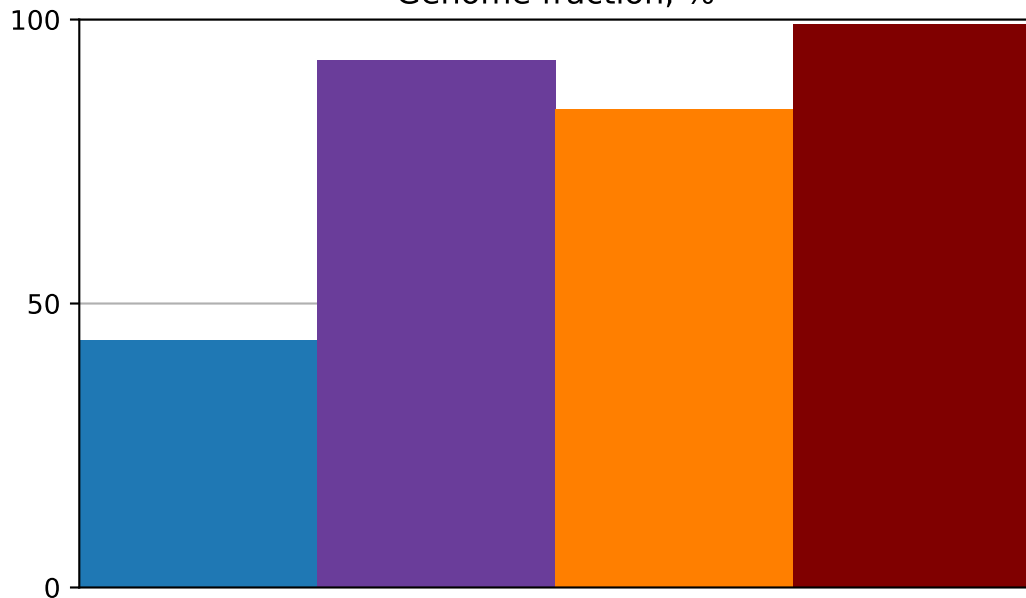


Genome fraction, %



sortie\_sequencage1  
sortie\_sequencageerreur

reads\_sequencage1\_in

reads\_contaminant\_in