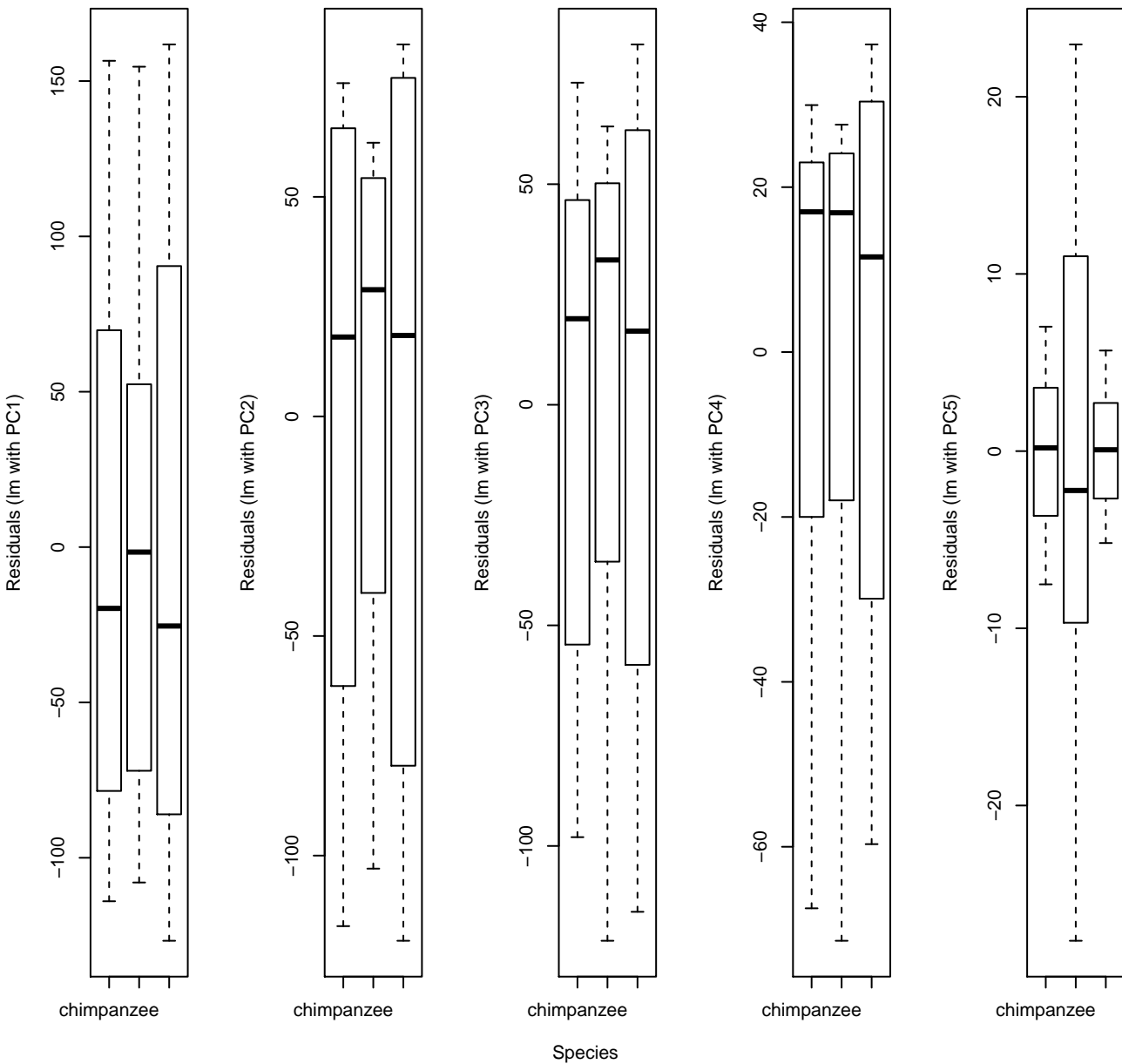
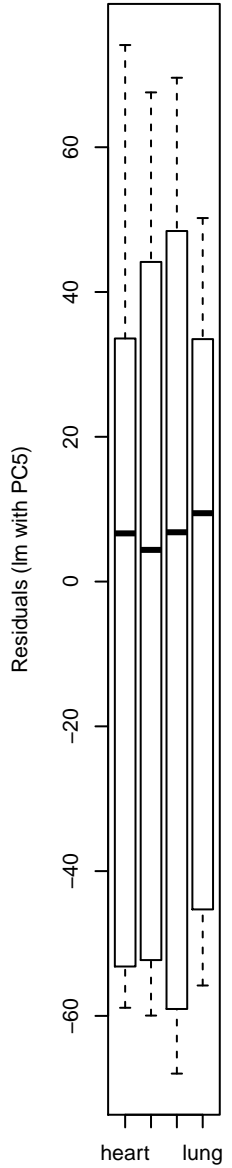
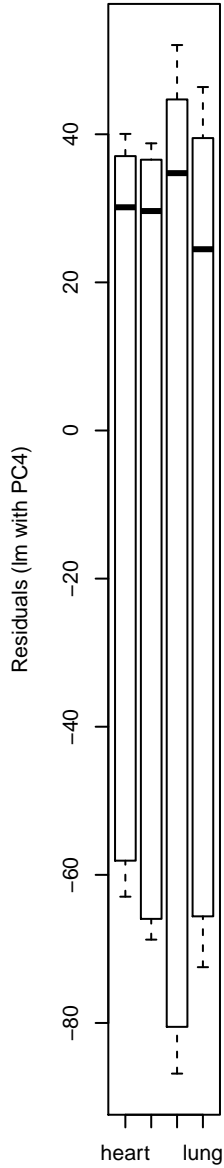
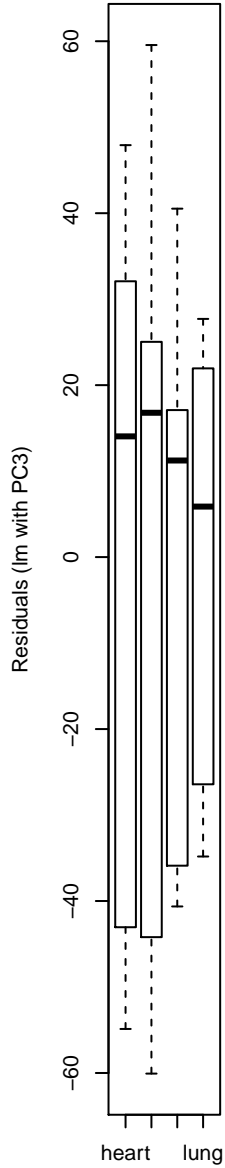
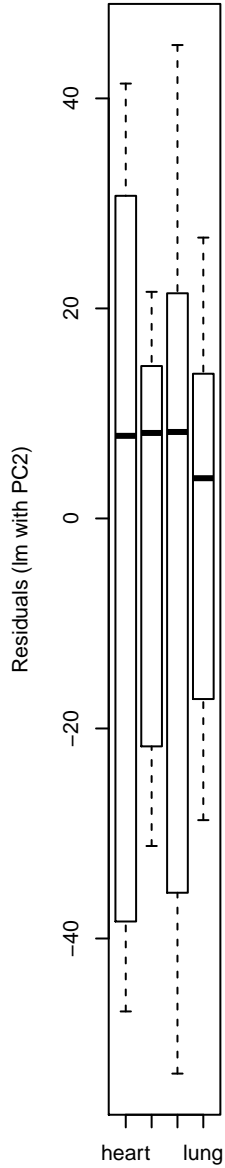
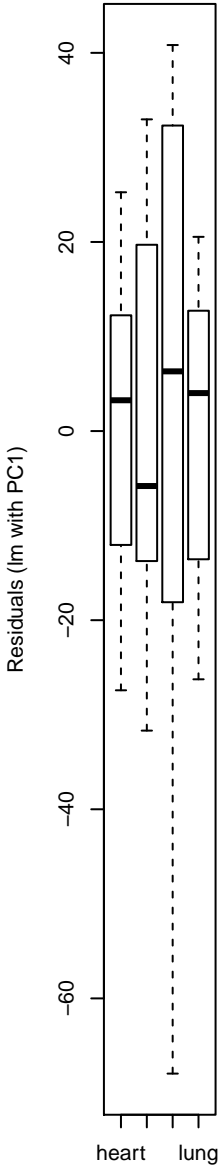


