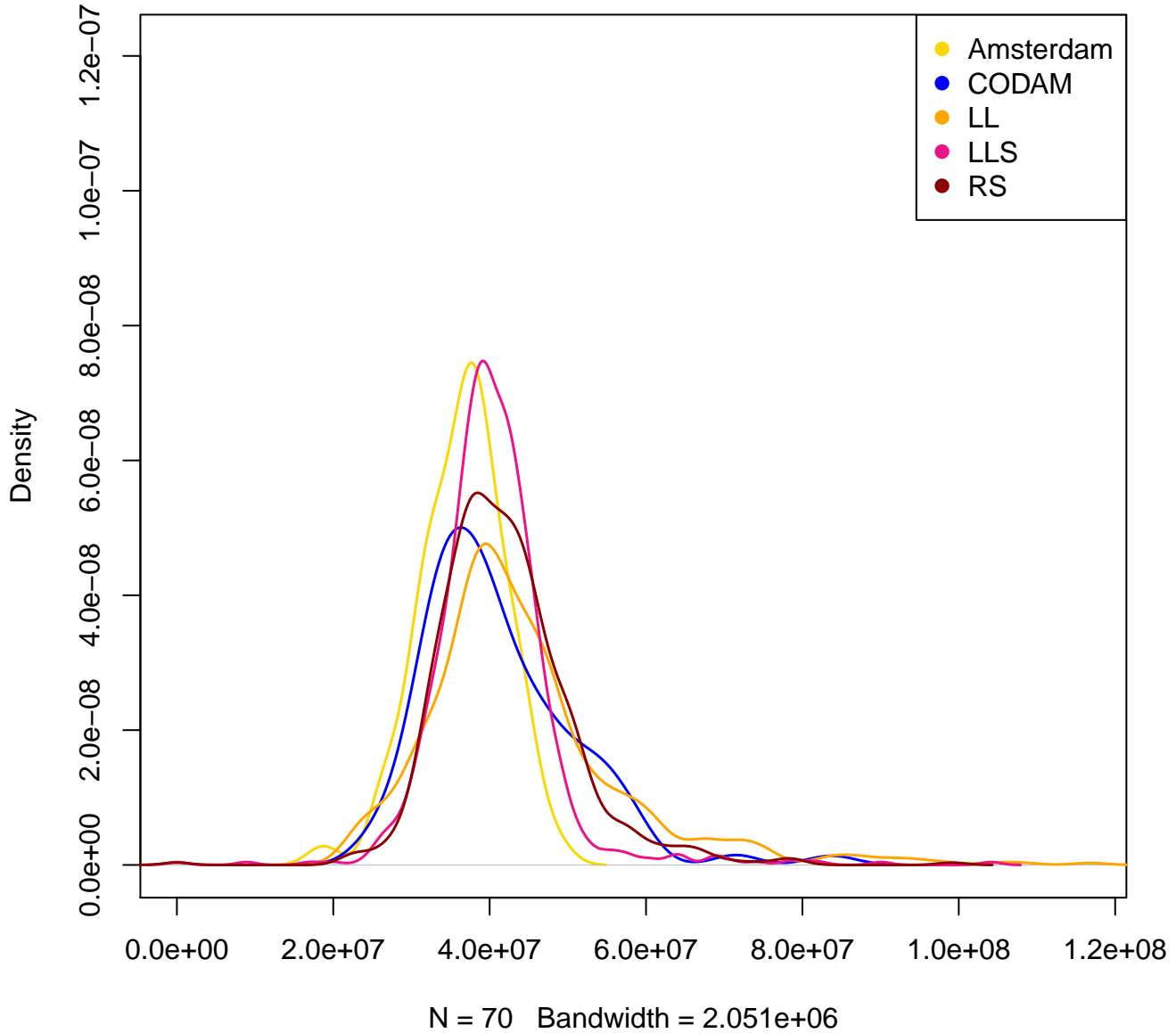
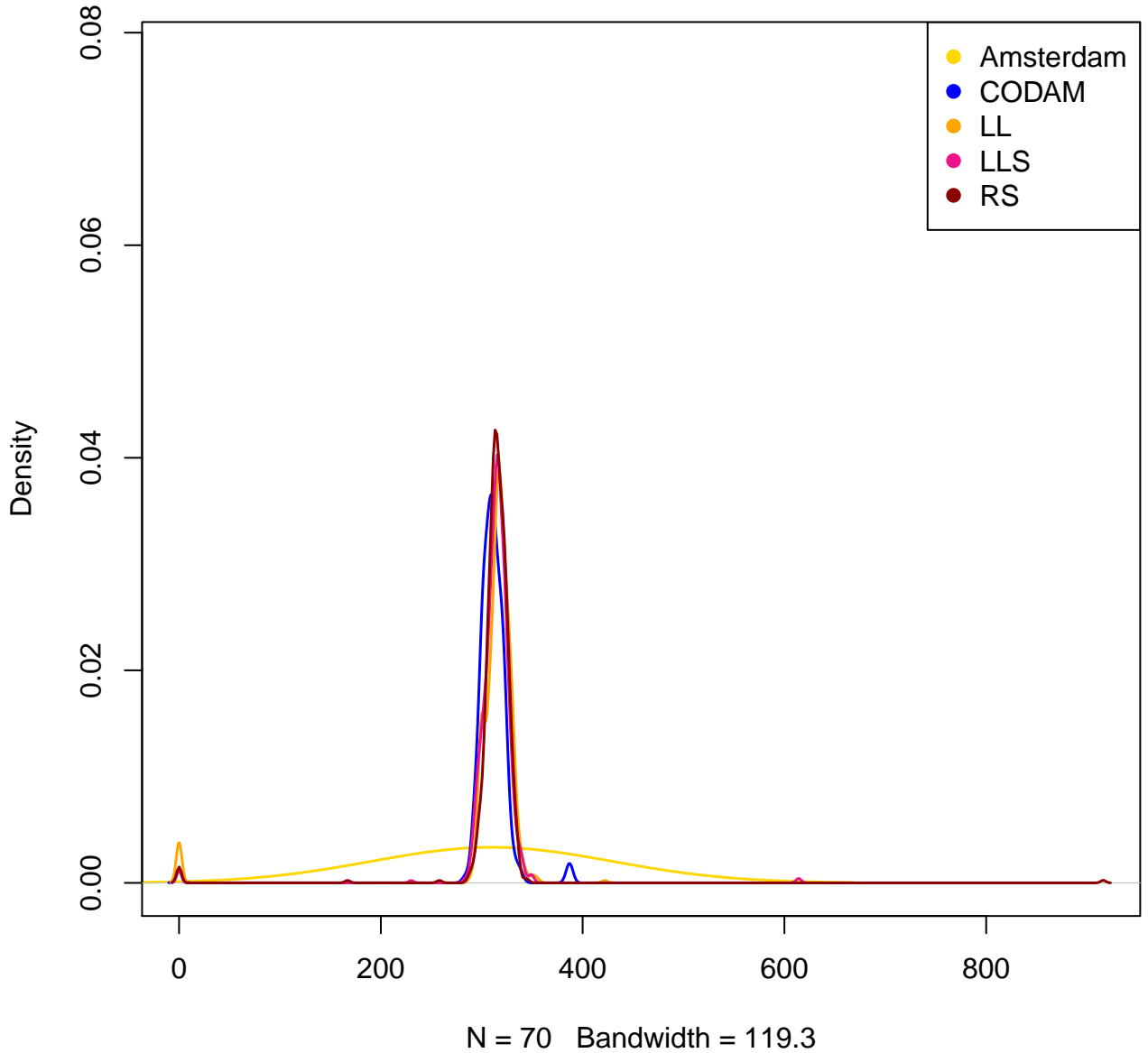


