IncRNA group = allLncRNA ::: data cols = bothPullDowns (91 / 6927) = (func/total IncRNA) ::: biotype = all_biotypes measures across all samples(cell-type/pulldown) sumExpr varianceExpr averageExpr 0.15 -0.075 0.10 -0.050 -0.05 0.025 0.000 0.00 0 -10 -5 Ö <u>-</u>5 -20 -10 -10 0 5 minExpr maxExpr nTimesRest 0.15 -0.75 withinSubset 0.10 -0.50 false true 0.05 -0.25 -0.00 0.00 -5 0 5 -8 -4 2.5 5.0 7.5 -10 0.0 tissSpec

0.15 -

0.10 -

0.05

0.00

0.20

0.15 -

0.05

0.00

1.25

1.00 -

0.75 -

0.50 -

0.25

0.00

-2.0 -1.5 -1.0 -0.5 0.0

density