

Description of Additional Supplementary Files:

Supplementary Data 1: Report of the plasmid sequences (n=4,569) (4,071 circular and 498 non-circular) assigned to a particular plasmid type (pT) after quality control. Each plasmid sequence is uniquely identified based on the 'Plasmid_ID' column and in the column 'Cluster' we provide its pT assignment. To contextualize each plasmid sequence with other typing schemes, we provide its PlasmidFinder, pmlst, MOBSuite, antibiotic resistance (reported by AMRFinderPlus) and virulence (ecoli_vf database) annotations.

Supplementary Data 2: Plasmid type (pT) statistics and contextualization. The number of sequences assigned to each type is reported after filtering out sequences initially predicted to belong to it, but differing by more than 2 standard-deviation of the average plasmid length reported. The reported predominant genes/categories are reported if they had a frequency of at least 0.3 and their exact frequency is reported in parenthesis. The name of the virulence genes reported by ecoli_vf (indexed in Abricate) was curated according to the annotation of well-known ExPEC plasmids

Supplementary Data 3: Acquisition dates of the most prevalent plasmid types among the four major ExPEC clones. Each acquisition is associated with a branch, but the exact time of introduction is unknown. For this reason, acquisitions are given as an interval date corresponding to the internal nodes flanking the branch. For each reported date, we provide the 95% confidence interval (CI) given by BactDating.

Supplementary Data 4: Isolates used in experiments. Internal collection numbers and NORM sequence identifiers (or alternative identifiers for lab strains) are given for each isolate, together with ST and clade information. Presence of a pColV plasmid is indicated according to its pT classification. Presence or absence of genes encoding microcin V (cvaC) and colicin Ia (Colla, also known as pECS88_0104) is indicated as + and -, respectively. The presence of genes encoding additional bacteriocins is indicated in the format "gene (location)". Presence or absence of genes encoding distinct siderophores is indicated respectively as + and -. Experimentally tested sensitivity to microcin V and colicin Ia is indicated as sensitivity (S) or insensitivity (I).

Supplementary Data 5: ENA genome accessions of the nucleotide sequences generated in this study.