IncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns (22 / 588) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, full range 30 -20 -10 factor(label) 0 count 0 1 6 -4 · 2 -0 -1.5 0.0 0.5 1.0

rank