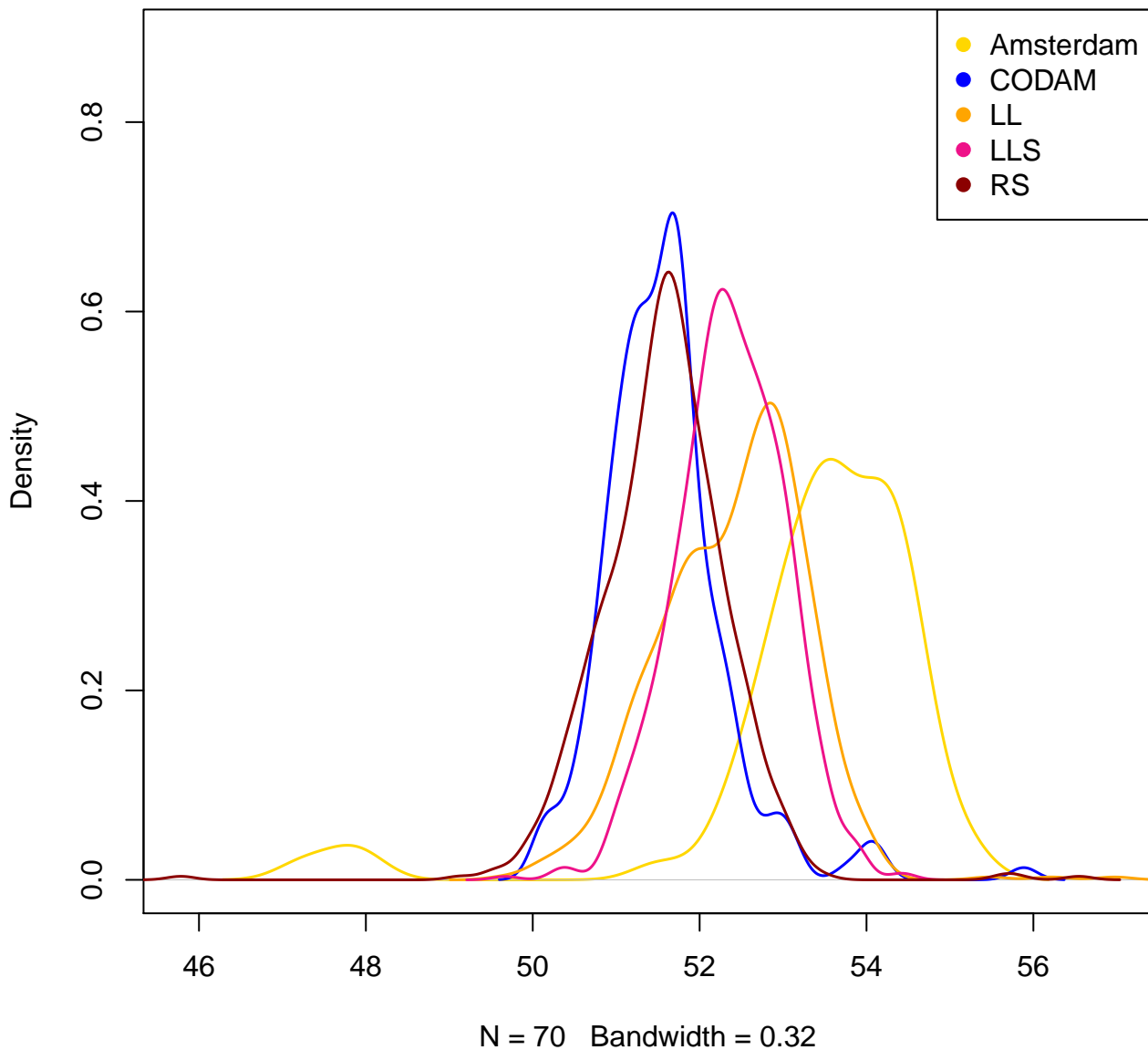
# num\_past\_filter



