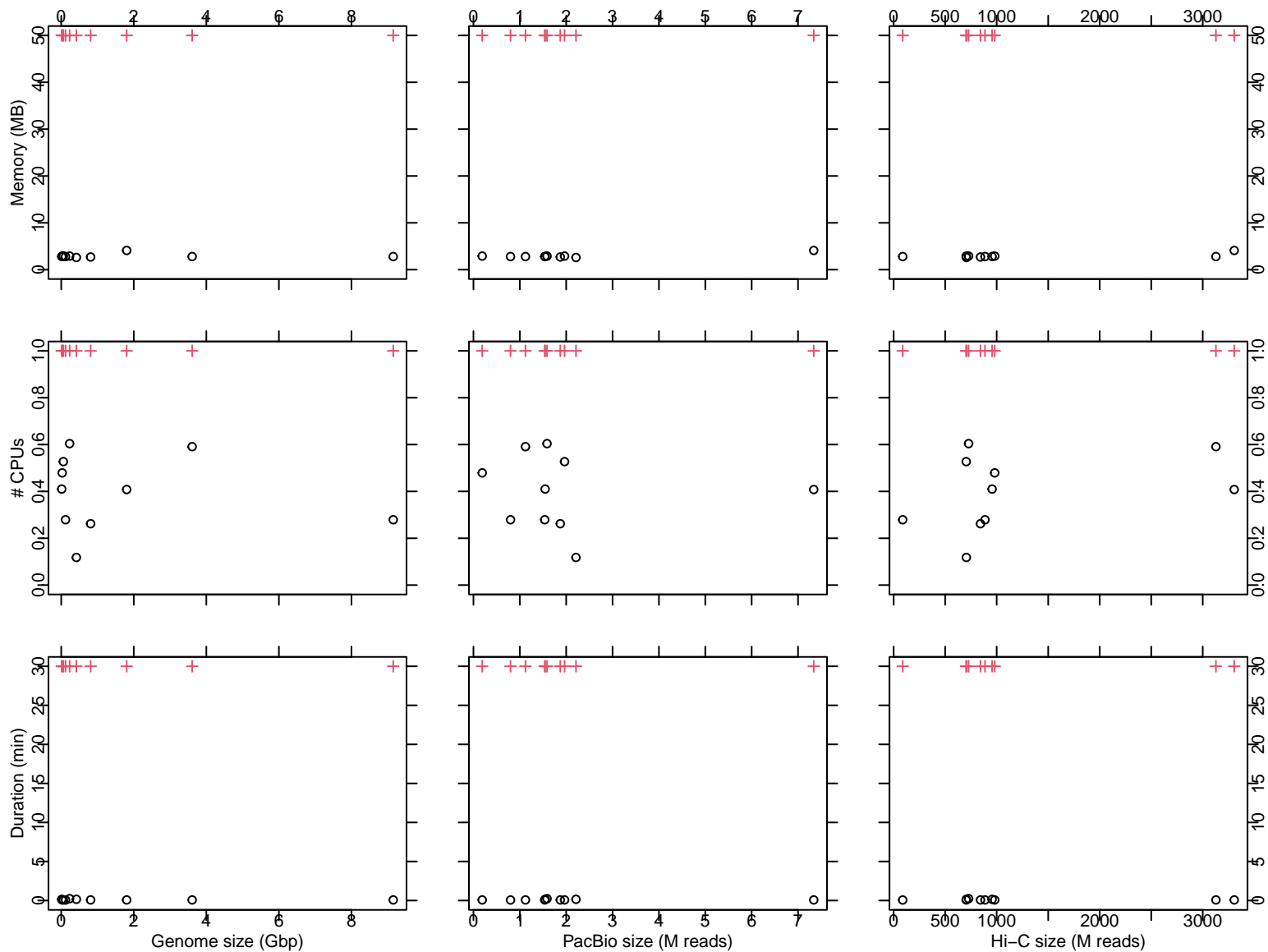
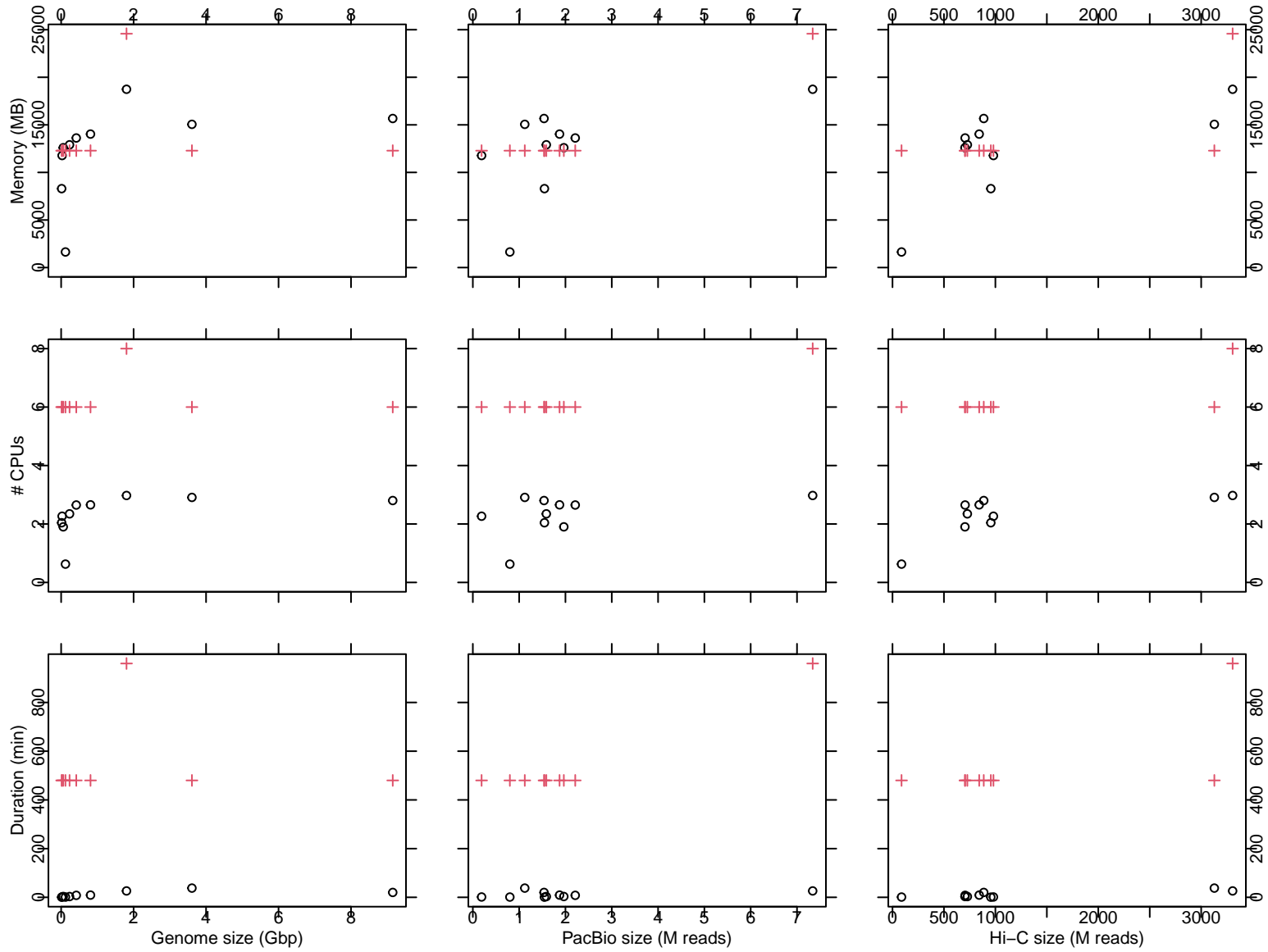


