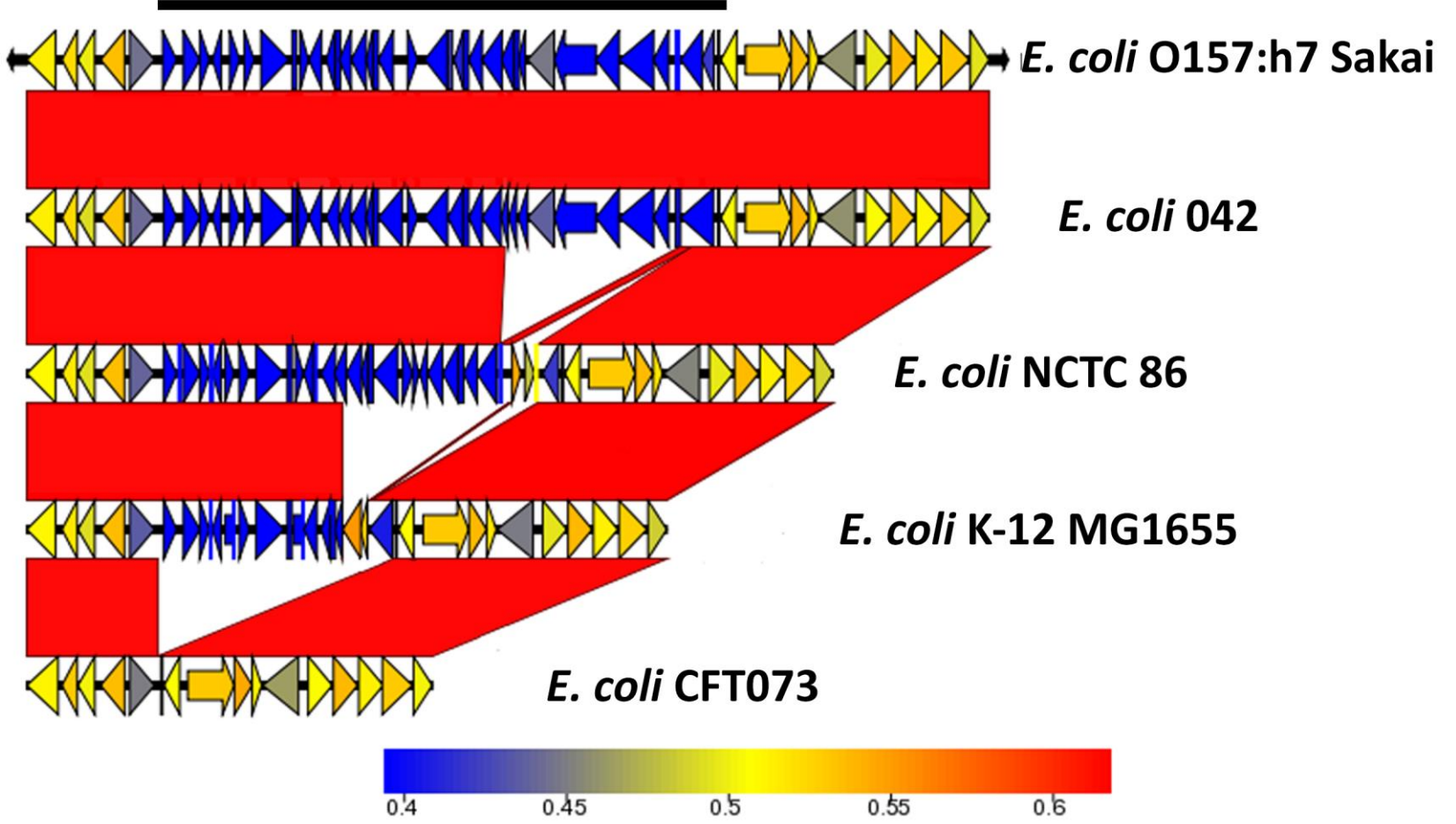


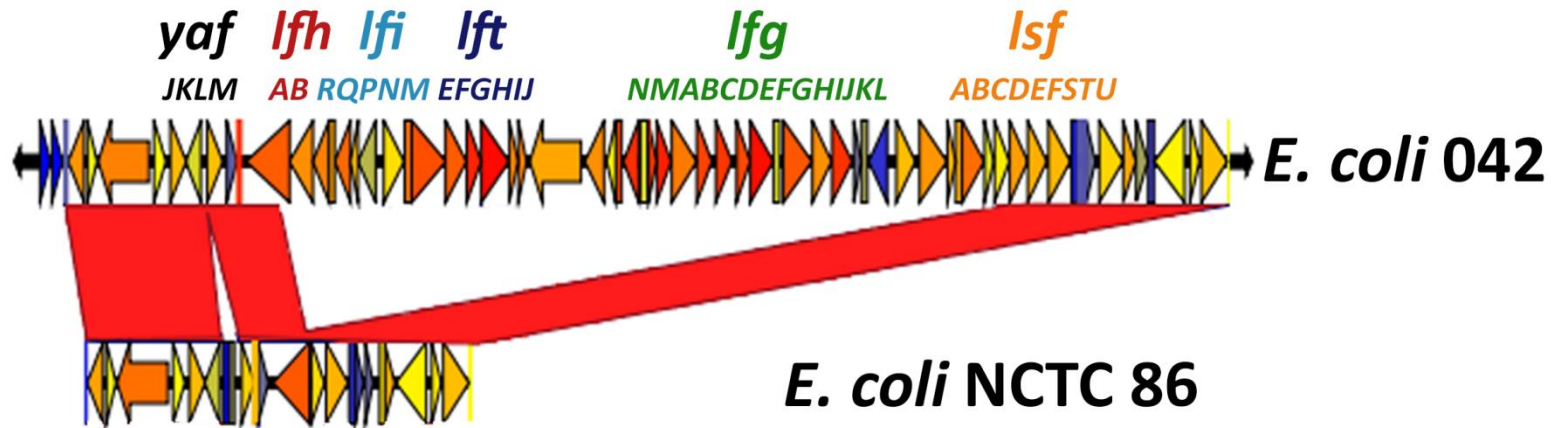
Supplemental Figure 1: Alignment of the *E. coli* Type Three secretion system. Alignments reveal the genetic attrition of *E. coli* Type Three secretion system 2 (ETT2). ETT2 is located on ROD 24 in *E. coli* NCTC 86. ETT2 is most complete in *E. coli* O157:H7 and *E. coli* 042 but is in various stages of degradation in *E. coli* NCTC 86 and *E. coli* K-12. ETT2 is completely absent in CFT073. The CDSs are indicated by arrows coloured according to the % GC content of the gene.

