Figure 1: overview of the Trycycler long-read assembly pipeline. Before Trycycler is run, the user must generate multiple different completed assemblies of the same genome, e.g. by assembling different subsets of the original long-read set. Trycycler then clusters contigs from different assemblies and produces a consensus contig for each cluster. These consensus contigs can then be polished (e.g. with Medaka) and combined into a final high-quality long-read assembly.