IncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns (22 / 587) = (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 -0.5 1.0 0.0 1.5

rank