sanger-tol/genomenote - opt3

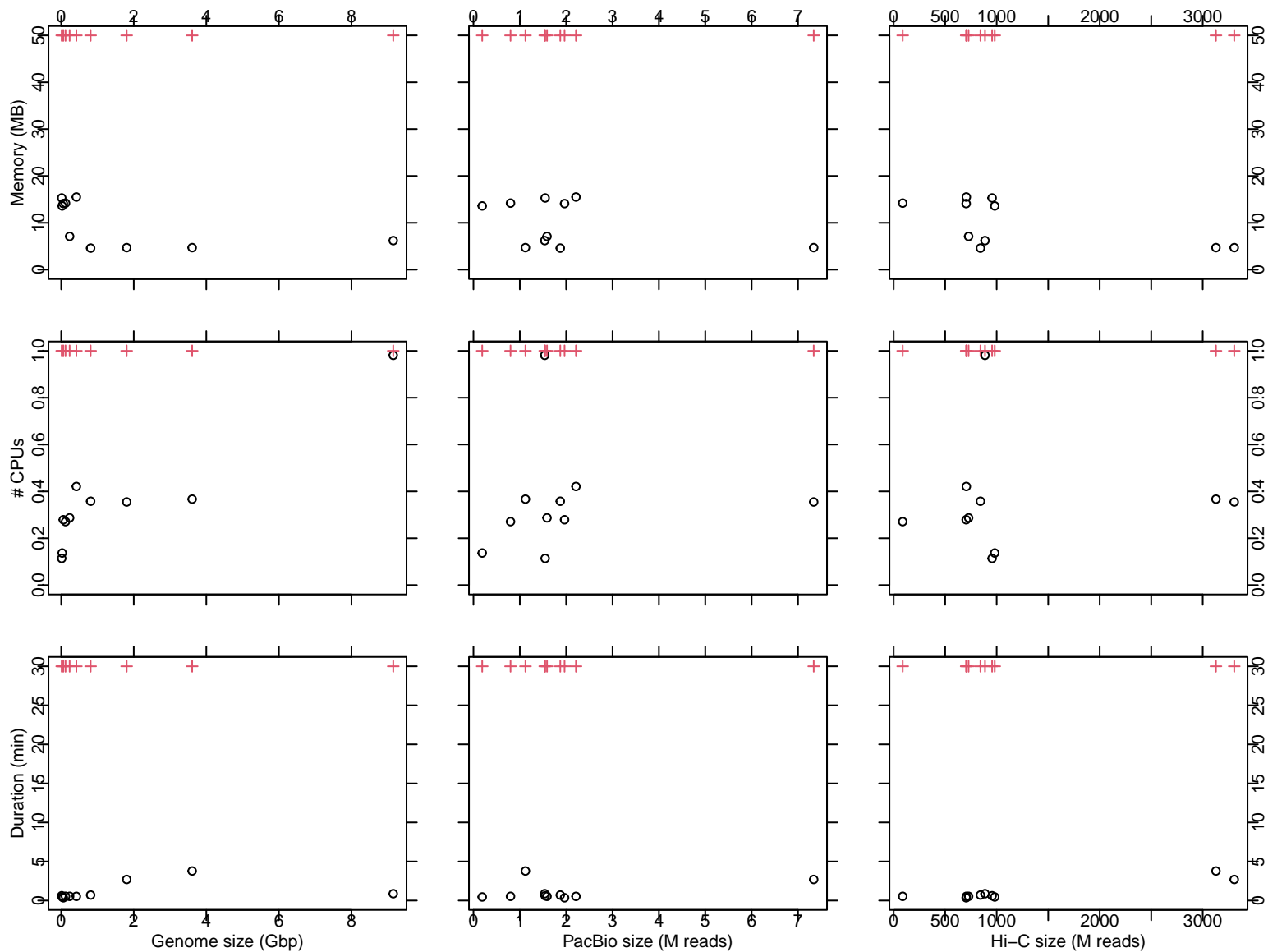
# CONTACT\_MAPS:FILTER\_GENOME



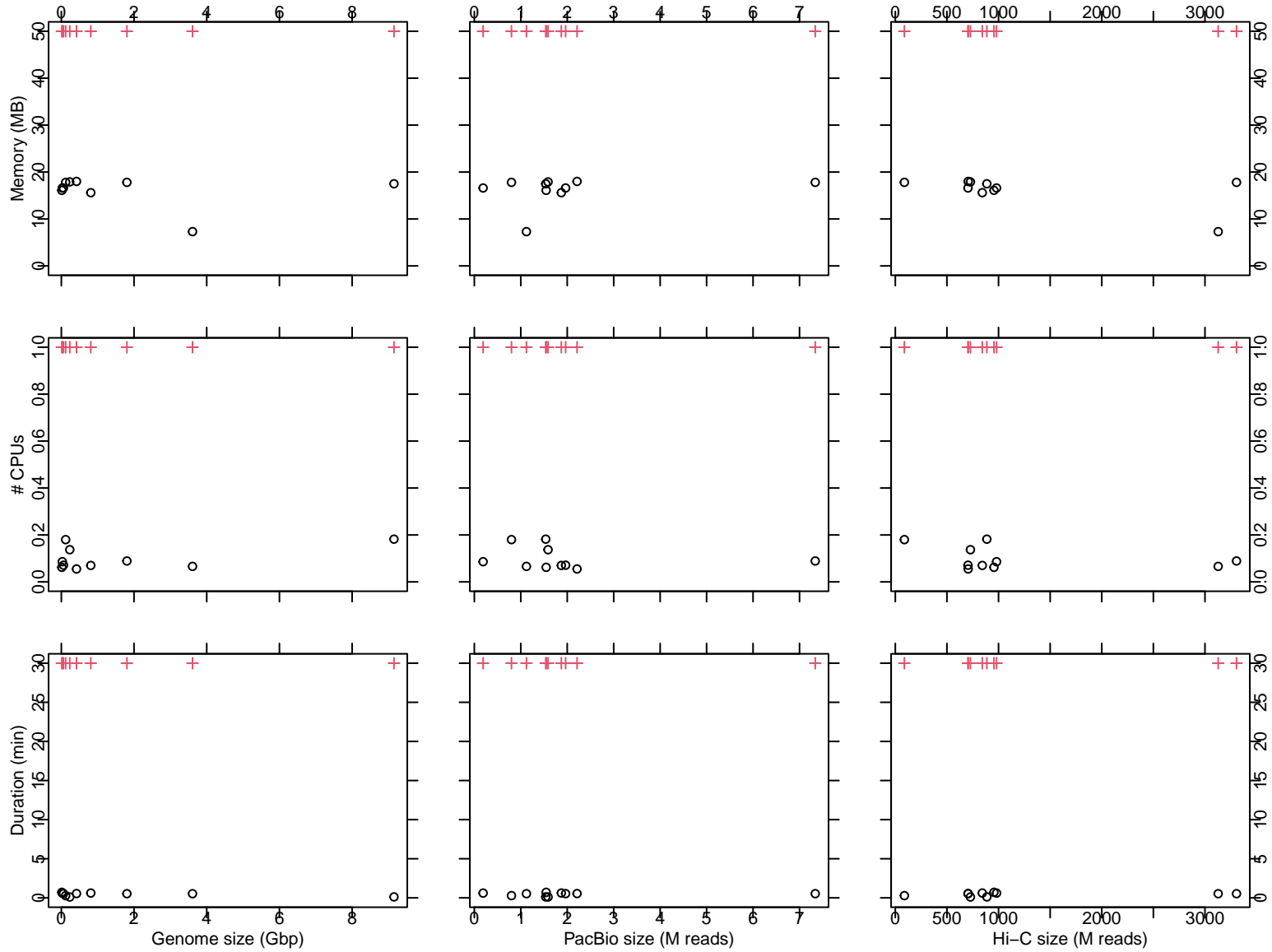
# CONTACT\_MAPS:COOLER\_ZOOMIFY



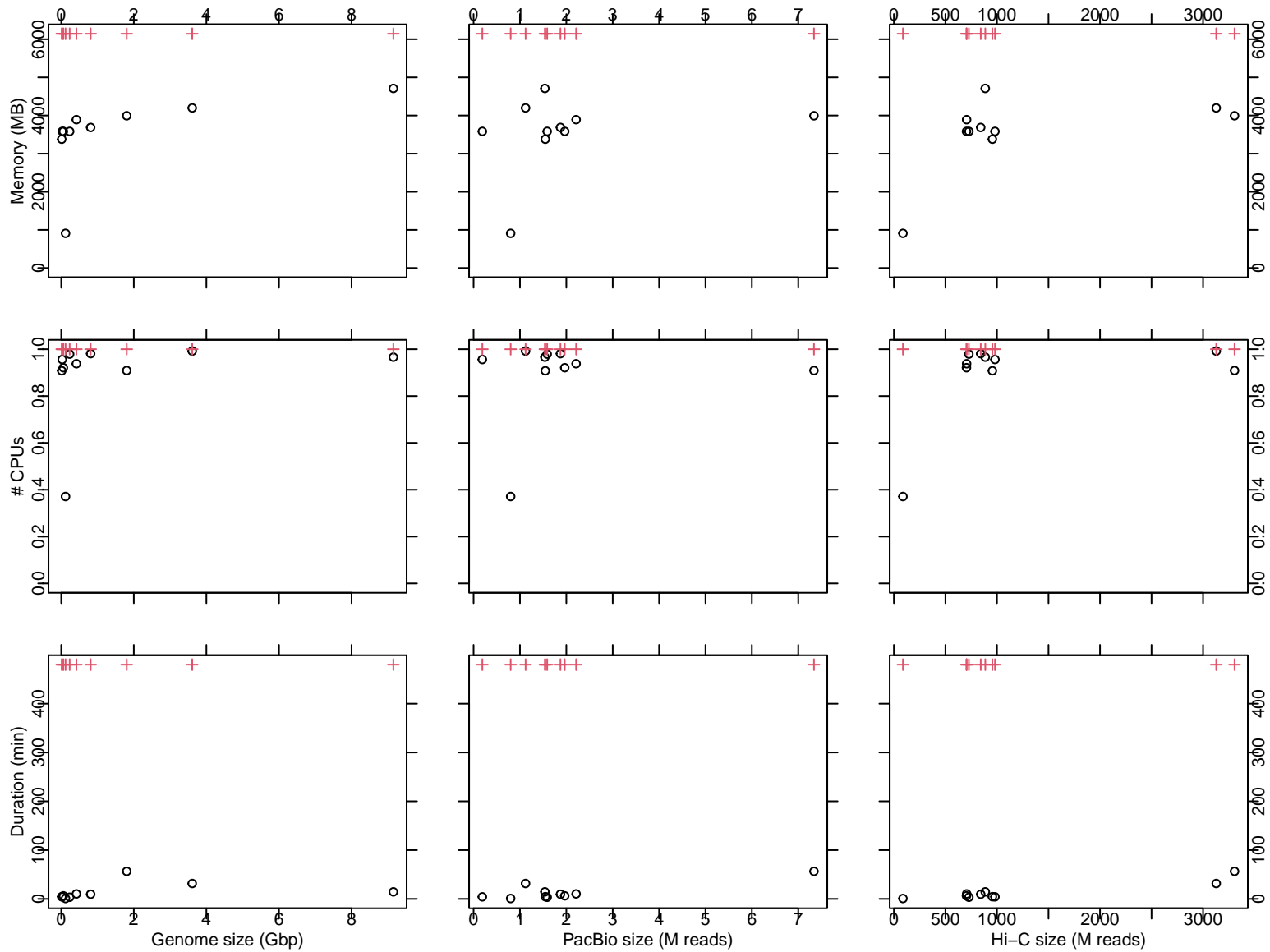
