Figure S1: Long read alignments to linear plasmids and one representative circular plasmid per Klebsiella genome. The total number of alignments shown is capped at 100 to improve visualisation. The plasmid sequence is the thick black line at the bottom, and reads aligning to the plasmid are shown in green if the alignment starts at the beginning or end of the plasmid sequence, or pink if the alignment starts elsewhere. Segments coloured dotted grey indicate regions of the read that do not align.
Figure S2: Maximum-likelihood phylogenies of type II toxin-antitoxin systems in various bacterial taxa. 

**a. RelE toxin**

- Mycobacterium tuberculosis H37Rv*
- Yersinia pestis*
- Yersinia pseudotuberculosis
- Photorhabdus luminescens*
- Escherichia coli K-12
- Salmonella enterica
- Mycobacterium tuberculosis CDC1551
- Staphylococcus aureus
- Shigella flexneri
- Pseudomonas aeruginosa
- Pseudomonas putida*
- Bordetella bronchiseptica*
- INF019 (A)
- INF102 (C)
- 1194/11 (B)

**b. RelB antitoxin**

- INF007 (D)
- Salmonella enterica
- Pseudomonas aeruginosa
- Escherichia coli K-12
- Pseudomonas putida*
- Staphylococcus aureus
- Shigella flexneri
- Mycobacterium tuberculosis CDC1551
- Escherichia coli CTF073
- Pseudomonas aeruginosa
- Pseudomonas putida*
- Bordetella bronchiseptica*
- INF019 (A)
- INF102 (C)
- 1194/11 (B)

**c. VapC toxin**

- Escherichia coli
- Ralstonia solanacearum
- Xanthomonas axonopodis
- Bordetella parapertussis
- Streptomyces avermitilis
- Haemophilus influenzae
- Salmonella enterica
- Leptospira interrogans
- INF352 (E)
- Neisseria meningitidis

**d. VapB antitoxin**

- Bordetella parapertussis
- Streptomyces avermitilis
- Escherichia coli
- Haemophilus influenzae
- Salmonella enterica
- Xanthomonas axonopodis
- Leptospira interrogans
- INF352 (E)
- Neisseria meningitidis

Species with asterisks indicate that these sequences come from the HigBA subfamily. Phylogroups for each linear plasmid are shown in brackets. Phylogenies for RelE toxins, RelB antitoxins, VapC toxins, and VapB antitoxins are shown in panels a, b, c, and d, respectively.
Figure S3: TIR sequence alignments within each phylogroup. Linear plasmid sequences are clustered by gene content, with the phylogroup indicated by tip colour and coloured as per legend. TIR sequences are aligned within each phylogroup, where each colour represents a different nucleotide as per legend. Colour intensity indicates level of conservation at that position (pale=low; intense=high).
Figure S4: Cluster dendrogram of trinucleotide frequencies for the 12 linear plasmids and their host Klebsiella chromosomes. Trinucleotide frequencies were clustered using hclust. Tips are coloured by phylogroup or chromosome (as per legend).