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

rank