# CONTACT\_MAPS:SAMTOOLS\_FAIDX



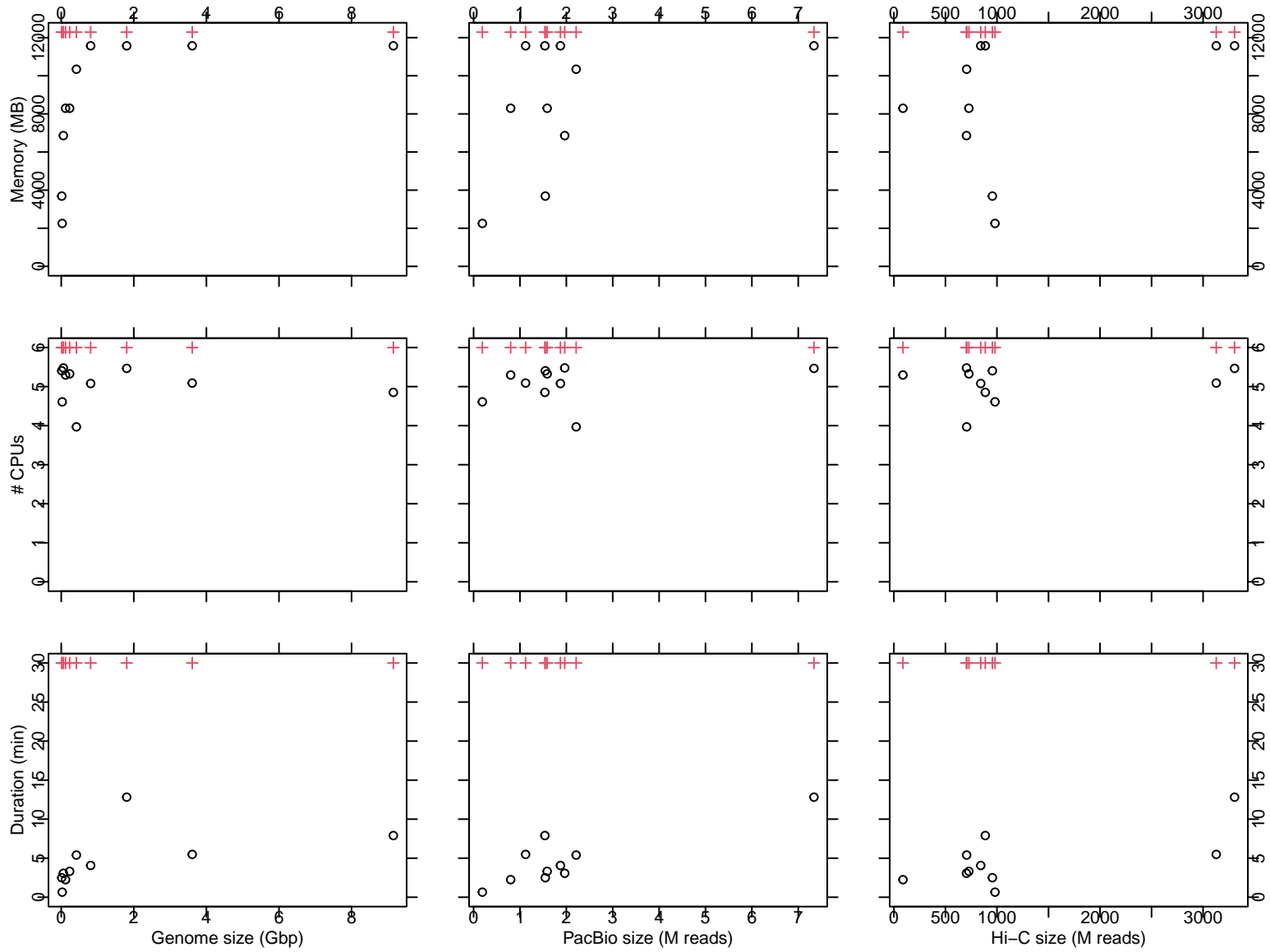
# GENOME\_STATISTICS:SUMMARYSEQUENCE



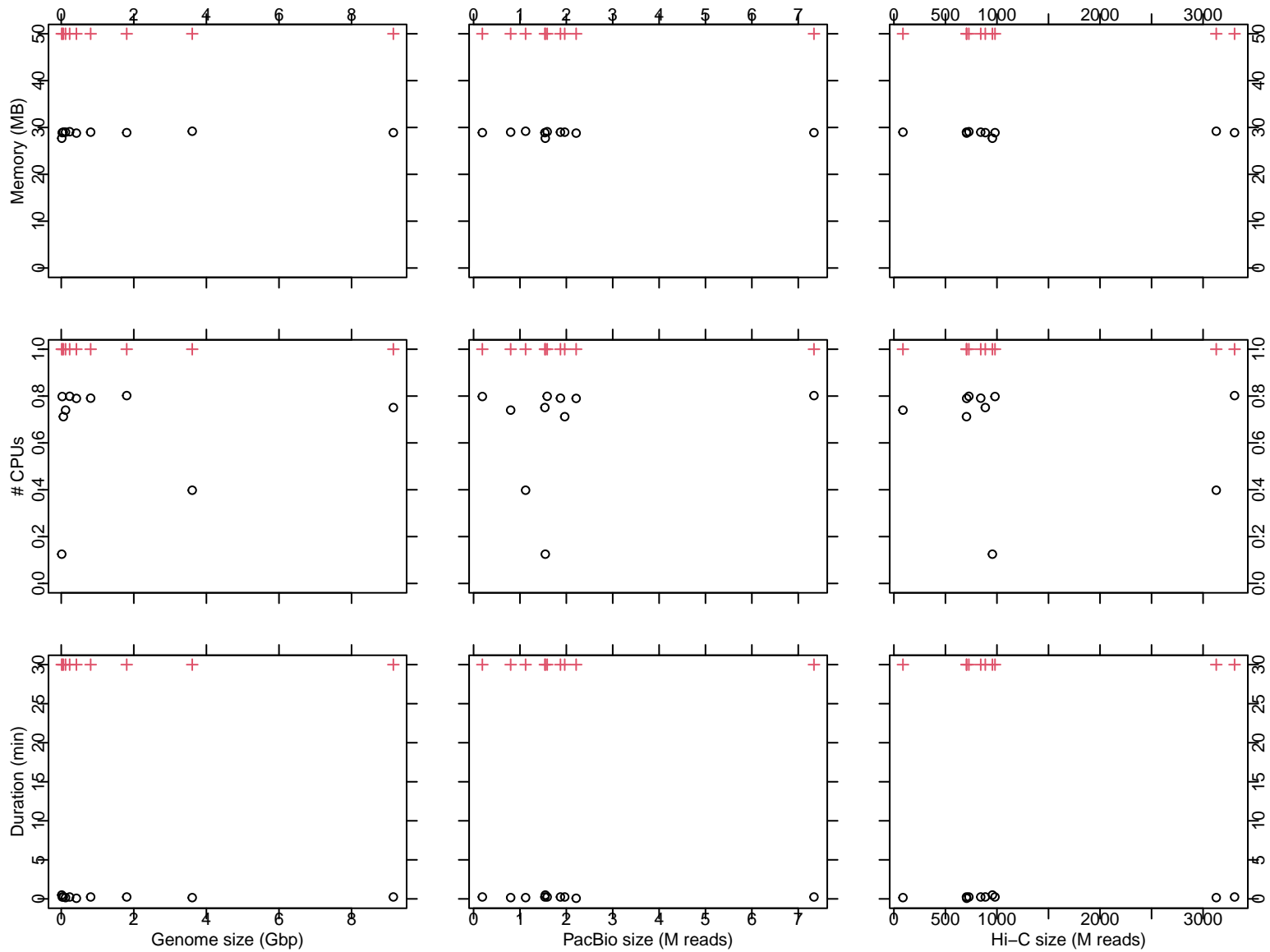
