Fig. S1

Flowchart for verification of strain clonality using comparative genomic analysis

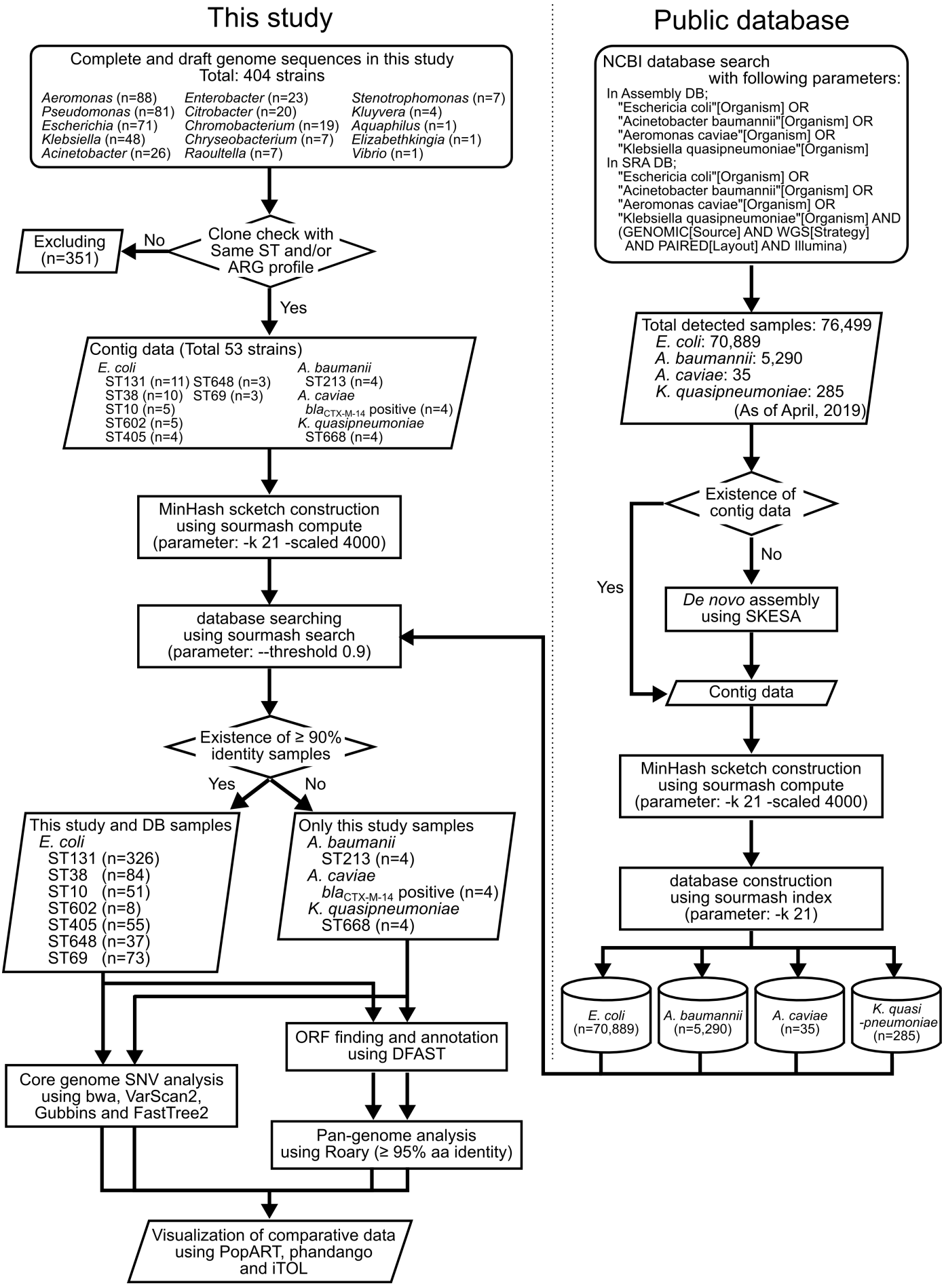
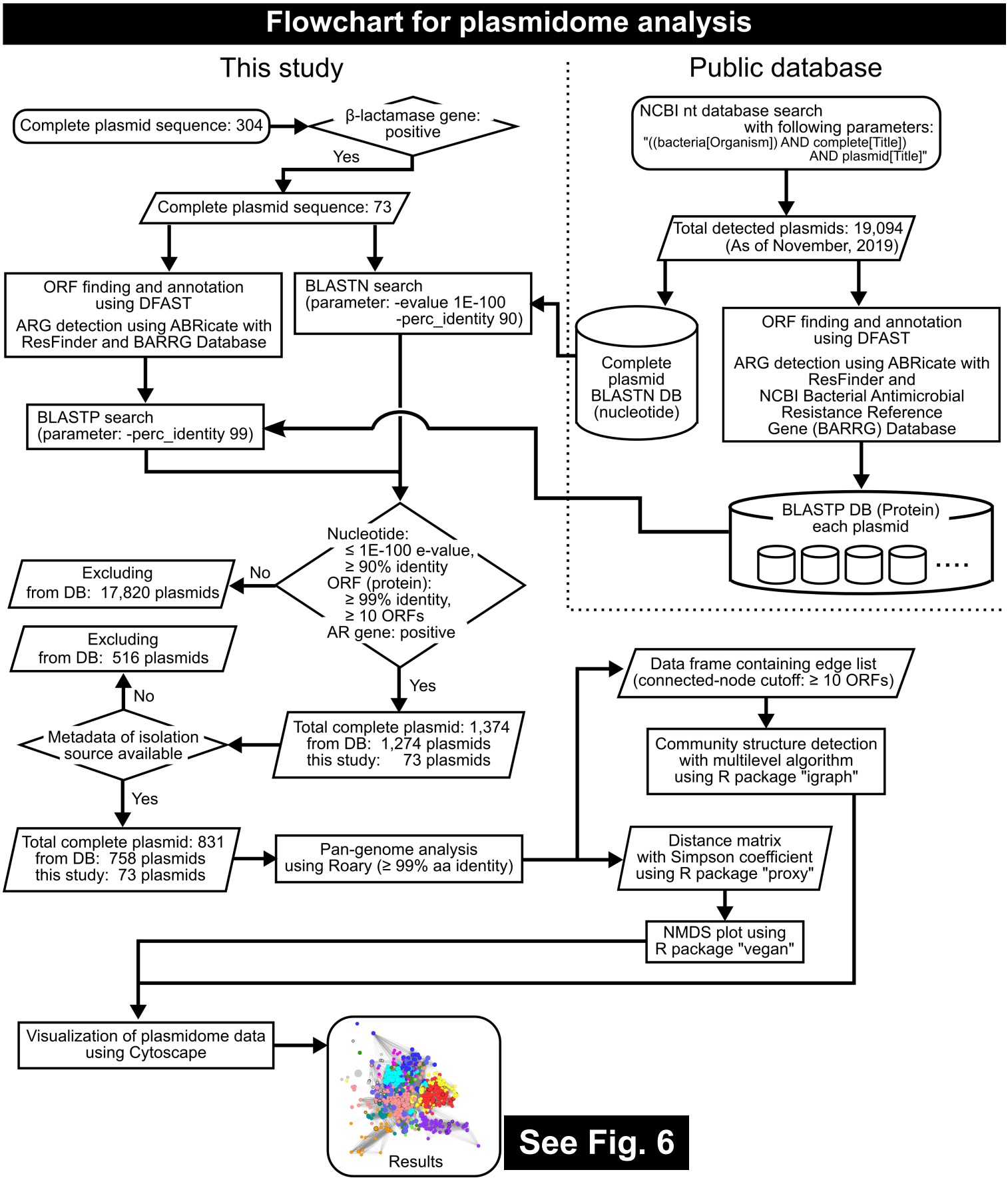


