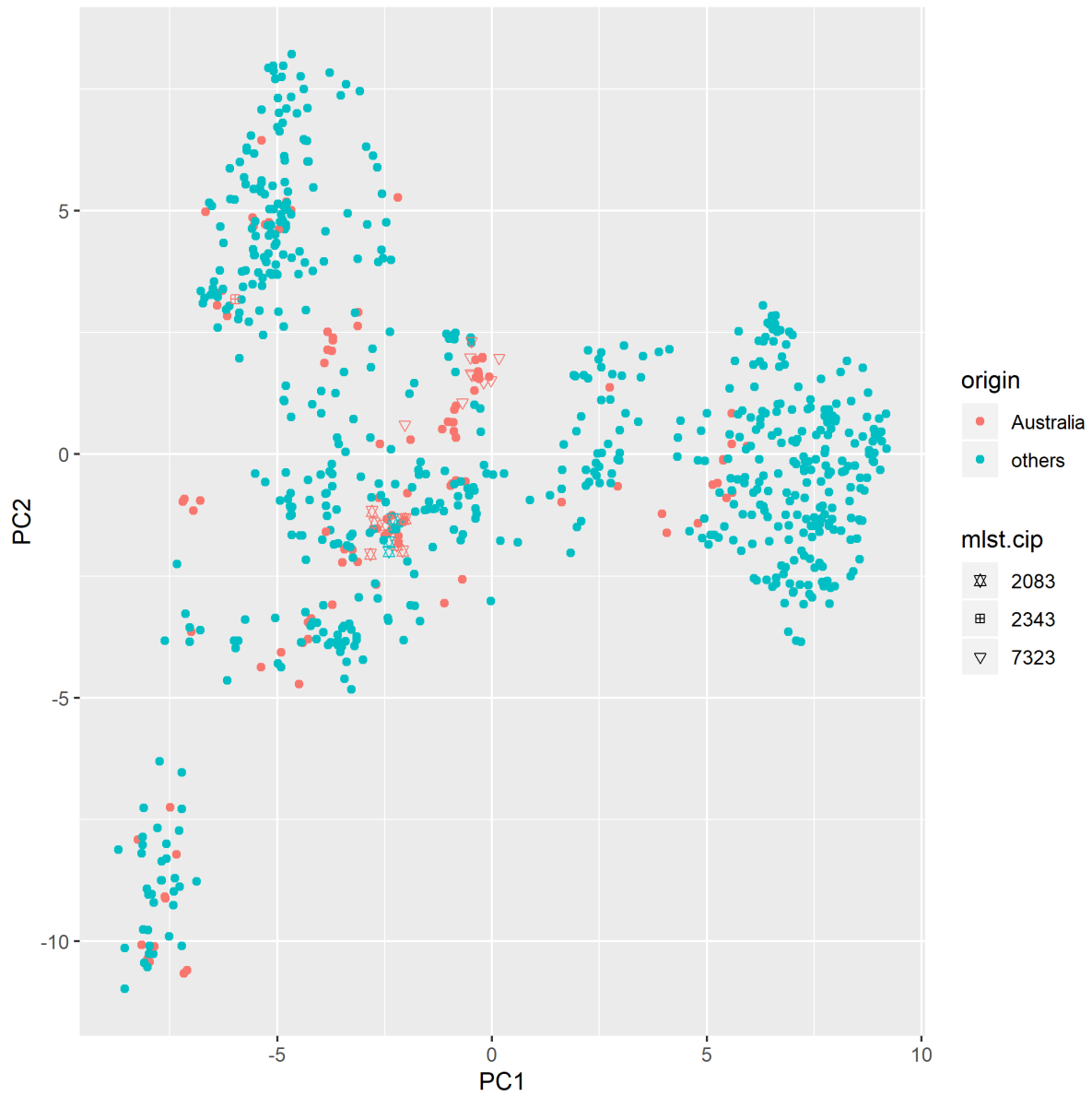
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22 **Table S5. MLST and resistance profile of *Campylobacter coli* (n=95)**

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Clonal Complex	MLST	Number of isolates	QRDR mutation	Ciprofloxacin (S/R)
828	860	5	yes	R
828	860	2		S
828	1181	14		S
-	9419	14		S
828	827	9		S
828	3985	9		S
828	825	8		S
828	832	6		S
