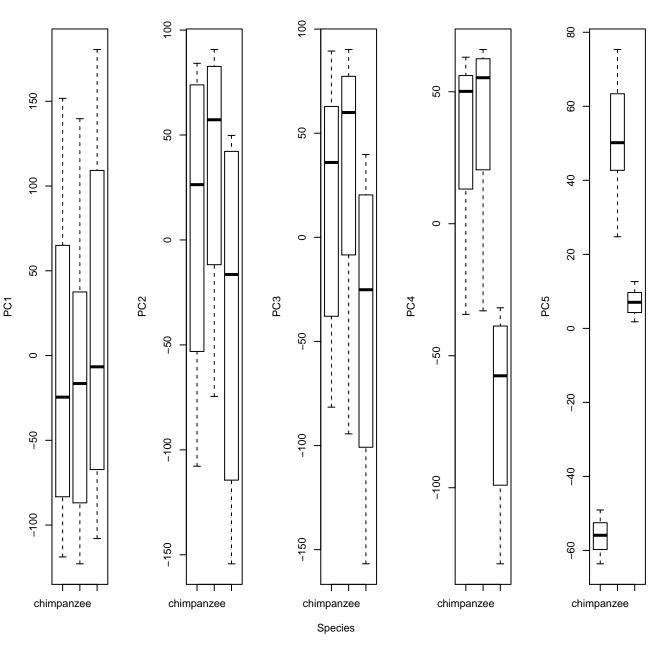
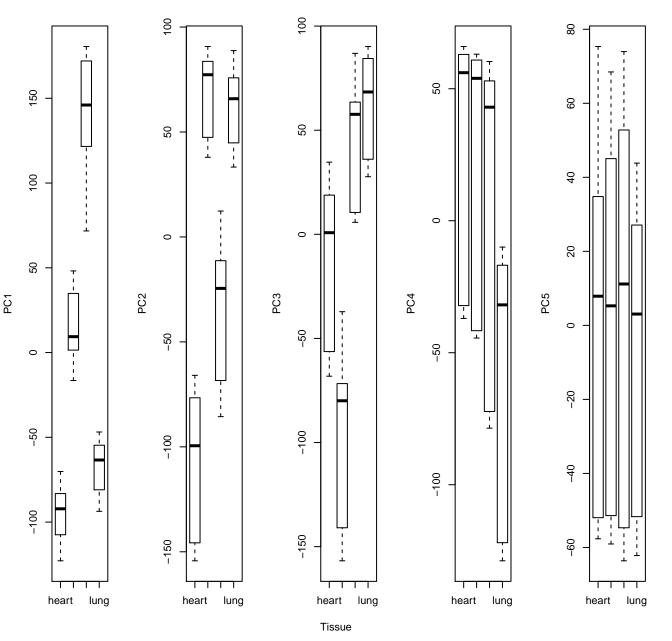
PCs vs. Species



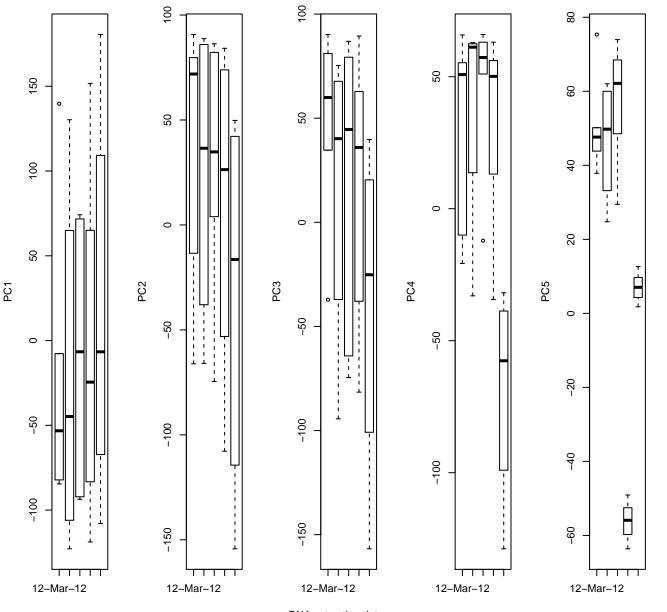
PCs vs. Tissue



PCs vs. Individual 100 100 8 20 150 9 20 20 4 100 20 20 PC2 PC3 PC5 0 -50 -50 -50 -20 -50 -100 -100 4 -100 -100 -150 -150 09-4x0516 4x0516 4x0516 4x0516 4x0516