Residuals vs. Species

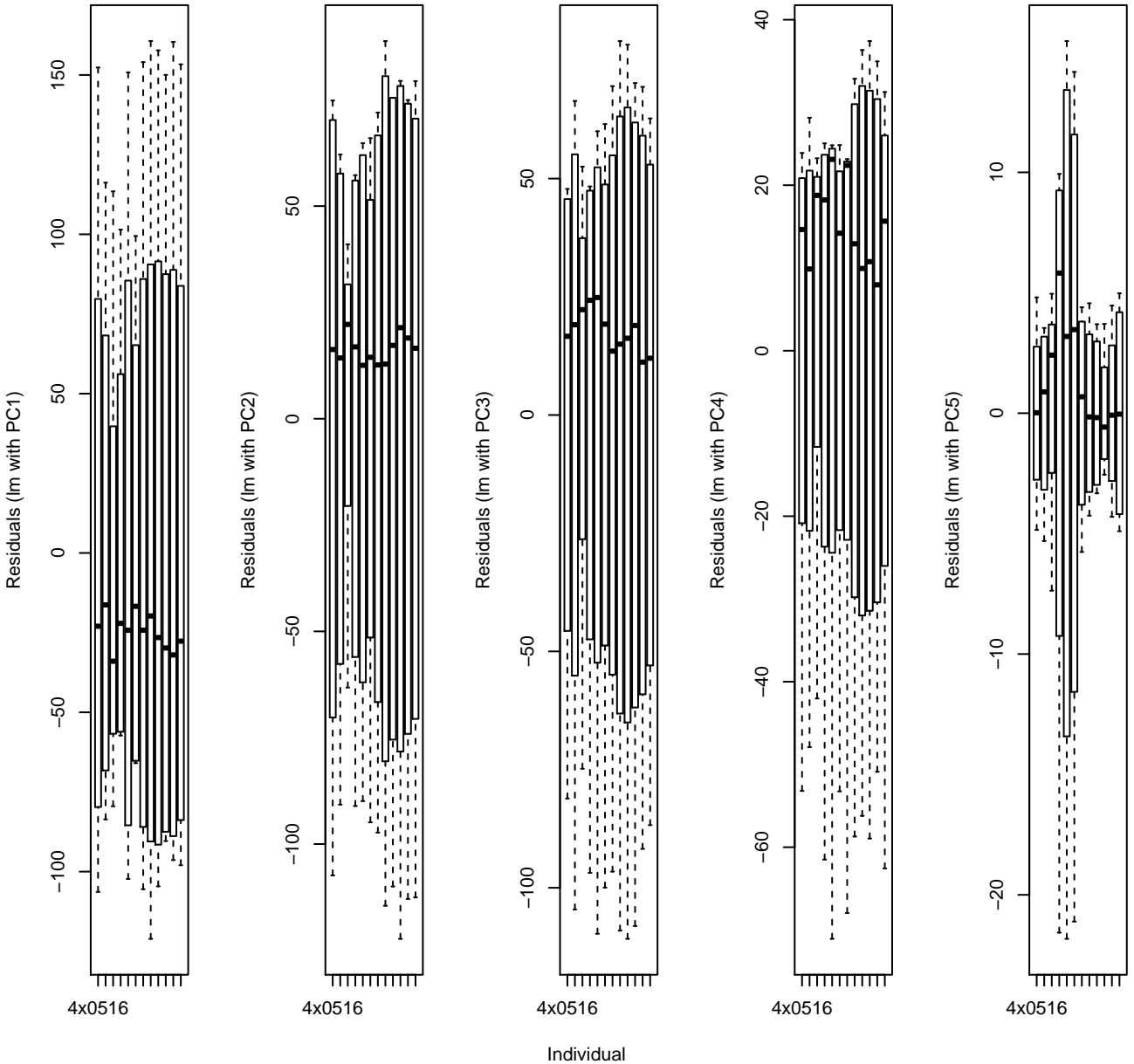


Residuals vs. Tissue

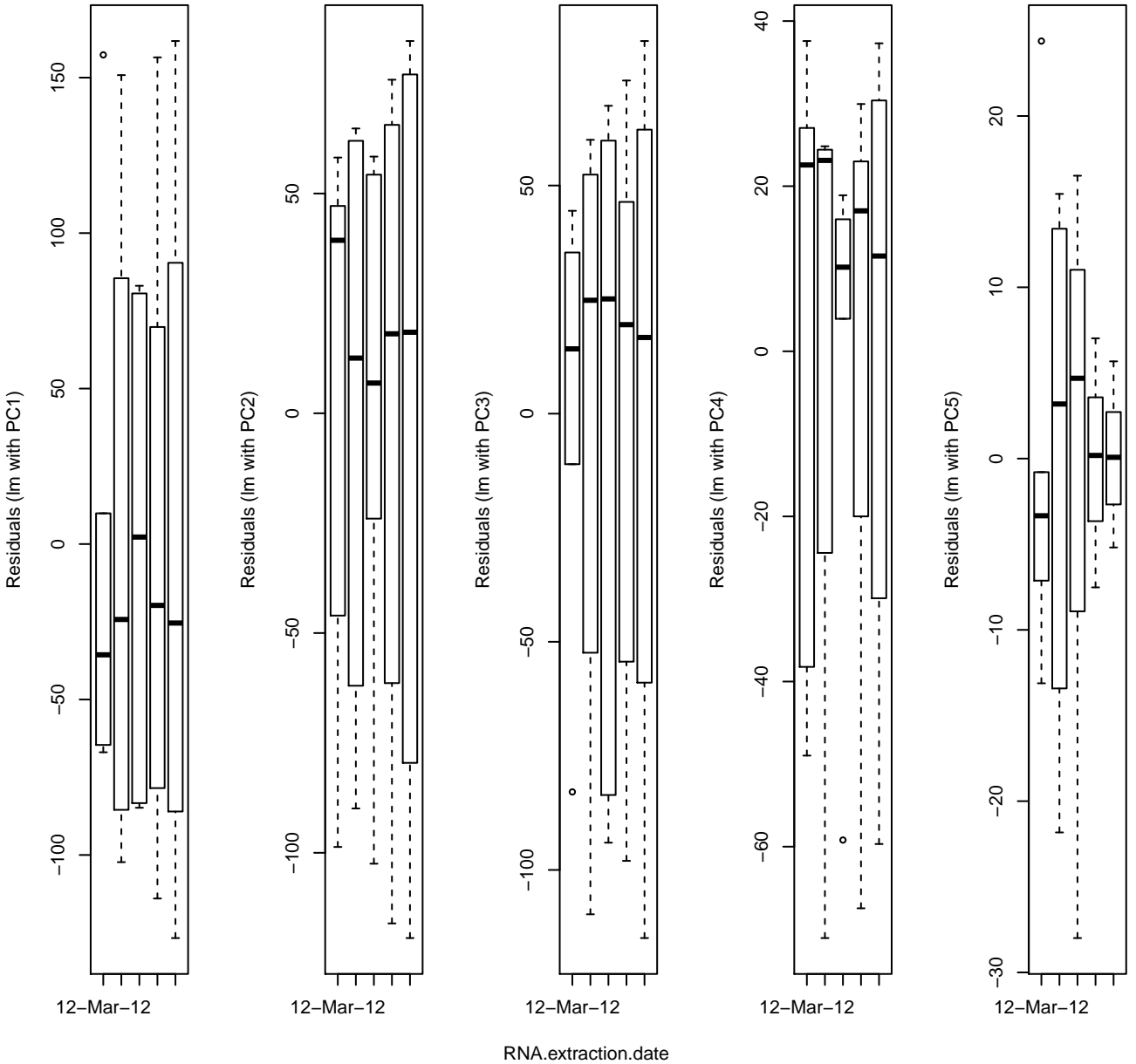


Tissue

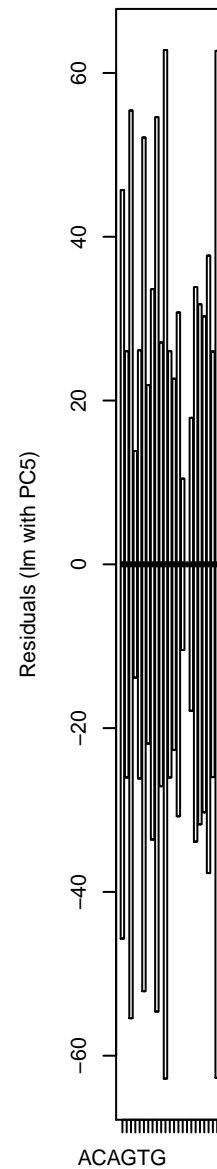
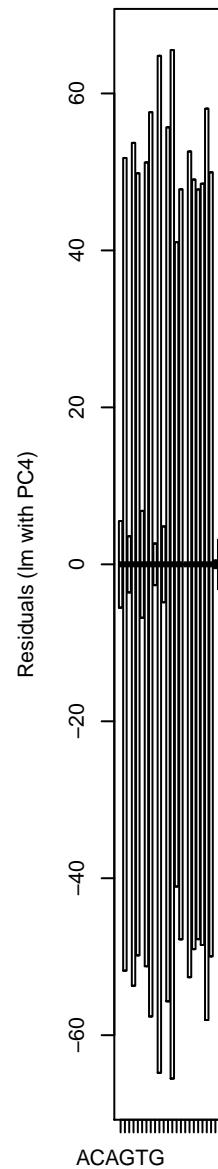
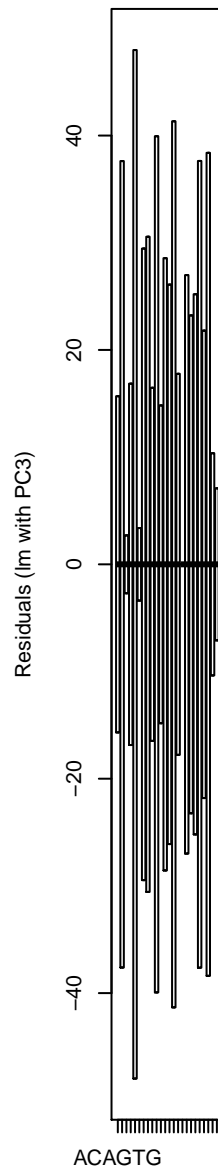
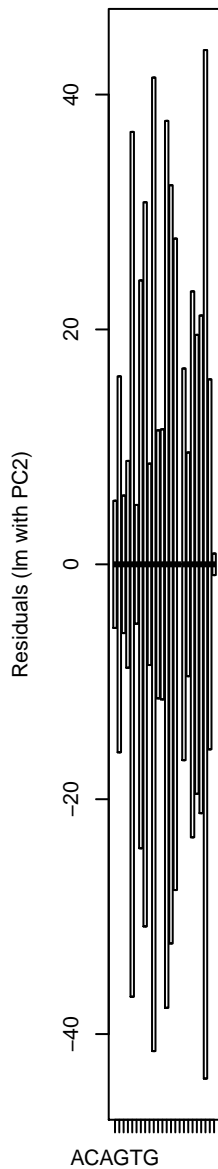
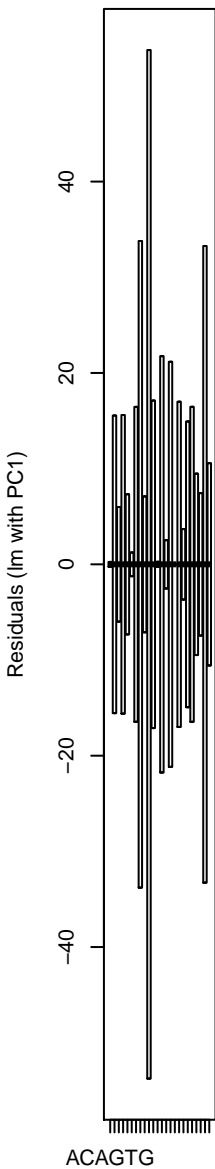
Residuals vs. Individual