-	9420	4		S
-	1243	3		S
-	1764	2		S
-	9418	2		S
-	9421	2		S
-	9436	2		S
-	2534	1		S
828	6755	1		S
	8714	1		S
-	9417	1		S
-	9423	1		S
-	9430	1		S
-	9433	1		S
-	9434	1		S
-	9435	1		S
-	-	3		S

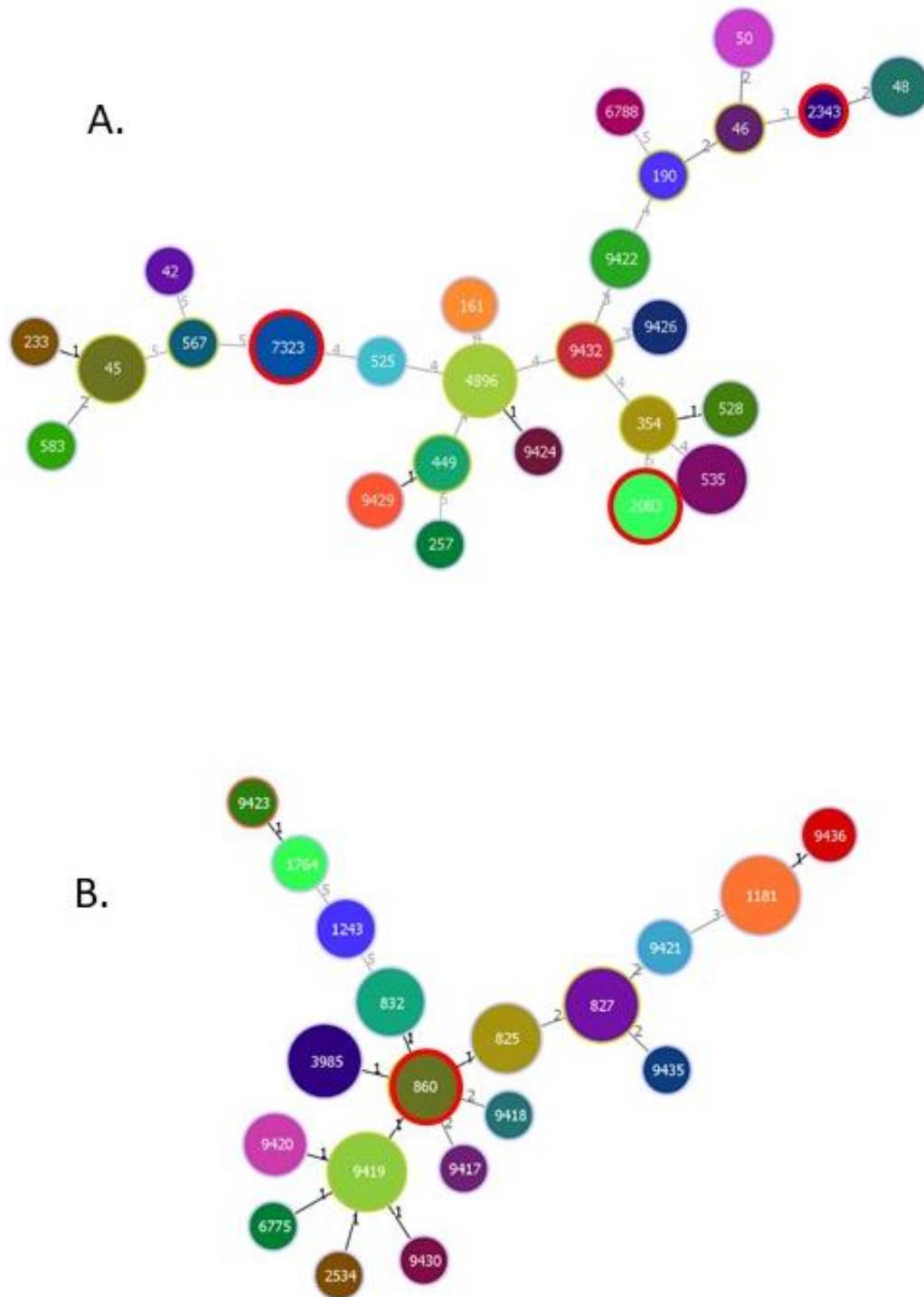
24 Isolates grouped by MLST with the resistant isolates above the line. Gaps represent no
 25 presence. S-sensitive; R-resistant. QRDR; quinolone resistance-determining region.



