**Figure 1 Genomic characterisation of antibiotic resistant determinants and clinically relevant antibiotic resistance mutations in the *P. aeruginosa* AUST-03 strains from the study. Brown squares denote genes that are present, green squares denote genes carrying non-synonymous (missense and frameshift) mutations, grey squares represent genes carrying wildtype/synonymous mutation with limited contribution to antibiotic resistance.**

**Figure 2 Dendrogram showing the genetic relationship between the 11 *P. aeruginosa* ST 242 (AUST-03) strains from the study and the 28 *P. aeruginosa* ST 242 isolates from other studies globally. Core SNP clusters were defined at a cut-off of 20 SNPs.**