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 –10 Ö -4 -5 -20 0 -12 -8 0 5 minExpr maxExpr nTimesRest 0.8 -0.20 -0.6 0.15 withinSubset false 0.4 0.10 true 0.2 -0.05 -0.00 0.0 0 -4 -5 2.5 -8 5.0 7.5 0 -10 0.0 tissSpec

0.20

0.15

0.10

0.05 -

0.00

0.20

0.15 -

0.05

0.00

0.6 -

0.4 -

0.2

0.0

-2.0 -1.5 -1.0 -0.5

density

value of facet label