Fig. S2


Flowchart for plasmidome analysis
This study
Public database
Complete plasmid sequence: 304
β-lactamase gene: positive
Yes
Complete plasmid sequence: 73
ORF finding and annotation using DFAST
ARG detection using ABRicate with ResFinder and BARRG Database
BLASTN search (parameter: -evalue 1E-100 -perc_identity 90)
BLASTP search (parameter: -perc_identity 99)
NCBI nt database search with following parameters: "((bacteria[Organism]) AND complete[Title]) AND plasmid[Title]"
Total detected plasmids: 19,094 (As of November, 2019)
Complete plasmid BLASTN DB (nucleotide)
ORF finding and annotation using DFAST
ARG detection using ABRicate with ResFinder and NCBI Bacterial Antimicrobial Resistance Reference Gene (BARRG) Database
BLASTP DB (Protein) each plasmid
Nucleotide: ≤ 1E-100 e-value, ≥ 90% identity
ORF (protein): ≥ 99% identity, ≥ 10 ORFs
AR gene: positive
No
Excluding from DB: 17,820 plasmids
Yes
Total complete plasmid: 1,374
from DB: 1,274 plasmids
this study: 73 plasmids
Metadata of isolation source available
No
Excluding from DB: 516 plasmids
Yes
Total complete plasmid: 831
from DB: 758 plasmids
this study: 73 plasmids
Pan-genome analysis using Roary (≥ 99% aa identity)
Data frame containing edge list (connected-node cutoff: ≥ 10 ORFs)
Community structure detection with multilevel algorithm using R package "igraph"
Distance matrix with Simpson coefficient using R package "proxy"
NMDS plot using R package "vegan"
Visualization of plasmidome data using Cytoscape
Results
See Fig. 6