# CONTACT\_MAPS:COOLER\_LOAD



# GENOME\_STATISTICS:FASTK\_FASTK

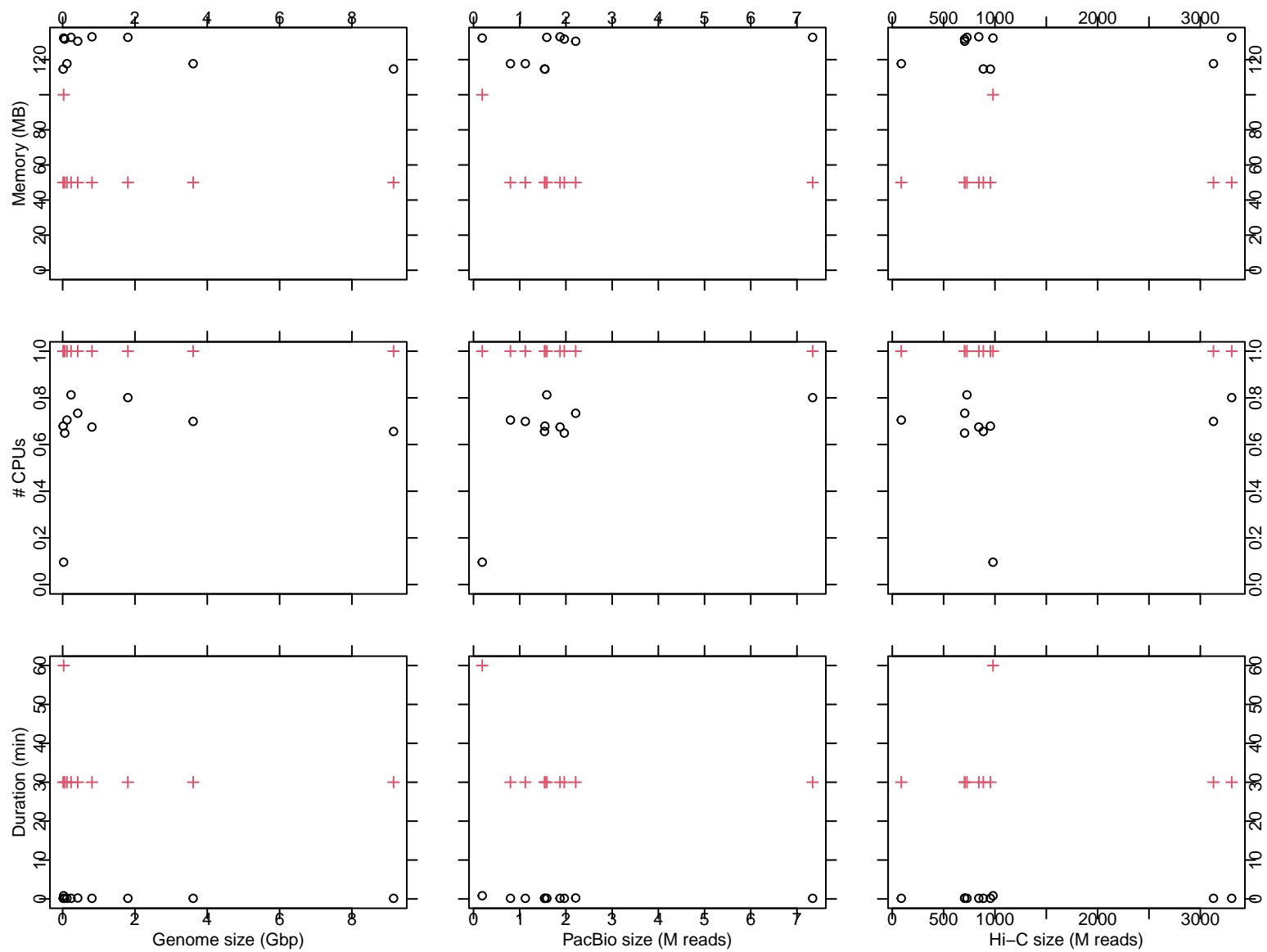


# GENOME\_STATISTICS:NCBI\_GET\_ODB

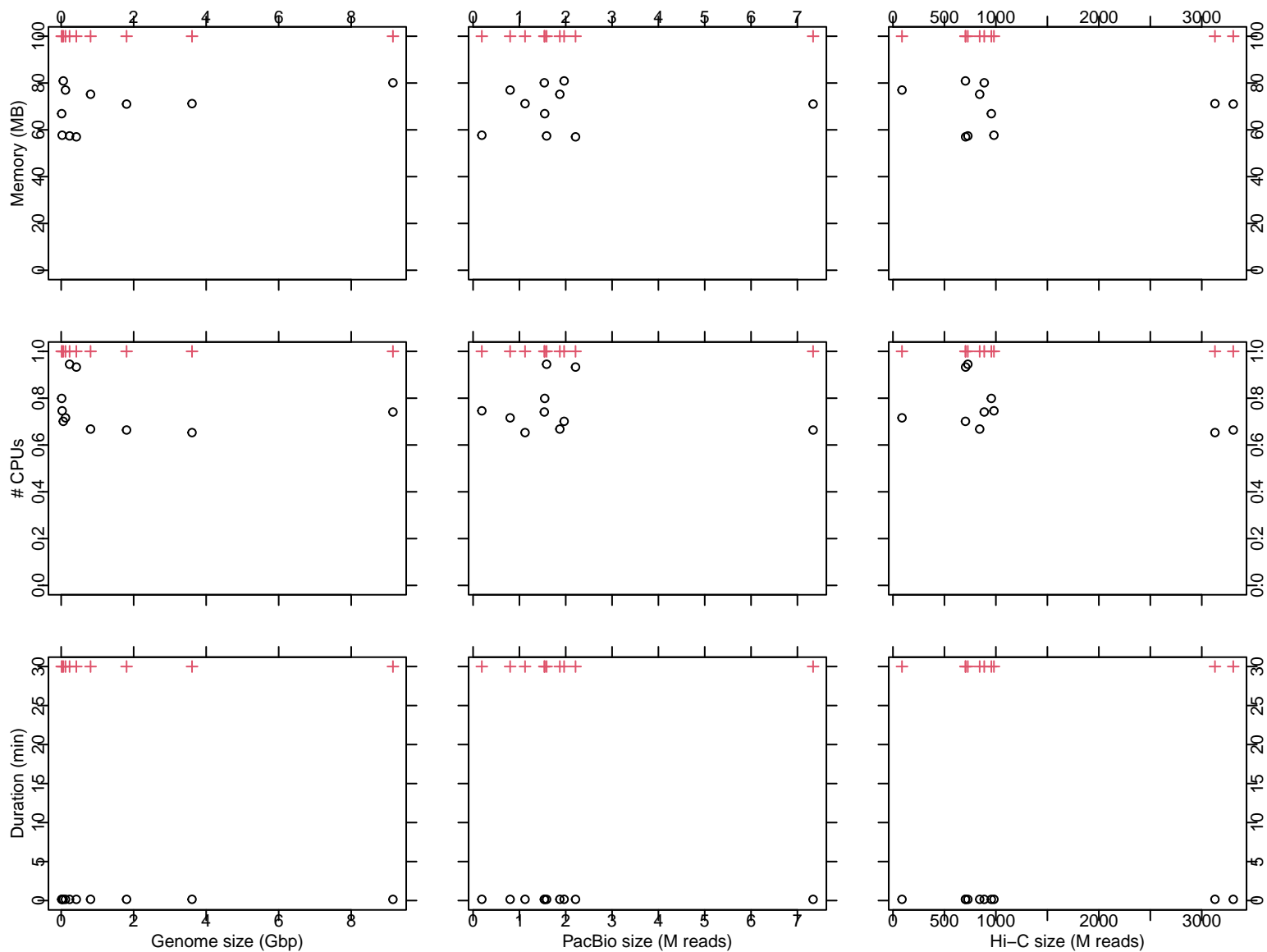




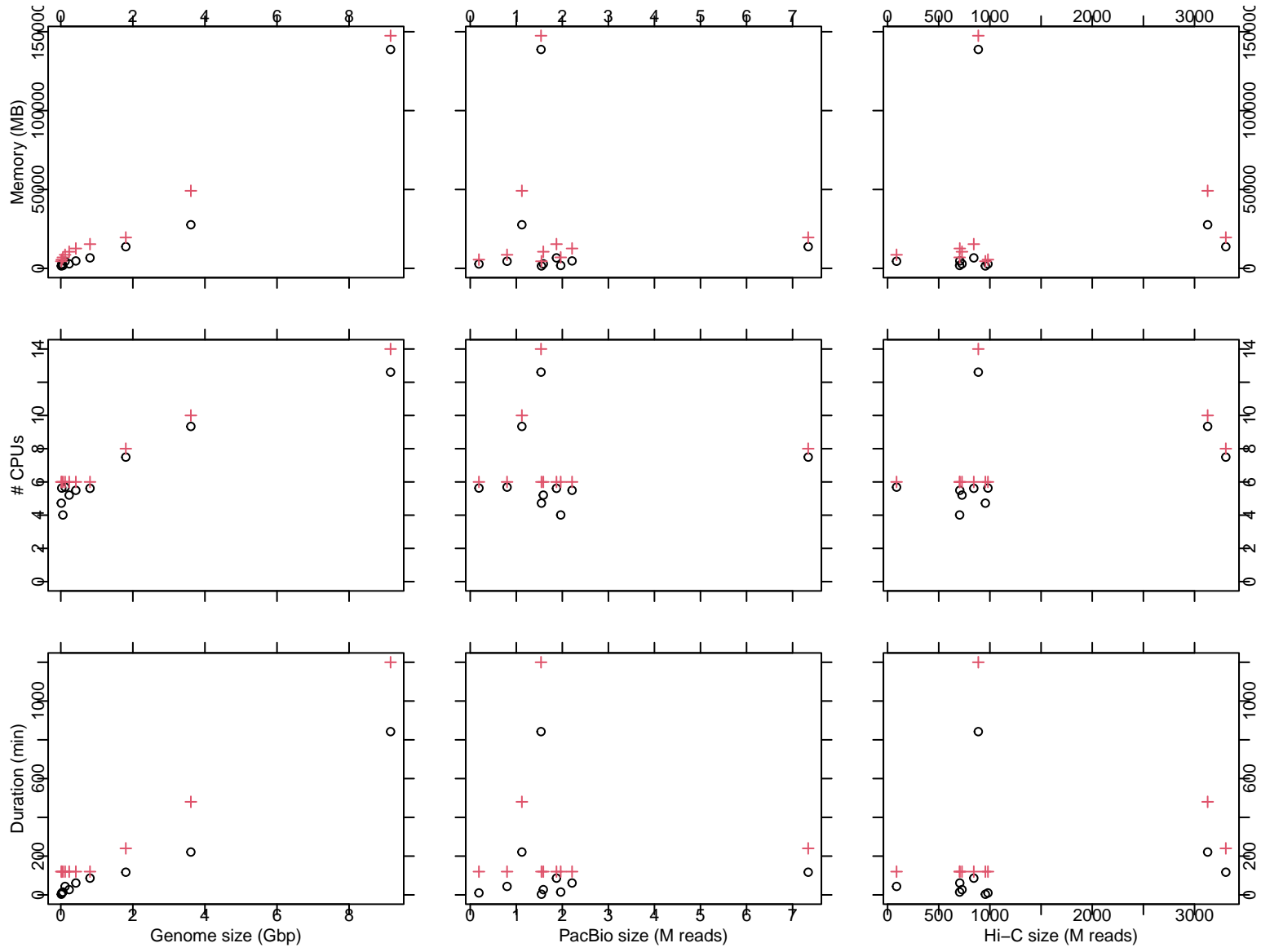