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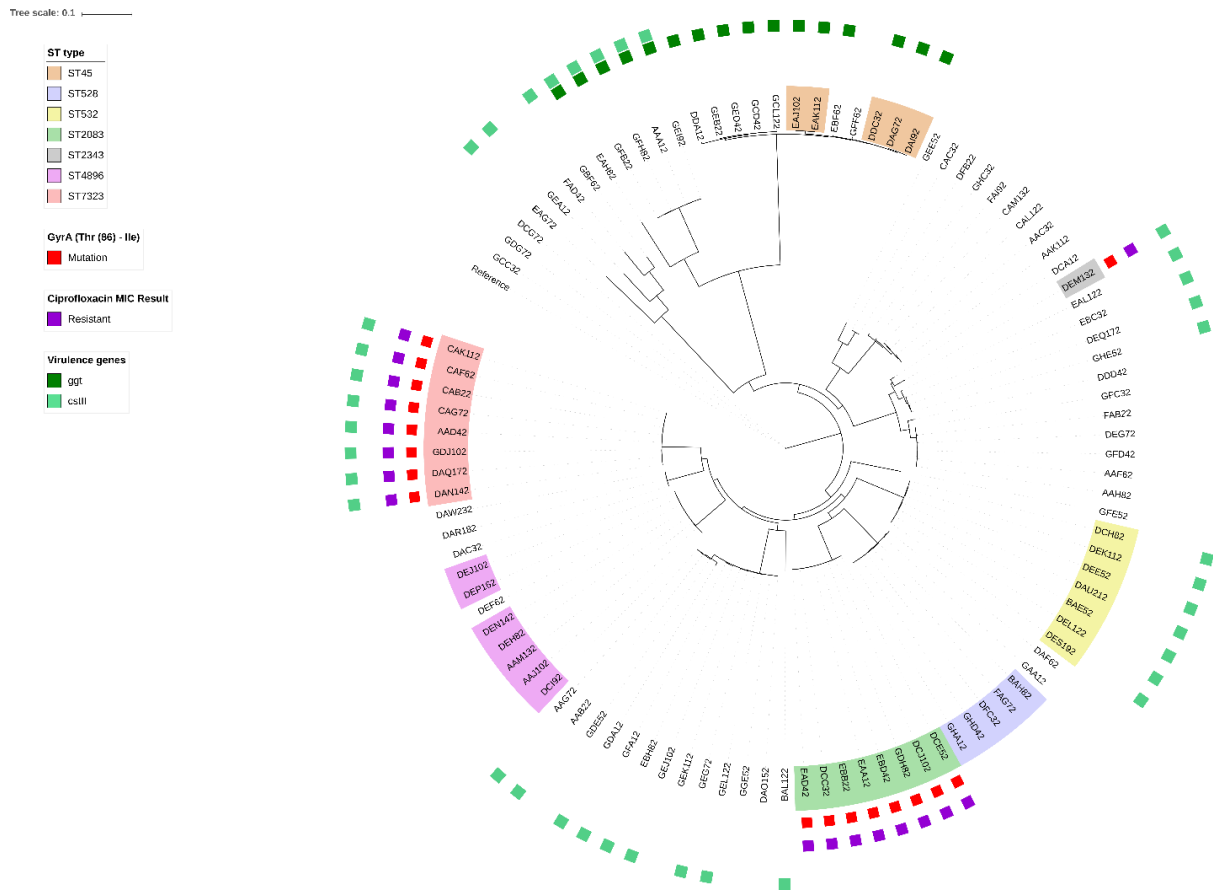
27 **Figure S1.** Principal component analysis ordination of total gene content for Australian *C. jejuni* and
 28 international collection where no distinct clustering is observed. Strain types resistant to ciprofloxacin
 29 are shown as mlst.cip.