Residuals vs. RNA.extraction.date

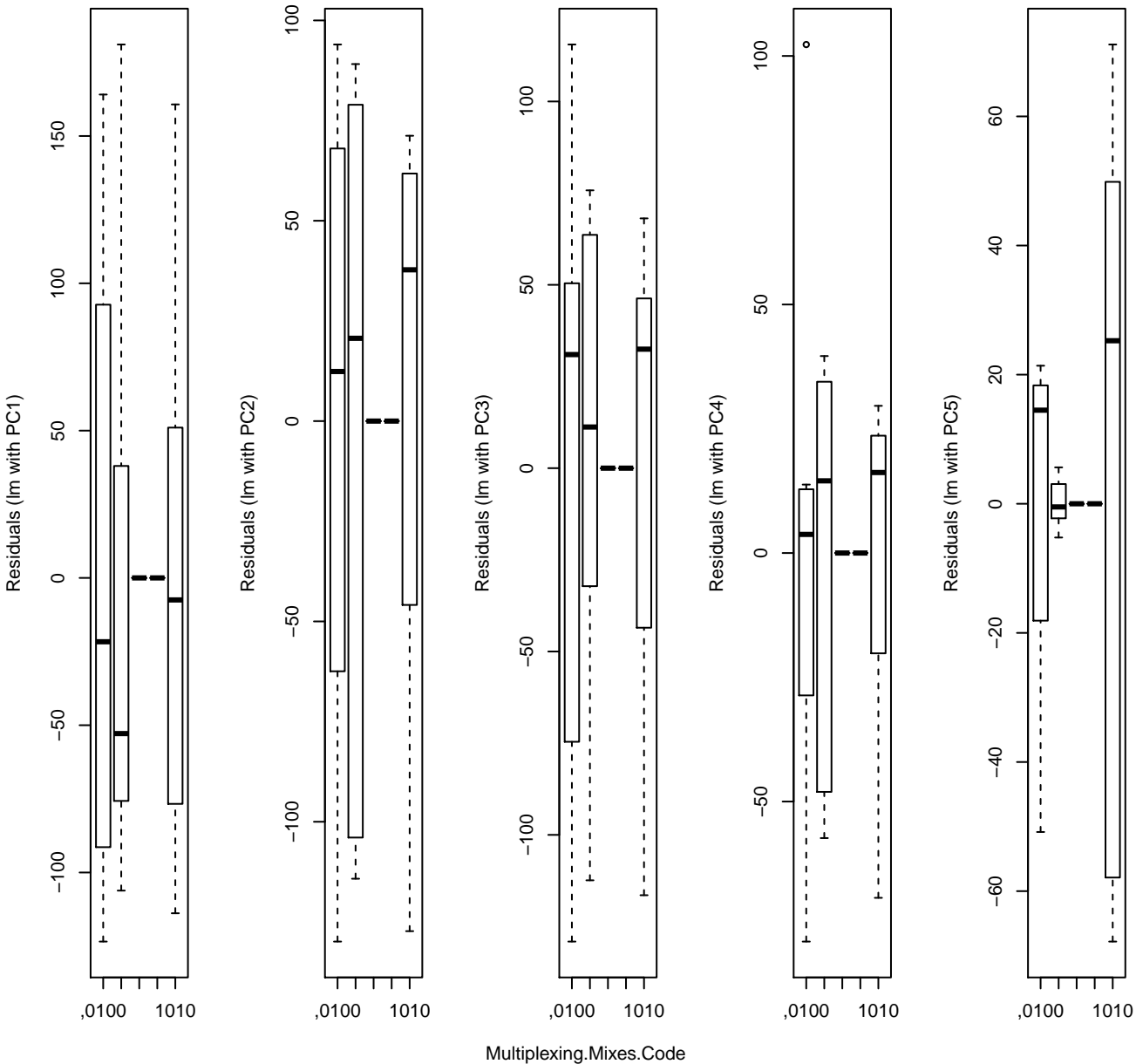


Residuals vs. Multiplexing.index.sequence

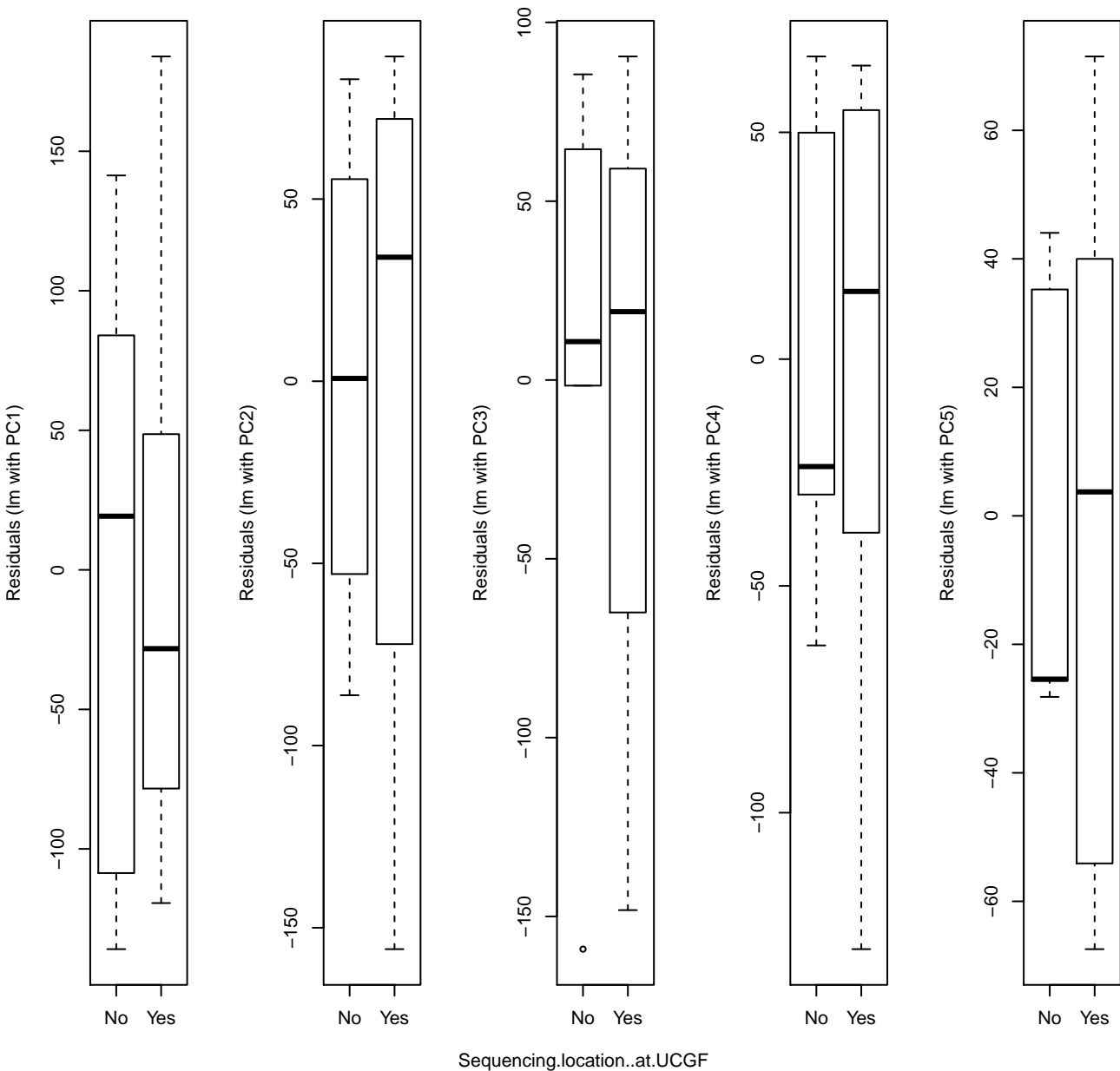


Multiplexing.index.sequence

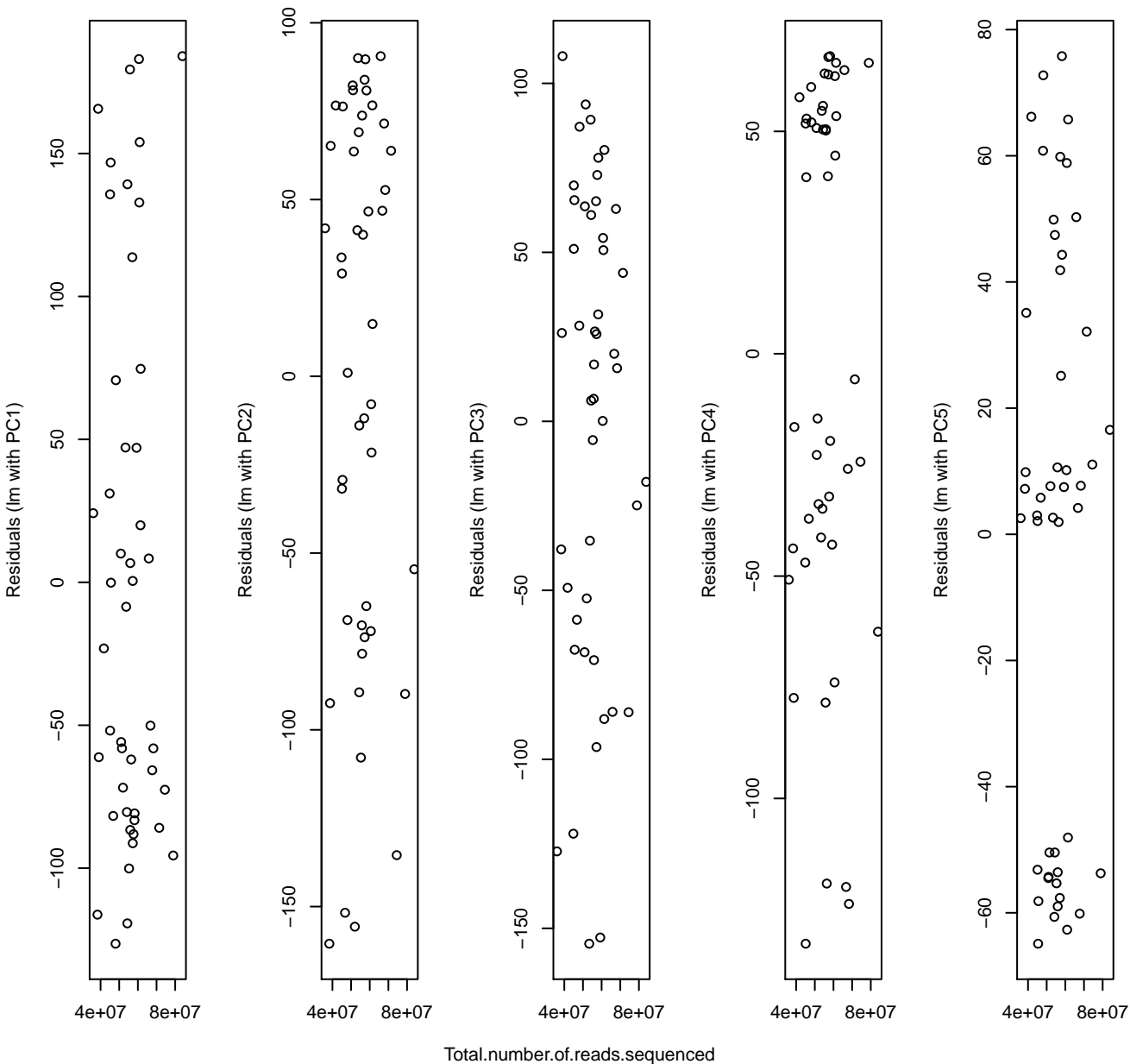
