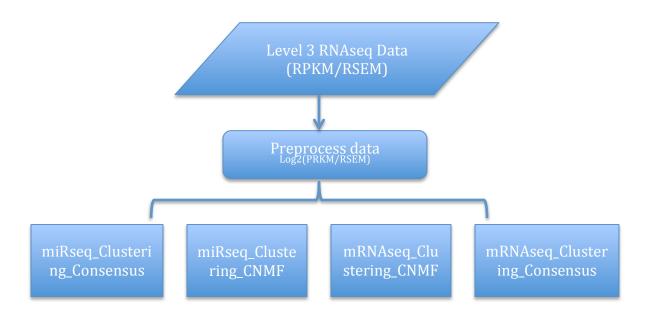
The flowchart of RNAseq clustering pipeline



*RPKM for a given GeneX is calculated by: (raw read counts \times 10^9) / (total reads \times length of GeneX). "Total reads" is the lane yield after removing poor quality reads and the length of GeneX is defined as the median length of all transcripts associated with GeneX.