### a

| Allele          | Forward primer (5' to 3') | Reverse primer (5' to 3') | Notes                                           |
|-----------------|---------------------------|---------------------------|-------------------------------------------------|
| blaKPC          | CCATCCGTACGCAAAAT         | TTATCAGTATTGAGACGCG       | For figure 2e and Additional file 2b/2c         |
| xylR-L4         | ACGTCCACCGACTACCA         | CCCGACCTCCTCTTGAAG        | For figure 5f                                   |
| xylR-WT (control for L4) | ACGTCCACCGACTACCG   | CCCGACCTCCTCTTGAAG        | For figure 5f                                   |
| xylR-Tn1        | GGTCCTATATCGGCAAGCG      | GAACACCCGAGAAAAATCATCG    | For figure 5c. Use PCR elongation time = 20 sec  |
| xylR-WT (control for Tn1) | GGTCCTATATCGGCAAGCG | GAACACCCGAGAAAAATCATCG    | For figure 5c. Use PCR elongation time = 20 sec  |

### b

| Bacterial strains | Description                                               | Source                                      |
|-------------------|-----------------------------------------------------------|---------------------------------------------|
| MKP103            | K. pneumoniae, ST258, blaKPC-, derived from KPNIH1 strain | (Ramage et al. 2017)                       |
| KPNIH1            | K. pneumoniae patient isolate, ST258, blaKPC+            | (Conlan et al. 2014)                       |
| KPNIH29           | K. pneumoniae patient isolate, ST1518, blaKPC+           | (Conlan et al. 2014)                       |
| KPNIH27           | K. pneumoniae patient isolate, ST34, blaKPC+             | (Conlan et al. 2014)                       |
| CRE-15            | K. pneumoniae patient isolate, ST45, blaKPC+             | NCBI accession: SAMN04014967                |
| ECONIH1           | E. coli patient isolate, ST648, blaKPC+                  | (Conlan et al. 2014)                       |
| ECONIH2           | E. coli patient isolate, ST127, blaKPC+                  | (Hardiman et al. 2016)                     |
| ECNIH6            | E. cloacae patient isolate, ST191, blaKPC+               | (Chen et al. 2017)                         |
| ECNIH7            | E. cloacae patient isolate, ST53, blaKPC+                | (Chen et al. 2017)                         |
| xylR-L1           | K. pneumoniae, from evolution lineage 1, contains a missense SNP at xylR gene | This study                                 |
| xylR-L2           | K. pneumoniae, from evolution lineage 2, contains a missense SNP at xylR gene | This study                                 |
| xylR-L3           | K. pneumoniae, from evolution lineage 3, contains a missense SNP at xylR gene | This study                                 |
| xylR-L4           | K. pneumoniae, from evolution lineage 4, contains a missense SNP at xylR gene | This study                                 |
| xylR-L5           | K. pneumoniae, from evolution lineage 5, contains a missense SNP at xylR gene | This study                                 |
| xylR-Tn1          | K. pneumoniae, loss-of-function mutant of xylR gene, from MKP103 transposon library #KP10497 | (Ramage et al. 2017)                       |
| xylR-Tn2          | K. pneumoniae, loss-of-function mutant of xylR gene, from MKP103 transposon library #KP10499 | (Ramage et al. 2017)                       |