IncRNA group = IDRlessthan0_1 ::: data cols = Inpa (16 / 231) = (func/total IncRNA) ::: biotype = processed_transcript average expression vs. tissue specificity (JSD) 0.75 factor(withinSubset) • false • true label • 0.00 • 0.25 • 0.50 0.75 1.00 -7.5 0.0 2.5 -5.0 log(averageExpr)