

CORRECTION

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Correction: Genomic islands and plasmid borne antimicrobial resistance genes drive the evolution of high-risk, ST-131 uropathogenic *E. coli* NS30

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Following publication of the original article [1], it was reported that, due to a figure processing error, the gene numbering was missing in Figs. 3, 4, 5 and 6.

The correct figures are given in this Correction and the originally published figures are available in the Supplementary material.

The original article has been corrected.

The original article can be found online at <https://doi.org/10.1186/s12864-025-12308-z>.

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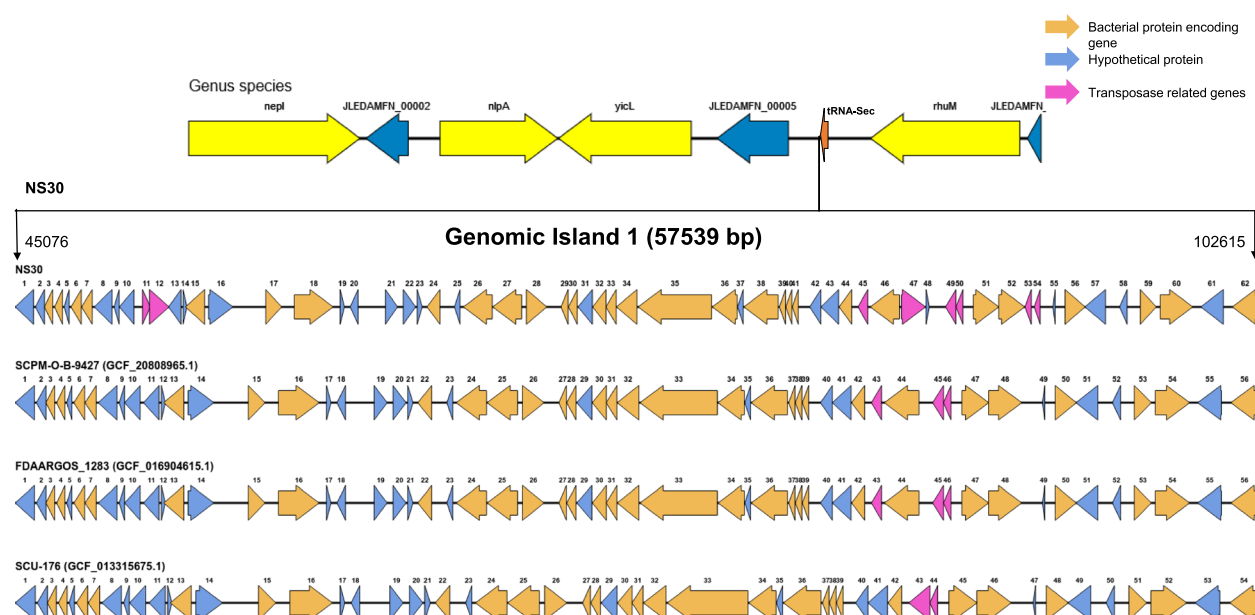


Fig. 3 GI-1 of NS30 has its origins from other STs. First ribbon represents the GI-1 of NS30, while the other three represent its homologs from ST678, ST144 and ST550. GI-1 of NS30 harboured efflux genes such as *emrE*, *qacN* and a type IV TA system, along with ORFs of unknown function. Additional pink arrows in the first ribbon view represent extra copies of IS3 and IS4, found in GI-1 of NS30. The labelling of all GI-1 ORFs is presented in Supplementary Table 2

