

1 **Supplementary Figure 1. Genetic characteristics of *Escherichia coli* carriage**
2 **isolates from A. subject IHD813; B. subject IHD1178; C. subject IHD717.**
3 Black circles at tree nodes indicate bootstrap values of > 95%. Colored circles
4 represent genetic similarity of isolates within STs, and are sized and labeled
5 according to the number of isolates sharing identity. Branches between circles
6 represent a core, single nucleotide variant. Labels adjacent to circles represent
7 *bla*_{CTX-M} variants (colored by variant type). Within-host resistance and virulence
8 gene profiles for all isolates in this individual are represented in the heatmap at the
9 bottom of each panel, with colored blocks representing presence, and gray blocks
10 absence of a gene. Resistance genes are represented as red blocks; virulence
11 factors are colored by functional category (sea-green = adhesins; olive = toxins;
12 light blue = nutritional factors; dark blue = immune evasion; lilac =
13 miscellaneous). Isolates from within the cefpodoxime zones are labelled _1-8;
14 from outside the zones _9-16, where applicable.

- Subject IHD717**
- 16 isolates
 - 5 STs
 - No CTX-M/ESBL positive isolates

- *Within-host diversity*
- Core variable sites = 70,933

3,100 SNVs

11,315 SNVs

