lncRNA group = IDRlessthan0_01 ::: data cols = Inpa (10 / 37) = (func/total lncRNA) ::: biotype = processed_transcript PageRank, full range 3 2 1 2.0 factor(label) 0 1 1.5 -1.0 0.5 0.0 0.5 1.0 1.5

rank