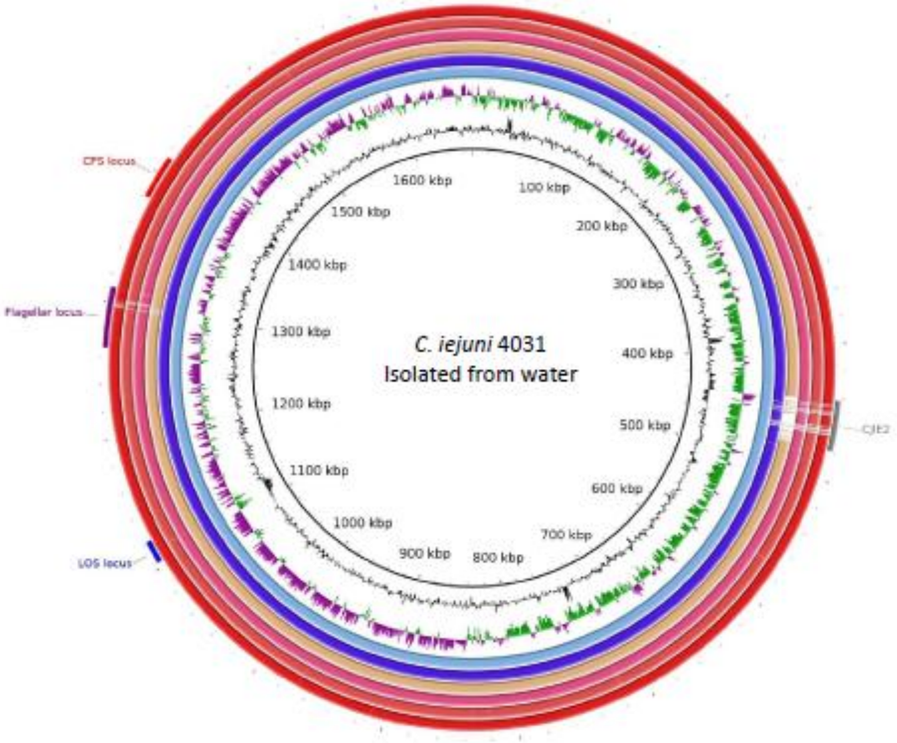
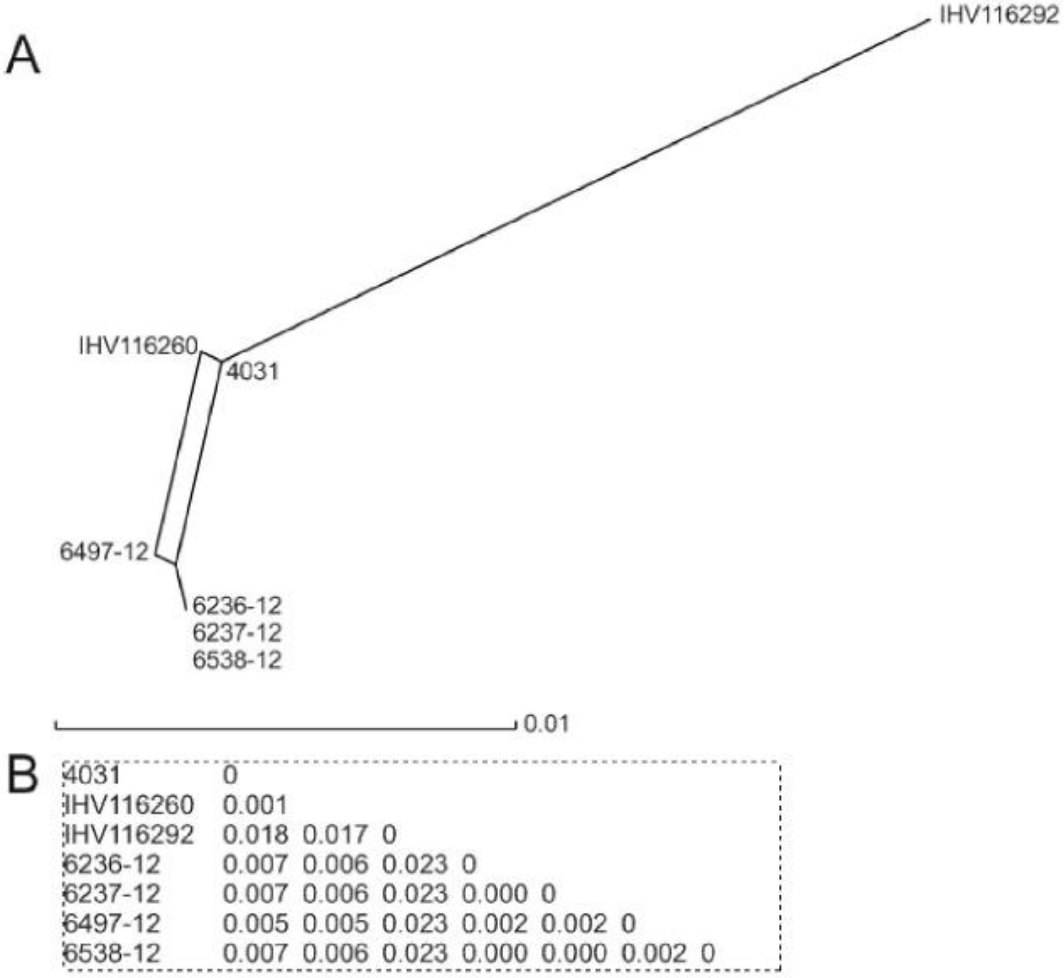
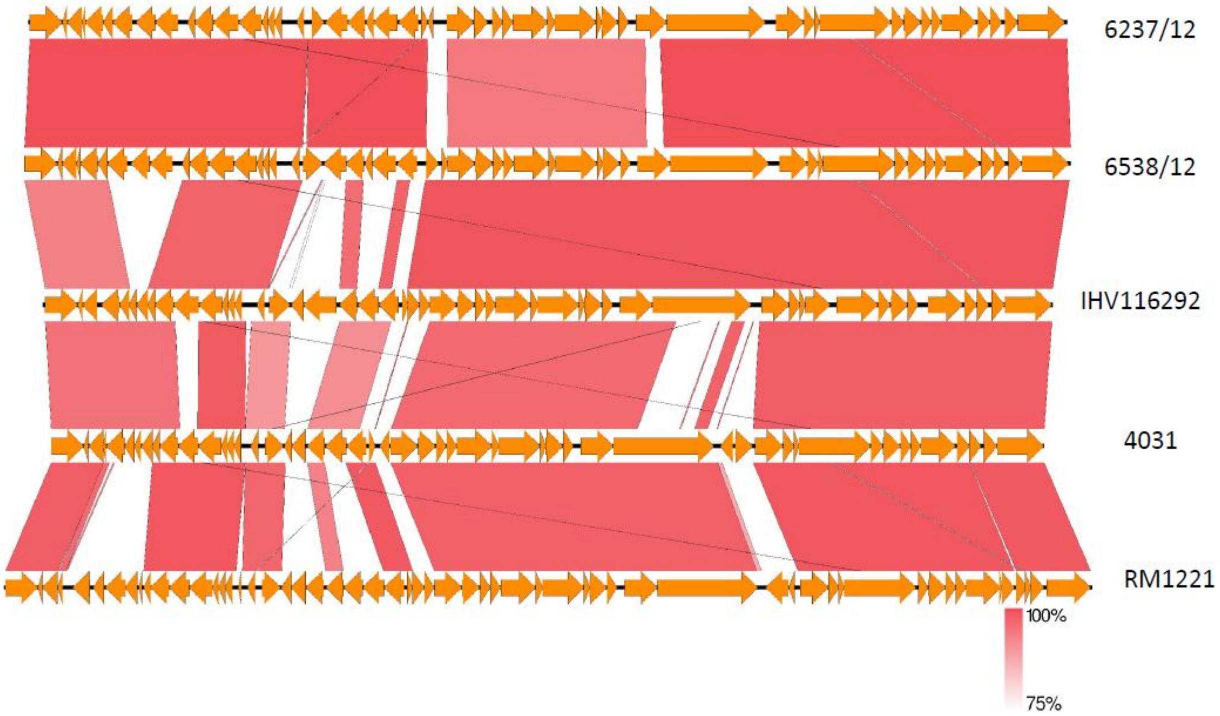


