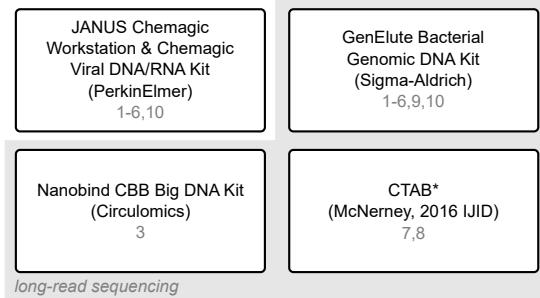


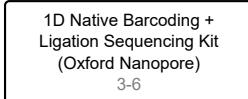
Genomic DNA Extraction



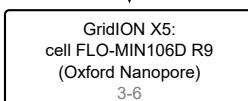
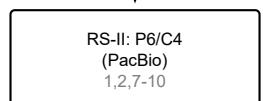
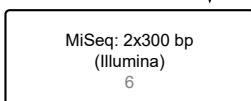
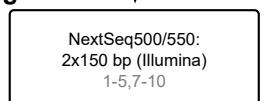
Assembly Groups

- L. pneumophila* (AUSMDU00010536); *L. monocytogenes* (AUSMDU00000224, AUSMDU00000235, AUSMDU00007774); *N. gonorrhoeae* (AUSMDU00010541); *N. meningitidis* (AUSMDU00005726); *S. enterica* (AUSMDU00010532, AUSMDU00010527, AUSMDU00010528, AUSMDU00010530, AUSMDU00010533); *S. pyogenes* (AUSMDU00010539)
- E. coli* (AUSMDU00002545); *S. enterica* (AUSMDU00010529), *S. pneumoniae* (AUSMDU00010538)
- E. coli* (AUSMDU00014361); *S. flexneri* (AUSMDU00010535); *S. sonnei* (AUSMDU00010534)
- S. enterica* (AUSMDU00010531, AUSMDU00008979)
- E. faecium* (AUSMDU00004167)
- K. pneumoniae* (AUSMDU00008079)
- M. chimaera* (AUSMDU00007395)
- M. tuberculosis* (AUSMDU00018547)
- N. meningitidis* (AUSMDU00010537)
- S. enterica* (AUSMDU00005056)

Library Construction



Sequencing

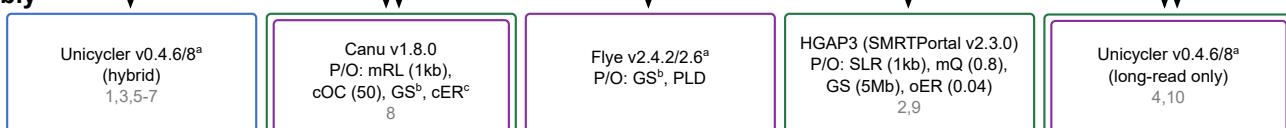


Quality Control

Depth: > 40x
Basecall Quality: > Q30
Match to expected organism: kraken2

Depth: >100x**
Basecall Quality: variable***
Match to expected organism: kraken2

Assembly



Hybrid

PacBio Only

Nanopore Only

Canu v1.8.0 P/O: mRL (1kb), cOC (50), GS^b, cER^c

Flye v2.4.2/2.6^a P/O: GS^b, PLD

HGAP3 (SMRTPortal v2.3.0)
P/O: SLR (1kb), mQ (0.8),
GS (5Mb), oER (0.04)

Unicycler v0.4.6/8^a
(long-read only)
4,10

Snippy v4.3/4^a
(correction)

Berokka v0.2.1
(circularisation)

Snippy v4.3/4.4^a (correction)

BridgeMapper (SMRTPortal v2.3.0)
(long-read correction)

Mauve 2.3.1 (assessment of assembly consensus)
Geneious v8.1.5 (orientation to start replicon^d)

Genome Characterisation: MLST: mlst v2.19.0; Resistome: abriTAMR v.0.2.2; *in silico* typing/serotyping:
emmytper v0.1.0 (*S. pyogenes*), Kleborate v0.3.0 (*K. pneumoniae*), legsta v0.3.2 (*L. pneumophila*),
LisSero v0.2 (*L. monocytogenes*), meningotyper v0.8.2-beta (*N. meningitidis*), ngmaster v0.5.5 (*N. gonorrhoeae*),
SeroBA v1.0.1 (*S. pneumoniae*), SISTR v1.0.2 (*S. enterica*), SRST2 v0.2.0 (*E. coli*, using EcOH DB)

Abbreviations and Footnotes: * Modifications to the published CTAB method are described in the methods section. **Nanopore data was filtered to 100x for the expected species size, preferring quality and length equally using Filtlong v0.2.0; *** PacBio data was filtered using a minimum read quality [mQ] = 0.80; ^a multiple versions used - refer to the methods section and supplementary tables; P/O = parameters/options (that differ from default); mRL = minimum read length; cOR = corOutCoverage; GS = genome size (^b set as Mb closest to species average); cER = correctedErrorRate (^c set as 0.144 for Nanopore or 0.045 for PacBio data); PLD = plasmid flag used; SLR = seed read length; oER = overlapper error rate;

^d start replicon was *dnaA* for chromosome sequences and *rep* for plasmid sequences, based on prokka annotations.