Supplementary Figure 8. Maximum likelihood phylogenetic tree using amino acid sequences of six concatenated gene alignments (*ENO1*, *ERG7*, *ERG10*, *GPD1*, *MDR1* and *UPC2*) of *Candida auris* one representative by clade, including clade V (B18474) and one representative from the *C. haemulonii* species complex. Phylogeny was constructed using RAxML v8.2.4