EET2 locus

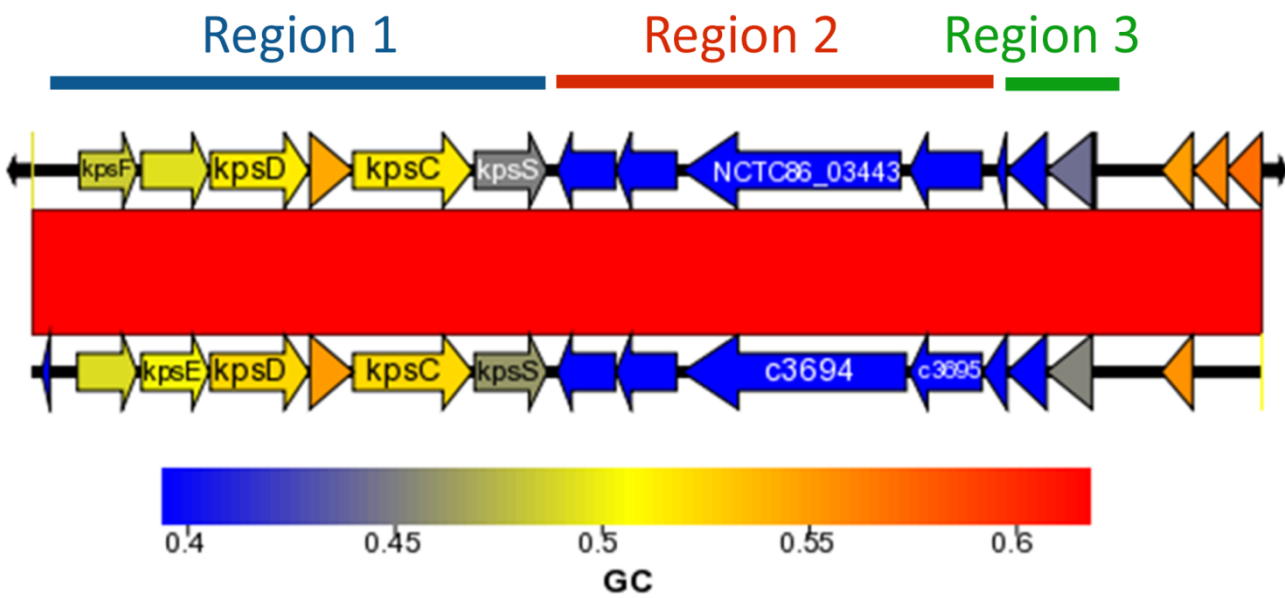


Supplemental Figure 2: Schematic representation of the Flag-2 gene cluster in *E. coli* 042.

Schematic representation of the 48.8-kb region of the *E. coli* 042 genome encoding Flag-2. The illustration shows the absence of the locus when in *E. coli* NCTC 86. CDSs are indicated by arrows coloured according to the GC content of the gene.



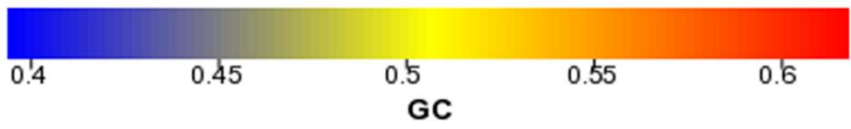
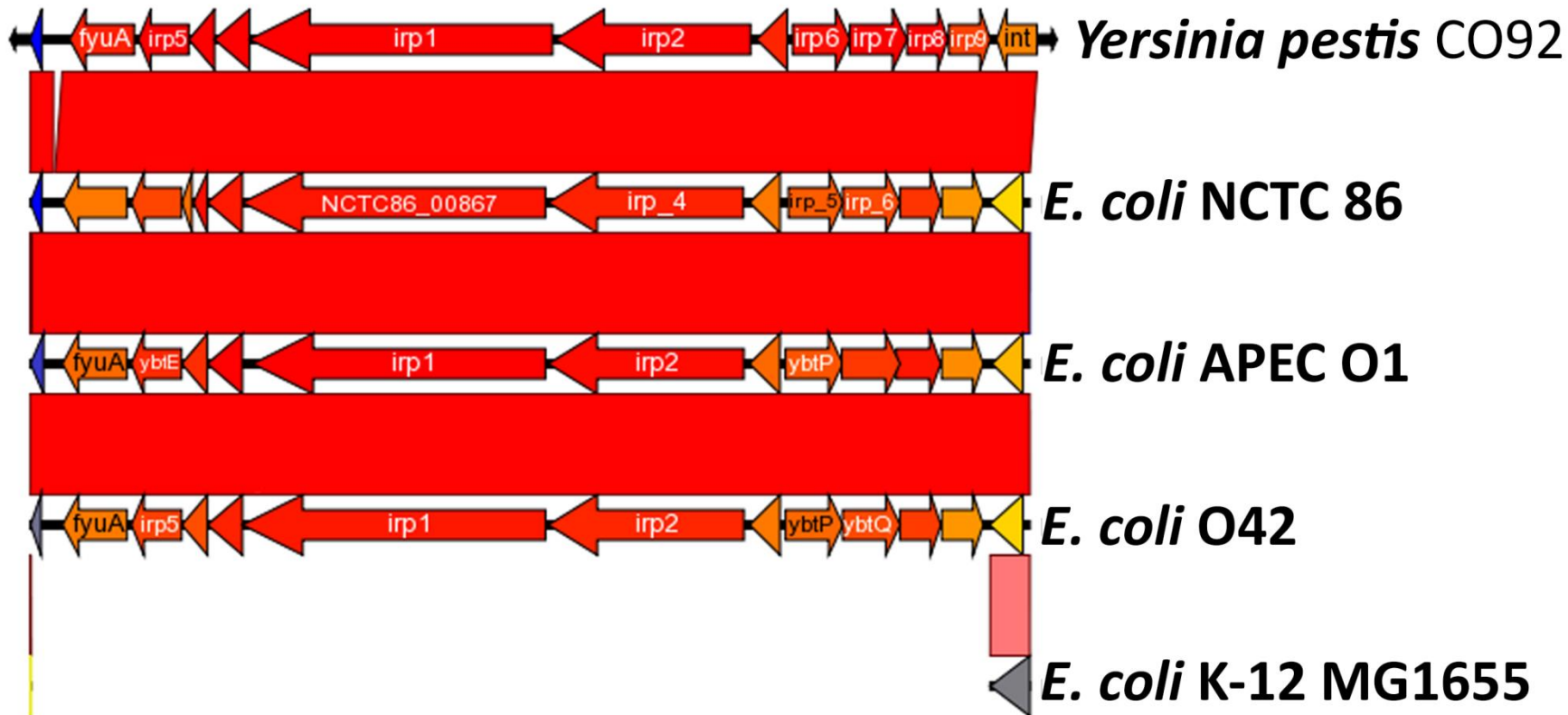
Supplemental Figure 3: Alignment of the capsular operon from of *E. coli* CFT073 with *E. coli* NCTC 86. Alignments reveal genetic lesions in the *E. coli* NCTC 86 contains the same *kps* locus found on ROD 31, which encodes the capsule found in *E. coli* CTF073. The locus is divided into three regions. The conserved regions 1 and the variable Region 2 that encode enzymes for polymer biosynthesis, and the complexity of this region corresponds UPEC *E. coli* CFT073 group two capsule indicating it possesses the K-2 antigen. CDSs are indicated by arrows and their colour represents the GG content according to the scale below.