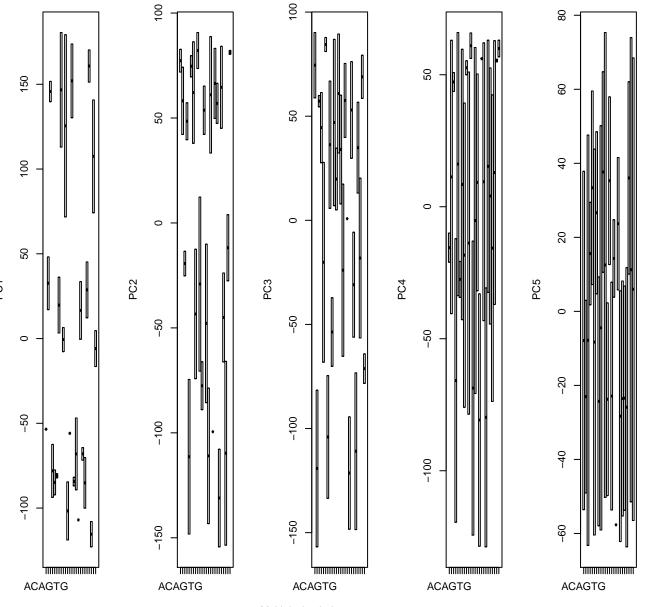
Individual

PCs vs. RNA.extraction.date



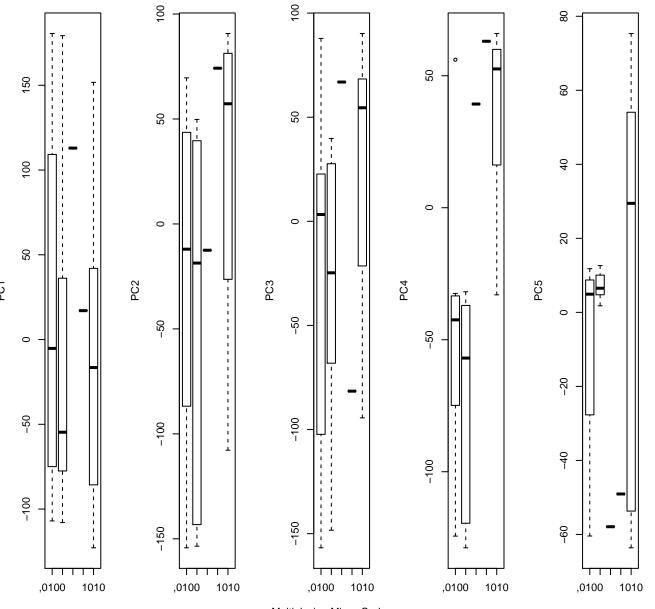
RNA.extraction.date

PCs vs. Multiplexing.index.sequence



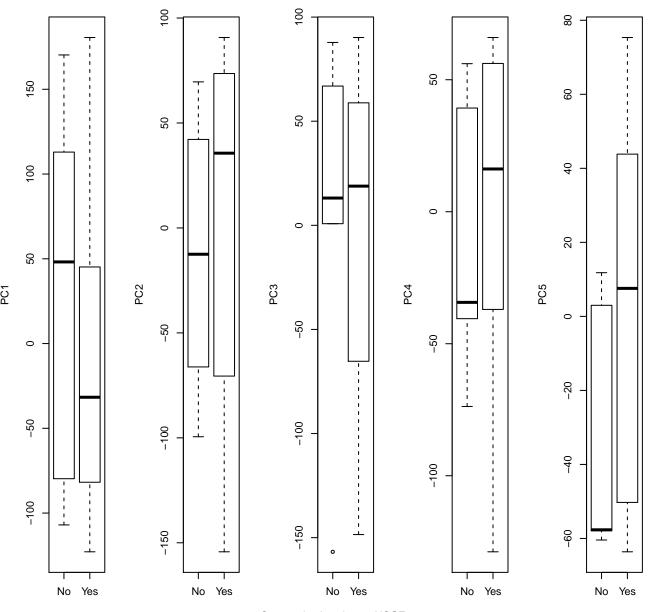
Multiplexing.index.sequence

PCs vs. Multiplexing.Mixes.Code



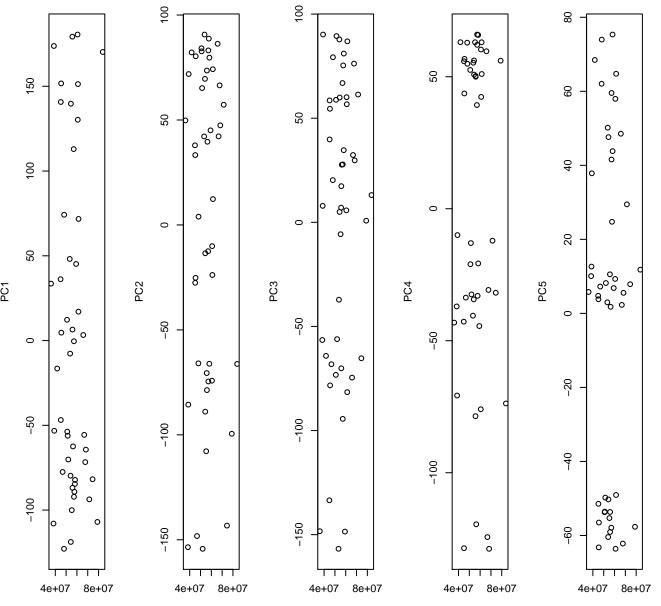