# MULTIQC



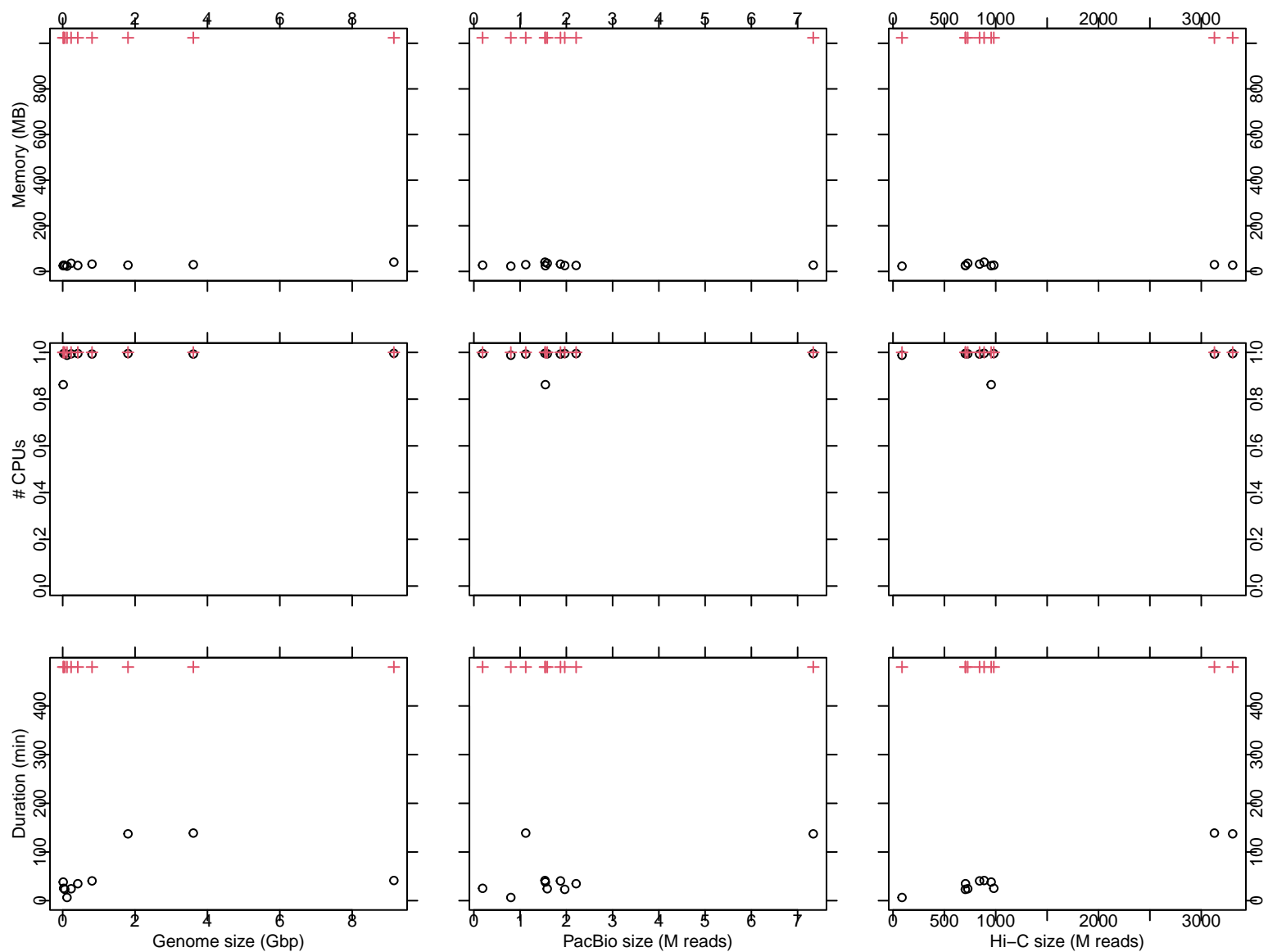
# CONTACT\_MAPS:COOLER\_DUMP



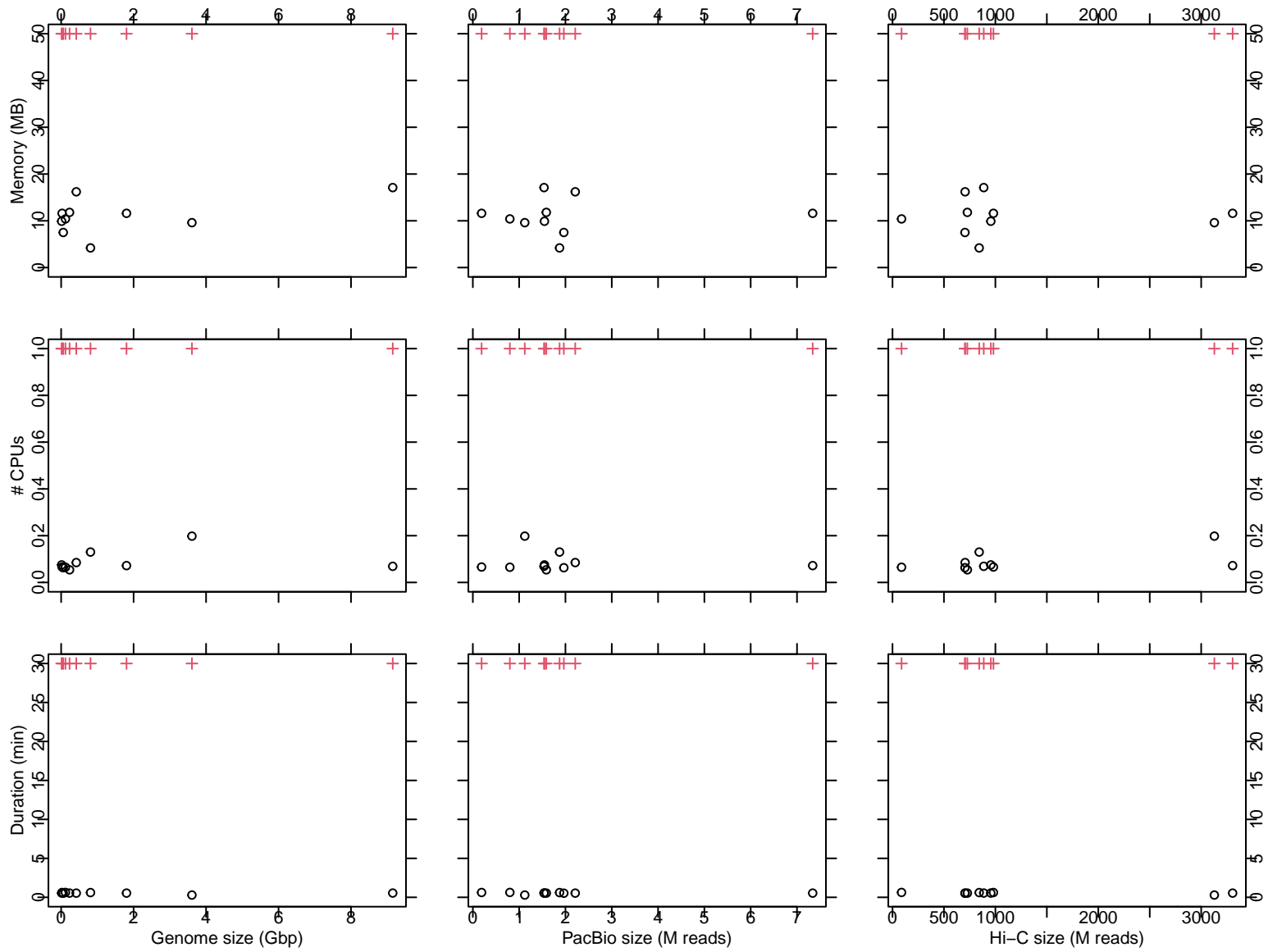
# GENOME\_STATISTICS:BUSCO



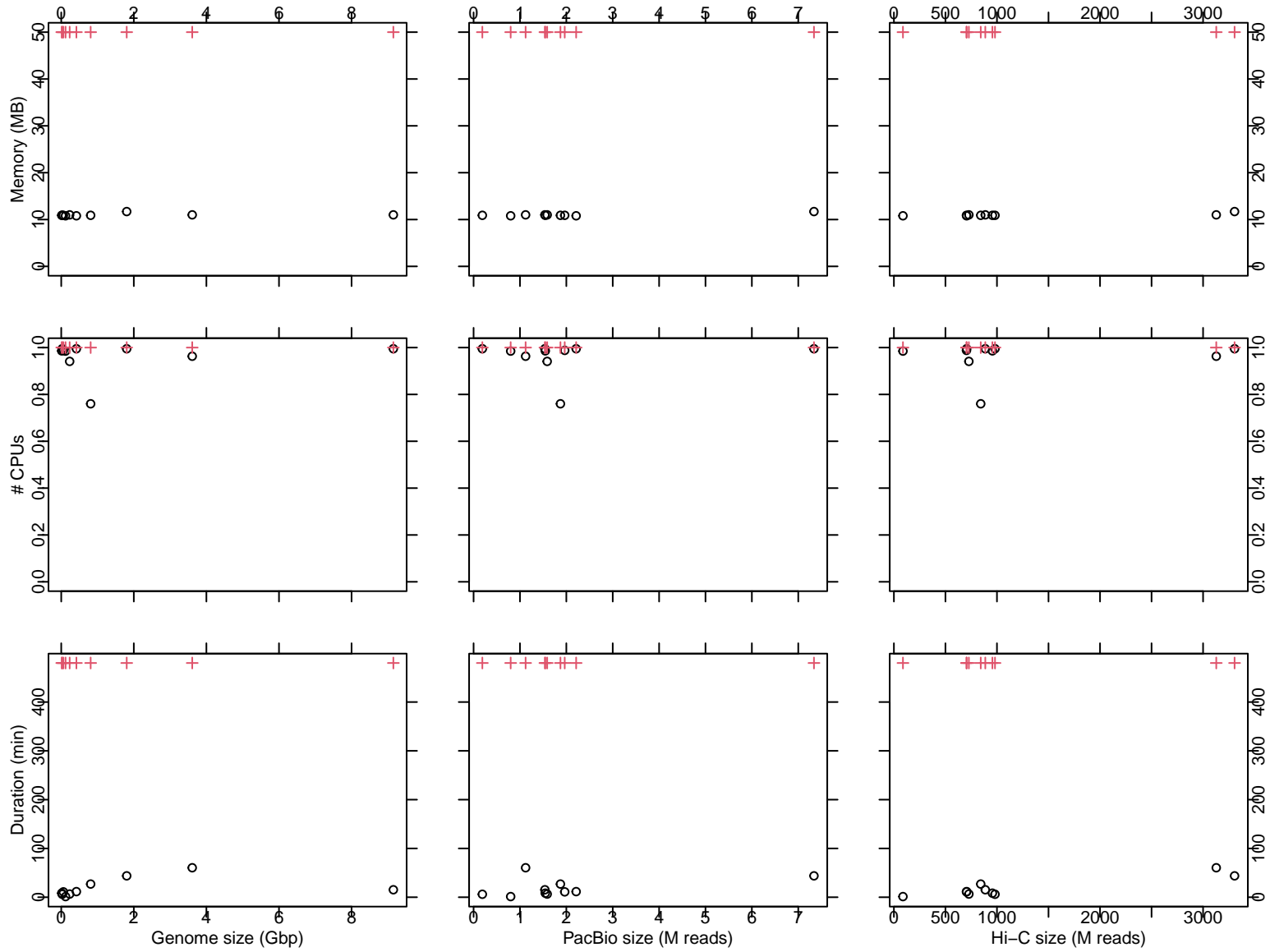