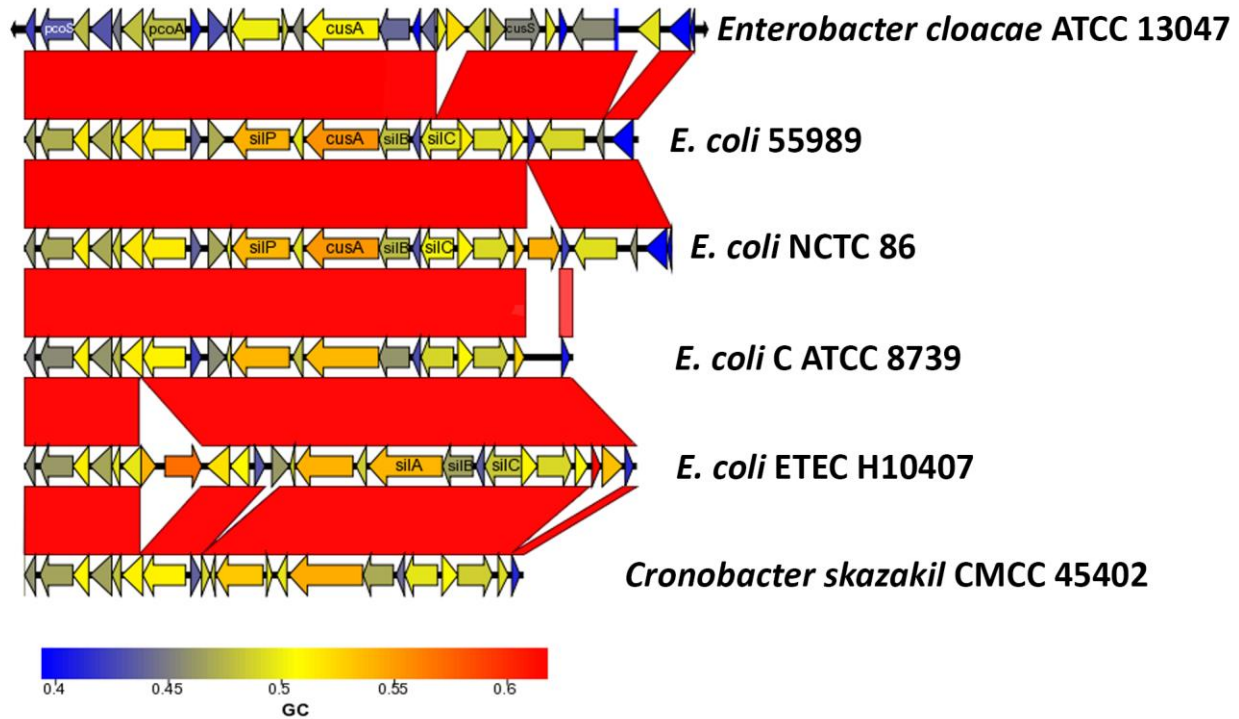
E. coli NCTC 86

E. coli CFT073

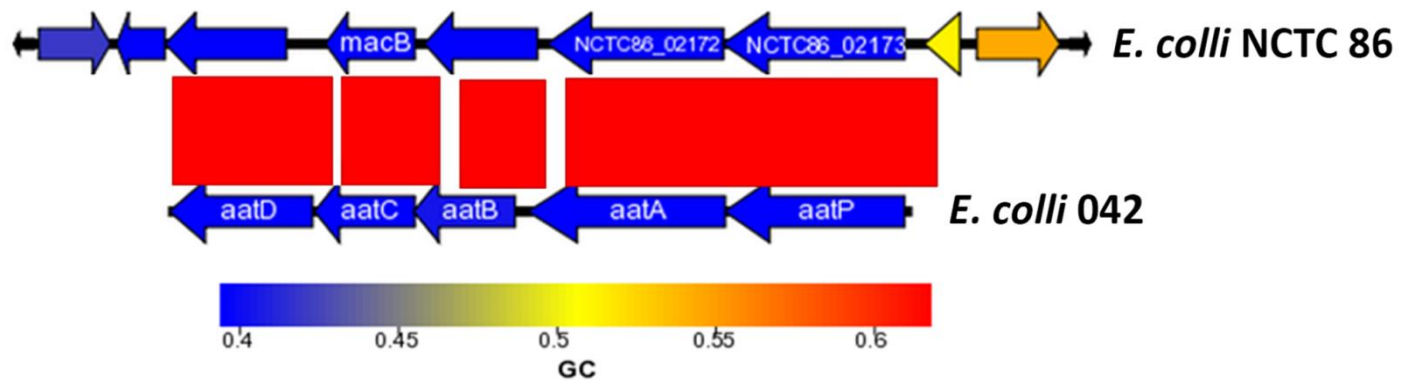
Supplemental Figure 4: Comparison of the Yersiniabactin locus. Alignment of the Yersiniabactin operon from *Yersinia pestis* with *E. coli* NCTC 86, *E. coli* APEC O1, *E. coli* EAEC 042 *E. coli* K-12. Alignments reveal the locus is present in all strains apart from in the *E. coli* K12. The yersiniabactin locus is located on ROD 5 in *E. coli* NCTC 86. CDSs are indicated by arrows coloured according to the GC content of the gene revealing a high GC content.