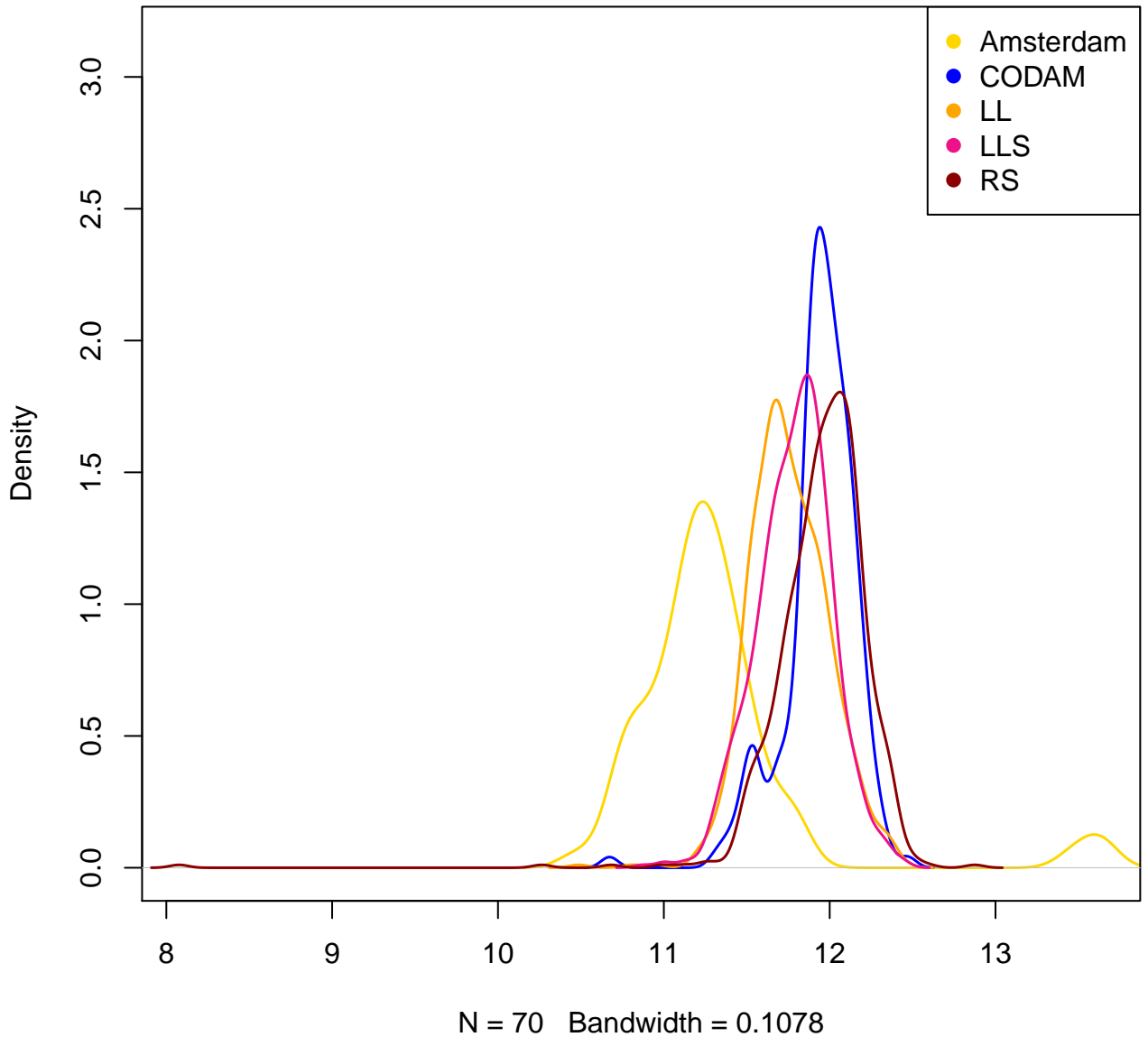
# insert\_size



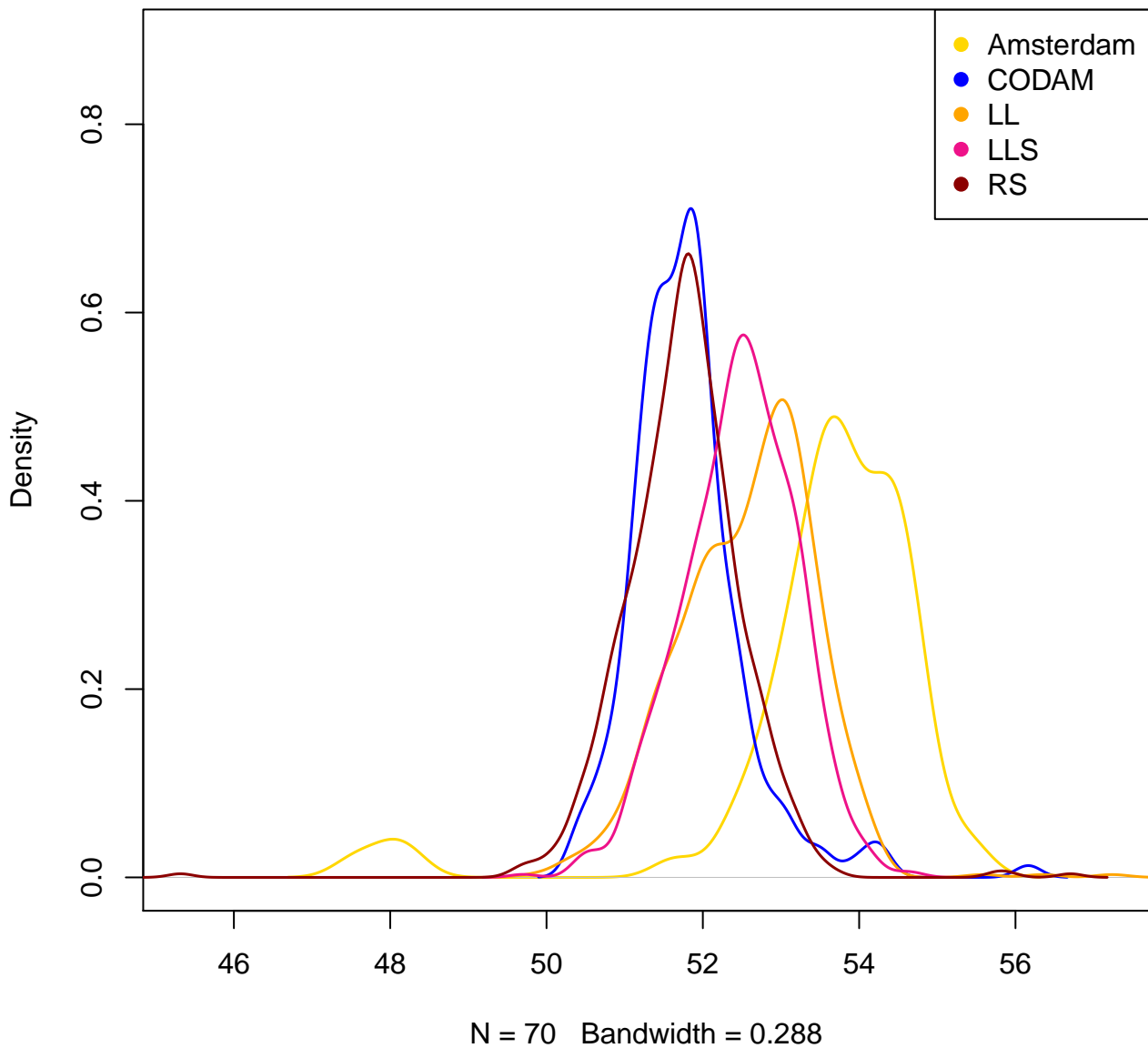
