



Supplementary FIG 1: Maximum likelihood phylogenetic tree using 80 *Acinetobacter* representative species genomes and ten South Australian environmental isolates. Tree was built using a core genome alignment (54,841 bp length). Bootstrap values > 0.9 shown as dots on branches. Isolates from this study highlighted in purple and are boxed to include each nearest representative *Acinetobacter* species. The potentially novel species is marked with a star.