

***Figure 1. Flow chart showing bactpipe.nf pipeline***. Analysis flow starts with pre-processing of paired end reads in fastq format, quality evaluation using FastQC, *de novo* assembly using SPAdes, assembly filtering using a customized Pearl script, contig ordering using Mauve, contig renaming using a customized python script and genome annotation using prokka. Intermediate output files from each analysis step are indicated by arrows.