Taxonomy classification of the input genome bins can be obtained with TCG, which is based on the Genome Taxonomy Database (GTDB). GTDB is a recently released database with standardized taxonomy based on the phylogeny inferred from 120 ubiquitous, SCGs covering 94,759 bacterial genomes. Briefly, TCG searches predicted proteins for input genome bins against the PFAM and TIGRFAM hmm profiles of the 120 SCG using HMMER. Identified protein sequences for each hmm profile are then searched with blastP against the relevant subset of reference sequences in GTDB. The taxonomic assignment to the input genome was then based on the last common ancestor that was found above a pre-defined threshold (e.g. 80%) in the taxonomy of the highest-bit score hit for each SCG.