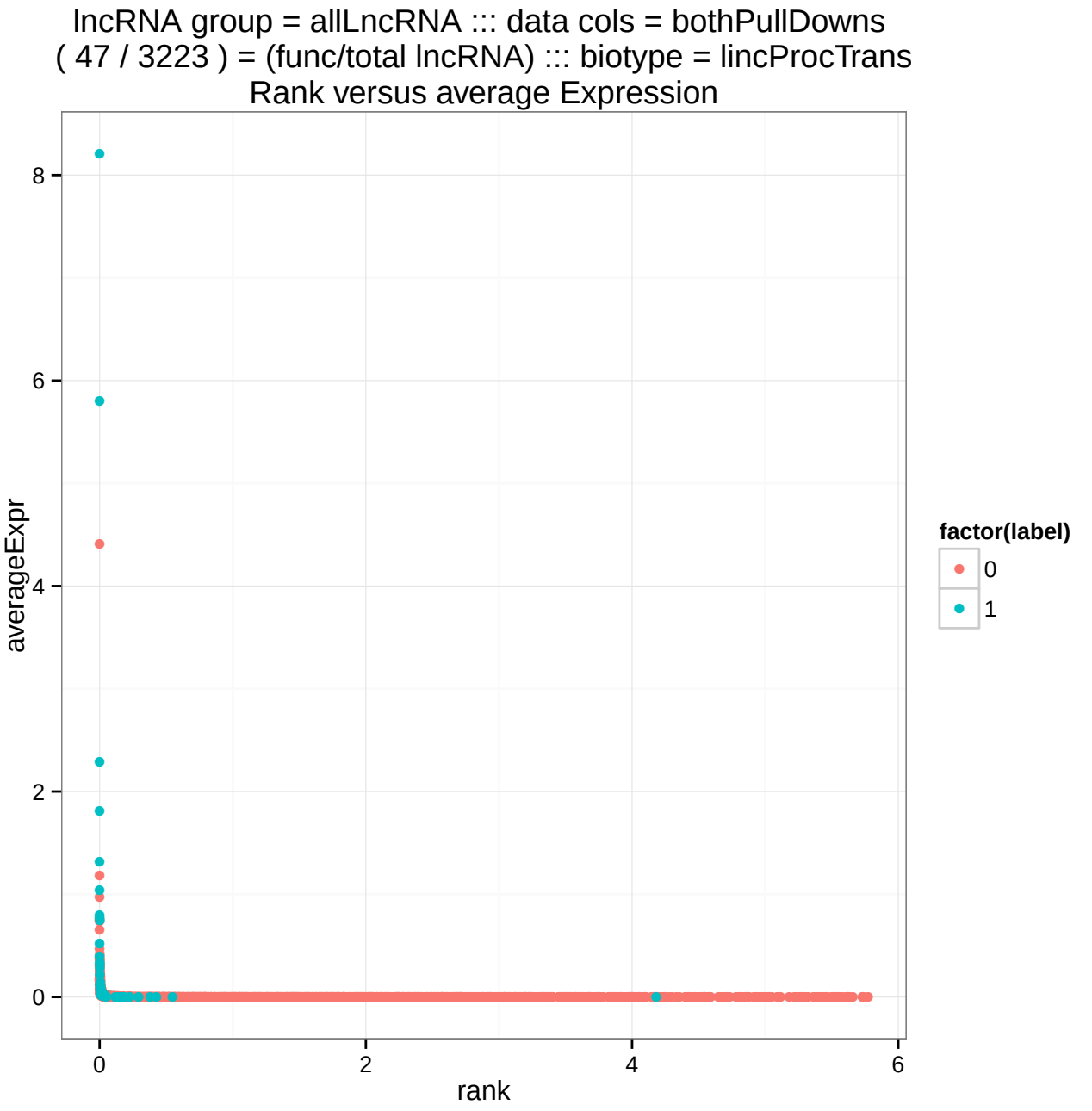
lncRNA group = allLncRNA ::: data cols = bothPullDowns
(47 / 3223) = (func/total lncRNA) ::: biotype = lincProcTrans
Rank versus average Expression
averageExpr
rank
0
2
4
6
8
factor(label)
0
1