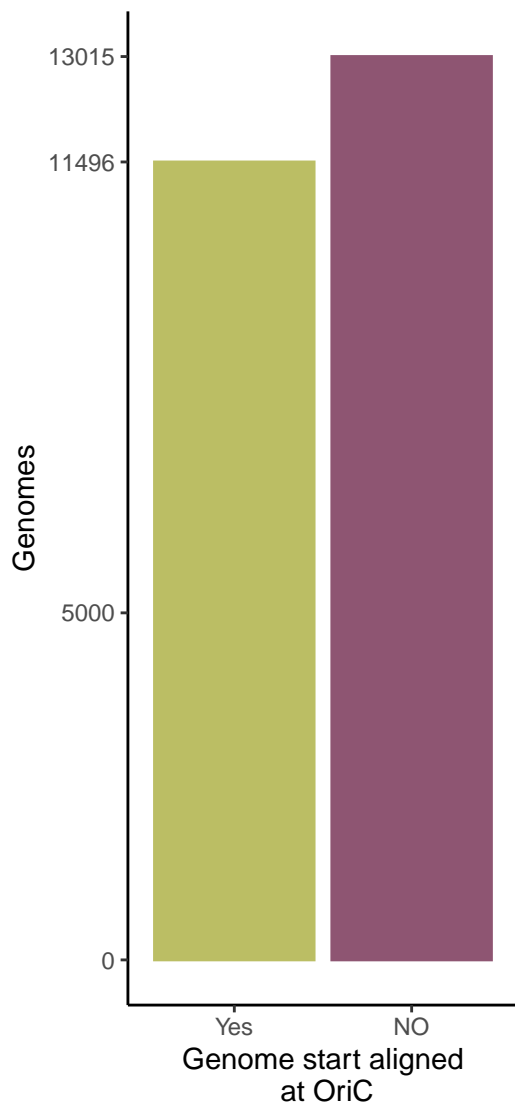
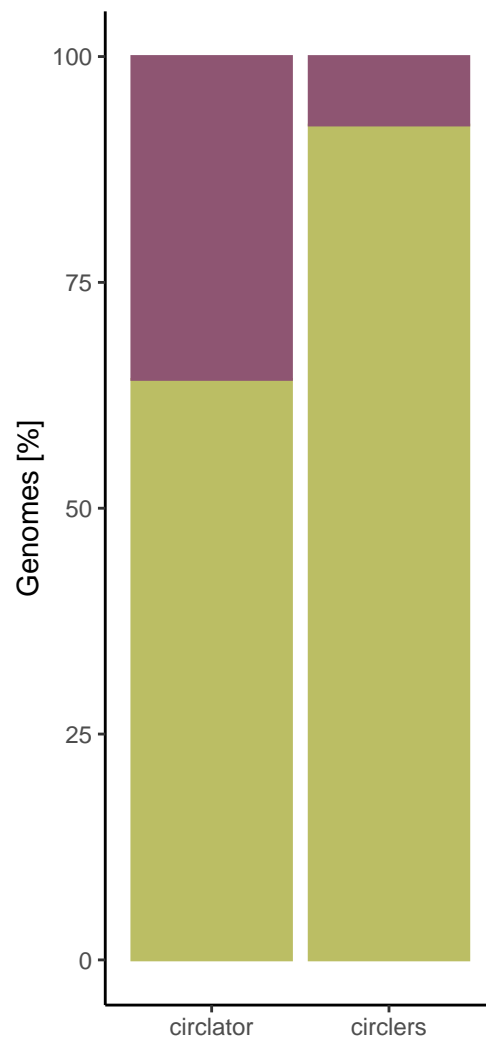


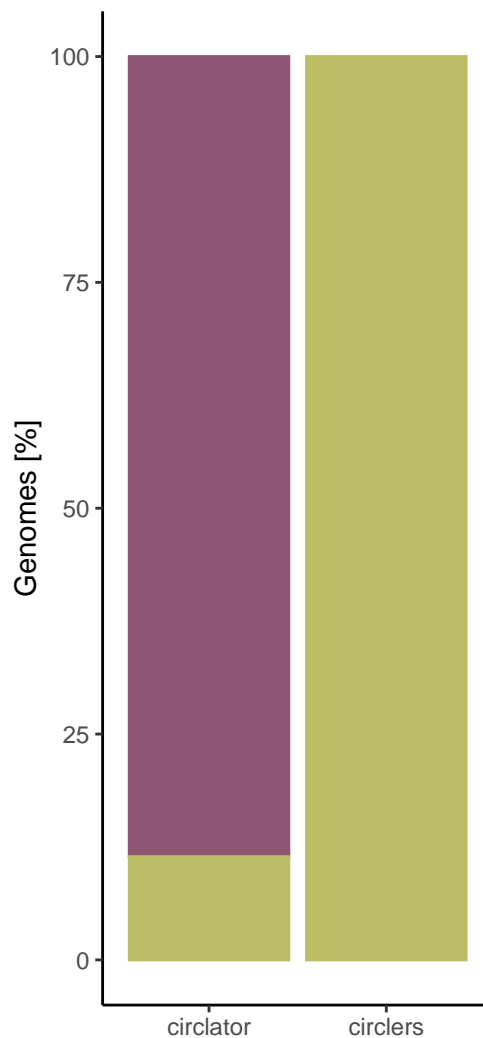
Chromosome-level
assemblies on RefSeq



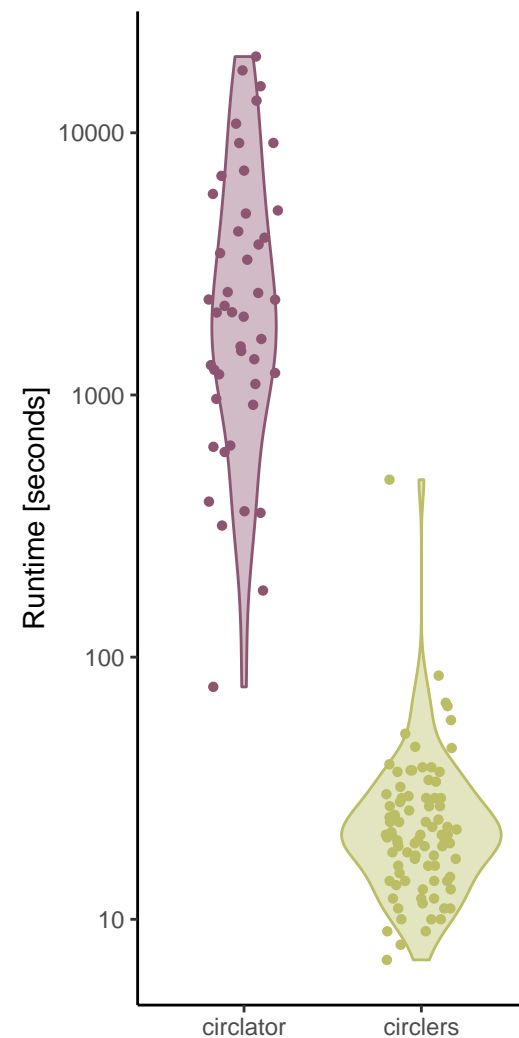
Correctly identified
circular contigs (n=277)



Start alignment of bacterial
chromosomes (n=35)



Runtime of the two tools
(n=87)



incorrect correct

not aligned startaligned