lncRNA group = allLncRNA ::: data cols = bothPullDowns (28 / 2998) = (func/total IncRNA) ::: biotype = lincRNA logAbsRank, range = all points 0.20 0.15 factor(label) 0.10 0.05 0.00

-2.5

0.0

density

-7.5

-5.0

log(abs(rank))