IncRNA group = allLncRNA ::: data cols = bothPullDowns (38 / 2538) = (func/total IncRNA) ::: biotype = antisense measures across all samples(cell-type/pulldown) varianceExpr sumExpr averageExpr 0.15 0.08 -0.06 -0.10 0.04 -0.05 0.02 -0.00 0.00 0 -20 -15 -10 *-*5 -5 -5 -10 0 0 5 minExpr nTimesRest maxExpr 0.15 -0.9 withinSubset 0.10 -0.6 false true 0.05 -0.3 0.00 0.0 т –4 0 2 <u>-</u>9 <u>-</u>7 -3 -8 4 6 -5 0 tissSpec

0.15 -

0.10

0.05

0.00

0.20

density 0.10 -

0.05

0.00

0.6 -

0.4 -

0.2

0.0

-2.0 -1.5 -1.0 -0.5 0.0

-11

-10

value of facet label