Additional file 2 Figure S1. BLAST atlas produced using BLAST Ring Image Generator v 0.95. In the middle, a genome atlas of *C. jejuni* 4031 strain is shown, around which BLAST lanes are shown. Every lane corresponds to a genome. From in to out: GC skew; GC content; BlastN pairwise comparison of *C. jejuni* genomes with ST-45: HV116260 (human waterborne outbreak); IHV116292 (human waterborne outbreak); 6497/12 (chicken); 6538/12 (chicken); 6236/12 (chicken); 6237/12 (chicken); annotation: red, CPS locus/genes; purple, Flagellar locus; blue, LOS locus; grey, *Campylobacter* integrate elements.



4031	0						
IHV116260	0.001						
IHV116292	0.018	0.017	0				
6236-12	0.007	0.006	0.023	0			
6237-12	0.007	0.006	0.023	0.000	0		
6497-12	0.005	0.005	0.023	0.002	0.002	0	
6538-12	0.007	0.006	0.023	0.000	0.000	0.002	0

Additional file 2: Figure S2. (A) Split decomposition and (B) Distance matrix of the allelic profiles of 1,287 genes obtained from PubMLST-*Campylobacter* database of *C. jejuni* strains 4031 (water), HV116260 (human waterborne outbreak), IHV116292 (human waterborne outbreak), 6497/12, ST-45 (chicken); 6538/12, ST-45 (chicken); 6236/12, ST-45 (chicken) and 6237/12, ST-45 (chicken).



Additional file 2: Figure S3. A collinear BLASTN comparison of the CJIE2 elements of *C. jejuni* strains RM1221, 4031, IHV116292, 6538/12 and 6236/12.