lncRNA group = IDRlessthan0\_2 ::: data cols = bothPullDowns (23 / 861) = (func/total lncRNA) ::: biotype = processed\_transcript logAbsRank, range = all points 0.25 0.20 0.15 factor(label) density 0.10 0.05 0.00 -5.0 -2.5 -7.5 0.0 2.5

log(abs(rank))