Table S1. Source and origin of *Enterobacteriaceae* isolates obtained from a pig farm in Shanghai, China

| Source                        | No. of samples | No. of isolates (no. of isolates obtained from agar with tigecycline) | *E. coli* | *E. cloacae* complex | *C. freundii* | *L. adecarboxylylate* | *P. cibarius* | *A. veronii* |
|-------------------------------|----------------|------------------------------------------------------------------------|-----------|---------------------|---------------|-----------------------|---------------|--------------|
| Pig feces                     | 51             | 37(1)                                                                  | 3(2)      | 1                   |               |                       |               |              |
| Pig nasal swabs               | 10             | 4                                                                      | 2(1)      |                     |               |                       |               |              |
| Feed                          | 24             | 3                                                                      | 7(1)      | 1                   | 2             |                       |               |              |
| Pig drinking water            | 17             |                                                                        | 3         |                     |               |                       | 1             |              |
| Vegetables                    | 5              |                                                                        | 4         |                     |               |                       |               |              |
| Vegetable field soil          | 5              |                                                                        | 2         |                     |               |                       |               |              |
| Floor swabs from pens         | 8              |                                                                        | 1         |                     |               |                       |               |              |
| Shoe sole from workers        | 9              |                                                                        |           |                     | 1             |                       | 1             |              |
| **Total**                     | **88**         | **45**                                                                 | **22**    | **3**               | **2**         | **1**                 | **1**         |              |

Table S2. Comparison between *E. hormaechei* strain SH19PTE2 and other tigecycline susceptible strains. The numbers depict amino acid differences using SH19PTE2 as a reference.

| Strains  | Species            | Accession no. | AcrA | AcrB | RamA | RamR | MarR | MarA | TolC |
|----------|--------------------|---------------|------|------|------|------|------|------|------|
| SH19PE4  | *E. hormaechei*    | PRJNA724799   | 1    | 0    | 0    | 0    | 0    | 1    | 1    |
| SH19PE5  | *E. hormaechei*    | PRJNA724799   | 1    | 0    | 0    | 0    | 0    | 0    | 1    |
| NCTC9394 | *E. cloacae*       | FP929040      | 0    | 3    | 0    | 0    | 0    | 0    | 0    |
| FY01     | *E. hormaechei*    | PRJNA623478   | 0    | 0    | 0    | 0    | 0    | 0    | 1    |
Table S3. MICs of tigecycline against parental strains and pUC57-*tet*(A)-variant transformations

| Strains                        | Tigecycline MIC (mg/L) |
|--------------------------------|------------------------|
| *E. coli* MG1655               | 0.5                    |
| MG1655-pUC57                   | 0.5                    |
| MG1655-pUC57-*tet*(A)-variant | 4                      |
| *E. hormaechei* SH19PE5        | 0.5                    |
| SH19PE5-pUC57                  | 0.5                    |
| SH19PE5-pUC57-*tet*(A)-variant | 4                      |
| *E. cloacae* CMCC45301         | 0.25                   |
| CMCC45301-pUC57                | 0.25                   |
| CMCC45301-pUC57-*tet*(A)-variant | 1                   |
| *Salmonella* Typhimurium SL1344 | 0.5                    |
| SL1344-pUC57                   | 0.5                    |
| SL1344-pUC57-*tet*(A)-variant  | 2                      |
| *K. pneumoniae* CMCC46117      | 0.125                  |
| CMCC46117-pUC57-*tet*(A)-variant | 1                    |
Figure S1. Sequence comparison of pYUSHP6-tetX in this study with other IncFIA18/IncFIB(K)/IncX1 plasmids pNT1F31-tetX4 (CP045188, pig), pYPE3-92k-tetX4 (CP041453, pork), pRF148-2_101k_tetX (MT219817, pig), pZF31-tetX-119kb (CP047460, pig), p54-tetX (CP041286, cow), pYPE12-101k-tetX4 (CP041443, pork), pRF10-1_119k_tetX (MT219823, pig), pRF108-2_97k_tetX (MT219820, pig), pRF148-1_119k-tetX (MT219818, pig), pRF52-1_119k_tetX (MT219819, pig), pRW8-1_122k_tetX (MT219826, wastewater), and pSTB20-1T (CP050174, pig) in China using BRIG.