IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (82 / 4643) = (func/total IncRNA) ::: biotype = all_biotypes measures across all samples(cell-type/pulldown) sumExpr varianceExpr averageExpr 0.12 -0.20 -0.09 -0.15 0.06 -0.10 0.03 -0.05 0.00 0.00 0 -10 -5 -5 **-10** -10 -20 0 0 5 minExpr nTimesRest maxExpr 1.00 -0.20 -0.75 withinSubset 0.15 false 0.50 -0.10 true 0.250.05 -0.00 0.00 2 0 <u>-3</u> -5 <u>-</u>9 -6 5 -10 6 0 tissSpec

0.20 -

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

value of facet label