# fastqc\_clean\_R1\_clean\_GC\_mean



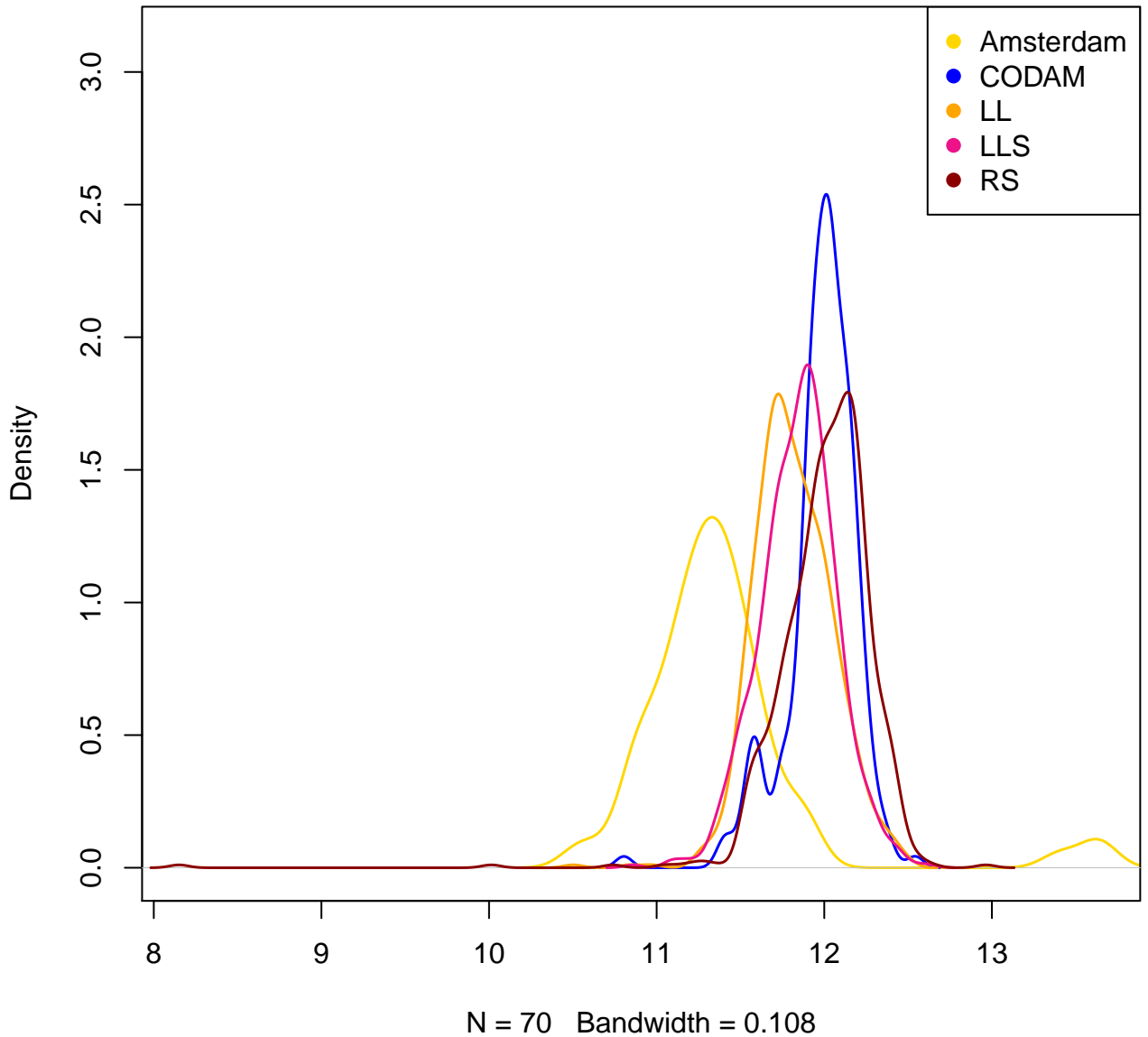
