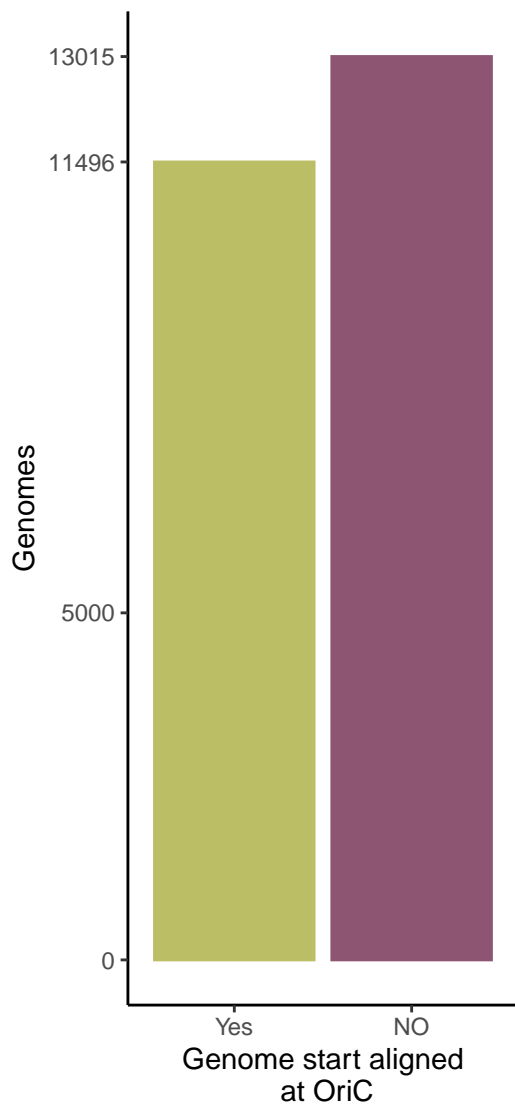
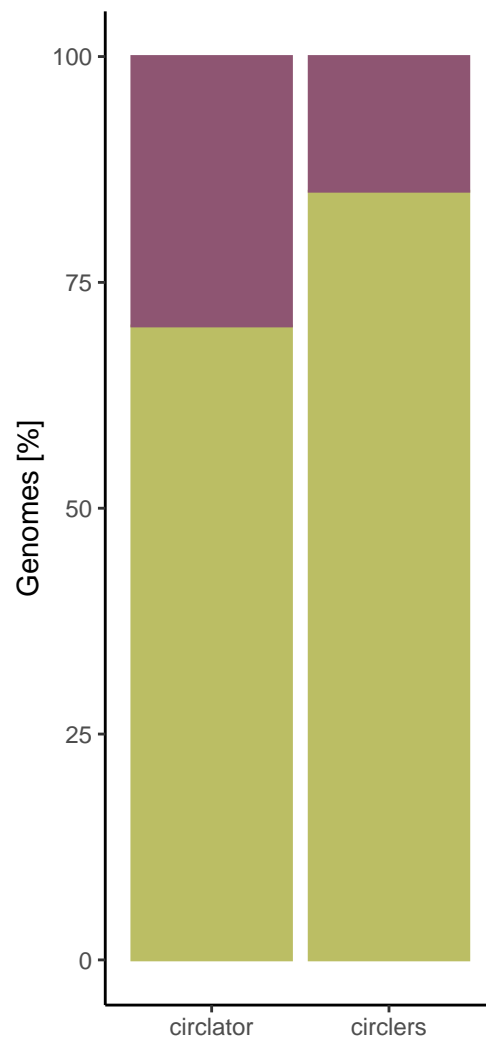


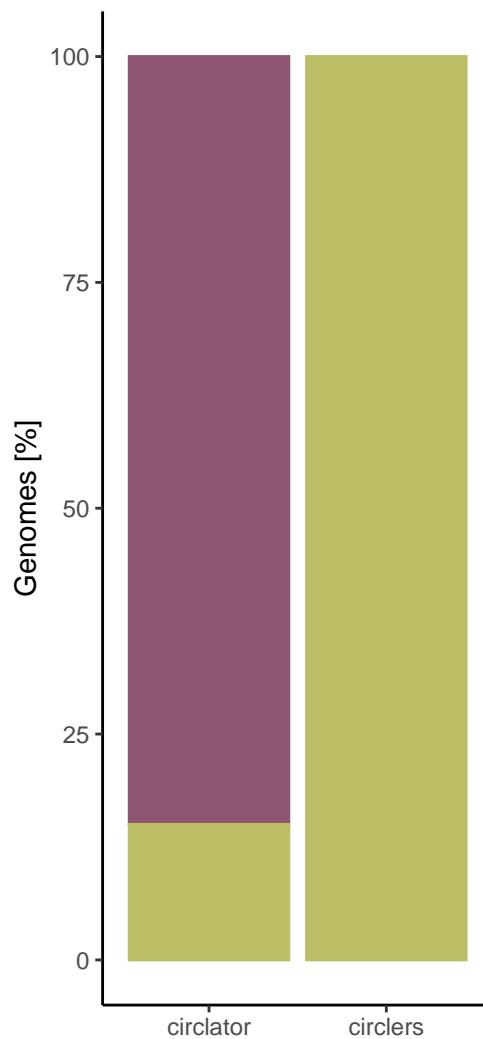
Chromosome-level assemblies on RefSeq



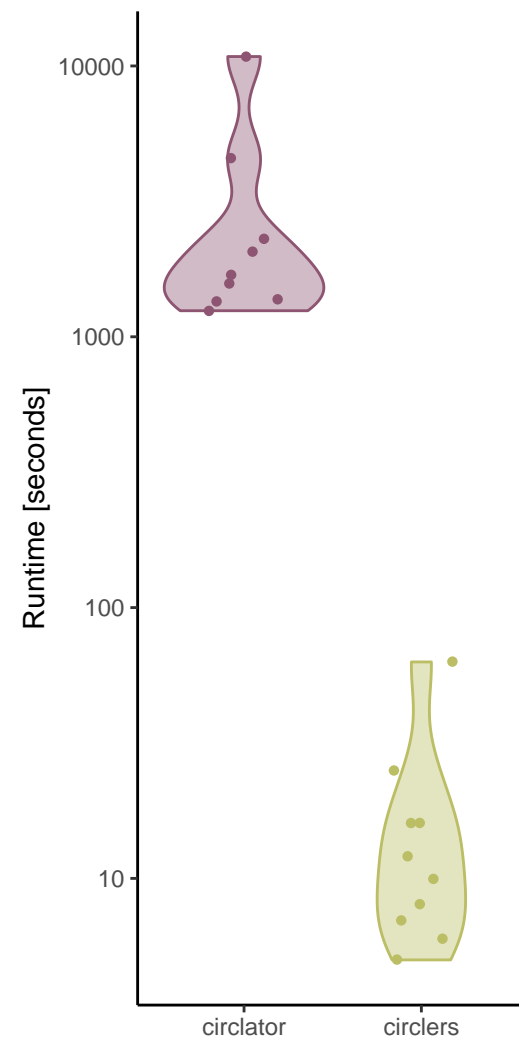
Correctly identified circular contigs (n=228)



Start alignment of bacterial chromosomes (n=20)



Runtime of the two tools (n=8)



incorrect correct

not aligned startaligned