Multiplexing.Mixes.Code

PCs vs. Sequencing.location..at.UCGF



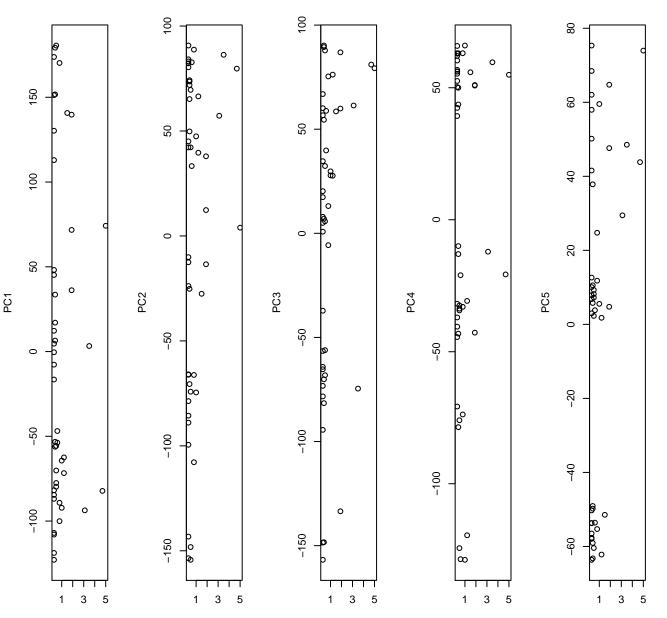
Sequencing.location..at.UCGF

PCs vs. Total.number.of.reads.sequenced



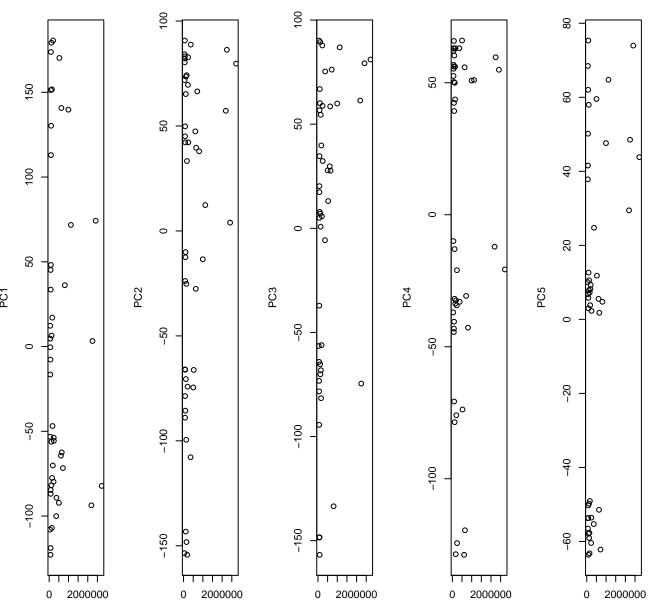
Total.number.of.reads.sequenced

PCs vs. Percentage.of.bps.trimmed..adapters.