# fastqc\_clean\_R1\_clean\_GC\_std



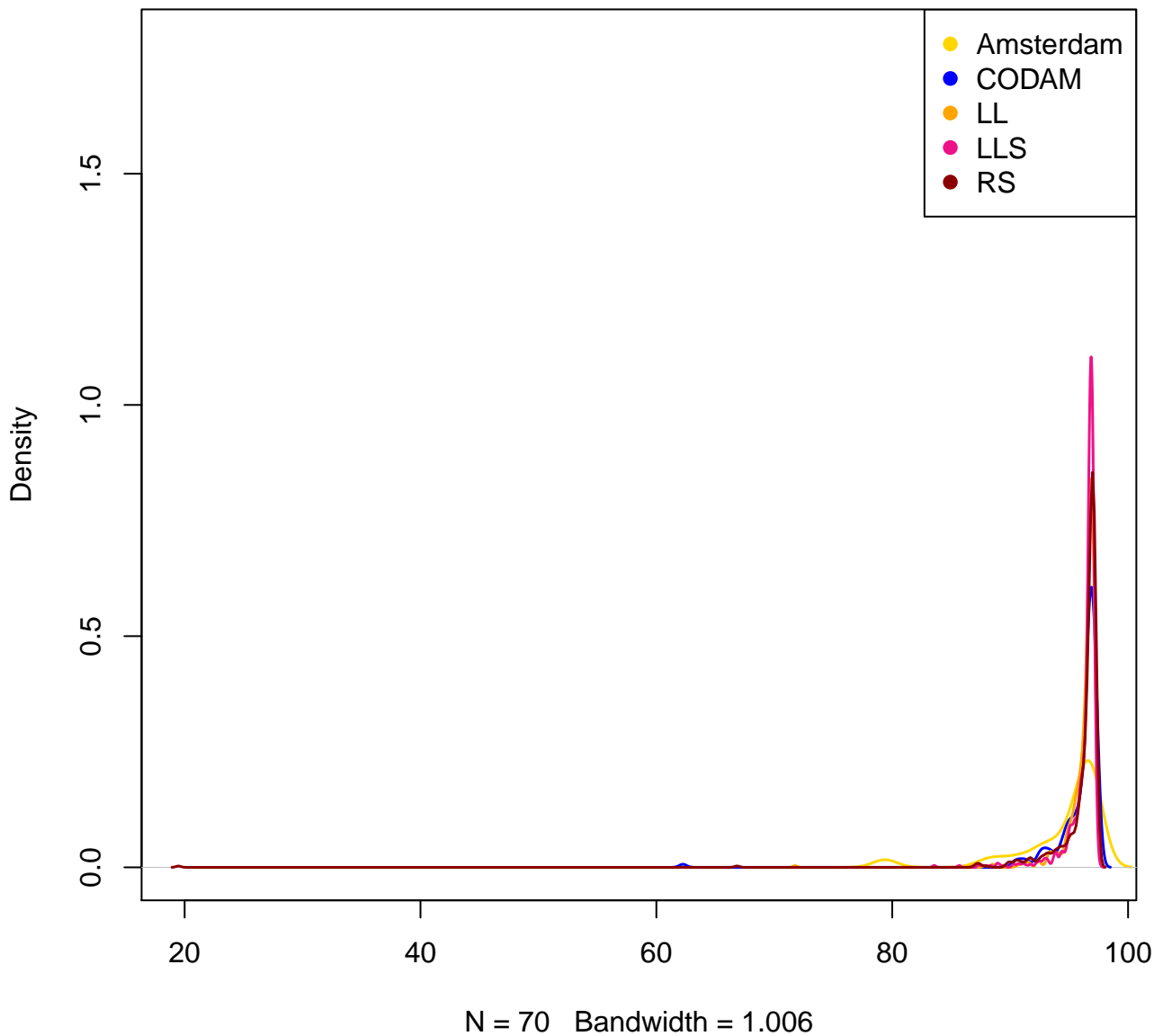
# fastqc\_clean\_R2\_clean\_GC\_mean



# fastqc\_clean\_R2\_clean\_GC\_std



# bam\_perc\_genome\_mapped



# bam\_perc\_exon\_mapped