Residuals vs. Multiplexing.Mixes.Code



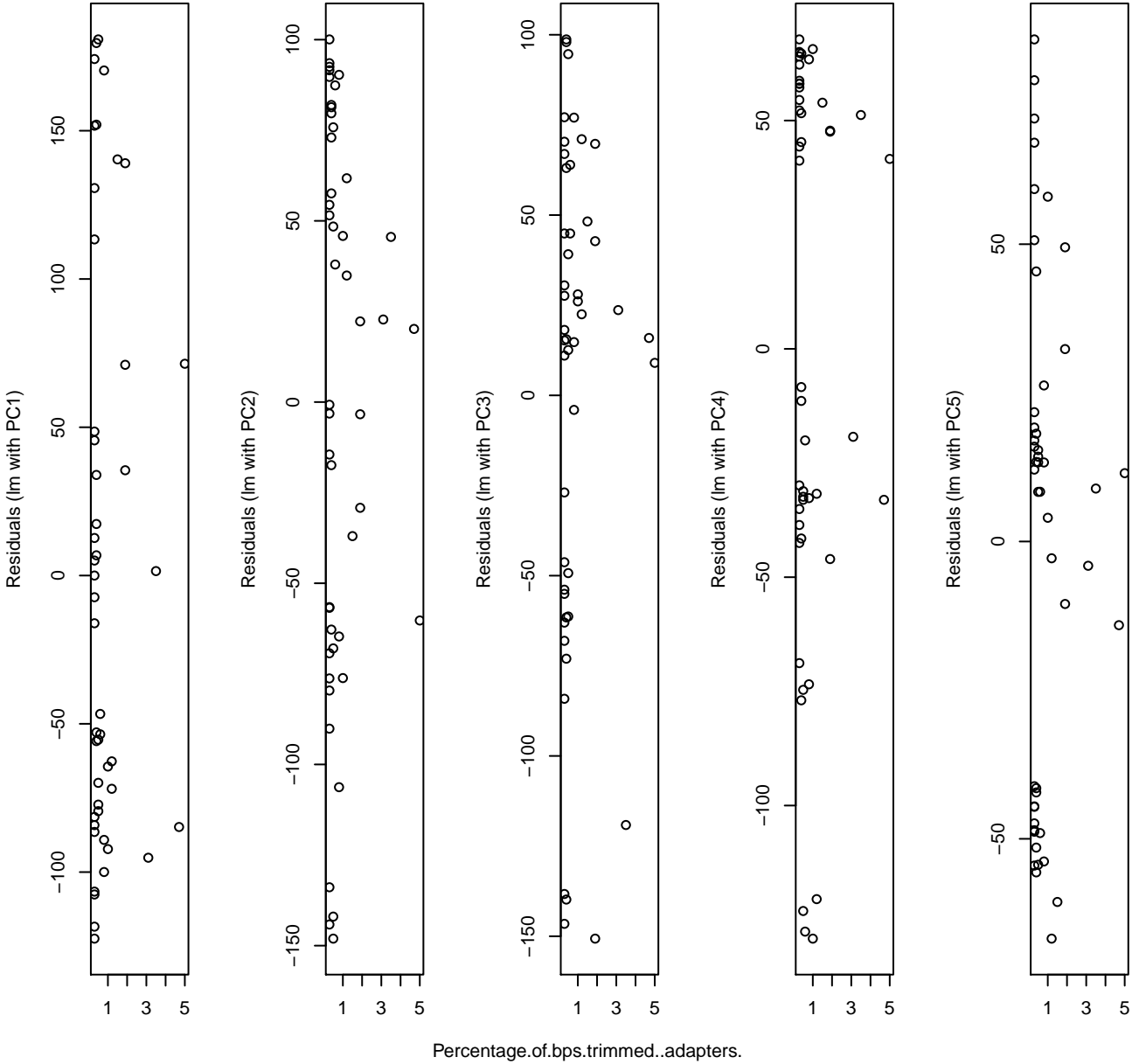
Residuals vs. Sequencing.location..at.UCGF



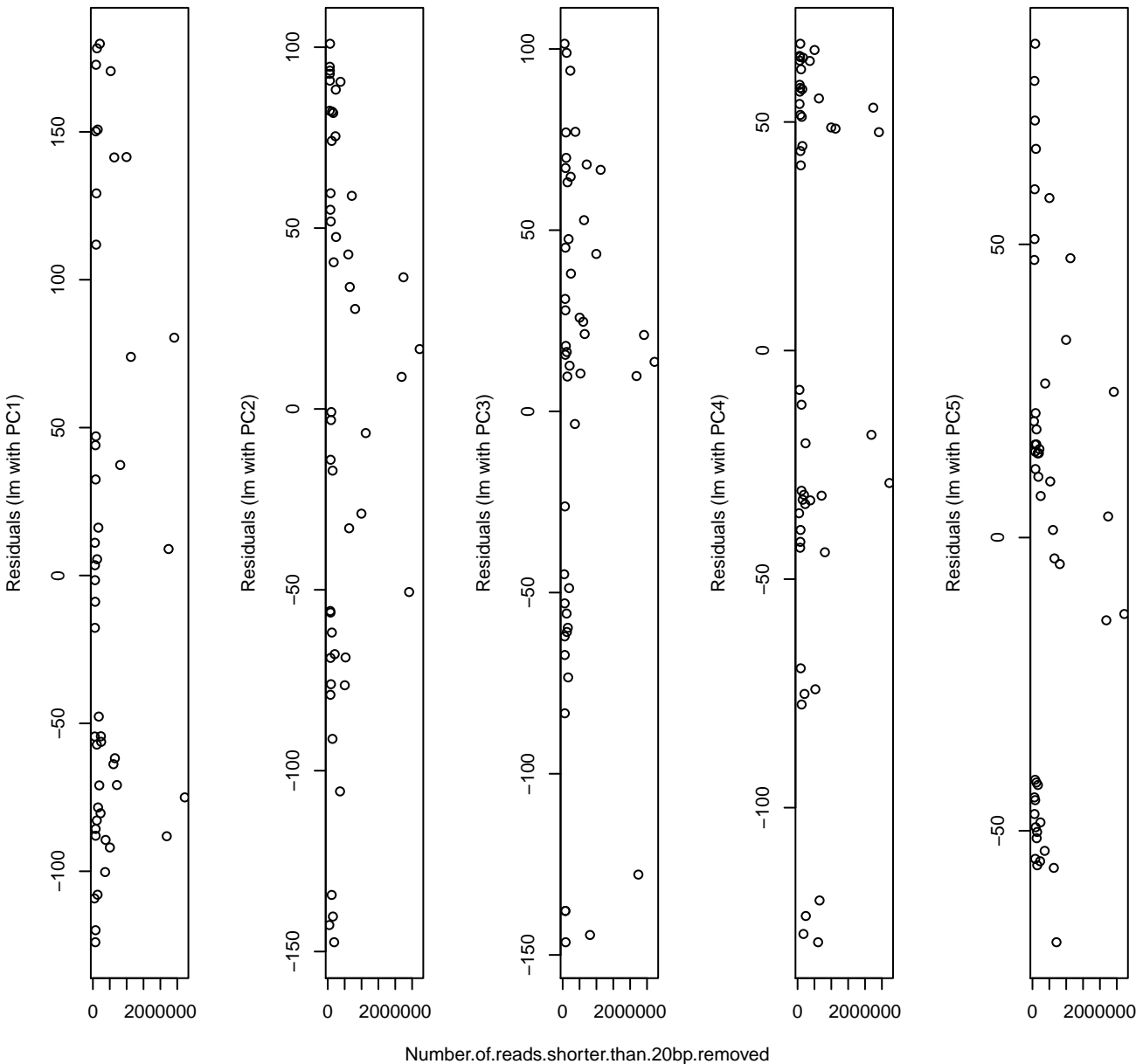
Residuals vs. Total.number.of.reads.sequenced



