IncRNA group = IDRlessthan0_01 ::: data cols = bothPullDowns (21 / 146) = (func/total IncRNA) ::: biotype = lincProcTrans measures across all samples(cell-type/pulldown) sumExpr varianceExpr averageExpr 0.25 -0.3 0.20 0.15 -0.2 0.10 -0.1 0.05 -0.00 0.0 -2.5 2 ò Ö 0.0 4 -4 2.5 4 8 minExpr nTimesRest maxExpr 0.75 0.4 withinSubset 0.50 false 0.2 true 0.25 0.0 0.00 2 <u>-4</u> Ö 2 -6 4 -2 4 6 0 -8 tissSpec

0.3

0.2

0.1

0.0

0.2

density 0.1

0.0

0.6

0.4

0.2

0.0

-2.0 -1.5 -1.0 -0.5

