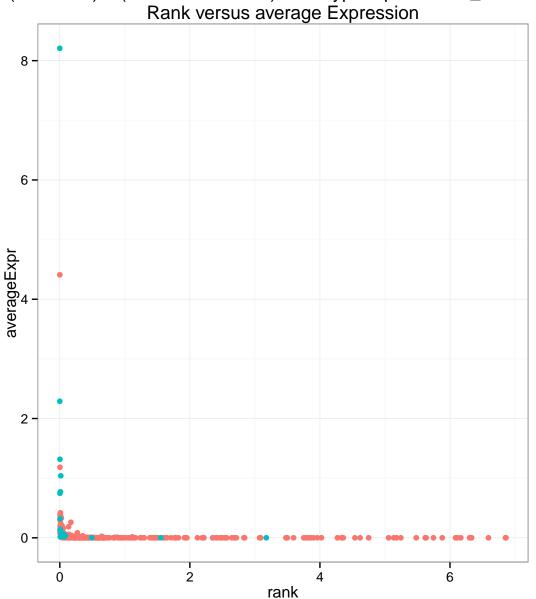
IncRNA group = allLncRNA ::: data cols = Inpa (17 / 366) = (func/total IncRNA) ::: biotype = processed_transcript Rank versus average Expression



factor(label)

0