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32 **Figure S2.** Minimum spanning trees based on MLST loci of *C. jejuni* (A) and *C. coli* (B). Branch
 33 numbers indicate number of loci variants, STs in bold red outlines are those with fluoroquinolone
 34 resistance.



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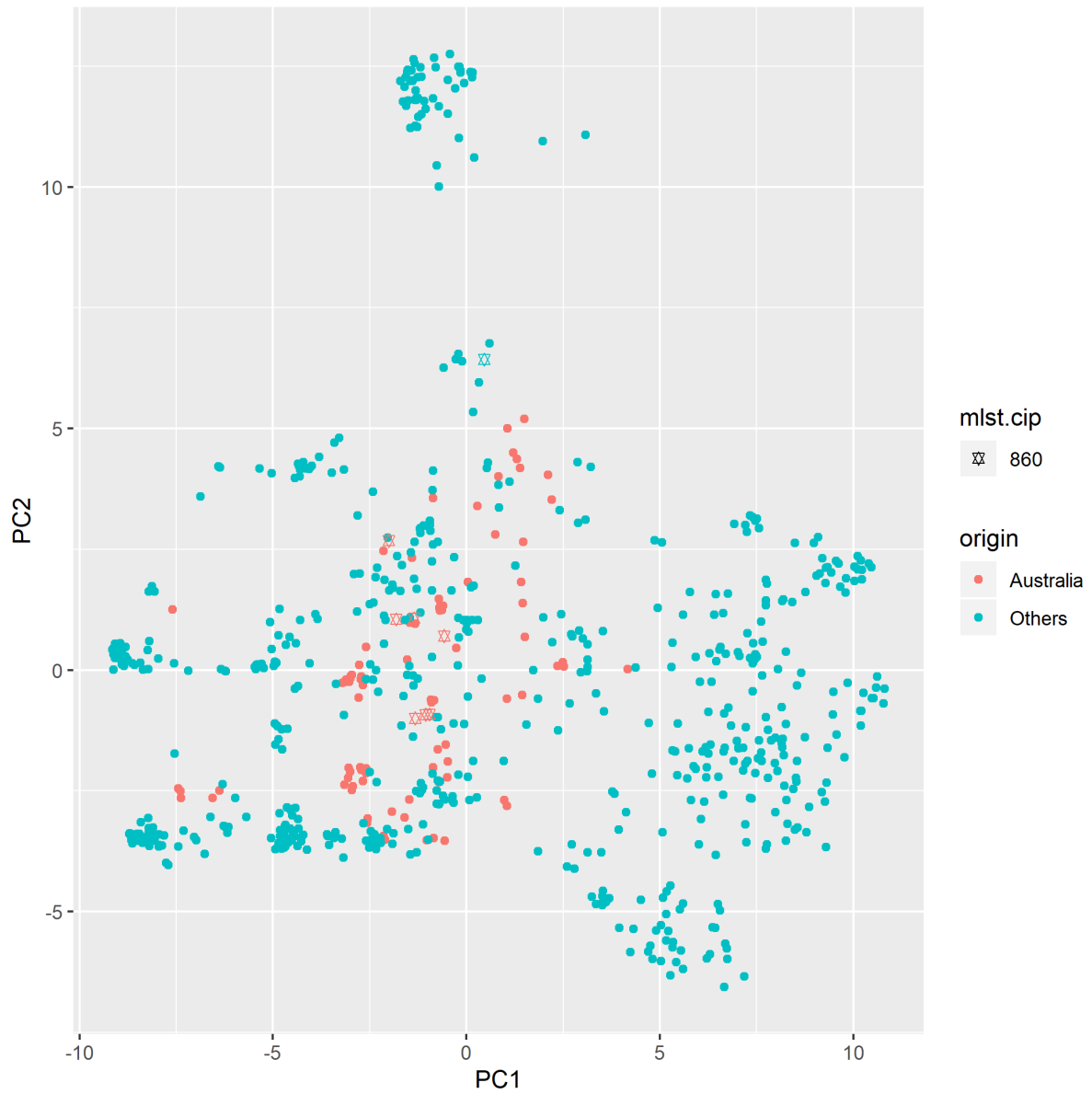
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37 **Figure S3.** A maximum likelihood phylogeny based on the single nucleotide polymorphisms
 38 (SNPs) in the core genome of all *C. jejuni* isolated from Australian chickens. The
 39 phylogenetic tree also displays multilocus sequence types, antimicrobial resistance genes,
 40 phenotypic and genotypic (mutation of *gyrA*) resistance to ciprofloxacin of each isolates.