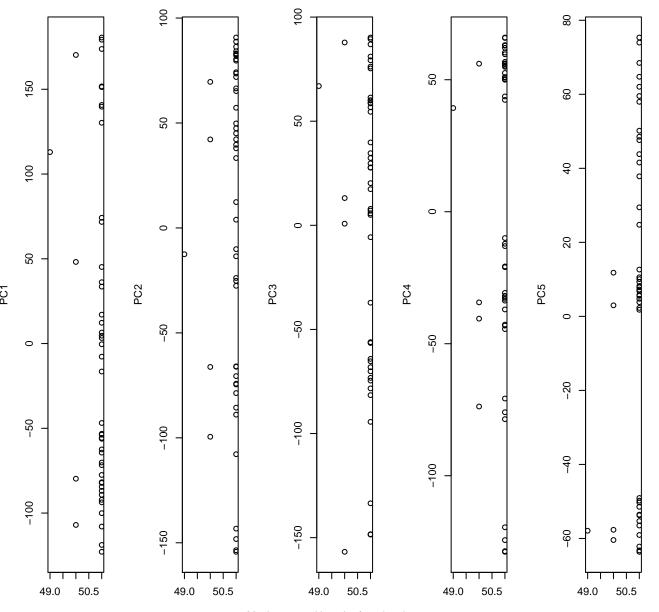


Percentage.of.bps.trimmed..adapters.