# CONTACT\_MAPS:SAMTOOLS\_VIEW



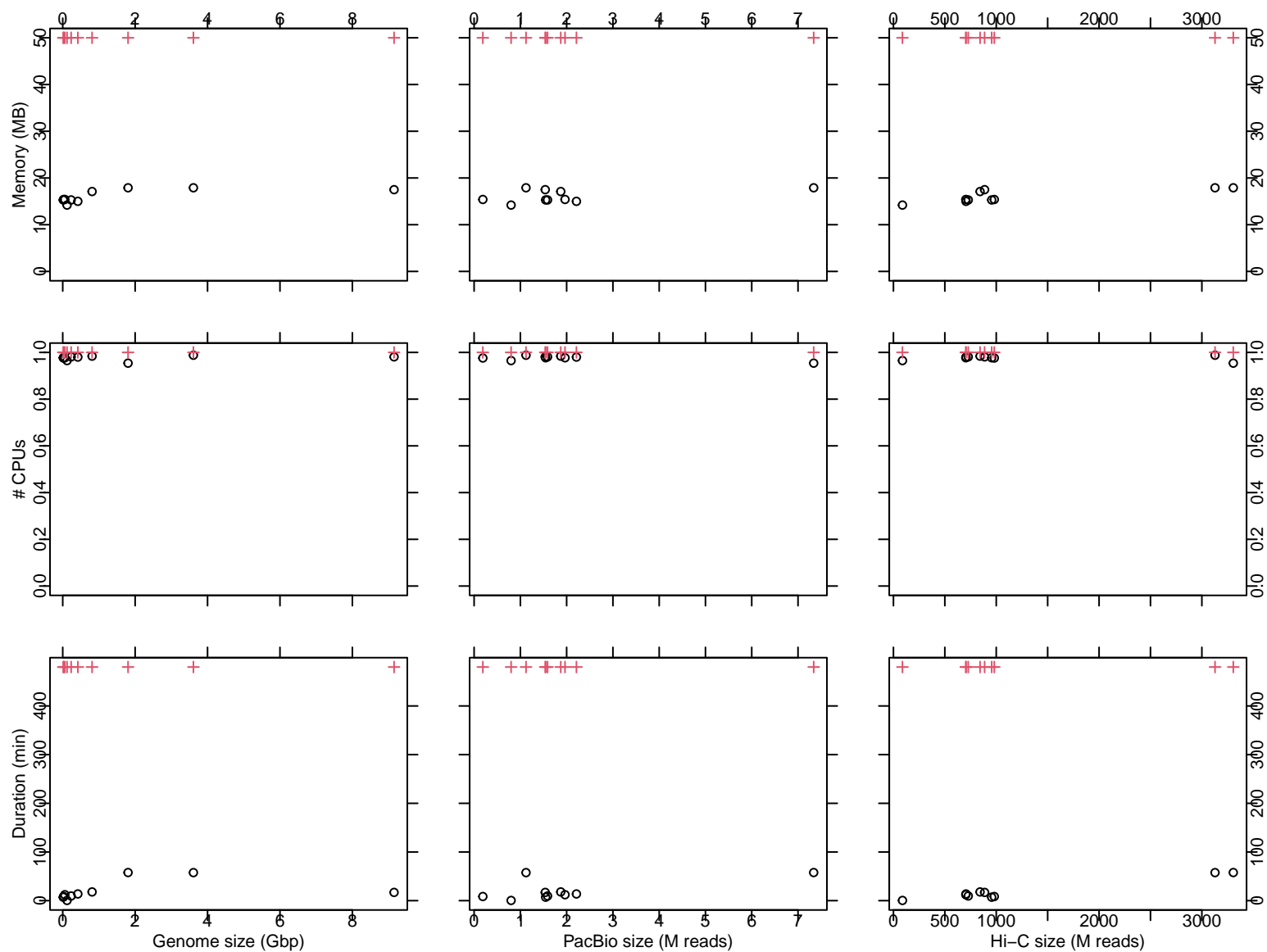
# GENOME\_STATISTICS:SUMMARYGENOME



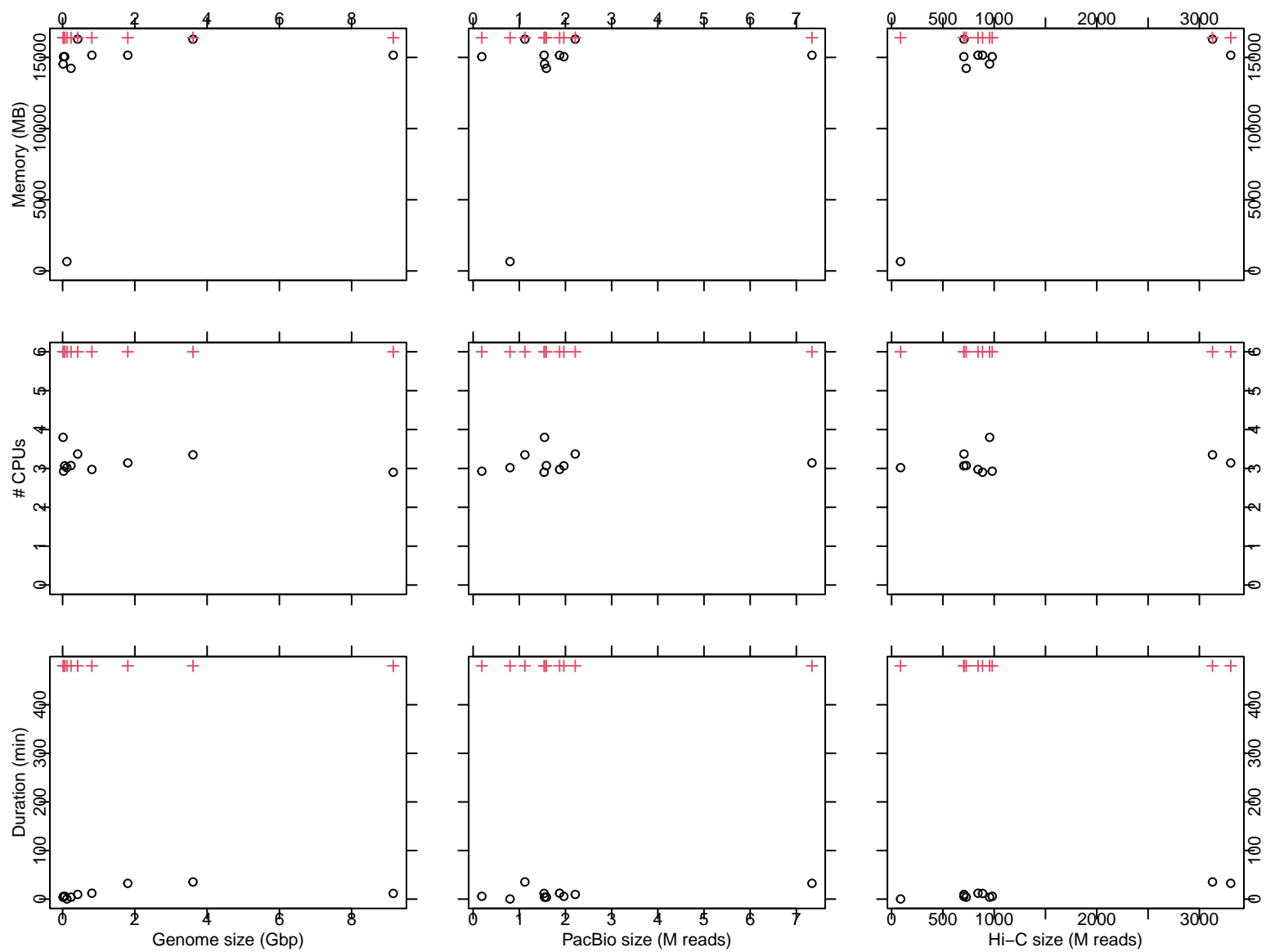
# CONTACT\_MAPS:BEDTOOLS\_BAMTOBED



