IncRNA group = IDRlessthan0_01 ::: data cols = Ipa (25 / 243) = (func/total IncRNA) ::: biotype = all_biotypes average expression vs. tissue specificity (JSD) 1.00 -0.75 factor(withinSubset) false true tissSpec label • 0.00 • 0.25 • 0.50 0.50 -0.75 1.00 0.25 --2.5 0.0 2.5 log(averageExpr)