1   Supplementary information

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3   Next generation ESKAPE-E superbugs: identifying transmissible locus of stress
4   tolerance and antibiotic resistance in pandemic bacterial lineages

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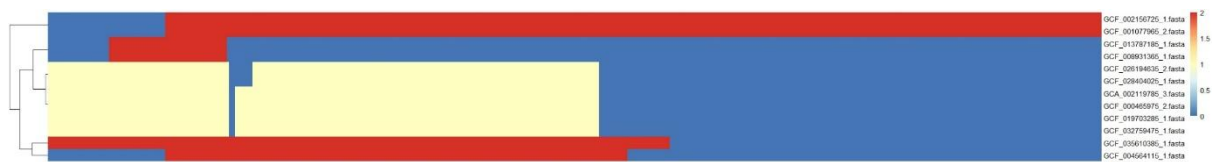
14   *Corresponding author: steven.djordjevic@uts.edu.au
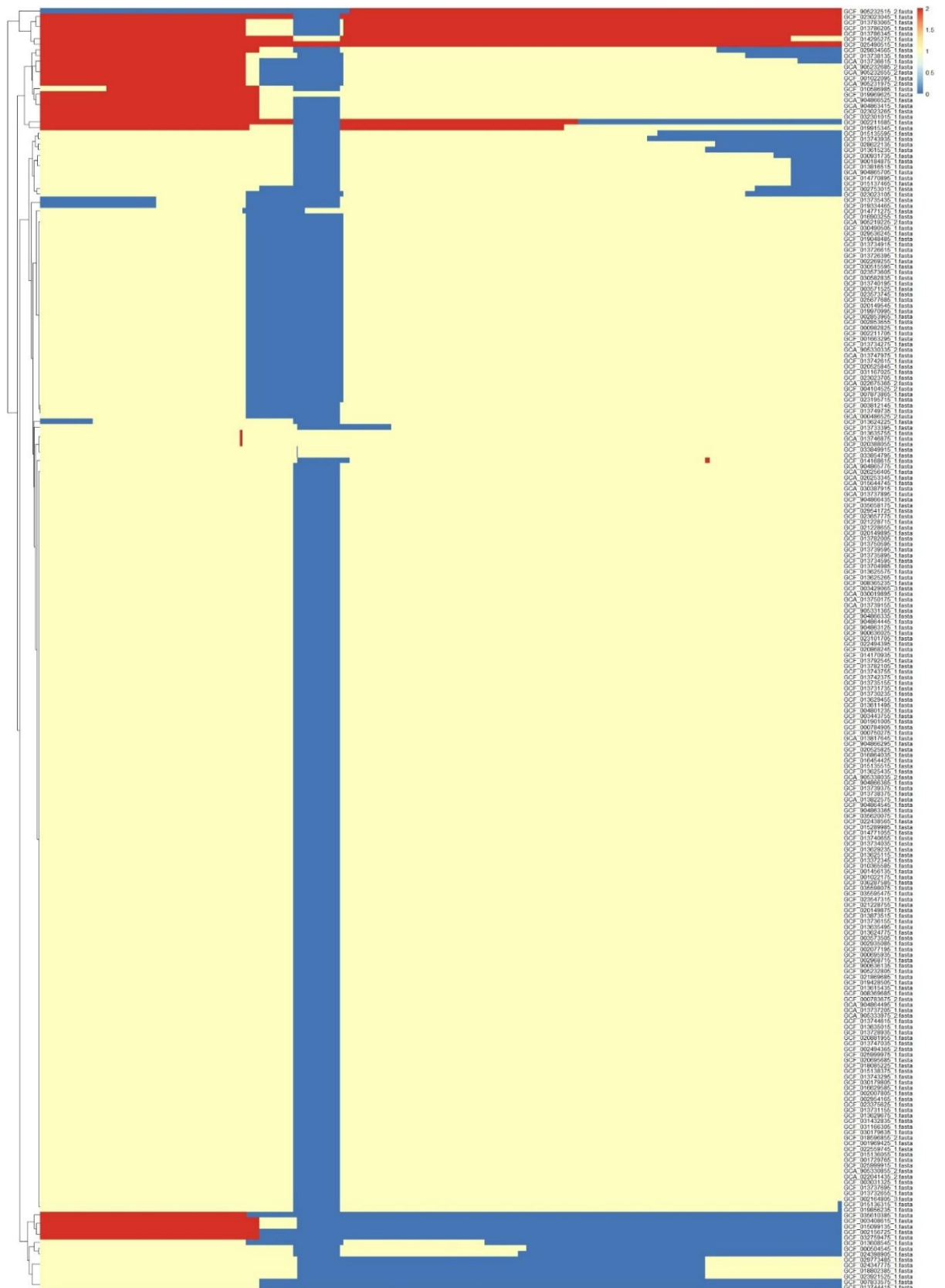
Supplementary Figure 1: tLST1 mapping figure for assemblies with more than one hit. Regions of BLUE colour represent NO hit, regions of YELLOW colour represent SINGLE hit and regions of RED colour represent DOUBLE hit. Assemblies are hierarchically clustered.
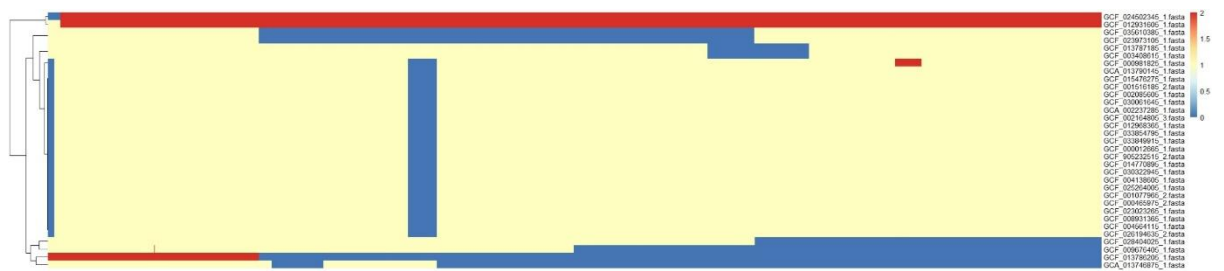
Supplementary figure 2: tLST2 mapping figure for assemblies with more than one hit. Regions of BLUE colour represent NO hit, regions of YELLOW colour represent SINGLE hit and regions of RED colour represent DOUBLE hit. Assemblies are hierarchically clustered.