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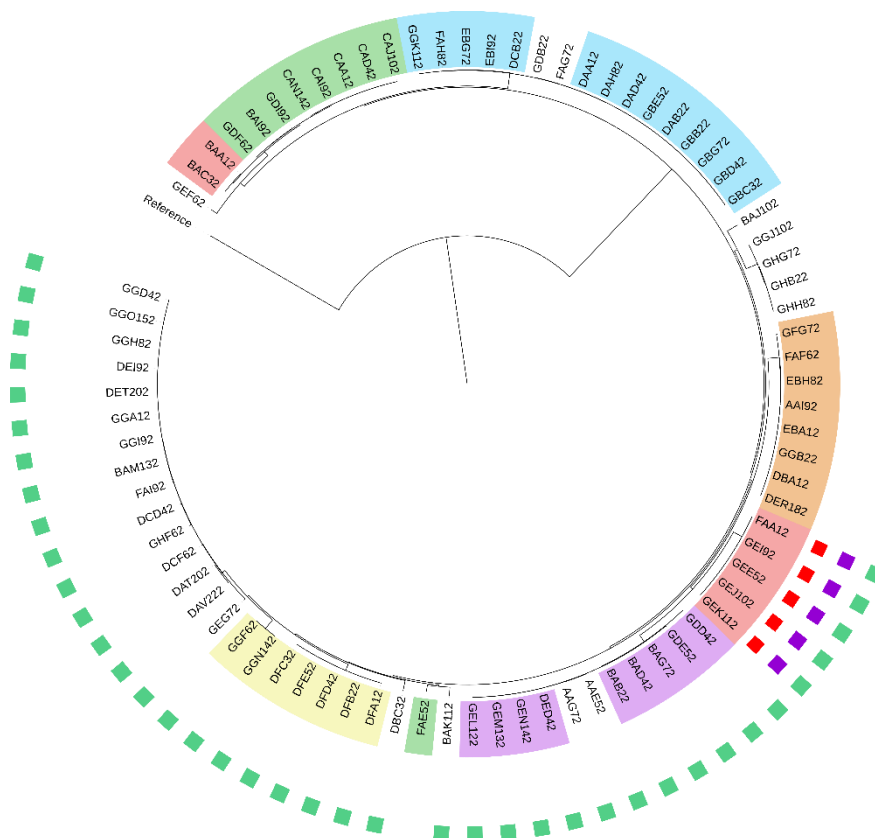
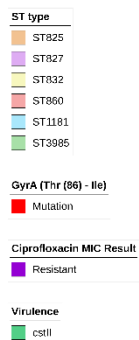
45 **Figure S4.** Principal component analysis ordination of total gene content for Australian *C.*
 46 *coli* and international collection where no distinct clustering is observed. Strain types
 47 resistant to ciprofloxacin are shown as mlst.cip.

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Tree scale: 0.1



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52 **Figure S5.** A maximum likelihood phylogeny based on the single nucleotide polymorphisms
53 (SNPs) in the core genome of *C. coli* isolates belonging to Australian clade 3. The
54 phylogenetic tree also displays multilocus sequence types, antimicrobial resistance genes,
55 phenotypic and genotypic (mutation of *gyrA*) resistance to ciprofloxacin of each isolates.