Table S1: Genome quality statistics for all the assembled genomes

| Isolate no. | No. of contigs | Largest contig | Size(bp) | GC (%) | N50 | L50 | Genome fraction (%) |
|-------------|---------------|---------------|---------|--------|-----|-----|-------------------|
| S44         | 40            | 517772        | 5482928 | 57.27  | 308712 | 7   | 92.224           |
| S54         | 46            | 1082409       | 5691332 | 57.15  | 435362 | 4   | 98.04            |
| S55         | 79            | 1010433       | 5752447 | 56.75  | 345690 | 6   | 92.898calc       |
| S56         | 86            | 992865        | 5708668 | 57.05  | 226397 | 5   | 90.508           |
| S57         | 101           | 605472        | 5718919 | 56.86  | 233432 | 9   | 90.207           |
| S58         | 104           | 584373        | 5839331 | 56.58  | 306551 | 8   | 91.983           |
| S59         | 70            | 698263        | 5769731 | 56.77  | 350190 | 6   | 93.125           |
| S60         | 72            | 851986        | 5714482 | 56.83  | 286886 | 6   | 93.1             |
| S61         | 34            | 512126        | 5352578 | 57.8   | 363661 | 7   | 33.733           |
| S62         | 2947          | 86358         | 7457857 | 56.15  | 4818  | 346 | 92.984           |
| S63         | 2187          | 71415         | 7190142 | 56.28  | 11256 | 176 | 93.917           |
| S65         | 83            | 698263        | 5745130 | 56.78  | 287340 | 7   | 93.105           |
| S66         | 335           | 357715        | 6494540 | 56.07  | 95700 | 19  | 93.42            |
| S67         | 115           | 504304        | 6062433 | 56.53  | 200969 | 11  | 93.098           |
Table S2: Sequence types of isolates based on MLST scheme

| Isolate | Chr_ST | gapA | infB | mdh | pgi | phoE | rpoB | tonB |
|---------|--------|------|------|-----|-----|------|------|------|
| S44     | ST86   | 9    | 4    | 2   | 1   | 1    | 1    | 27   |
| S54     | ST23   | 2    | 1    | 1   | 1   | 9    | 4    | 12   |
| S55     | ST2096 | 1    | 6    | 1   | 1   | 1    | 46   | 1    |
| S56     | ST147  | 3    | 4    | 6   | 1   | 7    | 4    | 38   |
| S57     | ST43   | 2    | 6    | 1   | 5   | 11   | 1    | 15   |
| S58     | ST231  | 2    | 6    | 1   | 3   | 26   | 1    | 77   |
| S59     | ST2096 | 1    | 6    | 1   | 1   | 1    | 46   | 1    |
| S60     | ST2096 | 1    | 6    | 1   | 1   | 1    | 46   | 1    |
| S61     | ST3857 | 18   | 23   | 56  | 260 | 25   | 92   | 548  |
| S62     | ST147-1LV | 3  | 4    | 6   | 1   | -    | 4    | 38   |
| S63     | ST336-1LV | 2 | 1    | 1   | 1   | 1    | 72   | 4    | -    |
| S65     | ST2096 | 1    | 6    | 1   | 1   | 1    | 46   | 1    |
| S66     | ST15   | 1    | 1    | 1   | 1   | 1    | 1    | 1    |
| S67     | ST15-1LV | 1 | 1    | 1   | 1   | 1*   | 1    | 1    |
Data Availability:

The genome sequenced files are submitted to NCBI SRA under the accession number SRR17640814, SRR17640813, SRR17640812, SRR17640811, SRR17640810, SRR17640809, SRR17640808, SRR17640807, SRR17640806, SRR17640805, SRR17640804, SRR17640803, SRR17640802, SRR17640801

Table S3: List of highly mutated genes with their respective functions (as found in UniProt and NCBI)

| Gene Names   | Function                                                                 |
|--------------|--------------------------------------------------------------------------|
| KP1_0403     | Putative secretion ATPase                                                |
| KP1_4102     | hypothetical protein                                                      |
| fimD         | Putative fimbrial usher protein                                           |
| mobB         | Mobilization protein, GTP binding                                         |
| wzi          | Surface assembly of capsule                                               |
| wzc          | ATP Binding and protein tyrosine kinase activity                          |
| KP1_0410     | Fimbrial biogenesis outer membrane usher protein                          |
| ardC         | Single-stranded DNA binding                                              |
| wza          | Polysaccharide transmembrane transporter activity                         |
| KP1_4970     | AsmA2 domain-containing protein YhdP                                     |
| RmpA         | DNA binding                                                              |
| WcaJ         | Transferase activity                                                     |
| entA         | 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity                 |
| entD         | holo-[acyl-carrier-protein] synthase activity, magnesium ion binding      |
| entC         | isochorismate synthase activity                                           |
