IncRNA group = allLncRNA ::: data cols = bothPullDowns (17/372) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, full range 100 -75 -50 -25 factor(label) 0 count 0 10 5 -0 -

1.5

1.0 rank 2.0

0.5

0.0