IncRNA group = allLncRNA ::: data cols = bothPullDowns (32 / 3319) = (func/total IncRNA) ::: biotype = lincRNA measures across all samples(cell-type/pulldown) varianceExpr sumExpr averageExpr 0.15 -0.075 -0.10 -0.050 -0.05 0.025 -0.000 0.00 -5 -25 -20 -15 -10 -5 Ö -5 -10 -10 0 5 minExpr maxExpr nTimesRest 0.6 -0.15 withinSubset 0.4 -0.10 false true 0.2 0.05 -0.00 0.0 -4 0 6 2 -10.0 -7.5 -5.0 -2.5 -8 0 tissSpec

0.15 -

0.10 -

0.05 -

0.00

0.20

0.15 -

density

0.05

0.00

1.0

0.5

0.0

-2.0 -1.5 -1.0 -0.5

0.0