IncRNA group = allLncRNA ::: data cols = bothPullDowns (52 / 4177) = (func/total IncRNA) ::: biotype = remove_antisense average expression vs. tissue specificity (JSD) 1.00 -0.75 tissSpec factor(withinSubset) • false • true 0.50 -0.25 -0.0 2.5 7.5 5.0 averageExpr