S2 Table. Selection of task-specific third party bioinformatics software tools. Third party bioinformatics software tools selected for each task within ASA³P along with a short argumentative reasoning for why was selected.

Task - Tool	Parameters
QC - Trimmomatic	- Published - Well performing (due to publication) - Community standards and best practices
QC - FiltLong	- Well performing (broad experience) - One of the first tools available, broadly used
QC - FastQC	- Well performing (broad experience) - Community standards and best practices - Broad applicability (all sequencing platforms) - Actively maintained
QC - FastQ Screen	- Well performing (broad experience) - Broad applicability (all sequencing platforms) - Actively maintained
Assembly Illumina - SPAdes	- Well performing (publication & broad experience) - Community standards and best practices - Actively maintained
Assembly PacBio - HGAP	- Well performing (publication & broad experience) - One of the first tools available - Actively maintained
Assembly NanoPore/Hybrid (Illumina) - Unicycler	- Well performing (publication & broad experience) - Unicycler combines trimming, polishing and dnaA rotation like no other assembly pipeline whilst still being easy to technically integrate
Scaffolding - MeDuSa	- Well performing (publication & broad experience) - Supporting multiple references - In contradiction to many other multi-reference scaffolders, MeDuSa is available as a locally executable tool
Annotation - Prokka	- Well performing (publication & broad experience) - Community standards and best practices - Actively maintained
ABR - CARD rgi	- Well designed AMR ontology - All-in-one AMR detection tool (acquired genes, mutation based, efflux pump mediated) - Actively maintained
Pan/Core Genome calculation - Roary	- Well performing (publication & broad experience) - Community standards and best practices - Computationally applicable for large cohorts - Actively maintained

Phylogenomics - FastTree	- Well performing (publication & broad experience) - Computationally applicable for large cohorts - Community standards and best practices