PCs vs. Number.of.reads.shorter.than.20bp.removed

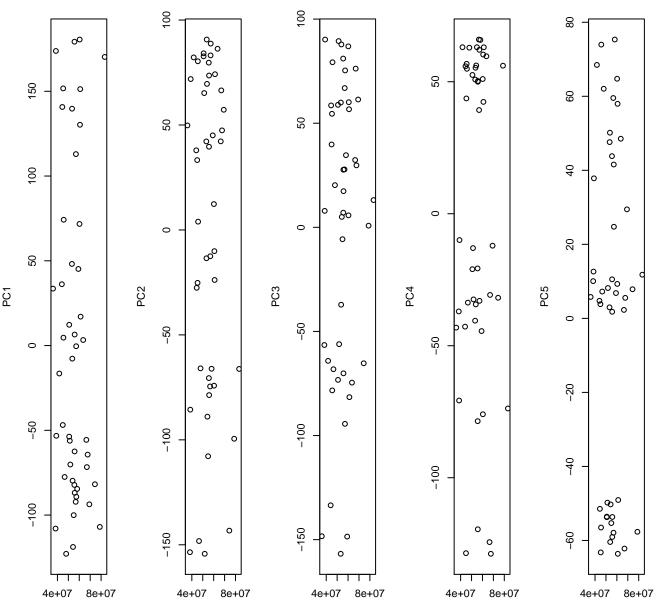


PCs vs. Maximum.read.length.after.trimming



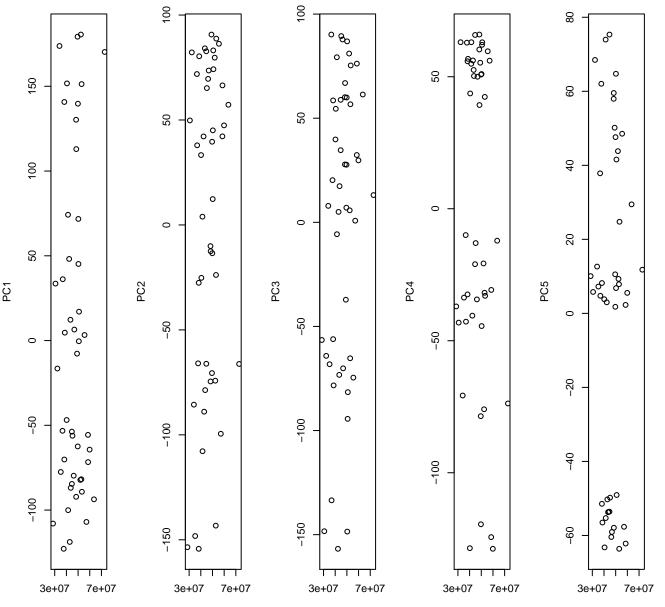
Maximum.read.length.after.trimming

PCs vs. Total.number.of.reads.processed.in.tophat



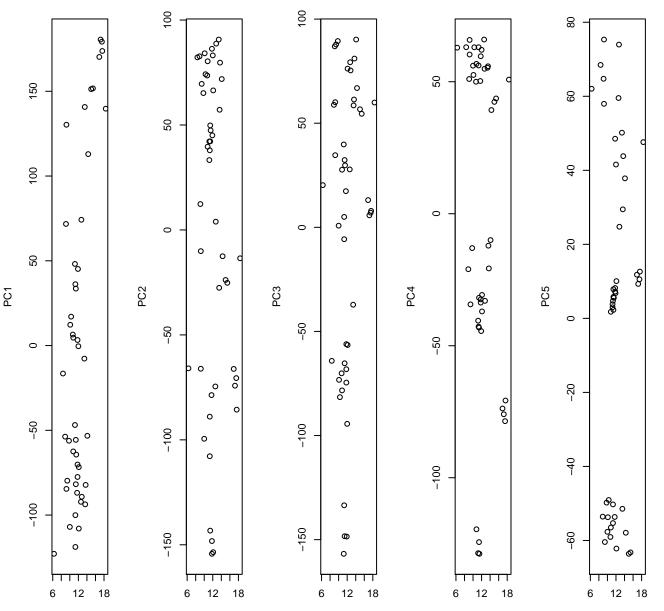
Total.number.of.reads.processed.in.tophat