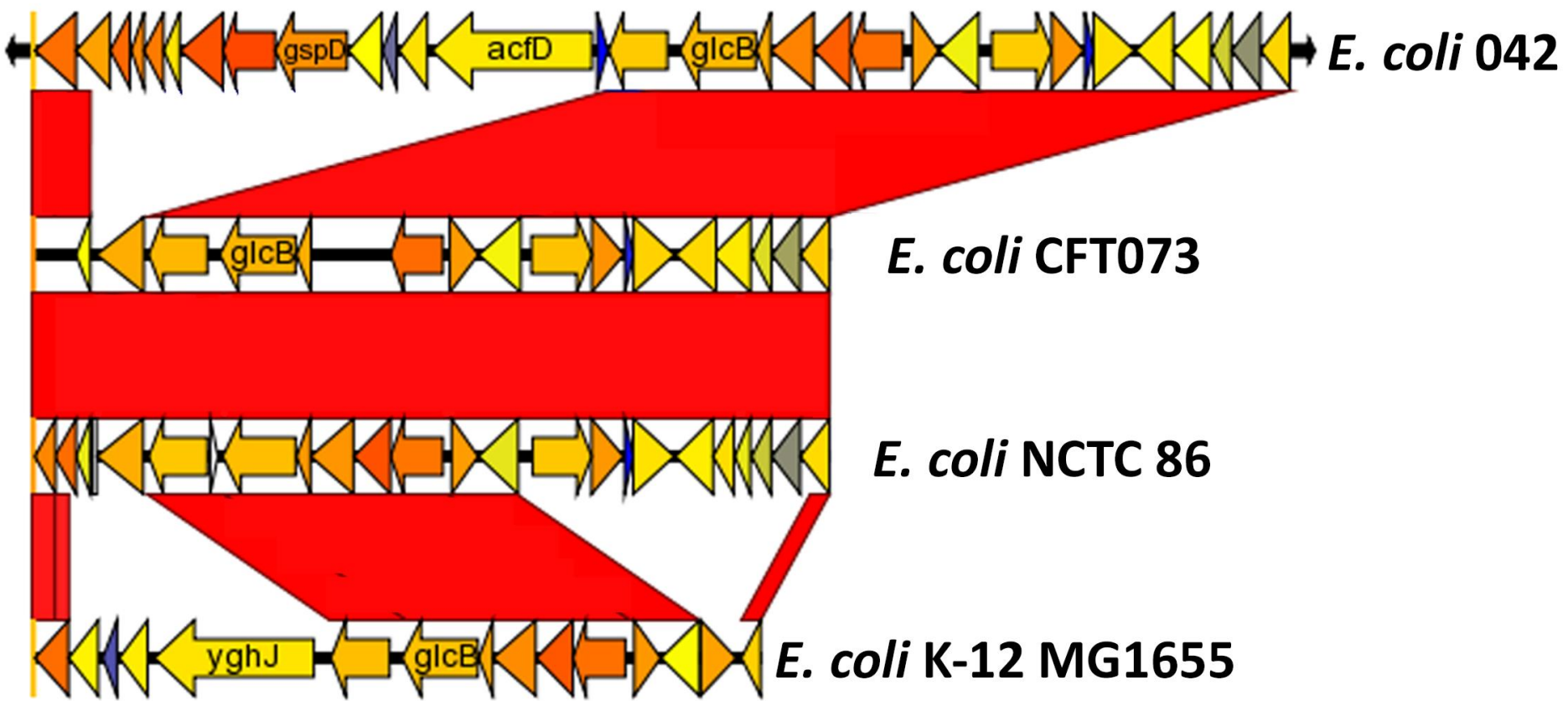
Supplemental Figure 5: Alignment of the *sil* locus confers resistance to silver. *E. coli* NCTC 86 *sil* locus that confers resistance to silver. Alignment of the *sil* locus shows that it is present in *E. coli* 55989, C str. ATTC 8739, H10407 as well as *E. coli* NCTC 86 where it is located on ROD 36. The *sil* operon is widespread and not confined to *E. coli*, it is also present in *Cronobacter sakazakii* and *Enterobacter cloacae*. CDSs are indicated by arrows coloured according to the GC content of the gene.