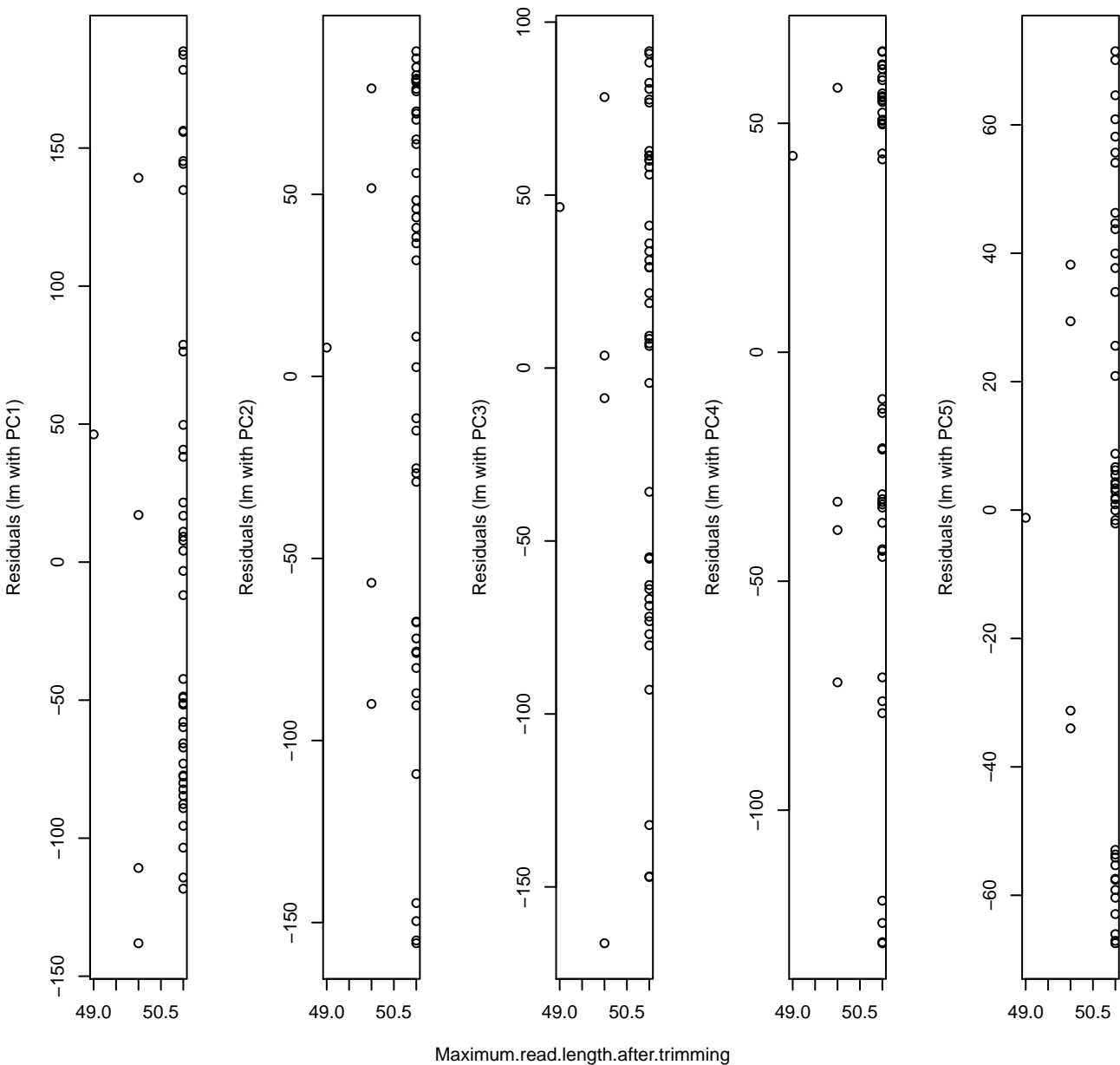
Residuals vs. Percentage.of.bps.trimmed..adapters.



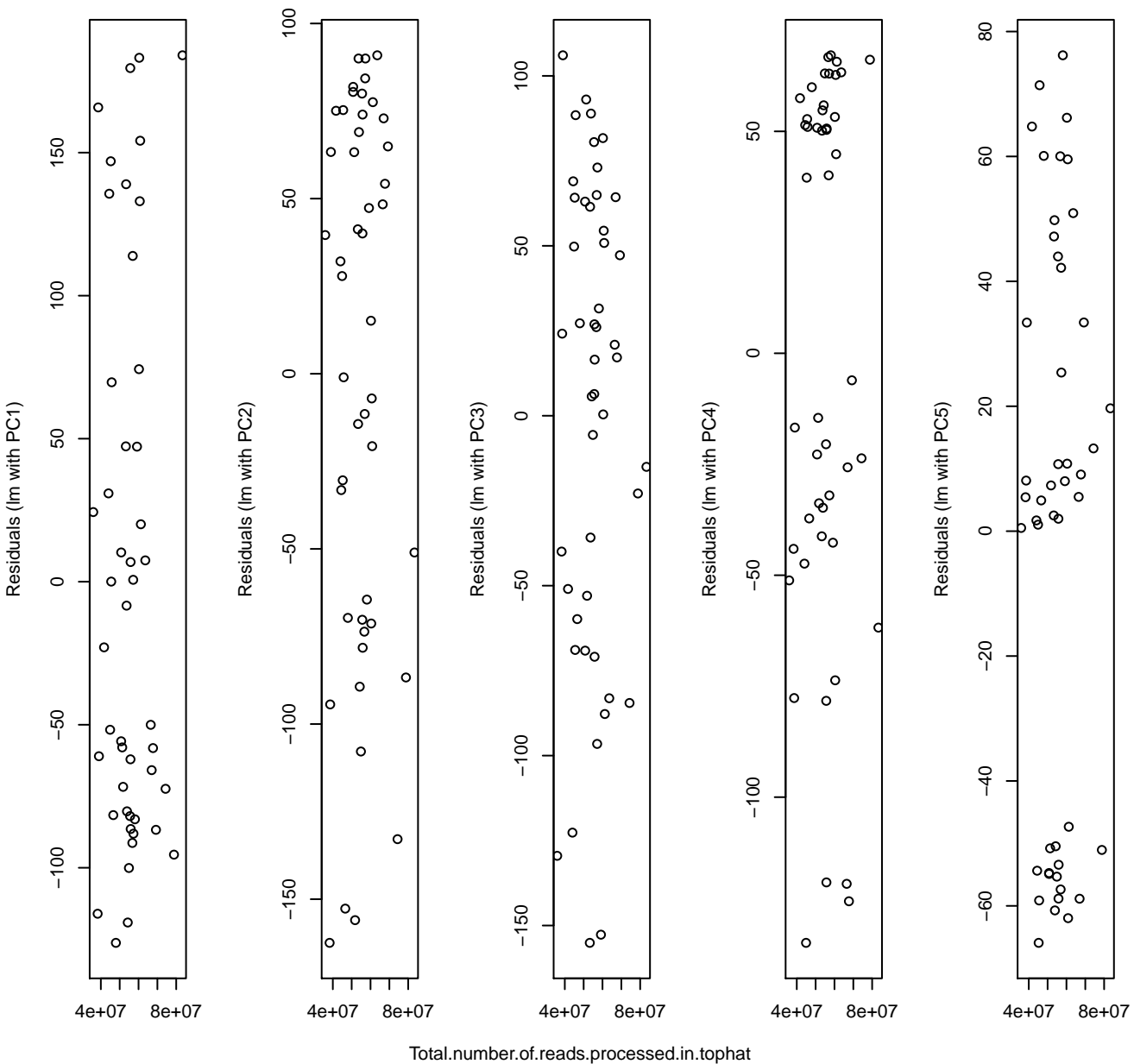
Residuals vs. Number.of.reads.shorter.than.20bp.removed



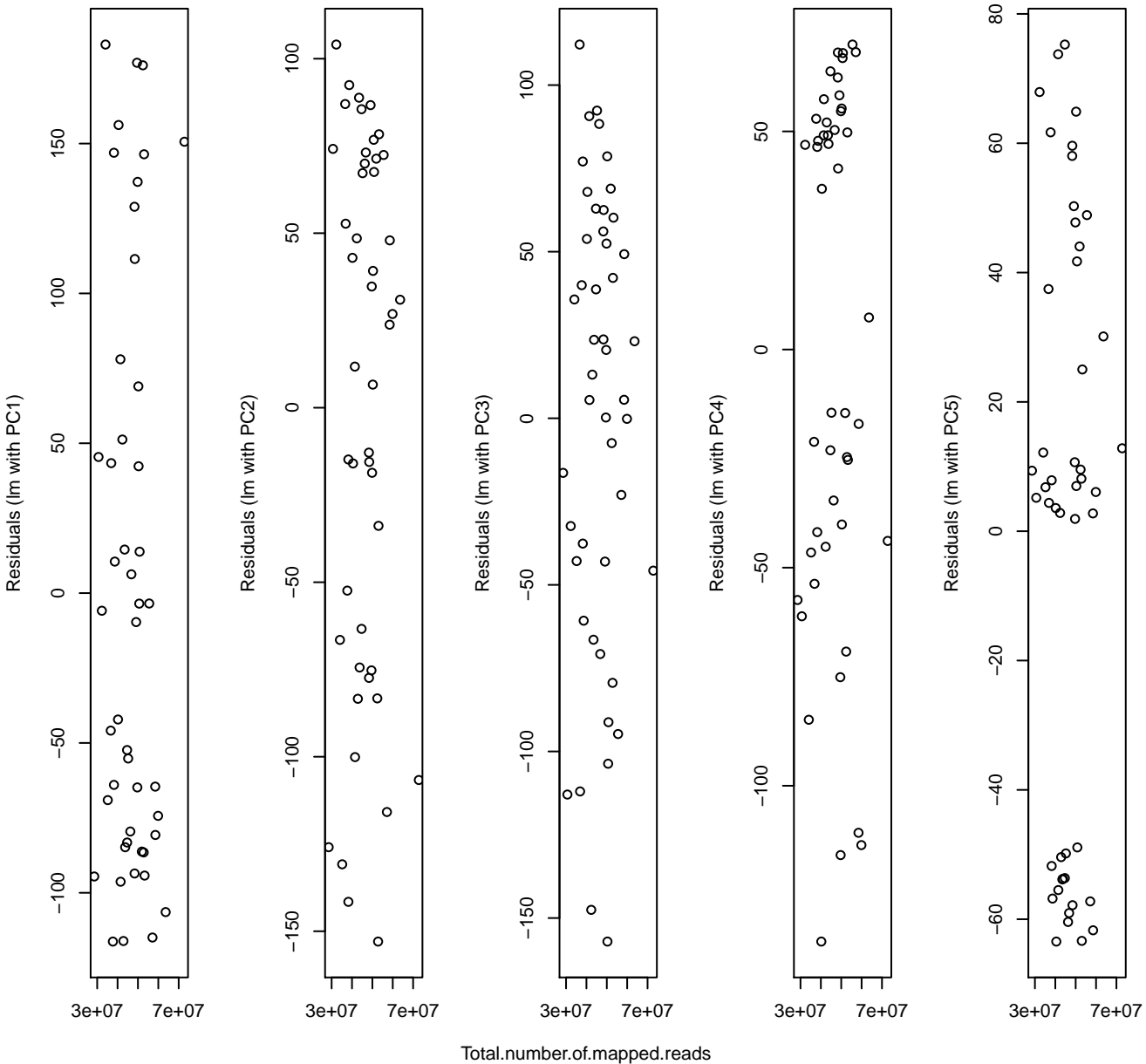
Residuals vs. Maximum.read.length.after.trimming