# CONTACT\_MAPS:FILTER\_BED

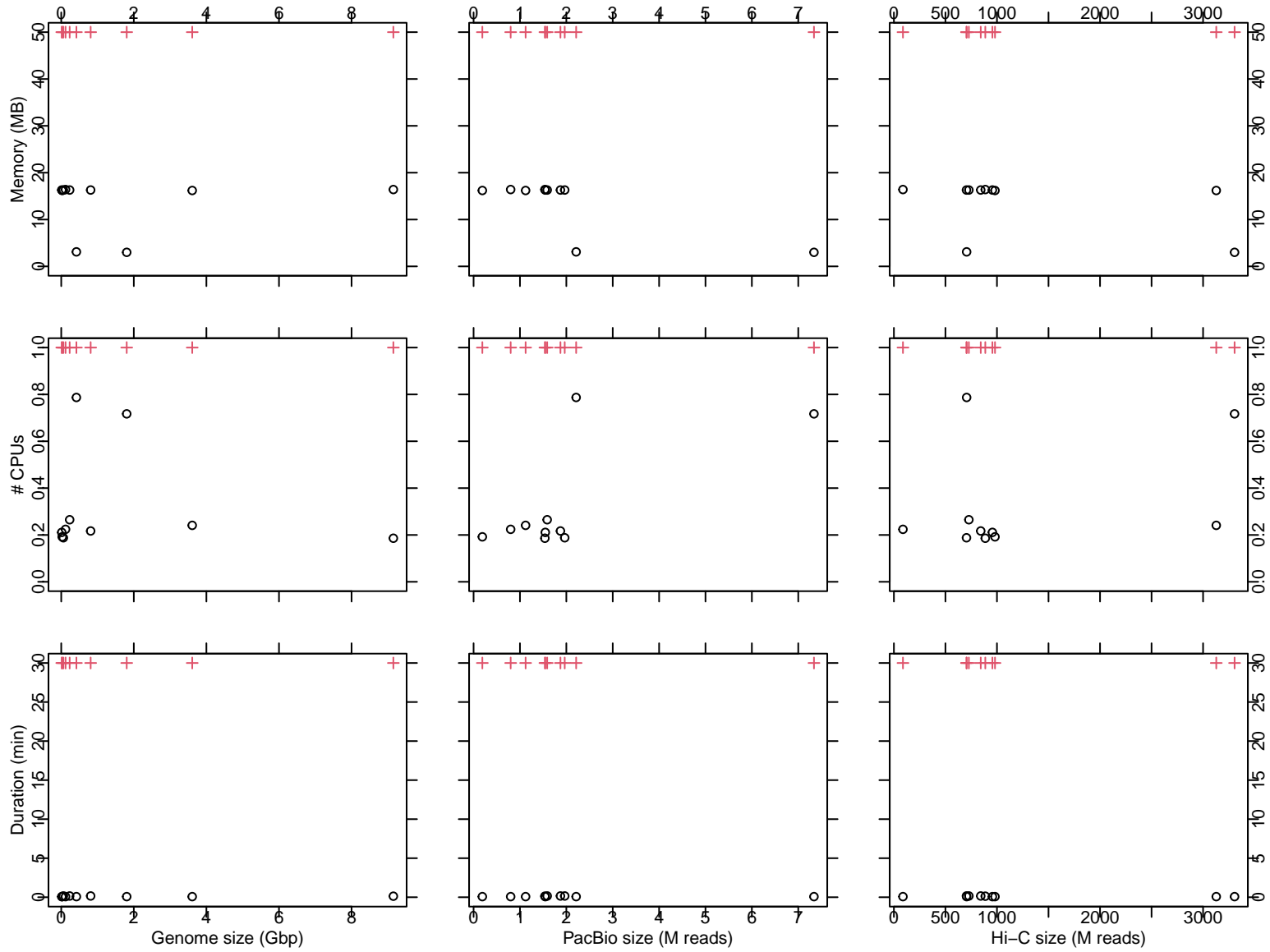


# CONTACT\_MAPS:FILTER\_SORT

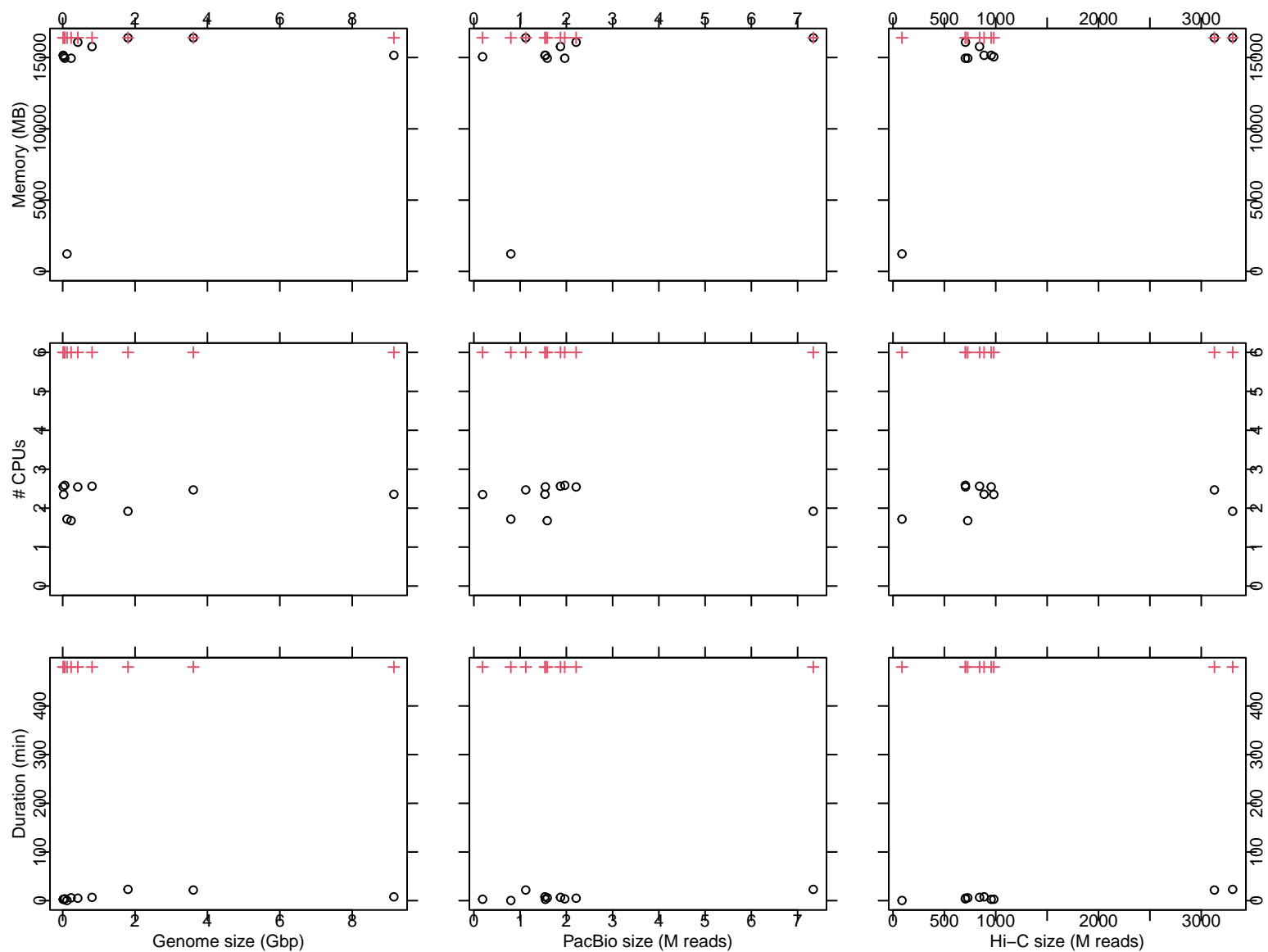




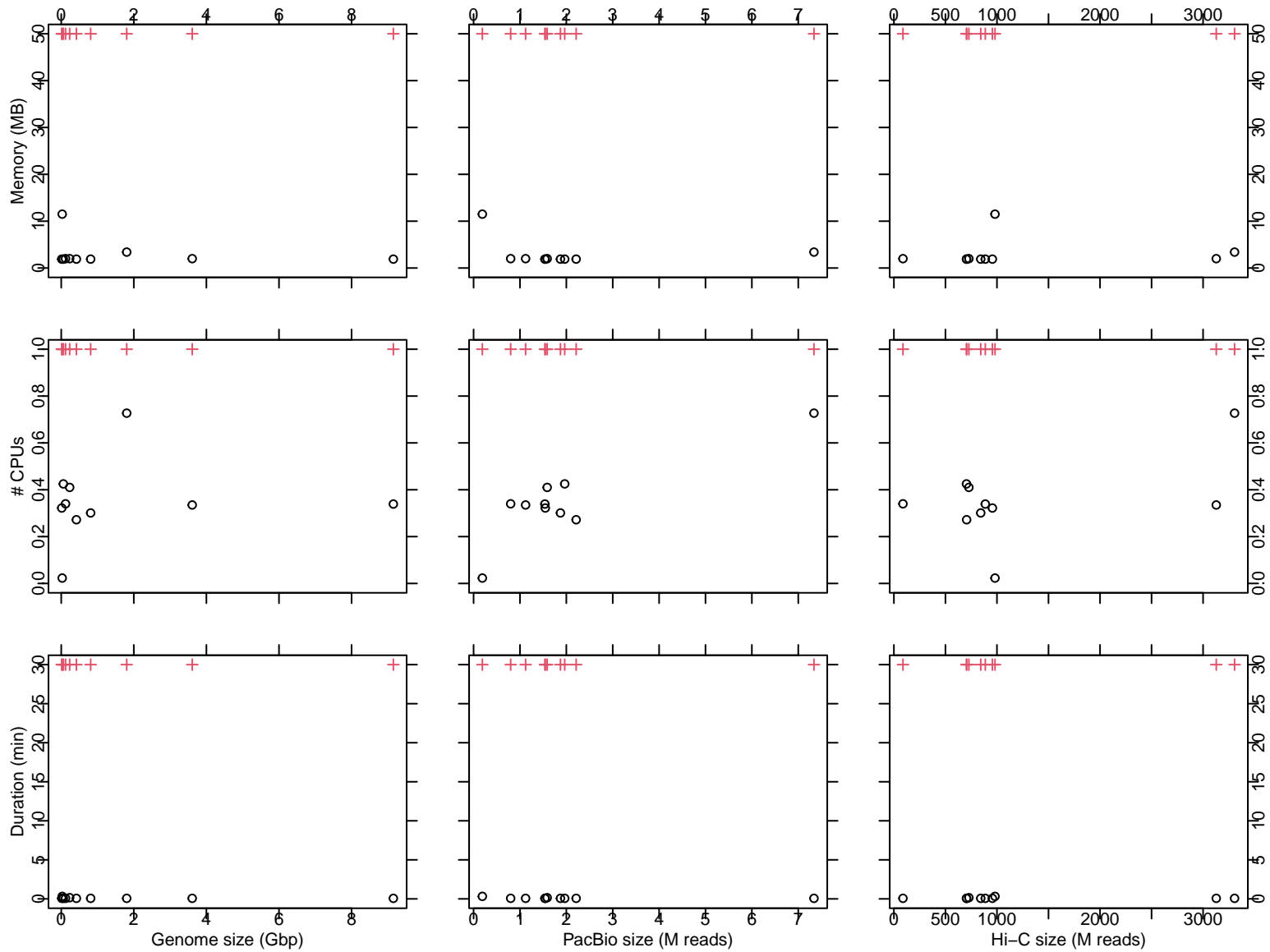