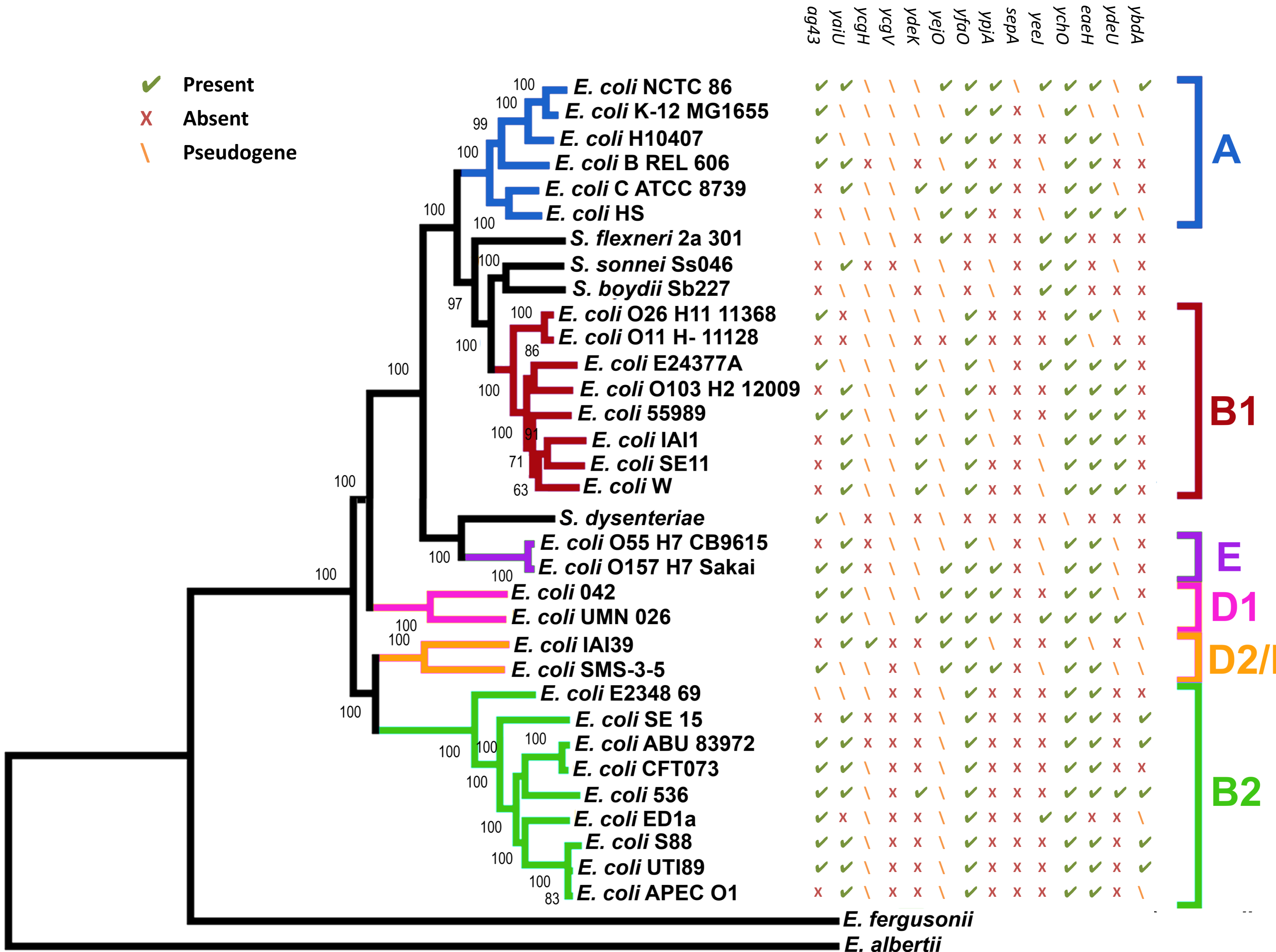
Supplemental Figure 6: Genomic architecture of the Type 1 Secretion System. Alignment of the *E. coli* NCTC 86 Type 1 secretion system to the EAEC 042 *aat* gene cluster. The loci share 63 - 81 % amino acid sequence identity and appear to differ in the efflux transporter/ *aatB* gene. CDSs are indicated by arrows coloured according to the GC content of the gene revealing a low GC content.



Supplemental Figure 7: Alignment Type 2 Secretion System *E. coli* NCTC 86 with *E. coli* 042, CFT073 an K-12. The *E. coli* NCTC 86 the type 2 secretion system is in a later stage of degradation in compared to *E. coli* K-12 however it does appear to still possess a set of acyl-CoA synthetase and permease genes absent from *E. coli* K-12 and appears to be in an identical state as the *E. coli* CFT073 genome. CDSs are indicated by arrows coloured according to the GC content of the gene.