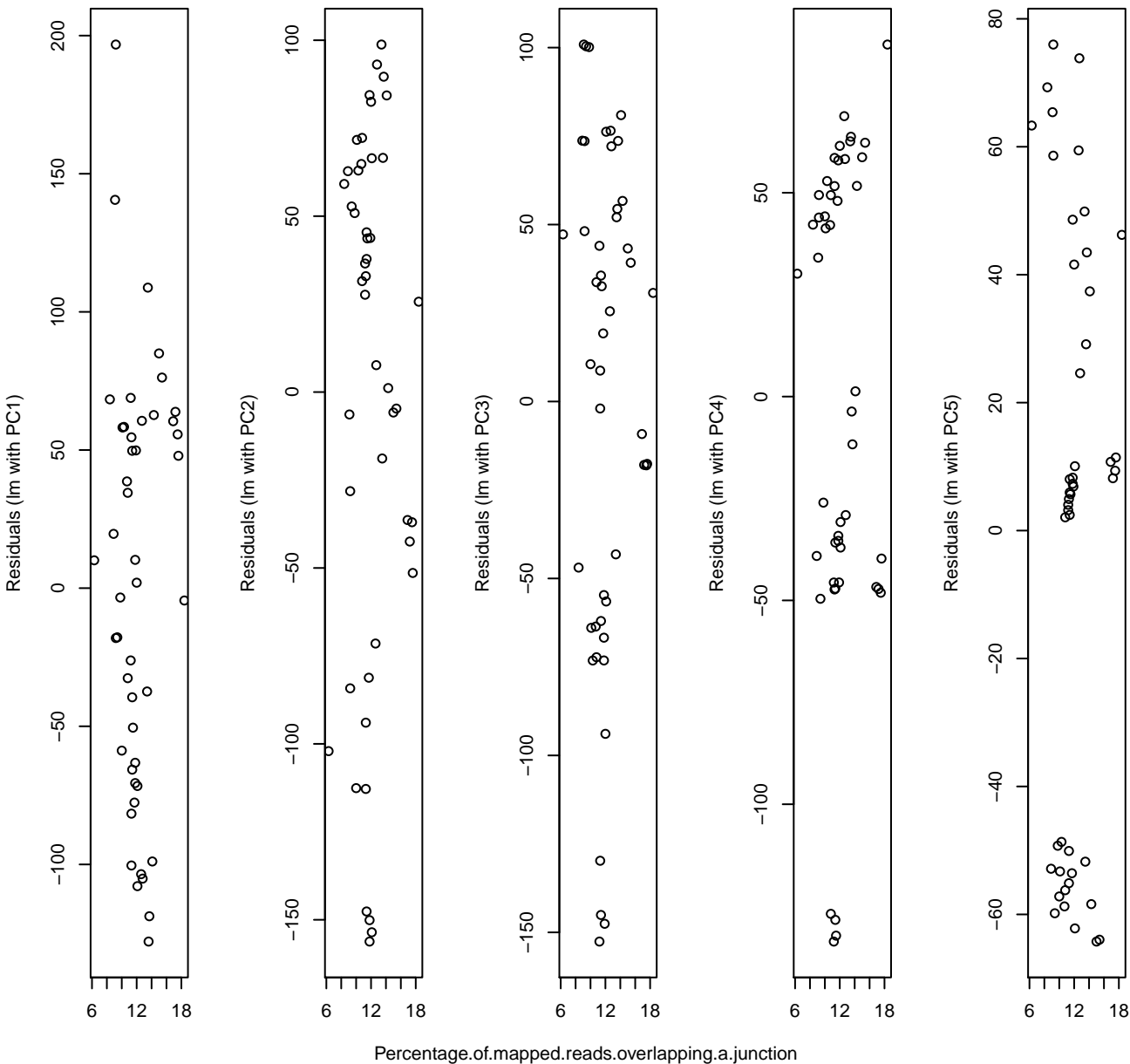
Residuals vs. Total.number.of.reads.processed.in.tophat



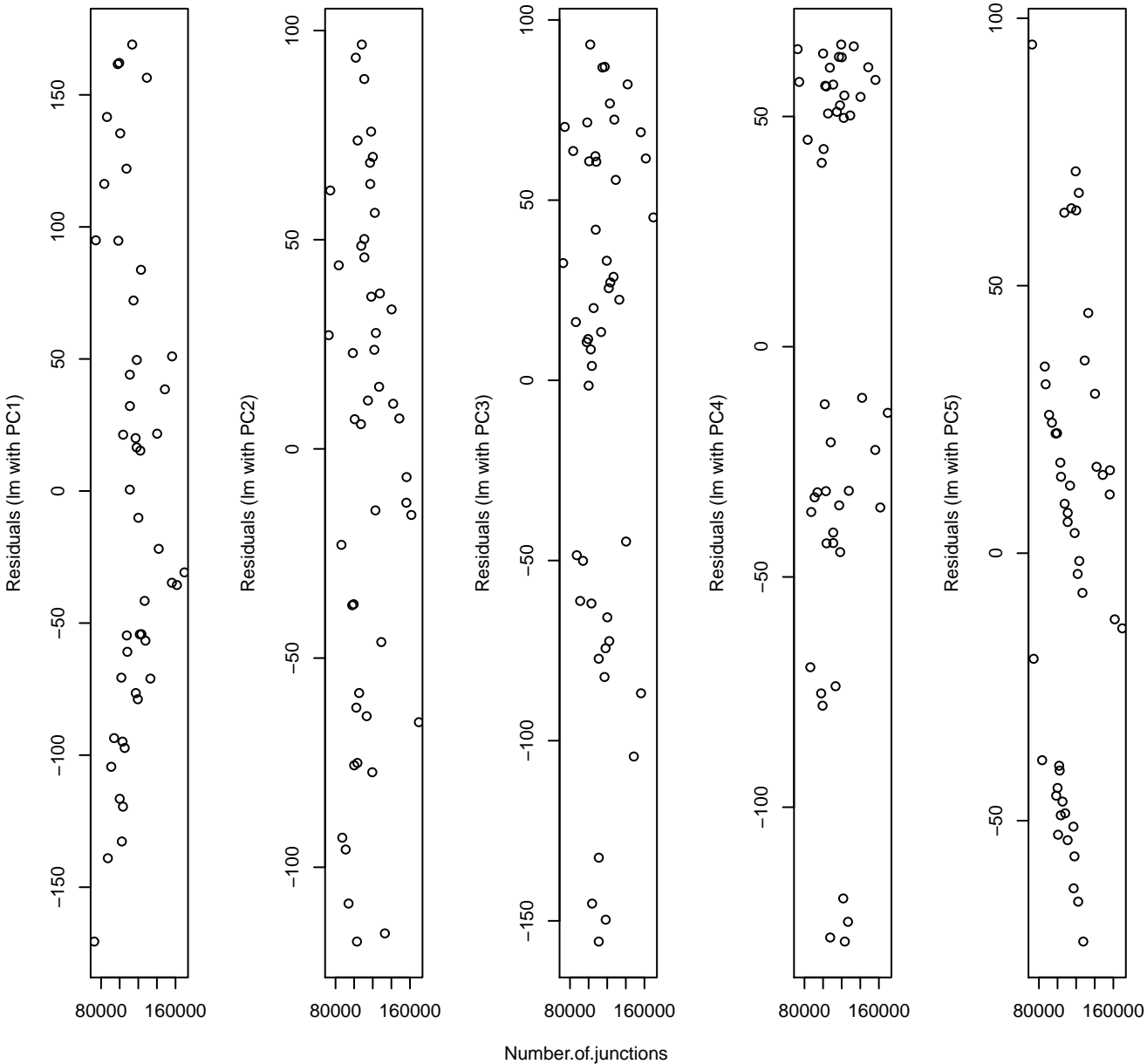
Residuals vs. Total.number.of.mapped.reads



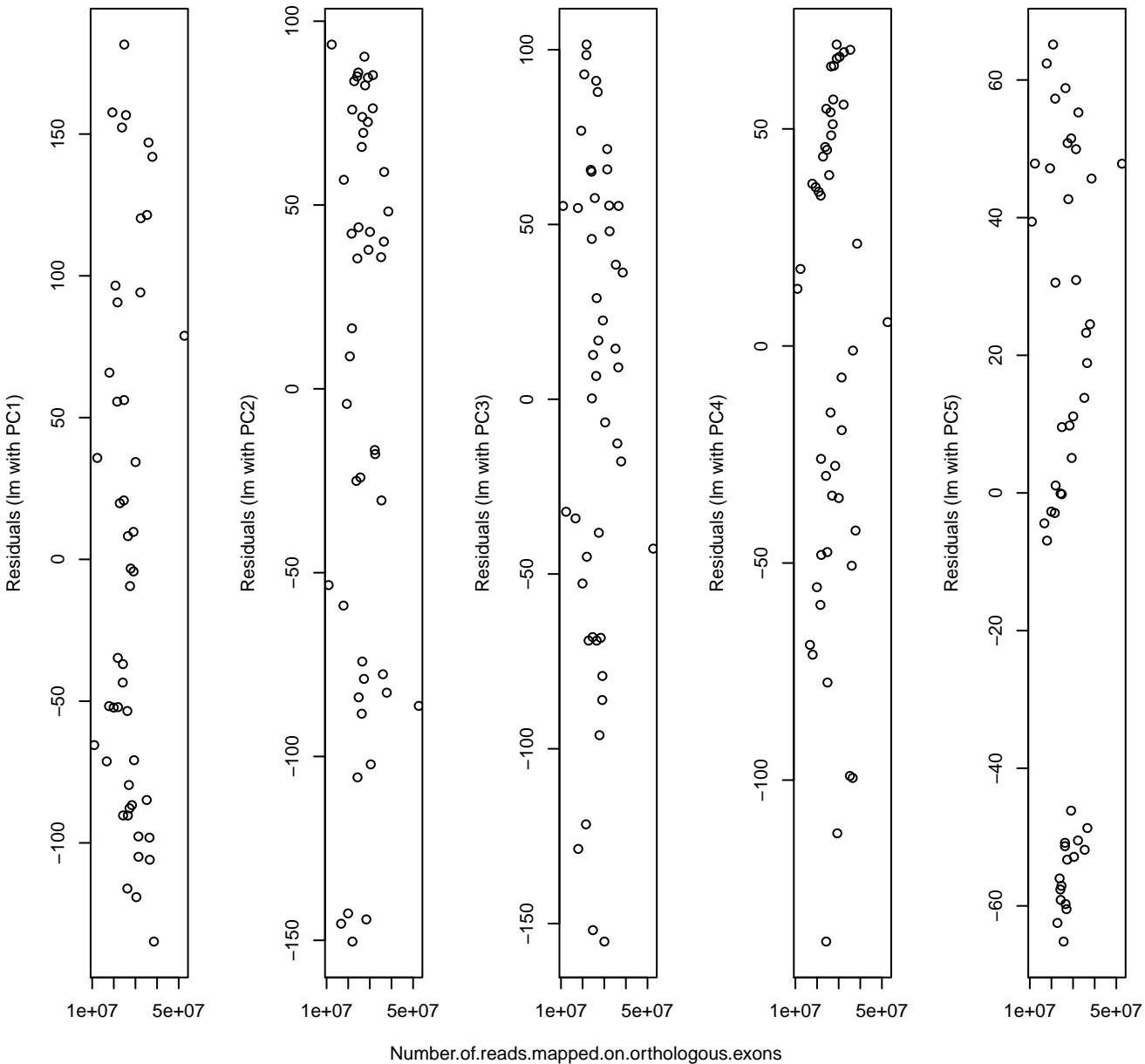
Residuals vs. Percentage.of.mapped.reads.overlapping.a.junction