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26 **Supplementary Figure 3: tLST3a mapping figure for assemblies with more**
27 **than one hit.** Regions of BLUE colour represent NO hit, regions of YELLOW
28 colour represent SINGLE hit and regions of RED colour represent DOUBLE hit.
29 Assemblies are hierarchically clustered.

30

31   **Supplementary Figure 4: tLST3b mapping figure for assemblies with more**

32   **than one hit.** Regions of BLUE colour represent NO hit, regions of YELLOW

33   colour represent SINGLE hit and regions of RED colour represent DOUBLE hit.

34   Assemblies are hierarchically clustered.
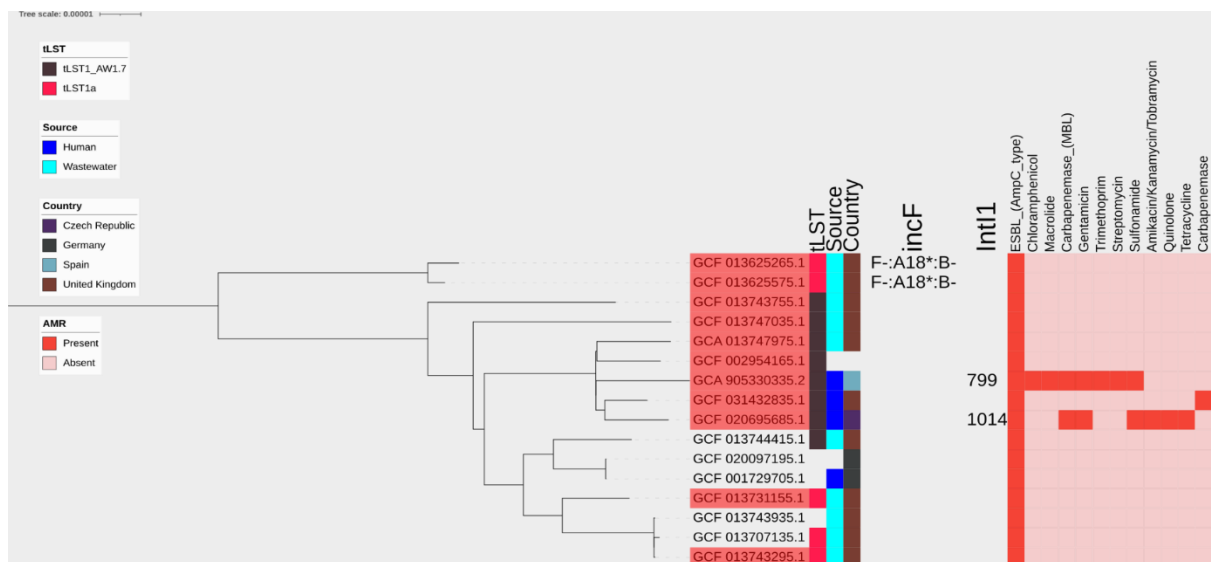
Supplementary Figure 5: Midpoint rooted, core genome phylogenetic tree of E. hormaechei ST108. Highlighted in red leaf names are complete genomes from earlier part of study. Coloured strips present, tLST variant, source and country of origin. Followed by IncF RST and length of IntI1 gene detected. Red heatmap represent antimicrobial resistance to groups of antibiotics.

41   Information of Supplementary Data:

42   **Supplementary data 1. Set of tables containing information about collection of**
43   **complete genomes used in this study.** A) Metadata of all complete genomes acquired
44   alongside as genome assemblies, after processing for ease of read and use. B)
45   Taxonomy information of complete genomes. C) Complete BLAST results of tLST
46   screening of all complete genomes. D) pMLST typing results. E) MLST results of tLST
47   positive genomes.

48   **Supplementary data 2. Set of tables containing information about *K. pneumoniae***
49   **ST20 isolates.** A) Metadata information of isolates. B) AMR profiling output from
50   AbritAMR. C) VAG and other resistances profiling output from AbritAMR. D) Kleborate
51   output.

52   **Supplementary data 3. Set of table containing information about *P. aeruginosa***
53   **ST111.** A) Metadata information of isolates. B) AMR profiling output from AbritAMR. C)
54   VAG and other resistances profiling output from AbritAMR.

55   **Supplementary data 4. Set of table containing information about *E. coli* ST399.** A)
56   Metadata information of isolates. B) AMR profiling output from AbritAMR. C) VAG and
57   other resistances profiling output from AbritAMR.

58   **Supplementary data 5. Set of table containing information about *E. coli* ST635.** A)
59   Metadata information of isolates. B) AMR profiling output from AbritAMR. C) VAG and
60   other resistances profiling output from AbritAMR.