# GENOME\_STATISTICS:CREATETABLE



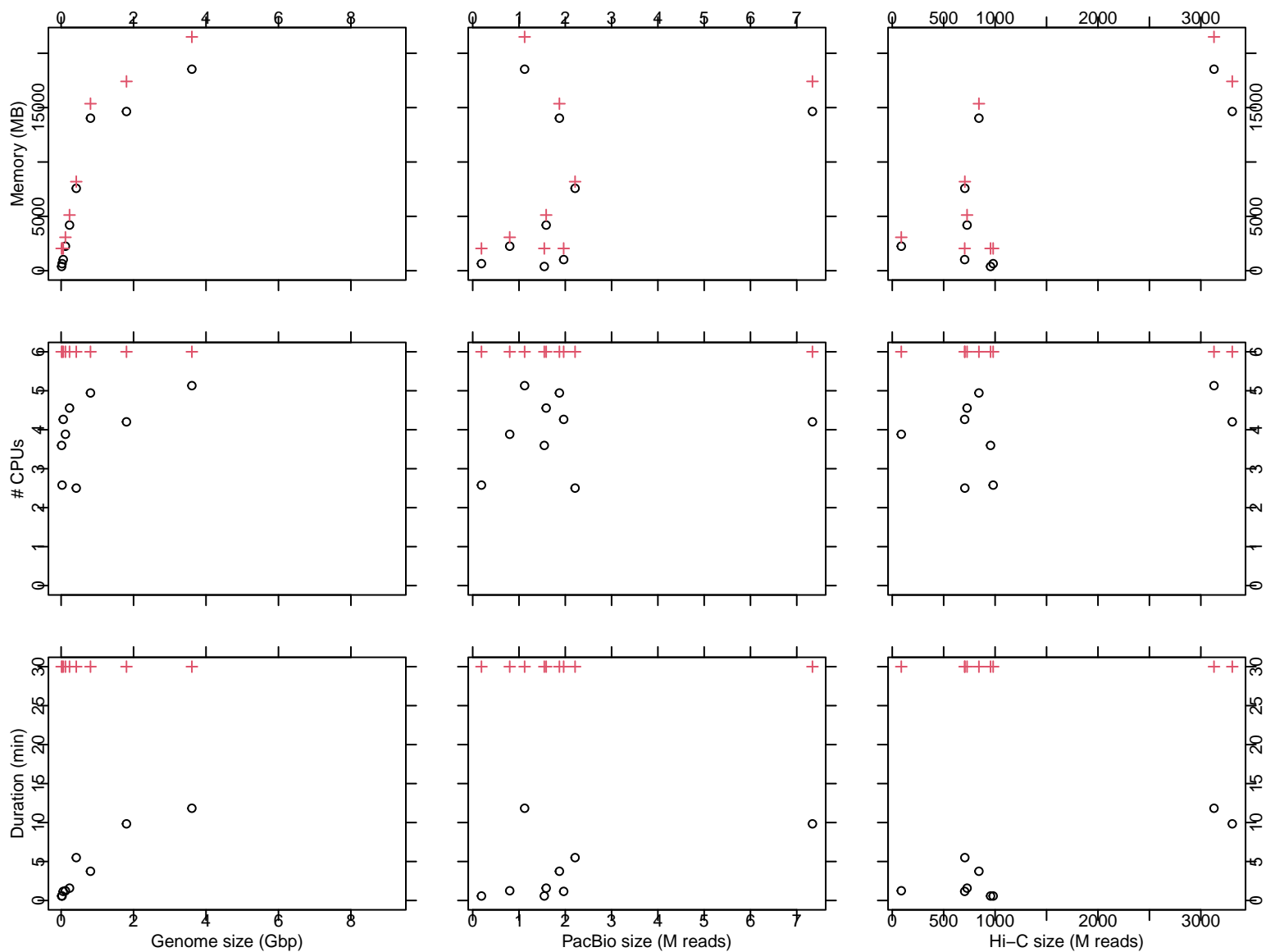
# CONTACT\_MAPS:BED\_SORT



# CUSTOM\_DUMPSOFTWAREVERSIONS



# GENOME\_STATISTICS:MERQURYFK\_MERQURYFK



# INPUT\_CHECK:SAMPLESHEET\_CHECK

