IncRNA group = IDRIessthan0_1 ::: data cols = Inpa (42 / 1350) = (func/total IncRNA) ::: biotype = lincProcTrans average expression vs. tissue specificity (JSD) 0.75 factor(withinSubset) false true tissSpec label • 0.00 • 0.25 0.50 -• 0.50 0.75 1.00 0.25 --6 -3 log(averageExpr)