IncRNA group = IDRlessthan0\_2 ::: data cols = bothPullDowns ( 31 / 2082 ) = (func/total IncRNA) ::: biotype = lincRNA 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 -4 -5 -20 -15 -10 -5 0 0 -12 -8 0 minExpr maxExpr nTimesRest 0.6 -0.20 withinSubset 0.15 -0.4 false 0.10 true 0.2 0.05 -0.00 0.0 -3 0 2 6 -6 3 -10.0 -7.5 -5.0 -2.5 0.0 0 tissSpec

0.20

0.15

0.10 -

0.05

0.00

0.20

0.15 -

density

0.05

0.00

0.6 -

0.4 -

0.2

0.0

-2.0 -1.5 -1.0 -0.5

value of facet label