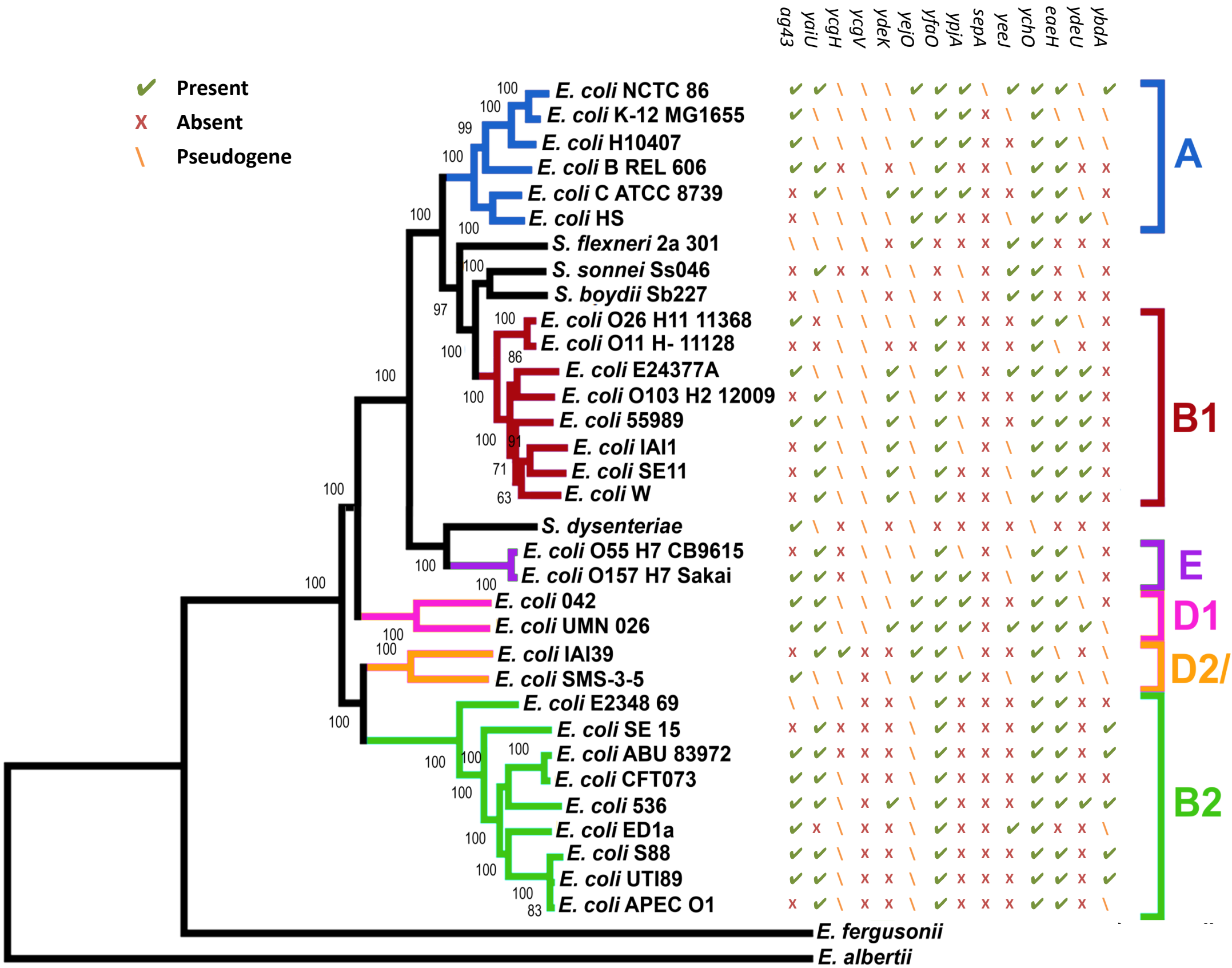
Supplemental Figure 8: Phylogenetic distribution of members of the Type 5 secretion system present in NCTC 86. The Autotransporters are differentially represented amongst the *E. coli* phylogeny, though several members of this group show phylogenetic clustering. Their presence in both commensal and pathogenic lineages suggesting autotransporters are not directly responsible for the ability of *E. coli* to mediate disease.



0.005

Supplemental Figure 9: Type 6 Secretion System. Alignment *E. coli* NCTC 86 with other *E. coli* that possess the Type 6 secretion system. *E. coli* NCTC 86 has the strongest homology with *E. coli* 55989. CDSs are indicated by arrows coloured according to the GC content of the gene

- ✓ Present
- ✗ Absent
- ∖ Pseudogene



0.005