PCs vs. Total.number.of.mapped.reads



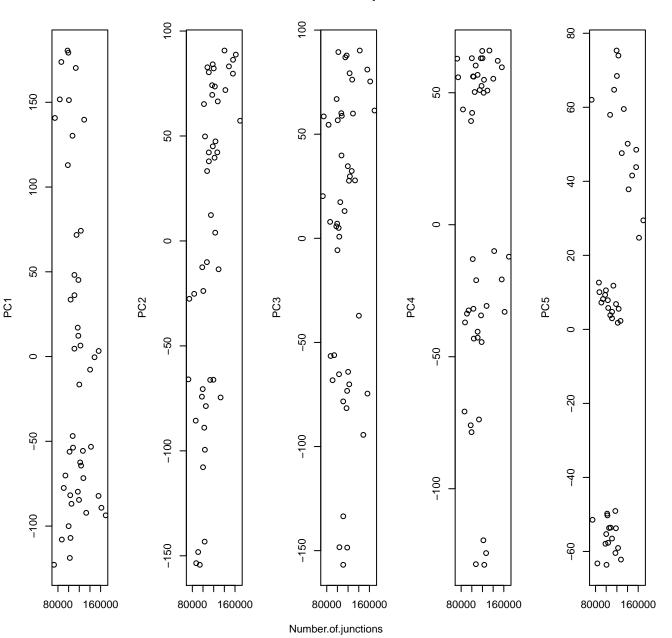
Total.number.of.mapped.reads

PCs vs. Percentage.of.mapped.reads.overlapping.a.junction

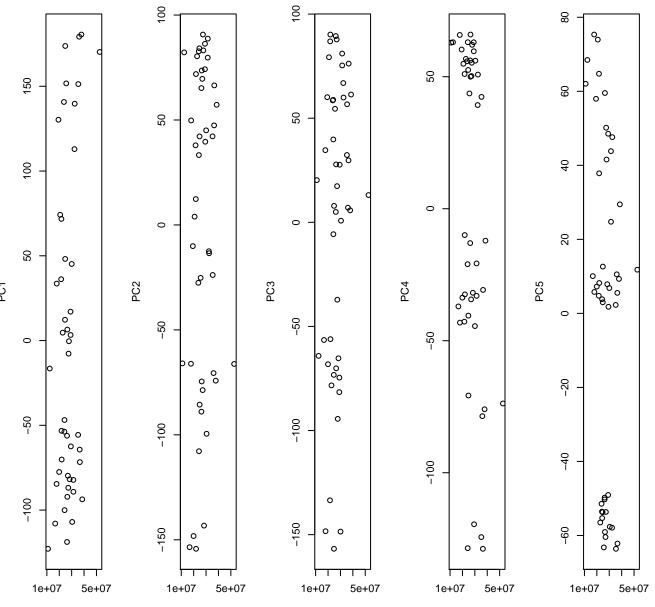


Percentage.of.mapped.reads.overlapping.a.junction

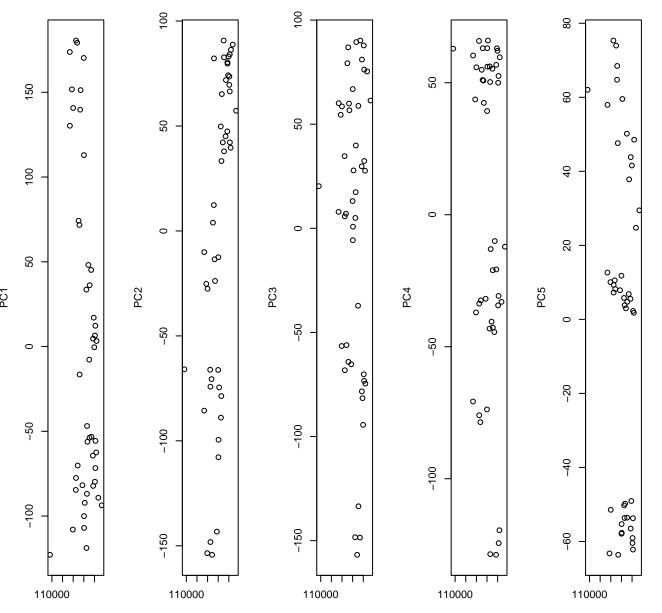
PCs vs. Number.of.junctions



PCs vs. Number.of.reads.mapped.on.orthologous.exons

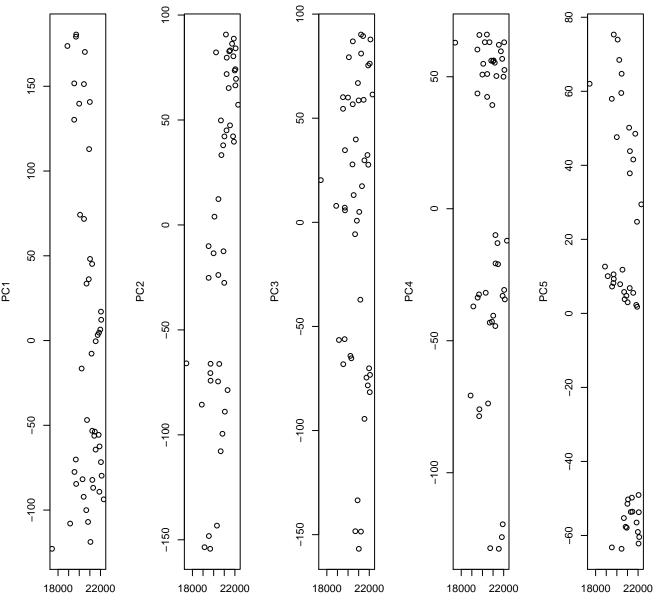


PCs vs. Number.of.orthologous.exons.with.at.least.1.mapped.read