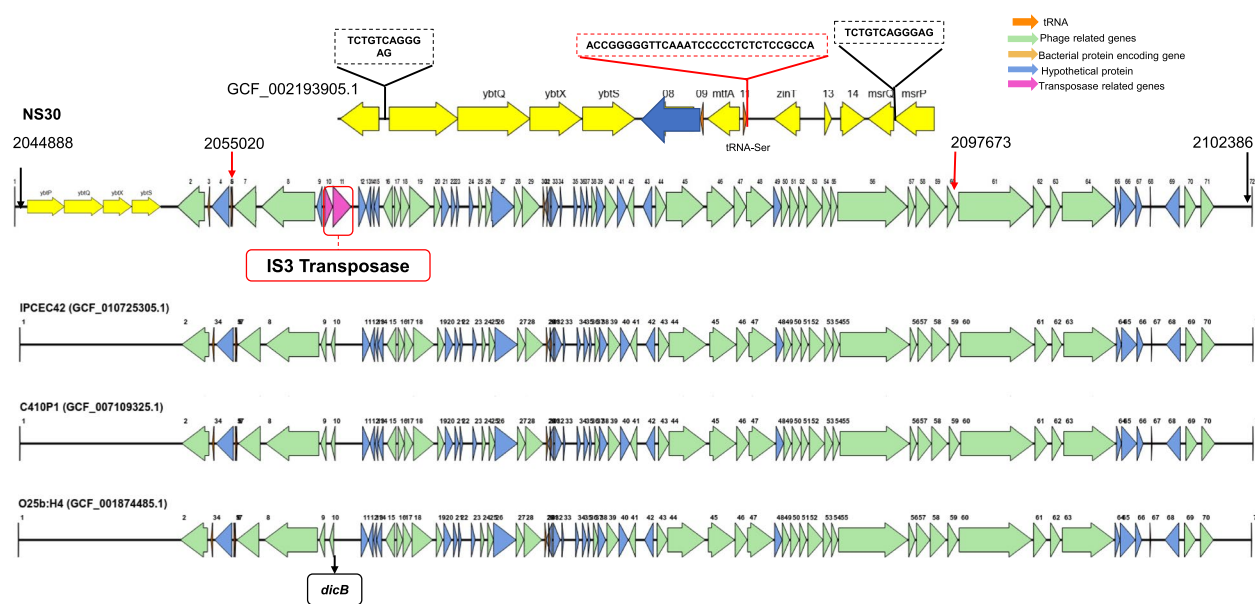


Fig. 4 GI-2 has an insertionally inactivated *dicB*. GI-2, a lambdoid Enterobacteria phage mEp460, is located downstream of *tRNA-Ser*. The red arrows represent the inner pair of *att* sites and the black arrows represent the outer pair of *att* sites. Sequences in the black boxes represent the outer *attL* and *attR* sites, while the sequence in the red dotted box represents the *att* site that was split for the insertion of GI-2. The first ribbon represents NS30, followed by its homologs from ST131 genomes. The *dicB* gene in GI-2 of NS30 is disrupted by an IS3 transposase indicated in red box. ORF data of GI-2 has been provided in Supplementary Table 3

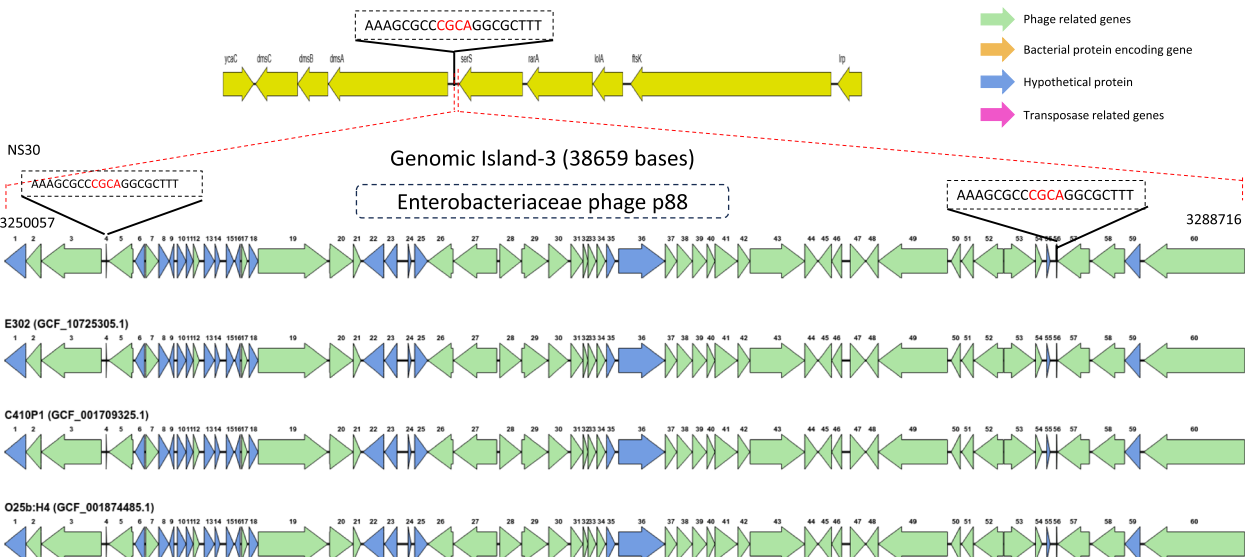


Fig. 5 GI-3 is a conserved phage. Escherichia p88 phage has inserted itself adjacent to SerS Serine Recombinase. The attL and attR sites are inverted repeats, except for the portion colored in red. GI-3 was present in other ST131 UPEC and is conserved across all the compared genomes, without any alterations. C410P1 and O25b:H4 genomes harboured both GI-2 and GI-3. The ORF data is provided in Supplementary Table 4

