IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (23 / 861) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, full range 120 90 60 30 factor(label) 0 count 0 10 5 · 0 -0.0 0.5 1.0 1.5 rank