

## **Supplementary data index:**

- **Table S1:** Genome assembly statistics.
- **Table S2:** List of publicly available genomes included in this study.
- **Table S3:** Predicted plasmid information including plasmid id, size (bp), replicon and relaxase types.
- **Table S4:** Results of ARGs screening on predicted plasmid sequences.

## **Supplementary figure titles and legends:**

**Figure S1: Species-wide ANI comparison.** Species-wide all-vs-all ANI comparison of all available genomes of *A. johnsonii*, PHSF-originating isolates (teal), and E154408A strain (orange). *A. johnsonii* reference genome and type strain are highlighted in respectively orange and purple.

**Figure S2: SNP analysis.** SNP analysis conducted on the 22 PHSF-derived isolates of *A. johnsonii* using 2P07AA strain as the earliest reference genome. PHSF-originating isolates form a tight cluster differing by 40–77 core SNPs, consistent with a dataset of closely related yet genetically distinct isolates.

**Figure S3: Species-wide characterization of putative virulence-associated genes of *A. johnsonii*.** Species-wide characterization of putative virulence-associated genes using VFDB of *A. johnsonii* (n= 112 strains), including PHSF-originating genomes (teal) and *A. johnsonii* E154408A (orange). *A. johnsonii* reference genome and type strain are highlighted in respectively red and purple. A total of eight known VFs were identified across all genomes. *pilT* and *pilG* were ubiquitously found in 100% (112/112) of the genomes and *ompA* was detected in 98.2% (110/112) of the genomes. *hcp/tssD* and *tssC* were detected in the same subset of 86.6% (97/112) of the genomes. *tssC* was individually detected in strains HNAS0100 (clinical source, Hunan, China) and GD03725 (environmental source, Pakistan). GD04060, GD04065 (both environmental source, US), and UN03-31 (human source, Shenzhen, China) strains were identified to encode the highest number of VFs (n=7). PHSF-originating *A. johnsonii* genomes were observed to carry the same subset of 6 VFs, namely *ompA*, *pilG*, *pilT*, *hcp/tssD*, *tssC*, and *tse4*. 3 VFs were identified in E154408A strain, namely *pilG*, *pilT*, and *ompA*.

**Figure S4: AST.** AST interpreted under EUCAST and CLSI guidelines to 12 clinically relevant antimicrobials including Piperacillin (PRL), Ampicillin-sulbactam (SAM), Cefepime (FEP), Cefotaxime (CTX), Imipenem (IPM), Meropenem (MEM), Gentamicin (GEN), Tobramycin (TOB), Amikacin (AK), Doxycycline (DO), Tetracycline (TET) and Ciprofloxacin (CIP). Strains E154408A, 3P2-tot-C, 3P5-tot-B, 3P6-tot-E, 3P8-tot-B, 3P04AE, 3P06AC, 3P06AD, 3P09AC showed intermediate susceptibility (highlighted yellow) to CTX. Five strains (i.e., 3P6-tot-E, 3P8-tot-B, 3P04AE, 3P06AD, 3P09AA) demonstrated intermediate susceptibility to piperacillin. *A. johnsonii* E154408A exhibited phenotypic resistance (highlighted in red) to tetracycline, piperacillin, cefepime, and ciprofloxacin as well as carbapenems imipenem and meropenem.