IncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns (22 / 588) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, range = median +/- 2 ds 0 30 -20 -10 factor(label) 0 count 0 1 6 -4 -2 -0 -

1.0

rank

1.5

0.5

0.0