IncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns (16 / 232) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, range = median +/- 2 ds 0 15 -10 -5 factor(label) 0 count 0 1 6 -4 -2 -0 -0.5 0.0 1.0 1.5

rank