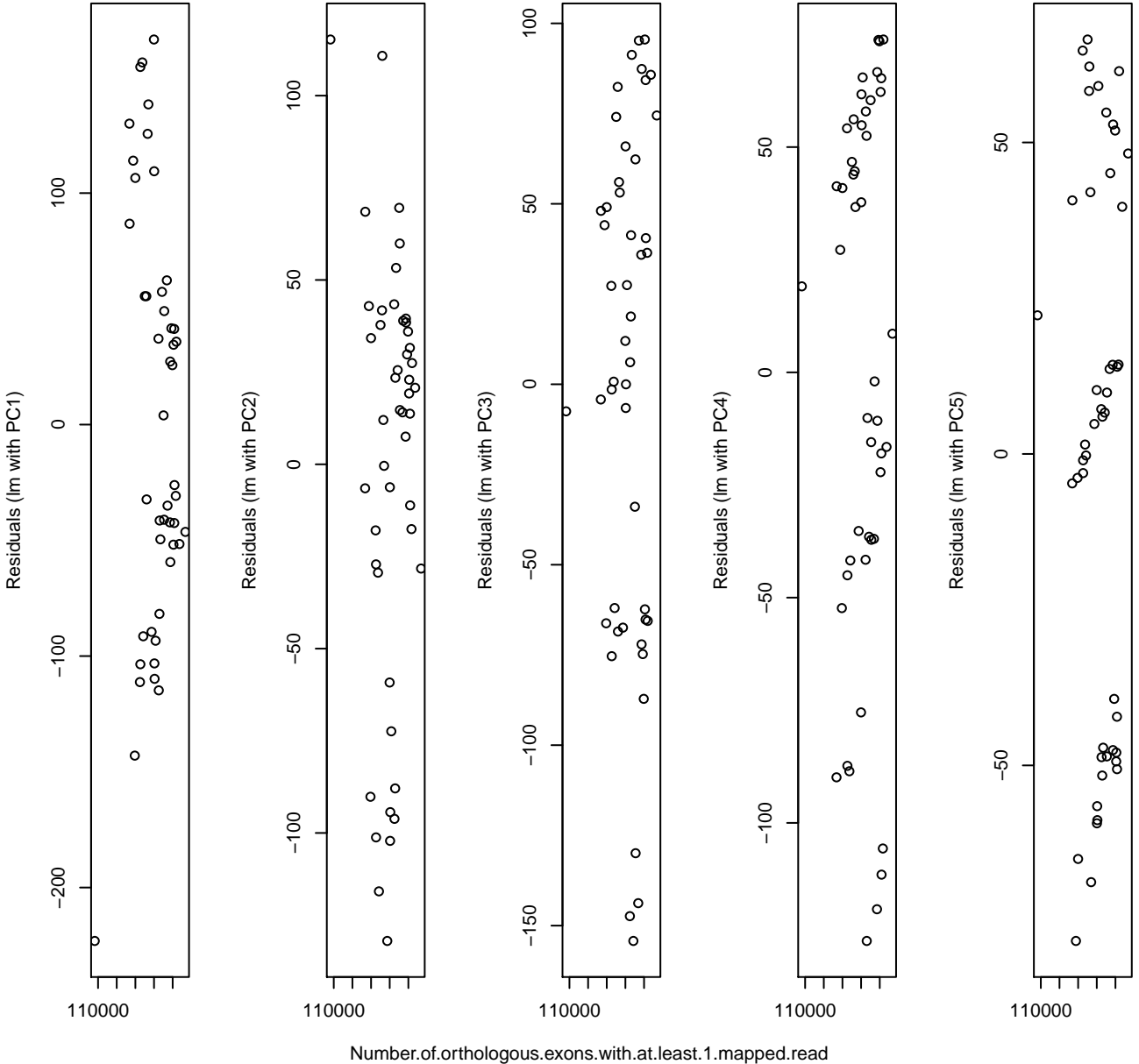
Residuals vs. Number.of.junctions



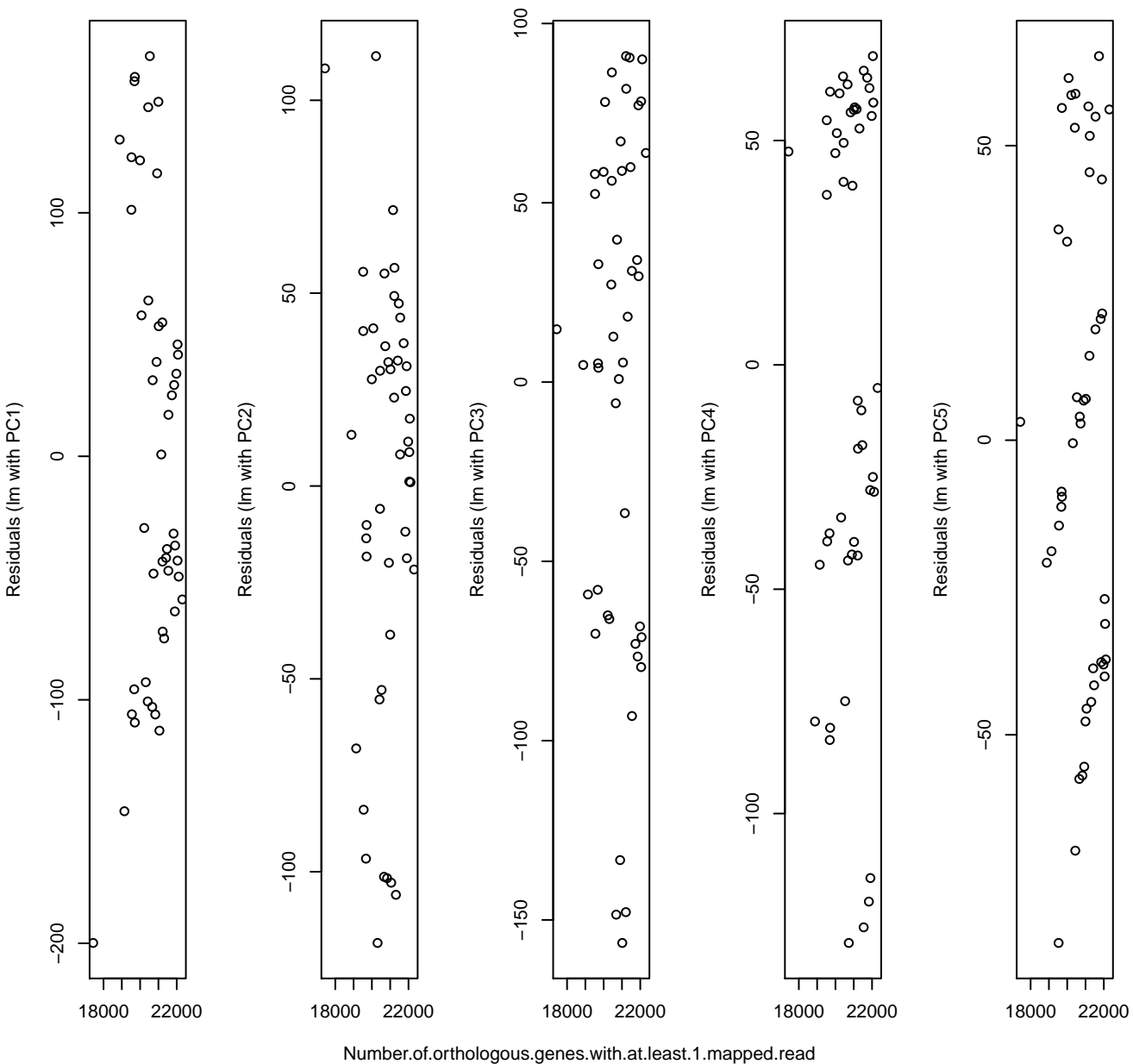
Residuals vs. Number.of.reads.mappped.on.orthologous.exons