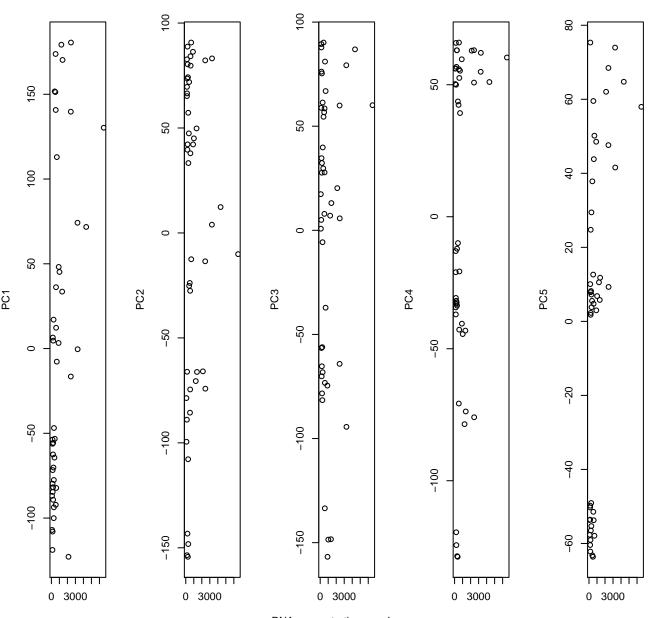


Number.of.orthologous.exons.with.at.least.1.mapped.read

PCs vs. Number.of.orthologous.genes.with.at.least.1.mapped.read

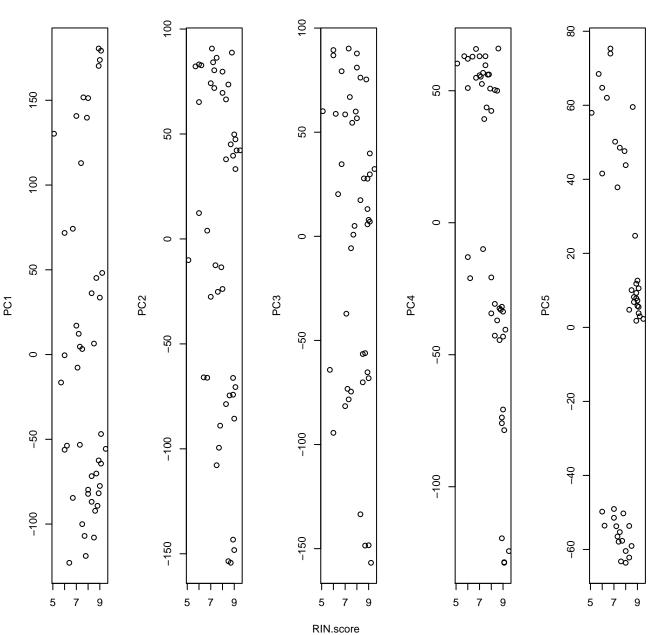


PCs vs. RNA.concentration..ng.uL.

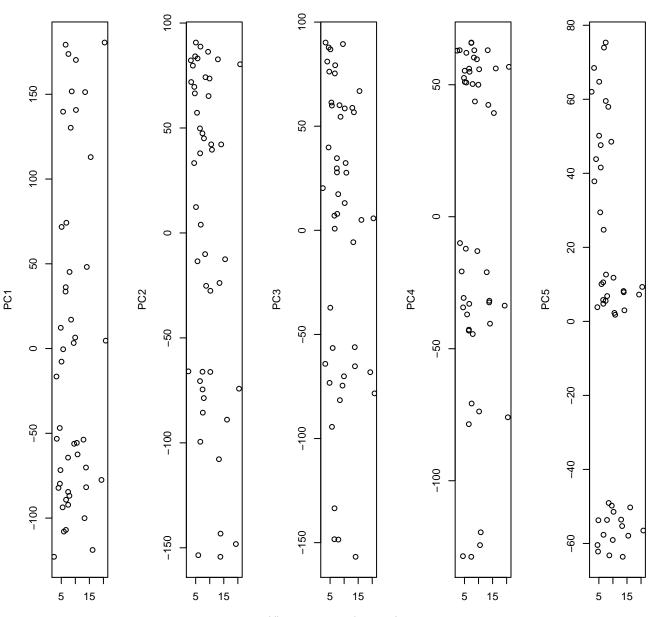


RNA.concentration..ng.uL.

PCs vs. RIN.score

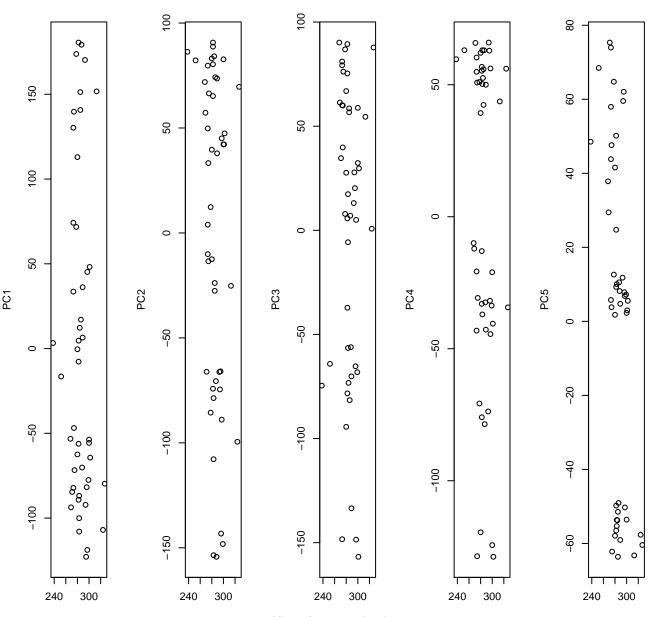


PCs vs. Library.concentration..ng.uL.



Library.concentration..ng.uL.

PCs vs. Library.fragments.size..bp.



Library. fragments. size..bp.