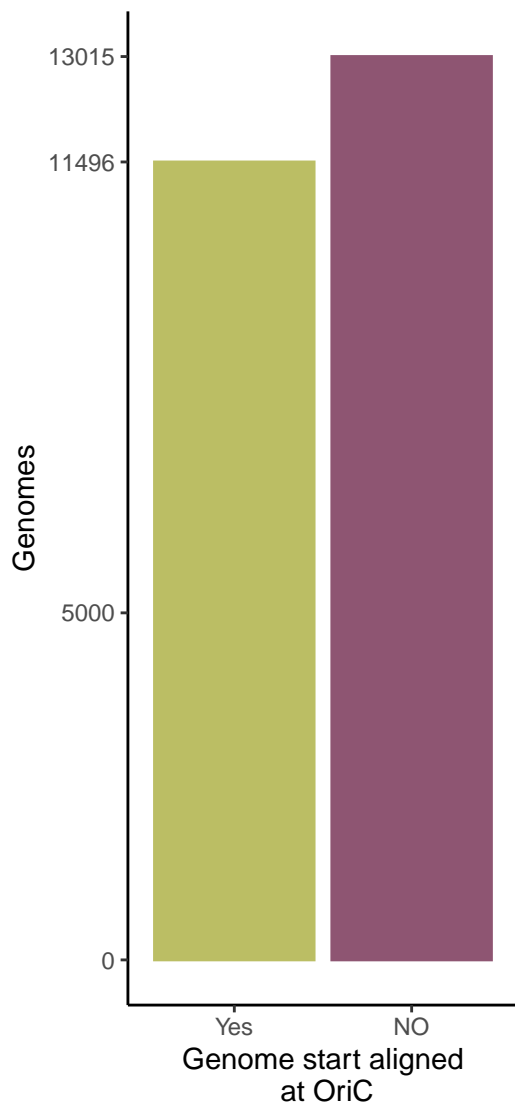
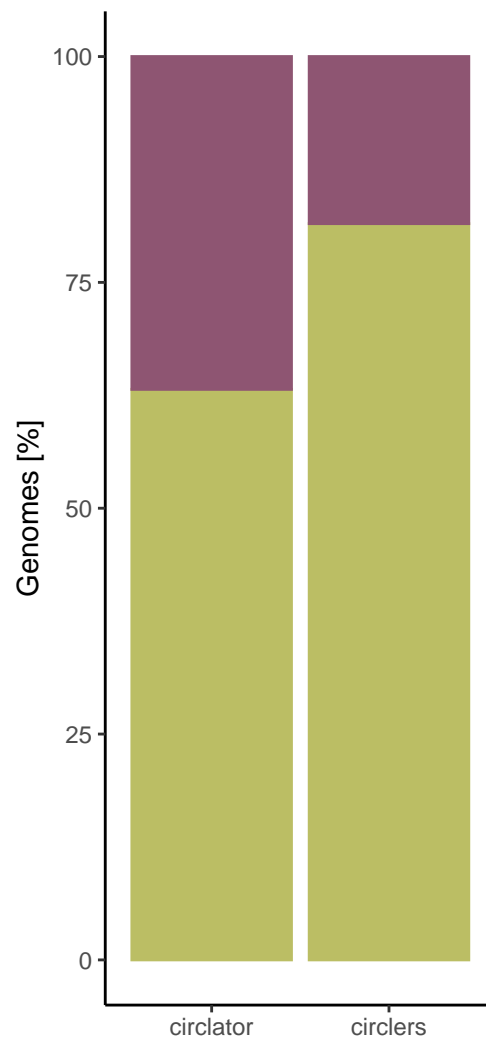


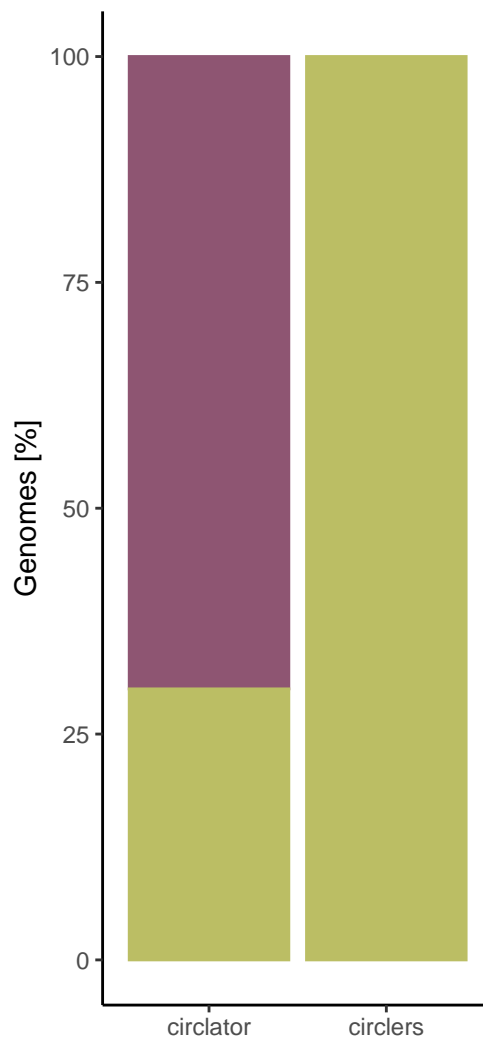
Chromosome-level assemblies on RefSeq



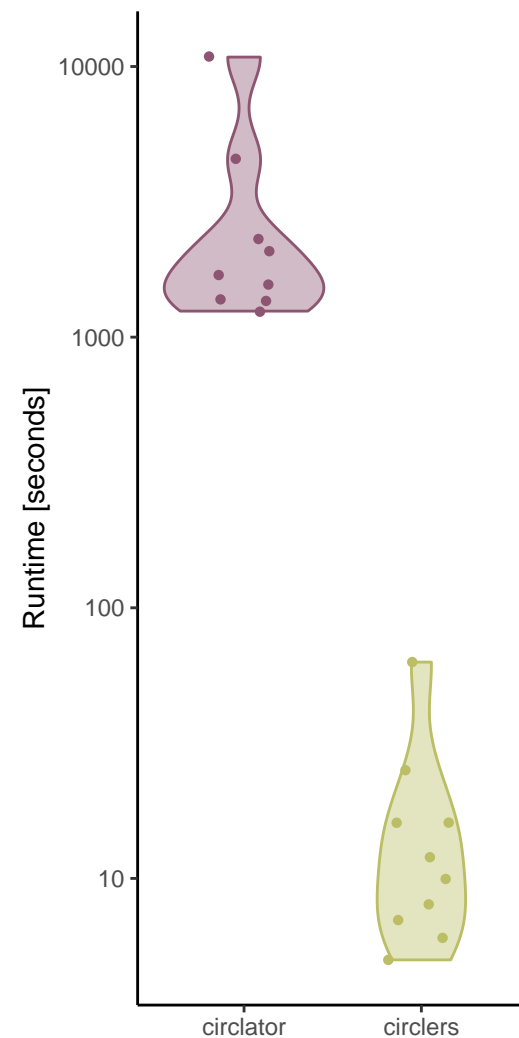
Correctly identified circular contigs (n=173)



Start alignment of bacterial chromosomes (n=10)



Runtime of the two tools (n=8)



incorrect correct

not aligned startaligned