



**Supplementary Figure 5. (a)** Shared synteny regions based on whole genome alignments between *C. auris* B11220 (contig2 and contig4) and JCM15448 (contig1). Blue circle indicates a mis-join in the genome assembly of JCM15448 between two telomeric contig ends. **(b).** Integrative Genomics Viewer (IGV) snapshot of short and long reads from *C. auris* isolates B11220 and JCM15448 aligned to the genome assembly of JCM15448 providing evidence of a mis-join in JCM15448 contig1 (BGX01000001.1).