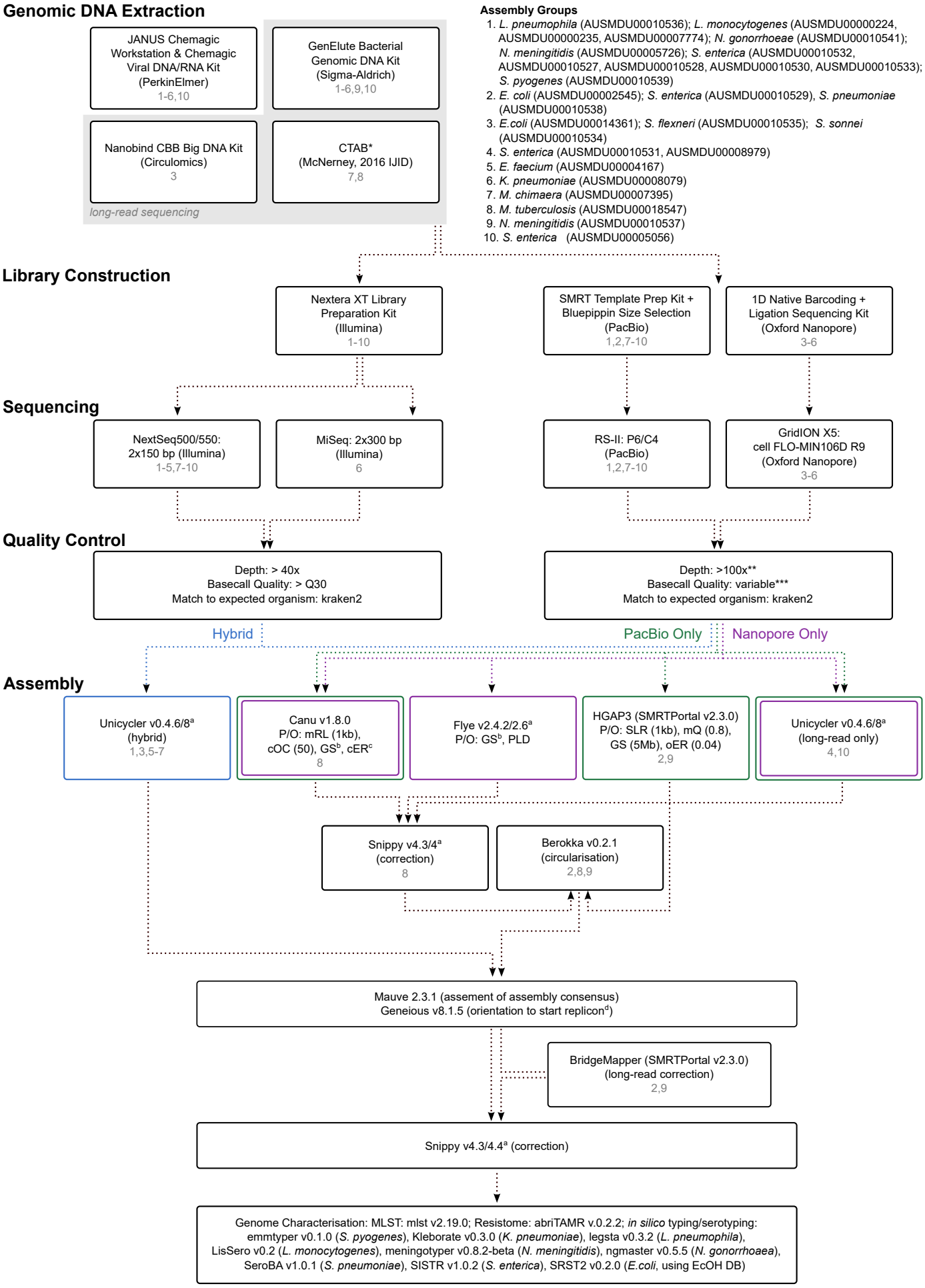

Abbreviations and Footnotes: * Modifications to the published CTAB method are decsribed in the methods section. **Nanopore data was filtered to 100x for the expected species size, preferencing quality and length equally using Filtlong v0.2.0; *** PacBio data was filtered using a minimum read quality [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.