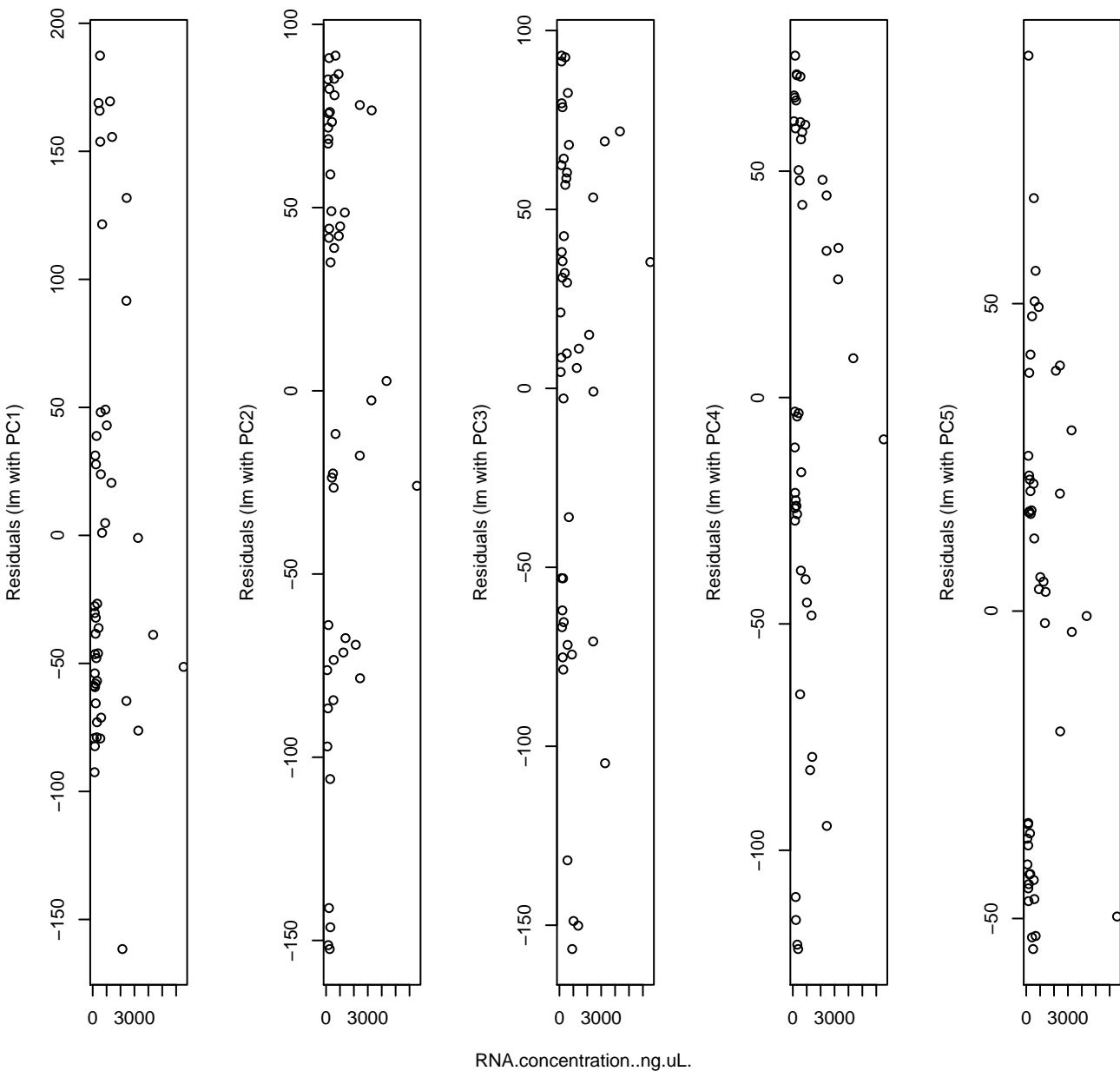
Residuals vs. Number.of.orthologous.exons.with.at.least.1.mapped.read



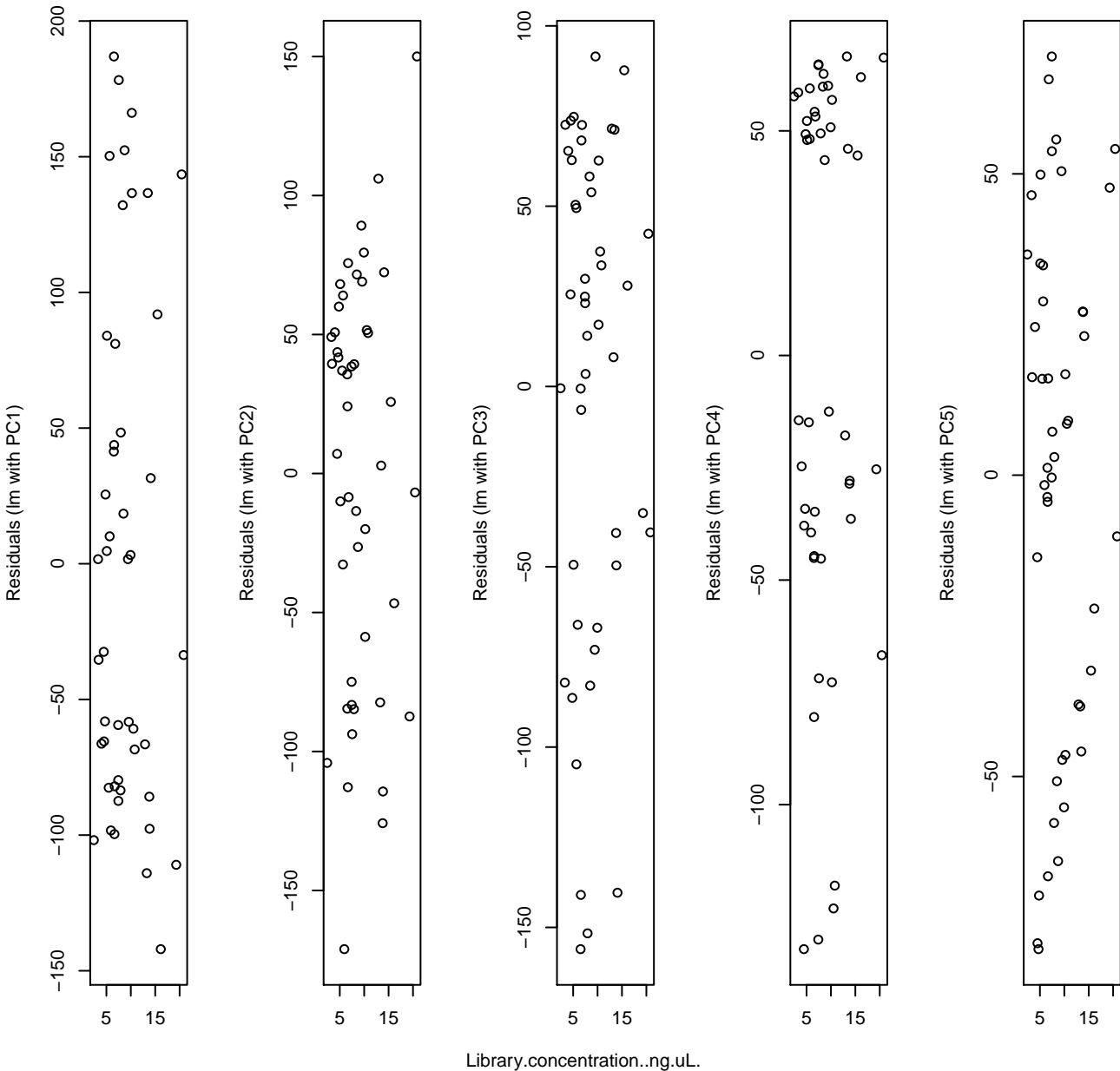
Residuals vs. Number.of.orthologous.genes.with.at.least.1.mapped.read



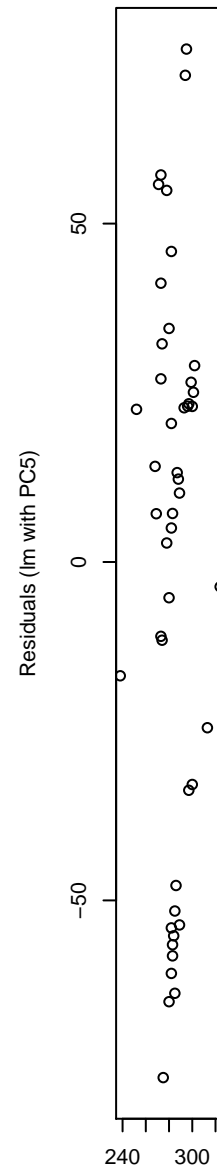
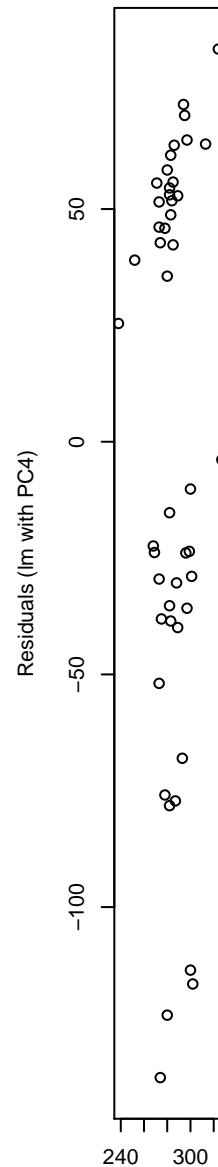
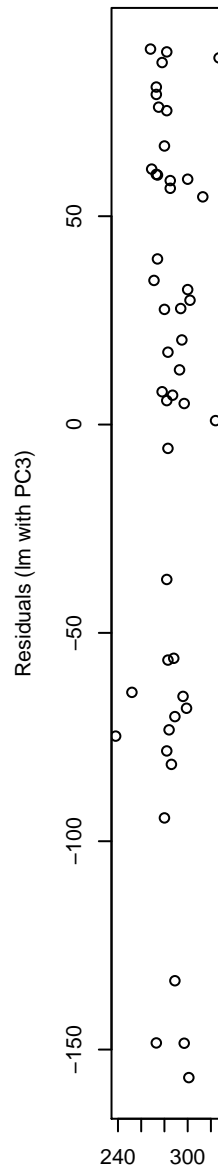
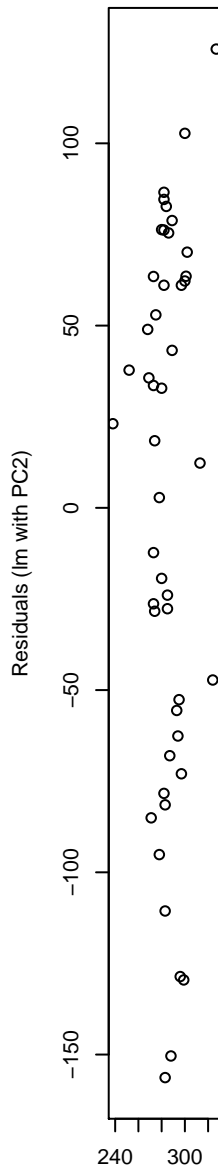
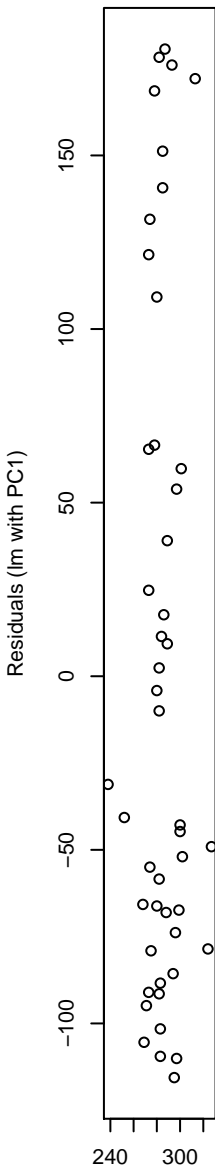
Residuals vs. RNA.concentration..ng.uL.



Residuals vs. Library.concentration..ng.uL.



Residuals vs. Library.fragments.size..bp.



Library.fragments.size..bp.