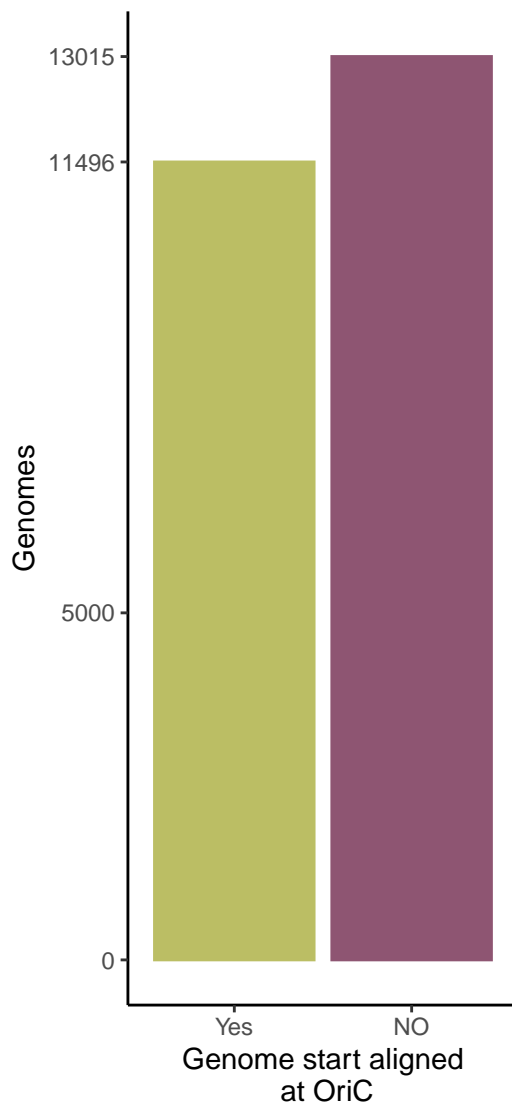
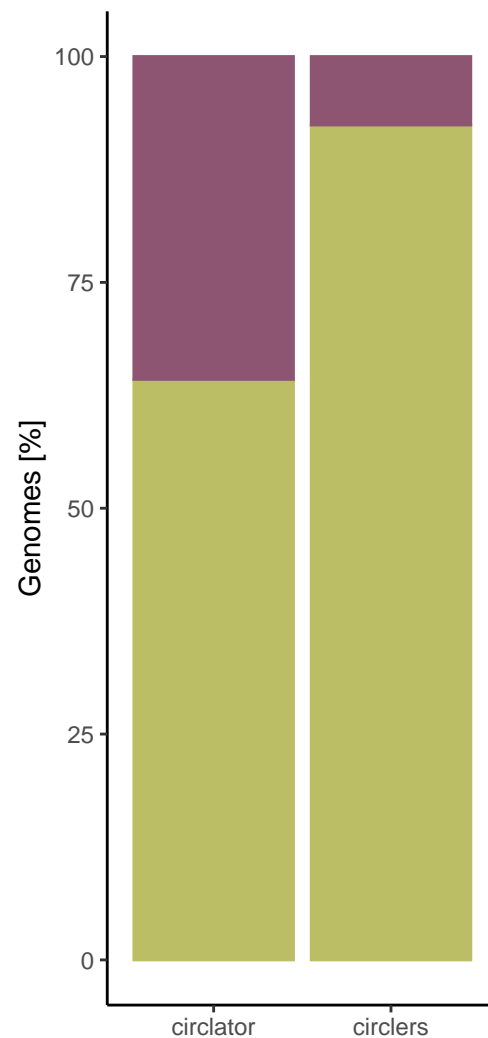


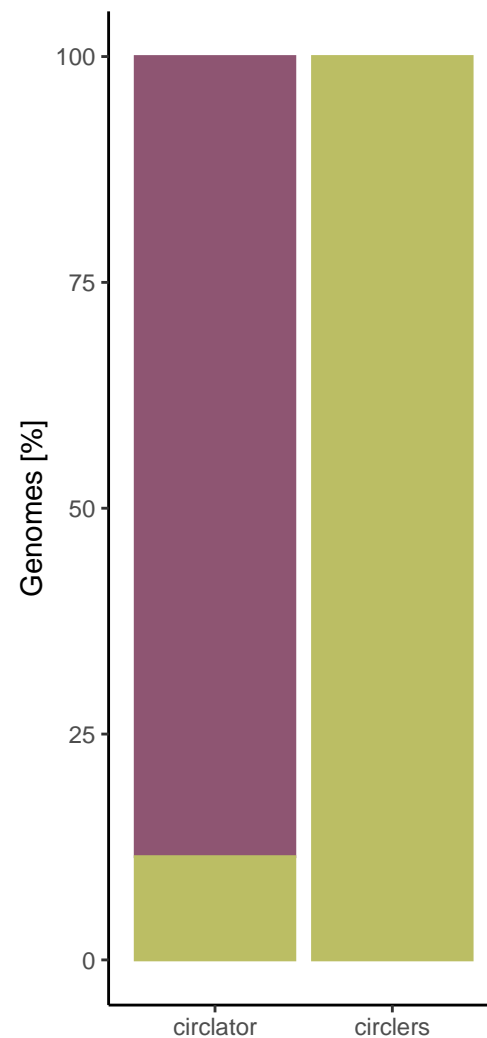
Chromosome-level  
assemblies on RefSeq



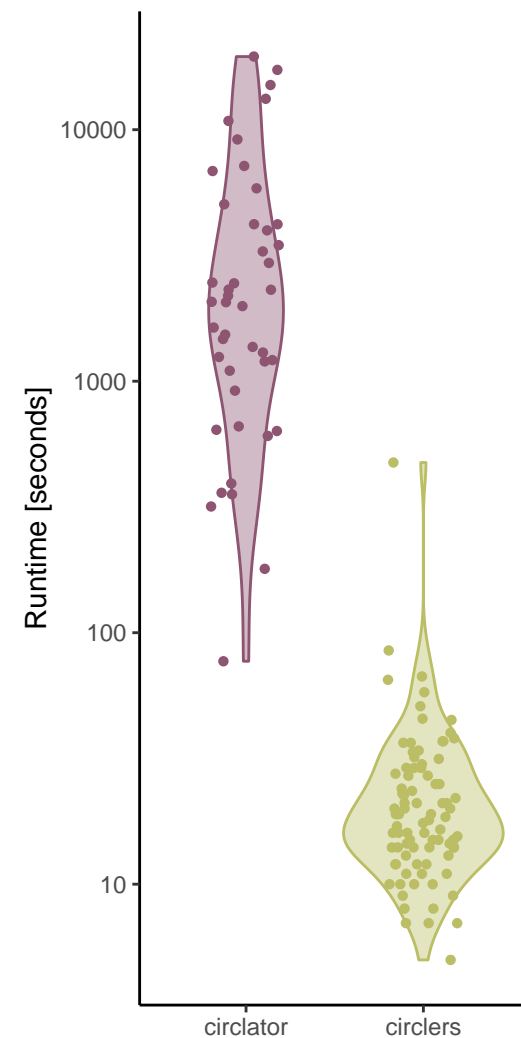
Correctly identified  
circular contigs (n=277)



Start alignment of bacterial  
chromosomes (n=35)



Runtime of the two tools  
(n=87)



incorrect correct

not aligned startaligned