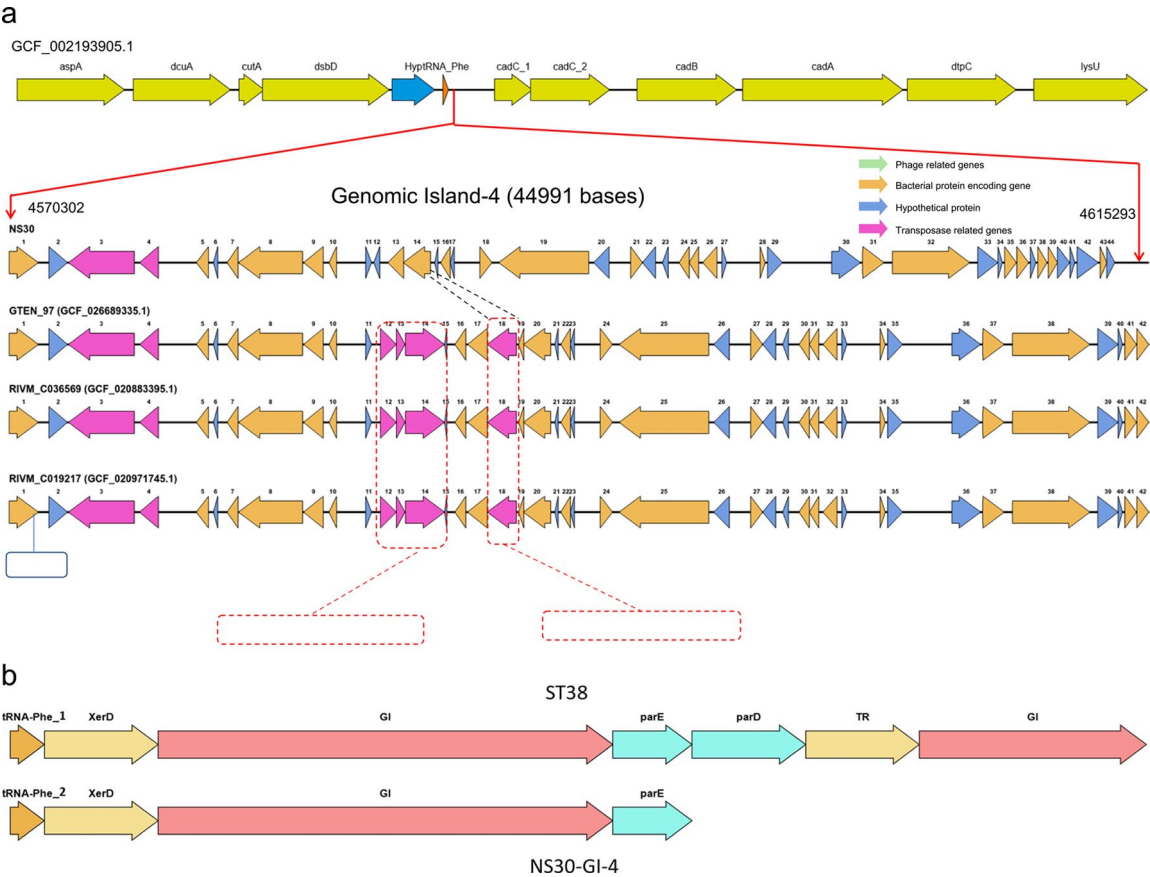


Fig. 6 a GI-4 is a PAI acquired from ST38 genomes. GI-4 is a PAI, inserted next to a tRNA-Phe Locus. The dotted lines represent the loci where GI-4 of NS30 lost the transposases IS66 and IS21. NS30's GI-4 is represented by the first ribbon and its homologs from ST38 genomes are represented as the other three ribbons. An orphan type II toxin parE was found at the 3' end of GI-4. A xerD recombinase is present at the 5' end, adjacent to tRNA-Phe. The ORF annotation of GI-4 is available in Supplementary Table 5. **b** GI-4 of NS30 is part of a larger PAI found in ST38 strains. ST38 genomes harbour a 110 Kb genomic region adjacent to tRNA-Phe. This region comprises a parDE TA module separating two GIs. GI-4 of NS30, along with an orphan parE toxin has inserted itself in a different tRNA-Phe locus, compared to its location in ST38 genomes

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12864-025-12413-z>.

Supplementary Material 1. Originally published figures.

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Reference

1. Peketi ASK, Nagaraja V, Bulagonda EP. Genomic islands and plasmid borne antimicrobial resistance genes drive the evolution of high-risk, ST-131 uropathogenic *E. coli* NS30. *BMC Genomics*. 2025;26:1065. <https://doi.org/10.1186/s12864-025-12308-z>.